



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 09:10 AM UTC

PDB ID : 5MYJ / pdb_00005myj
EMDB ID : EMD-3581
Title : Structure of 70S ribosome from *Lactococcus lactis*
Authors : Franken, L.E.; Oostergetel, G.T.; Pijning, T.; Puri, P.; Boekema, E.J.; Poolman, B.; Guskov, A.
Deposited on : 2017-01-26
Resolution : 5.60 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:

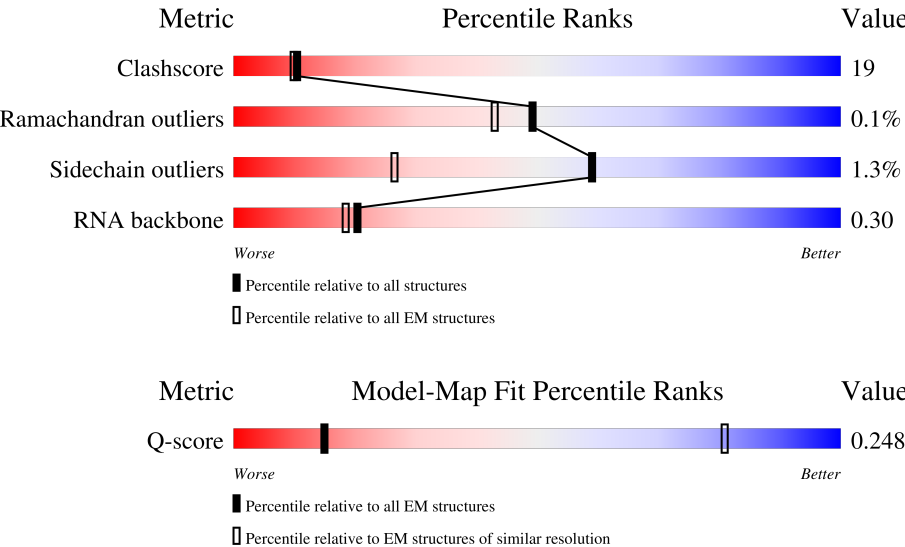
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 5.60 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	513 (5.10 - 6.10)

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	AA	1535	27% 49% 25%
2	AB	255	36% 58% 30% 12%
3	AC	217	17% 50% 46% ..

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Mol	Chain	Length	Quality of chain
4	AD	203	
5	AE	168	
6	AF	97	
7	AG	155	
8	AH	132	
9	AI	130	
10	AJ	102	
11	AK	127	
12	AL	137	
13	AM	121	
14	AN	61	
15	AO	89	
16	AP	90	
17	AQ	86	
18	AR	81	
19	AS	92	
20	AT	77	
21	AU	58	
22	B0	64	
23	B1	69	
24	B2	59	
25	B3	81	
26	B4	57	
27	B5	49	
28	B6	44	

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Mol	Chain	Length	Quality of chain
29	B7	66	
30	B8	38	
31	BA	2897	
32	BB	115	
33	BD	276	
34	BE	207	
35	BF	208	
36	BG	180	
37	BH	178	
38	BM	148	
39	BN	122	
40	BO	147	
41	BP	137	
42	BQ	126	
43	BR	115	
44	BS	114	
45	BT	119	
46	BU	104	
47	BV	115	
48	BW	97	
49	BX	101	
50	BZ	94	
51	A	185	

2 Entry composition

There are 51 unique types of molecules in this entry. The entry contains 140480 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 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	1535	Total	C	N	O	P	0	0
			32911	14689	6018	10669	1535		

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	224	Total	C	N	O	S	0	0
			1774	1129	311	326	8		

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	211	Total	C	N	O	S	0	0
			1648	1042	302	301	3		

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	200	Total	C	N	O	S	0	0
			1610	1014	298	294	4		

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	156	Total	C	N	O	S	0	0
			1133	711	212	209	1		

- Molecule 6 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	97	Total	C	N	O	S	0	0
			797	507	132	156	2		

- Molecule 7 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	152	Total	C	N	O	S	0	0
			1207	748	236	217	6		

- Molecule 8 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	130	Total	C	N	O	S	0	0
			1009	641	178	188	2		

- Molecule 9 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	129	Total	C	N	O	S	0	0
			983	606	199	176	2		

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	98	Total	C	N	O	S	0	0
			794	501	145	146	2		

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	118	Total	C	N	O	S	0	0
			857	530	165	160	2		

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	136	Total	C	N	O	S	0	0
			1054	656	215	180	3		

- Molecule 13 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	111	Total	C	N	O	S	0	0
			873	535	174	162	2		

- Molecule 14 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	59	Total	C	N	O	S	0	0
			471	296	94	76	5		

- Molecule 15 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	87	Total	C	N	O	S	0	0
			708	442	140	125	1		

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	86	Total	C	N	O	S	0	0
			688	433	127	126	2		

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	82	Total	C	N	O	S	0	0
			675	423	126	124	2		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	68	Total	C	N	O	S	0	0
			549	349	105	94	1		

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	82	Total	C	N	O	S	0	0
			660	419	121	118	2		

- Molecule 20 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	71	Total	C	N	O	S	0	0
			542	333	107	101	1		

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	AU	56	Total	C	N	O	0	0
			440	269	95	76		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	B0	61	Total	C	N	O	S	0	0
			477	299	91	86	1		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	B1	67	Total	C	N	O	0	0
			533	334	95	104		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	B2	58	Total	C	N	O	S	0	0
			424	269	77	77	1		

- Molecule 25 is a protein called 50S ribosomal protein L31 type B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	B3	79	Total	C	N	O	S	0	0
			642	408	110	122	2		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	B4	53	Total	C	N	O	0	0
			437	270	92	75		

- Molecule 27 is a protein called 50S ribosomal protein L33 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	B5	47	Total	C	N	O	S	0	0
			365	225	72	64	4		

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	B6	44	Total	C	N	O	S	0	0
			362	219	86	55	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	B7	64	Total	C	N	O	S	0	0
			530	327	120	80	3		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	B8	36	Total	C	N	O	S	0	0
			292	182	62	44	4		

- Molecule 31 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BA	2897	Total	C	N	O	P	0	0
			62143	27749	11409	20088	2897		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BA	135	U	C	conflict	GB 124491690
BA	376	A	G	conflict	GB 124491690
BA	1239	A	G	conflict	GB 124491690
BA	1489	C	U	conflict	GB 124491690

- Molecule 32 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BB	115	Total	C	N	O	P	0	0
			2455	1097	439	804	115		

- Molecule 33 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BD	272	Total	C	N	O	S	0	0
			2041	1264	397	371	9		

- Molecule 34 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BE	205	Total	C	N	O	S	0	0
			1522	957	282	279	4		

- Molecule 35 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BF	206	Total	C	N	O	S	0	0
			1563	980	284	299			

- Molecule 36 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BG	176	Total	C	N	O	S	0	0
			1367	867	238	256	6		

- Molecule 37 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BH	174	Total	C	N	O	S	0	0
			1303	811	237	251	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BM	147	Total	C	N	O	S	0	0
			1127	714	203	205	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BN	121	Total	C	N	O	S	0	0
			895	563	165	166	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	BO	146	Total	C	N	O	S	0	0
			1066	650	210	205	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BP	134	Total	C	N	O	S	0	0
			1061	675	206	174	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BQ	125	Total	C	N	O	S	0	0
			990	613	188	186	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BR	115	Total	C	N	O	S	0	0
			872	542	164	165	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BS	114	Total	C	N	O	S	0	0
			923	578	186	158	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BT	117	Total	C	N	O	S	0	0
			945	601	186	154	4		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
46	BU	101	Total	C	N	O	0	0
			783	501	138	144		

- Molecule 47 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BV	112	Total	C	N	O	S	0	0
			853	536	160	156	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BW	88	Total	C	N	O	S	0	0
			689	441	116	130	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BX	99	Total	C	N	O	S	0	0
			747	474	136	136	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BZ	75	Total	C	N	O	S	0	0
			562	345	110	106	1		

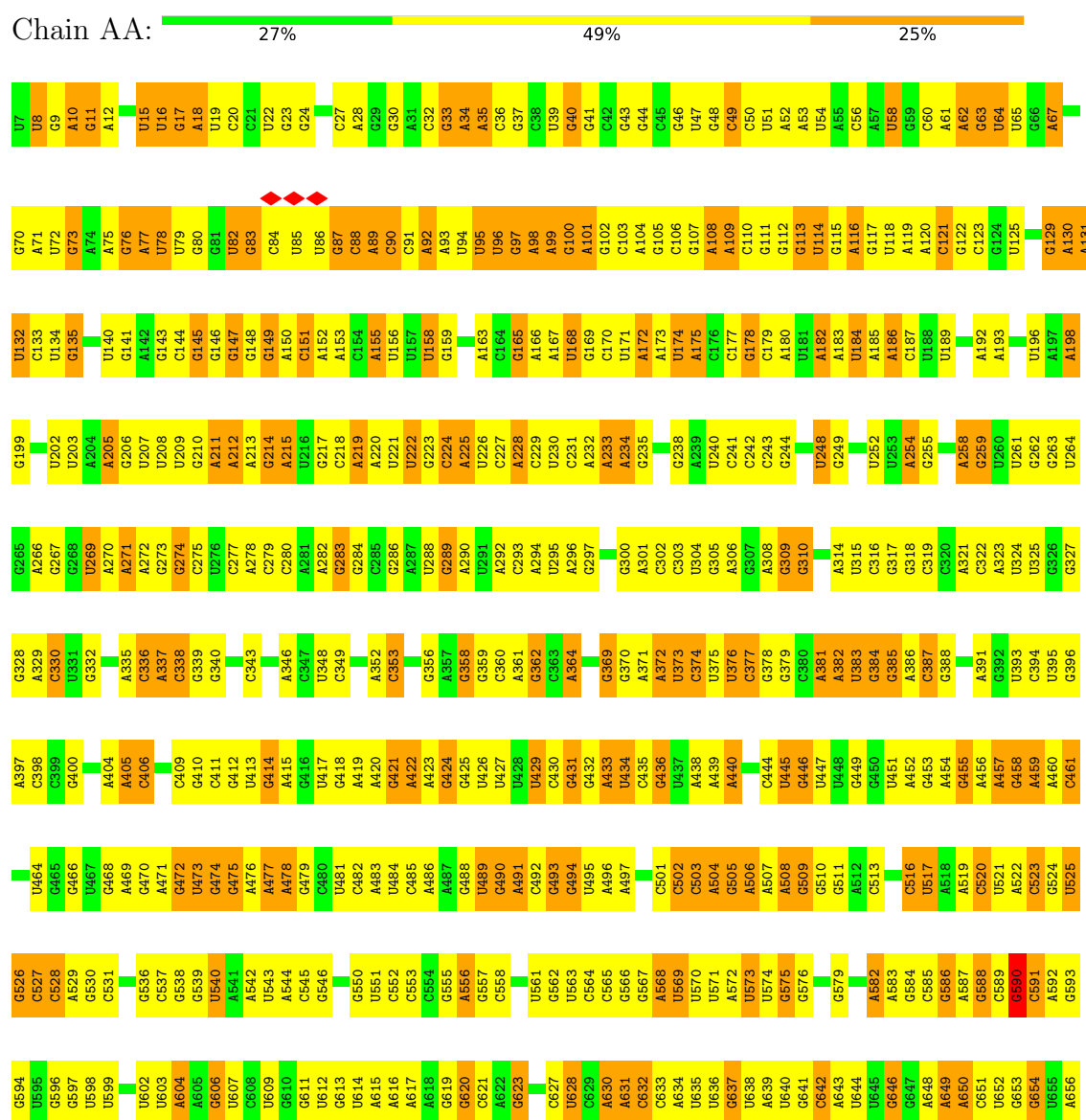
- Molecule 51 is a protein called Ribosome hibernation promotion factor.

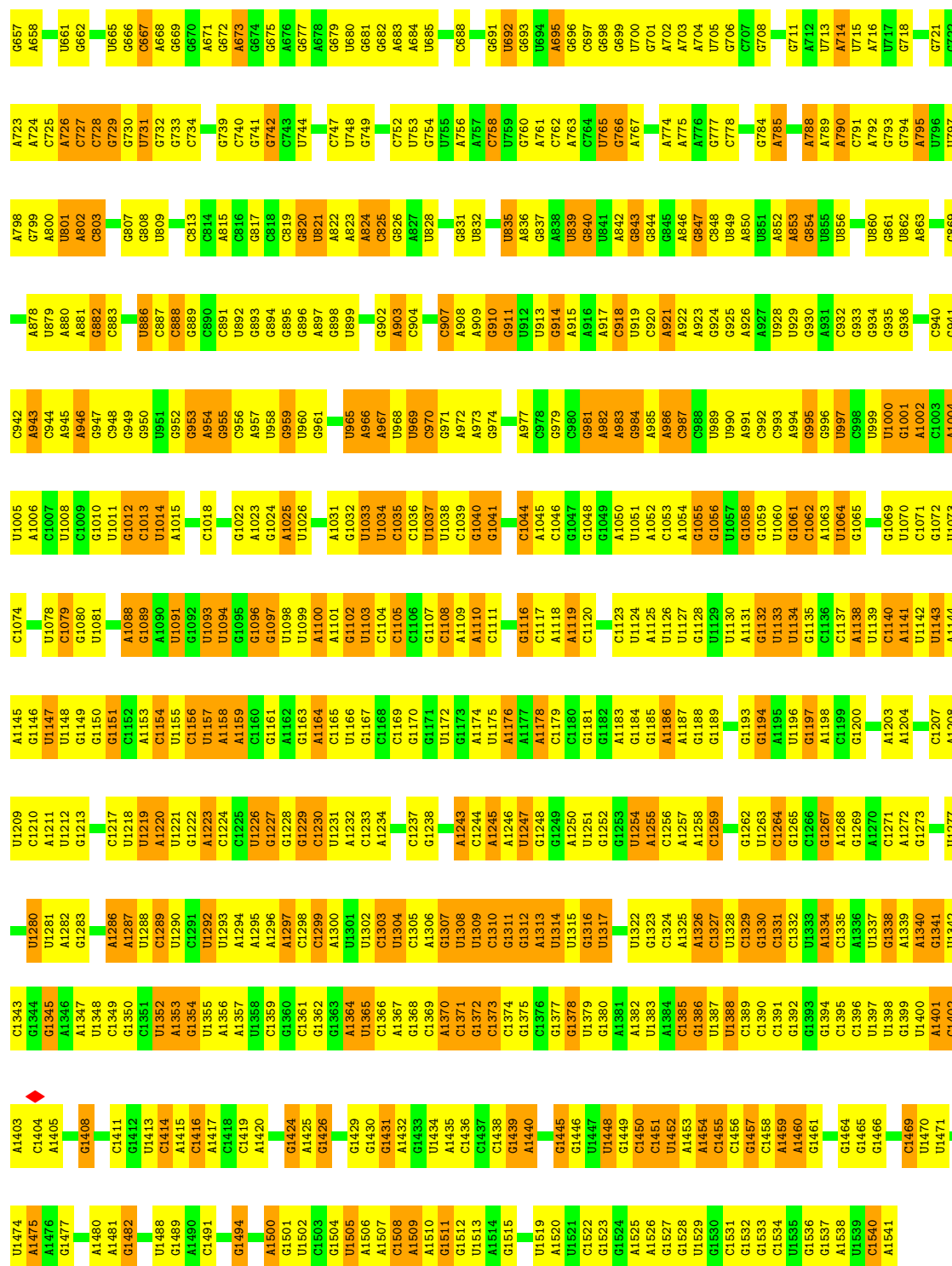
Mol	Chain	Residues	Atoms					AltConf	Trace
51	A	159	Total	C	N	O	S	0	0
			1128	698	209	218	3		

