



wwPDB EM Validation Summary Report ⓘ

Sep 23, 2026 – 06:48 pm BST

PDB ID : 9T69 / pdb_00009t69
EMDB ID : EMD-55610
Title : In vitro reconstituted METAP1-NAA40-NAC bound 80S - State 1
Authors : Guan, D.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-11-07
Resolution : 3.54 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:

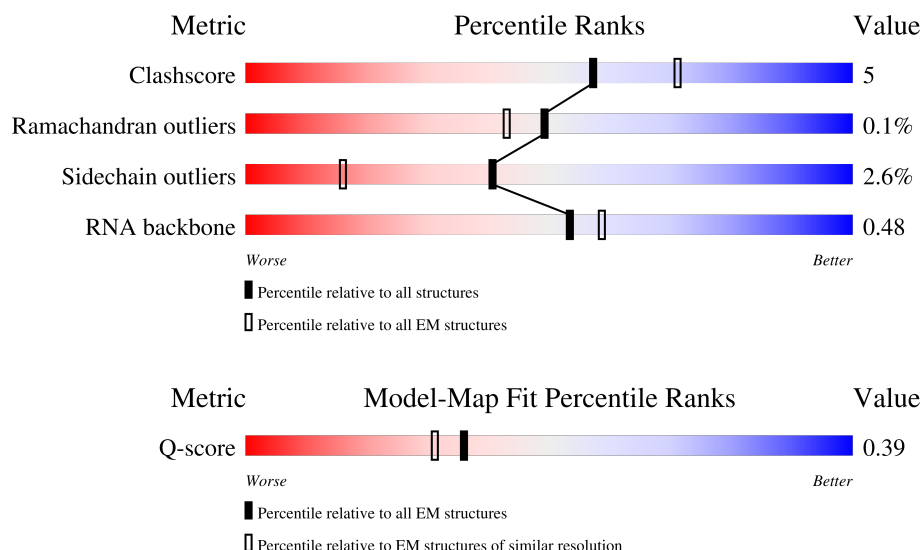
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

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

The reported resolution of this entry is 3.54 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.



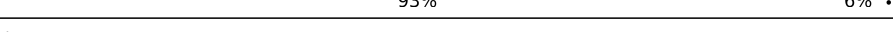
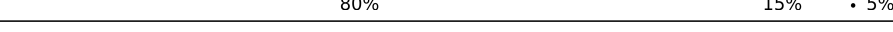
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12891 (3.04 - 4.04)

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	L5	5070	
2	L7	121	
3	L8	157	

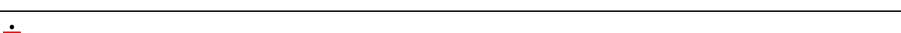
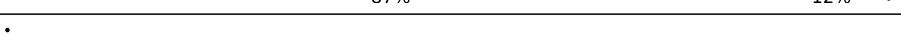
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

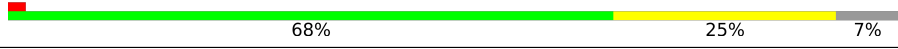
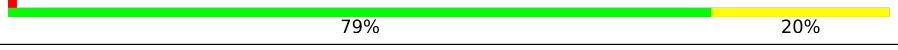
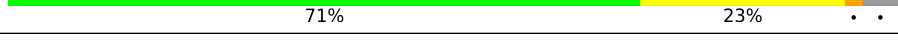
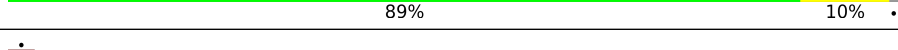
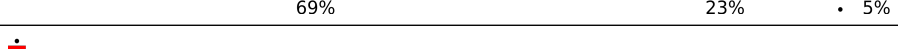
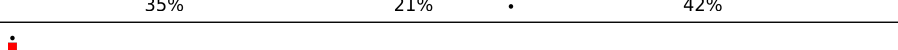
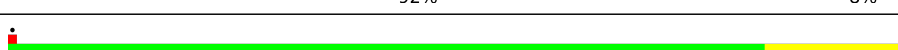
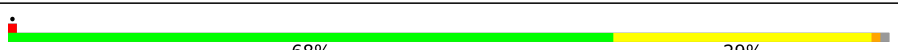
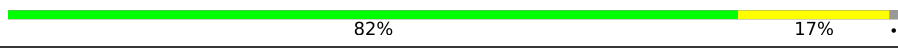
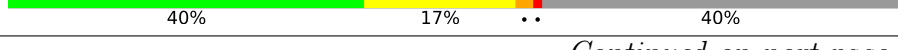
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Ls	317	
47	Lt	165	
48	MA	386	
49	N4	237	
50	NA	215	
51	NB	162	
52	S2	1869	
53	SA	295	

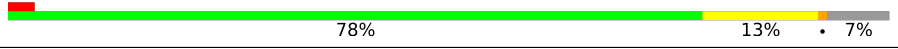
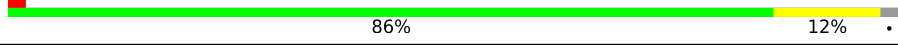
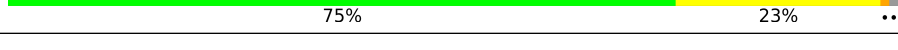
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Mol	Chain	Length	Quality of chain
54	SB	264	
55	SC	293	
56	SD	243	
57	SE	263	
58	SF	204	
59	SG	249	
60	SH	194	
61	SI	208	
62	SJ	194	
63	SK	165	
64	SL	158	
65	SM	132	
66	SN	151	
67	SO	151	
68	SP	145	
69	SQ	146	
70	SR	135	
71	SS	152	
72	ST	145	
73	SU	119	
74	SV	83	
75	SW	130	
76	SX	143	
77	SY	133	
78	SZ	125	

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Mol	Chain	Length	Quality of chain
79	Sa	115	
80	Sb	84	
81	Sc	69	
82	Sd	56	
83	Se	133	
84	Sf	156	
85	Sg	317	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 221535 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3670	Total	C	N	O	P	0	0
			78678	35036	14400	25573	3669		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	2113	C	G	conflict	GB 86475748

- Molecule 2 is a RNA chain called 5S rRNA.

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

- Molecule 3 is a RNA chain called 5.8S rRNA.

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

- Molecule 4 is a protein called 60S ribosomal protein L8.

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

- Molecule 5 is a protein called 60S ribosomal protein L3.

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

- Molecule 6 is a protein called 60S ribosomal protein L4.

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

- Molecule 7 is a protein called 60S ribosomal protein L5.

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

- Molecule 8 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 9 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 10 is a protein called 60S ribosomal protein L7a.

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

- Molecule 11 is a protein called 60S ribosomal protein L9.

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

- Molecule 12 is a protein called 60S ribosomal protein L10.

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

- Molecule 13 is a protein called 60S ribosomal protein L11.

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

- Molecule 14 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 15 is a protein called 60S ribosomal protein L14.

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

- Molecule 16 is a protein called 60S ribosomal protein L15.

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

- Molecule 17 is a protein called 60S ribosomal protein L13a.

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

- Molecule 18 is a protein called 60S ribosomal protein L17.

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

- Molecule 19 is a protein called 60S ribosomal protein L18.

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

- Molecule 20 is a protein called 60S ribosomal protein L19.

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

- Molecule 21 is a protein called 60S ribosomal protein L18a.

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

- Molecule 22 is a protein called 60S ribosomal protein L21.

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

- Molecule 23 is a protein called 60S ribosomal protein L22.

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

- Molecule 24 is a protein called 60S ribosomal protein L23.

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

- Molecule 25 is a protein called 60S ribosomal protein L24.

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

- Molecule 26 is a protein called 60S ribosomal protein L23a.

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

- Molecule 27 is a protein called 60S ribosomal protein L26.

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

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

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

- Molecule 30 is a protein called 60S ribosomal protein L29.

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

- Molecule 31 is a protein called 60S ribosomal protein L30.

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

- Molecule 32 is a protein called 60S ribosomal protein L31.

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

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

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

- Molecule 36 is a protein called 60S ribosomal protein L35.

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

- Molecule 37 is a protein called 60S ribosomal protein L36.

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 42 is a protein called 60S ribosomal protein L41.

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

- Molecule 43 is a protein called 60S ribosomal protein L36a.

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

- Molecule 44 is a protein called 60S ribosomal protein L37a.

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

- Molecule 45 is a protein called 60S ribosomal protein L28.

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

- Molecule 46 is a protein called 60S acidic ribosomal protein P0.

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

- Molecule 47 is a protein called Large ribosomal subunit protein uL11.

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

- Molecule 48 is a protein called Methionine aminopeptidase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	MA	315	Total	C	N	O	S	0	0
			2485	1562	443	462	18		

- Molecule 49 is a protein called N-alpha-acetyltransferase 40.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	N4	222	Total	C	N	O	S	0	0
			1805	1134	316	340	15		

- Molecule 50 is a protein called Nascent polypeptide-associated complex subunit alpha.

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

- Molecule 51 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	NB	105	Total	C	N	O	S	0	0
			813	508	152	150	3		

- Molecule 52 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	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 53 is a protein called 40S ribosomal protein SA.

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

- Molecule 54 is a protein called 40S ribosomal protein S3a.

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

- Molecule 55 is a protein called 40S ribosomal protein S2.

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

- Molecule 56 is a protein called 40S ribosomal protein S3.

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

- Molecule 57 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 58 is a protein called 40S ribosomal protein S5.

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

- Molecule 59 is a protein called 40S ribosomal protein S6.

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

- Molecule 60 is a protein called 40S ribosomal protein S7.

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

- Molecule 61 is a protein called 40S ribosomal protein S8.

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

- Molecule 62 is a protein called 40S ribosomal protein S9.

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

- Molecule 63 is a protein called 40S ribosomal protein S10.

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

- Molecule 64 is a protein called 40S ribosomal protein S11.

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

- Molecule 65 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms				AltConf	Trace
65	SM	122	Total	C	N	O	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 66 is a protein called 40S ribosomal protein S13.

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

- Molecule 67 is a protein called 40S ribosomal protein S14.

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

- Molecule 68 is a protein called 40S ribosomal protein S15.

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

- Molecule 69 is a protein called 40S ribosomal protein S16.

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

- Molecule 70 is a protein called 40S ribosomal protein S17.

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

- Molecule 71 is a protein called 40S ribosomal protein S18.

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

- Molecule 72 is a protein called 40S ribosomal protein S19.

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

- Molecule 73 is a protein called 40S ribosomal protein S20.

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

- Molecule 74 is a protein called 40S ribosomal protein S21.

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

- Molecule 75 is a protein called 40S ribosomal protein S15a.

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

- Molecule 76 is a protein called 40S ribosomal protein S23.

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

- Molecule 77 is a protein called 40S ribosomal protein S24.

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

- Molecule 78 is a protein called 40S ribosomal protein S25.

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

- Molecule 79 is a protein called 40S ribosomal protein S26.

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

- Molecule 80 is a protein called 40S ribosomal protein S27.

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

- Molecule 81 is a protein called 40S ribosomal protein S28.

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

- Molecule 82 is a protein called 40S ribosomal protein S29.

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

- Molecule 83 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

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

- Molecule 84 is a protein called Ubiquitin.

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

- Molecule 85 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 86 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
86	L5	214	Total	Mg	0
			214	214	
86	L7	3	Total	Mg	0
			3	3	
86	L8	4	Total	Mg	0
			4	4	
86	LA	1	Total	Mg	0
			1	1	
86	LI	1	Total	Mg	0
			1	1	
86	LP	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
86	LV	1	Total 1	Mg 1	0
86	Le	1	Total 1	Mg 1	0
86	Lj	1	Total 1	Mg 1	0
86	S2	27	Total 27	Mg 27	0
86	SG	1	Total 1	Mg 1	0
86	Sa	1	Total 1	Mg 1	0

- Molecule 87 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

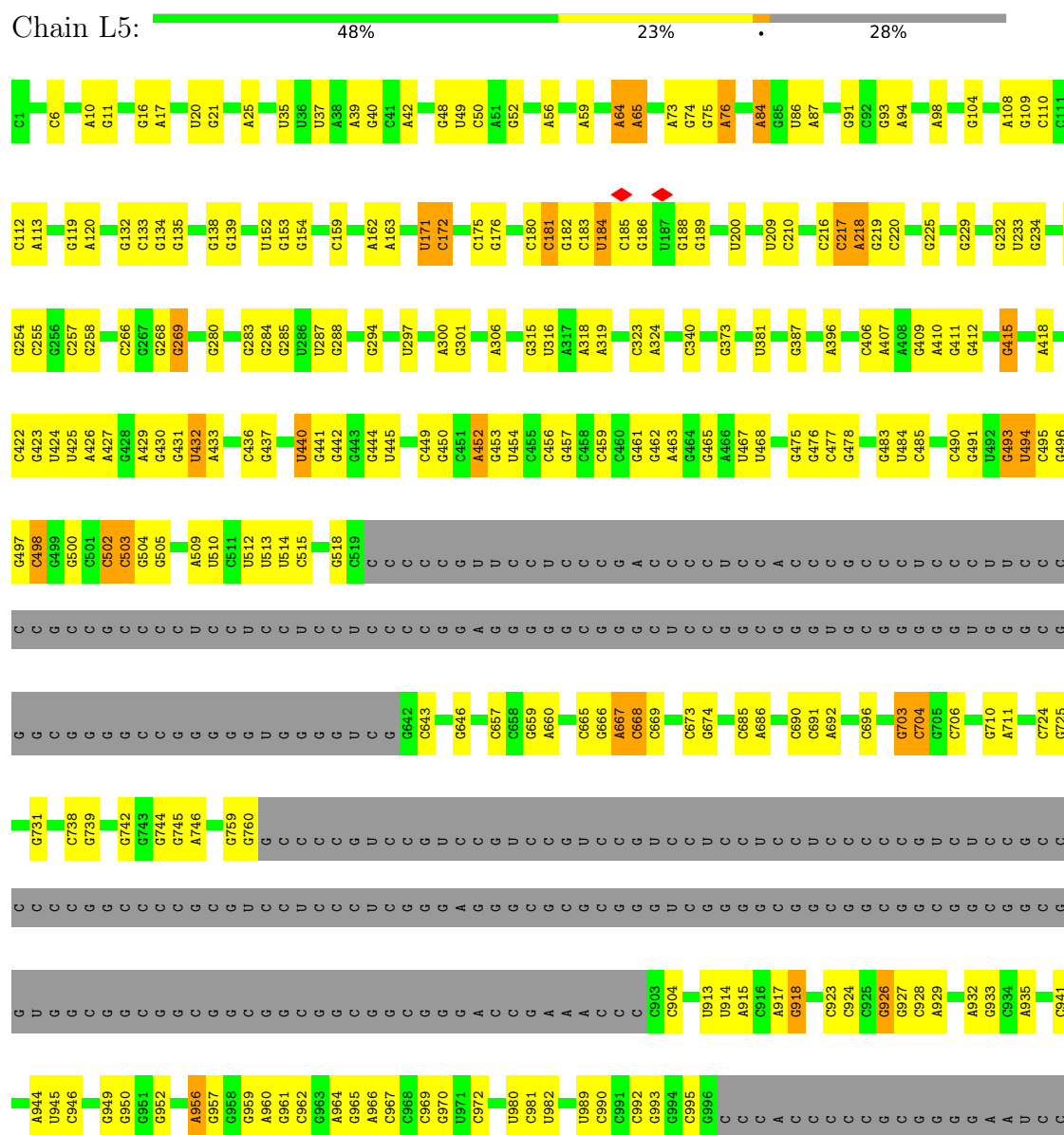
- Molecule 88 is water.

