



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:17 AM UTC

PDB ID : 9S3B / pdb_00009s3b
EMDB ID : EMD-54528
Title : NMT1-NAC bound human RNC with 58 amino acid ARF1-linker - State 1
Authors : Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-07-24
Resolution : 2.38 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

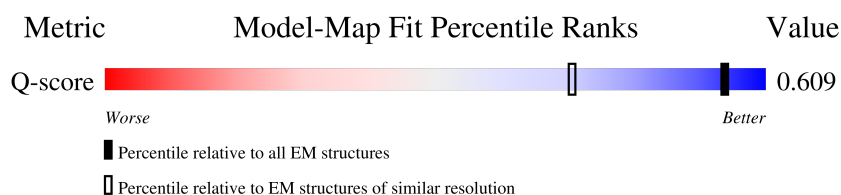
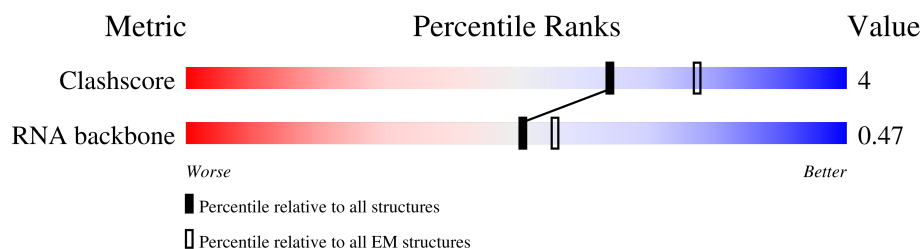
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

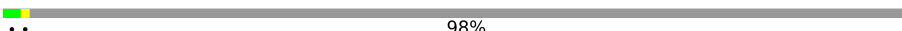



The reported resolution of this entry is 2.38 Å.

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.



















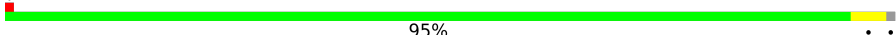








Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
RNA backbone	8273	3508	-
Q-score	-	25397	4811 (1.88 - 2.88)

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	CM	586	 98%
2	CP	75	 64% 36%
3	CR	437	 85% 10% 5%
4	L5	5070	 49% 20% 28%
5	L7	121	 79% 19% ..


























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Mol	Chain	Length	Quality of chain
6	L8	157	
7	LA	257	
8	LB	403	
9	LC	427	
10	LD	297	
11	LE	288	
12	LF	248	
13	LG	266	
14	LH	192	
15	LI	214	
16	LJ	178	
17	LL	211	
18	LM	215	
19	LN	204	
20	LO	203	
21	LP	184	
22	LQ	188	
23	LR	196	
24	LS	176	
25	LT	160	
26	LU	128	
27	LV	140	
28	LW	157	
29	LX	156	
30	LY	145	

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Mol	Chain	Length	Quality of chain
31	LZ	136	
32	La	148	
33	Lb	159	
34	Lc	115	
35	Ld	125	
36	Le	135	
37	Lf	110	
38	Lg	117	
39	Lh	123	
40	Li	105	
41	Lj	97	
42	Lk	70	
43	Ll	51	
44	Lm	128	
45	Ln	25	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	Ls	317	
50	Lt	165	
51	S2	1869	
52	SA	295	
53	SB	264	
54	SC	293	
55	SD	243	









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Mol	Chain	Length	Quality of chain
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	
79	Sb	84	
80	Sc	69	

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Mol	Chain	Length	Quality of chain
81	Sd	56	 79%16%5%
82	Se	133	 38%59%
83	Sf	156	 35%5%60%
84	Sg	317	 85%12%
85	NA	215	 6%20%11%69%
86	NB	162	 9%61%15%23%
87	NM	496	 63%16%21%
88	CZ	95	 32%79%17%

2 Entry composition [i](#)

There are 91 unique types of molecules in this entry. The entry contains 222378 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 58 amino acid ARF1-linker - V5 peptide - hCMV staller mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CM	12	Total	C	N	O	P	0	0
			247	111	37	87	12		

- Molecule 2 is a RNA chain called prolyl-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CP	75	Total	C	N	O	P	0	0
			1602	713	284	530	75		

- Molecule 3 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	CR	414	Total	C	N	O	S	0	0
			3269	2080	557	621	11		

- Molecule 4 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L5	3648	Total	C	N	O	P	0	0
			78199	34823	14307	25422	3647		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 6 is a RNA chain called 5.8S rRNA.

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

- Molecule 7 is a protein called 60S ribosomal protein L8.

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

- Molecule 8 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LB	395	Total	C	N	O	S	0	0
			3183	2027	597	545	14		

- Molecule 9 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LC	364	Total	C	N	O	S	0	0
			2884	1814	576	479	15		

- Molecule 10 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LD	293	Total	C	N	O	S	0	0
			2361	1496	430	421	14		

- Molecule 11 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	219	Total	C	N	O	S	0	0
			1754	1129	334	287	4		

- Molecule 12 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 13 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LG	229	Total	C	N	O	S	0	0
			1818	1157	351	306	4		

- Molecule 14 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LH	190	Total	C	N	O	S	0	0
			1510	950	282	272	6		

- Molecule 15 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LI	207	Total	C	N	O	S	0	0
			1666	1059	323	270	14		

- Molecule 16 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LJ	169	Total	C	N	O	S	0	0
			1329	841	250	232	6		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LL	205	Total	C	N	O	S	0	0
			1630	1020	340	266	4		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LM	139	Total	C	N	O	S	0	0
			1122	720	216	179	7		

- Molecule 19 is a protein called 60S ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LO	200	Total	C	N	O	S	0	0
			1633	1053	318	257	5		

- Molecule 21 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LP	153	Total	C	N	O	S	0	0
			1234	771	240	214	9		

- Molecule 22 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LQ	187	Total	C	N	O	S	0	0
			1502	939	313	245	5		

- Molecule 23 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LR	176	Total	C	N	O	S	0	0
			1452	898	318	227	9		

- Molecule 24 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LS	175	Total	C	N	O	S	0	0
			1452	925	283	234	10		

- Molecule 25 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LT	159	Total	C	N	O	S	0	0
			1282	813	250	213	6		

- Molecule 26 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LU	101	Total	C	N	O	S	0	0
			806	520	141	143	2		

- Molecule 27 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LV	131	Total	C	N	O	S	0	0
			971	613	183	170	5		

- Molecule 28 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LW	115	Total	C	N	O	S	0	0
			808	506	160	139	3		

- Molecule 29 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LX	120	Total	C	N	O	S	0	0
			981	627	184	169	1		

- Molecule 30 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LY	134	Total	C	N	O	S	0	0
			1111	697	225	186	3		

- Molecule 31 is a protein called 60S ribosomal protein L27.

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

- Molecule 32 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	La	147	Total	C	N	O	S	0	0
			1154	731	236	184	3		

- Molecule 33 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lb	75	Total	C	N	O	S	0	0
			590	367	123	97	3		

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lc	97	Total	C	N	O	S	0	0
			742	473	130	133	6		

- Molecule 35 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ld	107	Total	C	N	O	S	0	0
			874	554	171	147	2		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Le	128	Total	C	N	O	S	0	0
			1049	664	215	165	5		

- Molecule 37 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lf	109	Total	C	N	O	S	0	0
			872	552	173	144	3		

- Molecule 38 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lg	114	Total	C	N	O	S	0	0
			889	557	184	142	6		

- Molecule 39 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Lh	121	Total	C	N	O	S	0	0
			1006	635	203	167	1		

- Molecule 40 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Li	102	Total	C	N	O	S	0	0
			813	510	176	123	4		

- Molecule 41 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Lk	69	Total	C	N	O	S	0	0
			542	350	100	91	1		

- Molecule 43 is a protein called 60S ribosomal protein L39.

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

- Molecule 44 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Lm	52	Total	C	N	O	S	0	0
			425	264	90	65	6		

- Molecule 45 is a protein called 60S ribosomal protein L41.

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

- Molecule 46 is a protein called 60S ribosomal protein L36a.

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

- Molecule 47 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lp	91	Total	C	N	O	S	0	0
			696	440	135	114	7		

- Molecule 48 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lr	125	Total	C	N	O	S	0	0
			997	618	207	168	4		

- Molecule 49 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Ls	212	Total	C	N	O	S	0	0
			1640	1042	284	305	9		

- Molecule 50 is a protein called Large ribosomal subunit protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Lt	160	Total	C	N	O	S	0	0
			1208	749	226	229	4		

- Molecule 51 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S2	1713	Total	C	N	O	P	0	0
			36562	16320	6564	11966	1712		

- Molecule 52 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SA	216	Total	C	N	O	S	0	0
			1671	1068	297	298	8		

- Molecule 53 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SB	213	Total	C	N	O	S	0	0
			1718	1092	308	304	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SC	219	Total	C	N	O	S	0	0
			1661	1076	284	291	10		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SD	223	Total	C	N	O	S	0	0
			1594	1023	291	273	7		

- 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
			1972	1270	370	324	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SF	181	Total	C	N	O	S	0	0
			1403	879	269	248	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SG	231	Total	C	N	O	S	0	0
			1634	1026	332	269	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SH	183	Total	C	N	O		0	0
			1274	819	242	213			

- 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
			1574	989	308	272	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SJ	179	Total	C	N	O	S	0	0
			1431	915	290	224	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SK	96	Total	C	N	O	S	0	0
			726	479	127	115	5		

- 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
			1143	730	213	194	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
			950	596	168	177	9		

- 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
			1182	758	226	197	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SO	134	Total	C	N	O	S	0	0
			969	596	194	173	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
			990	626	190	168	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SQ	142	Total	C	N	O	S	0	0
			1075	689	204	179	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SR	131	Total	C	N	O	S	0	0
			942	600	179	159	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SS	141	Total	C	N	O	S	0	0
			1130	712	232	185	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
			1081	679	210	189	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SU	101	Total	C	N	O	S	0	0
			713	447	137	125	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
			618	385	115	113	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
			1026	655	193	172	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
			1078	682	212	181	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
76	SY	123	Total	C	N	O	S	0	0
			927	588	183	152	4		

- 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
			559	361	105	92	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sa	99	Total	C	N	O	S	0	0
			781	487	165	124	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
			618	386	118	107	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sc	63	Total	C	N	O	S	0	0
			472	289	92	89	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sd	53	Total	C	N	O	S	0	0
			433	271	87	70	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
82	Se	55	Total	C	N	O	S	0	0
			416	254	93	68	1		

- Molecule 83 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	Sf	63	Total	C	N	O	S	0	0
			515	324	98	86	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
84	Sg	308	Total	C	N	O	S	0	0
			2180	1393	381	395	11		

- Molecule 85 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	NA	67	Total	C	N	O	S	0	0
			531	335	97	98	1		

- Molecule 86 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	NB	124	Total	C	N	O	S	0	0
			963	597	175	188	3		

- Molecule 87 is a protein called Glycylpeptide N-tetradecanoyltransferase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	NM	393	Total	C	N	O	S	3	0
			3209	2075	544	573	17		

- Molecule 88 is a protein called nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	CZ	79	Total	C	N	O	S	0	0
			455	283	83	87	2		

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	CM	1	Total	Mg	0
			1	1	
89	L5	126	Total	Mg	0
			126	126	
89	L7	3	Total	Mg	0
			3	3	
89	L8	3	Total	Mg	0
			3	3	
89	LA	1	Total	Mg	0
			1	1	
89	LC	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
89	LI	1	Total 1	Mg 1	0
89	LN	1	Total 1	Mg 1	0
89	LP	1	Total 1	Mg 1	0
89	LV	1	Total 1	Mg 1	0
89	S2	51	Total 51	Mg 51	0
89	ST	1	Total 1	Mg 1	0

- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 91 is water.

Mol	Chain	Residues	Atoms		AltConf
91	L5	4	Total 4	O 4	0
91	L7	1	Total 1	O 1	0
91	LI	1	Total 1	O 1	0

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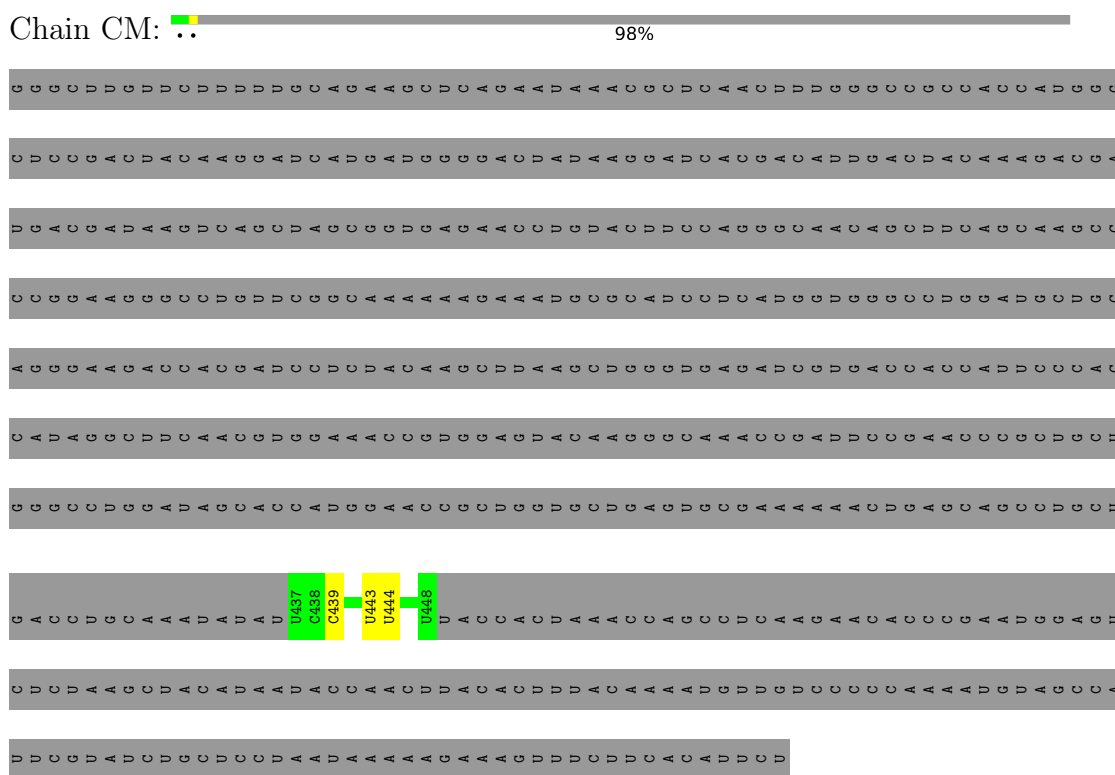
Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
91	LN	1	Total 1	O 1	0
91	La	1	Total 1	O 1	0
91	S2	3	Total 3	O 3	0

