



wwPDB EM Validation Summary Report ⓘ

Sep 23, 2026 – 06:57 pm BST

PDB ID : 9T6C / pdb_00009t6c
EMDB ID : EMD-55612
Title : NAA40-NAC bound active human 80S
Authors : Guan, D.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-11-07
Resolution : 2.91 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:

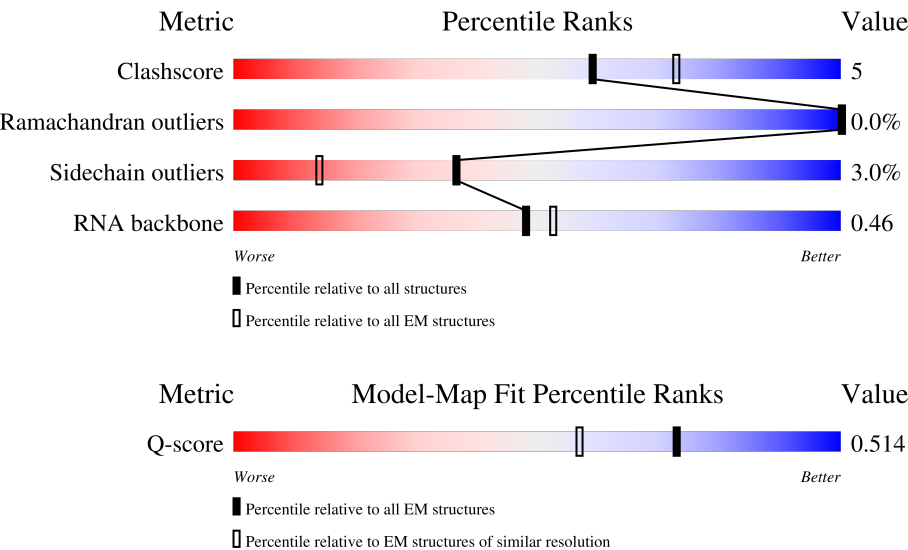
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.91 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.



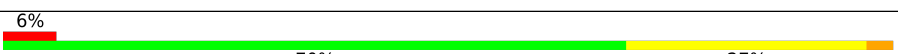
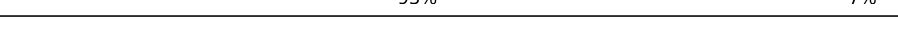
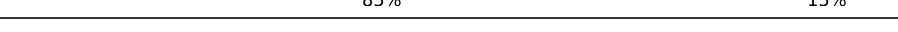
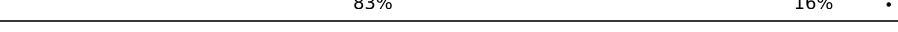
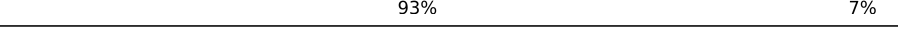
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	12972 (2.41 - 3.41)

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

Mol	Chain	Length	Quality of chain
1	LA	248	87%12%
2	NA	215	32% 42%8%50%
3	SA	216	77%22%

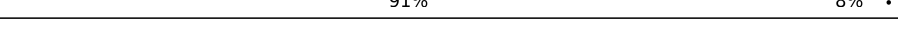
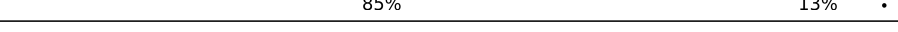
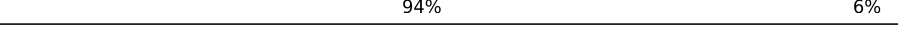
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Mol	Chain	Length	Quality of chain
4	LB	395	
5	NB	106	
6	SB	213	
7	Bv	76	
8	Bx	11	
9	Bw	76	
10	N4	221	
11	L5	5070	
12	L7	120	
13	L8	156	
14	LC	364	
15	LD	293	
16	LE	288	
17	LF	225	
18	LG	238	
19	LH	190	
20	LI	213	
21	LJ	169	
22	LL	205	
23	LM	139	
24	LN	203	
25	LO	200	
26	LP	153	
27	LQ	187	
28	LR	176	

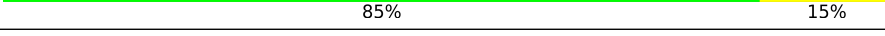
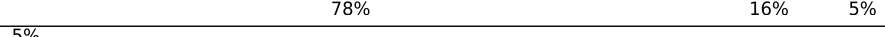
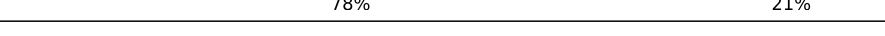
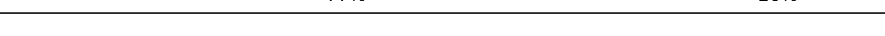
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Mol	Chain	Length	Quality of chain
29	LS	175	 89% 11% .
30	LT	159	 86% 13% .
31	LU	101	 73% 26% .
32	LV	131	 84% 16%
33	LW	119	 89% 8% .
34	LX	120	 85% 14% .
35	LY	134	 83% 16% .
36	LZ	135	 79% 21%
37	La	147	 86% 12% .
38	Lb	75	 89% 9% .
39	Lc	97	 85% 15%
40	Ld	107	 87% 13%
41	Le	128	 90% 10%
42	Lf	109	 88% 12%
43	Lg	114	 89% 11%
44	Lh	121	 91% 8% .
45	Li	102	 85% 13% .
46	Lj	86	 94% 6%
47	Lk	69	 81% 14% .
48	Ll	50	 92% 8%
49	Lm	52	 90% 10%
50	Ln	24	 88% 12%
51	Lo	105	 88% 10% .
52	Lp	91	 91% 9%
53	Lr	125	 85% 15%

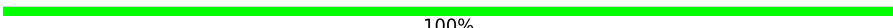
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Mol	Chain	Length	Quality of chain
54	S2	1869	
55	SC	219	
56	SD	225	
57	SE	262	
58	SF	187	
59	SG	231	
60	SH	185	
61	SI	206	
62	SJ	179	
63	SK	96	
64	SL	152	
65	SM	122	
66	SN	150	
67	SO	134	
68	SP	117	
69	SQ	142	
70	SR	131	
71	SS	141	
72	ST	143	
73	SU	101	
74	SV	83	
75	SW	129	
76	SX	141	
77	SY	123	
78	SZ	75	

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Mol	Chain	Length	Quality of chain
79	Sa	99	 80%19%.
80	Sb	83	 87%13%
81	Sc	63	 70%24%6%
82	Sd	53	 83%17%
83	Se	55	 87%13%
84	Sf	63	 73%27%
85	Sg	310	 70%27%..
86	NC	26	 100%

2 Entry composition

There are 89 unique types of molecules in this entry. The entry contains 215206 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L8.

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

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

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

- Molecule 3 is a protein called Small ribosomal subunit protein uS2.

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

- Molecule 4 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 5 is a protein called Isoform 2 of Transcription factor BTF3.

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

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

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

- Molecule 7 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Bv	76	Total	C	N	O	P	0	0
			1620	723	290	531	76		

- Molecule 8 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Bx	11	Total	C	N	O	P	0	0
			234	105	41	77	11		

- Molecule 9 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Bw	76	Total	C	N	O	P	0	0
			1627	725	294	532	76		

- Molecule 10 is a protein called N-alpha-acetyltransferase 40.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N4	221	Total	C	N	O	S	0	0
			1795	1128	313	339	15		

- Molecule 11 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L5	3600	Total	C	N	O	P	0	0
			77166	34362	14114	25091	3599		

- Molecule 12 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 13 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 14 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 15 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 16 is a protein called Large ribosomal subunit protein eL6.

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

- Molecule 17 is a protein called 60S ribosomal protein L7.

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

- Molecule 18 is a protein called Large ribosomal subunit protein eL8.

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

- Molecule 19 is a protein called 60S ribosomal protein L9.

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

- Molecule 20 is a protein called Ribosomal protein uL16-like.

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

- Molecule 21 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 22 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 23 is a protein called 60S ribosomal protein L14.

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

- Molecule 24 is a protein called 60S ribosomal protein L15.

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

- Molecule 25 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 26 is a protein called 60S ribosomal protein L17.

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

- Molecule 27 is a protein called 60S ribosomal protein L18.

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

- Molecule 28 is a protein called Large ribosomal subunit protein eL19.

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

- Molecule 29 is a protein called 60S ribosomal protein L18a.

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

- Molecule 30 is a protein called 60S ribosomal protein L21.

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

- Molecule 31 is a protein called 60S ribosomal protein L22.

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

- Molecule 32 is a protein called 60S ribosomal protein L23.

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

- Molecule 33 is a protein called Large ribosomal subunit protein eL24.

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

- Molecule 34 is a protein called 60S ribosomal protein L23a.

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

- Molecule 35 is a protein called 60S ribosomal protein L26.

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

- Molecule 36 is a protein called 60S ribosomal protein L27.

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

- Molecule 37 is a protein called 60S ribosomal protein L27a.

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

- Molecule 38 is a protein called Large ribosomal subunit protein eL29.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL30.

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

- Molecule 40 is a protein called 60S ribosomal protein L31.

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

- Molecule 41 is a protein called 60S ribosomal protein L32.

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

- Molecule 42 is a protein called 60S ribosomal protein L35a.

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

- Molecule 43 is a protein called 60S ribosomal protein L34.

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

- Molecule 44 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 45 is a protein called 60S ribosomal protein L36.

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

- Molecule 46 is a protein called 60S ribosomal protein L37.

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

- Molecule 47 is a protein called 60S ribosomal protein L38.

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

- Molecule 48 is a protein called 60S ribosomal protein L39.

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

- Molecule 49 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 50 is a protein called 60S ribosomal protein L41.

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

- Molecule 51 is a protein called 60S ribosomal protein L36a.

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

- Molecule 52 is a protein called 60S ribosomal protein L37a.

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

- Molecule 53 is a protein called 60S ribosomal protein L28.

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

- Molecule 54 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 55 is a protein called Small ribosomal subunit protein uS5.

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

- Molecule 56 is a protein called Small ribosomal subunit protein uS3.

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

- Molecule 57 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SE	262	Total	C	N	O	S	0	0
			1972	1270	370	324	8		

- Molecule 58 is a protein called Small ribosomal subunit protein uS7.

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

- Molecule 59 is a protein called Small ribosomal subunit protein eS6.

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

- Molecule 60 is a protein called Small ribosomal subunit protein eS7.

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

- 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
			1574	989	308	272	5		

- Molecule 62 is a protein called Small ribosomal subunit protein uS4.

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

- Molecule 63 is a protein called Small ribosomal subunit protein eS10.

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

- Molecule 64 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SL	144	Total	C	N	O	S	0	0
			1143	730	213	194	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SM	122	Total	C	N	O	S	0	0
			950	596	168	177	9		

- 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
			1182	758	226	197	1		

- Molecule 67 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SO	134	Total	C	N	O	S	0	0
			969	596	194	173	6		

- Molecule 68 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SP	117	Total	C	N	O	S	0	0
			907	578	170	153	6		

- Molecule 69 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 70 is a protein called Small ribosomal subunit protein eS17.

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

- Molecule 71 is a protein called Small ribosomal subunit protein uS13.

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

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

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

- Molecule 77 is a protein called Small ribosomal subunit protein eS24.

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

- 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
			559	361	105	92	1		

- Molecule 79 is a protein called Small ribosomal subunit protein eS26.

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

- Molecule 81 is a protein called Small ribosomal subunit protein eS28.

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

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

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

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

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

- Molecule 84 is a protein called Ubiquitin-ribosomal protein eS31 fusion protein.

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

- Molecule 85 is a protein called Small ribosomal subunit protein RACK1.

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

- Molecule 86 is a protein called nascent polypeptide chain.

Mol	Chain	Residues	Atoms				AltConf	Trace
86	NC	26	Total	C	N	O	0	0
			130	78	26	26		

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	LA	1	Total	Mg	0
			1	1	
87	L5	126	Total	Mg	0
			126	126	
87	L7	3	Total	Mg	0
			3	3	
87	L8	3	Total	Mg	0
			3	3	
87	LC	1	Total	Mg	0
			1	1	
87	LI	1	Total	Mg	0
			1	1	
87	LN	1	Total	Mg	0
			1	1	
87	LP	1	Total	Mg	0
			1	1	
87	LV	1	Total	Mg	0
			1	1	
87	S2	52	Total	Mg	0
			52	52	
87	ST	1	Total	Mg	0
			1	1	

- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

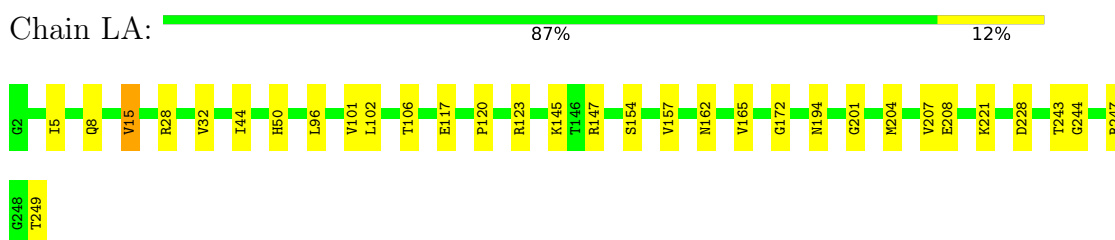
- Molecule 89 is water.

Mol	Chain	Residues	Atoms		AltConf
89	L5	3	Total 3	O 3	0
89	L7	1	Total 1	O 1	0
89	LI	1	Total 1	O 1	0
89	LN	1	Total 1	O 1	0
89	La	1	Total 1	O 1	0
89	Lp	1	Total 1	O 1	0
89	S2	3	Total 3	O 3	0

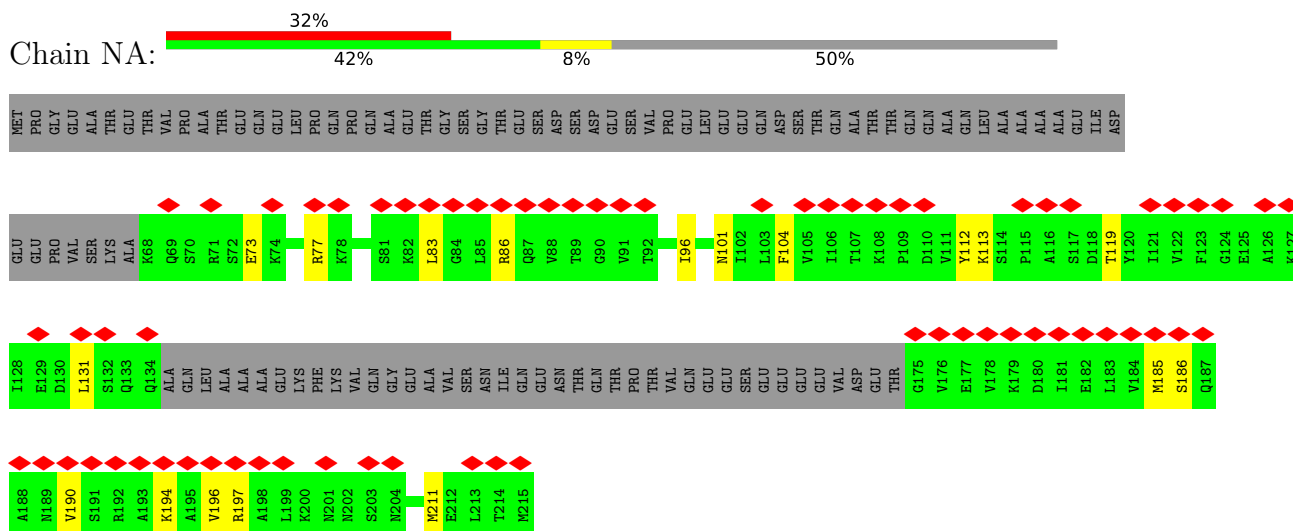
3 Residue-property plots

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.

