



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:44 PM UTC

PDB ID : 6I0Y / pdb_00006i0y
EMDB ID : EMD-0322
Title : TnaC-stalled ribosome complex with the titin I27 domain folding close to the ribosomal exit tunnel
Authors : Su, T.; Kudva, R.; von Heijne, G.; Beckmann, R.
Deposited on : 2018-10-26
Resolution : 3.20 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:

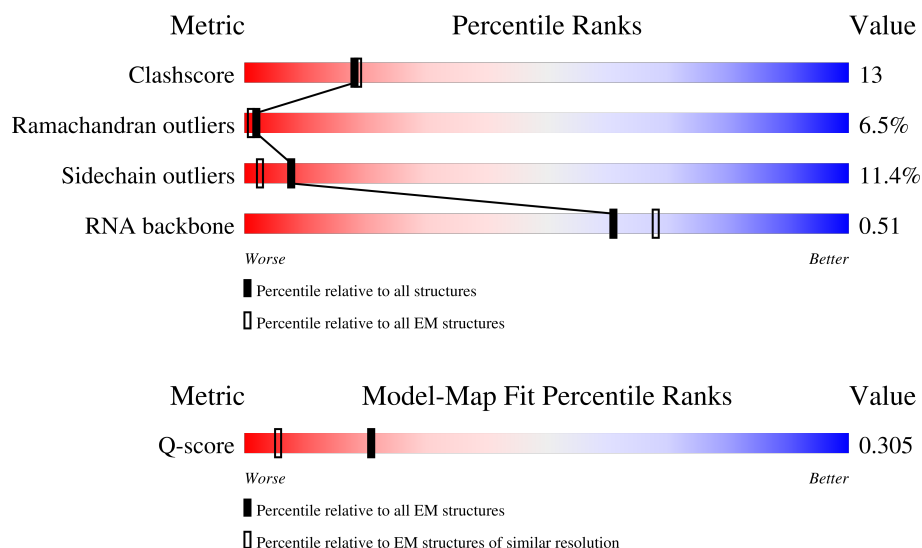
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.20 Å.

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



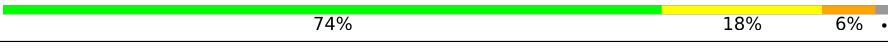
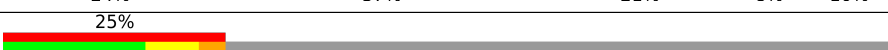
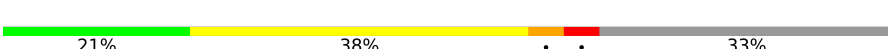
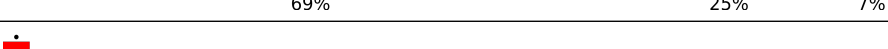
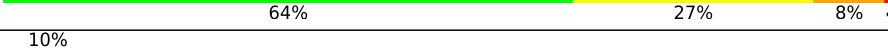
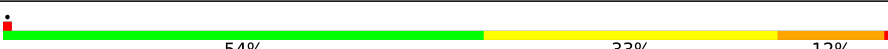
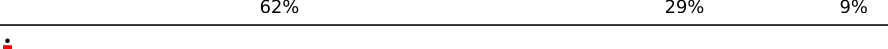
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	h	104	
2	0	57	
3	1	55	

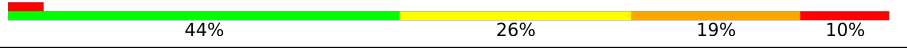
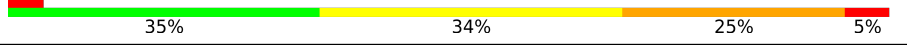
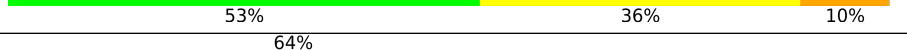
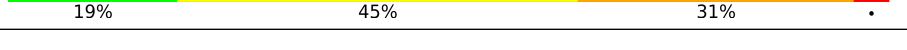
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Mol	Chain	Length	Quality of chain
4	2	46	
5	3	65	
6	4	38	
7	5	165	
8	6	121	
9	7	24	
10	8	94	
11	A	2903	
12	B	118	
13	C	273	
14	D	209	
15	E	201	
16	F	177	
17	G	176	
18	H	50	
19	I	141	
20	J	142	
21	K	122	
22	L	143	
23	M	136	
24	N	120	
25	O	116	
26	P	114	
27	Q	117	
28	R	103	

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Mol	Chain	Length	Quality of chain
29	S	110	
30	T	93	
31	V	77	
32	W	79	
33	X	77	
34	Y	63	
35	Z	58	
36	z	89	

2 Entry composition

There are 40 unique types of molecules in this entry. The entry contains 93619 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 L24.

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

- Molecule 2 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 3 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 4 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 5 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 6 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	5	148	Total	C	N	O	S	0	0
			1117	705	196	209	7		

- Molecule 8 is a protein called 50S ribosomal protein L7/L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	6	30	Total	C	N	O	S	0	0
			227	144	33	47	3		

- Molecule 9 is a protein called Tryptophanase operon leader peptide.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	7	16	Total	C	N	O	0	0
			139	89	26	24		

- Molecule 10 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	8	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 11 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	2854	Total	C	N	O	P	0	0
			61274	27334	11279	19807	2854		

- Molecule 12 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	B	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 13 is a protein called 50S ribosomal protein L2.

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

- Molecule 14 is a protein called 50S ribosomal protein L3.

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

- Molecule 15 is a protein called 50S ribosomal protein L4.

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

- Molecule 16 is a protein called 50S ribosomal protein L5.

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

- Molecule 17 is a protein called 50S ribosomal protein L6.

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

- Molecule 18 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	H	50	Total	C	N	O	S	0	0
			384	247	68	68	1		

- Molecule 19 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 20 is a protein called 50S ribosomal protein L13.

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

- Molecule 21 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 22 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 23 is a protein called 50S ribosomal protein L16.

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

- Molecule 24 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 25 is a protein called 50S ribosomal protein L18.

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

- Molecule 26 is a protein called 50S ribosomal protein L19.

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

- Molecule 27 is a protein called 50S ribosomal protein L20.

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

- Molecule 28 is a protein called 50S ribosomal protein L21.

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

- Molecule 29 is a protein called 50S ribosomal protein L22.

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

- Molecule 30 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 31 is a RNA chain called Proline tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	V	77	Total	C	N	O	P	0	0
			1649	733	297	542	77		

- Molecule 32 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	W	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 33 is a protein called 50S ribosomal protein L28.

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

- Molecule 34 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 35 is a protein called 50S ribosomal protein L30.

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

- Molecule 36 is a protein called Titin.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	z	89	Total	C	N	O	S	0	0
			688	439	113	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
z	3	GLU	LYS	conflict	UNP Q8WZ42

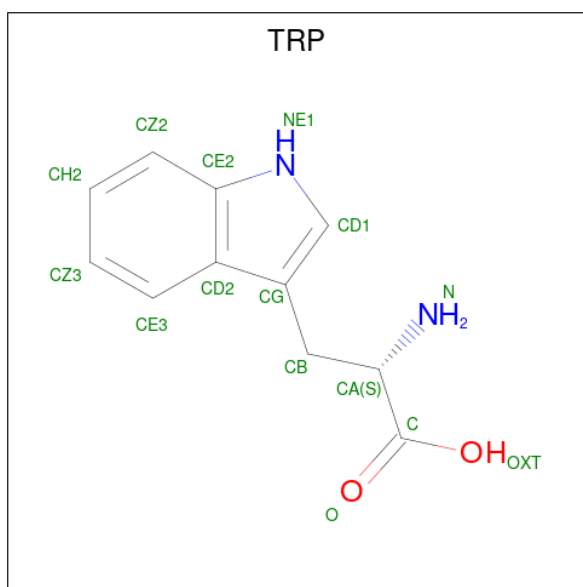
- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	4	1	Total	Mg	0
			1	1	
37	A	136	Total	Mg	0
			136	136	
37	B	4	Total	Mg	0
			4	4	
37	C	1	Total	Mg	0
			1	1	
37	E	1	Total	Mg	0
			1	1	

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

Mol	Chain	Residues	Atoms		AltConf
38	4	1	Total	Zn	0
			1	1	

- Molecule 39 is TRYPTOPHAN (CCD ID: TRP) (formula: C₁₁H₁₂N₂O₂).



Mol	Chain	Residues	Atoms				AltConf
39	A	1	Total	C	N	O	0
			15	11	2	2	

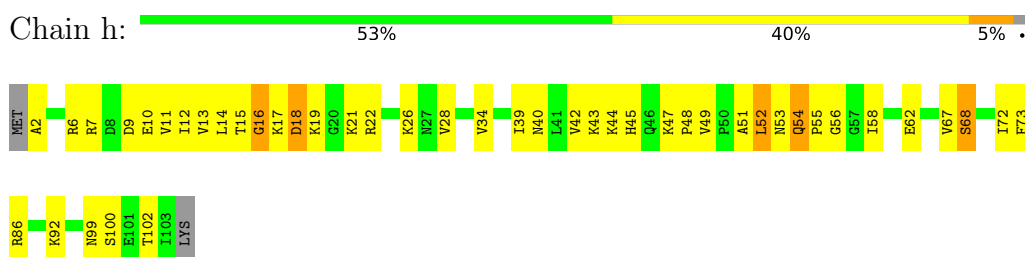
- Molecule 40 is water.

Mol	Chain	Residues	Atoms		AltConf
40	4	1	Total	O	0
			1	1	
40	A	415	Total	O	0
			415	415	
40	B	14	Total	O	0
			14	14	
40	C	2	Total	O	0
			2	2	
40	D	3	Total	O	0
			3	3	
40	E	1	Total	O	0
			1	1	
40	L	3	Total	O	0
			3	3	

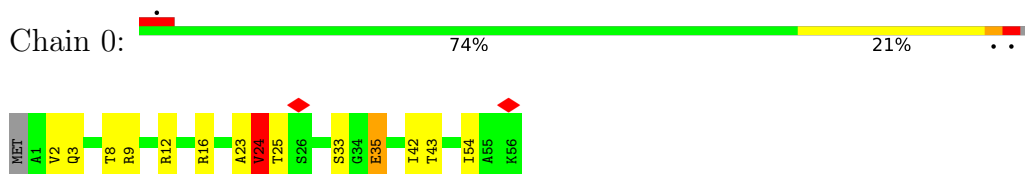
3 Residue-property plots [i](#)

