



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:53 AM UTC

PDB ID : 5GAF / pdb_00005gaf
EMDB ID : EMD-8002
Title : RNC in complex with SRP
Authors : Jomaa, A.; Boehringer, D.; Leibundgut, M.; Ban, N.
Deposited on : 2015-11-25
Resolution : 4.30 Å(reported)

This is a wwPDB EM Validation Summary 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:

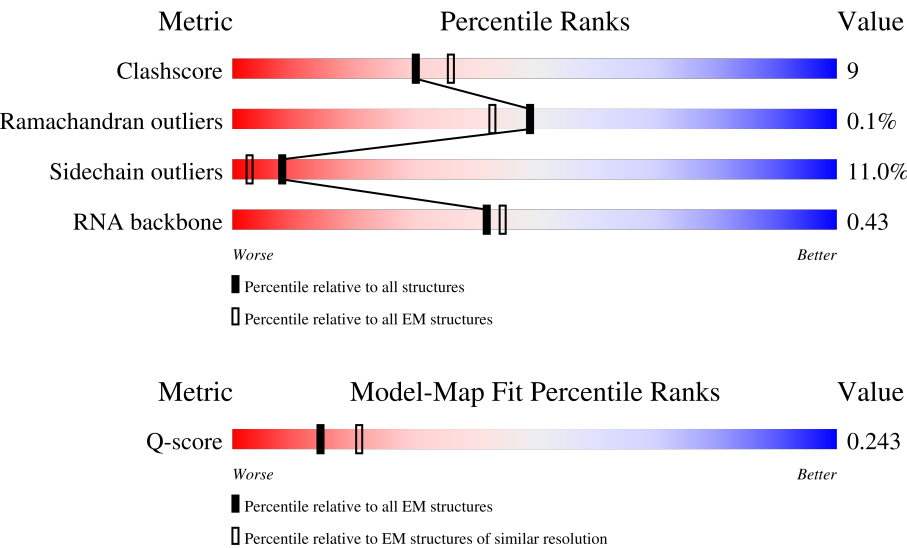
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 4.30 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.



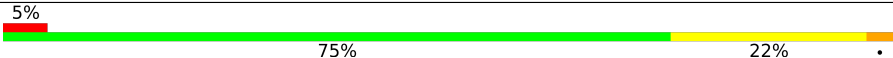
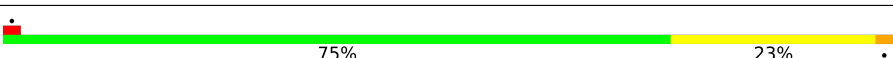
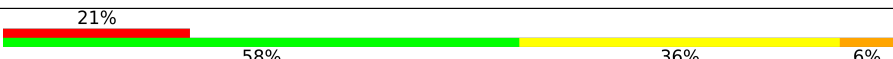
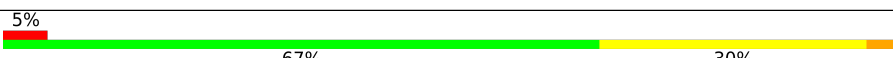
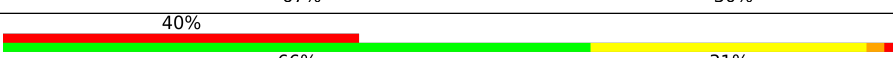
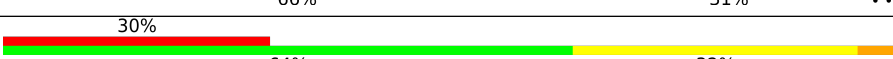
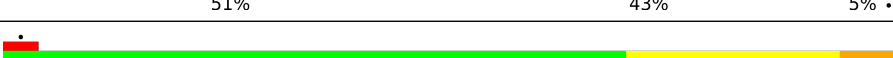
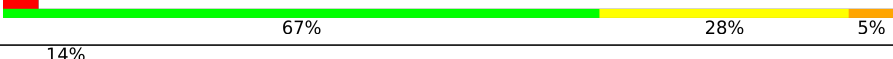
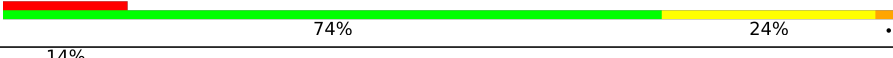
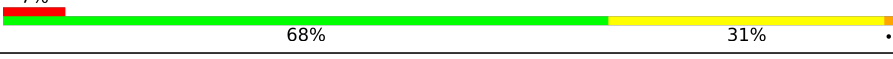
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4585 (3.80 - 4.80)

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	1	113	11% 7%21%10%62%
2	2	3	33%67%
3	A	2883	57%36%7%

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Mol	Chain	Length	Quality of chain
4	B	120	
5	C	271	
6	D	209	
7	E	201	
8	F	177	
9	G	176	
10	H	149	
11	I	125	
12	J	134	
13	K	142	
14	L	123	
15	M	144	
16	N	136	
17	O	125	
18	P	117	
19	Q	114	
20	R	117	
21	S	103	
22	T	110	
23	U	95	
24	V	102	
25	W	94	
26	X	76	
27	Y	77	
28	Z	62	

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Mol	Chain	Length	Quality of chain
29	a	58	10% 71% 28%
30	b	56	11% 57% 32% 11%
31	c	51	24% 76% 22%
32	d	46	7% 70% 26%
33	e	64	58% 41%
34	f	38	68% 24% 8%
35	i	398	68% 58% 37%
36	k	18	17% 94% 78% 6%

2 Entry composition [i](#)

There are 39 unique types of molecules in this entry. The entry contains 96182 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called SRP 4.5S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	43	Total	C	N	O	P	0	0
			926	413	174	296	43		

- Molecule 2 is a RNA chain called tRNA CCAend.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

- Molecule 3 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	2883	Total	C	N	O	P	0	0
			61902	27613	11397	20009	2883		

- Molecule 4 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	F	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 9 is a protein called 50S ribosomal protein L6.

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

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 11 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	125	Total	C	N	O	S	0	0
			946	599	169	175	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	85	VAL	SER	conflict	UNP P0A7J3
I	86	THR	MET	conflict	UNP P0A7J3

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	134	Total	C	N	O	S	0	0
			979	619	169	185	6		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	125	Total	C	N	O	S	0	0
			993	613	202	173	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	95	Total	C	N	O	S	0	0
			756	479	141	135	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	102	Total	C	N	O	0	0
			780	492	146	142		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	76	Total	C	N	O	S	0	0
			580	359	117	103	1		

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

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

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

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

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

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

- Molecule 30 is a protein called 50S ribosomal protein L32.

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

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	c	51	Total	C	N	O	0	0
			414	266	76	72		

- Molecule 32 is a protein called 50S ribosomal protein L34.

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

- Molecule 33 is a protein called 50S ribosomal protein L35.

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

- Molecule 34 is a protein called 50S ribosomal protein L36.

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

- Molecule 35 is a protein called Signal recognition particle protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	398	Total	C	N	O	S	0	0
			3036	1910	548	560	18		

- Molecule 36 is a protein called 1A9L SS.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	18	Total	C	N	O	S	0	0
			137	94	20	22	1		

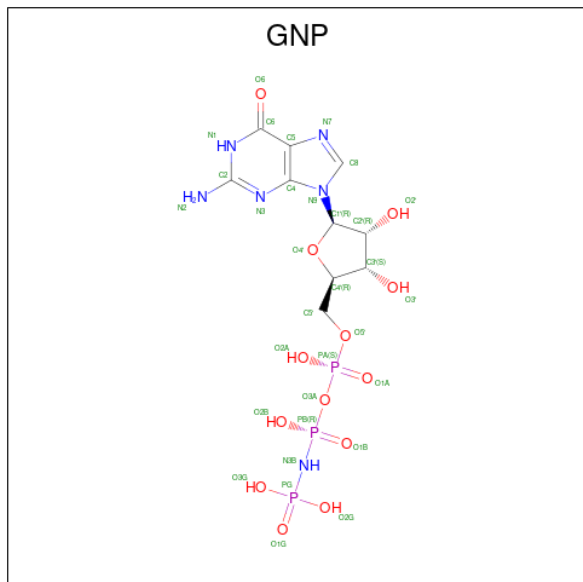
- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	2	1	Total	Mg	0
			1	1	
37	A	412	Total	Mg	0
			412	412	
37	B	11	Total	Mg	0
			11	11	
37	C	2	Total	Mg	0
			2	2	
37	D	1	Total	Mg	0
			1	1	
37	E	1	Total	Mg	0
			1	1	
37	P	1	Total	Mg	0
			1	1	
37	R	1	Total	Mg	0
			1	1	
37	b	1	Total	Mg	0
			1	1	

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

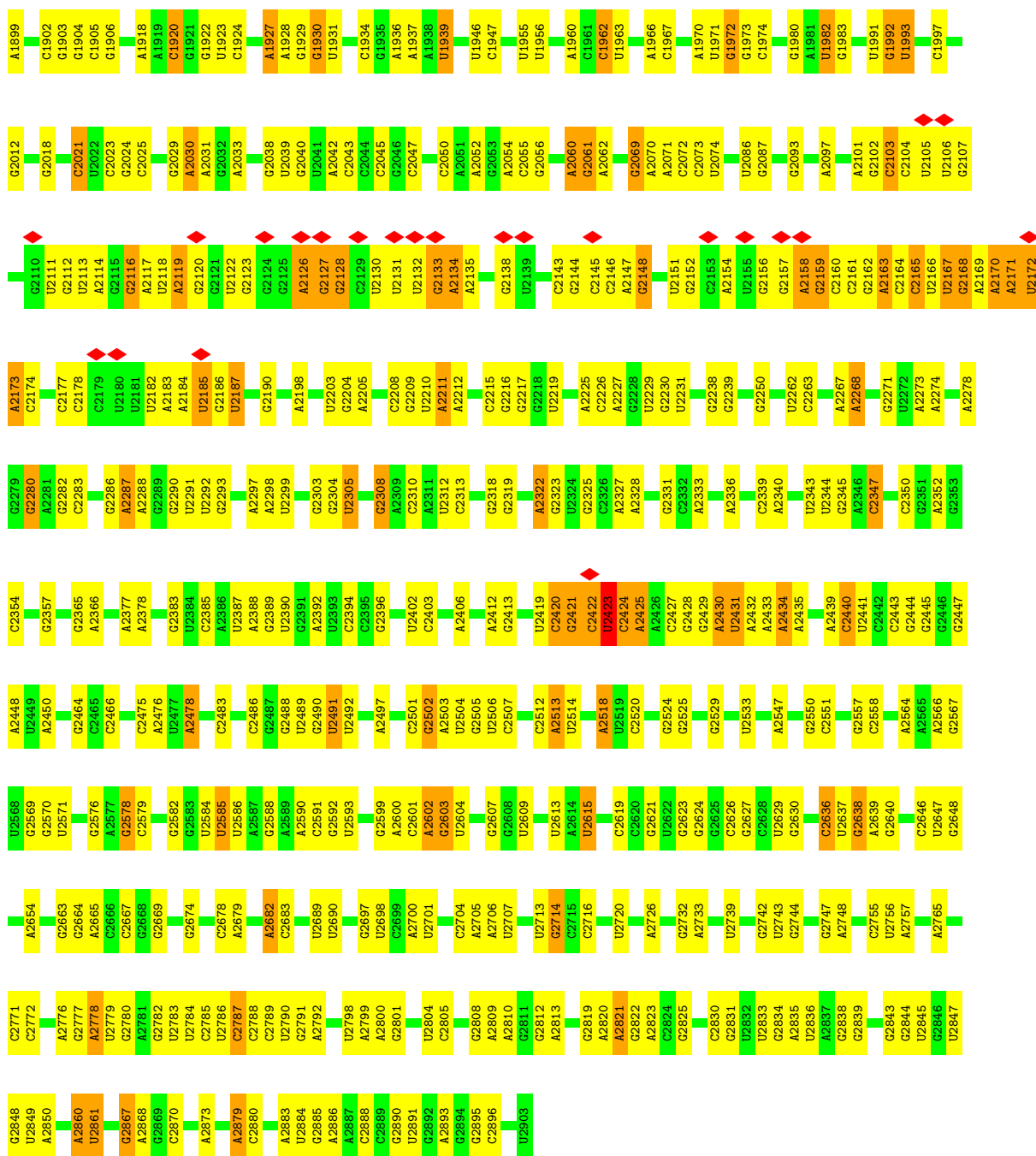
Mol	Chain	Residues	Atoms		AltConf
38	f	1	Total	Zn	0
			1	1	

