



wwPDB EM Validation Summary Report ⓘ

May 11, 2026 – 01:15 PM JST

PDB ID : 22TU / pdb_000022tu
EMDB ID : EMD-68666
Title : Human 80S ribosome in complex with DHX29
Authors : Goto-Ito, S.; Iwasaki, W.; Ito, T.
Deposited on : 2026-01-22
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

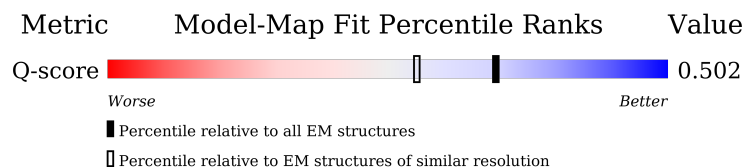
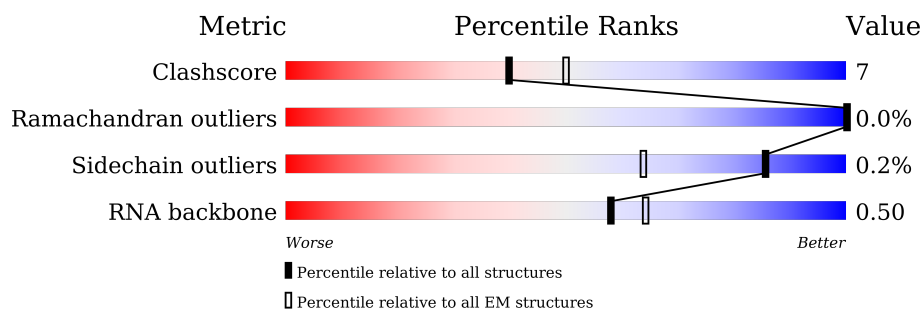
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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.






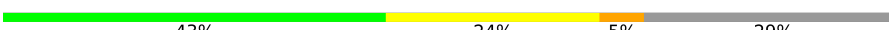






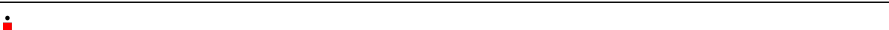

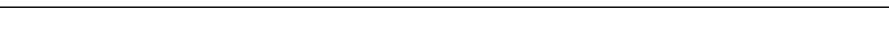
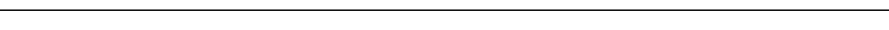











Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

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

Mol	Chain	Length	Quality of chain
1	LA	257	
2	SA	295	
3	LB	403	

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Mol	Chain	Length	Quality of chain
4	SB	264	
5	B4	75	
5	C4	75	
6	L5	5070	
7	L7	121	
8	L8	157	
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	






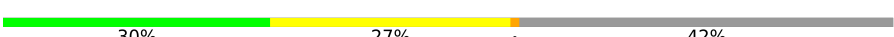




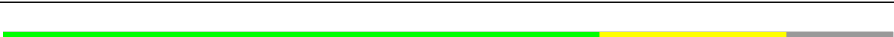


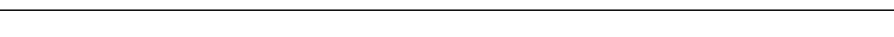
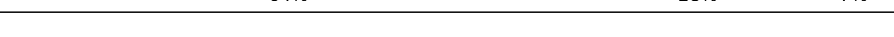
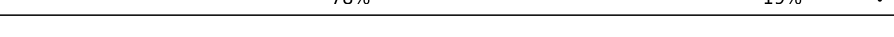



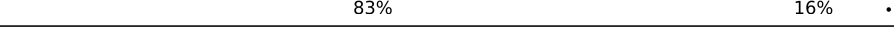

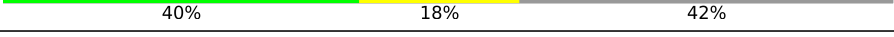



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Mol	Chain	Length	Quality of chain
28	LW	157	
29	LX	156	
30	LY	145	
31	LZ	136	
32	La	148	
33	Lb	159	
34	Lc	115	
35	Ld	125	
36	Le	135	
37	Lf	110	
38	Lg	117	
39	Lh	123	
40	Li	105	
41	Lj	97	
42	Lk	70	
43	Ll	51	
44	Lm	128	
45	Ln	25	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	S2	1869	
50	SC	293	
51	SD	243	
52	SE	263	



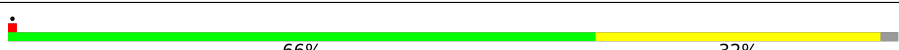
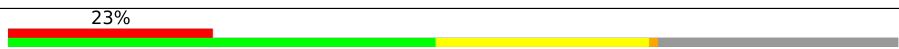

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Mol	Chain	Length	Quality of chain
53	SF	204	
54	SG	249	
55	SH	194	
56	SI	208	
57	SJ	194	
58	SK	165	
59	SL	158	
60	SM	132	
61	SN	151	
62	SO	151	
63	SP	145	
64	SQ	146	
65	SR	135	
66	SS	152	
67	ST	145	
68	SU	119	
69	SV	83	
70	SW	130	
71	SX	143	
72	SY	133	
73	SZ	125	
74	Sa	115	
75	Sb	84	
76	Sc	69	
77	Sd	56	

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Mol	Chain	Length	Quality of chain
78	Se	133	 36% 8% 56%
79	Sf	156	 10% 29% 12% 59%
80	Sg	317	 66% 32%
81	DH	1369	 23% 48% 24% 27%
82	zx	32	 53% 38% 6%

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 222283 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 Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SA	219	Total	C	N	O	S	0	0
			1727	1097	303	319	8		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	LB	395	Total	C	N	O	S	0	0
			3189	2030	600	545	14		

- Molecule 4 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 5 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B4	75	Total	C	N	O	P	0	0
			1599	713	284	528	74		
5	C4	75	Total	C	N	O	P	0	0
			1602	713	284	530	75		

- Molecule 6 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L5	3619	Total	C	N	O	P	0	0
			77578	34548	14191	25221	3618		

- Molecule 7 is a RNA chain called 5S rRNA.

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

- Molecule 8 is a RNA chain called 5.8S rRNA.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LC	362	Total	C	N	O	S	0	0
			2882	1814	576	478	14		

- 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
			2382	1507	434	427	14		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	222	Total	C	N	O	S	0	0
			1783	1148	338	293	4		

- Molecule 12 is a protein called 60S ribosomal protein L7.

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	228	Total	C	N	O	S	0	0
			1841	1174	354	309	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
			1518	956	284	272	6		

- Molecule 15 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LI	213	Total	C	N	O	S	0	0
			1716	1086	331	285	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LJ	168	Total	C	N	O	S	0	0
			1344	850	251	237	6		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LM	137	Total	C	N	O	S	0	0
			1125	722	216	180	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
			1641	1058	320	258	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LP	155	Total	C	N	O	S	0	0
			1259	787	244	219	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
			1513	944	314	250	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
			1472	910	320	233	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
			1294	821	252	215	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
			825	529	144	150	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LV	130	Total	C	N	O	S	0	0
			973	615	183	170	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LW	114	Total	C	N	O	S	0	0
			932	583	192	153	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LX	118	Total	C	N	O	S	0	0
			967	618	181	167	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
			1115	700	226	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	106	Total	C	N	O	S	0	0
			864	537	189	134	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	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
			888	560	171	155	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Le	130	Total	C	N	O	S	0	0
			1070	676	221	168	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
			876	555	174	144	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lg	112	Total	C	N	O	S	0	0
			888	555	183	144	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
			1010	638	204	167	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Li	101	Total	C	N	O	S	0	0
			823	515	175	128	5		

- Molecule 41 is a protein called 60S ribosomal protein L37.

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
			569	366	103	99	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
			429	266	90	67	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	89	Total	C	N	O	S	0	0
			690	436	133	114	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lr	123	Total	C	N	O	S	0	0
			987	612	205	166	4		

- Molecule 49 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	1683	Total	C	N	O	P	0	0
			35919	16035	6448	11754	1682		

- Molecule 50 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SC	219	Total	C	N	O	S	0	0
			1700	1100	292	298	10		

- Molecule 51 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SD	224	Total	C	N	O	S	0	0
			1740	1110	313	310	7		

- Molecule 52 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SE	259	Total	C	N	O	S	0	0
			2055	1314	383	350	8		

- Molecule 53 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SF	186	Total	C	N	O	S	0	0
			1475	923	278	267	7		

- Molecule 54 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SG	231	Total	C	N	O	S	0	0
			1853	1157	371	318	7		

- Molecule 55 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SH	186	Total	C	N	O	S	0	0
			1501	957	276	267	1		

- Molecule 56 is a protein called 40S ribosomal protein S8.

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

- Molecule 57 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SJ	180	Total	C	N	O	S	0	0
			1499	955	300	242	2		

- Molecule 58 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 59 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SL	143	Total	C	N	O	S	0	0
			1173	747	222	198	6		

- Molecule 60 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SM	120	Total	C	N	O	S	0	0
			925	580	162	175	8		

- Molecule 61 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SN	150	Total	C	N	O	S	0	0
			1204	771	229	203	1		

- Molecule 62 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SO	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 63 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SP	127	Total	C	N	O	S	0	0
			1043	662	197	177	7		

- Molecule 64 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SQ	140	Total	C	N	O	S	0	0
			1117	710	211	193	3		

- Molecule 65 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SR	133	Total	C	N	O	S	0	0
			1072	674	200	194	4		

- Molecule 66 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SS	141	Total	C	N	O	S	0	0
			1160	731	235	193	1		

- Molecule 67 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	ST	140	Total	C	N	O	S	0	0
			1086	681	208	194	3		

- Molecule 68 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SU	101	Total	C	N	O	S	0	0
			803	504	153	142	4		

- Molecule 69 is a protein called 40S ribosomal protein S21.

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

- Molecule 70 is a protein called 40S ribosomal protein S15a.

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

- Molecule 71 is a protein called 40S ribosomal protein S23.

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

- Molecule 72 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SY	122	Total	C	N	O	S	0	0
			994	630	195	164	5		

- Molecule 73 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SZ	73	Total	C	N	O	S	0	0
			583	374	106	102	1		

- Molecule 74 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Sa	99	Total	C	N	O	S	0	0
			788	490	165	128	5		

- Molecule 75 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Sb	83	Total	C	N	O	S	0	0
			647	406	121	113	7		

- Molecule 76 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sc	63	Total	C	N	O	S	0	0
			495	302	98	93	2		

- Molecule 77 is a protein called 40S ribosomal protein S29.

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

- Molecule 78 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

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

- Molecule 79 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sf	64	Total	C	N	O	S	0	0
			522	329	99	87	7		

- Molecule 80 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sg	311	Total	C	N	O	S	0	0
			2420	1526	422	460	12		

- Molecule 81 is a protein called ATP-dependent RNA helicase DHX29.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	DH	1004	Total	C	N	O	S	0	0
			8048	5136	1404	1473	35		

- Molecule 82 is a protein called nascent peptide.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	zx	32	Total	C	N	O	S	0	0
			246	164	36	45	1		

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	LA	2	Total 2	Mg 2	0
83	B4	1	Total 1	Mg 1	0
83	L5	124	Total 124	Mg 124	0
83	L7	3	Total 3	Mg 3	0
83	L8	4	Total 4	Mg 4	0
83	LC	1	Total 1	Mg 1	0
83	LN	1	Total 1	Mg 1	0
83	LP	1	Total 1	Mg 1	0
83	LV	1	Total 1	Mg 1	0
83	Lb	2	Total 2	Mg 2	0
83	S2	51	Total 51	Mg 51	0


- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

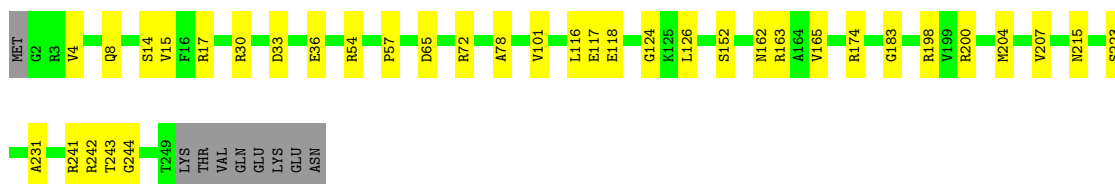
Mol	Chain	Residues	Atoms		AltConf
84	Lg	1	Total 1	Zn 1	0
84	Lj	1	Total 1	Zn 1	0
84	Lm	1	Total 1	Zn 1	0
84	Lo	1	Total 1	Zn 1	0
84	Lp	1	Total 1	Zn 1	0
84	Sa	1	Total 1	Zn 1	0
84	Sd	1	Total 1	Zn 1	0
84	Sf	1	Total 1	Zn 1	0

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.

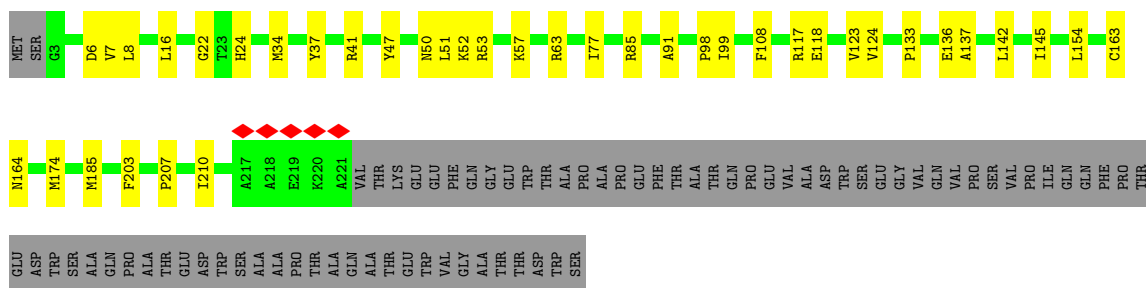
- Molecule 1: 60S ribosomal protein L8

Chain LA: 




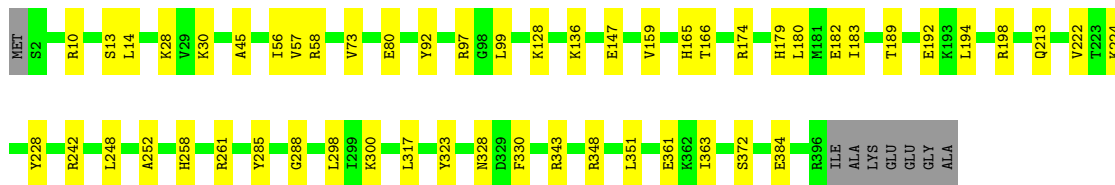
- Molecule 2: Small ribosomal subunit protein uS2

Chain SA: 



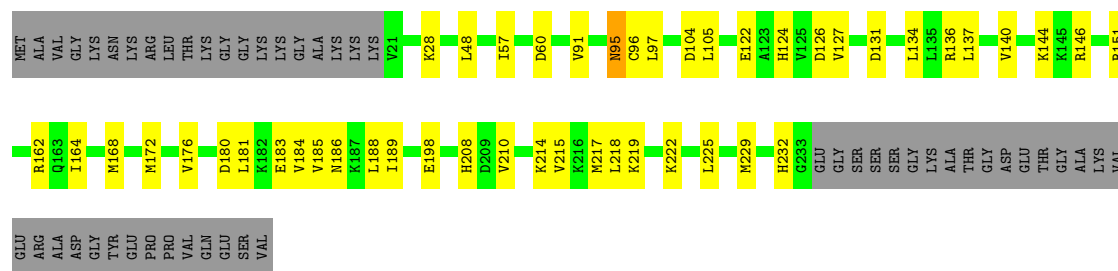
- Molecule 3: 60S ribosomal protein L3

Chain LB: 