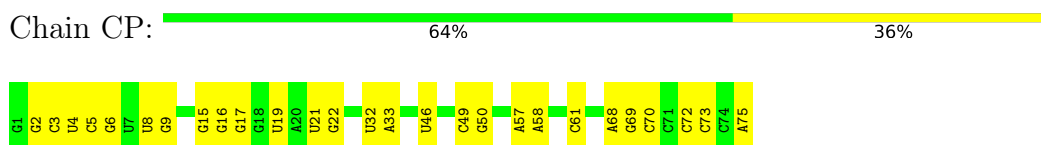
3 Residue-property plots

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

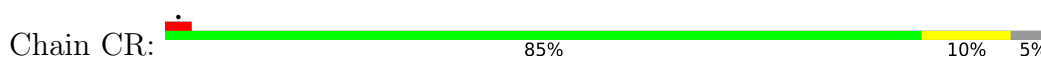
- Molecule 1: 58 amino acid ARF1-linker - V5 peptide - hCMV staller mRNA



- Molecule 2: prolyl-tRNA




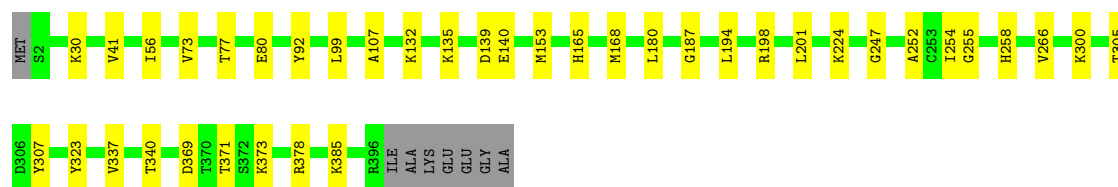
- Molecule 3: Eukaryotic peptide chain release factor subunit 1






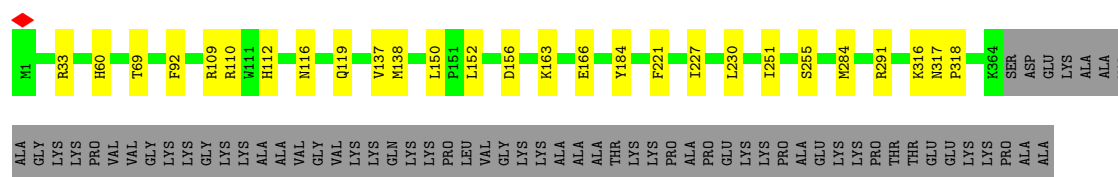


Chain LB:  88% 10%




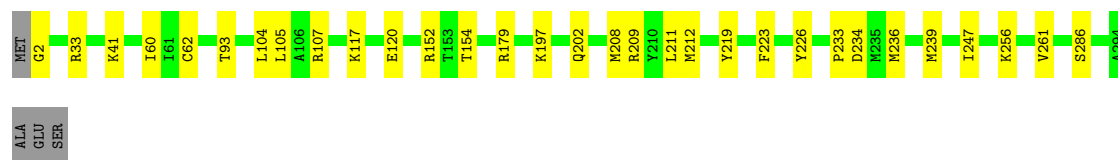
• Molecule 9: 60S ribosomal protein L4

Chain LC:  79% 6% 15%



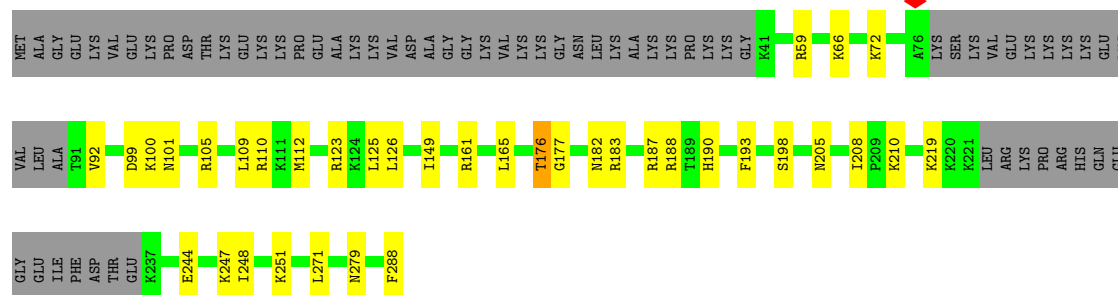
• Molecule 10: 60S ribosomal protein L5

Chain LD:  88% 10%




• Molecule 11: Large ribosomal subunit protein eL6

Chain LE:  63% 12% 24%



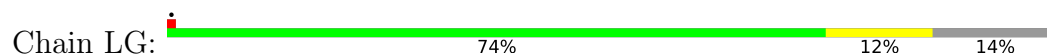
• Molecule 12: Large ribosomal subunit protein uL30

Chain LF:  80% 10% 9%





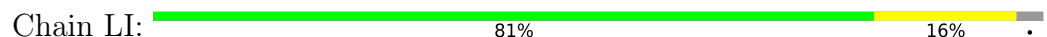
- Molecule 13: 60S ribosomal protein L7a



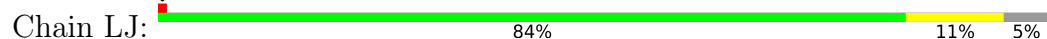
- Molecule 14: 60S ribosomal protein L9



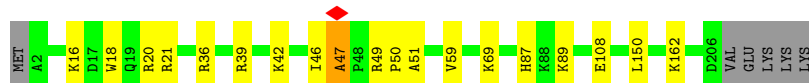
- Molecule 15: Ribosomal protein uL16-like



- Molecule 16: 60S ribosomal protein L11

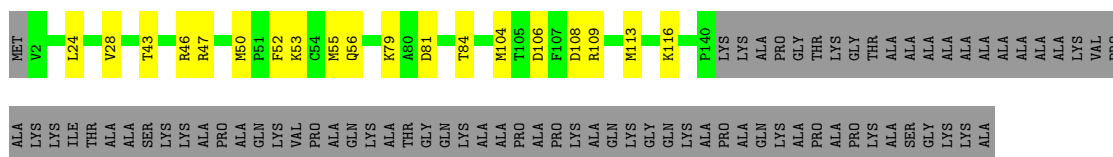


- Molecule 17: 60S ribosomal protein L13



- Molecule 18: 60S ribosomal protein L14





- Molecule 19: 60S ribosomal protein L15

Chain LN: 88% 12%



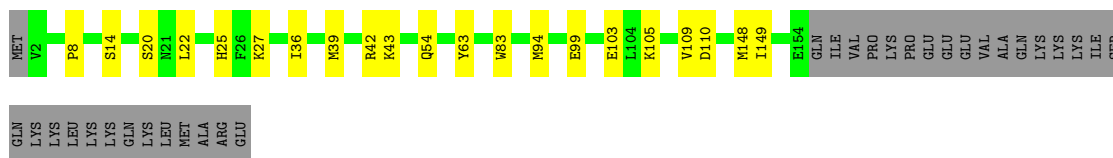
- Molecule 20: 60S ribosomal protein L13a

Chain LO: 87% 11%



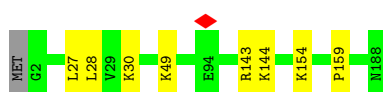
- Molecule 21: 60S ribosomal protein L17

Chain LP: 72% 11% 17%



- Molecule 22: 60S ribosomal protein L18

Chain LQ: 95%



- Molecule 23: 60S ribosomal protein L19

Chain LR: 82% 8% 10%



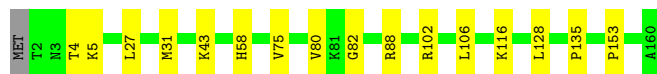
- Molecule 24: 60S ribosomal protein L18a

Chain LS: 88% 11%



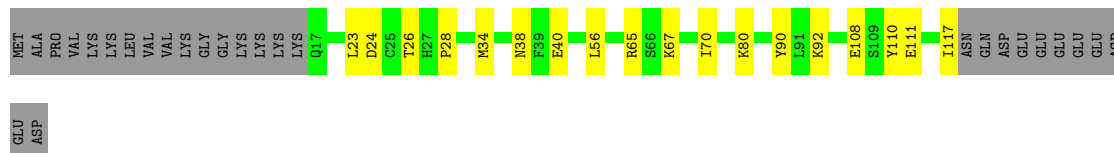
- Molecule 25: 60S ribosomal protein L21

Chain LT:  89% 10%




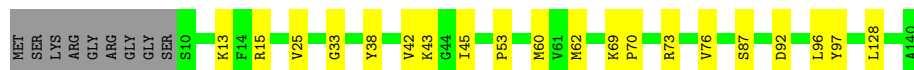
- Molecule 26: 60S ribosomal protein L22

Chain LU:  65% 14% 21%



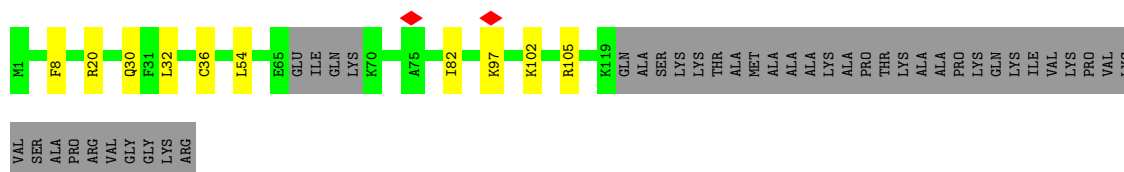
- Molecule 27: 60S ribosomal protein L23

Chain LV:  79% 14% 6%



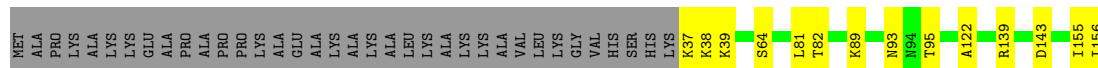
- Molecule 28: 60S ribosomal protein L24

Chain LW:  67% 6% 27%




- Molecule 29: 60S ribosomal protein L23a

Chain LX:  68% 9% 23%




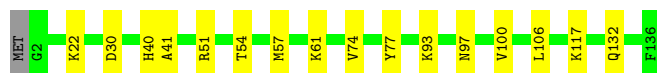
- Molecule 30: 60S ribosomal protein L26

Chain LY:  77% 15% 8%




- Molecule 31: 60S ribosomal protein L27

Chain LZ:  88% 12%



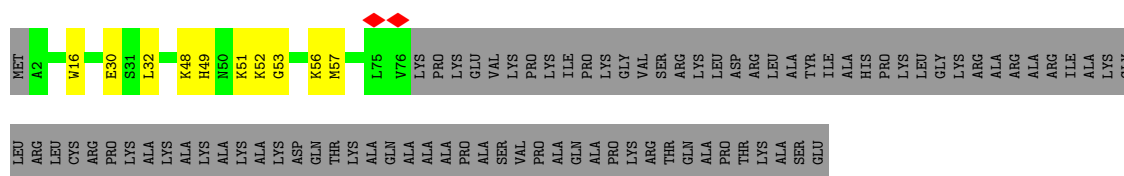
- Molecule 32: 60S ribosomal protein L27a

Chain La:  87% 12%



- Molecule 33: 60S ribosomal protein L29

Chain Lb:  41% 6% 53%



- Molecule 34: 60S ribosomal protein L30

Chain Lc:  70% 15% 16%




- Molecule 35: 60S ribosomal protein L31

Chain Ld:  75% 10% 14%




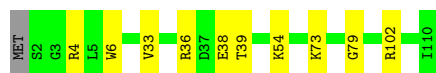
- Molecule 36: 60S ribosomal protein L32

Chain Le:  88% 7% 5%




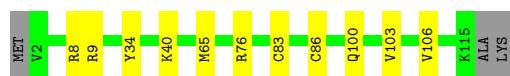
- Molecule 37: 60S ribosomal protein L35a

Chain Lf:  90% 9%



- Molecule 38: 60S ribosomal protein L34

Chain Lg:  88% 9%



- Molecule 39: 60S ribosomal protein L35

Chain Lh:  92% 7%




- Molecule 40: 60S ribosomal protein L36

Chain Li:  90% 7%




- Molecule 41: Large ribosomal subunit protein eL37

Chain Lj:  75% 13% 11%




- Molecule 42: 60S ribosomal protein L38

Chain Lk:  86% 13%



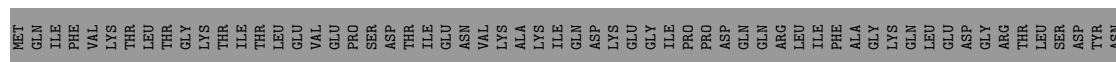
- Molecule 43: 60S ribosomal protein L39

