



wwPDB EM Validation Summary Report ⓘ

Dec 8, 2025 – 01:38 PM JST

PDB ID : 9KN6 / pdb_00009kn6
EMDB ID : EMD-62454
Title : Structure of the HCV IRES-dependent pre-48S translation initiation complex with eIF1A, eIF5B, and eIF3
Authors : Iwasaki, W.; Kashiwagi, K.; Sakamoto, A.; Nishimoto, M.; Takahashi, M.; Machida, K.; Imataka, H.; Matsumoto, A.; Shichino, Y.; Iwasaki, S.; Imami, K.; Ito, T.
Deposited on : 2024-11-18
Resolution : 3.30 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.dev129
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.47

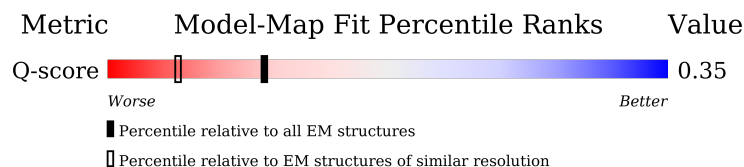
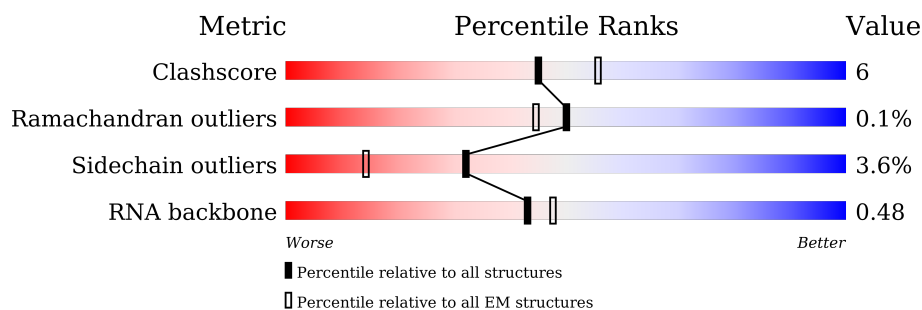
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	210492	15764	-
Ramachandran outliers	207382	16835	-
Sidechain outliers	206894	16415	-
RNA backbone	6643	2191	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	1A	144	
2	5B	621	

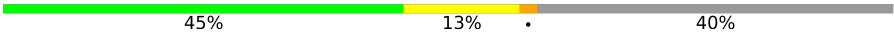







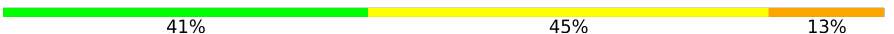
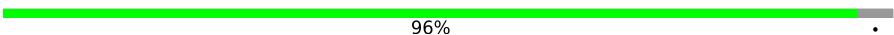
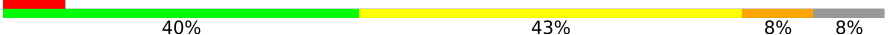










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Mol	Chain	Length	Quality of chain
3	SA	295	
4	SB	264	
5	SC	293	
6	SD	243	
7	SE	263	
8	SF	204	
9	SG	249	
10	SH	194	
11	SI	208	
12	SJ	194	
13	SK	165	
14	SL	158	
15	Sf	132	
16	SN	151	
17	SO	151	
18	SP	145	
19	SQ	146	
20	SR	135	
21	SS	152	
22	ST	145	
23	SU	119	
24	SV	83	
25	SW	130	
26	SX	143	
27	SY	133	

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Mol	Chain	Length	Quality of chain
28	SZ	125	
29	Sa	115	
30	Sb	84	
31	Sc	69	
32	Sd	56	
33	Se	59	
34	sh	156	
35	Sg	317	
36	zy	75	
37	Ln	25	
38	zz	332	
39	S2	1869	
40	3m	374	
41	3f	357	
42	3a	1382	
43	3e	445	
44	3c	913	
45	3h	352	
46	3d	548	
47	3k	218	
48	3l	564	

2 Entry composition [i](#)

There are 51 unique types of molecules in this entry. The entry contains 115376 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 Eukaryotic translation initiation factor 1A, X-chromosomal.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1A	98	Total	C	N	O	S	0	0
			783	494	139	146	4		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 5B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5B	621	Total	C	N	O	S	0	0
			4917	3135	847	913	22		

- 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
			1705	1083	299	315	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SB	212	Total	C	N	O	S	0	0
			1722	1093	308	307	14		

- Molecule 5 is a protein called 40S ribosomal protein S2.

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

- Molecule 6 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SD	226	Total	C	N	O	S	0	0
			1756	1119	316	314	7		

- Molecule 7 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	SE	260	Total	C	N	O	S	0	0
			2065	1319	384	354	8		

- Molecule 8 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SF	192	Total	C	N	O	S	0	0
			1518	948	287	276	7		

- Molecule 9 is a protein called 40S ribosomal protein S6.

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

- Molecule 10 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	SH	187	Total	C	N	O	S	0	0
			1506	961	277	267	1		

- Molecule 11 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	SI	205	Total	C	N	O	S	0	0
			1682	1056	331	290	5		

- Molecule 12 is a protein called 40S ribosomal protein S9.

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

- Molecule 13 is a protein called 40S ribosomal protein S10.

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

- Molecule 14 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SL	150	Total	C	N	O	S	0	0
			1220	776	228	210	6		

- Molecule 15 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	Sf	121	Total	C	N	O	S	0	0
			935	586	165	175	9		

- Molecule 16 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 17 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SO	135	Total	C	N	O	S	0	0
			1007	617	198	186	6		

- Molecule 18 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	SP	119	Total	C	N	O	S	0	0
			984	625	187	165	7		

- Molecule 19 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SQ	140	Total	C	N	O	S	0	0
			1116	710	211	192	3		

- Molecule 20 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 21 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	SS	143	Total	C	N	O	S	0	0
			1184	743	240	200	1		

- Molecule 22 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	ST	142	Total	C	N	O	S	0	0
			1103	691	212	197	3		

- Molecule 23 is a protein called 40S ribosomal protein S20.

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

- Molecule 24 is a protein called 40S ribosomal protein S21.

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

- Molecule 25 is a protein called 40S ribosomal protein S15a.

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

- Molecule 26 is a protein called 40S ribosomal protein S23.

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

- Molecule 27 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SY	124	Total	C	N	O	S	0	0
			1014	641	198	170	5		

- Molecule 28 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SZ	75	Total	C	N	O	S	0	0
			601	385	111	104	1		

- Molecule 29 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Sa	100	Total	C	N	O	S	0	0
			803	501	166	131	5		

- Molecule 30 is a protein called 40S ribosomal protein S27.

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

- Molecule 31 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Sc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 32 is a protein called 40S ribosomal protein S29.

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

- Molecule 33 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Se	52	Total	C	N	O	S	0	0
			417	259	92	65	1		

- Molecule 34 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 35 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 36 is a RNA chain called Initiator Met-tRNA-i.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	zy	75	Total	C	N	O	P	0	0
			1607	717	298	517	75		

- Molecule 37 is a protein called 60S ribosomal protein L41.

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

- Molecule 38 is a RNA chain called HCV-IRES RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	zz	306	Total	C	N	O	P	0	0
			6528	2909	1164	2149	306		

- Molecule 39 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	S2	1759	Total	C	N	O	P	4	0
			37626	16795	6759	12310	1762		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	3m	363	Total	C	N	O	S	0	0
			2639	1666	450	511	12		

- Molecule 41 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	3f	269	Total	C	N	O	S	0	0
			2063	1303	354	394	12		

- Molecule 42 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	3a	592	Total	C	N	O	S	0	0
			4470	2835	796	818	21		

- Molecule 43 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	3e	430	Total	C	N	O	S	0	0
			3224	2053	561	594	16		

- Molecule 44 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	3c	543	Total	C	N	O	S	0	0
			3907	2452	716	716	23		

- Molecule 45 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	3h	318	Total	C	N	O	S	0	0
			2520	1599	431	475	15		

- Molecule 46 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	3d	55	Total	C	N	O	S	0	0
			343	220	64	58	1		

- Molecule 47 is a protein called Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	3k	215	Total	C	N	O	S	0	0
			1475	932	251	282	10		

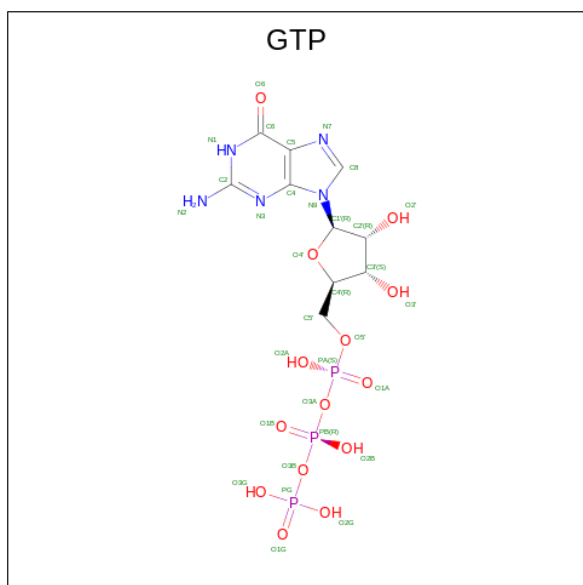
- Molecule 48 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	3l	520	Total	C	N	O	S	0	0
			4335	2808	715	793	19		

