



wwPDB EM Validation Summary Report ⓘ

Jun 8, 2026 – 03:35 pm BST

PDB ID : 9RG7 / pdb_00009rg7
EMDB ID : EMD-53944
Title : In vitro reconstituted NAA40-NAC bound 80S
Authors : Guan, D.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-06-05
Resolution : 2.72 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

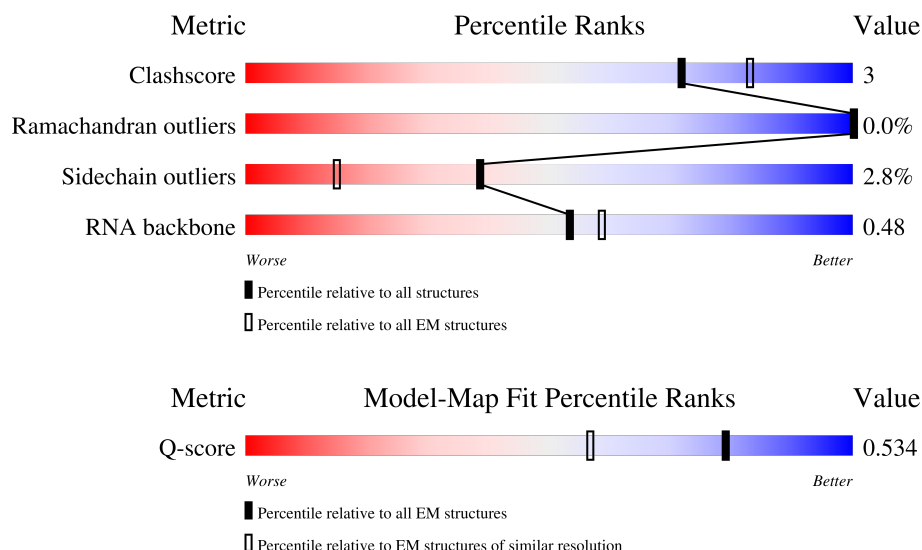
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal 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 2.72 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	10355 (2.22 - 3.22)

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	LA	257	<div> <div>87%</div> <div>9%</div> <div>.</div> </div>
2	NA	215	<div> <div>21%</div> <div>36%</div> <div>14%</div> <div>50%</div> </div>
3	SA	295	<div> <div>63%</div> <div>11%</div> <div>.</div> <div>25%</div> </div>

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Mol	Chain	Length	Quality of chain
4	LB	403	
5	NB	206	
6	SB	264	
7	L5	5070	
8	L7	121	
9	L8	157	
10	LC	427	
11	LD	297	
12	LE	288	
13	LF	248	
14	LG	266	
15	LH	192	
16	LI	214	
17	LJ	178	
18	LL	211	
19	LM	215	
20	LN	204	
21	LO	203	
22	LP	184	
23	LQ	188	
24	LR	196	
25	LS	176	
26	LT	160	
27	LU	128	
28	LV	140	







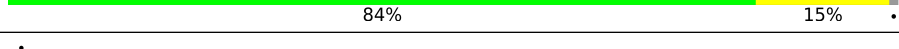
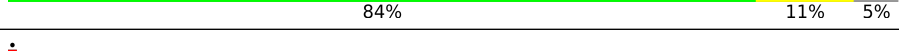
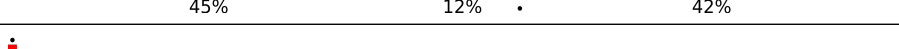

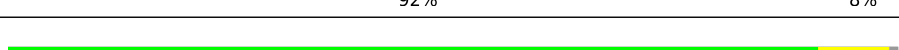
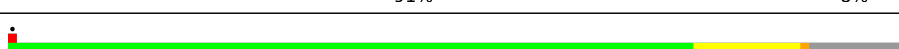
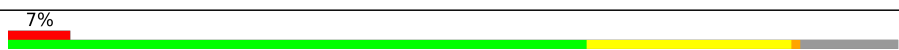

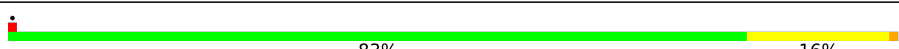





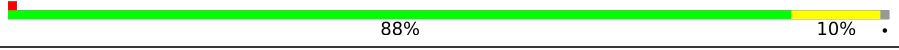
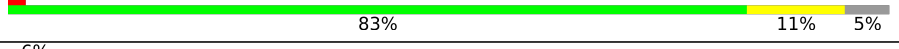
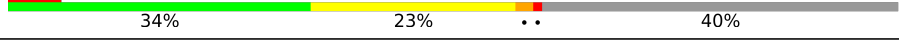


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Mol	Chain	Length	Quality of chain
29	LW	157	
30	LX	156	
31	LY	145	
32	LZ	136	
33	La	148	
34	Lb	159	
35	Lc	115	
36	Ld	125	
37	Le	135	
38	Lf	110	
39	Lg	117	
40	Lh	123	
41	Li	105	
42	Lj	97	
43	Lk	70	
44	Ll	51	
45	Lm	128	
46	Ln	25	
47	Lo	106	
48	Lp	92	
49	Lr	137	
50	Ls	317	
51	Lt	165	
52	N4	237	
53	S2	1869	




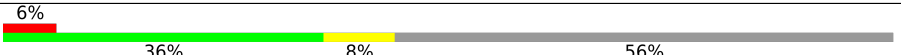

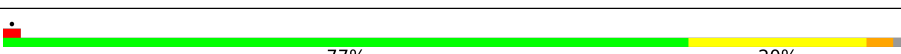
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Mol	Chain	Length	Quality of chain
54	SC	293	
55	SD	243	
56	SE	263	
57	SF	204	
58	SG	249	
59	SH	194	
60	SI	208	
61	SJ	194	
62	SK	165	
63	SL	158	
64	SM	132	
65	SN	151	
66	SO	151	
67	SP	145	
68	SQ	146	
69	SR	135	
70	SS	152	
71	ST	145	
72	SU	119	
73	SV	83	
74	SW	130	
75	SX	143	
76	SY	133	
77	SZ	125	
78	Sa	115	

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Mol	Chain	Length	Quality of chain
79	Sb	84	 87% 12% .
80	Sc	69	 6% 75% 16% . 7%
81	Sd	56	 88% 9% . .
82	Se	133	 6% 36% 8% 56%
83	Sf	156	 15% 38% 5% 57%
84	Sg	317	 77% 20% . .

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 219040 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 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 2 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	NA	108	Total	C	N	O	S	0	0
			841	524	153	160	4		

- Molecule 3 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 4 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 5 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	NB	106	Total	C	N	O	S	0	0
			821	514	153	151	3		

- Molecule 6 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SB	221	Total	C	N	O	S	0	0
			1791	1135	323	319	14		

- Molecule 7 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L5	3669	Total	C	N	O	P	0	0
			78658	35027	14397	25566	3668		

- Molecule 8 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 9 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 10 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LC	365	Total	C	N	O	S	0	0
			2908	1829	580	486	13		

- Molecule 11 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 12 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LE	221	Total	C	N	O	S	0	0
			1774	1142	336	292	4		

- Molecule 13 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 14 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 15 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 16 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LI	202	Total	C	N	O	S	0	0
			1639	1041	316	269	13		

- Molecule 17 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LJ	171	Total	C	N	O	S	0	0
			1371	867	256	242	6		

- Molecule 18 is a protein called Large ribosomal subunit protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LL	207	Total	C	N	O	S	0	0
			1673	1046	346	277	4		

- Molecule 19 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 20 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 21 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 22 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 23 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 24 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 25 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 26 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 27 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LU	100	Total	C	N	O	S	0	0
			816	524	142	148	2		

- Molecule 28 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 29 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 30 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 31 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LY	133	Total	C	N	O	S	0	0
			1106	694	224	185	3		

- Molecule 32 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 33 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 34 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lb	109	Total	C	N	O	S	0	0
			882	549	192	137	4		

- Molecule 35 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 36 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 37 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 38 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 39 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 40 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 41 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 42 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 43 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 44 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 45 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lm	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

- Molecule 46 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 47 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 48 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 49 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 50 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 51 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

- Molecule 52 is a protein called N-alpha-acetyltransferase 40.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	N4	223	Total	C	N	O	S	0	0
			1809	1136	317	341	15		

- Molecule 53 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S2	1719	Total	C	N	O	P	0	0
			36456	16264	6516	11958	1718		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S2	582	C	U	conflict	GB 36162
S2	583	C	A	conflict	GB 36162
S2	584	G	A	conflict	GB 36162
S2	798	A	G	conflict	GB 36162
S2	1095	U	C	conflict	GB 36162

- Molecule 54 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 55 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 56 is a protein called Small ribosomal subunit protein eS4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 57 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SF	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 58 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 59 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 60 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 61 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 62 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SK	95	Total	C	N	O	S	0	0
			799	524	139	130	6		

- Molecule 63 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SL	144	Total	C	N	O	S	0	0
			1182	752	224	200	6		

- Molecule 64 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SM	122	Total	C	N	O	S	0	0
			604	359	122	123			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P25398
SM	69	LEU	CYS	conflict	UNP P25398
SM	99	ASN	LYS	conflict	UNP P25398

- Molecule 65 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 66 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SO	135	Total	C	N	O	S	0	0
			1010	618	198	188	6		

- Molecule 67 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SP	129	Total	C	N	O	S	0	0
			1061	672	202	180	7		

- Molecule 68 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 69 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 70 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 71 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 72 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SU	103	Total	C	N	O	S	0	0
			817	511	155	147	4		

- Molecule 73 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 74 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 75 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 76 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SY	126	Total	C	N	O	S	0	0
			1027	648	201	173	5		

- Molecule 77 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 78 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 79 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 80 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 81 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 82 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 83 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 84 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	LA	1	Total	Mg	0
			1	1	
85	L5	210	Total	Mg	0
			210	210	
85	L7	3	Total	Mg	0
			3	3	
85	L8	6	Total	Mg	0
			6	6	
85	LI	1	Total	Mg	0
			1	1	
85	LP	1	Total	Mg	0
			1	1	
85	LV	1	Total	Mg	0
			1	1	
85	Le	2	Total	Mg	0
			2	2	
85	Lg	1	Total	Mg	0
			1	1	
85	S2	30	Total	Mg	0
			30	30	
85	SG	1	Total	Mg	0
			1	1	


- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

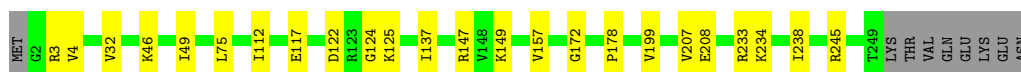
Mol	Chain	Residues	Atoms		AltConf
86	Lg	1	Total 1	Zn 1	0
86	Lj	1	Total 1	Zn 1	0
86	Lm	1	Total 1	Zn 1	0
86	Lo	1	Total 1	Zn 1	0
86	Lp	1	Total 1	Zn 1	0
86	Sa	1	Total 1	Zn 1	0
86	Sd	1	Total 1	Zn 1	0
86	Sf	1	Total 1	Zn 1	0

3 Residue-property plots [i](#)


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

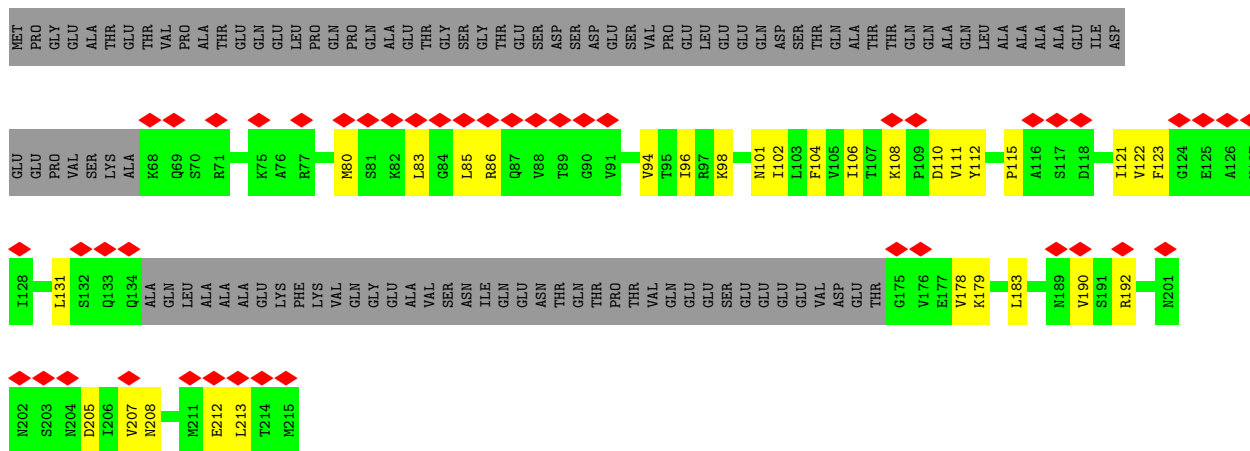
- Molecule 1: 60S ribosomal protein L8

Chain LA:  87% 9% .




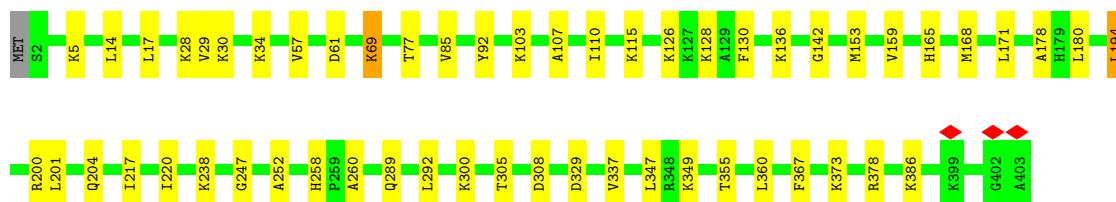
- Molecule 2: Nascent polypeptide-associated complex subunit alpha