- Molecule 4: 40S ribosomal protein S3a

Chain SB: 



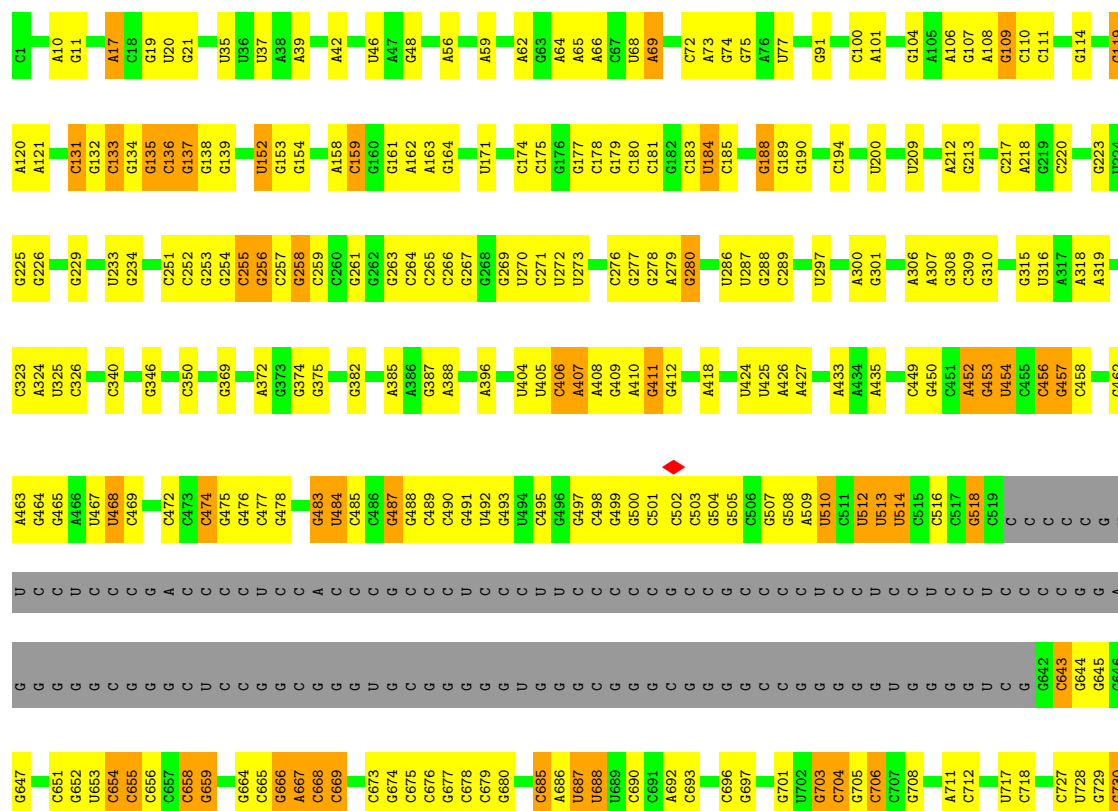
• Molecule 5: tRNA



• Molecule 5: tRNA



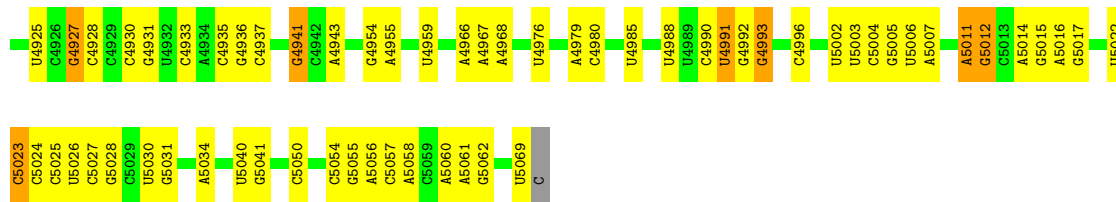
• Molecule 6: 28S rRNA





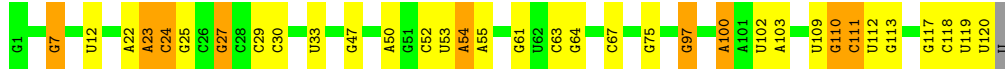






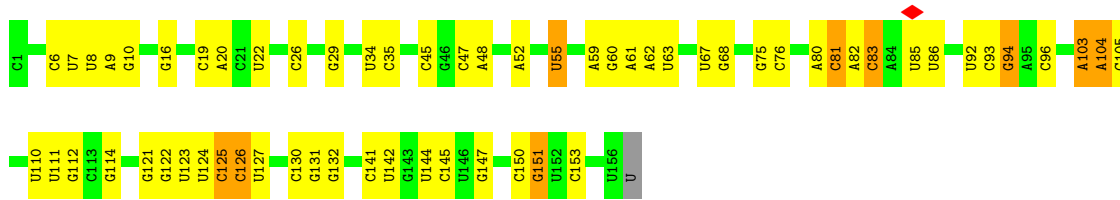
- Molecule 7: 5S rRNA

Chain L7: 71% 21% 7% .



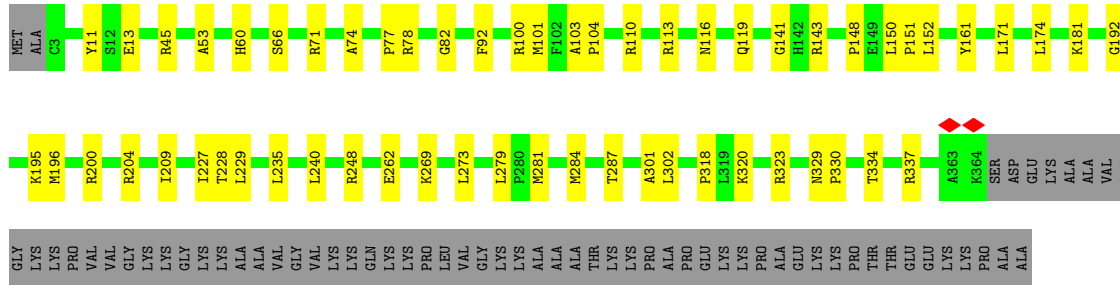
- Molecule 8: 5.8S rRNA

Chain L8: 60% 34% 6% .



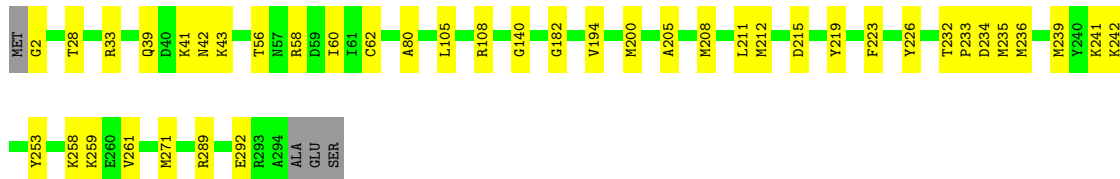
- Molecule 9: 60S ribosomal protein L4

Chain LC: 71% 14% 15%



- Molecule 10: 60S ribosomal protein L5

Chain LD: 85% 14% .



- Molecule 11: 60S ribosomal protein L6

[illegible]

- [illegible]

- | Protein | Residue | Score | Category |
|---------|---------|-------|----------|
| P00073 | ALA | 0.98 | High |
| | ALA | 0.96 | High |
| | GLY | 0.94 | High |
| | LYS | 0.92 | High |
| | GLY | 0.90 | High |
| | ASP | 0.88 | High |
| | VAL | 0.86 | High |
| | PRO | 0.84 | High |
| | THR | 0.82 | High |
| | LYS | 0.80 | High |
| P00074 | R132 | 0.78 | High |
| | F133 | 0.76 | High |
| | P134 | 0.74 | High |
| | V135 | 0.72 | High |
| | L136 | 0.70 | High |
| | V143 | 0.68 | High |
| | V161 | 0.66 | High |
| | D162 | 0.64 | High |
| | P163 | 0.62 | High |
| | K176 | 0.60 | High |
| P00075 | P180 | 0.58 | High |
| | I184 | 0.56 | High |
| | L190 | 0.54 | High |
| | G191 | 0.52 | High |
| | R192 | 0.50 | High |
| | H195 | 0.48 | High |
| | T200 | 0.46 | High |
| | T201 | 0.44 | High |
| | Q206 | 0.42 | High |
| | N227 | 0.40 | High |
| P00076 | Y230 | 0.38 | High |
| | I233 | 0.36 | High |
| | T263 | 0.34 | High |
| | K264 | 0.32 | High |
| | LEU | 0.30 | High |
| | GLY | 0.28 | High |
| | E103 | 0.26 | High |
| | P104 | 0.24 | High |
| | E105 | 0.22 | High |
| | E109 | 0.20 | High |
| P00077 | MET | 0.18 | High |
| | PRO | 0.16 | High |
| | LYS | 0.14 | High |
| | GLY | 0.12 | High |
| | LYS | 0.10 | High |
| | ALA | 0.08 | High |
| | GLY | 0.06 | High |
| | LYS | 0.04 | High |
| | VAL | 0.02 | High |
| | LYS | 0.00 | High |
| P00078 | L31 | -0.02 | Low |
| | F32 | -0.04 | Low |
| | R35 | -0.06 | Low |
| | L51 | -0.08 | Low |
| | V55 | -0.10 | Low |
| | L63 | -0.12 | Low |
| | G64 | -0.14 | Low |
| | H65 | -0.16 | Low |
| | Y71 | -0.18 | Low |
| | K72 | -0.20 | Low |
| R73 | -0.22 | Low | |
| P00079 | P77 | -0.24 | Low |
| | I80 | -0.26 | Low |
| | D88 | -0.28 | Low |
| | A99 | -0.30 | Low |
| | E103 | -0.32 | Low |
| | P104 | -0.34 | Low |
| | E105 | -0.36 | Low |
| | E109 | -0.38 | Low |
| | C110 | -0.40 | Low |
| | S111 | -0.42 | Low |

- [illegible]

- | |
|------|
| MET |
| G2 |
| R3 |
| K13 |
| K19 |
| V26 |
| I31 |
| R38 |
| A41 |
| K42 |
| V43 |
| D44 |
| E45 |
| F46 |
| P47 |
| L48 |
| H51 |
| D55 |
| S62 |
| M76 |
| F85 |
| H86 |
| I87 |
| P93 |
| M102 |
| L103 |
| D109 |
| R110 |
| L111 |
| Q112 |
| T125 |
| V134 |
| I138 |
| R139 |
| K145 |
| V148 |
| R162 |
| I191 |
| R193 |



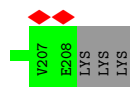
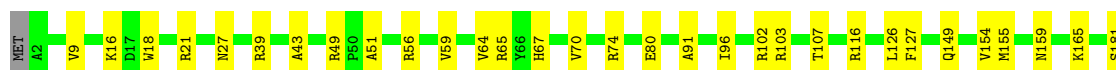
- Molecule 16: 60S ribosomal protein L11

Chain LJ: 78% 16% 6%



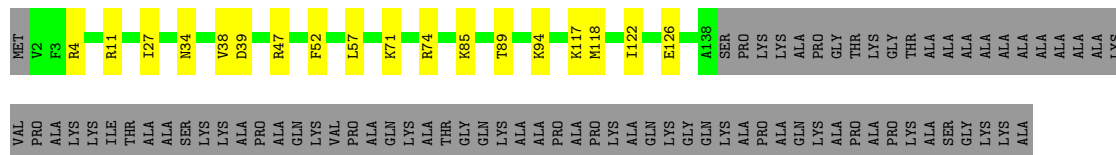
- Molecule 17: 60S ribosomal protein L13

Chain LL: 83% 15% .



- Molecule 18: 60S ribosomal protein L14

Chain LM: 55% 8% 36%



- Molecule 19: 60S ribosomal protein L15

Chain LN: 82% 18%




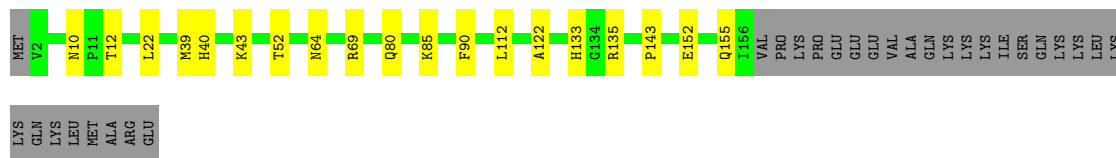
- Molecule 20: 60S ribosomal protein L13a

Chain LO: 85% 13% .




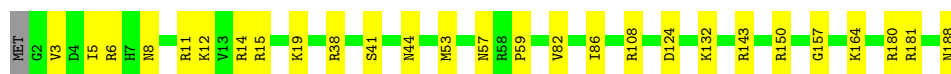
- Molecule 21: 60S ribosomal protein L17

Chain LP:  74% 10% 16%




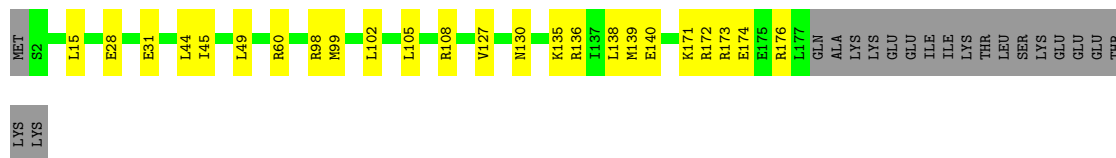
- Molecule 22: 60S ribosomal protein L18

Chain LQ:  85% 14%




- Molecule 23: 60S ribosomal protein L19

Chain LR:  78% 12% 10%




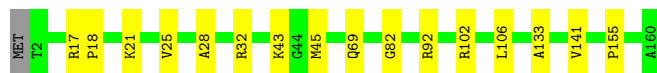
- Molecule 24: 60S ribosomal protein L18a

Chain LS:  86% 14%



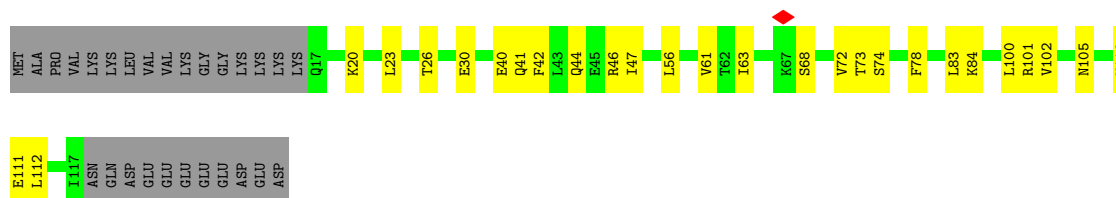
- Molecule 25: 60S ribosomal protein L21

Chain LT:  89% 10%




- Molecule 26: 60S ribosomal protein L22

Chain LU:  58% 21% 21%



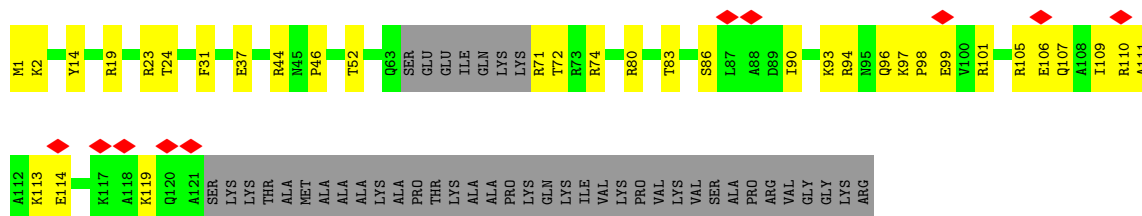
- Molecule 27: 60S ribosomal protein L23