3 Residue-property plots

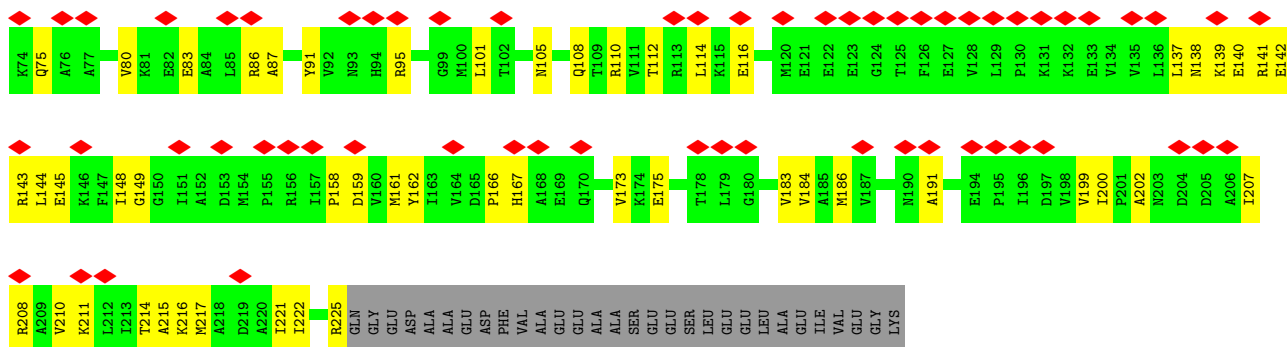
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 16S ribosomal RNA

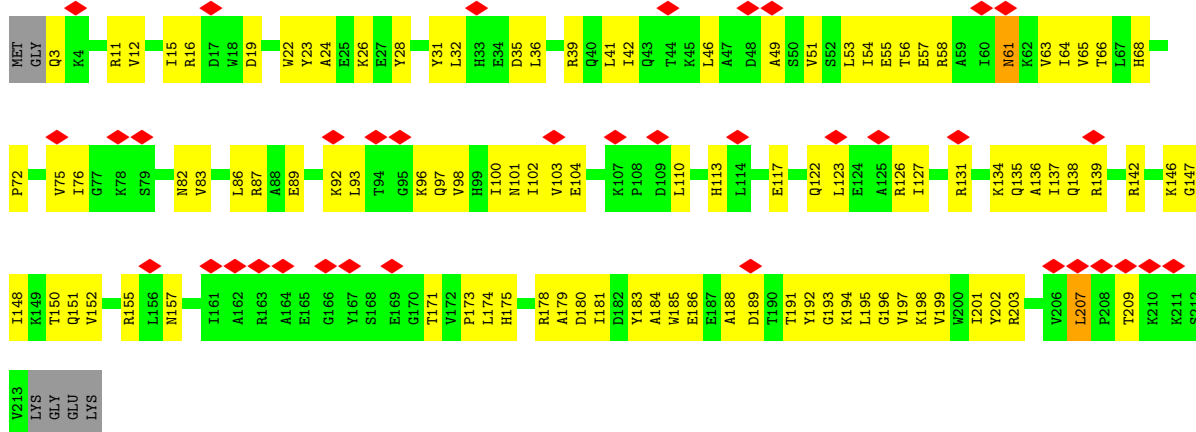




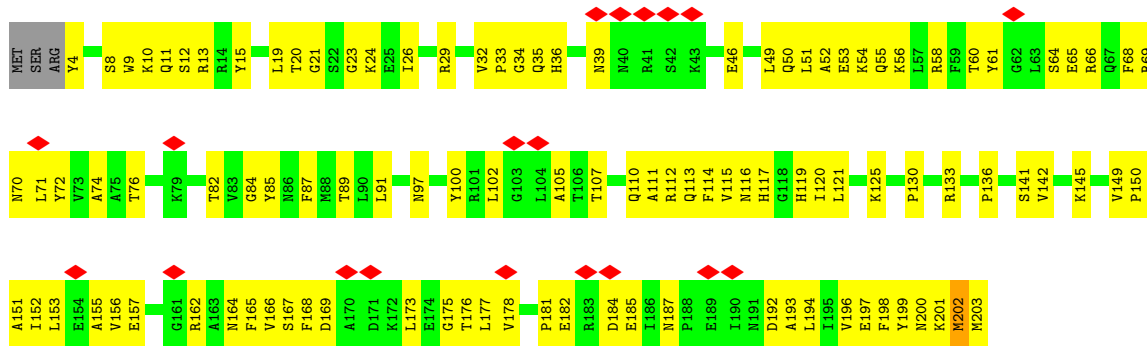
• Molecule 2: 30S ribosomal protein S2



• Molecule 3: 30S ribosomal protein S3

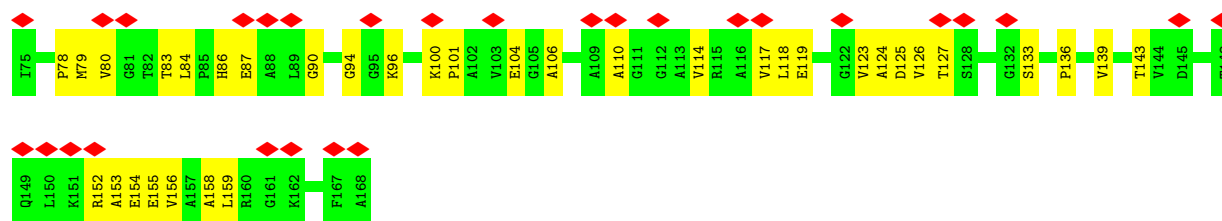


• Molecule 4: 30S ribosomal protein S4

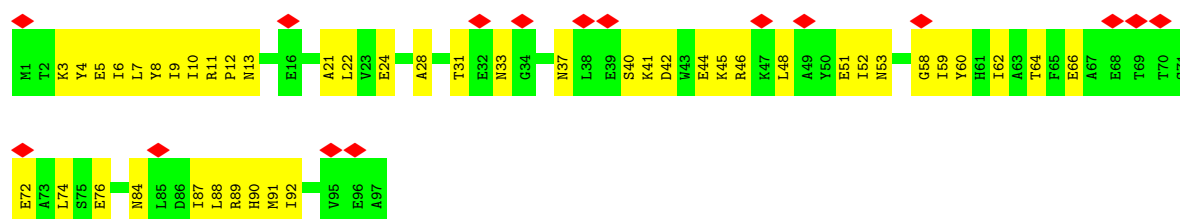


• Molecule 5: 30S ribosomal protein S5

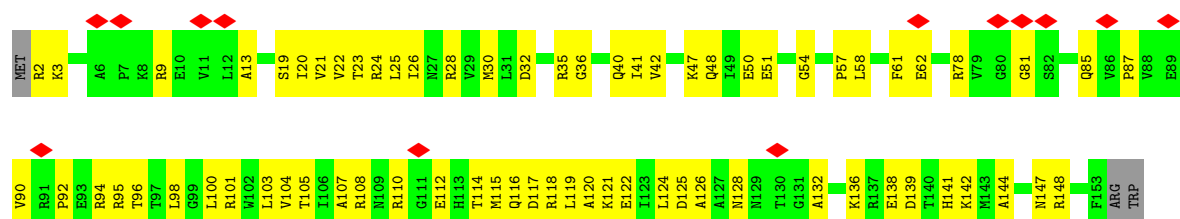




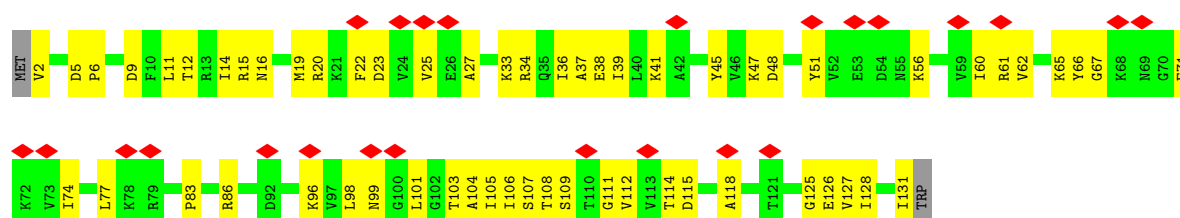
• Molecule 6: 30S ribosomal protein S6



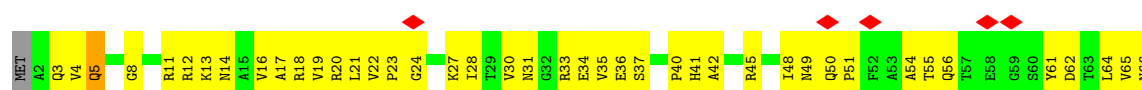
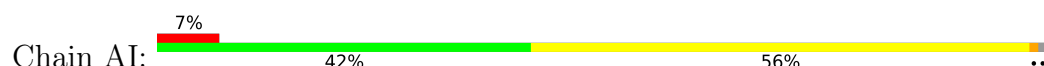
• Molecule 7: 30S ribosomal protein S7

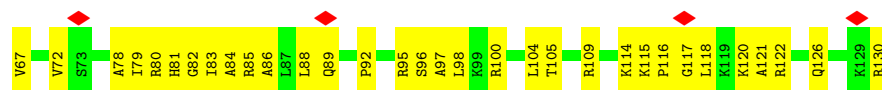


• Molecule 8: 30S ribosomal protein S8

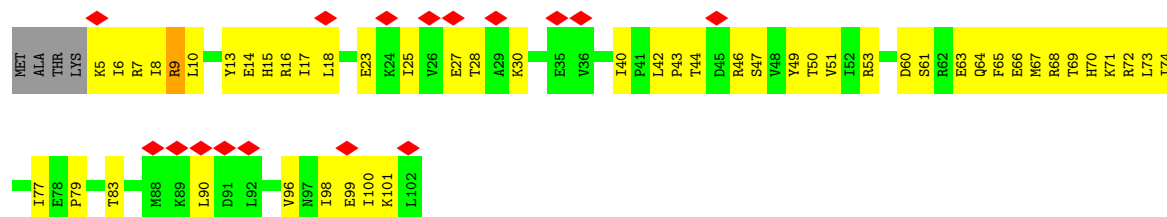


• Molecule 9: 30S ribosomal protein S9

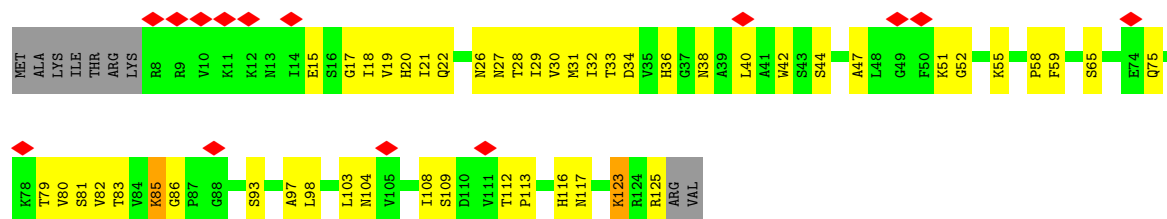




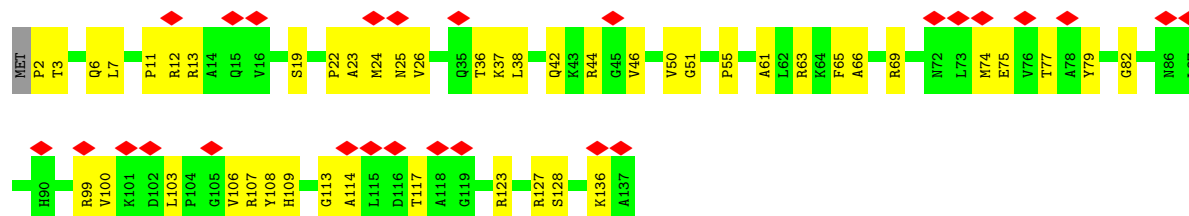
- Molecule 10: 30S ribosomal protein S10



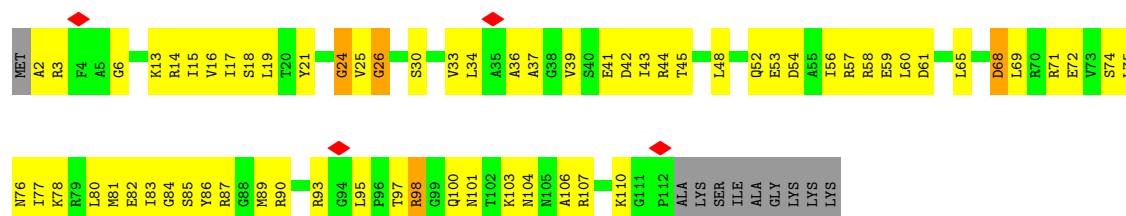
- Molecule 11: 30S ribosomal protein S11



- Molecule 12: 30S ribosomal protein S12



- Molecule 13: 30S ribosomal protein S13



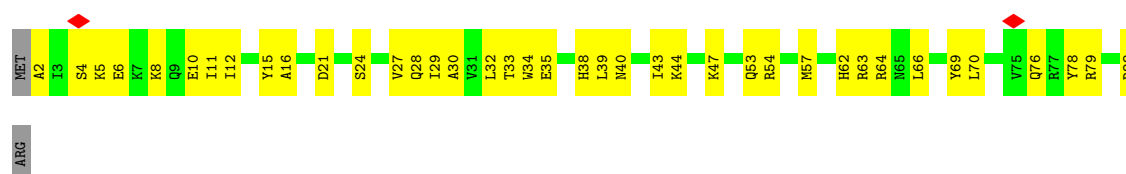
- Molecule 14: 30S ribosomal protein S14 type Z

Chain AN:  51% 46% .