- Molecule 39 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



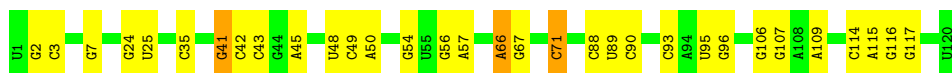
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
39	i	1	32	10	6	13	3	0

G1797	G1798	G1799	C1800	A1801	A1802	G1807	A1808	A1809	A1810	G1811	C1816	G1817	G1818	A1819	U1820	A1821	C1822	U1825	G1826	U1827	G1828	A1829	C1837	C1838	C1839	G1846	A1847	A1848	G1849	G1850	A1853	A1858	G1859	C1869	C1870	A1871	C1872	C1873	C1874	C1875	G1876	G1877	C1878	C1879	C1880	U1881	G1888	G1896			
C1706	G1707	C1708	G1709	G1710	A1711	G1715	G1721	A1722			U1725	U1729	U1730	G1731	C1732	A1735	U1736	G1737	G1738		G1743	U1751	C1752		G1756	A1757	G1758	A1759	C1760	G1761	A1762	G1763	C1764		G1770	A1773	C1774	U1775	A1780	U1781	U1782	A1785	A1786	U1789	C1790	A1791	A1794	C1795	U1796		
C1582	A1583	U1584	C1585	A1590	A1591	C1592	A1597	A1598		A1603	C1606	C1607	U1610	A1614	C1615	A1616	G1627	G1628	G1631		A1634	A1637	C1638	C1639	G1645	C1646	U1647	U1648	C1649		G1653	A1654	A1655	G1660	G1667	A1672	G1673	C1674	A1677		G1681	A1689		A1700							
C1493	A1494	A1495	A1496	U1497	C1498	C1499	G1500	G1501	A1502	U1506	C1507	A1508	A1509	U1510	G1511	A1515	G1516	G1517	G1524	A1525	C1526	G1527	A1528	C1533	U1534	A1535	C1536	G1537	U1542	G1543	A1544	A1545	G1546	U1554		G1560	U1563	C1564	C1565	A1566	A1569	A1570	A1571	A1572		U1576	C1577	U1578	G1581		
G1410	C1414	U1415	G1416	C1417	A1418	A1419	G1420	G1421	G1422	G1423	G1424	G1425	G1426	G1427	A1428	G1432	A1433	G1434	G1435	G1436	C1437	U1438	A1439	U1442	U1443	C1446	C1447	G1448	G1449	G1450	C1451	G1452	A1453	C1463	G1464	G1465	U1466	U1467	U1468	A1469	G1473	U1474	G1482	G1483	U1484	U1485	C1489	A1490	U1491	G1492	
A1301	A1302	A1308	U1313	G1324	A1327	A1328	U1329	G1332	G1337	G1338	G1339	U1340	G1341	A1342	G1343	U1344	G1345	C1346	C1351	A1354	G1355	C1363	G1364	A1365	A1366	A1367	G1374	U1379	A1383	C1386	A1387	G1388	U1394	A1395	U1396	U1397	C1398	C1399	U1400	G1401	U1402	A1403	C1404	U1405	U1406						
G1177	C1178	G1179	U1180	U1181	U1182	G1187	U1198	U1199	U1199	A1205	G1206	G1210	G1211	G1212	G1218	A1230	U1231	G1236	A1237	G1238	C1243	A1247	U1249	A1250	C1251	G1252	A1253	G1256	A1262	G1266	U1267	A1268	A1269	C1270	G1271	A1272	A1275	A1287	G1288	C1289	C1290	U1294		G1300							
U1083	A1084	A1085	A1086	G1087	A1088	A1089	A1090	G1093	U1094	A1095	A1096	A1098	G1099	C1100	U1101	A1103	U1105	C1104	G1106	G1110	A1111	G1112	U1113	C1114	G1115	G1116	G1125	A1126	A1127	G1128	A1129	U1130	G1131	U1132	A1133	A1134	C1135	G1136	G1139	U1141	A1142	A1143	G1149	C1150	G1154	A1155	G1168	U1173			
U999	A1000	A1001	G1002	C1005	C1006	C1007	A1008	A1009	U1012	C1013	A1021	G1022	U1023	G1024	G1025	G1026	A1028	U1033	G1038	A1039	A1040	C1044	C1045	A1046	G1047	A1048	A1056	A1057	U1060	U1061	G1062	G1063	C1064	U1065	U1066	A1067	G1068	A1069	A1070	G1071	C1072	A1073	G1074	C1075	G1076	A1077	C1079	U1082			
G881	G882	U884	U885	A886	C887	C888	A889	G897	C908	A909	A910	G914	C915	G916	A917	G930	U931	U932	A933	C946	A947	C948	G949	G953	C957	U958	A959	U960	C961	C968	G969	U970	G971	A972	A973	A975	G976	A983	A984	C987		A989	C994	C995	A996	G997	C998				
G801	A804	G805	C806	U807	G808	U811	C812	C908	U821	C814	A819	G822	C823	U824	A825	U826	U827	U828	G830	U831	U832	A833	C834	C835	U839	C840	A845	U846	G847	C848	A849	U850	G857	G858	G859	U860	A861	G862	A863	G864	C865	G869	U870	U871	A873	U872	C876	A877	A878	G879	G880
G707	G711	G712	G713	U714	A718	C719	U720	U721	A722	G729	A730	G738	A743	U747	A753	G757	C758	G759	G763	A764	C765	C772	U773	G774	G775	G776	G777	G778	G780	A781	A782	A783	G784	G785	A788	U789	C791	A792	A793	A794	C795	C796	G797	G798	U799	A800					
A608	A609	C610	A613	A614	U615	A616	G620	U621	A621	G622	A627	G628	G629	C630	A631	A632	A633	C634	A637	U639	C640	C645	U646	U647	C648	G649	C650	U653	A654	A655	G656	U657	U658	A668	G669	A670	C671	C672	G673	G674	A675	A676	A677	C678	C679	C680	G681	A685	U686	A706	
G518	U519	G520	U521	A526	C527	A528	U529	G530	C531	A532	G533	G543	C544	U545	G548	C549	C550	G551	U552	U558	G561	U562	A563	C564	C565	G566	U567	U568	U569	U570	U571	A572	U573	A574	U575	U576	U577	G577	C581	G585	A586	U591	A592	U593	U594	C595	C601	A602	A603	G604	G605



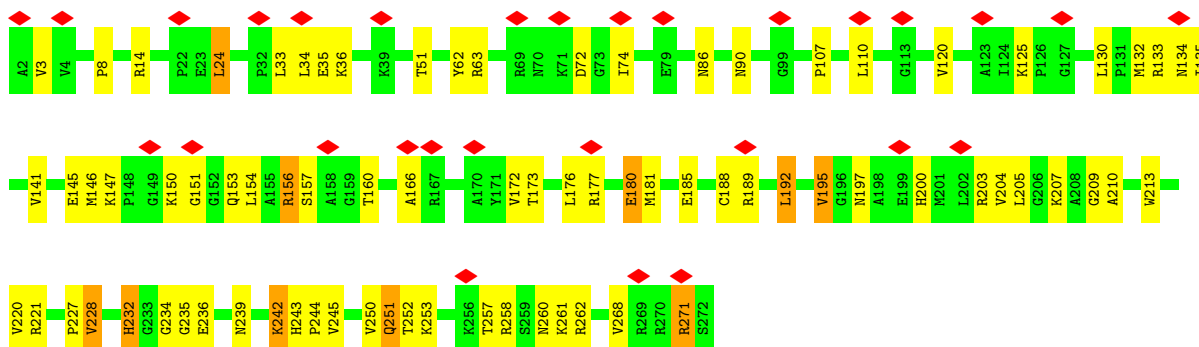
• Molecule 4: 5S ribosomal RNA

Chain B: 73% 24%

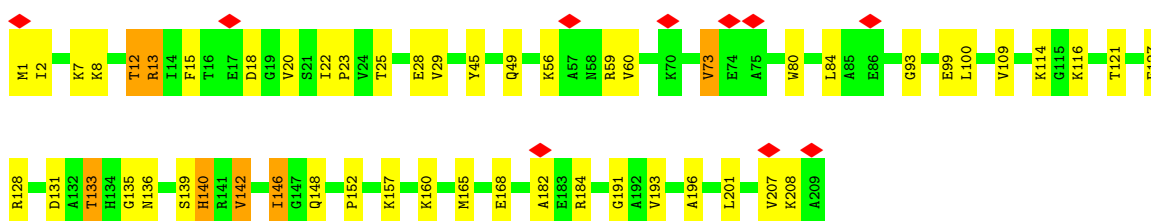
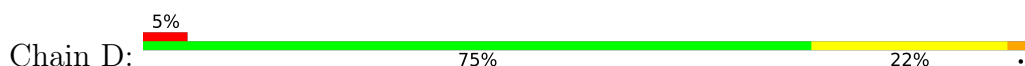


• Molecule 5: 50S ribosomal protein L2

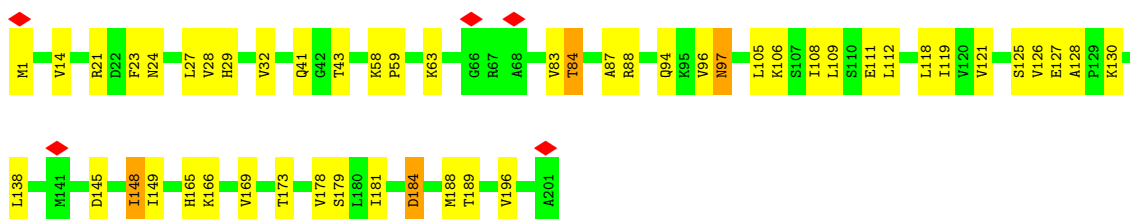
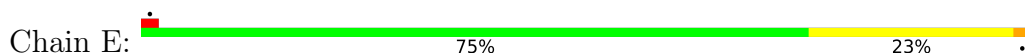
Chain C: 11% 70% 26%