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

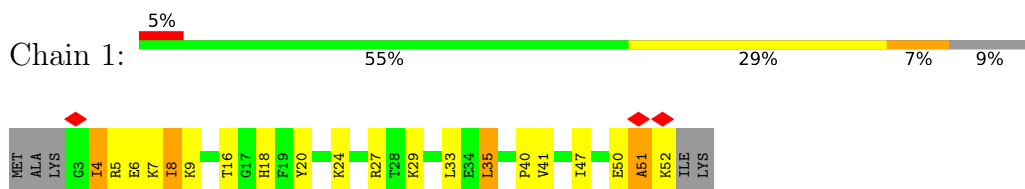
- Molecule 1: 50S ribosomal protein L24



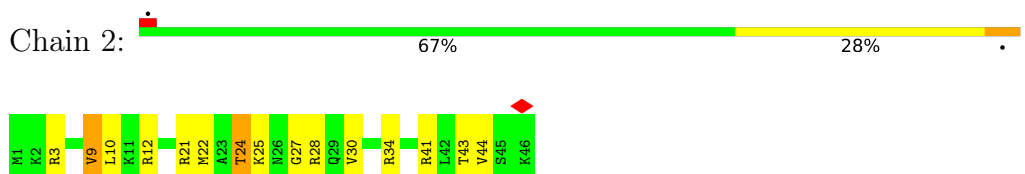
- Molecule 2: 50S ribosomal protein L32



- Molecule 3: 50S ribosomal protein L33



- Molecule 4: 50S ribosomal protein L34



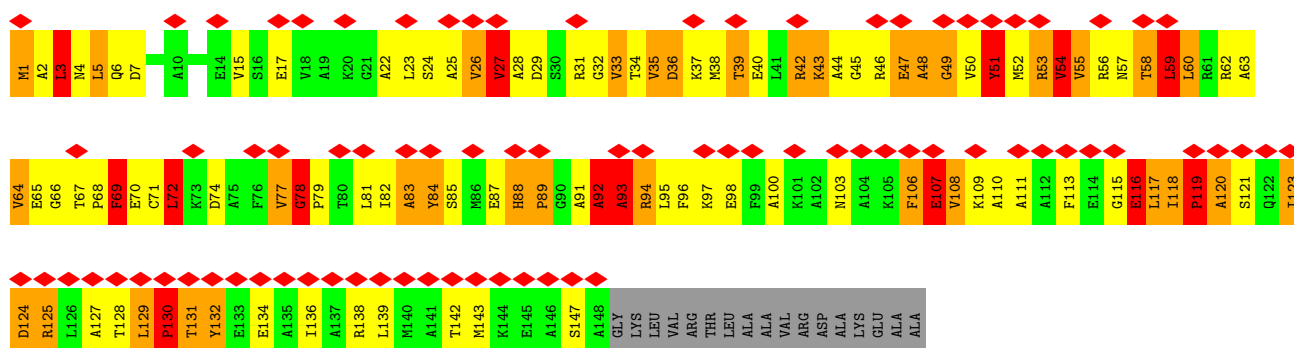
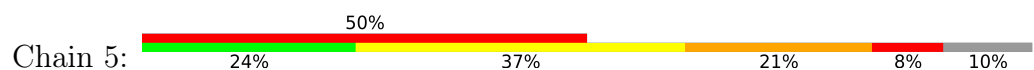
- Molecule 5: 50S ribosomal protein L35



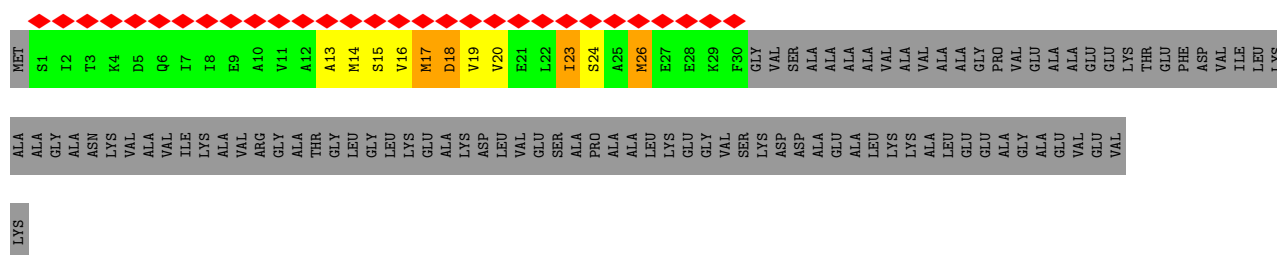
- Molecule 6: 50S ribosomal protein L36



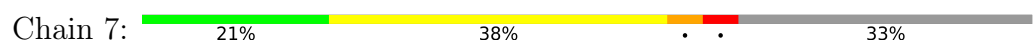
- Molecule 7: 50S ribosomal protein L10



- Molecule 8: 50S ribosomal protein L7/L12



- Molecule 9: Tryptophanase operon leader peptide



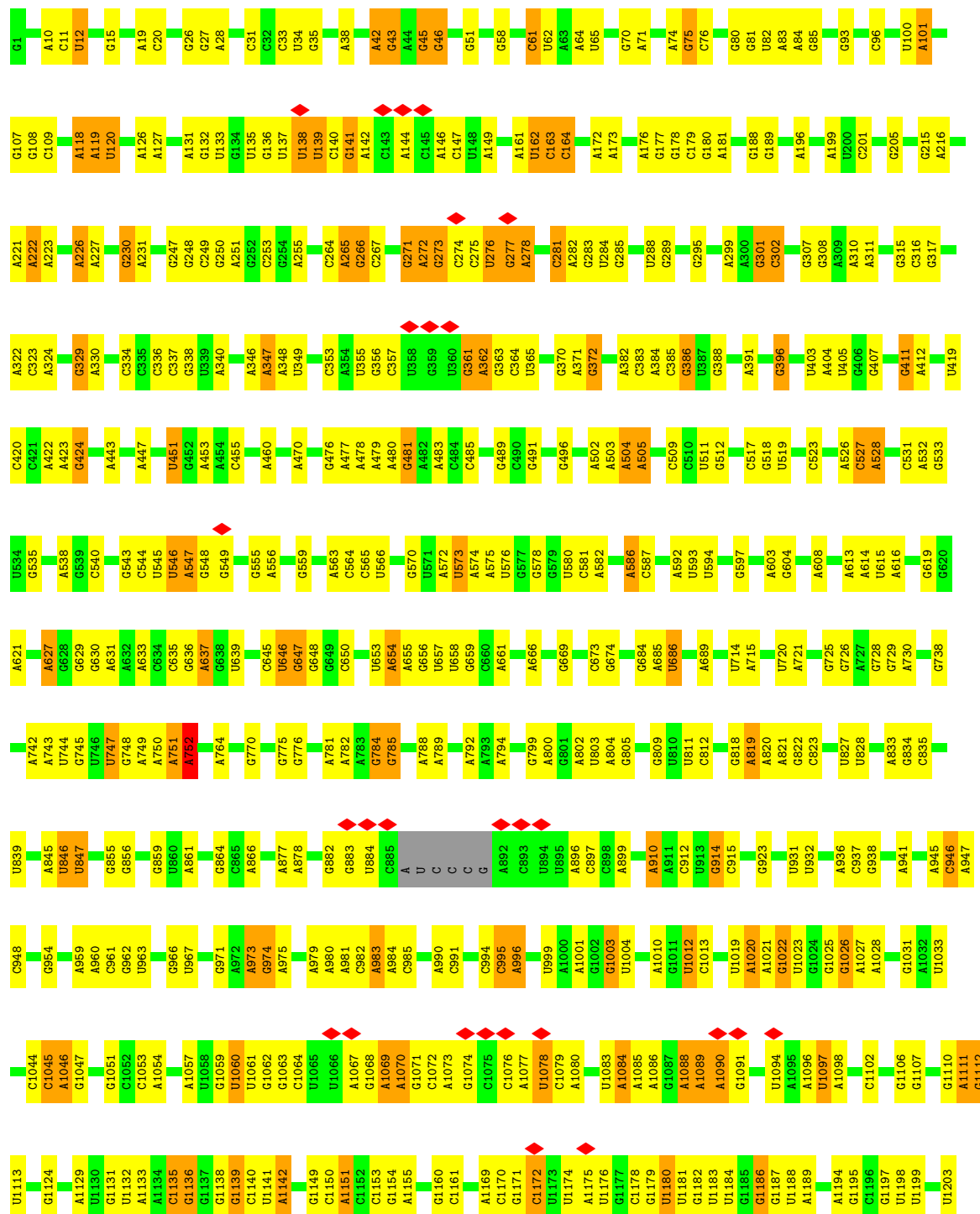
- Molecule 10: 50S ribosomal protein L25