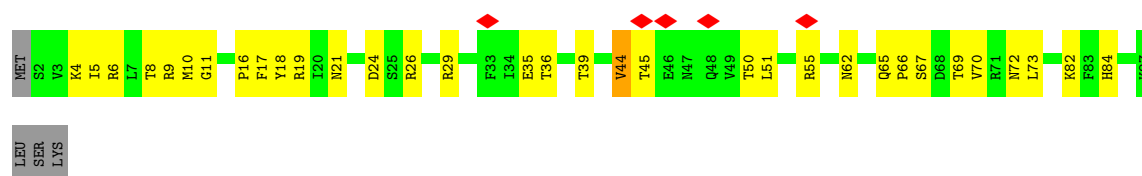
- Molecule 15: 30S ribosomal protein S15

Chain AO:  54% 44% .



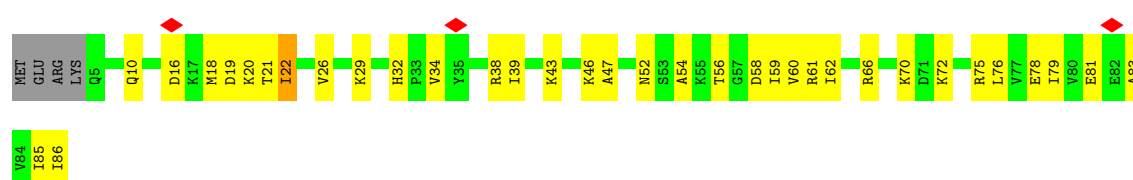
- Molecule 16: 30S ribosomal protein S16

Chain AP:  6% 59% 36% . .



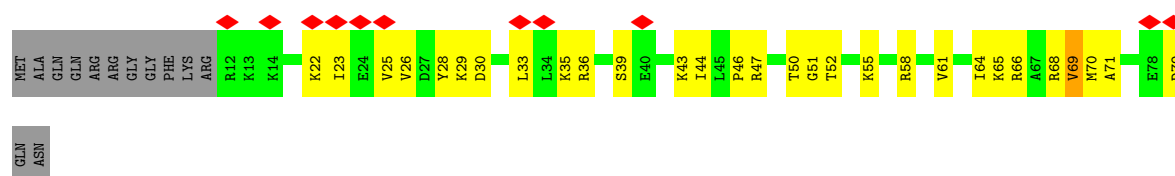
- Molecule 17: 30S ribosomal protein S17

Chain AQ:  55% 40% . 5%



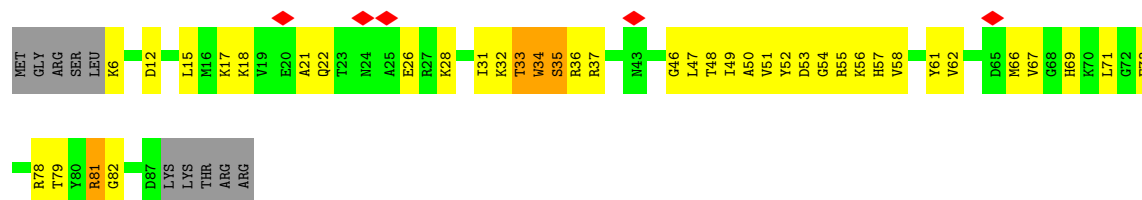
- Molecule 18: 30S ribosomal protein S18

Chain AR:  14% 48% 35% . 16%



- Molecule 19: 30S ribosomal protein S19

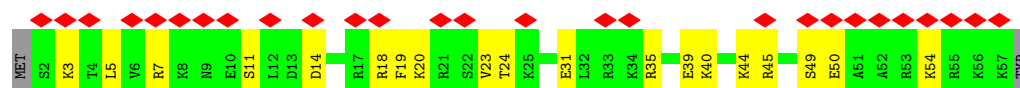
Chain AS:  5% 46% 39% . 11%



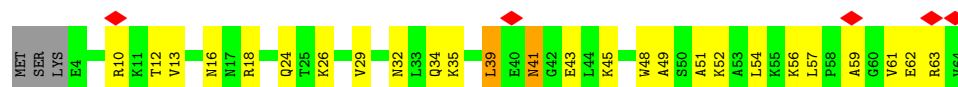
- Molecule 20: 30S ribosomal protein S20



- Molecule 21: 30S ribosomal protein S21



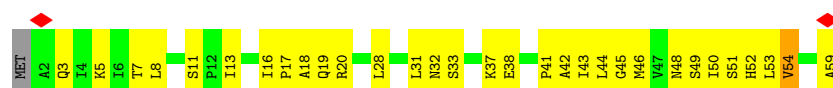
- Molecule 22: 50S ribosomal protein L28



- Molecule 23: 50S ribosomal protein L29

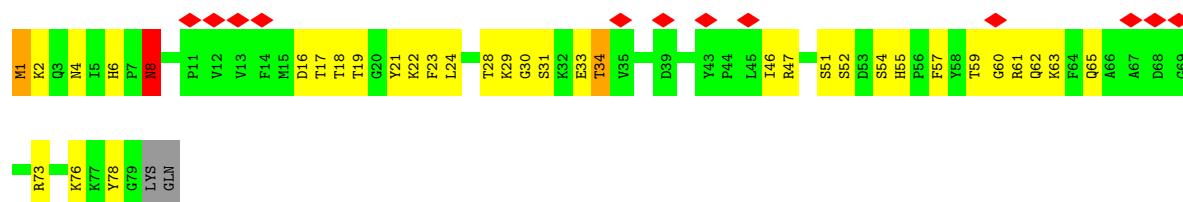


- Molecule 24: 50S ribosomal protein L30



- Molecule 25: 50S ribosomal protein L31 type B

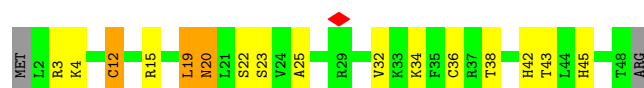




- Molecule 26: 50S ribosomal protein L32



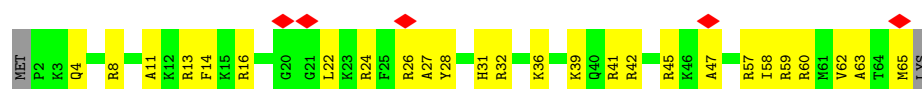
- Molecule 27: 50S ribosomal protein L33 3



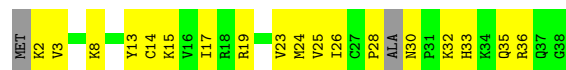
- Molecule 28: 50S ribosomal protein L34



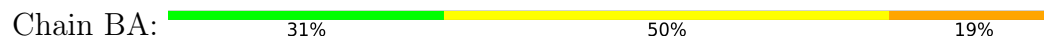
- Molecule 29: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L36

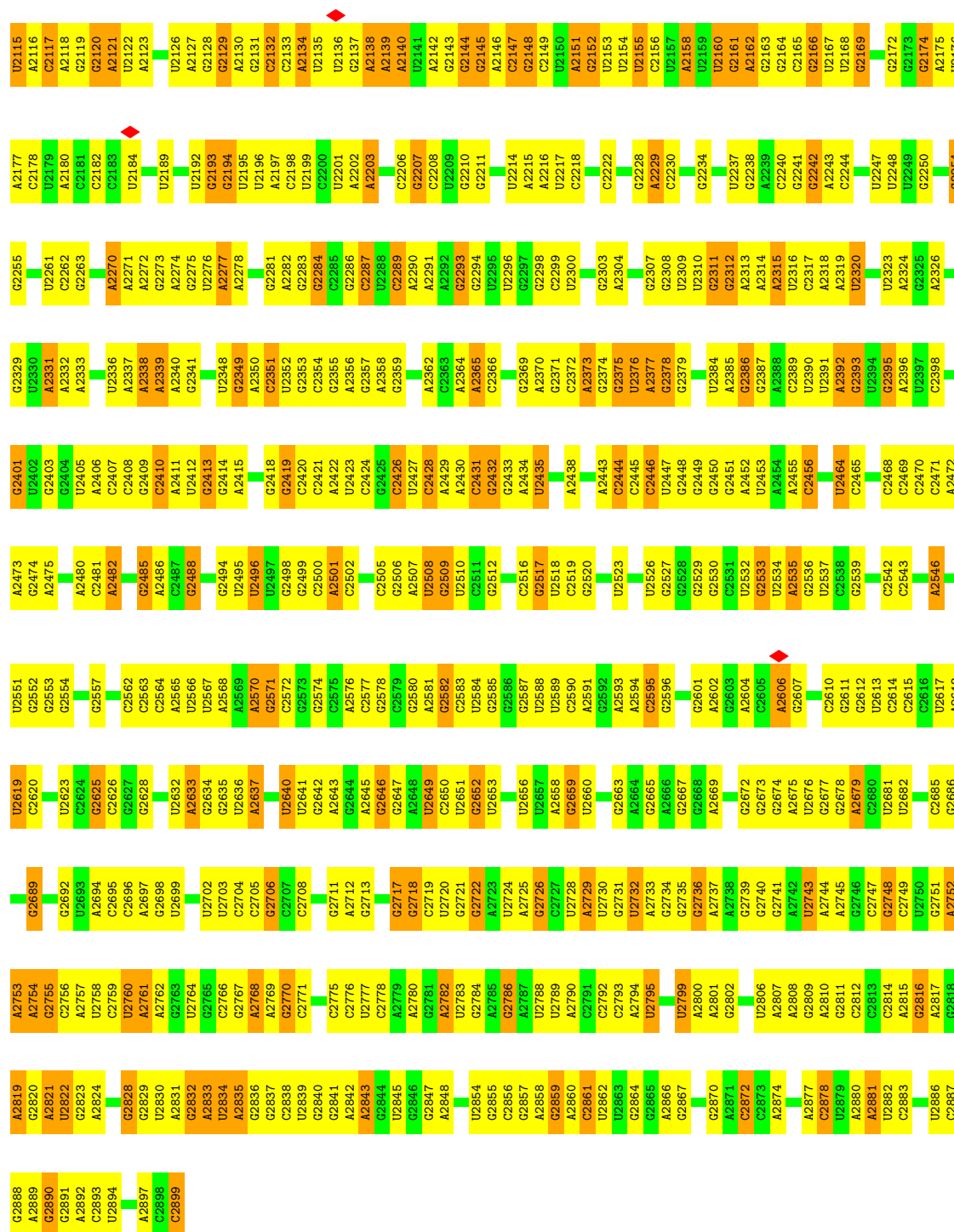


- Molecule 31: 23S ribosomal RNA



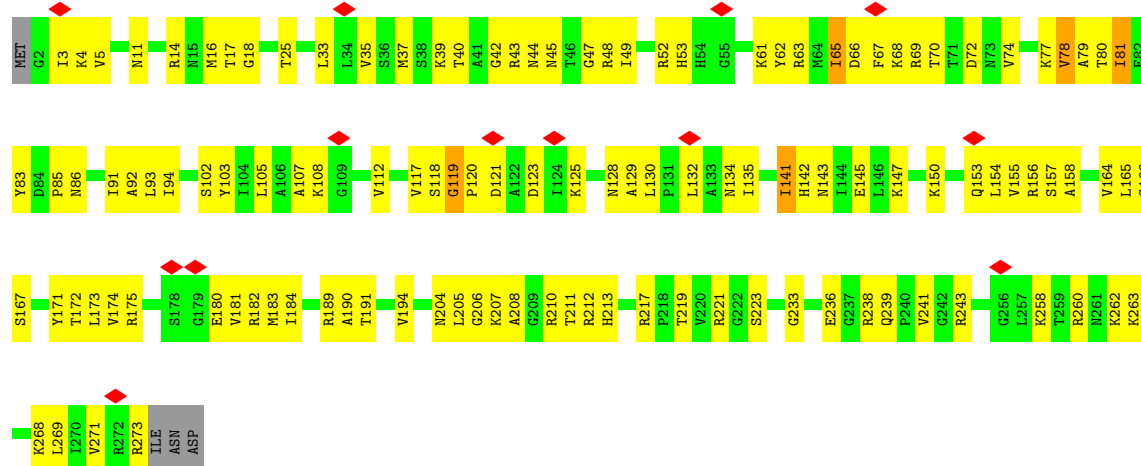
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C2048	G1108	G1172	A1246	A1306	G1372	U1435	G1499	A1561	U1706	A1706	C1769	G1837	G1908	C1971	C2048
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U2093	G1145	G1217	U1279	A1405	G1406	A1473	G1534	A1602	G1672	G1742	U1803	A1875	U1943	U2021	U2093
A2094	A1146	G1218	G1280	C1407	A1407	U1474	U1535	A1603	U1676	U1743	A1804	G1876	U1944	U2022	A2094
U2095	U1148	U1219	A1281	U1408	U1408	U1475	C1536	U1606	U1677	A1744	A1805	U1877	C1945	U2023	U2095
U2096	G1149	G1220	G1282	G1409	G1409	G1476	U1537	C1607	C1677	A1745	A1806	C1878	U1946	U2024	U2096
G2097	A1150	G1221	A1283	G1410	G1410	C1477	A1538	U1608	G1680	A1746	C1807	G1879	U1947	A2025	G2097
A2098	A1151	A1222	U1284	A1411	A1411	C1478	G1539	A1609	G1681	A1747	C1808	A1880	U1948	U2026	A2098
C2099	C1151	G1223	G1285	G1349	A1412	U1479	C1540	G1610	A1681	G1748	C1809	G1883	G1949	U2027	A2099
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G2105	C1153	U1228	C1287	A1351	A1414	U1480	G1541	G1612	A1683	C1750	U1815	U1885	C1951	U2104	U2104
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C2115	G1160	A1235	G1294	C1359	G1421	U1487	U1550	U1619	A1693	A1757	U1822	U1892	U1960	A2037	U2113
G2116	A1161	C1236	A1295	C1360	A1422	U1488	G1551	A1620	G1696	U1758	G1824	G1893	A1961	U2038	G2114