Chain Ll:  76% 22%

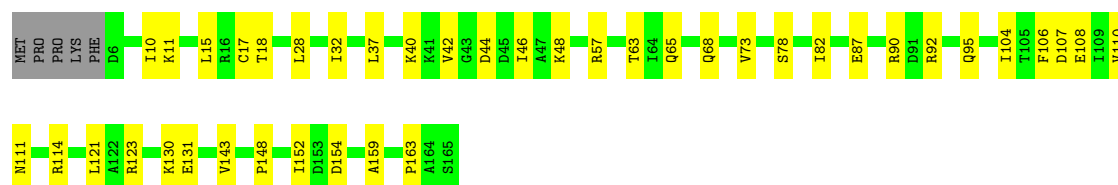


- Molecule 44: Ubiquitin-60S ribosomal protein L40

Chain Lm:  37% 59%

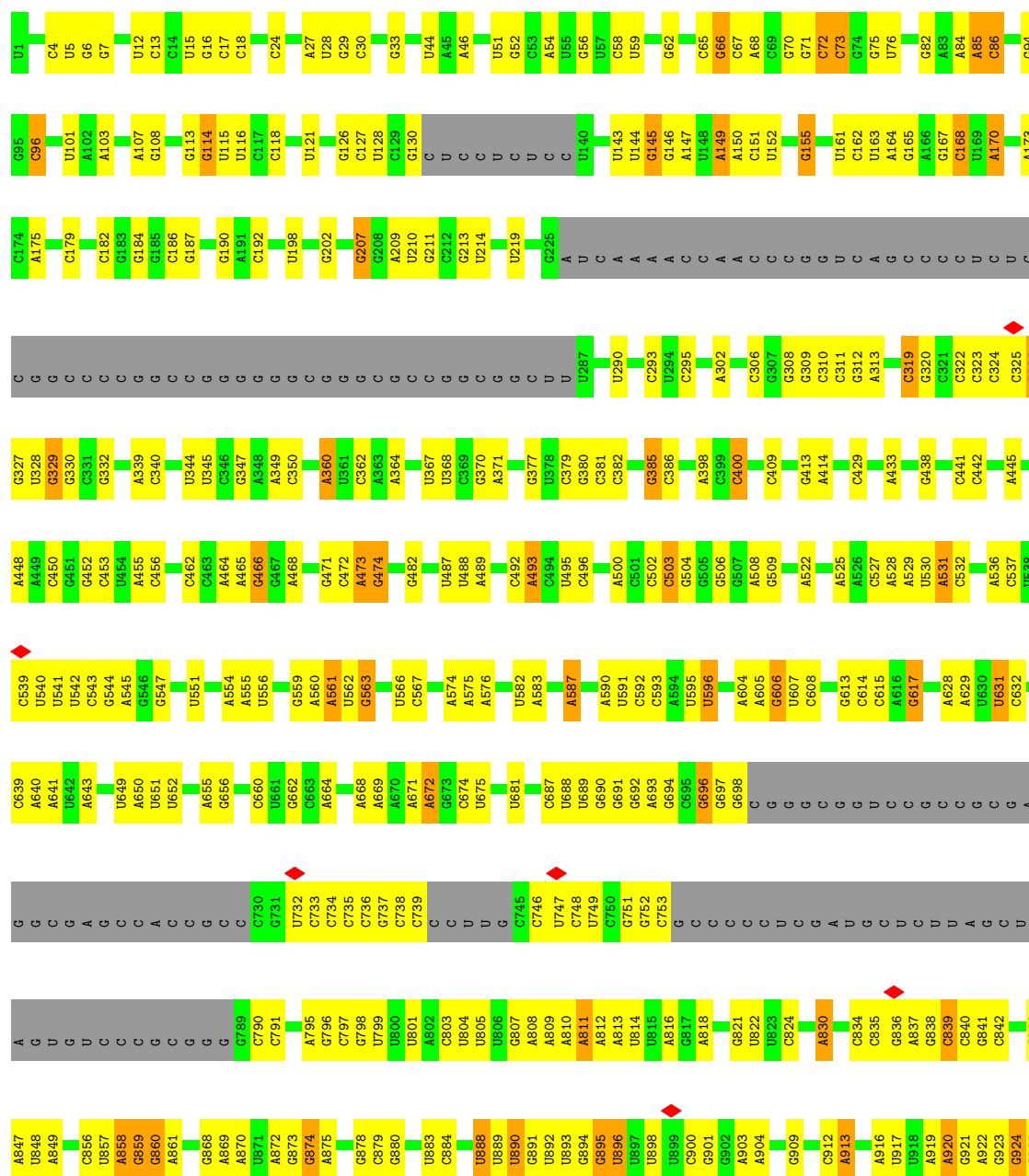


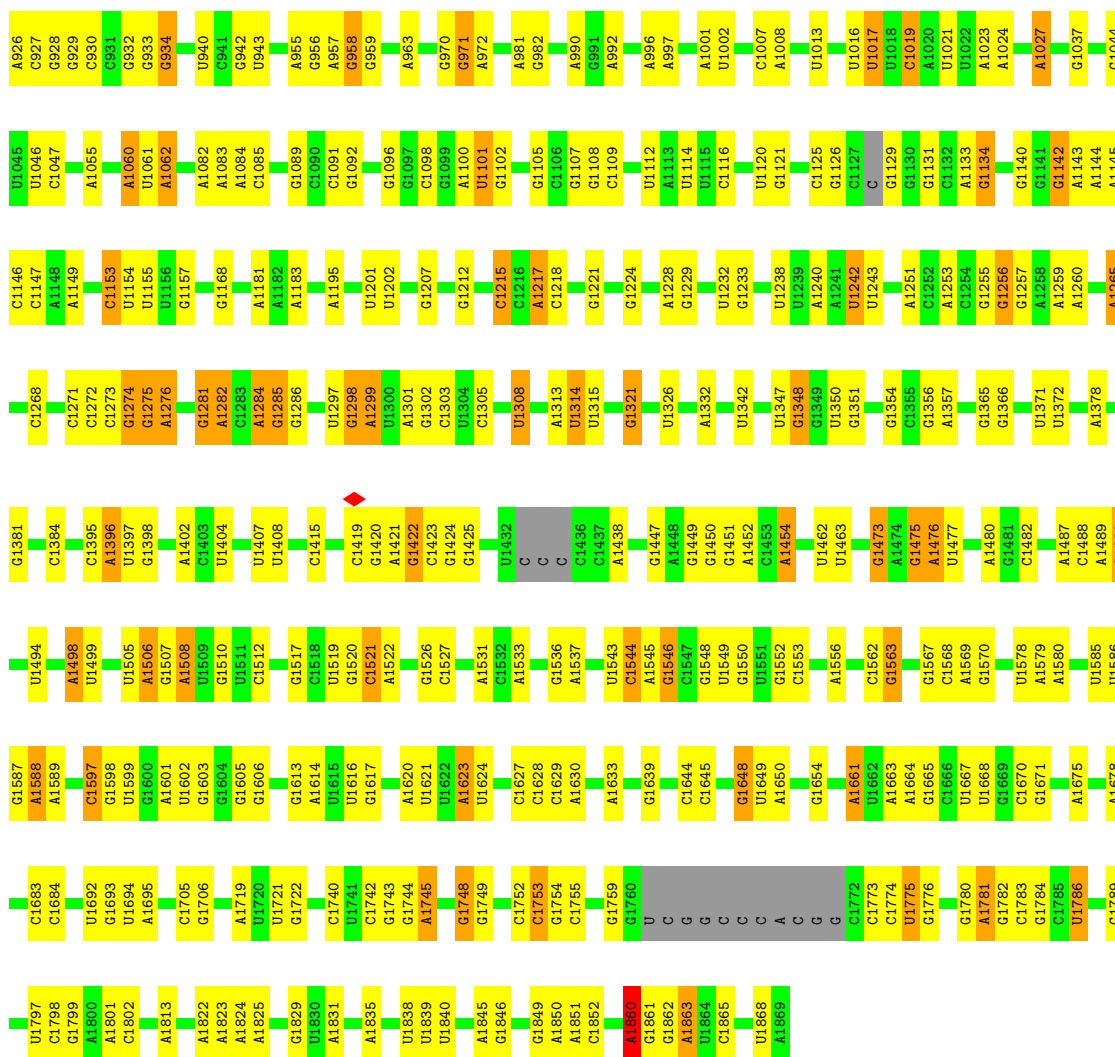
Chain Lt:  72% 25% .



• Molecule 51: 18S rRNA

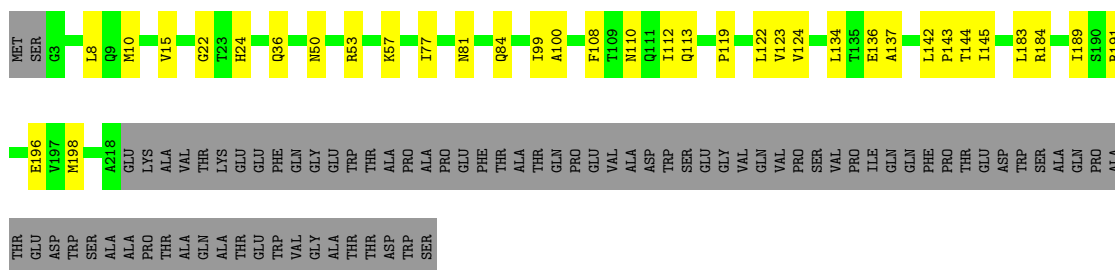
Chain S2:  55% 31% 6% 8%





• Molecule 52: 40S ribosomal protein SA

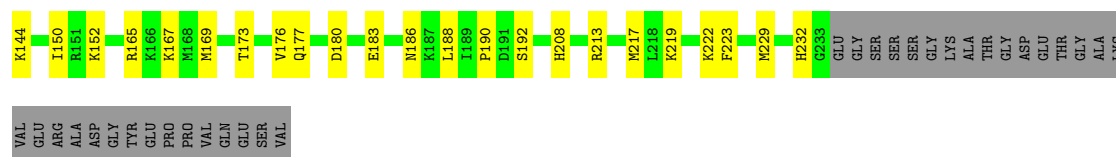
Chain SA: 61% 12% 27%



• Molecule 53: 40S ribosomal protein S3a

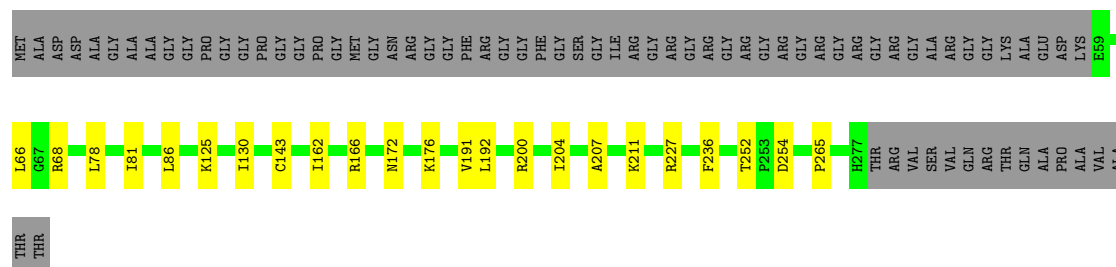
Chain SB: 64% 17% 19%





- Molecule 54: 40S ribosomal protein S2

Chain SC: 67% 8% 25%



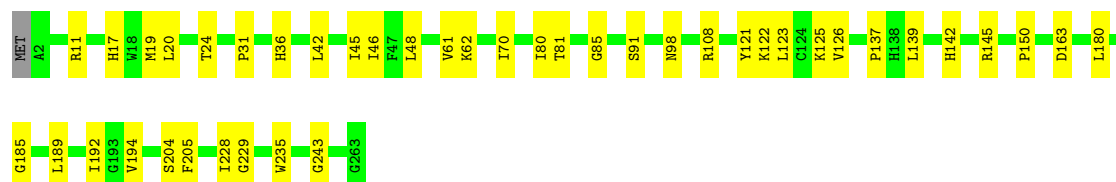
- Molecule 55: 40S ribosomal protein S3

Chain SD: 81% 11% 8%



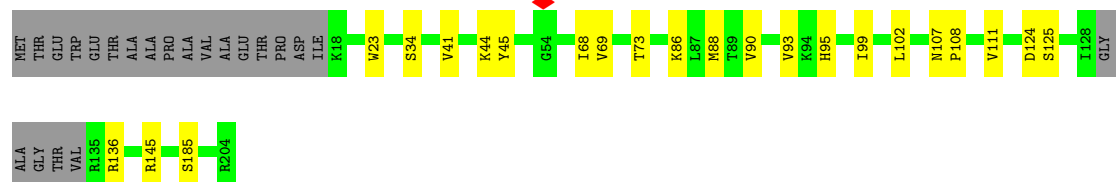
- Molecule 56: Small ribosomal subunit protein eS4, X isoform