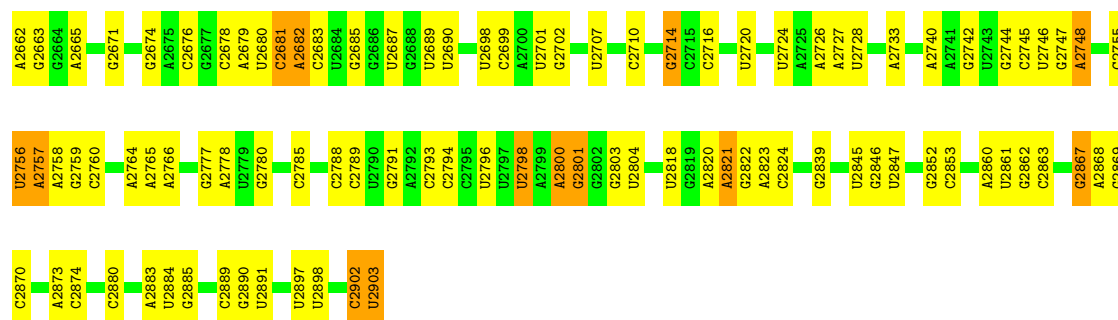


• Molecule 11: 23S ribosomal RNA

Chain A: 59% 31% 7%



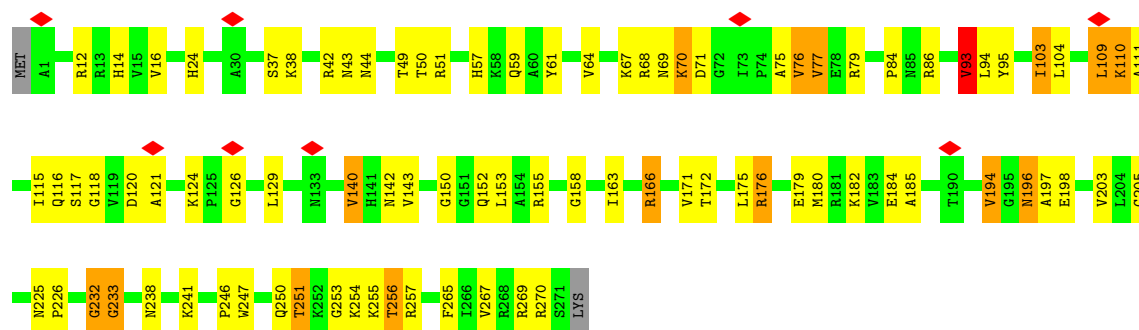
G2557	A2336	A2439	G2337	G2250	G2157	C2091	A1848	G1770	G1653	C1536	A1419	G1324	A1204
C2558	G2337	C2440	G2341	U2259	A	U2092	G1857	C1771	A1654	G1537	A1420	A1327	U1219
A2564	U2259	U2441	C2341	C	C	G2093	A1858	A1772	A1655	U1542	C1428	A1328	U1223
A2566	U2262	A2448	U2343	C	A2094	U1991	G1867	A1773	C1658	G1543	G1435	C1330	U1224
G2567	U2262		U2344	G		U1993	C1868	U1775	U1662	A1553	G1436	G1331	
	A2268		U2345	C	C2103	C2104	G1869	G1776	U1669	A1566	C1437	G1332	G1232
U2571	G2269	A2468	A2346	C	C2104	U2105	C1870	U1777	C1670	G1567	A1538	G1336	C1233
A2572	U2274	A2469	C2347	U	U2106	U2107	A1871	U1778	C1670	G1569	U1437	G1337	G1238
C2573	U2348	G2470	U2348	U	C2107	A2108	A1872	U1779	A1676	A1570	U1438	G1338	G1239
	G2275		G2275	G	A2109	U2109	G1873	U1782	G1674	A1571	U1439	G1339	U1240
G2576	G2276	A2476	G2276	A	U2110	U2110	G1884	A1785	A1677	U1576	G1450	G1340	
C2579	G2277	U2477	G2277	A	U		C1905	A1786	G1681	U1587	G1451	G1341	A1247
U2580	A2478		G2278	A	G	A2015	G1906	A1786	U1681	G1587	G1452	A1342	G1248
G2581	G2279		G2279	A	U	U2016	G1907	A1789	G1684	U1588	G1453	G1343	U1249
G2582	C2283	A2482	C2283	A	U	U2017	C1908	C1790	G1685	G1589	U1454	G1344	U1250
G2583	C2285		C2285	C	A	U2018	C1909	C1790	U1686	U1588	G1455	C1251	C1251
U2584	C2286		C2286	C	G	A2019	C1909	C1790	U1686	U1588	U1456	G1348	G1252
U2585	C2287		C2287	C	G	A2020	C1909	C1790	U1686	U1588	U1457	G1349	A1253
U2586	A2287		A2287	C	A	A2021	C1913	G1797	C1691	G1585	U1458	U1352	G1256
A2587	G2288		G2288	C	U	C2021	A1914	U1798	U1692	G1586	G1459	A1353	
G2588	G2289		G2289	C	A	U2022	U1915	G1798	U1692	U1586	G1460	A1359	
	A2297		A2297	C	G	C2023	U1915	G1798	G1703	G1587	G1461	U1262	U1263
G2589	A2298		A2298	C	U	C2024	U1915	G1798	G1704	U1587	U1466	U1266	
G2599	G2301		G2301	C	U	C2025	U1915	G1798	C1704	G1587	U1466	G1267	
A2600	U2181		U2181	C	U	A2030	A1927	A1801	A1591	U1469	U1469	G1268	
G2601	G2302		G2302	C	U	A2031	A1928	A1802	C1592	U1474	U1474	U1268	
G2602	U2302		U2302	C	U	G2032	A1928	A1803	A1593	U1475	U1475	A1268	
G2603	U2303		U2303	C	U	G2033	A1928	A1804	U1594	U1476	U1476	A1269	
U2604	U2304		U2304	C	U	A2033	A1930	A1805	G1715	U1477	U1477	G1270	
G2607	U2305		U2305	C	U	G2038	A1936	A1808	A1722	G1478	G1478	G1271	
G2608	G2306		G2306	C	U	U2039	A1937	G1811	G1723	G1479	G1479	A1272	
U2609	G2307		G2307	C	U	G2040	A1938	G1812	G1729	G1482	G1482	U1273	
G2610	U2198		U2198	C	U	C2043	U1939	G1813	U1730	U1485	U1485	G1277	
	A2199		A2199	C	U		U1940	G1814	G1737	U1486	U1486	G1281	
U2613	G2310		G2310	C	U	C2047	U1943	A1815	G1738	U1487	U1487	G1288	
A2614	U2311		U2311	C	U	G2048	U1944	A1816	A1739	C1493	C1493	G1289	
U2615	G2312		G2312	C	U	U2053	U1945	A1817	A1739	A1494	A1494	C1290	
G2616	U2313		U2313	C	U	G2054	U1946	A1818	A1744	A1495	A1495	C1298	
U2617	A2314		A2314	C	U	G2055	U1955	A1819	U1747	A1504	A1504	G1299	
G2618	U2315		U2315	C	U	C2056	U1956	U1820	U1748	A1509	A1509	A1301	
G2619	G2316		G2316	C	U	G2057	U1957	G1824	G1750	G1510	G1510	G1309	
	U2210		U2210	C	U	A2060	U1960	A1829	G1753	U1397	U1397	U1312	
U2629	A2211		A2211	C	U	G2061	U1963	C1833	A1754	G1626	G1626	C1313	
G2637	U2212		U2212	C	U	C2062	U1963	C1837	U1757	U1398	U1398	G1314	
G2638	U2213		U2213	C	U	C2063	U1966	C1838	U1758	A1403	A1403	C1404	
U2647	G2230		G2230	C	U	G2069	C1967	G1839	A1759	U1523	U1523	U1316	
C2649	U2231		U2231	C	U	A2070	C1968	G1839	C1760	G1524	G1524	G1317	
U2650	U2232		U2232	C	U	A2071	C1969	C1843	C1761	U1647	U1647	A1322	
	G2233		G2233	C	U	C2072	A1970	C1844	A1762	C1533	C1533	G1416	
A2654	U2234		U2234	C	U	G2073	U1971	G1763	A1763	U1534	U1534	A1322	
U2657	G2235		G2235	C	U	C2074	U1972	G1763	C1764	G1649	G1649	C1323	
G2661	U2236		U2236	C	U	U2075	U1972	A1847		A1652	A1652		



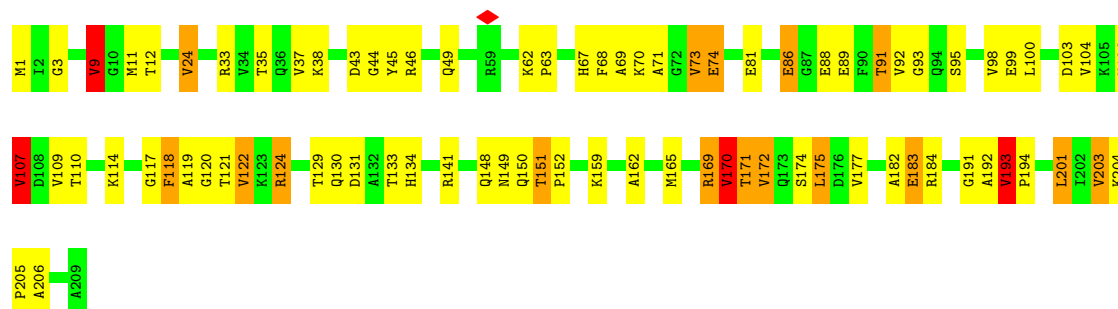
• Molecule 12: 5S ribosomal RNA



• Molecule 13: 50S ribosomal protein L2

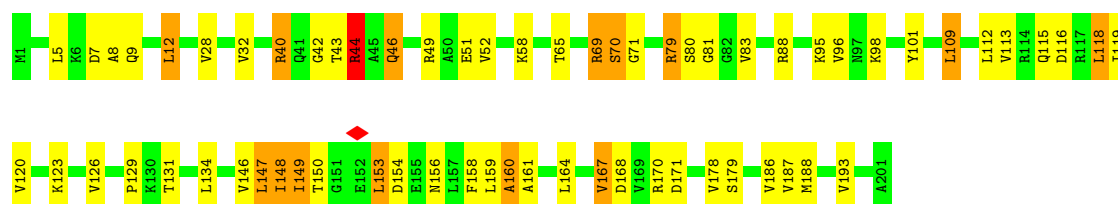


• Molecule 14: 50S ribosomal protein L3

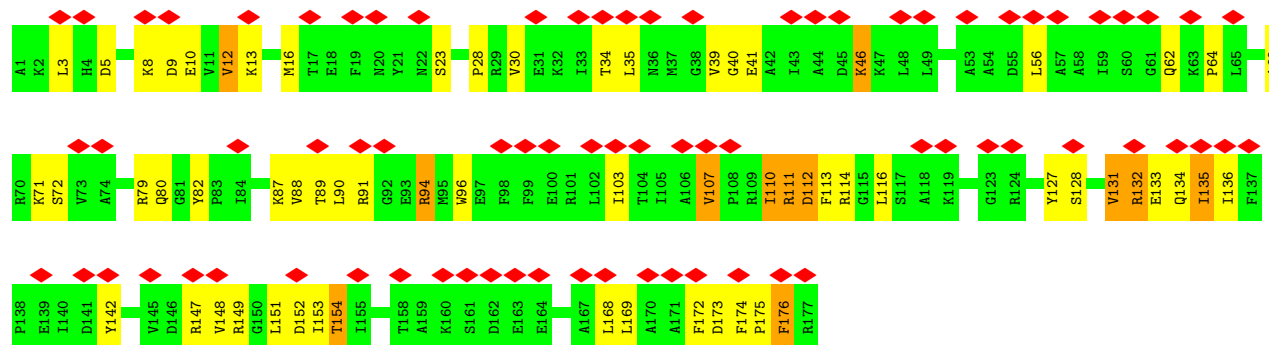
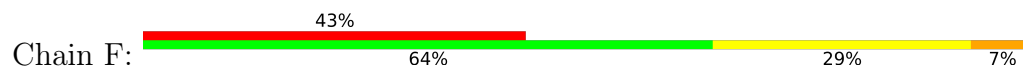