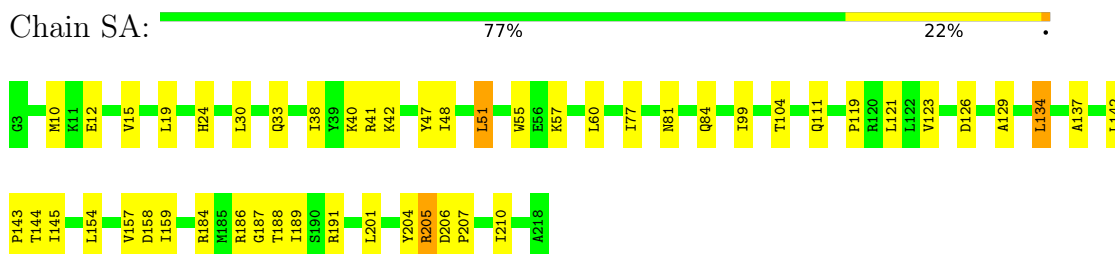
- Molecule 1: 60S ribosomal protein L8



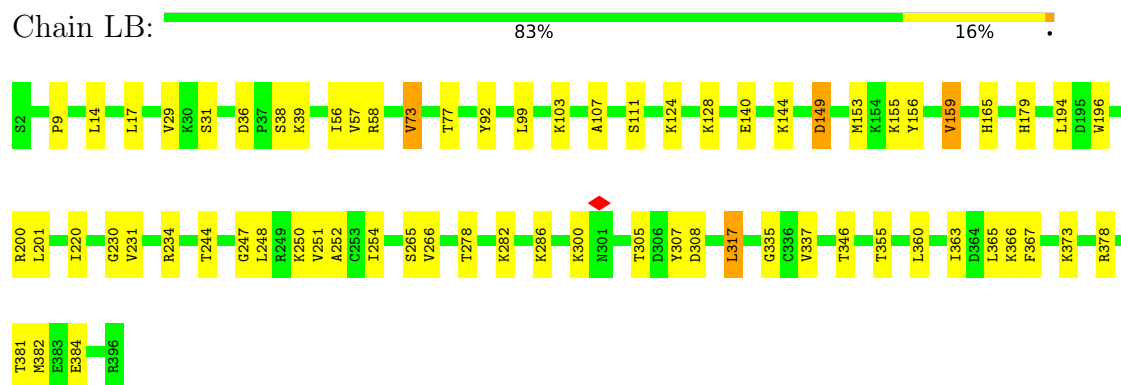
- Molecule 2: Nascent polypeptide-associated complex subunit alpha



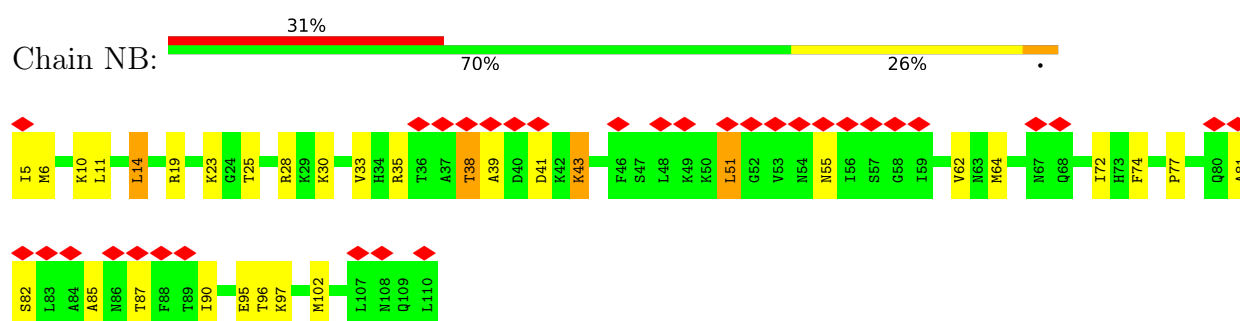
- Molecule 3: Small ribosomal subunit protein uS2



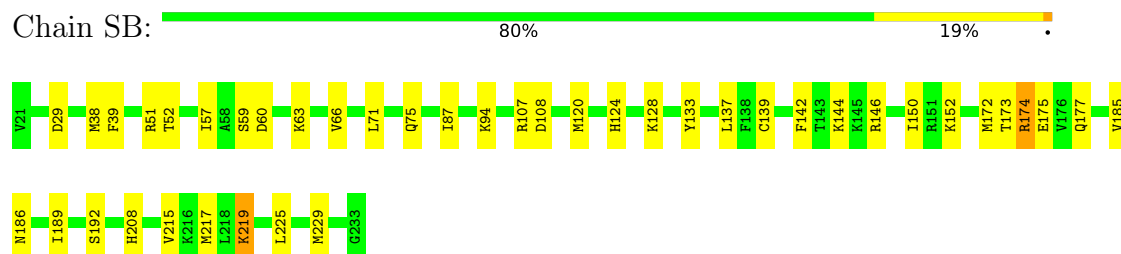
- Molecule 4: Large ribosomal subunit protein uL3



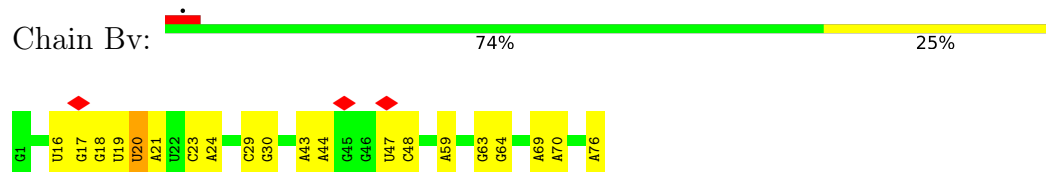
- Molecule 5: Isoform 2 of Transcription factor BTF3



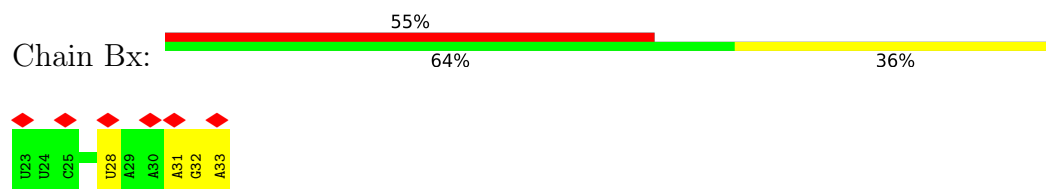
- Molecule 6: 40S ribosomal protein S3a



- Molecule 7: P-site tRNA



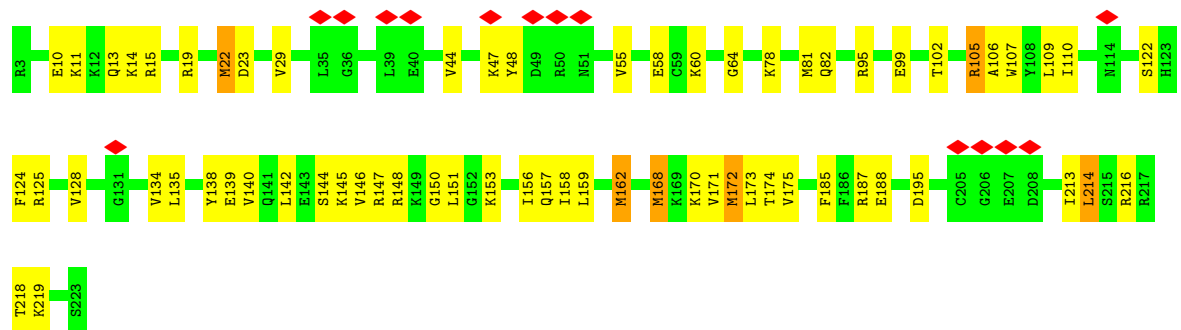
- Molecule 8: mRNA



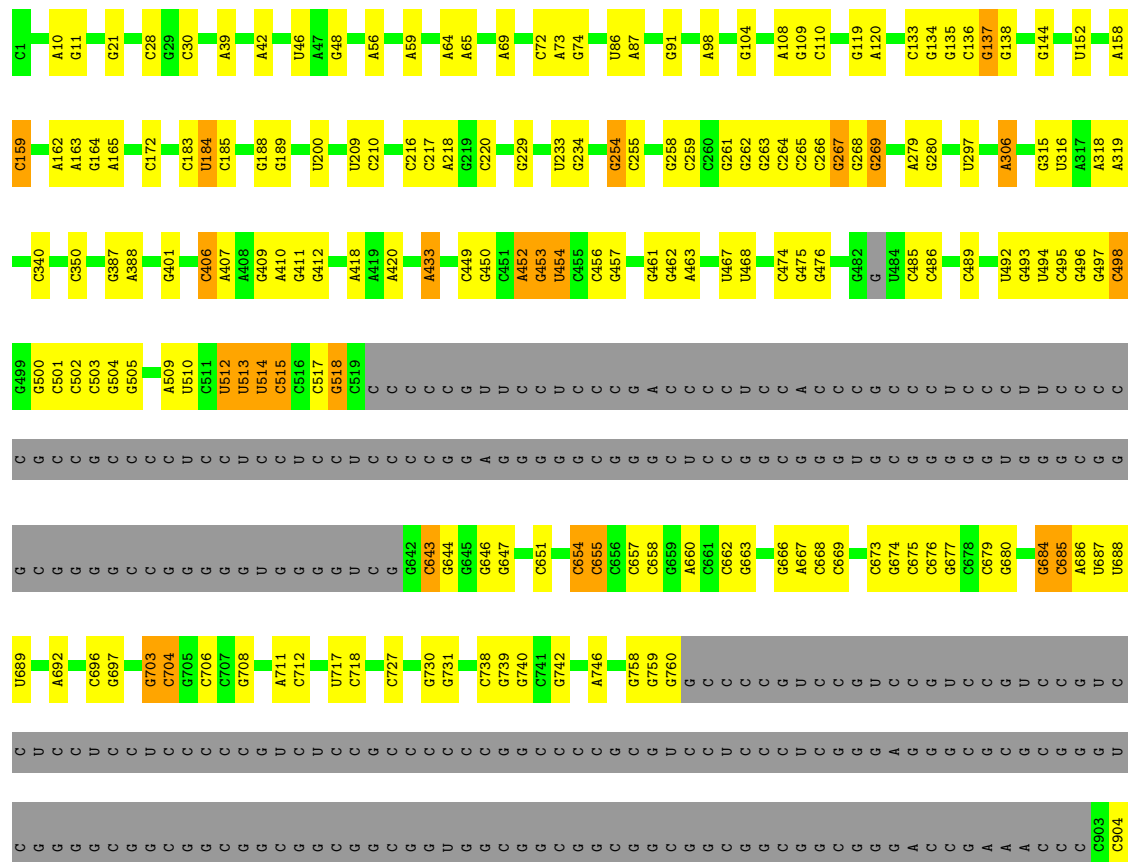
Chain Bw: 79% 21%



Chain N4:



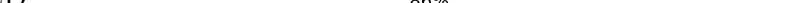
Chain L5: 50% 19% 1% 29%





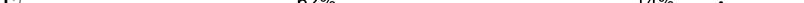


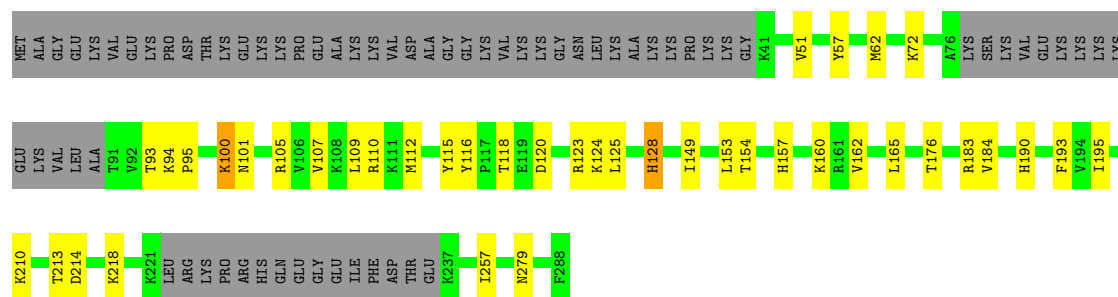
- Molecule 15: Large ribosomal subunit protein uL18

Chain LD:  86% 14%



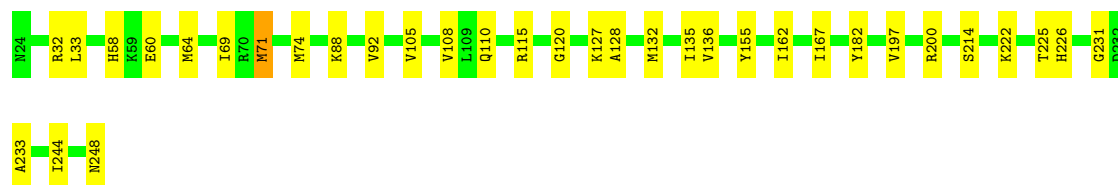
- Molecule 16: Large ribosomal subunit protein eL6

Chain LE: 



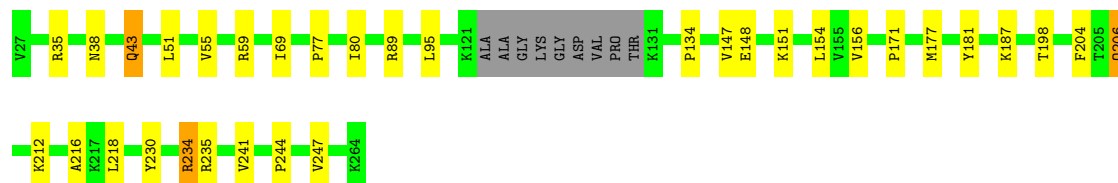
- Molecule 17: 60S ribosomal protein L7

Chain LF:  85% 15%

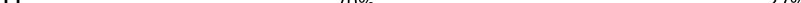


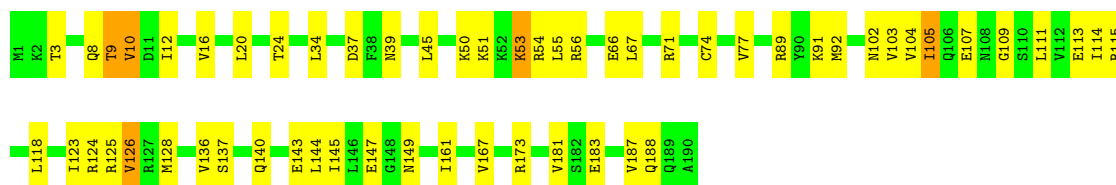
- Molecule 18: Large ribosomal subunit protein eL8

Chain LG:  82% 13% ..



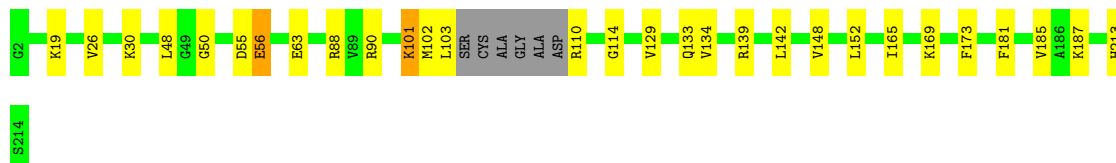
- Molecule 19: 60S ribosomal protein L9

Chain LH: 



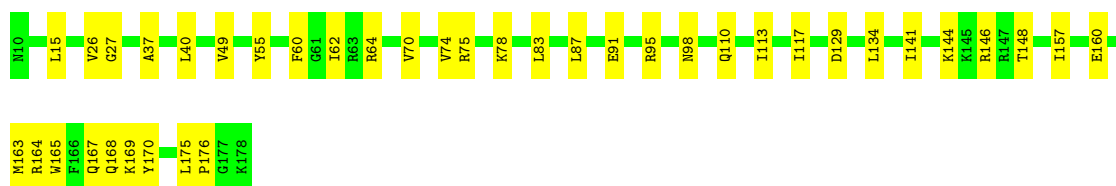
- Molecule 20: Ribosomal protein uL16-like

Chain LI: 84% 13% ..