Mol	Chain	Residues	Atoms		AltConf
88	L5	3	Total 3	O 3	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: 28S rRNA

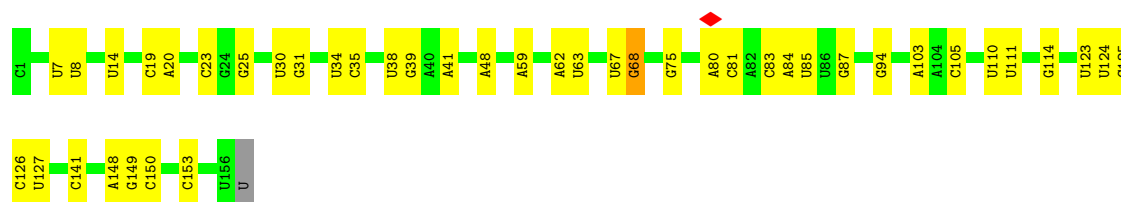




[illegible]

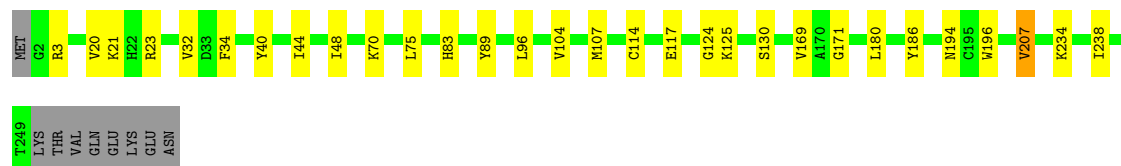


Chain L8:  72% 27% ..



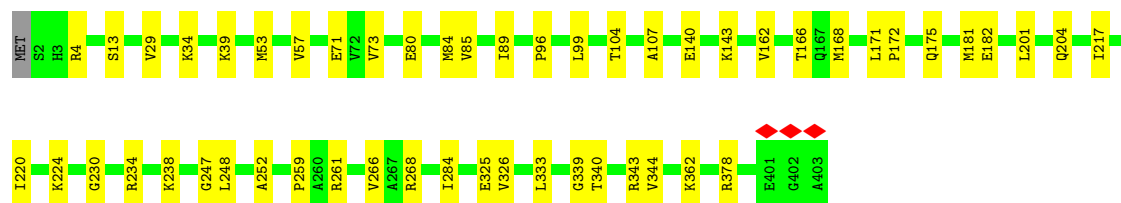
- Molecule 4: 60S ribosomal protein L8

Chain LA:  85% 11% .



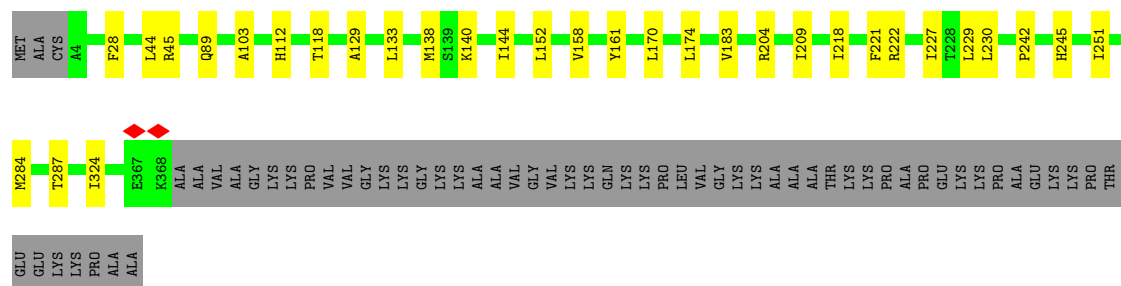
- Molecule 5: 60S ribosomal protein L3

Chain LB:  87% 13%



- Molecule 6: 60S ribosomal protein L4

Chain LC:  78% 7% 15%

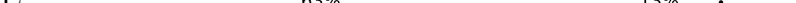


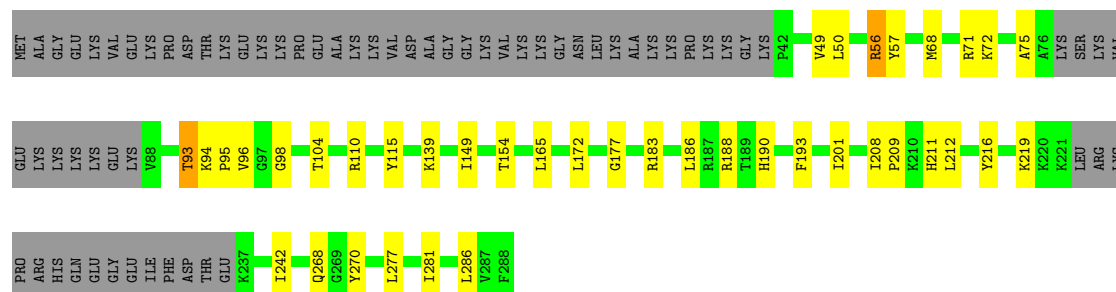
- Molecule 7: 60S ribosomal protein L5

Chain LD:  85% 12% ..

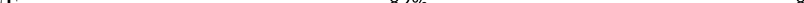


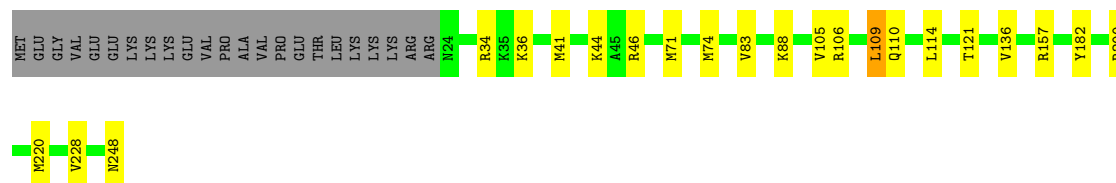
- Molecule 8: Large ribosomal subunit protein eL6

Chain LE: 

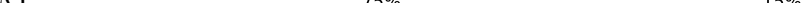


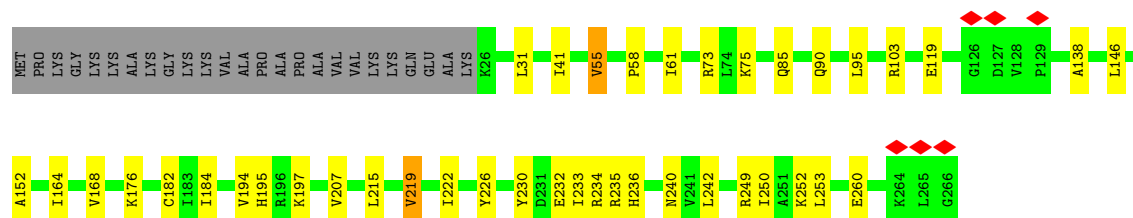
- Molecule 9: Large ribosomal subunit protein uL30

Chain LF: 

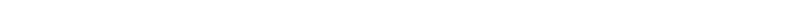


- Molecule 10: 60S ribosomal protein L7a

Chain LG:  75% 15% 9%



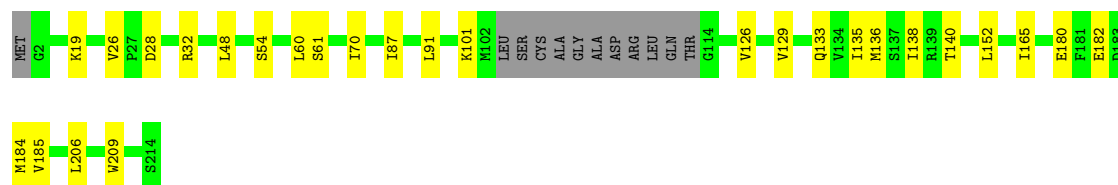
- Molecule 11: 60S ribosomal protein L9

Chain LH:  87% 12%



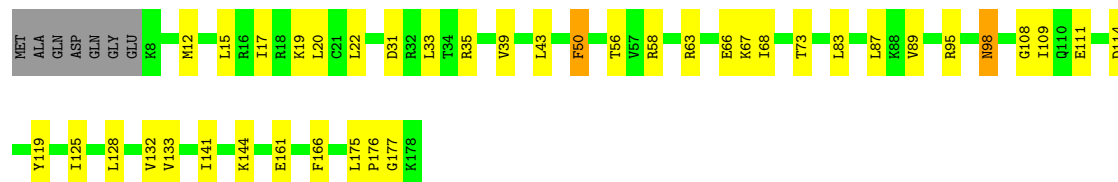
- Molecule 12: 60S ribosomal protein L10

Chain LI: 



- Molecule 13: 60S ribosomal protein L11

Chain LJ: 74% 21% . .



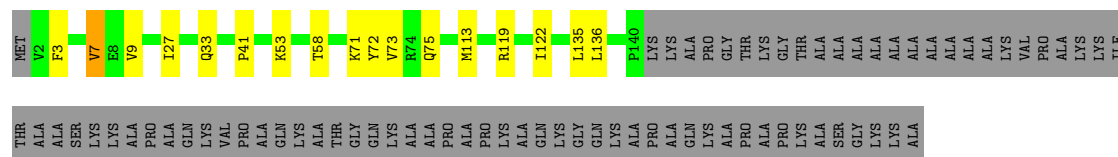
- Molecule 14: Large ribosomal subunit protein eL13

Chain LL: 89% 9% .



- Molecule 15: 60S ribosomal protein L14

Chain LM: 57% 7% 35%



- Molecule 16: 60S ribosomal protein L15

Chain LN: 86% 13%



- Molecule 17: 60S ribosomal protein L13a

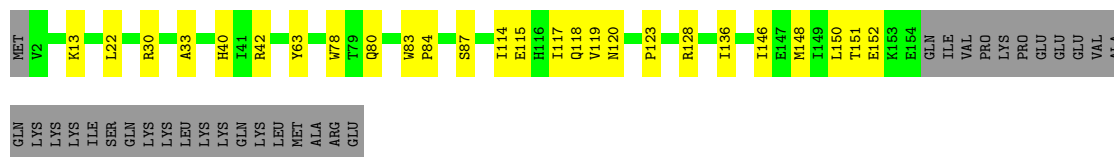
Chain LO: 85% 14% .





- Molecule 18: 60S ribosomal protein L17

Chain LP: 69% 14% 17%



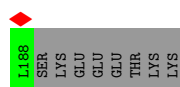
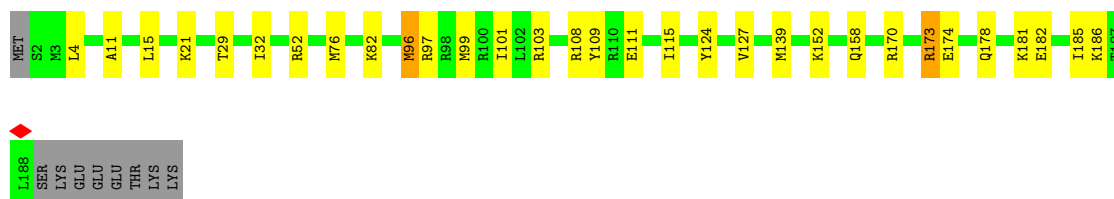
- Molecule 19: 60S ribosomal protein L18

Chain LQ: 93% 6% ..



- Molecule 20: 60S ribosomal protein L19

Chain LR: 80% 15% 5%



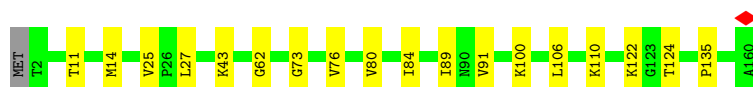
- Molecule 21: 60S ribosomal protein L18a

Chain LS: 84% 15% ..



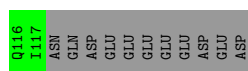
- Molecule 22: 60S ribosomal protein L21

Chain LT: 88% 11% .



- Molecule 23: 60S ribosomal protein L22

Chain LU: 59% 17% 22%



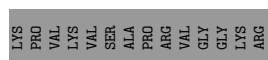
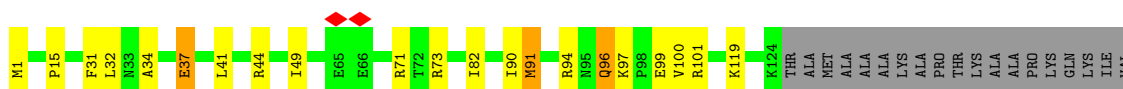
- Molecule 24: 60S ribosomal protein L23

Chain LV: 76% 16% 6%



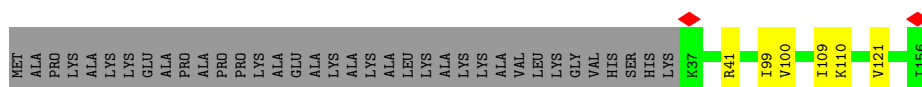
- Molecule 25: 60S ribosomal protein L24

Chain LW: 66% 11% 21%



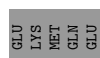
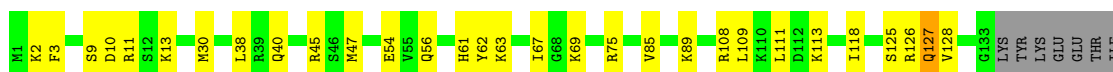
- Molecule 26: 60S ribosomal protein L23a

Chain LX: 73% 23%



- Molecule 27: 60S ribosomal protein L26

Chain LY: 71% 20% 8%



- Molecule 28: 60S ribosomal protein L27

Chain LZ: 89% 10%



- Molecule 29: 60S ribosomal protein L27a

Chain La: 81% 17%





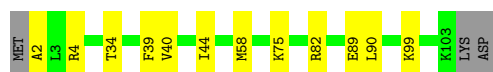
- Molecule 36: 60S ribosomal protein L35

Chain Lh: 85% 14% ..



- Molecule 37: 60S ribosomal protein L36

Chain Li: 86% 11% .



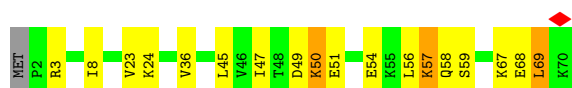
- Molecule 38: Large ribosomal subunit protein eL37

Chain Lj: 82% 6% 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk: 73% 21% . .



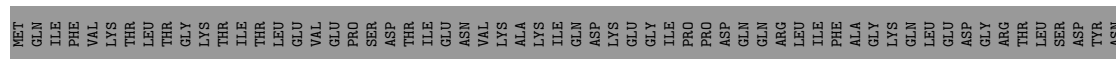
- Molecule 40: 60S ribosomal protein L39

Chain Ll: 92% 6% .