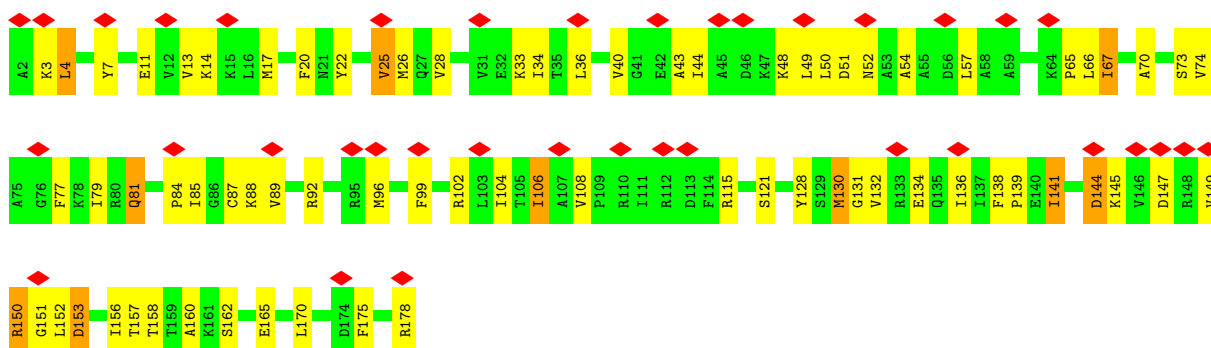
• Molecule 6: 50S ribosomal protein L3



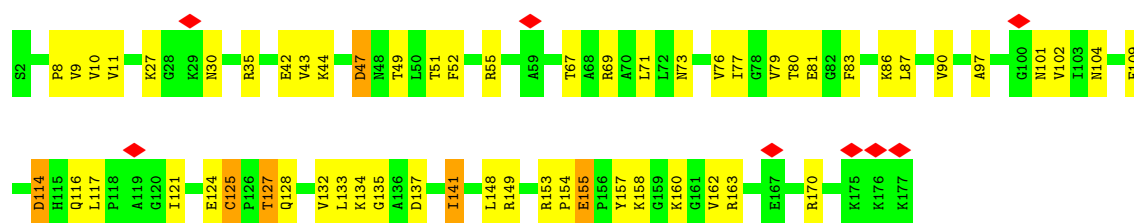
• Molecule 7: 50S ribosomal protein L4



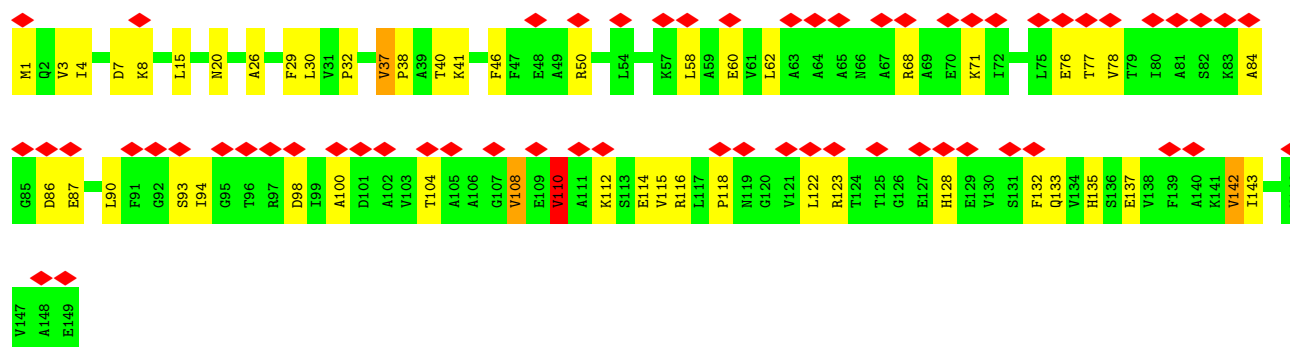
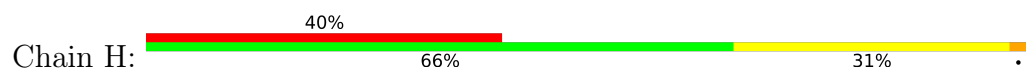
• Molecule 8: 50S ribosomal protein L5



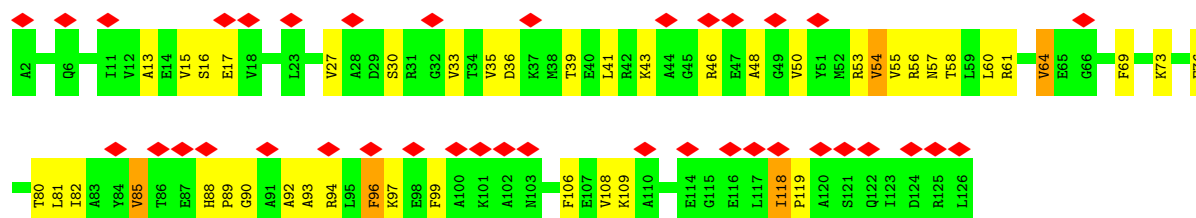
• Molecule 9: 50S ribosomal protein L6



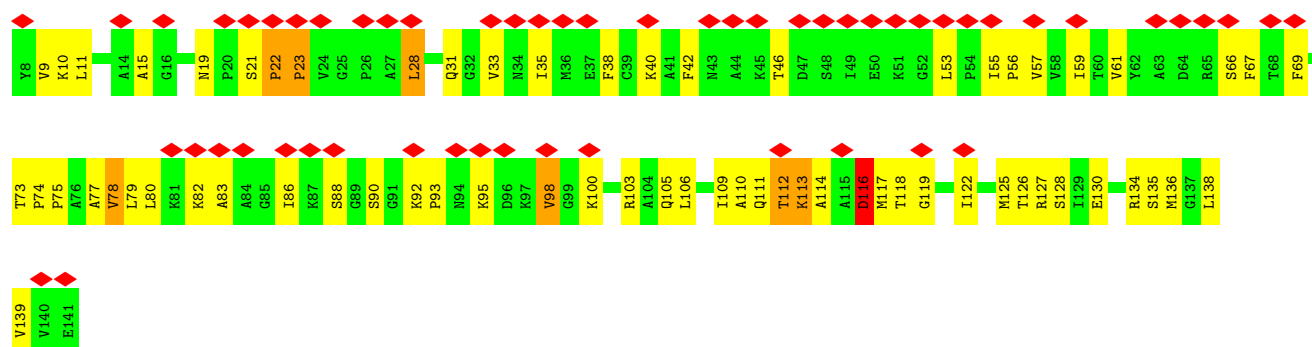
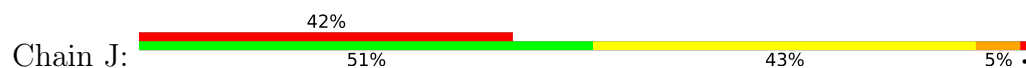
• Molecule 10: 50S ribosomal protein L9



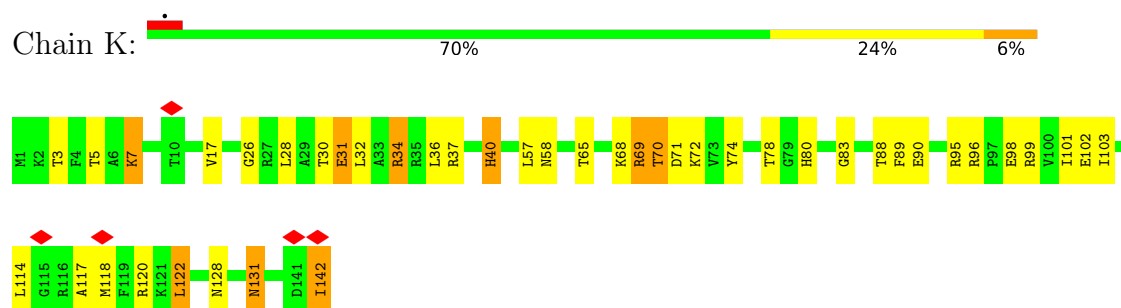
• Molecule 11: 50S ribosomal protein L10



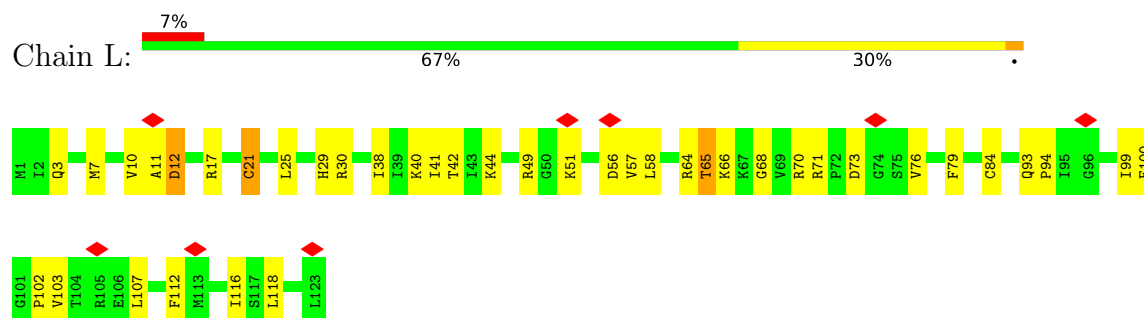
• Molecule 12: 50S ribosomal protein L11



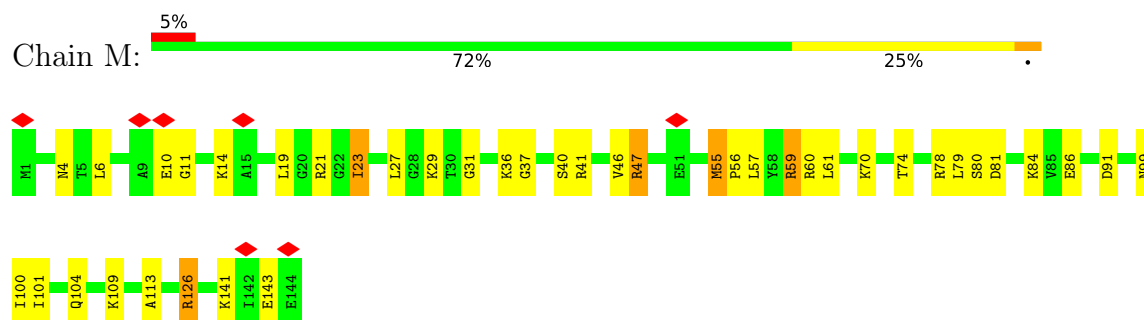
- Molecule 13: 50S ribosomal protein L13



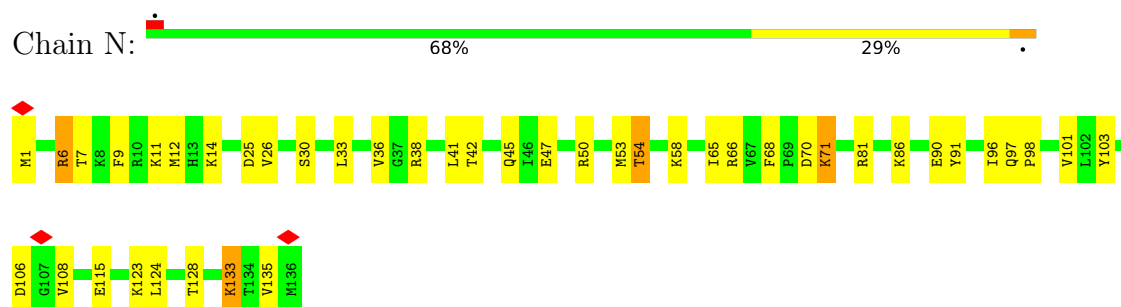
- Molecule 14: 50S ribosomal protein L14