• Molecule 15: 50S ribosomal protein L4

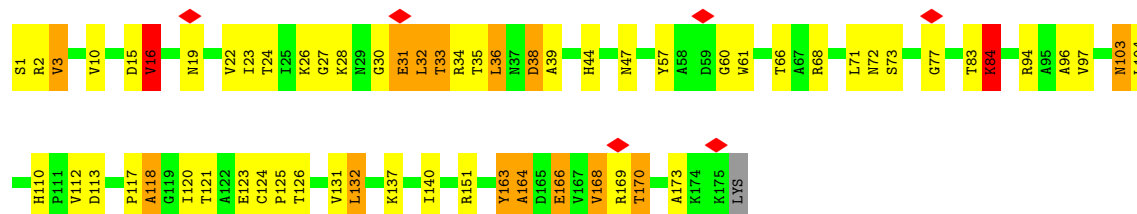




• Molecule 16: 50S ribosomal protein L5



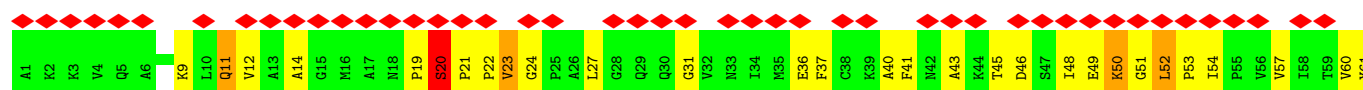
• Molecule 17: 50S ribosomal protein L6

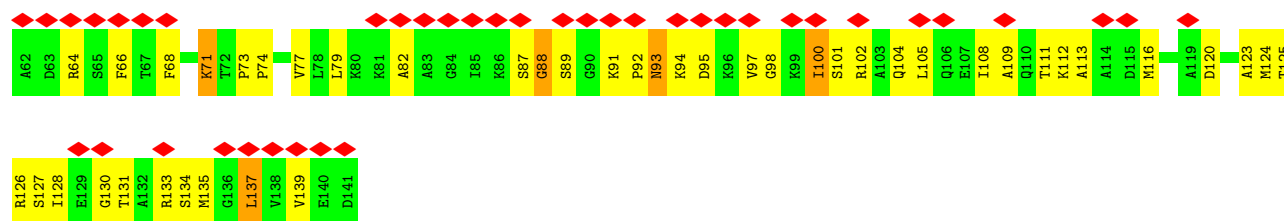


• Molecule 18: 50S ribosomal protein L9

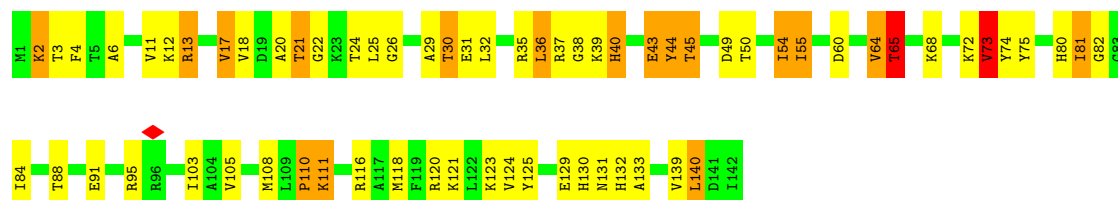


• Molecule 19: 50S ribosomal protein L11

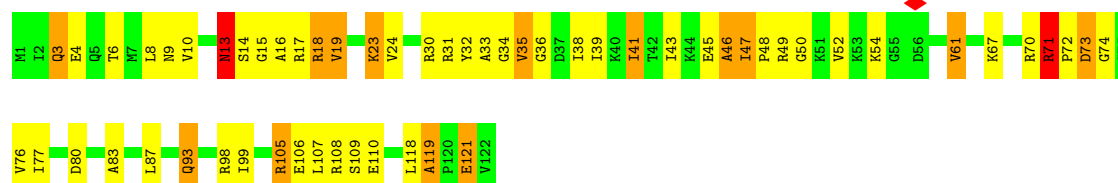




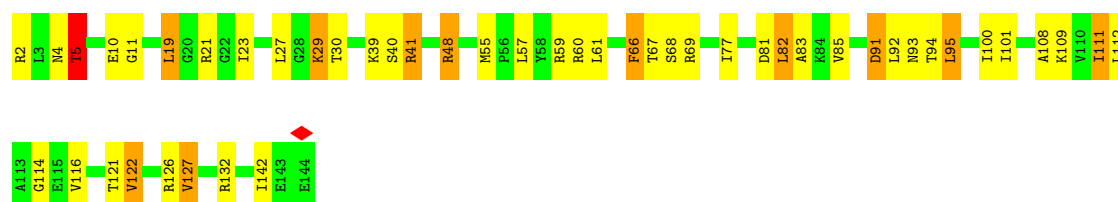
• Molecule 20: 50S ribosomal protein L13



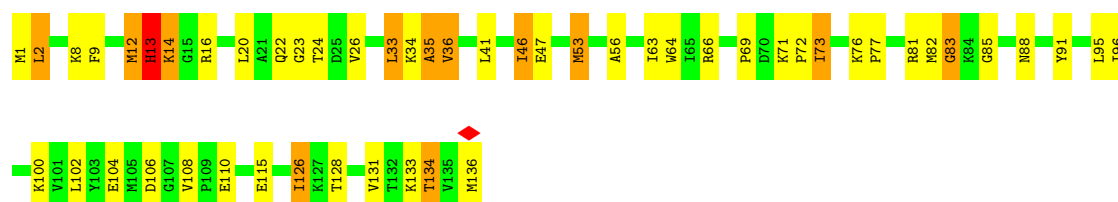
• Molecule 21: 50S ribosomal protein L14



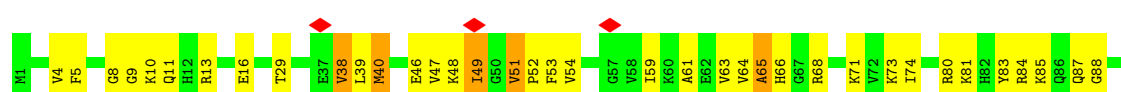
• Molecule 22: 50S ribosomal protein L15

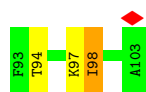


• Molecule 23: 50S ribosomal protein L16

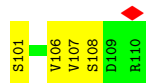


Chain N: 65% 30% 5%

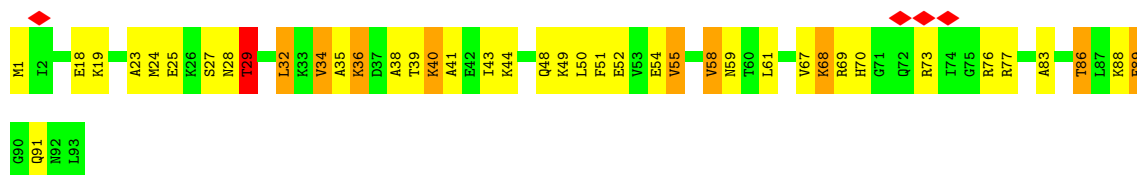




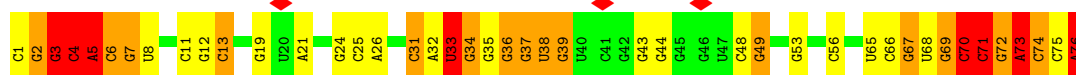
- Molecule 29: 50S ribosomal protein L22



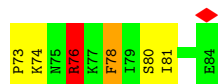
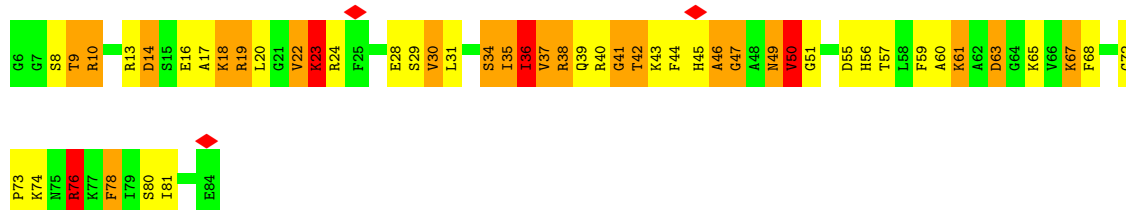
- Molecule 30: 50S ribosomal protein L23



- Molecule 31: Proline tRNA



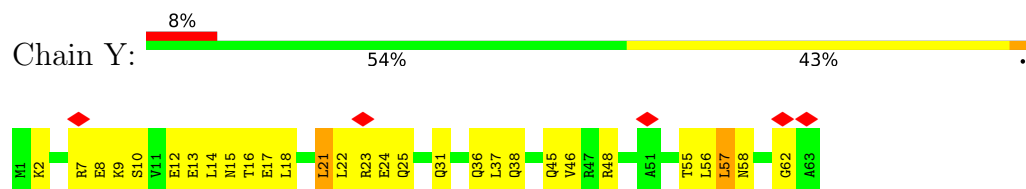
- Molecule 32: 50S ribosomal protein L27



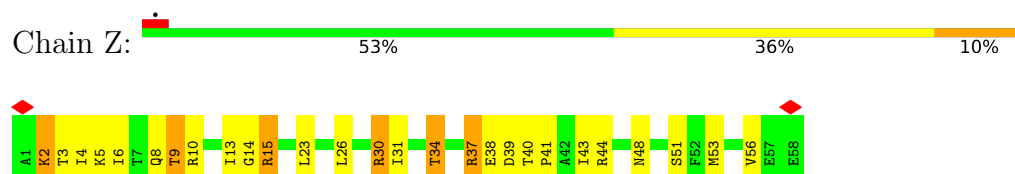
- Molecule 33: 50S ribosomal protein L28



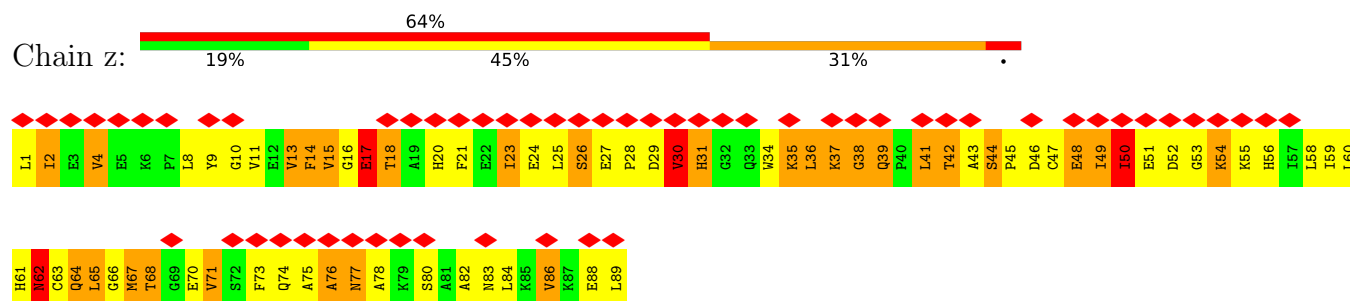
- Molecule 34: 50S ribosomal protein L29



- Molecule 35: 50S ribosomal protein L30



- Molecule 36: Titin



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	301510	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 ($e^-/\text{\AA}^2$)	0.926	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.240	Depositor
Minimum map value	-0.171	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.019	Depositor
Map size (Å)	394.31998, 394.31998, 394.31998	wwPDB
Map dimensions	372, 372, 372	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	h	0.85	1/787 (0.1%)	1.20	8/1051 (0.8%)
2	0	0.69	0/450	0.89	0/599
3	1	0.68	0/416	1.02	2/554 (0.4%)
4	2	0.73	0/380	0.99	0/498
5	3	0.72	0/513	0.96	1/676 (0.1%)
6	4	0.86	1/303 (0.3%)	1.19	1/397 (0.3%)
7	5	0.90	1/1131 (0.1%)	2.03	51/1524 (3.3%)
8	6	0.78	0/227	0.98	1/304 (0.3%)
9	7	0.73	0/143	1.45	3/193 (1.6%)
10	8	0.62	0/766	0.92	3/1025 (0.3%)
11	A	0.44	1/68626 (0.0%)	0.62	21/107056 (0.0%)
12	B	0.37	0/2828	0.55	0/4410
13	C	0.71	0/2121	1.10	8/2852 (0.3%)
14	D	0.75	0/1586	1.11	7/2134 (0.3%)
15	E	0.69	0/1571	1.00	3/2113 (0.1%)
16	F	0.60	0/1434	0.99	5/1926 (0.3%)
17	G	0.69	0/1333	0.99	1/1805 (0.1%)
18	H	0.69	0/389	1.05	1/523 (0.2%)
19	I	0.83	0/1046	1.23	12/1410 (0.9%)
20	J	0.81	1/1152 (0.1%)	1.07	3/1551 (0.2%)
21	K	0.83	0/947	1.03	2/1268 (0.2%)
22	L	0.74	0/1054	1.00	0/1403
23	M	0.79	0/1093	1.04	3/1460 (0.2%)
24	N	0.68	0/973	0.90	0/1301
25	O	0.59	0/902	0.96	1/1209 (0.1%)
26	P	0.68	0/929	1.03	2/1242 (0.2%)
27	Q	0.79	0/960	0.95	1/1278 (0.1%)
28	R	0.71	0/829	1.04	3/1107 (0.3%)
29	S	1.27	14/864 (1.6%)	1.40	10/1156 (0.9%)
30	T	0.74	0/744	1.11	3/994 (0.3%)
31	V	1.39	12/1842 (0.7%)	1.45	32/2870 (1.1%)
32	W	0.95	2/603 (0.3%)	1.28	4/797 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	X	0.66	0/635	0.98	1/848 (0.1%)
34	Y	0.55	0/510	0.98	0/677
35	Z	0.75	0/453	1.08	0/605
36	z	1.44	0/701	1.63	5/946 (0.5%)
All	All	0.59	33/101241 (0.0%)	0.80	198/151762 (0.1%)