Chain NA:  21% 36% 14% 50%




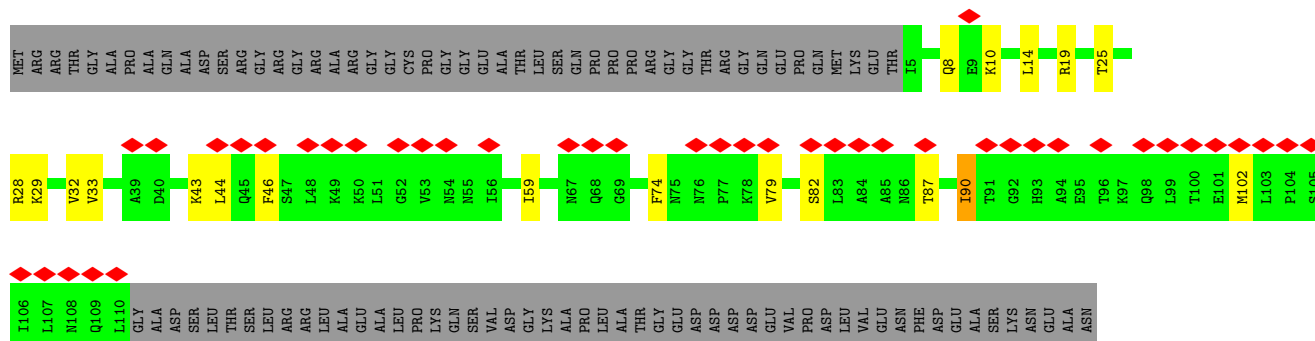
- Molecule 4: 60S ribosomal protein L3

Chain LB:  86% 13%



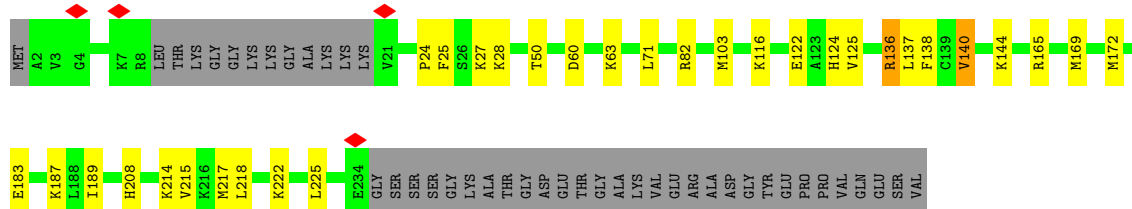
- Molecule 5: Transcription factor BTF3

Chain NB:  21% 42% 9% 49%



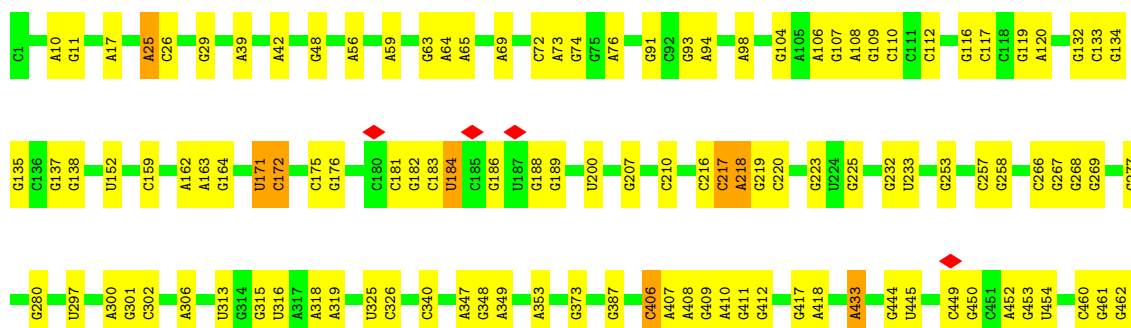
- Molecule 6: 40S ribosomal protein S3a

Chain SB:  72% 11% 16%



- Molecule 7: 28S rRNA

Chain L5:  51% 20% 28%










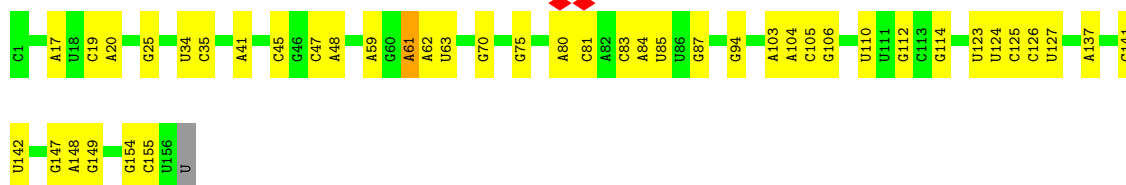
- Molecule 8: 5S rRNA

Chain L7:  84% 14% ..




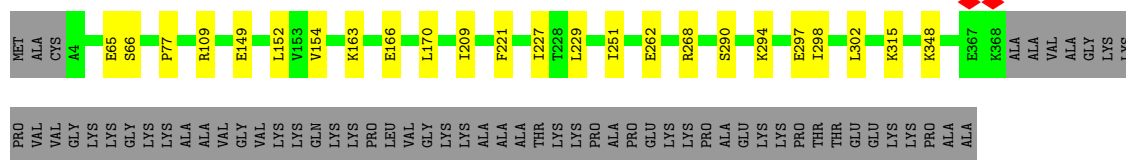
- Molecule 9: 5.8S rRNA

Chain L8:  72% 27% ..




- Molecule 10: 60S ribosomal protein L4

Chain LC:  80% 6% 15%



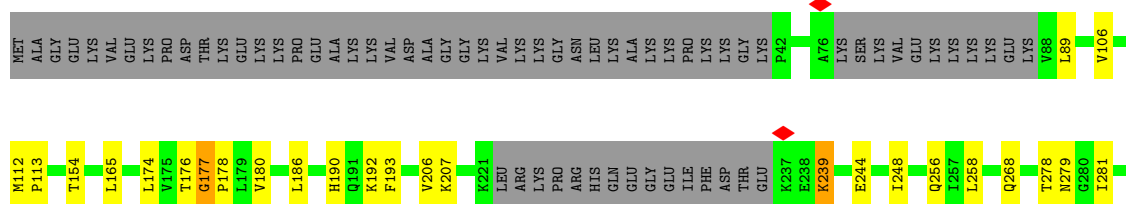
- Molecule 11: 60S ribosomal protein L5

Chain LD:  86% 12% .




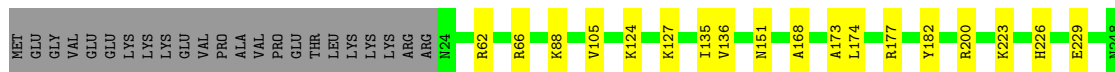
- Molecule 12: Large ribosomal subunit protein eL6

Chain LE:  68% 8% 23%




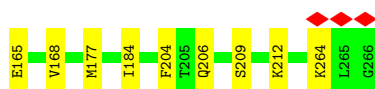
F288

- Molecule 13: Large ribosomal subunit protein uL30


Chain LF:  83% 7% 9%


- Molecule 14: 60S ribosomal protein L7a

Chain LG:  82% 8% 9%




- Molecule 15: 60S ribosomal protein L9

Chain LH:  83% 16% .


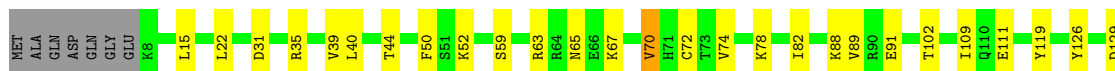


- Molecule 16: 60S ribosomal protein L10

Chain LI:  81% 13% 6%



- Molecule 17: 60S ribosomal protein L11

Chain LJ:  78% 18% . .




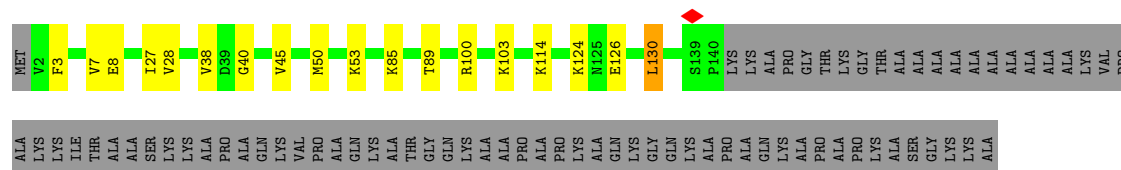
- Molecule 18: Large ribosomal subunit protein eL13

Chain LL: 91% 8%



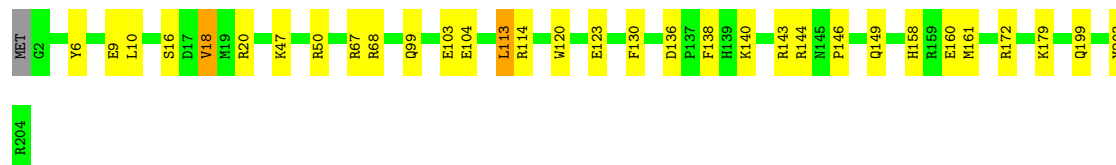
- Molecule 19: 60S ribosomal protein L14

Chain LM: 56% 8% 35%



- Molecule 20: 60S ribosomal protein L15

Chain LN: 84% 15%



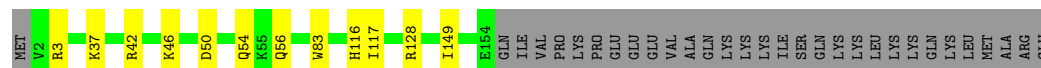
- Molecule 21: 60S ribosomal protein L13a

Chain LO: 93% 5%



- Molecule 22: 60S ribosomal protein L17

Chain LP: 77% 7% 17%

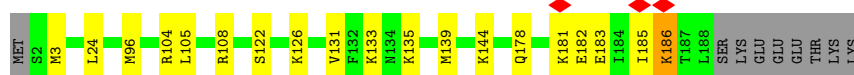
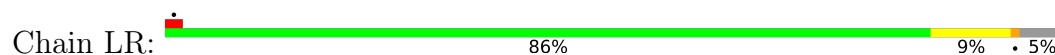


- Molecule 23: 60S ribosomal protein L18

Chain LQ: 95%



- Molecule 24: 60S ribosomal protein L19



- Molecule 25: 60S ribosomal protein L18a



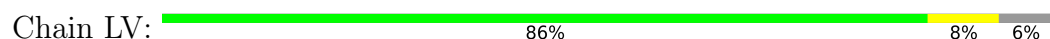
- Molecule 26: 60S ribosomal protein L21



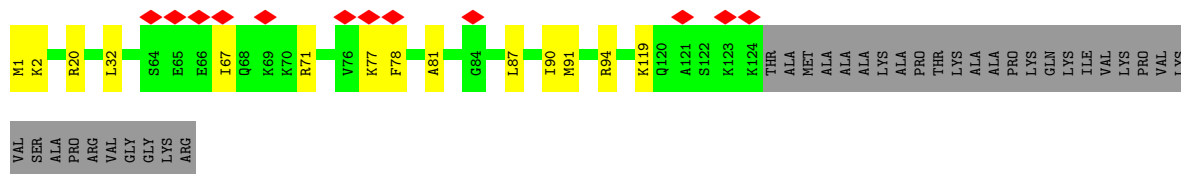
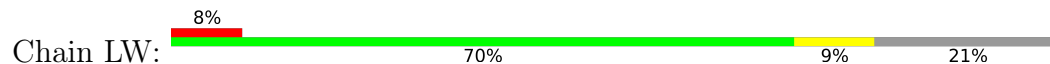
- Molecule 27: 60S ribosomal protein L22




- Molecule 28: 60S ribosomal protein L23

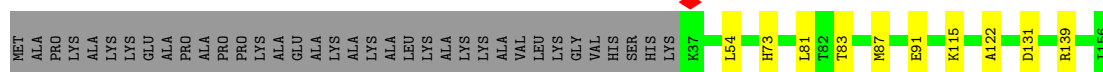


- Molecule 29: 60S ribosomal protein L24



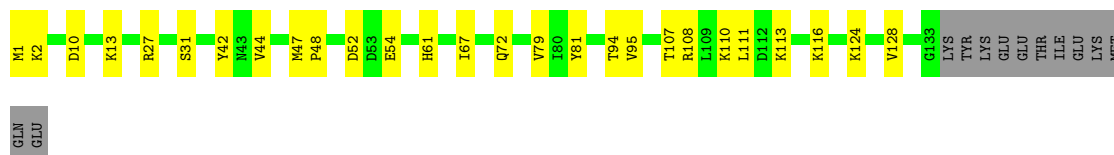
- Molecule 30: 60S ribosomal protein L23a

Chain LX:  71% 6% 23%




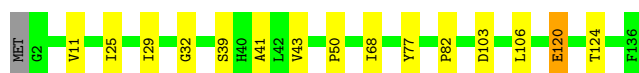
- Molecule 31: 60S ribosomal protein L26

Chain LY:  73% 19% 8%



- Molecule 32: 60S ribosomal protein L27

Chain LZ:  88% 10% ..



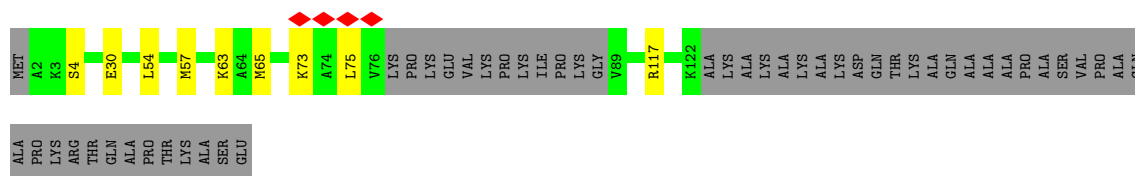
- Molecule 33: 60S ribosomal protein L27a

Chain La:  89% 11% .



- Molecule 34: 60S ribosomal protein L29

Chain Lb:  63% 6% 31%




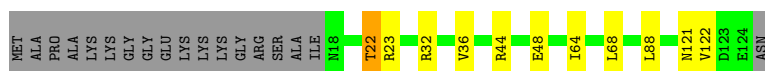
- Molecule 35: 60S ribosomal protein L30

Chain Lc:  70% 14% . 15%



- Molecule 36: 60S ribosomal protein L31

Chain Ld:  77% 8% . 14%



- Molecule 37: 60S ribosomal protein L32

Chain Le: 89% 6% 5%



- Molecule 38: 60S ribosomal protein L35a

Chain Lf: 91% 8% .



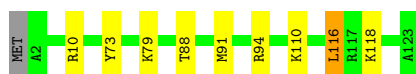
- Molecule 39: 60S ribosomal protein L34

Chain Lg: 92% 5% .



- Molecule 40: 60S ribosomal protein L35

Chain Lh: 92% 7% ..



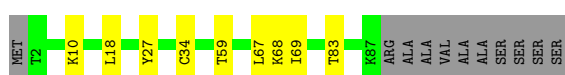
- Molecule 41: 60S ribosomal protein L36

Chain Li: 92% 5% .



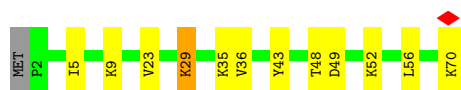
- Molecule 42: Large ribosomal subunit protein eL37

Chain Lj: 79% 9% 11%



- Molecule 43: 60S ribosomal protein L38

Chain Lk: 81% 16% ..



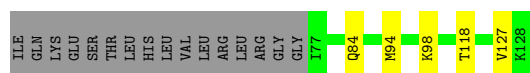
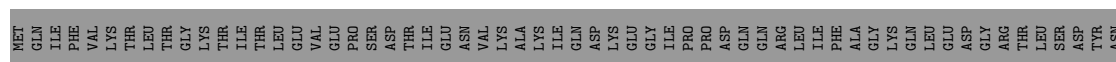
- Molecule 44: 60S ribosomal protein L39

Chain Ll: 78% 16% . .



- Molecule 45: Large ribosomal subunit protein eL40

Chain Lm: 37% . 59%



- Molecule 46: 60S ribosomal protein L41

Chain Ln: 84% 12% .



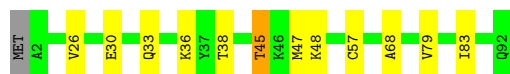
- Molecule 47: 60S ribosomal protein L36a

Chain Lo: 86% 13% .



- Molecule 48: 60S ribosomal protein L37a

Chain Lp: 86% 12% . .