Chain LV:  76% 16% 7%



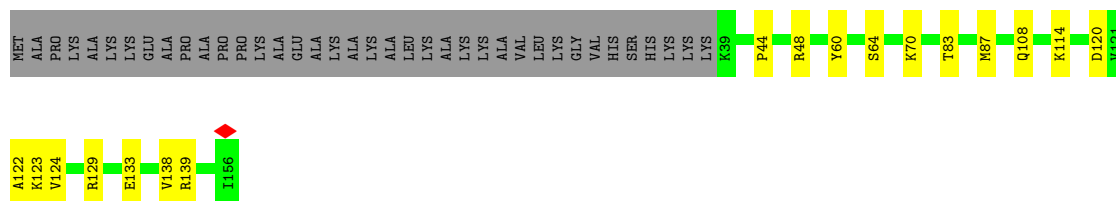
- Molecule 28: 60S ribosomal protein L24

Chain LW:  6% 51% 22% 27%



- Molecule 29: 60S ribosomal protein L23a

Chain LX:  65% 11% 24%




- Molecule 30: 60S ribosomal protein L26

Chain LY:  71% 21% 8%



- Molecule 31: 60S ribosomal protein L27

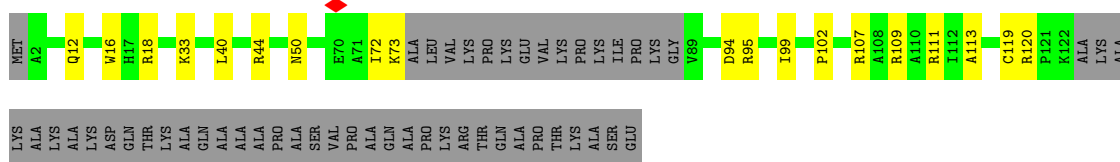
Chain LZ:  84% 15% 1%



- Molecule 32: 60S ribosomal protein L27a

Chain La:  91% 9% 0%

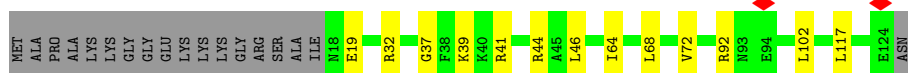
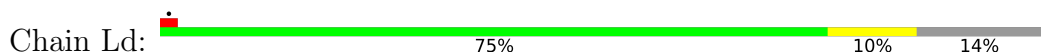
- Molecule 33: 60S ribosomal protein L29



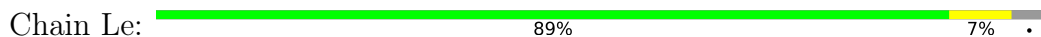
- Molecule 34: 60S ribosomal protein L30



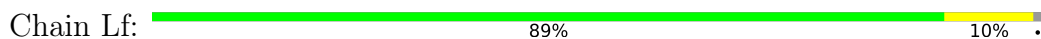
- Molecule 35: 60S ribosomal protein L31



- Molecule 36: 60S ribosomal protein L32




- Molecule 37: 60S ribosomal protein L35a



- Molecule 38: 60S ribosomal protein L34




- Molecule 39: 60S ribosomal protein L35

Chain Lh:  85% 13%



- Molecule 40: 60S ribosomal protein L36

Chain Li:  82% 14%




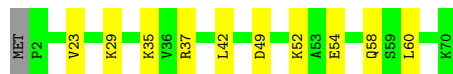
- Molecule 41: 60S ribosomal protein L37

Chain Lj:  74% 14% 11%




- Molecule 42: 60S ribosomal protein L38

Chain Lk:  84% 14%



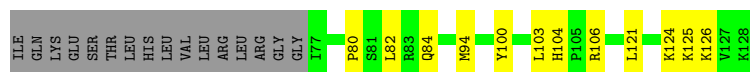
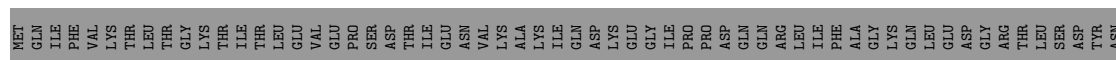
- Molecule 43: 60S ribosomal protein L39

Chain Ll:  78% 20%




- Molecule 44: Ubiquitin-60S ribosomal protein L40

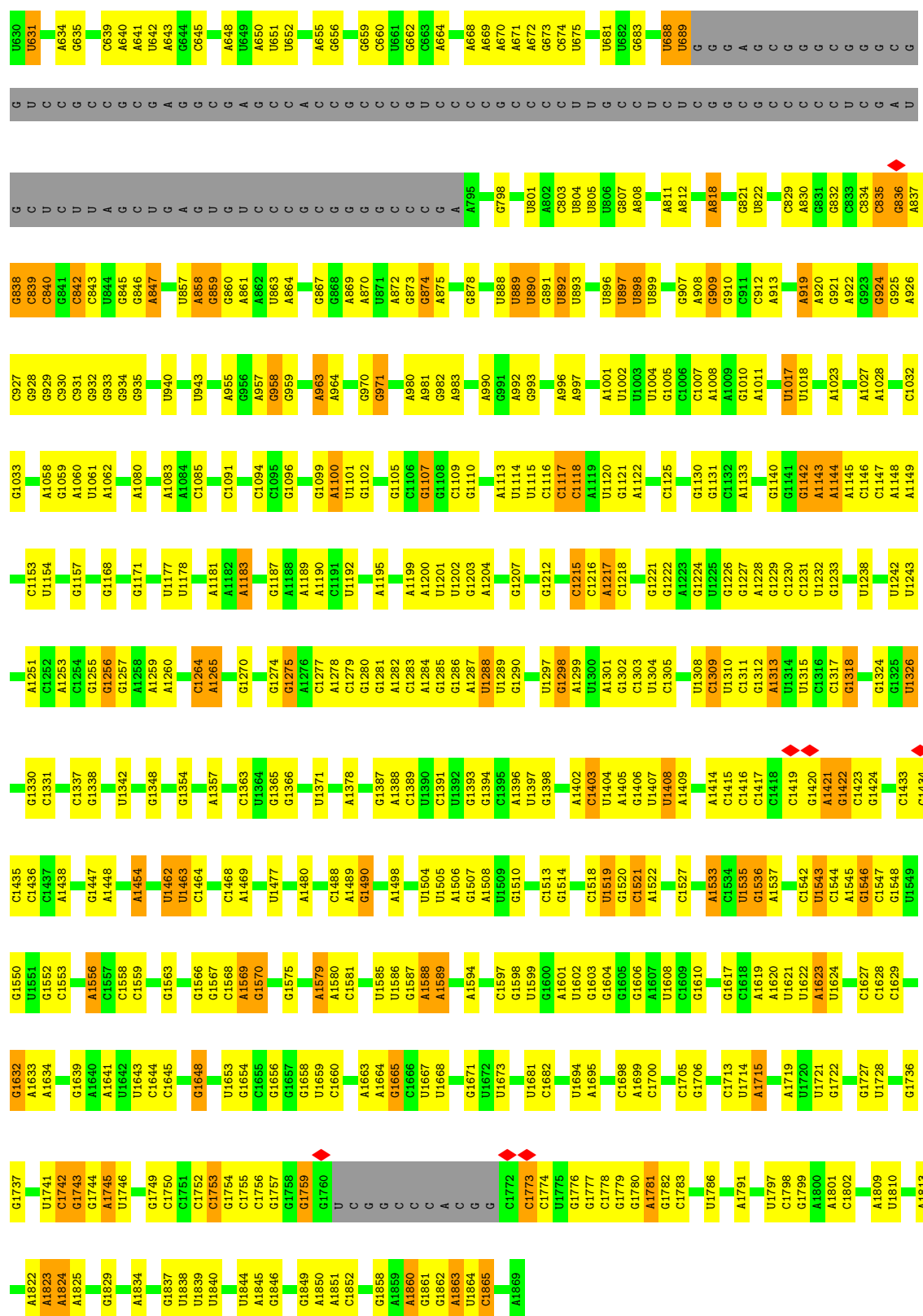
Chain Lm:  31% 9% 59%



- Molecule 45: 60S ribosomal protein L41

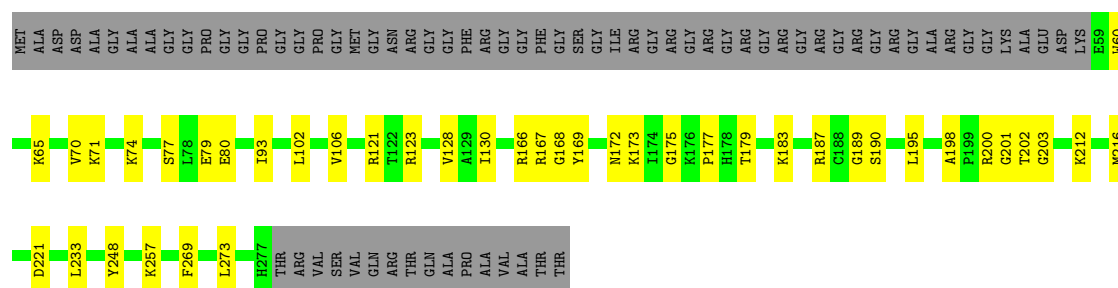
Chain Ln:  84% 12%





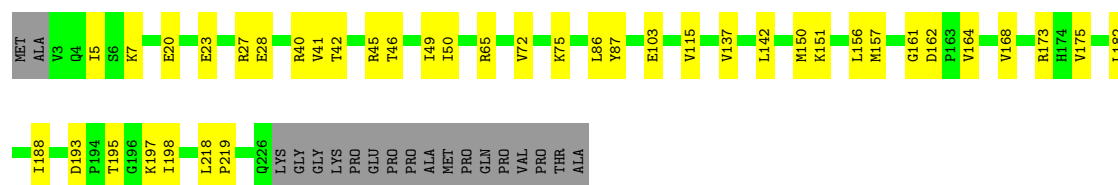
• Molecule 50: 40S ribosomal protein S2

Chain SC: 60% 14% 25%



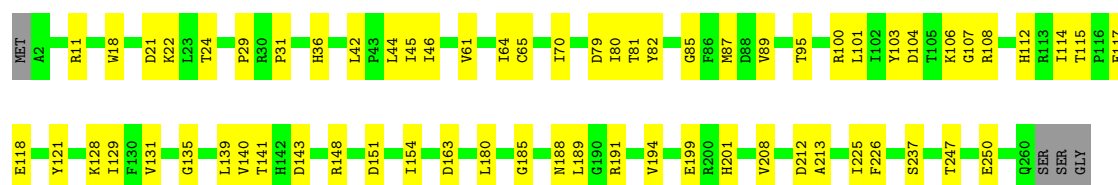
• Molecule 51: 40S ribosomal protein S3

Chain SD: 76% 16% 8%



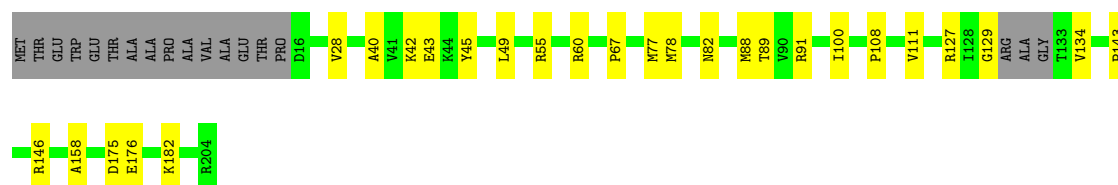
• Molecule 52: 40S ribosomal protein S4, X isoform

Chain SE: 74% 25% .