- Molecule 15: 50S ribosomal protein L15

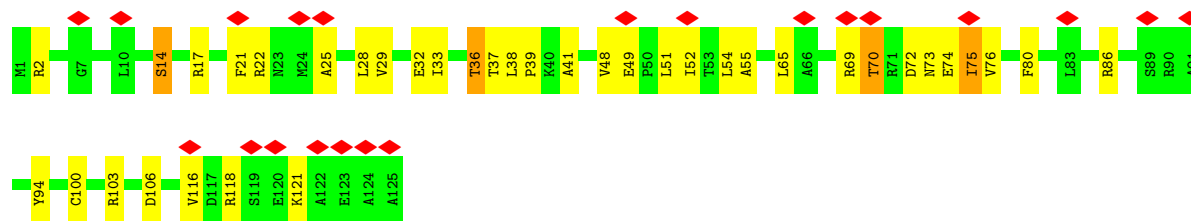


- Molecule 16: 50S ribosomal protein L16

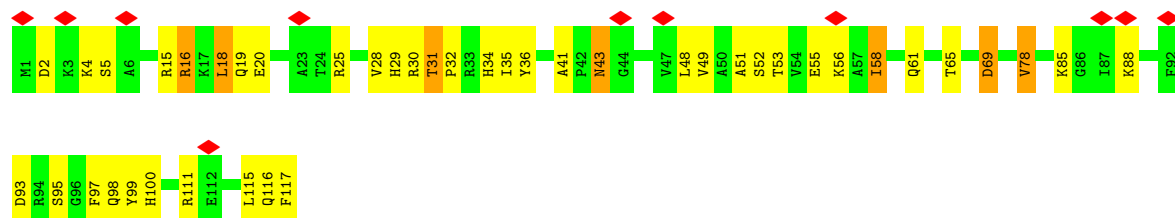


- Molecule 17: 50S ribosomal protein L17

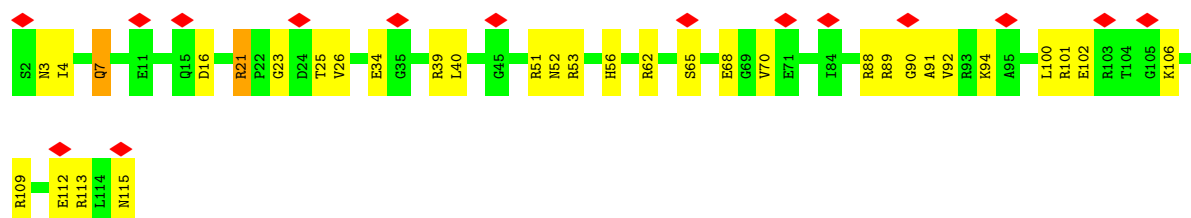




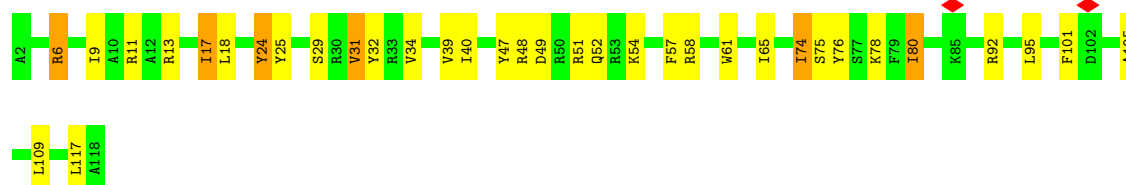
- Molecule 18: 50S ribosomal protein L18



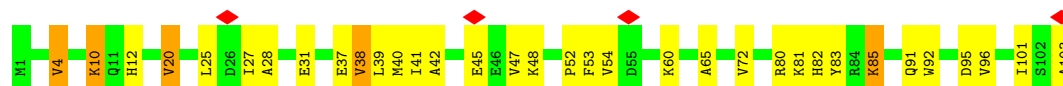
- Molecule 19: 50S ribosomal protein L19



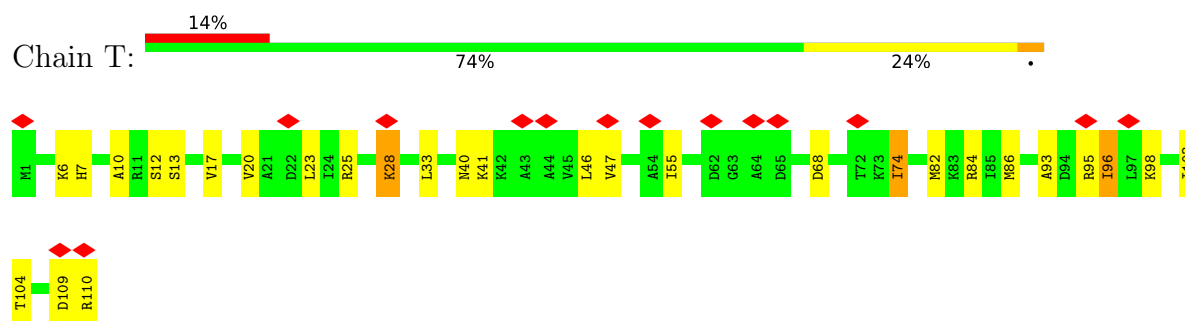
- Molecule 20: 50S ribosomal protein L20



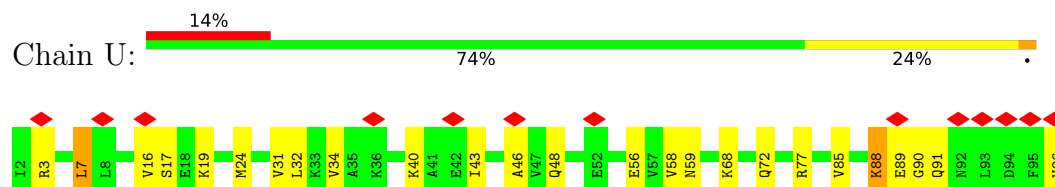
- Molecule 21: 50S ribosomal protein L21



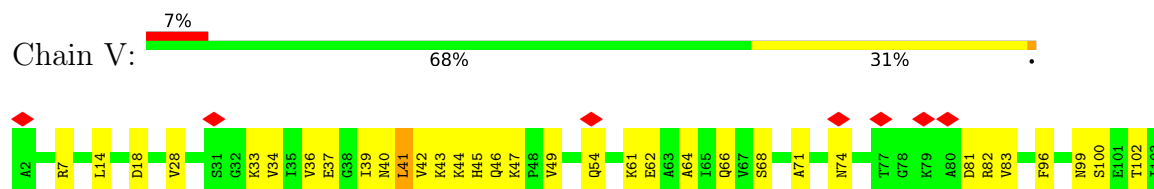
- Molecule 22: 50S ribosomal protein L22



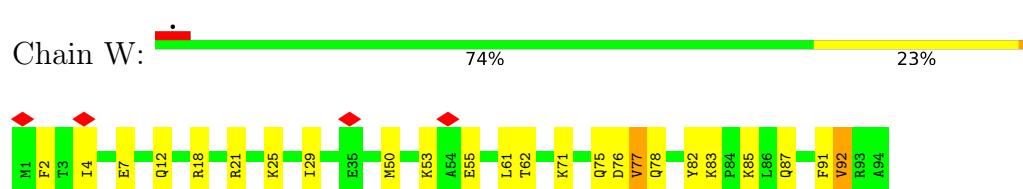
- Molecule 23: 50S ribosomal protein L23



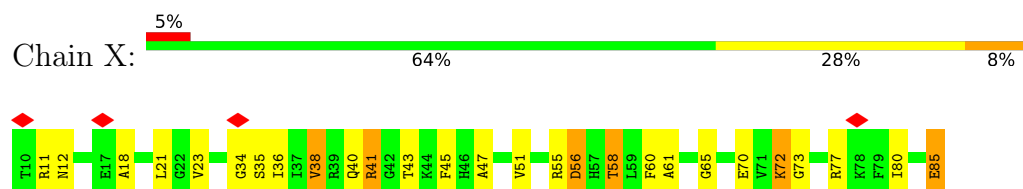
- Molecule 24: 50S ribosomal protein L24



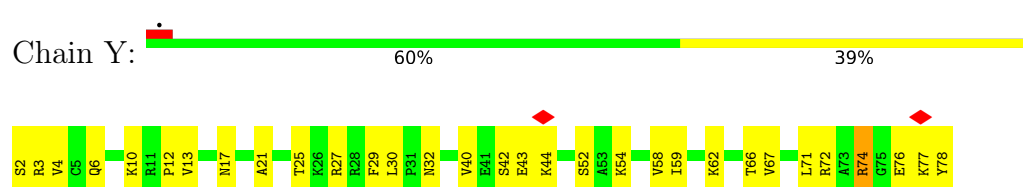
- Molecule 25: 50S ribosomal protein L25



- Molecule 26: 50S ribosomal protein L27

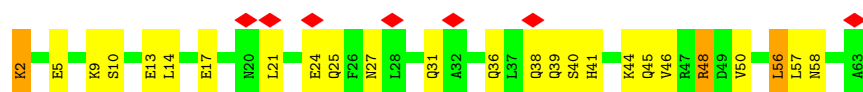


- Molecule 27: 50S ribosomal protein L28



- Molecule 28: 50S ribosomal protein L29

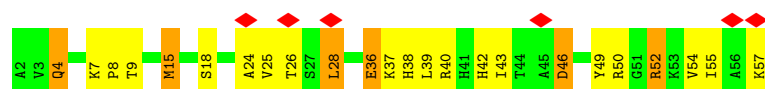




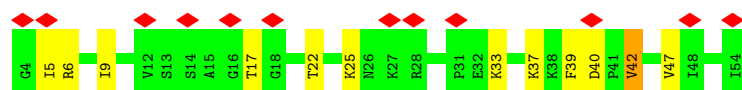
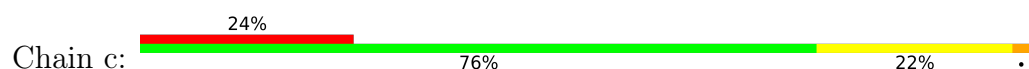
- Molecule 29: 50S ribosomal protein L30



- Molecule 30: 50S ribosomal protein L32



- Molecule 31: 50S ribosomal protein L33



- Molecule 32: 50S ribosomal protein L34



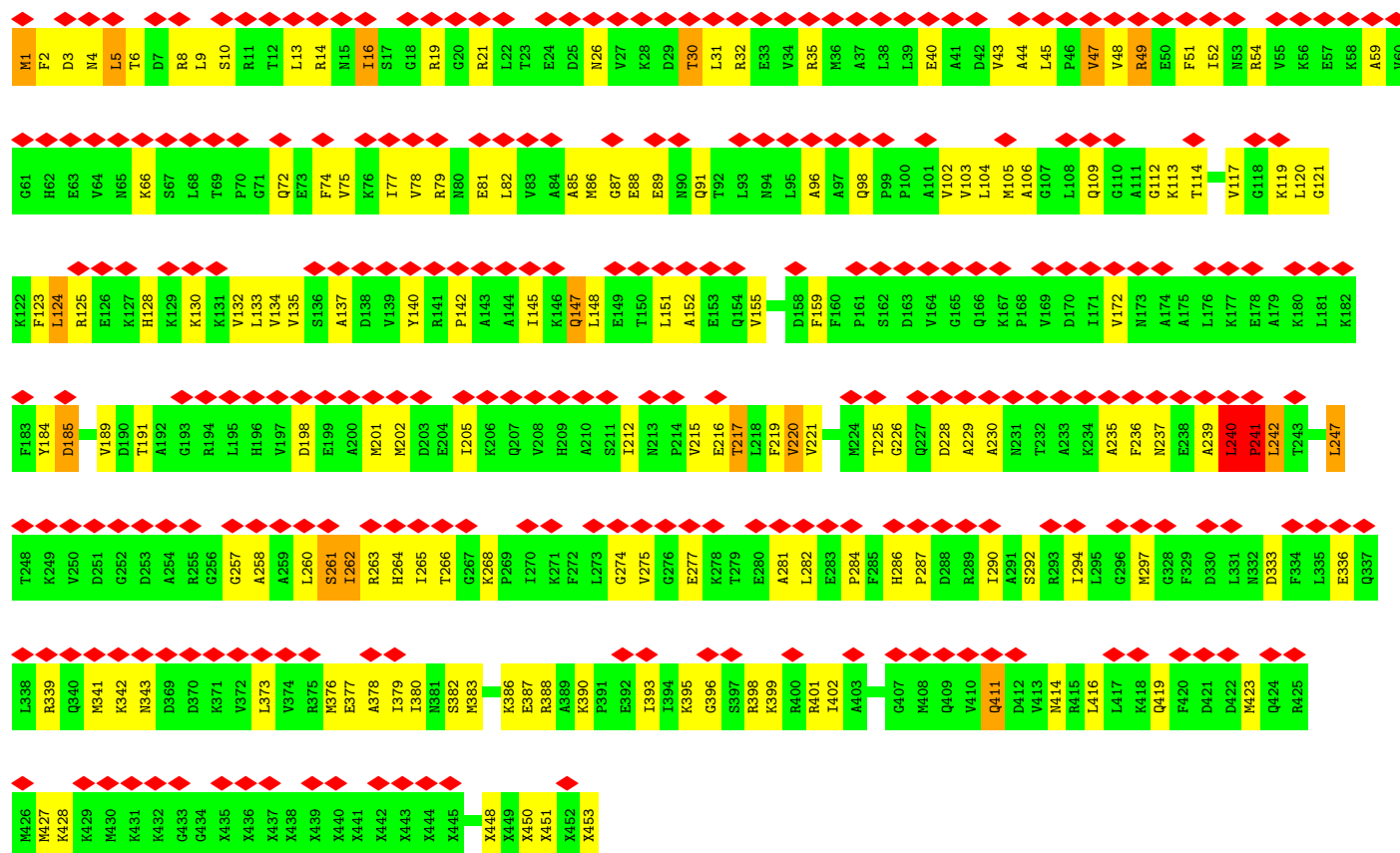
- Molecule 33: 50S ribosomal protein L35