- Molecule 49 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
49	5B	1	Total	Mg	0
			1	1	
49	S2	7	Total	Mg	0
			7	7	

- Molecule 50 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
50	5B	1	Total	C	N	O	P	0
			32	10	5	14	3	

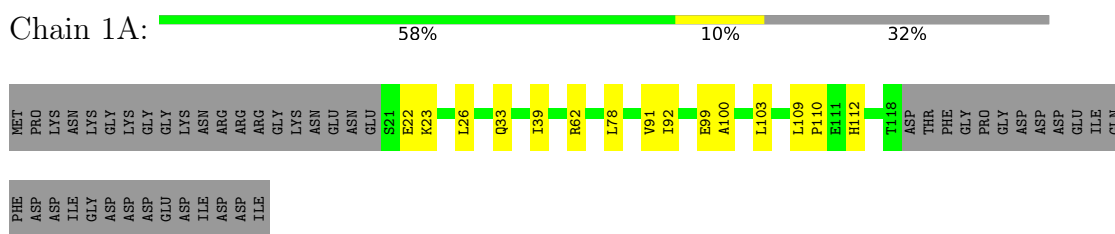
- Molecule 51 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
51	Sa	1	Total	Zn	0
			1	1	
51	sh	1	Total	Zn	0
			1	1	

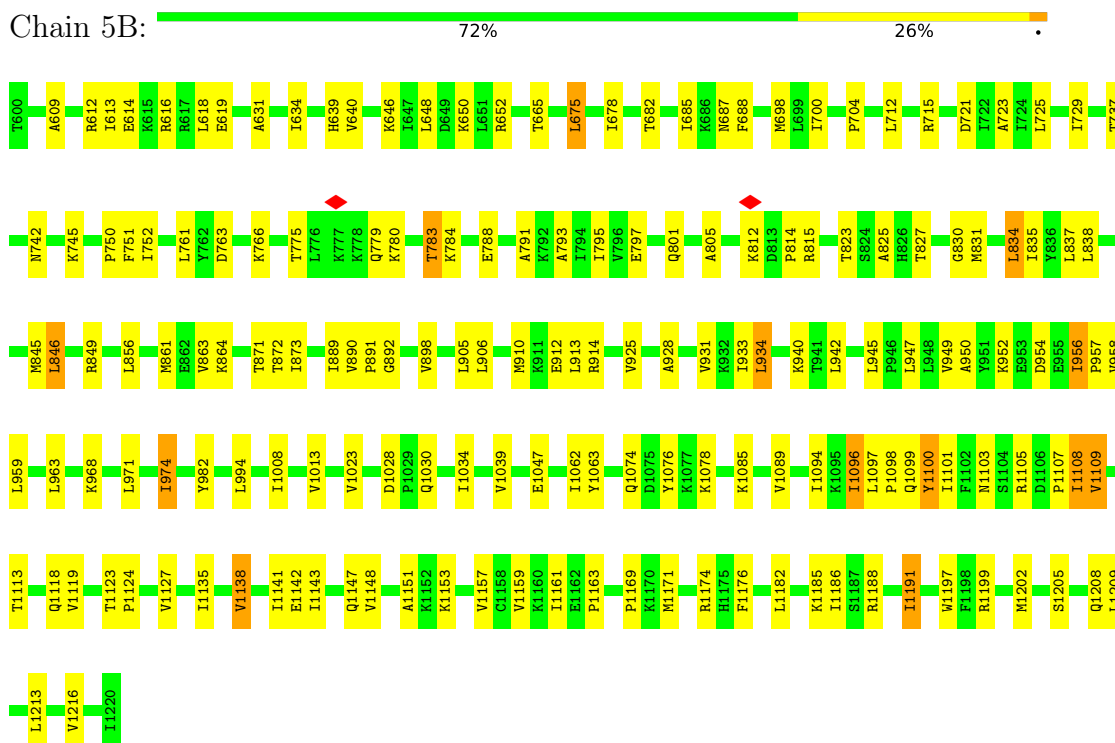
3 Residue-property plots [i](#)

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

- Molecule 1: Eukaryotic translation initiation factor 1A, X-chromosomal

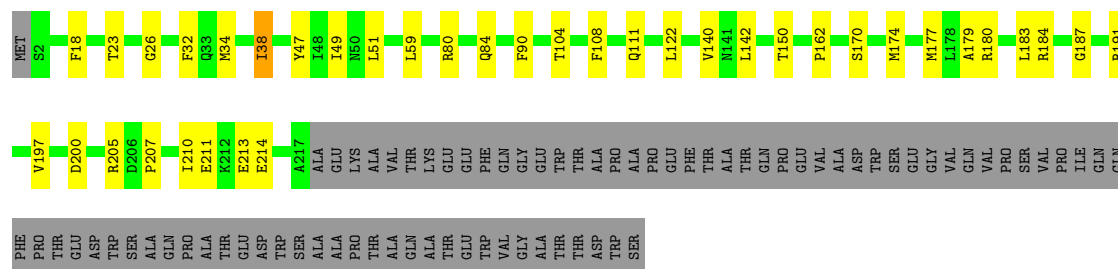


- Molecule 2: Eukaryotic translation initiation factor 5B

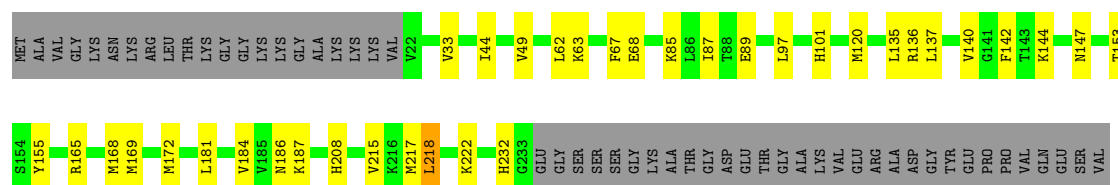


- Molecule 3: Small ribosomal subunit protein uS2

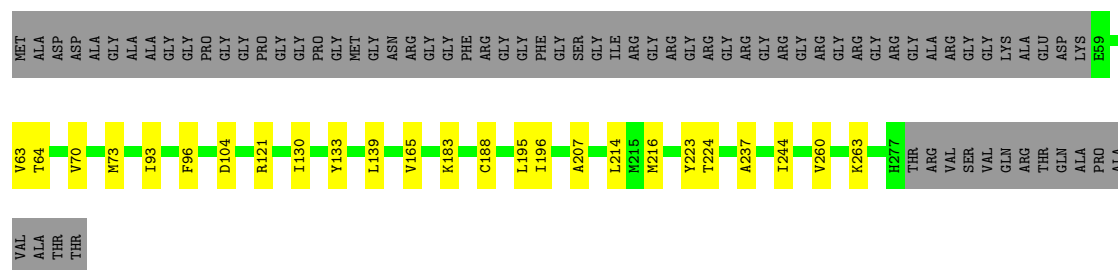




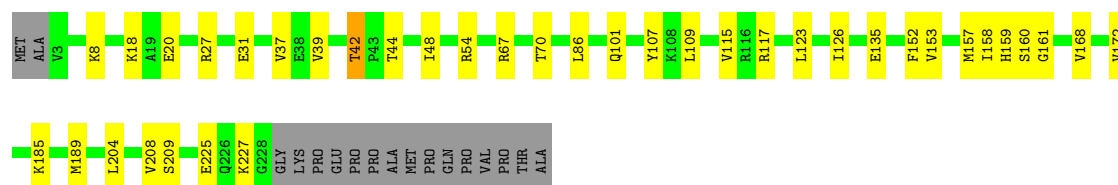
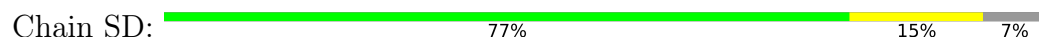
- Molecule 4: 40S ribosomal protein S3a