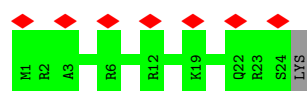


- Molecule 41: Large ribosomal subunit protein eL40

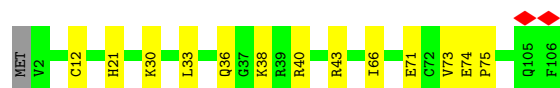
Chain Lm: 38% 59%



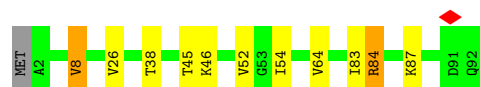
- Molecule 42: 60S ribosomal protein L41



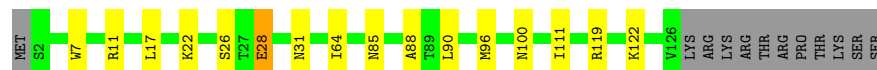
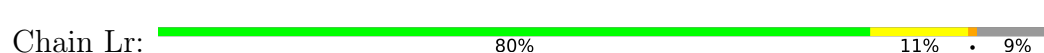
- Molecule 43: 60S ribosomal protein L36a



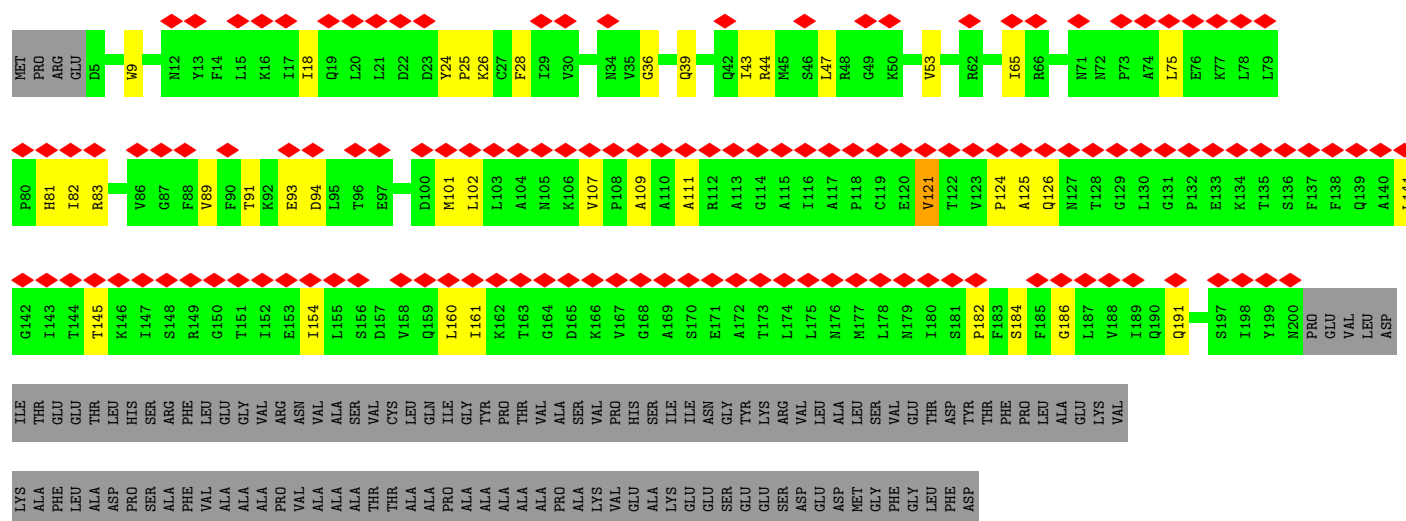
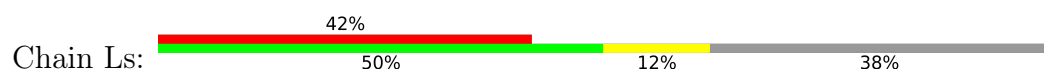
- Molecule 44: 60S ribosomal protein L37a



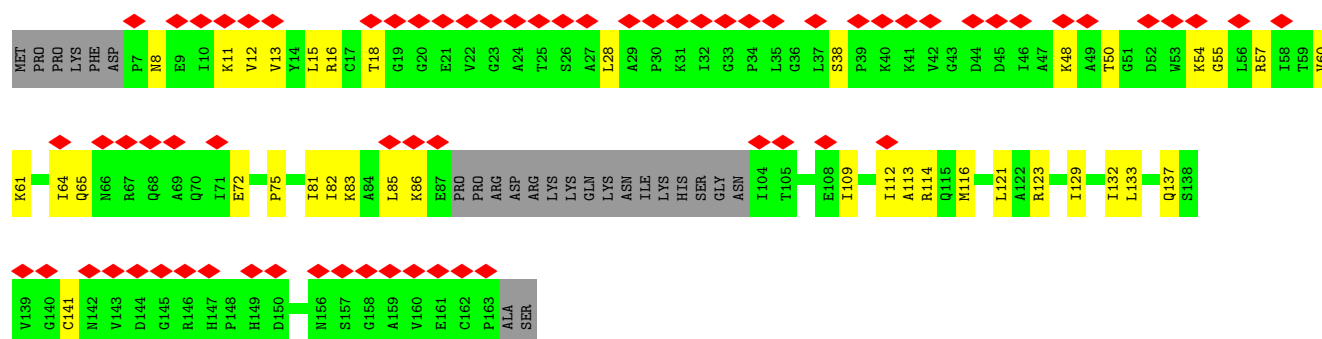
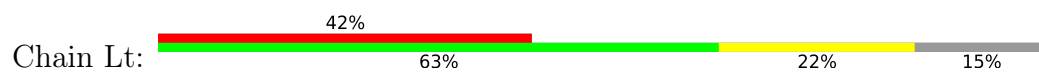
- Molecule 45: 60S ribosomal protein L28



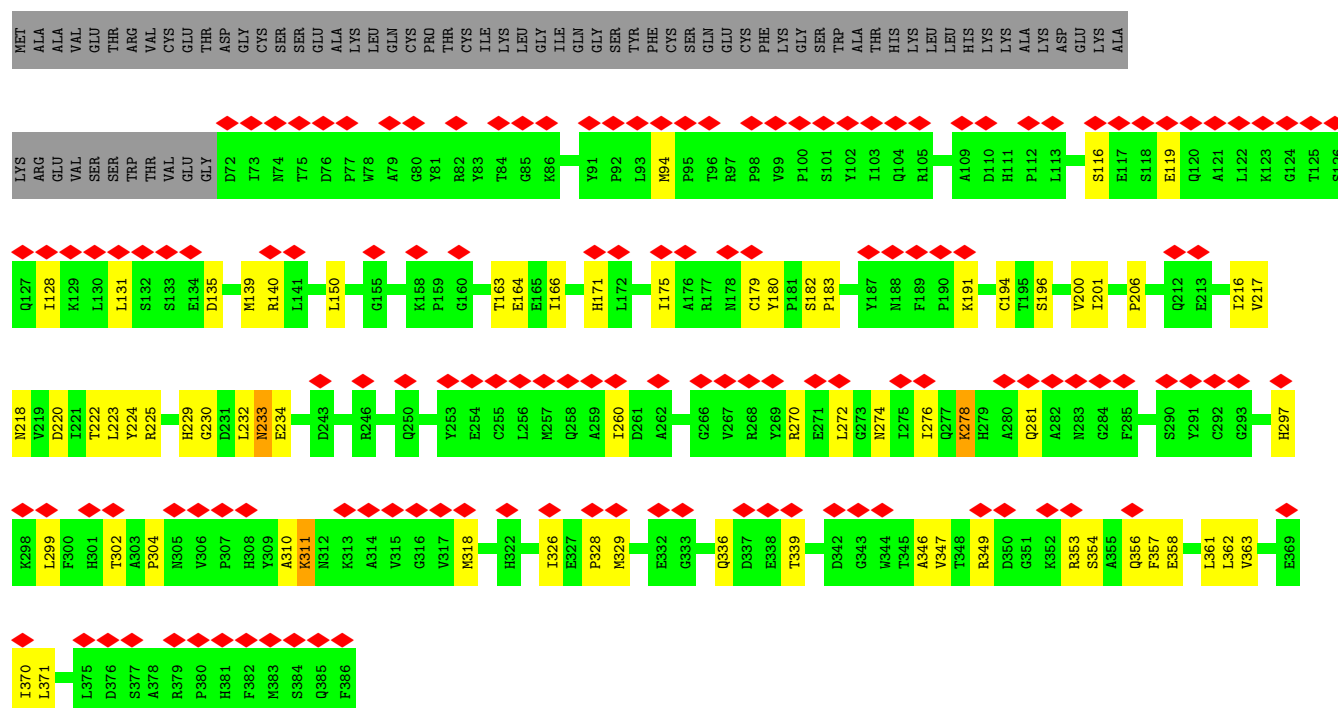
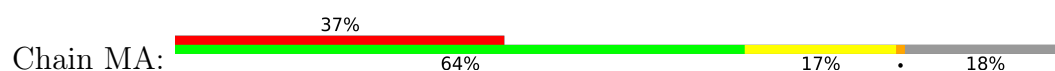
- Molecule 46: 60S acidic ribosomal protein P0



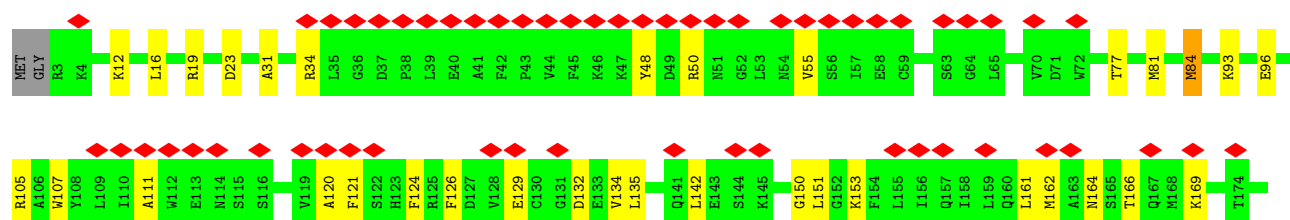
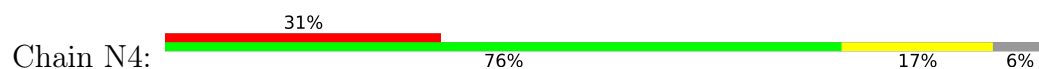
- Molecule 47: Large ribosomal subunit protein uL11



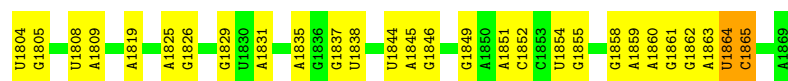
• Molecule 48: Methionine aminopeptidase 1



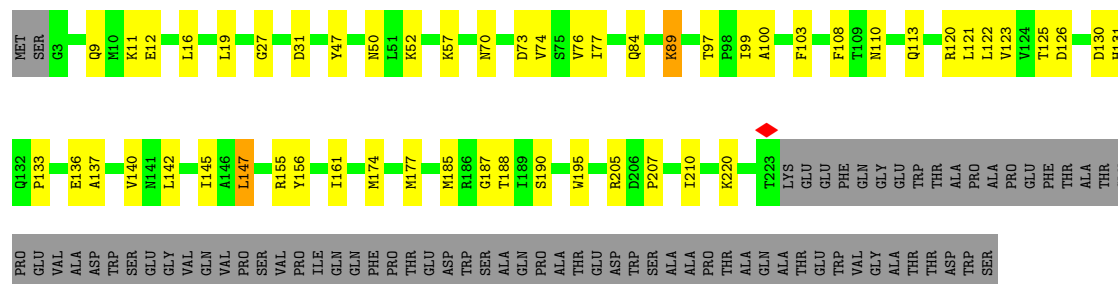
• Molecule 49: N-alpha-acetyltransferase 40



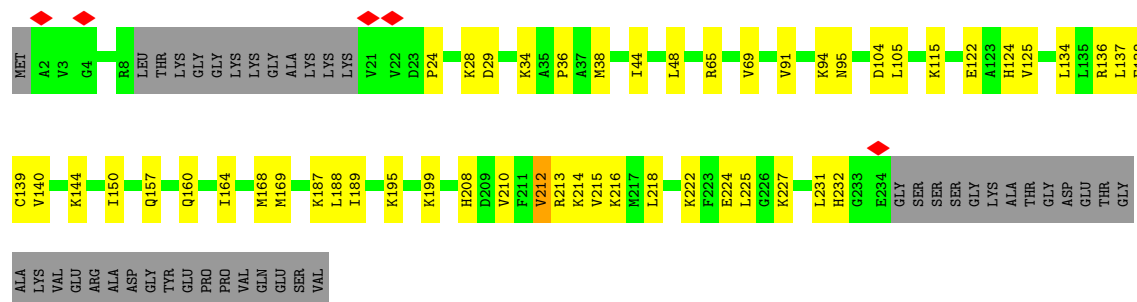
WORLDWIDE
PDB
PROTEIN DATA BANK



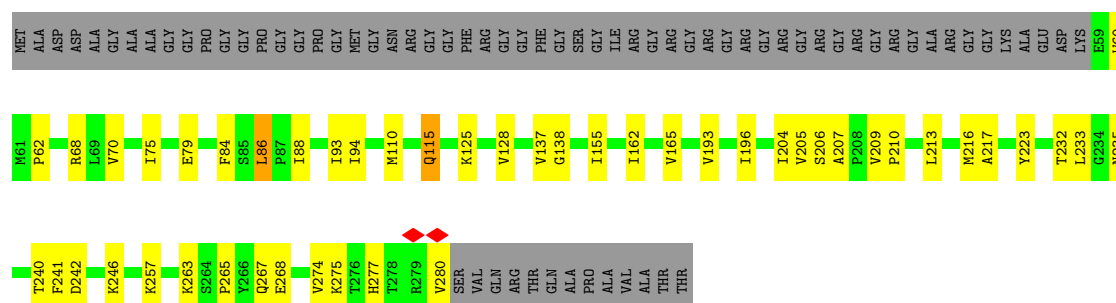
- Molecule 53: 40S ribosomal protein SA



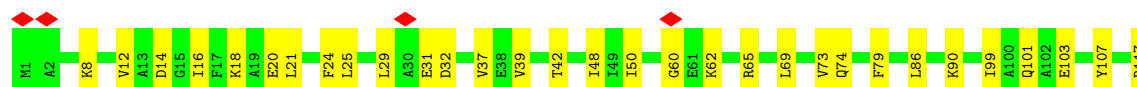
- Molecule 54: 40S ribosomal protein S3a

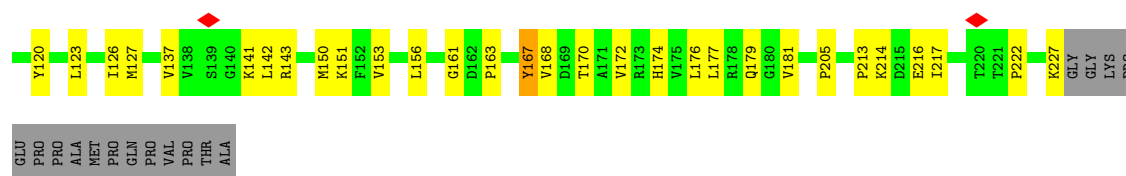


- Molecule 55: 40S ribosomal protein S2

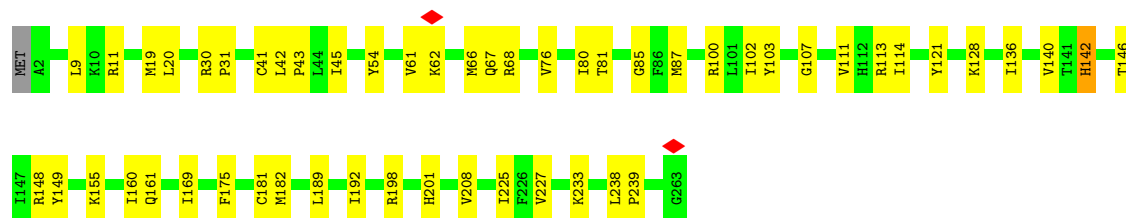
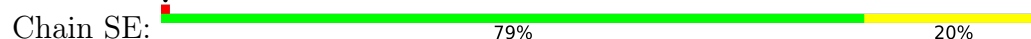


- Molecule 56: 40S ribosomal protein S3

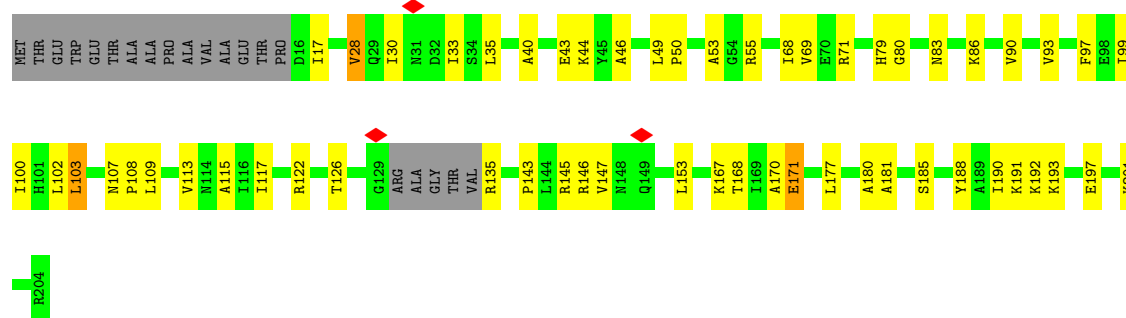




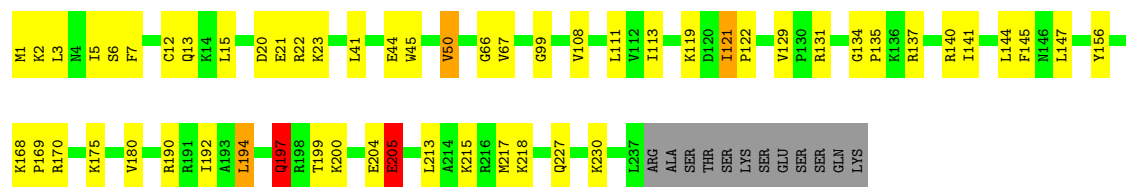
- Molecule 57: Small ribosomal subunit protein eS4, X isoform