- Molecule 21: Large ribosomal subunit protein uL5

Chain LJ: 77% 23%



- Molecule 22: Large ribosomal subunit protein eL13

Chain LL: 85% 14% .



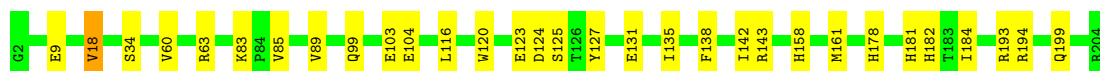
- Molecule 23: 60S ribosomal protein L14

Chain LM: 93% 7%



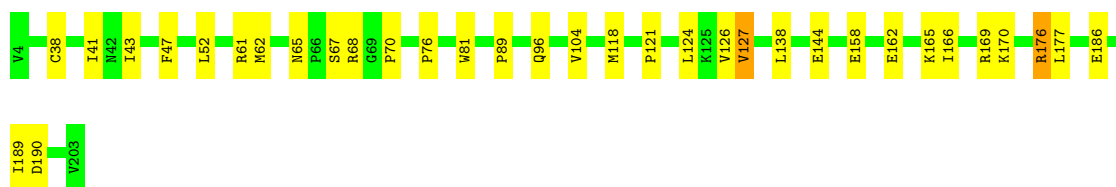
- Molecule 24: 60S ribosomal protein L15

Chain LN: 85% 15%



- Molecule 25: Large ribosomal subunit protein uL13

Chain LO:  83% 16%

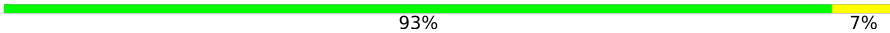


- Molecule 26: 60S ribosomal protein L17

Chain LP:  88% 10%



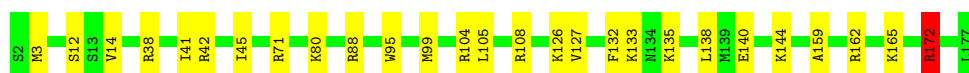
- Molecule 27: 60S ribosomal protein L18

Chain LQ:  93% 7%



- Molecule 28: Large ribosomal subunit protein eL19

Chain LR:  85% 15%



- Molecule 29: 60S ribosomal protein L18a

Chain LS:  89% 11%



- Molecule 30: 60S ribosomal protein L21

Chain LT:  86% 13%



- Molecule 31: 60S ribosomal protein L22

Chain LU:  73% 26%



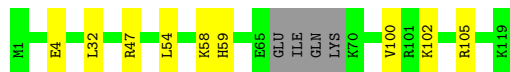
- Molecule 32: 60S ribosomal protein L23

Chain LV:  84% 16%



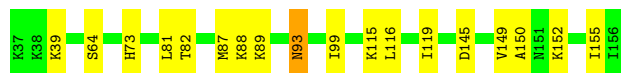
- Molecule 33: Large ribosomal subunit protein eL24

Chain LW:  89% 8%



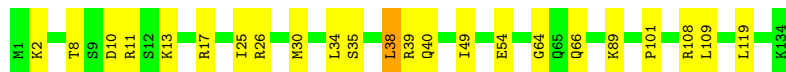
- Molecule 34: 60S ribosomal protein L23a

Chain LX:  85% 14%



- Molecule 35: 60S ribosomal protein L26

Chain LY:  83% 16%



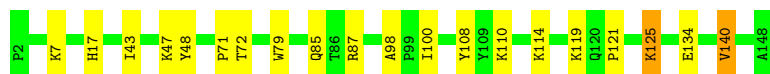
- Molecule 36: 60S ribosomal protein L27

Chain LZ:  79% 21%



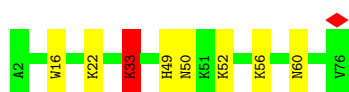
- Molecule 37: 60S ribosomal protein L27a

Chain La:  86% 12%



- Molecule 38: Large ribosomal subunit protein eL29

Chain Lb:  89% 9%



- Molecule 39: Large ribosomal subunit protein eL30

Chain Lc:  85% 15%



- Molecule 40: 60S ribosomal protein L31

Chain Ld:  87% 13%



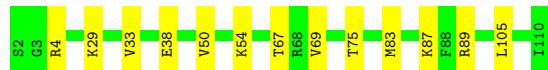
- Molecule 41: 60S ribosomal protein L32

Chain Le:  90% 10%



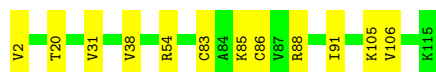
- Molecule 42: 60S ribosomal protein L35a

Chain Lf:  88% 12%

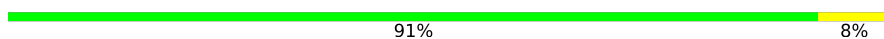


- Molecule 43: 60S ribosomal protein L34

Chain Lg:  89% 11%



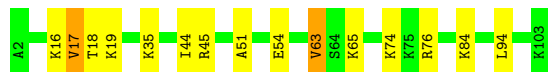
- Molecule 44: Large ribosomal subunit protein uL29

Chain Lh:  91% 8%



- Molecule 45: 60S ribosomal protein L36

Chain Li:  85% 13%



- Molecule 46: 60S ribosomal protein L37

Chain Lj:  94% 6%



- Molecule 47: 60S ribosomal protein L38

Chain Lk:  81% 14% .



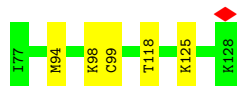
- Molecule 48: 60S ribosomal protein L39

Chain Ll:  92% 8%



- Molecule 49: Ubiquitin-60S ribosomal protein L40

Chain Lm:  90% 10%



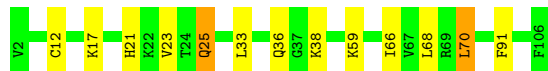
- Molecule 50: 60S ribosomal protein L41

Chain Ln:  88% 12%



- Molecule 51: 60S ribosomal protein L36a

Chain Lo:  88% 10% .



- Molecule 52: 60S ribosomal protein L37a

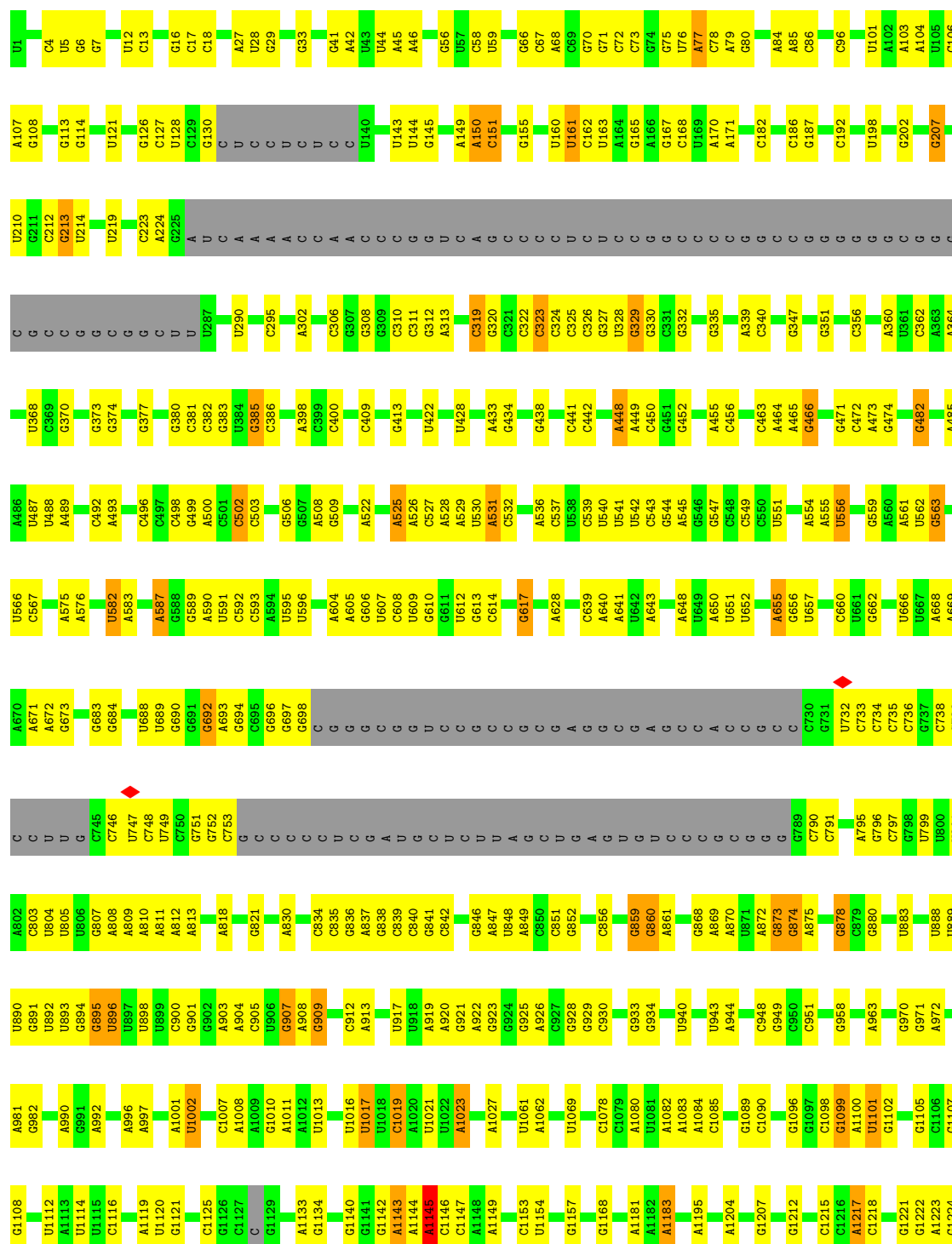
Chain Lp:  91% 9%

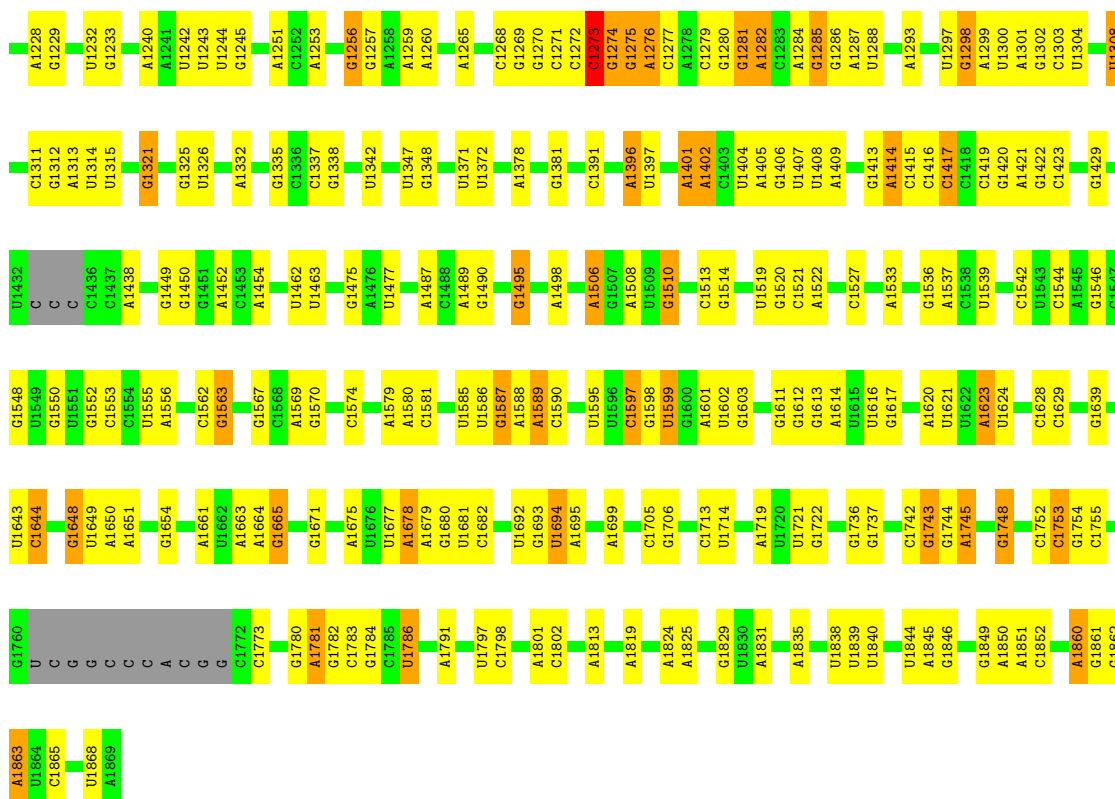


- Molecule 53: 60S ribosomal protein L28

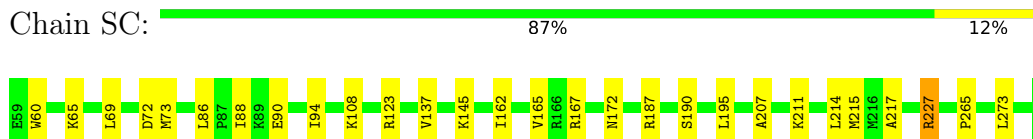
S2
 L17
 I18
 K19
 L32
 K33
 Y40
 E52
 V61
 R71
 K72
 S76
 T80
 R87
 A88
 T89
 I97
 R98
 K99
 R107
 M108
 S115
 L118
 V126

Chain S2: 56% 31% 0% 8%

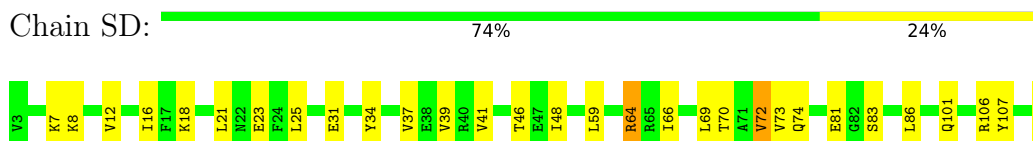




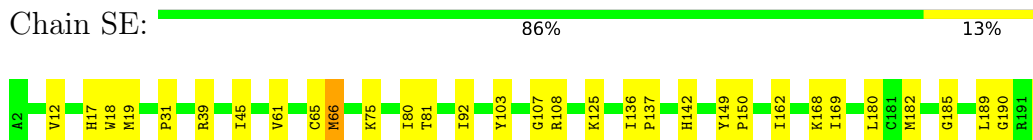
- Molecule 55: Small ribosomal subunit protein uS5

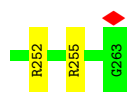


- Molecule 56: Small ribosomal subunit protein uS3



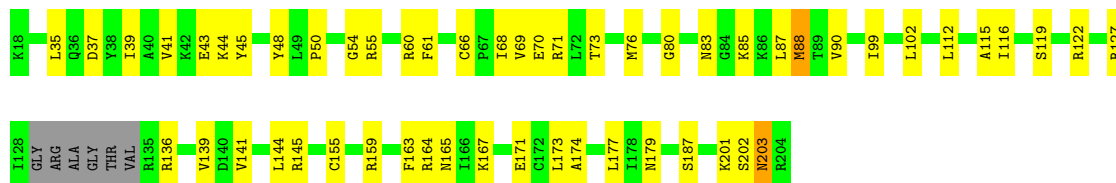
- Molecule 57: 40S ribosomal protein S4, X isoform





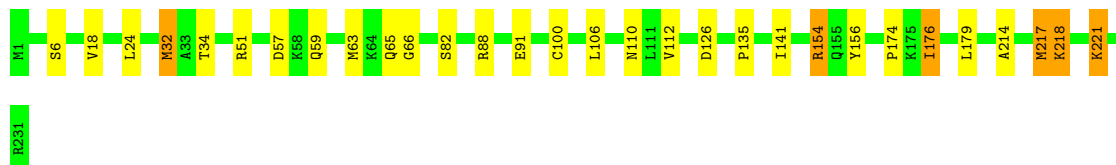
- Molecule 58: Small ribosomal subunit protein uS7

Chain SF: 68% 28% ..



