



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 04:44 AM UTC

PDB ID : 8BJQ / pdb_00008bjq
EMDB ID : EMD-16090
Title : Structure of a yeast 80S ribosome-bound N-Acetyltransferase B complex
Authors : Knorr, A.G.; Mackens-Kiani, T.; Musial, J.; Berninghausen, O.; Becker, T.;
Beatrix, B.; Beckmann, R.
Deposited on : 2022-11-05
Resolution : 3.80 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:

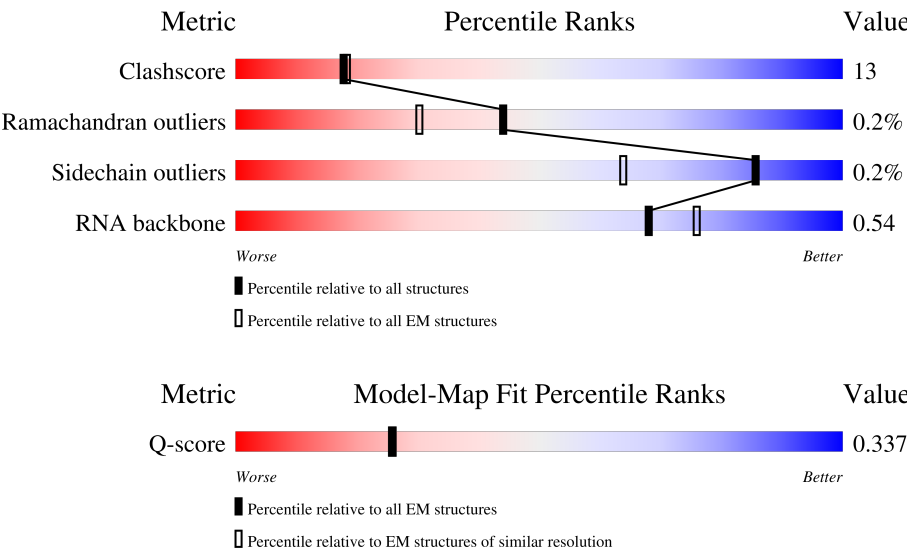
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	A	195	82% 65% 35%
1	C	195	29% 26% 8% 65%
2	B	796	41% 68% 31%

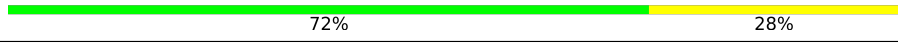
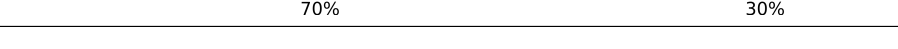
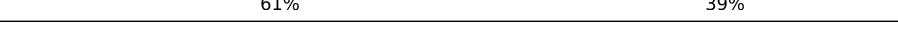
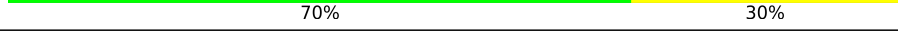
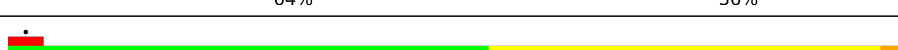
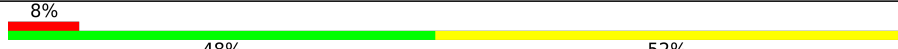
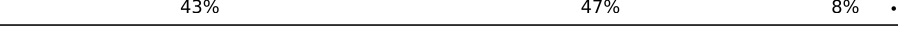
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Mol	Chain	Length	Quality of chain
2	D	796	
3	C4	121	
4	C3	158	
5	LA	251	
6	LB	386	
7	LC	361	
8	LD	294	
9	LE	175	
10	LF	222	
11	LG	233	
12	LH	191	
13	LI	218	
14	LJ	169	
15	LL	193	
16	LM	136	
17	LN	203	
18	LO	197	
19	LP	183	
20	LQ	185	
21	LR	188	
22	LS	171	
23	LT	159	
24	LU	100	
25	LV	136	
26	LW	126	

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Mol	Chain	Length	Quality of chain
27	LX	121	 75%25%
28	LY	125	 72%28%
29	LZ	135	 70%30%
30	La	148	 61%39%
31	Lb	58	 83%17%
32	Lc	96	 67%33%
33	Ld	109	 83%15%.
34	Le	127	 66%34%
35	Lf	106	 61%39%
36	Lg	112	 69%31%
37	Lh	119	 76%24%
38	Li	99	 77%23%
39	Lj	85	 79%21%
40	Lk	77	 70%30%
41	Ll	50	 64%36%
42	Lm	52	 54%44%.
43	Ln	25	 8%48%52%
44	Lo	103	 70%30%
45	Lp	91	 65%35%
46	1	3395	 43%47%8%.

2 Entry composition [i](#)

There are 48 unique types of molecules in this entry. The entry contains 141384 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 N-terminal acetyltransferase B complex catalytic subunit NAT3.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	195	Total	C	N	O	S	0	0
			1612	1030	273	297	12		
1	C	68	Total	C	N	O	S	0	0
			571	378	81	107	5		

- Molecule 2 is a protein called N-terminal acetyltransferase B complex subunit MDM20.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	796	Total	C	N	O	S	0	0
			6536	4195	1080	1231	30		
2	D	796	Total	C	N	O	S	0	0
			6536	4195	1080	1231	30		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C4	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 5 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	LA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LB	386	Total	C	N	O	S	0	0
			3075	1950	584	533	8		

- Molecule 7 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 9 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LE	132	ALA	THR	conflict	UNP P05739
LE	146	ILE	LEU	conflict	UNP P05739
LE	173	MET	LEU	conflict	UNP P05739

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LF	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 11 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LG	233	Total	C	N	O	S	0	0
			1804	1151	323	327	3		

- Molecule 12 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 13 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 14 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LL	193	Total	C	N	O		0	0
			1543	962	315	266			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 17 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 18 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LO	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 19 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	LP	183	Total	C	N	O	0	0
			1416	879	284	253		

- Molecule 20 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 21 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	LR	171	Total	C	N	O	0	0
			1378	850	294	234		

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LS	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 23 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LT	159	Total	C	N	O	S	0	0
			1276	805	246	221	4		

- Molecule 24 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	LU	100	Total	C	N	O	0	0
			796	516	131	149		

- Molecule 25 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LV	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LW	67	Total	C	N	O	S	0	0
			538	345	106	86	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
LW	104	GLN	ASN	conflict	UNP P04449
LW	109	GLN	LEU	conflict	UNP P04449
LW	112	ASP	ASN	conflict	UNP P04449
LW	119	ALA	GLU	conflict	UNP P04449

- Molecule 27 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LX	121	Total	C	N	O	S	0	0
			964	620	169	173	2		

- Molecule 28 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LY	125	Total	C	N	O		0	0
			984	620	191	173			

- Molecule 29 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LZ	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 30 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	La	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Lb	58	Total	C	N	O		0	0
			462	289	100	73			

- Molecule 32 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lc	96	Total	C	N	O	S	0	0
			737	476	123	137	1		

- Molecule 33 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ld	109	Total	C	N	O	S	0	0
			880	559	168	152	1		

- Molecule 34 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Le	127	Total	C	N	O	S	0	0
			1017	644	205	167	1		

- Molecule 35 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lf	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 36 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lg	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 37 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lh	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 38 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Li	99	Total	C	N	O	S	0	0
			766	478	154	132	2		

- Molecule 39 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lj	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lk	77	Total	C	N	O		0	0
			612	391	115	106			

- Molecule 41 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ll	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lm	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 43 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ln	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 44 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lo	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 45 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lp	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 46 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1	3301	Total	C	N	O	P	0	0
			70586	31525	12690	23070	3301		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	G	deletion	GB 1262303
1	1962	A	G	conflict	GB 1262303

- Molecule 47 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
47	C4	1	Total	Mg	0
			1	1	
47	C3	1	Total	Mg	0
			1	1	
47	LA	2	Total	Mg	0
			2	2	
47	LB	1	Total	Mg	0
			1	1	
47	LN	1	Total	Mg	0
			1	1	
47	LP	1	Total	Mg	0
			1	1	
47	LR	1	Total	Mg	0
			1	1	
47	LV	1	Total	Mg	0
			1	1	
47	La	1	Total	Mg	0
			1	1	
47	Le	1	Total	Mg	0
			1	1	
47	1	195	Total	Mg	0
			195	195	

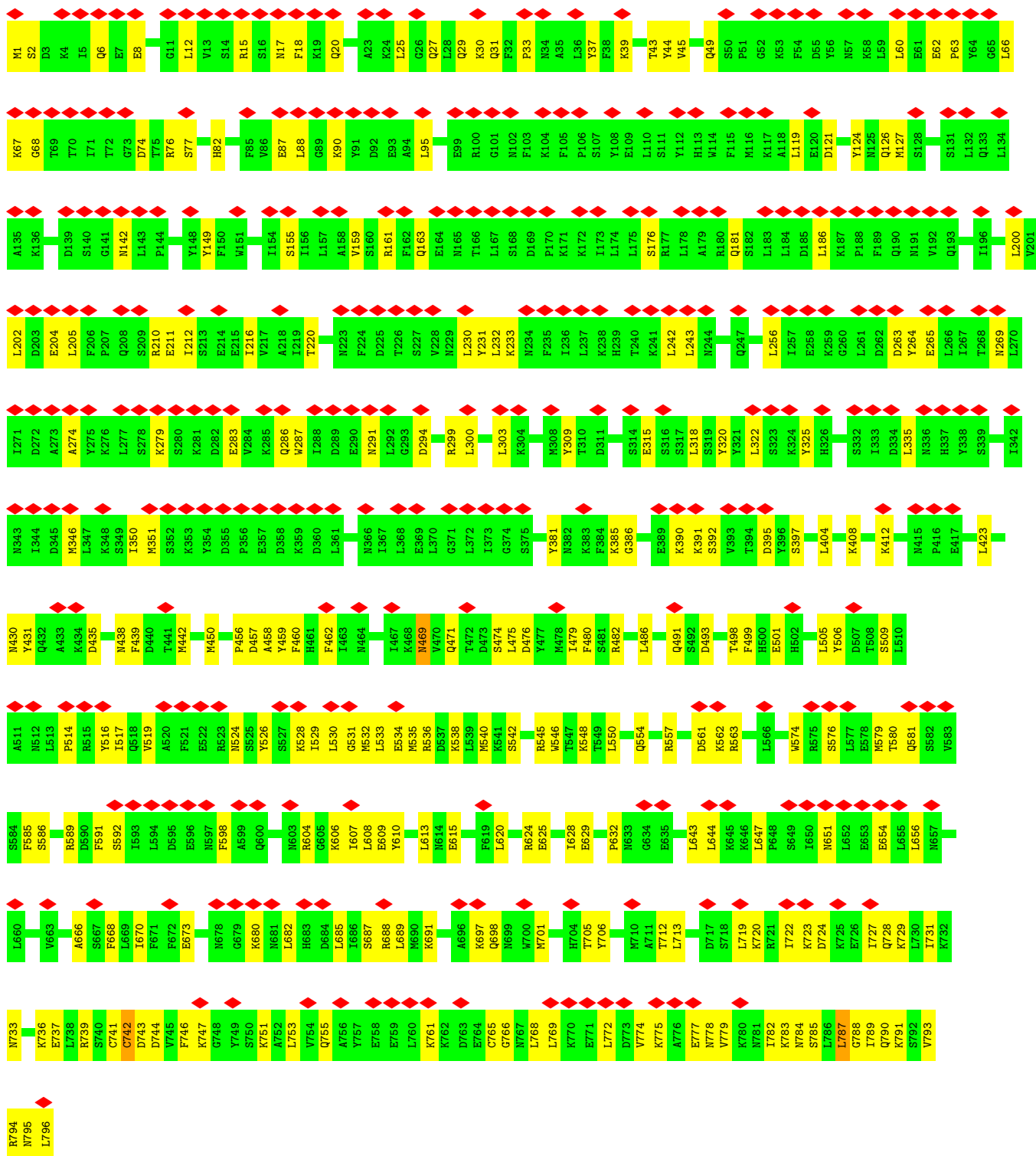
- Molecule 48 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
48	Lg	1	Total	Zn	0
			1	1	
48	Lj	1	Total	Zn	0
			1	1	

