



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 09:41 PM UTC

PDB ID : 8KAB / pdb_00008kab
EMDB ID : EMD-37007
Title : Mycobacterium smegmatis 50S ribosomal subunit-HflX complex
Authors : Srinivasan, K.; Banerjee, A.; Sengupta, J.
Deposited on : 2023-08-02
Resolution : 3.30 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

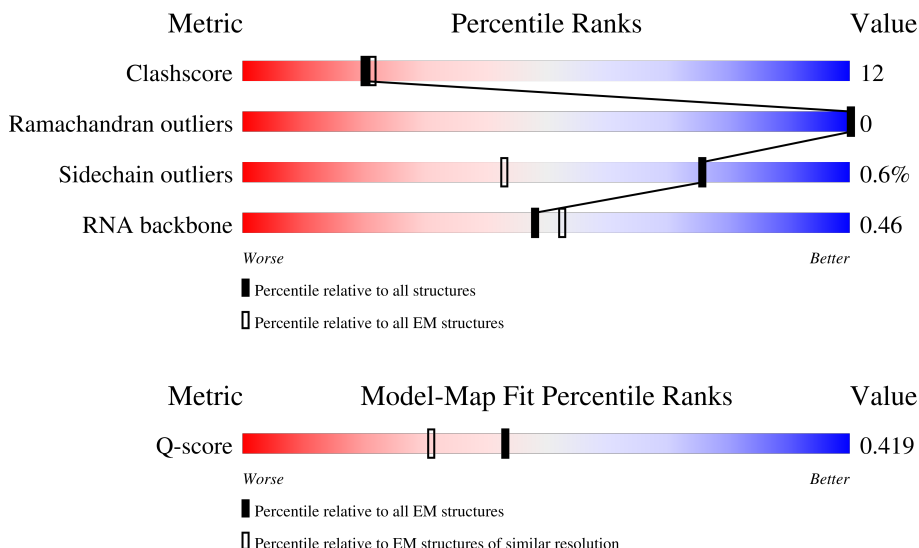
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.



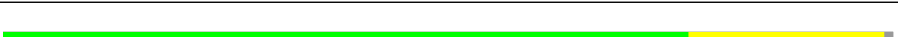
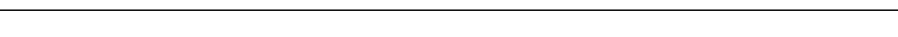
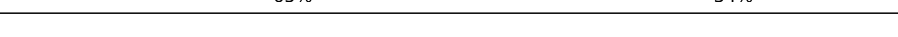
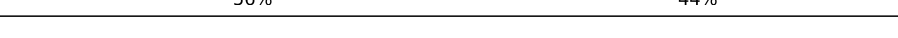
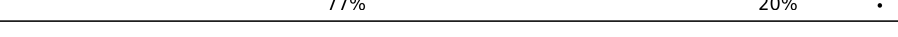
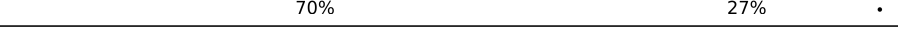
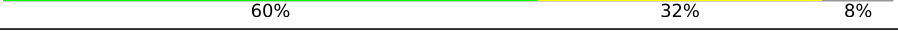
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	3	24	
2	A	3120	
3	B	118	

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Mol	Chain	Length	Quality of chain
4	C	278	
5	D	217	
6	E	215	
7	F	187	
8	G	179	
9	H	151	
10	I	175	
11	J	142	
12	K	147	
13	L	122	
14	M	147	
15	N	138	
16	O	199	
17	P	127	
18	Q	113	
19	R	129	
20	S	103	
21	T	153	
22	U	100	
23	V	105	
24	W	215	
25	X	88	
26	Y	64	
27	Z	77	
28	a	61	

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Mol	Chain	Length	Quality of chain
29	b	57	
30	c	55	
31	d	47	
32	e	64	
33	f	37	
34	g	75	
35	h	483	

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 100780 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein bL37.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	3111	Total	C	N	O	P	0	0
			66813	29778	12283	21641	3111		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	118	Total	C	N	O	P	0	0
			2522	1126	468	810	118		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 10 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 11 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 12 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 13 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 14 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 15 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 16 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 17 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	126	Total	C	N	O	S	0	0
			956	586	199	171			

- Molecule 18 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 19 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	124	Total	C	N	O	S	0	0
			988	613	203	172			

- Molecule 20 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	100	Total	C	N	O	S	0	0
			754	478	137	139			

- Molecule 21 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 22 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 23 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	97	Total	C	N	O	S	0	0
			732	456	137	137	2		

- Molecule 24 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	W	192	Total	C	N	O	0	0
			1428	881	255	292		

- Molecule 25 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 26 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 27 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 28 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	a	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 30 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	48	Total	C	N	O	S	0	0
			397	244	81	68	4		

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	e	63	Total	C	N	O	0	0
			502	302	115	85		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 34 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

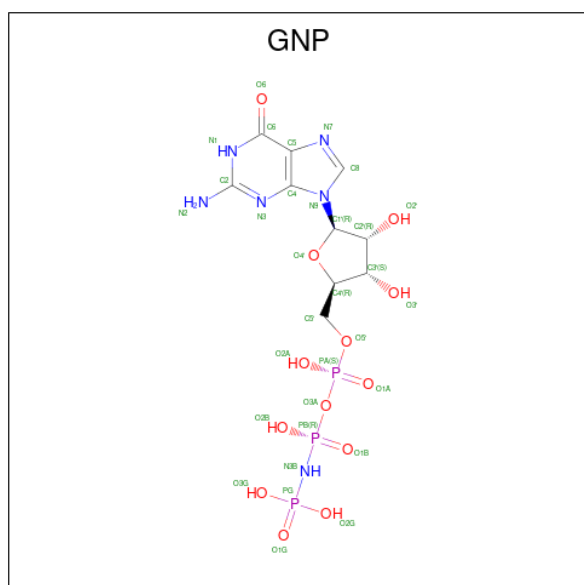
- Molecule 35 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	430	Total	C	N	O	S	0	0
			3256	2016	603	630	7		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	471	LYS	-	expression tag	UNP A0QVY1
h	472	LEU	-	expression tag	UNP A0QVY1
h	473	ALA	-	expression tag	UNP A0QVY1
h	474	ALA	-	expression tag	UNP A0QVY1
h	475	ALA	-	expression tag	UNP A0QVY1
h	476	LEU	-	expression tag	UNP A0QVY1
h	477	GLU	-	expression tag	UNP A0QVY1
h	478	HIS	-	expression tag	UNP A0QVY1
h	479	HIS	-	expression tag	UNP A0QVY1
h	480	HIS	-	expression tag	UNP A0QVY1
h	481	HIS	-	expression tag	UNP A0QVY1
h	482	HIS	-	expression tag	UNP A0QVY1
h	483	HIS	-	expression tag	UNP A0QVY1

- Molecule 36 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
36	h	1	Total	C	N	O	P	0
			32	10	6	13	3	

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.

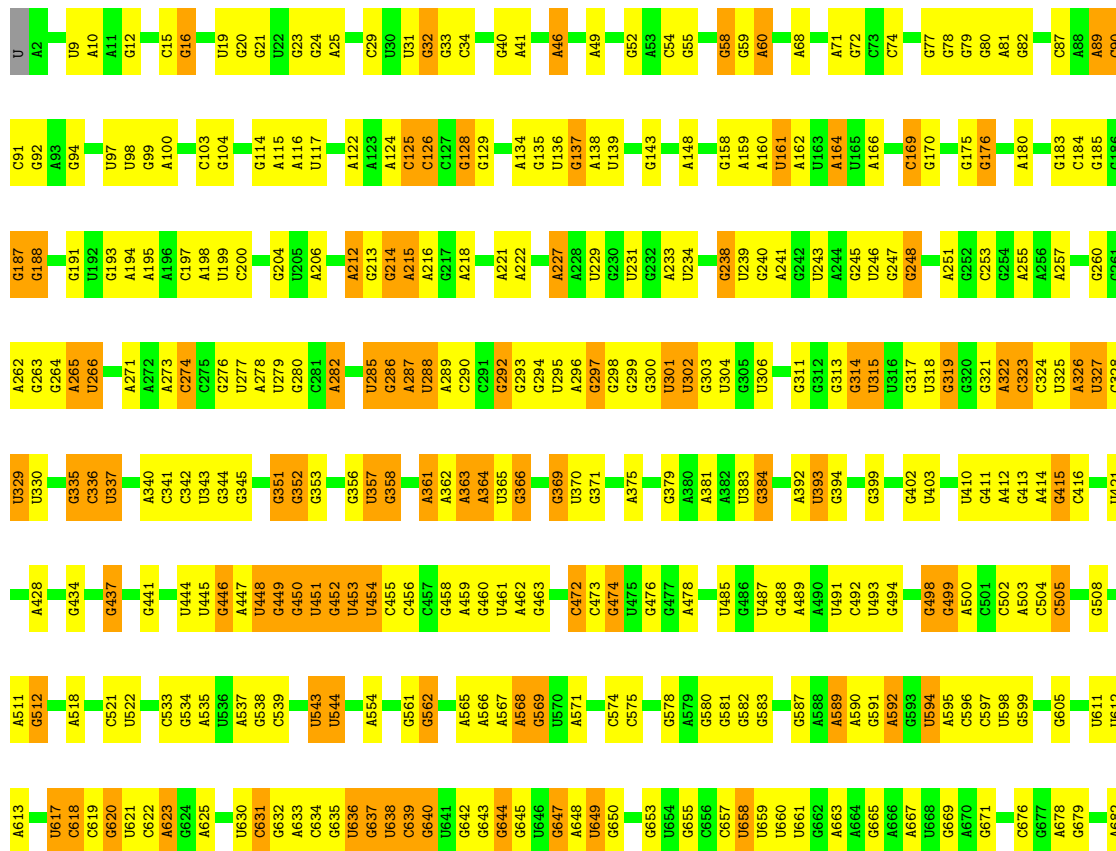
- Molecule 1: 50S ribosomal protein bL37

Chain 3: 

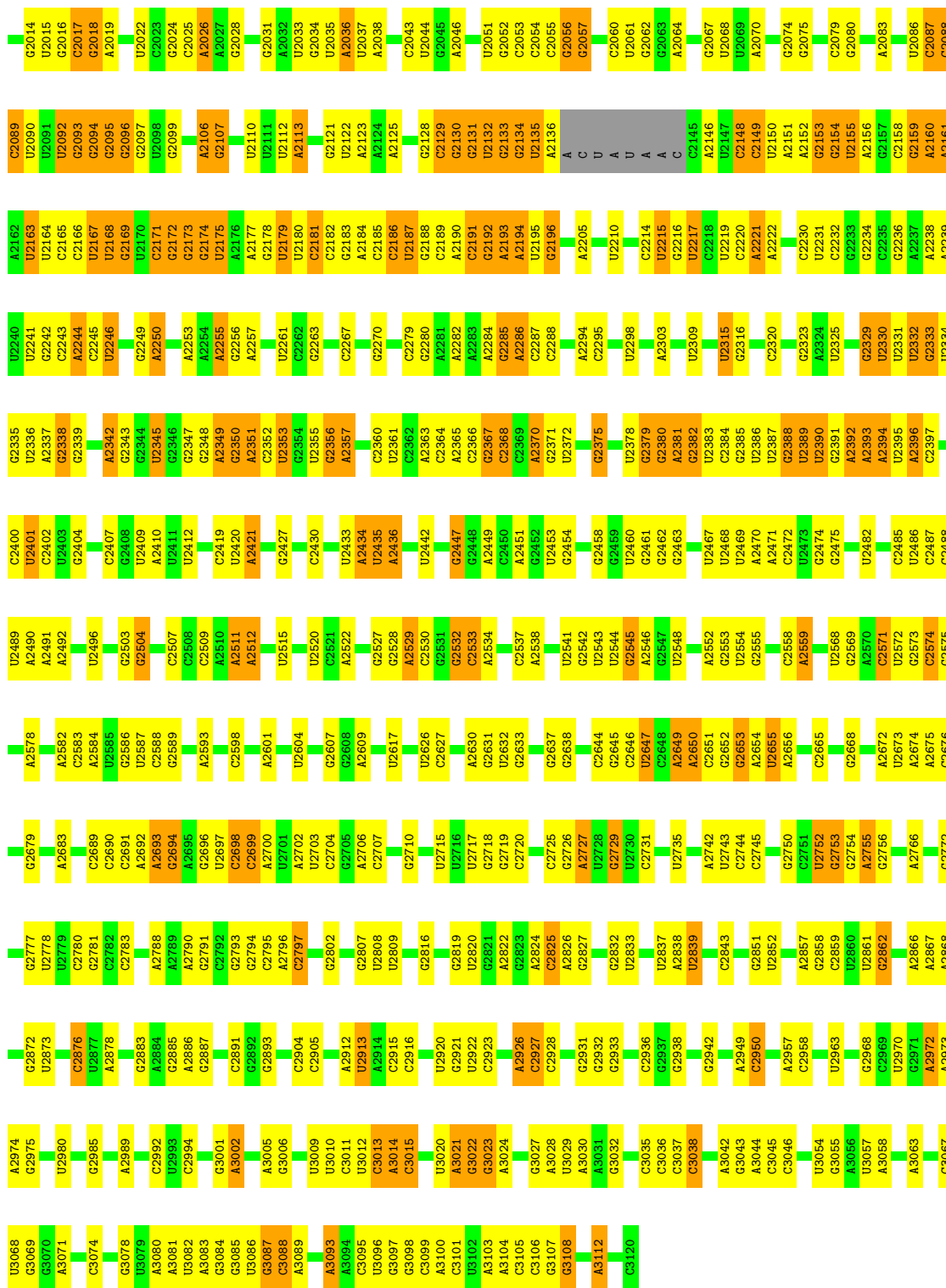


- Molecule 2: 23S rRNA

Chain A: 



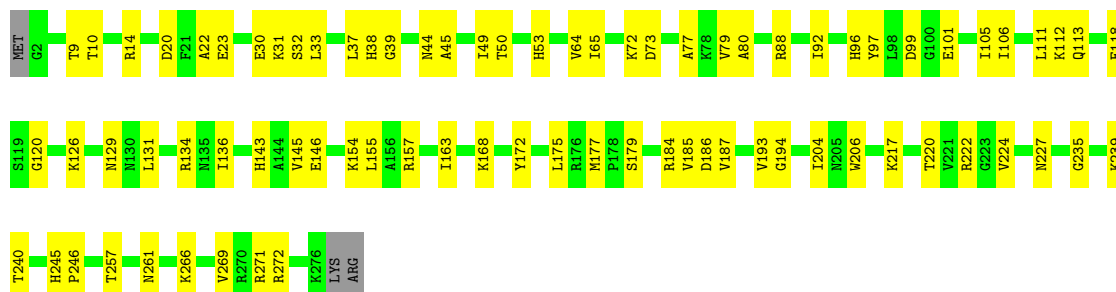
A1896	G1814	U1619	G1456	U1358	A1261	G1192	C1123	C1046	C964	G880	G771	G683
C1903	G1815	U1620	A1457	U1364	A1262	G1193	C1124	A1047	U965	C881	U772	G684
A1908	C1818	G1621	G1458	G1365	G1270	A1195	U1126	G1048	G970	U892	G774	G695
C1909	U1713	U1623	C1465	G1367	C1271	C1196	A1127	G1049	A972	G885	G792	U691
U1910	A1716	U1624	C1466	A1368	G1272	C1197	G1128	A1050	G973	G886	C793	G692
C1823	U1717	G1625	U1467	A1369	G1273	C1198	G1129	A1062	G974	G887	G794	G693
U1911	C1718	U1626	A1468	U1370	G1282	U1199	C1130	A1063	G975	U888	C795	A696
C1912	C1824	C1627	G1473	U1371	G1285	U1200	G1131	A1064	G976	G889	A800	G697
G1913	A1825	U1628	A1474	G1371	G1286	G1201	U1132	C1065	G979	G890	U800	G698
C1927	G1826	U1630	A1475	G1377	G1289	A1202	G1133	G1066	C980	G891	U699	A699
C1930	A1831	U1631	A1480	U1378	A1289	A1203	U1137	C1067	U981	U894	A808	G706
A1931	A1832	G1632	C1481	G1379	C1290	G1205	A1138	G1068	A982	G895	G819	G707
U1932	C1833	U1633	A1482	A1380	G1291	A1206	G1139	G1070	G986	A896	A820	G708
G1933	A1834	C1634	G1486	U1381	U1292	G1209	A1140	G1071	G987	A897	U709	U709
C1934	C1835	A1635	U1487	U1382	G1293	G1210	A1141	G1072	U988	A898	G824	G825
G1935	U1836	G1636	U1487	A1383	U1294	G1211	A1142	A1074	G989	G900	C826	U714
G1936	G1837	G1639	A1493	G1384	U1295	G1212	A1143	U1075	G992	U911	A721	A721
U1937	U1640	U1641	U1494	G1385	G1296	U1213	A1144	A1076	G993	C912	G722	G722
G1938	G1642	G1643	A1499	A1386	U1297	A1214	G1147	A1077	G994	G912	C723	C723
C1944	G1845	G1644	A1500	U1387	C1298	U1215	G1148	G1078	A995	A917	G832	G724
U1945	U1846	U1647	C1501	U1388	U1299	A1216	A1150	C1079	G996	A918	A725	A725
U1946	A1847	G1648	C1501	U1389	G1301	G1217	U1151	U1080	G997	A919	A726	A726
U1947	A1848	A1649	G1507	G1392	G1302	C1220	G1152	C1081	G998	G920	A727	A727
A1948	U1854	G1653	A1508	C1393	U1303	A1221	U1153	G1082	G999	C921	G836	G728
C1949	A1855	G1654	U1509	G1396	A1304	C1222	G1157	C1083	C1000	G922	C837	G729
G1950	G1856	G1654	A1510	U1397	G1305	U1223	G1158	U1084	C1001	G924	G838	C729
A1955	A1858	G1659	U1511	G1398	G1310	G1224	C1161	G1085	A1002	G924	U839	G730
A1956	A1859	U1661	U1512	C1403	G1314	G1225	G1162	G1086	C1003	C927	G840	A731
G1957	U1861	C1662	C1513	U1411	C1315	U1226	G1163	U1088	A1004	U928	G841	G732
U1960	U1665	U1665	A1518	G1411	G1316	C1227	A1164	C1089	A1005	C929	G844	U733
C1971	G1670	G1670	G1522	A1415	U1320	G1230	C1167	G1090	C1012	C931	G736	G736
A1972	A1755	A1673	U1523	A1416	G1323	U1231	U1171	A1091	U1013	C932	A737	A737
C1973	G1756	G1674	G1524	A1417	U1329	G1232	C1170	A1098	A1014	G933	A738	A738
A1974	U1757	U1675	G1528	U1427	G1329	A1233	A1172	A1099	A1015	A934	U739	U739
U1975	G1758	G1676	U1529	G1426	U1336	U1237	G1173	G1102	C1016	A936	G741	G741
A1976	U1870	U1677	G1530	U1427	G1336	U1247	A1174	G1103	A1020	A940	G742	G742
C1977	A1872	G1677	C1531	C1435	A1336	G1243	G1175	C1104	A1026	U941	G745	G745
U1981	U1876	A1678	G1532	C1436	G1337	A1244	A1176	C1105	A1027	U942	U746	U746
G1989	G1878	U1679	U1533	A1437	U1338	A1247	G1177	A1108	C1027	A944	A747	A747
A1990	G1879	U1681	C1534	G1438	G1339	A1249	U1178	A1091	G1031	U947	C754	C754
C1991	U1882	G1688	A1536	C1441	G1343	U1250	G1180	G1111	A1032	G948	A755	A755
U1996	A1883	G1692	G1538	A1442	A1344	A1251	G1181	G1112	A1033	G949	U756	U756
G1999	G1884	C1693	A1539	G1443	G1345	G1252	C1182	C1113	G1034	G951	G870	G870
U1999	A1885	U1683	U1540	U1444	G1346	C1253	G1184	G1114	A1035	G956	A871	A871
A2000	G1886	G1694	G1541	C1445	U1349	G1254	U1185	U1117	C1037	C957	G872	G872
A2001	A1887	U1695	U1541	C1445	G1350	G1255	A1186	U1118	A1041	G957	G874	G874
A2006	C1888	C1696	C1545	C1448	G1351	G1256	G1187	A1119	A1042	G960	G875	G875
C2007	G1892	U1704	A1546	C1449	A1352	G1257	A1188	A1119	A1043	U961	A876	A876
A2008	U1812	C1813	C1547	G1454	G1353	C1258	G1189	G1120	U1044	U962	U877	U877
			G1549	U1455	G1357	C1260	A1191	C1122	C1045	U963	G768	G768





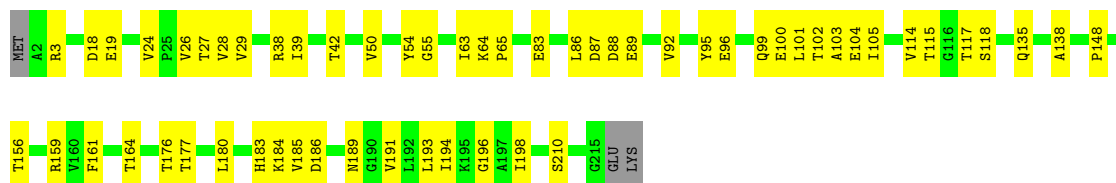
• Molecule 4: 50S ribosomal protein L2

Chain C: 71% 28%



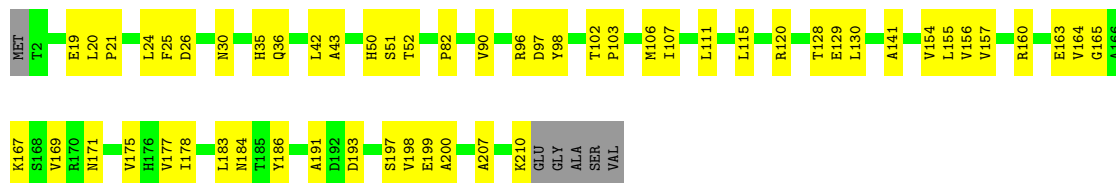
• Molecule 5: 50S ribosomal protein L3

Chain D: 72% 26%



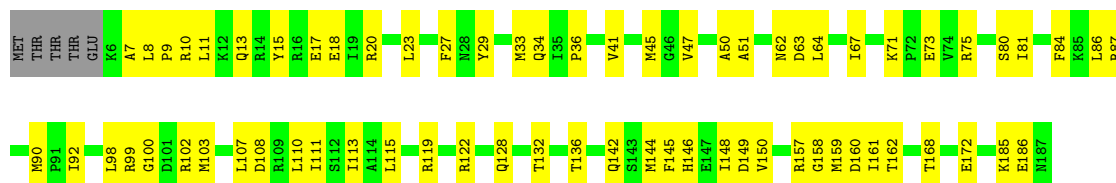
• Molecule 6: 50S ribosomal protein L4

Chain E: 72% 26%



• Molecule 7: 50S ribosomal protein L5

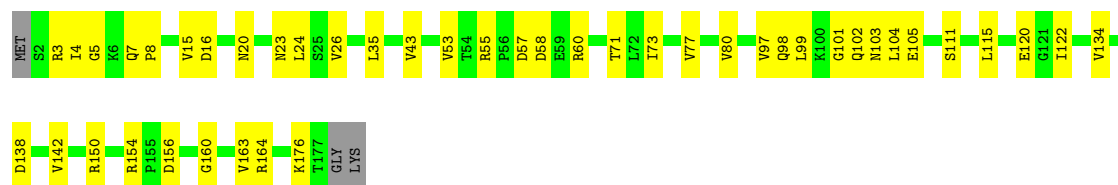
Chain F: 61% 36%



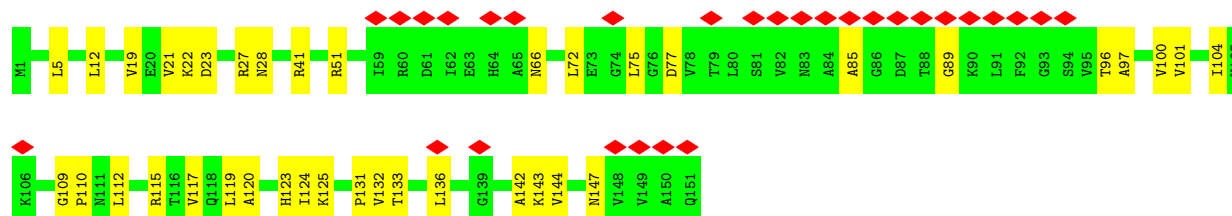
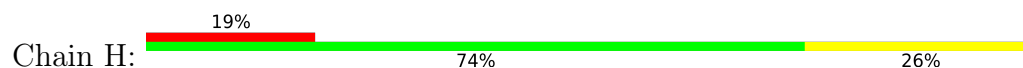
• Molecule 8: 50S ribosomal protein L6

Chain G: 74% 25%

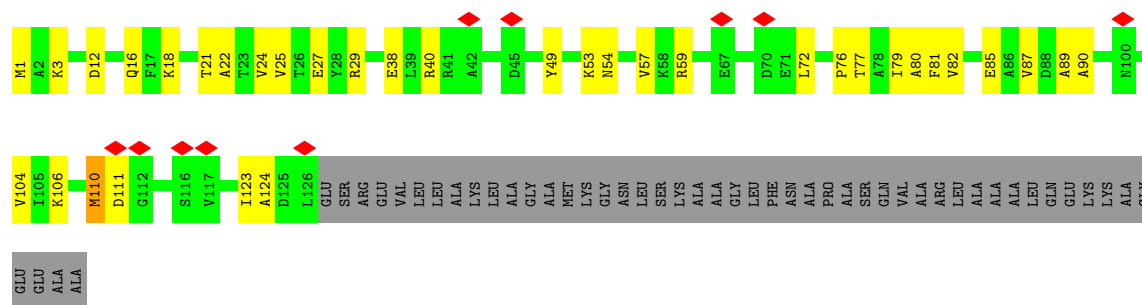




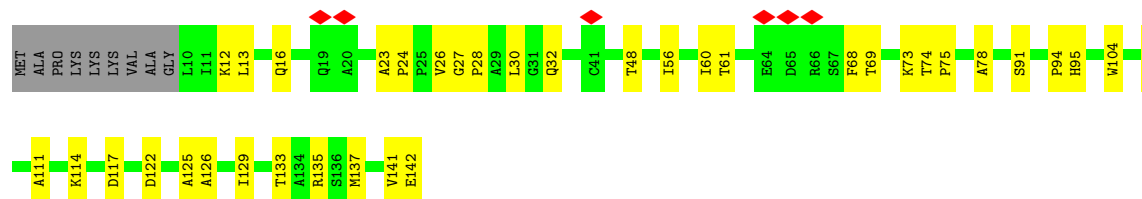
• Molecule 9: 50S ribosomal protein L9



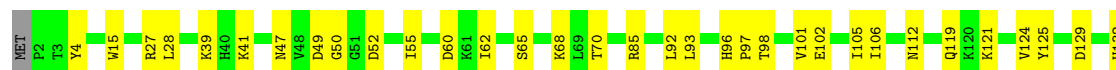
• Molecule 10: 50S ribosomal protein L10



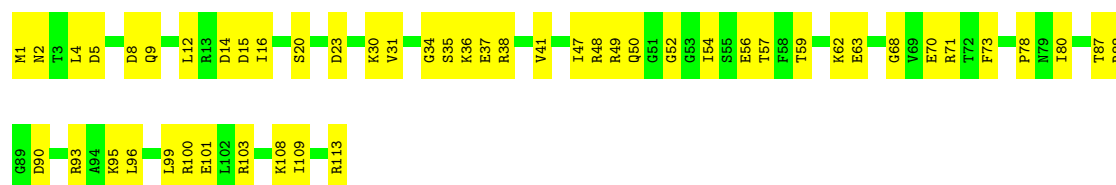
• Molecule 11: 50S ribosomal protein L11



• Molecule 12: 50S ribosomal protein L13



Chain Q:  56% 44%



- Molecule 19: 50S ribosomal protein L20

Chain R:  76% 20% .



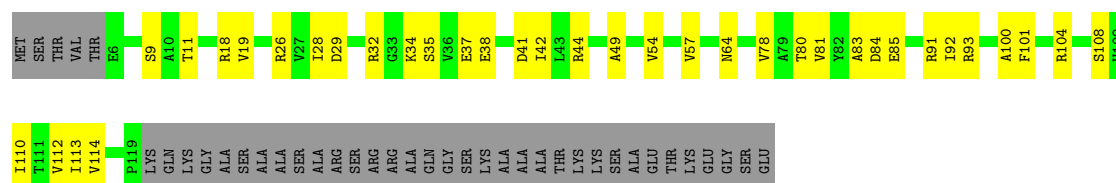
- Molecule 20: 50S ribosomal protein L21

Chain S:  77% 20% .



- Molecule 21: 50S ribosomal protein L22

Chain T:  51% 24% 25%



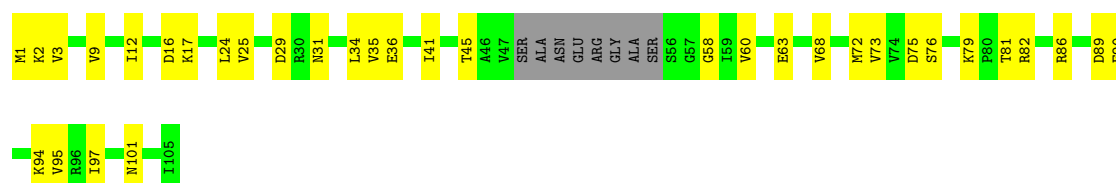
- Molecule 22: 50S ribosomal protein L23

Chain U:  70% 27% .