- Molecule 5: 40S ribosomal protein S2




- Molecule 6: 40S ribosomal protein S3



- Molecule 7: 40S ribosomal protein S4, X isoform




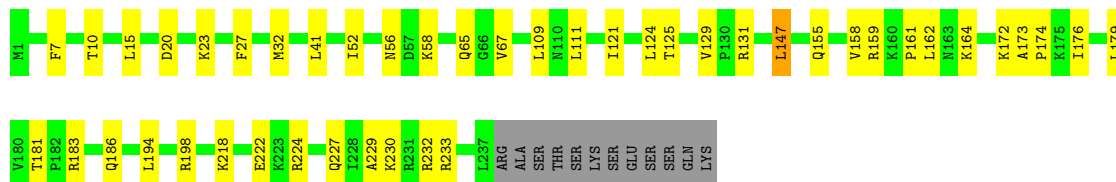
- Molecule 8: 40S ribosomal protein S5

Chain SF:  81% 13% 6%




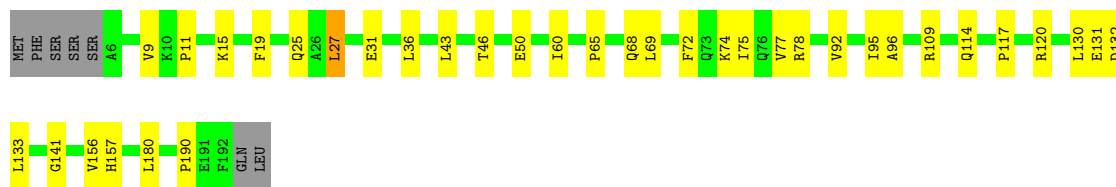
- Molecule 9: 40S ribosomal protein S6

Chain SG:  77% 18% 5%




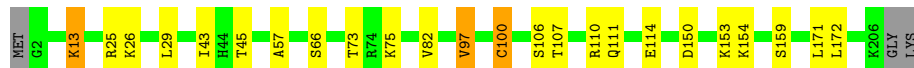
- Molecule 10: 40S ribosomal protein S7

Chain SH:  78% 18% 4%




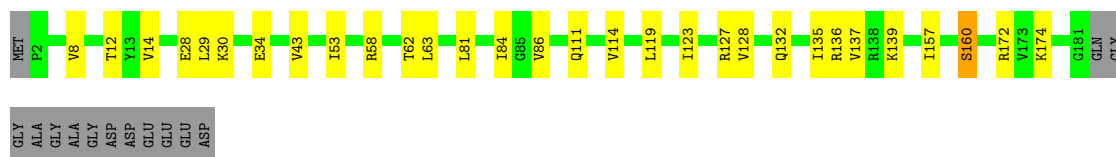
- Molecule 11: 40S ribosomal protein S8

Chain SI:  87% 10% 3%



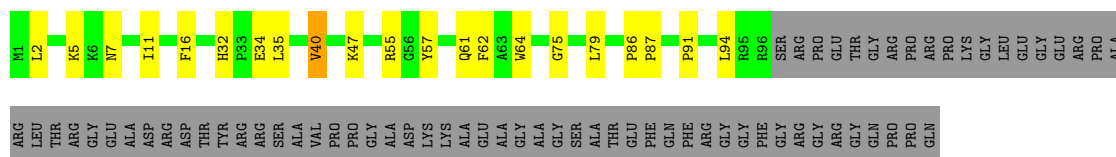
- Molecule 12: 40S ribosomal protein S9

Chain SJ:  77% 15% 8%

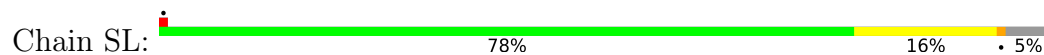


- Molecule 13: 40S ribosomal protein S10

Chain SK:  45% 12% 43%



- Molecule 14: 40S ribosomal protein S11



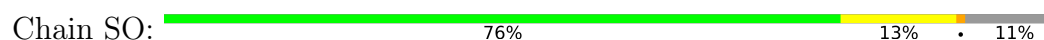
- Molecule 15: 40S ribosomal protein S12



- Molecule 16: 40S ribosomal protein S13




- Molecule 17: 40S ribosomal protein S14



- Molecule 18: 40S ribosomal protein S15



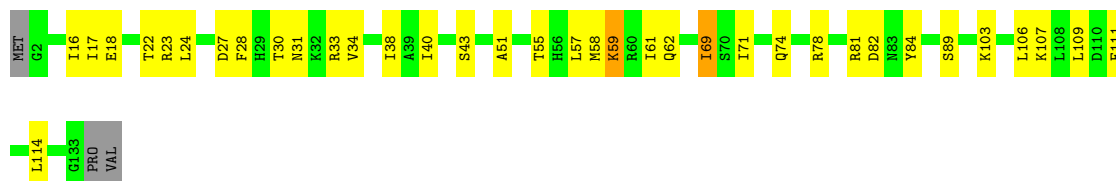
- Molecule 19: 40S ribosomal protein S16

Chain SQ:  84% 12% ..




- Molecule 20: 40S ribosomal protein S17

Chain SR:  71% 25% ..




- Molecule 21: 40S ribosomal protein S18

Chain SS:  80% 13% • 6%



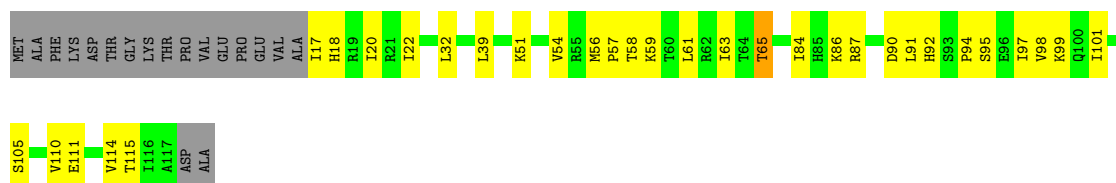
- Molecule 22: 40S ribosomal protein S19

Chain ST:  85% 13% •




- Molecule 23: 40S ribosomal protein S20

Chain SU:  58% 26% • 15%



- Molecule 24: 40S ribosomal protein S21

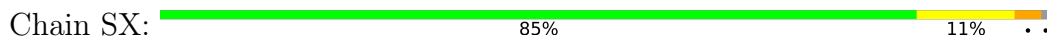
Chain SV:  84% 14% •



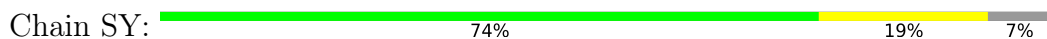
- Molecule 25: 40S ribosomal protein S15a

Chain SW:  87% 12% •

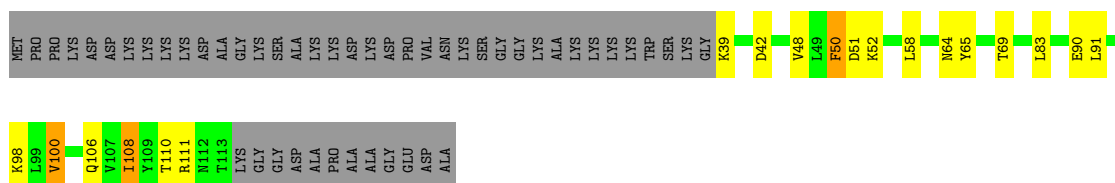
- Molecule 26: 40S ribosomal protein S23



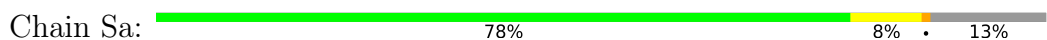
- Molecule 27: 40S ribosomal protein S24



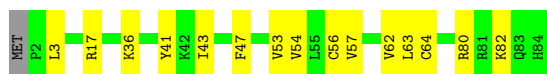
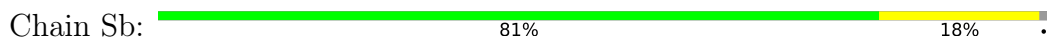
- Molecule 28: 40S ribosomal protein S25



- Molecule 29: 40S ribosomal protein S26



- Molecule 30: 40S ribosomal protein S27



- Molecule 31: 40S ribosomal protein S28



- Molecule 32: 40S ribosomal protein S29

Diagram illustrating the structure of a protein, showing residues MET, G2, R19, R22, V23, R32, K33, Y34, M38, K48, I53, and D56. The residues are connected by a black line representing the protein backbone.

- LYS VAL HIS GLY SER LEU A7 Q22 K25 R31 R40 R41 V45 N58 SER

- | | | |
|-----|------|-----|
| LYS | ILE | MET |
| PRO | GLN | GLN |
| GLU | LYS | ILE |
| ASP | GLU | PHE |
| LYS | SER | VAL |
| | THR | LYS |
| | LEU | THR |
| | HIS | LEU |
| | LEU | THR |
| | VAL | GLY |
| | LEU | LYS |
| | ARG | THR |
| | LEU | ILE |
| | ARG | THR |
| | GLY | LEU |
| | GLY | GLU |
| | ALA | VAL |
| | LYS | GLU |
| | LYS | PRO |
| | ARG | SER |
| | ARG | ASP |
| | LYS | THR |
| | LYS | THR |
| | LYS | ILE |
| | SER | GLU |
| | TYR | ASN |
| | THR | VAL |
| | THR | LYS |
| | THR | ALA |
| | P88 | LYS |
| | K99 | ILE |
| | H93 | GLN |
| | K94 | ASP |
| | R95 | LYS |
| | K96 | GLU |
| | K97 | GLY |
| | V98 | ILE |
| | K99 | PRO |
| | L100 | PRO |
| | L103 | ASP |
| | L103 | GLN |
| | Y106 | GLN |
| | K107 | ARG |
| | V108 | LEU |
| | D109 | ILE |
| | S115 | PHE |
| | R118 | ALA |
| | R119 | GLY |
| | C126 | LYS |
| | G129 | GLN |
| | V130 | LEU |
| | F131 | GLU |
| | Y148 | ASP |
| | | GLY |
| | | ARG |
| | | THR |
| | | LEU |
| | | SER |
| | | ASP |
| | | TYR |
| | | GLN |