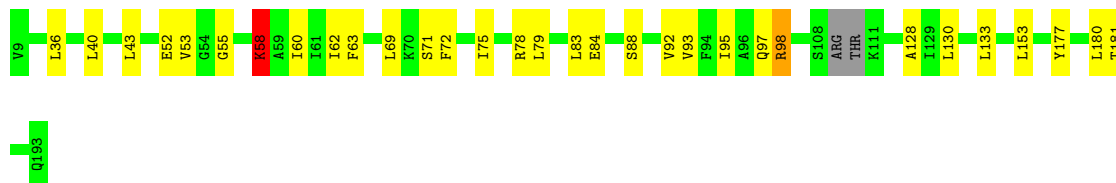
- Molecule 59: Small ribosomal subunit protein eS6

Chain SG: 87% 10% .



- Molecule 60: Small ribosomal subunit protein eS7

Chain SH: 82% 16% ...



- Molecule 61: 40S ribosomal protein S8

Chain SI: 89% 11%



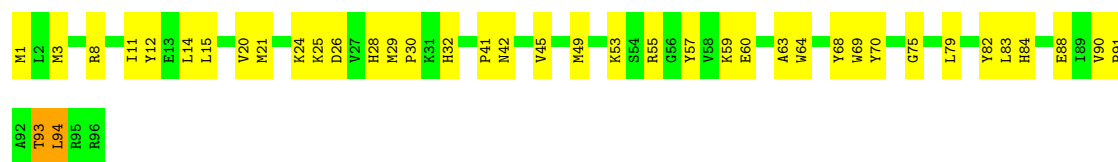
- Molecule 62: Small ribosomal subunit protein uS4

Chain SJ: 85% 15%



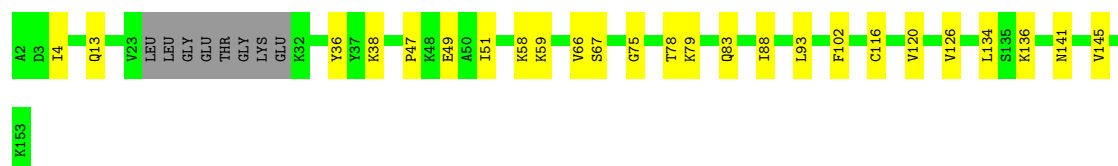
- Molecule 63: Small ribosomal subunit protein eS10

Chain SK:  58% 40%



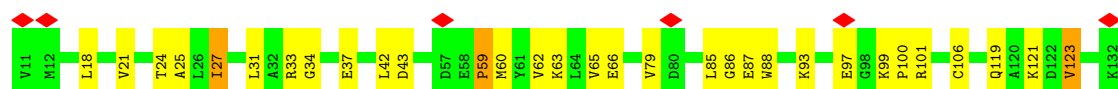
- Molecule 64: Small ribosomal subunit protein uS17

Chain SL:  78% 16% 5%



- Molecule 65: 40S ribosomal protein S12

Chain SM:  5% 75% 23%



- Molecule 66: 40S ribosomal protein S13

Chain SN:  89% 11%



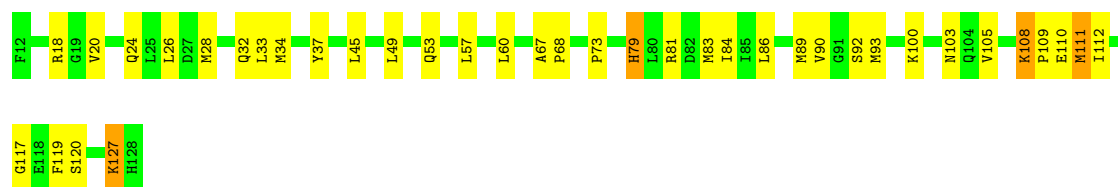
- Molecule 67: Small ribosomal subunit protein uS11

Chain SO:  78% 21%



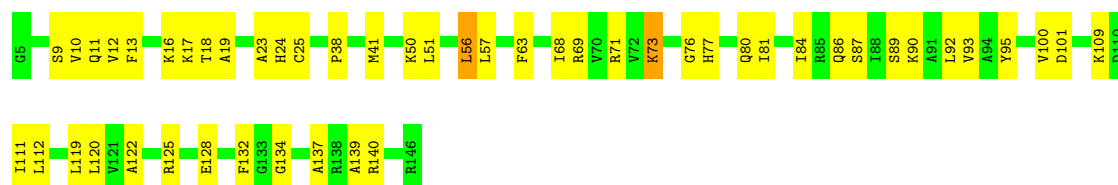
- Molecule 68: Small ribosomal subunit protein uS19

Chain SP:  68% 29%



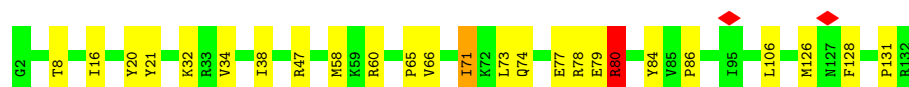
- Molecule 69: Small ribosomal subunit protein uS9

Chain SQ:  65% 34% .



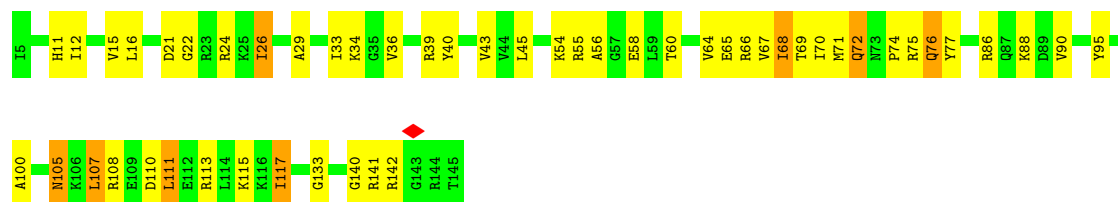
- Molecule 70: Small ribosomal subunit protein eS17

Chain SR:  81% 18% ..



- Molecule 71: Small ribosomal subunit protein uS13

Chain SS:  64% 30% 6%



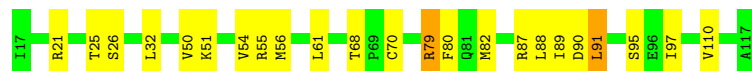
- Molecule 72: 40S ribosomal protein S19

Chain ST:  77% 20% .



- Molecule 73: 40S ribosomal protein S20

Chain SU:  77% 21% .



- Molecule 74: 40S ribosomal protein S21

Chain SV:  81% 17% ..



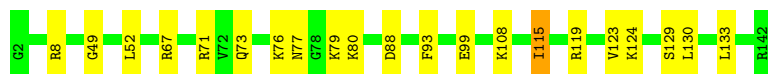
- Molecule 75: 40S ribosomal protein S15a

Chain SW:  91% 9%



- Molecule 76: 40S ribosomal protein S23

Chain SX:  85% 14%



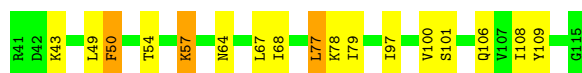
- Molecule 77: Small ribosomal subunit protein eS24

Chain SY:  85% 15%



- Molecule 78: 40S ribosomal protein S25

Chain SZ:  77% 19%



- Molecule 79: Small ribosomal subunit protein eS26

Chain Sa:  80% 19%



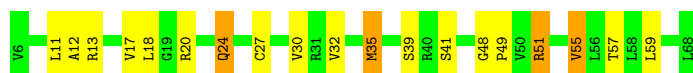
- Molecule 80: 40S ribosomal protein S27

Chain Sb:  87% 13%



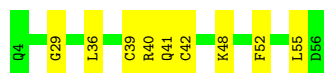
- Molecule 81: Small ribosomal subunit protein eS28

Chain Sc:  70% 24% 6%



- Molecule 82: 40S ribosomal protein S29

Chain Sd:  83% 17%



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

Chain Se:  87% 13%



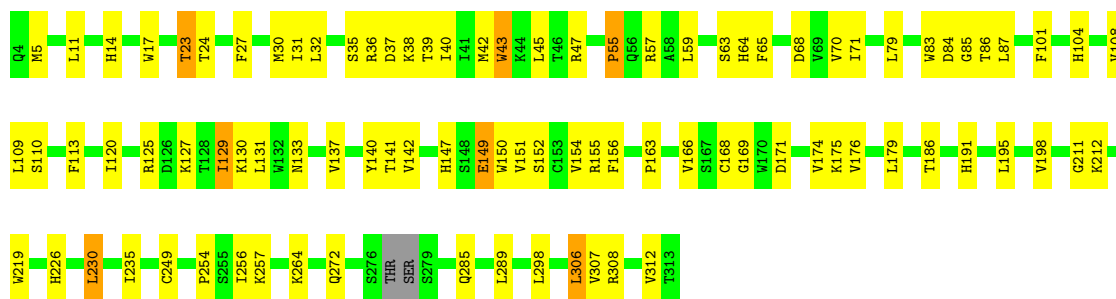
- Molecule 84: Ubiquitin-ribosomal protein eS31 fusion protein

Chain Sf:  73% 27%



- Molecule 85: Small ribosomal subunit protein RACK1

Chain Sg:  70% 27% ..



- Molecule 86: nascent polypeptide chain

Chain NC:  100%

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19178	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)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	3.394	Depositor
Minimum map value	-1.961	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.089	Depositor
Recommended contour level	0.07	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: MG, ZN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	LA	0.33	0/1936	0.64	2/2596 (0.1%)
2	NA	0.27	0/845	0.67	0/1128
3	SA	0.38	0/1708	0.71	0/2324
4	LB	0.34	0/3251	0.61	1/4352 (0.0%)
5	NB	0.37	0/829	0.84	1/1112 (0.1%)
6	SB	0.37	0/1745	0.69	1/2337 (0.0%)
7	Bv	0.18	0/1810	0.29	0/2817
8	Bx	0.25	0/261	0.55	2/404 (0.5%)
9	Bw	0.13	0/1819	0.27	0/2833
10	N4	0.40	1/1831 (0.1%)	0.85	8/2456 (0.3%)
11	L5	0.28	0/86312	0.38	2/134632 (0.0%)
12	L7	0.25	0/2858	0.35	0/4455
13	L8	0.27	0/3701	0.36	0/5766
14	LC	0.32	0/2938	0.58	1/3947 (0.0%)
15	LD	0.29	0/2407	0.60	2/3227 (0.1%)
16	LE	0.32	0/1788	0.68	3/2399 (0.1%)
17	LF	0.31	0/1905	0.55	0/2539
18	LG	0.39	1/1849 (0.1%)	0.68	2/2496 (0.1%)
19	LH	0.38	0/1529	0.71	1/2058 (0.0%)
20	LI	0.37	0/1705	0.67	3/2277 (0.1%)
21	LJ	0.42	0/1352	0.75	1/1813 (0.1%)
22	LL	0.36	1/1661 (0.1%)	0.57	1/2229 (0.0%)
23	LM	0.30	0/1145	0.59	0/1536
24	LN	0.30	0/1746	0.46	0/2338
25	LO	0.30	0/1665	0.55	0/2229
26	LP	0.27	0/1260	0.51	0/1692
27	LQ	0.34	0/1526	0.53	0/2038
28	LR	0.38	1/1468 (0.1%)	0.55	0/1945
29	LS	0.28	0/1492	0.47	0/2003
30	LT	0.29	0/1310	0.60	1/1752 (0.1%)
31	LU	0.46	0/820	0.87	1/1102 (0.1%)
32	LV	0.30	0/985	0.58	0/1323

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LW	0.26	0/820	0.54	0/1104
34	LX	0.31	0/998	0.58	0/1341
35	LY	0.31	0/1128	0.57	0/1500
36	LZ	0.29	0/1130	0.50	0/1507
37	La	0.30	0/1183	0.52	1/1582 (0.1%)
38	Lb	0.37	0/600	0.65	2/796 (0.3%)
39	Lc	0.29	0/752	0.52	0/1011
40	Ld	0.25	0/889	0.48	0/1198
41	Le	0.31	0/1067	0.53	0/1425
42	Lf	0.29	0/891	0.57	0/1194
43	Lg	0.34	0/899	0.57	1/1200 (0.1%)
44	Lh	0.27	0/1014	0.52	1/1340 (0.1%)
45	Li	0.24	0/824	0.52	1/1093 (0.1%)
46	Lj	0.30	0/720	0.51	0/952
47	Lk	0.28	0/548	0.60	0/730
48	Ll	0.31	0/454	0.53	0/599
49	Lm	0.23	0/431	0.49	0/570
50	Ln	0.34	0/231	0.51	0/294
51	Lo	0.28	0/876	0.51	0/1156
52	Lp	0.27	0/706	0.53	0/939
53	Lr	0.33	0/1012	0.58	0/1358
54	S2	0.25	1/40882 (0.0%)	0.41	2/63715 (0.0%)
55	SC	0.32	0/1697	0.59	0/2301
56	SD	0.41	0/1620	0.79	1/2198 (0.0%)
57	SE	0.37	1/2014 (0.0%)	0.78	3/2726 (0.1%)
58	SF	0.42	0/1423	0.82	3/1913 (0.2%)
59	SG	0.29	0/1657	0.71	6/2247 (0.3%)
60	SH	0.35	1/1295 (0.1%)	0.62	0/1763
61	SI	0.26	0/1603	0.50	0/2161
62	SJ	0.31	0/1456	0.63	0/1957
63	SK	0.50	1/750 (0.1%)	0.90	0/1026
64	SL	0.29	0/1163	0.52	0/1562
65	SM	0.57	1/960 (0.1%)	0.93	4/1286 (0.3%)
66	SN	0.27	0/1206	0.52	1/1626 (0.1%)
67	SO	0.42	0/982	0.77	2/1320 (0.2%)
68	SP	0.50	0/925	1.04	6/1248 (0.5%)
69	SQ	0.44	0/1093	0.84	2/1470 (0.1%)
70	SR	0.36	0/955	0.77	2/1294 (0.2%)
71	SS	0.55	1/1148 (0.1%)	1.06	5/1542 (0.3%)
72	ST	0.37	0/1100	0.74	2/1479 (0.1%)
73	SU	0.29	0/722	0.61	0/983
74	SV	0.55	2/625 (0.3%)	0.78	1/837 (0.1%)
75	SW	0.29	0/1043	0.54	0/1396

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SX	0.35	0/1096	0.68	1/1467 (0.1%)
77	SY	0.29	0/944	0.62	0/1271
78	SZ	0.41	0/565	0.89	3/764 (0.4%)
79	Sa	0.40	0/794	0.63	0/1065
80	Sb	0.38	0/632	0.62	0/851
81	Sc	0.33	0/474	0.83	1/638 (0.2%)
82	Sd	0.30	0/443	0.63	0/589
83	Se	0.25	0/420	0.68	1/554 (0.2%)
84	Sf	0.40	0/525	0.88	0/695
85	Sg	0.49	2/2235 (0.1%)	0.83	1/3068 (0.0%)
All	All	0.30	14/231077 (0.0%)	0.50	86/340056 (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
6	SB	0	1
10	N4	0	1
18	LG	0	1
20	LI	0	1
22	LL	0	1
25	LO	0	1
28	LR	0	1
55	SC	0	1
59	SG	0	2
70	SR	0	1
71	SS	0	2
72	ST	0	1
74	SV	0	1
78	SZ	0	1
81	Sc	0	1
All	All	0	17