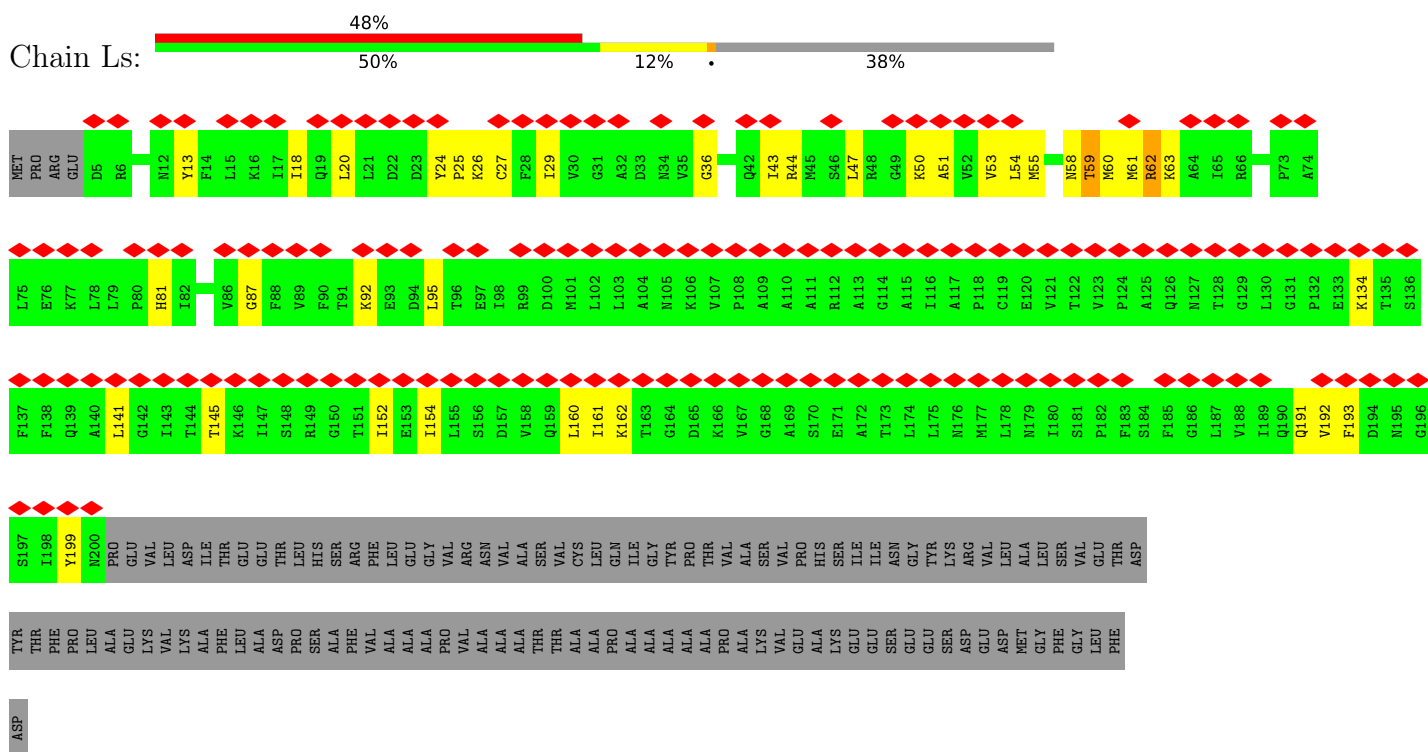


- Molecule 49: 60S ribosomal protein L28

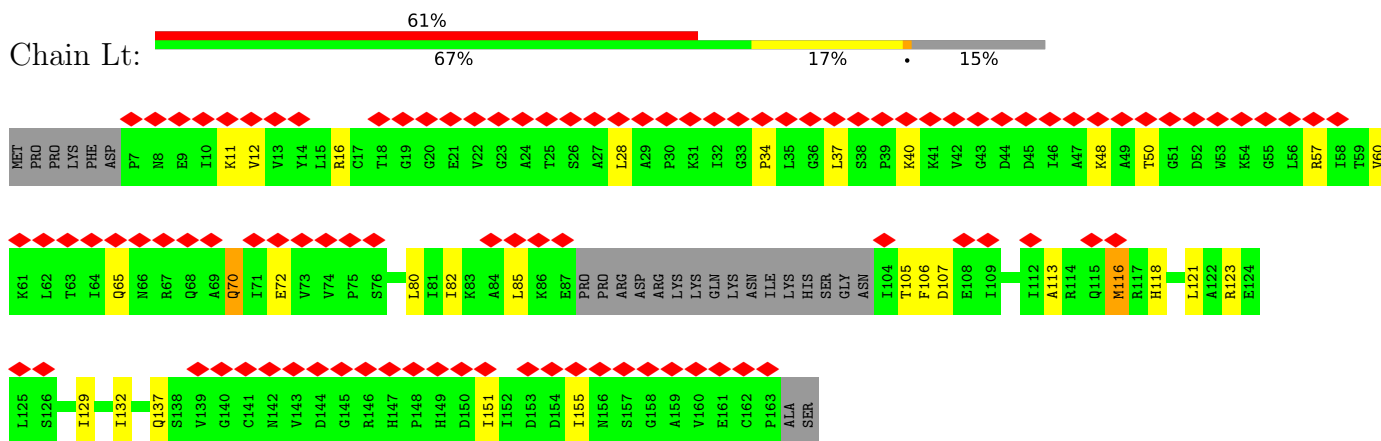
Chain Lr: 85% 6% 9%



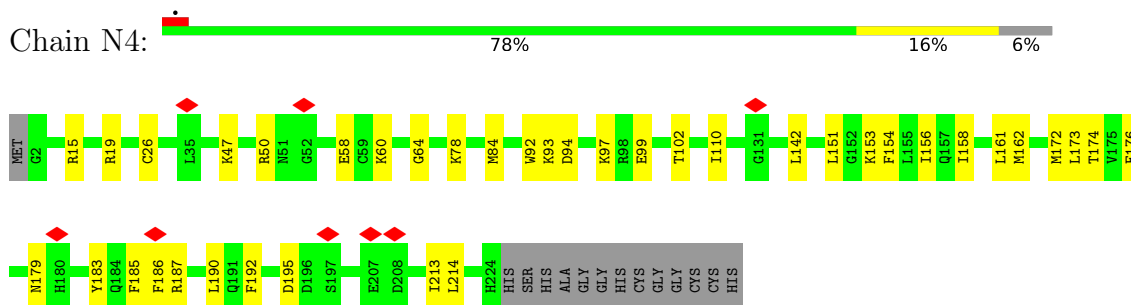
- Molecule 50: 60S acidic ribosomal protein P0



- Molecule 51: Large ribosomal subunit protein uL11



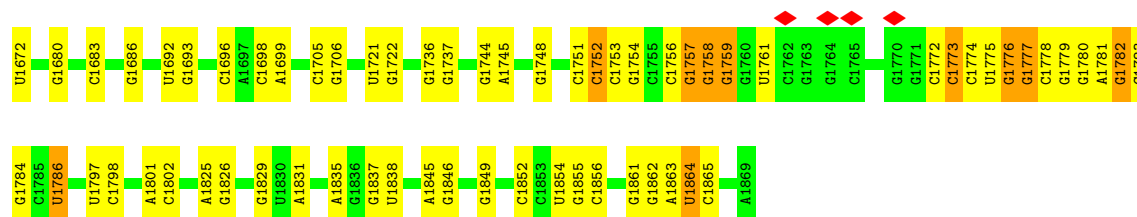
- Molecule 52: N-alpha-acetyltransferase 40



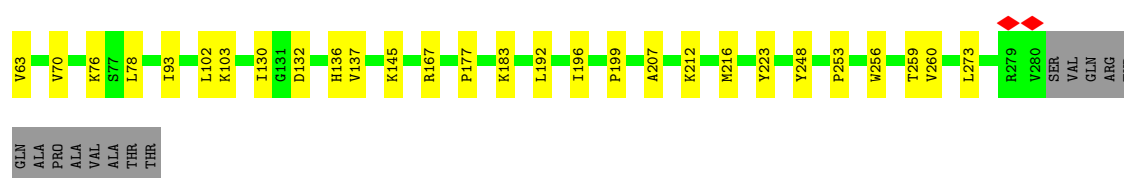
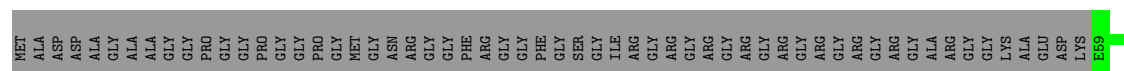
- Molecule 53: 18S rRNA



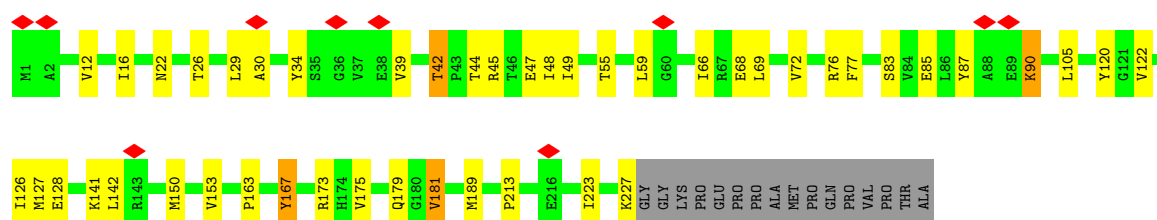
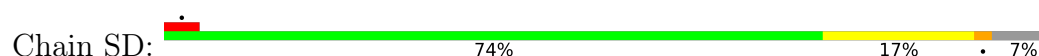
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C4	U115	C	A302	C409	A554	G673	C	A811	U917	A1028	C1219	C1436	A1569
G6	U116	C	U678	A433	A555	U678	U	G821	A920	G1037	G1220	C1437	G1570
C17	U121	A	G308	C434	U562	U681	G	U822	G921	A1060	G1224	A1438	A1579
C18	G126	C	C311	G438	G563	C887	C	A830	A922	A1067	U1227	A1439	A1580
U26	C129	C	G312	A448	A564	U888	U746	U822	G925	C1067	G1227	U1457	U1585
A27	G130	G	C319	A449	G565	U889	U747	A830	G926	A1080	A1228	G1458	U1586
U28	C133	U	C322	C450	C567	U890	U749	C833	G928	A1083	G1229	G1312	G1587
G29	C134	C	C323	G451	C568	G591	G750	C834	G929	A1084	U1232	U1462	A1588
G33	U135	A	C324	G452	A576	G	G751	C835	C930	C1085	G1233	U1463	C1593
U34	C136	G	C325	A455	C579	A	C753	G836	G933	C1086	U1239	C1468	A1594
C35	U143	C	C326	A456	C579	G	G	A837	G934	C1089	U1242	G1475	U1595
G41	U144	C	C327	A464	C583	C	C	G838	U940	G1098	U1243	A1476	G1598
A42	G145	U	U328	A465	G584	C	C	C839	U943	G1099	U1244	U1477	G1600
U43	G146	C	G329	G466	G588	C	C	C840	U944	G1100	G1245	C1487	A1601
U44	A147	U	C330	G468	G589	G	U	C841	A944	A1101	A1251	C1488	G1606
A45	A147	C	G331	G471	G590	G	G	C842	A947	G1102	C1252	A1489	C1618
A46	G155	C	G332	A473	U591	C	A	C847	C948	G1109	A1253	G1490	U1621
U51	U160	G	G333	G474	C592	G	U	G851	C949	C1115	G1256	G1495	U1622
G52	U161	C	A339	G482	C604	G	G	G852	A955	C1116	G1257	U1496	A1623
G56	C162	C	G347	A485	C614	U	C	G860	A963	C1117	A1258	G1497	U1632
U57	U163	C	G351	A486	C614	C	C	A861	U965	C1118	A1259	A1498	A1634
C58	G167	C	A360	U487	G623	C	U	A862	G971	G1121	U1263	U1504	A1630
U59	A171	C	U361	U488	G627	C	A	G873	A981	G1138	C1264	U1505	U1631
G62	A175	C	A362	C492	A628	G	G	A875	G982	A1133	G1274	G1507	A1632
C65	A182	G	A364	A493	U631	C	U	G878	A990	C1144	A1276	A1508	A1634
C67	U198	C	U367	C502	C638	G	A	C879	G991	A1145	C1277	U1509	C1644
A68	C199	C	U368	A508	C639	G	G	G880	A992	A1146	A1278	C1513	C1645
G71	G200	G	C369	G509	A640	C	U	A886	A996	C1153	C1283	G1514	C1646
C72	C201	G	G370	C517	U641	U	A	U887	A997	U1154	G1284	G1520	U1649
C73	G202	C	A371	A525	A643	C	C	U888	C998	C1172	G1285	C1521	A1650
G74	G203	C	U375	A526	G644	C	C	U889	G999	U1172	G1286	A1522	A1651
G75	G204	G	U376	A527	U649	C	A	U890	C1000	A1189	U1289	A1533	U1652
U76	U210	C	U377	C527	A650	C	C	G891	U1001	A1190	G1290	G1536	G1654
A77	G211	C	C379	A528	A655	C	G	G895	U1002	A1195	A1293	A1537	G1655
A91	C	G	G	A529	G656	C	G	U896	C1007	A1199	G1294	G1546	G1656
A102	U220	C	G383	G535	C660	C	G	U897	A1008	U1201	A1295	G1560	C1660
A103	A221	C	U384	A536	C660	C	C	U898	A1009	U1202	G1298	U1661	A1661
A104	U222	G	G385	C387	C663	G	C	U899	G1010	G1203	G1299	G1562	A1662
U105	C223	C	C386	U540	C664	U	U	C900	A1011	A1204	A1301	A1664	A1663
C106	A224	U	C387	U541	A664	C	C	A904	U1012	G1207	G1302	C1553	A1664
A107	G225	U	C391	U542	A668	C	C	A907	U1013	C1207	C1303	U1364	G1665
G108	A	C	A392	A545	A669	C	C	A908	U1016	C1215	U1364	C1305	U1668
U112	C	C	C400	G546	A670	G	G	A913	U1017	C1216	U1365	C1306	G1669
G113	A	C	G407	G547	C548	C	C	A913	A1023	A1217	U1367	C1433	C1670
													G1671



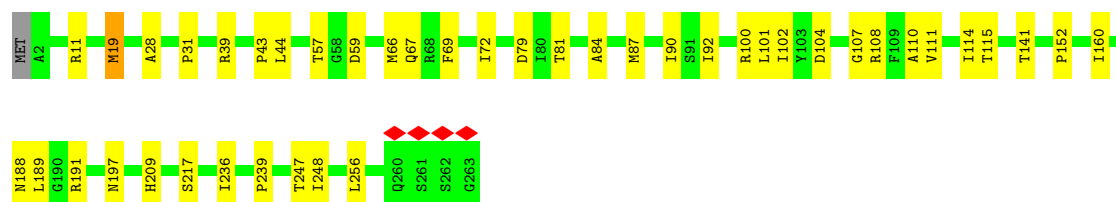
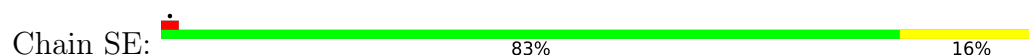
• Molecule 54: 40S ribosomal protein S2



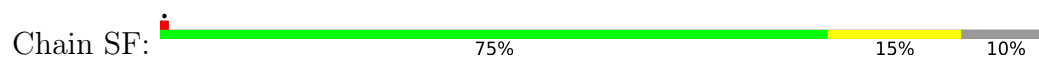
• Molecule 55: 40S ribosomal protein S3

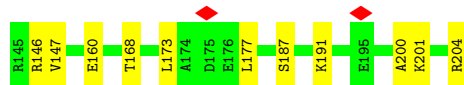


• Molecule 56: Small ribosomal subunit protein eS4, X isoform



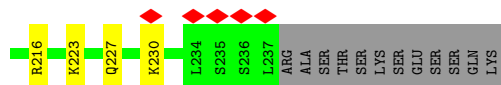
• Molecule 57: 40S ribosomal protein S5





- Molecule 58: 40S ribosomal protein S6

Chain SG: 80% 15% 5%



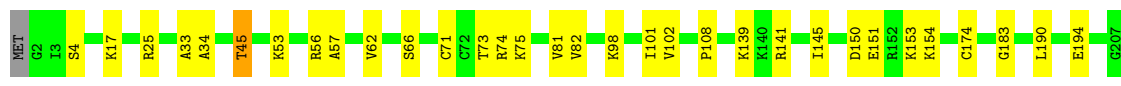
- Molecule 59: 40S ribosomal protein S7

Chain SH: 76% 19% . .



- Molecule 60: 40S ribosomal protein S8

Chain SI: 84% 15% .