- Molecule 58: 40S ribosomal protein S5



- Molecule 59: 40S ribosomal protein S6



- Molecule 60: 40S ribosomal protein S7





- Molecule 61: 40S ribosomal protein S8

Chain SI: 89% 10%



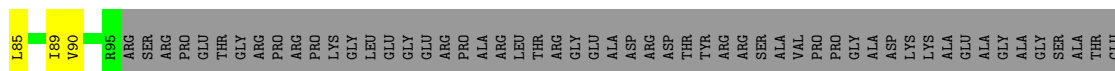
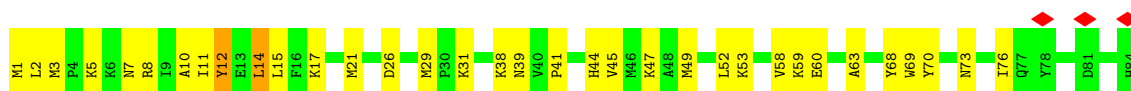
- Molecule 62: 40S ribosomal protein S9

Chain SJ: 69% 23% 5%



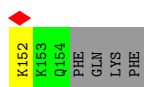
- Molecule 63: 40S ribosomal protein S10

Chain SK: 35% 21% 42%



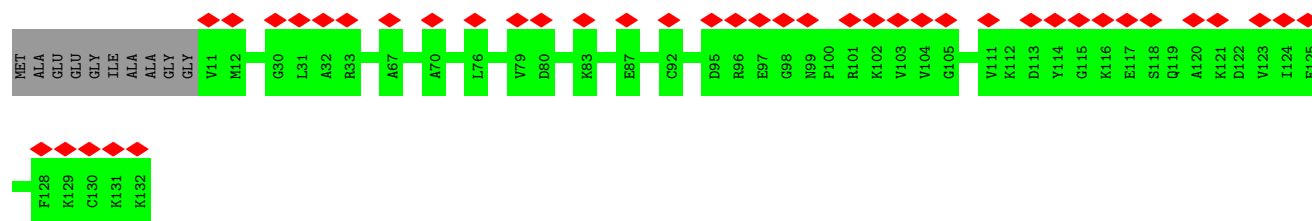
- Molecule 64: 40S ribosomal protein S11

Chain SL: 73% 17% 9%

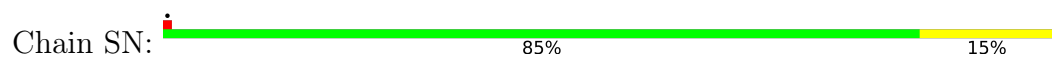


- Molecule 65: 40S ribosomal protein S12

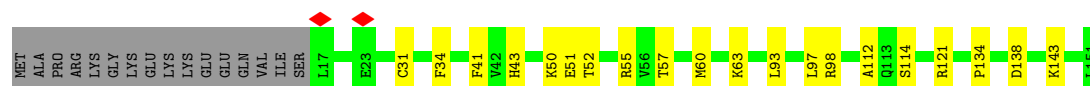
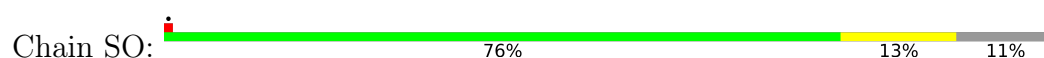
Chain SM: 31% 92% 8%



- Molecule 66: 40S ribosomal protein S13



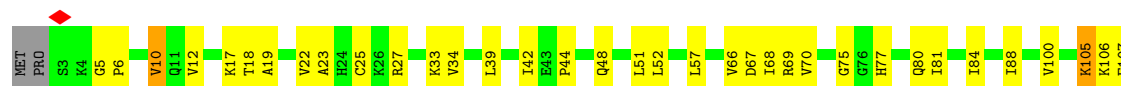
- Molecule 67: 40S ribosomal protein S14



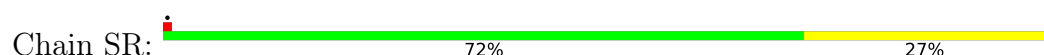
- Molecule 68: 40S ribosomal protein S15

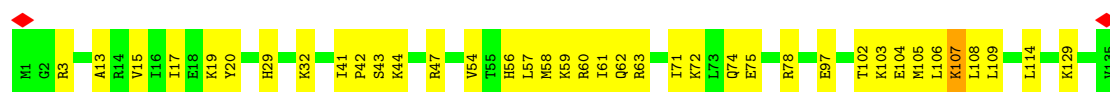


- Molecule 69: 40S ribosomal protein S16

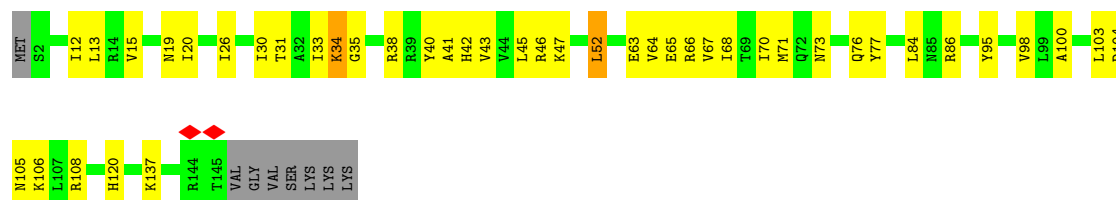


- Molecule 70: 40S ribosomal protein S17

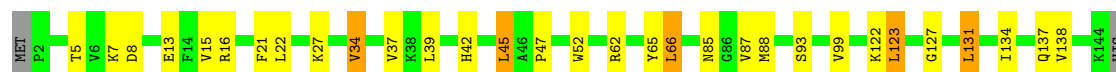
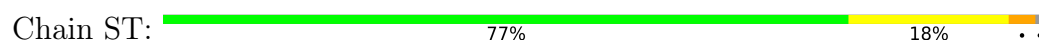




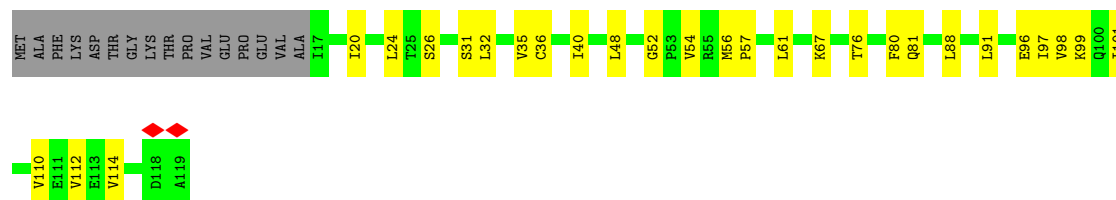
- Molecule 71: 40S ribosomal protein S18



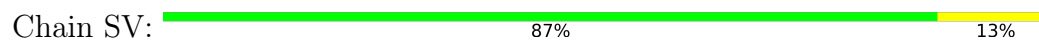
- Molecule 72: 40S ribosomal protein S19



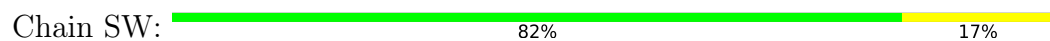
- Molecule 73: 40S ribosomal protein S20



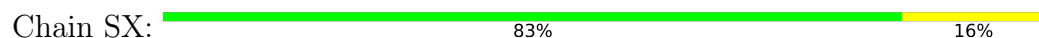
- Molecule 74: 40S ribosomal protein S21

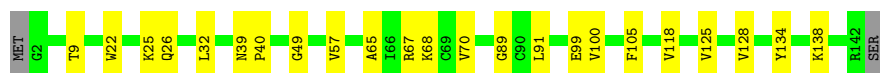


- Molecule 75: 40S ribosomal protein S15a

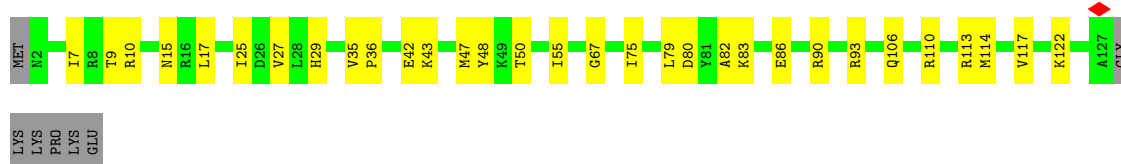


- Molecule 76: 40S ribosomal protein S23

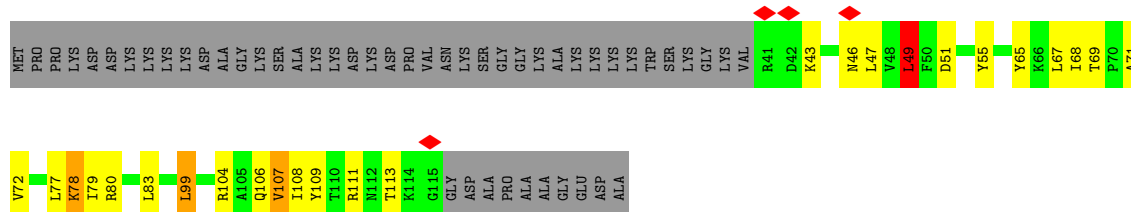




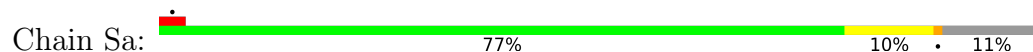
- Molecule 77: 40S ribosomal protein S24



- Molecule 78: 40S ribosomal protein S25



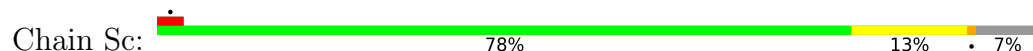
- Molecule 79: 40S ribosomal protein S26



- Molecule 80: 40S ribosomal protein S27

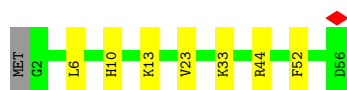


- Molecule 81: 40S ribosomal protein S28



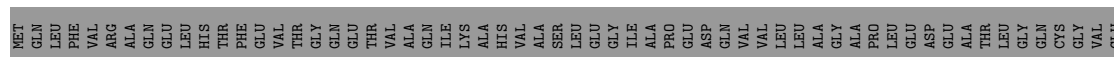
- Molecule 82: 40S ribosomal protein S29





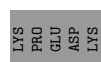
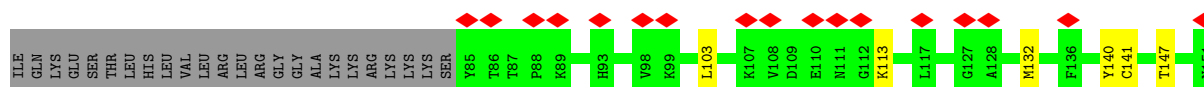
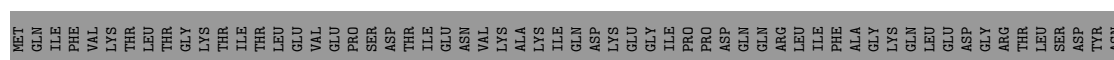
- Molecule 83: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

Chain Se: 36% 8% 56%



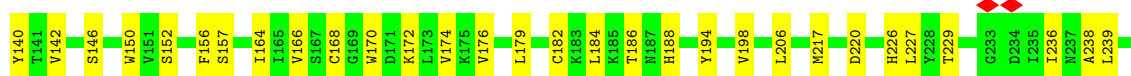
- Molecule 84: Ubiquitin

Chain Sf: 11% 39% 0% 57%



- Molecule 85: Receptor of activated protein C kinase 1

Chain Sg: 75% 23% 2%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11809	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	2.038	Depositor
Minimum map value	-1.371	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.070	Depositor
Recommended contour level	0.11	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

5.1 Standard geometry

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

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	L5	0.14	0/88012	0.33	0/137296
2	L7	0.14	0/2861	0.30	0/4459
3	L8	0.14	0/3701	0.32	0/5766
4	LA	0.20	0/1936	0.52	0/2596
5	LB	0.19	0/3306	0.49	1/4424 (0.0%)
6	LC	0.18	0/2962	0.45	0/3977
7	LD	0.22	0/2428	0.58	2/3252 (0.1%)
8	LE	0.23	0/1808	0.55	1/2425 (0.0%)
9	LF	0.20	0/1905	0.50	0/2539
10	LG	0.28	0/1960	0.74	5/2637 (0.2%)
11	LH	0.24	0/1537	0.56	0/2066
12	LI	0.17	0/1677	0.48	0/2237
13	LJ	0.27	0/1394	0.67	1/1863 (0.1%)
14	LL	0.22	0/1704	0.58	0/2282
15	LM	0.23	0/1161	0.60	2/1554 (0.1%)
16	LN	0.17	0/1746	0.43	0/2338
17	LO	0.19	0/1682	0.50	0/2250
18	LP	0.20	0/1268	0.46	0/1701
19	LQ	0.18	0/1537	0.45	0/2052
20	LR	0.23	0/1582	0.61	4/2091 (0.2%)
21	LS	0.21	0/1493	0.53	1/2003 (0.0%)
22	LT	0.19	0/1326	0.50	0/1770
23	LU	0.46	1/830 (0.1%)	0.76	2/1114 (0.2%)
24	LV	0.22	0/993	0.58	2/1332 (0.2%)
25	LW	0.22	0/1030	0.58	0/1364
26	LX	0.16	0/1002	0.42	0/1345
27	LY	0.21	0/1123	0.58	1/1493 (0.1%)
28	LZ	0.20	0/1130	0.50	0/1507
29	La	0.17	0/1191	0.44	0/1591
30	Lb	0.23	0/895	0.63	0/1182
31	Lc	0.20	0/774	0.54	0/1038
32	Ld	0.20	0/903	0.51	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.20	0/1071	0.54	0/1429
34	Lf	0.14	0/895	0.37	0/1198
35	Lg	0.18	0/916	0.50	0/1220
36	Lh	0.22	0/1023	0.62	1/1351 (0.1%)
37	Li	0.24	0/843	0.61	1/1115 (0.1%)
38	Lj	0.16	0/720	0.44	0/952
39	Lk	0.31	0/575	0.90	5/761 (0.7%)
40	Ll	0.19	0/454	0.45	0/599
41	Lm	0.20	0/425	0.54	0/561
42	Ln	0.14	0/231	0.37	0/294
43	Lo	0.20	0/876	0.49	0/1156
44	Lp	0.18	0/718	0.49	0/953
45	Lr	0.27	0/1017	0.54	0/1364
46	Ls	0.21	0/1519	0.56	0/2052
47	Lt	0.25	0/1058	0.73	2/1430 (0.1%)
48	MA	0.22	0/2549	0.57	1/3462 (0.0%)
49	N4	0.22	0/1842	0.60	0/2471
50	NA	0.19	0/845	0.50	0/1128
51	NB	0.24	0/821	0.67	0/1101
52	S2	0.14	0/40751	0.32	0/63496
53	SA	0.30	0/1778	0.72	2/2416 (0.1%)
54	SB	0.24	0/1817	0.67	1/2428 (0.0%)
55	SC	0.22	0/1762	0.57	0/2381
56	SD	0.21	0/1793	0.55	0/2414
57	SE	0.22	0/2118	0.61	4/2849 (0.1%)
58	SF	0.30	0/1481	0.79	1/1988 (0.1%)
59	SG	0.25	0/1946	0.76	4/2590 (0.2%)
60	SH	0.30	0/1519	0.72	2/2033 (0.1%)
61	SI	0.23	0/1715	0.58	2/2287 (0.1%)
62	SJ	0.24	0/1550	0.65	4/2069 (0.2%)
63	SK	0.32	0/823	0.87	0/1111
64	SL	0.26	0/1202	0.54	1/1606 (0.1%)
65	SM	0.10	0/603	0.29	0/837
66	SN	0.21	0/1232	0.56	0/1656
67	SO	0.21	0/1023	0.62	0/1372
68	SP	0.33	0/1082	0.99	7/1446 (0.5%)
69	SQ	0.29	0/1160	0.77	1/1553 (0.1%)
70	SR	0.30	0/1105	0.85	2/1484 (0.1%)
71	SS	0.29	0/1208	0.78	1/1618 (0.1%)
72	ST	0.29	0/1131	0.79	4/1515 (0.3%)
73	SU	0.28	0/827	0.71	0/1110
74	SV	0.19	0/643	0.56	0/860
75	SW	0.23	0/1051	0.53	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SX	0.21	0/1116	0.56	0/1490
77	SY	0.29	0/1044	0.77	4/1388 (0.3%)
78	SZ	0.31	0/604	0.87	0/810
79	Sa	0.24	0/836	0.67	1/1121 (0.1%)
80	Sb	0.22	0/665	0.56	0/891
81	Sc	0.25	0/508	0.65	0/680
82	Sd	0.29	0/470	0.64	0/623
83	Se	0.22	0/465	0.59	0/612
84	Sf	0.20	0/560	0.62	0/745
85	Sg	0.22	0/2493	0.61	1/3394 (0.0%)
All	All	0.18	1/237336 (0.0%)	0.46	74/347636 (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
8	LE	0	1
13	LJ	0	2
49	N4	0	1
53	SA	0	1
78	SZ	0	3
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	LU	94	ASN	CG-ND2	-6.24	1.20	1.33