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
85	Sg	149	GLU	CD-OE2	-10.68	1.05	1.25
65	SM	27	ILE	CG1-CD1	-8.83	1.17	1.51
57	SE	66	MET	CB-CG	-6.98	1.31	1.52
28	LR	172	ARG	CG-CD	-6.01	1.34	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
63	SK	93	THR	CB-CG2	-5.91	1.33	1.52

The worst 5 of 86 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	SE	66	MET	CG-SD-CE	-17.56	62.26	100.90
16	LE	95	PRO	CA-N-CD	-11.40	96.03	112.00
68	SP	111	MET	CG-SD-CE	-11.05	76.59	100.90
54	S2	1145	A	O4'-C1'-N9	9.88	123.32	108.50
65	SM	59	PRO	CA-N-CD	-9.21	99.11	112.00

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	LG	234	ARG	Sidechain
20	LI	110	ARG	Sidechain
22	LL	47	ALA	Peptide
10	N4	105	ARG	Sidechain
6	SB	174	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	LA	1898	0	1993	17	0
2	NA	841	0	898	15	0
3	SA	1671	0	1672	38	0
4	LB	3183	0	3316	49	0
5	NB	821	0	867	21	0
6	SB	1718	0	1786	25	0
7	Bv	1620	0	821	7	0
8	Bx	234	0	117	0	0
9	Bw	1627	0	821	3	0
10	N4	1795	0	1754	44	0
11	L5	77166	0	39006	288	0
12	L7	2558	0	1296	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	L8	3314	0	1683	14	0
14	LC	2884	0	3050	38	0
15	LD	2361	0	2378	24	0
16	LE	1754	0	1899	27	0
17	LF	1870	0	1996	25	0
18	LG	1818	0	1911	21	0
19	LH	1510	0	1579	34	0
20	LI	1666	0	1711	18	0
21	LJ	1329	0	1348	28	0
22	LL	1630	0	1715	17	0
23	LM	1122	0	1174	6	0
24	LN	1701	0	1749	17	0
25	LO	1633	0	1771	20	0
26	LP	1234	0	1254	7	0
27	LQ	1502	0	1616	9	0
28	LR	1452	0	1580	25	0
29	LS	1452	0	1490	13	0
30	LT	1282	0	1336	17	0
31	LU	806	0	826	20	0
32	LV	971	0	1024	15	0
33	LW	808	0	726	6	0
34	LX	981	0	1055	12	0
35	LY	1111	0	1194	16	0
36	LZ	1107	0	1182	17	0
37	La	1154	0	1198	12	0
38	Lb	590	0	613	8	0
39	Lc	742	0	774	10	0
40	Ld	874	0	918	6	0
41	Le	1049	0	1136	8	0
42	Lf	872	0	901	7	0
43	Lg	889	0	968	3	0
44	Lh	1006	0	1132	8	0
45	Li	813	0	887	9	0
46	Lj	705	0	737	2	0
47	Lk	542	0	590	7	0
48	Ll	444	0	483	2	0
49	Lm	425	0	462	3	0
50	Ln	230	0	276	3	0
51	Lo	862	0	929	7	0
52	Lp	696	0	744	5	0
53	Lr	997	0	1054	11	0
54	S2	36562	0	18470	209	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
55	SC	1661	0	1710	18	0
56	SD	1594	0	1568	44	0
57	SE	1972	0	2012	26	0
58	SF	1403	0	1421	49	0
59	SG	1634	0	1568	17	0
60	SH	1274	0	1196	18	0
61	SI	1574	0	1540	13	0
62	SJ	1431	0	1497	16	0
63	SK	726	0	674	46	0
64	SL	1143	0	1177	14	0
65	SM	950	0	987	26	0
66	SN	1182	0	1249	10	0
67	SO	969	0	982	24	0
68	SP	907	0	892	29	0
69	SQ	1075	0	1110	34	0
70	SR	942	0	913	21	0
71	SS	1130	0	1167	38	0
72	ST	1081	0	1093	25	0
73	SU	713	0	692	16	0
74	SV	618	0	617	18	0
75	SW	1026	0	1072	8	0
76	SX	1078	0	1130	11	0
77	SY	927	0	914	14	0
78	SZ	559	0	594	9	0
79	Sa	781	0	831	15	0
80	Sb	618	0	604	8	0
81	Sc	472	0	484	20	0
82	Sd	433	0	415	7	0
83	Se	416	0	439	3	0
84	Sf	515	0	521	12	0
85	Sg	2180	0	1968	68	0
86	NC	130	0	34	0	0
87	L5	126	0	0	0	0
87	L7	3	0	0	0	0
87	L8	3	0	0	0	0
87	LA	1	0	0	0	0
87	LC	1	0	0	0	0
87	LI	1	0	0	0	0
87	LN	1	0	0	0	0
87	LP	1	0	0	0	0
87	LV	1	0	0	0	0
87	S2	52	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	ST	1	0	0	0	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sd	1	0	0	0	0
88	Sf	1	0	0	0	0
89	L5	3	0	0	0	0
89	L7	1	0	0	0	0
89	LI	1	0	0	0	0
89	LN	1	0	0	0	0
89	La	1	0	0	0	0
89	Lp	1	0	0	0	0
89	S2	3	0	0	0	0
All	All	215206	0	156937	1692	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 1692 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)
54:S2:1287:A:H62	54:S2:1312:G:N2	1.53	1.06
54:S2:1287:A:N6	54:S2:1312:G:H21	1.59	0.99
54:S2:1748:G:H1	54:S2:1786:U:H3	1.11	0.98
21:LJ:55:TYR:HA	21:LJ:64:ARG:HD3	1.51	0.93
67:SO:56:VAL:HG12	67:SO:81:VAL:HG23	1.52	0.91

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	246/248 (99%)	229 (93%)	17 (7%)	0	100	100
2	NA	104/215 (48%)	99 (95%)	5 (5%)	0	100	100
3	SA	214/216 (99%)	205 (96%)	9 (4%)	0	100	100
4	LB	393/395 (100%)	375 (95%)	18 (5%)	0	100	100
5	NB	104/106 (98%)	95 (91%)	9 (9%)	0	100	100
6	SB	211/213 (99%)	204 (97%)	7 (3%)	0	100	100
10	N4	219/221 (99%)	215 (98%)	4 (2%)	0	100	100
14	LC	362/364 (100%)	339 (94%)	23 (6%)	0	100	100
15	LD	291/293 (99%)	273 (94%)	18 (6%)	0	100	100
16	LE	213/288 (74%)	194 (91%)	19 (9%)	0	100	100
17	LF	223/225 (99%)	211 (95%)	12 (5%)	0	100	100
18	LG	225/238 (94%)	211 (94%)	14 (6%)	0	100	100
19	LH	188/190 (99%)	174 (93%)	14 (7%)	0	100	100
20	LI	203/213 (95%)	190 (94%)	13 (6%)	0	100	100
21	LJ	167/169 (99%)	160 (96%)	7 (4%)	0	100	100
22	LL	203/205 (99%)	191 (94%)	12 (6%)	0	100	100
23	LM	137/139 (99%)	131 (96%)	6 (4%)	0	100	100
24	LN	201/203 (99%)	193 (96%)	8 (4%)	0	100	100
25	LO	198/200 (99%)	195 (98%)	3 (2%)	0	100	100
26	LP	151/153 (99%)	143 (95%)	7 (5%)	1 (1%)	18	46
27	LQ	185/187 (99%)	175 (95%)	10 (5%)	0	100	100
28	LR	174/176 (99%)	173 (99%)	1 (1%)	0	100	100
29	LS	173/175 (99%)	162 (94%)	11 (6%)	0	100	100
30	LT	157/159 (99%)	146 (93%)	10 (6%)	1 (1%)	21	50
31	LU	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
32	LV	129/131 (98%)	122 (95%)	7 (5%)	0	100	100
33	LW	111/119 (93%)	101 (91%)	10 (9%)	0	100	100
34	LX	118/120 (98%)	113 (96%)	5 (4%)	0	100	100
35	LY	132/134 (98%)	126 (96%)	6 (4%)	0	100	100
36	LZ	133/135 (98%)	125 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	La	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
38	Lb	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
39	Lc	95/97 (98%)	92 (97%)	3 (3%)	0	100	100
40	Ld	105/107 (98%)	103 (98%)	2 (2%)	0	100	100
41	Le	126/128 (98%)	123 (98%)	3 (2%)	0	100	100
42	Lf	107/109 (98%)	101 (94%)	6 (6%)	0	100	100
43	Lg	112/114 (98%)	102 (91%)	10 (9%)	0	100	100
44	Lh	119/121 (98%)	116 (98%)	3 (2%)	0	100	100
45	Li	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
46	Lj	84/86 (98%)	82 (98%)	2 (2%)	0	100	100
47	Lk	67/69 (97%)	63 (94%)	4 (6%)	0	100	100
48	Ll	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
49	Lm	50/52 (96%)	50 (100%)	0	0	100	100
50	Ln	22/24 (92%)	22 (100%)	0	0	100	100
51	Lo	103/105 (98%)	99 (96%)	4 (4%)	0	100	100
52	Lp	89/91 (98%)	86 (97%)	3 (3%)	0	100	100
53	Lr	123/125 (98%)	116 (94%)	7 (6%)	0	100	100
55	SC	217/219 (99%)	206 (95%)	11 (5%)	0	100	100
56	SD	219/225 (97%)	205 (94%)	14 (6%)	0	100	100
57	SE	260/262 (99%)	248 (95%)	12 (5%)	0	100	100
58	SF	177/187 (95%)	168 (95%)	8 (4%)	1 (1%)	21	50
59	SG	229/231 (99%)	204 (89%)	25 (11%)	0	100	100
60	SH	179/185 (97%)	170 (95%)	9 (5%)	0	100	100
61	SI	204/206 (99%)	202 (99%)	2 (1%)	0	100	100
62	SJ	177/179 (99%)	174 (98%)	3 (2%)	0	100	100
63	SK	94/96 (98%)	89 (95%)	5 (5%)	0	100	100
64	SL	140/152 (92%)	133 (95%)	7 (5%)	0	100	100
65	SM	120/122 (98%)	112 (93%)	8 (7%)	0	100	100
66	SN	148/150 (99%)	144 (97%)	4 (3%)	0	100	100
67	SO	132/134 (98%)	119 (90%)	13 (10%)	0	100	100
68	SP	115/117 (98%)	108 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	SQ	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
70	SR	129/131 (98%)	116 (90%)	13 (10%)	0	100	100
71	SS	139/141 (99%)	118 (85%)	21 (15%)	0	100	100
72	ST	141/143 (99%)	136 (96%)	5 (4%)	0	100	100
73	SU	99/101 (98%)	92 (93%)	7 (7%)	0	100	100
74	SV	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
75	SW	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
76	SX	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
77	SY	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
78	SZ	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
79	Sa	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
80	Sb	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
81	Sc	61/63 (97%)	53 (87%)	8 (13%)	0	100	100
82	Sd	51/53 (96%)	51 (100%)	0	0	100	100
83	Se	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
84	Sf	61/63 (97%)	53 (87%)	8 (13%)	0	100	100
85	Sg	304/310 (98%)	270 (89%)	34 (11%)	0	100	100
All	All	11540/11933 (97%)	10898 (94%)	639 (6%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
58	SF	80	GLY
26	LP	20	SER
30	LT	139	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	190/190 (100%)	181 (95%)	9 (5%)	23	55
2	NA	95/183 (52%)	94 (99%)	1 (1%)	65	86
3	SA	170/179 (95%)	163 (96%)	7 (4%)	27	60
4	LB	343/344 (100%)	337 (98%)	6 (2%)	53	80
5	NB	90/90 (100%)	83 (92%)	7 (8%)	11	33
6	SB	191/194 (98%)	185 (97%)	6 (3%)	35	67
10	N4	194/194 (100%)	191 (98%)	3 (2%)	57	82
14	LC	299/302 (99%)	295 (99%)	4 (1%)	61	84
15	LD	241/247 (98%)	237 (98%)	4 (2%)	53	80
16	LE	191/252 (76%)	183 (96%)	8 (4%)	26	59
17	LF	194/194 (100%)	191 (98%)	3 (2%)	57	82
18	LG	188/203 (93%)	184 (98%)	4 (2%)	47	76
19	LH	167/169 (99%)	156 (93%)	11 (7%)	15	41
20	LI	174/180 (97%)	170 (98%)	4 (2%)	44	74
21	LJ	136/142 (96%)	129 (95%)	7 (5%)	21	51
22	LL	164/171 (96%)	157 (96%)	7 (4%)	26	58
23	LM	114/118 (97%)	113 (99%)	1 (1%)	70	88
24	LN	171/171 (100%)	166 (97%)	5 (3%)	37	69
25	LO	170/172 (99%)	164 (96%)	6 (4%)	32	64
26	LP	132/134 (98%)	127 (96%)	5 (4%)	29	62
27	LQ	161/164 (98%)	160 (99%)	1 (1%)	78	92
28	LR	150/156 (96%)	147 (98%)	3 (2%)	48	77
29	LS	156/156 (100%)	154 (99%)	2 (1%)	61	84
30	LT	135/139 (97%)	130 (96%)	5 (4%)	30	63
31	LU	86/91 (94%)	85 (99%)	1 (1%)	63	85
32	LV	99/101 (98%)	95 (96%)	4 (4%)	28	61
33	LW	61/99 (62%)	60 (98%)	1 (2%)	55	81
34	LX	107/108 (99%)	104 (97%)	3 (3%)	38	70
35	LY	123/124 (99%)	120 (98%)	3 (2%)	43	73
36	LZ	117/117 (100%)	113 (97%)	4 (3%)	32	65
37	La	118/120 (98%)	114 (97%)	4 (3%)	32	65
38	Lb	59/63 (94%)	57 (97%)	2 (3%)	32	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	Lc	79/82 (96%)	77 (98%)	2 (2%)	42	73
40	Ld	94/98 (96%)	91 (97%)	3 (3%)	34	66
41	Le	113/114 (99%)	110 (97%)	3 (3%)	39	71
42	Lf	87/88 (99%)	84 (97%)	3 (3%)	32	65
43	Lg	93/98 (95%)	87 (94%)	6 (6%)	15	42
44	Lh	108/109 (99%)	108 (100%)	0	100	100
45	Li	81/86 (94%)	77 (95%)	4 (5%)	22	52
46	Lj	73/73 (100%)	71 (97%)	2 (3%)	39	71
47	Lk	57/64 (89%)	53 (93%)	4 (7%)	14	38
48	Ll	47/47 (100%)	46 (98%)	1 (2%)	47	76
49	Lm	47/48 (98%)	46 (98%)	1 (2%)	47	76
50	Ln	23/23 (100%)	23 (100%)	0	100	100
51	Lo	93/93 (100%)	89 (96%)	4 (4%)	26	58
52	Lp	71/74 (96%)	69 (97%)	2 (3%)	38	70
53	Lr	107/109 (98%)	103 (96%)	4 (4%)	30	63
55	SC	175/185 (95%)	173 (99%)	2 (1%)	65	86
56	SD	148/189 (78%)	142 (96%)	6 (4%)	27	60
57	SE	196/224 (88%)	194 (99%)	2 (1%)	68	87
58	SF	142/157 (90%)	139 (98%)	3 (2%)	47	76
59	SG	138/201 (69%)	134 (97%)	4 (3%)	37	69
60	SH	109/166 (66%)	102 (94%)	7 (6%)	16	43
61	SI	149/178 (84%)	147 (99%)	2 (1%)	61	84
62	SJ	143/160 (89%)	138 (96%)	5 (4%)	32	64
63	SK	65/87 (75%)	62 (95%)	3 (5%)	24	56
64	SL	121/136 (89%)	118 (98%)	3 (2%)	42	73
65	SM	104/104 (100%)	101 (97%)	3 (3%)	37	69
66	SN	123/130 (95%)	121 (98%)	2 (2%)	55	81
67	SO	95/104 (91%)	92 (97%)	3 (3%)	34	66
68	SP	90/107 (84%)	87 (97%)	3 (3%)	33	65
69	SQ	103/117 (88%)	98 (95%)	5 (5%)	22	52
70	SR	84/119 (71%)	82 (98%)	2 (2%)	43	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
71	SS	112/122 (92%)	108 (96%)	4 (4%)	31	63
72	ST	105/113 (93%)	104 (99%)	1 (1%)	68	87
73	SU	68/93 (73%)	62 (91%)	6 (9%)	9	28
74	SV	62/67 (92%)	62 (100%)	0	100	100
75	SW	110/112 (98%)	108 (98%)	2 (2%)	51	79
76	SX	109/113 (96%)	106 (97%)	3 (3%)	38	70
77	SY	86/108 (80%)	82 (95%)	4 (5%)	23	55
78	SZ	56/66 (85%)	52 (93%)	4 (7%)	13	38
79	Sa	83/86 (96%)	78 (94%)	5 (6%)	17	45
80	Sb	65/75 (87%)	63 (97%)	2 (3%)	35	67
81	Sc	51/56 (91%)	47 (92%)	4 (8%)	11	33
82	Sd	44/47 (94%)	43 (98%)	1 (2%)	44	74
83	Se	39/45 (87%)	37 (95%)	2 (5%)	21	51
84	Sf	56/56 (100%)	54 (96%)	2 (4%)	31	63
85	Sg	201/269 (75%)	196 (98%)	5 (2%)	42	73
All	All	9391/10265 (92%)	9111 (97%)	280 (3%)	37	68