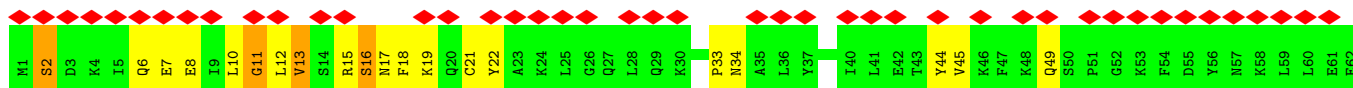
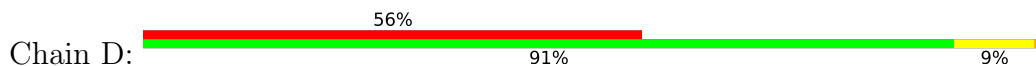
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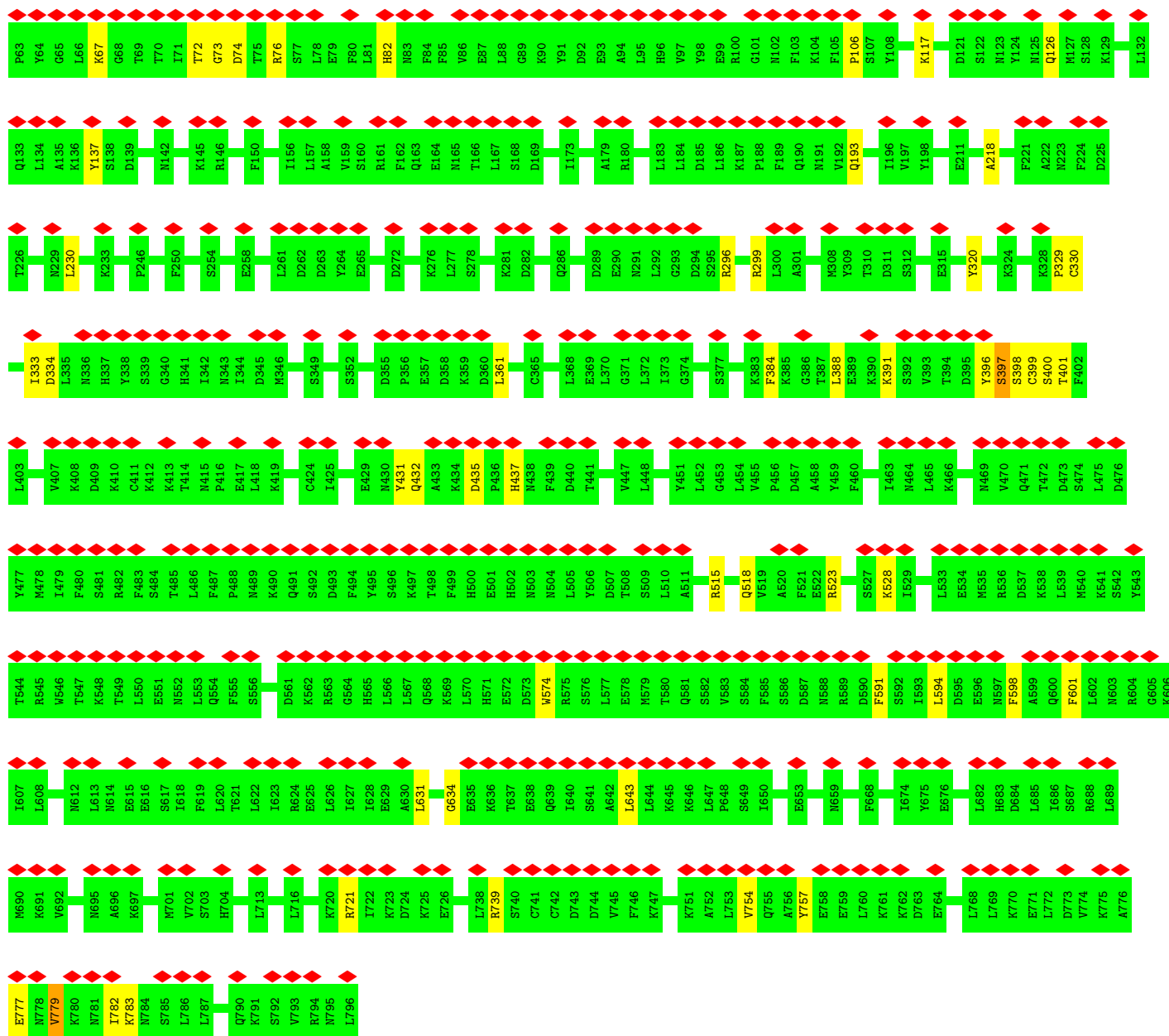
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Mol	Chain	Residues	Atoms		AltConf
48	Lm	1	Total 1	Zn 1	0
48	Lo	1	Total 1	Zn 1	0
48	Lp	1	Total 1	Zn 1	0



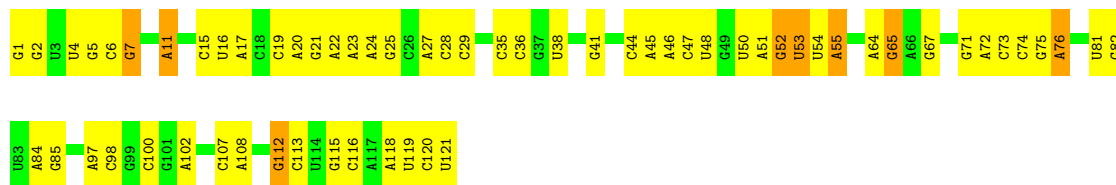
• Molecule 2: N-terminal acetyltransferase B complex subunit MDM20





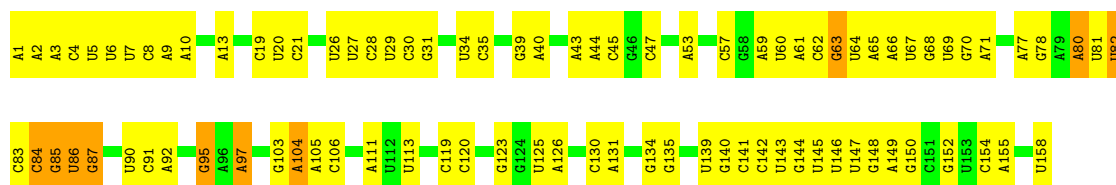
• Molecule 3: 5S rRNA

Chain C4: 49% 45% 7%

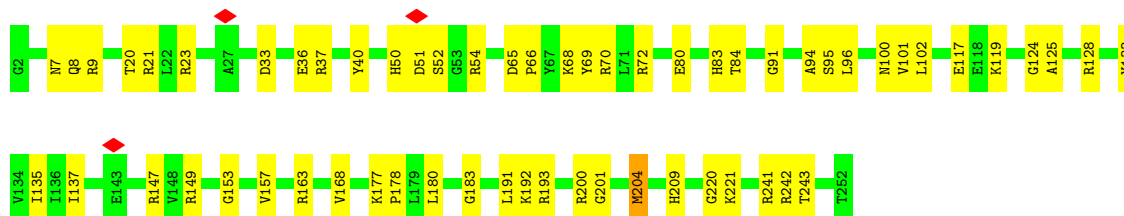
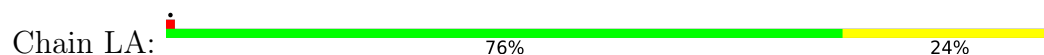


• Molecule 4: 5.8S rRNA

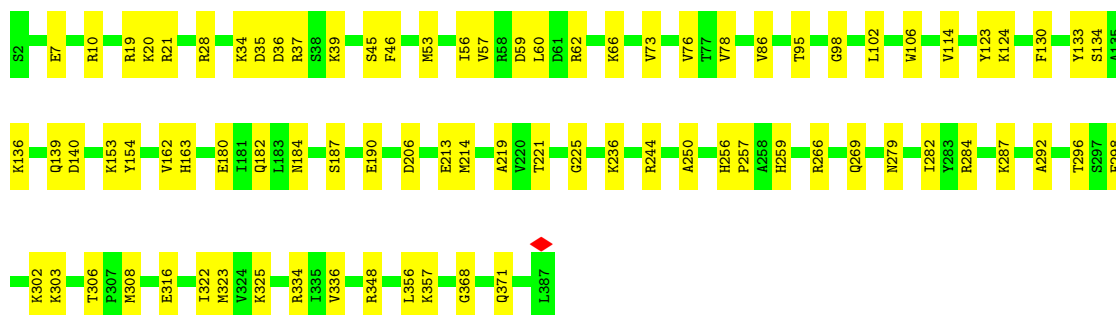
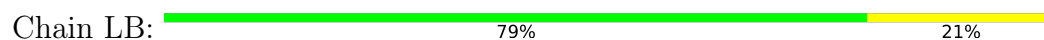
Chain C3: 44% 50% 6%



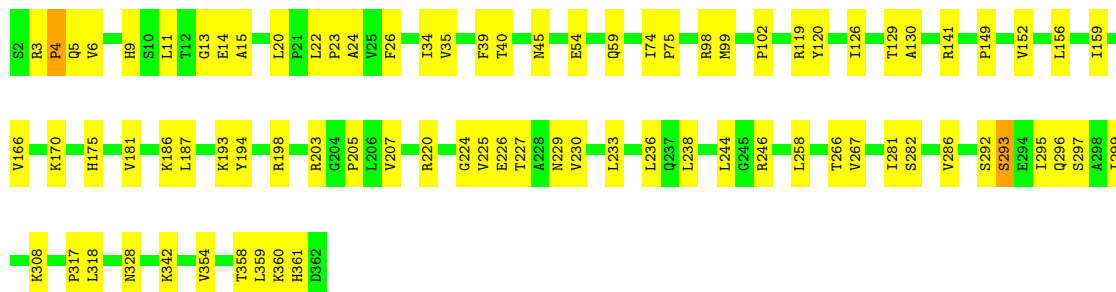
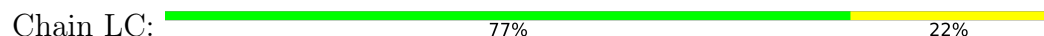
• Molecule 5: 60S ribosomal protein L2-A



• Molecule 6: 60S ribosomal protein L3

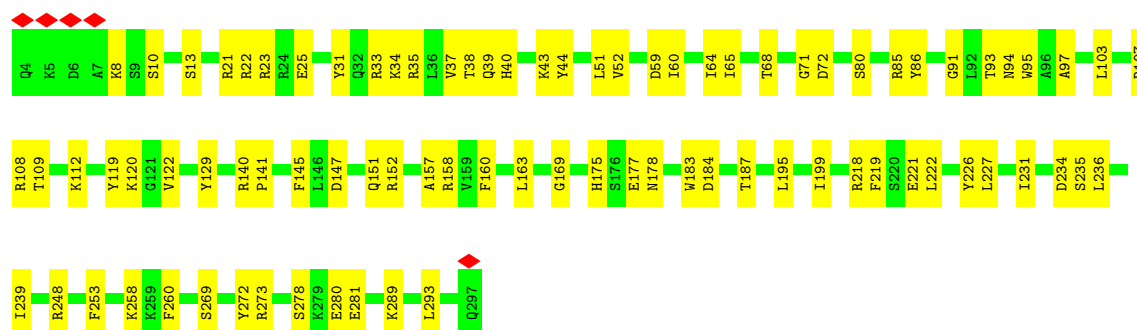


• Molecule 7: 60S ribosomal protein L4-A

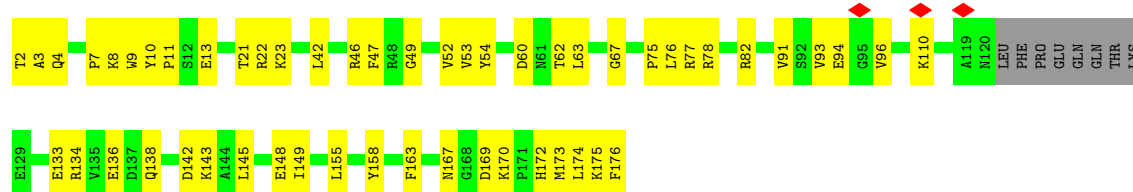


• Molecule 8: 60S ribosomal protein L5

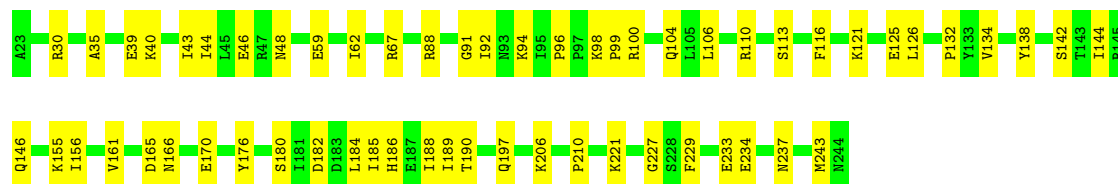




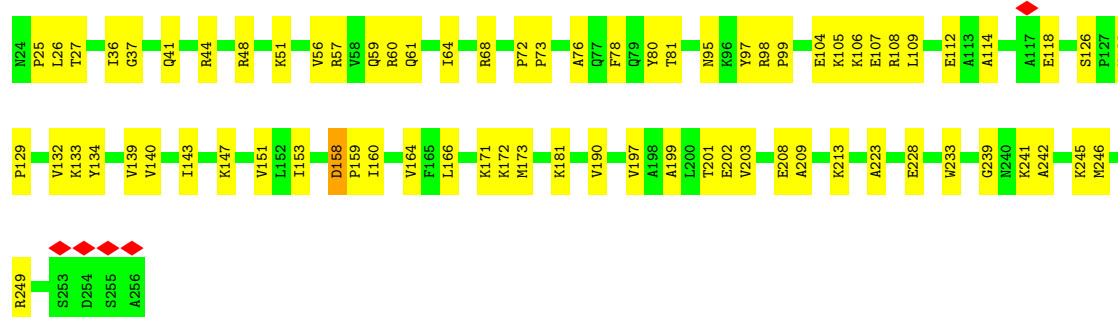
• Molecule 9: 60S ribosomal protein L6-B