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
7	5	0	1
13	C	0	1
14	D	0	1
20	J	0	1
21	K	0	1
29	S	0	3
31	V	0	13
All	All	0	21

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
29	S	88	ARG	CA-C	-11.94	1.37	1.52
29	S	86	MET	CA-C	-10.71	1.39	1.52
11	A	2602	A	O3'-P	-8.06	1.49	1.61
29	S	94	ASP	C-O	-7.67	1.14	1.23
29	S	89	ALA	C-O	-7.46	1.14	1.23

The worst 5 of 198 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	2608	G	C4'-C3'-O3'	18.96	141.45	113.00
29	S	86	MET	C-N-CD	-17.20	54.47	125.00
29	S	88	ARG	N-CA-C	-15.45	85.93	109.41
11	A	751	A	C4'-C3'-O3'	14.99	135.48	113.00
14	D	151	THR	CA-C-N	-14.28	104.05	119.19

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	5	130	PRO	Peptide
13	C	233	GLY	Peptide
14	D	9	VAL	Peptide
20	J	110	PRO	Peptide
21	K	71	ARG	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	h	779	0	829	81	0
2	0	444	0	461	18	0
3	1	409	0	440	17	0
4	2	377	0	418	10	0
5	3	504	0	574	11	0
6	4	302	0	340	18	0
7	5	1117	0	1155	135	0
8	6	227	0	237	6	0
9	7	139	0	134	12	0
10	8	753	0	780	15	0
11	A	61274	0	30816	843	0
12	B	2529	0	1281	20	0
13	C	2082	0	2157	55	0
14	D	1565	0	1616	55	0
15	E	1552	0	1619	41	0
16	F	1410	0	1445	46	0
17	G	1313	0	1361	40	0
18	H	384	0	405	14	0
19	I	1032	0	1088	59	0
20	J	1129	0	1162	58	0
21	K	938	0	1012	45	0
22	L	1045	0	1117	40	0
23	M	1074	0	1157	29	0
24	N	960	0	1000	30	0
25	O	892	0	923	23	0
26	P	917	0	965	44	0
27	Q	947	0	1022	51	0
28	R	816	0	839	35	0
29	S	857	0	922	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	T	738	0	807	38	0
31	V	1649	0	833	52	0
32	W	596	0	610	83	0
33	X	625	0	655	17	0
34	Y	509	0	543	20	0
35	Z	449	0	491	18	0
36	z	688	0	691	198	0
37	4	1	0	0	0	0
37	A	136	0	0	0	0
37	B	4	0	0	0	0
37	C	1	0	0	0	0
37	E	1	0	0	0	0
38	4	1	0	0	0	0
39	A	15	0	9	3	0
40	4	1	0	0	0	0
40	A	415	0	0	77	0
40	B	14	0	0	1	0
40	C	2	0	0	0	0
40	D	3	0	0	0	0
40	E	1	0	0	0	0
40	L	3	0	0	0	0
All	All	93619	0	61914	2002	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 13.

The worst 5 of 2002 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:52:LEU:HD21	36:z:67:MET:N	1.18	1.42
1:h:51:ALA:O	36:z:36:LEU:CD1	1.68	1.40
1:h:51:ALA:HB2	36:z:67:MET:CE	1.52	1.36
16:F:79:ARG:NH2	31:V:56:C:O2	1.62	1.30
11:A:2062:A:H2'	11:A:2063:C:C6	1.70	1.27

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	h	100/104 (96%)	92 (92%)	6 (6%)	2 (2%)	6	31
2	0	54/57 (95%)	43 (80%)	7 (13%)	4 (7%)	1	6
3	1	48/55 (87%)	42 (88%)	3 (6%)	3 (6%)	1	8
4	2	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
5	3	62/65 (95%)	53 (86%)	7 (11%)	2 (3%)	3	21
6	4	36/38 (95%)	29 (81%)	4 (11%)	3 (8%)	0	4
7	5	146/165 (88%)	77 (53%)	41 (28%)	28 (19%)	0	0
8	6	28/121 (23%)	20 (71%)	7 (25%)	1 (4%)	2	19
9	7	14/24 (58%)	13 (93%)	0	1 (7%)	1	6
10	8	92/94 (98%)	81 (88%)	11 (12%)	0	100	100
13	C	269/273 (98%)	211 (78%)	43 (16%)	15 (6%)	1	11
14	D	207/209 (99%)	163 (79%)	30 (14%)	14 (7%)	1	7
15	E	199/201 (99%)	162 (81%)	27 (14%)	10 (5%)	1	13
16	F	175/177 (99%)	141 (81%)	30 (17%)	4 (2%)	5	29
17	G	173/176 (98%)	126 (73%)	30 (17%)	17 (10%)	0	2
18	H	48/50 (96%)	29 (60%)	14 (29%)	5 (10%)	0	2
19	I	139/141 (99%)	97 (70%)	33 (24%)	9 (6%)	1	8
20	J	140/142 (99%)	113 (81%)	18 (13%)	9 (6%)	1	8
21	K	120/122 (98%)	95 (79%)	15 (12%)	10 (8%)	0	4
22	L	141/143 (99%)	104 (74%)	32 (23%)	5 (4%)	3	20
23	M	134/136 (98%)	107 (80%)	16 (12%)	11 (8%)	0	4
24	N	118/120 (98%)	101 (86%)	16 (14%)	1 (1%)	16	50
25	O	114/116 (98%)	95 (83%)	18 (16%)	1 (1%)	14	47
26	P	112/114 (98%)	86 (77%)	17 (15%)	9 (8%)	1	4
27	Q	115/117 (98%)	99 (86%)	12 (10%)	4 (4%)	3	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	R	101/103 (98%)	83 (82%)	15 (15%)	3 (3%)	3	23
29	S	108/110 (98%)	91 (84%)	10 (9%)	7 (6%)	1	8
30	T	91/93 (98%)	57 (63%)	24 (26%)	10 (11%)	0	2
32	W	77/79 (98%)	39 (51%)	21 (27%)	17 (22%)	0	0
33	X	75/77 (97%)	64 (85%)	8 (11%)	3 (4%)	2	17
34	Y	61/63 (97%)	39 (64%)	18 (30%)	4 (7%)	1	7
35	Z	56/58 (97%)	46 (82%)	8 (14%)	2 (4%)	2	19
36	z	87/89 (98%)	60 (69%)	14 (16%)	13 (15%)	0	1
All	All	3484/3678 (95%)	2699 (78%)	558 (16%)	227 (6%)	2	8

5 of 227 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	0	23	ALA
5	3	22	LYS
6	4	8	LYS
7	5	27	VAL
7	5	48	ALA

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	h	83/85 (98%)	79 (95%)	4 (5%)	23	56
2	0	47/48 (98%)	46 (98%)	1 (2%)	47	71
3	1	45/49 (92%)	42 (93%)	3 (7%)	15	47
4	2	38/38 (100%)	35 (92%)	3 (8%)	11	40
5	3	51/52 (98%)	45 (88%)	6 (12%)	5	23
6	4	34/34 (100%)	29 (85%)	5 (15%)	3	16
7	5	112/123 (91%)	93 (83%)	19 (17%)	2	11
8	6	26/85 (31%)	21 (81%)	5 (19%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	7	16/24 (67%)	12 (75%)	4 (25%)	0	3
10	8	78/78 (100%)	73 (94%)	5 (6%)	16	48
13	C	216/218 (99%)	199 (92%)	17 (8%)	11	40
14	D	164/164 (100%)	143 (87%)	21 (13%)	4	20
15	E	165/165 (100%)	146 (88%)	19 (12%)	5	24
16	F	148/148 (100%)	135 (91%)	13 (9%)	9	35
17	G	136/137 (99%)	122 (90%)	14 (10%)	7	28
18	H	40/40 (100%)	38 (95%)	2 (5%)	22	55
19	I	109/109 (100%)	106 (97%)	3 (3%)	38	68
20	J	116/116 (100%)	97 (84%)	19 (16%)	2	12
21	K	103/103 (100%)	88 (85%)	15 (15%)	3	16
22	L	102/102 (100%)	89 (87%)	13 (13%)	4	20
23	M	109/109 (100%)	93 (85%)	16 (15%)	3	16
24	N	100/100 (100%)	90 (90%)	10 (10%)	7	30
25	O	86/86 (100%)	78 (91%)	8 (9%)	8	33
26	P	99/99 (100%)	87 (88%)	12 (12%)	5	22
27	Q	89/89 (100%)	80 (90%)	9 (10%)	7	30
28	R	84/84 (100%)	74 (88%)	10 (12%)	5	23
29	S	93/93 (100%)	81 (87%)	12 (13%)	4	20
30	T	80/80 (100%)	75 (94%)	5 (6%)	16	48
32	W	59/59 (100%)	50 (85%)	9 (15%)	3	14
33	X	67/67 (100%)	59 (88%)	8 (12%)	5	23
34	Y	55/55 (100%)	51 (93%)	4 (7%)	13	43
35	Z	48/48 (100%)	39 (81%)	9 (19%)	1	9
36	z	75/75 (100%)	50 (67%)	25 (33%)	0	1
All	All	2873/2962 (97%)	2545 (89%)	328 (11%)	8	24

5 of 328 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	P	80	VAL
33	X	34	SER
27	Q	17	LEU

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Mol	Chain	Res	Type
29	S	45	VAL
35	Z	37	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
34	Y	38	GLN
34	Y	41	HIS
14	D	173	GLN
14	D	49	GLN
36	z	31	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	2850/2903 (98%)	459 (16%)	40 (1%)
12	B	117/118 (99%)	17 (14%)	0
31	V	76/77 (98%)	15 (19%)	0
All	All	3043/3098 (98%)	491 (16%)	40 (1%)

5 of 491 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	10	A
11	A	12	U
11	A	15	G
11	A	34	U
11	A	35	G

5 of 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	1847	A
11	A	2326	C
11	A	1870	C
11	A	2142	A
11	A	2756	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 [i](#)

Of 145 ligands modelled in this entry, 144 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	TRP	A	3001	-	15,16,16	0.89	0	18,22,22	0.45	0

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	TRP	A	3001	-	-	7/8/8/8	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
39	A	3001	TRP	OXT-C-CA-N
39	A	3001	TRP	OXT-C-CA-CB
39	A	3001	TRP	O-C-CA-CB
39	A	3001	TRP	O-C-CA-N

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Mol	Chain	Res	Type	Atoms
39	A	3001	TRP	CA-CB-CG-CD2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	A	3001	TRP	3	0

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.