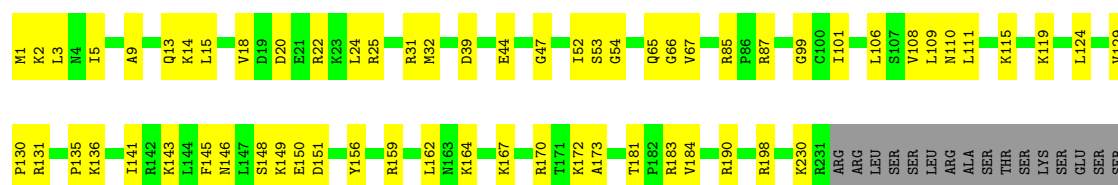
• Molecule 53: 40S ribosomal protein S5

Chain SF: 78% 13% 9%




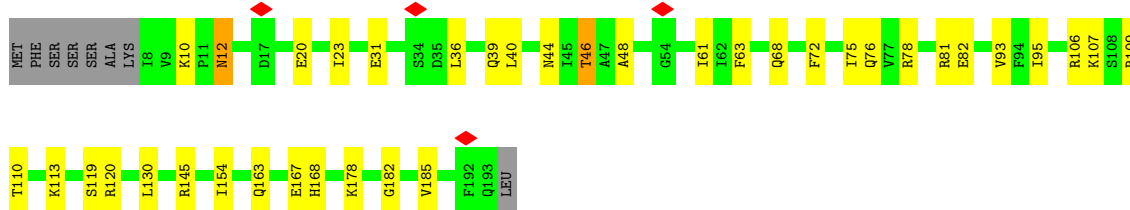
• Molecule 54: 40S ribosomal protein S6

Chain SG: 67% 25% 7%


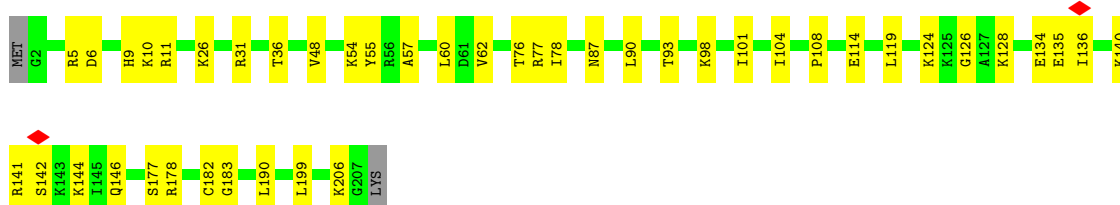


GLN
LYS


- Molecule 55: 40S ribosomal protein S7

Chain SH:  76% 19%


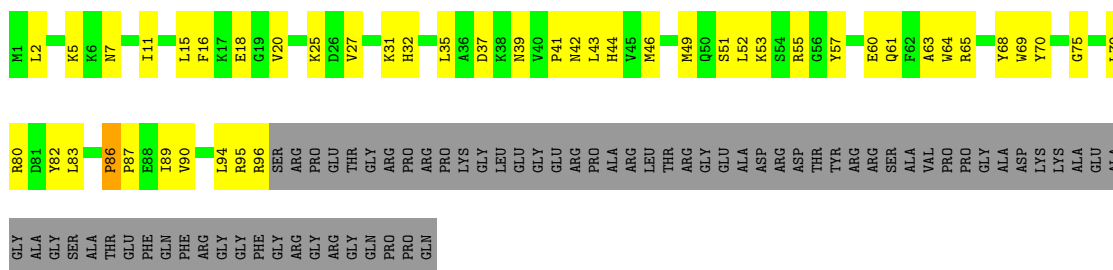
- Molecule 56: 40S ribosomal protein S8

Chain SI:  78% 21%


- Molecule 57: 40S ribosomal protein S9

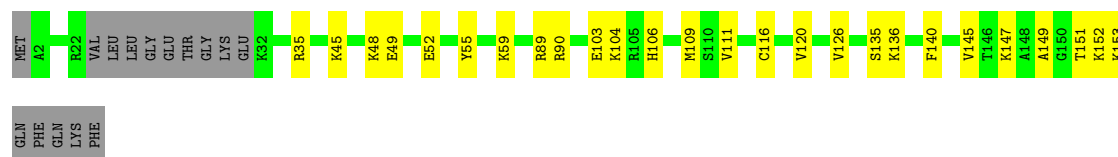
Chain SJ:  80% 13% 7%

- Molecule 58: 40S ribosomal protein S10

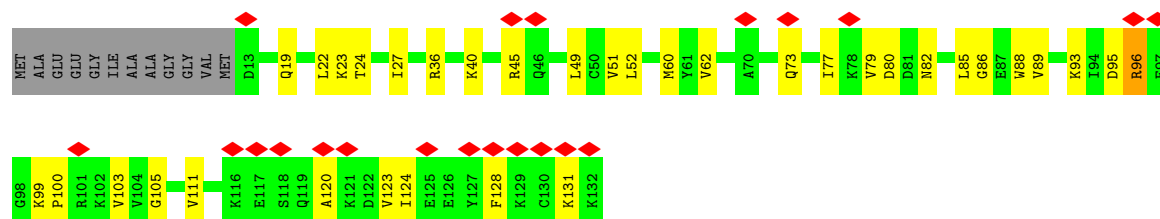
Chain SK:  30% 27% 42%

- Molecule 59: 40S ribosomal protein S11

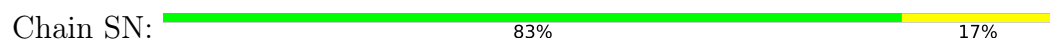
Chain SL:  74% 16% 9%



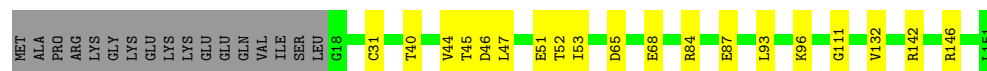
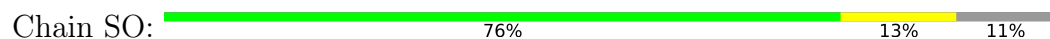
- Molecule 60: 40S ribosomal protein S12



- Molecule 61: 40S ribosomal protein S13



- Molecule 62: 40S ribosomal protein S14



- Molecule 63: 40S ribosomal protein S15

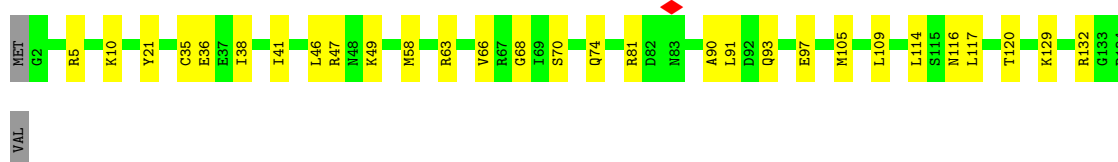
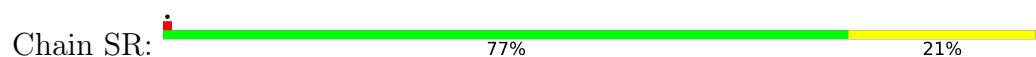


- Molecule 64: 40S ribosomal protein S16





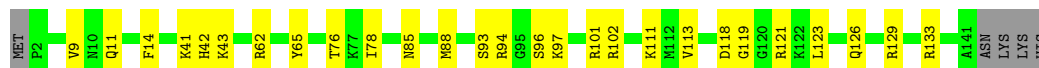
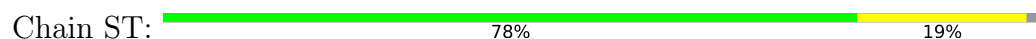
- Molecule 65: 40S ribosomal protein S17



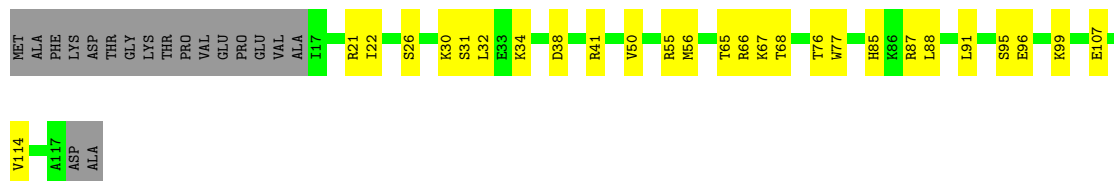
- Molecule 66: 40S ribosomal protein S18



- Molecule 67: 40S ribosomal protein S19




- Molecule 68: 40S ribosomal protein S20



- Molecule 69: 40S ribosomal protein S21




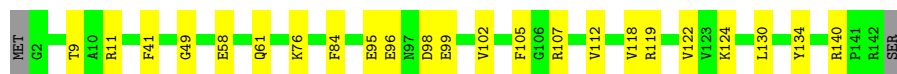
- Molecule 70: 40S ribosomal protein S15a

Chain SW:  85% 14%




- Molecule 71: 40S ribosomal protein S23

Chain SX:  83% 16%



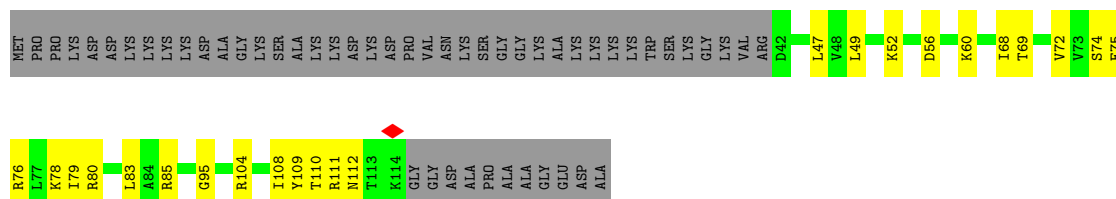
- Molecule 72: 40S ribosomal protein S24

Chain SY:  80% 11% 8%




- Molecule 73: 40S ribosomal protein S25

Chain SZ:  40% 18% 42%




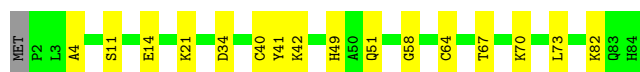
- Molecule 74: 40S ribosomal protein S26

Chain Sa:  73% 13% 14%




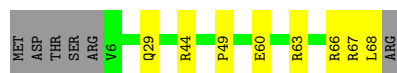
- Molecule 75: 40S ribosomal protein S27

Chain Sb:  80% 19%

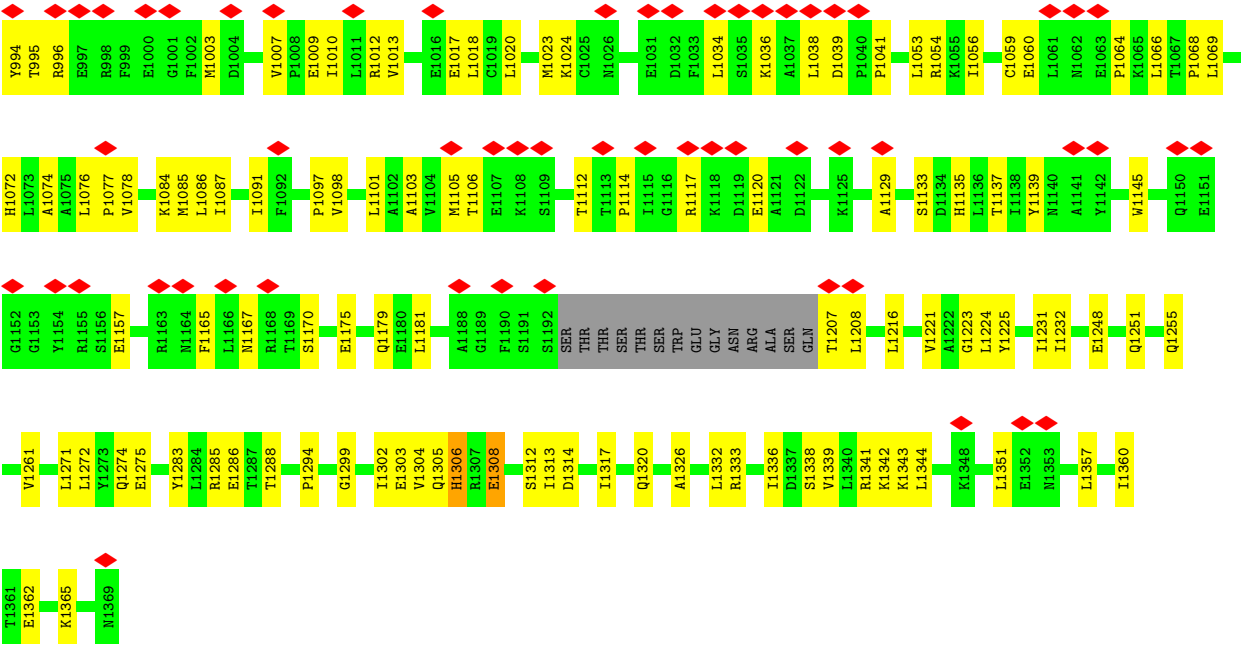


- Molecule 76: 40S ribosomal protein S28

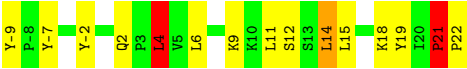
Chain Sc:  80% 12% 9%







● Molecule 82: nascent peptide



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	35668	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 ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.014	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.016	Depositor
Map size (Å)	508.8, 508.8, 508.8	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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	0.31	0/1936	0.37	0/2596
2	SA	0.27	0/1764	0.36	0/2396
3	LB	0.28	0/3257	0.35	0/4359
4	SB	0.26	0/1756	0.39	0/2350
5	B4	0.21	0/1786	0.26	0/2784
5	C4	0.18	0/1789	0.31	0/2788
6	L5	0.32	0/86777	0.30	0/135357
7	L7	0.32	0/2858	0.27	0/4455
8	L8	0.31	0/3701	0.28	0/5766
9	LC	0.29	0/2936	0.37	0/3943
10	LD	0.25	0/2428	0.37	0/3252
11	LE	0.24	0/1817	0.37	0/2437
12	LF	0.29	0/1905	0.35	0/2539
13	LG	0.55	2/1872 (0.1%)	0.50	2/2521 (0.1%)
14	LH	0.25	0/1537	0.36	0/2066
15	LI	0.28	0/1755	0.34	0/2344
16	LJ	0.23	0/1367	0.34	0/1829
17	LL	0.25	0/1704	0.33	0/2282
18	LM	0.26	0/1147	0.33	0/1534
19	LN	0.31	0/1746	0.33	0/2338
20	LO	0.29	0/1673	0.34	0/2238
21	LP	0.30	0/1285	0.34	0/1724
22	LQ	0.29	0/1537	0.32	0/2052
23	LR	0.27	0/1488	0.39	0/1968
24	LS	0.30	0/1492	0.35	0/2003
25	LT	0.28	0/1322	0.33	0/1765
26	LU	0.24	0/839	0.46	0/1126
27	LV	0.28	0/987	0.34	0/1324
28	LW	0.23	0/946	0.34	0/1254
29	LX	0.25	0/984	0.28	0/1323
30	LY	0.26	0/1132	0.35	0/1504
31	LZ	0.25	0/1130	0.33	0/1507

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	La	0.30	0/1183	0.33	0/1582
33	Lb	0.24	0/877	0.36	0/1157
34	Lc	0.28	0/774	0.35	0/1038
35	Ld	0.28	0/903	0.33	0/1216
36	Le	0.28	0/1088	0.31	0/1451
37	Lf	0.31	0/895	0.32	0/1198
38	Lg	0.26	0/898	0.35	0/1197
39	Lh	0.25	0/1018	0.35	0/1344
40	Li	0.23	0/834	0.36	0/1104
41	Lj	0.29	0/720	0.37	0/952
42	Lk	0.23	0/575	0.33	0/761
43	Ll	0.29	0/454	0.33	0/599
44	Lm	0.26	0/435	0.37	0/575
45	Ln	0.26	0/231	0.34	0/294
46	Lo	0.28	0/876	0.36	0/1156
47	Lp	0.29	0/700	0.43	0/930
48	Lr	0.28	0/1002	0.36	0/1344
49	S2	0.30	0/40168	0.31	0/62610
50	SC	0.28	0/1737	0.43	0/2347
51	SD	0.22	0/1768	0.34	0/2382
52	SE	0.26	0/2097	0.39	2/2823 (0.1%)
53	SF	0.25	0/1495	0.39	0/2008
54	SG	0.21	0/1876	0.36	0/2502
55	SH	0.33	2/1524 (0.1%)	0.39	0/2042
56	SI	0.27	0/1715	0.36	0/2287
57	SJ	0.24	0/1524	0.31	0/2035
58	SK	0.43	1/834 (0.1%)	0.50	1/1125 (0.1%)
59	SL	0.28	0/1193	0.36	0/1594
60	SM	0.17	0/935	0.40	0/1255
61	SN	0.25	0/1228	0.32	0/1651
62	SO	0.26	0/1015	0.35	0/1361
63	SP	0.23	0/1064	0.35	0/1422
64	SQ	0.24	0/1134	0.38	0/1517
65	SR	0.23	0/1087	0.44	0/1460
66	SS	0.23	0/1178	0.40	0/1578
67	ST	0.22	0/1105	0.35	0/1482
68	SU	0.22	0/813	0.42	0/1092
69	SV	0.26	0/643	0.37	0/860
70	SW	0.28	0/1051	0.33	0/1406
71	SX	0.27	0/1116	0.34	0/1490
72	SY	0.23	0/1011	0.34	0/1345
73	SZ	0.22	0/589	0.44	0/791
74	Sa	0.27	0/801	0.32	0/1074

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
75	Sb	0.24	0/661	0.35	0/886
76	Sc	0.23	0/497	0.32	0/666
77	Sd	0.27	0/470	0.39	0/623
78	Se	0.22	0/465	0.37	0/612
79	Sf	0.17	0/533	0.39	0/706
80	Sg	0.21	0/2477	0.39	0/3372
81	DH	0.32	6/8196 (0.1%)	0.47	5/11069 (0.0%)
82	zx	0.40	0/254	0.57	0/348
All	All	0.30	11/238370 (0.0%)	0.33	10/349443 (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
60	SM	0	1
81	DH	0	1
82	zx	0	1
All	All	0	3

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
13	LG	77	PRO	CA-C	20.47	1.63	1.51
58	SK	86	PRO	CA-C	-9.34	1.46	1.51
55	SH	12	ASN	CG-OD1	-6.82	1.10	1.23
81	DH	787	PHE	CG-CD2	-6.64	1.24	1.38
81	DH	839	TYR	C-O	-6.38	1.15	1.24

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	LG	77	PRO	O-C-N	16.78	129.03	121.31
81	DH	785	GLN	CA-CB-CG	10.60	135.31	114.10
81	DH	600	GLY	N-CA-C	7.54	127.10	115.72
58	SK	86	PRO	O-C-N	-6.79	118.19	121.31
81	DH	839	TYR	O-C-N	-6.18	114.32	122.42

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
81	DH	770	ILE	Mainchain
60	SM	96	ARG	Sidechain
82	zx	21	PRO	Peptide