- | | | | |
|------|------|------|-----|
| L298 | F156 | T2 | MET |
| F299 | S157 | T2 | |
| | | M5 | |
| T303 | I164 | T10 | |
| V309 | I165 | | |
| W310 | V166 | W17 | |
| | | V18 | |
| I314 | K172 | M30 | |
| GLY | L173 | | |
| THR | V174 | R36 | |
| ARG | K175 | T39 | |
| | V176 | I40 | |
| | N177 | | |
| | N178 | R57 | |
| | I179 | R60 | |
| | | H64 | |
| | K185 | V70 | |
| | T186 | L87 | |
| | N187 | R88 | |
| | I188 | L89 | |
| | I189 | G95 | |
| | G190 | R99 | |
| | H191 | R100 | |
| | T192 | F101 | |
| | G193 | K106 | |
| | Y194 | D107 | |
| | L195 | V108 | |
| | | S110 | |
| | D203 | V111 | |
| | G214 | V121 | |
| | M217 | R125 | |
| | | I129 | |
| | T229 | W132 | |
| | L230 | G136 | |
| | D234 | T141 | |
| | I235 | V142 | |
| | I236 | G143 | |
| | N237 | D144 | |
| | A238 | S288 | |
| | Y246 | L146 | |
| | A251 | V150 | |
| | T256 | | |
| | E262 | | |
| | L270 | | |
| | K271 | | |
| | T287 | | |
| | S288 | | |
| | L289 | | |
| | T307 | | |

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| A1 | A4 | G5 | A6 | G7 | U8 | G9 | G10 | G11 | G12 | G15 | C16 | G17 | G18 | A19 | A20 | G21 | U24 | G25 | C26 | U27 | G28 | A34 | U35 | C40 | A41 | G42 | A43 | C47 | G48 | A49 | U50 | G51 | G52 | A53 | U54 | C55 | G56 | A57 | A58 | C61 | A62 | C65 | U66 | C67 | U68 | G69 | C70 | U71 | A72 | C73 | G74 | A75 |
|----|----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