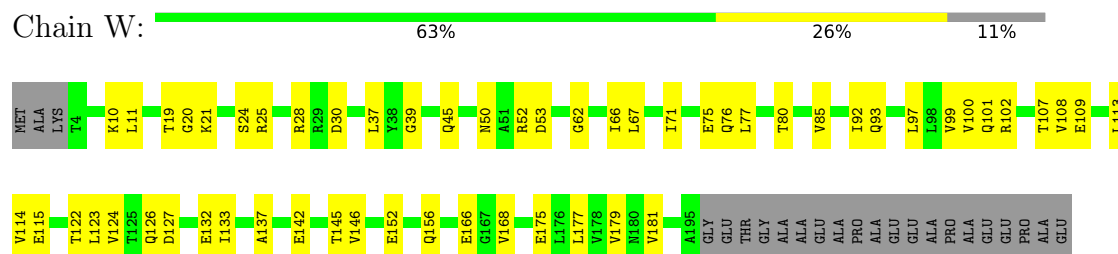


- Molecule 23: 50S ribosomal protein L24

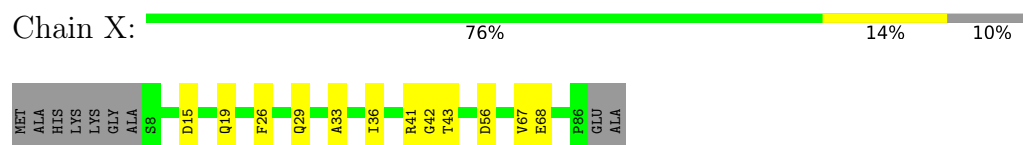
Chain V:  60% 32% 8%



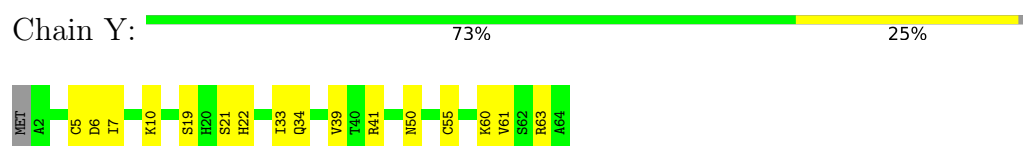
- Molecule 24: 50S ribosomal protein L25



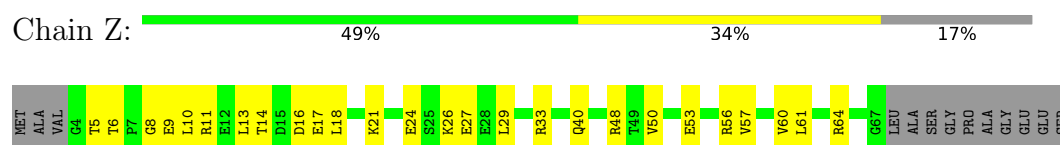
- Molecule 25: 50S ribosomal protein L27



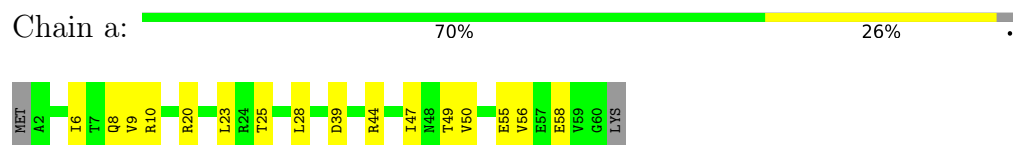
- Molecule 26: 50S ribosomal protein L28



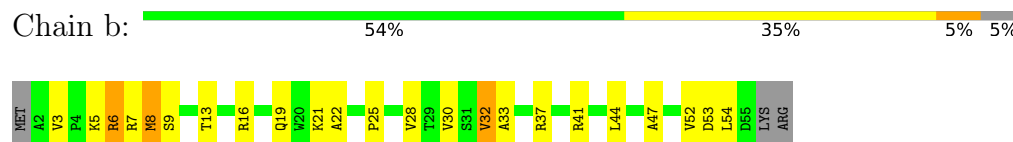
- Molecule 27: 50S ribosomal protein L29



- Molecule 28: 50S ribosomal protein L30



- Molecule 29: 50S ribosomal protein L32



- Molecule 30: 50S ribosomal protein L33 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	121211	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	28.26	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.086	Depositor
Minimum map value	-0.017	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	449.40002, 449.40002, 449.40002	wwPDB
Map dimensions	420, 420, 420	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

Bond lengths and bond angles in the following residue types are not validated in this section: GNP

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	3	0.23	0/191	0.44	0/247
2	A	0.26	0/74812	0.32	0/116731
3	B	0.20	0/2821	0.27	0/4396
4	C	0.24	0/2153	0.36	0/2895
5	D	0.25	0/1609	0.40	0/2165
6	E	0.24	0/1592	0.36	0/2153
7	F	0.15	0/1467	0.37	0/1973
8	G	0.16	0/1369	0.30	0/1848
9	H	0.14	0/1027	0.34	0/1398
10	I	0.14	0/925	0.31	0/1246
11	J	0.13	0/1006	0.32	0/1364
12	K	0.25	0/1157	0.36	0/1567
13	L	0.21	0/946	0.32	0/1268
14	M	0.24	0/1091	0.38	0/1457
15	N	0.21	0/1118	0.37	0/1506
16	O	0.25	0/945	0.42	0/1267
17	P	0.19	0/966	0.34	0/1298
18	Q	0.21	0/921	0.34	0/1236
19	R	0.30	0/1000	0.34	0/1341
20	S	0.22	0/764	0.29	0/1030
21	T	0.25	0/887	0.36	0/1204
22	U	0.21	0/766	0.32	0/1030
23	V	0.18	0/738	0.33	0/987
24	W	0.16	0/1443	0.33	0/1970
25	X	0.24	0/595	0.34	0/798
26	Y	0.24	0/478	0.38	0/641
27	Z	0.23	0/534	0.36	0/713
28	a	0.23	0/477	0.31	0/640
29	b	0.35	0/427	0.58	0/572
30	c	0.15	0/405	0.34	0/542
31	d	0.28	0/380	0.34	0/500
32	e	0.14	0/507	0.31	0/672

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	f	0.26	0/303	0.36	0/401
34	g	0.14	0/372	0.26	0/503
35	h	0.27	0/3297	0.50	2/4468 (0.0%)
All	All	0.25	0/109489	0.33	2/164027 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	h	198	VAL	N-CA-C	8.88	118.88	110.53
35	h	49	VAL	N-CA-C	5.92	118.15	108.97