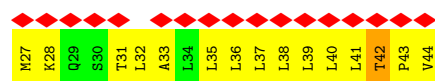
- Molecule 34: 50S ribosomal protein L36



- Molecule 35: Signal recognition particle protein



• Molecule 36: 1A9L SS



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	16407	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 ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.341	Depositor
Minimum map value	-0.183	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.05	Depositor
Map size ($\text{\AA}$)	398.88, 398.88, 398.88	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.385, 1.385, 1.385	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, 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	1	0.13	0/1037	0.32	0/1616
2	2	0.35	0/68	0.51	0/103
3	A	0.35	0/69329	0.48	1/108152 (0.0%)
4	B	0.27	0/2872	0.40	0/4478
5	C	0.60	0/2122	0.96	1/2852 (0.0%)
6	D	0.60	0/1586	0.95	5/2134 (0.2%)
7	E	0.57	0/1571	0.91	0/2113
8	F	0.51	1/1435 (0.1%)	0.93	3/1926 (0.2%)
9	G	0.51	0/1343	0.97	3/1816 (0.2%)
10	H	0.59	0/1121	0.89	1/1515 (0.1%)
11	I	0.72	0/958	0.95	2/1292 (0.2%)
12	J	0.94	1/993 (0.1%)	1.13	8/1341 (0.6%)
13	K	0.58	0/1152	0.88	2/1551 (0.1%)
14	L	0.57	0/955	0.97	2/1279 (0.2%)
15	M	0.57	0/1062	0.98	3/1413 (0.2%)
16	N	0.58	0/1093	0.96	6/1460 (0.4%)
17	O	0.61	0/1006	0.95	1/1345 (0.1%)
18	P	0.50	0/910	0.93	0/1219
19	Q	0.54	0/929	0.94	2/1242 (0.2%)
20	R	0.73	0/960	0.91	1/1278 (0.1%)
21	S	0.57	0/829	0.95	0/1107
22	T	0.66	0/864	1.05	2/1156 (0.2%)
23	U	0.97	5/763 (0.7%)	1.10	3/1021 (0.3%)
24	V	0.46	0/788	0.88	2/1051 (0.2%)
25	W	0.48	0/766	0.92	0/1025
26	X	0.59	0/587	0.98	2/776 (0.3%)
27	Y	0.61	0/635	0.92	0/848
28	Z	0.65	0/502	0.98	1/667 (0.1%)
29	a	0.53	0/453	0.87	0/605
30	b	0.54	0/450	0.89	0/599
31	c	0.54	0/421	1.01	2/561 (0.4%)
32	d	0.66	0/380	0.95	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.62	0/513	0.97	0/676
34	f	0.61	0/303	0.99	0/397
35	i	0.34	0/2954	0.85	6/3967 (0.2%)
36	k	0.53	0/137	1.01	2/186 (1.1%)
All	All	0.43	7/103847 (0.0%)	0.63	61/155265 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	C	0	1
9	G	0	1
12	J	0	1
35	i	0	2
All	All	0	5

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	U	88	LYS	CA-C	16.48	1.74	1.52
23	U	88	LYS	C-N	9.47	1.47	1.33
23	U	89	GLU	N-CA	6.35	1.54	1.46
12	J	22	PRO	CA-C	5.74	1.57	1.52
8	F	108	VAL	CA-CB	5.45	1.57	1.53

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	i	240	LEU	CA-C-N	10.67	133.17	119.84
35	i	240	LEU	C-N-CA	10.67	133.17	119.84
23	U	88	LYS	CB-CA-C	10.07	128.07	109.54
9	G	155	GLU	CA-C-N	9.39	129.02	119.82
9	G	155	GLU	C-N-CA	9.39	129.02	119.82

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	C	232	HIS	Peptide

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Mol	Chain	Res	Type	Group
9	G	47	ASP	Peptide
12	J	19	ASN	Peptide
35	i	240	LEU	Peptide
35	i	241	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	926	0	467	31	0
2	2	62	0	34	1	0
3	A	61902	0	31132	712	0
4	B	2569	0	1301	20	0
5	C	2083	0	2154	50	0
6	D	1565	0	1616	33	0
7	E	1552	0	1619	29	0
8	F	1411	0	1444	43	0
9	G	1323	0	1371	36	0
10	H	1110	0	1148	23	0
11	I	946	0	978	31	0
12	J	979	0	1028	42	0
13	K	1129	0	1162	24	0
14	L	946	0	1023	22	0
15	M	1053	0	1129	27	0
16	N	1074	0	1157	25	0
17	O	993	0	1034	26	0
18	P	900	0	935	23	0
19	Q	917	0	962	20	0
20	R	947	0	1019	26	0
21	S	816	0	839	23	0
22	T	857	0	922	16	0
23	U	756	0	817	19	0
24	V	780	0	831	18	0
25	W	753	0	780	16	0
26	X	580	0	594	16	0
27	Y	625	0	652	16	0
28	Z	501	0	531	34	0
29	a	449	0	488	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	b	444	0	458	18	0
31	c	414	0	442	5	0
32	d	377	0	418	7	0
33	e	504	0	572	15	0
34	f	302	0	340	13	0
35	i	3036	0	3154	127	0
36	k	137	0	168	13	0
37	2	1	0	0	0	0
37	A	412	0	0	0	0
37	B	11	0	0	0	0
37	C	2	0	0	0	0
37	D	1	0	0	0	0
37	E	1	0	0	0	0
37	P	1	0	0	0	0
37	R	1	0	0	0	0
37	b	1	0	0	0	0
38	f	1	0	0	0	0
39	i	32	0	13	3	0
All	All	96182	0	64732	1424	0

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

The worst 5 of 1424 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)
23:U:88:LYS:C	23:U:88:LYS:CA	1.74	1.58
28:Z:9:LYS:NZ	28:Z:17:GLU:HG3	1.61	1.15
3:A:96:C:OP1	28:Z:39:GLN:NE2	1.92	1.02
3:A:1818:U:OP2	5:C:156:ARG:NH1	2.00	0.95
35:i:342:LYS:NZ	35:i:377:GLU:OE2	2.00	0.94

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	C	269/271 (99%)	261 (97%)	8 (3%)	0	100	100
6	D	207/209 (99%)	201 (97%)	6 (3%)	0	100	100
7	E	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
8	F	175/177 (99%)	166 (95%)	9 (5%)	0	100	100
9	G	174/176 (99%)	171 (98%)	3 (2%)	0	100	100
10	H	147/149 (99%)	137 (93%)	9 (6%)	1 (1%)	18	55
11	I	123/125 (98%)	113 (92%)	9 (7%)	1 (1%)	16	52
12	J	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
13	K	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
14	L	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
15	M	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
16	N	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
17	O	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
18	P	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
19	Q	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
20	R	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
21	S	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
22	T	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
23	U	93/95 (98%)	89 (96%)	4 (4%)	0	100	100
24	V	100/102 (98%)	99 (99%)	1 (1%)	0	100	100
25	W	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
26	X	74/76 (97%)	73 (99%)	1 (1%)	0	100	100
27	Y	75/77 (97%)	72 (96%)	3 (4%)	0	100	100
28	Z	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
29	a	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
30	b	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
31	c	49/51 (96%)	48 (98%)	1 (2%)	0	100	100
32	d	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
33	e	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
34	f	36/38 (95%)	36 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	i	374/398 (94%)	357 (96%)	15 (4%)	2 (0%)	24	62
36	k	16/18 (89%)	11 (69%)	5 (31%)	0	100	100
All	All	3822/3908 (98%)	3685 (96%)	133 (4%)	4 (0%)	49	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
35	i	240	LEU
35	i	241	PRO
10	H	118	PRO
11	I	108	VAL

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	
5	C	216/216 (100%)	190 (88%)	26 (12%)	5	19
6	D	164/164 (100%)	148 (90%)	16 (10%)	7	25
7	E	165/165 (100%)	149 (90%)	16 (10%)	8	25
8	F	148/148 (100%)	127 (86%)	21 (14%)	3	15
9	G	137/137 (100%)	125 (91%)	12 (9%)	9	29
10	H	114/114 (100%)	100 (88%)	14 (12%)	4	18
11	I	95/95 (100%)	85 (90%)	10 (10%)	6	23
12	J	104/104 (100%)	88 (85%)	16 (15%)	2	13
13	K	116/116 (100%)	99 (85%)	17 (15%)	3	14
14	L	104/104 (100%)	96 (92%)	8 (8%)	12	33
15	M	103/103 (100%)	92 (89%)	11 (11%)	6	22
16	N	109/109 (100%)	99 (91%)	10 (9%)	8	28
17	O	102/102 (100%)	95 (93%)	7 (7%)	14	37
18	P	87/87 (100%)	70 (80%)	17 (20%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
19	Q	99/99 (100%)	88 (89%)	11 (11%)	6	21
20	R	89/89 (100%)	79 (89%)	10 (11%)	6	21
21	S	84/84 (100%)	73 (87%)	11 (13%)	4	17
22	T	93/93 (100%)	84 (90%)	9 (10%)	8	25
23	U	82/82 (100%)	76 (93%)	6 (7%)	13	34
24	V	83/83 (100%)	75 (90%)	8 (10%)	8	26
25	W	78/78 (100%)	72 (92%)	6 (8%)	12	33
26	X	57/58 (98%)	47 (82%)	10 (18%)	2	11
27	Y	67/67 (100%)	59 (88%)	8 (12%)	5	19
28	Z	54/54 (100%)	49 (91%)	5 (9%)	8	27
29	a	48/48 (100%)	45 (94%)	3 (6%)	16	38
30	b	47/47 (100%)	36 (77%)	11 (23%)	1	5
31	c	45/46 (98%)	40 (89%)	5 (11%)	6	21
32	d	38/38 (100%)	31 (82%)	7 (18%)	1	10
33	e	51/51 (100%)	47 (92%)	4 (8%)	11	32
34	f	34/34 (100%)	31 (91%)	3 (9%)	9	29
35	i	313/315 (99%)	286 (91%)	27 (9%)	10	30
36	k	17/17 (100%)	15 (88%)	2 (12%)	5	19
All	All	3143/3147 (100%)	2796 (89%)	347 (11%)	8	22

5 of 347 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
21	S	85	LYS
29	a	36	VAL
22	T	74	ILE
25	W	78	GLN
31	c	6	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 51 such sidechains are listed below:

Mol	Chain	Res	Type
20	R	37	GLN
23	U	59	ASN
35	i	264	HIS

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Mol	Chain	Res	Type
20	R	81	ASN
22	T	102	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	42/113 (37%)	16 (38%)	1 (2%)
2	2	2/3 (66%)	1 (50%)	0
3	A	2878/2883 (99%)	518 (17%)	19 (0%)
4	B	119/120 (99%)	13 (10%)	0
All	All	3041/3119 (97%)	548 (18%)	20 (0%)

5 of 548 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	33	C
1	1	34	U
1	1	37	U
1	1	39	A
1	1	41	C

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	A	2158	A
3	A	2430	A
3	A	2756	U
3	A	2602	A
3	A	827	U

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

Of 433 ligands modelled in this entry, 432 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
39	GNP	i	1400	-	34,34,34	1.56	8 (23%)	47,54,54	1.05	3 (6%)

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
39	GNP	i	1400	-	-	2/18/38/38	0/3/3/3

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	i	1400	GNP	PB-N3B	3.55	1.72	1.63
39	i	1400	GNP	PG-N3B	3.45	1.72	1.63
39	i	1400	GNP	PG-O1G	2.95	1.50	1.46
39	i	1400	GNP	PB-O2B	-2.55	1.50	1.56
39	i	1400	GNP	PB-O1B	2.43	1.49	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	i	1400	GNP	O2B-PB-O1B	4.05	118.56	109.87
39	i	1400	GNP	O1G-PG-N3B	-2.85	107.58	111.77
39	i	1400	GNP	O3A-PB-N3B	-2.29	100.23	106.59

There are no chirality outliers.