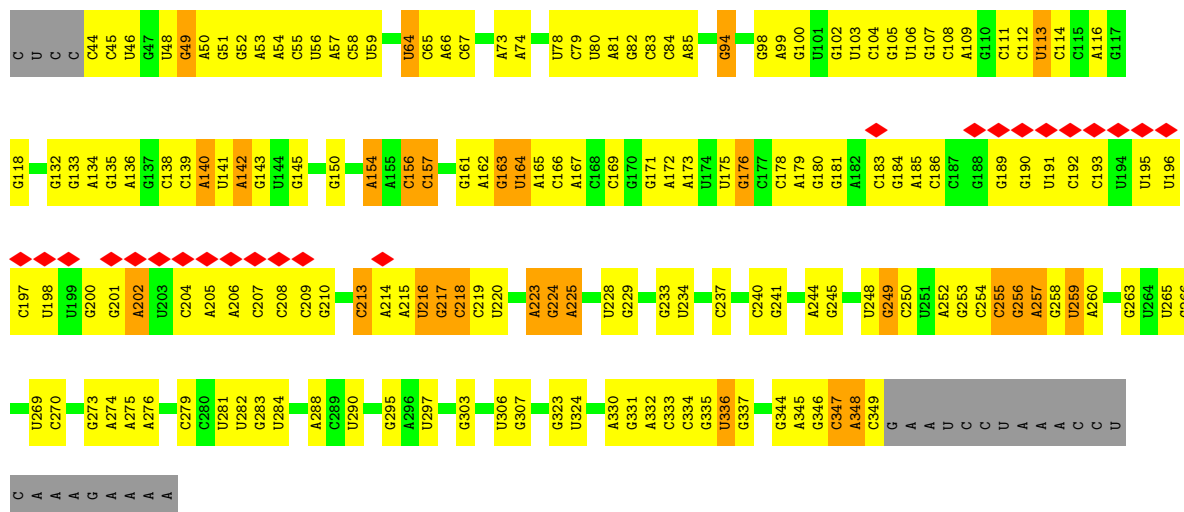
- 

Chain Ln:  96%



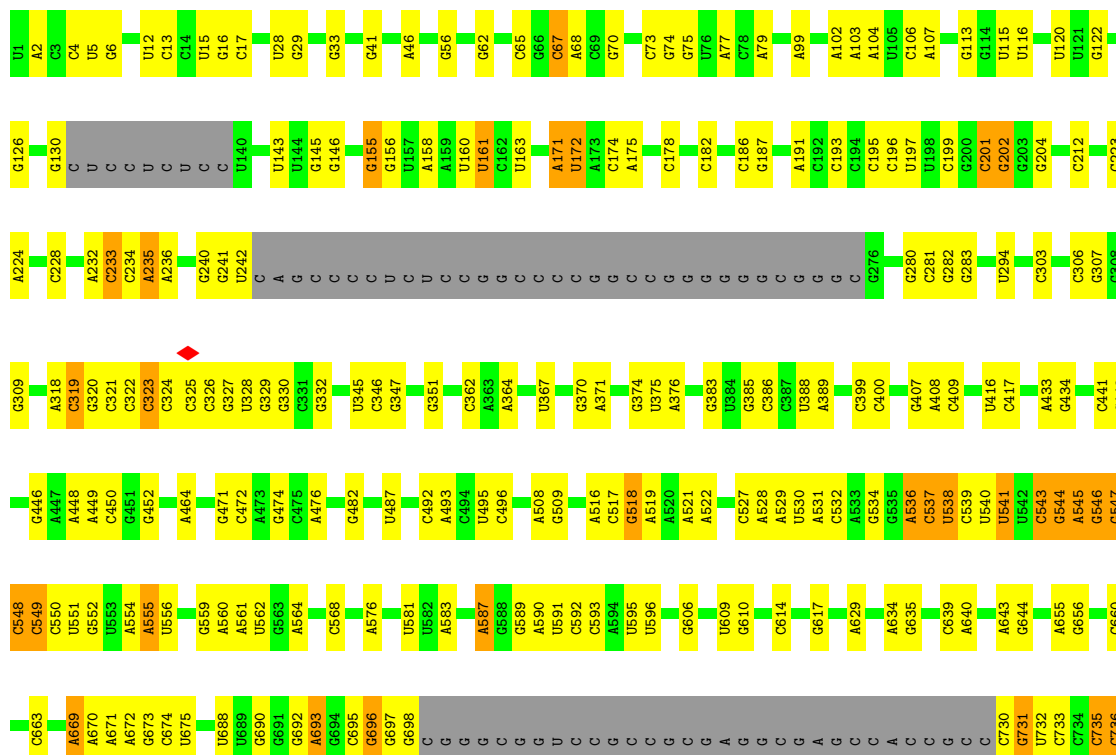
• Molecule 38: HCV-IRES RNA

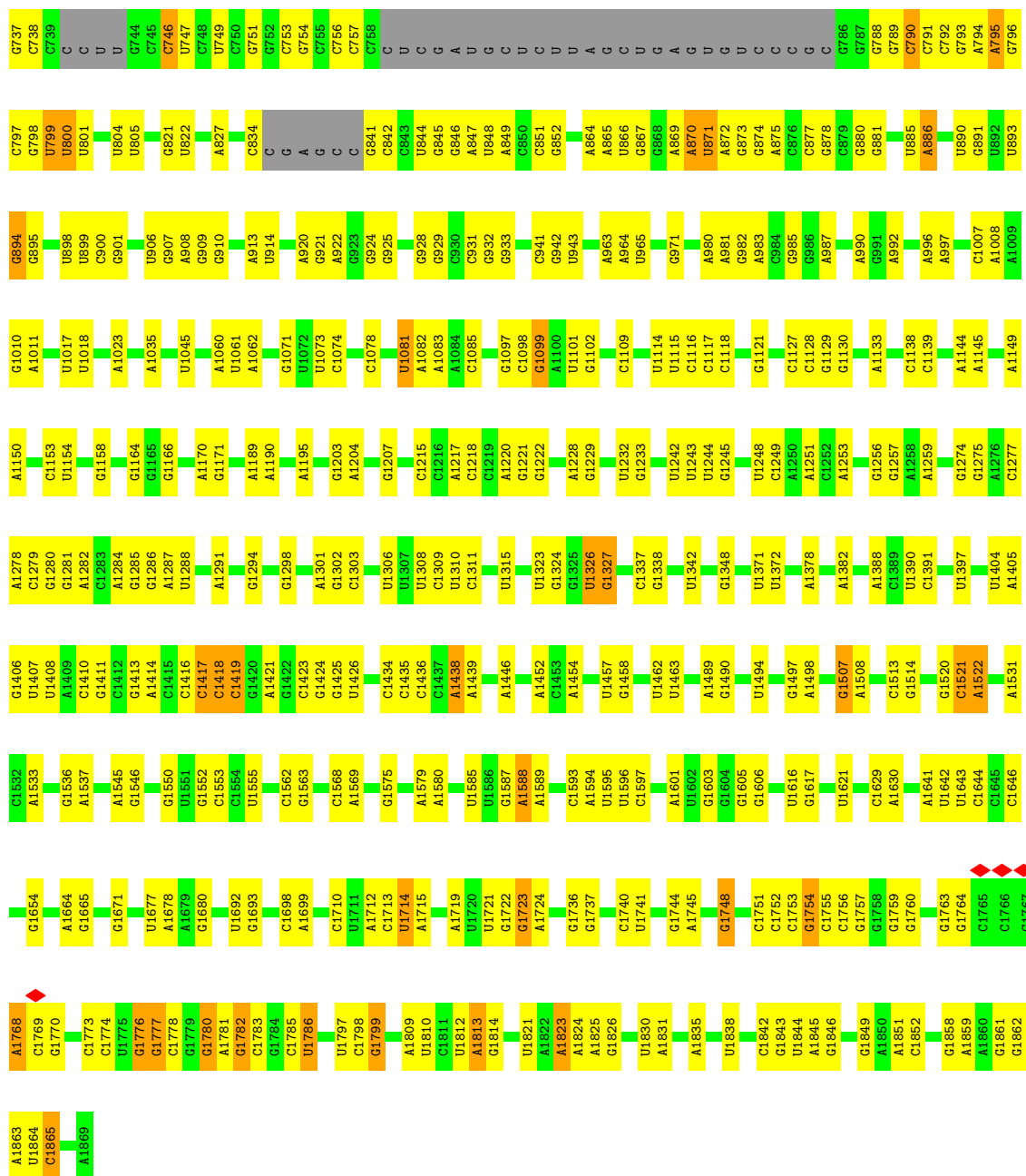
Chain zz:  7% 40% 43% 8% 8%



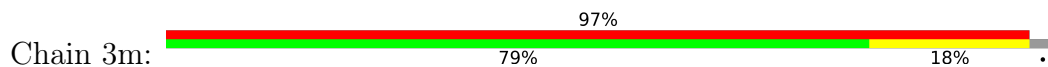
• Molecule 39: 18S ribosomal RNA

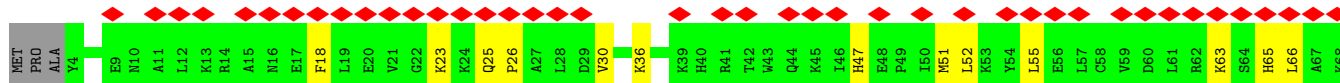
Chain S2:  61% 29% 6%





● Molecule 40: Eukaryotic translation initiation factor 3 subunit M

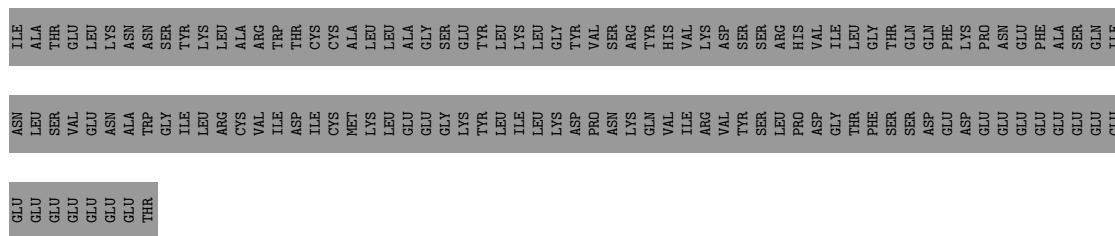




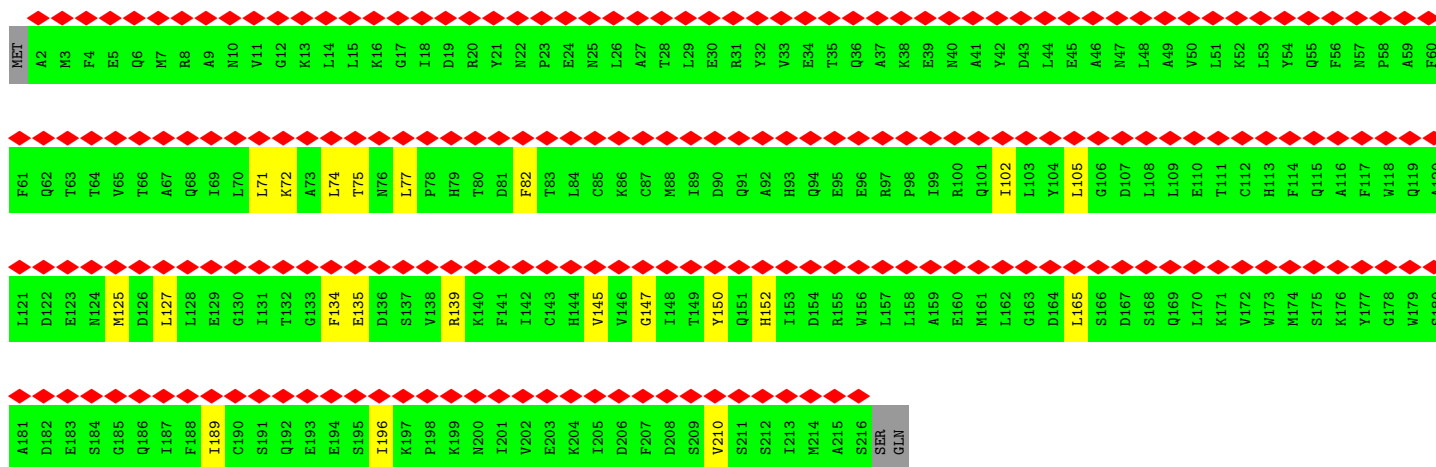
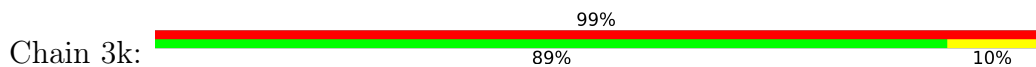