5 of 280 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
69	SQ	69	ARG
71	SS	105	ASN
79	Sa	40	VAL
25	LO	52	LEU
24	LN	89	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 86 such sidechains are listed below:

Mol	Chain	Res	Type
56	SD	74	GLN
66	SN	105	ASN
57	SE	188	ASN
61	SI	167	GLN
69	SQ	86	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	L5	3584/5070 (70%)	751 (20%)	15 (0%)
12	L7	119/120 (99%)	12 (10%)	0
13	L8	155/156 (99%)	29 (18%)	2 (1%)
54	S2	1704/1869 (91%)	475 (27%)	18 (1%)
7	Bv	75/76 (98%)	9 (12%)	0
8	Bx	10/11 (90%)	3 (30%)	0
9	Bw	75/76 (98%)	11 (14%)	0
All	All	5722/7378 (77%)	1290 (22%)	35 (0%)

5 of 1290 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	Bv	16	U
7	Bv	17	G
7	Bv	18	G
7	Bv	19	U
7	Bv	20	U

5 of 35 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	S2	1273	C
54	S2	1285	G
54	S2	1601	A
11	L5	4600	G
11	L5	3876	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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 [i](#)

There are no chain breaks in this entry.

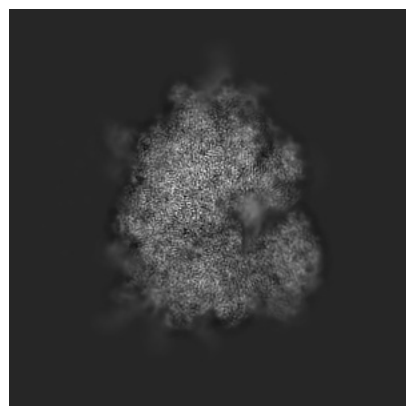
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55612. These allow visual inspection of the internal detail of the map and identification of artifacts.

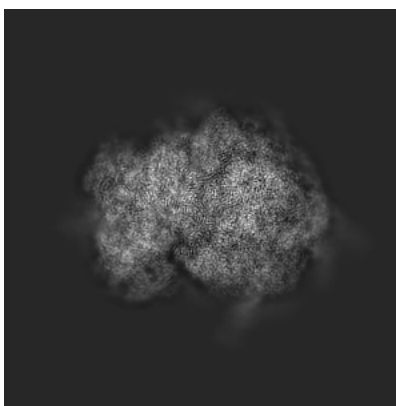
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

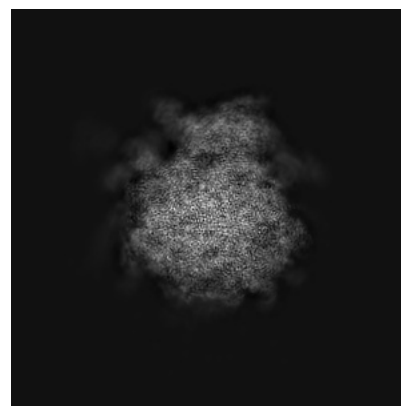
6.1.1 Primary map



X

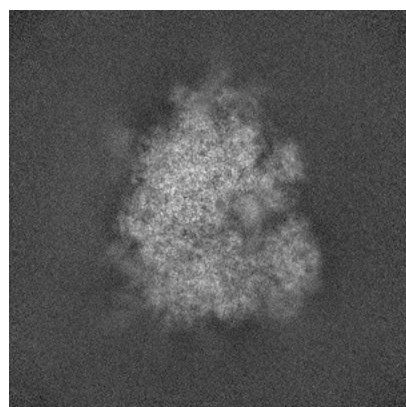


Y

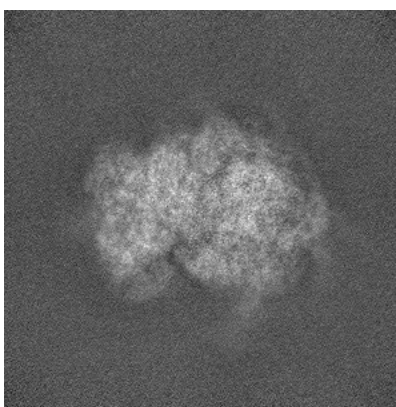


Z

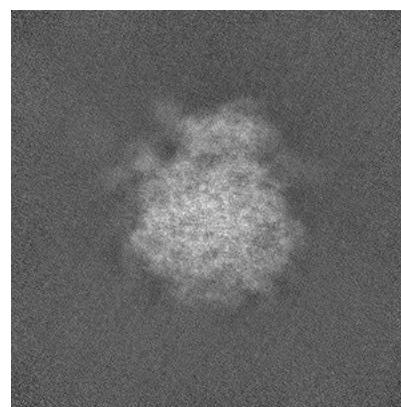
6.1.2 Raw map



X



Y

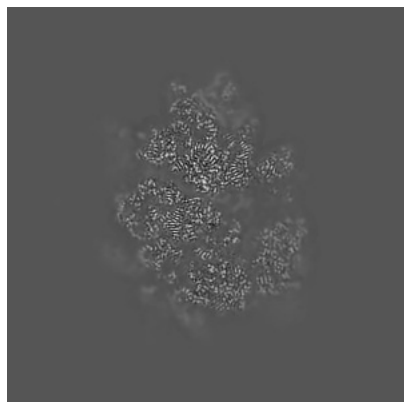


Z

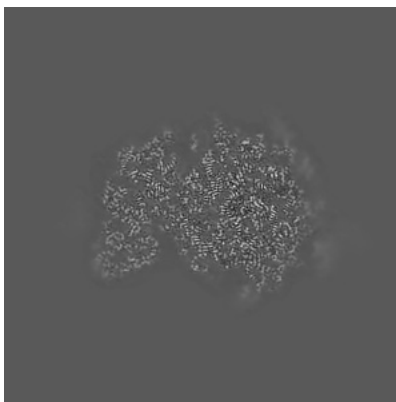
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

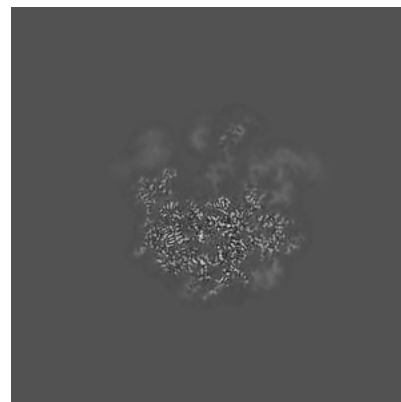
6.2.1 Primary map



X Index: 320

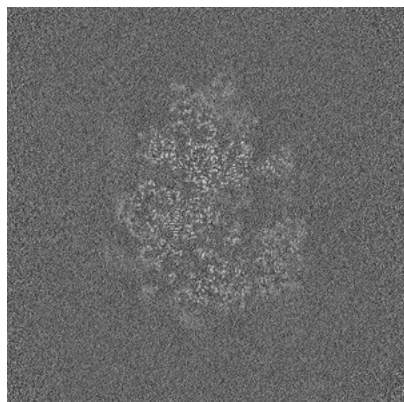


Y Index: 320

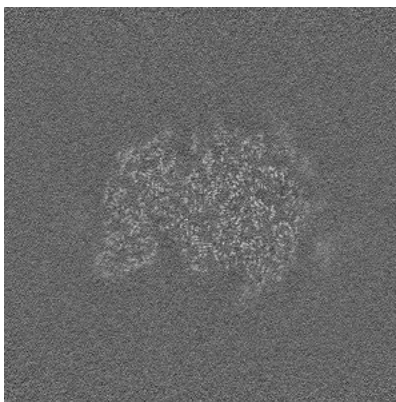


Z Index: 320

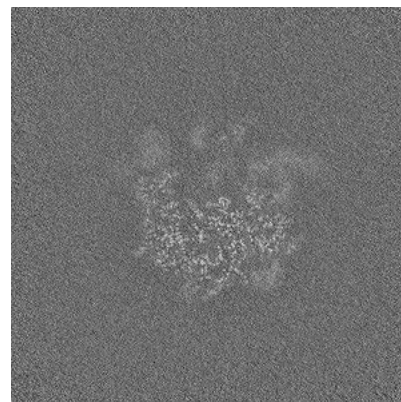
6.2.2 Raw map



X Index: 320



Y Index: 320

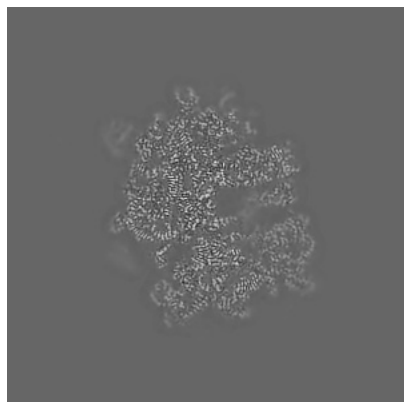


Z Index: 320

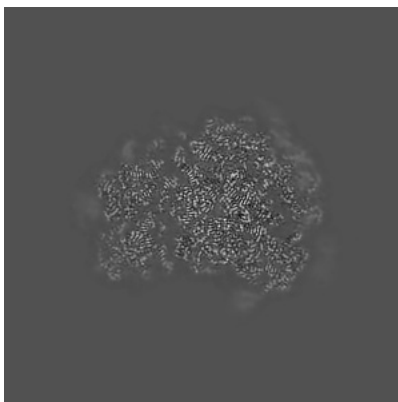
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

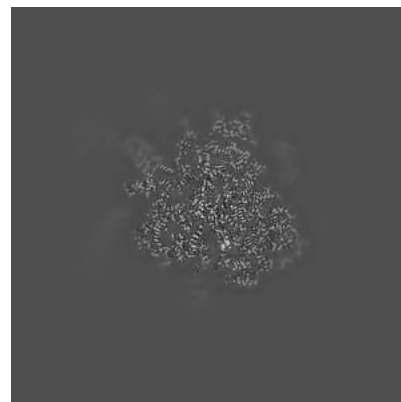
6.3.1 Primary map



X Index: 346

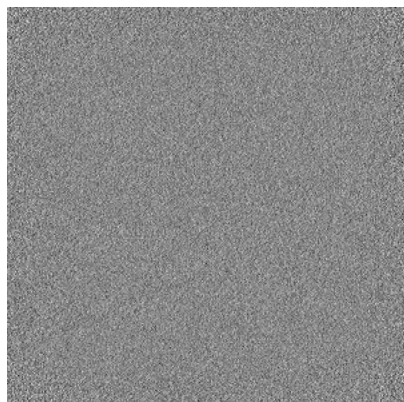


Y Index: 302

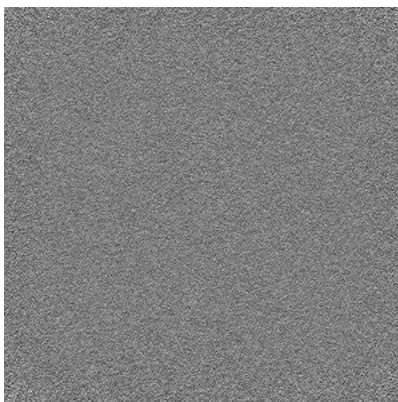


Z Index: 368

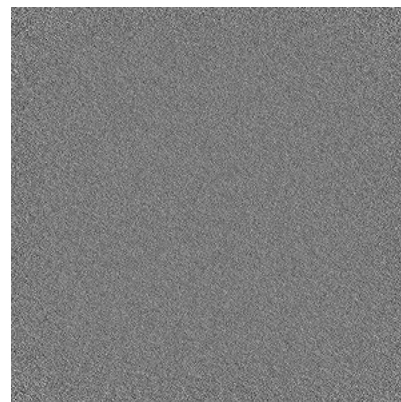
6.3.2 Raw map



X Index: 0



Y Index: 0

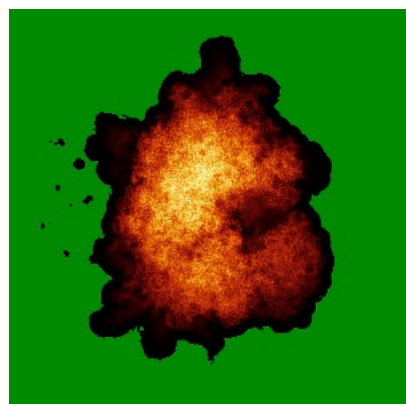


Z Index: 639

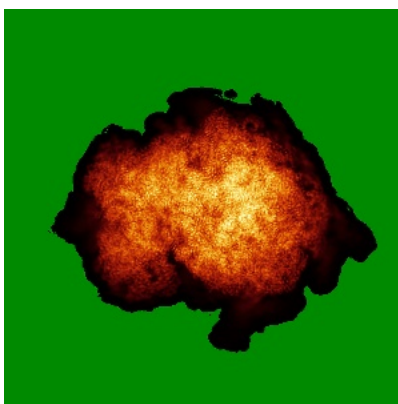
The images above show the largest variance slices of the map in three orthogonal directions.