- Molecule 61: 40S ribosomal protein S9

Chain SJ: 84% 11% 5%



- Molecule 62: 40S ribosomal protein S10

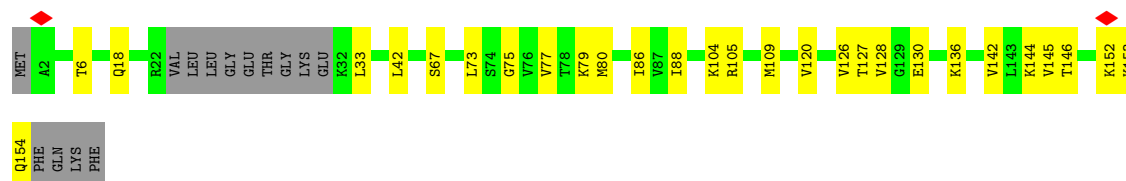
Chain SK: 45% 12% 42%



ARG GLY GLU ALA ASP ARG ASP THR TYR ARG ARG SER SER ALA VAL PRO PRO GLY ALA ASP LYS LYS ALA GLU GLY ALA GLY ALA GLY SER SER THR THR PHE GLN PHE ARG GLY PHE GLY ARG GLY GLN PRO PRO GLN

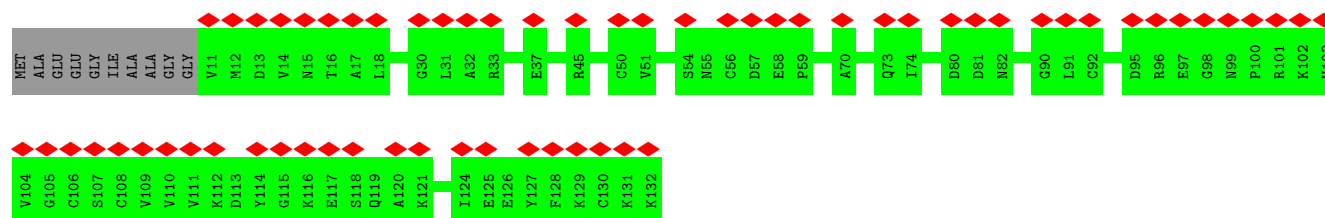
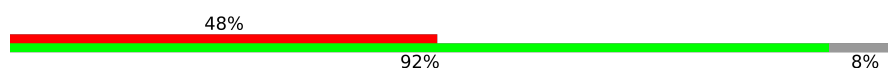
• Molecule 63: 40S ribosomal protein S11

Chain SL:



• Molecule 64: 40S ribosomal protein S12

Chain SM:



• Molecule 65: 40S ribosomal protein S13

Chain SN:



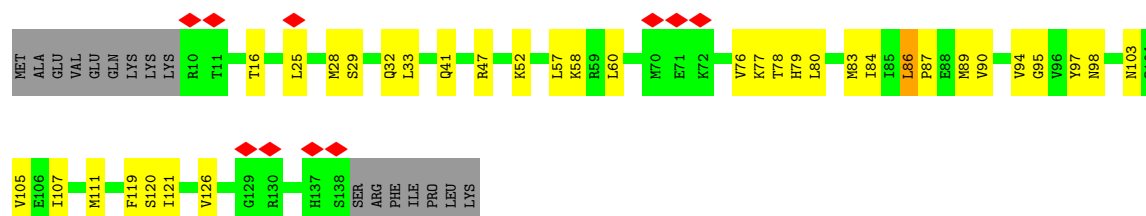
• Molecule 66: 40S ribosomal protein S14

Chain SO:

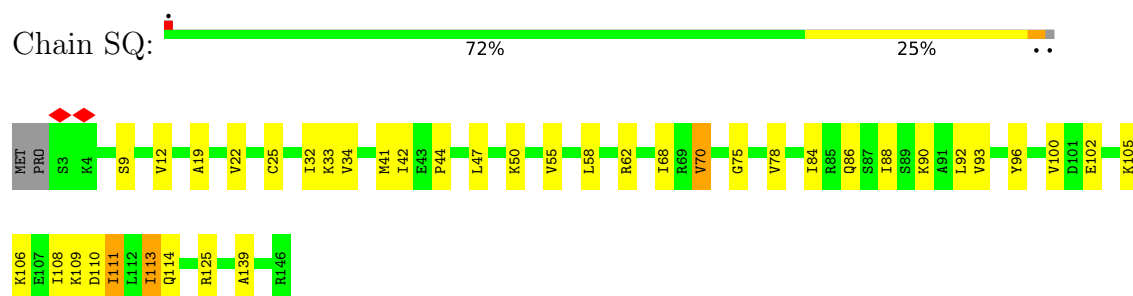


• Molecule 67: 40S ribosomal protein S15

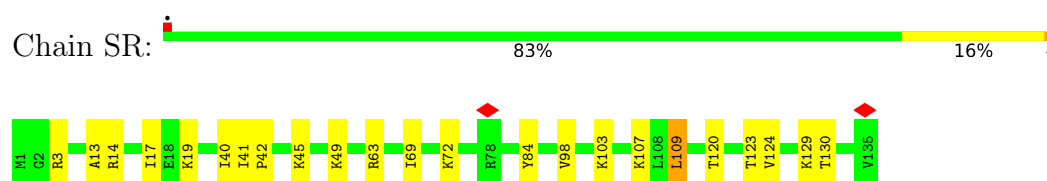
Chain SP:



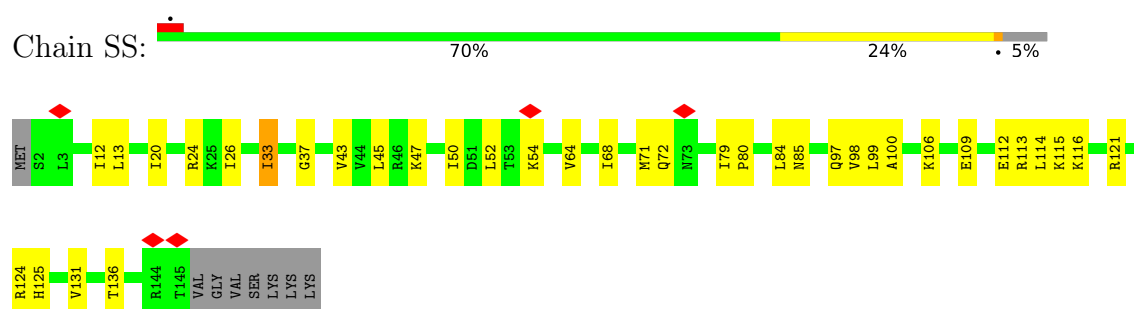
- Molecule 68: 40S ribosomal protein S16



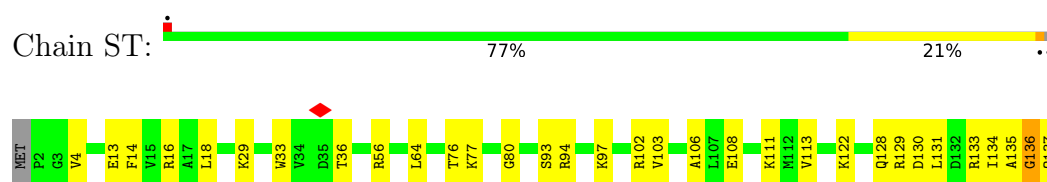
- Molecule 69: 40S ribosomal protein S17



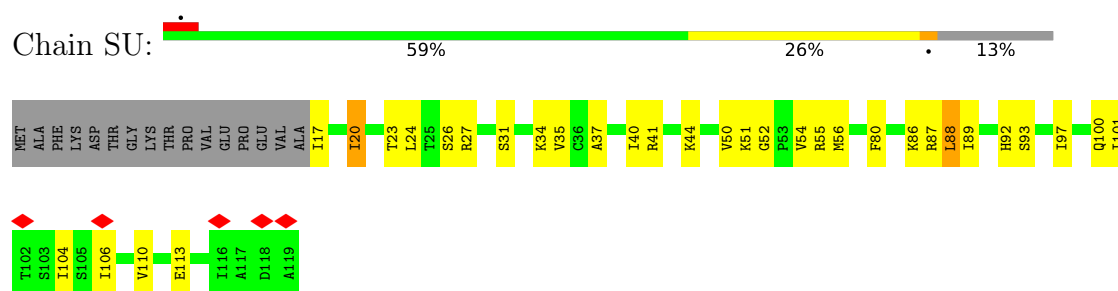
- Molecule 70: 40S ribosomal protein S18



- Molecule 71: 40S ribosomal protein S19



- Molecule 72: 40S ribosomal protein S20




- Molecule 73: 40S ribosomal protein S21

Chain SV:  90% 10%



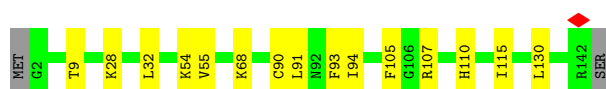
- Molecule 74: 40S ribosomal protein S15a

Chain SW:  85% 14%




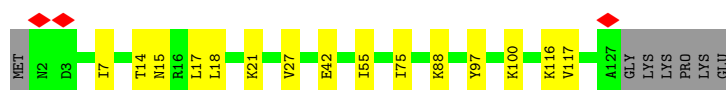
- Molecule 75: 40S ribosomal protein S23

Chain SX:  88% 10%

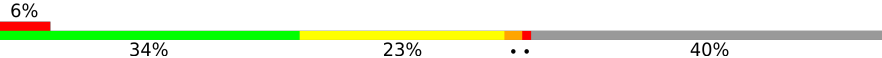


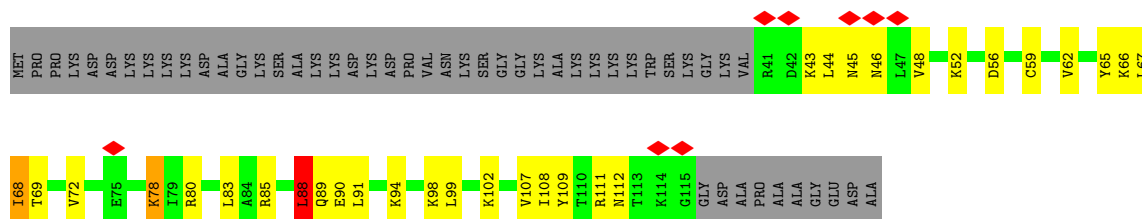
- Molecule 76: 40S ribosomal protein S24

Chain SY:  83% 11% 5%




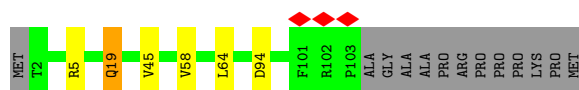
- Molecule 77: 40S ribosomal protein S25

Chain SZ:  6% 34% 23% 40%



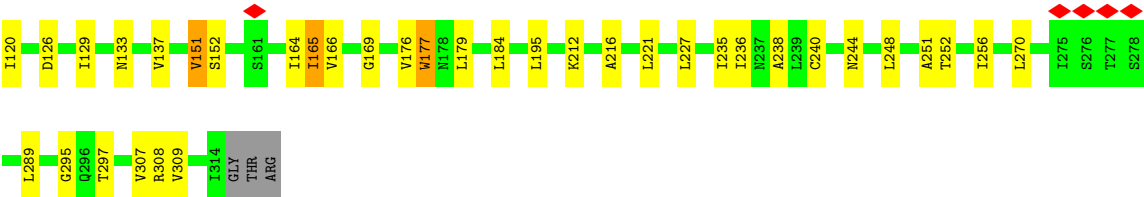
- Molecule 78: 40S ribosomal protein S26

Chain Sa:  83% 11%



- Molecule 79: 40S ribosomal protein S27

Chain Sb:  87% 12%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	26095	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	4.822	Depositor
Minimum map value	-2.416	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.106	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	465.28, 465.28, 465.28	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, MLZ, 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	LA	0.31	0/1936	0.49	0/2596
2	NA	0.18	0/845	0.56	0/1128
3	SA	0.25	0/1778	0.54	0/2416
4	LB	0.29	0/3306	0.49	0/4424
5	NB	0.26	0/829	0.69	1/1112 (0.1%)
6	SB	0.21	0/1817	0.49	0/2428
7	L5	0.33	0/87990	0.38	2/137262 (0.0%)
8	L7	0.31	0/2861	0.34	0/4459
9	L8	0.32	0/3701	0.34	0/5766
10	LC	0.29	0/2962	0.47	0/3977
11	LD	0.25	0/2428	0.46	0/3252
12	LE	0.25	0/1808	0.48	2/2425 (0.1%)
13	LF	0.29	0/1905	0.44	0/2539
14	LG	0.26	0/1960	0.53	0/2637
15	LH	0.26	0/1537	0.45	0/2066
16	LI	0.26	0/1677	0.43	0/2237
17	LJ	0.28	0/1394	0.65	2/1863 (0.1%)
18	LL	0.26	0/1704	0.44	0/2282
19	LM	0.25	0/1161	0.41	0/1554
20	LN	0.34	0/1746	0.43	0/2338
21	LO	0.30	0/1682	0.43	0/2250
22	LP	0.30	0/1268	0.46	0/1701
23	LQ	0.30	0/1537	0.41	0/2052
24	LR	0.27	0/1582	0.45	0/2091
25	LS	0.27	0/1493	0.41	0/2003
26	LT	0.27	0/1326	0.38	0/1770
27	LU	0.26	0/830	0.58	1/1114 (0.1%)
28	LV	0.29	0/993	0.46	0/1332
29	LW	0.25	0/1030	0.50	1/1364 (0.1%)
30	LX	0.25	0/1002	0.41	0/1345
31	LY	0.26	0/1123	0.43	0/1493
32	LZ	0.25	0/1130	0.40	0/1507

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	La	0.29	0/1191	0.42	0/1591
34	Lb	0.26	0/895	0.49	0/1182
35	Lc	0.28	0/774	0.51	0/1038
36	Ld	0.26	0/903	0.44	0/1216
37	Le	0.30	0/1071	0.45	0/1429
38	Lf	0.30	0/895	0.40	0/1198
39	Lg	0.29	0/916	0.45	0/1220
40	Lh	0.24	0/1023	0.43	0/1351
41	Li	0.23	0/843	0.47	0/1115
42	Lj	0.34	0/720	0.53	0/952
43	Lk	0.27	0/575	0.53	1/761 (0.1%)
44	Ll	0.32	0/454	0.39	0/599
45	Lm	0.24	0/425	0.40	0/561
46	Ln	0.20	0/231	0.40	0/294
47	Lo	0.26	0/876	0.42	0/1156
48	Lp	0.28	0/718	0.43	0/953
49	Lr	0.28	0/1017	0.42	0/1364
50	Ls	0.19	0/1519	0.55	0/2052
51	Lt	0.21	0/1058	0.69	2/1430 (0.1%)
52	N4	0.20	0/1846	0.58	0/2476
53	S2	0.22	0/40751	0.34	0/63496
54	SC	0.24	0/1762	0.52	0/2381
55	SD	0.26	0/1793	0.70	4/2414 (0.2%)
56	SE	0.21	0/2118	0.48	0/2849
57	SF	0.23	0/1481	0.61	1/1988 (0.1%)
58	SG	0.23	0/1946	0.58	1/2590 (0.0%)
59	SH	0.26	0/1519	0.65	0/2033
60	SI	0.24	0/1715	0.49	1/2287 (0.0%)
61	SJ	0.21	0/1550	0.47	0/2069
62	SK	0.29	0/823	0.86	0/1111
63	SL	0.23	0/1202	0.40	0/1606
64	SM	0.09	0/603	0.26	0/837
65	SN	0.25	0/1232	0.44	0/1656
66	SO	0.23	0/1023	0.52	1/1372 (0.1%)
67	SP	0.27	0/1082	0.75	0/1446
68	SQ	0.25	0/1160	0.68	0/1553
69	SR	0.30	0/1105	0.75	1/1484 (0.1%)
70	SS	0.30	0/1208	0.79	1/1618 (0.1%)
71	ST	0.29	0/1131	0.75	4/1515 (0.3%)
72	SU	0.29	0/827	0.80	0/1110
73	SV	0.22	0/643	0.48	1/860 (0.1%)
74	SW	0.25	0/1051	0.43	0/1406
75	SX	0.20	0/1116	0.39	0/1490

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	SY	0.25	0/1044	0.61	0/1388
77	SZ	0.33	0/604	1.06	2/810 (0.2%)
78	Sa	0.28	0/836	0.59	1/1121 (0.1%)
79	Sb	0.24	0/665	0.51	0/891
80	Sc	0.28	0/508	0.71	2/680 (0.3%)
81	Sd	0.31	0/470	0.73	0/623
82	Se	0.19	0/465	0.45	0/612
83	Sf	0.24	0/560	0.67	1/745 (0.1%)
84	Sg	0.21	0/2493	0.62	2/3394 (0.1%)
All	All	0.28	0/234777	0.44	35/344156 (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
12	LE	0	1
27	LU	0	1
51	Lt	0	1
59	SH	0	1
62	SK	0	1
72	SU	0	1
77	SZ	0	1
84	Sg	0	1
All	All	0	8

There are no bond length outliers.