Chain SE: 84% 16%



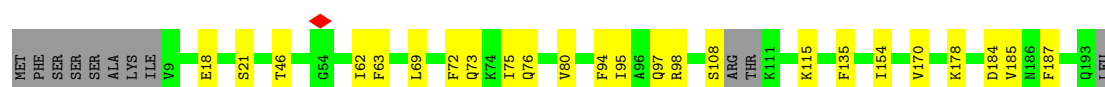
- Molecule 57: 40S ribosomal protein S5

Chain SF: 77% 11% 11%



- Molecule 58: 40S ribosomal protein S6

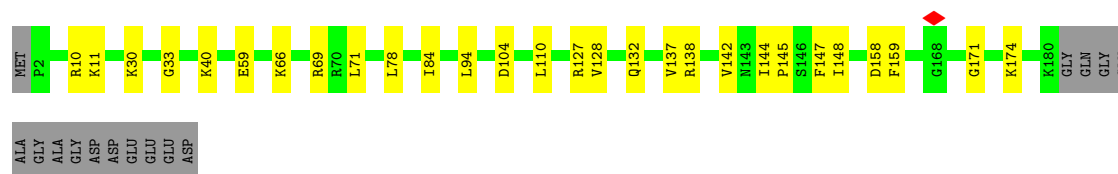
- Molecule 59: 40S ribosomal protein S7



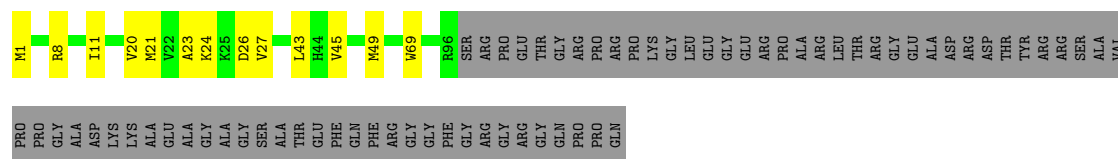
- Molecule 60: 40S ribosomal protein S8



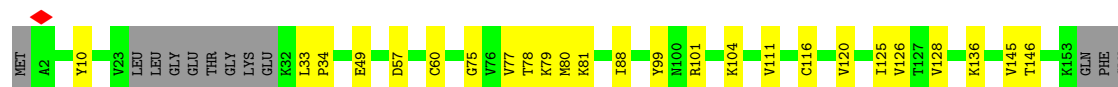
- Molecule 61: 40S ribosomal protein S9



- Molecule 62: 40S ribosomal protein S10

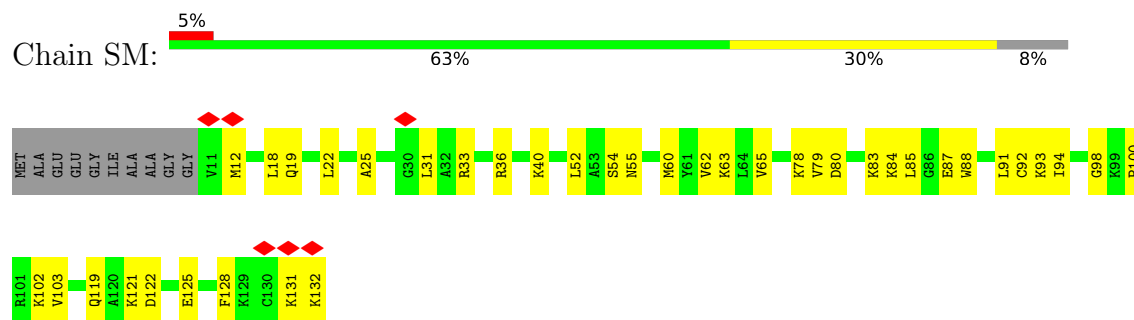


- Molecule 63: 40S ribosomal protein S11

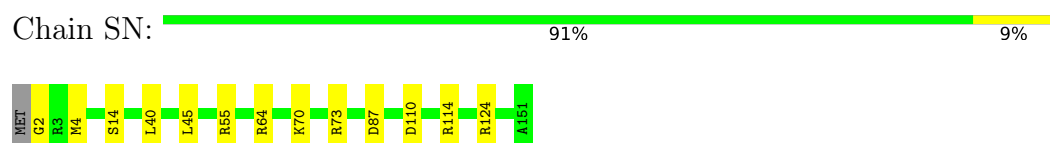


LYS
PHE

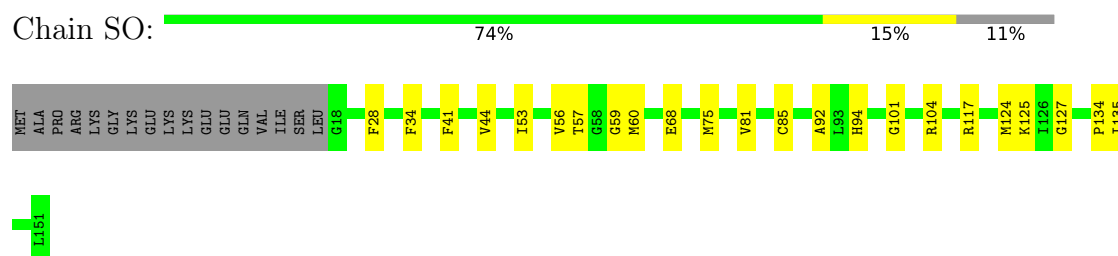
- Molecule 64: 40S ribosomal protein S12



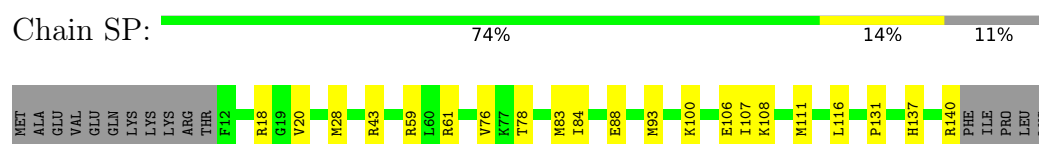
- Molecule 65: 40S ribosomal protein S13



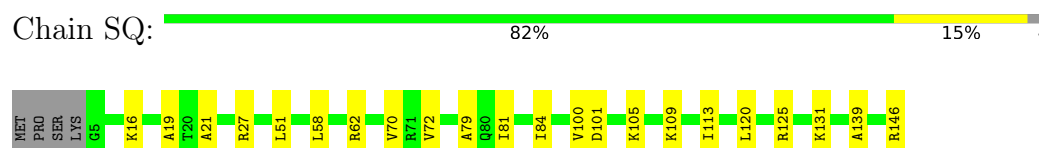
- Molecule 66: 40S ribosomal protein S14



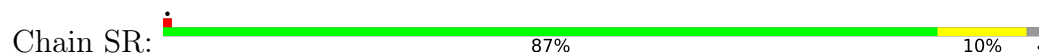
- Molecule 67: 40S ribosomal protein S15

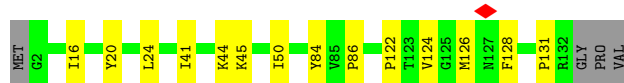


- Molecule 68: 40S ribosomal protein S16



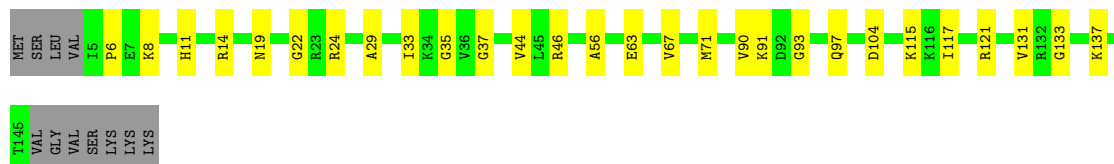
- Molecule 69: 40S ribosomal protein S17





- Molecule 70: 40S ribosomal protein S18

Chain SS: 74% 18% 7%



- Molecule 71: 40S ribosomal protein S19

Chain ST: 82% 17%



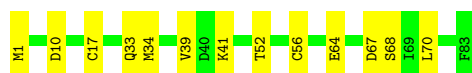
- Molecule 72: 40S ribosomal protein S20

Chain SU: 69% 16% 15%



- Molecule 73: 40S ribosomal protein S21

Chain SV: 84% 16%



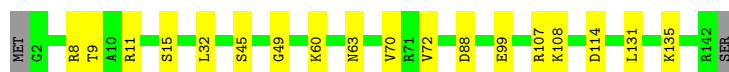
- Molecule 74: 40S ribosomal protein S15a

Chain SW: 88% 11%




- Molecule 75: 40S ribosomal protein S23

Chain SX: 86% 13%



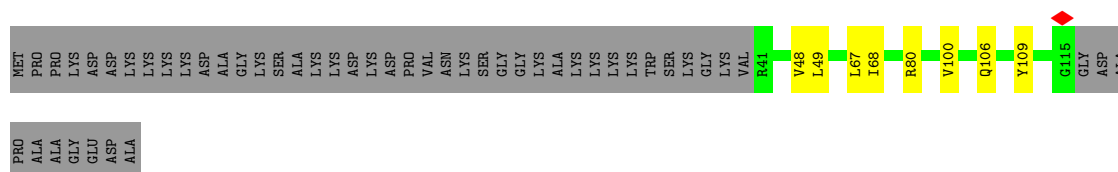
- Molecule 76: 40S ribosomal protein S24

Chain SY:  74% 18% 8%




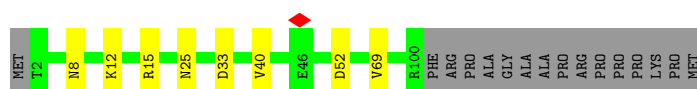
- Molecule 77: 40S ribosomal protein S25

Chain SZ:  54% 6% 40%




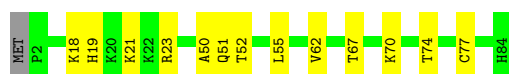
- Molecule 78: 40S ribosomal protein S26

Chain Sa:  79% 7% 14%




- Molecule 79: 40S ribosomal protein S27

Chain Sb:  83% 15% 2%




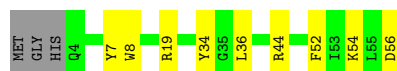
- Molecule 80: 40S ribosomal protein S28

Chain Sc:  80% 12% 9%



- Molecule 81: 40S ribosomal protein S29

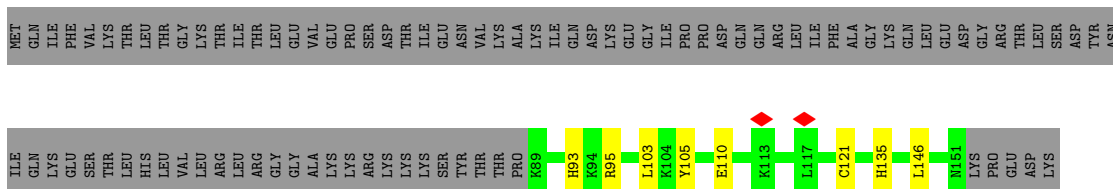
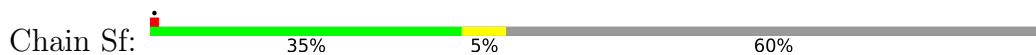
Chain Sd:  79% 16% 5%



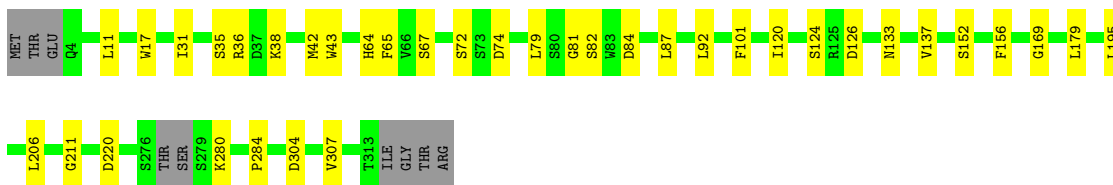
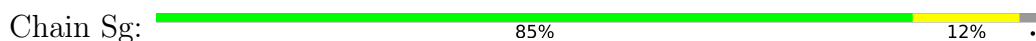
- Molecule 82: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

Chain Se:  38% 59%

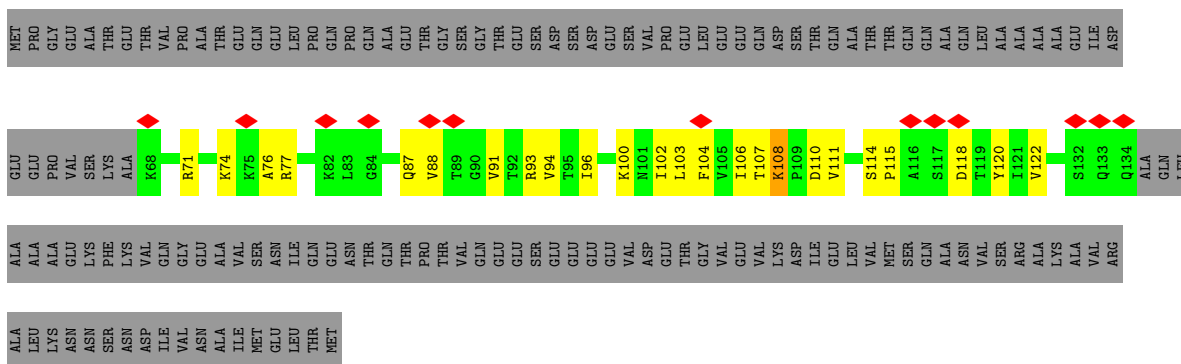
- Molecule 83: Ubiquitin



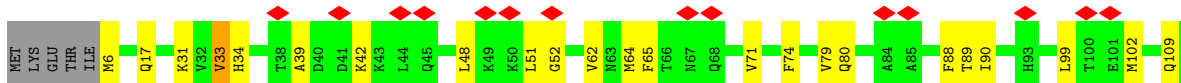
- Molecule 84: Receptor of activated protein C kinase 1



- Molecule 85: Nascent polypeptide-associated complex subunit alpha

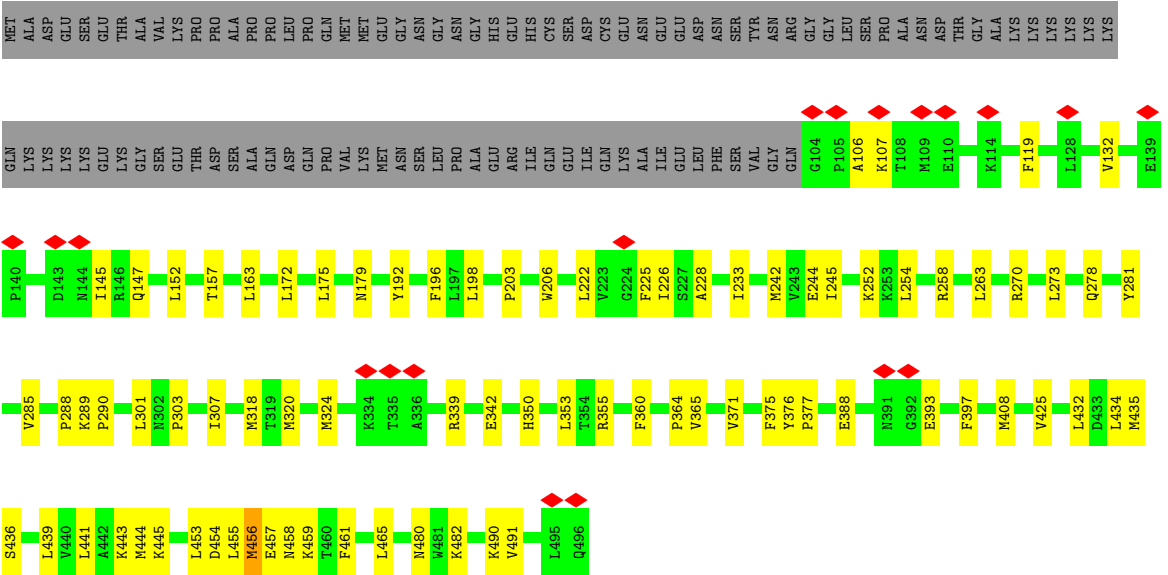


- Molecule 86: Isoform 2 of Transcription factor BTF3

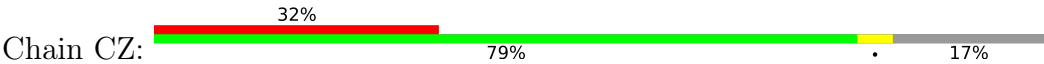




• Molecule 87: Glycylpeptide N-tetradecanoyltransferase 1



• Molecule 88: nascent chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	60443	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	5.209	Depositor
Minimum map value	-2.009	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.116	Depositor
Recommended contour level	0.1	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: ZN, LYO, 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	CM	0.36	0/273	0.48	0/421
2	CP	0.31	0/1789	0.47	0/2788
3	CR	0.27	0/3311	0.54	2/4452 (0.0%)
4	L5	0.36	0/87471	0.41	1/136443 (0.0%)
5	L7	0.35	0/2858	0.36	0/4455
6	L8	0.36	0/3701	0.38	0/5766
7	LA	0.36	0/1936	0.61	0/2596
8	LB	0.33	0/3251	0.55	1/4352 (0.0%)
9	LC	0.32	0/2938	0.56	2/3947 (0.1%)
10	LD	0.28	0/2407	0.52	0/3227
11	LE	0.31	0/1788	0.62	2/2399 (0.1%)
12	LF	0.33	0/1905	0.55	0/2539
13	LG	0.30	0/1849	0.60	1/2496 (0.0%)
14	LH	0.31	0/1529	0.55	0/2058
15	LI	0.31	0/1705	0.53	0/2277
16	LJ	0.30	0/1352	0.57	0/1813
17	LL	0.30	0/1661	0.53	0/2229
18	LM	0.28	0/1145	0.51	0/1536
19	LN	0.33	0/1746	0.48	0/2338
20	LO	0.35	0/1665	0.57	1/2229 (0.0%)
21	LP	0.32	0/1260	0.53	0/1692
22	LQ	0.33	0/1526	0.55	0/2038
23	LR	0.29	0/1468	0.54	0/1945
24	LS	0.33	0/1492	0.51	0/2003
25	LT	0.30	0/1310	0.60	0/1752
26	LU	0.27	0/820	0.65	0/1102
27	LV	0.31	0/985	0.58	0/1323
28	LW	0.29	0/820	0.56	0/1104
29	LX	0.29	0/998	0.50	0/1341
30	LY	0.34	0/1128	0.61	0/1500
31	LZ	0.30	0/1130	0.50	0/1507
32	La	0.32	0/1183	0.50	0/1582