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3	189	0	205	6	0
2	A	66813	0	33615	1159	0
3	B	2522	0	1285	41	0
4	C	2110	0	2165	65	0
5	D	1587	0	1630	45	0
6	E	1569	0	1607	46	0
7	F	1445	0	1476	66	0
8	G	1348	0	1399	35	0
9	H	1018	0	988	35	0
10	I	918	0	959	31	0
11	J	990	0	1021	42	0
12	K	1130	0	1167	33	0
13	L	938	0	1000	36	0
14	M	1078	0	1151	32	0
15	N	1092	0	1128	23	0
16	O	928	0	972	23	0
17	P	956	0	991	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Q	907	0	938	40	0
19	R	988	0	1038	21	0
20	S	754	0	802	17	0
21	T	873	0	909	34	0
22	U	756	0	802	23	0
23	V	732	0	782	29	0
24	W	1428	0	1443	46	0
25	X	586	0	601	13	0
26	Y	470	0	484	11	0
27	Z	531	0	541	27	0
28	a	474	0	500	17	0
29	b	423	0	463	26	0
30	c	397	0	407	9	0
31	d	377	0	411	17	0
32	e	502	0	541	17	0
33	f	299	0	324	6	0
34	g	364	0	352	11	0
35	h	3256	0	3311	166	0
36	h	32	0	13	0	0
All	All	100780	0	67421	2007	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (2007) 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)
6:E:102:THR:HG23	6:E:107:ILE:HD11	1.27	1.16
35:h:73:LEU:O	35:h:76:THR:HG22	1.46	1.14
21:T:92:ILE:HD11	21:T:100:ALA:HB1	1.39	1.01
12:K:125:TYR:HH	12:K:132:HIS:HE2	1.06	1.00
2:A:329:U:O2	2:A:446:G:O6	1.81	0.98
2:A:2706:A:HO2'	35:h:157:SER:HG	1.03	0.98
2:A:234:U:O4	2:A:263:G:N2	1.96	0.98
2:A:2130:G:OP1	2:A:2153:G:O2'	1.82	0.96
2:A:298:G:O2'	2:A:299:G:O4'	1.84	0.95
2:A:1411:G:OP1	2:A:2933:G:O2'	1.82	0.94
2:A:1186:G:O2'	2:A:1187:A:OP1	1.83	0.94
2:A:2777:G:N2	2:A:2807:G:O2'	2.01	0.94
2:A:1482:A:O3'	31:d:28:ARG:NH2	2.01	0.93
21:T:19:VAL:O	21:T:108:SER:OG	1.86	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:738:A:O2'	2:A:740:A:OP1	1.87	0.93
2:A:327:U:O2'	2:A:328:C:O4'	1.86	0.93
2:A:1597:G:O2'	2:A:1598:U:O4'	1.87	0.92
2:A:1002:C:O2'	2:A:1003:A:OP1	1.86	0.92
2:A:1201:G:O2'	2:A:1203:A:OP2	1.88	0.91
2:A:306:U:OP1	9:H:41:ARG:NH1	2.04	0.91
2:A:58:G:OP1	27:Z:48:ARG:NH1	2.03	0.90
3:B:41:U:O2'	3:B:44:C:OP2	1.90	0.90
12:K:125:TYR:OH	12:K:132:HIS:NE2	2.03	0.90
2:A:1825:C:N4	2:A:1840:G:OP2	2.04	0.89
2:A:286:G:N2	2:A:287:A:N7	2.19	0.89
35:h:46:LEU:HG	35:h:119:ILE:HD11	1.52	0.89
2:A:365:U:O2	2:A:437:G:O6	1.89	0.89
2:A:1163:A:OP1	10:I:3:LYS:NZ	2.05	0.89
2:A:2617:U:O4	2:A:2646:C:N4	2.06	0.89
2:A:2482:U:O2'	2:A:2651:C:OP2	1.91	0.88
2:A:1535:C:OP2	2:A:1536:A:N6	2.07	0.88
2:A:1540:U:O2'	2:A:1541:G:N7	2.07	0.88
1:3:8:LYS:NZ	2:A:2253:A:OP2	2.07	0.88
2:A:1711:G:O2'	4:C:101:GLU:OE2	1.91	0.88
2:A:2270:G:O2'	29:b:19:GLN:OE1	1.92	0.88
2:A:2270:G:O3'	29:b:19:GLN:NE2	2.07	0.87
2:A:273:A:H62	2:A:313:G:N2	1.71	0.87
2:A:1072:G:OP1	15:N:87:LYS:NZ	2.07	0.87
2:A:1623:U:O2'	2:A:1624:U:OP1	1.93	0.87
2:A:2008:A:OP1	4:C:217:LYS:NZ	2.07	0.87
2:A:2729:G:O2'	35:h:200:THR:CG2	2.23	0.87
2:A:2958:C:N4	2:A:2994:C:O2	2.06	0.87
3:B:44:C:O3'	7:F:102:ARG:NH2	2.07	0.86
2:A:1272:C:OP1	19:R:92:ARG:NH2	2.08	0.86
2:A:1137:U:OP1	2:A:1153:U:O2'	1.92	0.86
2:A:1578:G:O2'	2:A:1579:C:O5'	1.93	0.86
18:Q:48:ARG:NH1	18:Q:50:GLN:OE1	2.09	0.86
35:h:319:LEU:HD13	35:h:353:VAL:HG21	1.57	0.86
2:A:742:G:O2'	2:A:2575:G:OP1	1.93	0.86
2:A:1043:G:H21	28:a:25:THR:HG22	1.40	0.86
10:I:54:ASN:OD1	10:I:77:THR:OG1	1.94	0.85
2:A:188:G:O6	2:A:204:G:O2'	1.92	0.85
2:A:2584:A:OP1	32:e:24:ARG:NH2	2.09	0.85
2:A:2168:U:O2'	2:A:2185:C:OP2	1.95	0.85
2:A:199:U:O2	2:A:474:G:N2	2.09	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:27:ARG:NH1	9:H:28:ASN:OD1	2.10	0.85
2:A:1536:A:O2'	2:A:1537:U:O4'	1.94	0.84
2:A:2174:G:O2'	2:A:2210:U:O3'	1.95	0.84
2:A:2537:C:OP1	7:F:75:ARG:NE	2.09	0.84
7:F:9:PRO:O	7:F:13:GLN:NE2	2.10	0.84
2:A:1111:G:OP2	19:R:51:ARG:NH1	2.10	0.84
2:A:499:G:OP2	2:A:2630:A:O2'	1.95	0.84
2:A:2088:C:O2'	2:A:2089:C:OP1	1.94	0.84
2:A:2245:C:OP1	19:R:25:ARG:NH1	2.10	0.84
6:E:128:THR:OG1	6:E:129:GLU:OE1	1.96	0.84
2:A:248:G:O2'	2:A:2656:A:OP1	1.96	0.84
2:A:2196:G:OP2	4:C:239:LYS:NZ	2.10	0.84
2:A:2159:G:O2'	2:A:2186:C:N4	2.11	0.83
2:A:981:U:O2'	2:A:982:A:OP2	1.96	0.83
2:A:571:A:O2'	23:V:45:THR:O	1.94	0.83
2:A:740:A:O2'	2:A:741:G:OP2	1.95	0.83
28:a:58:GLU:N	28:a:58:GLU:OE2	2.11	0.83
2:A:2819:G:N2	2:A:2822:A:OP2	2.10	0.83
35:h:73:LEU:O	35:h:76:THR:CG2	2.27	0.83
2:A:2131:G:N2	2:A:2132:U:O2	2.12	0.83
2:A:2155:U:OP1	2:A:2192:G:N2	2.11	0.83
2:A:448:U:O2'	2:A:449:G:O4'	1.95	0.82
2:A:2255:A:N3	2:A:2679:G:O2'	2.12	0.82
2:A:313:G:O2'	2:A:314:G:O5'	1.98	0.82
2:A:1573:U:O2'	2:A:1575:A:N6	2.09	0.82
8:G:55:ARG:NH1	8:G:57:ASP:O	2.12	0.82
12:K:98:THR:OG1	12:K:124:VAL:HG13	1.78	0.82
2:A:2571:C:OP1	30:c:40:LYS:NZ	2.13	0.82
8:G:97:VAL:HG22	8:G:104:LEU:HD11	1.60	0.82
2:A:1125:C:OP1	12:K:39:LYS:NZ	2.13	0.82
15:N:27:VAL:HG23	15:N:105:GLU:OE2	1.80	0.82
6:E:129:GLU:OE1	6:E:129:GLU:N	2.12	0.81
2:A:745:G:OP1	32:e:19:THR:OG1	1.97	0.81
6:E:141:ALA:HB1	6:E:169:VAL:HG12	1.60	0.81
2:A:2653:G:O6	14:M:60:ARG:NH2	2.12	0.81
2:A:3068:U:OP1	18:Q:95:LYS:NZ	2.13	0.81
3:B:10:G:O2'	3:B:11:U:OP1	1.96	0.81
11:J:74:THR:OG1	11:J:117:ASP:OD2	1.99	0.81
11:J:23:ALA:HB3	11:J:24:PRO:HD3	1.62	0.81
2:A:1999:U:O2	2:A:2832:G:O2'	1.98	0.81
2:A:2674:A:N6	2:A:2725:C:O2	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:46:A:O4'	7:F:99:ARG:NE	2.14	0.81
35:h:43:GLN:HG2	35:h:44:LEU:H	1.45	0.81
2:A:2973:A:N3	8:G:60:ARG:NH2	2.27	0.81
8:G:102:GLN:OE1	8:G:102:GLN:N	2.13	0.81
34:g:27:THR:O	34:g:29:GLN:NE2	2.13	0.81
2:A:1884:G:HO2'	13:L:6:SER:HG	1.18	0.80
2:A:1996:U:OP2	2:A:2001:A:N6	2.14	0.80
2:A:52:G:O2'	2:A:124:A:N1	2.14	0.80
2:A:1854:U:O2'	2:A:1977:C:O2'	1.99	0.80
19:R:97:GLU:OE2	20:S:15:LYS:NZ	2.10	0.80
2:A:1223:U:OP2	10:I:1:MET:N	2.15	0.80
2:A:3009:U:O2'	5:D:38:ARG:NH2	2.15	0.80
2:A:2755:A:OP1	8:G:176:LYS:NZ	2.13	0.80
2:A:159:A:OP2	2:A:164:A:N6	2.15	0.80
2:A:747:A:N6	2:A:768:G:O2'	2.14	0.80
2:A:773:G:H21	6:E:106:MET:HE2	1.46	0.80
2:A:1577:C:N4	2:A:1593:U:O4	2.14	0.79
2:A:452:G:O2'	2:A:453:U:O4'	1.99	0.79
2:A:1577:C:N4	2:A:1578:G:O6	2.15	0.79
2:A:188:G:H8	2:A:206:A:H62	1.31	0.79
2:A:274:C:O2'	2:A:323:C:OP1	2.00	0.79
2:A:2393:A:O2'	2:A:2394:A:O4'	2.00	0.79
4:C:72:LYS:NZ	4:C:99:ASP:OD2	2.15	0.79
2:A:808:A:O2'	2:A:1468:A:N3	2.15	0.79
2:A:2315:U:OP1	26:Y:63:ARG:NH2	2.16	0.79
2:A:392:A:O2'	2:A:393:U:OP2	2.00	0.79
2:A:2447:G:OP1	4:C:172:TYR:OH	2.00	0.79
14:M:134:ARG:NH1	14:M:144:ALA:O	2.16	0.79
2:A:2729:G:O2'	35:h:200:THR:HG22	1.82	0.78
2:A:737:A:N1	2:A:2593:A:O2'	2.17	0.78
2:A:1541:G:O6	2:A:1629:G:O2'	2.01	0.78
2:A:2336:U:O4	2:A:2342:A:N6	2.16	0.78
2:A:336:C:O2'	2:A:337:U:OP1	2.01	0.78
2:A:2352:C:N3	2:A:2383:U:O4	2.16	0.78
2:A:183:G:O2'	2:A:216:A:N3	2.16	0.78
2:A:2352:C:C2	2:A:2383:U:N3	2.52	0.78
2:A:2487:C:N4	25:X:15:ASP:OD1	2.15	0.78
2:A:2571:C:O2'	30:c:23:TYR:OH	1.98	0.78
2:A:993:G:O2'	2:A:1015:A:N6	2.16	0.78
2:A:1831:A:O2'	31:d:6:ARG:NH1	2.17	0.78
2:A:2486:U:OP2	25:X:19:GLN:NE2	2.16	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:2859:C:O2'	5:D:83:GLU:OE1	2.00	0.78
12:K:41:LYS:NZ	12:K:52:ASP:OD1	2.16	0.78
2:A:729:C:O2'	2:A:733:U:OP1	2.02	0.77
2:A:1730:U:O2'	2:A:1731:A:OP2	2.03	0.77
2:A:1565:A:O2'	2:A:1566:A:O5'	2.02	0.77
7:F:142:GLN:OE1	7:F:157:ARG:N	2.16	0.77
24:W:175:GLU:OE1	24:W:175:GLU:N	2.16	0.77
2:A:485:U:O2'	2:A:2454:G:N2	2.18	0.77
2:A:1199:U:O2'	2:A:1200:U:OP1	2.01	0.77
2:A:2891:C:N3	8:G:111:SER:OG	2.16	0.77
2:A:363:A:O2'	2:A:364:A:OP1	2.02	0.76
4:C:30:GLU:OE1	4:C:32:SER:OG	2.03	0.76
6:E:102:THR:CG2	6:E:107:ILE:HD11	2.13	0.76
21:T:81:VAL:HG23	21:T:112:VAL:HG22	1.67	0.76
2:A:273:A:N6	2:A:313:G:N2	2.33	0.76
2:A:736:G:N2	2:A:739:U:OP2	2.16	0.76
8:G:122:ILE:HD11	8:G:134:VAL:CG1	2.14	0.76
8:G:23:ASN:OD1	8:G:24:LEU:N	2.18	0.76
22:U:34:HIS:ND1	22:U:36:ASP:OD1	2.14	0.76
2:A:2528:G:OP1	7:F:128:GLN:NE2	2.19	0.76
2:A:122:A:OP2	31:d:22:ARG:NH1	2.19	0.76
2:A:1578:G:O2'	2:A:1579:C:O4'	2.02	0.76
2:A:1171:C:O2	2:A:1172:A:N6	2.19	0.75
27:Z:11:ARG:O	27:Z:64:ARG:NH2	2.18	0.75
2:A:2333:G:OP1	2:A:2371:G:N2	2.20	0.75
25:X:26:PHE:N	25:X:29:GLN:OE1	2.17	0.75
35:h:200:THR:HG22	35:h:200:THR:O	1.85	0.75
27:Z:9:GLU:OE1	27:Z:9:GLU:N	2.19	0.75
35:h:46:LEU:HA	35:h:117:THR:HG21	1.68	0.75
2:A:1398:G:N2	2:A:1444:U:O4	2.19	0.75
2:A:103:C:O2'	2:A:375:A:O2'	1.94	0.75
2:A:273:A:N6	2:A:313:G:H21	1.84	0.75
2:A:2795:C:O2'	5:D:156:THR:OG1	2.05	0.75
2:A:1202:A:O2'	2:A:1203:A:OP2	2.04	0.75
2:A:2131:G:O2'	2:A:2154:G:O4'	2.03	0.75
6:E:103:PRO:O	6:E:107:ILE:HD12	1.86	0.75
13:L:105:GLU:N	13:L:105:GLU:OE1	2.19	0.75
2:A:1063:G:O6	2:A:1090:G:N2	2.20	0.74
2:A:724:G:OP1	32:e:47:ARG:NH2	2.19	0.74
2:A:2356:G:O2'	2:A:2381:A:N1	2.20	0.74
2:A:251:A:OP1	32:e:7:HIS:NE2	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:135:GLU:N	15:N:135:GLU:OE1	2.19	0.74
27:Z:10:LEU:HD22	27:Z:60:VAL:HG21	1.69	0.74
2:A:1379:G:OP1	29:b:16:ARG:NH2	2.20	0.74
2:A:1560:U:O2	4:C:134:ARG:NH2	2.19	0.74
2:A:3107:G:O2'	2:A:3108:G:OP2	2.04	0.74
2:A:227:A:N7	2:A:2631:G:O2'	2.19	0.74
2:A:1178:U:O4	11:J:133:THR:OG1	2.03	0.74
2:A:3078:G:N2	2:A:3081:A:OP2	2.18	0.74
2:A:2693:A:O2'	2:A:2694:G:OP1	2.06	0.74
2:A:218:A:N3	2:A:234:U:O2'	2.19	0.73
2:A:2128:G:N2	2:A:2153:G:O4'	2.21	0.73
2:A:1606:G:O2'	2:A:1607:C:O4'	2.06	0.73
4:C:118:GLU:OE1	4:C:129:ASN:ND2	2.21	0.73
2:A:636:U:O2'	2:A:637:G:OP1	2.07	0.73
2:A:1198:C:N4	2:A:1206:A:OP2	2.21	0.73
2:A:299:G:N2	2:A:301:U:O5'	2.21	0.73
2:A:2128:G:O2'	2:A:2130:G:N2	2.22	0.73
5:D:19:GLU:OE1	5:D:19:GLU:N	2.22	0.73
9:H:12:LEU:HD21	9:H:19:VAL:HG21	1.70	0.73
2:A:2394:A:O2'	2:A:2396:A:OP1	2.06	0.73
2:A:2447:G:O3'	4:C:266:LYS:NZ	2.22	0.73
2:A:727:A:OP1	14:M:72:ARG:NE	2.21	0.73
2:A:2475:G:OP2	15:N:82:ARG:NH1	2.22	0.73
27:Z:40:GLN:OE1	27:Z:40:GLN:N	2.22	0.73
2:A:2015:U:O2'	2:A:2019:A:N3	2.18	0.73
2:A:2181:C:O2'	2:A:2182:C:O4'	2.04	0.73
11:J:32:GLN:NE2	11:J:32:GLN:O	2.22	0.73
2:A:1675:U:O2'	2:A:1676:G:N7	2.22	0.72
8:G:7:GLN:NE2	8:G:8:PRO:O	2.22	0.72
2:A:1194:C:O2'	11:J:94:PRO:O	2.05	0.72
2:A:885:G:OP2	31:d:14:ARG:NH2	2.22	0.72
2:A:942:U:O2	2:A:2470:A:O2'	2.05	0.72
2:A:2515:U:OP1	2:A:2604:U:O2'	2.06	0.72
21:T:9:SER:OG	21:T:114:VAL:O	2.04	0.72
2:A:554:A:OP1	31:d:37:ARG:NH1	2.22	0.72
35:h:349:VAL:O	35:h:353:VAL:HG23	1.90	0.72
2:A:637:G:O2'	2:A:638:U:OP2	2.05	0.72
4:C:118:GLU:OE1	4:C:118:GLU:N	2.21	0.72
16:O:49:GLU:OE1	16:O:95:THR:OG1	2.06	0.72
2:A:2016:G:OP2	4:C:271:ARG:NH2	2.23	0.72
2:A:2932:G:O2'	16:O:71:ARG:NH1	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:27:A:N3	3:B:114:A:O2'	2.20	0.72
2:A:322:A:N6	2:A:454:U:O4	2.23	0.71
6:E:154:VAL:HG22	6:E:175:VAL:HG22	1.71	0.71
8:G:120:GLU:OE1	8:G:120:GLU:N	2.23	0.71
2:A:2729:G:O2'	35:h:200:THR:HG21	1.90	0.71
2:A:3021:A:O2'	2:A:3022:G:N7	2.16	0.71
2:A:31:U:O2'	2:A:32:G:O5'	2.08	0.71
2:A:1549:G:O2'	2:A:1550:G:O5'	2.08	0.71
5:D:29:VAL:HG11	5:D:194:ILE:HD11	1.71	0.71
2:A:329:U:O2	2:A:446:G:C6	2.42	0.71
2:A:2173:G:O2'	2:A:2174:G:O5'	2.06	0.71
7:F:149:ASP:OD1	7:F:150:VAL:N	2.23	0.71
35:h:73:LEU:C	35:h:76:THR:HG22	2.15	0.71
2:A:2230:C:O2'	2:A:3044:A:N3	2.23	0.71
16:O:57:LYS:O	16:O:62:ASN:ND2	2.24	0.71
16:O:87:TYR:OH	16:O:116:VAL:O	2.03	0.71
2:A:2095:G:O2'	2:A:2096:G:OP2	2.08	0.71
7:F:136:THR:OG1	7:F:162:THR:HG22	1.91	0.71
21:T:37:GLU:OE1	21:T:37:GLU:N	2.22	0.71
24:W:115:GLU:N	24:W:115:GLU:OE1	2.23	0.71
28:a:6:ILE:CD1	28:a:47:ILE:HD11	2.20	0.71
11:J:61:THR:OG1	11:J:69:THR:OG1	2.08	0.71
18:Q:16:ILE:O	18:Q:16:ILE:HD12	1.90	0.71
35:h:276:LEU:HD12	35:h:278:ALA:H	1.52	0.71
33:f:22:ARG:NH2	33:f:36:GLN:O	2.24	0.71
17:P:12:GLU:OE1	17:P:12:GLU:N	2.24	0.70
2:A:265:A:O2'	2:A:266:U:OP2	2.07	0.70
2:A:2178:G:O2'	2:A:2180:U:O4	2.08	0.70
4:C:77:ALA:HB2	4:C:97:TYR:CD1	2.26	0.70
2:A:1393:C:O2'	16:O:27:SER:OG	2.09	0.70
2:A:1164:A:O4'	10:I:59:ARG:NE	2.24	0.70
2:A:3083:A:O3'	18:Q:113:ARG:NH2	2.24	0.70
2:A:757:G:OP2	2:A:757:G:N2	2.15	0.70
2:A:1258:C:OP2	12:K:68:LYS:NZ	2.21	0.70
2:A:1551:U:O2'	2:A:1552:A:OP1	2.07	0.70
20:S:44:ASP:O	20:S:47:ASN:ND2	2.24	0.70
2:A:298:G:HO2'	2:A:299:G:C1'	2.04	0.70
2:A:3071:A:N7	2:A:3089:A:O2'	2.21	0.70
2:A:1165:G:OP2	10:I:53:LYS:NZ	2.25	0.69
4:C:143:HIS:ND1	4:C:194:GLY:O	2.24	0.69
23:V:75:ASP:OD1	23:V:76:SER:N	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:92:G:OP2	24:W:25:ARG:NH1	2.24	0.69
2:A:1568:C:O2	2:A:1604:G:N2	2.25	0.69
2:A:2155:U:H5''	2:A:2191:C:H42	1.57	0.69
24:W:156:GLN:OE1	24:W:156:GLN:N	2.24	0.69
2:A:844:G:OP1	4:C:10:THR:OG1	2.10	0.69
2:A:1756:G:O2'	2:A:1757:U:O2	2.10	0.69
2:A:1885:G:O2'	2:A:2215:U:O4	2.09	0.69
6:E:199:GLU:N	6:E:199:GLU:OE2	2.24	0.69
7:F:80:SER:OG	7:F:86:LEU:O	2.04	0.69
34:g:38:CYS:SG	34:g:40:GLN:NE2	2.66	0.69
2:A:894:U:OP1	4:C:49:ILE:HG22	1.91	0.69
2:A:2074:G:O6	2:A:2075:G:N1	2.25	0.69
2:A:1563:A:O2'	2:A:1564:A:OP2	2.07	0.68
2:A:2363:A:O2'	2:A:2364:C:O4'	2.06	0.68
2:A:2851:G:N2	2:A:3001:G:OP2	2.25	0.68
2:A:2070:A:N7	2:A:2113:A:N6	2.42	0.68
2:A:2674:A:N6	2:A:2725:C:C2	2.61	0.68
2:A:2802:G:OP1	2:A:2838:A:N6	2.26	0.68
22:U:59:THR:OG1	22:U:81:ARG:O	2.05	0.68
2:A:1458:G:O2'	2:A:1499:A:N1	2.23	0.68
2:A:2357:A:N6	2:A:2380:G:O3'	2.26	0.68
25:X:43:THR:HG23	25:X:43:THR:O	1.93	0.68
31:d:45:LEU:O	31:d:45:LEU:HD23	1.93	0.68
11:J:104:TRP:N	11:J:142:GLU:O	2.26	0.68
6:E:156:VAL:CG1	6:E:177:VAL:HG22	2.23	0.68
27:Z:14:THR:OG1	27:Z:16:ASP:OD1	2.12	0.68
2:A:2390:U:O2'	2:A:2392:A:N6	2.27	0.68
15:N:38:GLU:HB3	15:N:127:ILE:HD11	1.76	0.68
2:A:774:G:N2	6:E:36:GLN:OE1	2.22	0.68
2:A:1184:U:O2	2:A:1186:G:O2'	2.10	0.68
2:A:1364:U:O2'	2:A:1365:G:O5'	2.12	0.68
2:A:860:G:HO2'	2:A:863:G:HO2'	1.30	0.67
2:A:1579:C:N4	2:A:1588:G:OP1	2.27	0.67
2:A:2054:C:H2'	2:A:2123:A:H62	1.58	0.67
13:L:43:VAL:HG21	13:L:52:VAL:HG21	1.75	0.67
2:A:2698:C:O2'	2:A:2699:C:OP1	2.11	0.67
5:D:99:GLN:OE1	5:D:100:GLU:N	2.27	0.67
4:C:175:LEU:HD11	4:C:185:VAL:HG12	1.76	0.67
2:A:533:C:O2'	2:A:537:A:O2'	2.12	0.67
2:A:2851:G:O2'	2:A:3005:A:N1	2.25	0.67
6:E:26:ASP:O	6:E:120:ARG:NH2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:f:17:ILE:HD11	33:f:26:ILE:HD11	1.77	0.67
2:A:137:G:H21	2:A:1524:G:H1'	1.59	0.67
2:A:2474:G:O2'	2:A:2720:C:OP1	2.07	0.67
2:A:253:C:OP2	32:e:5:LYS:NZ	2.19	0.67
2:A:1867:G:O2'	16:O:106:ASP:OD2	2.09	0.67
2:A:582:G:O4'	21:T:64:ASN:ND2	2.28	0.67
2:A:2862:G:O2'	2:A:3002:A:N6	2.26	0.67
2:A:828:G:H21	2:A:833:A:H62	1.43	0.67
2:A:1199:U:H1'	11:J:125:ALA:HB1	1.76	0.67
2:A:2329:G:N2	2:A:2330:U:O2	2.27	0.67
2:A:191:G:OP2	2:A:191:G:N2	2.21	0.67
2:A:660:U:O5'	2:A:1062:A:N6	2.28	0.67
2:A:2239:A:C2	29:b:3:VAL:HG22	2.30	0.67
2:A:929:C:H1'	2:A:1339:G:H21	1.59	0.66
2:A:1248:U:O2	5:D:159:ARG:NH2	2.28	0.66
35:h:210:THR:HG23	35:h:213:ARG:HB2	1.76	0.66
24:W:107:THR:OG1	24:W:132:GLU:OE2	2.11	0.66
2:A:1676:G:O2'	2:A:3074:C:OP1	2.12	0.66
2:A:2489:U:OP2	2:A:2490:A:O2'	2.14	0.66
3:B:7:G:OP1	17:P:15:ARG:NH2	2.28	0.66
4:C:155:LEU:HB3	4:C:163:ILE:HD11	1.76	0.66
18:Q:2:ASN:N	18:Q:5:ASP:OD2	2.28	0.66
2:A:2074:G:N2	2:A:2110:U:O4	2.29	0.66
6:E:50:HIS:O	6:E:50:HIS:ND1	2.27	0.66
19:R:83:LEU:HD22	19:R:113:ALA:HB2	1.77	0.66
2:A:273:A:N6	2:A:313:G:C2	2.64	0.66
2:A:335:G:O2'	2:A:336:C:OP1	2.10	0.66
2:A:1467:U:O2'	2:A:1790:A:N3	2.29	0.66
2:A:2178:G:O2'	2:A:2179:U:OP2	2.13	0.66
2:A:2193:A:C2'	2:A:2196:G:H21	2.08	0.66
35:h:49:VAL:HG22	35:h:119:ILE:HG12	1.77	0.66
2:A:2381:A:O2'	2:A:2382:G:N3	2.27	0.66
27:Z:16:ASP:OD1	27:Z:17:GLU:N	2.29	0.66
32:e:55:ASN:OD1	32:e:56:SER:N	2.27	0.66
2:A:383:U:H1'	23:V:12:ILE:HD11	1.78	0.66
2:A:1199:U:HO2'	2:A:1200:U:P	2.17	0.66
2:A:369:G:O2'	2:A:371:G:O5'	2.14	0.66
2:A:2932:G:O2'	16:O:71:ARG:NH2	2.29	0.66
2:A:973:G:O2'	2:A:2492:A:N3	2.28	0.66
2:A:886:G:OP1	31:d:17:ARG:NE	2.29	0.65
2:A:1696:G:O2'	2:A:1736:G:O6	2.13	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:2193:A:O2'	2:A:2196:G:N3	2.26	0.65
2:A:24:G:O2'	2:A:25:A:OP2	2.14	0.65
2:A:351:G:O2'	2:A:352:G:OP1	2.09	0.65
2:A:1179:U:OP2	11:J:12:LYS:NZ	2.21	0.65
2:A:930:C:OP2	20:S:86:LYS:NZ	2.25	0.65
6:E:183:LEU:HD12	6:E:183:LEU:O	1.96	0.65
2:A:292:G:O5'	2:A:344:G:N2	2.28	0.65
2:A:451:U:H2'	2:A:452:G:C4	2.32	0.65
2:A:1002:C:HO2'	2:A:1003:A:P	2.20	0.65
3:B:4:A:N1	3:B:23:G:O2'	2.27	0.65
7:F:168:THR:N	7:F:172:GLU:OE2	2.30	0.65
35:h:47:GLU:H	35:h:117:THR:HG21	1.62	0.65
2:A:998:G:H1'	2:A:1011:A:H61	1.62	0.65
2:A:1074:A:N6	2:A:1076:A:N1	2.45	0.65
18:Q:108:LYS:NZ	18:Q:109:ILE:O	2.29	0.65
2:A:2586:G:OP2	32:e:44:LEU:HD21	1.96	0.65
6:E:20:LEU:HD23	6:E:25:PHE:CD2	2.32	0.65
35:h:326:ASP:OD2	35:h:411:VAL:HG13	1.97	0.65
2:A:2515:U:O2'	2:A:2598:C:O2	2.15	0.64
20:S:20:ASP:OD1	20:S:21:VAL:N	2.29	0.64
35:h:229:MET:SD	35:h:230:LYS:N	2.70	0.64
2:A:1947:U:O2'	2:A:1948:A:O4'	2.11	0.64
4:C:80:ALA:O	4:C:113:GLN:NE2	2.30	0.64
2:A:1037:C:O2'	25:X:29:GLN:NE2	2.31	0.64
2:A:2352:C:N3	2:A:2383:U:C4	2.66	0.64
5:D:50:VAL:HG11	5:D:95:TYR:HD2	1.62	0.64
2:A:920:G:OP2	14:M:44:LYS:NZ	2.30	0.64
2:A:1456:G:HO2'	2:A:1512:U:HO2'	1.42	0.64
6:E:154:VAL:CG2	6:E:175:VAL:HG22	2.28	0.64
2:A:1260:C:O2'	12:K:27:ARG:NH2	2.30	0.64
34:g:10:VAL:O	34:g:26:SER:N	2.30	0.64
4:C:105:ILE:HD12	4:C:106:ILE:O	1.97	0.64
9:H:77:ASP:OD2	9:H:147:ASN:ND2	2.30	0.64
7:F:47:VAL:HG21	7:F:50:ALA:HB2	1.80	0.64
2:A:2022:U:O2	4:C:50:THR:OG1	2.15	0.64
5:D:101:LEU:HD12	5:D:105:ILE:HD11	1.80	0.64
2:A:1539:A:C2'	2:A:1540:U:O5'	2.47	0.63
17:P:34:GLU:OE2	17:P:34:GLU:N	2.30	0.63
13:L:34:GLY:N	13:L:37:ASP:OD2	2.31	0.63
13:L:68:GLU:OE1	13:L:68:GLU:N	2.29	0.63
2:A:1545:C:N4	2:A:1626:G:O6	2.30	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:79:VAL:HG11	4:C:111:LEU:HD21	1.79	0.63
9:H:143:LYS:NZ	9:H:144:VAL:O	2.32	0.63
2:A:137:G:N2	2:A:1524:G:N3	2.45	0.63
2:A:1533:U:O2'	2:A:1534:C:OP1	2.11	0.63
2:A:1854:U:HO2'	2:A:1977:C:HO2'	1.41	0.63
2:A:2175:U:OP2	13:L:54:ARG:NH2	2.32	0.63
2:A:1427:U:O2'	22:U:65:LYS:NZ	2.21	0.63
21:T:92:ILE:HD12	21:T:101:PHE:O	1.97	0.63
23:V:3:VAL:HG12	23:V:73:VAL:HG23	1.81	0.63
2:A:125:C:O2'	2:A:126:C:OP2	2.11	0.63
2:A:365:U:O2	2:A:437:G:C6	2.52	0.63
2:A:287:A:O2'	2:A:288:U:OP2	2.14	0.63
2:A:485:U:OP2	26:Y:10:LYS:NZ	2.24	0.63
2:A:2555:G:O2'	25:X:43:THR:HG22	1.99	0.62
2:A:2883:G:N2	2:A:2886:A:OP2	2.30	0.62
7:F:132:THR:CG2	17:P:6:VAL:HG21	2.29	0.62
9:H:119:LEU:HD21	9:H:124:ILE:HD11	1.80	0.62
35:h:47:GLU:HB3	35:h:116:ASP:HB3	1.80	0.62
2:A:392:A:OP2	23:V:17:LYS:NZ	2.21	0.62
2:A:2345:U:OP1	2:A:2391:G:N1	2.30	0.62
35:h:140:VAL:C	35:h:141:ILE:HD12	2.23	0.62
35:h:354:VAL:HG23	35:h:359:ILE:HG13	1.81	0.62
2:A:1755:A:O2'	2:A:1758:G:N1	2.32	0.62
2:A:1554:U:O2'	2:A:1555:A:O5'	2.15	0.62
2:A:1067:G:O6	2:A:1086:C:N4	2.33	0.62
35:h:44:LEU:HB2	35:h:149:ASP:CG	2.24	0.62
35:h:303:PHE:HD2	35:h:346:VAL:HG12	1.65	0.62
2:A:383:U:C1'	23:V:12:ILE:HD11	2.30	0.62
2:A:1282:G:OP1	20:S:26:LYS:NZ	2.28	0.62
21:T:11:THR:OG1	21:T:112:VAL:O	2.08	0.62
35:h:123:GLU:OE1	35:h:123:GLU:N	2.32	0.62
2:A:31:U:HO2'	2:A:32:G:P	2.22	0.62
2:A:1547:G:N1	2:A:1623:U:O2'	2.32	0.62
2:A:1647:G:N7	4:C:31:LYS:NZ	2.44	0.62
2:A:2772:G:O2'	13:L:4:GLN:OE1	2.18	0.61
3:B:9:G:OP1	17:P:26:ARG:NH1	2.33	0.61
5:D:96:GLU:OE1	5:D:96:GLU:N	2.33	0.61
7:F:10:ARG:NH1	7:F:108:ASP:OD1	2.33	0.61
2:A:2242:G:O2'	19:R:34:LYS:NZ	2.21	0.61
2:A:1178:U:P	11:J:114:LYS:HZ2	2.24	0.61
16:O:101:GLU:OE2	21:T:44:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:96:LEU:HD23	18:Q:99:LEU:HD11	1.82	0.61
2:A:625:A:N6	2:A:647:G:O2'	2.33	0.61
1:3:20:LYS:NZ	2:A:1104:C:OP1	2.34	0.61
2:A:1087:G:OP1	28:a:20:ARG:NH2	2.33	0.61
17:P:67:GLU:OE1	17:P:91:ARG:NH2	2.34	0.61
2:A:461:U:O2'	2:A:511:A:N3	2.26	0.61
2:A:2163:U:O2'	2:A:2816:G:O2'	2.11	0.61
21:T:26:ARG:O	29:b:21:LYS:HE2	1.99	0.61
2:A:569:G:O2'	2:A:594:U:O4	2.15	0.61
2:A:2113:A:N3	2:A:2309:U:O2'	2.31	0.61
3:B:77:A:OP1	24:W:19:THR:OG1	2.19	0.61
35:h:276:LEU:HG	35:h:279:THR:HG23	1.82	0.61
2:A:2128:G:O3'	2:A:2130:G:N2	2.33	0.60
2:A:2135:U:O2'	35:h:101:GLY:N	2.34	0.60
4:C:136:ILE:O	4:C:168:LYS:NZ	2.33	0.60
4:C:186:ASP:OD1	4:C:187:VAL:N	2.34	0.60
10:I:12:ASP:O	10:I:16:GLN:NE2	2.33	0.60
2:A:49:A:OP2	2:A:114:G:N1	2.34	0.60
2:A:2093:G:N2	2:A:2094:G:O6	2.33	0.60
2:A:2932:G:O2'	16:O:71:ARG:CZ	2.49	0.60
11:J:32:GLN:OE1	35:h:427:GLY:N	2.34	0.60
34:g:13:THR:OG1	34:g:23:THR:OG1	2.07	0.60
2:A:2509:C:OP2	30:c:8:ARG:NH2	2.34	0.60
35:h:319:LEU:O	35:h:322:VAL:HG22	2.01	0.60
2:A:1435:C:N4	2:A:1445:C:OP2	2.35	0.60
11:J:16:GLN:OE1	11:J:16:GLN:N	2.33	0.60
2:A:1426:G:N2	2:A:1426:G:OP2	2.33	0.60
2:A:2435:U:O2'	2:A:2436:A:OP1	2.18	0.60
11:J:95:HIS:ND1	11:J:95:HIS:O	2.35	0.60
2:A:1579:C:H42	2:A:1592:G:N2	1.99	0.60
11:J:26:VAL:HG13	11:J:30:LEU:HD21	1.84	0.60
2:A:381:A:N1	2:A:415:G:O2'	2.31	0.60
2:A:738:A:O2'	2:A:739:U:O5'	2.19	0.60
35:h:76:THR:HG23	35:h:150:ILE:HD11	1.83	0.60
2:A:138:A:N1	2:A:1813:C:O2'	2.34	0.60
2:A:1565:A:O2'	2:A:1566:A:O4'	2.12	0.60
35:h:172:MET:O	35:h:176:LEU:N	2.35	0.60
5:D:102:THR:HG22	5:D:103:ALA:H	1.67	0.60
9:H:21:VAL:HG22	9:H:22:LYS:H	1.67	0.60
35:h:247:SER:O	35:h:326:ASP:N	2.34	0.60
2:A:2949:A:O2'	2:A:2950:C:OP2	2.19	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:93:LEU:HD12	12:K:97:PRO:HA	1.84	0.59
3:B:5:C:OP1	3:B:62:C:O2'	2.19	0.59
8:G:26:VAL:HG12	8:G:80:VAL:HG21	1.85	0.59
35:h:200:THR:HB	35:h:201:ARG:HE	1.67	0.59
2:A:1176:G:O2'	11:J:117:ASP:O	2.20	0.59
2:A:1436:C:O2'	21:T:18:ARG:NH2	2.34	0.59
6:E:163:GLU:OE1	6:E:163:GLU:N	2.31	0.59
2:A:639:C:O2'	2:A:640:G:O5'	2.20	0.59
2:A:2453:U:O2	26:Y:34:GLN:NE2	2.34	0.59
12:K:15:TRP:CE3	12:K:55:ILE:HD11	2.37	0.59
2:A:1147:A:N1	2:A:2689:C:O2'	2.32	0.59
23:V:16:ASP:OD1	23:V:16:ASP:N	2.35	0.59
24:W:109:GLU:OE1	24:W:109:GLU:N	2.35	0.59
2:A:997:G:N2	2:A:998:G:N7	2.51	0.59
2:A:1076:A:O2'	2:A:1077:A:O4'	2.18	0.59
2:A:2158:C:O2'	2:A:2159:G:OP2	2.17	0.59
7:F:45:MET:HG2	7:F:64:LEU:HD11	1.83	0.59
2:A:1113:C:OP1	19:R:53:ARG:NH1	2.36	0.59
13:L:75:SER:OG	18:Q:71:ARG:NH2	2.36	0.59
2:A:2970:U:N3	2:A:2980:U:O4	2.36	0.59
6:E:43:ALA:HB1	6:E:98:TYR:O	2.01	0.59
2:A:1098:A:N3	2:A:2261:U:O2'	2.32	0.59
2:A:1603:G:C6	2:A:1604:G:O6	2.56	0.59
2:A:2352:C:C2	2:A:2383:U:C4	2.89	0.59
2:A:2795:C:O3'	5:D:156:THR:OG1	2.20	0.59
2:A:741:G:N2	2:A:2574:C:O2'	2.36	0.59
31:d:34:VAL:HG13	31:d:45:LEU:HD21	1.85	0.59
2:A:730:G:N1	14:M:77:VAL:HG11	2.17	0.58
2:A:1337:G:O6	20:S:74:ARG:NH1	2.34	0.58
20:S:14:TYR:CE2	20:S:24:VAL:HG12	2.37	0.58
35:h:336:ASP:OD2	35:h:342:GLN:NE2	2.35	0.58
5:D:39:ILE:HG13	5:D:50:VAL:HG12	1.85	0.58
7:F:158:GLY:C	7:F:159:MET:HE3	2.29	0.58
22:U:8:ARG:CZ	27:Z:27:GLU:OE1	2.51	0.58
35:h:51:LEU:HD23	35:h:67:LEU:HG	1.83	0.58
2:A:21:G:O2'	21:T:84:ASP:OD1	2.08	0.58
12:K:112:ASN:OD1	12:K:112:ASN:N	2.37	0.58
17:P:82:VAL:HG12	17:P:86:GLN:OE1	2.02	0.58
35:h:47:GLU:H	35:h:117:THR:CG2	2.16	0.58
2:A:2015:U:OP2	4:C:272:ARG:NH2	2.33	0.58
3:B:43:C:OP1	7:F:71:LYS:NZ	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:10:LYS:O	24:W:11:LEU:HD22	2.03	0.58
2:A:1885:G:N2	2:A:2216:G:OP2	2.33	0.58
6:E:21:PRO:HG2	6:E:24:LEU:HD23	1.86	0.58
14:M:64:LEU:HD12	14:M:64:LEU:C	2.29	0.58
27:Z:14:THR:N	27:Z:17:GLU:OE2	2.36	0.58
2:A:2193:A:H2'	2:A:2196:G:H21	1.67	0.58
2:A:2044:U:OP2	4:C:222:ARG:NE	2.37	0.58
2:A:2382:G:O2'	2:A:2383:U:O4'	2.22	0.58
2:A:2693:A:HO2'	2:A:2694:G:P	2.26	0.58
2:A:894:U:P	4:C:49:ILE:HG22	2.44	0.58
2:A:1027:C:P	15:N:8:LYS:HZ3	2.27	0.58
2:A:222:A:O2'	2:A:508:G:N3	2.32	0.57
2:A:351:G:HO2'	2:A:352:G:P	2.26	0.57
11:J:78:ALA:HA	11:J:137:MET:HE1	1.85	0.57
12:K:15:TRP:HE3	12:K:55:ILE:HD11	1.68	0.57
2:A:80:G:N2	2:A:100:A:OP2	2.37	0.57
2:A:1592:G:O2'	2:A:1593:U:O4'	2.21	0.57
5:D:3:ARG:NH1	5:D:210:SER:O	2.36	0.57
5:D:183:HIS:N	5:D:193:LEU:O	2.37	0.57
35:h:338:ASN:O	35:h:342:GLN:NE2	2.37	0.57
2:A:271:A:N7	2:A:315:U:O4	2.37	0.57
2:A:402:G:N3	6:E:171:ASN:ND2	2.52	0.57
2:A:620:G:H2'	2:A:621:U:C6	2.39	0.57
2:A:1547:G:N2	2:A:1624:U:OP1	2.36	0.57
2:A:2745:C:O2'	2:A:2788:A:N3	2.30	0.57
7:F:41:VAL:HG13	7:F:98:LEU:HD13	1.86	0.57
8:G:97:VAL:CG2	8:G:104:LEU:HD11	2.33	0.57
2:A:2975:G:O4'	8:G:4:ILE:HD11	2.05	0.57
13:L:112:MET:HE2	13:L:112:MET:HA	1.86	0.57
2:A:1179:U:O2'	2:A:1181:G:OP2	2.22	0.57
2:A:1566:A:N1	2:A:1606:G:N2	2.53	0.57
21:T:28:ILE:HD12	21:T:83:ALA:HB2	1.85	0.57
21:T:78:VAL:HG13	21:T:78:VAL:O	2.04	0.57
24:W:37:LEU:HD23	24:W:45:GLN:NE2	2.20	0.57
2:A:1225:G:N3	10:I:29:ARG:NH2	2.53	0.57
2:A:2972:A:OP1	8:G:71:THR:HG21	2.04	0.57
15:N:48:GLU:OE1	15:N:52:ILE:HD11	2.05	0.57
18:Q:101:GLU:N	18:Q:101:GLU:OE1	2.37	0.57
26:Y:39:VAL:HG12	26:Y:41:ARG:O	2.04	0.57
2:A:1710:A:N6	2:A:1716:A:OP2	2.38	0.57
2:A:2727:A:O2'	2:A:2729:G:OP2	2.22	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:33:MET:HE2	7:F:33:MET:C	2.30	0.57
9:H:12:LEU:CD2	9:H:19:VAL:HG21	2.34	0.57
12:K:145:VAL:HG13	19:R:73:ASP:OD1	2.04	0.57
14:M:72:ARG:NH1	14:M:74:GLU:OE2	2.38	0.57
15:N:71:ASP:C	15:N:71:ASP:OD1	2.46	0.57
28:a:23:LEU:HD22	28:a:50:VAL:HG11	1.86	0.57
30:c:25:THR:OG1	30:c:26:LYS:N	2.38	0.57
2:A:1913:G:N7	4:C:14:ARG:NH2	2.52	0.56
2:A:2134:G:OP1	2:A:2149:C:N4	2.37	0.56
2:A:2352:C:O2	2:A:2383:U:N3	2.38	0.56
7:F:71:LYS:NZ	7:F:73:GLU:OE1	2.38	0.56
23:V:29:ASP:OD1	23:V:29:ASP:N	2.35	0.56
6:E:207:ALA:O	6:E:210:LYS:NZ	2.23	0.56
2:A:29:C:N4	2:A:535:A:OP2	2.39	0.56
2:A:89:A:O2'	2:A:90:C:OP1	2.23	0.56
2:A:103:C:HO2'	2:A:375:A:HO2'	1.15	0.56
2:A:773:G:N2	6:E:106:MET:HE2	2.16	0.56
2:A:2016:G:N7	4:C:179:SER:OG	2.39	0.56
2:A:2095:G:O2'	2:A:2096:G:P	2.63	0.56
2:A:2824:A:H2'	2:A:2825:C:O4'	2.06	0.56
2:A:3084:G:OP1	18:Q:113:ARG:NH1	2.39	0.56
24:W:124:VAL:HG23	24:W:181:VAL:HG22	1.88	0.56
35:h:132:LEU:HD23	35:h:140:VAL:HG11	1.86	0.56
35:h:212:ARG:HB3	35:h:216:ARG:CZ	2.35	0.56
35:h:223:ARG:HA	35:h:226:ILE:HD12	1.86	0.56
35:h:327:LEU:HD22	35:h:411:VAL:HG23	1.88	0.56
2:A:326:A:N6	2:A:449:G:O6	2.36	0.56
2:A:1253:C:O2'	2:A:1254:G:OP1	2.20	0.56
2:A:1577:C:C4	2:A:1578:G:O6	2.58	0.56
2:A:1628:A:O4'	2:A:1630:U:O2'	2.16	0.56
2:A:2698:C:HO2'	2:A:2699:C:P	2.28	0.56
9:H:97:ALA:O	9:H:101:VAL:HG23	2.05	0.56
17:P:65:SER:O	17:P:65:SER:OG	2.24	0.56
2:A:2675:A:N3	35:h:197:GLY:O	2.39	0.56
12:K:92:LEU:HD12	12:K:96:HIS:NE2	2.21	0.56
16:O:36:THR:O	16:O:110:MET:HE3	2.06	0.56
23:V:72:MET:SD	23:V:81:THR:N	2.79	0.56
2:A:1769:G:O3'	2:A:1957:G:N2	2.39	0.56
2:A:1927:C:O2'	2:A:3080:A:N3	2.38	0.56
15:N:75:THR:HG22	15:N:90:PRO:HA	1.87	0.56
2:A:1566:A:N1	2:A:1606:G:C2	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:42:ARG:HH11	17:P:113:ILE:HD11	1.70	0.56
35:h:143:ARG:NH2	35:h:306:HIS:O	2.36	0.56
35:h:260:SER:OG	35:h:369:ASN:ND2	2.39	0.56
2:A:379:G:N1	2:A:421:U:OP2	2.33	0.55
2:A:2193:A:O2'	2:A:2196:G:N2	2.40	0.55
2:A:2839:U:H4'	29:b:8:MET:HE2	1.88	0.55
2:A:3043:G:O2'	2:A:3045:C:OP2	2.14	0.55
2:A:1149:G:N3	33:f:36:GLN:NE2	2.55	0.55
2:A:2338:G:O2'	2:A:2388:G:O6	2.24	0.55
21:T:28:ILE:HD11	21:T:110:ILE:HG23	1.89	0.55
21:T:92:ILE:HD11	21:T:100:ALA:CB	2.26	0.55
22:U:17:SER:N	22:U:20:SER:OG	2.39	0.55
34:g:10:VAL:N	34:g:26:SER:O	2.37	0.55
35:h:130:ASN:OD1	35:h:134:LYS:NZ	2.32	0.55
2:A:636:U:HO2'	2:A:637:G:P	2.30	0.55
2:A:971:G:H2'	2:A:972:A:C8	2.42	0.55
2:A:1381:G:O2'	2:A:2236:G:O6	2.14	0.55
2:A:2394:A:H3'	2:A:2397:C:H41	1.71	0.55
2:A:1456:G:O2'	2:A:1512:U:O2'	2.18	0.55
2:A:1938:G:N2	2:A:1955:A:OP2	2.38	0.55
8:G:138:ASP:O	8:G:142:VAL:HG23	2.06	0.55
14:M:55:MET:N	14:M:55:MET:SD	2.76	0.55
2:A:313:G:C2'	2:A:314:G:O5'	2.55	0.55
2:A:561:G:H2'	2:A:562:G:H5'	1.88	0.55
2:A:1031:G:O2'	2:A:1032:A:O4'	2.25	0.55
3:B:50:C:O3'	17:P:78:LYS:NZ	2.27	0.55
6:E:157:VAL:HG22	6:E:178:ILE:CG2	2.37	0.55
2:A:160:A:H3'	2:A:161:U:H5''	1.87	0.55
2:A:659:U:OP2	14:M:31:LYS:NZ	2.39	0.55
2:A:3057:U:O4	2:A:3104:A:N6	2.40	0.55
19:R:125:SER:O	19:R:125:SER:OG	2.17	0.55
2:A:1027:C:OP1	15:N:8:LYS:NZ	2.34	0.55
2:A:2173:G:H2'	2:A:2174:G:C8	2.42	0.55
7:F:122:ARG:O	7:F:185:LYS:NZ	2.24	0.55
14:M:63:LYS:HZ1	32:e:12:LYS:C	2.15	0.55
24:W:30:ASP:C	24:W:30:ASP:OD1	2.49	0.55
35:h:270:VAL:HG12	35:h:274:ASN:ND2	2.22	0.55
2:A:974:G:O2'	2:A:975:U:P	2.65	0.55
2:A:2435:U:HO2'	2:A:2436:A:P	2.30	0.55
7:F:160:ASP:C	7:F:161:ILE:HD12	2.31	0.55
18:Q:48:ARG:NH2	18:Q:59:THR:HG21	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:12:LYS:NZ	20:S:25:GLU:OE2	2.39	0.55
2:A:1232:G:O6	2:A:1233:A:N6	2.39	0.54
2:A:2347:G:N7	2:A:2348:G:N2	2.51	0.54
2:A:2350:G:N2	2:A:2385:G:O2'	2.33	0.54
3:B:46:A:C4	3:B:47:A:C8	2.95	0.54
11:J:75:PRO:O	11:J:114:LYS:NZ	2.40	0.54
12:K:60:ASP:OD1	12:K:60:ASP:O	2.24	0.54
2:A:706:G:O2'	6:E:160:ARG:NH2	2.37	0.54
2:A:2171:C:O2'	2:A:2172:G:P	2.65	0.54
2:A:2753:G:N3	35:h:236:GLN:NE2	2.56	0.54
7:F:63:ASP:OD2	7:F:142:GLN:NE2	2.35	0.54
11:J:60:ILE:HD11	11:J:68:PHE:CD2	2.42	0.54
13:L:71:ARG:NH1	13:L:122:LEU:O	2.40	0.54
27:Z:61:LEU:HD23	27:Z:61:LEU:C	2.32	0.54
8:G:105:GLU:OE2	8:G:115:LEU:HD13	2.08	0.54
18:Q:4:LEU:O	18:Q:8:ASP:OD1	2.25	0.54
21:T:37:GLU:O	21:T:41:ASP:OD1	2.25	0.54
35:h:47:GLU:N	35:h:117:THR:HG21	2.22	0.54
35:h:257:GLY:O	35:h:261:LEU:HD12	2.07	0.54
35:h:271:LEU:CD1	35:h:272:VAL:HG23	2.37	0.54
2:A:2087:C:H2'	2:A:2088:C:C1'	2.38	0.54
2:A:2353:U:O2'	2:A:2381:A:N1	2.33	0.54
7:F:67:ILE:HD13	7:F:145:PHE:CE2	2.42	0.54
13:L:80:ASP:OD2	18:Q:68:GLY:N	2.41	0.54
2:A:741:G:N2	2:A:2574:C:O3'	2.40	0.54
14:M:133:ALA:O	14:M:137:ILE:HG22	2.07	0.54
35:h:198:VAL:CG1	35:h:202:GLY:HA2	2.37	0.54
2:A:21:G:O2'	21:T:85:GLU:O	2.26	0.54
2:A:998:G:N2	2:A:1011:A:OP1	2.41	0.54
2:A:1121:G:N2	2:A:1272:C:C2	2.76	0.54
20:S:7:VAL:CG2	20:S:60:VAL:HG21	2.38	0.54
2:A:2587:U:OP2	32:e:43:ARG:NH2	2.35	0.54
2:A:3036:C:C4	2:A:3037:C:C5	2.96	0.54
8:G:98:GLN:O	8:G:104:LEU:HD12	2.08	0.54
2:A:1561:C:H42	2:A:1610:C:N4	2.06	0.53
2:A:3096:U:O2'	18:Q:1:MET:O	2.26	0.53
8:G:24:LEU:HD21	8:G:43:VAL:HG21	1.90	0.53
13:L:86:ILE:HD11	13:L:94:ARG:CZ	2.37	0.53
14:M:57:ILE:HD11	32:e:58:ILE:HD11	1.90	0.53
18:Q:30:LYS:NZ	18:Q:78:PRO:O	2.35	0.53
23:V:86:ARG:HB3	23:V:97:ILE:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:100:VAL:HG11	24:W:137:ALA:HB2	1.90	0.53
28:a:8:GLN:NE2	28:a:10:ARG:O	2.39	0.53
35:h:262:LEU:HD23	35:h:262:LEU:C	2.33	0.53
2:A:1069:G:C6	2:A:1083:G:C6	2.95	0.53
2:A:2797:C:N3	35:h:206:THR:HG21	2.23	0.53
23:V:34:LEU:HD21	23:V:63:GLU:HG3	1.89	0.53