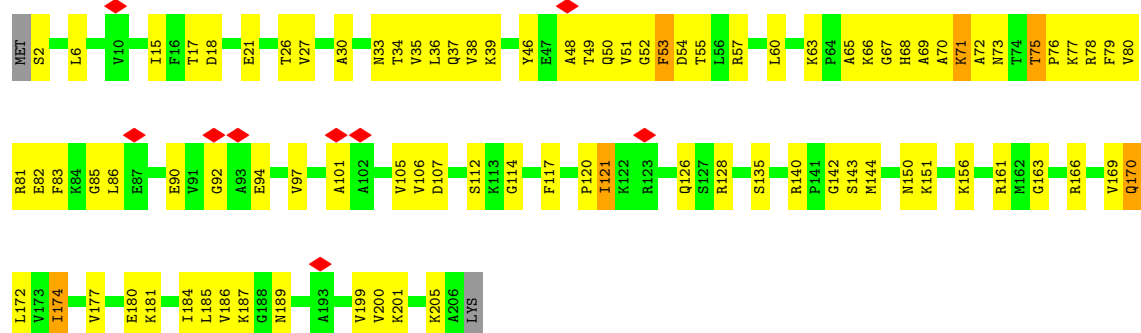




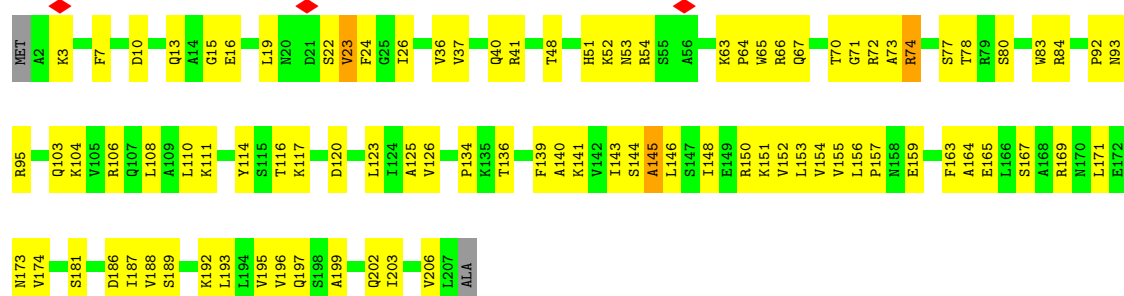
• Molecule 33: 50S ribosomal protein L2



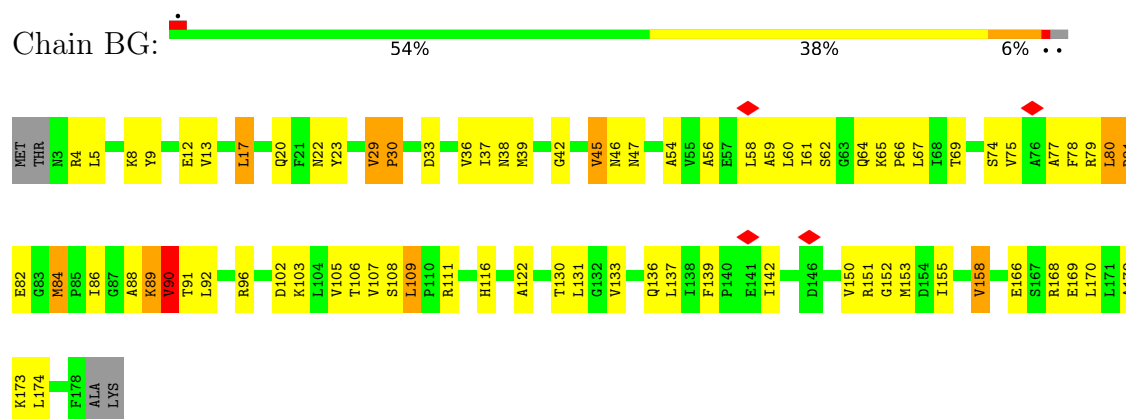
• Molecule 34: 50S ribosomal protein L3



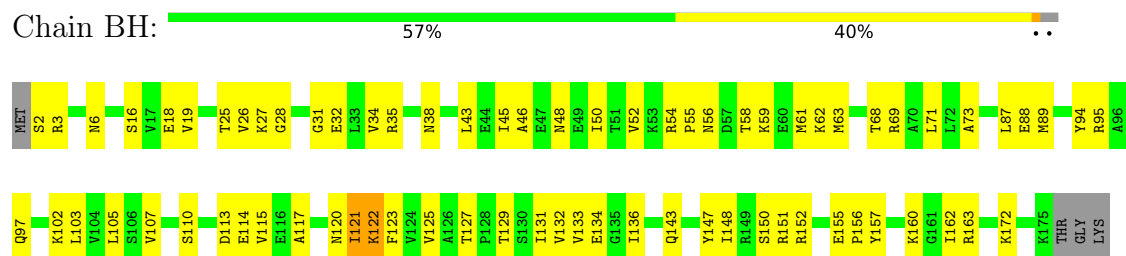
• Molecule 35: 50S ribosomal protein L4



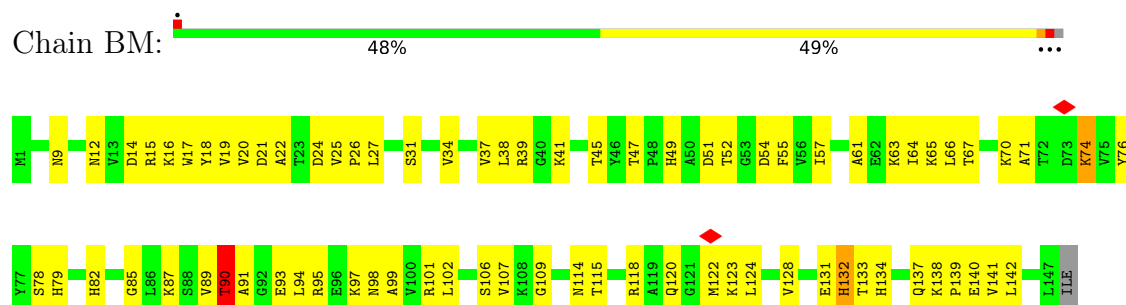
- Molecule 36: 50S ribosomal protein L5



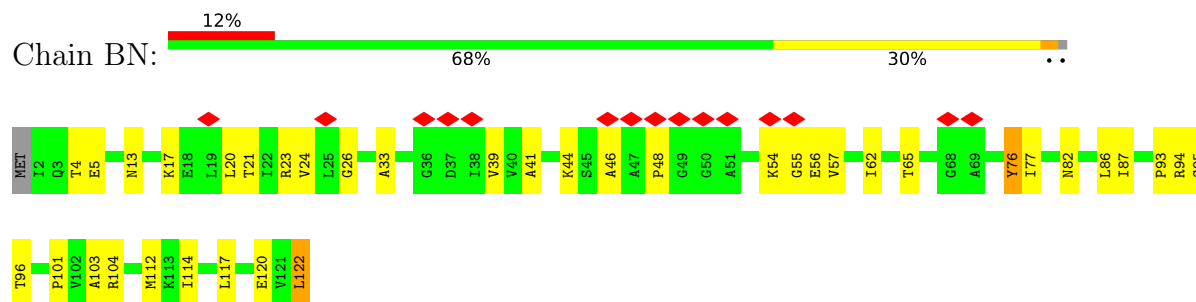
- Molecule 37: 50S ribosomal protein L6



- Molecule 38: 50S ribosomal protein L13

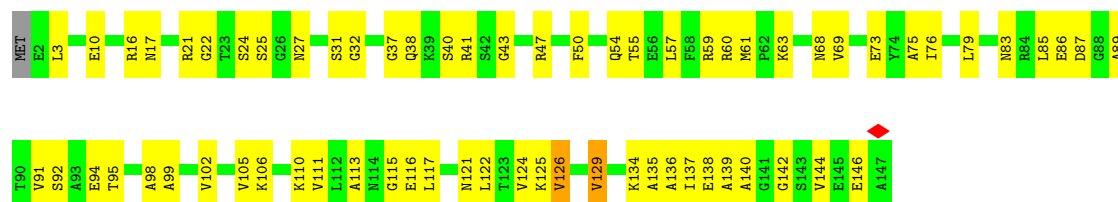


- Molecule 39: 50S ribosomal protein L14

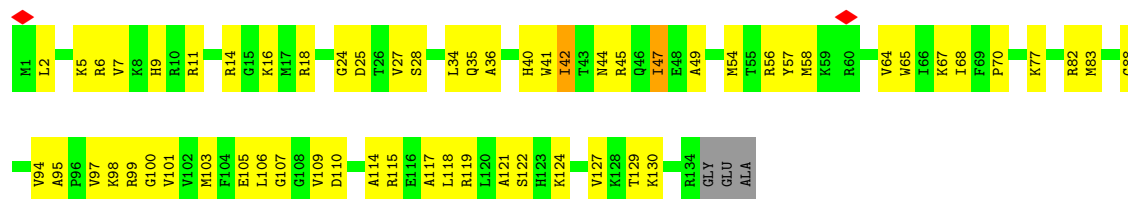


- Molecule 40: 50S ribosomal protein L15

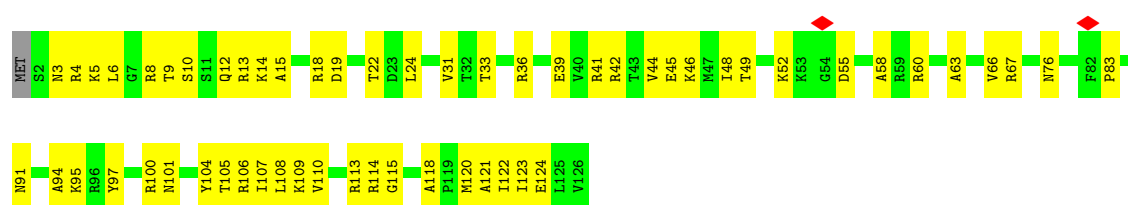




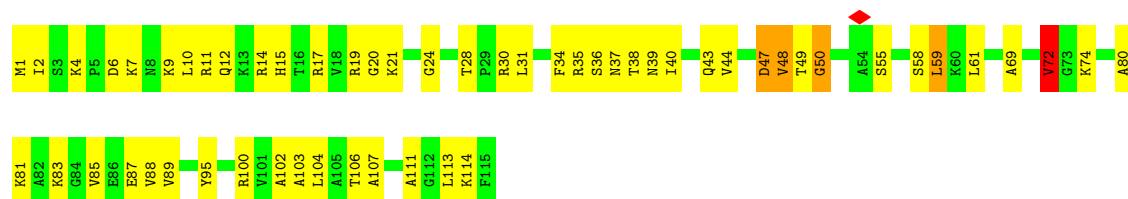
- Molecule 41: 50S ribosomal protein L16



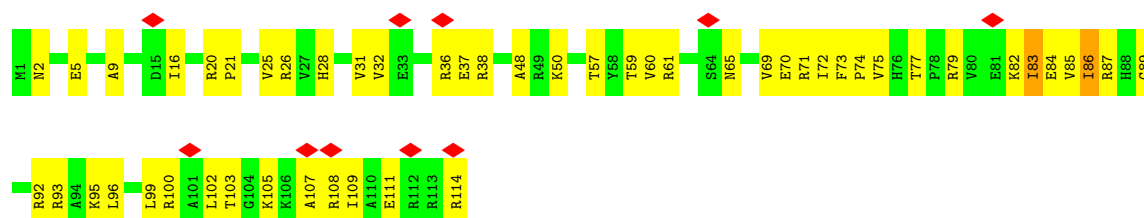
- Molecule 42: 50S ribosomal protein L17



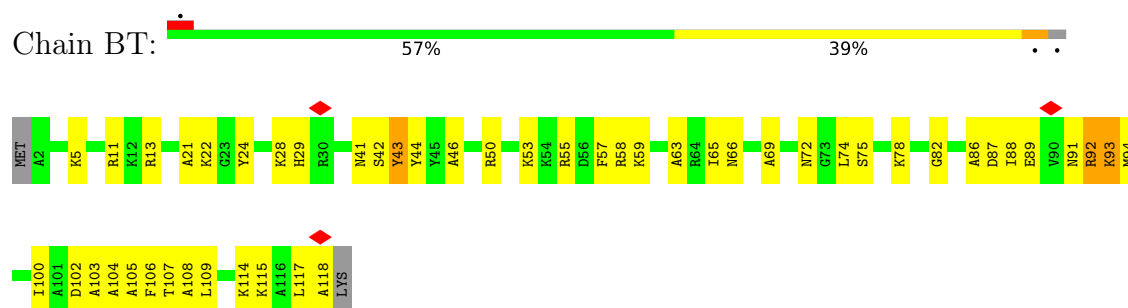
- Molecule 43: 50S ribosomal protein L18