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lb	0.29	0/600	0.53	0/796
34	Lc	0.32	0/752	0.53	0/1011
35	Ld	0.31	0/889	0.48	0/1198
36	Le	0.33	0/1067	0.55	0/1425
37	Lf	0.35	0/891	0.59	0/1194
38	Lg	0.30	0/899	0.52	0/1200
39	Lh	0.28	0/1014	0.52	0/1340
40	Li	0.24	0/824	0.45	0/1093
41	Lj	0.34	0/720	0.57	0/952
42	Lk	0.30	0/548	0.62	0/730
43	Ll	0.33	0/454	0.48	0/599
44	Lm	0.27	0/431	0.42	0/570
45	Ln	0.34	0/231	0.41	0/294
46	Lo	0.33	0/876	0.53	0/1156
47	Lp	0.31	0/706	0.54	0/939
48	Lr	0.32	0/1012	0.55	0/1358
49	Ls	0.33	0/1666	0.78	2/2250 (0.1%)
50	Lt	0.32	0/1224	0.87	3/1651 (0.2%)
51	S2	0.35	0/40882	0.44	1/63715 (0.0%)
52	SA	0.32	0/1708	0.57	0/2324
53	SB	0.28	0/1745	0.51	0/2337
54	SC	0.31	0/1697	0.56	0/2301
55	SD	0.44	2/1620 (0.1%)	0.67	4/2198 (0.2%)
56	SE	0.28	0/2014	0.52	0/2726
57	SF	0.31	0/1423	0.61	3/1913 (0.2%)
58	SG	0.24	0/1657	0.54	0/2247
59	SH	0.24	0/1295	0.50	0/1763
60	SI	0.29	0/1603	0.52	0/2161
61	SJ	0.28	0/1456	0.53	1/1957 (0.1%)
62	SK	0.27	0/750	0.56	0/1026
63	SL	0.35	0/1163	0.51	0/1562
64	SM	0.35	0/960	0.91	3/1286 (0.2%)
65	SN	0.28	0/1206	0.45	0/1626
66	SO	0.32	0/982	0.62	0/1320
67	SP	0.25	0/1010	0.48	0/1362
68	SQ	0.27	0/1093	0.61	0/1470
69	SR	0.31	0/955	0.67	1/1294 (0.1%)
70	SS	0.30	0/1148	0.69	2/1542 (0.1%)
71	ST	0.26	0/1100	0.44	0/1479
72	SU	0.27	0/722	0.59	0/983
73	SV	0.31	0/625	0.55	0/837
74	SW	0.31	0/1043	0.51	0/1396
75	SX	0.33	0/1096	0.63	0/1467

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SY	0.34	1/944 (0.1%)	0.70	2/1271 (0.2%)
77	SZ	0.26	0/565	0.56	0/764
78	Sa	0.35	0/794	0.64	0/1065
79	Sb	0.32	0/632	0.68	0/851
80	Sc	0.27	0/474	0.61	0/638
81	Sd	0.31	0/443	0.52	0/589
82	Se	0.26	0/420	0.54	0/554
83	Sf	0.30	0/525	0.73	1/695 (0.1%)
84	Sg	0.26	0/2235	0.63	0/3068
85	NA	0.43	0/536	1.03	6/715 (0.8%)
86	NB	0.32	0/972	0.71	1/1304 (0.1%)
87	NM	0.25	0/3299	0.69	7/4483 (0.2%)
88	CZ	0.24	0/459	0.45	0/629
All	All	0.34	3/238455 (0.0%)	0.49	47/349924 (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
11	LE	0	1
17	LL	0	1
25	LT	0	1
58	SG	0	1
68	SQ	0	1
70	SS	0	1
86	NB	0	2
87	NM	0	1
All	All	0	9

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	SD	219	PRO	CG-CD	-10.58	1.14	1.50
55	SD	219	PRO	N-CD	6.77	1.57	1.47
76	SY	52	PRO	CG-CD	-5.21	1.33	1.50

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
76	SY	52	PRO	CA-N-CD	-13.23	93.47	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	SD	219	PRO	CA-N-CD	-12.40	94.64	112.00
55	SD	219	PRO	N-CD-CG	-12.01	85.18	103.20
49	Ls	124	PRO	CA-N-CD	-10.16	97.78	112.00
87	NM	456	MET	CB-CG-SD	8.74	138.91	112.70

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
11	LE	176	THR	Peptide
17	LL	47	ALA	Peptide
25	LT	135	PRO	Peptide
58	SG	32	MET	Peptide
68	SQ	27	ARG	Sidechain

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	CM	247	0	128	1	0
2	CP	1602	0	809	2	0
3	CR	3269	0	3312	28	0
4	L5	78199	0	39525	374	0
5	L7	2558	0	1296	9	0
6	L8	3314	0	1683	17	0
7	LA	1898	0	1993	21	0
8	LB	3183	0	3316	28	0
9	LC	2884	0	3050	19	0
10	LD	2361	0	2378	21	0
11	LE	1754	0	1899	32	0
12	LF	1870	0	1996	17	0
13	LG	1818	0	1911	23	0
14	LH	1510	0	1579	8	0
15	LI	1666	0	1711	21	0
16	LJ	1329	0	1348	12	0
17	LL	1630	0	1715	15	0
18	LM	1122	0	1174	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	LN	1701	0	1749	20	0
20	LO	1633	0	1771	13	0
21	LP	1234	0	1254	13	0
22	LQ	1502	0	1616	6	0
23	LR	1452	0	1580	13	0
24	LS	1452	0	1490	12	0
25	LT	1282	0	1336	13	0
26	LU	806	0	826	14	0
27	LV	971	0	1023	12	0
28	LW	808	0	726	8	0
29	LX	981	0	1055	14	0
30	LY	1111	0	1194	16	0
31	LZ	1107	0	1182	11	0
32	La	1154	0	1198	12	0
33	Lb	590	0	613	9	0
34	Lc	742	0	774	10	0
35	Ld	874	0	918	9	0
36	Le	1049	0	1136	7	0
37	Lf	872	0	901	7	0
38	Lg	889	0	968	8	0
39	Lh	1006	0	1132	6	0
40	Li	813	0	887	6	0
41	Lj	705	0	737	10	0
42	Lk	542	0	590	7	0
43	Ll	444	0	483	8	0
44	Lm	425	0	461	5	0
45	Ln	230	0	276	1	0
46	Lo	862	0	929	8	0
47	Lp	696	0	744	8	0
48	Lr	997	0	1054	10	0
49	Ls	1640	0	1687	41	0
50	Lt	1208	0	1257	26	0
51	S2	36562	0	18472	257	0
52	SA	1671	0	1672	27	0
53	SB	1718	0	1786	29	0
54	SC	1661	0	1710	15	0
55	SD	1594	0	1568	19	0
56	SE	1972	0	2012	25	0
57	SF	1403	0	1421	15	0
58	SG	1634	0	1568	21	0
59	SH	1274	0	1196	17	0
60	SI	1574	0	1540	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	SJ	1431	0	1497	21	0
62	SK	726	0	674	9	0
63	SL	1143	0	1177	16	0
64	SM	950	0	987	21	0
65	SN	1182	0	1249	11	0
66	SO	969	0	982	16	0
67	SP	990	0	974	16	0
68	SQ	1075	0	1110	15	0
69	SR	942	0	913	12	0
70	SS	1130	0	1167	19	0
71	ST	1081	0	1093	19	0
72	SU	713	0	692	14	0
73	SV	618	0	617	9	0
74	SW	1026	0	1072	12	0
75	SX	1078	0	1130	16	0
76	SY	927	0	914	17	0
77	SZ	559	0	594	7	0
78	Sa	781	0	831	6	0
79	Sb	618	0	604	8	0
80	Sc	472	0	484	5	0
81	Sd	433	0	415	11	0
82	Se	416	0	439	4	0
83	Sf	515	0	521	5	0
84	Sg	2180	0	1968	22	0
85	NA	531	0	573	15	0
86	NB	963	0	982	18	0
87	NM	3209	0	3185	47	0
88	CZ	455	0	338	3	0
89	CM	1	0	0	0	0
89	L5	126	0	0	0	0
89	L7	3	0	0	0	0
89	L8	3	0	0	0	0
89	LA	1	0	0	0	0
89	LC	1	0	0	0	0
89	LI	1	0	0	0	0
89	LN	1	0	0	0	0
89	LP	1	0	0	0	0
89	LV	1	0	0	0	0
89	S2	51	0	0	0	0
89	ST	1	0	0	0	0
90	Lg	1	0	0	0	0
90	Lj	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
90	Lm	1	0	0	0	0
90	Lo	1	0	0	0	0
90	Lp	1	0	0	0	0
90	Sa	1	0	0	0	0
90	Sd	1	0	0	0	0
90	Sf	1	0	0	0	0
91	L5	4	0	0	0	0
91	L7	1	0	0	0	0
91	LI	1	0	0	0	0
91	LN	1	0	0	0	0
91	La	1	0	0	0	0
91	S2	3	0	0	0	0
All	All	222378	0	164497	1563	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 4.

The worst 5 of 1563 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)
51:S2:1748:G:H1	51:S2:1786:U:H3	1.14	0.89
4:L5:3751:G:H21	4:L5:3775:A:H8	1.18	0.88
1:CM:443:U:H3	2:CP:33:A:H61	1.26	0.84
51:S2:1098:C:H5	51:S2:1134:G:H1	1.30	0.80
51:S2:1142:G:H21	51:S2:1145:A:H2	1.30	0.80

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	CM	11/586 (1%)	2 (18%)	0
2	CP	74/75 (98%)	23 (31%)	2 (2%)
4	L5	3633/5070 (71%)	750 (20%)	21 (0%)
5	L7	119/121 (98%)	14 (11%)	0
51	S2	1704/1869 (91%)	458 (26%)	18 (1%)
6	L8	155/157 (98%)	27 (17%)	3 (1%)
All	All	5696/7878 (72%)	1274 (22%)	44 (0%)

5 of 1274 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	CM	439	C
1	CM	444	U
2	CP	2	G
2	CP	4	U
2	CP	5	C

5 of 44 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	S2	213	G
51	S2	1273	C
51	S2	465	A
51	S2	912	C
51	S2	1395	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	$\# Z > 2$
3	LYO	CR	63	3	7,9,10	0.80	0	7,10,12	1.15	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
3	LYO	CR	63	3	-	2/8/9/11	-

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
3	CR	63	LYO	N-CA-CB-CG
3	CR	63	LYO	C-CA-CB-CG

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 199 ligands modelled in this entry, 199 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

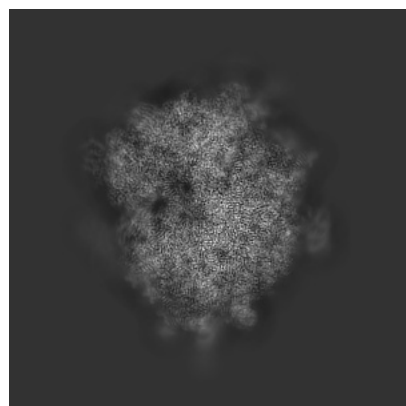
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-54528. These allow visual inspection of the internal detail of the map and identification of artifacts.