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

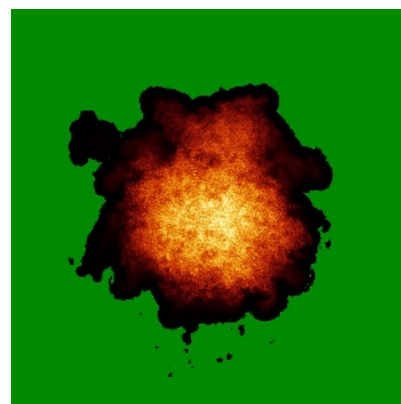
6.4.1 Primary map



X

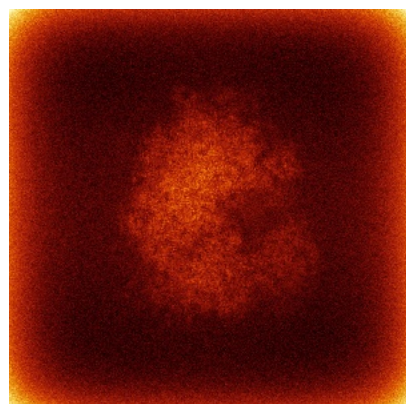


Y

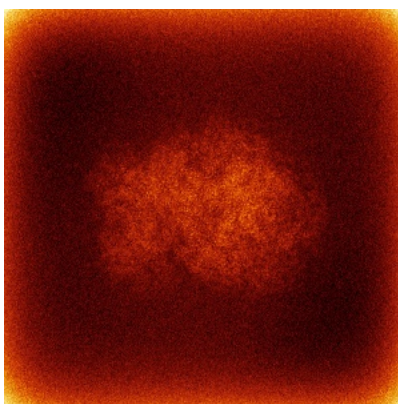


Z

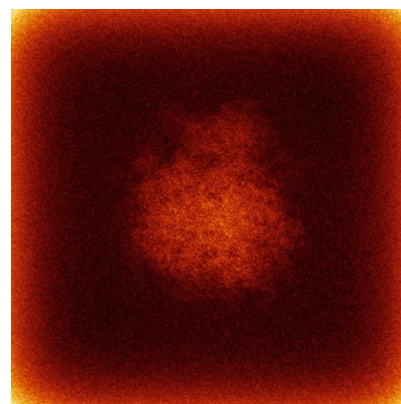
6.4.2 Raw map



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



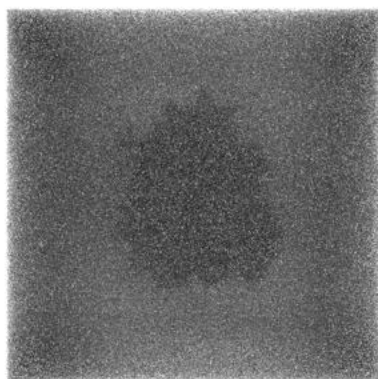
Y



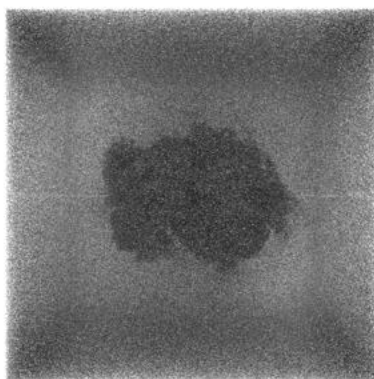
Z

The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

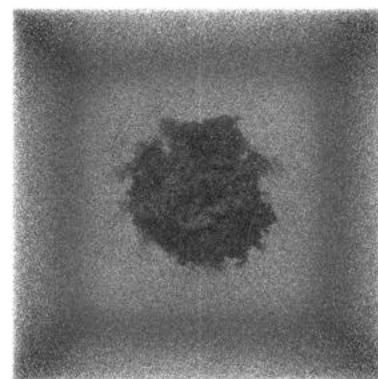
6.5.2 Raw map



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.

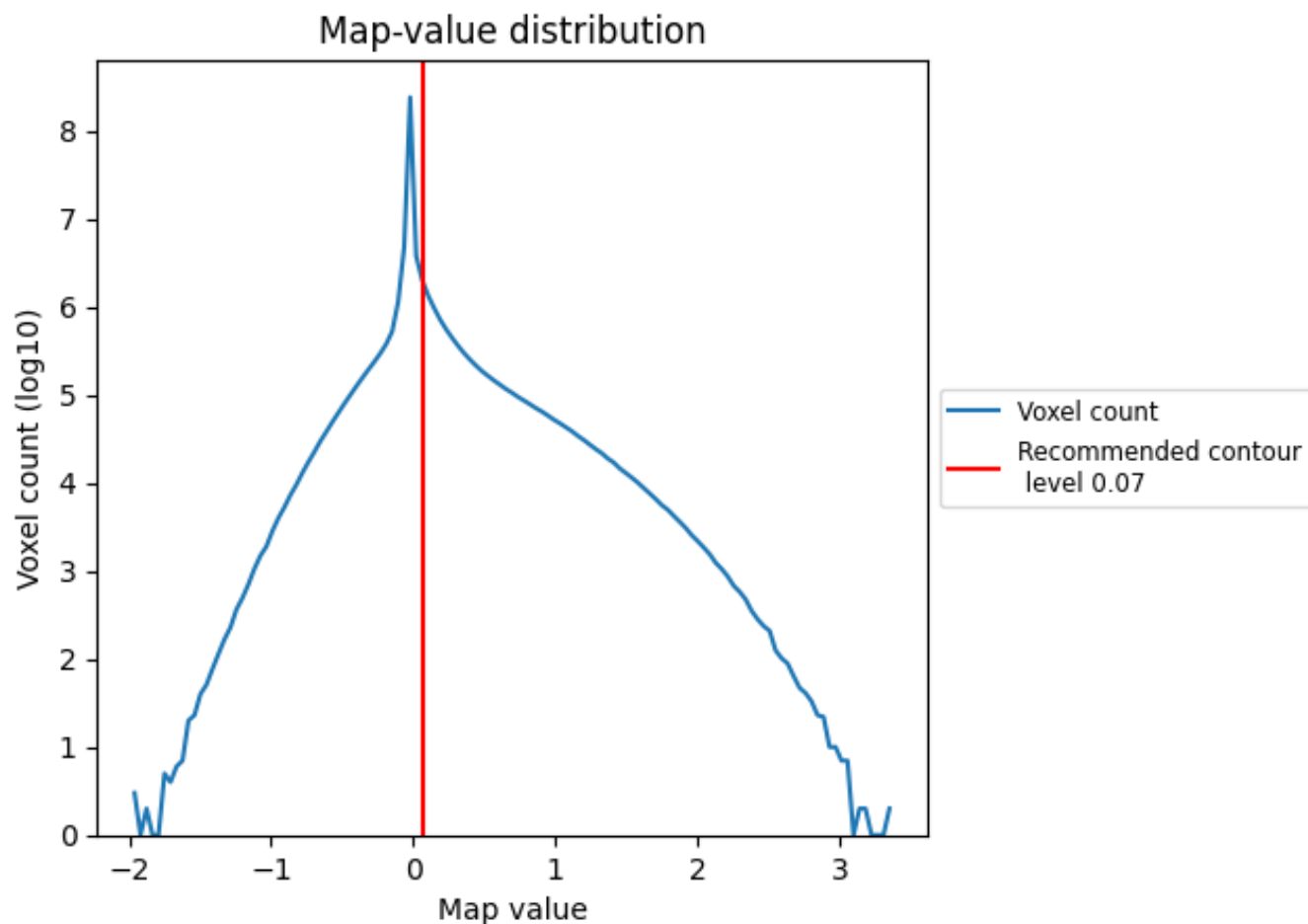
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

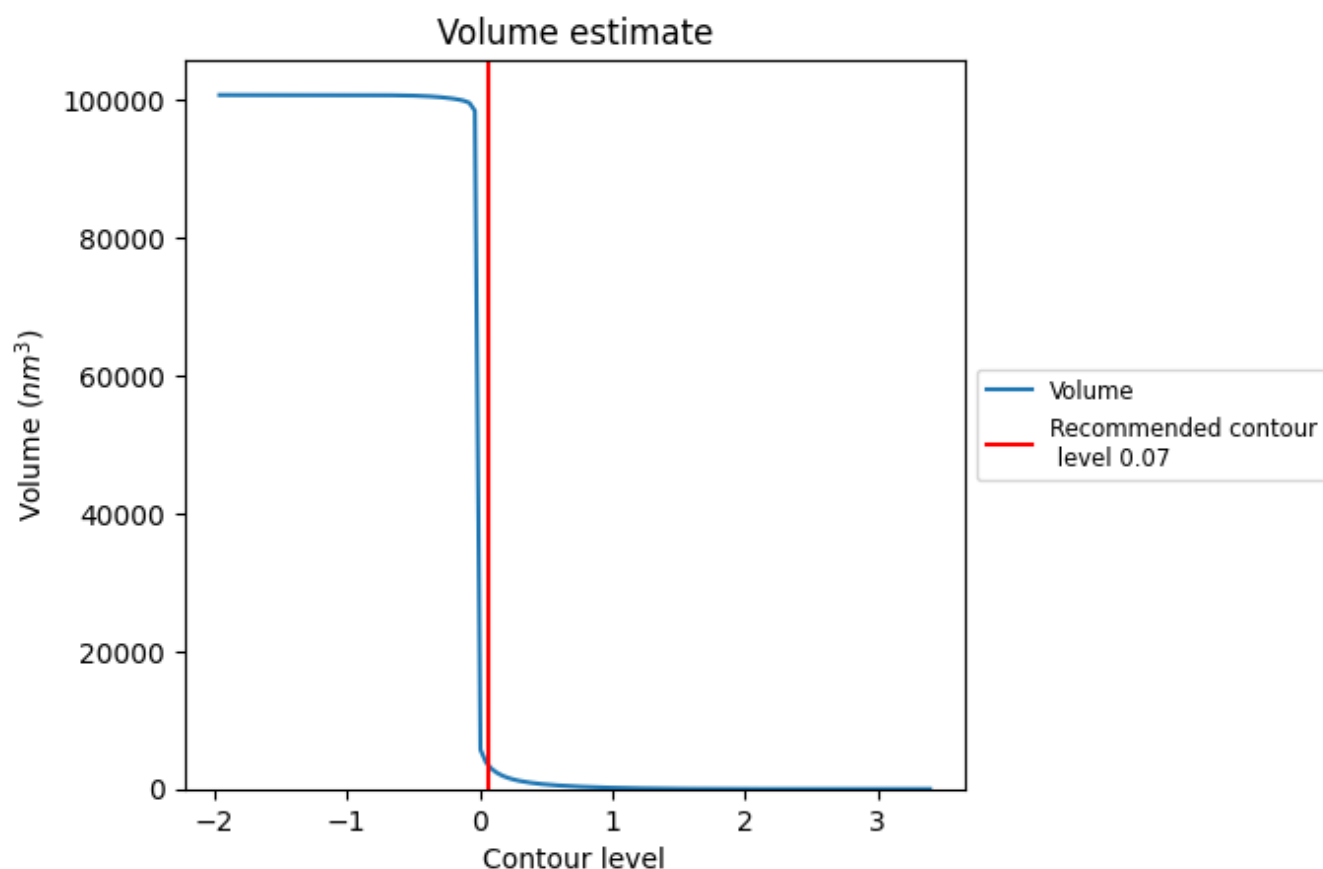
This section contains the results of statistical analysis of the map.

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.

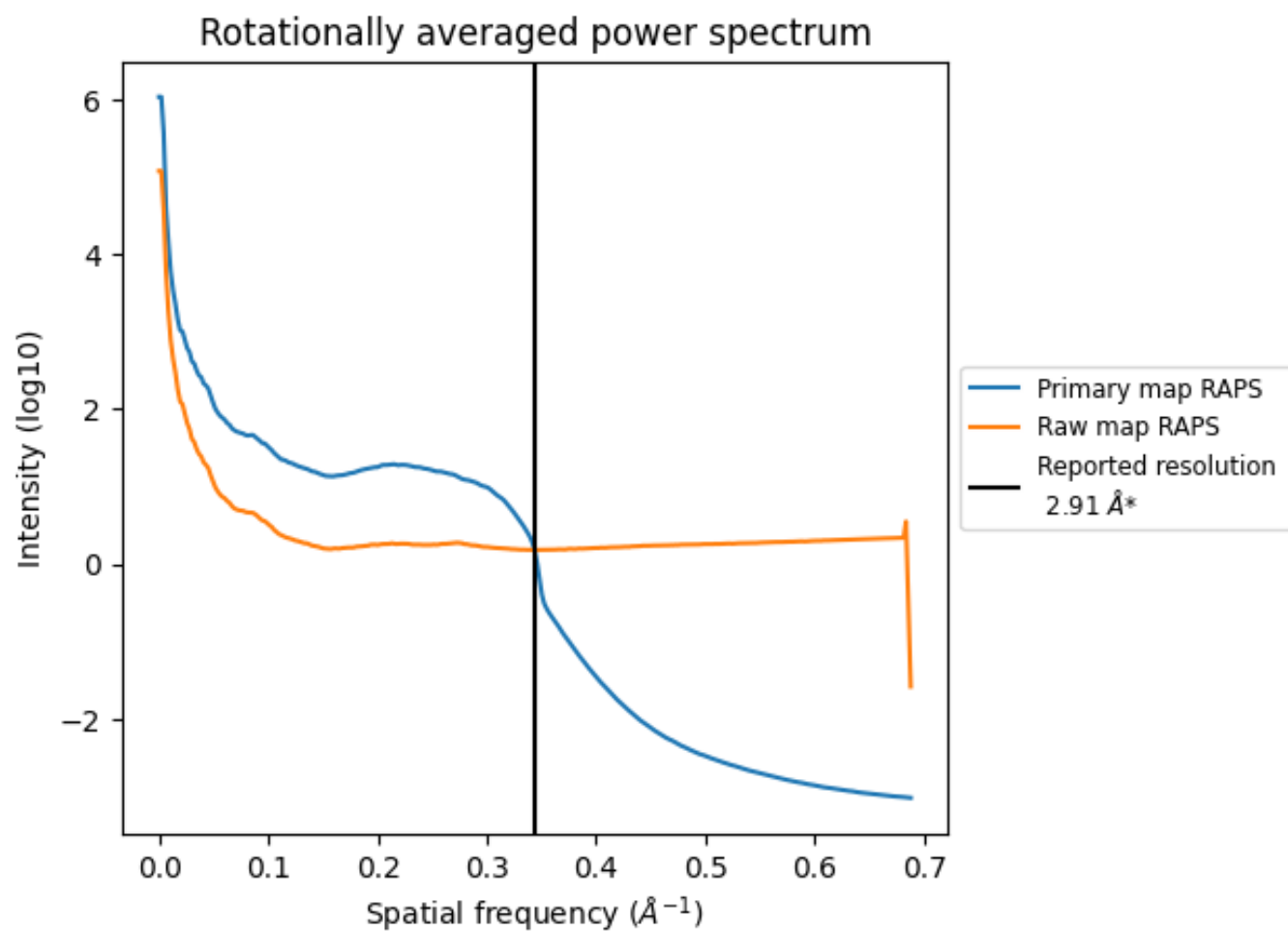
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3348 nm^3 ; this corresponds to an approximate mass of 3025 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 ⓘ