• Molecule 10: 60S ribosomal protein L7-A

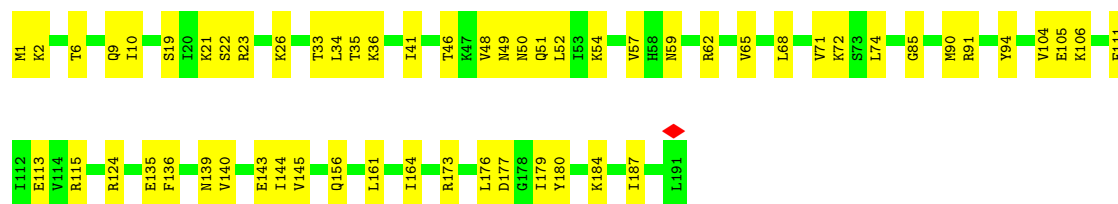


• Molecule 11: 60S ribosomal protein L8-A

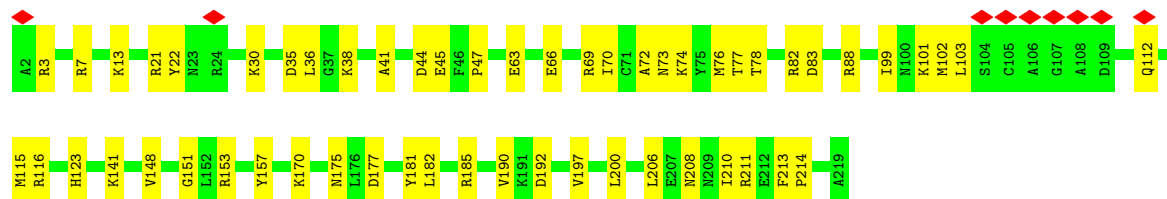
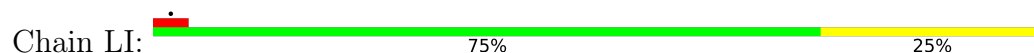


• Molecule 12: 60S ribosomal protein L9-A

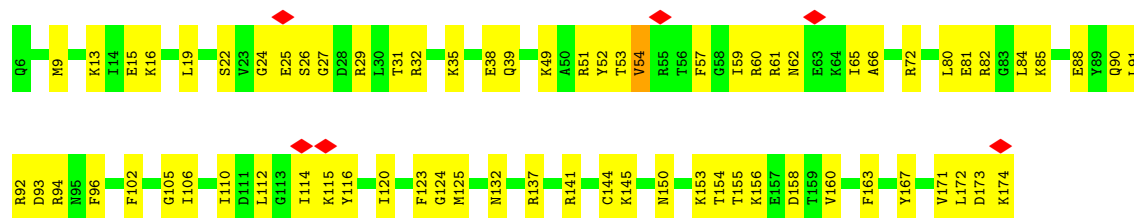




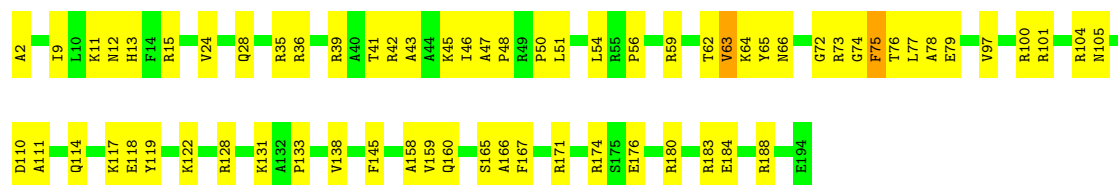
- Molecule 13: 60S ribosomal protein L10



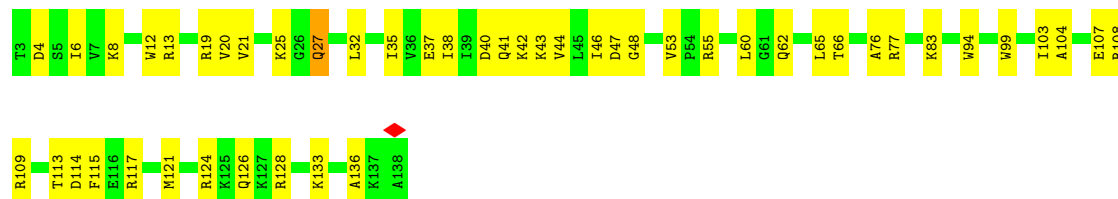
- Molecule 14: 60S ribosomal protein L11-B



- Molecule 15: 60S ribosomal protein L13-A

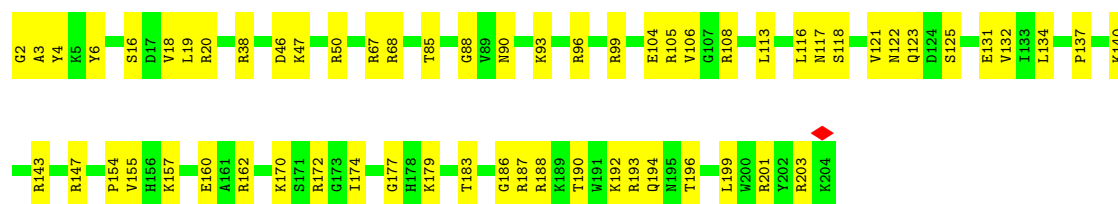


- Molecule 16: 60S ribosomal protein L14-A



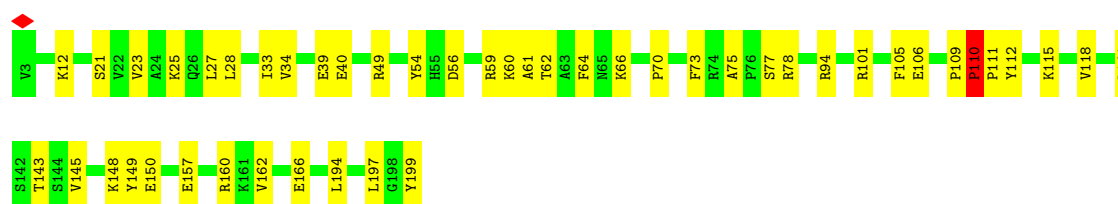
- Molecule 17: 60S ribosomal protein L15-A

Chain LN:  70% 30%



- Molecule 18: 60S ribosomal protein L16-A

Chain LO:  76% 23%



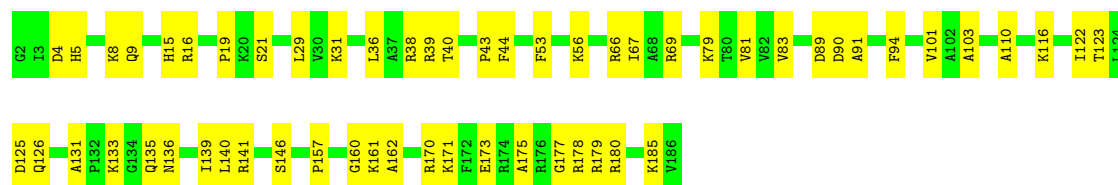
- Molecule 19: 60S ribosomal protein L17-A

Chain LP:  7% 85% 15%



- Molecule 20: 60S ribosomal protein L18-A

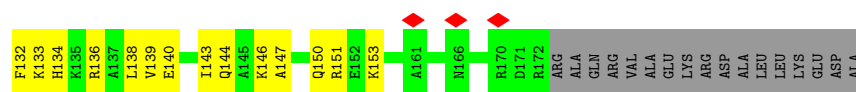
Chain LQ:  69% 31%



- Molecule 21: 60S ribosomal protein L19-A

Chain LR:  66% 25% 9%





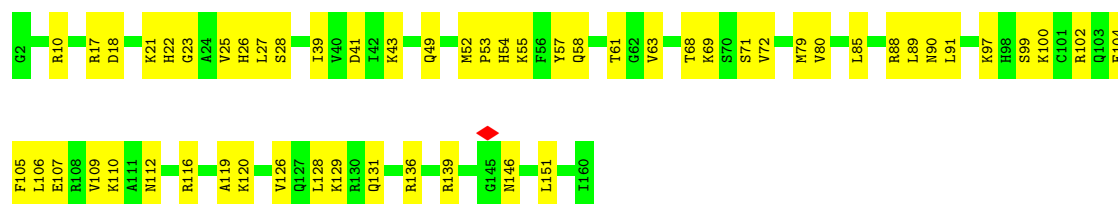
- Molecule 22: 60S ribosomal protein L20-A

Chain LS: 76% 24%



- Molecule 23: 60S ribosomal protein L21-A

Chain LT: 65% 35%



- Molecule 24: 60S ribosomal protein L22-A

Chain LU: 70% 30%



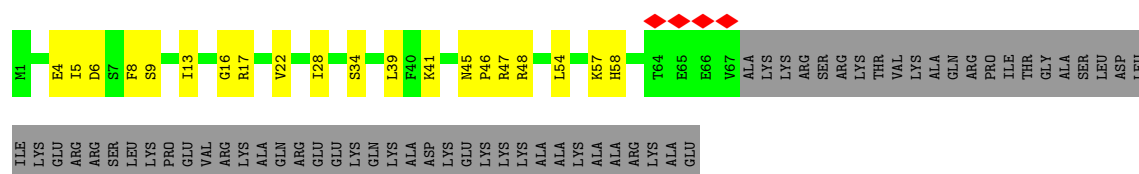
- Molecule 25: 60S ribosomal protein L23-A

Chain LV: 82% 18%



- Molecule 26: 60S ribosomal protein L24-A

Chain LW: 37% 16% 47%



- Molecule 27: 60S ribosomal protein L25

Chain LX:  75% 25%



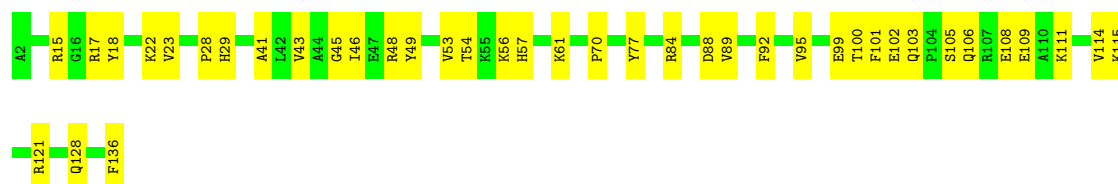
- Molecule 28: 60S ribosomal protein L26-A

Chain LY:  72% 28%



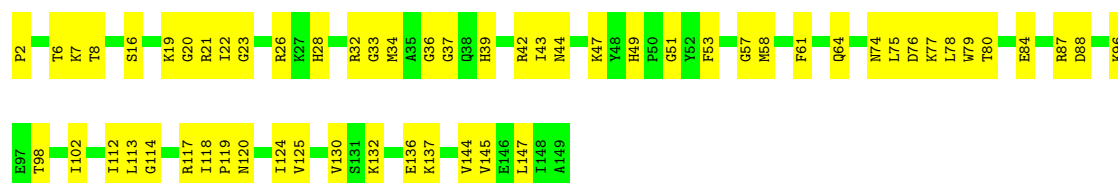
- Molecule 29: 60S ribosomal protein L27-A

Chain LZ:  70% 30%



- Molecule 30: 60S ribosomal protein L28

Chain La:  61% 39%



- Molecule 31: 60S ribosomal protein L29

Chain Lb:  83% 17%



- Molecule 32: 60S ribosomal protein L30

Chain Lc:  67% 33%



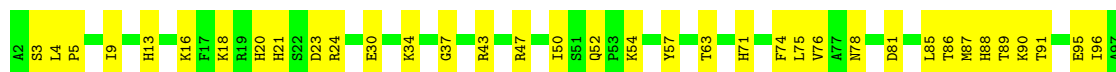
- Molecule 33: 60S ribosomal protein L31-A

Chain Ld:  83% 15%



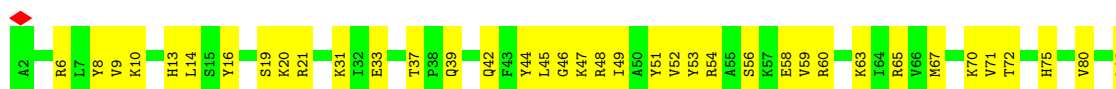
- Molecule 34: 60S ribosomal protein L32

Chain Le:  66% 34%



- Molecule 35: 60S ribosomal protein L33-A

Chain Lf:  61% 39%



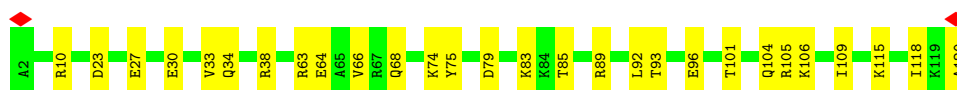
- Molecule 36: 60S ribosomal protein L34-A

Chain Lg:  69% 31%



- Molecule 37: 60S ribosomal protein L35-A

Chain Lh:  76% 24%

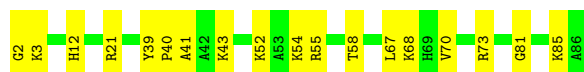
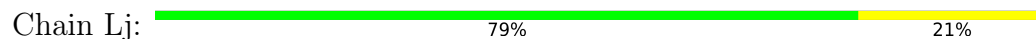


- Molecule 38: 60S ribosomal protein L36-A

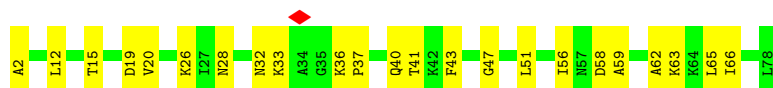
Chain Li:  77% 23%



- Molecule 39: 60S ribosomal protein L37-A



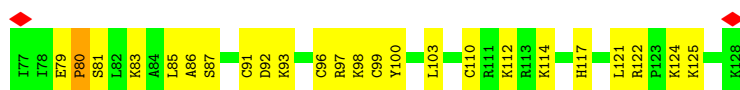
- Molecule 40: 60S ribosomal protein L38