5.2 Too-close contacts [i](#)

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	31	0
2	SA	1727	0	1730	28	0
3	LB	3189	0	3327	38	0
4	SB	1729	0	1803	33	0
5	B4	1599	0	809	12	0
5	C4	1602	0	809	30	0
6	L5	77578	0	39204	842	0
7	L7	2558	0	1296	19	0
8	L8	3314	0	1683	42	0
9	LC	2882	0	3059	44	0
10	LD	2382	0	2410	30	0
11	LE	1783	0	1942	41	0
12	LF	1870	0	1996	28	0
13	LG	1841	0	1975	29	0
14	LH	1518	0	1601	23	0
15	LI	1716	0	1765	30	0
16	LJ	1344	0	1380	21	0
17	LL	1673	0	1779	27	0
18	LM	1125	0	1192	14	0
19	LN	1701	0	1749	26	0
20	LO	1641	0	1788	21	0
21	LP	1259	0	1288	14	0
22	LQ	1513	0	1628	22	0
23	LR	1472	0	1614	19	0
24	LS	1452	0	1490	17	0
25	LT	1294	0	1362	14	0
26	LU	825	0	850	17	0
27	LV	973	0	1034	19	0
28	LW	932	0	985	36	0
29	LX	967	0	1040	13	0
30	LY	1115	0	1205	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	LZ	1107	0	1182	15	0
32	La	1154	0	1198	11	0
33	Lb	864	0	941	17	0
34	Lc	764	0	804	8	0
35	Ld	888	0	930	11	0
36	Le	1070	0	1165	9	0
37	Lf	876	0	912	8	0
38	Lg	888	0	977	6	0
39	Lh	1010	0	1143	16	0
40	Li	823	0	904	16	0
41	Lj	705	0	737	14	0
42	Lk	569	0	637	7	0
43	Ll	444	0	483	9	0
44	Lm	429	0	466	10	0
45	Ln	230	0	276	3	0
46	Lo	862	0	929	11	0
47	Lp	690	0	745	11	0
48	Lr	987	0	1050	20	0
49	S2	35919	0	18142	426	0
50	SC	1700	0	1784	28	0
51	SD	1740	0	1833	28	0
52	SE	2055	0	2160	41	0
53	SF	1475	0	1527	21	0
54	SG	1853	0	1988	51	0
55	SH	1501	0	1593	26	0
56	SI	1686	0	1772	34	0
57	SJ	1499	0	1618	22	0
58	SK	810	0	836	34	0
59	SL	1173	0	1245	22	0
60	SM	925	0	947	22	0
61	SN	1204	0	1290	18	0
62	SO	1002	0	1023	11	0
63	SP	1043	0	1087	22	0
64	SQ	1117	0	1185	29	0
65	SR	1072	0	1126	23	0
66	SS	1160	0	1220	38	0
67	ST	1086	0	1114	23	0
68	SU	803	0	873	21	0
69	SV	636	0	637	5	0
70	SW	1034	0	1080	14	0
71	SX	1098	0	1167	21	0
72	SY	994	0	1060	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
73	SZ	583	0	640	22	0
74	Sa	788	0	837	12	0
75	Sb	647	0	668	12	0
76	Sc	495	0	523	5	0
77	Sd	459	0	449	11	0
78	Se	459	0	503	11	0
79	Sf	522	0	529	17	0
80	Sg	2420	0	2380	65	0
81	DH	8048	0	8253	262	0
82	zx	246	0	253	25	0
83	B4	1	0	0	0	0
83	L5	124	0	0	0	0
83	L7	3	0	0	0	0
83	L8	4	0	0	0	0
83	LA	2	0	0	0	0
83	LC	1	0	0	0	0
83	LN	1	0	0	0	0
83	LP	1	0	0	0	0
83	LV	1	0	0	0	0
83	Lb	2	0	0	0	0
83	S2	51	0	0	0	0
84	Lg	1	0	0	0	0
84	Lj	1	0	0	0	0
84	Lm	1	0	0	0	0
84	Lo	1	0	0	0	0
84	Lp	1	0	0	0	0
84	Sa	1	0	0	0	0
84	Sd	1	0	0	0	0
84	Sf	1	0	0	0	0
All	All	222283	0	166607	2691	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 7.

The worst 5 of 2691 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)
81:DH:785:GLN:HG2	81:DH:839:TYR:HA	1.28	1.11
81:DH:785:GLN:N	81:DH:839:TYR:O	1.86	1.07
81:DH:785:GLN:HB3	81:DH:841:ASN:OD1	1.56	1.04
49:S2:540:U:H3	49:S2:543:C:N4	1.54	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
81:DH:125:GLN:HG2	81:DH:488:ARG:NH1	1.83	0.93

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	LA	246/257 (96%)	235 (96%)	11 (4%)	0	100	100
2	SA	217/295 (74%)	206 (95%)	11 (5%)	0	100	100
3	LB	393/403 (98%)	386 (98%)	7 (2%)	0	100	100
4	SB	211/264 (80%)	204 (97%)	7 (3%)	0	100	100
9	LC	360/427 (84%)	339 (94%)	21 (6%)	0	100	100
10	LD	291/297 (98%)	277 (95%)	13 (4%)	1 (0%)	36	70
11	LE	216/288 (75%)	207 (96%)	9 (4%)	0	100	100
12	LF	223/248 (90%)	215 (96%)	8 (4%)	0	100	100
13	LG	224/266 (84%)	219 (98%)	5 (2%)	0	100	100
14	LH	188/192 (98%)	185 (98%)	3 (2%)	0	100	100
15	LI	211/214 (99%)	204 (97%)	7 (3%)	0	100	100
16	LJ	166/178 (93%)	166 (100%)	0	0	100	100
17	LL	205/211 (97%)	199 (97%)	6 (3%)	0	100	100
18	LM	135/215 (63%)	132 (98%)	3 (2%)	0	100	100
19	LN	201/204 (98%)	199 (99%)	2 (1%)	0	100	100
20	LO	198/203 (98%)	194 (98%)	4 (2%)	0	100	100
21	LP	153/184 (83%)	146 (95%)	7 (5%)	0	100	100
22	LQ	185/188 (98%)	179 (97%)	6 (3%)	0	100	100
23	LR	174/196 (89%)	172 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	LS	173/176 (98%)	160 (92%)	13 (8%)	0	100	100
25	LT	157/160 (98%)	152 (97%)	5 (3%)	0	100	100
26	LU	99/128 (77%)	93 (94%)	6 (6%)	0	100	100
27	LV	128/140 (91%)	124 (97%)	4 (3%)	0	100	100
28	LW	110/157 (70%)	108 (98%)	2 (2%)	0	100	100
29	LX	116/156 (74%)	114 (98%)	2 (2%)	0	100	100
30	LY	132/145 (91%)	129 (98%)	3 (2%)	0	100	100
31	LZ	133/136 (98%)	129 (97%)	4 (3%)	0	100	100
32	La	145/148 (98%)	138 (95%)	7 (5%)	0	100	100
33	Lb	102/159 (64%)	96 (94%)	6 (6%)	0	100	100
34	Lc	96/115 (84%)	94 (98%)	2 (2%)	0	100	100
35	Ld	105/125 (84%)	102 (97%)	3 (3%)	0	100	100
36	Le	128/135 (95%)	126 (98%)	2 (2%)	0	100	100
37	Lf	107/110 (97%)	106 (99%)	1 (1%)	0	100	100
38	Lg	110/117 (94%)	109 (99%)	1 (1%)	0	100	100
39	Lh	119/123 (97%)	114 (96%)	5 (4%)	0	100	100
40	Li	99/105 (94%)	93 (94%)	6 (6%)	0	100	100
41	Lj	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
42	Lk	67/70 (96%)	67 (100%)	0	0	100	100
43	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
44	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
45	Ln	22/25 (88%)	21 (96%)	1 (4%)	0	100	100
46	Lo	103/106 (97%)	95 (92%)	8 (8%)	0	100	100
47	Lp	87/92 (95%)	83 (95%)	4 (5%)	0	100	100
48	Lr	121/137 (88%)	115 (95%)	6 (5%)	0	100	100
50	SC	217/293 (74%)	204 (94%)	13 (6%)	0	100	100
51	SD	222/243 (91%)	213 (96%)	9 (4%)	0	100	100
52	SE	257/263 (98%)	239 (93%)	18 (7%)	0	100	100
53	SF	182/204 (89%)	167 (92%)	15 (8%)	0	100	100
54	SG	229/249 (92%)	219 (96%)	10 (4%)	0	100	100
55	SH	184/194 (95%)	169 (92%)	15 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
56	SI	204/208 (98%)	192 (94%)	12 (6%)	0	100	100
57	SJ	178/194 (92%)	174 (98%)	4 (2%)	0	100	100
58	SK	94/165 (57%)	91 (97%)	3 (3%)	0	100	100
59	SL	139/158 (88%)	134 (96%)	5 (4%)	0	100	100
60	SM	118/132 (89%)	110 (93%)	8 (7%)	0	100	100
61	SN	148/151 (98%)	145 (98%)	3 (2%)	0	100	100
62	SO	132/151 (87%)	129 (98%)	3 (2%)	0	100	100
63	SP	125/145 (86%)	123 (98%)	2 (2%)	0	100	100
64	SQ	138/146 (94%)	130 (94%)	8 (6%)	0	100	100
65	SR	131/135 (97%)	123 (94%)	8 (6%)	0	100	100
66	SS	139/152 (91%)	128 (92%)	11 (8%)	0	100	100
67	ST	138/145 (95%)	132 (96%)	6 (4%)	0	100	100
68	SU	99/119 (83%)	97 (98%)	2 (2%)	0	100	100
69	SV	81/83 (98%)	80 (99%)	1 (1%)	0	100	100
70	SW	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
71	SX	139/143 (97%)	134 (96%)	5 (4%)	0	100	100
72	SY	120/133 (90%)	117 (98%)	3 (2%)	0	100	100
73	SZ	71/125 (57%)	71 (100%)	0	0	100	100
74	Sa	97/115 (84%)	95 (98%)	2 (2%)	0	100	100
75	Sb	81/84 (96%)	80 (99%)	1 (1%)	0	100	100
76	Sc	61/69 (88%)	60 (98%)	1 (2%)	0	100	100
77	Sd	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
78	Se	56/133 (42%)	55 (98%)	1 (2%)	0	100	100
79	Sf	62/156 (40%)	60 (97%)	2 (3%)	0	100	100
80	Sg	309/317 (98%)	279 (90%)	30 (10%)	0	100	100
81	DH	990/1369 (72%)	955 (96%)	33 (3%)	2 (0%)	43	76
82	zx	30/32 (94%)	24 (80%)	4 (13%)	2 (7%)	1	5
All	All	12189/14163 (86%)	11711 (96%)	473 (4%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
81	DH	775	PHE

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Mol	Chain	Res	Type
81	DH	831	SER
82	zx	21	PRO
10	LD	235	MET
82	zx	4	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	LA	190/199 (96%)	190 (100%)	0	100	100
2	SA	181/243 (74%)	181 (100%)	0	100	100
3	LB	344/349 (99%)	344 (100%)	0	100	100
4	SB	194/231 (84%)	193 (100%)	1 (0%)	81	89
9	LC	301/348 (86%)	301 (100%)	0	100	100
10	LD	246/250 (98%)	246 (100%)	0	100	100
11	LE	196/252 (78%)	196 (100%)	0	100	100
12	LF	194/215 (90%)	194 (100%)	0	100	100
13	LG	196/223 (88%)	196 (100%)	0	100	100
14	LH	169/171 (99%)	169 (100%)	0	100	100
15	LI	180/181 (99%)	178 (99%)	2 (1%)	65	83
16	LJ	141/149 (95%)	141 (100%)	0	100	100
17	LL	173/177 (98%)	173 (100%)	0	100	100
18	LM	116/161 (72%)	116 (100%)	0	100	100
19	LN	171/172 (99%)	171 (100%)	0	100	100
20	LO	172/174 (99%)	172 (100%)	0	100	100
21	LP	136/163 (83%)	136 (100%)	0	100	100
22	LQ	164/165 (99%)	164 (100%)	0	100	100
23	LR	155/175 (89%)	155 (100%)	0	100	100
24	LS	156/157 (99%)	156 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	LT	138/140 (99%)	138 (100%)	0	100	100
26	LU	91/115 (79%)	91 (100%)	0	100	100
27	LV	100/107 (94%)	99 (99%)	1 (1%)	68	84
28	LW	93/126 (74%)	93 (100%)	0	100	100
29	LX	106/133 (80%)	106 (100%)	0	100	100
30	LY	124/135 (92%)	124 (100%)	0	100	100
31	LZ	117/118 (99%)	117 (100%)	0	100	100
32	La	118/121 (98%)	118 (100%)	0	100	100
33	Lb	88/126 (70%)	88 (100%)	0	100	100
34	Lc	83/97 (86%)	83 (100%)	0	100	100
35	Ld	98/110 (89%)	98 (100%)	0	100	100
36	Le	116/121 (96%)	116 (100%)	0	100	100
37	Lf	88/89 (99%)	88 (100%)	0	100	100
38	Lg	96/100 (96%)	96 (100%)	0	100	100
39	Lh	109/110 (99%)	109 (100%)	0	100	100
40	Li	85/89 (96%)	85 (100%)	0	100	100
41	Lj	73/80 (91%)	73 (100%)	0	100	100
42	Lk	64/65 (98%)	64 (100%)	0	100	100
43	Ll	47/48 (98%)	47 (100%)	0	100	100
44	Lm	48/116 (41%)	48 (100%)	0	100	100
45	Ln	23/24 (96%)	23 (100%)	0	100	100
46	Lo	93/94 (99%)	93 (100%)	0	100	100
47	Lp	72/75 (96%)	72 (100%)	0	100	100
48	Lr	107/121 (88%)	107 (100%)	0	100	100
50	SC	185/225 (82%)	185 (100%)	0	100	100
51	SD	187/202 (93%)	187 (100%)	0	100	100
52	SE	221/225 (98%)	221 (100%)	0	100	100
53	SF	158/170 (93%)	158 (100%)	0	100	100
54	SG	196/218 (90%)	196 (100%)	0	100	100
55	SH	167/174 (96%)	167 (100%)	0	100	100
56	SI	178/180 (99%)	176 (99%)	2 (1%)	65	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	SJ	160/168 (95%)	160 (100%)	0	100	100
58	SK	87/136 (64%)	87 (100%)	0	100	100
59	SL	129/142 (91%)	129 (100%)	0	100	100
60	SM	100/108 (93%)	100 (100%)	0	100	100
61	SN	129/131 (98%)	129 (100%)	0	100	100
62	SO	104/119 (87%)	104 (100%)	0	100	100
63	SP	113/130 (87%)	113 (100%)	0	100	100
64	SQ	116/121 (96%)	116 (100%)	0	100	100
65	SR	119/122 (98%)	119 (100%)	0	100	100
66	SS	120/132 (91%)	120 (100%)	0	100	100
67	ST	110/115 (96%)	110 (100%)	0	100	100
68	SU	93/107 (87%)	93 (100%)	0	100	100
69	SV	67/67 (100%)	67 (100%)	0	100	100
70	SW	112/113 (99%)	112 (100%)	0	100	100
71	SX	113/115 (98%)	113 (100%)	0	100	100
72	SY	105/115 (91%)	105 (100%)	0	100	100
73	SZ	65/103 (63%)	65 (100%)	0	100	100
74	Sa	85/98 (87%)	85 (100%)	0	100	100
75	Sb	74/76 (97%)	74 (100%)	0	100	100
76	Sc	56/62 (90%)	56 (100%)	0	100	100
77	Sd	48/49 (98%)	48 (100%)	0	100	100
78	Se	47/104 (45%)	47 (100%)	0	100	100
79	Sf	57/140 (41%)	57 (100%)	0	100	100
80	Sg	270/275 (98%)	270 (100%)	0	100	100
81	DH	898/1208 (74%)	890 (99%)	8 (1%)	70	85
82	zx	28/29 (97%)	23 (82%)	5 (18%)	2	10
All	All	10649/12094 (88%)	10630 (100%)	19 (0%)	85	92

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
82	zx	-9	TYR
82	zx	4	LEU

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Mol	Chain	Res	Type
82	zx	14	LEU
82	zx	-2	TYR
81	DH	830	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
57	SJ	124	HIS
70	SW	120	HIS
58	SK	73	ASN
65	SR	118	GLN
75	Sb	51	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
49	S2	1678/1869 (89%)	368 (21%)	10 (0%)
5	B4	74/75 (98%)	14 (18%)	0
5	C4	74/75 (98%)	19 (25%)	2 (2%)
6	L5	3603/5070 (71%)	719 (19%)	20 (0%)
7	L7	119/121 (98%)	18 (15%)	0
8	L8	155/157 (98%)	26 (16%)	0
All	All	5703/7367 (77%)	1164 (20%)	32 (0%)

5 of 1164 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	B4	13	U
5	B4	16	G
5	B4	17	G
5	B4	18	G
5	B4	19	U

5 of 32 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	S2	1434	C
49	S2	1519	U
6	L5	2095	A
6	L5	1633	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
49	S2	1664	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 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.