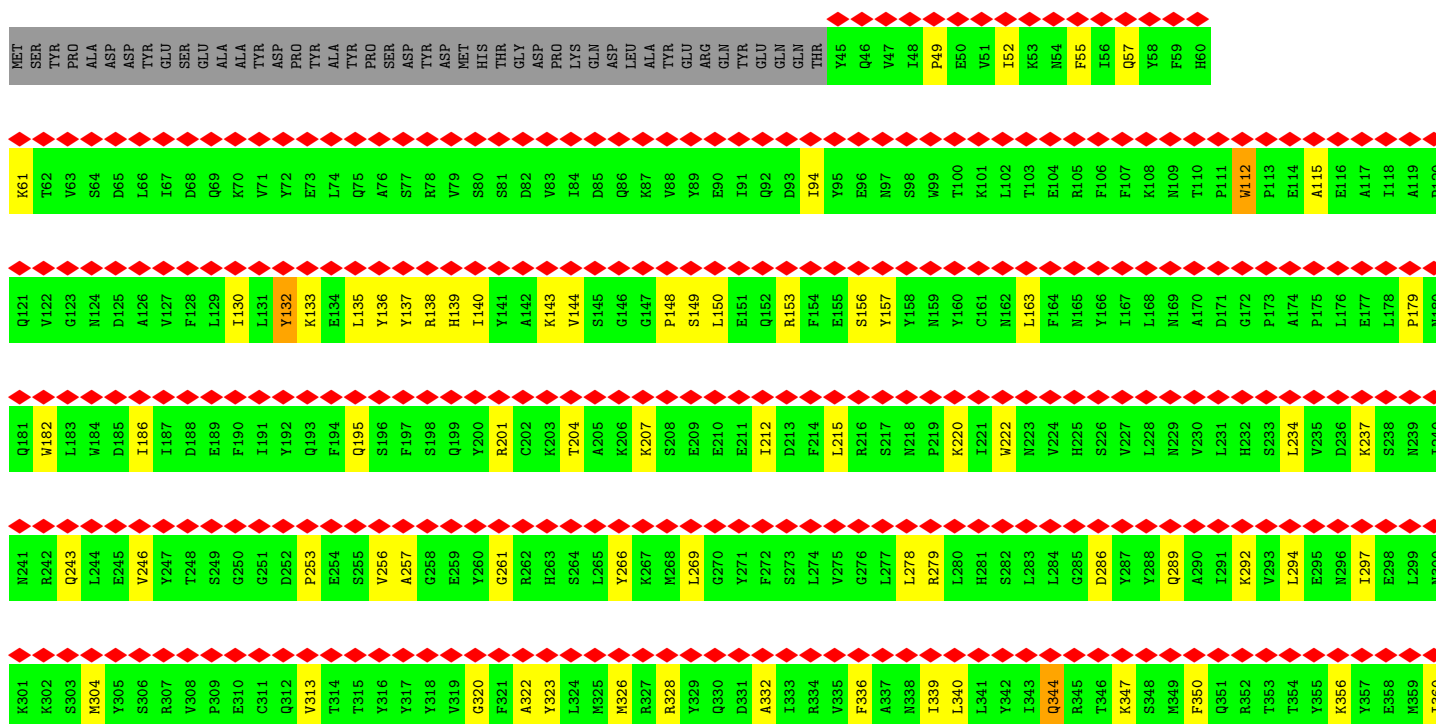
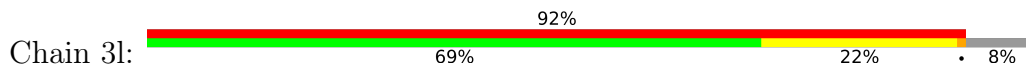
MET	THR	TRP	SER	ASP	TRP	G421	A361	G421	A481	G541	A601	E661	R723	T783	V643
SER	ASN	GLU	SER	GLU	GLU	E422	A362	E422	I482	E542	D602	Q662	Q724	Q784	M644
ARG	LEU	ASP	ARG	GLU	VAL	N423	E363	N423	I483	D543	P603	E663	P725	E785	M645
PHE	ILE	LYS	ARG	GLU	ARG	I424	N364	I424	E484	S544	P604	K664	L726	E786	M646
THR	THR	GLY	THR	GLY	GLY	I425	N365	I425	R485	A545	V605	V665	G728	S787	M647
GLY	ILE	LYS	ILE	ASP	VAL	E426	N366	E426	R486	V546	Q606	E666	P729	L788	E648
SER	ASN	LYS	ASN	GLU	PRO	E427	G367	E427	Q487	L547	I607	R667	P730	R789	P649
SER	GLU	LYS	SER	LEU	LEU	S428	E368	S428	R488	M548	L608	R668	E731	T790	T650
LEU	ALA	ASN	ALA	VAL	VAL	E429	G369	E429	Y489	E549	Y609	R669	E732	T791	A651
SER	ILE	ASN	ILE	ALA	LYS	N430	V370	N430	L490	R550	N610	R670	S733	L792	Q652
GLU	ARG	ASN	ARG	ALA	LYS	L431	I371	L431	E491	L551	R611	V671	R734	F793	Q653
SER	ASP	LYS	ASP	THR	PHE	H432	V372	H432	E492	C552	M613	P672	E735	T794	M654
LEU	VAL	LEU	VAL	LEU	ALA	N433	K373	N433	K493	K553	V614	F673	H736	L795	L655
SER	THR	LYS	THR	LEU	LYS	A434	I374	A434	G494	Y554	Q615	H674	V737	S796	A656
GLY	CYS	LYS	CYS	LYS	LYS	D435	K375	D435	T495	I555	Q616	L675	V738	S797	L657
GLU	LEU	THR	LEU	LYS	ALA	Q436	F376	Q436	T496	Y556	G617	H676	A739	V798	Q658
LEU	GLU	ARG	GLU	LEU	THR	P437	N377	P437	E497	A557	I618	I677	A740	V799	L659
LEU	GLU	ILE	LEU	LEU	ASP	R438	I378	R438	K558	D559	C619	G678	S741	D800	A660
PRO	LYS	ARG	PRO	GLY	GLU	V440	I379	V440	V499	R560	A620	L679	K742	S801	E661
VAL	LYS	ARG	VAL	ASP	THR	R441	I381	R441	C500	T561	F621	L681	A743	I802	K662
GLY	LYS	LYS	GLY	GLY	GLU	G442	S382	G442	R501	R622	Q623	E680	H744	L803	L663
ASN	ALA	ALA	ASN	ALA	ALA	C443	K383	C443	Y503	D562	G624	E683	K745	M804	S665
GLY	GLY	GLY	GLY	GLY	GLY	I444	D384	I444	L504	R563	T626	C684	G747	E805	L666
TYR	LYS	PHE	TYR	PHE	PHE	L505	Y385	L505	L505	I564	K627	H685	D748	T806	V667
GLY	LYS	PHE	GLY	PHE	LEU	R506	Y386	R506	R506	R565	R628	Y686	M749	L807	E668
LYS	LYS	GLU	LYS	GLU	LYS	T446	N386	T446	I507	C567	D628	L687	K750	S808	N669
GLN	LYS	SER	GLN	SER	LYS	L447	P387	L447	I507	C567	A629	V688	K751	D809	N670
PRO	ILE	ILE	PRO	ILE	LYS	V448	N388	V448	L508	A568	H630	S689	T751	M810	E671
LEU	VAL	THR	LEU	VAL	LYS	E449	L389	E449	H509	I569	N631	I669	C752	F811	R672
LEU	ASP	SER	LEU	ASP	ALA	R450	A390	R450	T510	L570	A632	G636	M753	H812	V673
SER	GLU	THR	SER	GLU	LYS	M451	T391	M451	Y511	C571	A633	Q637	M758	E813	M674
GLU	LYS	LYS	GLU	LYS	LYS	D452	K392	D452	Y512	H572	L633	S638	E759	E814	G675
ASP	GLN	GLY	ASP	GLN	ASP	E453	M393	E453	K513	L573	L634	G639	K760	S820	L676
GLU	PRO	GLU	GLU	PRO	ASP	F454	K394	F454	F514	Y574	D635	G640	M761	T821	G677
ASP	GLU	GLU	ASP	GLU	ARG	F455	P395	F455	D515	H575	G636	G641	N762	E822	H678
THR	GLN	SER	THR	GLN	THR	T456	E396	T456	Y516	A577	L637	R642	M763	S823	L679
LYS	LYS	GLU	LYS	LYS	ALA	K457	M397	K457	K517	L578	A642	Q643	G764	K824	M680
ARG	VAL	ASP	ARG	VAL	VAL	M459	W398	M459	A518	H579	S580	R643	V765	M825	T681
VAL	ILE	ASP	VAL	ILE	GLU	Q460	G399	Q460	H519	H579	S580	R644	V766	I826	Q682
ARG	ASP	ASP	ARG	ASP	ALA	N461	K400	N461	Q520	R581	Q522	Q645	M767	T827	L683
SER	ASP	ALA	SER	ASP	ALA	T462	C401	T462	R521	W582	L645	L646	F769	N828	V684
GLU	LEU	GLU	GLU	LEU	GLU	D463	D403	D463	LEU	Y583	L646	L646	P770	E829	L685
ASP	THR	GLU	ASP	THR	THR	P464	C404	P464	THR	Q584	L646	L646	E771	E830	L686
GLY	LEU	GLU	GLY	LEU	GLU	H465	I405	H465	PRO	A585	G647	Q648	T772	L831	Q687
LEU	LEU	ASP	LEU	LEU	GLY	S466	N406	S466	GLU	R586	Q649	Q649	F773	M832	L688
GLU	ASP	ASP	GLU	ASP	ASP	Q467	E407	Q467	GLY	D587	G649	G649	V775	A633	L689
LEU	THR	GLU	LEU	THR	THR	E468	L408	E468	SER	L588	L650	L650	F776	S834	L690
ASP	GLU	GLU	ASP	GLU	GLU	Y469	M409	Y469	SER	M589	L651	L651	T777	L835	L691
GLY	GLU	GLU	GLY	GLU	GLU	V470	D410	V470	LYS	L590	ARG	LEU	T778	E836	L692
GLY	GLU	GLU	GLY	GLU	GLU	E471	I411	E471	GLU	M591	THR	LEU	V779	T837	L693
GLY	GLU	GLU	GLY	GLU	GLU	H472	L412	H472	ASP	S592	GLU	GLU	F780	E838	L694
GLY	GLU	GLU	GLY	GLU	GLU	L473	F413	L473	GLN	H593	L594	L594	M781	T839	L695
GLY	GLU	GLU	GLY	GLU	GLU	K474	N415	K474	ALA	L594	L594	L594	L782	Q840	L696
GLY	GLU	GLU	GLY	GLU	GLU	D475	N416	D475	GLN	H595	L594	L594	L783	Q841	L697
GLY	GLU	GLU	GLY	GLU	GLU	E476	P416	E476	ALA	Q595	L594	L594	L784	T842	L698
GLY	GLU	GLU	GLY	GLU	GLU	A477	N417	A477	GLU	N597	L594	L594	L785	Q843	L699
GLY	GLU	GLU	GLY	GLU	GLU	Q478	I418	Q478	GLU	I598	L594	L594	L786	T844	L700
GLY	GLU	GLU	GLY	GLU	GLU	V479	F419	V479	GLU	Q599	L594	L594	L787	Q845	L701
GLY	GLU	GLU	GLY	GLU	GLU	C480	V420	C480	GLU	H600	L594	L594	L788	V846	L702



- Molecule 47: Eukaryotic translation initiation factor 3 subunit K



- Molecule 48: Eukaryotic translation initiation factor 3 subunit L





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	19430	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.103	Depositor
Minimum map value	-0.016	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.011	Depositor
Map size (\AA)	636.0, 636.0, 636.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.272, 1.272, 1.272	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, 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	1A	0.15	0/793	0.41	0/1061
2	5B	0.20	0/4999	0.54	0/6740
3	SA	0.19	0/1742	0.38	0/2367
4	SB	0.19	0/1749	0.36	0/2340
5	SC	0.20	0/1737	0.43	0/2347
6	SD	0.18	0/1784	0.40	0/2402
7	SE	0.20	0/2107	0.38	0/2836
8	SF	0.20	0/1540	0.42	0/2071
9	SG	0.17	0/1946	0.37	0/2590
10	SH	0.19	0/1529	0.42	0/2048
11	SI	0.18	0/1711	0.35	0/2282
12	SJ	0.18	0/1524	0.36	0/2035
13	SK	0.18	0/834	0.45	0/1125
14	SL	0.20	0/1241	0.37	0/1662
15	Sf	0.20	0/945	0.57	0/1269
16	SN	0.20	0/1226	0.39	0/1649
17	SO	0.19	0/1020	0.40	0/1368
18	SP	0.20	0/1003	0.49	0/1340
19	SQ	0.23	0/1133	0.49	0/1517
20	SR	0.22	0/1082	0.54	0/1452
21	SS	0.18	0/1202	0.42	0/1610
22	ST	0.20	0/1122	0.42	0/1504
23	SU	0.18	0/813	0.45	0/1092
24	SV	0.17	0/643	0.36	0/860
25	SW	0.21	0/1051	0.38	0/1406
26	SX	0.20	0/1116	0.43	0/1490
27	SY	0.19	0/1031	0.46	0/1370
28	SZ	0.24	0/607	0.58	0/815
29	Sa	0.22	0/817	0.39	0/1095
30	Sb	0.20	0/665	0.39	0/891
31	Sc	0.23	0/490	0.49	0/656
32	Sd	0.20	0/470	0.41	0/623