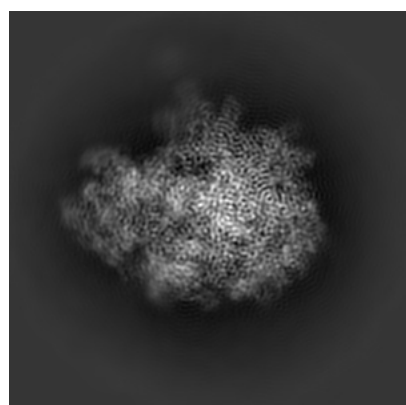
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0322. These allow visual inspection of the internal detail of the map and identification of artifacts.

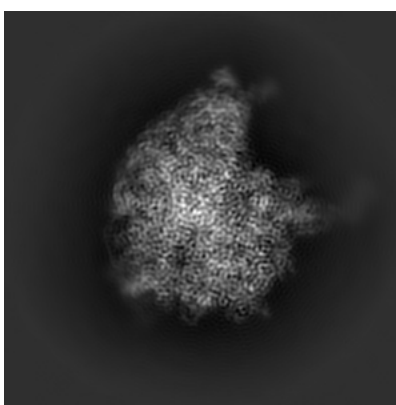
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

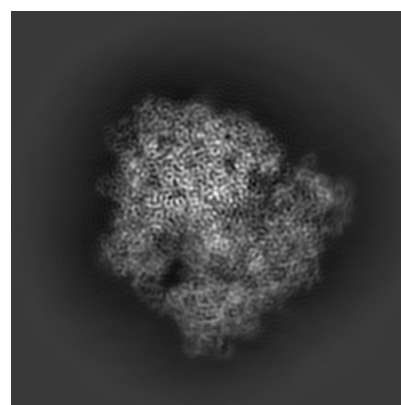
6.1.1 Primary map



X



Y

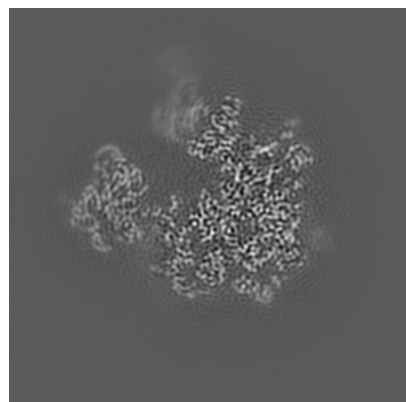


Z

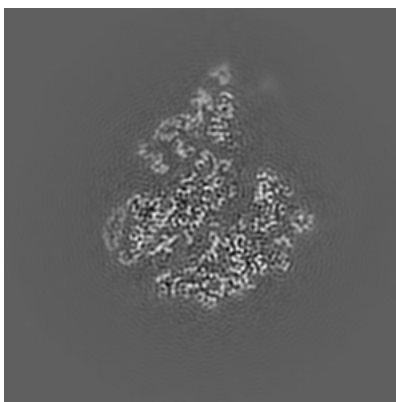
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

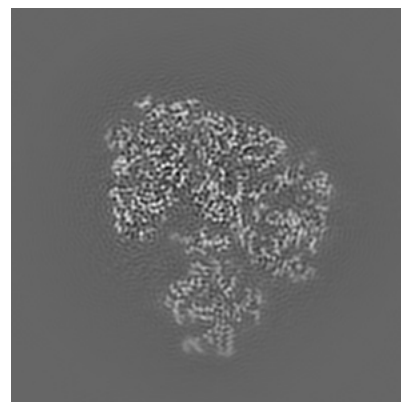
6.2.1 Primary map



X Index: 186



Y Index: 186

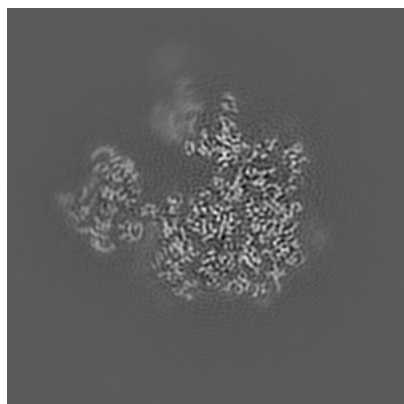


Z Index: 186

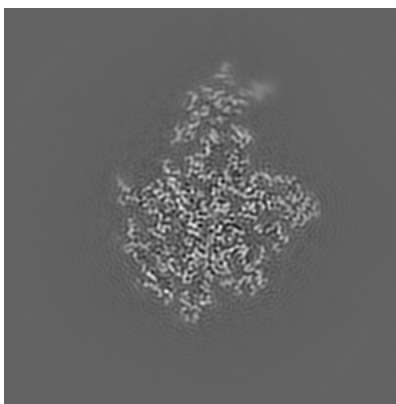
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

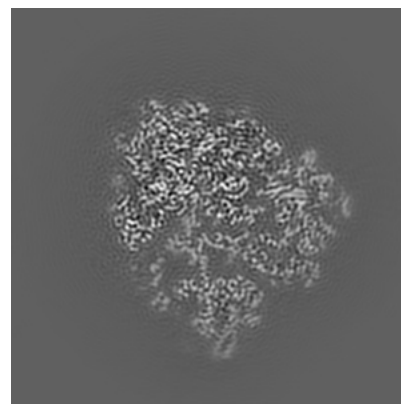
6.3.1 Primary map



X Index: 190



Y Index: 204

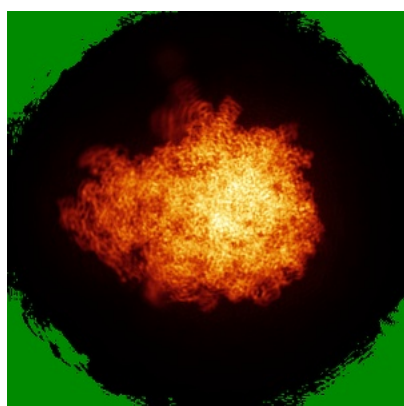


Z Index: 194

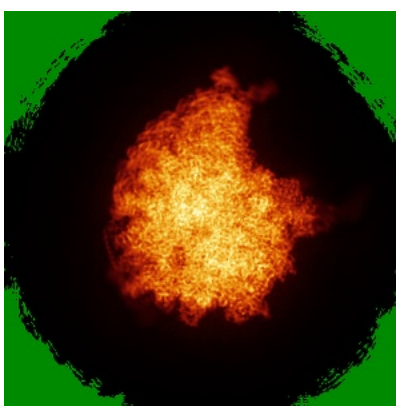
The images above show the largest variance slices of the map in three orthogonal directions.

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

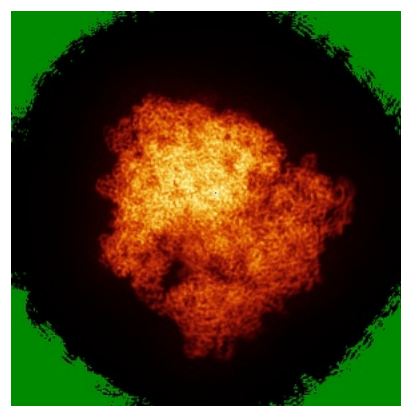
6.4.1 Primary map



X



Y

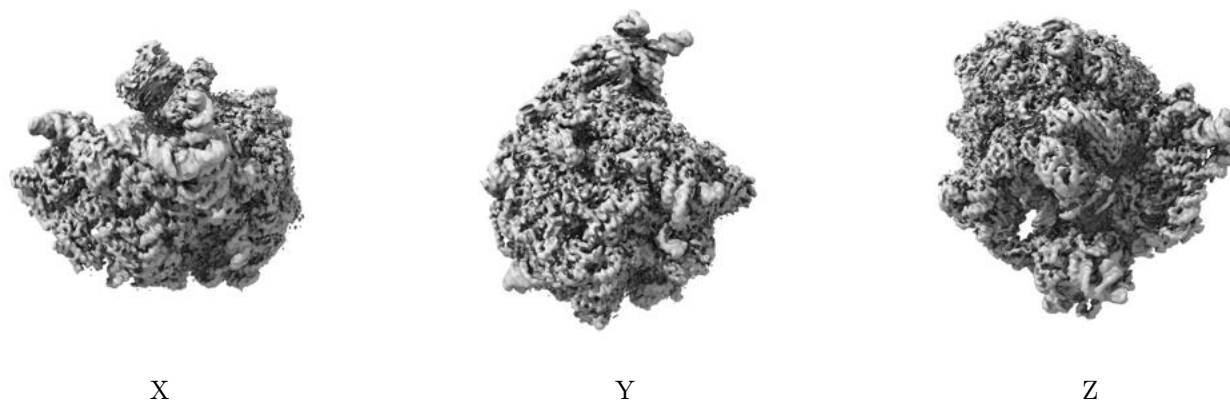


Z

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

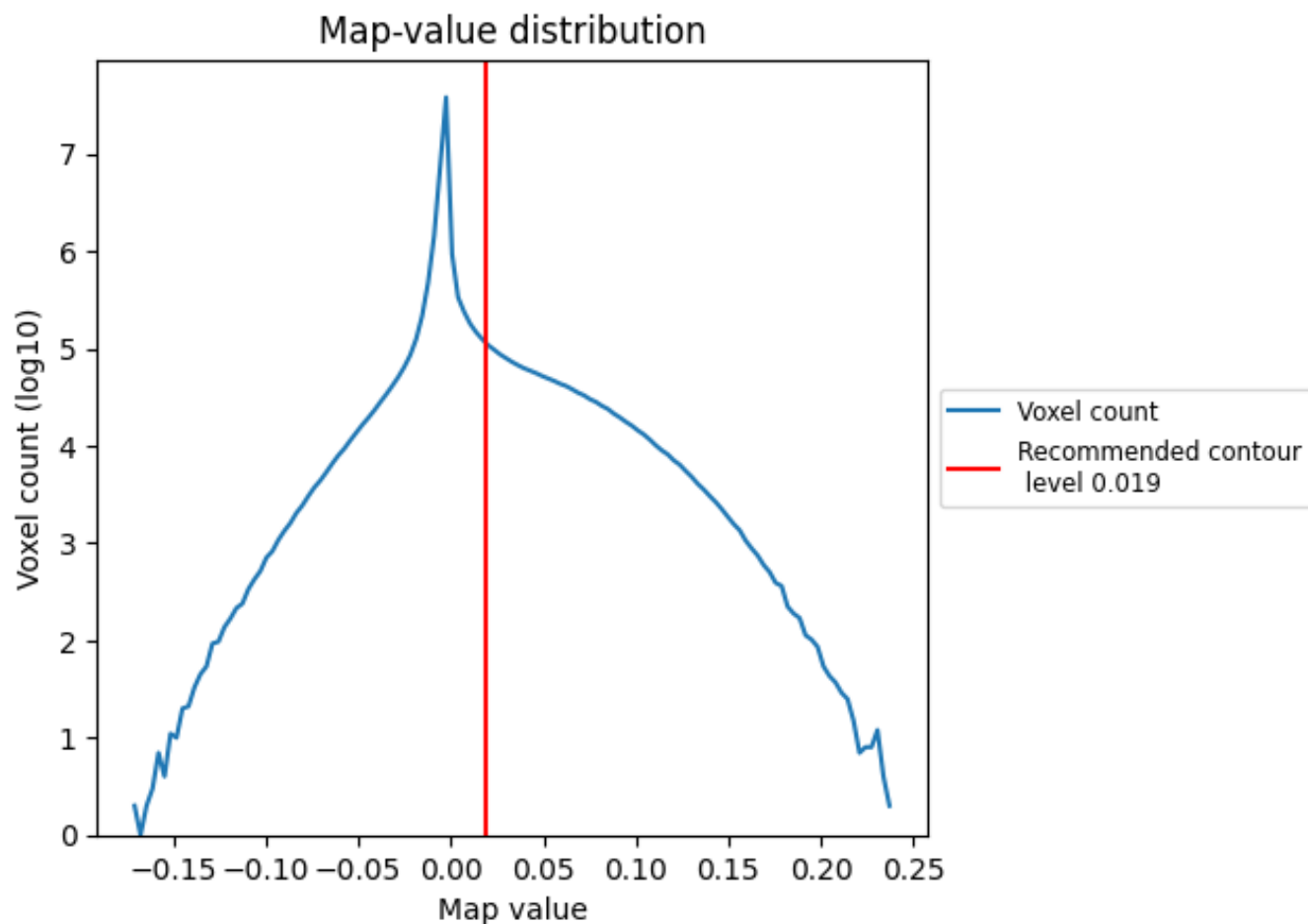
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