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	SY	42	GLU	CA-CB-CG	7.95	130.00	114.10
57	SE	66	MET	CA-C-N	-7.83	109.66	122.65
57	SE	66	MET	C-N-CA	-7.83	109.66	122.65
39	Lk	58	GLN	CA-CB-CG	7.17	128.45	114.10
61	SI	111	GLN	CA-CB-CG	7.17	128.44	114.10

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	LE	177	GLY	Peptide
13	LJ	114	ASP	Peptide
13	LJ	58	ARG	Sidechain
49	N4	84	MET	Peptide
53	SA	195	TRP	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	L5	78678	0	39757	446	0
2	L7	2561	0	1295	13	0
3	L8	3314	0	1683	11	0
4	LA	1898	0	1993	20	0
5	LB	3238	0	3376	31	0
6	LC	2908	0	3082	21	0
7	LD	2382	0	2410	25	0
8	LE	1774	0	1930	25	0
9	LF	1870	0	1996	15	0
10	LG	1927	0	2074	20	0
11	LH	1518	0	1601	14	0
12	LI	1639	0	1687	14	0
13	LJ	1371	0	1412	23	0
14	LL	1673	0	1779	11	0
15	LM	1138	0	1204	9	0
16	LN	1701	0	1749	18	0
17	LO	1650	0	1794	22	0
18	LP	1242	0	1269	17	0
19	LQ	1513	0	1628	7	0
20	LR	1566	0	1729	16	0
21	LS	1453	0	1490	13	0
22	LT	1298	0	1366	10	0
23	LU	816	0	842	14	0
24	LV	979	0	1039	17	0
25	LW	1015	0	1079	17	0
26	LX	985	0	1066	4	0
27	LY	1106	0	1192	18	0
28	LZ	1107	0	1182	10	0
29	La	1162	0	1213	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Lb	882	0	959	9	0
31	Lc	764	0	804	10	0
32	Ld	888	0	930	12	0
33	Le	1053	0	1147	11	0
34	Lf	876	0	912	5	0
35	Lg	906	0	998	6	0
36	Lh	1015	0	1148	10	0
37	Li	832	0	917	8	0
38	Lj	705	0	737	4	0
39	Lk	569	0	637	10	0
40	Ll	444	0	483	3	0
41	Lm	430	0	465	2	0
42	Ln	230	0	276	0	0
43	Lo	862	0	929	10	0
44	Lp	708	0	756	11	0
45	Lr	1002	0	1068	7	0
46	Ls	1496	0	1540	22	0
47	Lt	1046	0	1076	22	0
48	MA	2485	0	2416	41	0
49	N4	1805	0	1761	25	0
50	NA	841	0	898	13	0
51	NB	813	0	856	14	0
52	S2	36456	0	18381	241	0
53	SA	1741	0	1746	30	0
54	SB	1791	0	1870	28	0
55	SC	1725	0	1813	28	0
56	SD	1765	0	1865	35	0
57	SE	2076	0	2177	37	0
58	SF	1461	0	1511	39	0
59	SG	1923	0	2088	39	0
60	SH	1497	0	1590	30	0
61	SI	1686	0	1772	11	0
62	SJ	1525	0	1640	35	0
63	SK	799	0	823	24	0
64	SL	1182	0	1253	19	0
65	SM	604	0	281	0	0
66	SN	1208	0	1294	13	0
67	SO	1010	0	1034	12	0
68	SP	1061	0	1107	34	0
69	SQ	1142	0	1213	29	0
70	SR	1090	0	1149	28	0
71	SS	1190	0	1249	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	ST	1112	0	1146	18	0
73	SU	817	0	882	18	0
74	SV	636	0	637	8	0
75	SW	1034	0	1080	12	0
76	SX	1098	0	1167	12	0
77	SY	1027	0	1093	19	0
78	SZ	598	0	656	14	0
79	Sa	821	0	870	8	0
80	Sb	651	0	672	6	0
81	Sc	506	0	536	7	0
82	Sd	459	0	448	6	0
83	Se	459	0	503	9	0
84	Sf	548	0	551	4	0
85	Sg	2436	0	2393	45	0
86	L5	214	0	0	0	0
86	L7	3	0	0	0	0
86	L8	4	0	0	0	0
86	LA	1	0	0	0	0
86	LI	1	0	0	0	0
86	LP	1	0	0	0	0
86	LV	1	0	0	0	0
86	Le	1	0	0	0	0
86	Lj	1	0	0	0	0
86	S2	27	0	0	0	0
86	SG	1	0	0	0	0
86	Sa	1	0	0	0	0
87	Lg	1	0	0	0	0
87	Lj	1	0	0	0	0
87	Lm	1	0	0	0	0
87	Lo	1	0	0	0	0
87	Lp	1	0	0	0	0
87	Sa	1	0	0	0	0
87	Sd	1	0	0	0	0
87	Sf	1	0	0	0	0
88	L5	3	0	0	0	0
All	All	221535	0	166120	1855	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 5.

The worst 5 of 1855 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)
52:S2:1756:C:H42	52:S2:1776:G:N2	1.50	1.07
52:S2:1756:C:N4	52:S2:1776:G:H22	1.52	1.06
1:L5:1762:C:N4	1:L5:1770:A:C2	2.36	0.94
1:L5:2557:G:H1	1:L5:2570:U:H3	0.98	0.92
1:L5:2483:G:H1	1:L5:2495:U:H3	0.97	0.90

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	
4	LA	246/257 (96%)	235 (96%)	11 (4%)	0	100	100
5	LB	400/403 (99%)	387 (97%)	13 (3%)	0	100	100
6	LC	363/427 (85%)	345 (95%)	18 (5%)	0	100	100
7	LD	291/297 (98%)	282 (97%)	9 (3%)	0	100	100
8	LE	215/288 (75%)	204 (95%)	11 (5%)	0	100	100
9	LF	223/248 (90%)	218 (98%)	5 (2%)	0	100	100
10	LG	239/266 (90%)	222 (93%)	17 (7%)	0	100	100
11	LH	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
12	LI	198/214 (92%)	191 (96%)	7 (4%)	0	100	100
13	LJ	169/178 (95%)	160 (95%)	9 (5%)	0	100	100
14	LL	205/211 (97%)	197 (96%)	6 (3%)	2 (1%)	12	45
15	LM	137/215 (64%)	131 (96%)	6 (4%)	0	100	100
16	LN	201/204 (98%)	197 (98%)	4 (2%)	0	100	100
17	LO	199/203 (98%)	197 (99%)	2 (1%)	0	100	100
18	LP	151/184 (82%)	146 (97%)	5 (3%)	0	100	100
19	LQ	185/188 (98%)	181 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	LR	185/196 (94%)	183 (99%)	2 (1%)	0	100	100
21	LS	173/176 (98%)	163 (94%)	10 (6%)	0	100	100
22	LT	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
23	LU	98/128 (77%)	97 (99%)	1 (1%)	0	100	100
24	LV	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
25	LW	122/157 (78%)	119 (98%)	3 (2%)	0	100	100
26	LX	118/156 (76%)	116 (98%)	2 (2%)	0	100	100
27	LY	131/145 (90%)	125 (95%)	6 (5%)	0	100	100
28	LZ	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
29	La	145/148 (98%)	138 (95%)	7 (5%)	0	100	100
30	Lb	105/159 (66%)	99 (94%)	6 (6%)	0	100	100
31	Lc	96/115 (84%)	95 (99%)	1 (1%)	0	100	100
32	Ld	105/125 (84%)	104 (99%)	1 (1%)	0	100	100
33	Le	126/135 (93%)	124 (98%)	2 (2%)	0	100	100
34	Lf	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
35	Lg	112/117 (96%)	109 (97%)	3 (3%)	0	100	100
36	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	99 (99%)	1 (1%)	0	100	100
38	Lj	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
39	Lk	67/70 (96%)	67 (100%)	0	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	49/128 (38%)	49 (100%)	0	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	98 (95%)	5 (5%)	0	100	100
44	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
45	Lr	123/137 (90%)	118 (96%)	5 (4%)	0	100	100
46	Ls	194/317 (61%)	183 (94%)	11 (6%)	0	100	100
47	Lt	137/165 (83%)	114 (83%)	22 (16%)	1 (1%)	18	52
48	MA	313/386 (81%)	302 (96%)	11 (4%)	0	100	100
49	N4	220/237 (93%)	212 (96%)	8 (4%)	0	100	100
50	NA	104/215 (48%)	100 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	NB	103/162 (64%)	93 (90%)	10 (10%)	0	100	100
53	SA	219/295 (74%)	208 (95%)	11 (5%)	0	100	100
54	SB	217/264 (82%)	208 (96%)	8 (4%)	1 (0%)	24	58
55	SC	220/293 (75%)	214 (97%)	6 (3%)	0	100	100
56	SD	225/243 (93%)	214 (95%)	11 (5%)	0	100	100
57	SE	260/263 (99%)	247 (95%)	13 (5%)	0	100	100
58	SF	180/204 (88%)	171 (95%)	9 (5%)	0	100	100
59	SG	235/249 (94%)	232 (99%)	2 (1%)	1 (0%)	30	61
60	SH	182/194 (94%)	178 (98%)	4 (2%)	0	100	100
61	SI	204/208 (98%)	197 (97%)	7 (3%)	0	100	100
62	SJ	183/194 (94%)	180 (98%)	3 (2%)	0	100	100
63	SK	93/165 (56%)	86 (92%)	7 (8%)	0	100	100
64	SL	140/158 (89%)	133 (95%)	7 (5%)	0	100	100
65	SM	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
66	SN	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
67	SO	133/151 (88%)	117 (88%)	15 (11%)	1 (1%)	16	50
68	SP	127/145 (88%)	117 (92%)	10 (8%)	0	100	100
69	SQ	142/146 (97%)	131 (92%)	11 (8%)	0	100	100
70	SR	133/135 (98%)	127 (96%)	5 (4%)	1 (1%)	16	50
71	SS	142/152 (93%)	137 (96%)	5 (4%)	0	100	100
72	ST	141/145 (97%)	133 (94%)	8 (6%)	0	100	100
73	SU	101/119 (85%)	94 (93%)	7 (7%)	0	100	100
74	SV	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
75	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
76	SX	139/143 (97%)	132 (95%)	7 (5%)	0	100	100
77	SY	124/133 (93%)	124 (100%)	0	0	100	100
78	SZ	73/125 (58%)	60 (82%)	12 (16%)	1 (1%)	9	38
79	Sa	100/115 (87%)	95 (95%)	5 (5%)	0	100	100
80	Sb	81/84 (96%)	79 (98%)	2 (2%)	0	100	100
81	Sc	62/69 (90%)	61 (98%)	1 (2%)	0	100	100
82	Sd	53/56 (95%)	48 (91%)	5 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
83	Se	56/133 (42%)	54 (96%)	2 (4%)	0	100	100
84	Sf	65/156 (42%)	56 (86%)	9 (14%)	0	100	100
85	Sg	311/317 (98%)	281 (90%)	30 (10%)	0	100	100
All	All	12345/14244 (87%)	11811 (96%)	526 (4%)	8 (0%)	49	79

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
47	Lt	141	CYS
78	SZ	49	LEU
54	SB	222	LYS
59	SG	12	CYS
67	SO	138	ASP