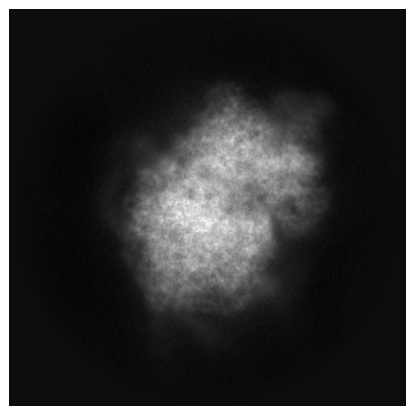
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-68666. These allow visual inspection of the internal detail of the map and identification of artifacts.

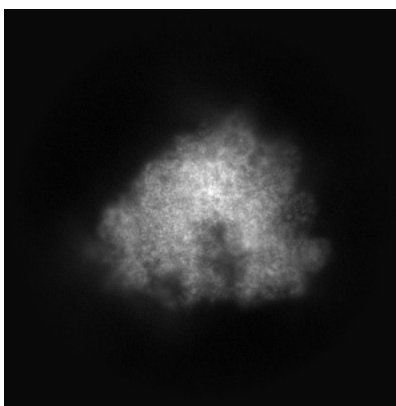
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

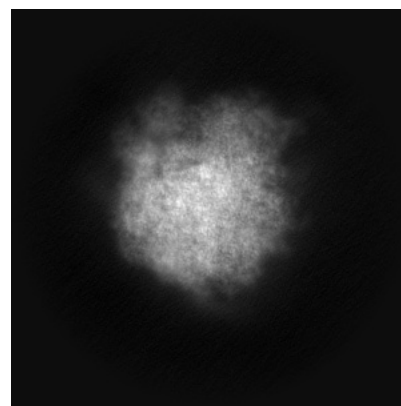
6.1.1 Primary map



X

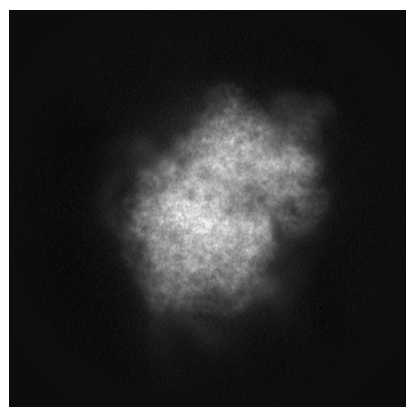


Y

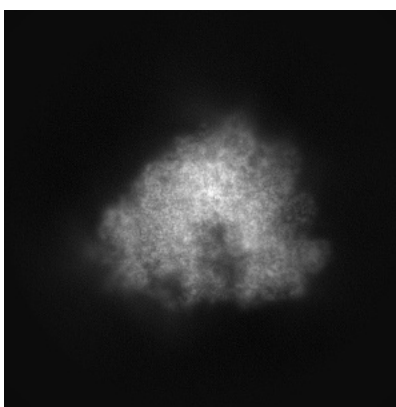


Z

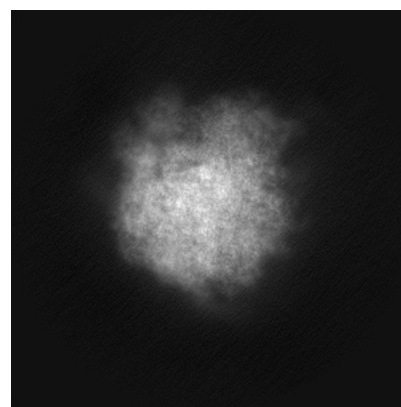
6.1.2 Raw map



X



Y

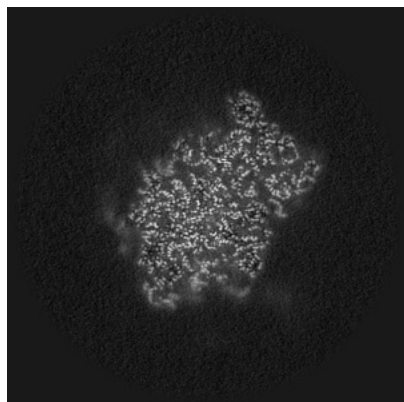


Z

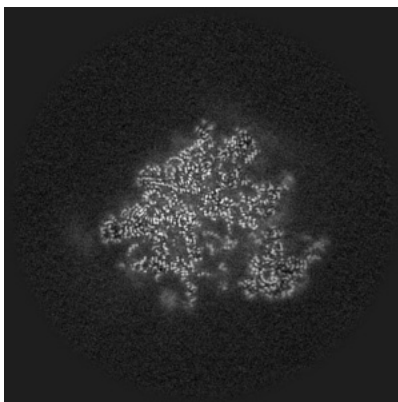
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

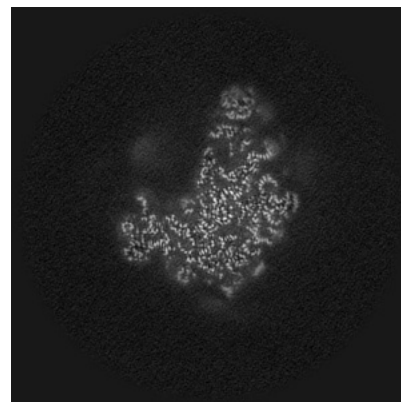
6.2.1 Primary map



X Index: 240

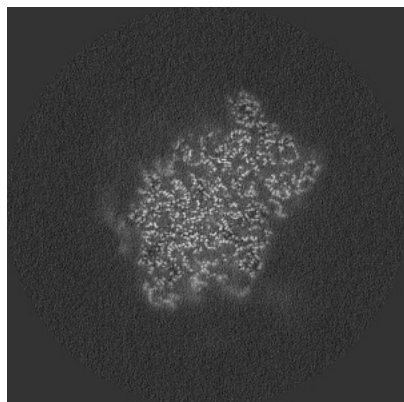


Y Index: 240

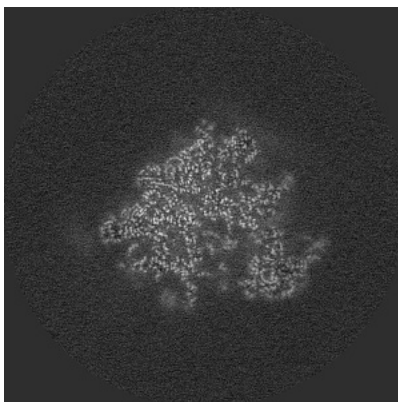


Z Index: 240

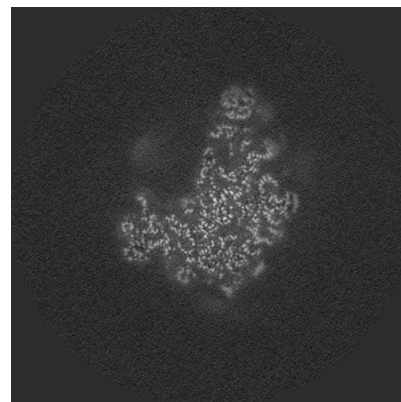
6.2.2 Raw map



X Index: 240



Y Index: 240

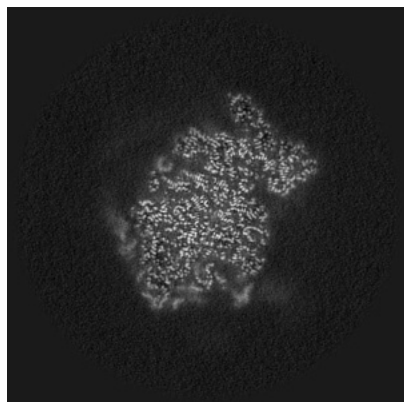


Z Index: 240

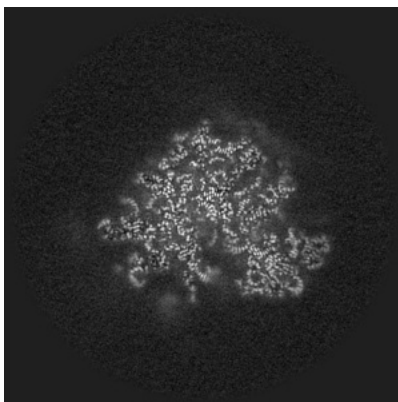
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

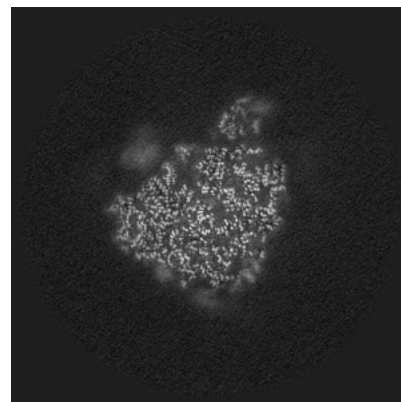
6.3.1 Primary map



X Index: 234

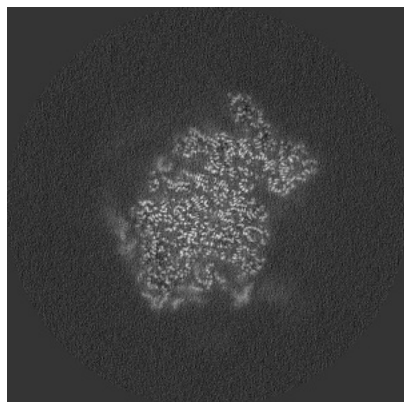


Y Index: 250

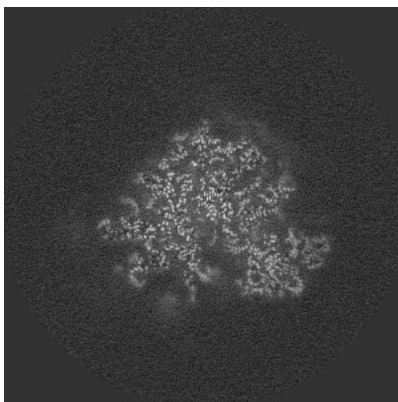


Z Index: 225

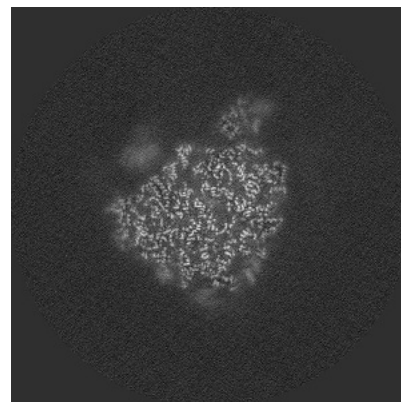
6.3.2 Raw map



X Index: 234



Y Index: 250

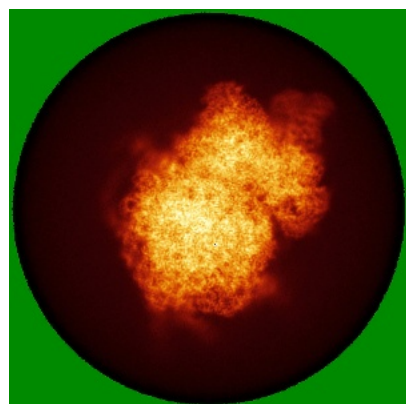


Z Index: 223

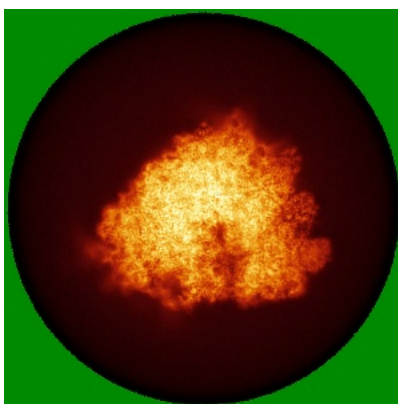
The images above show the largest variance slices of the map in three orthogonal directions.

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

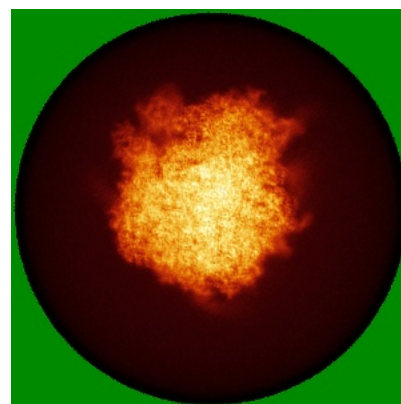
6.4.1 Primary map



X

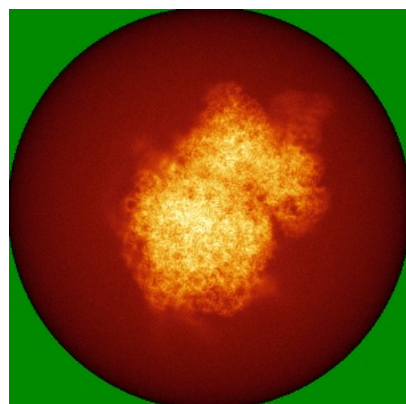


Y

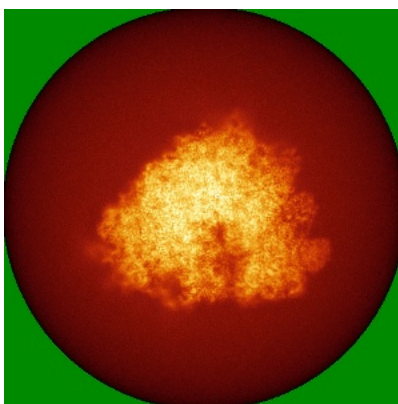


Z

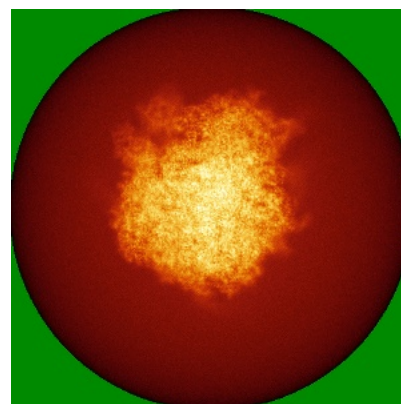
6.4.2 Raw map



X



Y

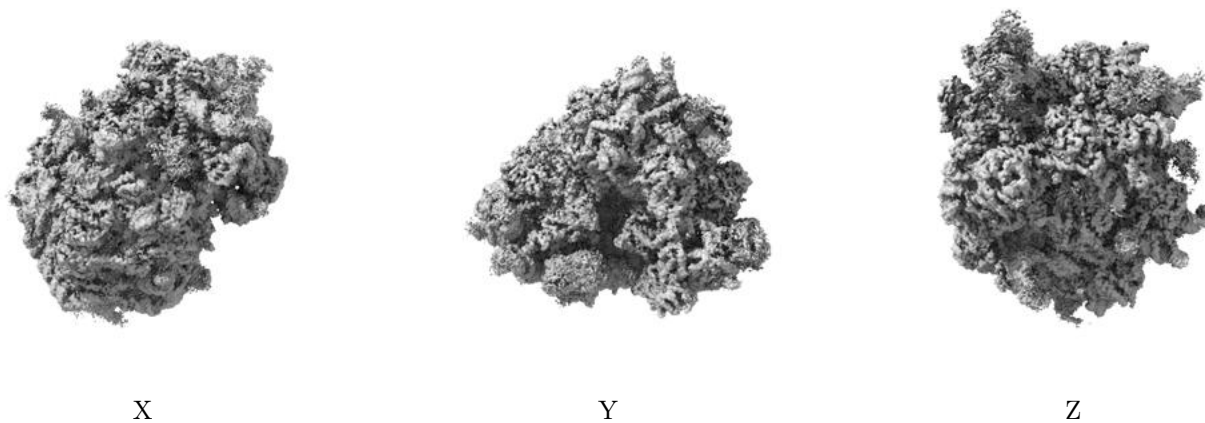


Z

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.