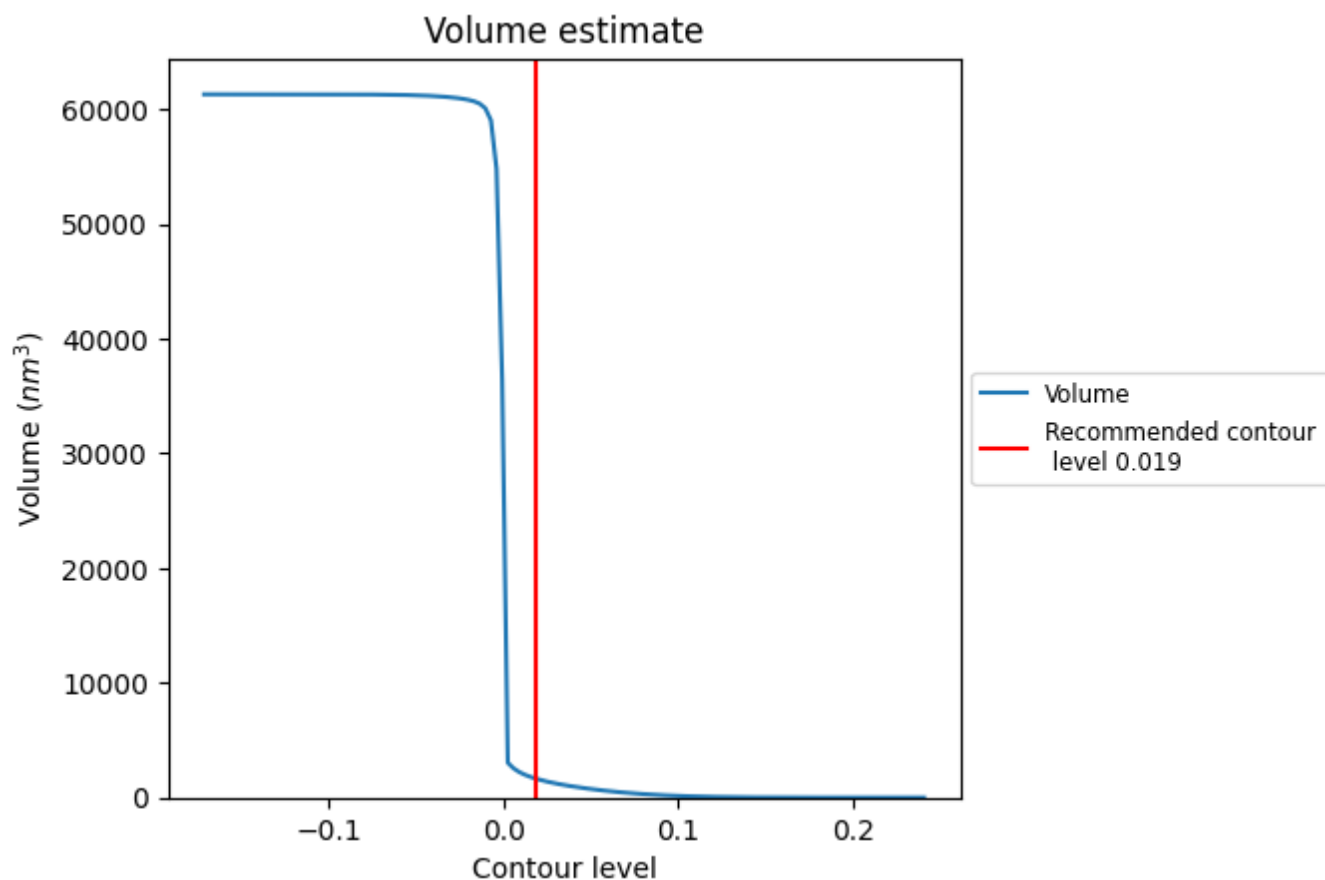
This section contains the results of statistical analysis of the map.

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.

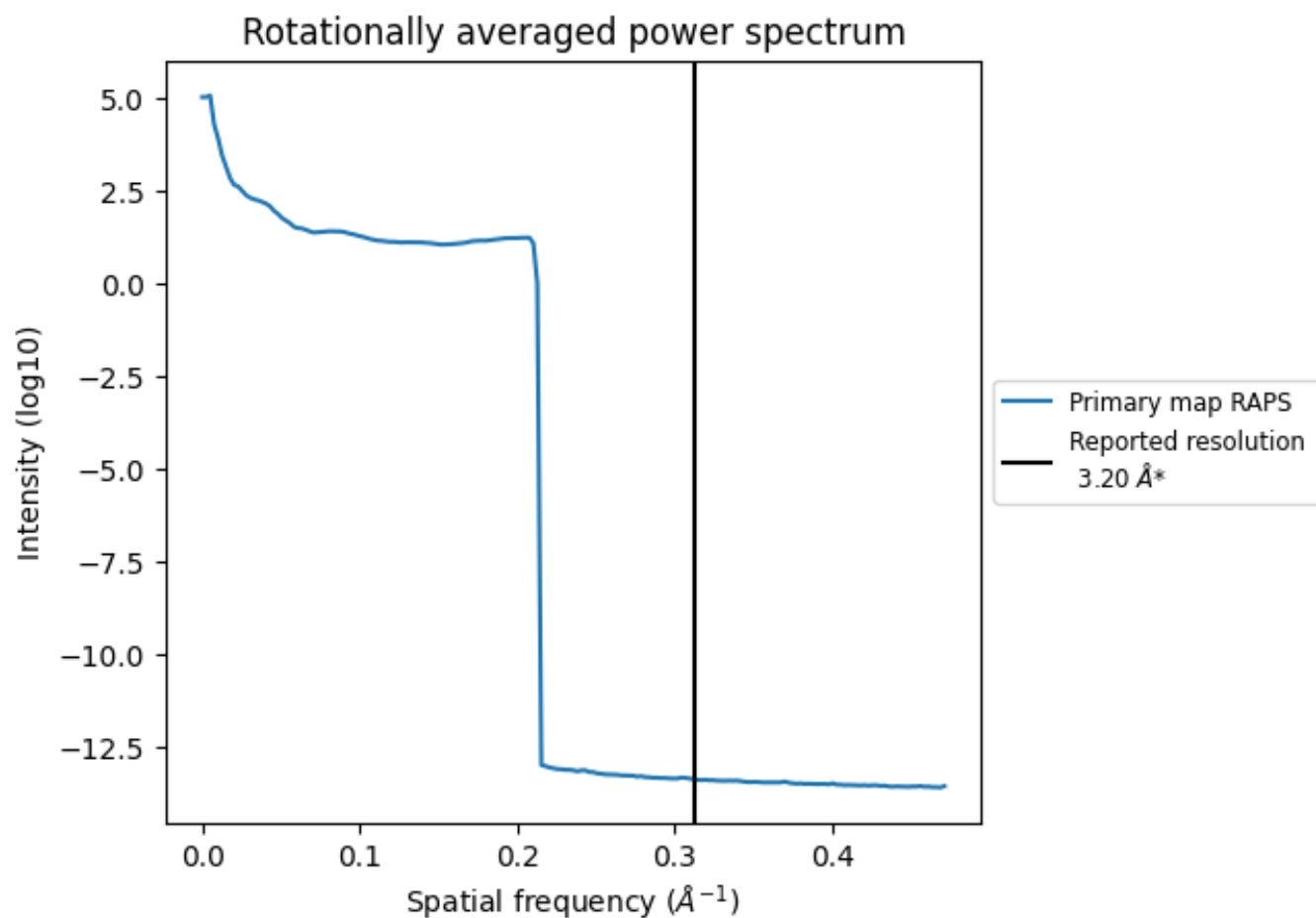
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1634 nm³; this corresponds to an approximate mass of 1476 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