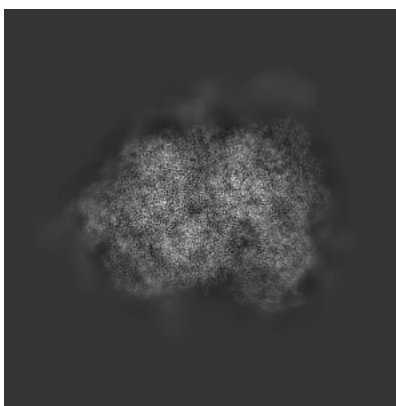
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

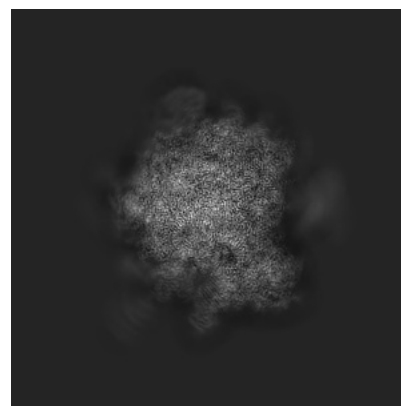
6.1.1 Primary map



X

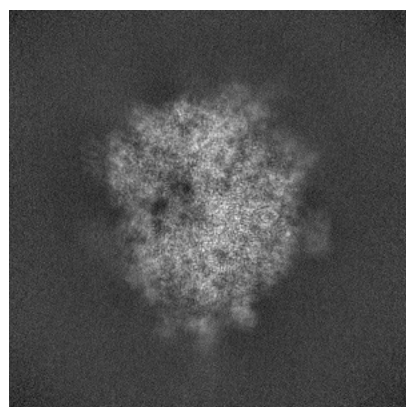


Y

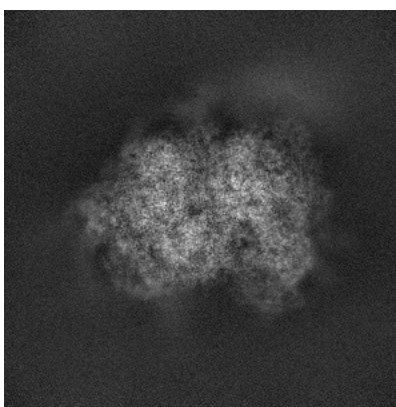


Z

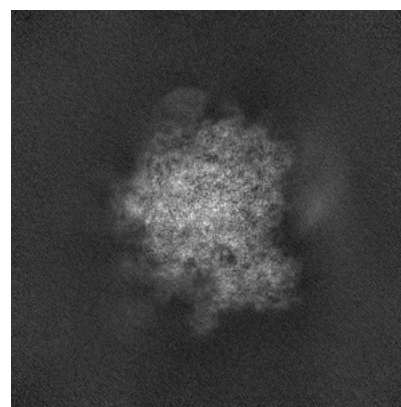
6.1.2 Raw map



X



Y

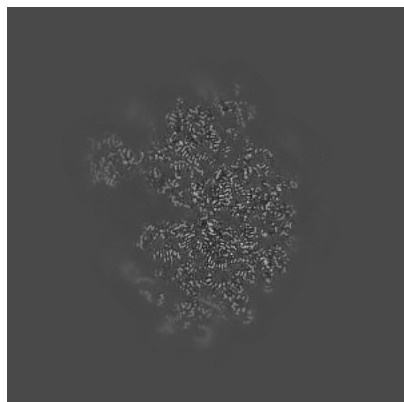


Z

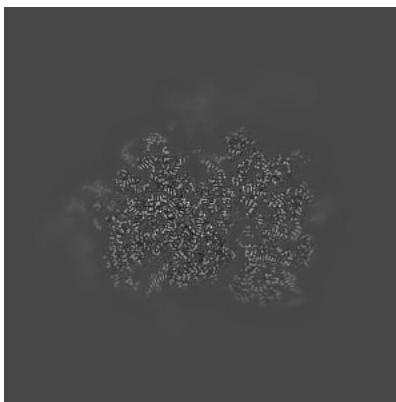
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

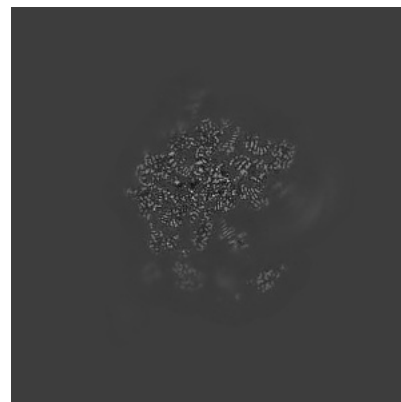
6.2.1 Primary map



X Index: 320

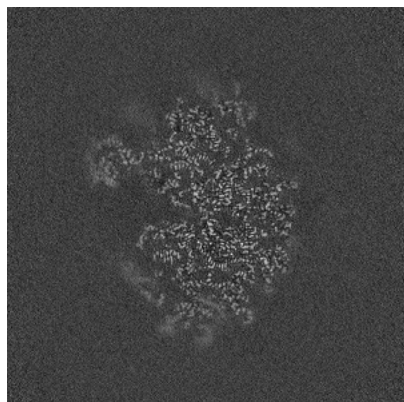


Y Index: 320

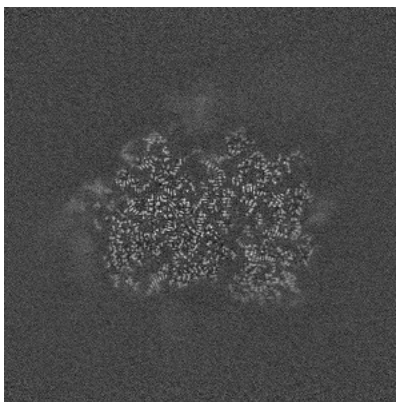


Z Index: 320

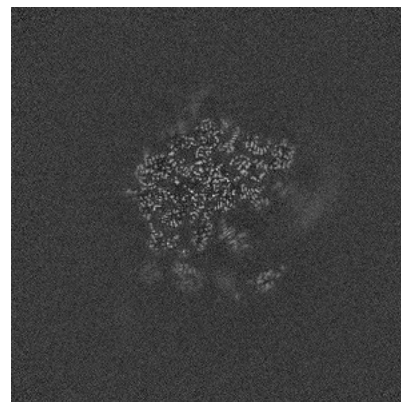
6.2.2 Raw map



X Index: 320



Y Index: 320

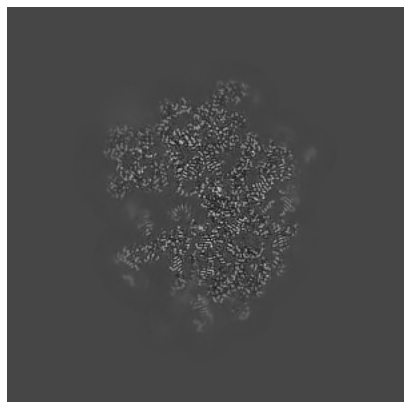


Z Index: 320

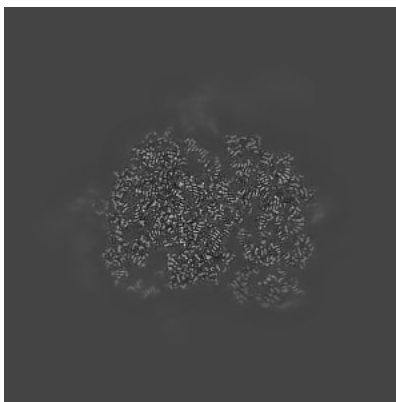
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

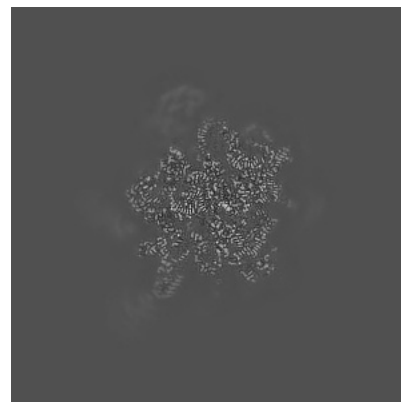
6.3.1 Primary map



X Index: 344

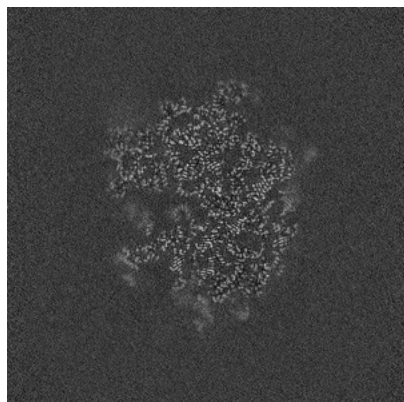


Y Index: 329

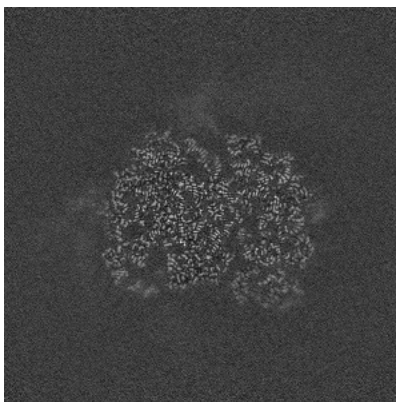


Z Index: 267

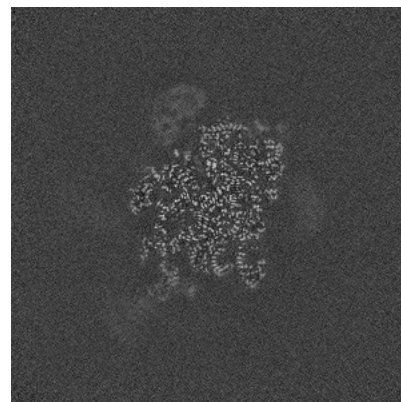
6.3.2 Raw map



X Index: 344



Y Index: 329

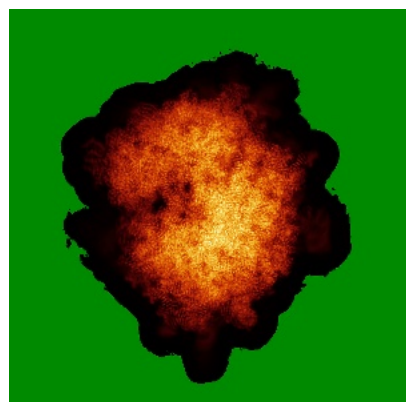


Z Index: 282

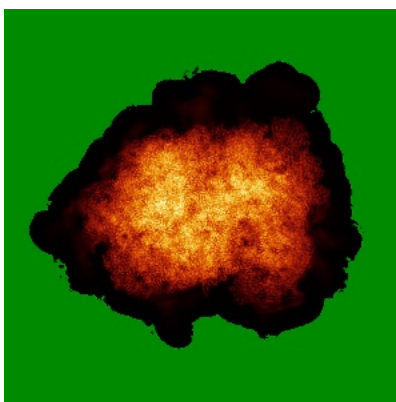
The images above show the largest variance slices of the map in three orthogonal directions.

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

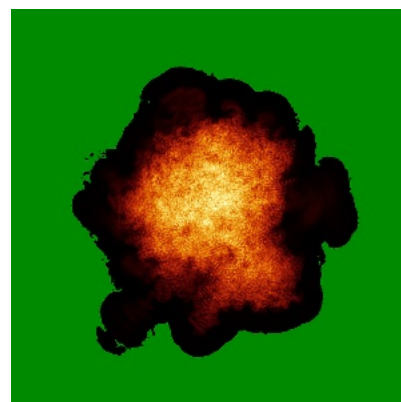
6.4.1 Primary map



X

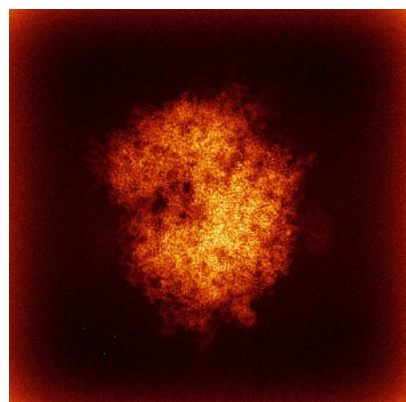


Y

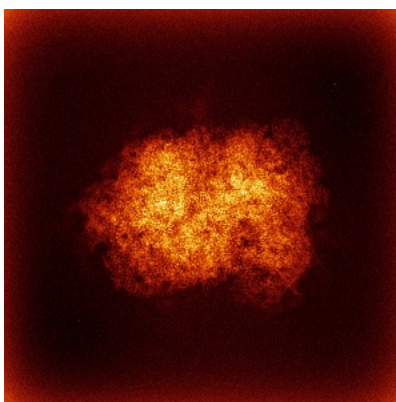


Z

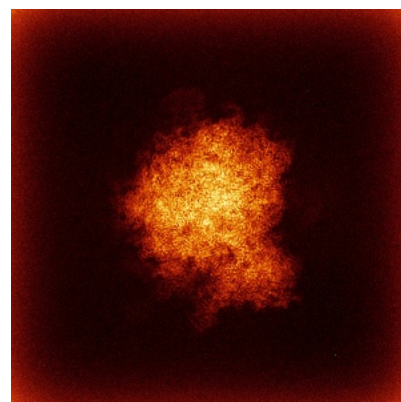
6.4.2 Raw map



X



Y

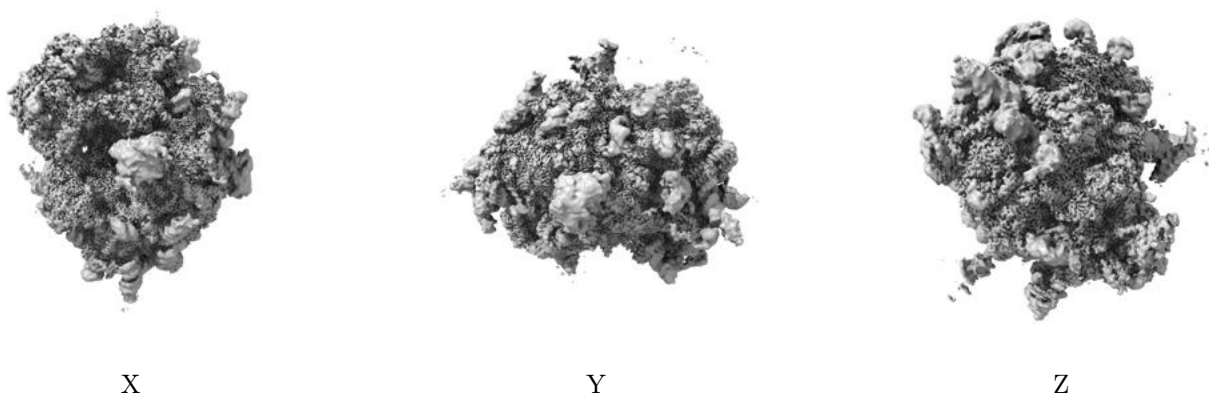


Z

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.

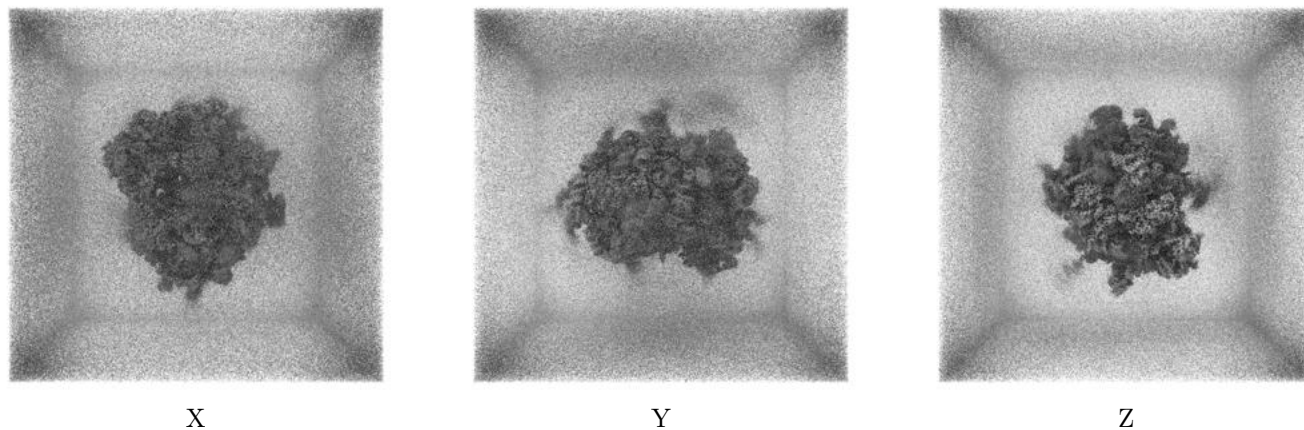
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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



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.