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	NB	8	GLN	CA-CB-CG	7.14	128.38	114.10
55	SD	128	GLU	CA-CB-CG	6.54	127.17	114.10
51	Lt	37	LEU	CA-CB-CG	6.37	138.59	116.30
55	SD	127	MET	CA-C-N	-6.12	113.06	122.60
55	SD	127	MET	C-N-CA	-6.12	113.06	122.60

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	LE	177	GLY	Peptide
27	LU	107	LYS	Peptide
51	Lt	118	HIS	Peptide
59	SH	32	MET	Peptide
62	SK	17	LYS	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	LA	1898	0	1993	15	0
2	NA	841	0	898	17	0
3	SA	1741	0	1746	19	0
4	LB	3238	0	3376	31	0
5	NB	821	0	867	10	0
6	SB	1791	0	1870	16	0
7	L5	78658	0	39747	270	0
8	L7	2561	0	1295	5	0
9	L8	3314	0	1683	12	0
10	LC	2908	0	3082	13	0
11	LD	2382	0	2410	20	0
12	LE	1774	0	1930	17	0
13	LF	1870	0	1996	12	0
14	LG	1927	0	2074	16	0
15	LH	1518	0	1601	16	0
16	LI	1639	0	1687	14	0
17	LJ	1371	0	1412	17	0
18	LL	1673	0	1779	9	0
19	LM	1138	0	1204	11	0
20	LN	1701	0	1749	21	0
21	LO	1650	0	1794	8	0
22	LP	1242	0	1269	5	0
23	LQ	1513	0	1628	3	0
24	LR	1566	0	1729	10	0
25	LS	1453	0	1490	13	0
26	LT	1298	0	1366	11	0
27	LU	816	0	842	4	0
28	LV	979	0	1039	6	0
29	LW	1015	0	1079	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	LX	985	0	1066	4	0
31	LY	1106	0	1192	13	0
32	LZ	1107	0	1182	8	0
33	La	1162	0	1213	7	0
34	Lb	882	0	959	6	0
35	Lc	764	0	804	10	0
36	Ld	888	0	930	6	0
37	Le	1053	0	1147	3	0
38	Lf	876	0	912	5	0
39	Lg	906	0	998	5	0
40	Lh	1015	0	1148	6	0
41	Li	832	0	917	2	0
42	Lj	705	0	737	5	0
43	Lk	569	0	637	9	0
44	Ll	444	0	483	7	0
45	Lm	430	0	466	2	0
46	Ln	230	0	276	2	0
47	Lo	862	0	929	8	0
48	Lp	708	0	756	8	0
49	Lr	1002	0	1068	4	0
50	Ls	1496	0	1540	24	0
51	Lt	1046	0	1076	17	0
52	N4	1809	0	1764	25	0
53	S2	36456	0	18381	174	0
54	SC	1725	0	1813	13	0
55	SD	1765	0	1865	29	0
56	SE	2076	0	2177	22	0
57	SF	1461	0	1511	19	0
58	SG	1923	0	2089	25	0
59	SH	1497	0	1590	23	0
60	SI	1686	0	1772	18	0
61	SJ	1525	0	1640	13	0
62	SK	799	0	823	15	0
63	SL	1182	0	1253	12	0
64	SM	604	0	281	0	0
65	SN	1208	0	1294	6	0
66	SO	1010	0	1034	7	0
67	SP	1061	0	1107	25	0
68	SQ	1142	0	1213	22	0
69	SR	1090	0	1149	12	0
70	SS	1190	0	1249	20	0
71	ST	1112	0	1146	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	SU	817	0	882	22	0
73	SV	636	0	637	3	0
74	SW	1034	0	1080	12	0
75	SX	1098	0	1167	8	0
76	SY	1027	0	1093	9	0
77	SZ	598	0	656	17	0
78	Sa	821	0	870	4	0
79	Sb	651	0	672	5	0
80	Sc	506	0	536	6	0
81	Sd	459	0	448	4	0
82	Se	459	0	503	7	0
83	Sf	548	0	551	5	0
84	Sg	2436	0	2393	38	0
85	L5	210	0	0	0	0
85	L7	3	0	0	0	0
85	L8	6	0	0	0	0
85	LA	1	0	0	0	0
85	LI	1	0	0	0	0
85	LP	1	0	0	0	0
85	LV	1	0	0	0	0
85	Le	2	0	0	0	0
85	Lg	1	0	0	0	0
85	S2	30	0	0	0	0
85	SG	1	0	0	0	0
86	Lg	1	0	0	0	0
86	Lj	1	0	0	0	0
86	Lm	1	0	0	0	0
86	Lo	1	0	0	0	0
86	Lp	1	0	0	0	0
86	Sa	1	0	0	0	0
86	Sd	1	0	0	0	0
86	Sf	1	0	0	0	0
All	All	219040	0	163710	1280	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 3.

The worst 5 of 1280 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)
53:S2:1756:C:N4	53:S2:1776:G:H22	1.53	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
53:S2:1756:C:H42	53:S2:1776:G:N2	1.52	1.06
7:L5:1762:C:N4	7:L5:1770:A:C2	2.35	0.94
7:L5:1996:C:H42	7:L5:2000:G:N2	1.73	0.86
7:L5:2557:G:H1	7:L5:2570:U:H3	1.19	0.86

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	246/257 (96%)	235 (96%)	11 (4%)	0	100	100
2	NA	104/215 (48%)	102 (98%)	2 (2%)	0	100	100
3	SA	219/295 (74%)	211 (96%)	8 (4%)	0	100	100
4	LB	400/403 (99%)	381 (95%)	19 (5%)	0	100	100
5	NB	104/206 (50%)	95 (91%)	9 (9%)	0	100	100
6	SB	217/264 (82%)	212 (98%)	5 (2%)	0	100	100
10	LC	363/427 (85%)	348 (96%)	14 (4%)	1 (0%)	36	59
11	LD	291/297 (98%)	287 (99%)	4 (1%)	0	100	100
12	LE	215/288 (75%)	201 (94%)	14 (6%)	0	100	100
13	LF	223/248 (90%)	216 (97%)	7 (3%)	0	100	100
14	LG	239/266 (90%)	229 (96%)	10 (4%)	0	100	100
15	LH	188/192 (98%)	175 (93%)	13 (7%)	0	100	100
16	LI	198/214 (92%)	194 (98%)	4 (2%)	0	100	100
17	LJ	169/178 (95%)	166 (98%)	3 (2%)	0	100	100
18	LL	205/211 (97%)	195 (95%)	8 (4%)	2 (1%)	12	30
19	LM	137/215 (64%)	134 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	LN	201/204 (98%)	191 (95%)	10 (5%)	0	100	100
21	LO	199/203 (98%)	197 (99%)	2 (1%)	0	100	100
22	LP	151/184 (82%)	147 (97%)	4 (3%)	0	100	100
23	LQ	185/188 (98%)	178 (96%)	7 (4%)	0	100	100
24	LR	185/196 (94%)	184 (100%)	1 (0%)	0	100	100
25	LS	173/176 (98%)	166 (96%)	7 (4%)	0	100	100
26	LT	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
27	LU	98/128 (77%)	97 (99%)	1 (1%)	0	100	100
28	LV	129/140 (92%)	125 (97%)	4 (3%)	0	100	100
29	LW	122/157 (78%)	117 (96%)	5 (4%)	0	100	100
30	LX	118/156 (76%)	115 (98%)	3 (2%)	0	100	100
31	LY	131/145 (90%)	128 (98%)	3 (2%)	0	100	100
32	LZ	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
33	La	145/148 (98%)	139 (96%)	6 (4%)	0	100	100
34	Lb	105/159 (66%)	101 (96%)	4 (4%)	0	100	100
35	Lc	96/115 (84%)	96 (100%)	0	0	100	100
36	Ld	105/125 (84%)	103 (98%)	2 (2%)	0	100	100
37	Le	126/135 (93%)	125 (99%)	1 (1%)	0	100	100
38	Lf	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
39	Lg	112/117 (96%)	112 (100%)	0	0	100	100
40	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
41	Li	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
42	Lj	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
43	Lk	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
44	Ll	48/51 (94%)	48 (100%)	0	0	100	100
45	Lm	49/128 (38%)	49 (100%)	0	0	100	100
46	Ln	22/25 (88%)	22 (100%)	0	0	100	100
47	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
48	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
49	Lr	123/137 (90%)	123 (100%)	0	0	100	100
50	Ls	194/317 (61%)	181 (93%)	13 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	Lt	137/165 (83%)	115 (84%)	22 (16%)	0	100	100
52	N4	221/237 (93%)	211 (96%)	10 (4%)	0	100	100
54	SC	220/293 (75%)	217 (99%)	3 (1%)	0	100	100
55	SD	225/243 (93%)	212 (94%)	13 (6%)	0	100	100
56	SE	260/263 (99%)	250 (96%)	10 (4%)	0	100	100
57	SF	180/204 (88%)	171 (95%)	9 (5%)	0	100	100
58	SG	235/249 (94%)	230 (98%)	5 (2%)	0	100	100
59	SH	182/194 (94%)	176 (97%)	6 (3%)	0	100	100
60	SI	204/208 (98%)	194 (95%)	10 (5%)	0	100	100
61	SJ	183/194 (94%)	181 (99%)	2 (1%)	0	100	100
62	SK	93/165 (56%)	84 (90%)	9 (10%)	0	100	100
63	SL	140/158 (89%)	134 (96%)	6 (4%)	0	100	100
64	SM	120/132 (91%)	115 (96%)	5 (4%)	0	100	100
65	SN	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
66	SO	133/151 (88%)	123 (92%)	9 (7%)	1 (1%)	16	35
67	SP	127/145 (88%)	121 (95%)	6 (5%)	0	100	100
68	SQ	142/146 (97%)	131 (92%)	11 (8%)	0	100	100
69	SR	133/135 (98%)	128 (96%)	4 (3%)	1 (1%)	16	35
70	SS	142/152 (93%)	127 (89%)	15 (11%)	0	100	100
71	ST	141/145 (97%)	137 (97%)	4 (3%)	0	100	100
72	SU	101/119 (85%)	95 (94%)	6 (6%)	0	100	100
73	SV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
74	SW	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
75	SX	139/143 (97%)	136 (98%)	3 (2%)	0	100	100
76	SY	124/133 (93%)	122 (98%)	2 (2%)	0	100	100
77	SZ	73/125 (58%)	59 (81%)	14 (19%)	0	100	100
78	Sa	100/115 (87%)	97 (97%)	3 (3%)	0	100	100
79	Sb	81/84 (96%)	78 (96%)	3 (4%)	0	100	100
80	Sc	62/69 (90%)	61 (98%)	1 (2%)	0	100	100
81	Sd	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
82	Se	56/133 (42%)	55 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
83	Sf	65/156 (42%)	56 (86%)	9 (14%)	0	100	100
84	Sg	311/317 (98%)	282 (91%)	29 (9%)	0	100	100
All	All	12034/13902 (87%)	11554 (96%)	475 (4%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
66	SO	138	ASP
18	LL	97	SER
10	LC	149	GLU
18	LL	136	LYS
69	SR	129	LYS

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	LA	190/199 (96%)	188 (99%)	2 (1%)	65	84
2	NA	95/183 (52%)	93 (98%)	2 (2%)	47	73
3	SA	183/243 (75%)	178 (97%)	5 (3%)	39	68
4	LB	348/349 (100%)	339 (97%)	9 (3%)	40	69
5	NB	90/165 (54%)	83 (92%)	7 (8%)	11	28
6	SB	200/231 (87%)	195 (98%)	5 (2%)	42	69
10	LC	304/348 (87%)	300 (99%)	4 (1%)	61	81
11	LD	246/250 (98%)	239 (97%)	7 (3%)	38	67
12	LE	195/252 (77%)	193 (99%)	2 (1%)	68	85
13	LF	194/215 (90%)	193 (100%)	1 (0%)	81	91
14	LG	203/223 (91%)	199 (98%)	4 (2%)	48	74
15	LH	169/171 (99%)	164 (97%)	5 (3%)	36	64
16	LI	172/181 (95%)	169 (98%)	3 (2%)	53	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	LJ	144/149 (97%)	137 (95%)	7 (5%)	22	47
18	LL	173/177 (98%)	168 (97%)	5 (3%)	37	65
19	LM	118/161 (73%)	115 (98%)	3 (2%)	42	69
20	LN	171/172 (99%)	168 (98%)	3 (2%)	51	76
21	LO	173/174 (99%)	170 (98%)	3 (2%)	53	77
22	LP	134/163 (82%)	132 (98%)	2 (2%)	57	79
23	LQ	164/165 (99%)	160 (98%)	4 (2%)	43	70
24	LR	166/175 (95%)	162 (98%)	4 (2%)	43	70
25	LS	156/157 (99%)	151 (97%)	5 (3%)	34	62
26	LT	139/140 (99%)	138 (99%)	1 (1%)	76	89
27	LU	90/115 (78%)	87 (97%)	3 (3%)	33	61
28	LV	101/107 (94%)	100 (99%)	1 (1%)	68	85
29	LW	103/126 (82%)	101 (98%)	2 (2%)	50	75
30	LX	108/133 (81%)	105 (97%)	3 (3%)	38	67
31	LY	123/135 (91%)	117 (95%)	6 (5%)	22	47
32	LZ	117/118 (99%)	116 (99%)	1 (1%)	70	86
33	La	120/121 (99%)	117 (98%)	3 (2%)	42	69
34	Lb	89/126 (71%)	86 (97%)	3 (3%)	32	60
35	Lc	83/97 (86%)	81 (98%)	2 (2%)	43	70
36	Ld	98/110 (89%)	96 (98%)	2 (2%)	48	74
37	Le	114/121 (94%)	110 (96%)	4 (4%)	32	59
38	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	84
39	Lg	98/100 (98%)	97 (99%)	1 (1%)	68	85
40	Lh	109/110 (99%)	107 (98%)	2 (2%)	51	76
41	Li	86/89 (97%)	83 (96%)	3 (4%)	32	59
42	Lj	73/80 (91%)	71 (97%)	2 (3%)	39	68
43	Lk	64/65 (98%)	63 (98%)	1 (2%)	55	78
44	Ll	47/48 (98%)	45 (96%)	2 (4%)	26	52
45	Lm	47/115 (41%)	45 (96%)	2 (4%)	26	52
46	Ln	23/24 (96%)	22 (96%)	1 (4%)	26	52
47	Lo	93/94 (99%)	91 (98%)	2 (2%)	45	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	Lp	74/75 (99%)	73 (99%)	1 (1%)	59	80
49	Lr	109/121 (90%)	107 (98%)	2 (2%)	51	76
50	Ls	162/258 (63%)	158 (98%)	4 (2%)	42	69
51	Lt	112/137 (82%)	110 (98%)	2 (2%)	51	76
52	N4	195/204 (96%)	192 (98%)	3 (2%)	57	79
54	SC	188/225 (84%)	179 (95%)	9 (5%)	23	48
55	SD	190/202 (94%)	183 (96%)	7 (4%)	30	57
56	SE	224/225 (100%)	216 (96%)	8 (4%)	31	58
57	SF	156/170 (92%)	154 (99%)	2 (1%)	61	81
58	SG	207/218 (95%)	203 (98%)	4 (2%)	50	75
59	SH	166/174 (95%)	162 (98%)	4 (2%)	43	70
60	SI	178/180 (99%)	174 (98%)	4 (2%)	45	72
61	SJ	161/168 (96%)	157 (98%)	4 (2%)	42	69
62	SK	86/136 (63%)	83 (96%)	3 (4%)	32	59
63	SL	130/142 (92%)	121 (93%)	9 (7%)	14	33
65	SN	130/131 (99%)	126 (97%)	4 (3%)	35	63
66	SO	105/119 (88%)	99 (94%)	6 (6%)	18	41
67	SP	115/130 (88%)	111 (96%)	4 (4%)	32	59
68	SQ	119/121 (98%)	109 (92%)	10 (8%)	10	24
69	SR	122/122 (100%)	116 (95%)	6 (5%)	22	47
70	SS	125/132 (95%)	118 (94%)	7 (6%)	19	42
71	ST	113/115 (98%)	113 (100%)	0	100	100
72	SU	94/107 (88%)	91 (97%)	3 (3%)	34	62
73	SV	67/67 (100%)	64 (96%)	3 (4%)	24	50
74	SW	112/113 (99%)	109 (97%)	3 (3%)	39	68
75	SX	113/115 (98%)	109 (96%)	4 (4%)	32	59
76	SY	109/115 (95%)	105 (96%)	4 (4%)	30	57
77	SZ	66/103 (64%)	60 (91%)	6 (9%)	9	21
78	Sa	89/98 (91%)	87 (98%)	2 (2%)	45	72
79	Sb	75/76 (99%)	72 (96%)	3 (4%)	28	55
80	Sc	57/62 (92%)	56 (98%)	1 (2%)	51	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
81	Sd	48/49 (98%)	46 (96%)	2 (4%)	26	53
82	Se	47/104 (45%)	46 (98%)	1 (2%)	47	73
83	Sf	60/140 (43%)	58 (97%)	2 (3%)	33	61
84	Sg	272/275 (99%)	259 (95%)	13 (5%)	23	48
All	All	10377/11695 (89%)	10087 (97%)	290 (3%)	38	67