2:A:1566:A:N6	2:A:1606:G:N1	2.57	0.53
2:A:3023:G:H2'	2:A:3024:A:O4'	2.09	0.53
6:E:35:HIS:HA	14:M:9:LEU:HD21	1.90	0.53
10:I:53:LYS:O	10:I:57:VAL:HG23	2.08	0.53
2:A:449:G:C2'	2:A:450:G:OP1	2.56	0.53
2:A:1177:G:N3	11:J:129:ILE:HG23	2.23	0.53
2:A:2148:C:O2'	2:A:2149:C:O5'	2.26	0.53
2:A:2159:G:O6	2:A:2186:C:O2'	2.27	0.53
2:A:2992:C:OP1	12:K:85:ARG:NH1	2.41	0.53
3:B:48:C:OP2	17:P:14:ARG:NH2	2.38	0.53
8:G:5:GLY:O	8:G:53:VAL:HG23	2.08	0.53
10:I:21:THR:HG22	10:I:110:MET:HE1	1.91	0.53
17:P:74:ASP:O	17:P:74:ASP:OD1	2.27	0.53
19:R:14:ARG:O	19:R:18:LEU:HD23	2.08	0.53
5:D:185:VAL:HG22	5:D:185:VAL:O	2.08	0.53
17:P:43:SER:OG	17:P:46:HIS:N	2.41	0.53
23:V:89:ASP:OD1	23:V:90:GLU:N	2.42	0.53
28:a:6:ILE:HD13	28:a:47:ILE:HD11	1.91	0.53
35:h:320:GLU:N	35:h:320:GLU:OE1	2.42	0.53
2:A:1604:G:O2'	2:A:1605:G:O4'	2.10	0.53
7:F:33:MET:HE1	7:F:34:GLN:HG2	1.91	0.53
21:T:81:VAL:CG2	21:T:112:VAL:HG22	2.36	0.53
27:Z:10:LEU:O	27:Z:10:LEU:HD23	2.09	0.53
2:A:1539:A:O2'	2:A:1540:U:O5'	2.26	0.53
2:A:1576:C:H2'	2:A:1577:C:C6	2.43	0.53
2:A:1896:A:N3	2:A:2214:C:O2'	2.37	0.53
35:h:236:GLN:OE1	35:h:240:ARG:NH2	2.41	0.53
2:A:2632:U:N3	2:A:2633:G:N7	2.56	0.53
6:E:111:LEU:O	6:E:115:LEU:HD23	2.09	0.53
2:A:326:A:N1	2:A:450:G:C6	2.77	0.53
2:A:543:U:O2'	2:A:544:U:OP1	2.18	0.53
2:A:1200:U:H5''	2:A:1201:G:OP2	2.09	0.53
11:J:60:ILE:HD11	11:J:68:PHE:HD2	1.74	0.53
12:K:28:LEU:CD2	12:K:62:ILE:HD11	2.39	0.53
35:h:259:SER:HB2	35:h:275:ALA:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:452:G:O2'	2:A:453:U:O5'	2.27	0.53
7:F:11:LEU:HD11	7:F:111:ILE:HD11	1.91	0.53
7:F:161:ILE:HD12	7:F:161:ILE:N	2.24	0.53
31:d:46:THR:OG1	31:d:47:ALA:N	2.42	0.53
35:h:46:LEU:CG	35:h:119:ILE:HD11	2.32	0.53
35:h:261:LEU:HD12	35:h:261:LEU:H	1.74	0.53
2:A:262:A:O2'	2:A:518:A:O2'	2.23	0.52
2:A:928:U:O2'	2:A:1339:G:O2'	2.24	0.52
2:A:1539:A:N6	2:A:1632:G:H21	2.07	0.52
2:A:2185:C:O2'	2:A:2186:C:O5'	2.21	0.52
4:C:131:LEU:HD23	4:C:131:LEU:H	1.73	0.52
15:N:102:VAL:HG11	15:N:105:GLU:OE1	2.09	0.52
2:A:449:G:O2'	2:A:450:G:OP1	2.26	0.52
2:A:2014:G:O2'	4:C:257:THR:HG22	2.08	0.52
2:A:2243:C:O5'	19:R:27:GLN:NE2	2.42	0.52
3:B:14:A:N1	3:B:70:G:O2'	2.32	0.52
2:A:730:G:H1	14:M:77:VAL:HG11	1.72	0.52
15:N:58:ILE:HG21	15:N:61:GLY:O	2.09	0.52
35:h:209:GLU:HA	35:h:213:ARG:HD2	1.91	0.52
7:F:159:MET:HE3	7:F:159:MET:N	2.25	0.52
28:a:6:ILE:HD11	28:a:47:ILE:HD11	1.90	0.52
2:A:287:A:O2'	2:A:288:U:P	2.68	0.52
2:A:844:G:O2'	2:A:878:G:H4'	2.09	0.52
2:A:2270:G:C3'	29:b:19:GLN:HE22	2.20	0.52
6:E:155:LEU:HB2	6:E:191:ALA:HB2	1.92	0.52
6:E:191:ALA:HB1	6:E:193:ASP:O	2.10	0.52
7:F:11:LEU:HD12	7:F:108:ASP:CG	2.35	0.52
8:G:160:GLY:O	8:G:164:ARG:NH1	2.42	0.52
10:I:22:ALA:HB2	10:I:110:MET:HE3	1.92	0.52
35:h:262:LEU:HD22	35:h:270:VAL:HG22	1.92	0.52
2:A:1249:G:HO2'	2:A:2249:G:HO2'	1.53	0.52
2:A:1323:G:O2'	2:A:1352:A:N1	2.31	0.52
2:A:1911:U:O2'	4:C:14:ARG:NH1	2.39	0.52
2:A:2174:G:OP1	13:L:54:ARG:NH2	2.39	0.52
7:F:13:GLN:O	7:F:17:GLU:HG3	2.10	0.52
17:P:10:ILE:N	17:P:10:ILE:HD12	2.25	0.52
35:h:41:TYR:CE2	35:h:42:ARG:HD2	2.45	0.52
2:A:970:G:C6	2:A:971:G:N7	2.78	0.52
7:F:67:ILE:HD13	7:F:145:PHE:HE2	1.74	0.52
17:P:116:LEU:O	17:P:116:LEU:HD12	2.10	0.52
27:Z:5:THR:HG21	27:Z:10:LEU:HD12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:e:63:ASN:OD1	32:e:64:GLY:N	2.42	0.52
2:A:1556:A:H2	2:A:1615:G:H22	1.58	0.52
7:F:23:LEU:HD23	7:F:36:PRO:HG2	1.92	0.52
35:h:49:VAL:HG12	35:h:81:VAL:HA	1.92	0.52
35:h:276:LEU:HD13	35:h:277:PHE:CE2	2.44	0.52
2:A:271:A:H62	2:A:315:U:H3	1.57	0.52
2:A:1147:A:N6	2:A:1243:G:O2'	2.42	0.52
2:A:1594:G:H2'	2:A:1595:G:C8	2.45	0.52
2:A:3063:A:N6	2:A:3097:G:O6	2.43	0.52
7:F:18:GLU:O	7:F:18:GLU:HG2	2.10	0.52
11:J:12:LYS:O	11:J:13:LEU:HD22	2.10	0.52
2:A:240:G:OP2	2:A:241:A:O2'	2.17	0.52
2:A:587:G:N1	2:A:590:A:OP2	2.42	0.52
2:A:1118:A:H2'	2:A:1119:A:C8	2.45	0.52
4:C:131:LEU:HD23	4:C:131:LEU:N	2.25	0.52
6:E:19:GLU:HA	6:E:19:GLU:OE2	2.09	0.52
35:h:46:LEU:HD21	35:h:119:ILE:HG13	1.92	0.52
35:h:258:LYS:CD	35:h:275:ALA:HB1	2.39	0.52
10:I:40:ARG:NH2	10:I:49:TYR:O	2.43	0.51
2:A:313:G:HO2'	2:A:314:G:P	2.30	0.51
2:A:450:G:H2'	2:A:451:U:C6	2.46	0.51
2:A:2160:A:O4'	2:A:2161:A:H2'	2.10	0.51
2:A:2927:C:C2	2:A:2928:C:C5	2.98	0.51
2:A:3036:C:O2	29:b:41:ARG:NH1	2.43	0.51
9:H:66:ASN:CB	9:H:136:LEU:HD13	2.39	0.51
21:T:80:THR:OG1	21:T:113:ILE:HG22	2.10	0.51
2:A:2155:U:O4'	2:A:2191:C:N4	2.43	0.51
2:A:1604:G:H2'	2:A:1605:G:C8	2.46	0.51
2:A:2244:A:O2'	2:A:2246:U:OP2	2.14	0.51
2:A:2294:A:H2'	2:A:2295:C:C6	2.45	0.51
18:Q:37:GLU:C	18:Q:37:GLU:OE1	2.53	0.51
2:A:286:G:N2	2:A:299:G:O2'	2.43	0.51
2:A:2331:U:O2'	2:A:2332:U:O5'	2.29	0.51
16:O:33:ARG:NE	16:O:114:GLU:OE2	2.40	0.51
18:Q:34:GLY:O	18:Q:35:SER:OG	2.19	0.51
35:h:50:VAL:O	35:h:50:VAL:HG13	2.11	0.51
35:h:205:GLU:HA	35:h:207:LYS:HE3	1.92	0.51
2:A:543:U:H3'	2:A:544:U:H5''	1.93	0.51
2:A:1329:G:O6	2:A:1350:G:C2	2.64	0.51
13:L:9:LYS:HD2	13:L:9:LYS:N	2.25	0.51
35:h:214:ARG:HE	35:h:218:ARG:HG2	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:792:G:H2'	2:A:793:C:H5'	1.93	0.51
4:C:44:ASN:OD1	4:C:45:ALA:N	2.44	0.51
6:E:21:PRO:CG	6:E:24:LEU:HD23	2.40	0.51
35:h:46:LEU:HD11	35:h:141:ILE:HG21	1.93	0.51
2:A:1301:G:H2'	2:A:1302:G:O4'	2.11	0.51
2:A:1377:A:N3	29:b:7:ARG:CZ	2.74	0.51
2:A:2174:G:HO2'	2:A:2210:U:C3'	2.19	0.51
9:H:101:VAL:HG22	9:H:112:LEU:HD11	1.92	0.51
12:K:49:ASP:OD1	12:K:121:LYS:NZ	2.43	0.51
14:M:137:ILE:HG21	14:M:144:ALA:HB2	1.92	0.51
20:S:64:VAL:O	20:S:64:VAL:HG13	2.10	0.51
21:T:29:ASP:C	21:T:29:ASP:OD1	2.54	0.51
29:b:47:ALA:HA	29:b:52:VAL:HG22	1.93	0.51
35:h:148:LEU:HD12	35:h:168:GLN:HG2	1.93	0.51
1:3:10:ASP:OD2	2:A:1252:G:N2	2.43	0.51
2:A:473:C:O2'	2:A:478:A:N1	2.40	0.51
2:A:1971:C:OP1	18:Q:93:ARG:NH1	2.39	0.51
2:A:2094:G:H1'	2:A:2095:G:C8	2.46	0.51
11:J:23:ALA:O	11:J:27:GLY:N	2.42	0.51
15:N:119:THR:HA	15:N:122:ILE:HG22	1.93	0.51
19:R:89:GLU:N	19:R:89:GLU:OE1	2.42	0.51
24:W:133:ILE:HG23	24:W:168:VAL:HG13	1.92	0.51
2:A:727:A:P	14:M:72:ARG:HE	2.34	0.51
2:A:1531:C:O2'	2:A:1532:G:OP1	2.24	0.51
3:B:10:G:HO2'	3:B:11:U:P	2.30	0.51
6:E:42:LEU:HD11	6:E:186:TYR:CE2	2.46	0.51
21:T:34:LYS:O	21:T:78:VAL:HG12	2.11	0.51
8:G:58:ASP:OD1	8:G:58:ASP:O	2.29	0.50
35:h:48:ARG:HD2	35:h:115:ALA:HA	1.93	0.50
9:H:109:GLY:N	9:H:110:PRO:CD	2.74	0.50
18:Q:47:ILE:HG22	18:Q:99:LEU:HD12	1.93	0.50
21:T:29:ASP:OD1	29:b:21:LYS:HE3	2.11	0.50
4:C:77:ALA:HB2	4:C:97:TYR:CE1	2.46	0.50
8:G:150:ARG:NE	8:G:163:VAL:O	2.44	0.50
18:Q:41:VAL:HG23	18:Q:41:VAL:O	2.11	0.50
35:h:212:ARG:O	35:h:213:ARG:C	2.54	0.50
35:h:275:ALA:N	35:h:279:THR:HG21	2.26	0.50
2:A:33:G:N3	2:A:538:G:O2'	2.41	0.50
2:A:302:U:HO2'	2:A:304:U:H5	1.60	0.50
2:A:2916:C:O2	2:A:3068:U:O2'	2.27	0.50
4:C:49:ILE:O	4:C:49:ILE:HG23	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:166:GLU:OE1	24:W:166:GLU:HA	2.12	0.50
26:Y:55:CYS:SG	26:Y:60:LYS:HE2	2.52	0.50
35:h:50:VAL:CG1	35:h:118:VAL:HG22	2.42	0.50
2:A:137:G:OP1	2:A:137:G:C8	2.64	0.50
2:A:326:A:C6	2:A:327:U:O2	2.65	0.50
2:A:1165:G:N2	2:A:1229:A:OP2	2.45	0.50
2:A:2703:U:O2	35:h:233:ARG:NH1	2.44	0.50
4:C:154:LYS:C	4:C:155:LEU:HD12	2.37	0.50
2:A:403:U:O2	6:E:167:LYS:NZ	2.44	0.50
2:A:1227:C:O3'	2:A:1228:A:O4'	2.29	0.50
2:A:2054:C:O2	2:A:2123:A:N6	2.44	0.50
4:C:235:GLY:O	4:C:240:THR:HG21	2.12	0.50
35:h:95:SER:OG	35:h:96:THR:N	2.44	0.50
35:h:110:VAL:HG11	35:h:138:VAL:HG11	1.94	0.50
2:A:669:G:O2'	2:A:1369:A:OP1	2.30	0.50
2:A:1593:U:N3	2:A:1594:G:O6	2.45	0.50
2:A:1605:G:C5	2:A:1606:G:C6	3.00	0.50
2:A:2180:U:C2'	2:A:2181:C:H5'	2.42	0.50
2:A:2926:A:C5	2:A:2927:C:C5	2.99	0.50
19:R:27:GLN:OE1	19:R:31:LEU:HD11	2.11	0.50
35:h:382:LEU:HD23	35:h:382:LEU:O	2.11	0.50
2:A:2578:A:O2'	25:X:36:ILE:HD12	2.12	0.50
7:F:45:MET:HG2	7:F:64:LEU:HD21	1.94	0.50
13:L:25:LEU:O	13:L:30:ARG:NH1	2.45	0.50
23:V:34:LEU:HD23	23:V:35:VAL:N	2.27	0.50
2:A:1130:C:O2	12:K:27:ARG:NH1	2.45	0.49
2:A:2367:G:OP1	2:A:2368:C:N4	2.38	0.49
2:A:3022:G:H2'	2:A:3023:G:O4'	2.12	0.49
5:D:104:GLU:CD	5:D:104:GLU:H	2.20	0.49
2:A:895:G:C2	2:A:897:A:C2	3.00	0.49
18:Q:90:ASP:C	18:Q:90:ASP:OD1	2.53	0.49
2:A:1329:G:O6	2:A:1350:G:N2	2.45	0.49
2:A:2378:U:C2'	2:A:2379:G:O5'	2.61	0.49
2:A:2756:G:N2	2:A:2887:G:O2'	2.45	0.49
35:h:141:ILE:HD12	35:h:141:ILE:N	2.27	0.49
2:A:487:U:H2'	2:A:488:G:O4'	2.11	0.49
2:A:1688:G:C6	2:A:1748:A:C2	2.99	0.49
3:B:58:A:N3	7:F:33:MET:HE3	2.26	0.49
3:B:94:G:O6	24:W:21:LYS:NZ	2.42	0.49
5:D:115:THR:OG1	5:D:176:THR:OG1	2.26	0.49
9:H:124:ILE:HG22	9:H:125:LYS:N	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
28:a:49:THR:HG23	28:a:50:VAL:HG13	1.94	0.49
35:h:200:THR:CG2	35:h:200:THR:O	2.56	0.49
35:h:330:HIS:ND1	35:h:330:HIS:O	2.46	0.49
18:Q:49:ARG:NE	18:Q:49:ARG:O	2.44	0.49
24:W:66:ILE:HG22	24:W:77:LEU:HD11	1.95	0.49
27:Z:10:LEU:HD11	27:Z:57:VAL:CG2	2.42	0.49
2:A:2180:U:H2'	2:A:2181:C:H5'	1.94	0.49
2:A:2718:G:C2	2:A:2719:G:C8	3.01	0.49
27:Z:24:GLU:C	27:Z:24:GLU:OE1	2.55	0.49
3:B:31:C:O2	3:B:31:C:H2'	2.13	0.49
12:K:70:THR:O	12:K:70:THR:HG22	2.11	0.49
15:N:122:ILE:HD12	15:N:129:ALA:HB3	1.95	0.49
29:b:28:VAL:HG21	29:b:44:LEU:HD11	1.95	0.49
2:A:774:G:H21	6:E:36:GLN:CD	2.17	0.49
2:A:2219:U:O2	13:L:3:GLN:NE2	2.43	0.49
22:U:94:ASP:OD1	22:U:95:LEU:N	2.45	0.49
35:h:307:LEU:HD13	35:h:312:VAL:HG22	1.95	0.49
2:A:618:C:OP1	2:A:653:G:N1	2.44	0.49
2:A:981:U:O2'	2:A:982:A:P	2.71	0.49
2:A:1173:G:C6	2:A:1224:G:N2	2.81	0.49
2:A:2743:U:C6	2:A:2766:A:N6	2.81	0.49
2:A:2876:C:N4	2:A:2893:G:O6	2.45	0.49
5:D:186:ASP:C	5:D:186:ASP:OD1	2.56	0.49
7:F:47:VAL:HG22	7:F:92:ILE:O	2.13	0.49
10:I:25:VAL:HG13	10:I:106:LYS:HG2	1.94	0.49
15:N:84:GLY:O	15:N:85:SER:OG	2.21	0.49
24:W:113:LEU:HD22	24:W:145:THR:HG22	1.95	0.49
2:A:450:G:O2'	2:A:451:U:O5'	2.31	0.49
2:A:503:A:H2'	2:A:504:C:C6	2.48	0.49
2:A:1607:C:H3'	2:A:1608:U:C6	2.48	0.49
2:A:1930:C:OP2	2:A:1931:A:O2'	2.21	0.49
2:A:2717:U:C4	2:A:2718:G:C8	3.00	0.49
3:B:85:C:OP1	28:a:10:ARG:NH1	2.38	0.49
4:C:184:ARG:HD3	4:C:269:VAL:HG23	1.95	0.49
7:F:113:ILE:HD13	34:g:35:VAL:HG11	1.95	0.49
9:H:101:VAL:HG22	9:H:112:LEU:CD1	2.43	0.49
17:P:118:ASP:O	17:P:122:GLU:OE1	2.31	0.49
18:Q:52:GLY:N	18:Q:56:GLU:OE1	2.45	0.49
23:V:31:ASN:O	23:V:68:VAL:HG12	2.13	0.49
4:C:9:THR:OG1	4:C:10:THR:HG23	2.12	0.48
5:D:29:VAL:CG1	5:D:194:ILE:HD11	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1629:G:H4'	2:A:1630:U:O4'	2.11	0.48
2:A:1815:G:OP1	22:U:40:THR:HG22	2.12	0.48
5:D:88:ASP:O	5:D:92:VAL:HG23	2.13	0.48
7:F:51:ALA:HA	7:F:90:MET:HE2	1.94	0.48
10:I:38:GLU:OE1	10:I:38:GLU:N	2.38	0.48
18:Q:35:SER:OG	18:Q:36:LYS:NZ	2.45	0.48
22:U:94:ASP:OD1	22:U:94:ASP:C	2.56	0.48
35:h:70:LEU:HD11	35:h:119:ILE:CG2	2.43	0.48
2:A:543:U:H3'	2:A:544:U:C5'	2.43	0.48
2:A:1224:G:N3	2:A:1225:G:N7	2.61	0.48
17:P:113:ILE:H	17:P:113:ILE:HD12	1.77	0.48
2:A:1146:A:N3	2:A:2710:G:O2'	2.43	0.48
7:F:45:MET:HE2	7:F:64:LEU:HD11	1.93	0.48
31:d:27:THR:HG22	31:d:28:ARG:N	2.28	0.48
2:A:336:C:O2'	2:A:337:U:P	2.70	0.48
2:A:1204:A:H4'	2:A:1205:G:OP1	2.13	0.48
2:A:1256:G:C5	2:A:1257:G:H1'	2.49	0.48
2:A:2973:A:OP2	2:A:2974:A:O2'	2.26	0.48
9:H:5:LEU:HD11	9:H:12:LEU:HD22	1.95	0.48
22:U:68:ARG:O	22:U:68:ARG:HG3	2.13	0.48
29:b:30:VAL:HG13	29:b:32:VAL:HG13	1.95	0.48
33:f:12:ASP:OD1	33:f:12:ASP:N	2.45	0.48
35:h:276:LEU:HD13	35:h:277:PHE:CD2	2.49	0.48
2:A:290:C:H42	2:A:299:G:H1	1.62	0.48
2:A:352:G:H2'	2:A:353:G:O4'	2.13	0.48
2:A:361:A:N1	2:A:441:G:H1'	2.28	0.48
2:A:992:C:H2'	2:A:993:G:O4'	2.14	0.48
2:A:1064:A:H2'	2:A:1065:C:C6	2.49	0.48
2:A:1438:G:OP1	21:T:91:ARG:NH1	2.47	0.48
2:A:2777:G:H21	2:A:2807:G:H1'	1.78	0.48
29:b:32:VAL:HG11	29:b:54:LEU:HD11	1.95	0.48
2:A:725:A:C2'	2:A:726:A:O5'	2.62	0.48
2:A:1120:G:C6	2:A:1273:G:N2	2.82	0.48
2:A:1213:A:N6	11:J:28:PRO:O	2.47	0.48
2:A:1528:G:H2'	2:A:1529:U:C6	2.49	0.48
2:A:2054:C:C2'	2:A:2123:A:H62	2.24	0.48
2:A:2092:U:O2'	2:A:2093:G:OP2	2.20	0.48
2:A:3037:C:C2'	2:A:3038:C:H5'	2.44	0.48
7:F:84:PHE:HB2	7:F:86:LEU:HG	1.96	0.48
13:L:66:VAL:HG12	13:L:66:VAL:O	2.13	0.48
14:M:39:GLY:O	14:M:42:ALA:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:h:262:LEU:HD22	35:h:270:VAL:CG2	2.44	0.48
2:A:321:G:N1	2:A:456:C:N3	2.62	0.48
2:A:357:U:H4'	2:A:358:G:O5'	2.14	0.48
2:A:1604:G:C5	2:A:1605:G:C6	3.02	0.48
2:A:2171:C:O2'	2:A:2172:G:OP1	2.32	0.48
2:A:2288:C:H5'	35:h:197:GLY:HA2	1.94	0.48
2:A:2522:A:N6	2:A:2542:G:O2'	2.45	0.48
17:P:47:ILE:HD12	17:P:116:LEU:HD22	1.95	0.48
35:h:272:VAL:HG12	35:h:276:LEU:CD2	2.44	0.48
2:A:89:A:HO2'	2:A:90:C:P	2.35	0.48
13:L:43:VAL:HG21	13:L:52:VAL:CG2	2.41	0.48
35:h:258:LYS:HD3	35:h:275:ALA:HB1	1.96	0.48
2:A:323:C:O2	2:A:454:U:N3	2.45	0.48
2:A:1132:U:N3	2:A:1133:G:N7	2.62	0.48
2:A:1367:G:O2'	2:A:1368:A:C8	2.67	0.48
2:A:1553:C:O4'	2:A:1618:C:N4	2.47	0.48
2:A:1631:A:N1	2:A:1632:G:H1'	2.29	0.48
2:A:2368:C:N4	2:A:2370:A:N1	2.62	0.48
4:C:38:HIS:ND1	4:C:39:GLY:O	2.46	0.48
5:D:114:VAL:HG11	5:D:198:ILE:HD12	1.96	0.48
7:F:11:LEU:HD11	7:F:111:ILE:CD1	2.44	0.48
13:L:86:ILE:HD11	13:L:94:ARG:NE	2.29	0.48
15:N:75:THR:HG22	15:N:90:PRO:CA	2.44	0.48
26:Y:61:VAL:HG13	26:Y:61:VAL:O	2.14	0.48
35:h:351:ASN:HA	35:h:354:VAL:HG12	1.95	0.48
2:A:77:G:C6	2:A:104:G:C6	3.02	0.47
2:A:159:A:C5	2:A:166:A:C2	3.01	0.47
2:A:313:G:HO2'	2:A:314:G:C5'	2.18	0.47
2:A:2172:G:H3'	2:A:2173:G:C4'	2.44	0.47
10:I:87:VAL:HG23	10:I:123:ILE:O	2.14	0.47
13:L:17:LYS:NZ	13:L:47:ILE:HG23	2.28	0.47
35:h:307:LEU:HD22	35:h:315:PHE:CE2	2.49	0.47
2:A:2843:C:H4'	5:D:161:PHE:O	2.13	0.47
3:B:9:G:OP1	17:P:37:ARG:NH1	2.47	0.47
16:O:20:LEU:O	16:O:24:LEU:HD23	2.14	0.47
19:R:77:ASN:OD1	19:R:78:ARG:N	2.46	0.47
23:V:3:VAL:HG12	23:V:73:VAL:CG2	2.44	0.47
24:W:67:LEU:O	24:W:77:LEU:HD12	2.14	0.47
35:h:70:LEU:HD11	35:h:119:ILE:HG21	1.96	0.47
2:A:187:G:H3'	2:A:188:G:H5''	1.95	0.47
2:A:319:G:C6	2:A:492:C:C2	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:589:A:O2'	2:A:592:A:OP1	2.15	0.47
2:A:714:U:O2	2:A:714:U:H2'	2.14	0.47
2:A:745:G:H5'	32:e:19:THR:HG23	1.96	0.47
2:A:1507:G:O2'	2:A:1508:A:O5'	2.25	0.47
13:L:12:ASP:OD1	13:L:85:VAL:HG13	2.15	0.47
13:L:14:THR:HG21	13:L:86:ILE:HG21	1.96	0.47
14:M:37:THR:HG23	14:M:38:LYS:N	2.29	0.47
2:A:279:U:H2'	2:A:280:G:H8	1.79	0.47
2:A:1379:G:O2'	2:A:1380:A:OP1	2.25	0.47
6:E:184:ASN:N	6:E:184:ASN:OD1	2.46	0.47
7:F:62:ASN:C	7:F:62:ASN:OD1	2.56	0.47
9:H:85:ALA:O	9:H:89:GLY:N	2.45	0.47
35:h:203:PRO:O	35:h:204:GLY:C	2.55	0.47
2:A:965:U:H1'	28:a:25:THR:HG21	1.95	0.47
2:A:1124:C:C2	2:A:1256:G:N2	2.83	0.47
2:A:2106:A:C2'	2:A:2107:G:OP1	2.63	0.47
24:W:39:GLY:HA3	24:W:99:VAL:HG22	1.97	0.47
35:h:326:ASP:O	35:h:363:PRO:HD2	2.15	0.47
2:A:932:C:C2	2:A:933:G:C8	3.02	0.47
2:A:1530:G:H2'	2:A:1531:C:C6	2.49	0.47
2:A:1539:A:H2'	2:A:1540:U:O4'	2.15	0.47
2:A:1934:G:O6	2:A:1960:U:O2	2.31	0.47
2:A:2270:G:H4'	29:b:19:GLN:CD	2.40	0.47
2:A:2303:A:P	26:Y:21:SER:HG	2.38	0.47
2:A:2750:G:OP2	8:G:154:ARG:NH2	2.47	0.47
20:S:65:LEU:HB2	20:S:96:VAL:HG13	1.97	0.47
28:a:39:ASP:OD1	28:a:44:ARG:NE	2.47	0.47
35:h:89:ARG:NH1	35:h:93:ASP:OD2	2.47	0.47
2:A:298:G:H2'	2:A:299:G:C8	2.50	0.47
2:A:598:U:O4	2:A:599:G:C2	2.67	0.47
2:A:636:U:H3'	2:A:637:G:O4'	2.14	0.47
2:A:1074:A:N6	2:A:1076:A:C2	2.83	0.47
2:A:1084:U:H5''	2:A:1085:G:OP1	2.14	0.47
2:A:1532:G:O2'	2:A:1803:A:N1	2.33	0.47
2:A:1535:C:P	2:A:1536:A:H62	2.37	0.47
2:A:1818:C:OP1	22:U:80:LYS:NZ	2.47	0.47
2:A:1848:A:N6	2:A:1855:A:N6	2.62	0.47
2:A:2553:G:N2	25:X:41:ARG:HB3	2.30	0.47
11:J:111:ALA:HB1	11:J:126:ALA:C	2.40	0.47
12:K:28:LEU:HD23	12:K:62:ILE:HD11	1.95	0.47
17:P:16:ASN:HA	17:P:19:LEU:HD12	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:66:GLU:O	20:S:96:VAL:HG12	2.15	0.47
22:U:9:ASP:OD1	27:Z:26:LYS:HE3	2.14	0.47
24:W:37:LEU:HD23	24:W:45:GLN:HE22	1.78	0.47
26:Y:19:SER:O	26:Y:22:HIS:N	2.43	0.47
35:h:76:THR:HG23	35:h:150:ILE:CD1	2.44	0.47
2:A:34:C:H4'	2:A:539:C:OP1	2.15	0.47
2:A:1224:G:C2	2:A:1225:G:N7	2.83	0.47
2:A:2018:G:H22	2:A:2028:G:P	2.38	0.47
2:A:2697:U:O2'	35:h:286:ARG:N	2.45	0.47
11:J:114:LYS:O	11:J:117:ASP:N	2.48	0.47
18:Q:37:GLU:OE1	18:Q:38:ARG:N	2.48	0.47
35:h:404:ARG:HD3	35:h:407:MET:HE2	1.97	0.47
2:A:296:A:N6	2:A:340:A:H61	2.13	0.47
2:A:722:G:H2'	2:A:723:C:H6	1.80	0.47
2:A:740:A:HO2'	2:A:741:G:P	2.35	0.47
2:A:974:G:O2'	2:A:975:U:O5'	2.32	0.47
2:A:1132:U:C2	2:A:1133:G:C8	3.03	0.47
5:D:50:VAL:HG22	5:D:86:LEU:HD21	1.95	0.47
15:N:112:LYS:HA	15:N:112:LYS:HE3	1.95	0.47
17:P:114:ALA:O	17:P:118:ASP:OD2	2.33	0.47
35:h:46:LEU:CA	35:h:117:THR:HG21	2.41	0.47
35:h:76:THR:HG23	35:h:77:ALA:N	2.30	0.47
35:h:401:ASP:N	35:h:401:ASP:OD1	2.45	0.47
2:A:90:C:H2'	2:A:91:C:O4'	2.15	0.47
2:A:285:U:H3'	2:A:286:G:H4'	1.96	0.47
2:A:621:U:H2'	2:A:622:C:C6	2.50	0.47
2:A:1337:G:N2	2:A:1340:A:OP2	2.42	0.47
2:A:2056:G:H2'	2:A:2057:G:H5'	1.96	0.47
2:A:2185:C:HO2'	2:A:2186:C:P	2.38	0.47
2:A:2676:C:H5'	35:h:203:PRO:HA	1.96	0.47
2:A:2922:U:H2'	2:A:2923:C:C6	2.50	0.47
9:H:104:ILE:HG21	9:H:112:LEU:HD21	1.95	0.47
18:Q:14:ASP:O	18:Q:15:ASP:OD1	2.32	0.47
22:U:36:ASP:OD1	22:U:36:ASP:N	2.36	0.47
29:b:32:VAL:HG21	29:b:37:ARG:HD3	1.97	0.47
2:A:620:G:H2'	2:A:621:U:H6	1.80	0.46
2:A:691:U:H2'	2:A:692:C:C6	2.51	0.46
2:A:1025:A:N3	2:A:2488:C:O2'	2.40	0.46
2:A:1785:C:HO2'	2:A:1786:G:P	2.38	0.46
2:A:2034:G:H2'	2:A:2034:G:N3	2.30	0.46
2:A:2515:U:H4'	2:A:2604:U:O2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:17:LYS:HZ1	13:L:47:ILE:HG23	1.81	0.46
15:N:91:GLU:HG3	15:N:92:TRP:CE3	2.50	0.46
34:g:15:GLN:NE2	34:g:16:CYS:O	2.47	0.46
35:h:266:THR:HG22	35:h:268:ALA:H	1.80	0.46
2:A:54:C:C2	2:A:55:G:C8	3.03	0.46
2:A:365:U:H2'	2:A:366:G:C8	2.51	0.46
2:A:1147:A:C2	2:A:2690:C:O4'	2.69	0.46
2:A:1554:U:O2'	2:A:1555:A:H8	1.98	0.46
2:A:2409:U:O4	2:A:2410:A:N6	2.47	0.46
2:A:2752:U:H2'	2:A:2754:G:O5'	2.15	0.46
9:H:27:ARG:O	9:H:27:ARG:HG2	2.14	0.46
29:b:21:LYS:NZ	29:b:22:ALA:H	2.13	0.46
35:h:142:ASP:OD1	35:h:142:ASP:N	2.47	0.46
2:A:59:G:H5'	2:A:60:A:P	2.54	0.46
2:A:89:A:O2'	2:A:90:C:P	2.73	0.46
2:A:363:A:O2'	2:A:364:A:P	2.74	0.46
2:A:819:G:O2'	2:A:820:A:OP2	2.32	0.46
2:A:1944:C:H2'	2:A:1945:U:O4'	2.16	0.46
2:A:2323:G:N2	2:A:2412:U:O2	2.47	0.46
2:A:3014:A:N6	2:A:3112:A:C8	2.83	0.46
2:A:3046:C:O2	2:A:3046:C:O5'	2.33	0.46
12:K:4:TYR:O	19:R:64:ARG:NH2	2.40	0.46
35:h:113:THR:O	35:h:113:THR:HG22	2.16	0.46
35:h:308:PRO:HD2	35:h:311:LEU:HD12	1.97	0.46
35:h:334:GLY:N	35:h:369:ASN:O	2.47	0.46
2:A:46:A:N6	2:A:176:G:C4	2.83	0.46
2:A:733:U:C2	2:A:734:C:C5	3.03	0.46
2:A:1392:G:H4'	16:O:20:LEU:HD11	1.98	0.46
2:A:1580:A:H62	2:A:1592:G:H21	1.62	0.46
2:A:2133:G:H3'	2:A:2134:G:H5''	1.96	0.46
2:A:2148:C:HO2'	2:A:2149:C:C5'	2.26	0.46
2:A:3014:A:O2'	2:A:3015:C:H5''	2.16	0.46
2:A:3021:A:O3'	2:A:3022:G:C8	2.69	0.46
6:E:156:VAL:HG11	6:E:177:VAL:HG22	1.98	0.46
12:K:102:GLU:OE1	12:K:124:VAL:HG11	2.16	0.46
18:Q:9:GLN:HA	18:Q:12:LEU:HD12	1.98	0.46
19:R:107:THR:HA	19:R:110:VAL:HG12	1.96	0.46
24:W:152:GLU:OE1	24:W:152:GLU:N	2.48	0.46
35:h:210:THR:HG23	35:h:213:ARG:CB	2.44	0.46
2:A:1214:A:H3'	2:A:1215:U:H5''	1.97	0.46
2:A:1541:G:N1	2:A:1630:U:O4	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1752:C:H3'	2:A:1753:C:H5''	1.98	0.46
2:A:2129:C:O2'	2:A:2192:G:H3'	2.15	0.46
2:A:2329:G:N3	2:A:2329:G:H2'	2.31	0.46
5:D:177:THR:HB	5:D:180:LEU:HD11	1.98	0.46
5:D:189:ASN:OD1	5:D:189:ASN:N	2.48	0.46
7:F:146:HIS:CD2	7:F:146:HIS:C	2.93	0.46
27:Z:6:THR:HG22	27:Z:8:GLY:H	1.81	0.46
34:g:38:CYS:SG	34:g:39:SER:N	2.88	0.46
2:A:322:A:O2'	2:A:323:C:OP1	2.33	0.46
2:A:2006:A:H2'	2:A:2007:C:O4'	2.15	0.46
10:I:82:VAL:HG23	10:I:89:ALA:HB2	1.98	0.46
13:L:85:VAL:HG11	13:L:114:ILE:CD1	2.46	0.46
14:M:122:VAL:HG23	14:M:137:ILE:HD11	1.98	0.46
22:U:50:PHE:O	22:U:52:VAL:HG13	2.15	0.46
22:U:84:VAL:O	22:U:84:VAL:HG13	2.15	0.46
28:a:9:VAL:HG11	28:a:55:GLU:HG2	1.97	0.46
30:c:35:ARG:HB3	30:c:52:LYS:HE3	1.97	0.46
2:A:1071:G:C6	2:A:1081:C:N3	2.84	0.46
2:A:1168:A:C4	2:A:1169:A:C8	3.04	0.46
2:A:1539:A:H2'	2:A:1540:U:O5'	2.15	0.46
2:A:1989:G:N2	2:A:1991:C:H5''	2.30	0.46
2:A:2572:U:N3	2:A:2573:G:N7	2.64	0.46
9:H:100:VAL:HG21	9:H:117:VAL:HG11	1.98	0.46
16:O:63:ARG:HA	16:O:80:PHE:CZ	2.51	0.46
17:P:118:ASP:O	17:P:121:ARG:N	2.48	0.46
2:A:325:U:H2'	2:A:326:A:C8	2.51	0.46
2:A:693:G:N2	2:A:698:G:O3'	2.49	0.46
2:A:1129:G:C5	2:A:1131:G:C8	3.03	0.46
2:A:1703:G:C6	2:A:1727:A:C6	3.04	0.46
2:A:3087:G:H4'	2:A:3088:C:O5'	2.16	0.46
4:C:23:GLU:OE1	4:C:23:GLU:HA	2.16	0.46
10:I:25:VAL:HG23	10:I:79:ILE:HD13	1.97	0.46
11:J:23:ALA:HB3	11:J:24:PRO:CD	2.40	0.46
16:O:100:VAL:HG22	16:O:101:GLU:N	2.31	0.46
18:Q:87:THR:HG22	18:Q:88:ARG:O	2.16	0.46
35:h:148:LEU:HD13	35:h:311:LEU:HD21	1.97	0.46
35:h:340:LEU:HD23	35:h:340:LEU:H	1.81	0.46
2:A:658:U:H2'	2:A:659:U:O4'	2.16	0.46
2:A:944:A:N7	2:A:2471:A:O2'	2.49	0.46
2:A:1181:G:O2'	11:J:91:SER:N	2.49	0.46
2:A:1747:C:H2'	2:A:1748:A:O4'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:2007:C:H2'	2:A:2008:A:C8	2.51	0.46
2:A:2172:G:C6	2:A:2183:G:C6	3.04	0.46
7:F:67:ILE:HG13	7:F:148:ILE:HD11	1.97	0.46
7:F:103:MET:O	7:F:107:LEU:HG	2.15	0.46
14:M:63:LYS:NZ	32:e:12:LYS:O	2.40	0.46
23:V:25:VAL:HG12	23:V:34:LEU:HB3	1.98	0.46
35:h:255:ASN:HA	35:h:258:LYS:HE2	1.98	0.46
35:h:270:VAL:CB	35:h:274:ASN:HD22	2.29	0.46
2:A:187:G:O2'	2:A:188:G:OP1	2.27	0.46
2:A:1129:G:C6	2:A:1270:G:C6	3.03	0.46
2:A:1630:U:C6	2:A:1631:A:C8	3.04	0.46
3:B:81:U:H2'	3:B:82:A:C8	2.51	0.46
5:D:27:THR:OG1	5:D:196:GLY:O	2.30	0.46
7:F:119:ARG:NH1	7:F:144:MET:SD	2.89	0.46
13:L:24:VAL:HA	13:L:39:ILE:HG22	1.98	0.46
21:T:35:SER:HB3	21:T:38:GLU:OE1	2.15	0.46
2:A:184:C:C2	2:A:185:G:C8	3.04	0.45
2:A:1121:G:C2	2:A:1272:C:N3	2.84	0.45
2:A:1575:A:HO2'	2:A:1576:C:C5'	2.29	0.45
2:A:2017:C:H5	2:A:2036:A:H62	1.64	0.45
2:A:2337:A:N6	2:A:2389:U:O4	2.50	0.45
2:A:2485:C:C2	2:A:2504:G:N2	2.84	0.45
2:A:2552:A:H2'	2:A:2553:G:C8	2.50	0.45
7:F:113:ILE:CD1	34:g:35:VAL:HG11	2.46	0.45
18:Q:8:ASP:OD2	18:Q:54:ILE:HG21	2.15	0.45
21:T:113:ILE:O	21:T:113:ILE:HG23	2.17	0.45
28:a:23:LEU:CD2	28:a:50:VAL:HG11	2.45	0.45
2:A:708:G:N3	2:A:709:U:C5	2.84	0.45
2:A:964:C:C2	2:A:965:U:C5	3.03	0.45
2:A:1545:C:H2'	2:A:1546:A:C8	2.51	0.45
2:A:1753:C:H2'	2:A:1754:G:C8	2.51	0.45
2:A:2729:G:H1'	35:h:200:THR:HG21	1.98	0.45
21:T:32:ARG:NH1	21:T:81:VAL:O	2.43	0.45
22:U:8:ARG:NH2	27:Z:27:GLU:OE1	2.49	0.45
26:Y:5:CYS:SG	26:Y:7:ILE:HD12	2.57	0.45
35:h:251:VAL:HG23	35:h:251:VAL:O	2.15	0.45
2:A:574:C:C2	2:A:575:C:C5	3.05	0.45
2:A:1225:G:C2	2:A:1226:U:C4	3.04	0.45
2:A:2034:G:OP1	4:C:88:ARG:NH1	2.44	0.45
2:A:2866:A:C2	2:A:2867:A:C8	3.05	0.45
3:B:10:G:O2'	3:B:11:U:H5'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:44:C:O2'	7:F:102:ARG:NH2	2.49	0.45
9:H:96:THR:OG1	9:H:97:ALA:N	2.49	0.45
10:I:110:MET:SD	10:I:111:ASP:N	2.89	0.45
19:R:17:VAL:O	19:R:21:SER:OG	2.19	0.45
26:Y:5:CYS:N	26:Y:33:ILE:HD11	2.32	0.45
30:c:7:VAL:O	30:c:7:VAL:HG12	2.16	0.45
2:A:410:U:O2'	2:A:411:G:OP1	2.27	0.45
2:A:1673:A:C5	2:A:2926:A:C8	3.04	0.45
2:A:2035:U:H2'	4:C:157:ARG:HB2	1.98	0.45
4:C:79:VAL:HG11	4:C:111:LEU:CD2	2.45	0.45
11:J:48:THR:HG21	11:J:56:ILE:HD13	1.98	0.45
2:A:944:A:N7	2:A:2472:C:H5'	2.32	0.45
2:A:1578:G:C2'	2:A:1579:C:O4'	2.64	0.45
2:A:1822:C:N3	2:A:1823:C:C4	2.85	0.45
2:A:2509:C:P	30:c:8:ARG:HH21	2.38	0.45
3:B:41:U:H3'	3:B:42:C:H4'	1.98	0.45
5:D:117:THR:HG22	5:D:118:SER:N	2.31	0.45
9:H:12:LEU:HD23	9:H:12:LEU:O	2.17	0.45
35:h:246:PRO:HG2	35:h:411:VAL:HG11	1.98	0.45
2:A:1163:A:N3	2:A:1165:G:N1	2.65	0.45
2:A:1396:G:H2'	2:A:1397:U:C6	2.51	0.45
2:A:1860:G:O2'	2:A:1861:G:H5'	2.17	0.45
2:A:2645:G:OP2	30:c:10:LYS:NZ	2.49	0.45
11:J:122:ASP:HB2	11:J:125:ALA:HB3	1.97	0.45
12:K:129:ASP:C	12:K:129:ASP:OD1	2.60	0.45
17:P:22:HIS:NE2	17:P:103:ASP:OD2	2.41	0.45
17:P:46:HIS:ND1	17:P:65:SER:OG	2.47	0.45
22:U:21:TYR:O	22:U:24:ILE:HG22	2.17	0.45
35:h:323:VAL:HG23	35:h:359:ILE:HG21	1.99	0.45
2:A:23:G:H2'	2:A:24:G:O4'	2.17	0.45
2:A:161:U:O4	2:A:2442:U:H4'	2.16	0.45
2:A:682:A:OP1	6:E:96:ARG:NH1	2.50	0.45
2:A:998:G:N3	2:A:998:G:H2'	2.32	0.45
2:A:1305:G:H2'	2:A:1306:G:H8	1.82	0.45
2:A:1349:U:H2'	2:A:1350:G:O5'	2.16	0.45
2:A:2093:G:H2'	2:A:2093:G:N3	2.32	0.45
2:A:2270:G:H4'	29:b:19:GLN:NE2	2.32	0.45
2:A:2735:U:O2'	5:D:148:PRO:O	2.26	0.45
2:A:2992:C:OP1	12:K:85:ARG:NH2	2.50	0.45
5:D:135:GLN:OE1	5:D:135:GLN:N	2.44	0.45
6:E:183:LEU:HD12	6:E:183:LEU:C	2.41	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:186:GLU:OE1	7:F:186:GLU:N	2.40	0.45
13:L:66:VAL:HG23	13:L:82:ASN:OD1	2.17	0.45
14:M:57:ILE:CD1	32:e:58:ILE:HD11	2.47	0.45
17:P:49:VAL:HG11	17:P:116:LEU:HD21	1.98	0.45
17:P:69:ASP:OD1	17:P:69:ASP:N	2.48	0.45
2:A:1090:G:C6	2:A:1091:A:C6	3.05	0.45
2:A:1165:G:O4'	2:A:1229:A:N6	2.38	0.45
2:A:1358:U:O3'	14:M:10:LYS:NZ	2.42	0.45
2:A:1513:C:OP1	22:U:58:ASN:ND2	2.42	0.45
2:A:1589:G:N1	2:A:1590:G:O6	2.50	0.45
2:A:2644:C:OP1	32:e:34:GLU:HB3	2.17	0.45
3:B:46:A:O4'	7:F:99:ARG:CZ	2.64	0.45
4:C:65:ILE:HD11	4:C:92:ILE:HG21	1.98	0.45
8:G:23:ASN:OD1	8:G:23:ASN:C	2.60	0.45
2:A:137:G:H22	2:A:1812:A:H2	1.62	0.45
2:A:473:C:O2	2:A:478:A:C2	2.70	0.45
2:A:1117:U:O2	2:A:1118:A:C8	2.69	0.45
2:A:1295:U:N3	2:A:1296:G:N7	2.64	0.45
2:A:1403:C:O2	2:A:1403:C:H2'	2.16	0.45
2:A:1548:C:N3	2:A:1623:U:O2	2.50	0.45
2:A:2490:A:N3	2:A:2496:U:C4	2.85	0.45
11:J:107:VAL:HG21	11:J:141:VAL:HG13	1.99	0.45
23:V:3:VAL:HG23	23:V:3:VAL:O	2.16	0.45
27:Z:5:THR:HB	27:Z:53:GLU:OE1	2.17	0.45
35:h:250:ILE:HD12	35:h:329:ILE:HB	1.99	0.45
35:h:420:VAL:HG13	35:h:422:ILE:HD11	1.99	0.45
2:A:643:G:C2'	2:A:644:G:OP1	2.65	0.45
2:A:1077:A:H5''	2:A:1078:G:P	2.57	0.45
2:A:1180:G:H2'	2:A:1180:G:N3	2.32	0.45
2:A:1180:G:H3'	2:A:1181:G:H8	1.82	0.45
2:A:1606:G:C2'	2:A:1607:C:O4'	2.65	0.45
2:A:1784:C:H2'	2:A:1785:C:C6	2.52	0.45
2:A:1886:A:N3	2:A:1888:C:N4	2.64	0.45
2:A:1886:A:N3	2:A:1888:C:C4	2.85	0.45
2:A:2155:U:C5'	2:A:2191:C:H42	2.27	0.45
2:A:2217:U:H4'	5:D:138:ALA:HB3	1.99	0.45
2:A:2234:G:H5''	21:T:49:ALA:HB3	1.99	0.45
2:A:2555:G:HO2'	25:X:43:THR:HG22	1.81	0.45
2:A:2653:G:O6	14:M:60:ARG:CZ	2.65	0.45
2:A:2696:G:C6	2:A:2699:C:H2'	2.52	0.45
23:V:101:ASN:OD1	23:V:101:ASN:N	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:963:U:C2	2:A:964:C:C6	3.05	0.44
2:A:1289:A:H2'	2:A:1290:C:C6	2.52	0.44
2:A:2420:U:H1'	2:A:2421:A:C8	2.51	0.44
2:A:2904:C:O2'	2:A:2905:C:H5'	2.17	0.44
2:A:2913:U:O2	2:A:2913:U:O4'	2.35	0.44
3:B:22:A:C6	3:B:64:G:C6	3.05	0.44
7:F:84:PHE:N	7:F:84:PHE:CD1	2.84	0.44
10:I:90:ALA:HB1	10:I:124:ALA:HB2	1.99	0.44
13:L:115:VAL:HG13	13:L:121:VAL:HG21	2.00	0.44
35:h:214:ARG:NE	35:h:218:ARG:HG2	2.32	0.44
35:h:236:GLN:O	35:h:240:ARG:HG2	2.17	0.44
2:A:722:G:H2'	2:A:723:C:C6	2.52	0.44
2:A:853:C:OP1	31:d:3:LYS:CE	2.65	0.44
2:A:1087:G:H2'	2:A:1088:U:C6	2.52	0.44
2:A:1833:C:OP2	2:A:1835:C:N4	2.41	0.44
2:A:3071:A:P	2:A:3087:G:H22	2.41	0.44
5:D:24:VAL:O	5:D:24:VAL:HG23	2.16	0.44
35:h:280:LEU:HD23	35:h:280:LEU:C	2.42	0.44
2:A:414:A:O2'	2:A:416:C:OP2	2.31	0.44
2:A:503:A:H2'	2:A:504:C:H6	1.82	0.44
2:A:1123:C:C2	2:A:1124:C:C5	3.06	0.44
2:A:1259:U:OP2	12:K:65:SER:OG	2.17	0.44
2:A:1580:A:N6	2:A:1592:G:H21	2.16	0.44
2:A:2007:C:C3'	2:A:2008:A:C8	3.00	0.44
2:A:2857:A:H2'	2:A:2858:G:H8	1.81	0.44
5:D:18:ASP:CG	5:D:19:GLU:N	2.75	0.44
6:E:130:LEU:HD11	6:E:156:VAL:HG21	2.00	0.44
17:P:103:ASP:OD1	17:P:105:GLY:N	2.47	0.44
18:Q:100:ARG:O	18:Q:103:ARG:NH2	2.50	0.44
1:3:4:ARG:O	1:3:8:LYS:HG3	2.17	0.44
2:A:363:A:H2'	2:A:364:A:O4'	2.17	0.44
2:A:1455:U:OP2	22:U:62:ARG:NH2	2.50	0.44
2:A:1538:G:O6	2:A:1635:A:N6	2.50	0.44
2:A:1845:G:C6	2:A:1858:A:N7	2.85	0.44
2:A:2053:C:H1'	2:A:2153:G:H5''	1.99	0.44
2:A:2992:C:OP1	12:K:85:ARG:CZ	2.66	0.44
6:E:42:LEU:CD1	6:E:186:TYR:CE2	3.00	0.44
6:E:197:SER:O	6:E:200:ALA:N	2.50	0.44
9:H:21:VAL:HG22	9:H:22:LYS:N	2.32	0.44
24:W:19:THR:OG1	24:W:20:GLY:N	2.50	0.44
2:A:24:G:C2	2:A:599:G:N3	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:940:A:H2'	2:A:941:U:O4'	2.18	0.44
2:A:1002:C:O2'	2:A:1003:A:P	2.74	0.44
2:A:1174:G:H1'	2:A:1221:A:H61	1.83	0.44
2:A:1243:G:O6	2:A:1244:A:N6	2.50	0.44
2:A:1291:G:N2	2:A:1293:G:C4	2.86	0.44
2:A:1554:U:O2'	2:A:1555:A:C5'	2.65	0.44
2:A:2588:C:H2'	2:A:2589:G:O4'	2.17	0.44
2:A:2637:G:H2'	2:A:2638:G:O4'	2.18	0.44
3:B:47:A:C6	3:B:48:C:C4	3.06	0.44
23:V:81:THR:HG22	23:V:82:ARG:O	2.17	0.44
2:A:684:G:H3'	2:A:685:G:C5'	2.47	0.44
2:A:979:G:H2'	2:A:980:C:H6	1.83	0.44
2:A:1937:U:H2'	2:A:1938:G:O4'	2.17	0.44
2:A:2193:A:O2'	2:A:2196:G:C2	2.70	0.44
7:F:86:LEU:O	7:F:87:ARG:NE	2.51	0.44
7:F:132:THR:HG22	17:P:6:VAL:HG21	1.99	0.44
12:K:106:ILE:HD11	12:K:119:GLN:HG3	1.99	0.44
23:V:86:ARG:CB	23:V:97:ILE:HD11	2.48	0.44
2:A:571:A:N3	23:V:58:GLY:N	2.66	0.44
2:A:1138:A:C2	2:A:1259:U:C2	3.06	0.44
2:A:1144:A:C2	2:A:1145:A:C8	3.05	0.44
2:A:2285:G:H1'	2:A:2286:A:C8	2.53	0.44
2:A:2451:A:O3'	4:C:261:ASN:ND2	2.44	0.44
2:A:3011:C:C2	2:A:3012:U:C5	3.06	0.44
4:C:37:LEU:HD23	4:C:37:LEU:C	2.42	0.44
24:W:10:LYS:C	24:W:11:LEU:HD22	2.43	0.44
2:A:661:U:O2'	2:A:1101:A:N1	2.44	0.44
2:A:678:A:N1	2:A:924:G:O2'	2.46	0.44
2:A:759:G:O6	25:X:33:ALA:N	2.40	0.44
2:A:921:C:O2	2:A:2668:G:O2'	2.35	0.44
2:A:1582:C:H2'	2:A:1583:U:O4'	2.18	0.44
2:A:2350:G:O2'	2:A:2351:A:N9	2.49	0.44
2:A:2364:C:H2'	2:A:2365:A:C8	2.53	0.44
2:A:2647:U:O2	2:A:2647:U:O4'	2.35	0.44
5:D:87:ASP:OD1	5:D:87:ASP:N	2.51	0.44
9:H:124:ILE:CG2	9:H:125:LYS:N	2.80	0.44
23:V:24:LEU:HD11	23:V:36:GLU:HB3	1.99	0.44
27:Z:10:LEU:HD23	27:Z:10:LEU:C	2.42	0.44
2:A:246:U:C2	2:A:247:G:C8	3.06	0.44
2:A:293:G:C2	2:A:343:U:O4	2.70	0.44
2:A:361:A:O2'	2:A:362:A:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:693:G:OP1	6:E:30:ASN:ND2	2.51	0.44
2:A:933:G:N2	2:A:1303:U:C5	2.84	0.44
2:A:1180:G:C6	2:A:1195:A:N6	2.86	0.44
2:A:1212:U:H3'	2:A:1213:A:H5''	1.99	0.44
2:A:1248:U:N3	2:A:2249:G:OP1	2.41	0.44
2:A:1673:A:C6	2:A:2926:A:C5	3.05	0.44
2:A:1831:A:C2	2:A:1837:G:O6	2.71	0.44
2:A:2169:G:N2	2:A:2185:C:H41	2.15	0.44
2:A:2583:C:O2'	2:A:2584:A:H5'	2.18	0.44