- Molecule 41: 60S ribosomal protein L39



- Molecule 42: 60S ribosomal protein L40-A



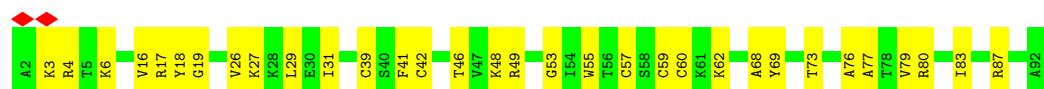
- Molecule 43: 60S ribosomal protein L41-A



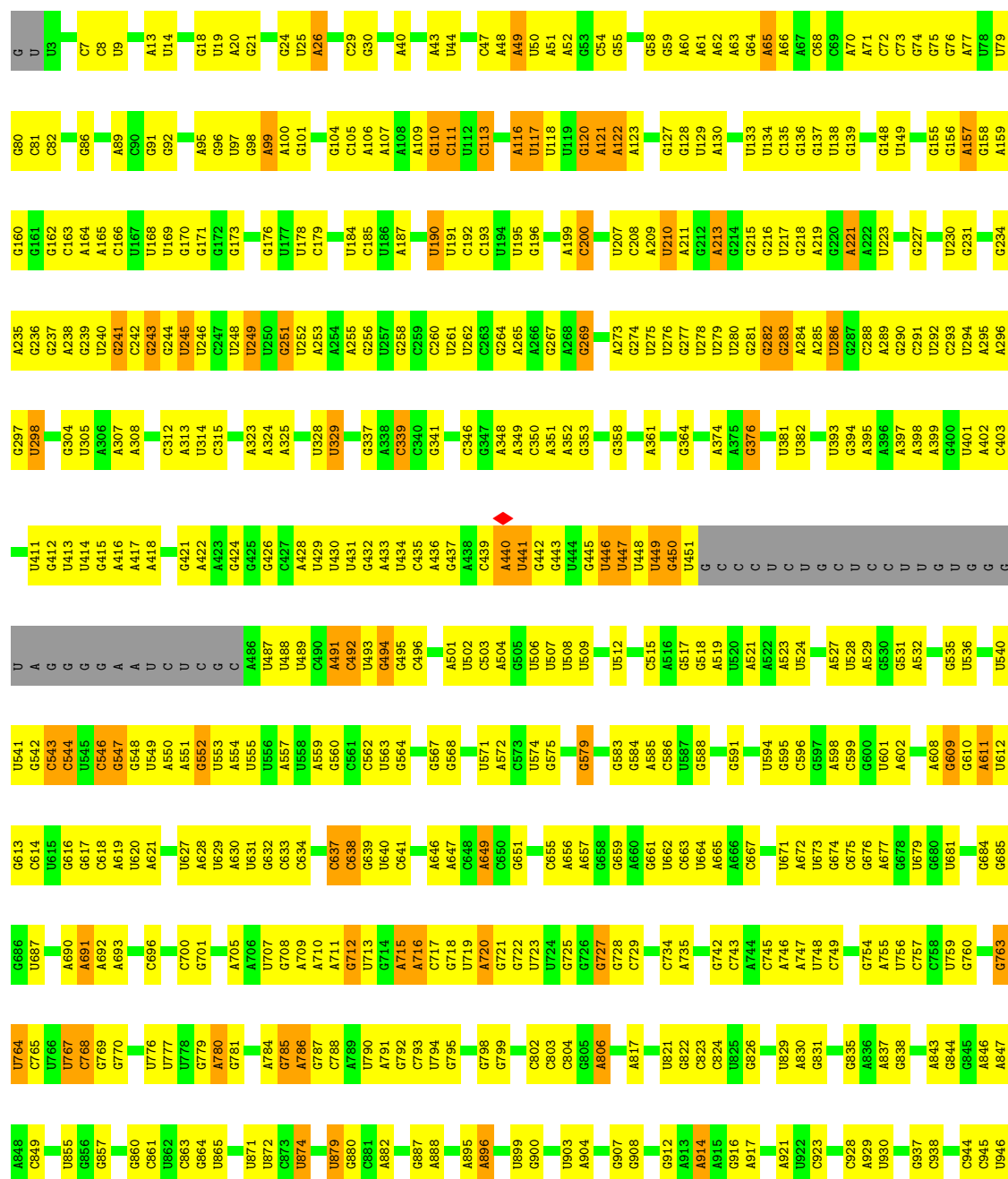
- Molecule 44: 60S ribosomal protein L42-A



- Molecule 45: 60S ribosomal protein L43-A



• Molecule 46: 25S rRNA



G2002	G1934	G1833	A1760	A1676	G1500	G1412	C1353	C1255	A1182	G1104	G1029	G947
G2003	G1935	U1834	C1761	G1677	U1501	G1413	C1333	G1256	C1183	A1105	A1030	C948
U2004	A1835	A1835	U1762	G1678	C1596	G1414	U1335	A1184	C1185	C1107	C1031	C949
G2005	U1938	G1838	U1763	G1679	C1505	U1415	U1336	U1257	C1189	U1108	C1032	G950
G2006	G1939	A1839	U1764	U1681	A1506	G1416	A1337	G1261	U1190	U1109	U1033	A951
G2007	G1940	U1765	U1765	U1682	G1507	G1417	C1338	G1262	U1191	U1110	U1034	A952
G2008	C1941	A1841	G1766	A1683	C1508	A1418	G1339	A1263	U1192	U1111	G1035	G953
G2009	U1942	A1842	G1770	U1684	G1509	A1419	G1340	U1264	A1193	U1112	A1036	U954
U2010	A1945	C1846	G1775	U1685	U1517	G1420	G1341	U1265	A1194	U1113	C1037	U955
C2013	A1946	A1847	G1776	U1686	U1522	G1421	C1342	G1266	A1195	U1114	U1038	U956
U2014	G1947	A1848	G1778	U1688	U1523	G1422	A1343	U1269	C1196	G1115	A1040	C959
C2015	G1948	C1849	G1779	U1689	U1524	C1426	U1348	A1270	U1196	G1116	U960	U960
U2016	U1950	A1850	G1780	U1694	G1525	C1432	C1349	A1271	C1201	G1117	C1043	U966
G2017	C1951	G1781	C1780	U1695	C1532	A1433	A1350	C1272	A1202	C1118	A1046	A967
C2018	U1855	U1782	U1782	A1696	U1534	G1434	A1351	A1273	A1203	C1119	A1047	G968
G2019	G1952	U1783	U1783	A1697	A1535	A1435	A1352	A1274	A1204	U1121	A1048	C969
A2020	G1954	C1857	U1784	C1698	U1536	U1436	U1353	G1281	G1208	G1126	C1049	A970
G2021	U1855	U1785	U1785	A1699	G1544	G1437	C1354	G1282	U1209	G1127	U1060	G971
G2022	A1956	G1786	G1786	G1623	G1544	G1443	A1355	A1277	G1209	U1128	A1054	G974
G2023	G1863	A1787	G1787	G1624	G1547	G1444	U1356	C1279	U1210	U1129	A1055	C975
G2024	A1864	G1788	C1788	A1625	U1553	G1445	G1357	G1280	U1211	A1130	U1060	A980
G2025	U1865	C1789	C1789	U1629	U1554	A1446	C1358	G1281	A1212	G1131	A1061	U981
A2026	A1866	C1790	C1790	U1630	U1555	G1447	G1362	G1282	U1214	C1132	A1062	C982
C2027	A1867	G1711	G1712	C1631	C1556	G1450	A1363	G1286	U1215	G1133	G1063	U987
G1963	U1871	G1717	U1717	G1634	A1557	A1460	G1367	U1287	A1216	A1135	A1064	A989
C1964	G1878	G1718	U1718	U1635	A1558	A1461	U1368	U1288	A1217	G1134	A1065	U990
C1965	U1795	G1719	G1719	U1636	A1559	G1470	A1369	G1289	G1222	G1139	U1070	G991
U1966	U1879	G1796	U1796	U1637	U1560	U1471	U1370	A1290	A1225	U1144	U1071	A992
U1967	U1880	U1797	U1797	A1637	G1561	U1472	G1371	A1291	C1226	U1143	G1072	A993
C2034	A1881	A1798	A1798	A1638	C1562	U1473	A1372	U1293	C1227	U1144	U1073	G994
G2035	G1882	C1725	C1725	C1639	C1563	G1473	G1373	U1294	C1228	G1152	U1074	U995
C2039	A1893	A1729	A1729	A1642	U1564	A1477	U1378	G1295	G1230	A1153	U1077	G999
U2040	U1894	G1730	G1730	A1643	G1565	U1478	G1379	U1296	A1231	A1154	A1080	C1000
U2041	A1895	C1805	C1805	C1644	A1566	U1479	G1380	U1299	C1232	C1155	U1081	G1001
C1974	A1896	G1807	G1807	U1645	U1567	G1480	A1381	G1300	G1233	G1156	A1084	A1002
U2043	G1897	G1734	G1734	G1646	U1568	A1481	G1382	A1301	G1234	G1157	A1085	A1003
G2044	G1899	G1735	G1735	G1650	U1570	G1482	G1383	A1302	U1235	A1158	A1086	U1008
G2045	G1906	A1810	A1810	U1651	A1571	A1483	A1386	G1306	G1236	G1160	C1086	U1009
U2046	A1909	U1814	U1814	A1654	U1572	U1484	U1387	G1307	G1237	G1161	U1087	G1010
A2047	A1910	U1815	U1815	G1655	G1573	G1485	A1388	A1308	C1238	U1162	G1088	U1015
A2049	G1983	A1816	A1816	A1656	C1574	G1486	U1388	U1309	C1239	U1241	G1090	C1016
C2050	A1913	G1817	G1817	C1657	A1575	G1487	G1389	U1315	U1242	A1169	C1092	C1017
G2051	G1914	U1818	U1818	G1658	G1576	G1488	A1390	U1322	A1243	G1174	A1093	G1018
U1986	A1915	U1819	U1819	U1659	C1579	A1489	A1399	G1323	A1244	G1175	U1094	G1019
G1967	U1916	U1820	U1820	C1660	A1580	A1490	G1400	U1324	A1245	C1176	U1095	G1020
C1988	U1920	U1821	U1821	G1661	C1581	A1491	U1407	U1325	G1243	U1168	G1097	G1024
U1989	A1921	G1751	G1751	C1662	C1582	G1492	G1408	C1327	A1252	A1178	A1088	A1025
U1990	A1922	A1752	G1753	C1663	A1583	U1494	G1409	U1326	U1247	G1179	A1102	A1026
G1991	G1991	C1827	G1827	G1666	A1587	U1495	U1410	A1327	A1251	U1181	A1103	U1027
U1992	U1992	G1828	G1828	A1667	A1588	G1496	A1407	C1327	A1252			
G1993	G1993	G1829	G1829	G1668	A1589	C1497	G1408	U1329	U1253			
G1994	A1932	U1831	U1831	G1675	G1590	U1498	U1409	A1330	C1254			
G1998		C1832	C1832		G1591	C1499	C1411					
U2001												
G												
A												
G												
U												
C												
U												
C												
U												
U												
G												



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	9645	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 ($e^-/\text{\AA}^2$)	45.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.382	Depositor
Minimum map value	-0.498	Depositor
Average map value	0.011	Depositor
Map value standard deviation	0.093	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	417.99997, 417.99997, 417.99997	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	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	A	0.15	0/1654	0.40	0/2237
1	C	0.67	0/589	1.09	0/800
2	B	0.14	0/6665	0.39	1/8979 (0.0%)
2	D	0.70	0/6665	1.20	9/8979 (0.1%)
3	C4	0.18	0/2883	0.22	0/4491
4	C3	0.21	0/3746	0.28	0/5832
5	LA	0.23	0/1933	0.42	2/2598 (0.1%)
6	LB	0.21	0/3146	0.36	0/4228
7	LC	0.20	0/2800	0.39	0/3790
8	LD	0.17	0/2400	0.38	0/3239
9	LE	0.18	0/1327	0.38	0/1790
10	LF	0.21	0/1821	0.37	0/2451
11	LG	0.21	0/1836	0.46	0/2481
12	LH	0.21	0/1529	0.43	0/2060
13	LI	0.19	0/1801	0.37	0/2416
14	LJ	0.18	0/1371	0.50	1/1838 (0.1%)
15	LL	0.21	0/1568	0.50	0/2106
16	LM	0.20	0/1068	0.41	0/1438
17	LN	0.21	0/1757	0.39	0/2354
18	LO	0.21	0/1585	0.39	0/2128
19	LP	0.21	0/1439	0.35	0/1938
20	LQ	0.20	0/1465	0.36	0/1965
21	LR	0.21	0/1395	0.36	0/1861
22	LS	0.23	0/1473	0.45	0/1980
23	LT	0.21	0/1300	0.40	0/1743
24	LU	0.19	0/812	0.46	0/1099
25	LV	0.21	0/1018	0.37	0/1369
26	LW	0.21	0/550	0.37	0/731
27	LX	0.21	0/979	0.34	0/1321
28	LY	0.23	0/995	0.46	0/1329
29	LZ	0.22	0/1118	0.46	0/1497
30	La	0.22	0/1204	0.47	0/1612