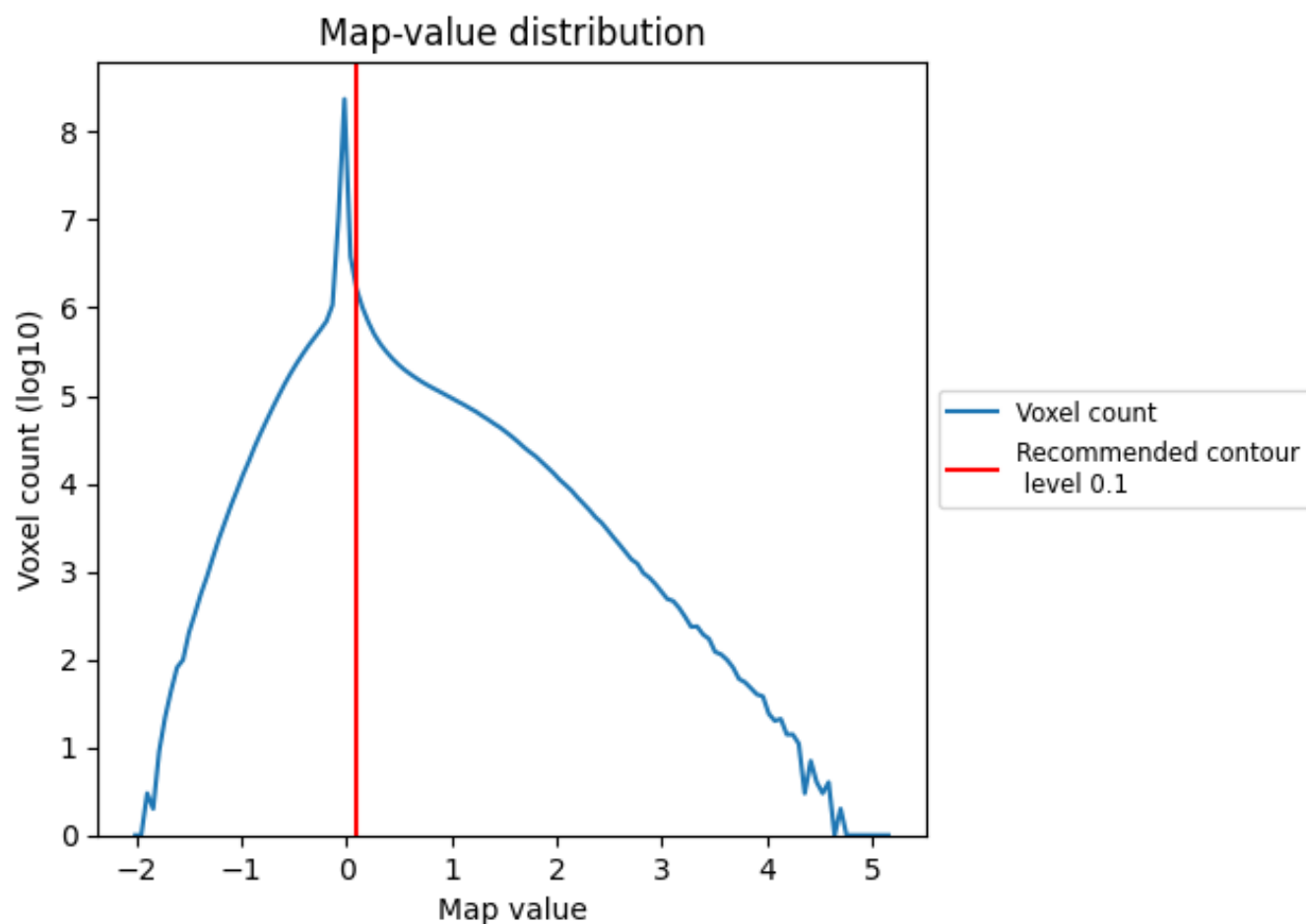
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

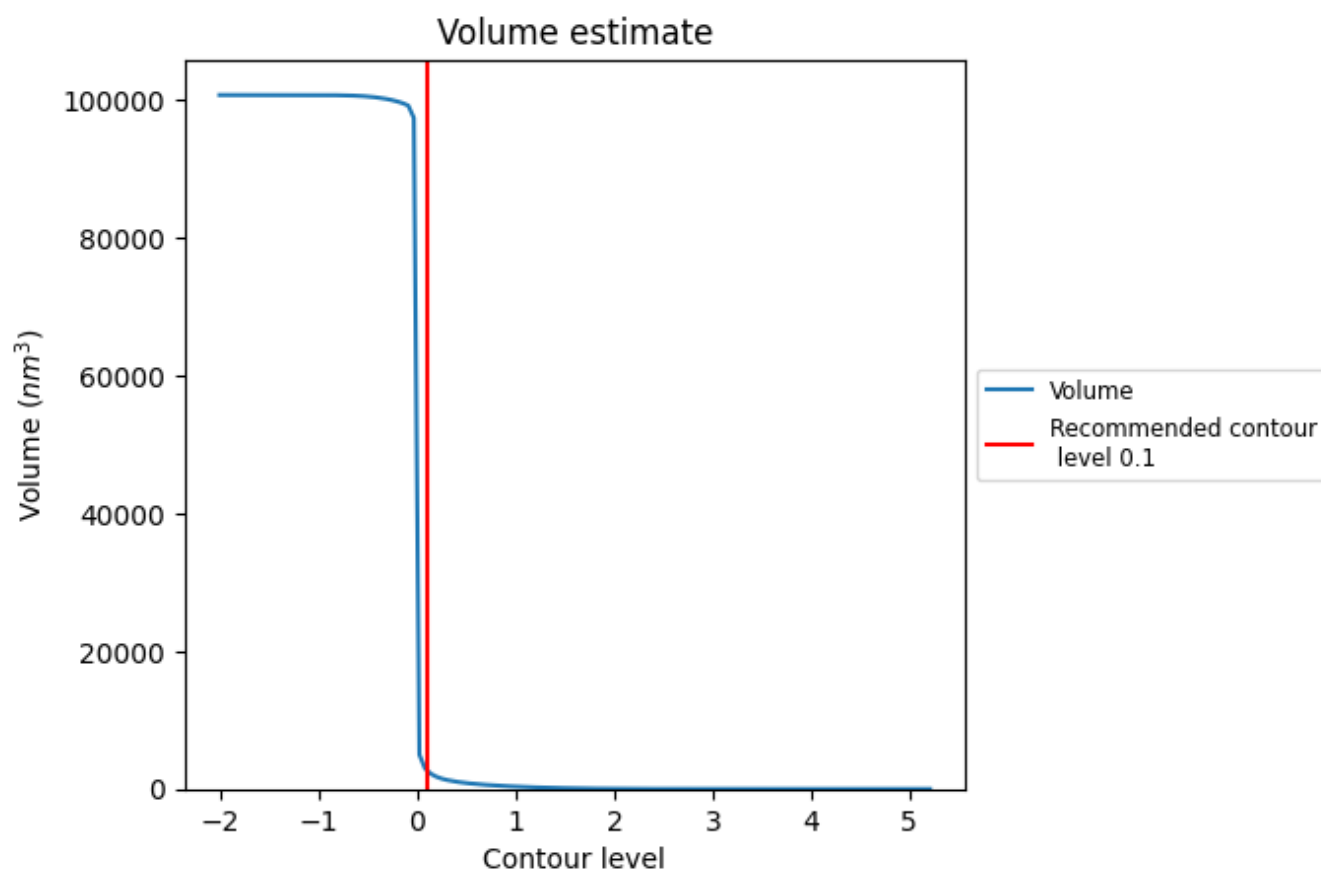
This section contains the results of statistical analysis of the map.

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.

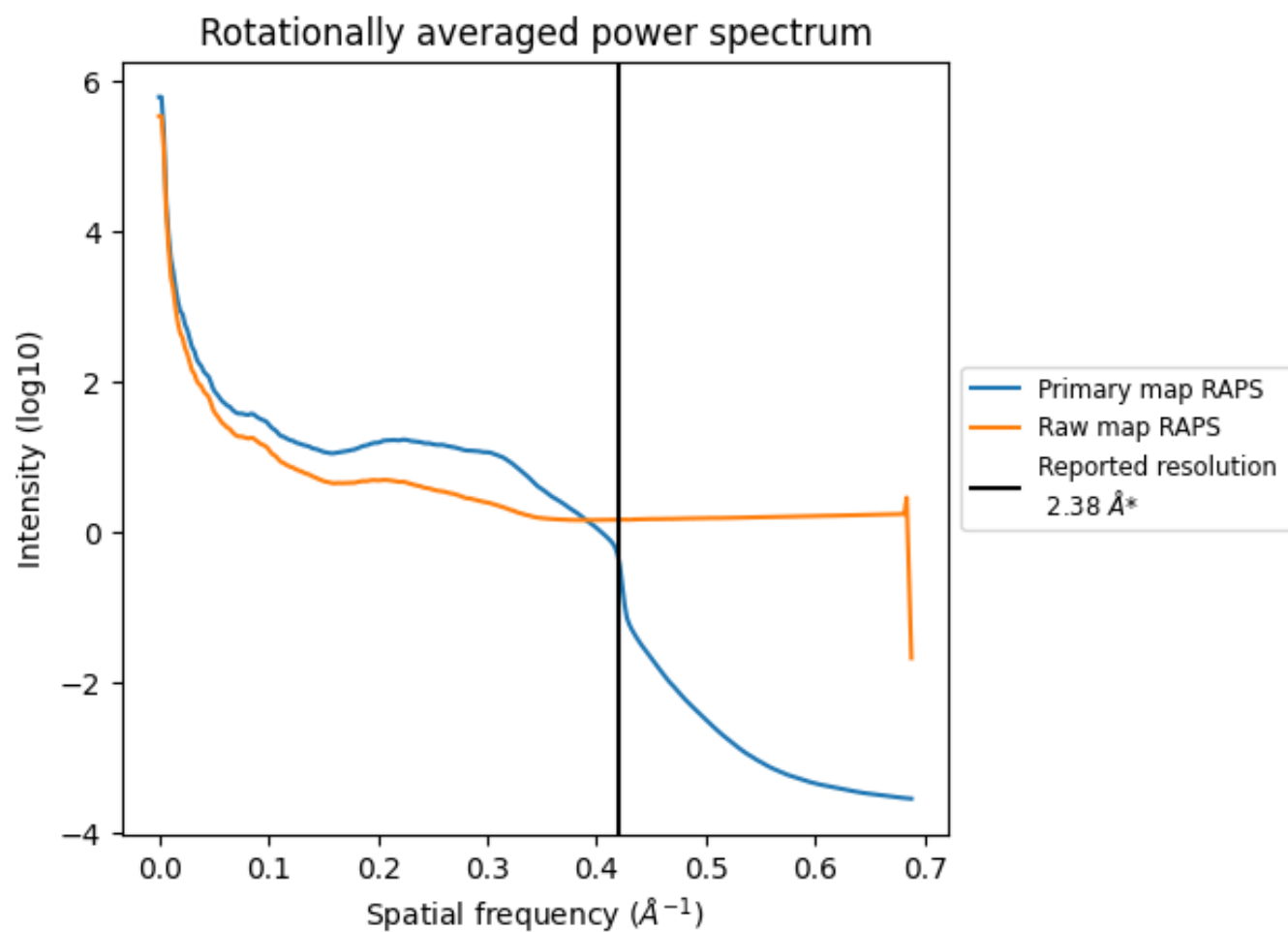
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2692 nm^3 ; this corresponds to an approximate mass of 2432 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 ⓘ