8:G:35:LEU:HD22	8:G:73:ILE:CD1	2.48	0.44
24:W:113:LEU:HD23	24:W:114:VAL:N	2.33	0.44
35:h:270:VAL:HB	35:h:274:ASN:HD22	1.83	0.44
2:A:828:G:H21	2:A:833:A:N6	2.13	0.43
2:A:1089:C:OP1	2:A:1092:G:C8	2.71	0.43
2:A:1296:G:H2'	2:A:1297:G:H8	1.83	0.43
2:A:2702:A:C8	2:A:2753:G:N7	2.86	0.43
23:V:9:VAL:CG1	23:V:35:VAL:HG21	2.48	0.43
27:Z:26:LYS:O	27:Z:26:LYS:HD3	2.18	0.43
29:b:53:ASP:N	29:b:53:ASP:OD1	2.39	0.43
35:h:214:ARG:O	35:h:215:ILE:C	2.61	0.43
35:h:463:LEU:HD12	35:h:463:LEU:O	2.17	0.43
2:A:383:U:H3'	2:A:384:G:C5'	2.48	0.43
2:A:623:A:C6	2:A:650:G:C6	3.06	0.43
2:A:1859:A:H2'	2:A:1860:G:O4'	2.18	0.43
2:A:2400:C:N4	2:A:2401:U:O2	2.51	0.43
2:A:2852:U:O2'	2:A:3006:G:OP1	2.17	0.43
2:A:2932:G:H4'	16:O:71:ARG:NH2	2.32	0.43
2:A:2975:G:OP1	2:A:2975:G:N2	2.47	0.43
4:C:111:LEU:HD23	4:C:112:LYS:N	2.33	0.43
10:I:79:ILE:HG21	10:I:81:PHE:CZ	2.53	0.43
20:S:7:VAL:HG22	20:S:60:VAL:HG21	1.99	0.43
35:h:307:LEU:HD22	35:h:315:PHE:HE2	1.82	0.43
2:A:58:G:C6	2:A:92:G:C2	3.06	0.43
2:A:263:G:H2'	2:A:264:G:O4'	2.17	0.43
2:A:1157:G:O3'	24:W:52:ARG:NH2	2.51	0.43
2:A:1555:A:H3'	2:A:1556:A:H8	1.83	0.43
2:A:1755:A:H2'	2:A:1758:G:O6	2.18	0.43
2:A:2177:A:O2'	2:A:2783:C:O2	2.35	0.43
2:A:2181:C:H2'	2:A:2182:C:C6	2.53	0.43
4:C:129:ASN:O	4:C:193:VAL:HG23	2.18	0.43
4:C:145:VAL:HG12	4:C:146:GLU:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:28:VAL:HG13	5:D:191:VAL:HG13	2.01	0.43
8:G:122:ILE:HD11	8:G:134:VAL:HG11	1.96	0.43
11:J:23:ALA:HB1	35:h:444:HIS:CE1	2.53	0.43
23:V:89:ASP:OD1	23:V:89:ASP:C	2.61	0.43
35:h:43:GLN:HG2	35:h:44:LEU:N	2.22	0.43
35:h:204:GLY:O	35:h:206:THR:HG23	2.18	0.43
2:A:733:U:H2'	2:A:734:C:C6	2.53	0.43
2:A:848:G:N2	2:A:849:A:N7	2.67	0.43
2:A:898:A:N3	2:A:898:A:H2'	2.33	0.43
2:A:1181:G:O2'	11:J:91:SER:O	2.31	0.43
2:A:1569:A:C6	2:A:1603:G:N1	2.86	0.43
2:A:2238:A:P	21:T:104:ARG:HH12	2.41	0.43
2:A:2287:C:O2	2:A:2287:C:H2'	2.18	0.43
2:A:2520:U:OP2	17:P:20:ARG:NH1	2.47	0.43
2:A:2867:A:C4	2:A:2868:A:C8	3.06	0.43
2:A:2883:G:C4	2:A:2885:G:OP2	2.71	0.43
6:E:164:VAL:HG23	6:E:165:GLY:N	2.34	0.43
7:F:27:PHE:HB2	7:F:29:TYR:CE2	2.53	0.43
7:F:100:GLY:N	7:F:103:MET:HE2	2.34	0.43
10:I:72:LEU:HD13	10:I:106:LYS:O	2.18	0.43
13:L:89:ASN:OD1	13:L:89:ASN:N	2.51	0.43
29:b:32:VAL:HG21	29:b:37:ARG:HB2	1.99	0.43
35:h:148:LEU:CD1	35:h:311:LEU:HD21	2.48	0.43
2:A:193:G:H2'	2:A:194:A:O4'	2.18	0.43
2:A:617:U:O2	2:A:617:U:C2'	2.66	0.43
2:A:934:A:C4	2:A:1304:A:C2	3.07	0.43
2:A:1250:U:H3'	2:A:1251:A:H5''	2.00	0.43
2:A:1349:U:O2'	2:A:1350:G:H5'	2.18	0.43
2:A:1847:U:O4	2:A:1848:A:N6	2.52	0.43
2:A:1909:C:H2'	2:A:1910:U:O4'	2.18	0.43
2:A:2025:C:O2	2:A:2025:C:O4'	2.35	0.43
4:C:33:LEU:O	4:C:64:VAL:HG22	2.19	0.43
6:E:82:PRO:HB3	6:E:90:VAL:CG2	2.48	0.43
9:H:133:THR:OG1	9:H:142:ALA:O	2.30	0.43
13:L:24:VAL:HG23	13:L:24:VAL:O	2.18	0.43
21:T:38:GLU:O	21:T:42:ILE:HG22	2.18	0.43
26:Y:6:ASP:OD2	26:Y:50:ASN:O	2.36	0.43
27:Z:10:LEU:HD11	27:Z:57:VAL:HG22	1.99	0.43
29:b:21:LYS:HA	29:b:21:LYS:HD2	1.91	0.43
32:e:48:THR:HG22	32:e:49:THR:N	2.33	0.43
35:h:210:THR:O	35:h:211:ASP:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:498:G:H5''	2:A:498:G:H8	1.84	0.43
2:A:582:G:C4	2:A:583:G:C8	3.07	0.43
2:A:1454:G:N2	2:A:1821:A:H1'	2.33	0.43
2:A:1592:G:H2'	2:A:1593:U:C6	2.54	0.43
2:A:2128:G:H3'	2:A:2129:C:C5'	2.48	0.43
2:A:2690:C:N4	2:A:2691:C:H41	2.16	0.43
2:A:3068:U:C2'	2:A:3069:G:H5'	2.49	0.43
5:D:102:THR:HB	5:D:104:GLU:OE1	2.19	0.43
7:F:160:ASP:C	7:F:160:ASP:OD1	2.61	0.43
9:H:23:ASP:OD1	9:H:23:ASP:N	2.52	0.43
9:H:119:LEU:CG	9:H:124:ILE:HD11	2.48	0.43
11:J:32:GLN:OE1	35:h:428:ASP:N	2.38	0.43
24:W:62:GLY:N	24:W:142:GLU:OE2	2.51	0.43
35:h:212:ARG:CB	35:h:216:ARG:CZ	2.96	0.43
35:h:215:ILE:HG22	35:h:219:MET:HE2	2.00	0.43
2:A:169:C:C2	2:A:170:G:C8	3.07	0.43
2:A:568:A:O4'	23:V:41:ILE:HG12	2.18	0.43
2:A:636:U:O2'	2:A:637:G:P	2.76	0.43
2:A:1145:A:O2'	2:A:1146:A:O5'	2.36	0.43
2:A:1876:A:O2'	2:A:1877:U:H5'	2.18	0.43
2:A:1882:A:C2	2:A:1883:A:C5	3.07	0.43
2:A:2067:G:C5	2:A:2068:U:C4	3.06	0.43
2:A:2363:A:C2	2:A:2375:G:O6	2.71	0.43
2:A:2389:U:O4	2:A:2393:A:C6	2.72	0.43
2:A:2460:U:H2'	2:A:2461:G:C5'	2.48	0.43
4:C:224:VAL:HB	4:C:240:THR:HG23	2.01	0.43
5:D:185:VAL:O	5:D:186:ASP:C	2.62	0.43
12:K:101:VAL:HG12	12:K:105:ILE:HD12	2.01	0.43
13:L:35:ILE:HD11	13:L:65:THR:HG22	2.00	0.43
30:c:39:LYS:HE2	30:c:39:LYS:HB3	1.93	0.43
2:A:411:G:C2	2:A:565:A:C2	3.06	0.43
2:A:1230:G:H2'	2:A:1231:U:O4'	2.19	0.43
2:A:1933:G:C6	2:A:1934:G:N7	2.87	0.43
2:A:2379:G:H2'	2:A:2380:G:C5	2.54	0.43
2:A:2780:C:H2'	2:A:2781:G:O4'	2.18	0.43
2:A:3021:A:H5'	2:A:3022:G:OP1	2.18	0.43
3:B:28:A:OP1	17:P:71:ARG:NH2	2.45	0.43
7:F:81:ILE:HG21	7:F:84:PHE:CE2	2.53	0.43
15:N:3:ILE:HG23	15:N:3:ILE:O	2.18	0.43
18:Q:31:VAL:HG23	18:Q:31:VAL:O	2.18	0.43
23:V:75:ASP:N	23:V:79:LYS:O	2.40	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:85:VAL:HG23	24:W:92:ILE:HD13	2.00	0.43
2:A:128:G:C2	2:A:129:G:N7	2.87	0.43
2:A:504:C:H2'	2:A:505:C:C6	2.54	0.43
2:A:533:C:O2'	2:A:534:G:H5'	2.19	0.43
2:A:1291:G:C2	2:A:1293:G:C2	3.07	0.43
2:A:1296:G:C2	2:A:1297:G:C5	3.07	0.43
2:A:1381:G:O2'	2:A:1382:U:OP2	2.37	0.43
2:A:1382:U:O2	2:A:1382:U:H2'	2.18	0.43
2:A:1533:U:C2'	2:A:1534:C:OP1	2.67	0.43
2:A:1565:A:C2	2:A:1566:A:C6	3.06	0.43
2:A:1733:C:H2'	2:A:1734:C:C6	2.54	0.43
2:A:1848:A:N6	2:A:1855:A:H61	2.17	0.43
2:A:2060:C:C2	2:A:2061:U:C5	3.07	0.43
5:D:164:THR:HG23	5:D:164:THR:O	2.18	0.43
13:L:96:THR:O	13:L:96:THR:HG22	2.18	0.43
24:W:99:VAL:HG23	24:W:99:VAL:O	2.18	0.43
35:h:256:ALA:C	35:h:370:LYS:HZ3	2.27	0.43
2:A:248:G:C2	2:A:2655:U:H4'	2.53	0.43
2:A:1180:G:O6	2:A:1195:A:N6	2.51	0.43
2:A:1632:G:N3	2:A:1633:U:O4	2.52	0.43
2:A:1653:G:H2'	2:A:1654:G:O4'	2.18	0.43
2:A:2511:A:O2'	2:A:2512:A:OP2	2.32	0.43
2:A:2912:A:H3'	2:A:2913:U:C5'	2.49	0.43
7:F:102:ARG:H	7:F:102:ARG:HD3	1.84	0.43
14:M:57:ILE:HA	14:M:60:ARG:HB3	1.99	0.43
23:V:94:LYS:O	23:V:95:VAL:HG23	2.19	0.43
24:W:122:THR:HG22	24:W:123:LEU:N	2.33	0.43
35:h:160:GLY:HA2	35:h:280:LEU:HD11	2.01	0.43
2:A:255:A:O2'	2:A:472:C:OP2	2.30	0.42
2:A:502:C:N4	2:A:503:A:H62	2.17	0.42
2:A:873:G:O2'	2:A:2205:A:N3	2.49	0.42
2:A:885:G:H4'	31:d:13:ARG:NH2	2.34	0.42
2:A:928:U:C2	2:A:1310:G:N2	2.87	0.42
2:A:947:U:H2'	2:A:948:G:H8	1.84	0.42
2:A:974:G:O2'	2:A:975:U:C6	2.72	0.42
2:A:986:G:H2'	2:A:987:A:O4'	2.19	0.42
2:A:994:A:N7	2:A:1014:G:O2'	2.45	0.42
2:A:1129:G:OP2	19:R:66:ASN:ND2	2.52	0.42
2:A:1152:G:H2'	2:A:1153:U:O4'	2.19	0.42
2:A:2037:U:H4'	2:A:2038:A:OP2	2.18	0.42
2:A:2051:U:O2'	2:A:2194:A:OP2	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:2367:G:O2'	2:A:2370:A:N6	2.50	0.42
2:A:2532:G:H2'	2:A:2532:G:N3	2.34	0.42
2:A:3035:C:C4	2:A:3036:C:C5	3.07	0.42
5:D:42:THR:HG23	5:D:89:GLU:OE2	2.19	0.42
10:I:18:LYS:HA	10:I:18:LYS:HE3	2.01	0.42
10:I:24:VAL:HG23	10:I:80:ALA:HB3	2.01	0.42
10:I:25:VAL:HG23	10:I:79:ILE:CD1	2.48	0.42
11:J:73:LYS:NZ	11:J:117:ASP:O	2.46	0.42
11:J:133:THR:O	11:J:137:MET:HG3	2.18	0.42
14:M:61:LEU:HD12	14:M:62:PRO:O	2.19	0.42
18:Q:50:GLN:HB3	18:Q:57:THR:HG22	2.01	0.42
35:h:70:LEU:HD22	35:h:121:ASP:HA	1.99	0.42
35:h:169:MET:HB3	35:h:212:ARG:CG	2.49	0.42
35:h:261:LEU:HD11	35:h:331:VAL:HG21	2.01	0.42
35:h:303:PHE:HZ	35:h:319:LEU:HD21	1.84	0.42
35:h:413:SER:OG	35:h:454:ARG:NH1	2.52	0.42
2:A:296:A:N6	2:A:297:G:O6	2.51	0.42
2:A:580:G:H2'	2:A:581:G:O4'	2.19	0.42
2:A:838:G:C4	2:A:839:U:C5	3.07	0.42
2:A:1001:C:OP1	2:A:1001:C:H4'	2.19	0.42
2:A:1048:A:C6	2:A:1050:A:C8	3.07	0.42
2:A:1200:U:H4'	2:A:1201:G:OP2	2.19	0.42
2:A:1473:G:N1	2:A:1487:U:OP2	2.43	0.42
6:E:197:SER:O	6:E:198:VAL:C	2.61	0.42
7:F:81:ILE:HG21	7:F:84:PHE:CD2	2.54	0.42
11:J:135:ARG:HB3	11:J:135:ARG:CZ	2.48	0.42
27:Z:21:LYS:HA	27:Z:24:GLU:HG3	2.01	0.42
35:h:144:THR:O	35:h:148:LEU:HD23	2.19	0.42
35:h:251:VAL:HG23	35:h:330:HIS:HA	2.01	0.42
2:A:136:U:N3	2:A:139:U:OP2	2.49	0.42
2:A:184:C:N3	2:A:185:G:N7	2.67	0.42
2:A:671:G:C8	2:A:2241:U:C4	3.07	0.42
2:A:709:U:O2	2:A:709:U:O4'	2.36	0.42
2:A:1063:G:O6	2:A:1090:G:C2	2.72	0.42
2:A:1166:A:H1'	2:A:1230:G:N2	2.35	0.42
2:A:1195:A:OP2	2:A:1196:C:N4	2.52	0.42
2:A:1295:U:C2	2:A:1296:G:C8	3.06	0.42
2:A:1383:A:H2'	2:A:1384:G:O4'	2.19	0.42
2:A:1597:G:C2'	2:A:1598:U:O4'	2.65	0.42
2:A:2008:A:C2	2:A:2046:A:H4'	2.54	0.42
2:A:2285:G:N2	2:A:2286:A:C6	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:2559:A:OP1	17:P:27:LYS:NZ	2.44	0.42
7:F:160:ASP:OD1	7:F:160:ASP:O	2.37	0.42
10:I:21:THR:HG21	10:I:85:GLU:H	1.84	0.42
18:Q:73:PHE:HB3	18:Q:80:ILE:HD11	2.00	0.42
24:W:133:ILE:CG2	24:W:168:VAL:HG13	2.49	0.42
27:Z:5:THR:CG2	27:Z:10:LEU:HD12	2.49	0.42
33:f:30:PRO:O	33:f:33:LYS:HG2	2.18	0.42
2:A:239:U:H2'	2:A:240:G:O4'	2.19	0.42
2:A:292:G:O4'	2:A:344:G:C2	2.73	0.42
2:A:451:U:H5''	2:A:452:G:P	2.60	0.42
2:A:499:G:OP1	2:A:2631:G:OP1	2.37	0.42
2:A:2529:A:O2'	2:A:2530:C:O4'	2.35	0.42
2:A:2533:C:H2'	2:A:2534:A:O4'	2.20	0.42
2:A:3037:C:C2	2:A:3038:C:C5	3.07	0.42
2:A:3093:A:H1'	16:O:4:PRO:HD3	2.00	0.42
5:D:64:LYS:CB	5:D:65:PRO:HD3	2.49	0.42
14:M:98:LEU:HB3	14:M:104:VAL:HG22	2.02	0.42
16:O:20:LEU:HD21	16:O:40:LYS:HE2	2.02	0.42
21:T:92:ILE:HD12	21:T:93:ARG:H	1.83	0.42
27:Z:13:LEU:HD22	27:Z:18:LEU:HD23	2.02	0.42
2:A:78:G:O2'	2:A:79:G:H5'	2.20	0.42
2:A:162:A:N3	9:H:115:ARG:NE	2.67	0.42
2:A:714:U:O2	2:A:714:U:C2'	2.67	0.42
2:A:1285:G:C2	2:A:1299:U:O2	2.73	0.42
2:A:2298:U:HO2'	2:A:2820:U:H3	1.64	0.42
2:A:2419:C:H2'	2:A:2420:U:C6	2.54	0.42
2:A:2554:U:O2	25:X:42:GLY:CA	2.67	0.42
7:F:7:ALA:C	7:F:8:LEU:HD22	2.44	0.42
7:F:110:LEU:HG	7:F:115:LEU:HD21	2.01	0.42
9:H:119:LEU:CD2	9:H:124:ILE:HD11	2.46	0.42
10:I:22:ALA:HB2	10:I:110:MET:CE	2.49	0.42
16:O:91:ASN:OD1	16:O:91:ASN:N	2.52	0.42
20:S:65:LEU:HD13	20:S:96:VAL:HG22	2.02	0.42
2:A:188:G:N3	2:A:188:G:O4'	2.53	0.42
2:A:238:G:C6	2:A:260:G:C6	3.06	0.42
2:A:341:C:N4	2:A:342:C:N4	2.68	0.42
2:A:352:G:H2'	2:A:353:G:C1'	2.49	0.42
2:A:885:G:O3'	31:d:13:ARG:NH2	2.50	0.42
2:A:1343:G:H2'	2:A:1345:G:C8	2.55	0.42
2:A:1349:U:C2'	2:A:1350:G:O5'	2.67	0.42
2:A:1448:C:C2	2:A:1449:C:C5	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1740:G:C4	2:A:1741:G:C8	3.08	0.42
2:A:2132:U:C5'	2:A:2153:G:H21	2.33	0.42
2:A:2135:U:P	2:A:2135:U:H3'	2.59	0.42
2:A:2288:C:H5'	35:h:197:GLY:CA	2.49	0.42
2:A:2706:A:C5	2:A:2707:C:C5	3.07	0.42
7:F:86:LEU:O	7:F:87:ARG:NH2	2.52	0.42
8:G:26:VAL:HG11	8:G:77:VAL:HG12	2.00	0.42
11:J:94:PRO:HB3	11:J:137:MET:HA	2.01	0.42
24:W:177:LEU:HD21	24:W:179:VAL:O	2.20	0.42
29:b:32:VAL:O	29:b:33:ALA:HB3	2.20	0.42
35:h:336:ASP:OD1	35:h:337:VAL:N	2.53	0.42
35:h:371:ILE:HG21	35:h:391:PHE:HB3	2.02	0.42
2:A:521:C:O2'	2:A:522:U:H5'	2.19	0.42
2:A:824:G:C6	2:A:838:G:C6	3.07	0.42
2:A:1167:C:N3	2:A:1168:A:C8	2.88	0.42
2:A:2163:U:O4'	2:A:2816:G:H4'	2.20	0.42
2:A:2866:A:C4	2:A:2867:A:C8	3.07	0.42
8:G:156:ASP:O	8:G:160:GLY:N	2.46	0.42
2:A:164:A:OP2	9:H:120:ALA:N	2.46	0.42
2:A:322:A:N1	2:A:455:C:N3	2.67	0.42
2:A:911:U:H2'	2:A:912:C:C6	2.55	0.42
2:A:1304:A:N7	2:A:1305:G:C8	2.87	0.42
2:A:1563:A:HO2'	2:A:1564:A:P	2.37	0.42
2:A:2008:A:C2	2:A:2046:A:C4'	3.02	0.42
2:A:2088:C:H3'	2:A:2089:C:C6	2.54	0.42
2:A:2357:A:H62	2:A:2380:G:H1'	1.84	0.42
2:A:2468:U:H2'	2:A:2469:U:O4'	2.19	0.42
2:A:3098:G:C2	2:A:3099:C:O2	2.72	0.42
3:B:47:A:C5	3:B:48:C:C5	3.08	0.42
18:Q:20:SER:O	18:Q:23:ASP:OD1	2.38	0.42
19:R:6:ARG:O	19:R:10:ALA:HB3	2.19	0.42
35:h:345:ALA:O	35:h:348:THR:HG22	2.19	0.42
35:h:404:ARG:CD	35:h:407:MET:HE2	2.49	0.42
2:A:97:U:OP1	2:A:98:U:O2'	2.29	0.42
2:A:800:A:C8	2:A:888:U:O4	2.72	0.42
2:A:886:G:OP1	31:d:17:ARG:CD	2.67	0.42
2:A:1127:A:O2'	19:R:62:ILE:HG21	2.19	0.42
2:A:1184:U:H2'	2:A:1186:G:H2'	2.02	0.42
2:A:1198:C:H1'	11:J:129:ILE:HD13	2.02	0.42
2:A:1675:U:O4	16:O:73:LYS:NZ	2.47	0.42
2:A:1885:G:N1	2:A:2216:G:OP2	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:2079:C:O2	2:A:2080:G:C8	2.73	0.42
2:A:2750:G:P	8:G:154:ARG:HH22	2.42	0.42
2:A:3071:A:N3	16:O:61:HIS:CE1	2.88	0.42
4:C:20:ASP:O	4:C:22:ALA:N	2.51	0.42
4:C:53:HIS:CD2	4:C:220:THR:HG22	2.54	0.42
7:F:45:MET:CG	7:F:64:LEU:HD11	2.47	0.42
9:H:97:ALA:HA	9:H:100:VAL:HG22	2.01	0.42
10:I:104:VAL:O	10:I:104:VAL:CG1	2.67	0.42
12:K:98:THR:HG1	12:K:124:VAL:HG13	1.80	0.42
28:a:6:ILE:HG12	28:a:56:VAL:HG12	2.01	0.42
35:h:250:ILE:HD12	35:h:250:ILE:HA	1.96	0.42
1:3:20:LYS:O	2:A:1103:C:O2'	2.30	0.42
2:A:392:A:C4	2:A:394:G:C8	3.07	0.42
2:A:993:G:N3	2:A:1016:C:N4	2.68	0.42
2:A:1173:G:C6	2:A:1174:G:C6	3.08	0.42
2:A:1365:G:OP2	14:M:24:ARG:NH1	2.53	0.42
2:A:1403:C:C2	2:A:1442:A:C2	3.08	0.42
2:A:1694:C:C2	2:A:1695:U:C6	3.08	0.42
2:A:1785:C:O2'	2:A:1786:G:O5'	2.28	0.42
2:A:2239:A:C6	29:b:3:VAL:HG13	2.54	0.42
2:A:2249:G:H2'	2:A:2250:A:C8	2.54	0.42
2:A:2349:A:H4'	2:A:2349:A:OP1	2.20	0.42
2:A:2527:G:C6	2:A:2538:A:C6	3.07	0.42
2:A:2541:U:C4	2:A:2542:G:C5	3.08	0.42
2:A:2717:U:C5'	35:h:207:LYS:HA	2.50	0.42
2:A:3022:G:O2'	2:A:3023:G:O5'	2.35	0.42
2:A:3067:C:OP2	18:Q:49:ARG:NH2	2.49	0.42
3:B:47:A:C4	3:B:48:C:C5	3.08	0.42
3:B:49:C:P	17:P:42:ARG:HH12	2.43	0.42
5:D:26:VAL:O	5:D:26:VAL:HG23	2.19	0.42
12:K:41:LYS:NZ	12:K:50:GLY:O	2.29	0.42
13:L:5:GLU:HA	13:L:20:LEU:HD21	2.01	0.42
13:L:112:MET:HE2	13:L:112:MET:CA	2.50	0.42
18:Q:23:ASP:OD1	18:Q:23:ASP:N	2.52	0.42
23:V:1:MET:O	23:V:2:LYS:HB2	2.19	0.42
35:h:198:VAL:HG12	35:h:202:GLY:HA2	2.01	0.42
2:A:40:G:O2'	2:A:41:A:H5'	2.20	0.41
2:A:81:A:C2	2:A:100:A:C5	3.07	0.41
2:A:240:G:O2'	2:A:257:A:N6	2.53	0.41
2:A:611:U:H2'	2:A:612:U:C6	2.55	0.41
2:A:649:U:O2	12:K:47:ASN:ND2	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:825:C:H2'	2:A:826:G:C8	2.55	0.41
2:A:865:A:OP1	2:A:1833:C:N4	2.42	0.41
2:A:993:G:C2'	2:A:1015:A:N6	2.82	0.41
2:A:1041:A:H2'	2:A:1042:A:O4'	2.19	0.41
2:A:1568:C:H2'	2:A:1569:A:C8	2.55	0.41
2:A:1623:U:HO2'	2:A:1624:U:P	2.37	0.41
2:A:2365:A:H2'	2:A:2366:C:O4'	2.20	0.41
5:D:86:LEU:H	5:D:86:LEU:HD22	1.84	0.41
12:K:141:GLU:OE1	12:K:142:ILE:N	2.47	0.41
17:P:83:ARG:O	17:P:86:GLN:HG2	2.20	0.41
21:T:54:VAL:HA	21:T:57:VAL:HG12	2.02	0.41
35:h:277:PHE:CD1	35:h:278:ALA:N	2.88	0.41
35:h:339:PRO:HG2	35:h:382:LEU:HD12	2.01	0.41
35:h:368:VAL:HG11	35:h:391:PHE:CE2	2.55	0.41
2:A:462:A:C4	2:A:463:G:C8	3.08	0.41
2:A:996:G:H2'	2:A:997:G:O4'	2.19	0.41
2:A:1211:G:C2	2:A:1217:G:O6	2.73	0.41
2:A:1739:A:C5	2:A:1740:G:C8	3.08	0.41
2:A:1878:G:C6	2:A:1879:G:N7	2.87	0.41
2:A:2121:G:H2'	2:A:2122:U:O4'	2.21	0.41
2:A:2950:C:O4'	13:L:1:MET:HE1	2.20	0.41
4:C:155:LEU:HD23	4:C:177:MET:SD	2.59	0.41
7:F:45:MET:SD	7:F:159:MET:HB3	2.60	0.41
9:H:109:GLY:N	9:H:110:PRO:HD2	2.35	0.41
11:J:133:THR:O	11:J:137:MET:HE3	2.18	0.41
24:W:50:ASN:O	24:W:53:ASP:OD1	2.38	0.41
24:W:80:THR:HA	24:W:97:LEU:HD23	2.02	0.41
24:W:126:GLN:OE1	24:W:127:ASP:N	2.53	0.41
2:A:134:A:O2'	2:A:135:G:H5'	2.20	0.41
2:A:214:G:H4'	2:A:215:A:OP1	2.20	0.41
2:A:276:G:H2'	2:A:277:U:O4'	2.19	0.41
2:A:458:G:H4'	2:A:459:A:OP2	2.20	0.41
2:A:928:U:C2	2:A:1310:G:C2	3.08	0.41
2:A:1296:G:H2'	2:A:1297:G:C8	2.54	0.41
2:A:1580:A:N6	2:A:1592:G:N2	2.68	0.41
2:A:1831:A:HO2'	31:d:6:ARG:HH11	1.59	0.41
2:A:3022:G:H2'	2:A:3023:G:C8	2.55	0.41
2:A:3057:U:C4	2:A:3104:A:N1	2.89	0.41
3:B:113:G:C2	3:B:114:A:C8	3.08	0.41
5:D:54:TYR:CG	5:D:55:GLY:N	2.88	0.41
10:I:49:TYR:CE1	10:I:80:ALA:HB2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:22:VAL:HG22	14:M:23:GLY:N	2.35	0.41
24:W:113:LEU:HD23	24:W:113:LEU:C	2.46	0.41
24:W:146:VAL:O	24:W:146:VAL:HG23	2.20	0.41
25:X:67:VAL:HG12	25:X:68:GLU:N	2.36	0.41
35:h:270:VAL:HG12	35:h:274:ASN:HD22	1.84	0.41
2:A:60:A:H4'	22:U:76:ARG:NH1	2.36	0.41
2:A:87:C:O2'	22:U:70:ARG:NH2	2.54	0.41
2:A:194:A:C6	2:A:197:C:C5	3.08	0.41
2:A:273:A:O2'	2:A:455:C:O2	2.38	0.41
2:A:899:G:H5''	4:C:227:ASN:HD21	1.84	0.41
2:A:1226:U:C4	2:A:1227:C:C4	3.07	0.41
2:A:1357:G:O2'	2:A:1358:U:H5'	2.21	0.41
2:A:1474:A:OP2	2:A:1486:G:N2	2.50	0.41
2:A:1665:U:C4	2:A:1687:G:C2	3.07	0.41
2:A:2088:C:HO2'	2:A:2089:C:P	2.38	0.41
2:A:2350:G:C4'	2:A:2351:A:OP1	2.68	0.41
2:A:2434:A:N7	2:A:2435:U:C4	2.88	0.41
2:A:2588:C:C5'	25:X:56:ASP:OD1	2.68	0.41
27:Z:29:LEU:HB2	27:Z:50:VAL:HG11	2.02	0.41
29:b:5:LYS:C	29:b:6:ARG:HG3	2.44	0.41
31:d:26:ARG:HG3	31:d:26:ARG:O	2.19	0.41
2:A:356:G:H5'	2:A:358:G:N2	2.36	0.41
2:A:771:G:H2'	2:A:772:U:O4'	2.20	0.41
2:A:898:A:O2'	2:A:900:G:OP1	2.27	0.41
2:A:1291:G:H2'	2:A:1292:U:O4'	2.21	0.41
2:A:1518:A:O2'	2:A:1692:G:O2'	1.87	0.41
2:A:1938:G:N1	2:A:1955:A:OP2	2.51	0.41
2:A:2488:C:H2'	2:A:2489:U:O4'	2.21	0.41
2:A:2717:U:H4'	35:h:207:LYS:HD3	2.02	0.41
3:B:8:C:OP1	17:P:18:ARG:NH1	2.53	0.41
3:B:34:G:C6	3:B:51:G:O6	2.74	0.41
4:C:204:ILE:HG21	4:C:206:TRP:CH2	2.55	0.41
14:M:137:ILE:HG23	14:M:138:THR:N	2.36	0.41
17:P:35:VAL:HG12	17:P:101:VAL:HG13	2.03	0.41
20:S:16:VAL:HB	20:S:99:VAL:HG21	2.02	0.41
24:W:101:GLN:OE1	24:W:102:ARG:O	2.38	0.41
35:h:169:MET:HG3	35:h:215:ILE:HG13	2.02	0.41
2:A:212:A:C2'	2:A:213:G:O5'	2.68	0.41
2:A:453:U:H5'	2:A:454:U:P	2.61	0.41
2:A:935:A:C2	2:A:936:A:C4	3.08	0.41
2:A:1077:A:C8	2:A:1079:C:C6	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1194:C:O2	11:J:94:PRO:HB2	2.21	0.41
2:A:1243:G:C6	2:A:1244:A:N6	2.88	0.41
2:A:1534:C:O2	2:A:1534:C:O4'	2.39	0.41
2:A:2016:G:OP2	4:C:271:ARG:CZ	2.69	0.41
2:A:2090:U:N3	2:A:2093:G:O2'	2.47	0.41
2:A:2646:C:H5'	2:A:2647:U:P	2.61	0.41
2:A:2649:A:H4'	2:A:2650:A:H5''	2.02	0.41
2:A:3029:U:C2	2:A:3030:A:C8	3.09	0.41
8:G:15:VAL:HG12	8:G:16:ASP:N	2.35	0.41
8:G:99:LEU:HD11	8:G:101:GLY:O	2.20	0.41
23:V:45:THR:HG21	23:V:60:VAL:HB	2.03	0.41
24:W:24:SER:OG	24:W:28:ARG:NH2	2.54	0.41
31:d:26:ARG:O	31:d:26:ARG:CG	2.68	0.41
33:f:26:ILE:HG22	33:f:27:CYS:N	2.36	0.41
35:h:46:LEU:CD2	35:h:119:ILE:HG13	2.49	0.41
35:h:169:MET:HB3	35:h:212:ARG:HG3	2.02	0.41
35:h:420:VAL:HG22	35:h:421:THR:N	2.36	0.41
1:3:3:LYS:O	1:3:7:LYS:HG3	2.20	0.41
2:A:633:A:H2'	2:A:634:C:O4'	2.21	0.41
2:A:1000:C:H3'	2:A:1001:C:H5''	2.02	0.41
2:A:1140:G:C6	2:A:1258:C:C4	3.08	0.41
2:A:1166:A:N7	2:A:1229:A:C4	2.88	0.41
2:A:1184:U:O2'	2:A:1187:A:N6	2.52	0.41
2:A:1200:U:H5''	2:A:1201:G:H5''	2.03	0.41
2:A:1563:A:O2'	2:A:1564:A:P	2.79	0.41
2:A:1564:A:N7	2:A:1565:A:C6	2.89	0.41
2:A:1597:G:H2'	2:A:1598:U:C6	2.55	0.41
2:A:1704:U:H2'	2:A:1705:C:C6	2.56	0.41
2:A:1934:G:C5	2:A:1935:C:C5	3.08	0.41
2:A:2287:C:O2'	35:h:198:VAL:N	2.54	0.41
2:A:2360:C:N3	2:A:2378:U:O4	2.53	0.41
2:A:2920:U:N3	2:A:2921:G:N7	2.68	0.41
2:A:3010:U:N3	2:A:3011:C:C5	2.88	0.41
2:A:3027:G:H2'	2:A:3028:A:O4'	2.21	0.41
8:G:122:ILE:HD11	8:G:134:VAL:HG12	2.01	0.41
11:J:114:LYS:NZ	11:J:117:ASP:OD2	2.53	0.41
13:L:2:ILE:CD1	13:L:8:LEU:HD21	2.50	0.41
17:P:103:ASP:OD1	17:P:103:ASP:C	2.62	0.41
24:W:66:ILE:CG2	24:W:77:LEU:HD11	2.51	0.41
24:W:80:THR:O	24:W:80:THR:HG23	2.19	0.41
24:W:100:VAL:CG1	24:W:137:ALA:HB2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:h:185:ARG:O	35:h:186:GLN:CB	2.69	0.41
2:A:337:U:O2	2:A:344:G:O6	2.39	0.41
2:A:598:U:O4	2:A:599:G:N1	2.54	0.41
2:A:919:A:H5'	2:A:920:G:P	2.60	0.41
2:A:962:U:H5'	2:A:963:U:OP2	2.21	0.41
2:A:974:G:C2'	2:A:975:U:OP2	2.69	0.41
2:A:1202:A:O2'	2:A:1203:A:H5'	2.20	0.41
2:A:1442:A:O2'	2:A:1443:G:H5'	2.21	0.41
2:A:1719:C:C4	2:A:1720:G:N7	2.89	0.41
2:A:2056:G:H2'	2:A:2057:G:C5'	2.50	0.41
2:A:2350:G:O2'	2:A:2351:A:O4'	2.38	0.41
2:A:2743:U:C4	2:A:2766:A:C5	3.08	0.41
5:D:184:LYS:HA	5:D:184:LYS:HD3	1.94	0.41
6:E:51:SER:OG	6:E:52:THR:N	2.54	0.41
18:Q:62:LYS:HG2	18:Q:63:GLU:N	2.36	0.41
21:T:42:ILE:HD11	29:b:25:PRO:HD2	2.02	0.41
21:T:78:VAL:O	21:T:78:VAL:CG1	2.67	0.41
22:U:43:LYS:O	22:U:47:GLU:HG3	2.21	0.41
24:W:100:VAL:HG11	24:W:137:ALA:CB	2.51	0.41
24:W:108:VAL:N	24:W:132:GLU:OE2	2.54	0.41
28:a:6:ILE:CG1	28:a:56:VAL:HG12	2.51	0.41
28:a:23:LEU:HD13	28:a:28:LEU:HD12	2.01	0.41
2:A:15:C:N3	2:A:16:G:N7	2.68	0.41
2:A:74:C:OP1	27:Z:56:ARG:NH2	2.54	0.41
2:A:187:G:C2'	2:A:188:G:OP1	2.68	0.41
2:A:450:G:C2	2:A:451:U:C4	3.09	0.41
2:A:617:U:O2	2:A:617:U:H2'	2.21	0.41
2:A:657:C:H5'	2:A:1368:A:H61	1.86	0.41
2:A:699:U:C4	2:A:714:U:O4	2.74	0.41
2:A:747:A:N6	2:A:768:G:C2'	2.84	0.41
2:A:754:C:C2	2:A:755:A:C8	3.09	0.41
2:A:1104:C:N3	2:A:1105:C:C5	2.88	0.41
2:A:1171:C:O2'	2:A:1174:G:O6	2.32	0.41
2:A:1214:A:H2'	2:A:1215:U:H4'	2.03	0.41
2:A:1226:U:C5	2:A:1227:C:C4	3.09	0.41
2:A:1272:C:H2'	2:A:1273:G:O4'	2.21	0.41
2:A:1291:G:N2	2:A:1293:G:N3	2.68	0.41
2:A:1456:G:C2	22:U:83:ILE:HG21	2.56	0.41
2:A:1545:C:H2'	2:A:1546:A:O4'	2.21	0.41
2:A:1555:A:H2'	2:A:1556:A:O4'	2.21	0.41
2:A:1642:G:C2	2:A:1643:G:N7	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1661:G:H2'	2:A:1662:C:O4'	2.21	0.41
2:A:1823:C:C5	2:A:1824:C:C4	3.09	0.41
2:A:2245:C:OP1	19:R:25:ARG:CZ	2.68	0.41
2:A:2378:U:H2'	2:A:2379:G:O5'	2.21	0.41
2:A:2545:G:H5'	2:A:2546:A:OP2	2.21	0.41
2:A:2793:G:C2	2:A:2794:G:C8	3.09	0.41
2:A:2872:G:H2'	2:A:2873:U:C6	2.56	0.41
2:A:2975:G:C1'	8:G:4:ILE:HD11	2.51	0.41
2:A:3063:A:C6	2:A:3097:G:C6	3.09	0.41
3:B:27:A:O2'	3:B:114:A:O3'	2.30	0.41
3:B:41:U:N3	3:B:45:G:OP2	2.46	0.41
3:B:78:U:O4	3:B:96:A:C2	2.74	0.41
4:C:126:LYS:N	4:C:129:ASN:OD1	2.53	0.41
4:C:245:HIS:O	4:C:246:PRO:C	2.63	0.41
8:G:103:ASN:HB3	8:G:115:LEU:HD11	2.02	0.41
13:L:66:VAL:O	13:L:66:VAL:CG1	2.69	0.41
14:M:32:THR:O	14:M:32:THR:HG22	2.20	0.41
15:N:122:ILE:CD1	15:N:129:ALA:HB3	2.51	0.41
18:Q:1:MET:N	18:Q:5:ASP:OD2	2.34	0.41
22:U:12:LEU:O	27:Z:33:ARG:HG2	2.21	0.41
29:b:8:MET:HB3	29:b:13:THR:CG2	2.51	0.41
34:g:35:VAL:HG12	34:g:36:GLU:N	2.36	0.41
2:A:276:G:C6	2:A:311:G:N1	2.89	0.41
2:A:282:A:H4'	9:H:51:ARG:CB	2.51	0.41
2:A:533:C:C2'	2:A:534:G:H5'	2.51	0.41
2:A:865:A:C2	2:A:868:C:C1'	3.05	0.41
2:A:935:A:H4'	2:A:951:G:N2	2.36	0.41
2:A:956:G:O2'	2:A:957:C:H5'	2.21	0.41
2:A:989:G:C6	2:A:1020:A:N1	2.89	0.41
2:A:1201:G:P	10:I:40:ARG:HH22	2.44	0.41
2:A:1379:G:OP2	2:A:1380:A:H2'	2.20	0.41
2:A:1596:C:OP2	2:A:1597:G:C5	2.75	0.41
2:A:1908:A:H2'	2:A:1909:C:O4'	2.21	0.41
2:A:2131:G:H3'	2:A:2132:U:H4'	2.03	0.41
2:A:2350:G:H22	2:A:2385:G:HO2'	1.63	0.41
2:A:2808:U:H2'	2:A:2809:U:H2'	2.03	0.41
2:A:2861:U:C2	2:A:3006:G:N2	2.88	0.41
2:A:2866:A:N3	2:A:2867:A:C8	2.89	0.41
2:A:2975:G:N7	8:G:3:ARG:NH2	2.68	0.41
2:A:3085:G:H2'	2:A:3086:U:C6	2.56	0.41
15:N:118:LEU:CD2	15:N:131:ILE:HG23	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:66:VAL:O	16:O:70:ILE:HG22	2.21	0.41
17:P:48:HIS:CE1	17:P:64:SER:HG	2.27	0.41
2:A:1314:C:H2'	2:A:1315:C:H6	1.85	0.40
2:A:1336:A:OP1	20:S:91:ARG:NH2	2.53	0.40
2:A:1415:A:H4'	2:A:1416:A:H5''	2.04	0.40
2:A:1551:U:HO2'	2:A:1552:A:P	2.37	0.40
2:A:1620:U:H3'	2:A:1621:C:C5	2.56	0.40
2:A:1633:U:H3'	2:A:1633:U:H6	1.87	0.40
2:A:1831:A:C2	2:A:1837:G:C6	3.09	0.40
2:A:2231:U:C2	2:A:2232:C:C5	3.09	0.40
2:A:2394:A:HO2'	2:A:2396:A:P	2.32	0.40
2:A:2691:C:O2'	2:A:2692:A:H5'	2.21	0.40
2:A:2931:G:H2'	2:A:2932:G:O4'	2.20	0.40
3:B:115:A:C6	3:B:116:C:C4	3.09	0.40
4:C:80:ALA:HB2	4:C:96:HIS:CD2	2.55	0.40
17:P:37:ARG:NE	17:P:54:ASP:OD2	2.52	0.40
17:P:118:ASP:O	17:P:122:GLU:CD	2.65	0.40
18:Q:15:ASP:OD1	18:Q:15:ASP:C	2.63	0.40
18:Q:70:GLU:OE2	18:Q:100:ARG:NE	2.48	0.40
35:h:81:VAL:O	35:h:81:VAL:HG13	2.21	0.40
2:A:158:G:OP2	9:H:123:HIS:NE2	2.55	0.40
2:A:278:A:H2'	2:A:279:U:O4'	2.22	0.40
2:A:357:U:H1'	2:A:358:G:OP2	2.20	0.40
2:A:458:G:O2'	2:A:512:G:OP1	2.39	0.40
2:A:663:A:N3	2:A:663:A:H2'	2.37	0.40
2:A:869:U:C2'	2:A:870:G:H5'	2.51	0.40
2:A:899:G:C8	4:C:227:ASN:ND2	2.89	0.40
2:A:1120:G:O6	2:A:1273:G:N2	2.55	0.40
2:A:1178:U:C2	2:A:1180:G:C4'	3.04	0.40
2:A:1225:G:C4	2:A:1226:U:C5	3.09	0.40
2:A:1298:C:H2'	2:A:1299:U:O4'	2.21	0.40
2:A:1739:A:C4	2:A:1740:G:C8	3.09	0.40
2:A:2024:G:C2	2:A:2026:A:OP2	2.74	0.40
2:A:3097:G:N1	2:A:3098:G:C6	2.89	0.40
7:F:15:TYR:OH	7:F:20:ARG:NH1	2.54	0.40
9:H:72:LEU:O	9:H:75:LEU:HB2	2.21	0.40
10:I:104:VAL:O	10:I:104:VAL:HG13	2.21	0.40
14:M:51:GLU:OE1	32:e:57:ARG:NH2	2.54	0.40
17:P:6:VAL:HG23	17:P:7:GLY:N	2.37	0.40
17:P:101:VAL:O	17:P:101:VAL:HG23	2.20	0.40
24:W:28:ARG:HE	24:W:93:GLN:HA	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:h:124:LEU:HD21	35:h:129:LEU:HD13	2.04	0.40
2:A:187:G:C3'	2:A:188:G:H5''	2.51	0.40
2:A:213:G:O2'	2:A:214:G:O4'	2.36	0.40
2:A:245:G:H21	2:A:472:C:HO2'	1.66	0.40
2:A:294:G:C5	2:A:295:U:C5	3.09	0.40
2:A:644:G:C5	2:A:645:G:N7	2.90	0.40
2:A:1161:C:C4	2:A:1162:G:N7	2.89	0.40
2:A:1493:A:O2'	2:A:1494:U:O5'	2.35	0.40
2:A:1554:U:O2'	2:A:1555:A:O4'	2.39	0.40
2:A:1870:U:C5	16:O:8:PRO:HG2	2.56	0.40
2:A:2092:U:O3'	2:A:2093:G:H4'	2.22	0.40
2:A:3012:U:C2'	2:A:3013:C:O5'	2.70	0.40
2:A:3012:U:H2'	2:A:3013:C:O5'	2.21	0.40
4:C:79:VAL:CG1	4:C:111:LEU:HD21	2.47	0.40
6:E:97:ASP:OD1	6:E:98:TYR:N	2.55	0.40
14:M:39:GLY:H	14:M:42:ALA:HB3	1.87	0.40
15:N:118:LEU:HD23	15:N:131:ILE:HG23	2.03	0.40
20:S:65:LEU:H	20:S:65:LEU:HD12	1.87	0.40
24:W:71:ILE:O	24:W:71:ILE:HG13	2.21	0.40
2:A:10:A:C2	2:A:613:A:N7	2.89	0.40
2:A:319:G:O6	2:A:492:C:O2'	2.37	0.40
2:A:327:U:C2'	2:A:328:C:O4'	2.68	0.40
2:A:363:A:HO2'	2:A:364:A:P	2.44	0.40
2:A:598:U:H2'	2:A:599:G:H5'	2.03	0.40
2:A:630:U:O2'	2:A:631:C:H5'	2.22	0.40
2:A:875:G:H2'	2:A:876:A:O4'	2.21	0.40
2:A:973:G:N3	2:A:2492:A:H2'	2.37	0.40
2:A:1180:G:N2	11:J:94:PRO:HG2	2.36	0.40
2:A:1203:A:H2'	2:A:1204:A:C4	2.56	0.40
2:A:1536:A:H2'	2:A:1537:U:C6	2.56	0.40
2:A:1694:C:C4	2:A:1695:U:C5	3.09	0.40
2:A:2159:G:H3'	2:A:2160:A:H5''	2.04	0.40
2:A:2364:C:N4	2:A:2367:G:H22	2.19	0.40
2:A:3032:G:OP1	5:D:63:ILE:CD1	2.70	0.40
2:A:3058:A:N6	2:A:3103:A:N6	2.69	0.40
2:A:3063:A:C6	2:A:3097:G:O6	2.75	0.40
3:B:30:G:O2'	3:B:59:A:N1	2.44	0.40
10:I:27:GLU:HA	10:I:76:PRO:O	2.22	0.40
12:K:102:GLU:OE1	12:K:124:VAL:CG1	2.69	0.40
35:h:148:LEU:HD22	35:h:311:LEU:HD11	2.03	0.40
35:h:328:LEU:HD12	35:h:364:GLU:OE1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:137:G:N2	2:A:1524:G:H1'	2.32	0.40
2:A:450:G:H2'	2:A:451:U:C5	2.57	0.40
2:A:682:A:O2'	2:A:683:G:H5'	2.21	0.40
2:A:731:A:N1	2:A:745:G:O2'	2.52	0.40
2:A:826:G:C6	2:A:836:G:C6	3.10	0.40
2:A:881:C:C2	2:A:882:U:C6	3.10	0.40
2:A:975:U:C5	2:A:1031:G:N2	2.89	0.40
2:A:1549:G:HO2'	2:A:1550:G:P	2.41	0.40
2:A:1554:U:HO2'	2:A:1555:A:C5'	2.31	0.40
2:A:1558:C:H2'	2:A:1559:A:C8	2.57	0.40
2:A:1560:U:C2	2:A:1561:C:C5	3.10	0.40
2:A:1604:G:C5	2:A:1605:G:O6	2.74	0.40
2:A:1758:G:H2'	2:A:1759:A:C8	2.57	0.40
2:A:2167:U:O2	2:A:2187:U:N3	2.55	0.40
2:A:2221:A:O2'	2:A:2222:A:H5'	2.22	0.40
2:A:2676:C:C5'	35:h:203:PRO:HA	2.51	0.40
2:A:2926:A:C2	2:A:2927:C:C6	3.10	0.40
4:C:73:ASP:OD1	4:C:120:GLY:HA2	2.21	0.40
7:F:159:MET:N	7:F:159:MET:SD	2.95	0.40
9:H:131:PRO:O	9:H:132:VAL:C	2.65	0.40
10:I:22:ALA:O	10:I:82:VAL:HG12	2.20	0.40
15:N:119:THR:HA	15:N:122:ILE:CG2	2.52	0.40
24:W:75:GLU:OE1	24:W:76:GLN:N	2.52	0.40
34:g:12:THR:HG22	34:g:26:SER:HB3	2.04	0.40
35:h:296:VAL:O	35:h:296:VAL:HG23	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	3	21/24 (88%)	18 (86%)	3 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	C	273/278 (98%)	244 (89%)	29 (11%)	0	100	100
5	D	212/217 (98%)	188 (89%)	24 (11%)	0	100	100
6	E	207/215 (96%)	195 (94%)	12 (6%)	0	100	100
7	F	180/187 (96%)	172 (96%)	8 (4%)	0	100	100
8	G	174/179 (97%)	170 (98%)	4 (2%)	0	100	100
9	H	149/151 (99%)	137 (92%)	12 (8%)	0	100	100
10	I	124/175 (71%)	122 (98%)	2 (2%)	0	100	100
11	J	131/142 (92%)	122 (93%)	9 (7%)	0	100	100
12	K	144/147 (98%)	135 (94%)	9 (6%)	0	100	100
13	L	120/122 (98%)	111 (92%)	9 (8%)	0	100	100
14	M	143/147 (97%)	134 (94%)	9 (6%)	0	100	100
15	N	134/138 (97%)	127 (95%)	7 (5%)	0	100	100
16	O	116/199 (58%)	108 (93%)	8 (7%)	0	100	100
17	P	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
18	Q	111/113 (98%)	104 (94%)	7 (6%)	0	100	100
19	R	122/129 (95%)	116 (95%)	6 (5%)	0	100	100
20	S	98/103 (95%)	93 (95%)	5 (5%)	0	100	100
21	T	112/153 (73%)	105 (94%)	7 (6%)	0	100	100
22	U	95/100 (95%)	91 (96%)	4 (4%)	0	100	100
23	V	93/105 (89%)	92 (99%)	1 (1%)	0	100	100
24	W	190/215 (88%)	185 (97%)	5 (3%)	0	100	100
25	X	77/88 (88%)	70 (91%)	7 (9%)	0	100	100
26	Y	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
27	Z	62/77 (80%)	62 (100%)	0	0	100	100
28	a	57/61 (93%)	56 (98%)	1 (2%)	0	100	100
29	b	52/57 (91%)	49 (94%)	3 (6%)	0	100	100
30	c	46/55 (84%)	44 (96%)	2 (4%)	0	100	100
31	d	44/47 (94%)	39 (89%)	5 (11%)	0	100	100
32	e	61/64 (95%)	61 (100%)	0	0	100	100
33	f	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
34	g	46/75 (61%)	45 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	h	428/483 (89%)	388 (91%)	40 (9%)	0	100	100
All	All	4042/4474 (90%)	3786 (94%)	256 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	3	18/19 (95%)	18 (100%)	0	100	100
4	C	215/218 (99%)	215 (100%)	0	100	100
5	D	160/163 (98%)	160 (100%)	0	100	100
6	E	169/173 (98%)	169 (100%)	0	100	100
7	F	151/156 (97%)	151 (100%)	0	100	100
8	G	148/150 (99%)	147 (99%)	1 (1%)	76	80
9	H	90/116 (78%)	90 (100%)	0	100	100
10	I	89/120 (74%)	88 (99%)	1 (1%)	65	76
11	J	102/108 (94%)	102 (100%)	0	100	100
12	K	119/120 (99%)	119 (100%)	0	100	100
13	L	100/100 (100%)	100 (100%)	0	100	100
14	M	112/114 (98%)	111 (99%)	1 (1%)	70	78
15	N	114/116 (98%)	114 (100%)	0	100	100
16	O	97/158 (61%)	97 (100%)	0	100	100
17	P	93/94 (99%)	93 (100%)	0	100	100
18	Q	100/100 (100%)	100 (100%)	0	100	100
19	R	97/99 (98%)	97 (100%)	0	100	100
20	S	81/83 (98%)	81 (100%)	0	100	100
21	T	90/117 (77%)	90 (100%)	0	100	100
22	U	83/85 (98%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	V	81/86 (94%)	81 (100%)	0	100	100
24	W	155/168 (92%)	155 (100%)	0	100	100
25	X	58/63 (92%)	58 (100%)	0	100	100
26	Y	50/51 (98%)	50 (100%)	0	100	100
27	Z	58/66 (88%)	58 (100%)	0	100	100
28	a	52/54 (96%)	52 (100%)	0	100	100
29	b	43/46 (94%)	39 (91%)	4 (9%)	8	30
30	c	46/52 (88%)	46 (100%)	0	100	100
31	d	35/36 (97%)	35 (100%)	0	100	100
32	e	53/54 (98%)	53 (100%)	0	100	100
33	f	35/35 (100%)	35 (100%)	0	100	100
34	g	43/63 (68%)	43 (100%)	0	100	100
35	h	339/382 (89%)	326 (96%)	13 (4%)	29	57
All	All	3276/3565 (92%)	3256 (99%)	20 (1%)	76	81