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	Lb	0.19	0/473	0.38	0/629
32	Lc	0.22	0/745	0.47	0/1001
33	Ld	0.23	0/894	0.46	2/1200 (0.2%)
34	Le	0.20	0/1038	0.40	0/1390
35	Lf	0.23	0/868	0.41	0/1168
36	Lg	0.22	0/890	0.41	0/1189
37	Lh	0.19	0/978	0.37	0/1301
38	Li	0.18	0/772	0.37	0/1026
39	Lj	0.22	0/685	0.37	0/908
40	Lk	0.18	0/618	0.35	0/826
41	Ll	0.25	0/443	0.51	0/588
42	Lm	0.23	0/423	0.54	0/562
43	Ln	0.18	0/230	0.56	0/296
44	Lo	0.20	0/836	0.44	0/1104
45	Lp	0.23	0/701	0.49	0/934
46	1	0.21	2/79000 (0.0%)	0.31	5/123166 (0.0%)
All	All	0.25	2/151486 (0.0%)	0.42	20/221968 (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
7	LC	0	1
11	LG	0	2
15	LL	0	1
18	LO	0	1
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	1	2094	C	O3'-P	-13.53	1.40	1.61
46	1	1950	U	O3'-P	-11.87	1.43	1.61

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	1	1950	U	O3'-P-O5'	34.87	156.31	104.00
46	1	1950	U	OP2-P-O3'	-10.33	77.02	108.00
46	1	1950	U	P-O3'-C3'	-9.44	106.03	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	15	ARG	CA-C-N	7.40	135.67	121.54
2	D	15	ARG	C-N-CA	7.40	135.67	121.54

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	LC	13	GLY	Peptide
11	LG	158	ASP	Peptide
11	LG	76	ALA	Peptide
15	LL	75	PHE	Peptide
18	LO	110[A]	PRO	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1612	0	1577	97	0
1	C	571	0	549	159	0
2	B	6536	0	6587	273	0
2	D	6536	0	6587	284	0
3	C4	2579	0	1304	54	0
4	C3	3353	0	1695	73	0
5	LA	1899	0	1956	55	0
6	LB	3075	0	3142	66	0
7	LC	2748	0	2859	70	0
8	LD	2351	0	2294	74	0
9	LE	1305	0	1373	70	0
10	LF	1784	0	1862	45	0
11	LG	1804	0	1877	54	0
12	LH	1508	0	1572	43	0
13	LI	1764	0	1804	37	0
14	LJ	1350	0	1381	63	0
15	LL	1543	0	1608	75	0
16	LM	1053	0	1149	64	0
17	LN	1720	0	1779	52	0
18	LO	1555	0	1659	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	LP	1416	0	1433	23	0
20	LQ	1441	0	1543	68	0
21	LR	1378	0	1462	63	0
22	LS	1437	0	1475	41	0
23	LT	1276	0	1323	50	0
24	LU	796	0	812	21	0
25	LV	1003	0	1048	17	0
26	LW	538	0	550	18	0
27	LX	964	0	1025	30	0
28	LY	984	0	1075	30	0
29	LZ	1092	0	1155	32	0
30	La	1173	0	1215	72	0
31	Lb	462	0	491	10	0
32	Lc	737	0	792	23	0
33	Ld	880	0	923	17	0
34	Le	1017	0	1081	37	0
35	Lf	850	0	880	33	0
36	Lg	880	0	942	30	0
37	Lh	969	0	1078	30	0
38	Li	766	0	844	26	0
39	Lj	670	0	673	15	0
40	Lk	612	0	682	24	0
41	Ll	436	0	475	26	0
42	Lm	417	0	455	23	0
43	Ln	229	0	273	8	0
44	Lo	824	0	888	21	0
45	Lp	694	0	736	30	0
46	1	70586	0	35465	1569	0
47	1	195	0	0	0	0
47	C3	1	0	0	0	0
47	C4	1	0	0	0	0
47	LA	2	0	0	0	0
47	LB	1	0	0	0	0
47	LN	1	0	0	0	0
47	LP	1	0	0	0	0
47	LR	1	0	0	0	0
47	LV	1	0	0	0	0
47	La	1	0	0	0	0
47	Le	1	0	0	0	0
48	Lg	1	0	0	0	0
48	Lj	1	0	0	0	0
48	Lm	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	Lo	1	0	0	0	0
48	Lp	1	0	0	0	0
All	All	141384	0	105408	3260	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 3260 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:C:50:THR:CA	2:D:333:ILE:HB	1.20	1.62
1:C:42:LEU:CD2	2:D:528:LYS:HE2	1.15	1.57
1:C:42:LEU:HD23	2:D:528:LYS:CE	1.30	1.55
1:C:48:GLU:CD	2:D:296:ARG:HH12	1.04	1.54
1:C:51:VAL:CG2	2:D:330:CYS:CB	1.85	1.50

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	
1	A	193/195 (99%)	192 (100%)	1 (0%)	0	100	100
1	C	66/195 (34%)	66 (100%)	0	0	100	100
2	B	794/796 (100%)	790 (100%)	3 (0%)	1 (0%)	48	79
2	D	794/796 (100%)	770 (97%)	22 (3%)	2 (0%)	36	67
5	LA	249/251 (99%)	234 (94%)	15 (6%)	0	100	100
6	LB	384/386 (100%)	358 (93%)	26 (7%)	0	100	100
7	LC	359/361 (99%)	329 (92%)	28 (8%)	2 (1%)	21	54
8	LD	292/294 (99%)	274 (94%)	17 (6%)	1 (0%)	36	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	LE	163/175 (93%)	155 (95%)	8 (5%)	0	100	100
10	LF	220/222 (99%)	205 (93%)	15 (7%)	0	100	100
11	LG	231/233 (99%)	221 (96%)	10 (4%)	0	100	100
12	LH	189/191 (99%)	176 (93%)	13 (7%)	0	100	100
13	LI	216/218 (99%)	208 (96%)	8 (4%)	0	100	100
14	LJ	167/169 (99%)	152 (91%)	15 (9%)	0	100	100
15	LL	191/193 (99%)	174 (91%)	15 (8%)	2 (1%)	12	43
16	LM	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
17	LN	201/203 (99%)	191 (95%)	10 (5%)	0	100	100
18	LO	195/197 (99%)	185 (95%)	8 (4%)	2 (1%)	12	43
19	LP	181/183 (99%)	171 (94%)	10 (6%)	0	100	100
20	LQ	183/185 (99%)	176 (96%)	7 (4%)	0	100	100
21	LR	169/188 (90%)	163 (96%)	6 (4%)	0	100	100
22	LS	169/171 (99%)	157 (93%)	12 (7%)	0	100	100
23	LT	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
24	LU	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
25	LV	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
26	LW	65/126 (52%)	61 (94%)	4 (6%)	0	100	100
27	LX	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
28	LY	123/125 (98%)	117 (95%)	6 (5%)	0	100	100
29	LZ	133/135 (98%)	123 (92%)	10 (8%)	0	100	100
30	La	146/148 (99%)	133 (91%)	13 (9%)	0	100	100
31	Lb	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
32	Lc	94/96 (98%)	93 (99%)	1 (1%)	0	100	100
33	Ld	107/109 (98%)	99 (92%)	7 (6%)	1 (1%)	14	45
34	Le	125/127 (98%)	120 (96%)	5 (4%)	0	100	100
35	Lf	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
36	Lg	110/112 (98%)	106 (96%)	4 (4%)	0	100	100
37	Lh	117/119 (98%)	110 (94%)	7 (6%)	0	100	100
38	Li	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
39	Lj	83/85 (98%)	80 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	Lk	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
41	Ll	48/50 (96%)	48 (100%)	0	0	100	100
42	Lm	50/52 (96%)	47 (94%)	2 (4%)	1 (2%)	6	32
43	Ln	23/25 (92%)	23 (100%)	0	0	100	100
44	Lo	101/103 (98%)	96 (95%)	5 (5%)	0	100	100
45	Lp	89/91 (98%)	88 (99%)	1 (1%)	0	100	100
All	All	7994/8297 (96%)	7629 (95%)	353 (4%)	12 (0%)	44	73

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	742	CYS
7	LC	293	SER
33	Ld	6	ASP
2	D	16	SER
2	D	777	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	
1	A	180/180 (100%)	180 (100%)	0	100	100
1	C	66/180 (37%)	65 (98%)	1 (2%)	57	69
2	B	743/743 (100%)	741 (100%)	2 (0%)	86	84
2	D	743/743 (100%)	737 (99%)	6 (1%)	73	76
5	LA	190/193 (98%)	190 (100%)	0	100	100
6	LB	318/322 (99%)	318 (100%)	0	100	100
7	LC	288/288 (100%)	288 (100%)	0	100	100
8	LD	241/243 (99%)	241 (100%)	0	100	100
9	LE	138/153 (90%)	138 (100%)	0	100	100
10	LF	186/186 (100%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	LG	187/191 (98%)	187 (100%)	0	100	100
12	LH	168/171 (98%)	168 (100%)	0	100	100
13	LI	185/185 (100%)	185 (100%)	0	100	100
14	LJ	146/147 (99%)	146 (100%)	0	100	100
15	LL	154/154 (100%)	154 (100%)	0	100	100
16	LM	107/107 (100%)	106 (99%)	1 (1%)	70	74
17	LN	175/175 (100%)	175 (100%)	0	100	100
18	LO	160/160 (100%)	160 (100%)	0	100	100
19	LP	138/145 (95%)	138 (100%)	0	100	100
20	LQ	150/150 (100%)	150 (100%)	0	100	100
21	LR	139/153 (91%)	139 (100%)	0	100	100
22	LS	155/155 (100%)	155 (100%)	0	100	100
23	LT	136/136 (100%)	136 (100%)	0	100	100
24	LU	87/87 (100%)	87 (100%)	0	100	100
25	LV	104/104 (100%)	104 (100%)	0	100	100
26	LW	54/107 (50%)	54 (100%)	0	100	100
27	LX	104/105 (99%)	104 (100%)	0	100	100
28	LY	108/108 (100%)	108 (100%)	0	100	100
29	LZ	115/115 (100%)	115 (100%)	0	100	100
30	La	118/118 (100%)	117 (99%)	1 (1%)	73	76
31	Lb	46/46 (100%)	46 (100%)	0	100	100
32	Lc	81/81 (100%)	81 (100%)	0	100	100
33	Ld	93/96 (97%)	93 (100%)	0	100	100
34	Le	108/109 (99%)	108 (100%)	0	100	100
35	Lf	90/90 (100%)	90 (100%)	0	100	100
36	Lg	95/95 (100%)	95 (100%)	0	100	100
37	Lh	104/104 (100%)	104 (100%)	0	100	100
38	Li	80/81 (99%)	80 (100%)	0	100	100
39	Lj	69/69 (100%)	69 (100%)	0	100	100
40	Lk	68/68 (100%)	68 (100%)	0	100	100
41	Ll	45/45 (100%)	45 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	Lm	47/47 (100%)	47 (100%)	0	100	100
43	Ln	22/23 (96%)	22 (100%)	0	100	100
44	Lo	87/88 (99%)	87 (100%)	0	100	100
45	Lp	71/71 (100%)	71 (100%)	0	100	100
All	All	6889/7117 (97%)	6878 (100%)	11 (0%)	85	87

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	401	THR
2	D	601	PHE
2	D	782	ILE
2	D	779	VAL
1	C	54	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	34	ASN
2	D	163	GLN
12	LH	51	GLN
11	LG	59	GLN
2	D	471	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C4	120/121 (99%)	11 (9%)	1 (0%)
4	C3	157/158 (99%)	26 (16%)	1 (0%)
46	1	3297/3395 (97%)	609 (18%)	39 (1%)
All	All	3574/3674 (97%)	646 (18%)	41 (1%)

5 of 646 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	C4	7	G
3	C4	11	A
3	C4	53	U

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Mol	Chain	Res	Type
3	C4	54	U
3	C4	55	A

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	1	2537	U
46	1	3228	C
46	1	2541	U
46	1	3154	C
46	1	3275	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 211 ligands modelled in this entry, 211 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

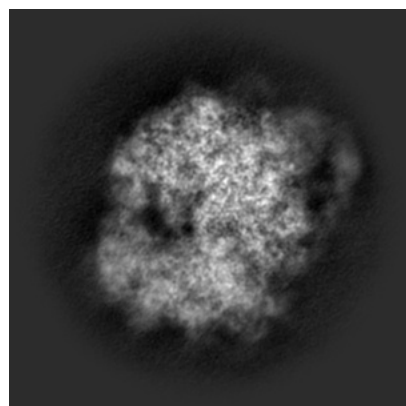
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16090. These allow visual inspection of the internal detail of the map and identification of artifacts.