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	
4	LA	190/199 (96%)	186 (98%)	4 (2%)	47	66
5	LB	348/349 (100%)	344 (99%)	4 (1%)	65	74
6	LC	304/348 (87%)	301 (99%)	3 (1%)	68	75
7	LD	246/250 (98%)	241 (98%)	5 (2%)	48	67
8	LE	195/252 (77%)	191 (98%)	4 (2%)	47	66
9	LF	194/215 (90%)	192 (99%)	2 (1%)	68	75
10	LG	203/223 (91%)	198 (98%)	5 (2%)	42	63
11	LH	169/171 (99%)	166 (98%)	3 (2%)	51	69
12	LI	172/181 (95%)	170 (99%)	2 (1%)	63	73
13	LJ	144/149 (97%)	139 (96%)	5 (4%)	32	57
14	LL	173/177 (98%)	172 (99%)	1 (1%)	78	80
15	LM	118/161 (73%)	113 (96%)	5 (4%)	26	52
16	LN	171/172 (99%)	168 (98%)	3 (2%)	51	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	LO	173/174 (99%)	171 (99%)	2 (1%)	63	73
18	LP	134/163 (82%)	133 (99%)	1 (1%)	76	78
19	LQ	164/165 (99%)	158 (96%)	6 (4%)	30	56
20	LR	166/175 (95%)	161 (97%)	5 (3%)	36	60
21	LS	156/157 (99%)	147 (94%)	9 (6%)	18	45
22	LT	139/140 (99%)	136 (98%)	3 (2%)	45	65
23	LU	90/115 (78%)	84 (93%)	6 (7%)	15	41
24	LV	101/107 (94%)	100 (99%)	1 (1%)	68	75
25	LW	103/126 (82%)	99 (96%)	4 (4%)	28	54
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	123/135 (91%)	119 (97%)	4 (3%)	33	58
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	116 (97%)	4 (3%)	33	58
30	Lb	89/126 (71%)	85 (96%)	4 (4%)	24	51
31	Lc	83/97 (86%)	79 (95%)	4 (5%)	23	49
32	Ld	98/110 (89%)	95 (97%)	3 (3%)	35	60
33	Le	114/121 (94%)	109 (96%)	5 (4%)	25	51
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	98/100 (98%)	97 (99%)	1 (1%)	68	75
36	Lh	109/110 (99%)	106 (97%)	3 (3%)	38	61
37	Li	86/89 (97%)	84 (98%)	2 (2%)	44	64
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	61 (95%)	3 (5%)	23	50
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	47/115 (41%)	47 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	91 (98%)	2 (2%)	45	65
44	Lp	74/75 (99%)	72 (97%)	2 (3%)	39	62
45	Lr	109/121 (90%)	105 (96%)	4 (4%)	30	56
46	Ls	162/258 (63%)	158 (98%)	4 (2%)	42	63
47	Lt	112/137 (82%)	110 (98%)	2 (2%)	51	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
48	MA	270/330 (82%)	264 (98%)	6 (2%)	45	65
49	N4	195/204 (96%)	193 (99%)	2 (1%)	68	75
50	NA	95/183 (52%)	92 (97%)	3 (3%)	34	59
51	NB	89/136 (65%)	87 (98%)	2 (2%)	45	65
53	SA	183/243 (75%)	174 (95%)	9 (5%)	22	49
54	SB	200/231 (87%)	191 (96%)	9 (4%)	24	51
55	SC	188/225 (84%)	182 (97%)	6 (3%)	34	59
56	SD	190/202 (94%)	180 (95%)	10 (5%)	20	47
57	SE	224/225 (100%)	220 (98%)	4 (2%)	51	69
58	SF	156/170 (92%)	151 (97%)	5 (3%)	34	59
59	SG	207/218 (95%)	200 (97%)	7 (3%)	32	58
60	SH	166/174 (95%)	160 (96%)	6 (4%)	31	57
61	SI	178/180 (99%)	175 (98%)	3 (2%)	53	69
62	SJ	161/168 (96%)	152 (94%)	9 (6%)	19	46
63	SK	86/136 (63%)	81 (94%)	5 (6%)	18	45
64	SL	130/142 (92%)	129 (99%)	1 (1%)	73	77
66	SN	130/131 (99%)	127 (98%)	3 (2%)	44	64
67	SO	105/119 (88%)	102 (97%)	3 (3%)	37	60
68	SP	115/130 (88%)	108 (94%)	7 (6%)	17	44
69	SQ	119/121 (98%)	112 (94%)	7 (6%)	18	45
70	SR	122/122 (100%)	119 (98%)	3 (2%)	42	63
71	SS	125/132 (95%)	122 (98%)	3 (2%)	43	64
72	ST	113/115 (98%)	109 (96%)	4 (4%)	32	57
73	SU	94/107 (88%)	91 (97%)	3 (3%)	34	59
74	SV	67/67 (100%)	66 (98%)	1 (2%)	57	71
75	SW	112/113 (99%)	110 (98%)	2 (2%)	51	69
76	SX	113/115 (98%)	110 (97%)	3 (3%)	39	62
77	SY	109/115 (95%)	107 (98%)	2 (2%)	51	69
78	SZ	66/103 (64%)	60 (91%)	6 (9%)	9	32
79	Sa	89/98 (91%)	87 (98%)	2 (2%)	45	65
80	Sb	75/76 (99%)	73 (97%)	2 (3%)	39	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
81	Sc	57/62 (92%)	55 (96%)	2 (4%)	32	57
82	Sd	48/49 (98%)	47 (98%)	1 (2%)	47	66
83	Se	47/104 (45%)	47 (100%)	0	100	100
84	Sf	60/140 (43%)	60 (100%)	0	100	100
85	Sg	272/275 (99%)	266 (98%)	6 (2%)	45	65
All	All	10646/11996 (89%)	10369 (97%)	277 (3%)	41	63

5 of 277 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
69	SQ	12	VAL
70	SR	97	GLU
78	SZ	99	LEU
31	Lc	71	VAL
30	Lb	119	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
64	SL	108	ASN
70	SR	31	ASN
79	Sa	7	ASN
20	LR	178	GLN
20	LR	40	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3658/5070 (72%)	750 (20%)	16 (0%)
2	L7	119/121 (98%)	10 (8%)	0
3	L8	155/157 (98%)	31 (20%)	0
52	S2	1696/1869 (90%)	368 (21%)	5 (0%)
All	All	5628/7217 (77%)	1159 (20%)	21 (0%)

5 of 1159 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	17	A

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Mol	Chain	Res	Type
1	L5	25	A
1	L5	39	A
1	L5	40	G
1	L5	42	A

5 of 21 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	4699	U
52	S2	291	G
52	S2	1434	C
52	S2	563	G
52	S2	112	U

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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	$\# Z > 2$
41	MLZ	Lm	98	41	8,9,10	0.77	0	4,9,11	0.64	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
41	MLZ	Lm	98	41	-	2/7/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
41	Lm	98	MLZ	C-CA-CB-CG
41	Lm	98	MLZ	CE-CD-CG-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 264 ligands modelled in this entry, 264 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.

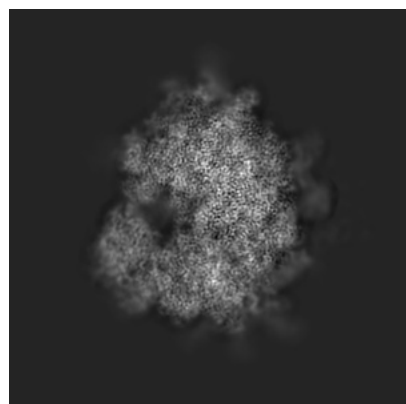
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55610. These allow visual inspection of the internal detail of the map and identification of artifacts.

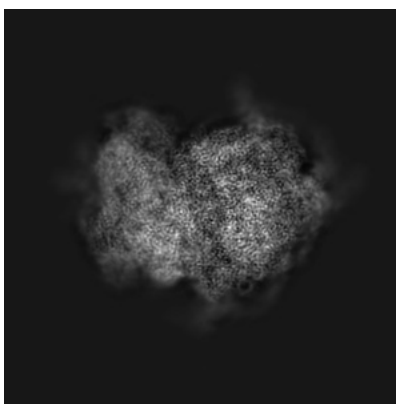
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

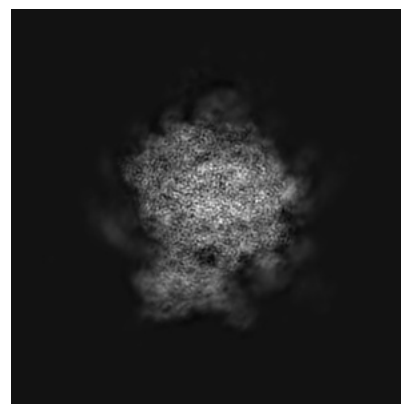
6.1.1 Primary map



X

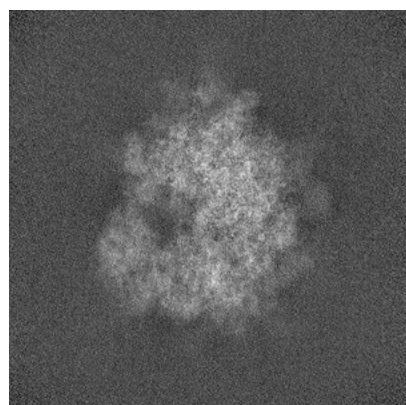


Y

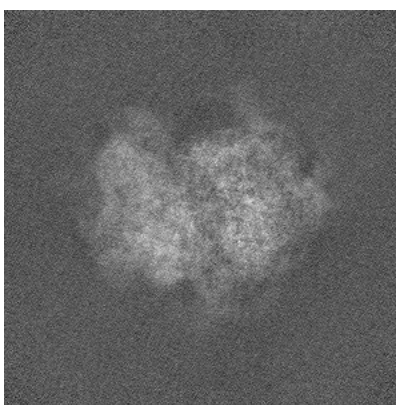


Z

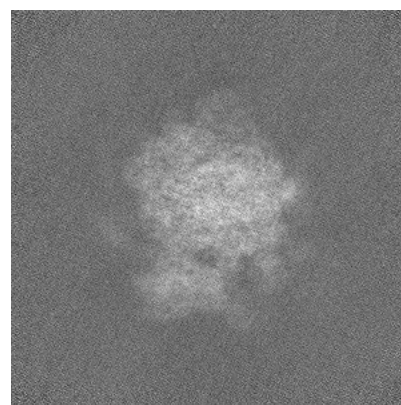
6.1.2 Raw map



X



Y

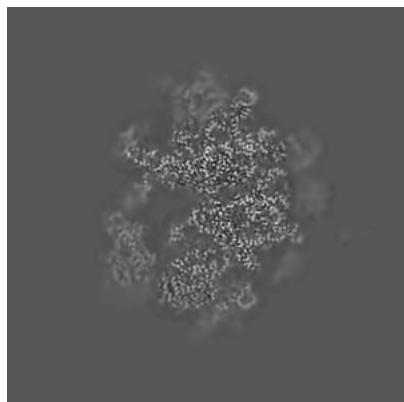


Z

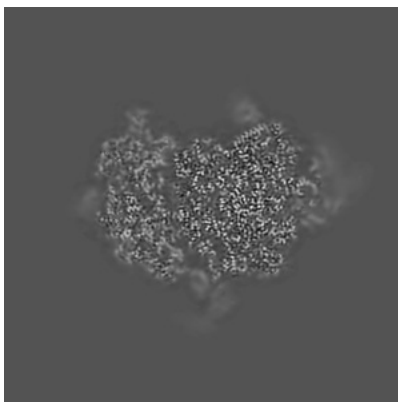
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

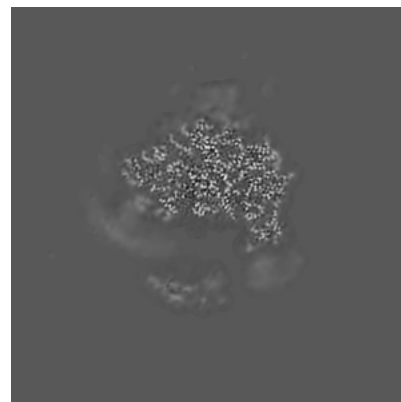
6.2.1 Primary map



X Index: 320

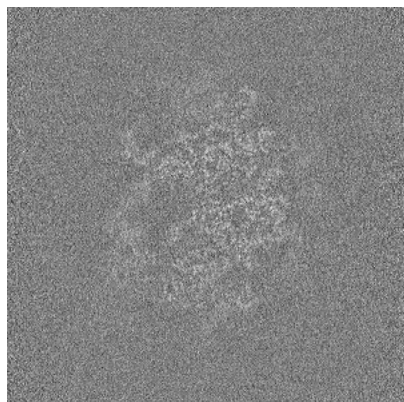


Y Index: 320

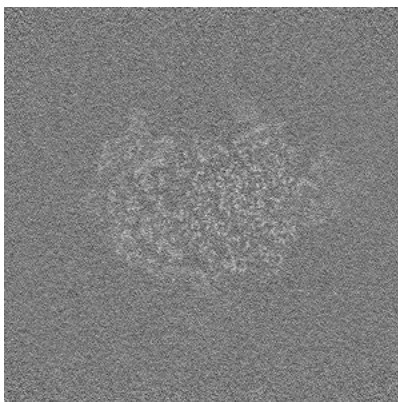


Z Index: 320

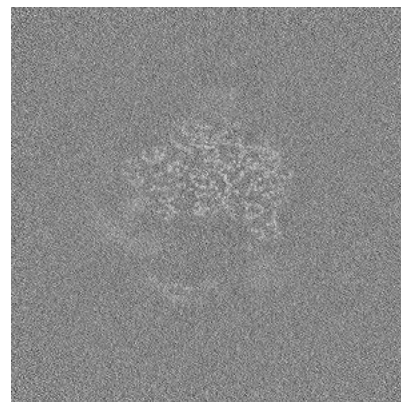
6.2.2 Raw map



X Index: 320



Y Index: 320

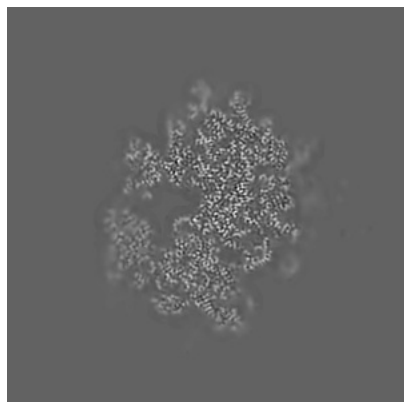


Z Index: 320

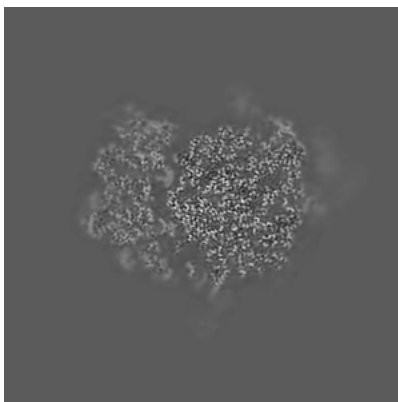
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

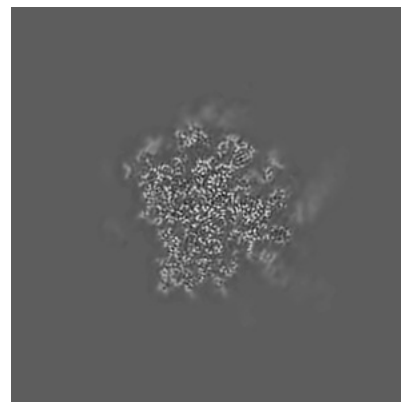
6.3.1 Primary map



X Index: 299

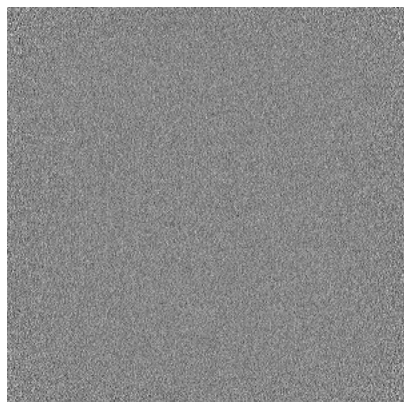


Y Index: 336

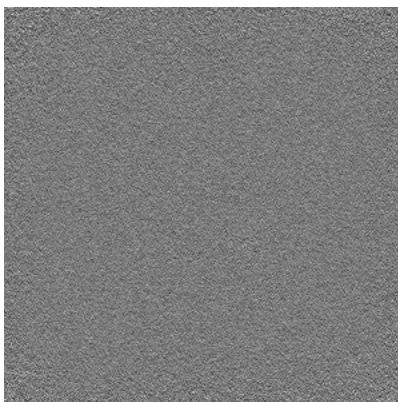


Z Index: 385

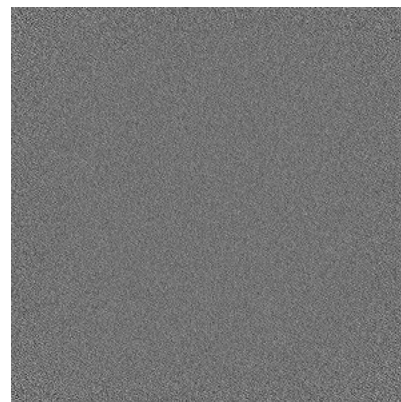
6.3.2 Raw map



X Index: 0



Y Index: 0

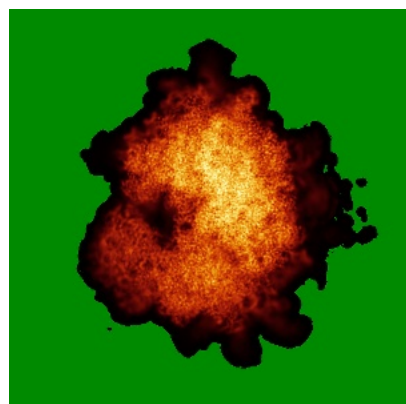


Z Index: 0

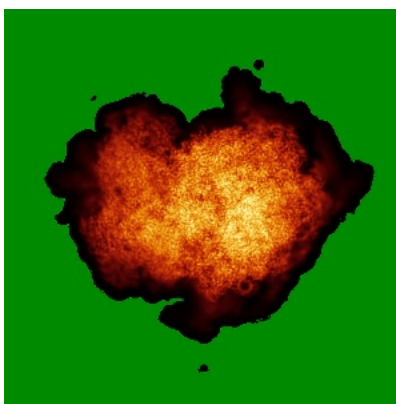
The images above show the largest variance slices of the map in three orthogonal directions.