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	G	20	ASN
10	I	110	MET
14	M	135	GLU
29	b	6	ARG
29	b	8	MET
29	b	9	SER
29	b	32	VAL
35	h	49	VAL
35	h	198	VAL
35	h	201	ARG
35	h	208	ILE
35	h	210	THR
35	h	211	ASP
35	h	212	ARG
35	h	213	ARG
35	h	217	GLU
35	h	218	ARG
35	h	258	LYS
35	h	270	VAL
35	h	307	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
4	C	201	GLN
4	C	227	ASN
5	D	34	ASN
8	G	66	HIS
9	H	130	HIS
10	I	100	ASN
11	J	36	ASN
11	J	119	ASN
14	M	45	ASN
16	O	17	GLN
17	P	3	HIS
18	Q	9	GLN
18	Q	28	HIS
18	Q	76	HIS
20	S	85	HIS
22	U	27	ASN
24	W	61	HIS
24	W	129	ASN
25	X	44	HIS
29	b	36	GLN
30	c	20	HIS
30	c	44	ASN
30	c	51	HIS
32	e	25	GLN
34	g	6	HIS
35	h	274	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	A	3109/3120 (99%)	669 (21%)	54 (1%)
3	B	117/118 (99%)	14 (11%)	1 (0%)
All	All	3226/3238 (99%)	683 (21%)	55 (1%)