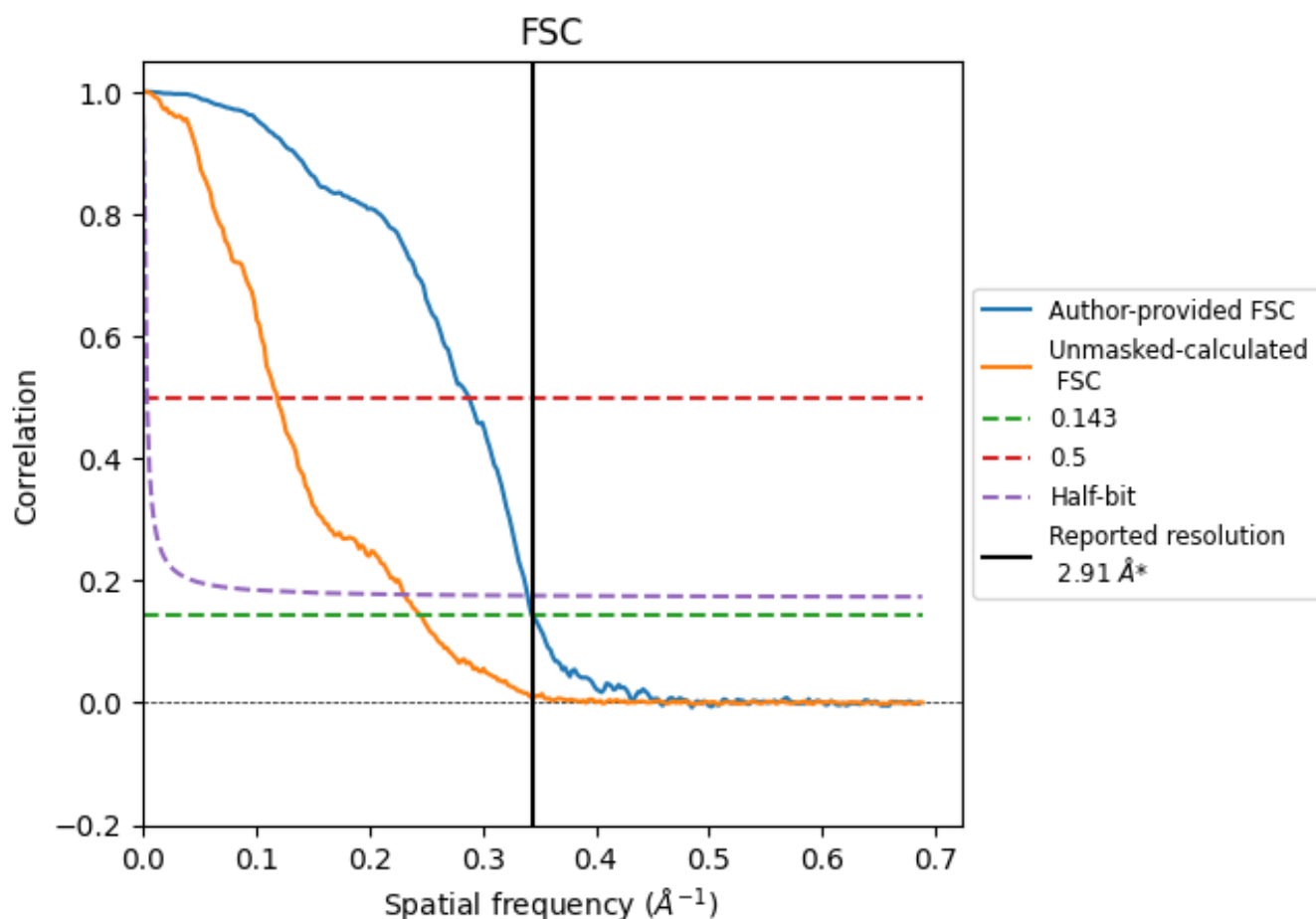


*Reported resolution corresponds to spatial frequency of 0.344 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.344 Å⁻¹

8.2 Resolution estimates [i](#)

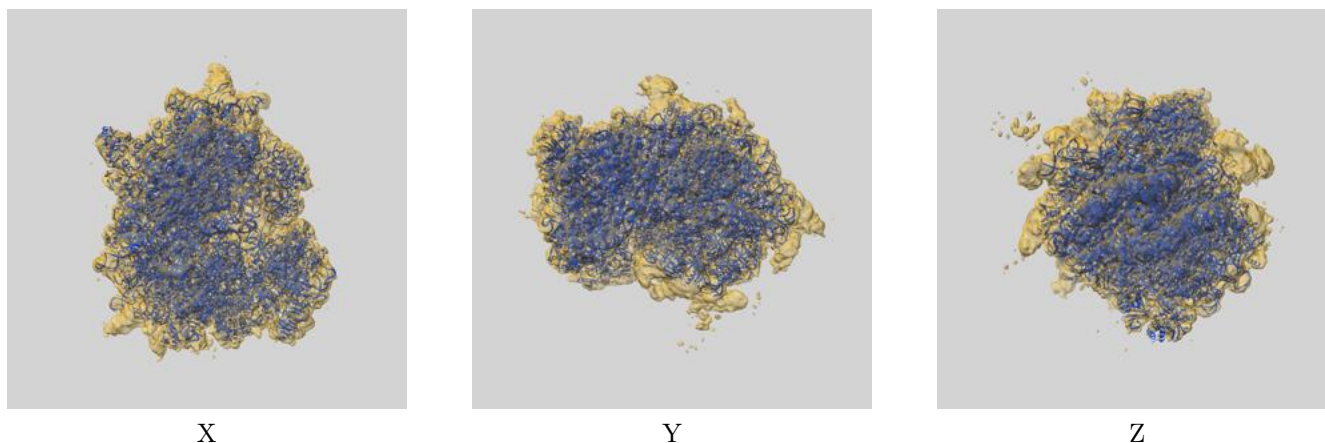
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.91	-	-
Author-provided FSC curve	2.91	3.47	2.94
Unmasked-calculated*	4.07	8.40	4.33

*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 4.07 differs from the reported value 2.91 by more than 10 %

9 Map-model fit [i](#)

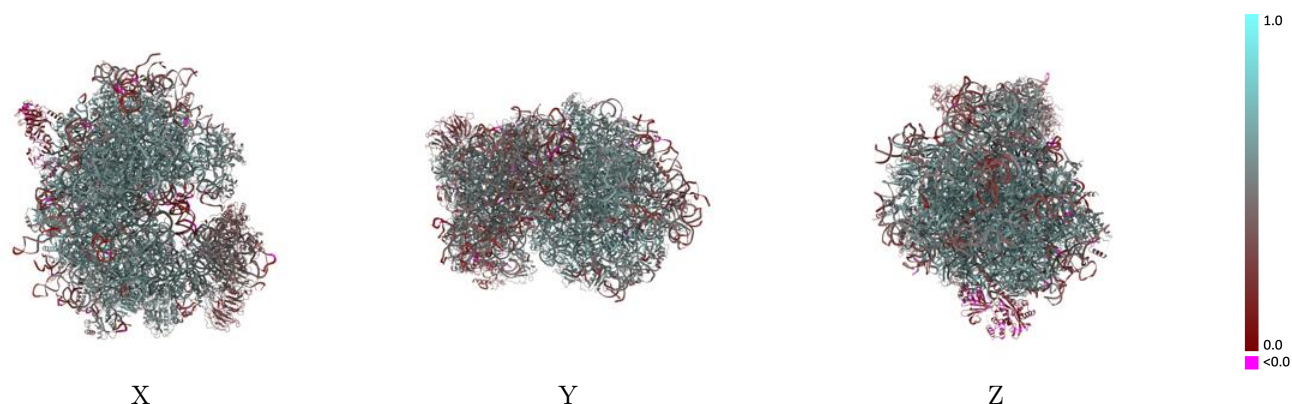
This section contains information regarding the fit between EMDB map EMD-55612 and PDB model 9T6C. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



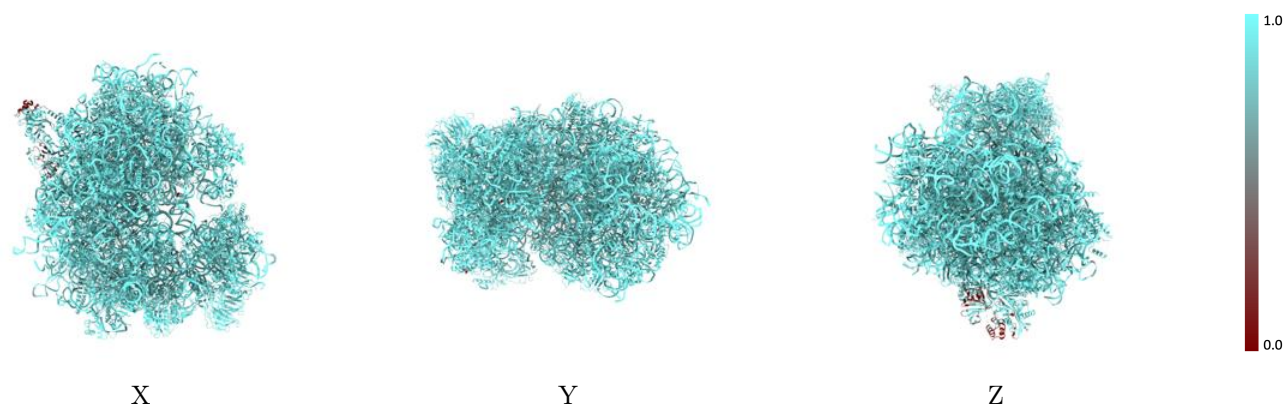
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



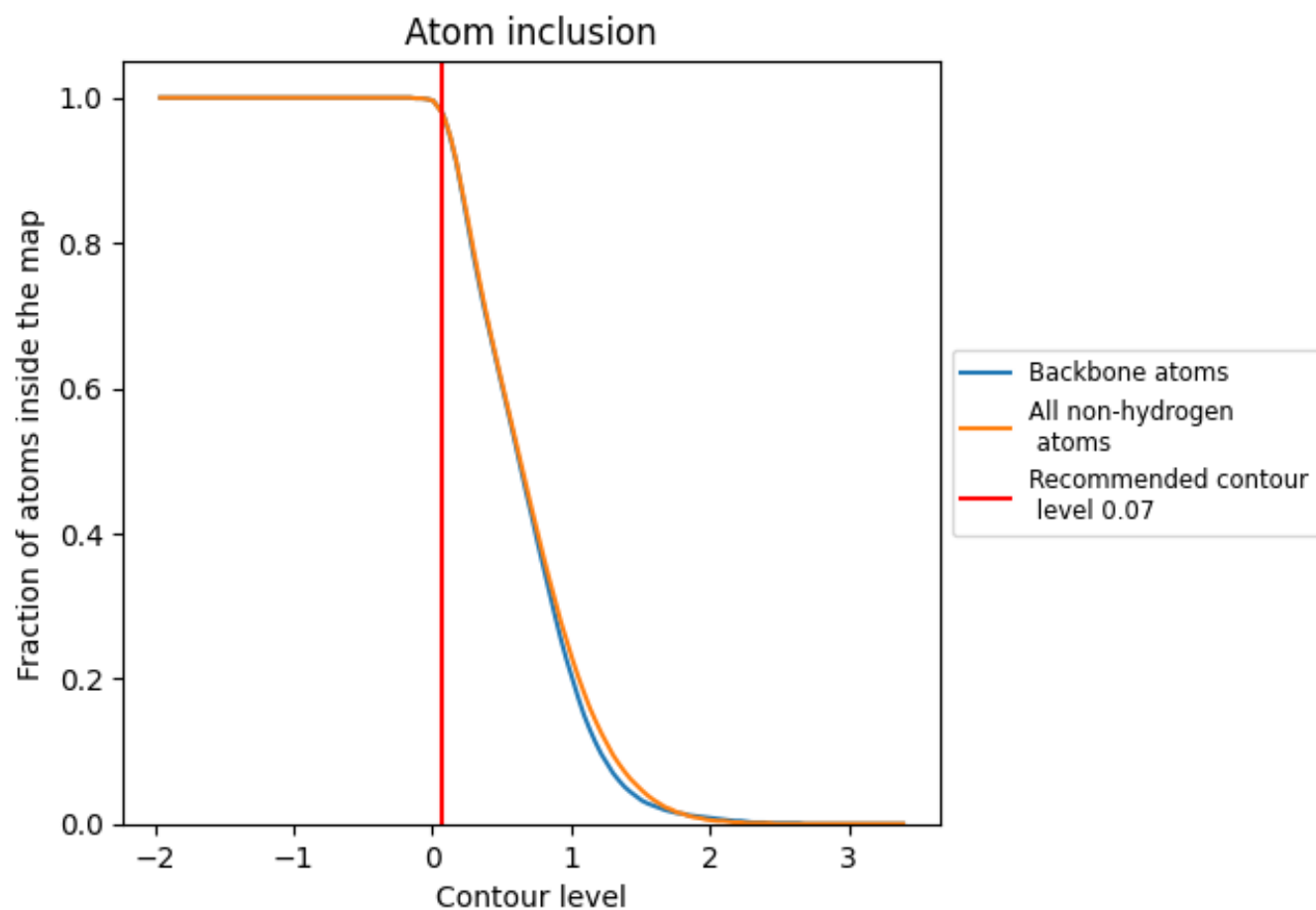
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9790	 0.5140
Bv	 0.9020	 0.2570
Bw	 0.8770	 0.1690
Bx	 0.3380	 0.0540
L5	 0.9920	 0.5410
L7	 0.9980	 0.5830
L8	 0.9940	 0.5590
LA	 0.9920	 0.6100
LB	 0.9880	 0.5850
LC	 0.9860	 0.5850
LD	 0.9870	 0.5170
LE	 0.9880	 0.5270
LF	 0.9880	 0.5880
LG	 0.9850	 0.5130
LH	 0.9890	 0.5380
LI	 0.9700	 0.5480
LJ	 0.9750	 0.4750
LL	 0.9790	 0.5520
LM	 0.9930	 0.5490
LN	 0.9930	 0.6170
LO	 0.9870	 0.5900
LP	 0.9880	 0.6040
LQ	 0.9910	 0.6060
LR	 0.9850	 0.5720
LS	 0.9910	 0.6000
LT	 0.9830	 0.5550
LU	 0.9820	 0.4620
LV	 0.9920	 0.5960
LW	 0.9780	 0.4710
LX	 0.9840	 0.5630
LY	 0.9840	 0.5640
LZ	 0.9900	 0.5600
La	 0.9950	 0.6040
Lb	 0.9620	 0.5030
Lc	 0.9850	 0.5730



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Chain	Atom inclusion	Q-score
Ld	 0.9910	 0.5690
Le	 0.9960	 0.6150
Lf	 0.9810	 0.6060
Lg	 0.9890	 0.5780
Lh	 0.9850	 0.5570
Li	 0.9770	 0.5400
Lj	 0.9850	 0.6030
Lk	 0.9660	 0.5140
Ll	 0.9930	 0.5960
Lm	 0.9710	 0.5700
Ln	 0.9810	 0.5910
Lo	 0.9760	 0.5590
Lp	 0.9910	 0.5990
Lr	 0.9930	 0.5870
N4	 0.8570	 0.1580
NA	 0.3180	 0.0910
NB	 0.6360	 0.1790
NC	 0.9390	 0.3610
S2	 0.9870	 0.4880
SA	 0.9870	 0.5190
SB	 0.9690	 0.5250
SC	 0.9850	 0.5520
SD	 0.9830	 0.4470
SE	 0.9800	 0.5200
SF	 0.9440	 0.4170
SG	 0.9840	 0.4350
SH	 0.9880	 0.4790
SI	 0.9900	 0.5440
SJ	 0.9900	 0.5350
SK	 0.9800	 0.3510
SL	 0.9830	 0.5700
SM	 0.8780	 0.1610
SN	 0.9850	 0.5630
SO	 0.9830	 0.5410
SP	 0.9600	 0.3360
SQ	 0.9620	 0.4350
SR	 0.9720	 0.4530
SS	 0.9510	 0.3590
ST	 0.9550	 0.3840
SU	 0.9810	 0.4280
SV	 0.9880	 0.5370
SW	 0.9870	 0.5810

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Chain	Atom inclusion	Q-score
SX	 0.9760	 0.5500
SY	 0.9860	 0.4670
SZ	 0.9580	 0.3370
Sa	 0.9880	 0.5650
Sb	 0.9820	 0.4900
Sc	 0.9670	 0.4450
Sd	 0.9830	 0.4690
Se	 0.9850	 0.4900
Sf	 0.9660	 0.1940
Sg	 0.9770	 0.3250