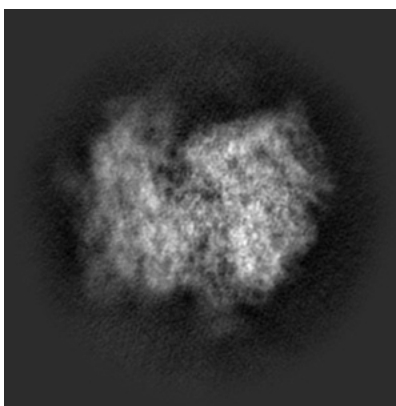
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

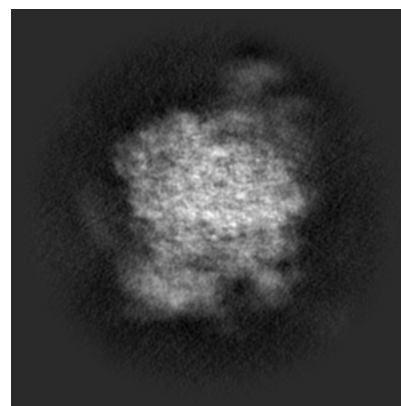
6.1.1 Primary map



X

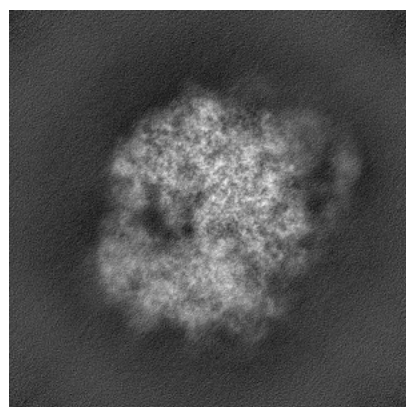


Y

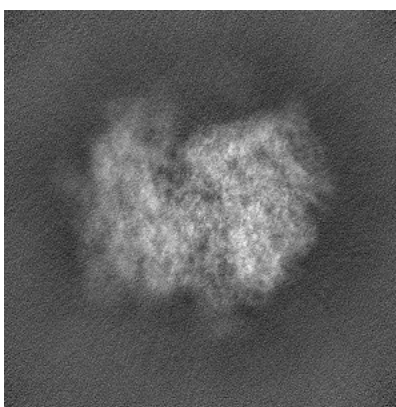


Z

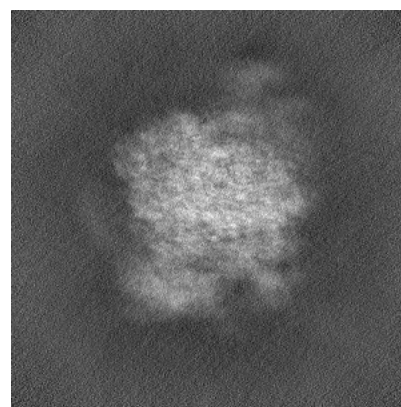
6.1.2 Raw map



X



Y

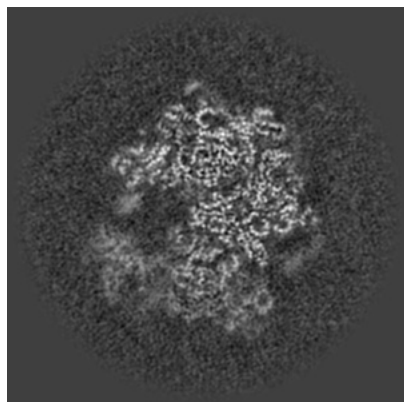


Z

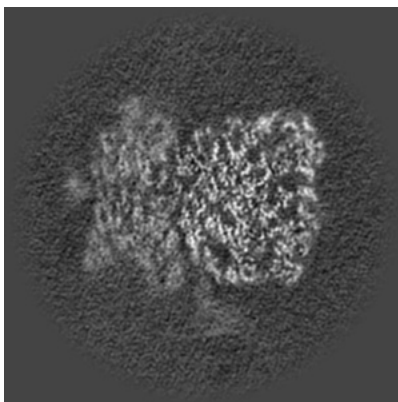
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

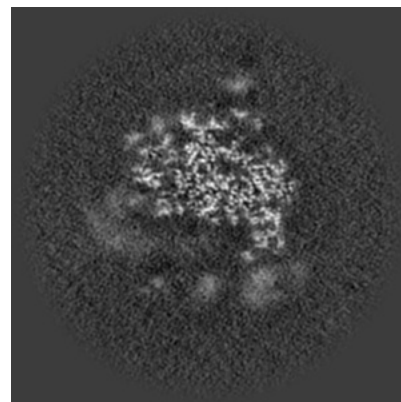
6.2.1 Primary map



X Index: 200

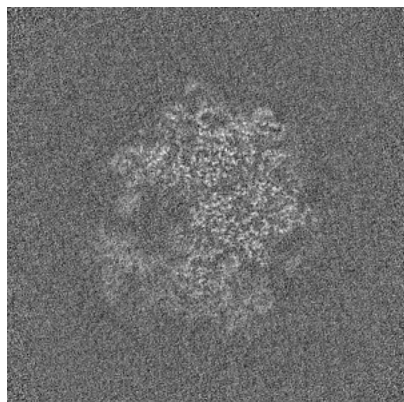


Y Index: 200

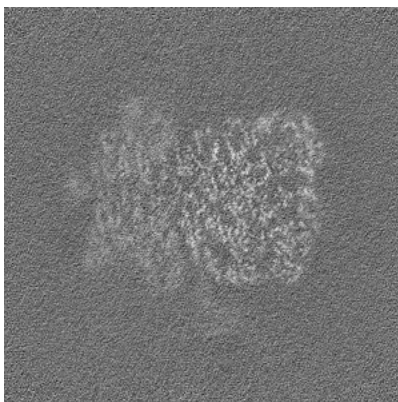


Z Index: 200

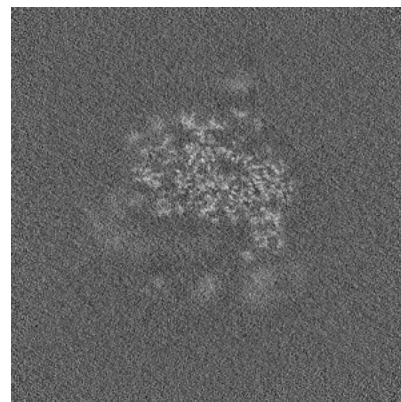
6.2.2 Raw map



X Index: 200



Y Index: 200

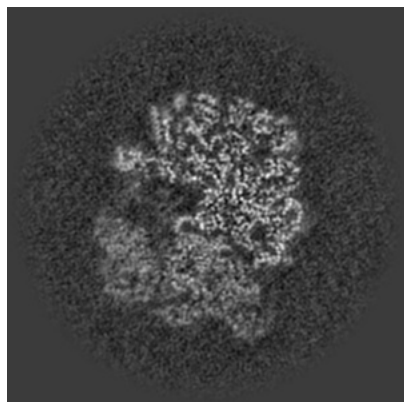


Z Index: 200

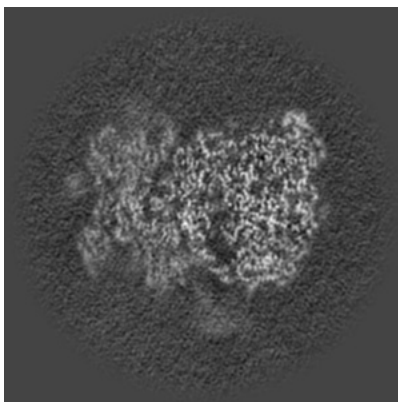
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

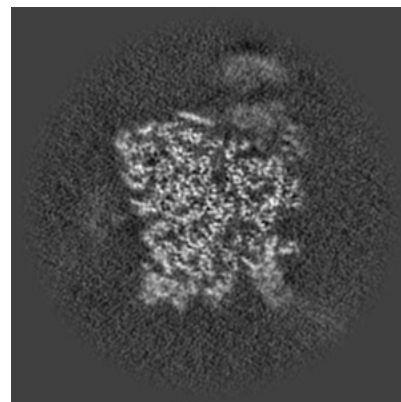
6.3.1 Primary map



X Index: 182

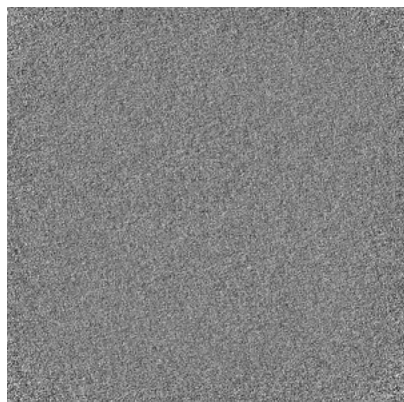


Y Index: 194

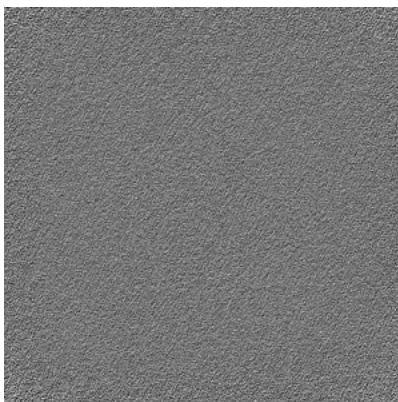


Z Index: 237

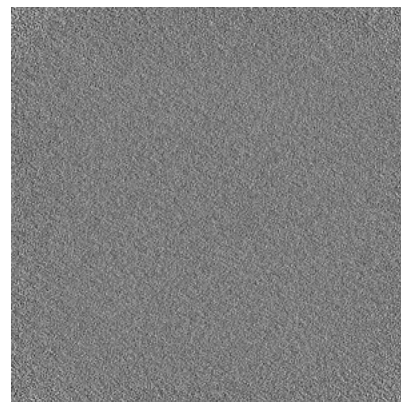
6.3.2 Raw map



X Index: 0



Y Index: 0

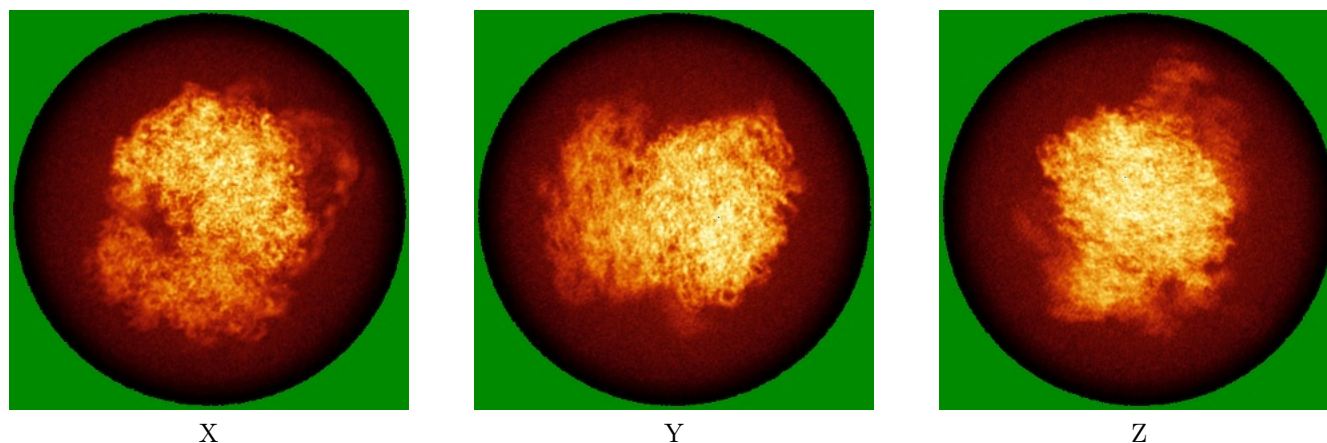


Z Index: 0

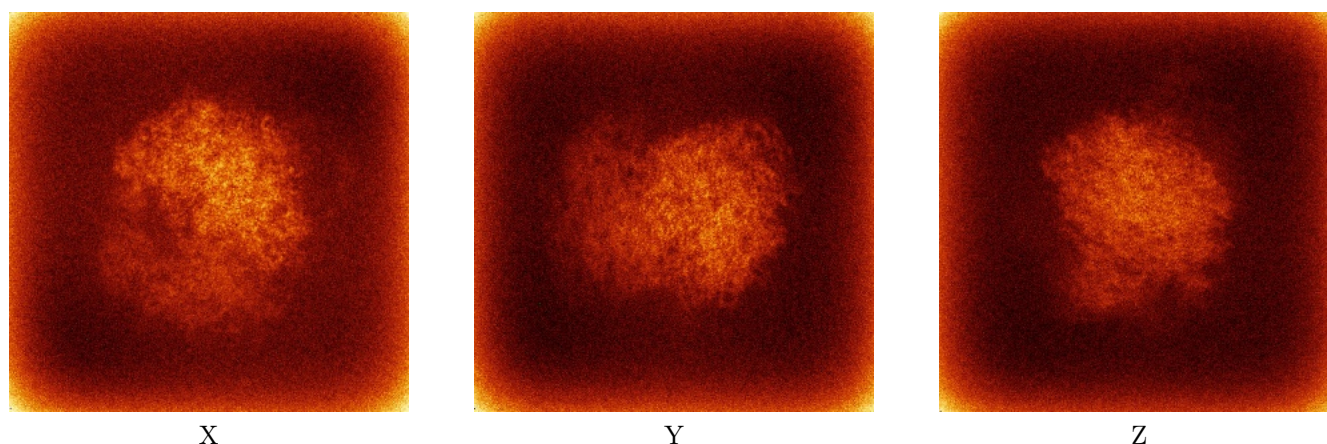
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