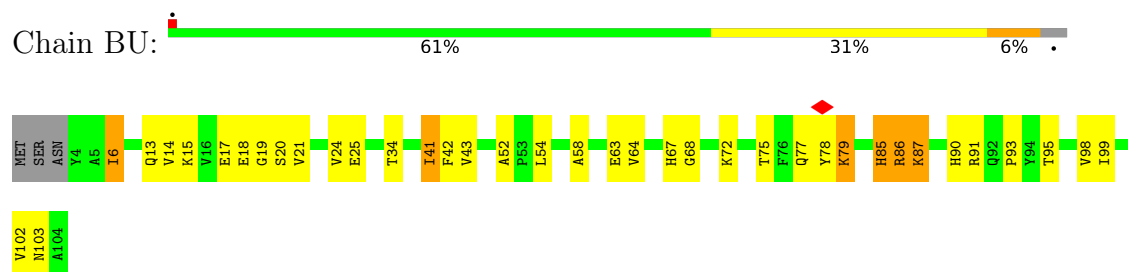
- Molecule 44: 50S ribosomal protein L19



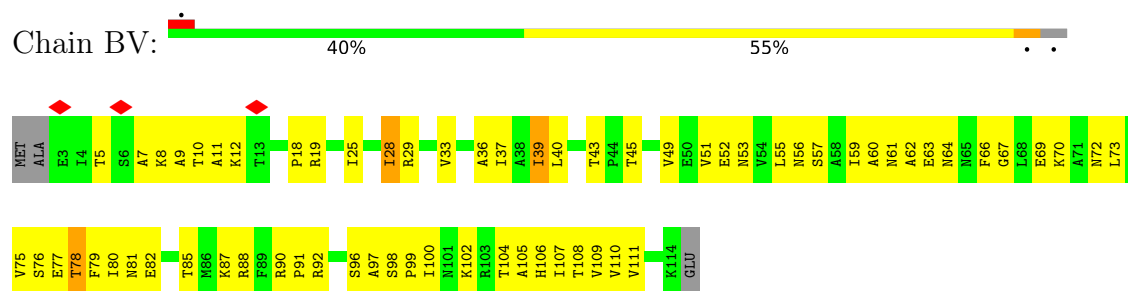
- Molecule 45: 50S ribosomal protein L20



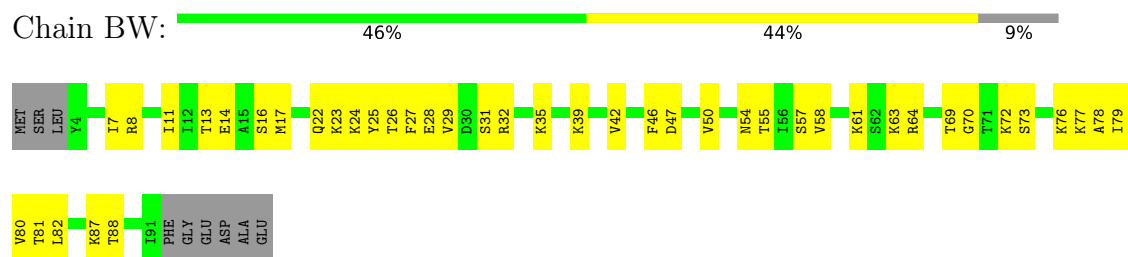
- Molecule 46: 50S ribosomal protein L21



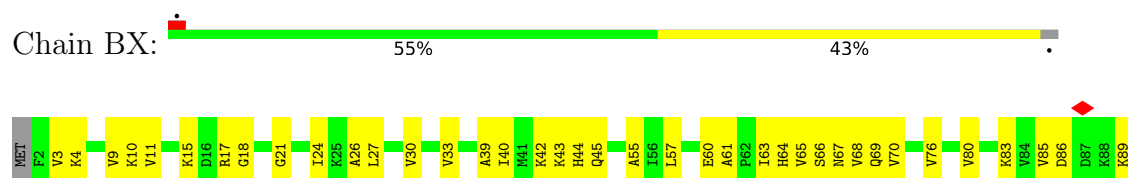
- Molecule 47: 50S ribosomal protein L22



- Molecule 48: 50S ribosomal protein L23



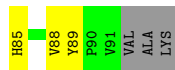
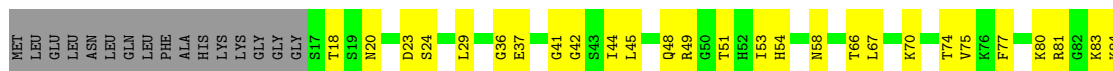
- Molecule 49: 50S ribosomal protein L24





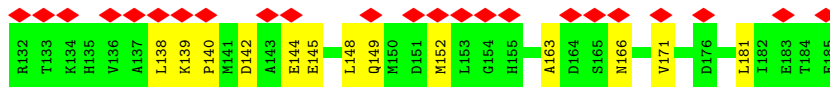
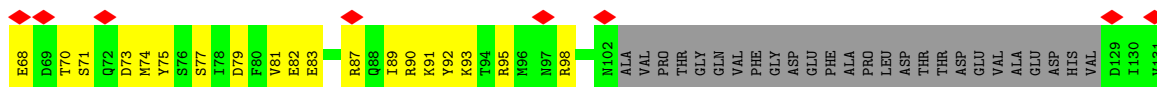
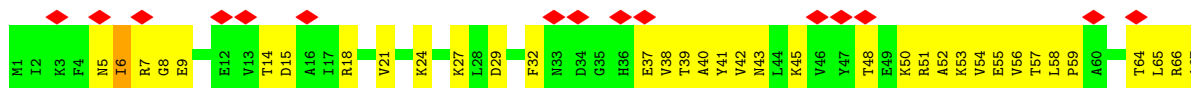
- Molecule 50: 50S ribosomal protein L27

Chain BZ: 48% 32% 20%



- Molecule 51: Ribosome hibernation promotion factor

Chain A: 25% 49% 36% 14%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	43530	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 ($e^-/\text{\AA}^2$)	25	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	0.161	Depositor
Minimum map value	-0.064	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.035	Depositor
Map size (Å)	663.0, 663.0, 663.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.105, 1.105, 1.105	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.32	0/36854	0.52	1/57482 (0.0%)
2	AB	0.27	0/1805	0.67	3/2442 (0.1%)
3	AC	0.26	0/1674	0.66	2/2259 (0.1%)
4	AD	0.28	0/1639	0.67	0/2205
5	AE	0.27	0/1143	0.64	0/1540
6	AF	0.36	0/809	0.83	0/1089
7	AG	0.28	0/1224	0.66	0/1649
8	AH	0.26	0/1020	0.60	0/1374
9	AI	0.28	0/995	0.84	4/1334 (0.3%)
10	AJ	0.27	0/805	0.72	0/1084
11	AK	0.33	0/870	0.71	2/1175 (0.2%)
12	AL	0.29	0/1070	0.74	0/1433
13	AM	0.37	0/880	0.92	2/1176 (0.2%)
14	AN	0.26	0/479	0.67	0/637
15	AO	0.27	0/718	0.70	0/958
16	AP	0.26	0/699	0.60	0/938
17	AQ	0.29	0/684	0.72	0/915
18	AR	0.34	0/554	0.87	0/740
19	AS	0.29	0/676	0.70	0/911
20	AT	0.28	0/545	0.68	0/723
21	AU	0.29	0/443	0.65	0/583
22	B0	0.36	0/483	0.80	0/649
23	B1	0.39	0/534	1.06	1/713 (0.1%)
24	B2	0.35	0/427	0.75	0/575
25	B3	0.38	0/659	1.00	4/888 (0.5%)
26	B4	0.38	0/447	0.68	0/599
27	B5	0.37	0/368	0.81	0/489
28	B6	0.42	0/366	0.85	0/481
29	B7	0.38	0/538	0.96	0/704
30	B8	0.34	0/297	0.78	0/396
31	BA	0.40	0/69612	0.54	3/108576 (0.0%)
32	BB	0.37	0/2746	0.52	0/4278
33	BD	0.39	0/2071	0.91	5/2789 (0.2%)
34	BE	0.46	1/1544 (0.1%)	0.92	6/2079 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	BF	0.37	0/1586	0.86	2/2145 (0.1%)
36	BG	0.43	1/1385 (0.1%)	1.03	6/1866 (0.3%)
37	BH	0.32	0/1317	0.79	2/1776 (0.1%)
38	BM	0.36	0/1147	0.83	0/1549
39	BN	0.36	0/904	0.80	0/1215
40	BO	0.36	0/1072	0.81	0/1430
41	BP	0.36	0/1084	0.67	0/1450
42	BQ	0.36	0/998	0.85	0/1338
43	BR	0.38	0/881	0.92	4/1184 (0.3%)
44	BS	0.34	0/935	0.75	0/1255
45	BT	0.43	0/958	0.88	3/1273 (0.2%)
46	BU	0.43	0/796	1.03	3/1070 (0.3%)
47	BV	0.36	0/862	0.86	1/1164 (0.1%)
48	BW	0.31	0/697	0.60	0/935
49	BX	0.37	0/755	0.90	0/1013
50	BZ	0.33	0/570	0.74	0/760
51	A	0.29	0/1138	0.70	0/1538
All	All	0.37	2/152763 (0.0%)	0.61	54/228824 (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
2	AB	0	1
3	AC	0	1
4	AD	0	2
6	AF	0	1
9	AI	0	1
10	AJ	0	1
11	AK	0	2
13	AM	0	4
14	AN	0	2
19	AS	0	3
22	B0	0	1
23	B1	0	3
24	B2	0	2
25	B3	0	3
26	B4	0	1
27	B5	0	1
33	BD	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
34	BE	0	4
35	BF	0	2
36	BG	0	3
37	BH	0	1
38	BM	0	4
39	BN	0	2
43	BR	0	2
44	BS	0	1
45	BT	0	1
46	BU	0	4
47	BV	0	2
48	BW	0	1
49	BX	0	1
All	All	0	61

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	BE	75	THR	C-N	6.95	1.42	1.33
36	BG	84	MET	C-N	5.67	1.38	1.33

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	BU	86	ARG	N-CA-C	10.40	126.40	109.96
43	BR	72	VAL	N-CA-C	-8.38	103.06	111.77
36	BG	90	VAL	CA-C-N	8.09	136.26	121.70
36	BG	90	VAL	C-N-CA	8.09	136.26	121.70
13	AM	41	GLU	CA-C-N	7.39	135.00	121.70

There are no chirality outliers.

5 of 61 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AB	4	ILE	Peptide
3	AC	207	LEU	Peptide
4	AD	187	ASN	Peptide
4	AD	201	LYS	Peptide
6	AF	51	GLU	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	AA	32911	0	16551	939	0
2	AB	1774	0	1820	85	0
3	AC	1648	0	1704	81	0
4	AD	1610	0	1632	98	0
5	AE	1133	0	1205	50	0
6	AF	797	0	795	36	0
7	AG	1207	0	1235	63	0
8	AH	1009	0	1068	47	0
9	AI	983	0	1025	61	0
10	AJ	794	0	841	49	0
11	AK	857	0	886	46	0
12	AL	1054	0	1141	39	0
13	AM	873	0	912	70	0
14	AN	471	0	499	25	0
15	AO	708	0	737	33	0
16	AP	688	0	716	32	0
17	AQ	675	0	704	28	0
18	AR	549	0	599	27	0
19	AS	660	0	658	36	0
20	AT	542	0	577	27	0
21	AU	440	0	448	14	0
22	B0	477	0	503	18	0
23	B1	533	0	572	25	0
24	B2	424	0	471	20	0
25	B3	642	0	620	31	0
26	B4	437	0	444	17	0
27	B5	365	0	389	14	0
28	B6	362	0	400	31	0
29	B7	530	0	573	28	0
30	B8	292	0	320	15	0
31	BA	62143	0	31234	1426	0
32	BB	2455	0	1236	59	0
33	BD	2041	0	2142	105	0
34	BE	1522	0	1608	72	0
35	BF	1563	0	1606	78	0
36	BG	1367	0	1417	62	0
37	BH	1303	0	1343	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	BM	1127	0	1176	52	0
39	BN	895	0	951	29	0
40	BO	1066	0	1109	60	0
41	BP	1061	0	1111	48	0
42	BQ	990	0	1037	52	0
43	BR	872	0	911	52	0
44	BS	923	0	983	41	0
45	BT	945	0	1012	40	0
46	BU	783	0	818	32	0
47	BV	853	0	915	57	0
48	BW	689	0	738	33	0
49	BX	747	0	808	32	0
50	BZ	562	0	567	29	0
51	A	1128	0	992	94	0
All	All	140480	0	93759	4036	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 19.