All (2) torsion outliers are listed below:

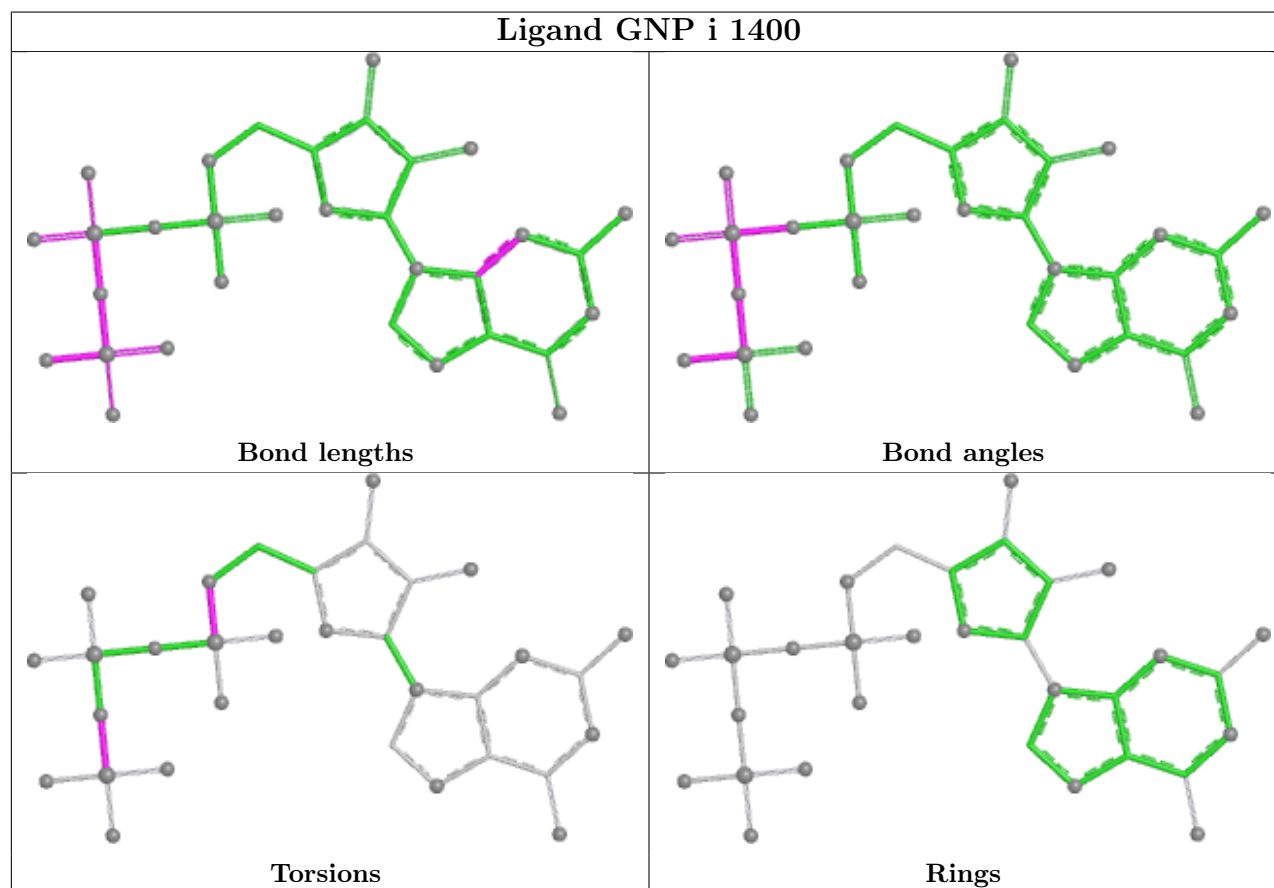
Mol	Chain	Res	Type	Atoms
39	i	1400	GNP	PB-N3B-PG-O1G
39	i	1400	GNP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	i	1400	GNP	3	0

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	A	4
35	i	2

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	i	297:MET	C	328:GLY	N	35.34
1	A	882:G	O3'	894:U	P	17.07
1	A	545:U	O3'	548:G	P	16.33
1	A	1912:A	O3'	1917:U	P	16.01
1	i	343:ASN	C	369:ASP	N	12.86

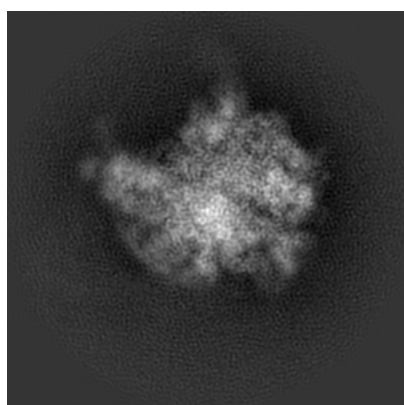
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8002. These allow visual inspection of the internal detail of the map and identification of artifacts.

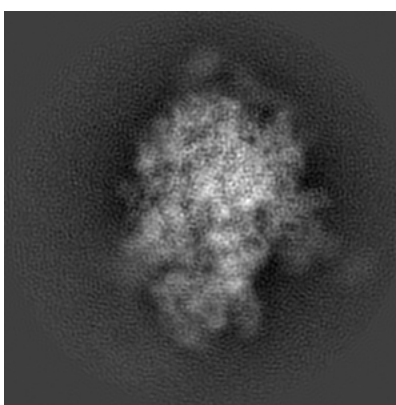
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

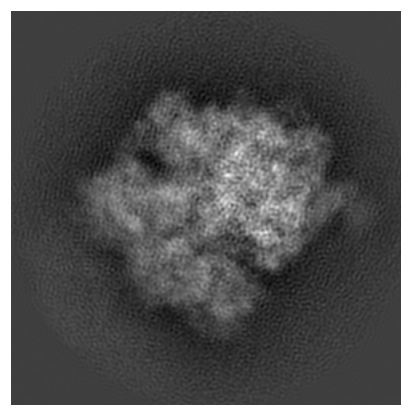
6.1.1 Primary map



X



Y

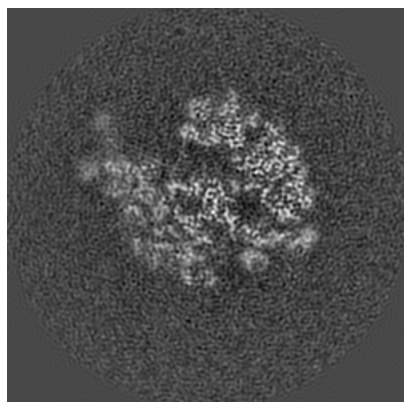


Z

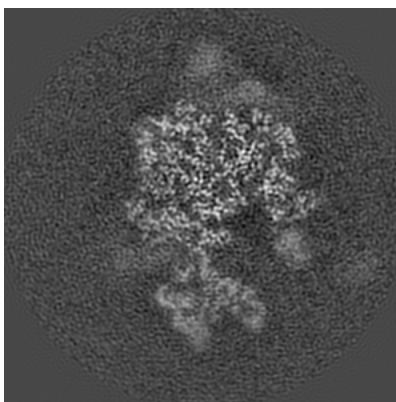
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

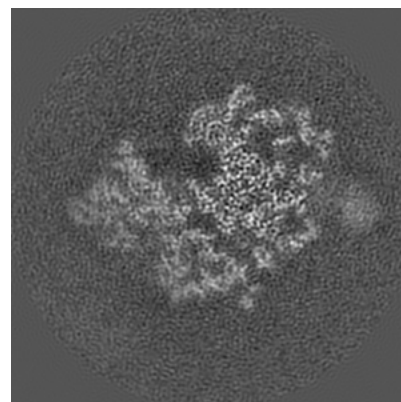
6.2.1 Primary map



X Index: 144



Y Index: 144

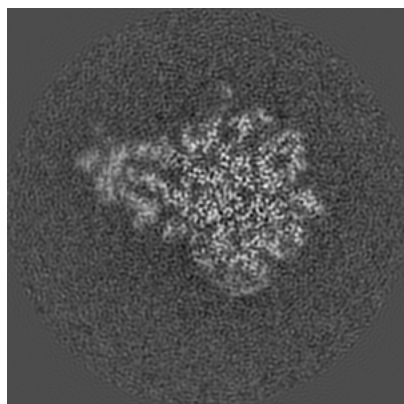


Z Index: 144

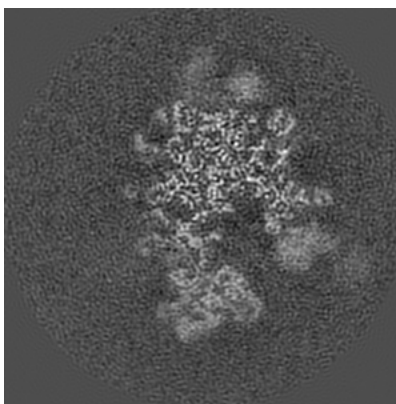
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

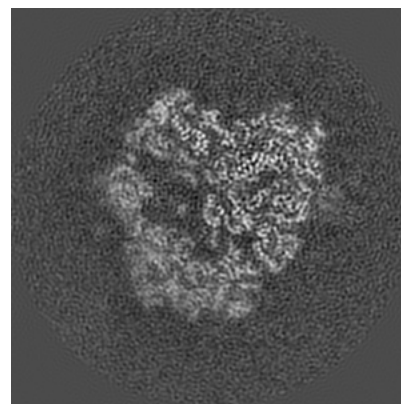
6.3.1 Primary map



X Index: 160



Y Index: 152

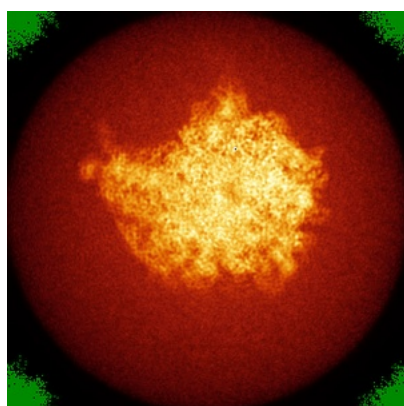


Z Index: 162

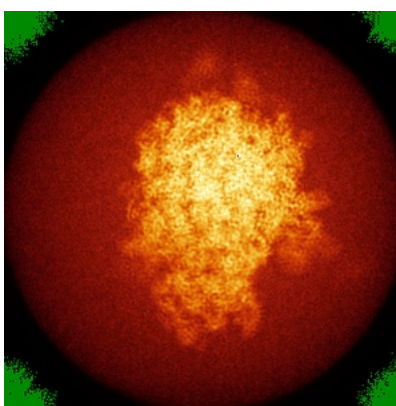
The images above show the largest variance slices of the map in three orthogonal directions.