5 of 290 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
69	SR	98	VAL
84	Sg	177	TRP
70	SS	50	ILE
77	SZ	43	LYS
29	LW	1	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
49	Lr	85	ASN
60	SI	7	ASN
50	Ls	190	GLN
56	SE	197	ASN
63	SL	19	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
53	S2	1696/1869 (90%)	346 (20%)	5 (0%)
7	L5	3657/5070 (72%)	760 (20%)	19 (0%)
8	L7	119/121 (98%)	11 (9%)	0
9	L8	155/157 (98%)	29 (18%)	0
All	All	5627/7217 (77%)	1146 (20%)	24 (0%)

5 of 1146 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	L5	17	A
7	L5	25	A

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Mol	Chain	Res	Type
7	L5	39	A
7	L5	42	A
7	L5	48	G

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	L5	3673	C
7	L5	4699	U
7	L5	4378	A
7	L5	4913	G
7	L5	1590	C

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
45	MLZ	Lm	98	45	8,9,10	0.81	0	4,9,11	0.67	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
45	MLZ	Lm	98	45	-	0/7/8/10	-

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
45	Lm	98	MLZ	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 265 ligands modelled in this entry, 265 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 [i](#)

There are no chain breaks in this entry.

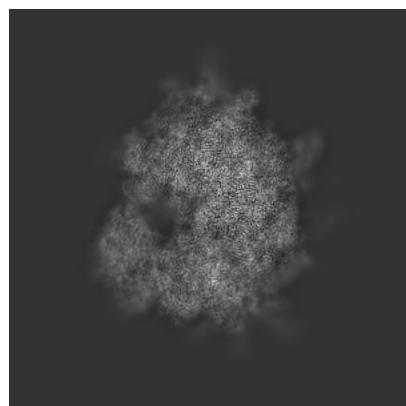
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-53944. These allow visual inspection of the internal detail of the map and identification of artifacts.

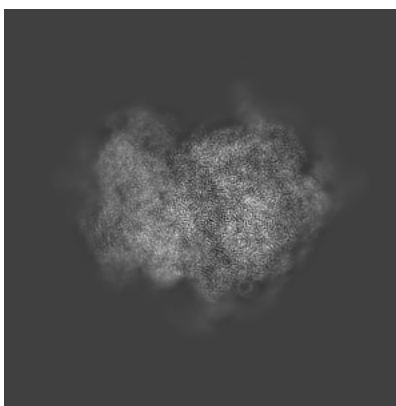
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

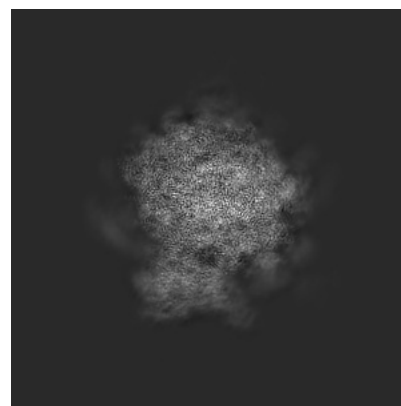
6.1.1 Primary map



X

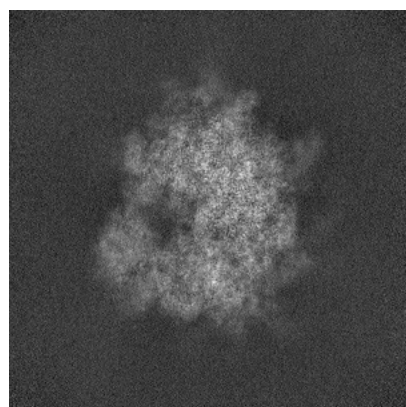


Y

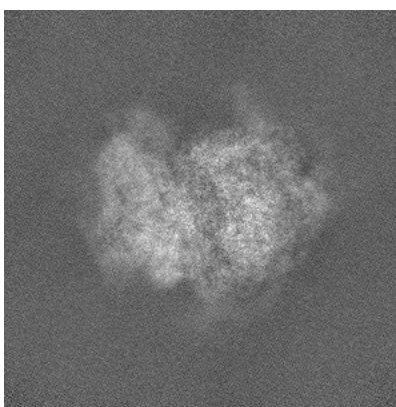


Z

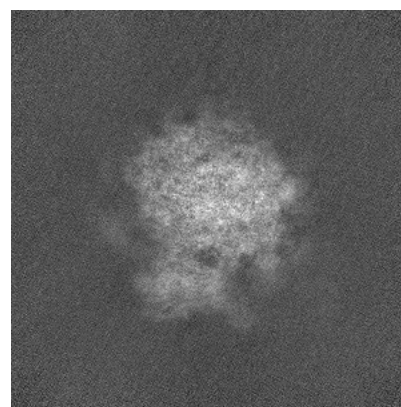
6.1.2 Raw map



X



Y

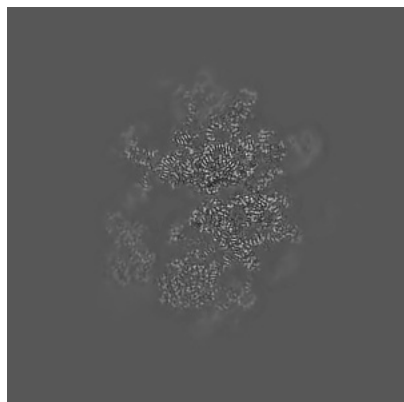


Z

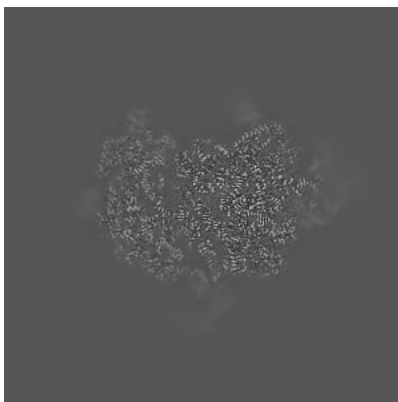
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

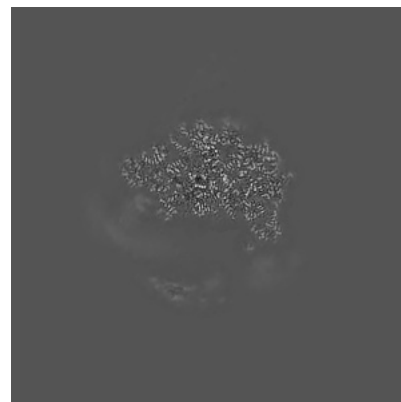
6.2.1 Primary map



X Index: 320

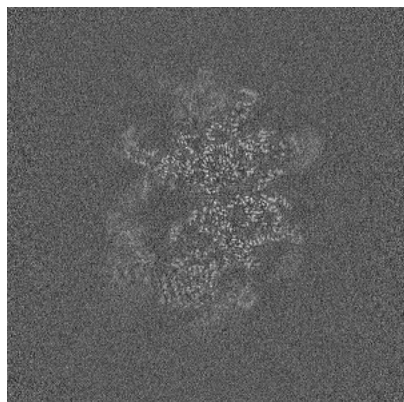


Y Index: 320

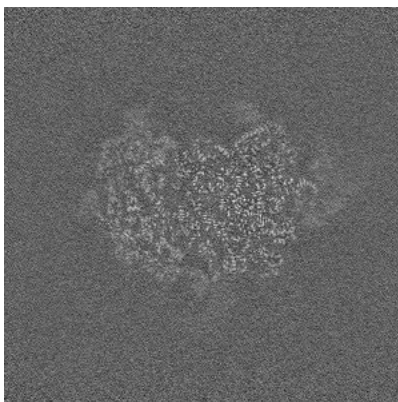


Z Index: 320

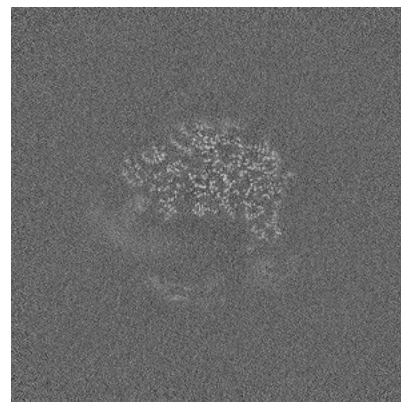
6.2.2 Raw map



X Index: 320



Y Index: 320

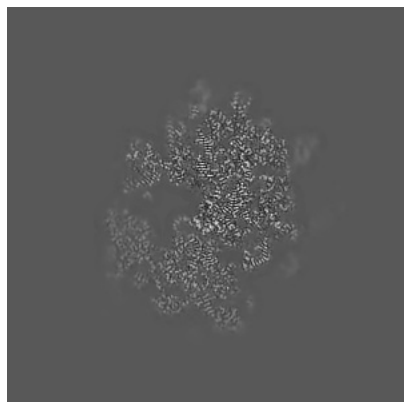


Z Index: 320

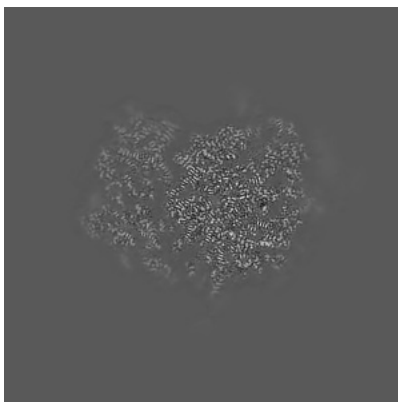
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

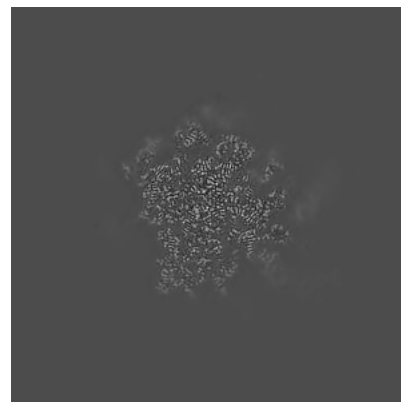
6.3.1 Primary map



X Index: 299

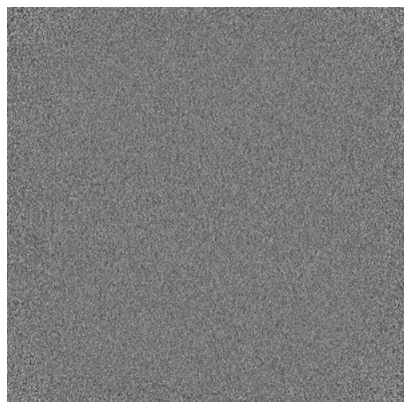


Y Index: 339

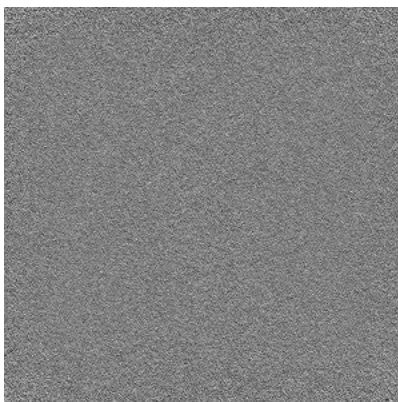


Z Index: 385

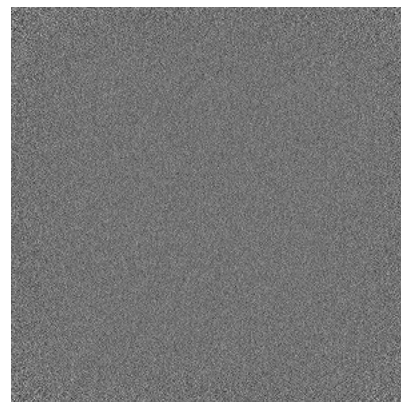
6.3.2 Raw map



X Index: 0



Y Index: 0

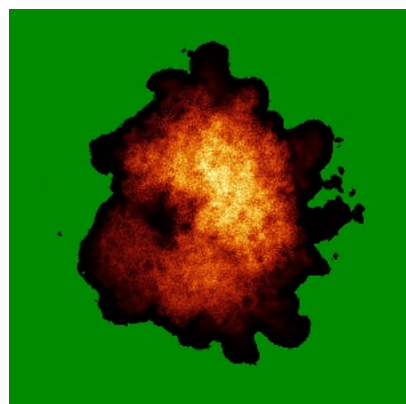


Z Index: 0

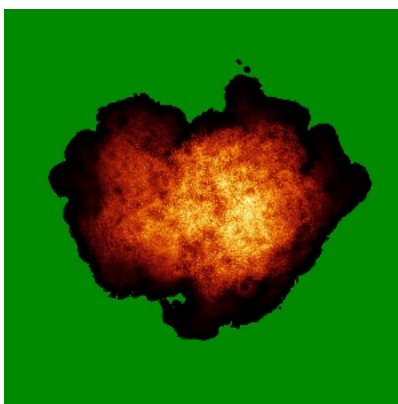
The images above show the largest variance slices of the map in three orthogonal directions.