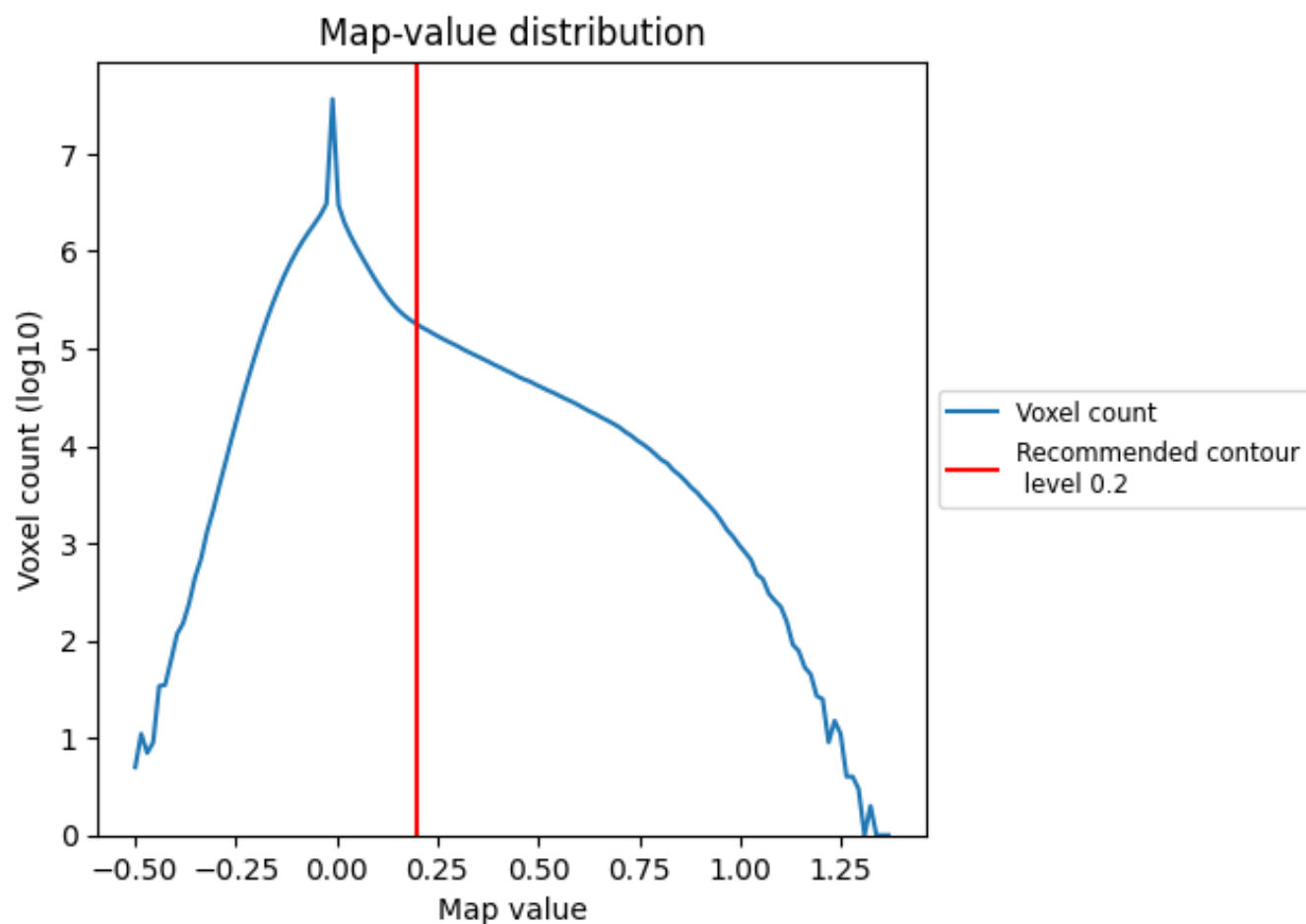
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

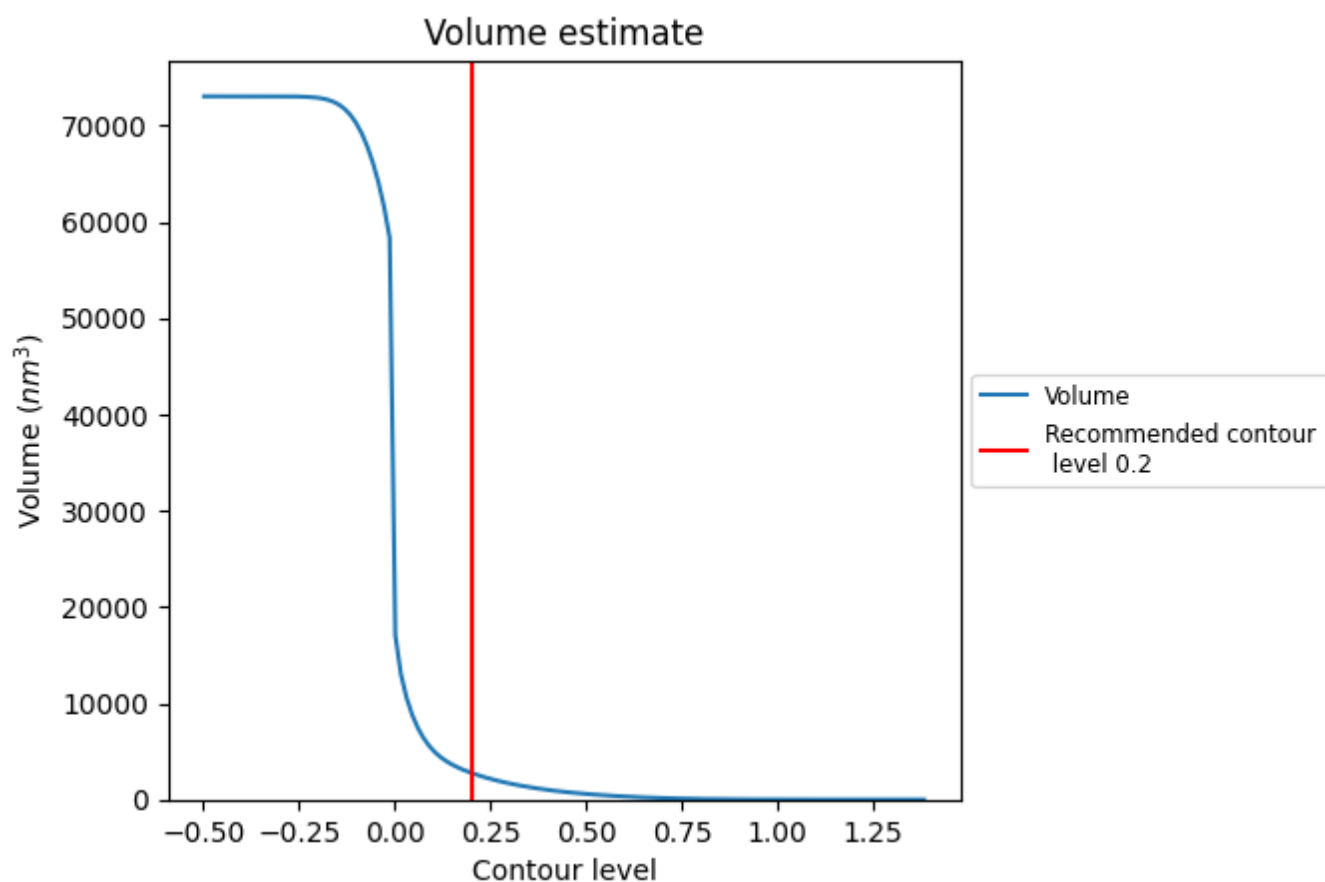
This section contains the results of statistical analysis of the map.

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.

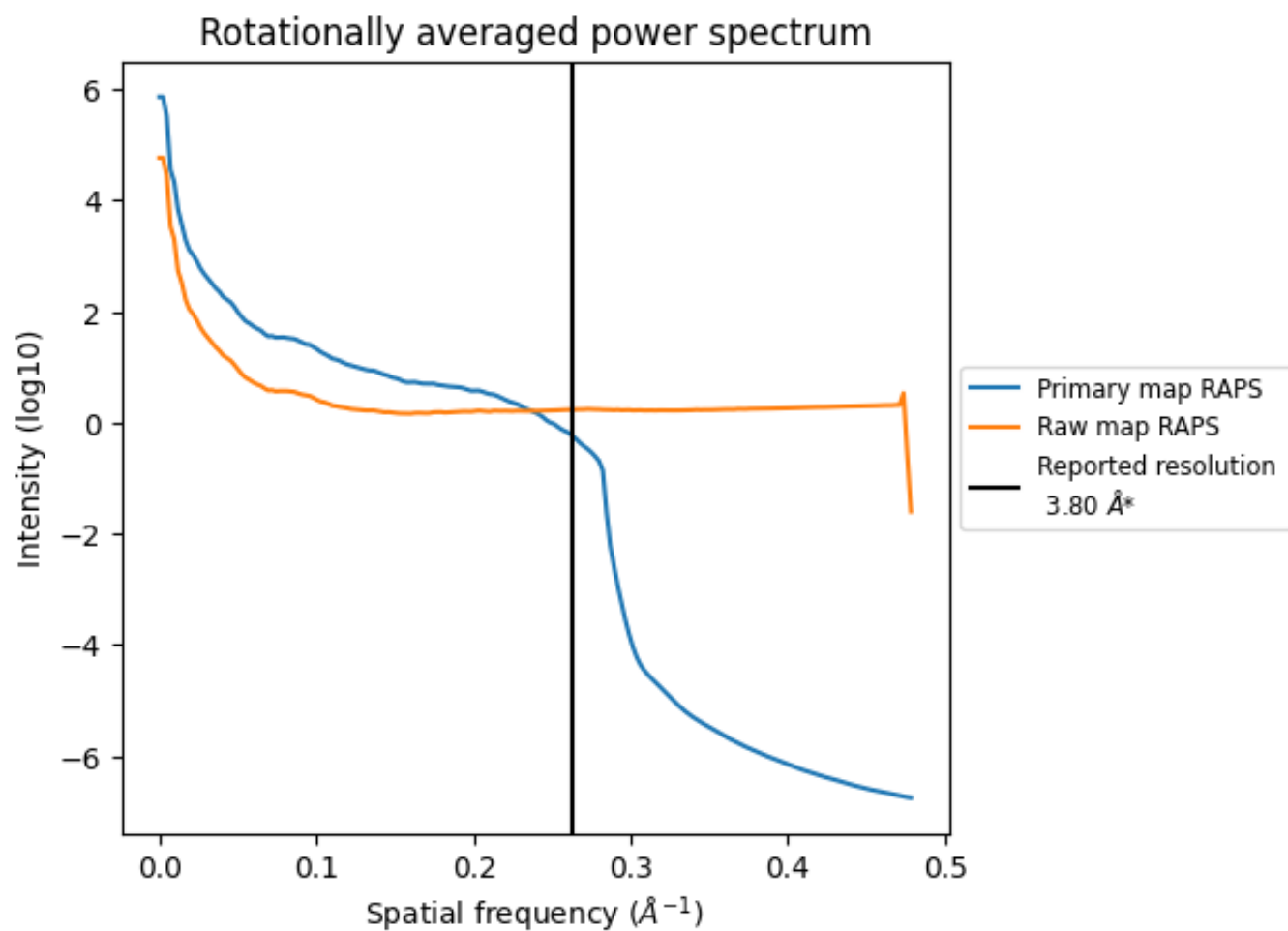
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2769 nm³; this corresponds to an approximate mass of 2501 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 ⓘ