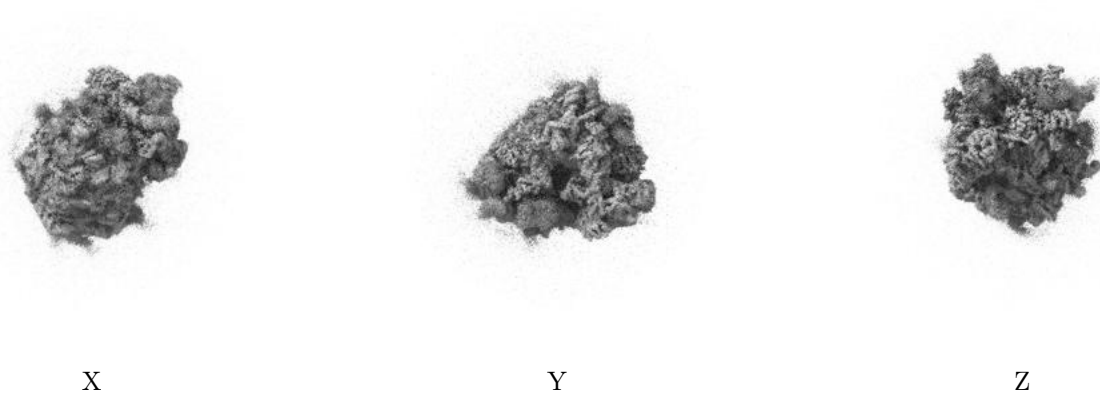
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.016. 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.

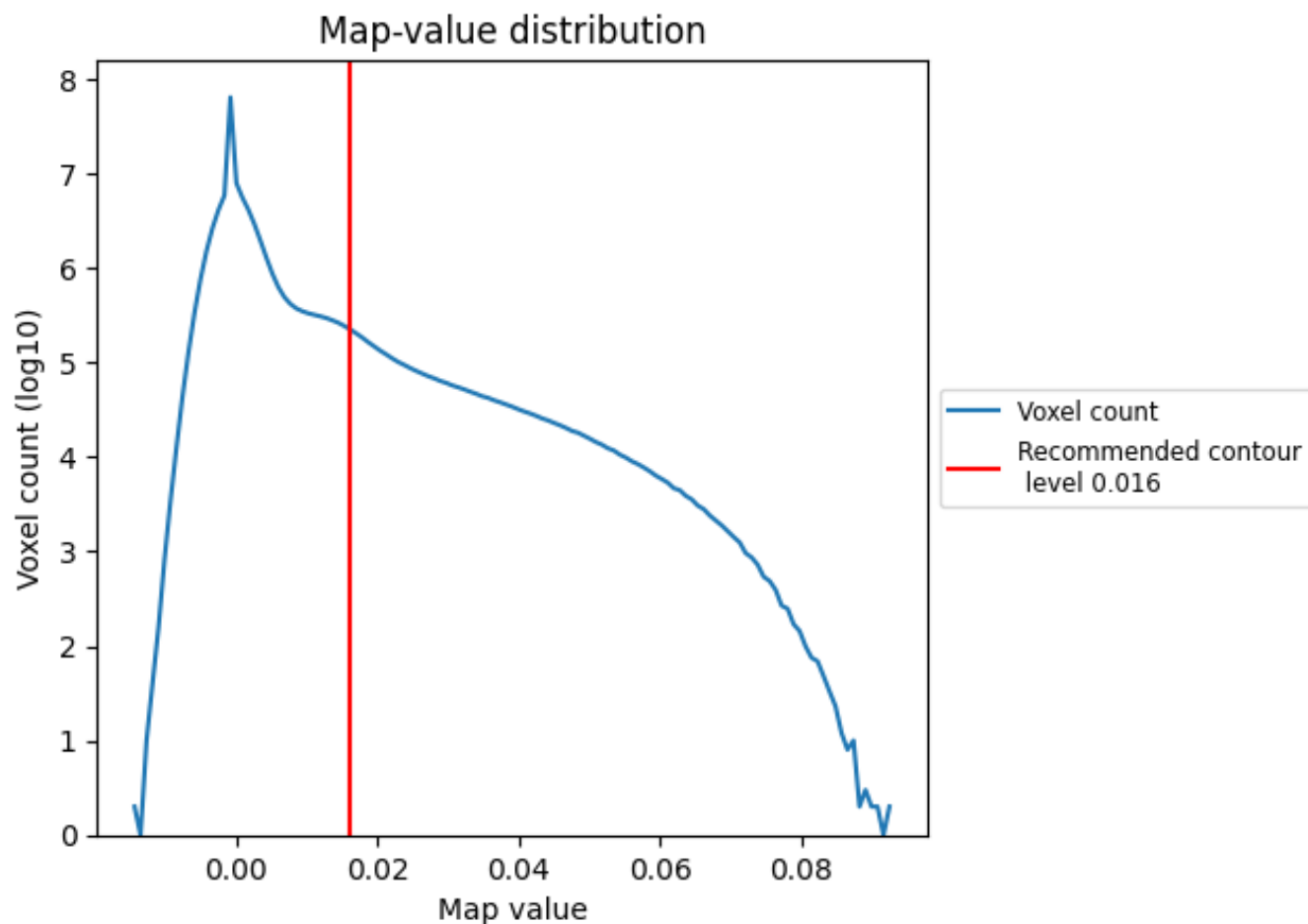
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

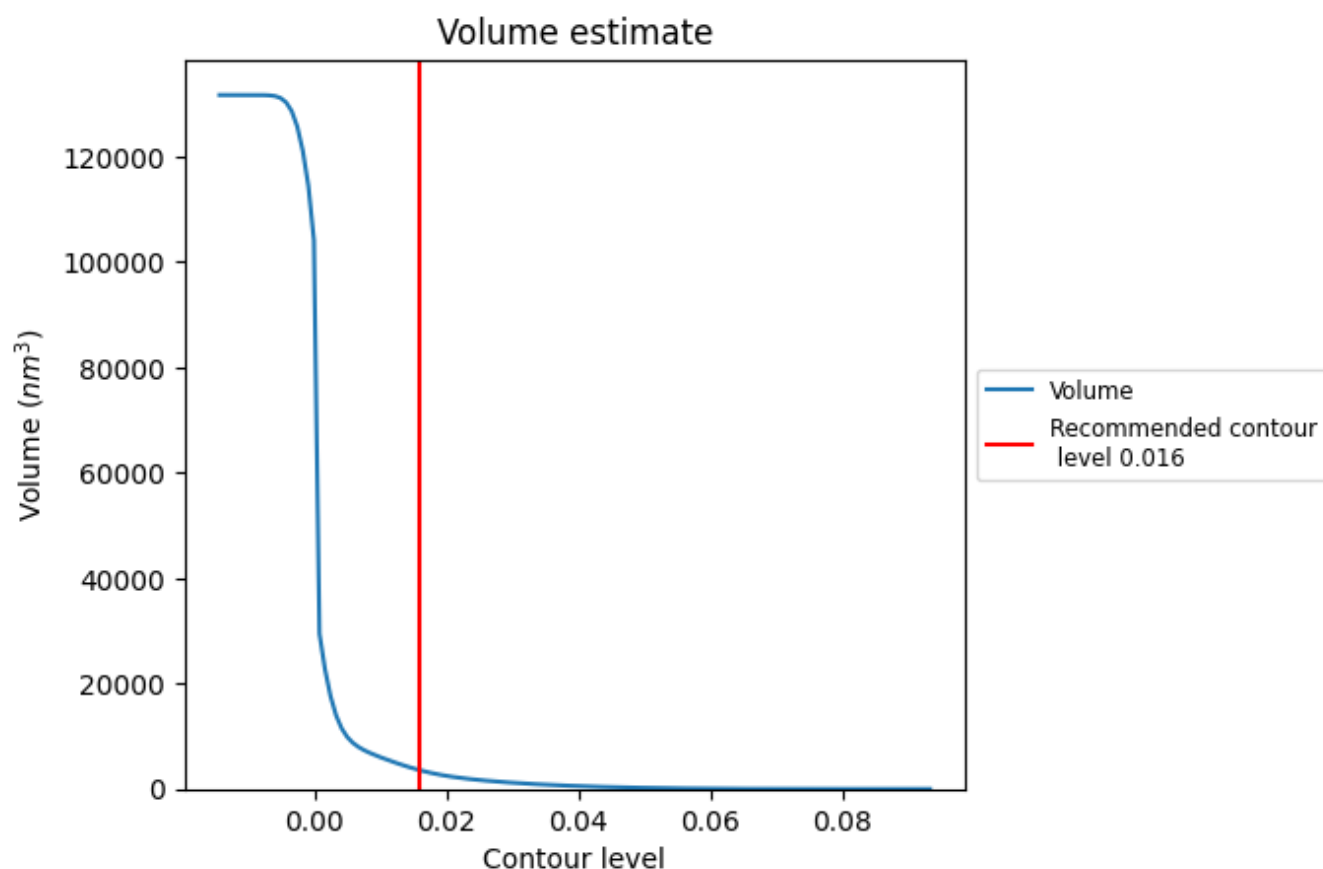
This section contains the results of statistical analysis of the map.

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.

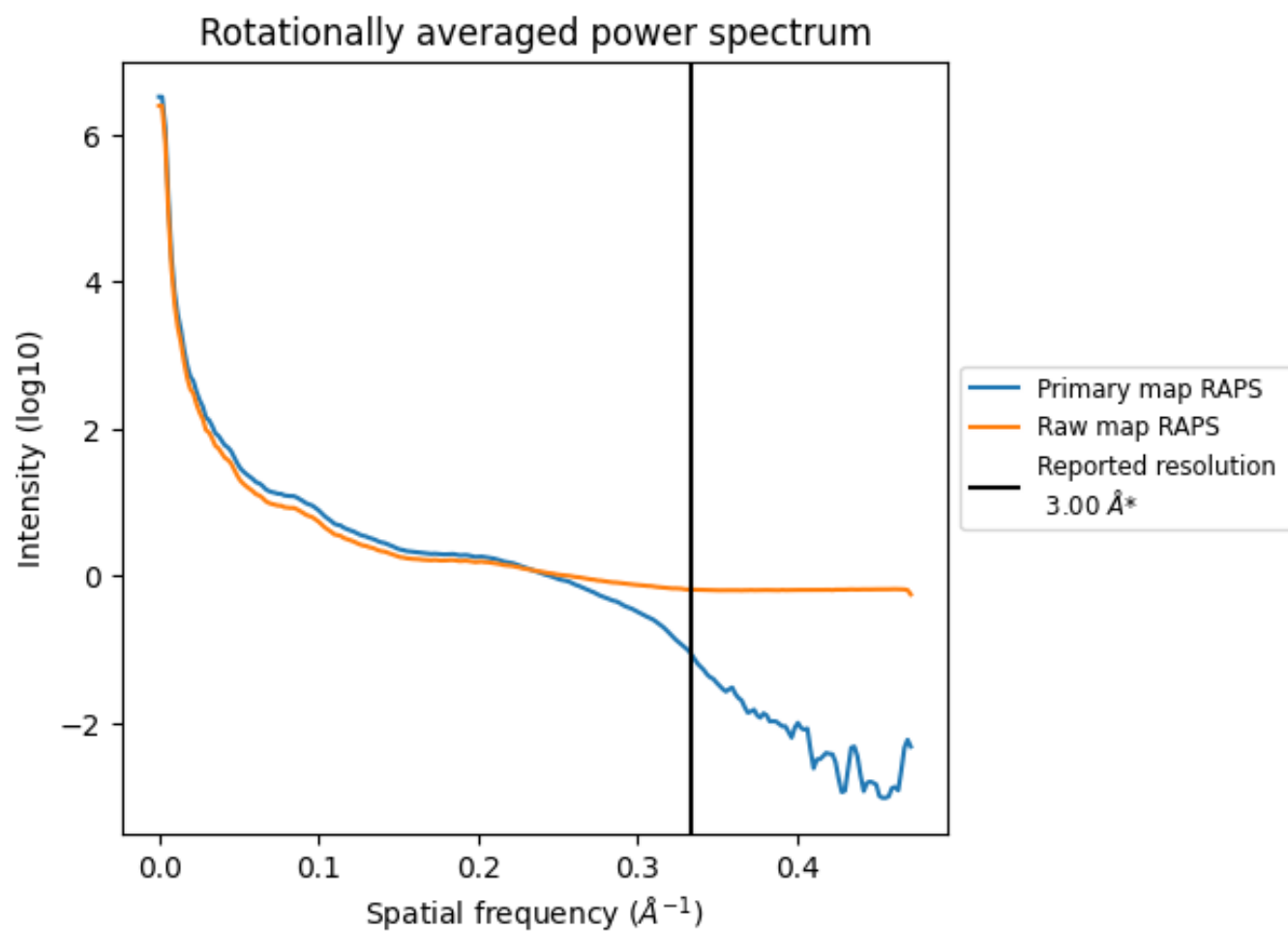
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3562 nm^3 ; this corresponds to an approximate mass of 3218 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 ⓘ