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

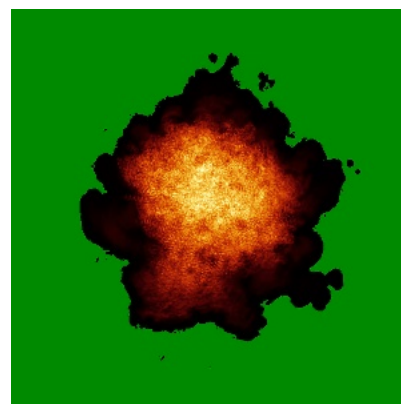
6.4.1 Primary map



X

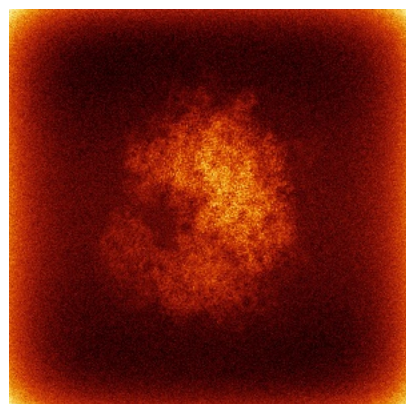


Y

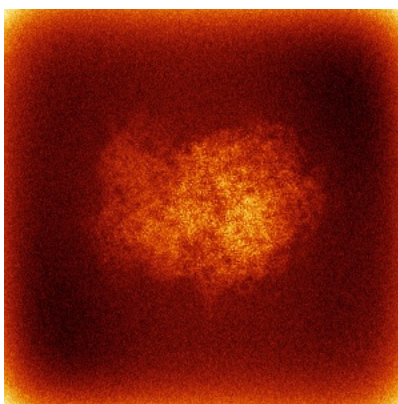


Z

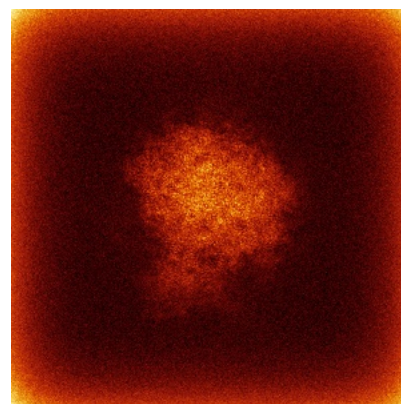
6.4.2 Raw map



X



Y

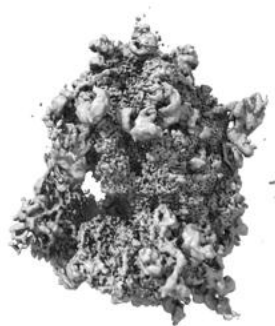


Z

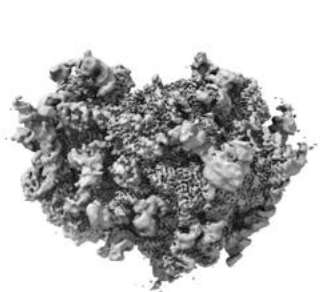
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



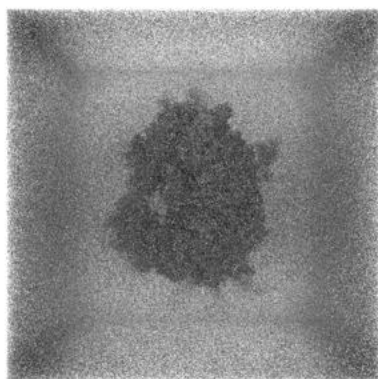
Y



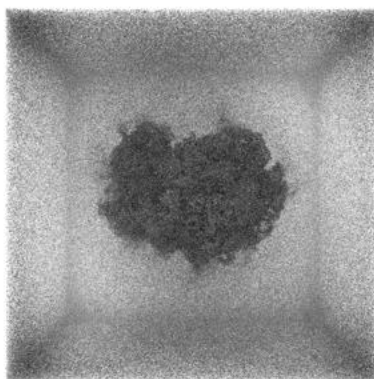
Z

The images above show the 3D surface view of the map at the recommended contour level 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

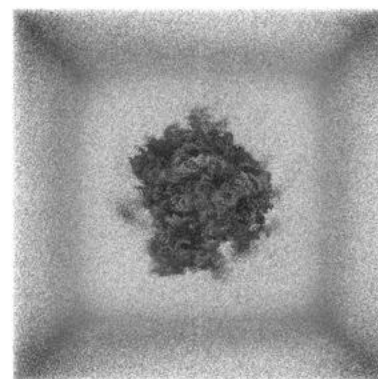
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

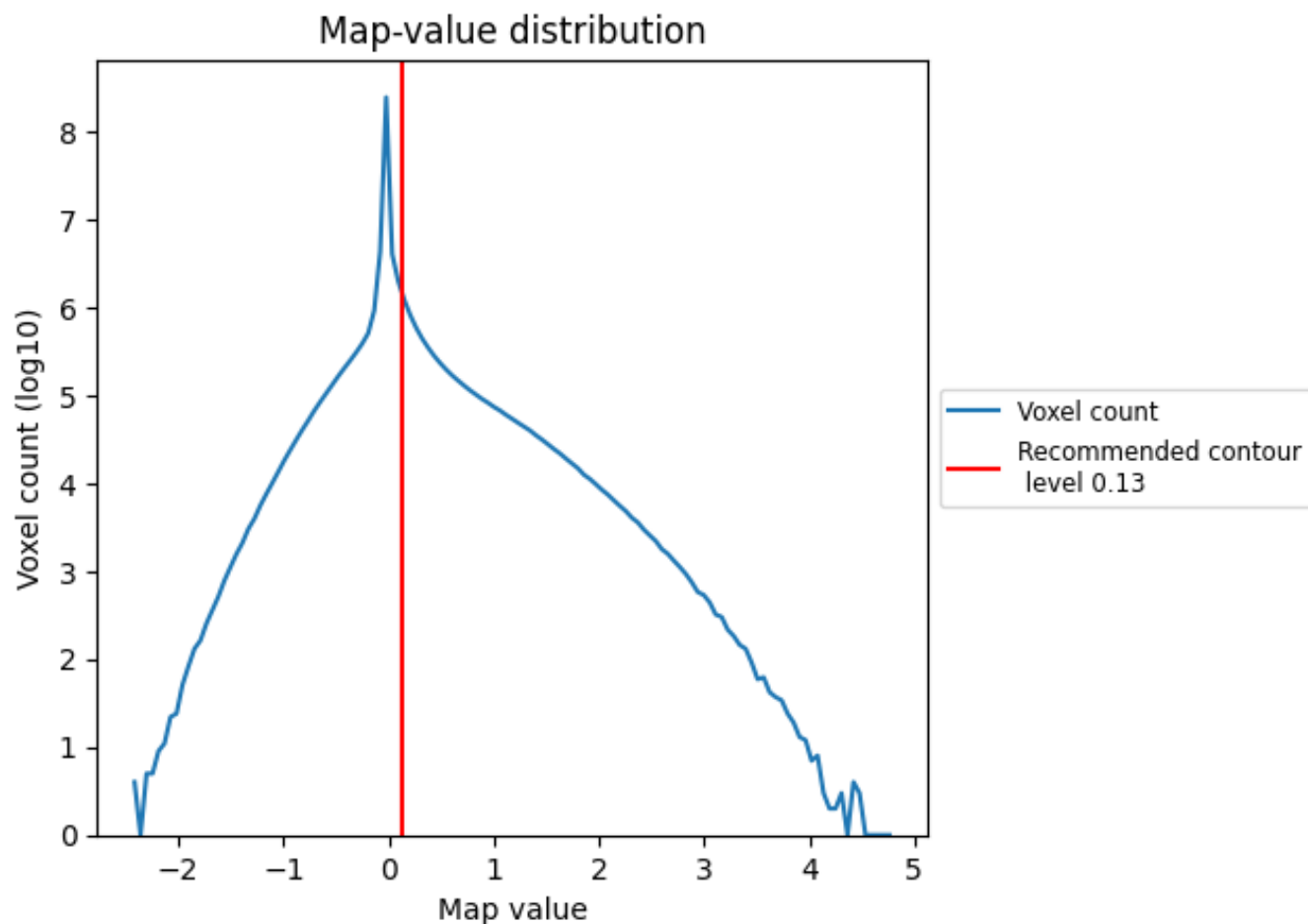
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

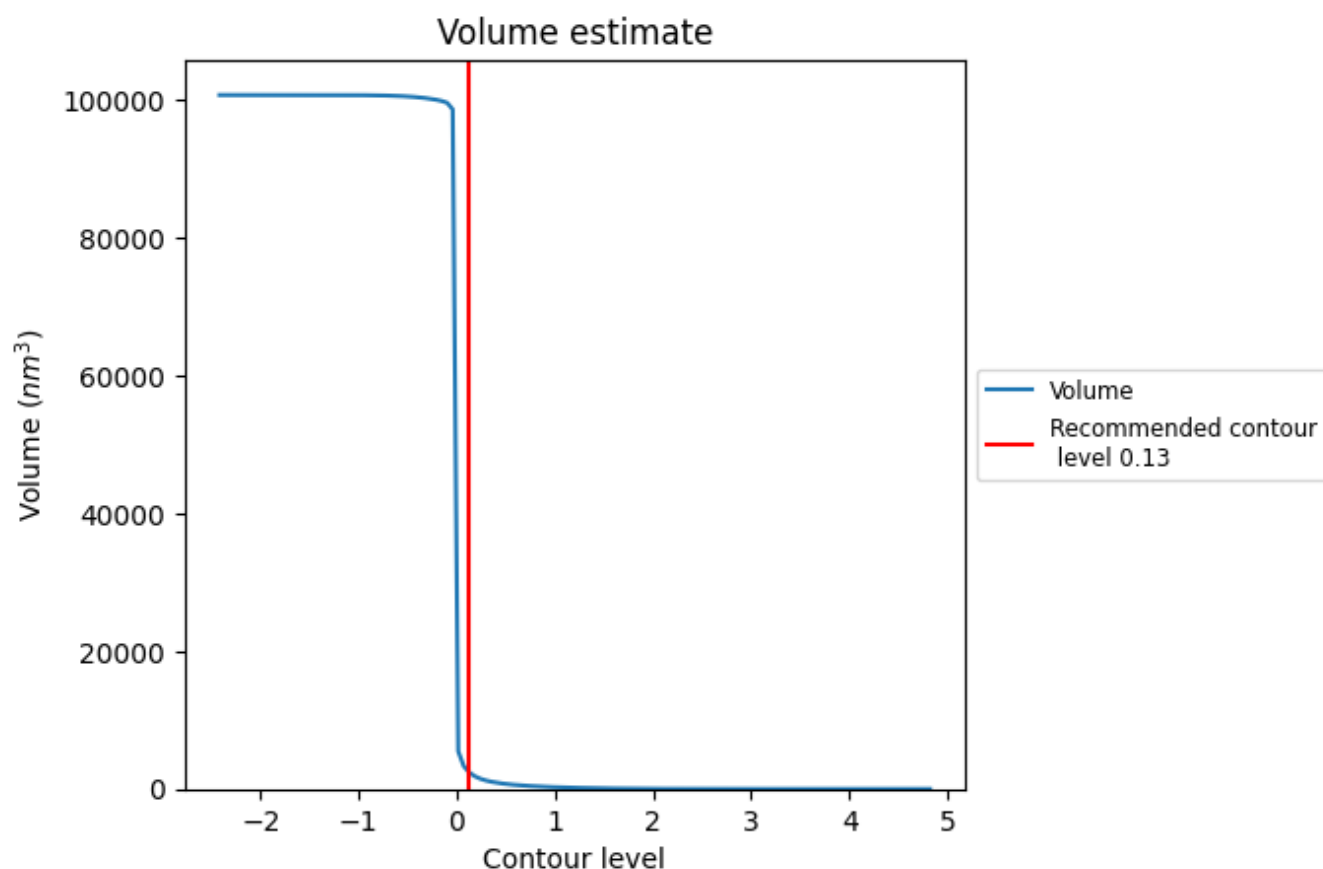
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

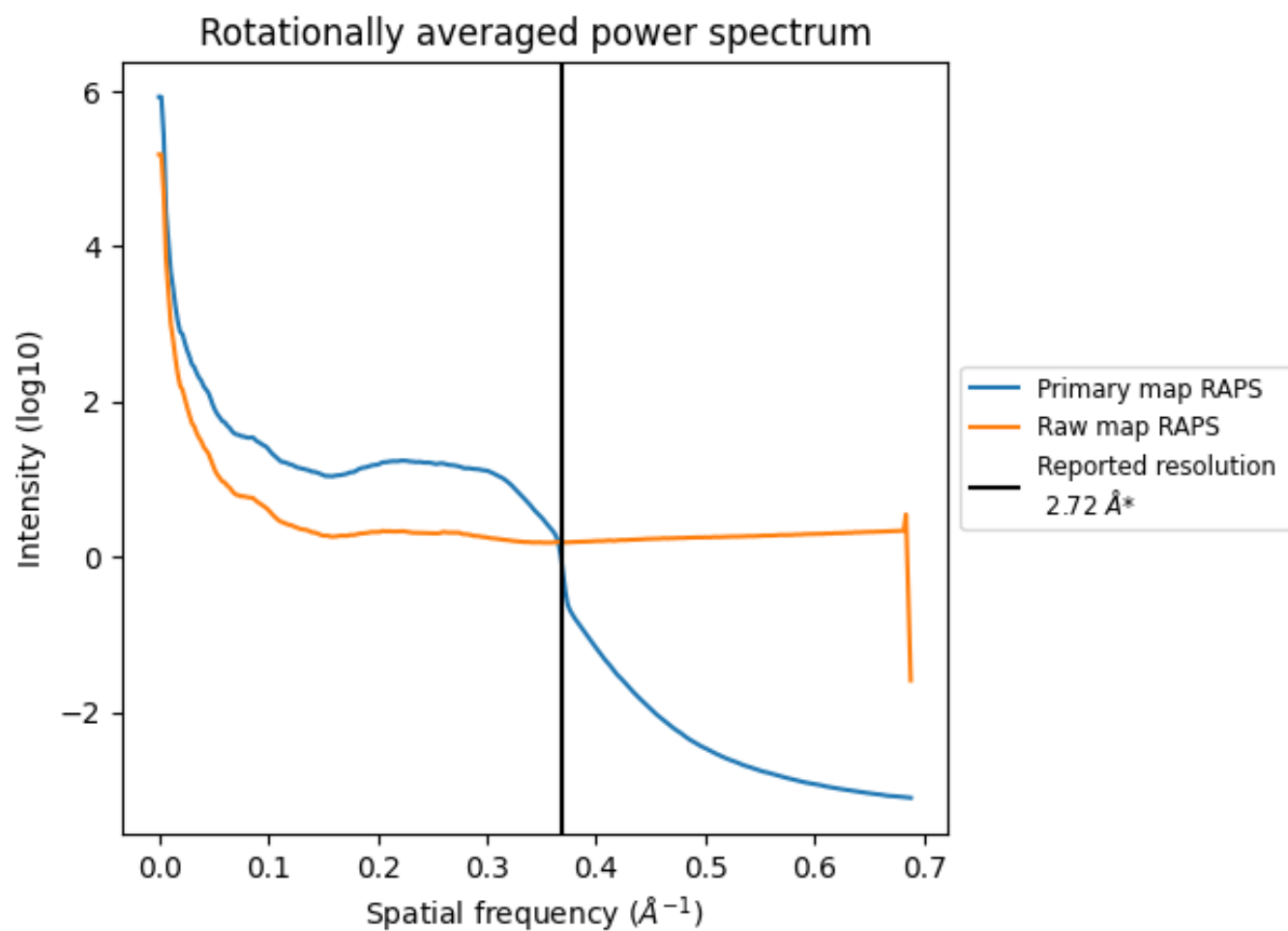
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2367 nm^3 ; this corresponds to an approximate mass of 2138 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 ⓘ