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Se	0.15	0/422	0.41	0/555
34	sh	0.18	0/533	0.44	0/706
35	Sg	0.16	0/2493	0.42	0/3394
36	zy	0.15	0/1798	0.32	0/2802
37	Ln	0.19	0/231	0.42	0/294
38	zz	0.16	0/7294	0.35	0/11371
39	S2	0.19	0/42073	0.31	0/65576
40	3m	0.14	0/2676	0.40	0/3635
41	3f	0.15	0/2099	0.40	0/2856
42	3a	0.16	0/4556	0.39	0/6205
43	3e	0.15	0/3288	0.39	0/4475
44	3c	0.15	0/3973	0.41	0/5406
45	3h	0.15	0/2571	0.39	0/3484
46	3d	0.14	0/354	0.36	0/488
47	3k	0.12	0/1502	0.36	0/2052
48	3l	0.15	0/4446	0.40	0/6013
All	All	0.18	0/121981	0.38	0/175225

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1A	783	0	793	8	0
2	5B	4917	0	5099	102	0
3	SA	1705	0	1706	21	0
4	SB	1722	0	1794	22	0
5	SC	1700	0	1784	11	0
6	SD	1756	0	1851	22	0
7	SE	2065	0	2169	14	0
8	SF	1518	0	1569	17	0
9	SG	1923	0	2089	25	0

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Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	SH	1506	0	1603	18	0
11	SI	1682	0	1769	14	0
12	SJ	1499	0	1618	14	0
13	SK	810	0	836	19	0
14	SL	1220	0	1289	16	0
15	Sf	935	0	964	29	0
16	SN	1202	0	1289	16	0
17	SO	1007	0	1032	10	0
18	SP	984	0	1033	15	0
19	SQ	1116	0	1185	9	0
20	SR	1068	0	1121	21	0
21	SS	1184	0	1244	11	0
22	ST	1103	0	1133	12	0
23	SU	803	0	873	16	0
24	SV	636	0	637	7	0
25	SW	1034	0	1080	12	0
26	SX	1098	0	1167	10	0
27	SY	1014	0	1082	15	0
28	SZ	601	0	662	12	0
29	Sa	803	0	850	7	0
30	Sb	651	0	672	7	0
31	Sc	488	0	514	10	0
32	Sd	459	0	452	5	0
33	Se	417	0	463	3	0
34	sh	522	0	530	9	0
35	Sg	2436	0	2393	43	0
36	zy	1607	0	815	25	0
37	Ln	230	0	276	0	0
38	zz	6528	0	3303	74	0
39	S2	37626	0	19015	268	0
40	3m	2639	0	2442	44	0
41	3f	2063	0	2054	53	0
42	3a	4470	0	4177	71	0
43	3e	3224	0	2925	45	0
44	3c	3907	0	3472	67	0
45	3h	2520	0	2445	53	0
46	3d	343	0	253	3	0
47	3k	1475	0	1239	14	0
48	3l	4335	0	4272	81	0
49	5B	1	0	0	0	0
49	S2	7	0	0	0	0
50	5B	32	0	11	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	Sa	1	0	0	0	0
51	sh	1	0	0	0	0
All	All	115376	0	93044	1275	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 6.

The worst 5 of 1275 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)
38:zz:259:U:H3	38:zz:274:A:N6	1.73	0.87
38:zz:256:G:N1	38:zz:276:A:N6	2.26	0.83
38:zz:259:U:H3	38:zz:274:A:H62	1.26	0.83
39:S2:885:U:H3	39:S2:901:G:H1	0.85	0.83
39:S2:1710:C:H42	39:S2:1823:A:H61	1.26	0.82

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	1A	96/144 (67%)	88 (92%)	8 (8%)	0	100	100
2	5B	619/621 (100%)	580 (94%)	35 (6%)	4 (1%)	22	53
3	SA	214/295 (72%)	209 (98%)	5 (2%)	0	100	100
4	SB	210/264 (80%)	199 (95%)	11 (5%)	0	100	100
5	SC	217/293 (74%)	210 (97%)	7 (3%)	0	100	100
6	SD	224/243 (92%)	218 (97%)	6 (3%)	0	100	100
7	SE	258/263 (98%)	248 (96%)	10 (4%)	0	100	100
8	SF	190/204 (93%)	182 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	SG	235/249 (94%)	232 (99%)	3 (1%)	0	100	100
10	SH	185/194 (95%)	180 (97%)	5 (3%)	0	100	100
11	SI	203/208 (98%)	194 (96%)	9 (4%)	0	100	100
12	SJ	178/194 (92%)	175 (98%)	3 (2%)	0	100	100
13	SK	94/165 (57%)	86 (92%)	8 (8%)	0	100	100
14	SL	148/158 (94%)	144 (97%)	4 (3%)	0	100	100
15	Sf	119/132 (90%)	109 (92%)	10 (8%)	0	100	100
16	SN	147/151 (97%)	141 (96%)	6 (4%)	0	100	100
17	SO	133/151 (88%)	120 (90%)	13 (10%)	0	100	100
18	SP	117/145 (81%)	112 (96%)	5 (4%)	0	100	100
19	SQ	138/146 (94%)	133 (96%)	5 (4%)	0	100	100
20	SR	130/135 (96%)	123 (95%)	7 (5%)	0	100	100
21	SS	141/152 (93%)	134 (95%)	7 (5%)	0	100	100
22	ST	140/145 (97%)	139 (99%)	1 (1%)	0	100	100
23	SU	99/119 (83%)	94 (95%)	4 (4%)	1 (1%)	13	42
24	SV	81/83 (98%)	81 (100%)	0	0	100	100
25	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
26	SX	139/143 (97%)	132 (95%)	7 (5%)	0	100	100
27	SY	122/133 (92%)	119 (98%)	3 (2%)	0	100	100
28	SZ	73/125 (58%)	69 (94%)	3 (4%)	1 (1%)	9	34
29	Sa	98/115 (85%)	95 (97%)	3 (3%)	0	100	100
30	Sb	81/84 (96%)	77 (95%)	4 (5%)	0	100	100
31	Sc	60/69 (87%)	58 (97%)	2 (3%)	0	100	100
32	Sd	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
33	Se	50/59 (85%)	47 (94%)	3 (6%)	0	100	100
34	sh	62/156 (40%)	56 (90%)	6 (10%)	0	100	100
35	Sg	311/317 (98%)	292 (94%)	19 (6%)	0	100	100
37	Ln	22/25 (88%)	21 (96%)	1 (4%)	0	100	100
40	3m	361/374 (96%)	343 (95%)	18 (5%)	0	100	100
41	3f	267/357 (75%)	263 (98%)	4 (2%)	0	100	100
42	3a	590/1382 (43%)	563 (95%)	27 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	3e	428/445 (96%)	413 (96%)	15 (4%)	0	100	100
44	3c	537/913 (59%)	517 (96%)	20 (4%)	0	100	100
45	3h	316/352 (90%)	304 (96%)	12 (4%)	0	100	100
46	3d	53/548 (10%)	49 (92%)	4 (8%)	0	100	100
47	3k	213/218 (98%)	206 (97%)	7 (3%)	0	100	100
48	3l	518/564 (92%)	503 (97%)	15 (3%)	0	100	100
All	All	8797/11419 (77%)	8431 (96%)	360 (4%)	6 (0%)	50	76

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	5B	1099	GLN
2	5B	1108	ILE
2	5B	1098	PRO
23	SU	54	VAL
28	SZ	42	ASP

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1A	82/123 (67%)	80 (98%)	2 (2%)	44	68
2	5B	546/546 (100%)	523 (96%)	23 (4%)	25	53
3	SA	180/243 (74%)	173 (96%)	7 (4%)	27	55
4	SB	193/231 (84%)	189 (98%)	4 (2%)	48	70
5	SC	185/225 (82%)	180 (97%)	5 (3%)	40	65
6	SD	189/202 (94%)	180 (95%)	9 (5%)	21	50
7	SE	223/225 (99%)	215 (96%)	8 (4%)	30	57
8	SF	162/170 (95%)	154 (95%)	8 (5%)	21	49
9	SG	207/218 (95%)	199 (96%)	8 (4%)	27	55
10	SH	167/174 (96%)	160 (96%)	7 (4%)	25	53