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

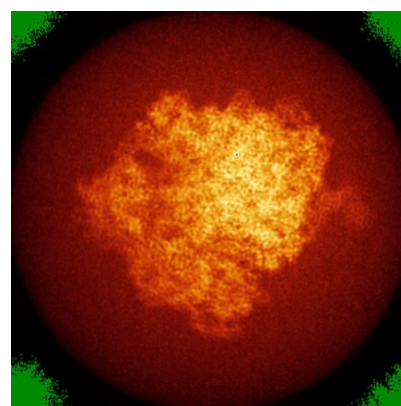
6.4.1 Primary map



X



Y

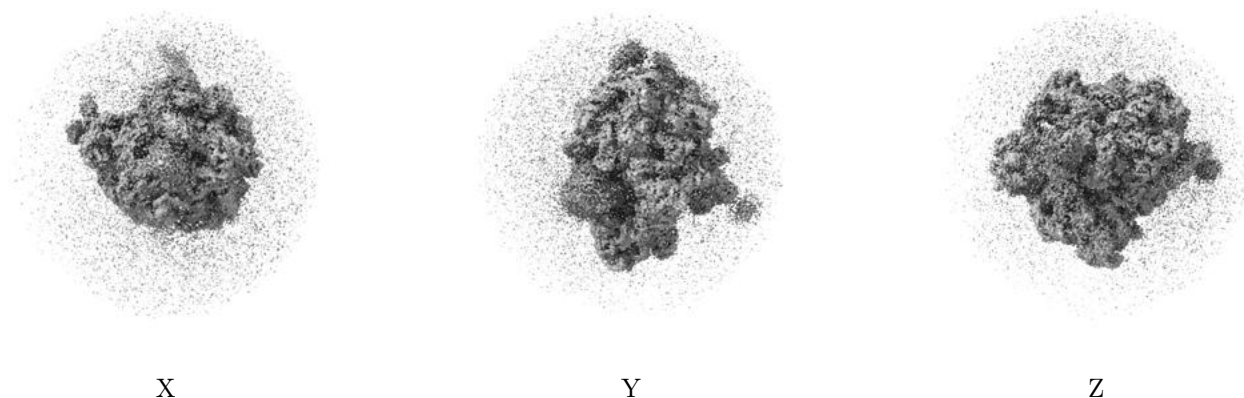


Z

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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

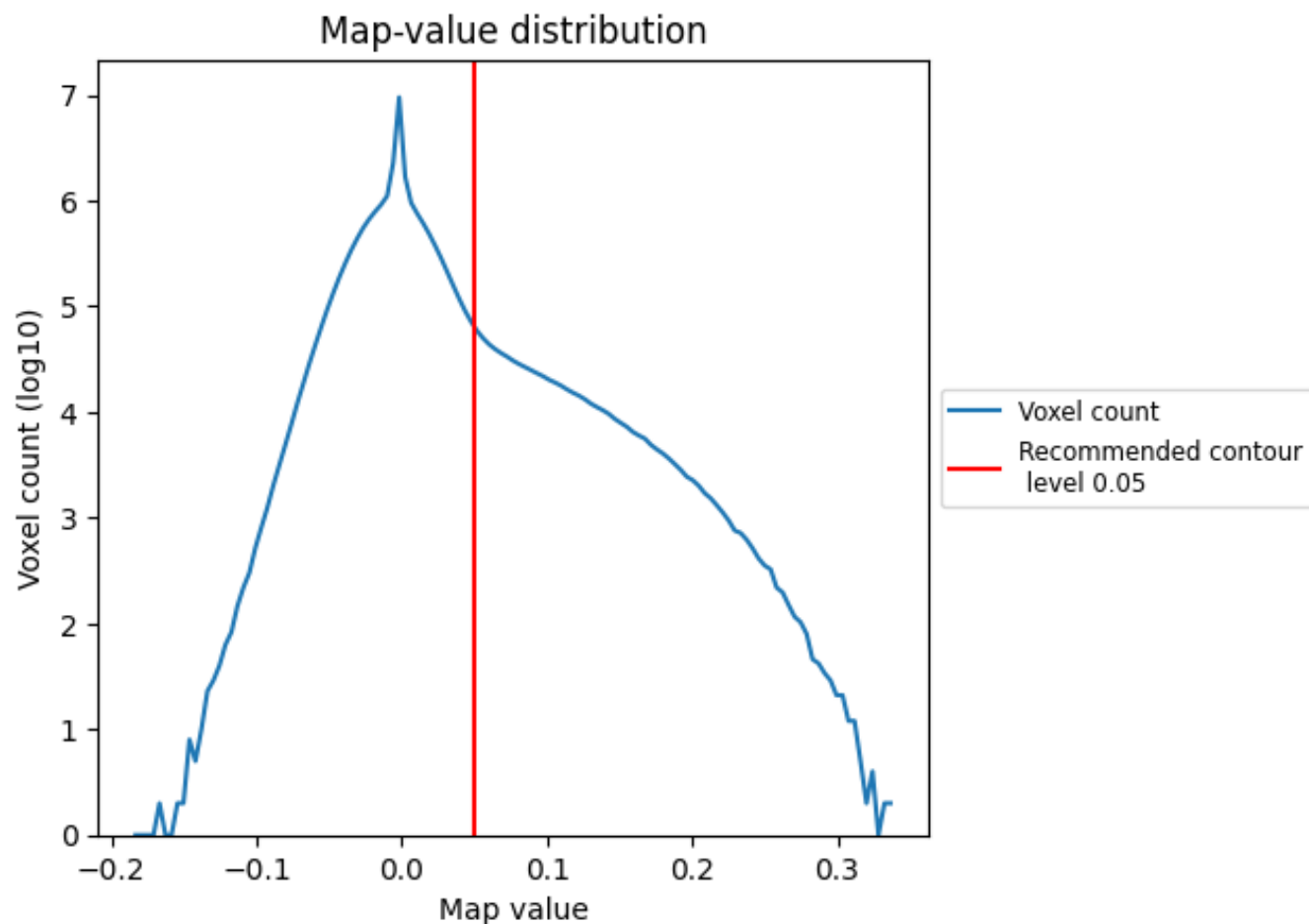
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

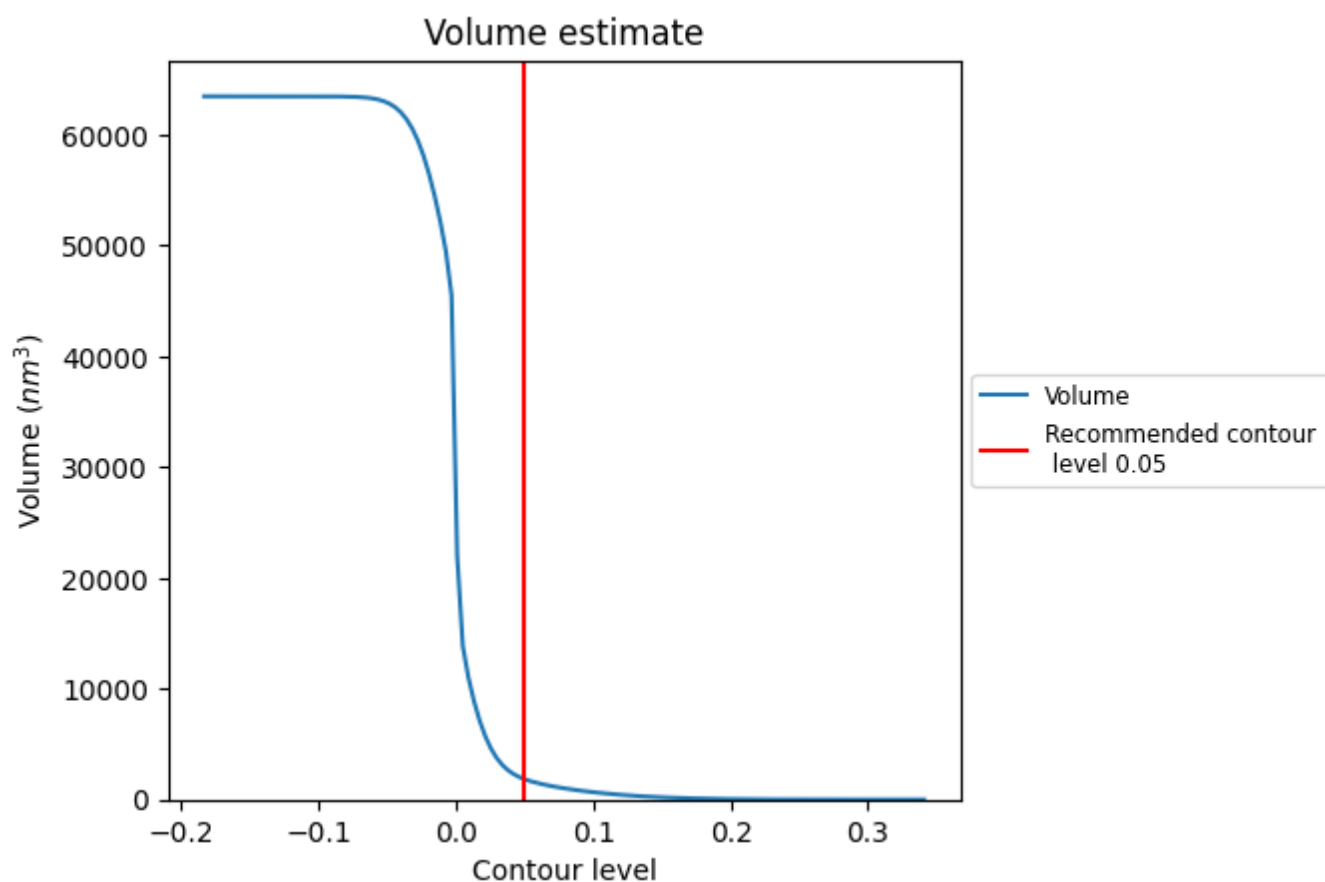
This section contains the results of statistical analysis of the map.

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.

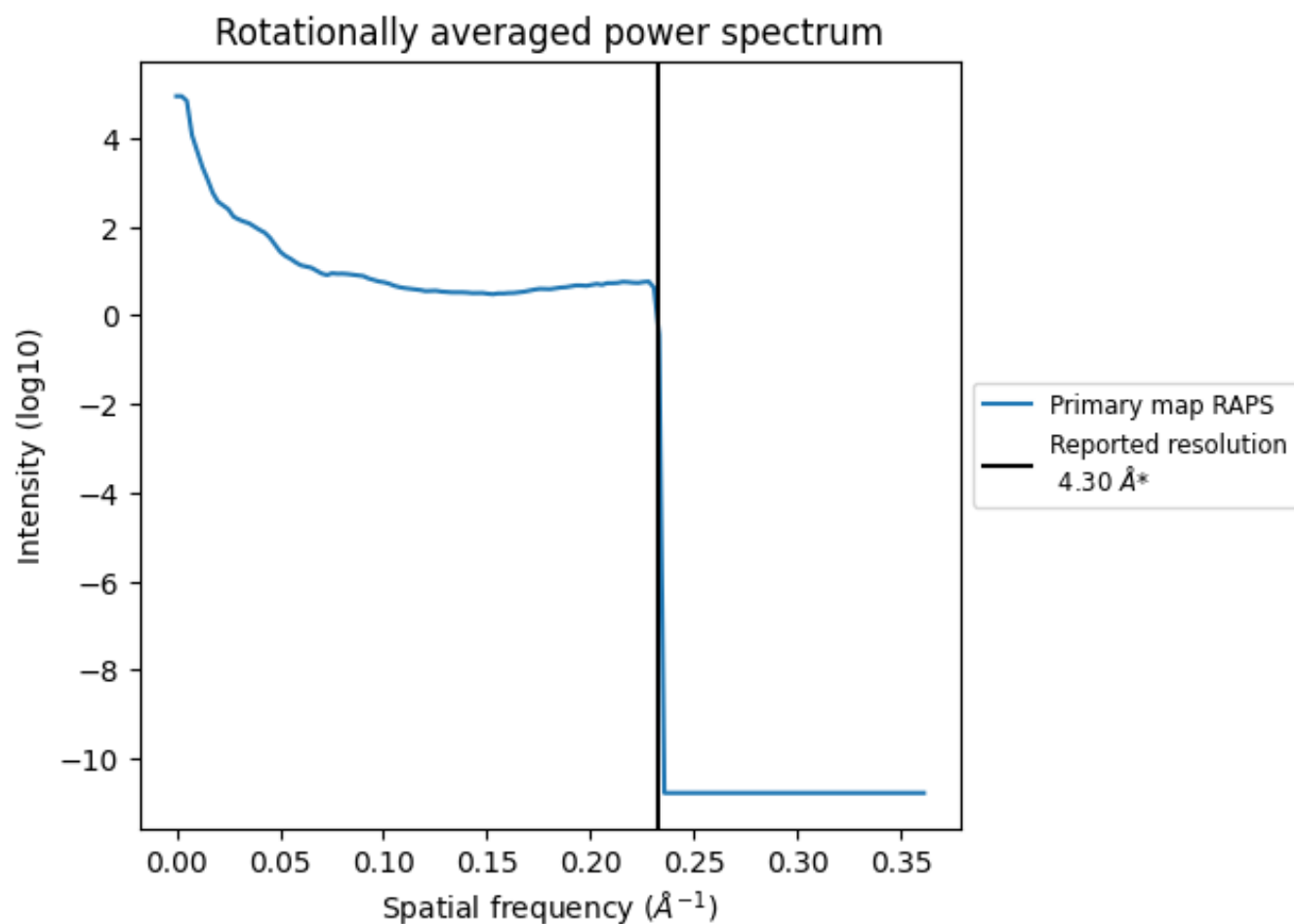
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1835 nm³; this corresponds to an approximate mass of 1658 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 0.233 $\text{\AA}^{-1}$