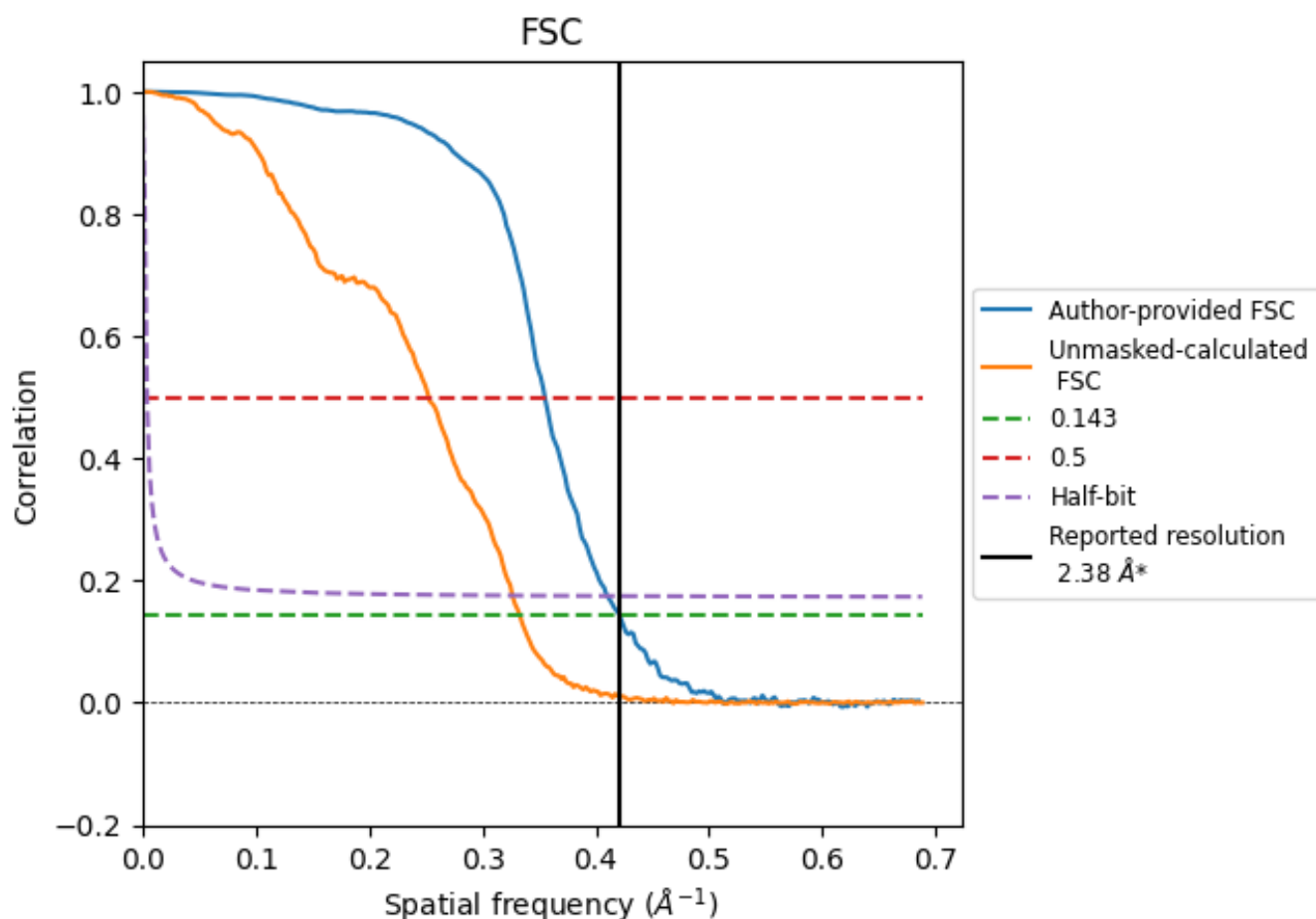


*Reported resolution corresponds to spatial frequency of 0.420 \AA^{-1}

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 0.420 Å⁻¹

8.2 Resolution estimates [i](#)

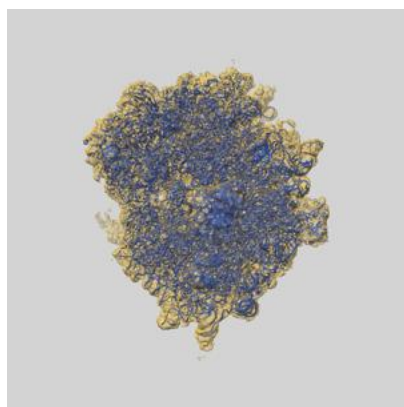
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.38	-	-
Author-provided FSC curve	2.38	2.82	2.44
Unmasked-calculated*	3.00	3.96	3.06

*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 3.00 differs from the reported value 2.38 by more than 10 %

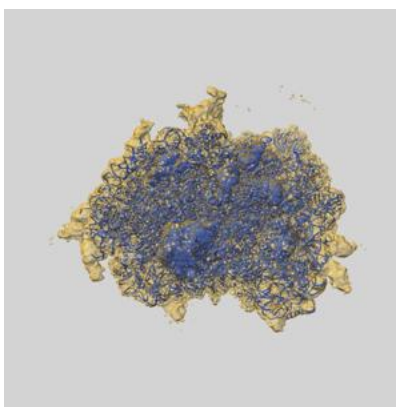
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-54528 and PDB model 9S3B. Per-residue inclusion information can be found in [section 3](#) on [page 22](#).

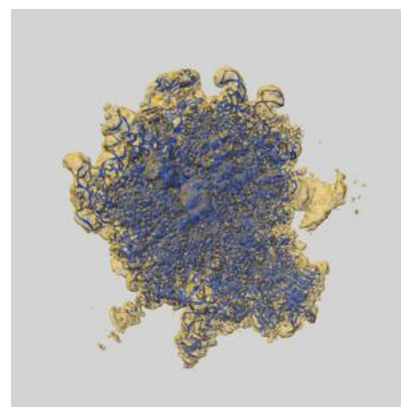
9.1 Map-model overlay [i](#)



X



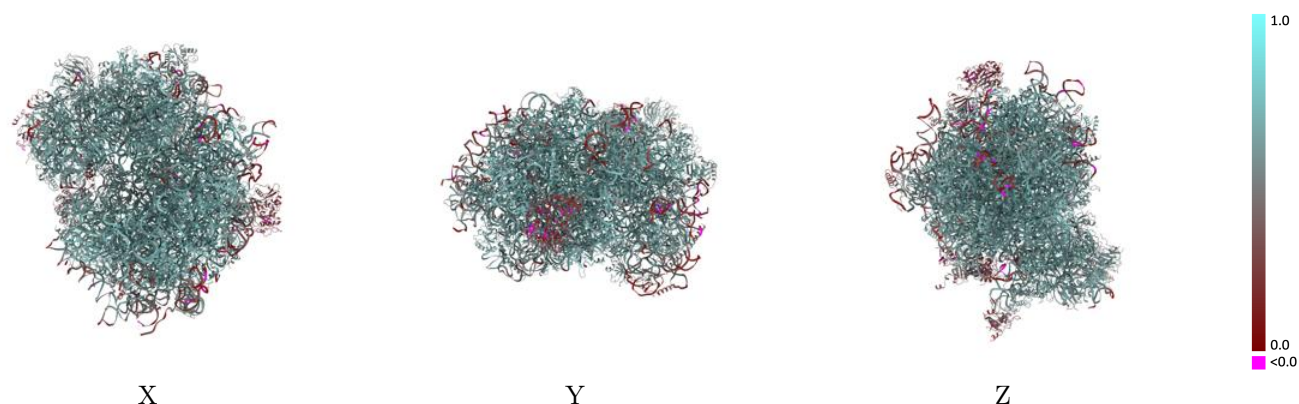
Y



Z

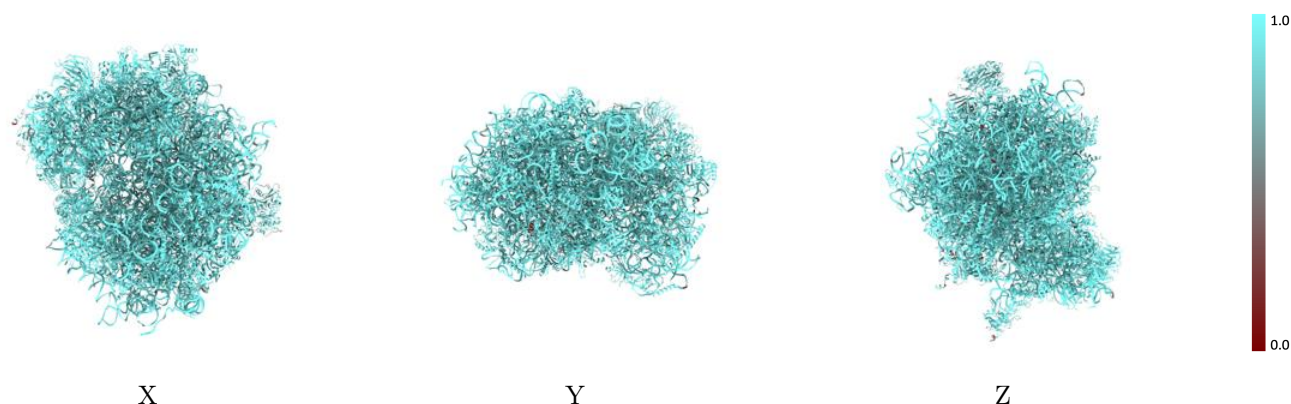
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



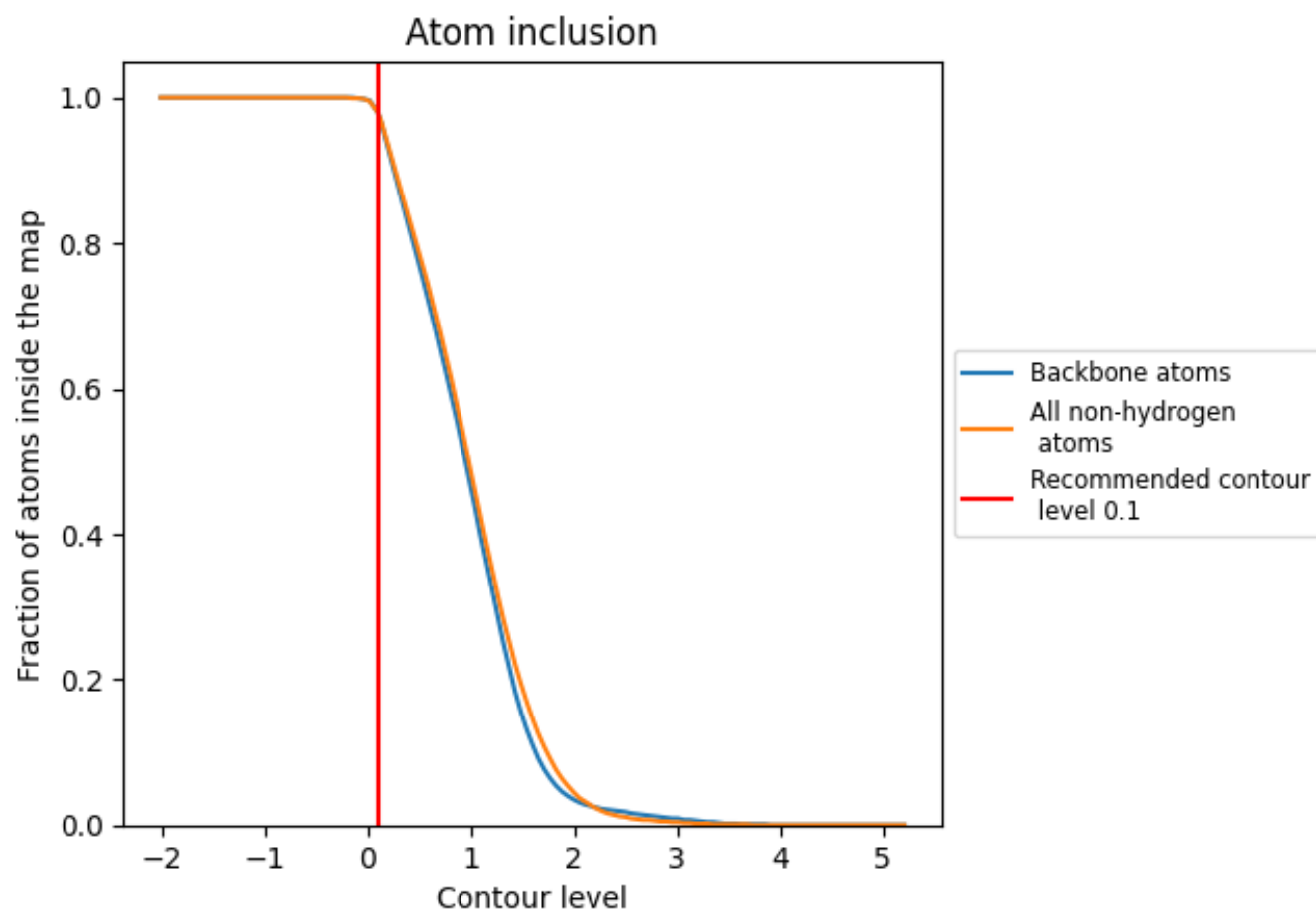
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 98% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9800	 0.6090
CM	 0.9880	 0.6080
CP	 0.9890	 0.5940
CR	 0.9230	 0.5290
CZ	 0.6670	 0.3350
L5	 0.9890	 0.6200
L7	 0.9950	 0.6690
L8	 0.9860	 0.6360
LA	 0.9940	 0.6970
LB	 0.9920	 0.6760
LC	 0.9890	 0.6720
LD	 0.9870	 0.6300
LE	 0.9860	 0.6200
LF	 0.9860	 0.6730
LG	 0.9770	 0.6140
LH	 0.9900	 0.6430
LI	 0.9850	 0.6490
LJ	 0.9810	 0.6120
LL	 0.9800	 0.6420
LM	 0.9960	 0.6510
LN	 0.9960	 0.7030
LO	 0.9940	 0.6860
LP	 0.9880	 0.6830
LQ	 0.9940	 0.6880
LR	 0.9880	 0.6610
LS	 0.9960	 0.6800
LT	 0.9820	 0.6410
LU	 0.9820	 0.5780
LV	 0.9930	 0.6860
LW	 0.9590	 0.5280
LX	 0.9790	 0.6560
LY	 0.9900	 0.6500
LZ	 0.9880	 0.6470
La	 0.9910	 0.6880
Lb	 0.9710	 0.5960



























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Chain	Atom inclusion	Q-score
Lc	 0.9840	 0.6610
Ld	 0.9890	 0.6610
Le	 0.9970	 0.6950
Lf	 0.9880	 0.6870
Lg	 0.9800	 0.6650
Lh	 0.9900	 0.6520
Li	 0.9950	 0.6490
Lj	 0.9910	 0.6880
Lk	 0.9510	 0.5770
Ll	 0.9880	 0.6640
Lm	 0.9760	 0.6660
Ln	 0.9950	 0.6940
Lo	 0.9920	 0.6680
Lp	 0.9960	 0.6920
Lr	 0.9950	 0.6690
Ls	 0.8520	 0.3050
Lt	 0.9390	 0.3680
NA	 0.6760	 0.1570
NB	 0.8010	 0.2540
NM	 0.8720	 0.2240
S2	 0.9850	 0.6000
SA	 0.9900	 0.6440
SB	 0.9860	 0.6340
SC	 0.9910	 0.6550
SD	 0.9860	 0.6020
SE	 0.9910	 0.6230
SF	 0.9750	 0.6080
SG	 0.9880	 0.5440
SH	 0.9890	 0.5770
SI	 0.9900	 0.6270
SJ	 0.9920	 0.6250
SK	 0.9870	 0.5870
SL	 0.9890	 0.6570
SM	 0.8710	 0.3010
SN	 0.9940	 0.6670
SO	 0.9920	 0.6550
SP	 0.9840	 0.5970
SQ	 0.9790	 0.6210
SR	 0.9620	 0.5660
SS	 0.9760	 0.5980
ST	 0.9870	 0.6230
SU	 0.9780	 0.5630

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Chain	Atom inclusion	Q-score
SV	 0.9880	 0.6390
SW	 0.9940	 0.6760
SX	 0.9840	 0.6480
SY	 0.9910	 0.5910
SZ	 0.9760	 0.5800
Sa	 0.9870	 0.6480
Sb	 0.9800	 0.6000
Sc	 0.9340	 0.5500
Sd	 0.9900	 0.6480
Se	 0.9900	 0.5960
Sf	 0.8490	 0.3210
Sg	 0.9770	 0.5450