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

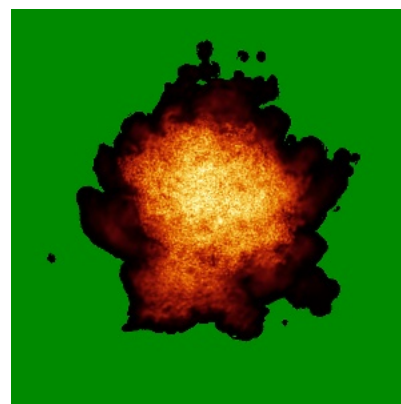
6.4.1 Primary map



X

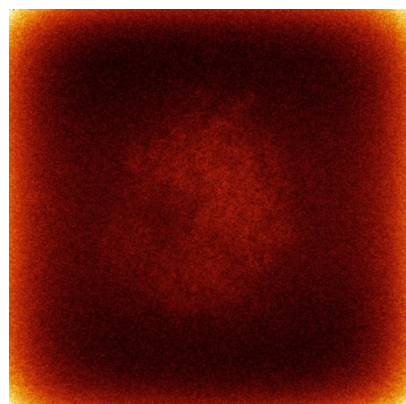


Y

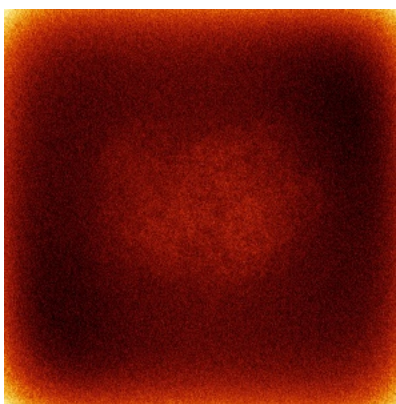


Z

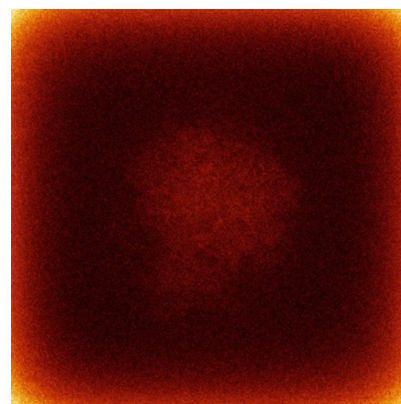
6.4.2 Raw map



X



Y

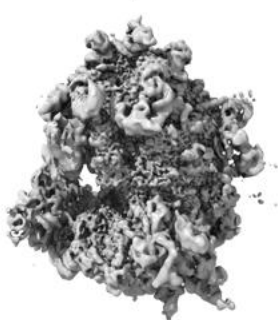


Z

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



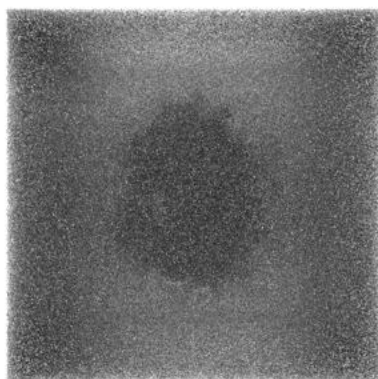
Y



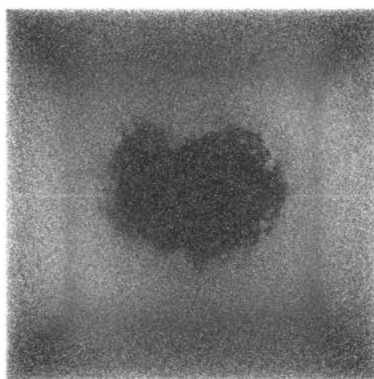
Z

The images above show the 3D surface view of the map at the recommended contour level 0.11. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

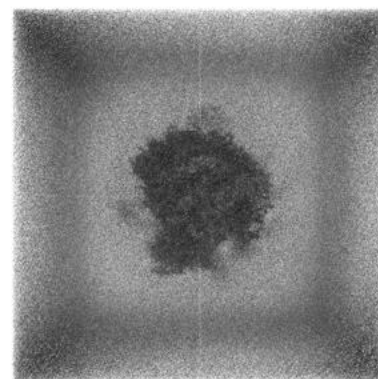
6.5.2 Raw map



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.

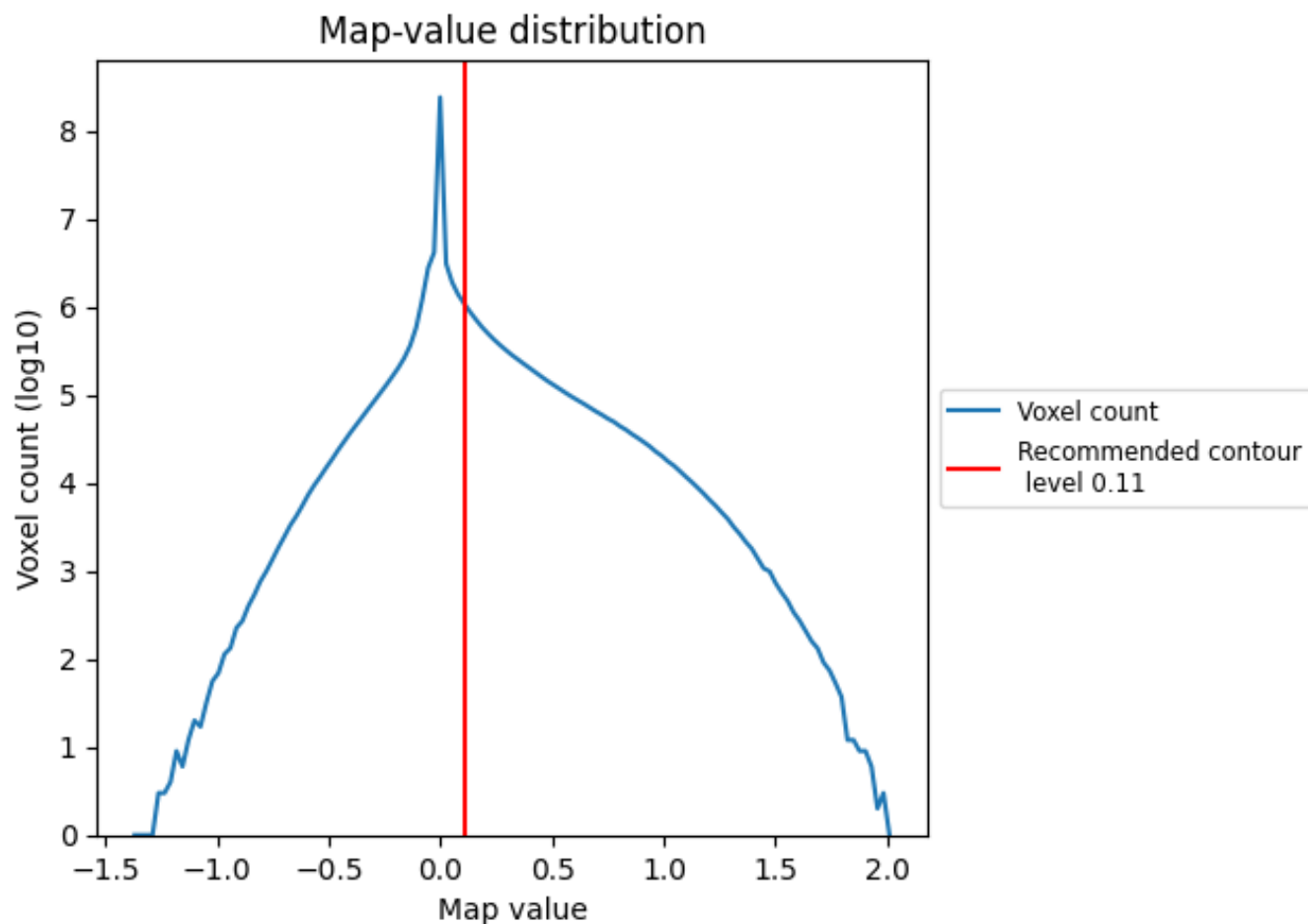
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

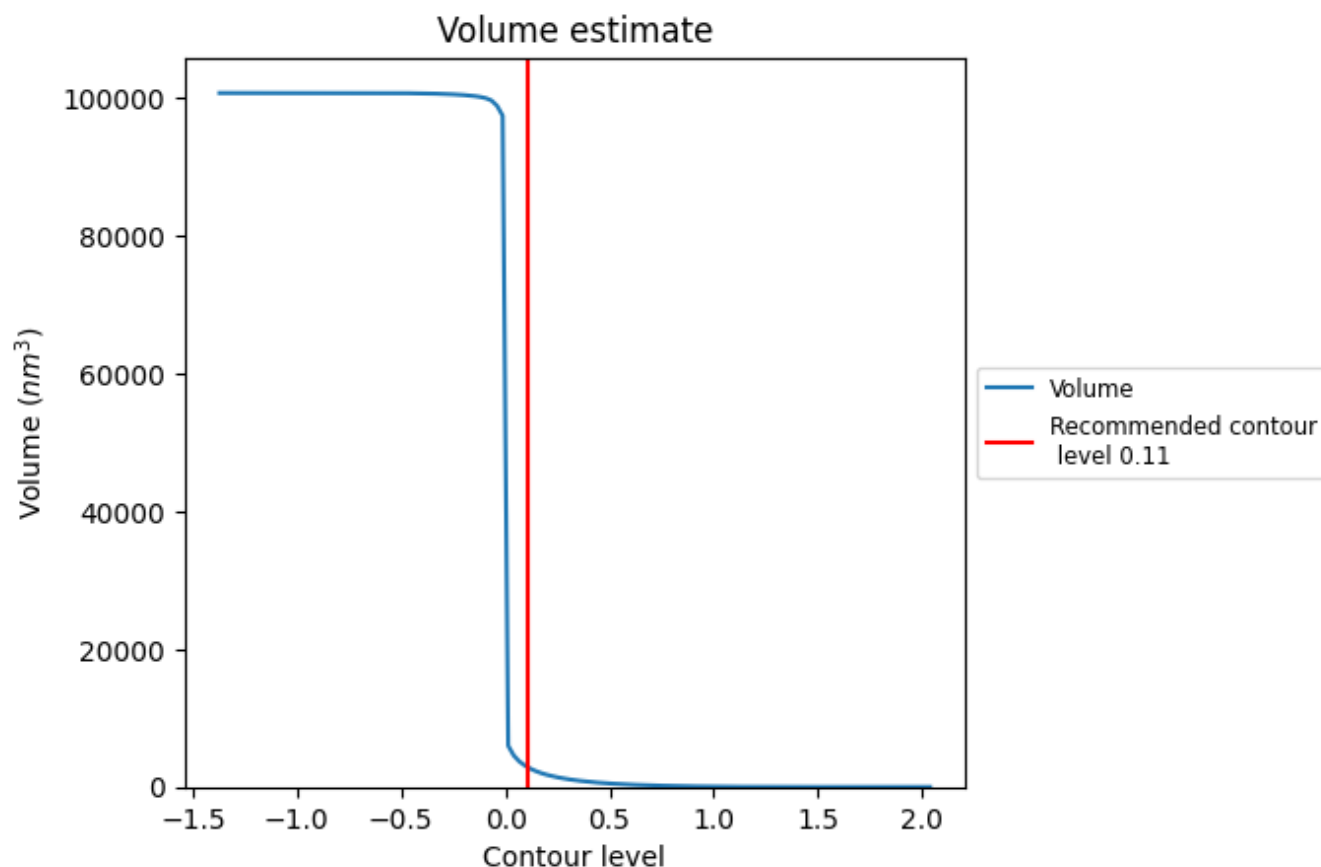
This section contains the results of statistical analysis of the map.

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.

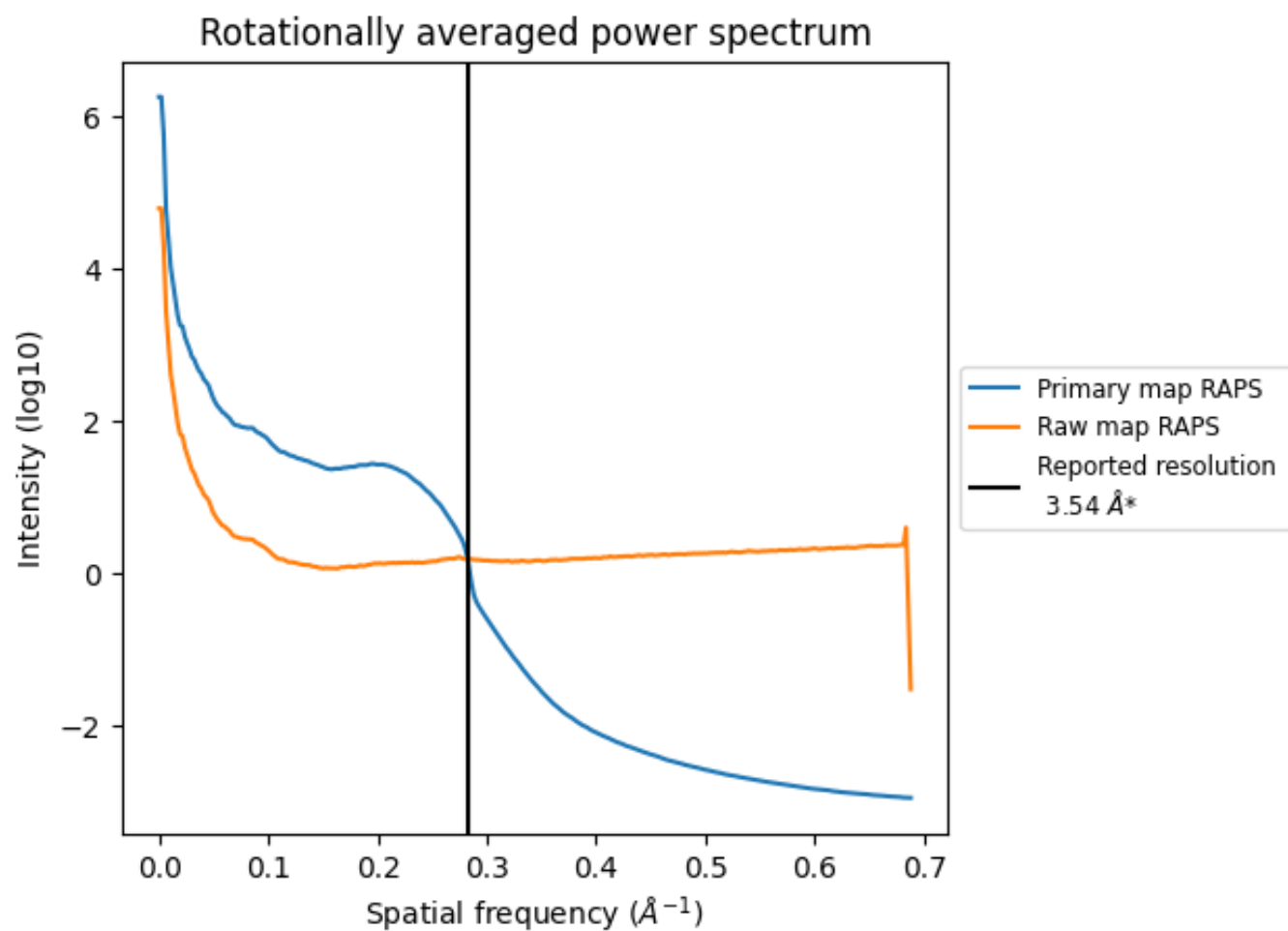
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2839 nm³; this corresponds to an approximate mass of 2564 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 ⓘ