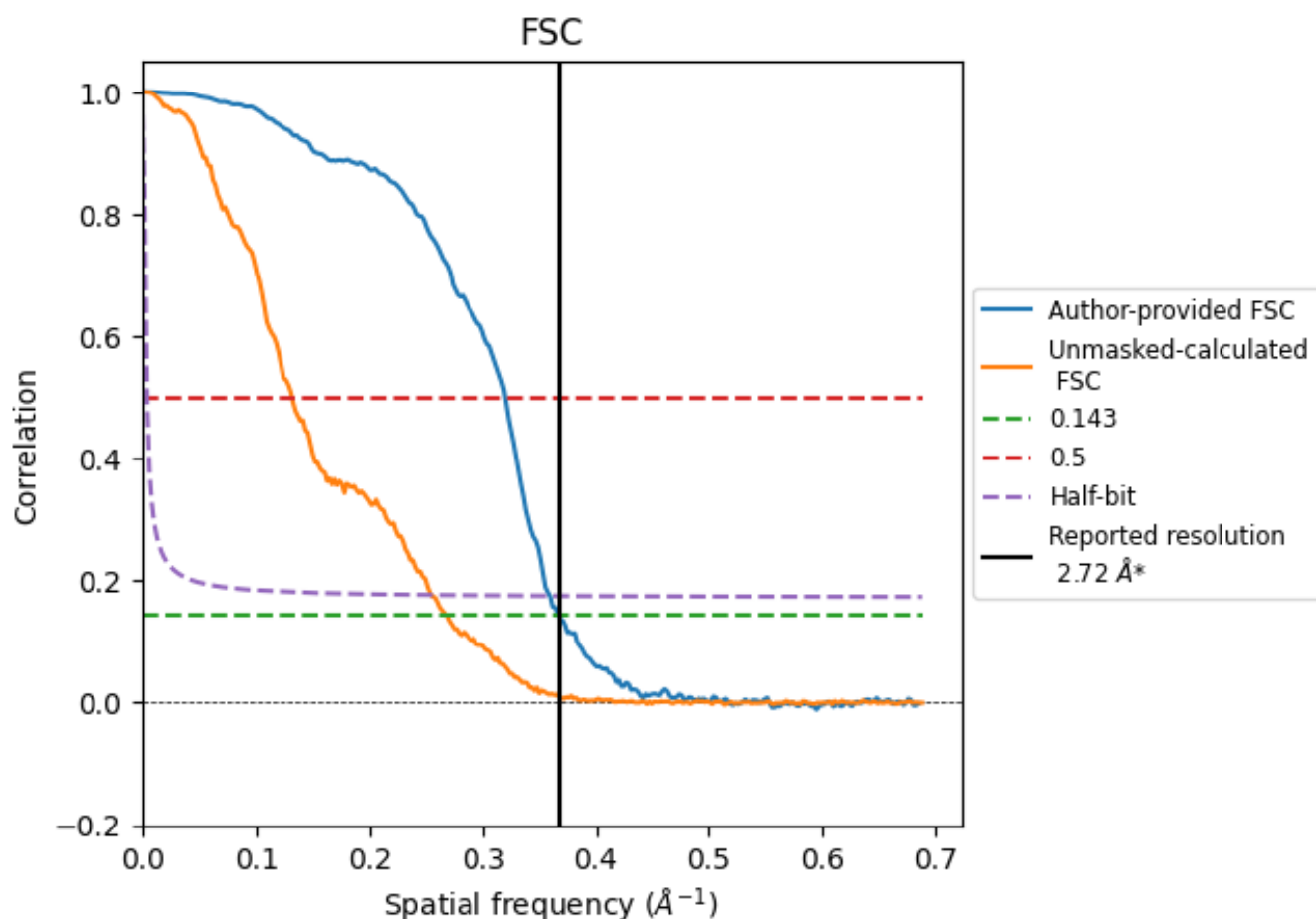


*Reported resolution corresponds to spatial frequency of 0.368 Å⁻¹

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 0.368 Å⁻¹

8.2 Resolution estimates [i](#)

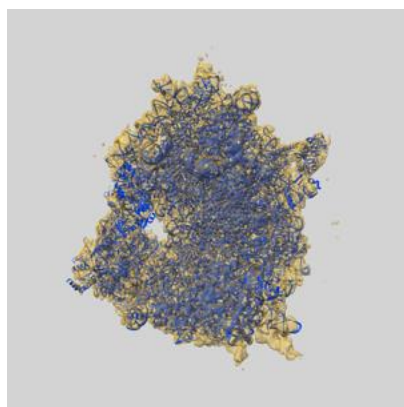
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.72	-	-
Author-provided FSC curve	2.72	3.12	2.78
Unmasked-calculated*	3.73	7.56	3.93

*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 3.73 differs from the reported value 2.72 by more than 10 %

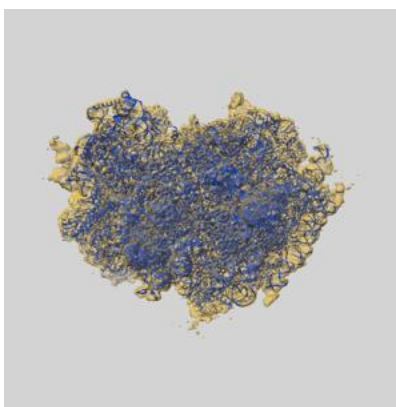
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-53944 and PDB model 9RG7. Per-residue inclusion information can be found in section [3](#) on page [21](#).

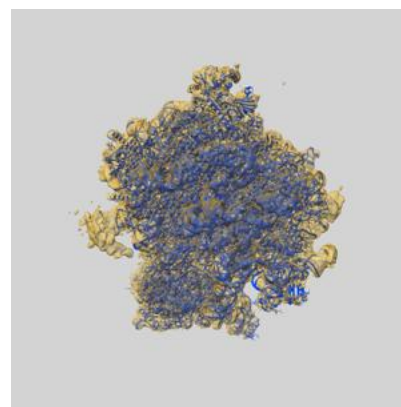
9.1 Map-model overlay [i](#)



X



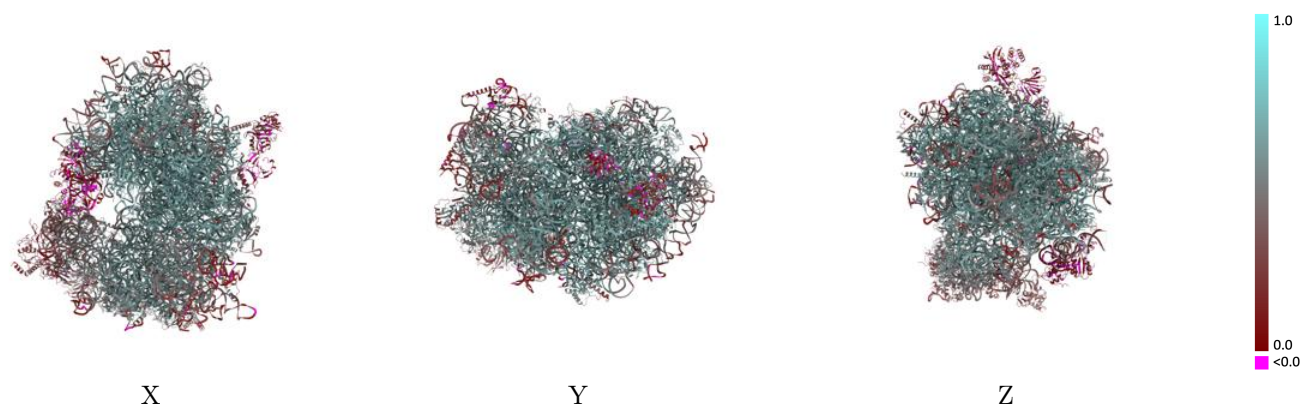
Y



Z

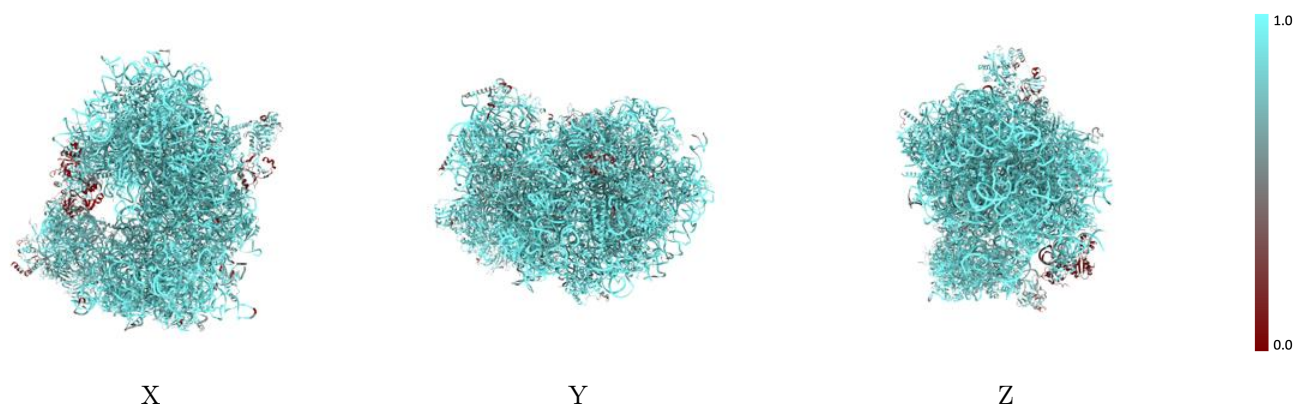
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



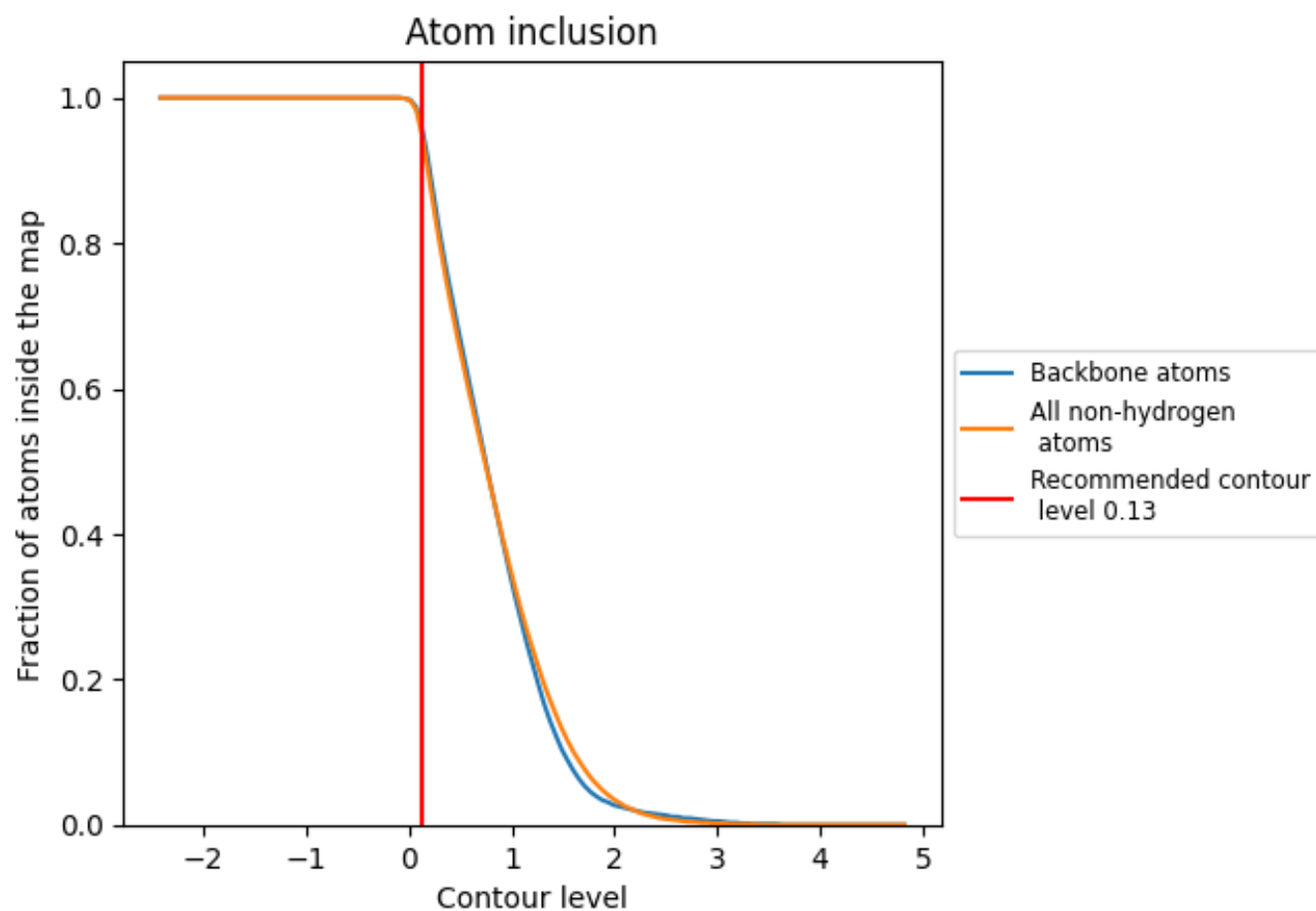
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.13).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9470	 0.5340
L5	 0.9750	 0.5660
L7	 0.9970	 0.6200
L8	 0.9790	 0.6030
LA	 0.9910	 0.6550
LB	 0.9800	 0.6260
LC	 0.9780	 0.6300
LD	 0.9750	 0.5700
LE	 0.9750	 0.5800
LF	 0.9870	 0.6360
LG	 0.9230	 0.5390
LH	 0.9750	 0.5940
LI	 0.9800	 0.6120
LJ	 0.9390	 0.5140
LL	 0.9780	 0.6040
LM	 0.9740	 0.6050
LN	 0.9960	 0.6560
LO	 0.9880	 0.6360
LP	 0.9880	 0.6440
LQ	 0.9910	 0.6520
LR	 0.9430	 0.5840
LS	 0.9910	 0.6420
LT	 0.9700	 0.6090
LU	 0.9470	 0.5400
LV	 0.9840	 0.6280
LW	 0.8170	 0.4230
LX	 0.9730	 0.6060
LY	 0.9790	 0.6170
LZ	 0.9870	 0.6110
La	 0.9900	 0.6460
Lb	 0.9210	 0.5330
Lc	 0.9680	 0.6070
Ld	 0.9690	 0.6040
Le	 0.9920	 0.6500
Lf	 0.9930	 0.6570



















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Chain	Atom inclusion	Q-score
Lg	 0.9680	 0.6120
Lh	 0.9730	 0.6000
Li	 0.9670	 0.5810
Lj	 0.9910	 0.6470
Lk	 0.9370	 0.5340
Ll	 0.9930	 0.6400
Lm	 0.9640	 0.6050
Ln	 0.8280	 0.5350
Lo	 0.9590	 0.6070
Lp	 0.9780	 0.6270
Lr	 0.9840	 0.6310
Ls	 0.2110	 0.0890
Lt	 0.2720	 0.0700
N4	 0.8380	 0.1820
NA	 0.5260	 0.1200
NB	 0.5500	 0.2060
S2	 0.9690	 0.4980
SA	 0.9400	 0.5250
SB	 0.9370	 0.5360
SC	 0.9620	 0.5560
SD	 0.8420	 0.3770
SE	 0.9420	 0.5330
SF	 0.8780	 0.4040
SG	 0.8940	 0.4270
SH	 0.9050	 0.4590
SI	 0.9440	 0.5360
SJ	 0.9340	 0.5170
SK	 0.8280	 0.3070
SL	 0.9490	 0.5720
SM	 0.4620	 0.2250
SN	 0.9740	 0.5890
SO	 0.9410	 0.5530
SP	 0.7940	 0.2940
SQ	 0.8950	 0.3960
SR	 0.8990	 0.4360
SS	 0.8480	 0.3220
ST	 0.8940	 0.3700
SU	 0.8510	 0.3630
SV	 0.9440	 0.5220
SW	 0.9720	 0.5910
SX	 0.9540	 0.5700
SY	 0.9200	 0.4650

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Chain	Atom inclusion	Q-score
SZ	 0.7980	 0.2670
Sa	 0.9330	 0.5460
Sb	 0.9360	 0.5290
Sc	 0.9010	 0.4180
Sd	 0.9160	 0.4210
Se	 0.8360	 0.4520
Sf	 0.5750	 0.1840
Sg	 0.8720	 0.2870