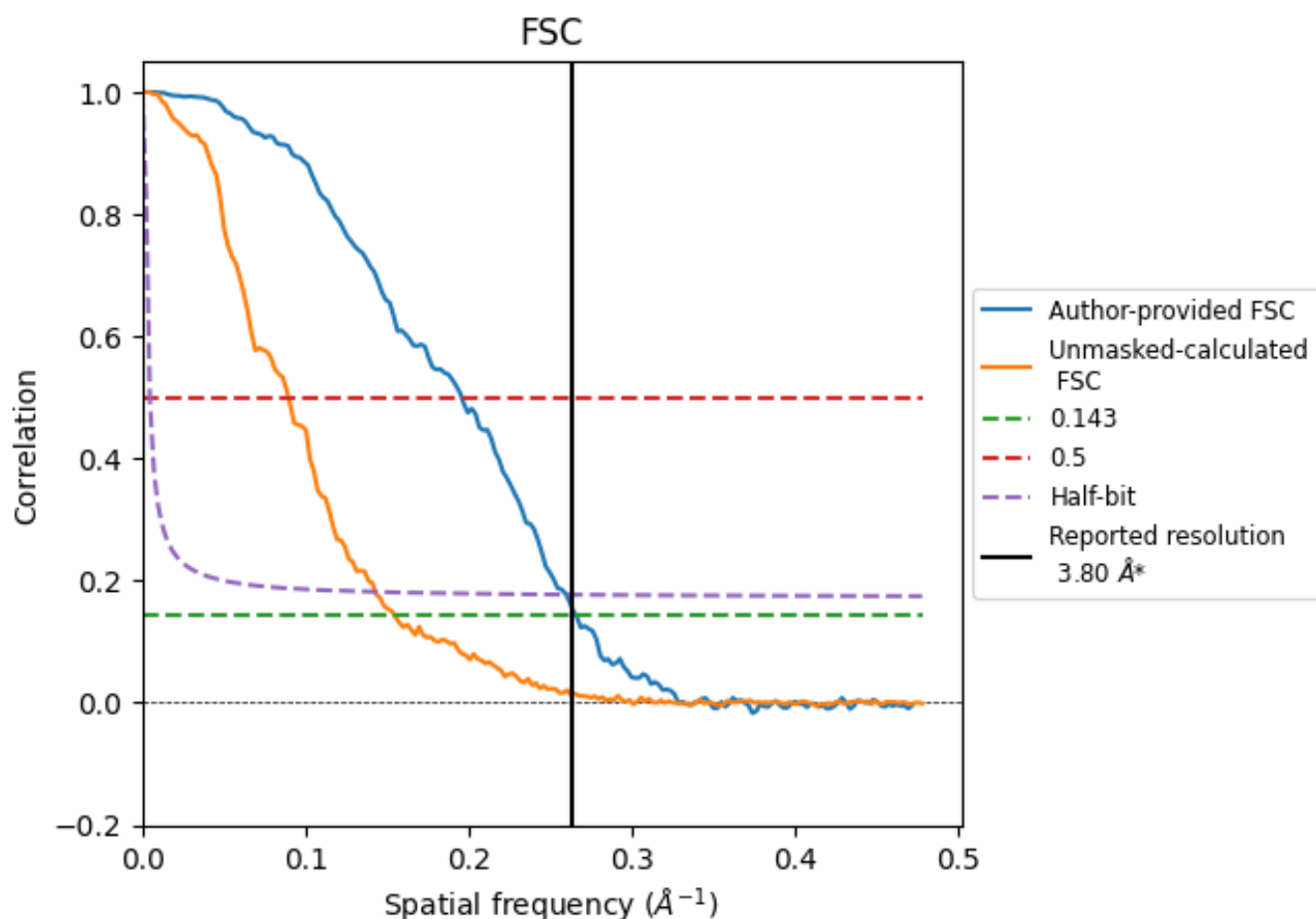


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

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 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

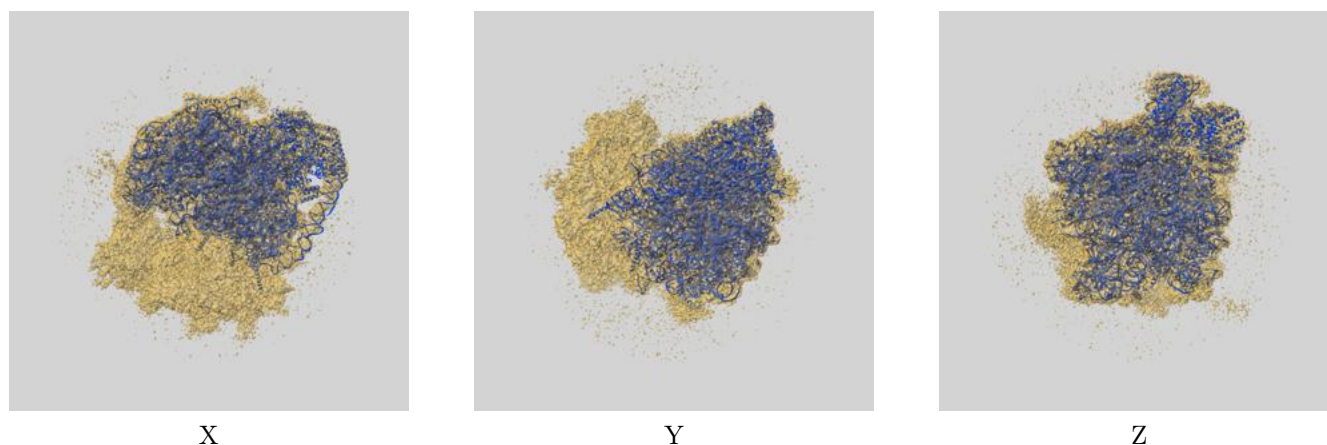
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.76	5.10	3.85
Unmasked-calculated*	6.46	11.15	6.99

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.46 differs from the reported value 3.8 by more than 10 %

9 Map-model fit [i](#)

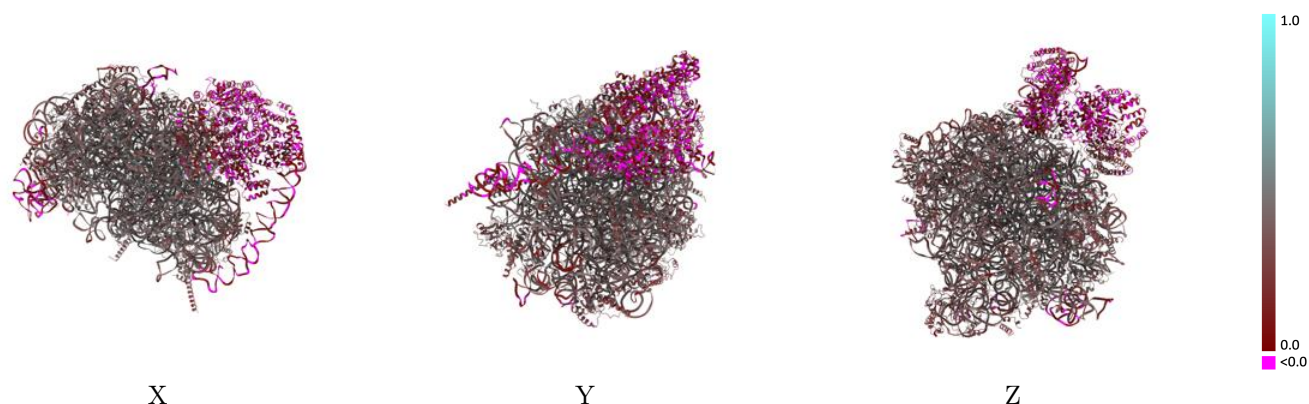
This section contains information regarding the fit between EMDB map EMD-16090 and PDB model 8BJQ. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



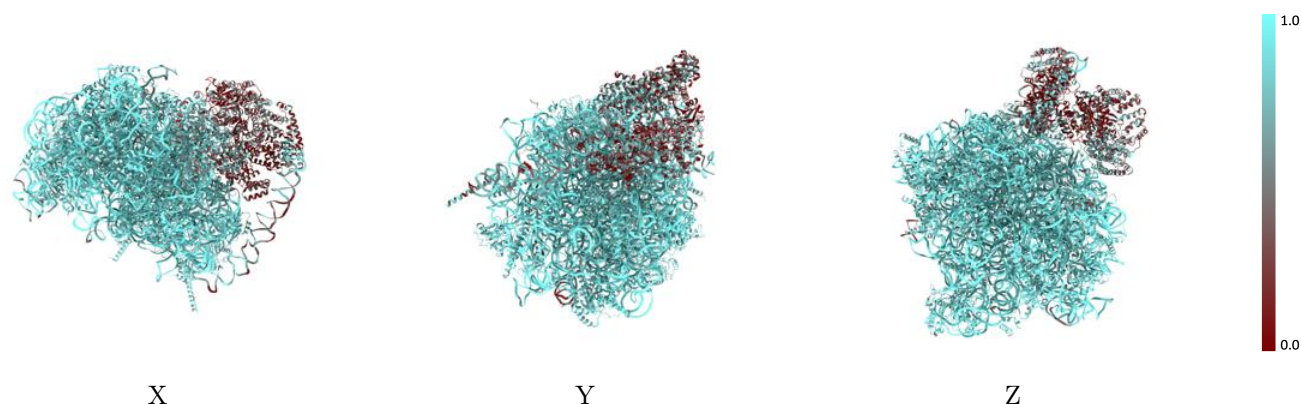
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



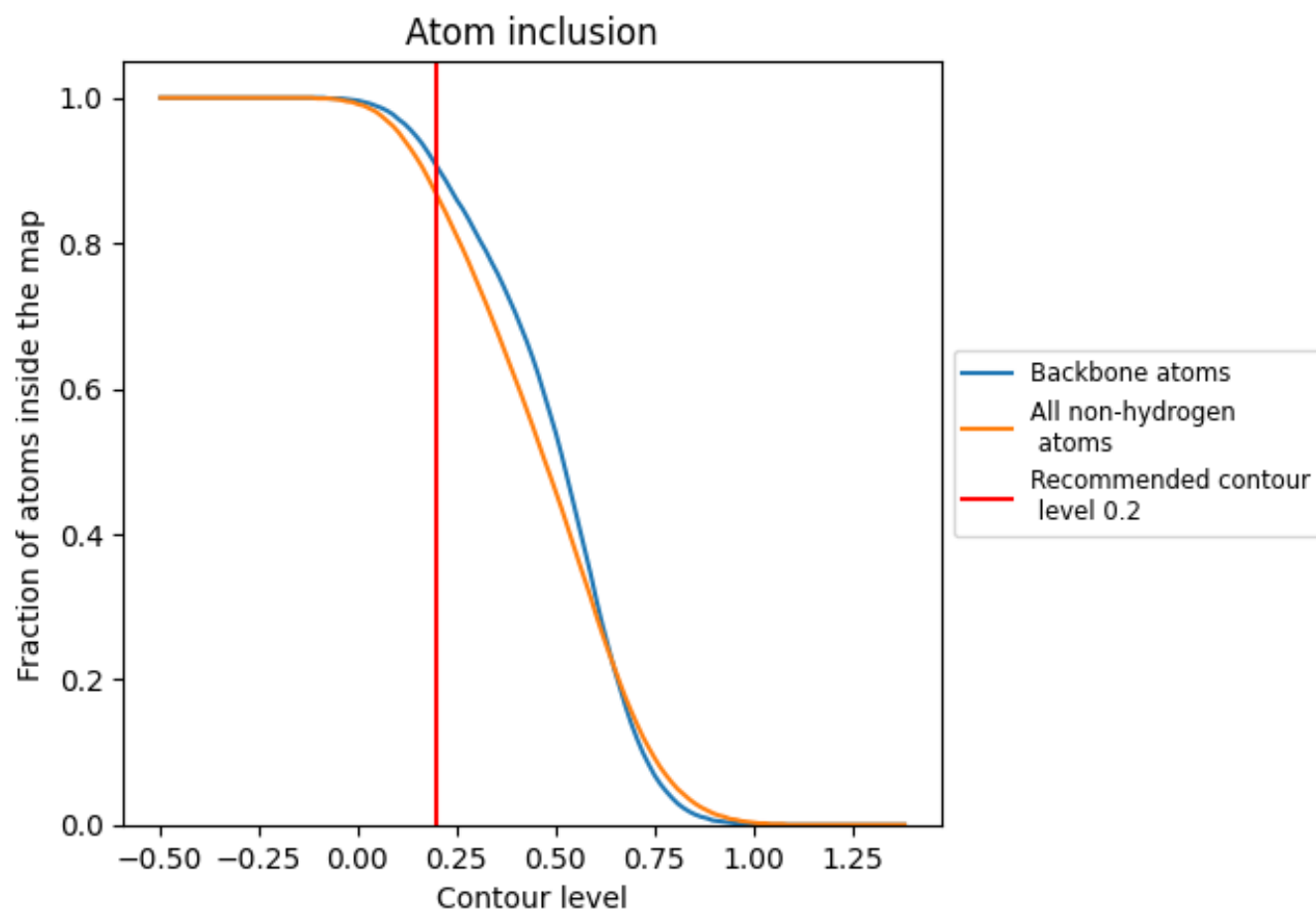
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion ⓘ



At the recommended contour level, 91% of all backbone atoms, 87% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8660	 0.3370
1	 0.9560	 0.3660
A	 0.1720	 0.0460
B	 0.4710	 0.1120
C	 0.1710	 0.0510
C3	 0.9890	 0.3920
C4	 0.9940	 0.3720
D	 0.3710	 0.0800
LA	 0.8480	 0.4090
LB	 0.9000	 0.4110
LC	 0.8880	 0.3830
LD	 0.8750	 0.2840
LE	 0.8540	 0.2940
LF	 0.8850	 0.3770
LG	 0.8540	 0.3350
LH	 0.8950	 0.3730
LI	 0.8570	 0.3560
LJ	 0.8060	 0.2790
LL	 0.8630	 0.3360
LM	 0.8920	 0.3610
LN	 0.8650	 0.3780
LO	 0.8940	 0.4090
LP	 0.8370	 0.3760
LQ	 0.8890	 0.3760
LR	 0.8480	 0.3690
LS	 0.8840	 0.3990
LT	 0.8800	 0.3910
LU	 0.8340	 0.3000
LV	 0.8140	 0.4190
LW	 0.8200	 0.3950
LX	 0.8710	 0.3860
LY	 0.8640	 0.3510
LZ	 0.8950	 0.3510
La	 0.8760	 0.3470
Lb	 0.8430	 0.3460



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Chain	Atom inclusion	Q-score
Lc	 0.8880	 0.3450
Ld	 0.8760	 0.4000
Le	 0.8780	 0.4100
Lf	 0.8990	 0.4200
Lg	 0.8770	 0.3860
Lh	 0.8810	 0.3370
Li	 0.8260	 0.3310
Lj	 0.9180	 0.4140
Lk	 0.8330	 0.3420
Ll	 0.8580	 0.3570
Lm	 0.8740	 0.3840
Ln	 0.8120	 0.3120
Lo	 0.8610	 0.3750
Lp	 0.8390	 0.3730