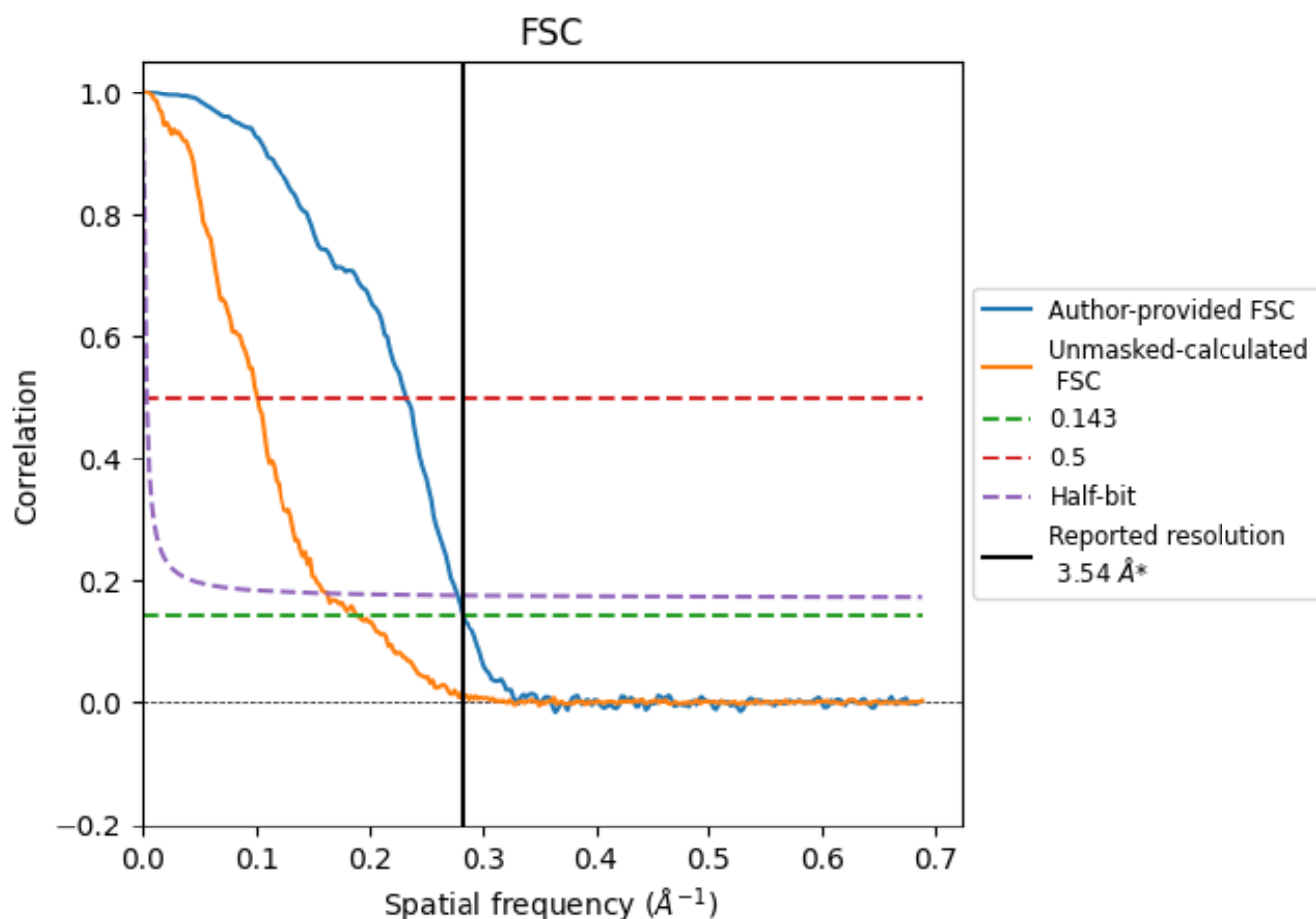


*Reported resolution corresponds to spatial frequency of 0.282 $\text{\AA}^{-1}$

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 0.282 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

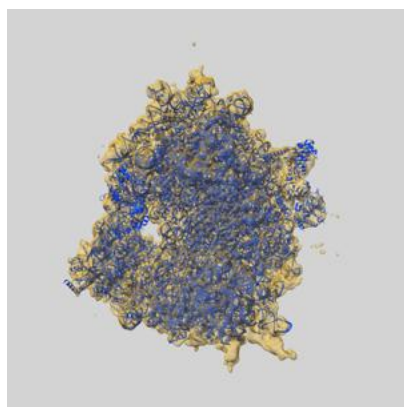
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.54	-	-
Author-provided FSC curve	3.54	4.30	3.60
Unmasked-calculated*	5.28	9.88	6.11

*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 5.28 differs from the reported value 3.54 by more than 10 %

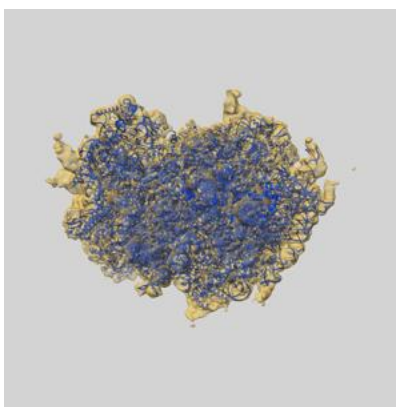
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55610 and PDB model 9T69. Per-residue inclusion information can be found in section [3](#) on page [21](#).

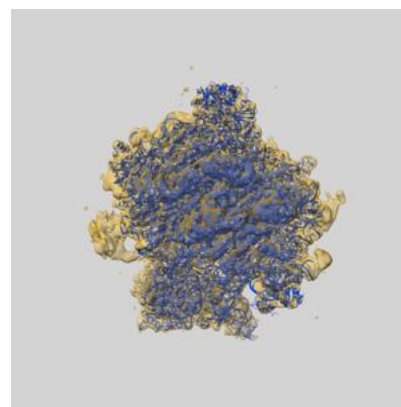
9.1 Map-model overlay [i](#)



X



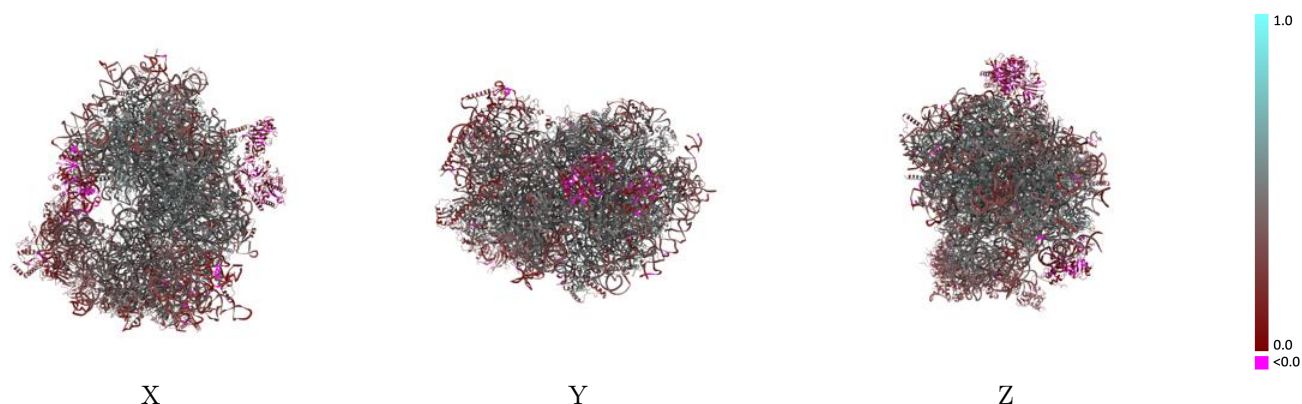
Y



Z

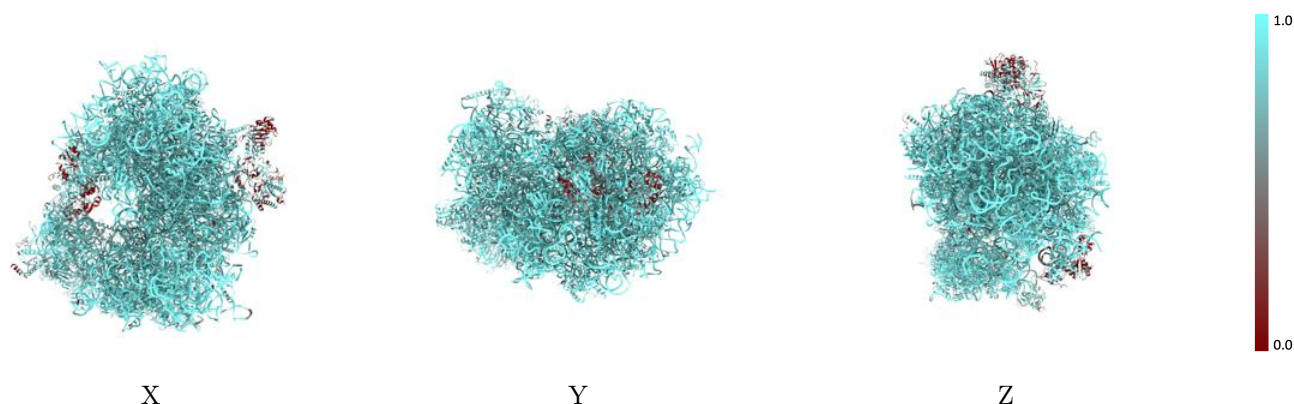
The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



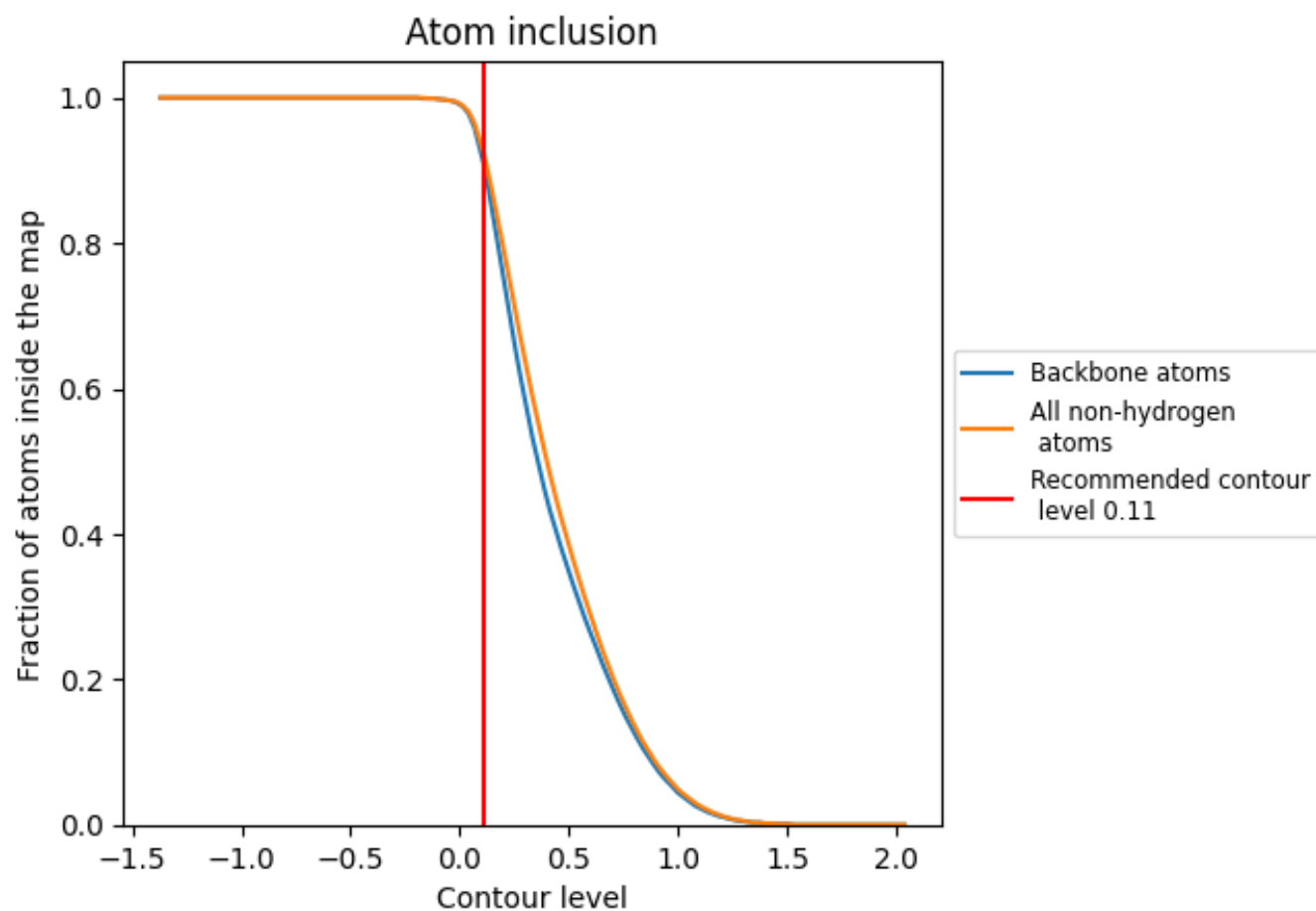
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.11).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 92% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9230	 0.3900
L5	 0.9630	 0.4140
L7	 0.9810	 0.4490
L8	 0.9620	 0.4250
LA	 0.9430	 0.5120
LB	 0.9510	 0.4910
LC	 0.9510	 0.4970
LD	 0.9530	 0.4170
LE	 0.9510	 0.4400
LF	 0.9420	 0.4840
LG	 0.9090	 0.4090
LH	 0.9390	 0.4760
LI	 0.9400	 0.4860
LJ	 0.9230	 0.3960
LL	 0.9280	 0.4600
LM	 0.9510	 0.4660
LN	 0.9490	 0.5110
LO	 0.9400	 0.4930
LP	 0.9550	 0.5080
LQ	 0.9570	 0.5180
LR	 0.9180	 0.4390
LS	 0.9650	 0.5080
LT	 0.9290	 0.4750
LU	 0.9340	 0.4020
LV	 0.9380	 0.5110
LW	 0.8440	 0.3280
LX	 0.9050	 0.4660
LY	 0.9390	 0.4680
LZ	 0.9620	 0.4580
La	 0.9510	 0.5020
Lb	 0.8780	 0.3770
Lc	 0.9290	 0.4550
Ld	 0.9310	 0.4630
Le	 0.9650	 0.5120
Lf	 0.9550	 0.5200



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Chain	Atom inclusion	Q-score
Lg	 0.9330	 0.4730
Lh	 0.9290	 0.4470
Li	 0.9350	 0.4530
Lj	 0.9750	 0.5190
Lk	 0.9100	 0.3950
Ll	 0.9530	 0.5020
Lm	 0.9350	 0.4850
Ln	 0.6410	 0.3090
Lo	 0.9200	 0.4710
Lp	 0.9240	 0.4980
Lr	 0.9540	 0.4980
Ls	 0.3030	 0.0660
Lt	 0.4630	 0.0750
MA	 0.4850	 0.0770
N4	 0.5500	 0.1300
NA	 0.3590	 0.1020
NB	 0.7110	 0.1670
S2	 0.9670	 0.3590
SA	 0.9030	 0.3740
SB	 0.9020	 0.3850
SC	 0.9120	 0.4050
SD	 0.8430	 0.2580
SE	 0.9210	 0.3880
SF	 0.8590	 0.2420
SG	 0.8990	 0.2790
SH	 0.8720	 0.3260
SI	 0.9120	 0.4050
SJ	 0.8940	 0.3580
SK	 0.8370	 0.1950
SL	 0.8970	 0.4350
SM	 0.6190	 0.1950
SN	 0.8930	 0.4090
SO	 0.9010	 0.4200
SP	 0.8350	 0.2140
SQ	 0.8640	 0.2470
SR	 0.8770	 0.2870
SS	 0.8470	 0.2290
ST	 0.8890	 0.2460
SU	 0.8510	 0.2510
SV	 0.9320	 0.4000
SW	 0.9210	 0.4400
SX	 0.9200	 0.4410

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Chain	Atom inclusion	Q-score
SY	 0.8840	 0.2830
SZ	 0.8610	 0.1860
Sa	 0.9010	 0.4090
Sb	 0.9150	 0.3950
Sc	 0.8870	 0.2900
Sd	 0.8910	 0.2960
Se	 0.8540	 0.3320
Sf	 0.6650	 0.1440
Sg	 0.9100	 0.1880