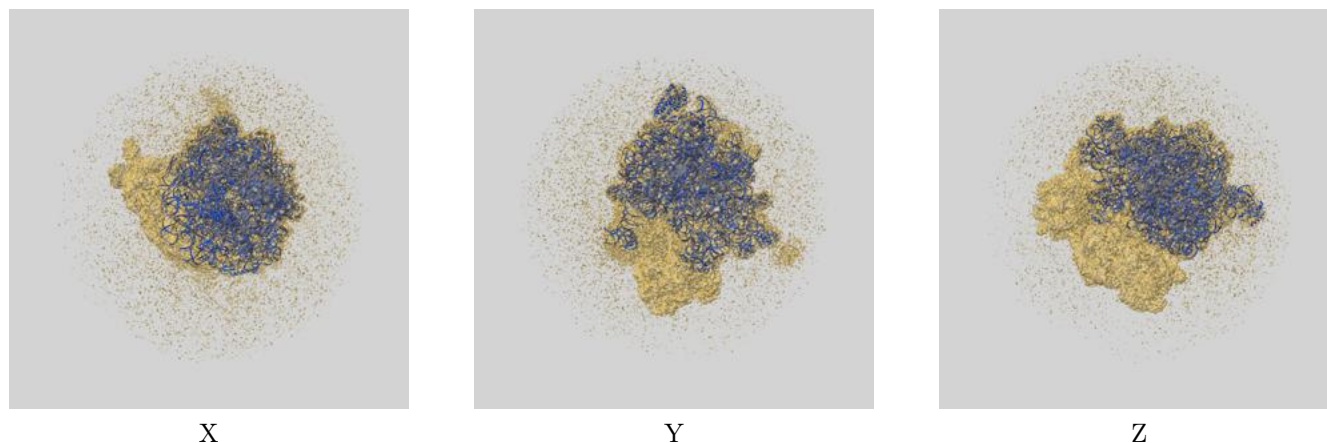
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

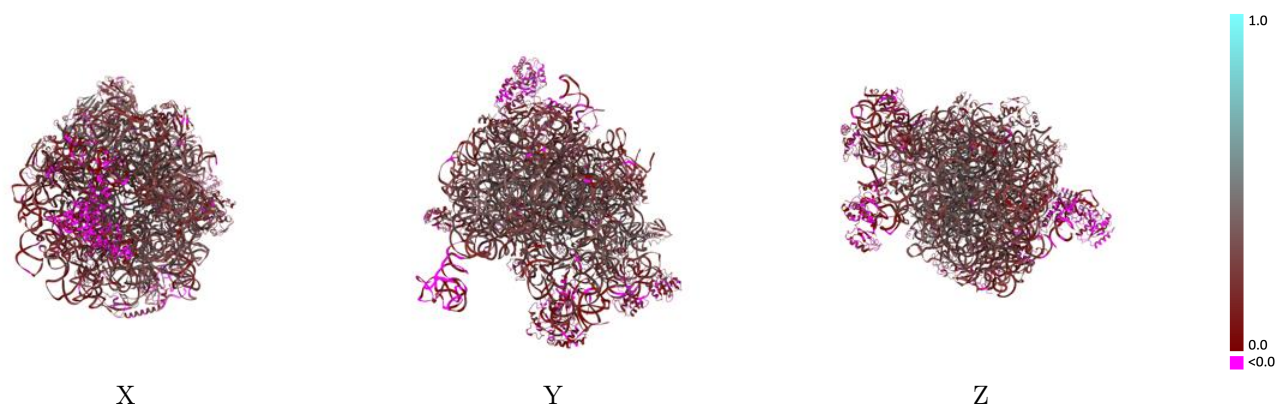
This section contains information regarding the fit between EMDB map EMD-8002 and PDB model 5GAF. Per-residue inclusion information can be found in section [3](#) on page [12](#).

9.1 Map-model overlay [i](#)



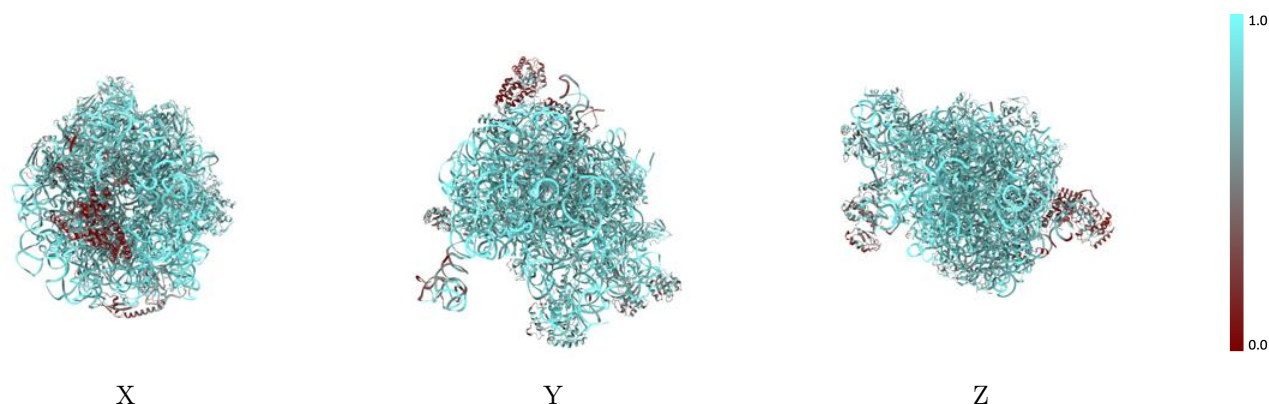
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



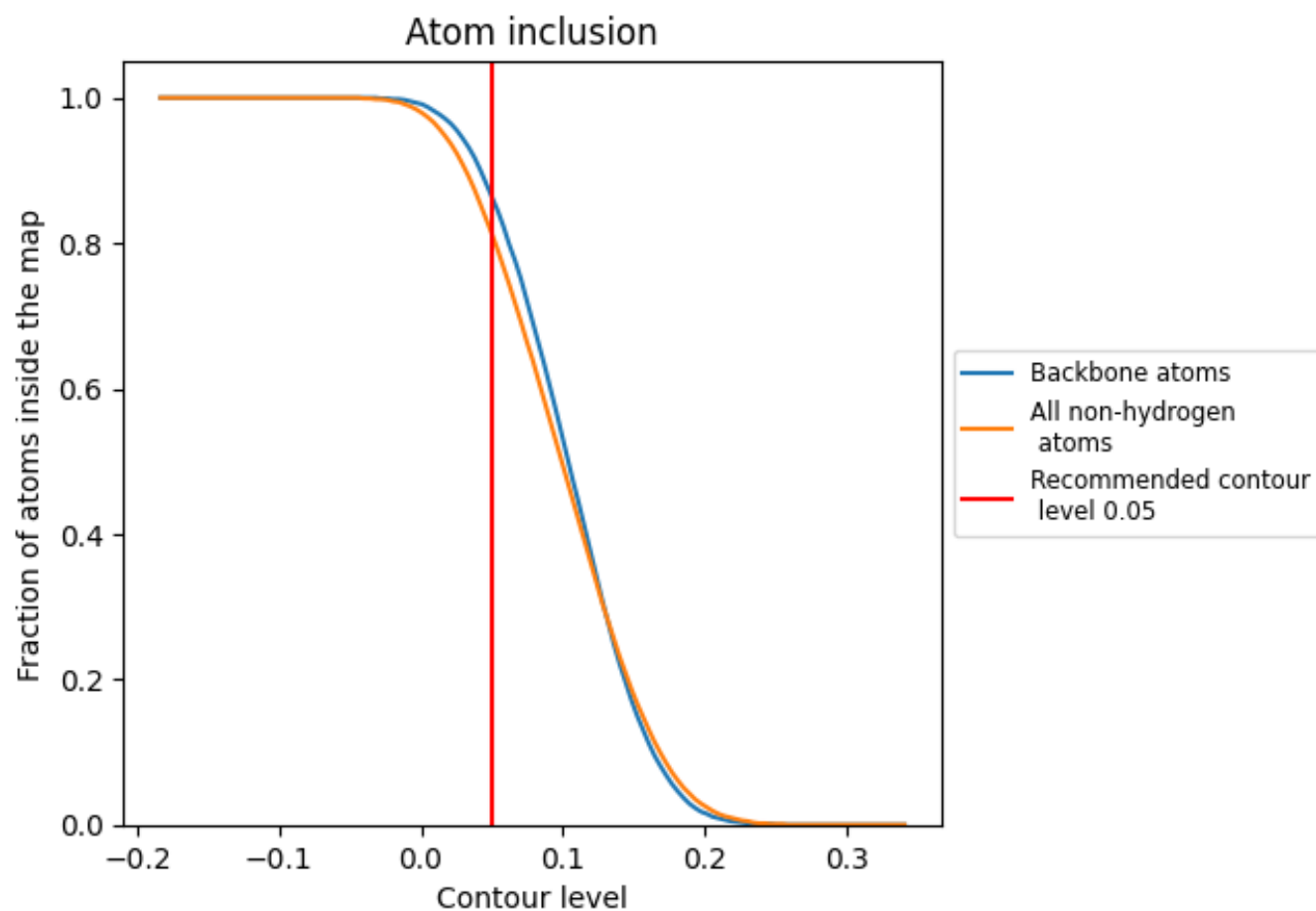
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 81% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8130	 0.2430
1	 0.5750	 0.0390
2	 0.8730	 0.3750
A	 0.8900	 0.2700
B	 0.8710	 0.1820
C	 0.6900	 0.2180
D	 0.7430	 0.2820
E	 0.7530	 0.2670
F	 0.6320	 0.1030
G	 0.7800	 0.2850
H	 0.4690	 0.1480
I	 0.5400	 0.1020
J	 0.4470	 0.0500
K	 0.7810	 0.2830
L	 0.6910	 0.2590
M	 0.7800	 0.2670
N	 0.7680	 0.3270
O	 0.6750	 0.1690
P	 0.7110	 0.0850
Q	 0.6490	 0.1780
R	 0.7910	 0.2680
S	 0.7570	 0.2320
T	 0.6650	 0.2390
U	 0.6490	 0.1850
V	 0.7330	 0.1930
W	 0.7520	 0.2130
X	 0.7360	 0.2240
Y	 0.7790	 0.3260
Z	 0.6970	 0.2150
a	 0.7230	 0.2410
b	 0.7090	 0.2110
c	 0.6480	 0.2380
d	 0.7630	 0.3160
e	 0.7640	 0.3080
f	 0.8190	 0.3640



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Chain	Atom inclusion	Q-score
i	 0.2910	 0.0140
k	 0.1020	 0.0500