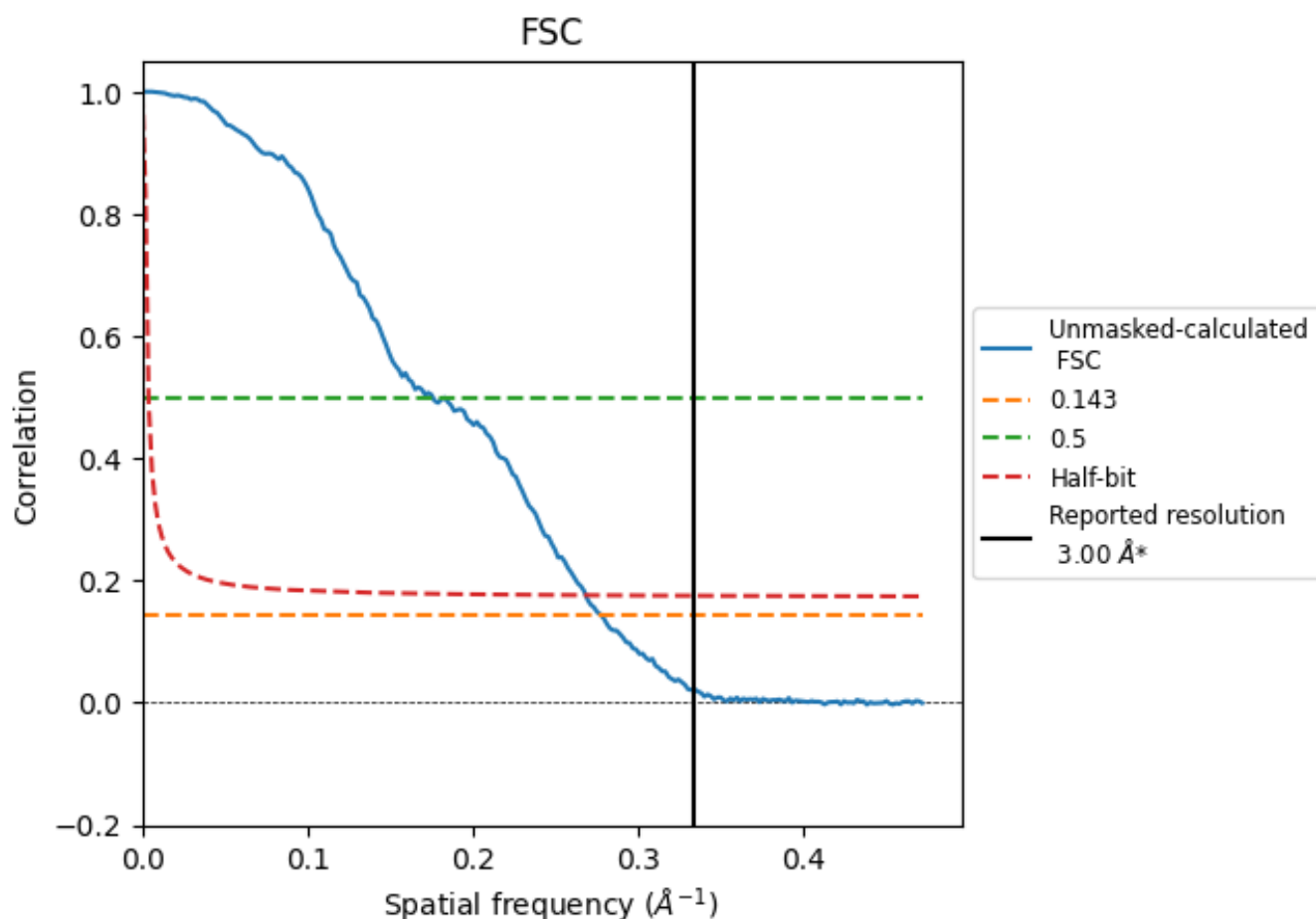


*Reported resolution corresponds to spatial frequency of 0.333 \AA^{-1}

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

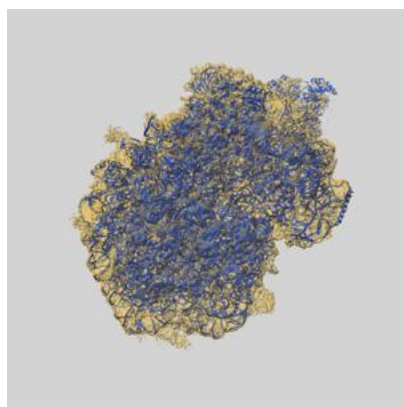
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.60	5.69	3.73

*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 3.60 differs from the reported value 3.0 by more than 10 %

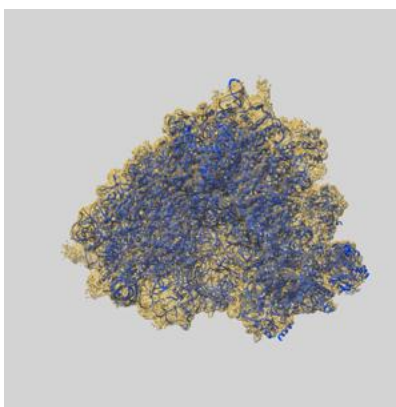
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-68666 and PDB model 22TU. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

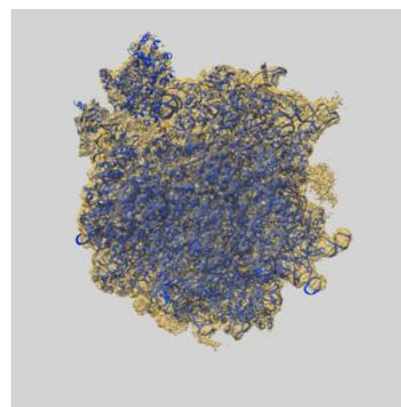
9.1 Map-model overlay [i](#)



X



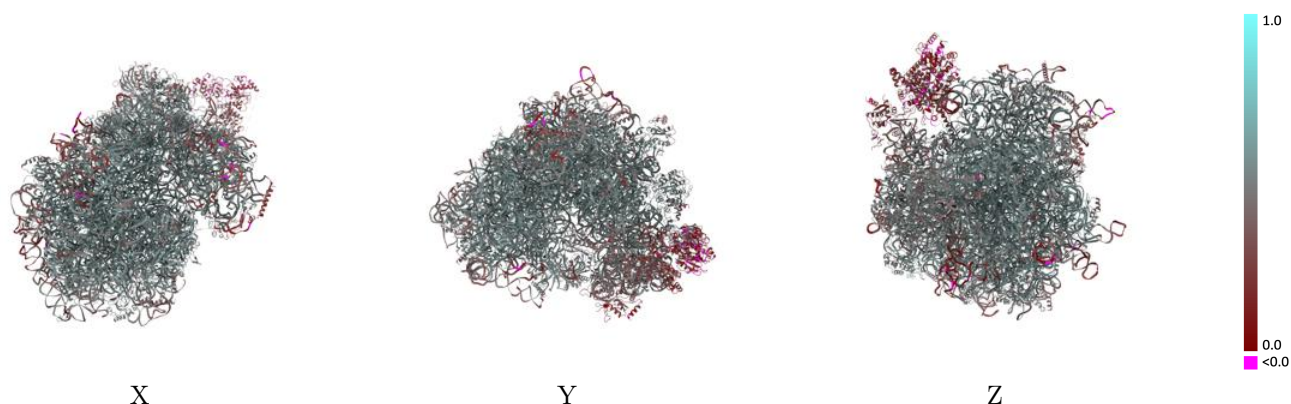
Y



Z

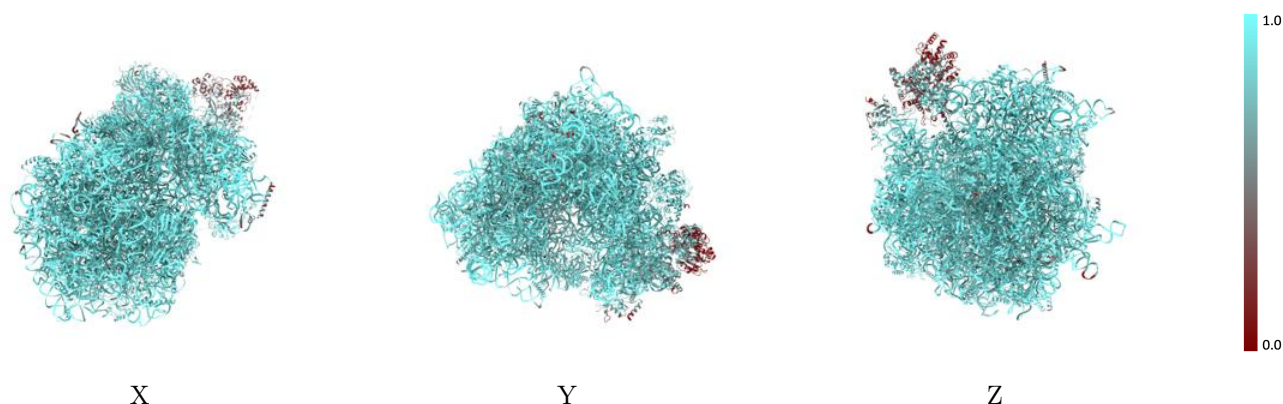
The images above show the 3D surface view of the map at the recommended contour level 0.016 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



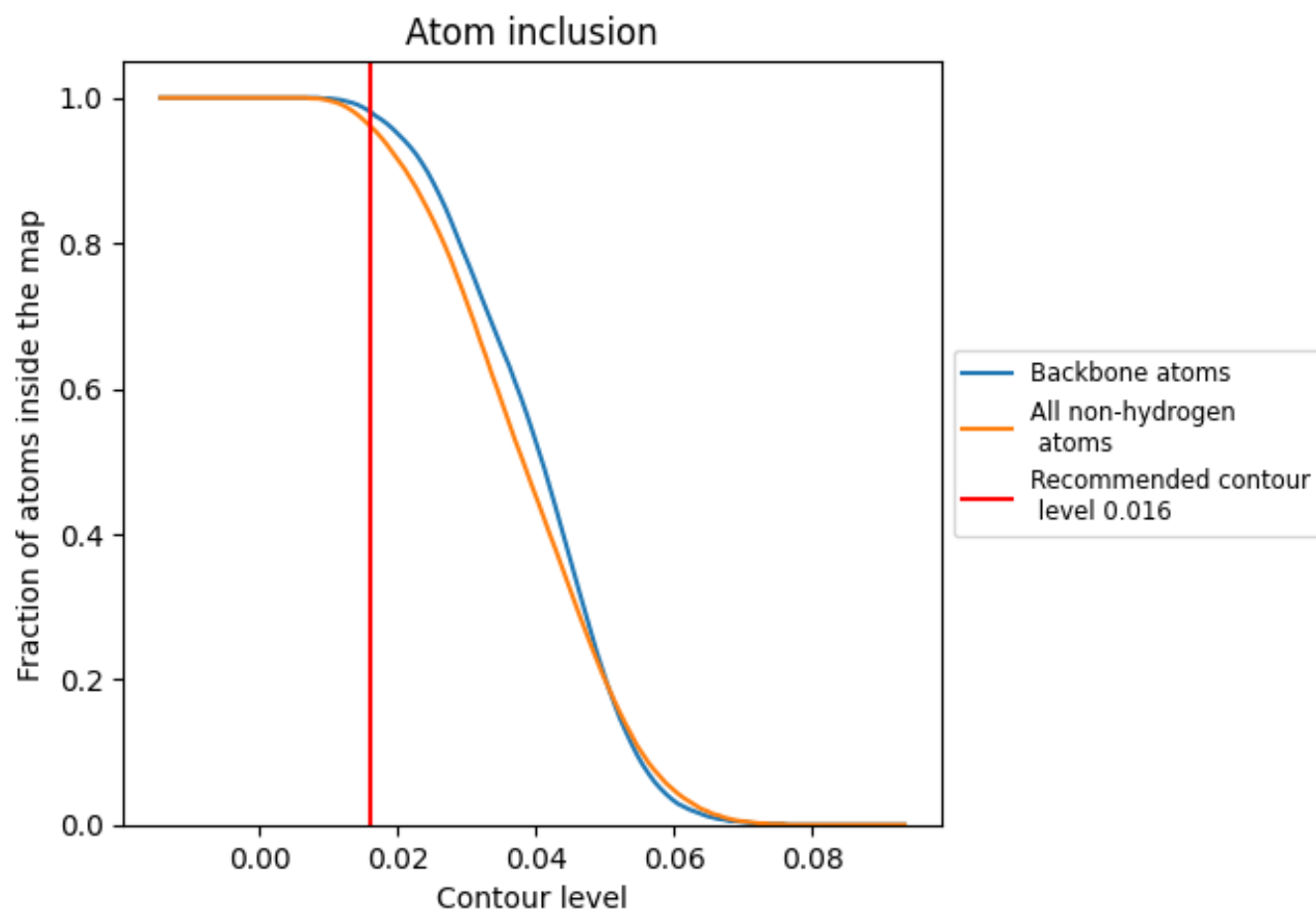
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.016).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 96% 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 (0.016) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9610	 0.5020
B4	 0.9890	 0.4770
C4	 0.9890	 0.3430
DH	 0.5770	 0.2560
L5	 0.9900	 0.5120
L7	 0.9980	 0.5540
L8	 0.9870	 0.5150
LA	 0.9990	 0.5770
LB	 0.9780	 0.5500
LC	 0.9850	 0.5480
LD	 0.9630	 0.5170
LE	 0.9790	 0.5140
LF	 0.9920	 0.5420
LG	 0.9230	 0.5020
LH	 0.9700	 0.5360
LI	 0.9800	 0.5400
LJ	 0.9590	 0.5140
LL	 0.9590	 0.5240
LM	 0.9780	 0.5310
LN	 0.9980	 0.5740
LO	 0.9820	 0.5420
LP	 0.9920	 0.5530
LQ	 0.9970	 0.5590
LR	 0.9750	 0.5270
LS	 0.9920	 0.5660
LT	 0.9820	 0.5270
LU	 0.9340	 0.4720
LV	 0.9880	 0.5670
LW	 0.8290	 0.4030
LX	 0.9830	 0.5370
LY	 0.9750	 0.5200
LZ	 0.9750	 0.5340
La	 0.9910	 0.5690
Lb	 0.9690	 0.4960
Lc	 0.9760	 0.5330

















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Chain	Atom inclusion	Q-score
Ld	 0.9670	 0.5240
Le	 0.9980	 0.5630
Lf	 0.9930	 0.5730
Lg	 0.9850	 0.5540
Lh	 0.9700	 0.5190
Li	 0.9580	 0.4740
Lj	 0.9990	 0.5660
Lk	 0.8850	 0.4850
Ll	 0.9980	 0.5310
Lm	 0.9710	 0.5410
Ln	 1.0000	 0.5690
Lo	 0.9820	 0.5500
Lp	 0.9970	 0.5460
Lr	 0.9870	 0.5520
S2	 0.9880	 0.5120
SA	 0.9260	 0.5150
SB	 0.9650	 0.5250
SC	 0.9650	 0.5390
SD	 0.9300	 0.4590
SE	 0.9670	 0.5190
SF	 0.9670	 0.4920
SG	 0.9190	 0.4620
SH	 0.8700	 0.4510
SI	 0.9450	 0.4960
SJ	 0.9610	 0.5140
SK	 0.9250	 0.4240
SL	 0.9810	 0.5450
SM	 0.6160	 0.2490
SN	 0.9800	 0.5260
SO	 0.9780	 0.5370
SP	 0.9220	 0.4330
SQ	 0.9570	 0.5150
SR	 0.8970	 0.4820
SS	 0.9260	 0.4470
ST	 0.9460	 0.4790
SU	 0.9100	 0.4500
SV	 0.9440	 0.5230
SW	 0.9880	 0.5500
SX	 0.9920	 0.5420
SY	 0.9680	 0.4960
SZ	 0.8960	 0.3960
Sa	 0.9910	 0.5470

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Chain	Atom inclusion	Q-score
Sb	 0.9540	 0.5160
Sc	 0.9710	 0.5020
Sd	 0.9800	 0.5120
Se	 0.9440	 0.4720
Sf	 0.6500	 0.1930
Sg	 0.8710	 0.4370
zx	 0.9790	 0.3380