All (683) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	A	9	U
2	A	12	G
2	A	16	G

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Mol	Chain	Res	Type
2	A	19	U
2	A	20	G
2	A	32	G
2	A	46	A
2	A	58	G
2	A	60	A
2	A	68	A
2	A	71	A
2	A	72	G
2	A	82	G
2	A	89	A
2	A	90	C
2	A	94	G
2	A	99	G
2	A	115	A
2	A	116	A
2	A	117	U
2	A	125	C
2	A	126	C
2	A	128	G
2	A	137	G
2	A	143	G
2	A	148	A
2	A	161	U
2	A	164	A
2	A	169	C
2	A	175	G
2	A	176	G
2	A	180	A
2	A	188	G
2	A	195	A
2	A	198	A
2	A	200	C
2	A	212	A
2	A	214	G
2	A	215	A
2	A	221	A
2	A	227	A
2	A	229	U
2	A	231	U
2	A	233	A
2	A	238	G

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Mol	Chain	Res	Type
2	A	243	U
2	A	248	G
2	A	265	A
2	A	266	U
2	A	274	C
2	A	282	A
2	A	285	U
2	A	286	G
2	A	287	A
2	A	288	U
2	A	289	A
2	A	292	G
2	A	297	G
2	A	300	G
2	A	301	U
2	A	302	U
2	A	303	G
2	A	314	G
2	A	315	U
2	A	317	G
2	A	318	U
2	A	319	G
2	A	322	A
2	A	323	C
2	A	324	C
2	A	326	A
2	A	327	U
2	A	329	U
2	A	330	U
2	A	336	C
2	A	337	U
2	A	345	G
2	A	351	G
2	A	352	G
2	A	357	U
2	A	358	G
2	A	361	A
2	A	364	A
2	A	366	G
2	A	369	G
2	A	370	U
2	A	384	G

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Mol	Chain	Res	Type
2	A	393	U
2	A	399	G
2	A	412	A
2	A	413	G
2	A	415	G
2	A	428	A
2	A	434	G
2	A	437	G
2	A	444	U
2	A	445	U
2	A	446	G
2	A	447	A
2	A	448	U
2	A	450	G
2	A	451	U
2	A	452	G
2	A	454	U
2	A	460	G
2	A	472	C
2	A	474	G
2	A	476	G
2	A	489	A
2	A	491	U
2	A	493	U
2	A	494	G
2	A	498	G
2	A	499	G
2	A	500	A
2	A	505	C
2	A	512	G
2	A	543	U
2	A	544	U
2	A	562	G
2	A	566	A
2	A	567	A
2	A	568	A
2	A	569	G
2	A	578	G
2	A	589	A
2	A	591	G
2	A	592	A
2	A	594	U

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Mol	Chain	Res	Type
2	A	595	A
2	A	596	C
2	A	597	C
2	A	605	G
2	A	617	U
2	A	618	C
2	A	619	C
2	A	620	G
2	A	623	A
2	A	631	C
2	A	632	G
2	A	635	G
2	A	636	U
2	A	637	G
2	A	638	U
2	A	639	C
2	A	640	G
2	A	642	G
2	A	644	G
2	A	647	G
2	A	648	A
2	A	649	U
2	A	655	G
2	A	658	U
2	A	665	G
2	A	667	A
2	A	676	C
2	A	679	G
2	A	684	G
2	A	685	G
2	A	696	A
2	A	706	G
2	A	707	G
2	A	708	G
2	A	709	U
2	A	721	A
2	A	726	A
2	A	731	A
2	A	739	U
2	A	740	A
2	A	741	G
2	A	755	A

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Mol	Chain	Res	Type
2	A	760	U
2	A	765	G
2	A	766	G
2	A	768	G
2	A	793	C
2	A	794	G
2	A	801	U
2	A	832	G
2	A	839	U
2	A	841	G
2	A	845	C
2	A	862	U
2	A	863	G
2	A	870	G
2	A	871	A
2	A	872	G
2	A	878	G
2	A	879	A
2	A	880	G
2	A	890	G
2	A	891	G
2	A	897	A
2	A	899	G
2	A	900	G
2	A	917	A
2	A	920	G
2	A	927	C
2	A	942	U
2	A	960	G
2	A	961	U
2	A	973	G
2	A	974	G
2	A	975	U
2	A	981	U
2	A	982	A
2	A	994	A
2	A	1001	C
2	A	1002	C
2	A	1003	A
2	A	1004	C
2	A	1005	A
2	A	1011	A

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Mol	Chain	Res	Type
2	A	1012	C
2	A	1014	G
2	A	1025	A
2	A	1034	U
2	A	1044	U
2	A	1047	A
2	A	1048	A
2	A	1049	G
2	A	1063	G
2	A	1069	G
2	A	1075	U
2	A	1076	A
2	A	1078	G
2	A	1085	G
2	A	1092	G
2	A	1099	A
2	A	1101	A
2	A	1108	A
2	A	1114	G
2	A	1124	C
2	A	1130	C
2	A	1131	G
2	A	1140	G
2	A	1144	A
2	A	1151	U
2	A	1152	G
2	A	1164	A
2	A	1165	G
2	A	1166	A
2	A	1171	C
2	A	1175	A
2	A	1178	U
2	A	1179	U
2	A	1181	G
2	A	1184	U
2	A	1186	G
2	A	1187	A
2	A	1188	A
2	A	1190	C
2	A	1191	A
2	A	1192	G
2	A	1196	C

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Mol	Chain	Res	Type
2	A	1197	C
2	A	1200	U
2	A	1201	G
2	A	1202	A
2	A	1203	A
2	A	1205	G
2	A	1209	G
2	A	1212	U
2	A	1213	A
2	A	1215	U
2	A	1220	C
2	A	1223	U
2	A	1224	G
2	A	1230	G
2	A	1237	U
2	A	1244	A
2	A	1247	A
2	A	1250	U
2	A	1251	A
2	A	1253	C
2	A	1254	G
2	A	1260	C
2	A	1261	A
2	A	1262	A
2	A	1293	G
2	A	1320	U
2	A	1335	G
2	A	1344	A
2	A	1353	G
2	A	1364	U
2	A	1365	G
2	A	1368	A
2	A	1371	G
2	A	1379	G
2	A	1380	A
2	A	1384	G
2	A	1386	G
2	A	1387	A
2	A	1389	U
2	A	1415	A
2	A	1416	A
2	A	1417	A

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Mol	Chain	Res	Type
2	A	1436	C
2	A	1440	C
2	A	1444	U
2	A	1448	C
2	A	1456	G
2	A	1465	C
2	A	1467	U
2	A	1474	A
2	A	1480	A
2	A	1493	A
2	A	1494	U
2	A	1499	A
2	A	1500	A
2	A	1501	C
2	A	1507	G
2	A	1508	A
2	A	1509	U
2	A	1510	A
2	A	1511	U
2	A	1522	G
2	A	1529	U
2	A	1531	C
2	A	1532	G
2	A	1533	U
2	A	1534	C
2	A	1535	C
2	A	1536	A
2	A	1538	G
2	A	1539	A
2	A	1540	U
2	A	1541	G
2	A	1545	C
2	A	1548	C
2	A	1550	G
2	A	1552	A
2	A	1553	C
2	A	1554	U
2	A	1555	A
2	A	1564	A
2	A	1565	A
2	A	1566	A
2	A	1572	G

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Mol	Chain	Res	Type
2	A	1574	G
2	A	1575	A
2	A	1578	G
2	A	1579	C
2	A	1584	U
2	A	1594	G
2	A	1598	U
2	A	1599	U
2	A	1604	G
2	A	1609	G
2	A	1610	C
2	A	1619	U
2	A	1624	U
2	A	1625	G
2	A	1628	A
2	A	1629	G
2	A	1631	A
2	A	1632	G
2	A	1633	U
2	A	1635	A
2	A	1639	G
2	A	1640	A
2	A	1641	U
2	A	1649	C
2	A	1670	G
2	A	1678	U
2	A	1679	A
2	A	1680	A
2	A	1681	U
2	A	1688	G
2	A	1703	G
2	A	1713	U
2	A	1716	A
2	A	1717	U
2	A	1723	U
2	A	1724	G
2	A	1727	A
2	A	1728	U
2	A	1729	A
2	A	1730	U
2	A	1731	A
2	A	1737	A

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Mol	Chain	Res	Type
2	A	1738	G
2	A	1753	C
2	A	1754	G
2	A	1756	G
2	A	1757	U
2	A	1758	G
2	A	1787	A
2	A	1789	A
2	A	1798	U
2	A	1802	G
2	A	1803	A
2	A	1825	C
2	A	1826	A
2	A	1834	A
2	A	1845	G
2	A	1864	U
2	A	1866	C
2	A	1867	G
2	A	1871	G
2	A	1872	A
2	A	1892	G
2	A	1895	A
2	A	1903	C
2	A	1933	G
2	A	1947	U
2	A	1949	C
2	A	1950	G
2	A	1973	C
2	A	1975	A
2	A	1981	U
2	A	1990	A
2	A	1999	U
2	A	2001	A
2	A	2008	A
2	A	2017	C
2	A	2018	G
2	A	2026	A
2	A	2031	G
2	A	2033	U
2	A	2036	A
2	A	2043	C
2	A	2052	G

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Mol	Chain	Res	Type
2	A	2055	C
2	A	2056	G
2	A	2057	G
2	A	2062	G
2	A	2064	A
2	A	2083	A
2	A	2086	U
2	A	2087	C
2	A	2088	C
2	A	2089	C
2	A	2092	U
2	A	2093	G
2	A	2095	G
2	A	2096	G
2	A	2097	G
2	A	2099	G
2	A	2106	A
2	A	2107	G
2	A	2112	U
2	A	2113	A
2	A	2125	A
2	A	2129	C
2	A	2130	G
2	A	2131	G
2	A	2132	U
2	A	2133	G
2	A	2134	G
2	A	2135	U
2	A	2136	A
2	A	2146	A
2	A	2148	C
2	A	2149	C
2	A	2150	U
2	A	2151	A
2	A	2152	A
2	A	2153	G
2	A	2154	G
2	A	2155	U
2	A	2156	A
2	A	2159	G
2	A	2160	A
2	A	2161	A

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Mol	Chain	Res	Type
2	A	2163	U
2	A	2164	U
2	A	2165	C
2	A	2166	C
2	A	2167	U
2	A	2168	U
2	A	2169	G
2	A	2171	C
2	A	2172	G
2	A	2173	G
2	A	2174	G
2	A	2175	U
2	A	2179	U
2	A	2181	C
2	A	2184	A
2	A	2186	C
2	A	2187	U
2	A	2188	G
2	A	2189	C
2	A	2190	A
2	A	2191	C
2	A	2192	G
2	A	2193	A
2	A	2194	A
2	A	2195	U
2	A	2196	G
2	A	2215	U
2	A	2217	U
2	A	2220	C
2	A	2221	A
2	A	2244	A
2	A	2246	U
2	A	2250	A
2	A	2255	A
2	A	2256	G
2	A	2257	A
2	A	2263	G
2	A	2267	C
2	A	2279	C
2	A	2280	G
2	A	2282	A
2	A	2284	A

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Mol	Chain	Res	Type
2	A	2285	G
2	A	2286	A
2	A	2315	U
2	A	2316	G
2	A	2320	C
2	A	2325	U
2	A	2329	G
2	A	2330	U
2	A	2332	U
2	A	2333	G
2	A	2334	U
2	A	2335	G
2	A	2338	G
2	A	2339	G
2	A	2342	A
2	A	2343	G
2	A	2345	U
2	A	2349	A
2	A	2350	G
2	A	2351	A
2	A	2353	U
2	A	2355	U
2	A	2356	G
2	A	2357	A
2	A	2361	U
2	A	2367	G
2	A	2368	C
2	A	2370	A
2	A	2372	U
2	A	2375	G
2	A	2379	G
2	A	2380	G
2	A	2382	G
2	A	2384	C
2	A	2386	U
2	A	2387	U
2	A	2388	G
2	A	2389	U
2	A	2390	U
2	A	2392	A
2	A	2393	A
2	A	2394	A

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Mol	Chain	Res	Type
2	A	2395	U
2	A	2396	A
2	A	2401	U
2	A	2402	C
2	A	2404	G
2	A	2407	C
2	A	2421	A
2	A	2427	G
2	A	2430	C
2	A	2433	U
2	A	2434	A
2	A	2436	A
2	A	2447	G
2	A	2449	A
2	A	2458	G
2	A	2462	G
2	A	2463	G
2	A	2467	U
2	A	2491	A
2	A	2503	G
2	A	2504	G
2	A	2507	C
2	A	2511	A
2	A	2512	A
2	A	2529	A
2	A	2532	G
2	A	2533	C
2	A	2543	U
2	A	2544	U
2	A	2545	G
2	A	2548	U
2	A	2558	C
2	A	2559	A
2	A	2568	U
2	A	2569	G
2	A	2571	C
2	A	2574	C
2	A	2582	A
2	A	2601	A
2	A	2607	G
2	A	2609	A
2	A	2626	U

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Mol	Chain	Res	Type
2	A	2627	C
2	A	2647	U
2	A	2649	A
2	A	2650	A
2	A	2652	G
2	A	2653	G
2	A	2654	A
2	A	2655	U
2	A	2665	C
2	A	2672	A
2	A	2673	U
2	A	2683	A
2	A	2693	A
2	A	2694	G
2	A	2699	C
2	A	2700	A
2	A	2704	C
2	A	2715	U
2	A	2726	G
2	A	2727	A
2	A	2729	G
2	A	2731	C
2	A	2742	A
2	A	2744	C
2	A	2752	U
2	A	2753	G
2	A	2755	A
2	A	2778	U
2	A	2790	A
2	A	2791	G
2	A	2796	A
2	A	2797	C
2	A	2825	C
2	A	2826	A
2	A	2827	G
2	A	2833	U
2	A	2837	U
2	A	2839	U
2	A	2862	G
2	A	2876	C
2	A	2878	A
2	A	2913	U

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Mol	Chain	Res	Type
2	A	2915	C
2	A	2926	A
2	A	2927	C
2	A	2936	C
2	A	2938	G
2	A	2942	G
2	A	2950	C
2	A	2957	A
2	A	2963	U
2	A	2968	G
2	A	2972	A
2	A	2985	G
2	A	2989	A
2	A	3002	A
2	A	3013	C
2	A	3014	A
2	A	3015	C
2	A	3020	U
2	A	3021	A
2	A	3022	G
2	A	3023	G
2	A	3038	C
2	A	3042	A
2	A	3054	U
2	A	3055	G
2	A	3082	U
2	A	3087	G
2	A	3088	C
2	A	3093	A
2	A	3095	C
2	A	3100	A
2	A	3101	C
2	A	3105	C
2	A	3106	C
2	A	3108	G
2	A	3112	A
3	B	4	A
3	B	7	G
3	B	11	U
3	B	13	C
3	B	24	G
3	B	25	G

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Mol	Chain	Res	Type
3	B	31	C
3	B	42	C
3	B	85	C
3	B	87	U
3	B	89	C
3	B	90	G
3	B	103	G
3	B	107	A

All (55) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	A	89	A
2	A	187	G
2	A	322	A
2	A	335	G
2	A	336	C
2	A	351	G
2	A	357	U
2	A	363	A
2	A	445	U
2	A	449	G
2	A	451	U
2	A	453	U
2	A	567	A
2	A	636	U
2	A	919	A
2	A	974	G
2	A	981	U
2	A	1002	C
2	A	1004	C
2	A	1046	C
2	A	1077	A
2	A	1186	G
2	A	1199	U
2	A	1200	U
2	A	1204	A
2	A	1253	C
2	A	1473	G
2	A	1531	C
2	A	1533	U
2	A	1537	U

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Mol	Chain	Res	Type
2	A	1538	G
2	A	1539	A
2	A	1551	U
2	A	1554	U
2	A	1565	A
2	A	1578	G
2	A	1628	A
2	A	1730	U
2	A	1753	C
2	A	2088	C
2	A	2094	G
2	A	2095	G
2	A	2112	U
2	A	2129	C
2	A	2130	G
2	A	2163	U
2	A	2166	C
2	A	2171	C
2	A	2342	A
2	A	2350	G
2	A	2381	A
2	A	2435	U
2	A	2693	A
2	A	2698	C
3	B	10	G

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](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	GNP	h	501	-	34,34,34	1.35	5 (14%)	47,54,54	0.94	1 (2%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
36	GNP	h	501	-	-	9/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	h	501	GNP	PB-O3A	4.82	1.65	1.59
36	h	501	GNP	PB-O1B	3.24	1.51	1.46
36	h	501	GNP	PG-N3B	3.02	1.71	1.63
36	h	501	GNP	PG-O1G	2.79	1.50	1.46
36	h	501	GNP	PB-O2B	-2.19	1.51	1.56

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	h	501	GNP	O4'-C4'-C3'	-2.00	101.18	105.15

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	h	501	GNP	PB-N3B-PG-O1G
36	h	501	GNP	PG-N3B-PB-O1B
36	h	501	GNP	C5'-O5'-PA-O3A
36	h	501	GNP	C5'-O5'-PA-O2A
36	h	501	GNP	C3'-C4'-C5'-O5'
36	h	501	GNP	C4'-C5'-O5'-PA
36	h	501	GNP	O4'-C4'-C5'-O5'
36	h	501	GNP	PB-O3A-PA-O5'

Continued on next page...

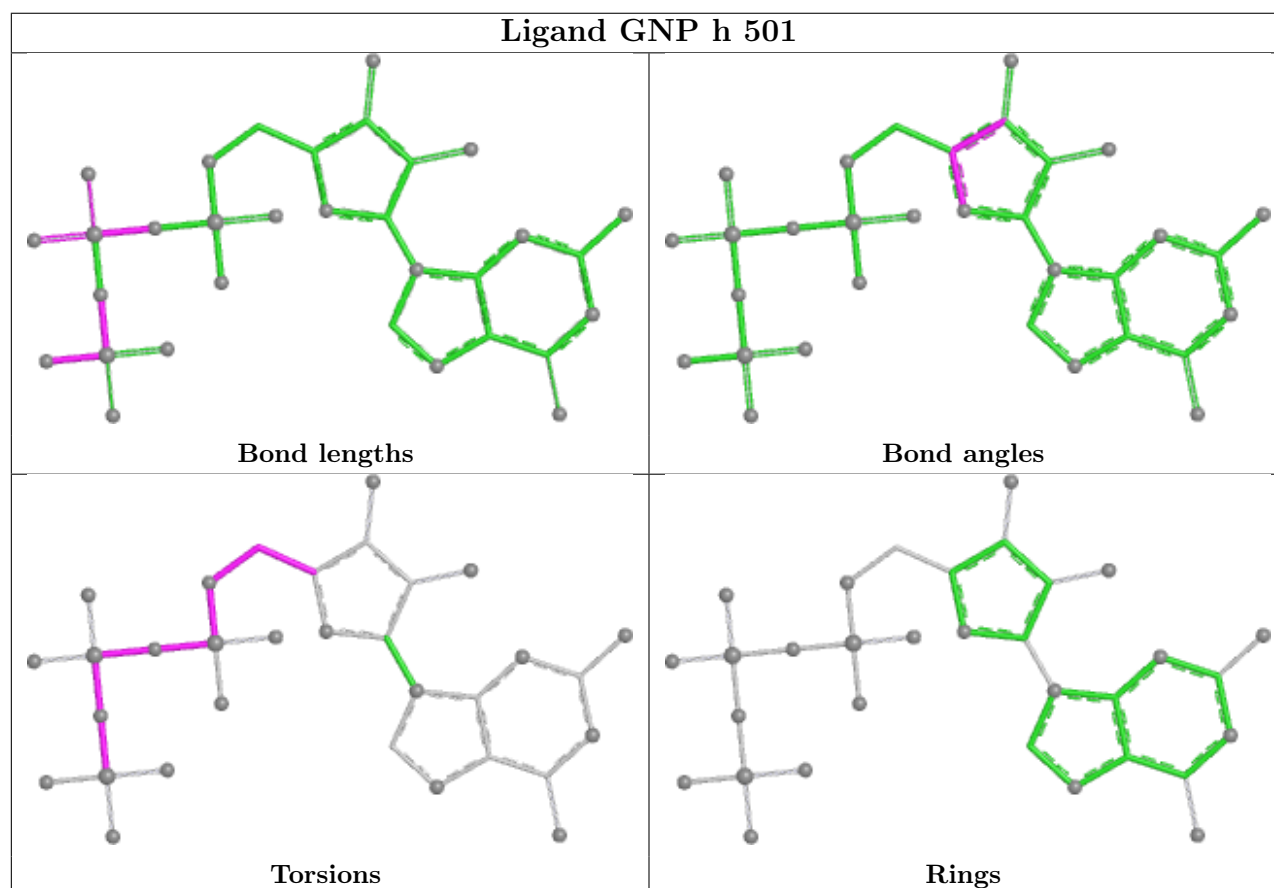
Continued from previous page...

Mol	Chain	Res	Type	Atoms
36	h	501	GNP	PA-O3A-PB-O1B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

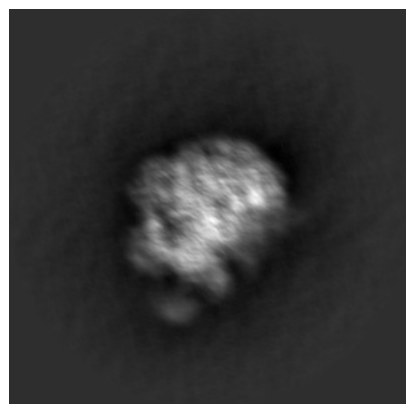
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37007. These allow visual inspection of the internal detail of the map and identification of artifacts.

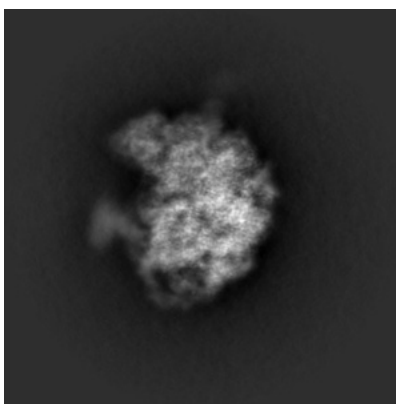
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

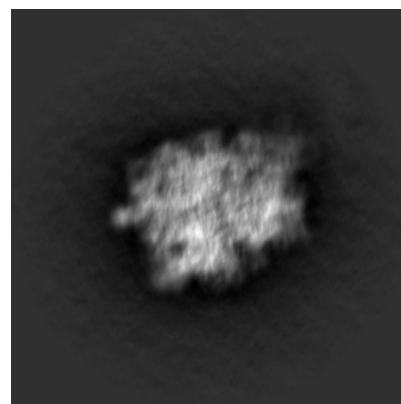
6.1.1 Primary map



X

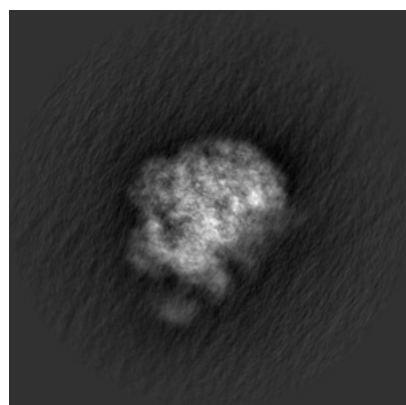


Y

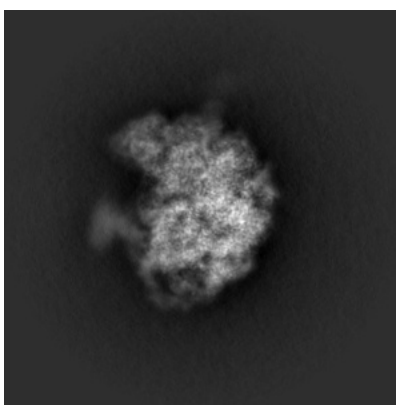


Z

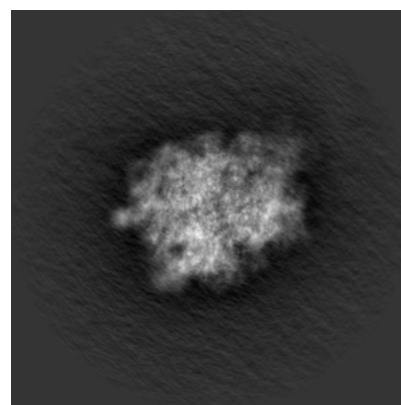
6.1.2 Raw map



X



Y

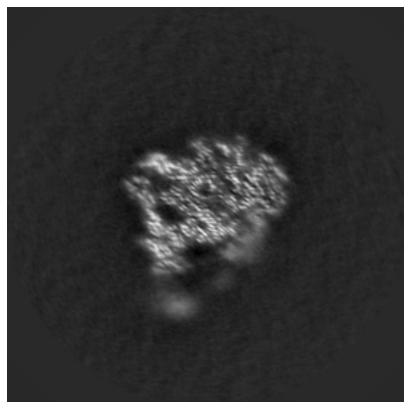


Z

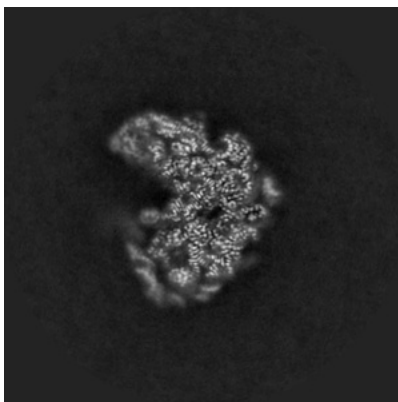
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

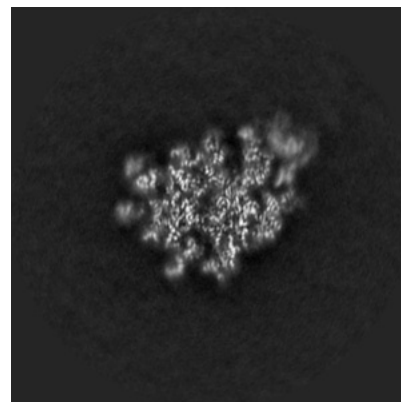
6.2.1 Primary map



X Index: 210

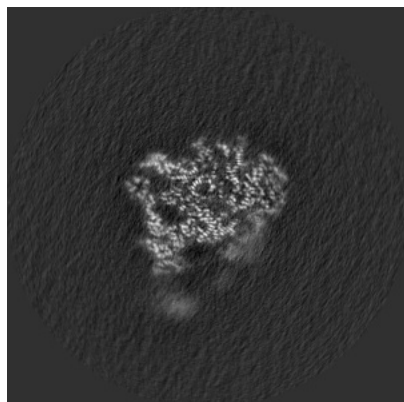


Y Index: 210

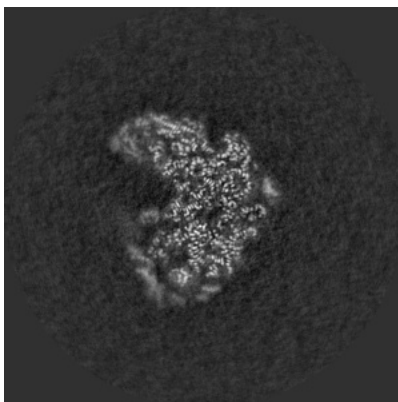


Z Index: 210

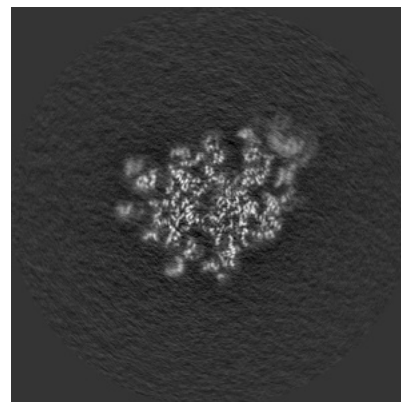
6.2.2 Raw map



X Index: 210



Y Index: 210

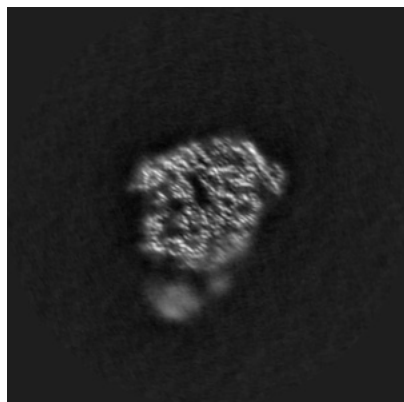


Z Index: 210

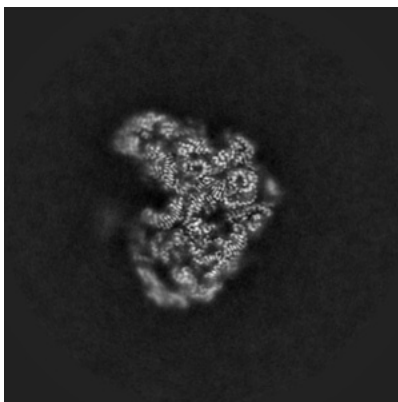
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

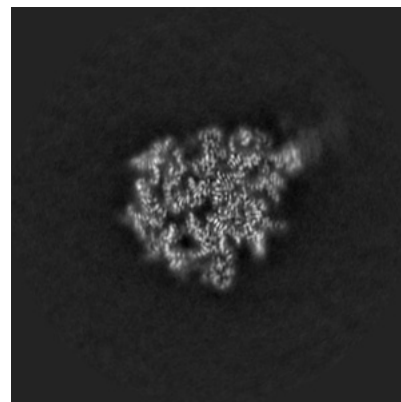
6.3.1 Primary map



X Index: 197

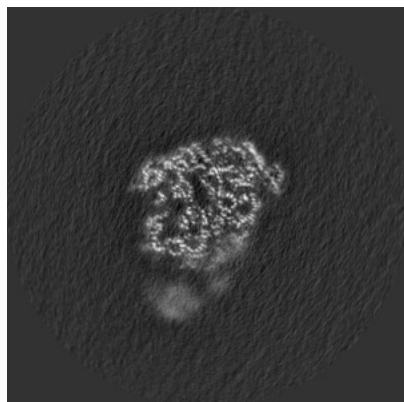


Y Index: 205

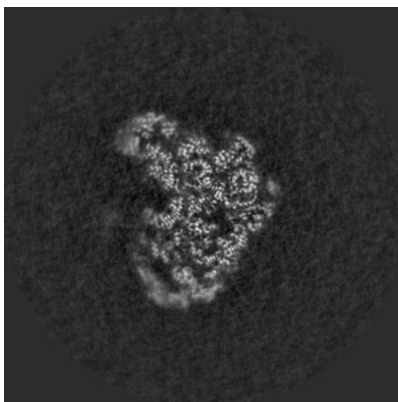


Z Index: 224

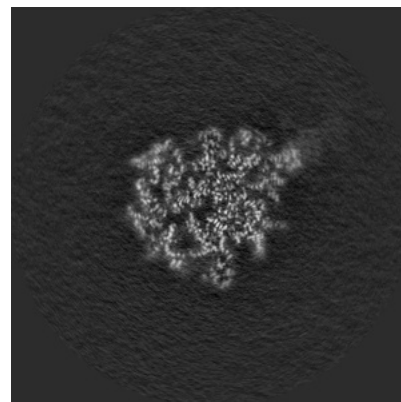
6.3.2 Raw map



X Index: 197



Y Index: 204

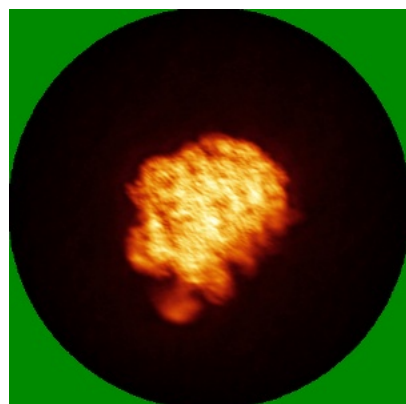


Z Index: 224

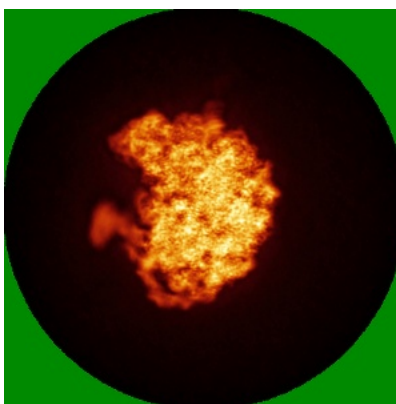
The images above show the largest variance slices of the map in three orthogonal directions.