The worst 5 of 4036 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:AA:1439:G:N2	1:AA:1475:A:N7	1.81	1.28
31:BA:1487:A:C2	31:BA:2706:G:N1	2.06	1.23
2:AB:207:ILE:HD11	51:A:144:GLU:O	1.48	1.11
2:AB:207:ILE:CD1	51:A:145:GLU:HA	1.84	1.07
31:BA:2312:G:N1	31:BA:2315:A:C2	2.22	1.06

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	
2	AB	222/255 (87%)	194 (87%)	28 (13%)	0	100	100
3	AC	209/217 (96%)	177 (85%)	32 (15%)	0	100	100
4	AD	198/203 (98%)	163 (82%)	34 (17%)	1 (0%)	24	63
5	AE	154/168 (92%)	138 (90%)	16 (10%)	0	100	100
6	AF	95/97 (98%)	73 (77%)	22 (23%)	0	100	100
7	AG	150/155 (97%)	136 (91%)	14 (9%)	0	100	100
8	AH	128/132 (97%)	110 (86%)	18 (14%)	0	100	100
9	AI	127/130 (98%)	104 (82%)	23 (18%)	0	100	100
10	AJ	96/102 (94%)	82 (85%)	14 (15%)	0	100	100
11	AK	116/127 (91%)	102 (88%)	14 (12%)	0	100	100
12	AL	134/137 (98%)	110 (82%)	24 (18%)	0	100	100
13	AM	109/121 (90%)	82 (75%)	27 (25%)	0	100	100
14	AN	57/61 (93%)	44 (77%)	13 (23%)	0	100	100
15	AO	85/89 (96%)	72 (85%)	13 (15%)	0	100	100
16	AP	84/90 (93%)	74 (88%)	10 (12%)	0	100	100
17	AQ	80/86 (93%)	65 (81%)	15 (19%)	0	100	100
18	AR	66/81 (82%)	53 (80%)	13 (20%)	0	100	100
19	AS	80/92 (87%)	61 (76%)	19 (24%)	0	100	100
20	AT	69/77 (90%)	57 (83%)	12 (17%)	0	100	100
21	AU	54/58 (93%)	46 (85%)	8 (15%)	0	100	100
22	B0	59/64 (92%)	45 (76%)	14 (24%)	0	100	100
23	B1	65/69 (94%)	51 (78%)	14 (22%)	0	100	100
24	B2	56/59 (95%)	45 (80%)	11 (20%)	0	100	100
25	B3	77/81 (95%)	52 (68%)	25 (32%)	0	100	100
26	B4	51/57 (90%)	43 (84%)	8 (16%)	0	100	100
27	B5	45/49 (92%)	32 (71%)	12 (27%)	1 (2%)	5	28
28	B6	42/44 (96%)	35 (83%)	7 (17%)	0	100	100
29	B7	62/66 (94%)	51 (82%)	11 (18%)	0	100	100
30	B8	34/38 (90%)	32 (94%)	2 (6%)	0	100	100
33	BD	270/276 (98%)	193 (72%)	77 (28%)	0	100	100
34	BE	203/207 (98%)	164 (81%)	39 (19%)	0	100	100
35	BF	204/208 (98%)	157 (77%)	46 (22%)	1 (0%)	24	63

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	BG	174/180 (97%)	137 (79%)	36 (21%)	1 (1%)	21	59
37	BH	172/178 (97%)	144 (84%)	28 (16%)	0	100	100
38	BM	145/148 (98%)	119 (82%)	25 (17%)	1 (1%)	18	55
39	BN	119/122 (98%)	99 (83%)	20 (17%)	0	100	100
40	BO	144/147 (98%)	117 (81%)	27 (19%)	0	100	100
41	BP	132/137 (96%)	120 (91%)	12 (9%)	0	100	100
42	BQ	123/126 (98%)	109 (89%)	14 (11%)	0	100	100
43	BR	113/115 (98%)	90 (80%)	22 (20%)	1 (1%)	14	50
44	BS	112/114 (98%)	95 (85%)	17 (15%)	0	100	100
45	BT	115/119 (97%)	103 (90%)	12 (10%)	0	100	100
46	BU	99/104 (95%)	67 (68%)	32 (32%)	0	100	100
47	BV	110/115 (96%)	99 (90%)	11 (10%)	0	100	100
48	BW	86/97 (89%)	78 (91%)	8 (9%)	0	100	100
49	BX	97/101 (96%)	73 (75%)	24 (25%)	0	100	100
50	BZ	73/94 (78%)	64 (88%)	9 (12%)	0	100	100
51	A	155/185 (84%)	130 (84%)	25 (16%)	0	100	100
All	All	5450/5778 (94%)	4487 (82%)	957 (18%)	6 (0%)	49	83

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
38	BM	132	HIS
4	AD	202	MET
27	B5	12	CYS
35	BF	23	VAL
36	BG	82	GLU

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	
2	AB	190/213 (89%)	188 (99%)	2 (1%)	65	75
3	AC	168/172 (98%)	167 (99%)	1 (1%)	78	82
4	AD	172/175 (98%)	172 (100%)	0	100	100
5	AE	115/126 (91%)	115 (100%)	0	100	100
6	AF	84/84 (100%)	84 (100%)	0	100	100
7	AG	125/128 (98%)	125 (100%)	0	100	100
8	AH	111/113 (98%)	111 (100%)	0	100	100
9	AI	99/100 (99%)	99 (100%)	0	100	100
10	AJ	89/92 (97%)	89 (100%)	0	100	100
11	AK	89/97 (92%)	87 (98%)	2 (2%)	45	64
12	AL	113/114 (99%)	113 (100%)	0	100	100
13	AM	93/100 (93%)	93 (100%)	0	100	100
14	AN	50/53 (94%)	50 (100%)	0	100	100
15	AO	74/76 (97%)	74 (100%)	0	100	100
16	AP	77/81 (95%)	76 (99%)	1 (1%)	61	73
17	AQ	76/80 (95%)	75 (99%)	1 (1%)	61	73
18	AR	59/69 (86%)	58 (98%)	1 (2%)	53	68
19	AS	70/79 (89%)	67 (96%)	3 (4%)	26	47
20	AT	53/58 (91%)	53 (100%)	0	100	100
21	AU	42/53 (79%)	42 (100%)	0	100	100
22	B0	52/56 (93%)	51 (98%)	1 (2%)	50	66
23	B1	58/60 (97%)	57 (98%)	1 (2%)	53	68
24	B2	48/49 (98%)	47 (98%)	1 (2%)	47	65
25	B3	69/71 (97%)	68 (99%)	1 (1%)	59	71
26	B4	46/50 (92%)	46 (100%)	0	100	100
27	B5	41/43 (95%)	40 (98%)	1 (2%)	43	63
28	B6	37/37 (100%)	37 (100%)	0	100	100
29	B7	54/56 (96%)	53 (98%)	1 (2%)	50	66
30	B8	34/35 (97%)	34 (100%)	0	100	100
33	BD	219/223 (98%)	216 (99%)	3 (1%)	59	71
34	BE	162/164 (99%)	158 (98%)	4 (2%)	42	62
35	BF	170/171 (99%)	168 (99%)	2 (1%)	63	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	BG	150/154 (97%)	144 (96%)	6 (4%)	28	49
37	BH	140/147 (95%)	139 (99%)	1 (1%)	76	80
38	BM	122/123 (99%)	119 (98%)	3 (2%)	42	62
39	BN	93/95 (98%)	91 (98%)	2 (2%)	45	64
40	BO	107/109 (98%)	104 (97%)	3 (3%)	38	59
41	BP	106/107 (99%)	103 (97%)	3 (3%)	38	59
42	BQ	104/105 (99%)	104 (100%)	0	100	100
43	BR	90/90 (100%)	88 (98%)	2 (2%)	45	64
44	BS	98/98 (100%)	94 (96%)	4 (4%)	27	48
45	BT	90/92 (98%)	88 (98%)	2 (2%)	45	64
46	BU	85/88 (97%)	84 (99%)	1 (1%)	63	74
47	BV	92/94 (98%)	90 (98%)	2 (2%)	45	64
48	BW	77/84 (92%)	77 (100%)	0	100	100
49	BX	83/85 (98%)	82 (99%)	1 (1%)	63	74
50	BZ	59/73 (81%)	59 (100%)	0	100	100
51	A	93/163 (57%)	92 (99%)	1 (1%)	65	75
All	All	4528/4785 (95%)	4471 (99%)	57 (1%)	59	73

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
36	BG	45	VAL
49	BX	76	VAL
38	BM	138	LYS
47	BV	39	ILE
44	BS	102	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
39	BN	82	ASN
44	BS	55	ASN
40	BO	38	GLN
41	BP	123	HIS
46	BU	85	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	AA	1534/1535 (99%)	663 (43%)	8 (0%)
31	BA	2896/2897 (99%)	1094 (37%)	20 (0%)
32	BB	114/115 (99%)	45 (39%)	0
All	All	4544/4547 (99%)	1802 (39%)	28 (0%)

5 of 1802 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	8	U
1	AA	9	G
1	AA	10	A
1	AA	11	G
1	AA	15	U

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
31	BA	1281	A
31	BA	2760	U
31	BA	1317	U
31	BA	2065	G
31	BA	1313	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

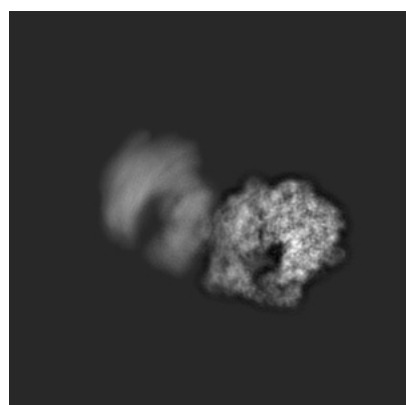
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3581. These allow visual inspection of the internal detail of the map and identification of artifacts.

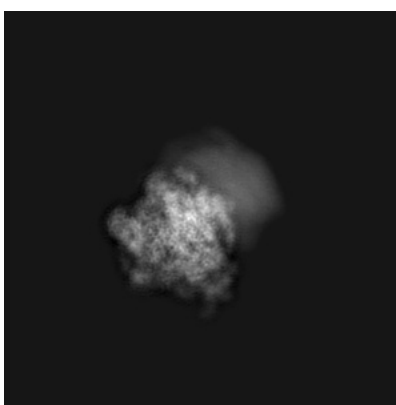
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

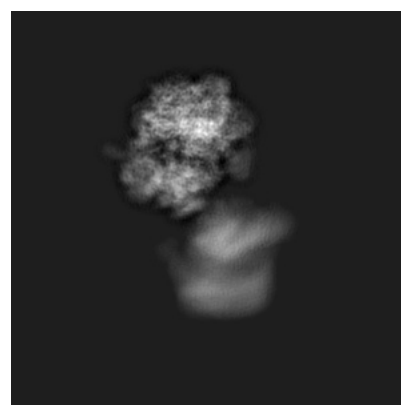
6.1.1 Primary map



X



Y

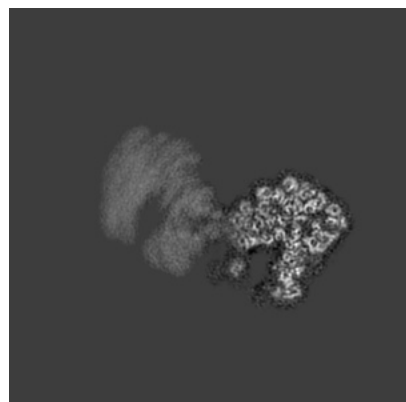


Z

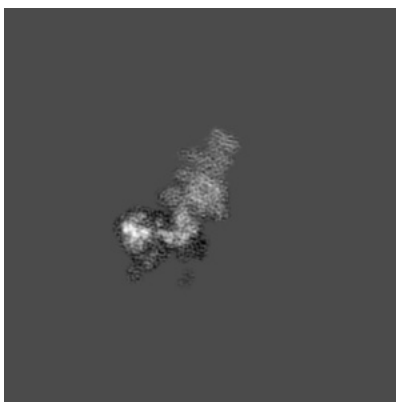
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

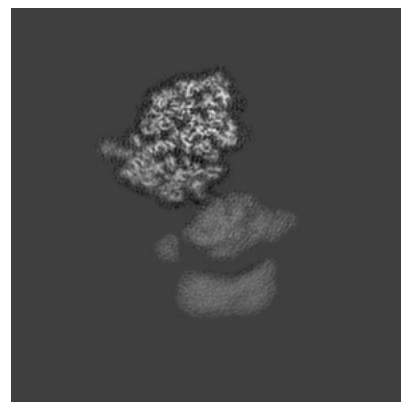
6.2.1 Primary map



X Index: 300



Y Index: 300

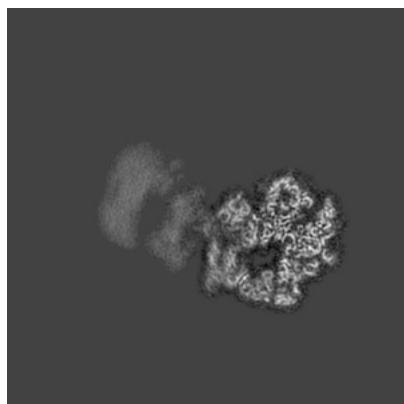


Z Index: 300

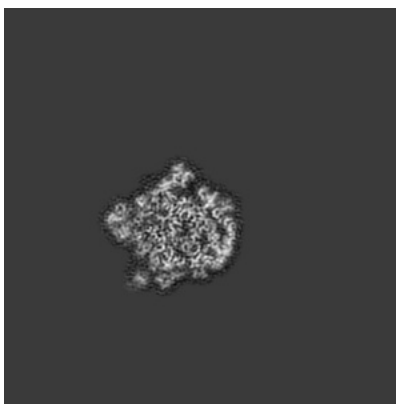
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

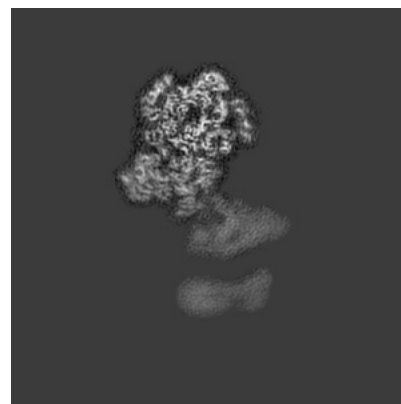
6.3.1 Primary map



X Index: 278



Y Index: 428

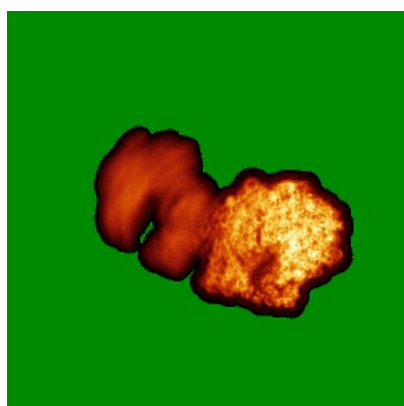


Z Index: 277

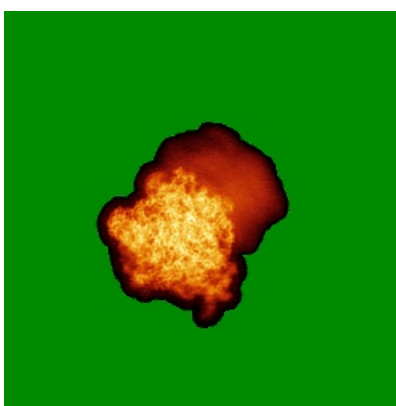
The images above show the largest variance slices of the map in three orthogonal directions.