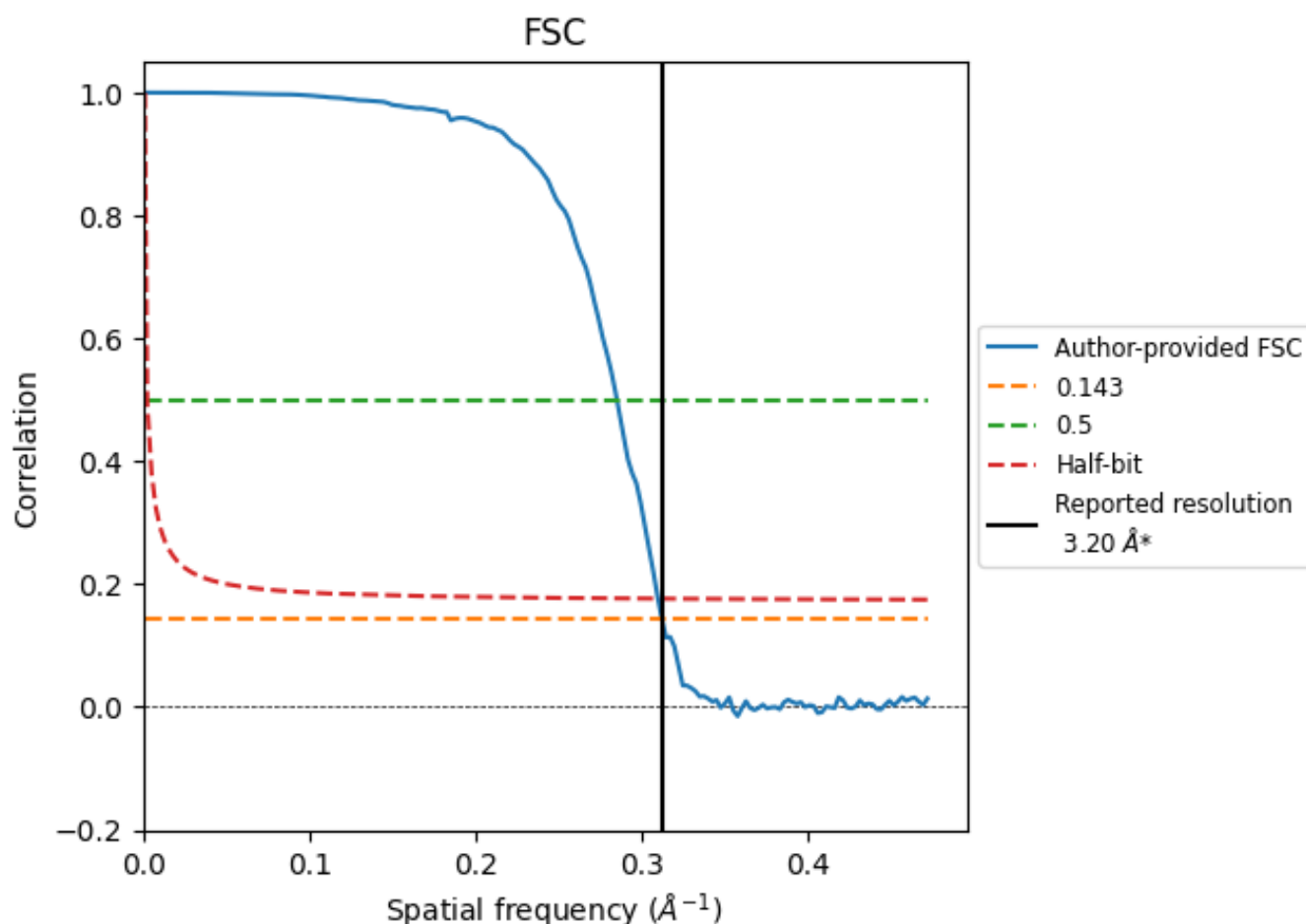


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

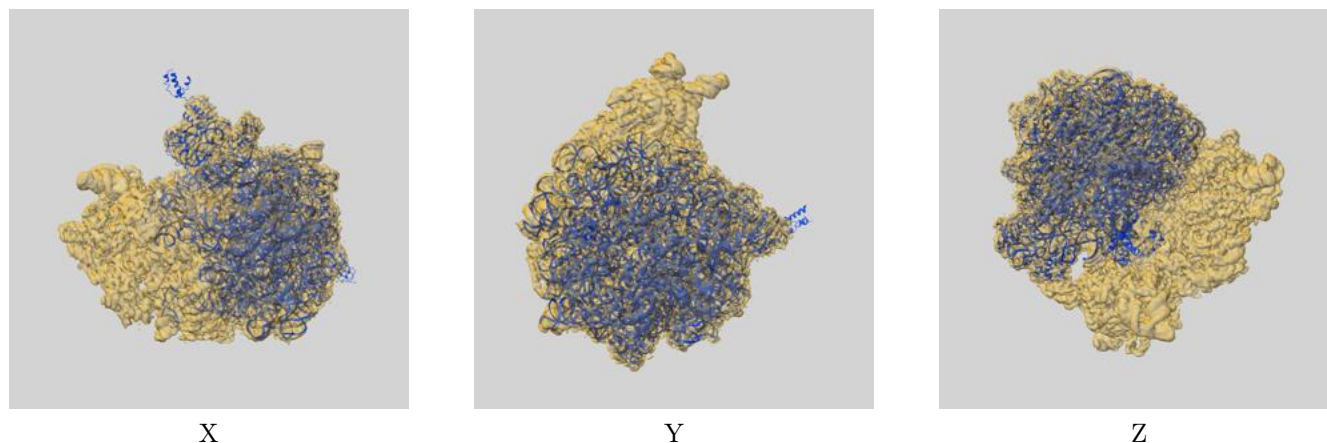
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.20	3.51	3.23
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

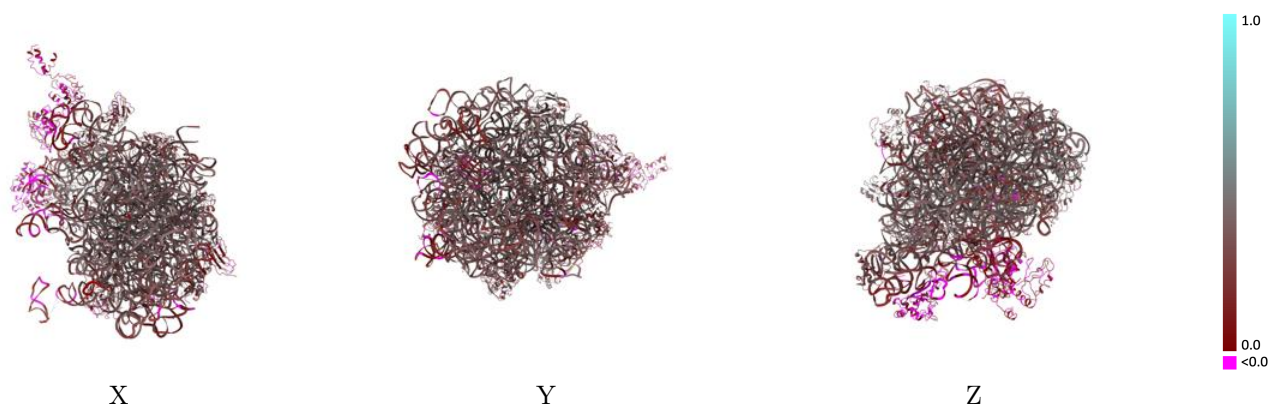
This section contains information regarding the fit between EMDB map EMD-0322 and PDB model 6I0Y. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.019 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

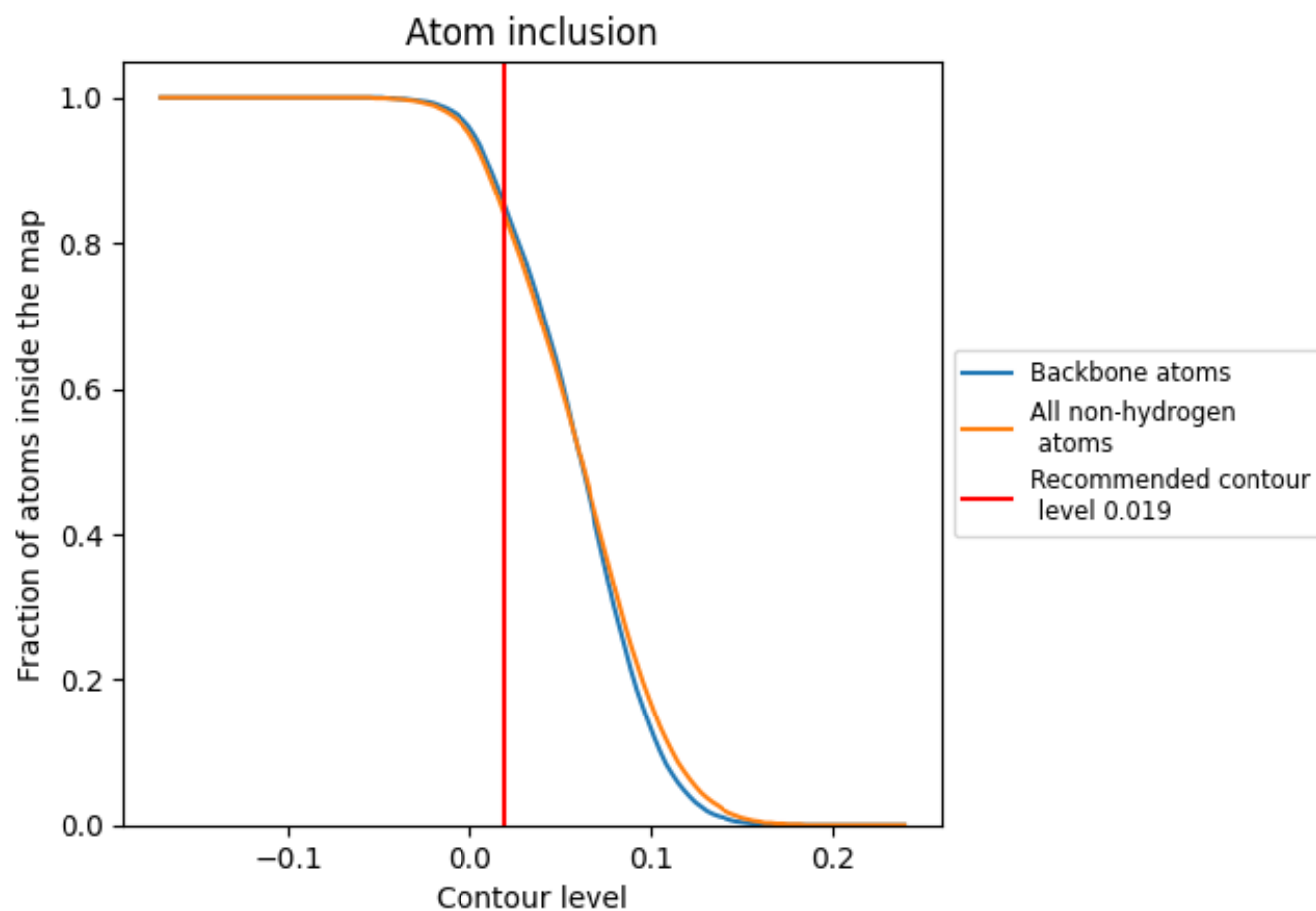


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 85% of all backbone atoms, 84% 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 (0.019) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8410	 0.3050
0	 0.8150	 0.3330
1	 0.8160	 0.3060
2	 0.8280	 0.3250
3	 0.8660	 0.3850
4	 0.8130	 0.3330
5	 0.3820	 0.0800
6	 0.0000	 0.0630
7	 0.7210	 0.2810
8	 0.7970	 0.3240
A	 0.8930	 0.3250
B	 0.8800	 0.2830
C	 0.7870	 0.2870
D	 0.8260	 0.3490
E	 0.7920	 0.3250
F	 0.4680	 -0.0220
G	 0.7860	 0.2640
H	 0.6890	 0.2060
I	 0.3160	 0.0540
J	 0.8040	 0.3010
K	 0.8010	 0.3460
L	 0.8260	 0.3420
M	 0.8170	 0.3460
N	 0.8590	 0.3490
O	 0.8260	 0.3090
P	 0.7960	 0.3310
Q	 0.7950	 0.2860
R	 0.8030	 0.3110
S	 0.8040	 0.3410
T	 0.7670	 0.3200
V	 0.7110	 0.1310
W	 0.7690	 0.2990
X	 0.8400	 0.3390
Y	 0.7890	 0.2610
Z	 0.7920	 0.3030



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Chain	Atom inclusion	Q-score
h	 0.7990	 0.3170
z	 0.3020	 0.1300