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

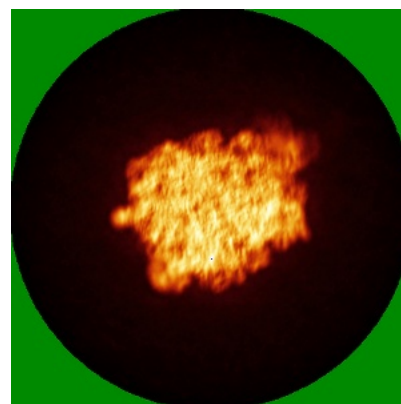
6.4.1 Primary map



X

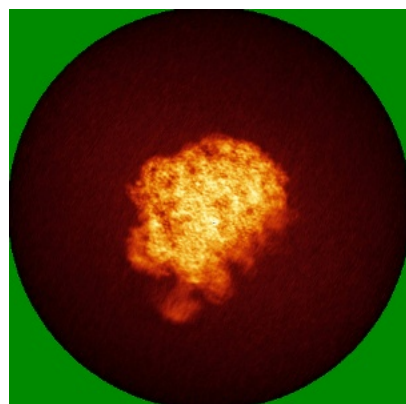


Y

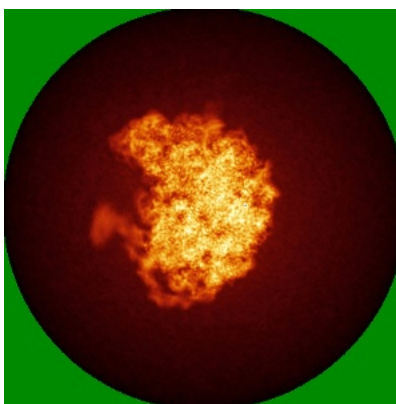


Z

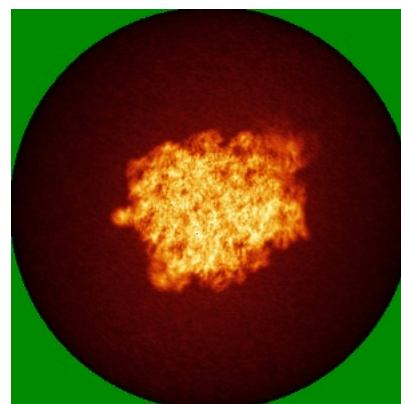
6.4.2 Raw map



X



Y

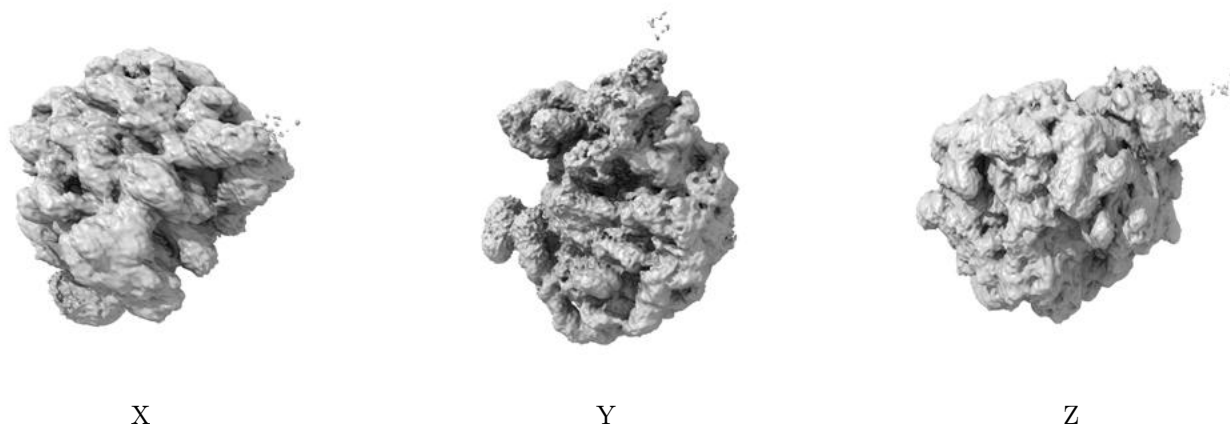


Z

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

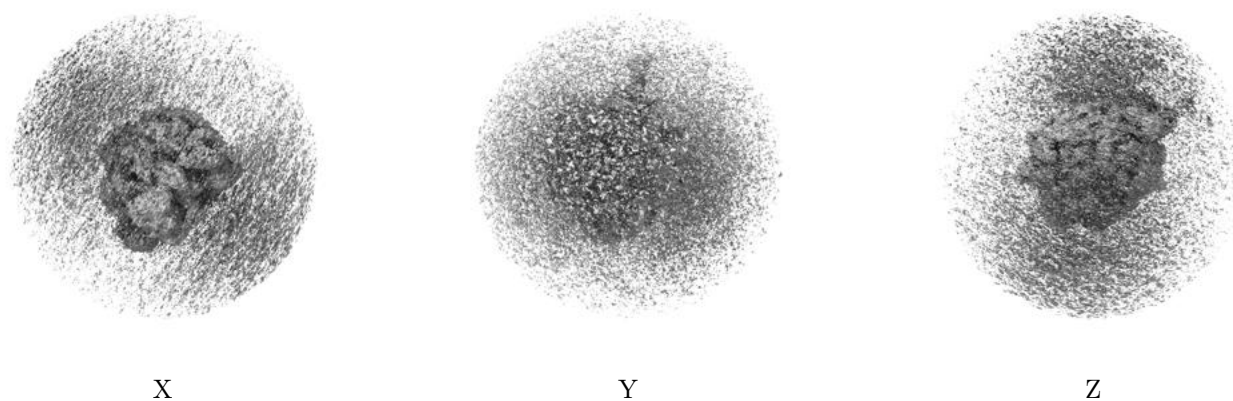
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. 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.

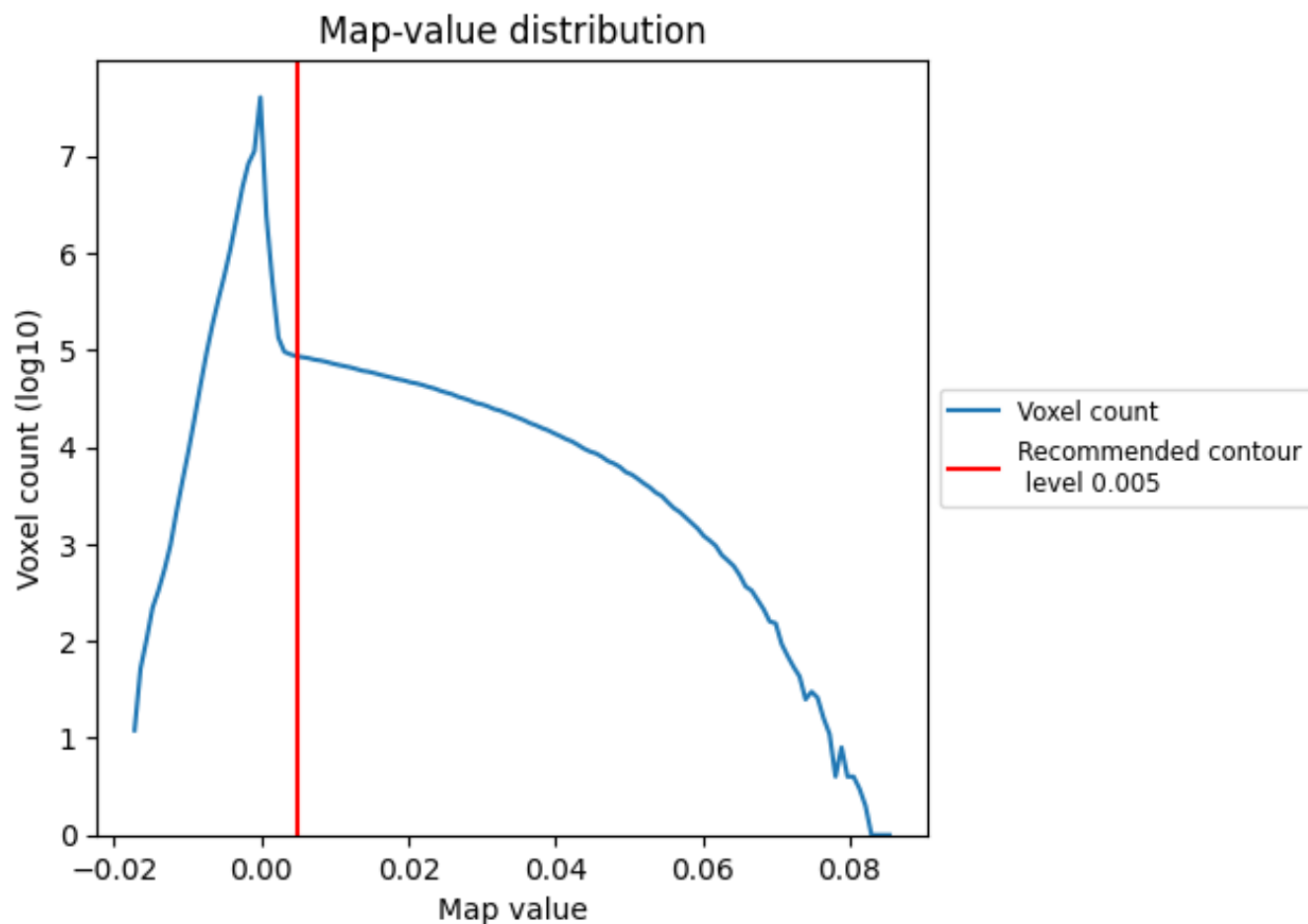
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

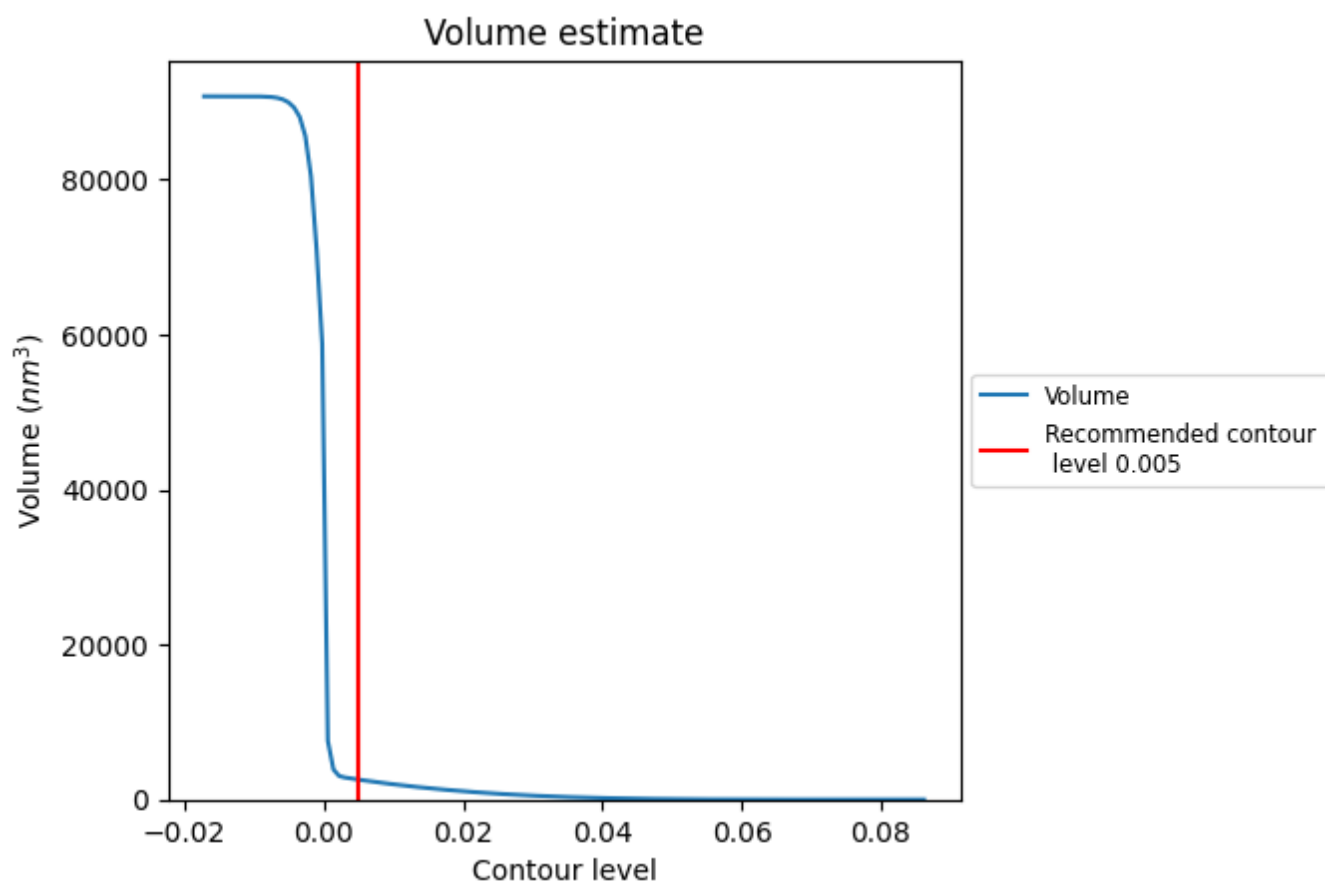
This section contains the results of statistical analysis of the map.

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.

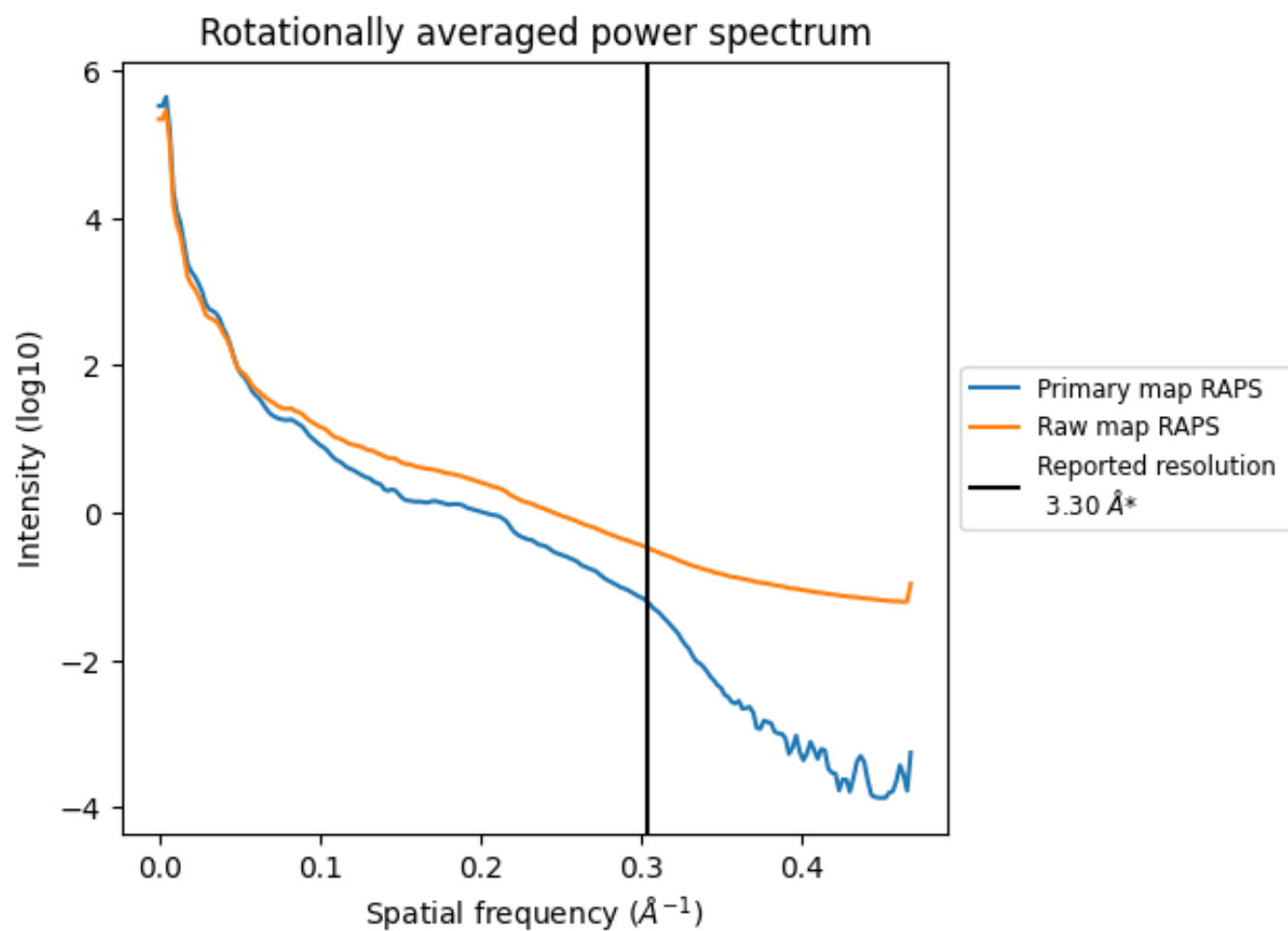
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2573 nm³; this corresponds to an approximate mass of 2324 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 ⓘ

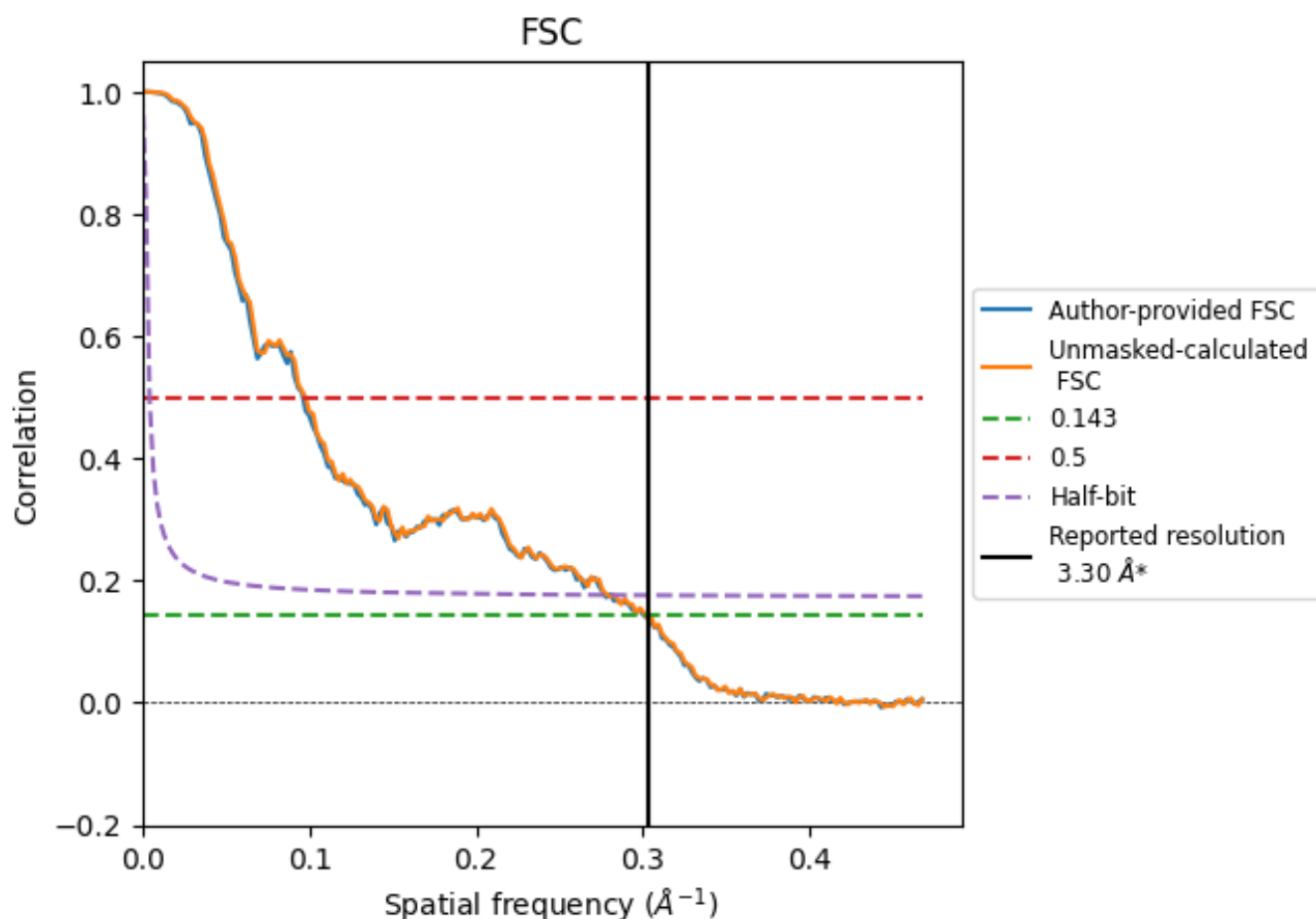


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.303 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

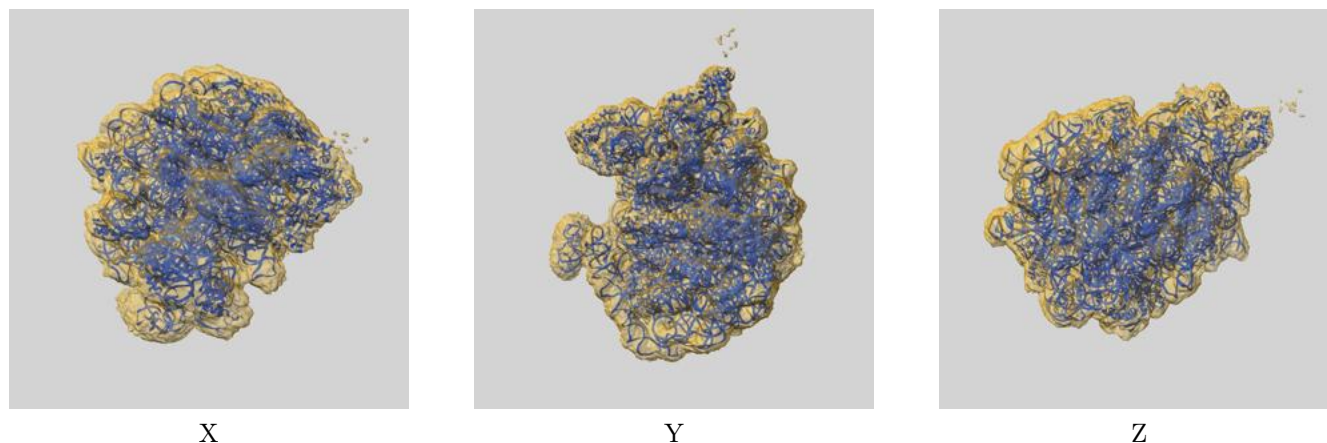
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.33	10.38	3.61
Unmasked-calculated*	3.32	10.24	3.58

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

9 Map-model fit [i](#)

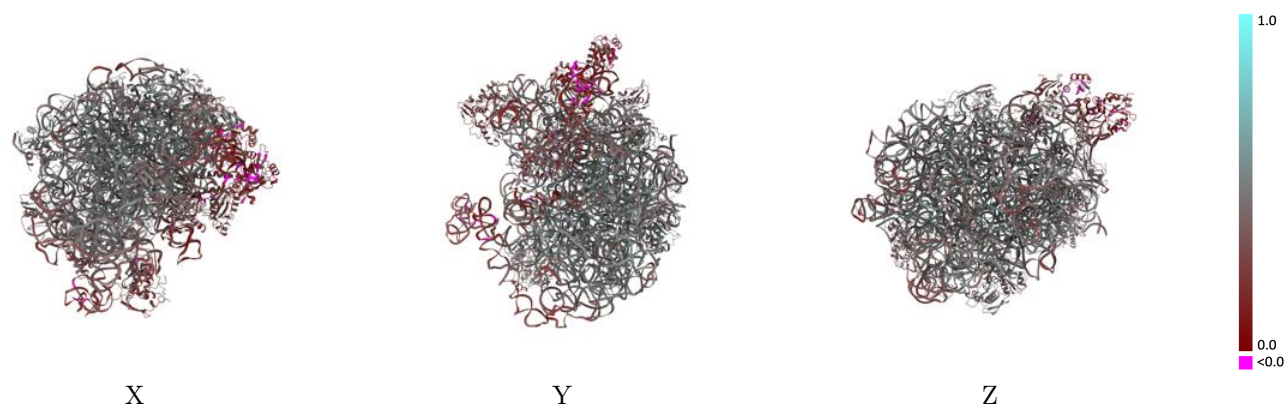
This section contains information regarding the fit between EMDB map EMD-37007 and PDB model 8KAB. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

9.1 Map-model overlay [i](#)



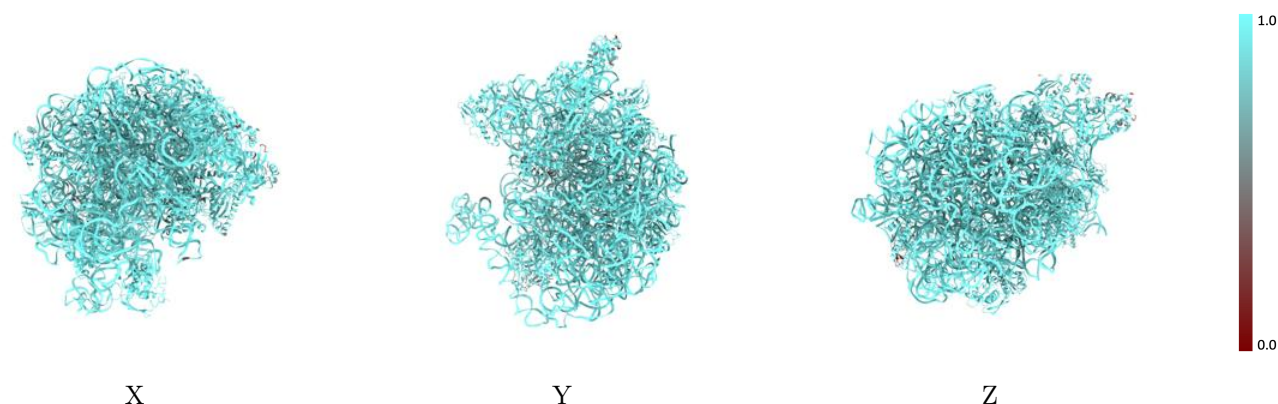
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



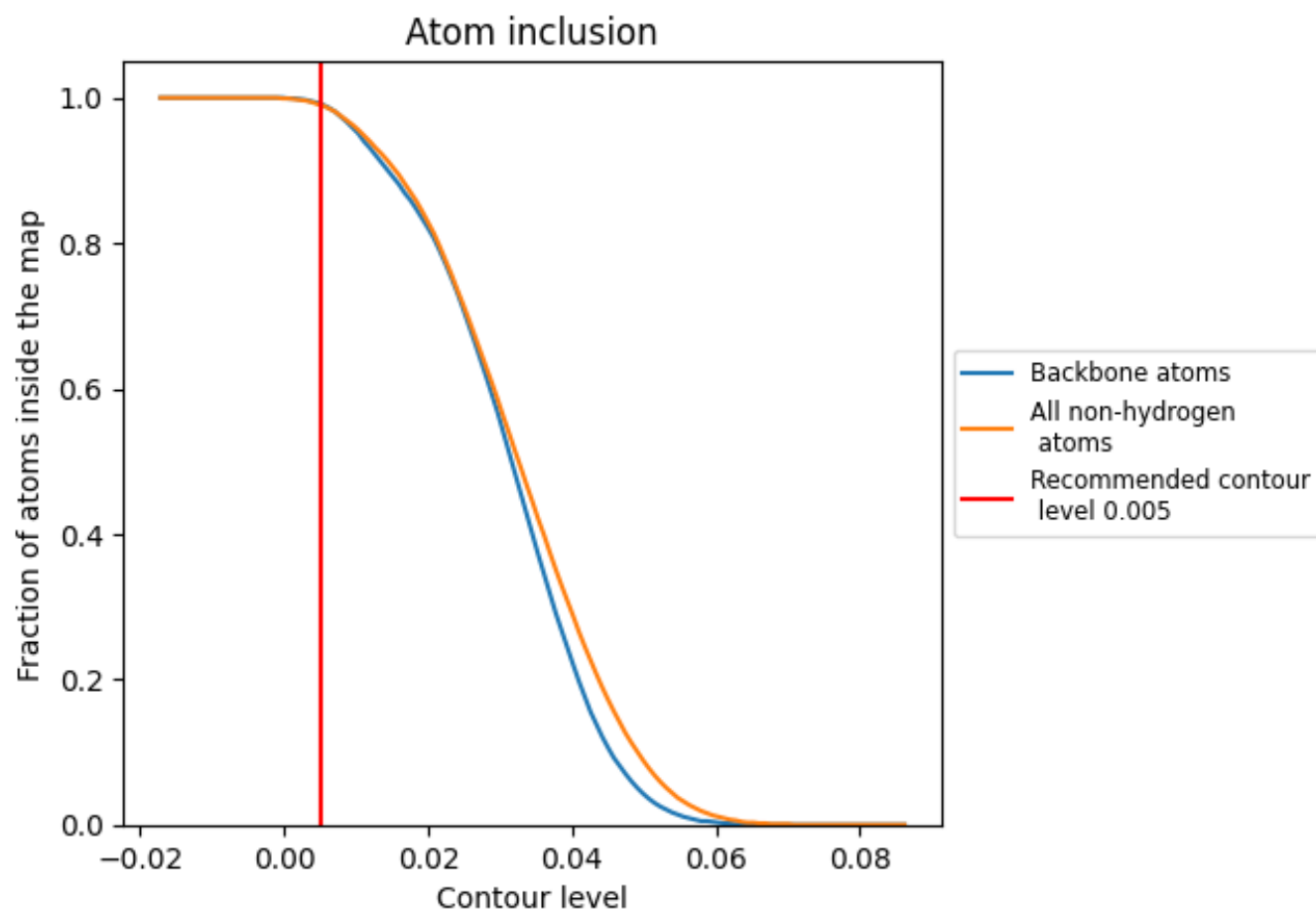
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9900	 0.4190
3	 1.0000	 0.4790
A	 0.9990	 0.4260
B	 1.0000	 0.4180
C	 1.0000	 0.4780
D	 1.0000	 0.4760
E	 0.9990	 0.4580
F	 0.9980	 0.3130
G	 1.0000	 0.3980
H	 0.7220	 0.3200
I	 0.8850	 0.1820
J	 0.9370	 0.1360
K	 0.9980	 0.4870
L	 0.9990	 0.4590
M	 0.9990	 0.4500
N	 0.9950	 0.4680
O	 1.0000	 0.4900
P	 1.0000	 0.3950
Q	 0.9990	 0.4340
R	 1.0000	 0.4790
S	 0.9990	 0.4820
T	 0.9990	 0.4710
U	 1.0000	 0.4510
V	 1.0000	 0.4150
W	 0.9960	 0.4070
X	 1.0000	 0.4940
Y	 1.0000	 0.4760
Z	 1.0000	 0.4120
a	 0.9940	 0.4870
b	 1.0000	 0.4460
c	 0.9720	 0.4180
d	 1.0000	 0.5050
e	 0.8520	 0.3900
f	 1.0000	 0.4680
g	 0.9970	 0.2610
h	 0.8900	 0.2670