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

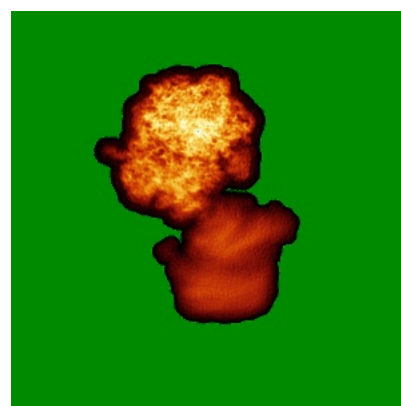
6.4.1 Primary map



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

This section was not generated.

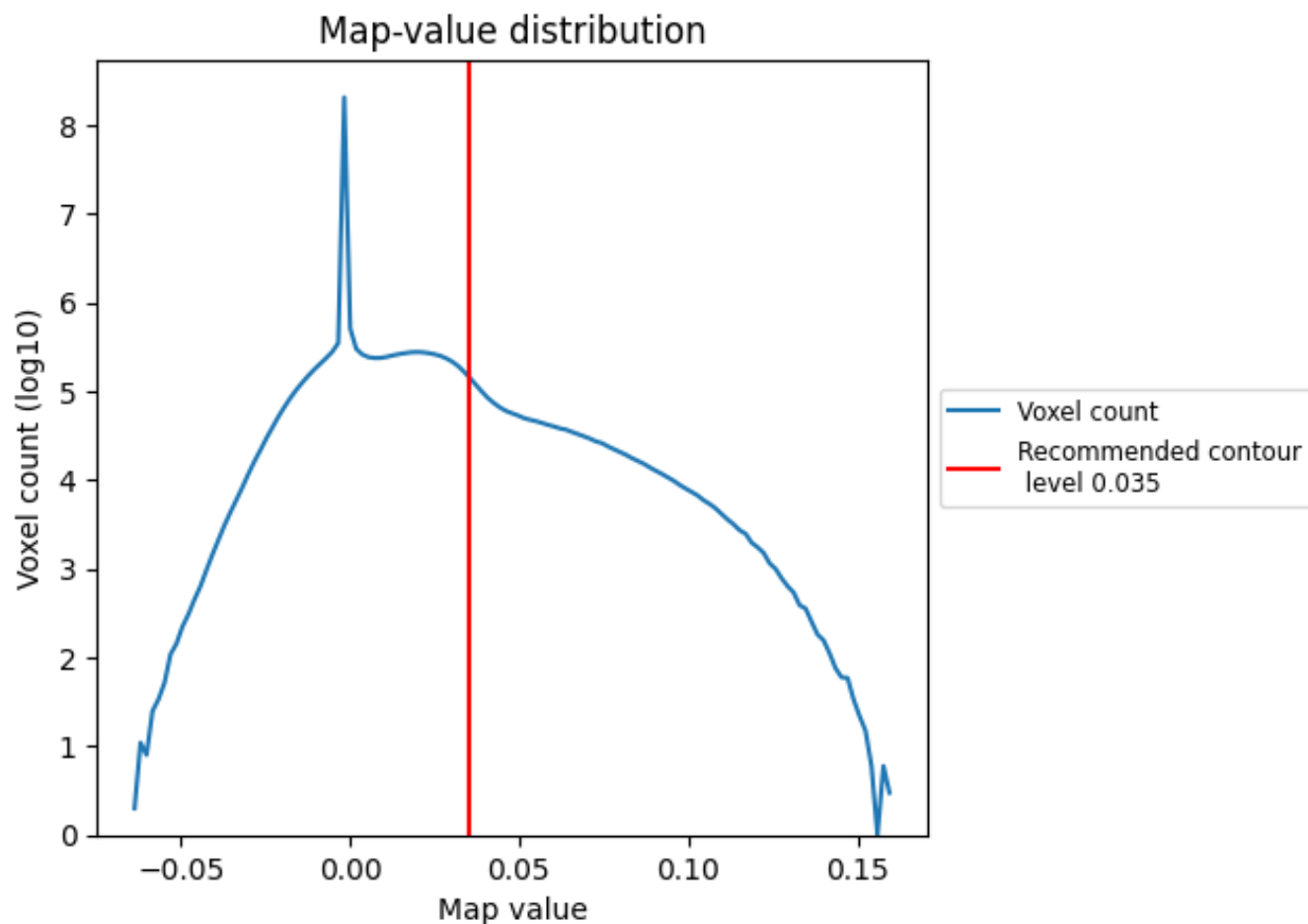
6.6 Mask visualisation

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

7 Map analysis [i](#)

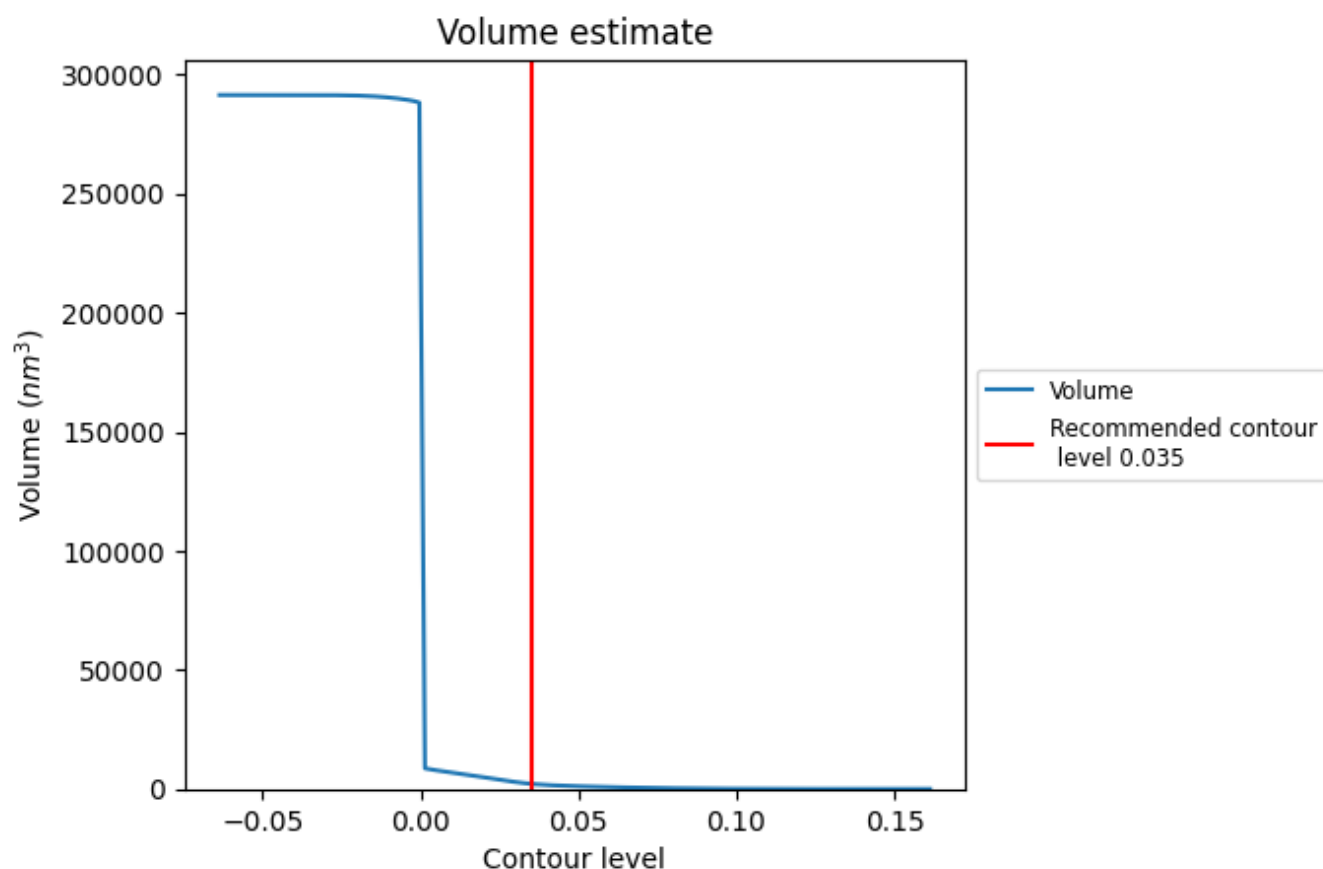
This section contains the results of statistical analysis of the map.

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.

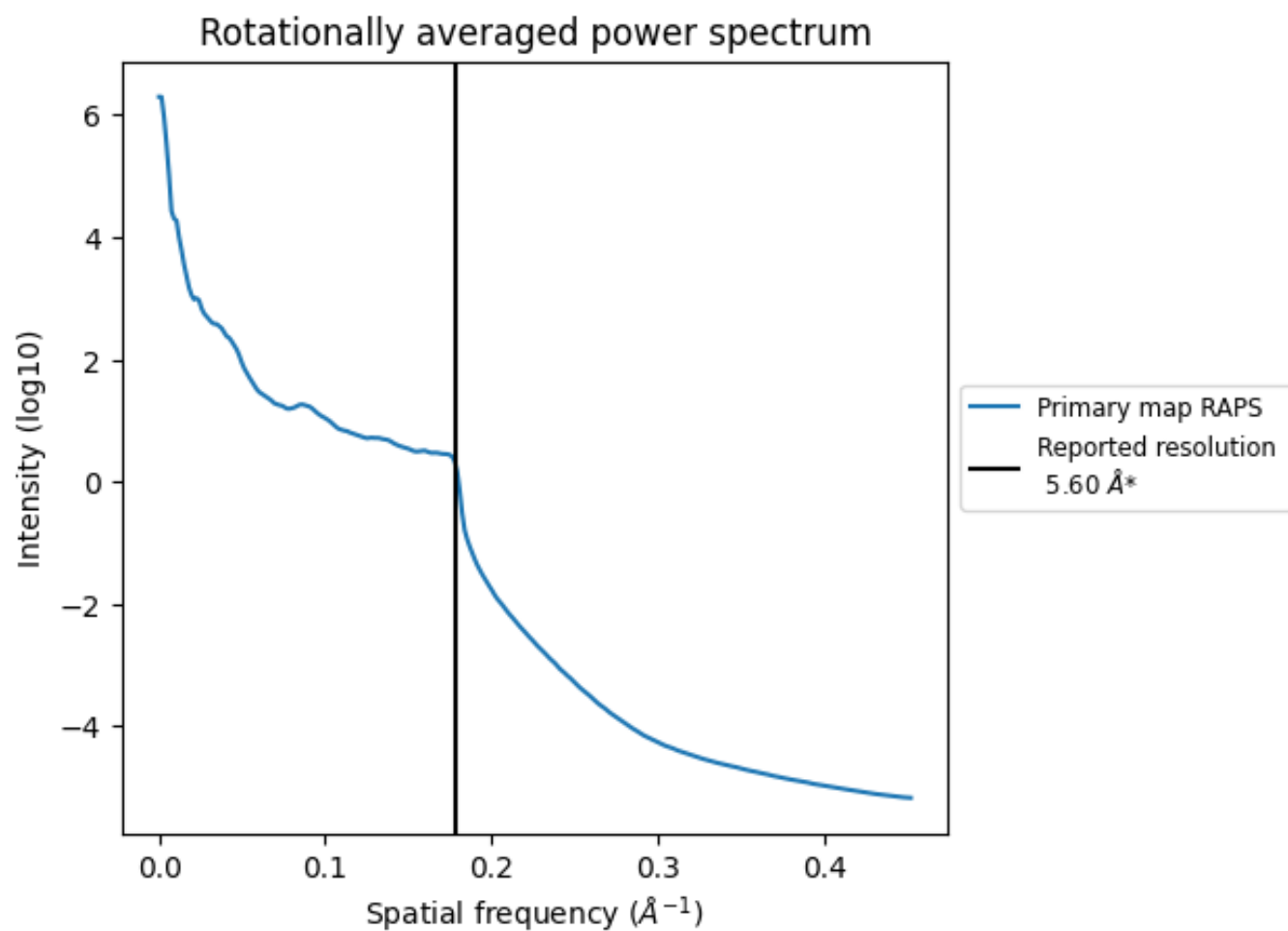
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2160 nm³; this corresponds to an approximate mass of 1951 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 ⓘ

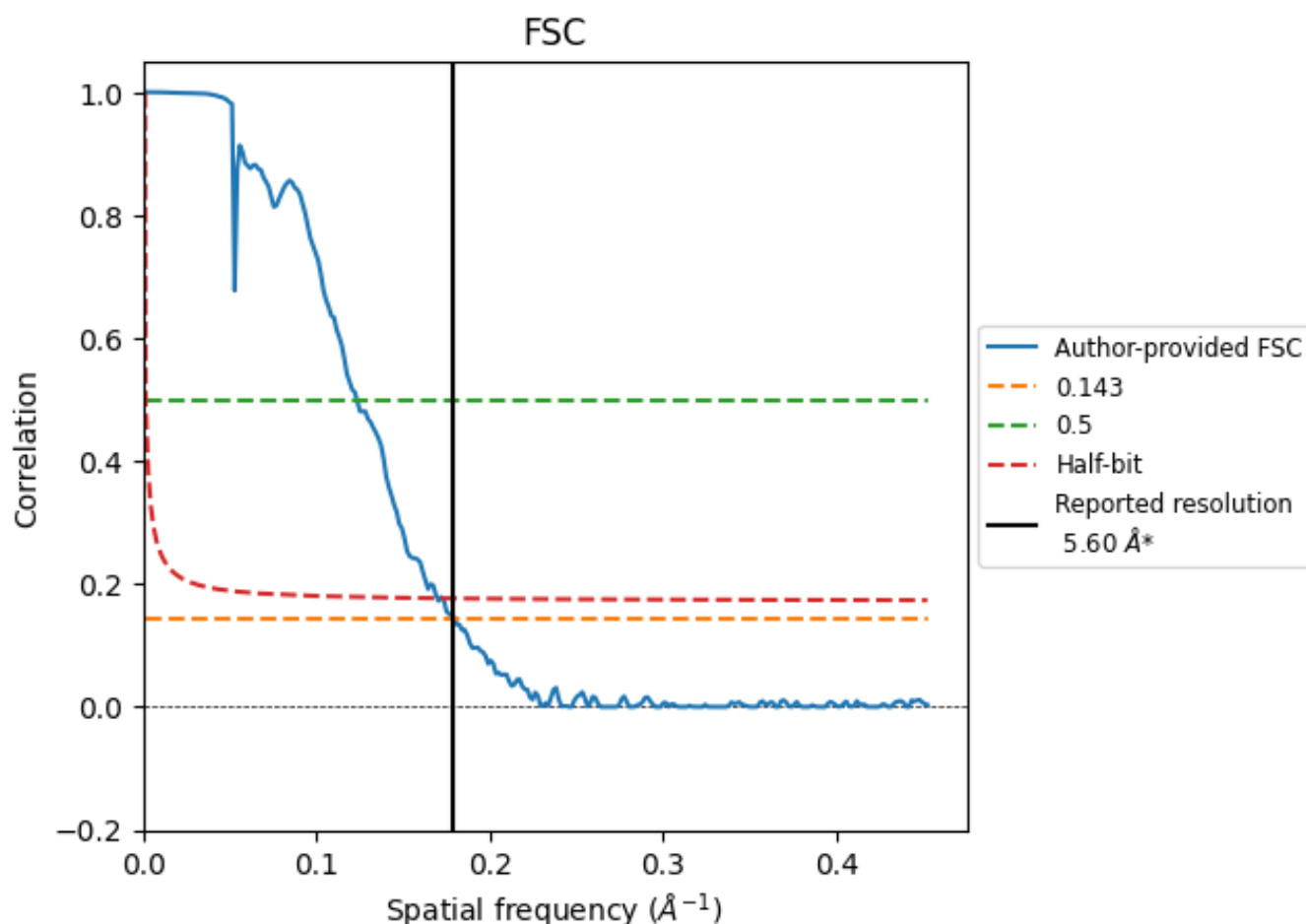


*Reported resolution corresponds to spatial frequency of 0.179 Å⁻¹

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 0.179 Å⁻¹

8.2 Resolution estimates [i](#)

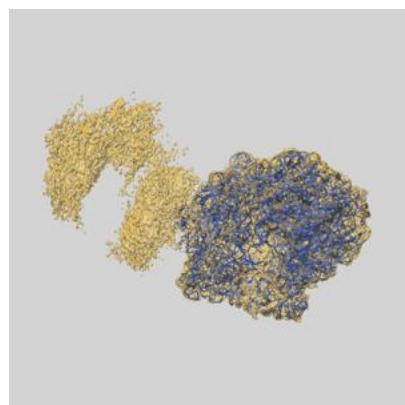
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.60	-	-
Author-provided FSC curve	5.56	8.11	5.89
Unmasked-calculated*	-	-	-

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

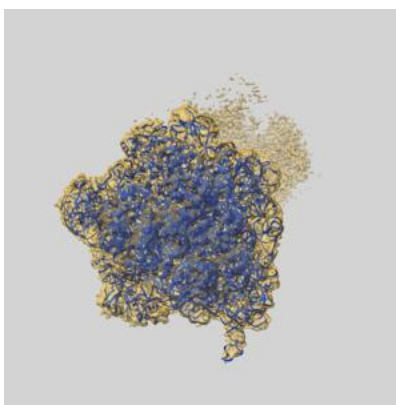
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3581 and PDB model 5MYJ. Per-residue inclusion information can be found in section 3 on page 13.

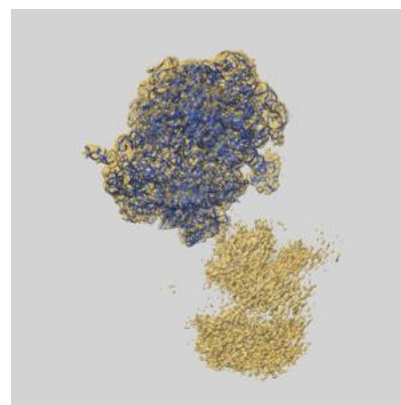
9.1 Map-model overlay [i](#)



X



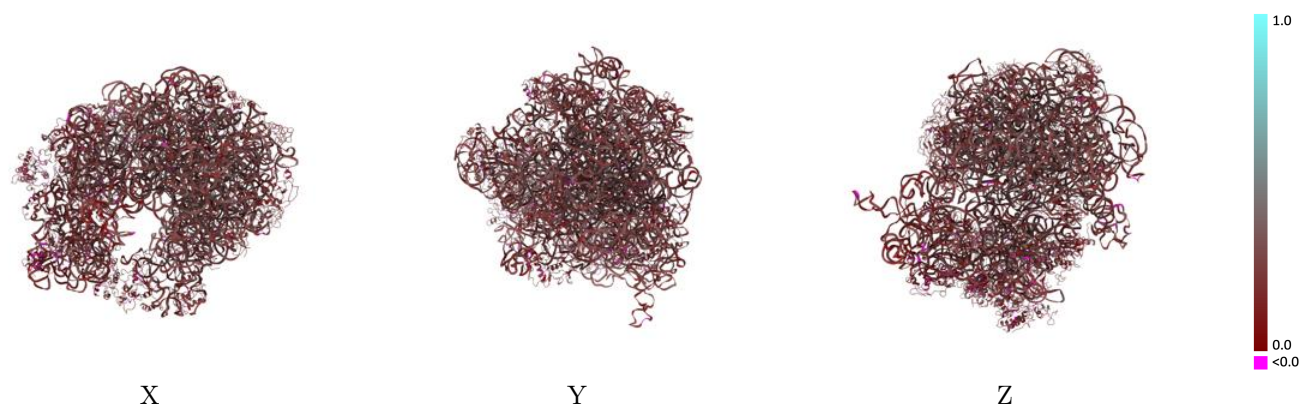
Y



Z

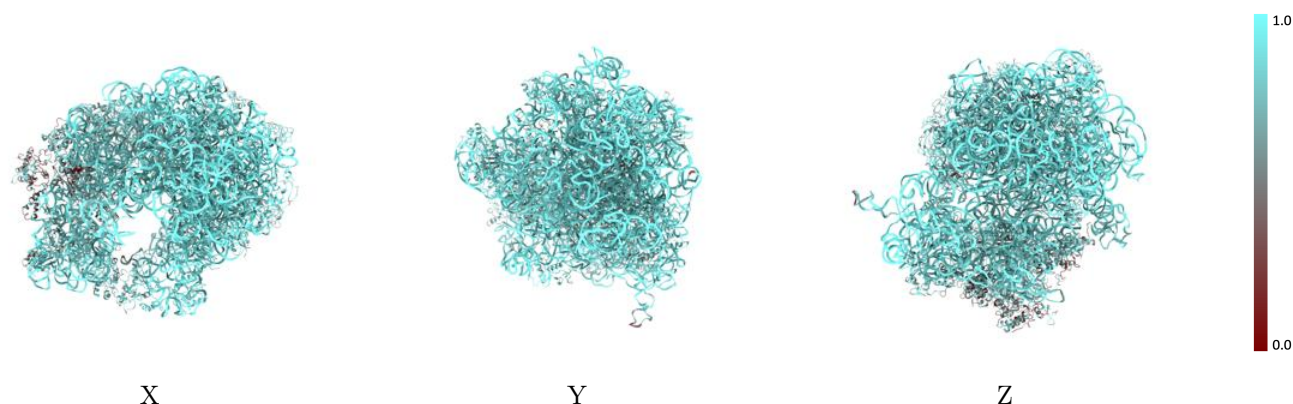
The images above show the 3D surface view of the map at the recommended contour level 0.035 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



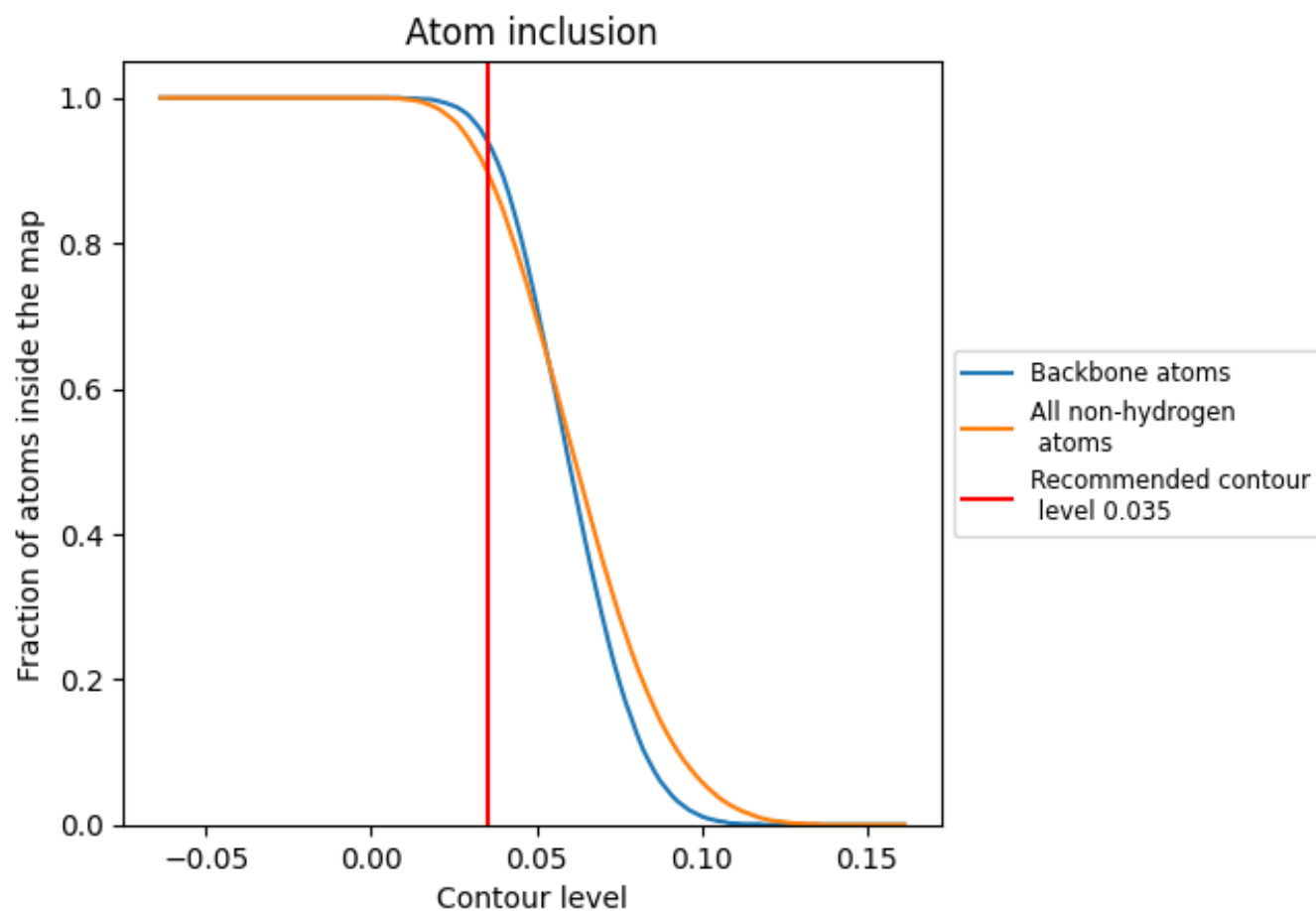
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.035).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% 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 (0.035) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9000	 0.2480
A	 0.5440	 0.2100
AA	 0.9500	 0.2270
AB	 0.4760	 0.2060
AC	 0.6560	 0.1880
AD	 0.7400	 0.1680
AE	 0.5600	 0.2170
AF	 0.6500	 0.2120
AG	 0.7110	 0.2150
AH	 0.6340	 0.1770
AI	 0.7760	 0.1630
AJ	 0.7060	 0.1710
AK	 0.6970	 0.2320
AL	 0.6410	 0.2190
AM	 0.8010	 0.2000
AN	 0.8500	 0.1690
AO	 0.7640	 0.2070
AP	 0.7780	 0.1640
AQ	 0.7170	 0.2110
AR	 0.6260	 0.2300
AS	 0.8070	 0.1760
AT	 0.7940	 0.1940
AU	 0.3920	 0.2390
B0	 0.7500	 0.2530
B1	 0.8070	 0.2010
B2	 0.8170	 0.2620
B3	 0.7750	 0.2060
B4	 0.8420	 0.2820
B5	 0.7950	 0.2340
B6	 0.8390	 0.2630
B7	 0.7940	 0.2500
B8	 0.8930	 0.2530
BA	 0.9730	 0.2760
BB	 0.9900	 0.2650
BD	 0.7660	 0.2590



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Chain	Atom inclusion	Q-score
BE	 0.8260	 0.2460
BF	 0.8280	 0.2400
BG	 0.8210	 0.2190
BH	 0.8580	 0.2290
BM	 0.8110	 0.2500
BN	 0.6980	 0.2490
BO	 0.8350	 0.2450
BP	 0.8350	 0.2580
BQ	 0.8010	 0.2240
BR	 0.9000	 0.2090
BS	 0.7350	 0.2520
BT	 0.7980	 0.1910
BU	 0.8230	 0.2520
BV	 0.7840	 0.2540
BW	 0.8230	 0.2550
BX	 0.8530	 0.2200
BZ	 0.8560	 0.2660