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	SI	178/180 (99%)	173 (97%)	5 (3%)	38	64
12	SJ	160/168 (95%)	151 (94%)	9 (6%)	17	45
13	SK	87/136 (64%)	84 (97%)	3 (3%)	32	59
14	SL	134/142 (94%)	130 (97%)	4 (3%)	36	62
15	Sf	102/108 (94%)	100 (98%)	2 (2%)	50	71
16	SN	130/131 (99%)	129 (99%)	1 (1%)	79	87
17	SO	104/119 (87%)	100 (96%)	4 (4%)	28	56
18	SP	107/130 (82%)	104 (97%)	3 (3%)	38	64
19	SQ	116/121 (96%)	113 (97%)	3 (3%)	41	66
20	SR	119/122 (98%)	110 (92%)	9 (8%)	11	34
21	SS	124/132 (94%)	118 (95%)	6 (5%)	21	50
22	ST	112/115 (97%)	110 (98%)	2 (2%)	54	74
23	SU	93/107 (87%)	86 (92%)	7 (8%)	11	34
24	SV	67/67 (100%)	65 (97%)	2 (3%)	36	62
25	SW	112/113 (99%)	111 (99%)	1 (1%)	75	85
26	SX	113/115 (98%)	103 (91%)	10 (9%)	8	28
27	SY	108/115 (94%)	105 (97%)	3 (3%)	38	64
28	SZ	67/103 (65%)	62 (92%)	5 (8%)	11	34
29	Sa	87/98 (89%)	85 (98%)	2 (2%)	45	68
30	Sb	75/76 (99%)	69 (92%)	6 (8%)	10	32
31	Sc	55/62 (89%)	53 (96%)	2 (4%)	30	57
32	Sd	48/49 (98%)	48 (100%)	0	100	100
33	Se	42/48 (88%)	40 (95%)	2 (5%)	21	50
34	sh	57/140 (41%)	53 (93%)	4 (7%)	12	37
35	Sg	272/275 (99%)	257 (94%)	15 (6%)	18	45
37	Ln	23/24 (96%)	23 (100%)	0	100	100
40	3m	252/335 (75%)	246 (98%)	6 (2%)	44	68
41	3f	229/289 (79%)	221 (96%)	8 (4%)	31	58
42	3a	433/1259 (34%)	421 (97%)	12 (3%)	38	64
43	3e	302/406 (74%)	294 (97%)	8 (3%)	41	66
44	3c	343/811 (42%)	336 (98%)	7 (2%)	50	71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	3h	272/310 (88%)	262 (96%)	10 (4%)	29	56
46	3d	19/494 (4%)	18 (95%)	1 (5%)	19	47
47	3k	121/193 (63%)	119 (98%)	2 (2%)	56	74
48	3l	475/515 (92%)	460 (97%)	15 (3%)	34	61
All	All	7272/9965 (73%)	7012 (96%)	260 (4%)	32	57

5 of 260 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
44	3c	779	LEU
45	3h	219	GLU
13	SK	79	LEU
12	SJ	172	ARG
47	3k	127	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
44	3c	623	GLN
47	3k	76	ASN
44	3c	648	GLN
45	3h	80	ASN
48	3l	218	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
36	zy	74/75 (98%)	26 (35%)	0
38	zz	305/332 (91%)	118 (38%)	0
39	S2	1748/1869 (93%)	325 (18%)	9 (0%)
All	All	2127/2276 (93%)	469 (22%)	9 (0%)

5 of 469 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
36	zy	5	G
36	zy	6	A
36	zy	8	U

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Mol	Chain	Res	Type
36	zy	9	G
36	zy	10	G

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
39	S2	1326	U
39	S2	1434	C
39	S2	517	C
39	S2	531	A
39	S2	871	U

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 11 ligands modelled in this entry, 10 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
50	GTP	5B	1302	49	26,34,34	3.54	13 (50%)	32,54,54	1.50	6 (18%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	GTP	5B	1302	49	-	5/18/38/38	0/3/3/3

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	5B	1302	GTP	C3'-C4'	-8.76	1.30	1.53
50	5B	1302	GTP	O4'-C4'	7.59	1.62	1.45
50	5B	1302	GTP	O4'-C1'	-7.10	1.31	1.41
50	5B	1302	GTP	C2-N3	5.42	1.46	1.33
50	5B	1302	GTP	C4-N3	4.97	1.49	1.37

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	5B	1302	GTP	PA-O3A-PB	-3.44	121.02	132.83
50	5B	1302	GTP	C5-C6-N1	3.28	119.75	113.95
50	5B	1302	GTP	PB-O3B-PG	-2.86	123.02	132.83
50	5B	1302	GTP	C8-N7-C5	2.73	108.20	102.99
50	5B	1302	GTP	C2-N1-C6	-2.71	120.11	125.10

There are no chirality outliers.

All (5) torsion outliers are listed below:

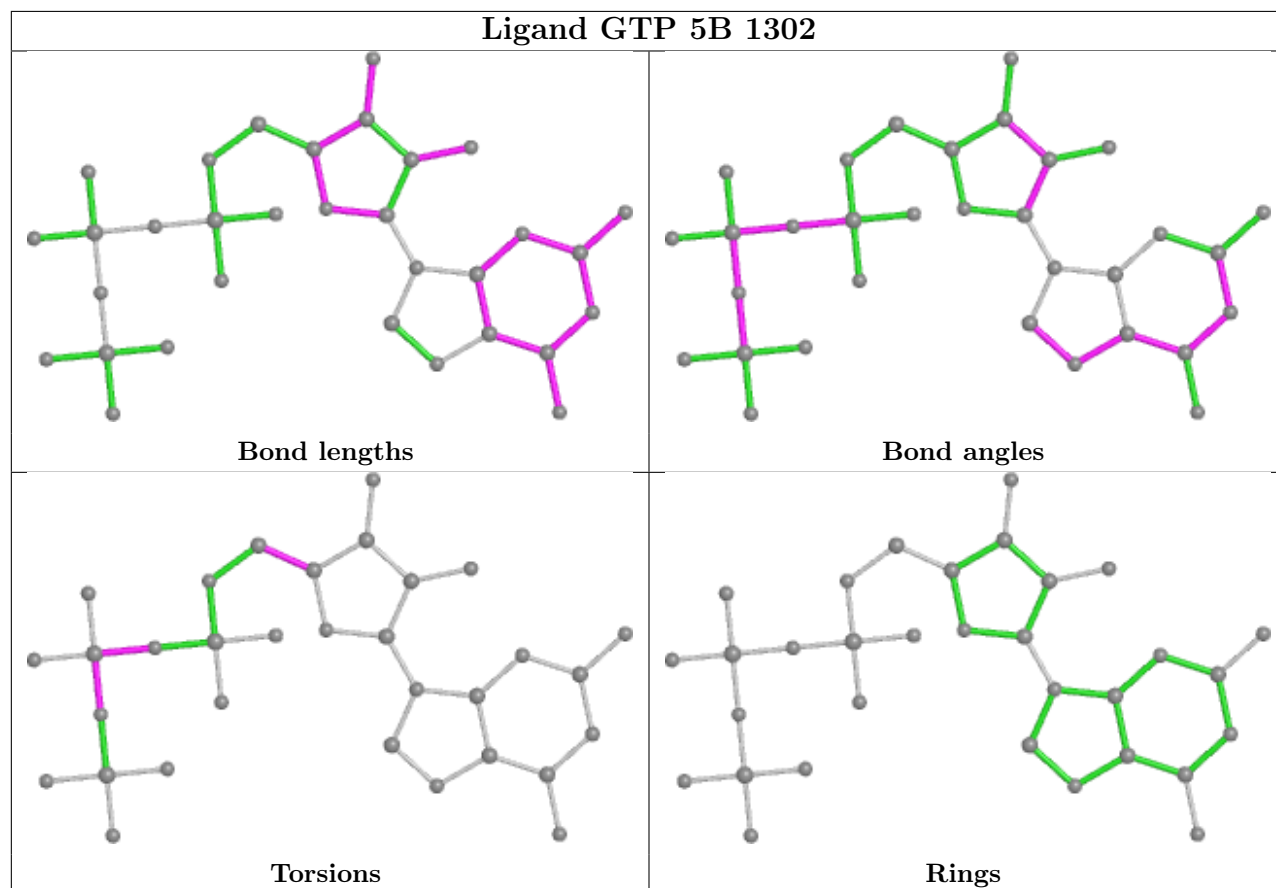
Mol	Chain	Res	Type	Atoms
50	5B	1302	GTP	PA-O3A-PB-O3B
50	5B	1302	GTP	PG-O3B-PB-O2B
50	5B	1302	GTP	O4'-C4'-C5'-O5'
50	5B	1302	GTP	PG-O3B-PB-O1B
50	5B	1302	GTP	PA-O3A-PB-O1B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

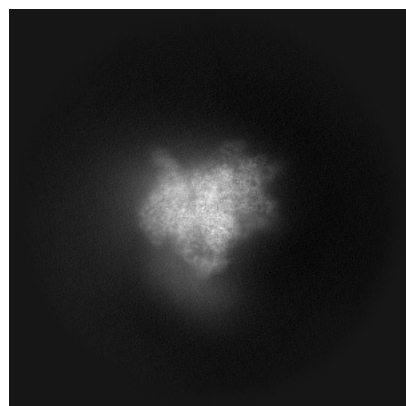
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62454. These allow visual inspection of the internal detail of the map and identification of artifacts.

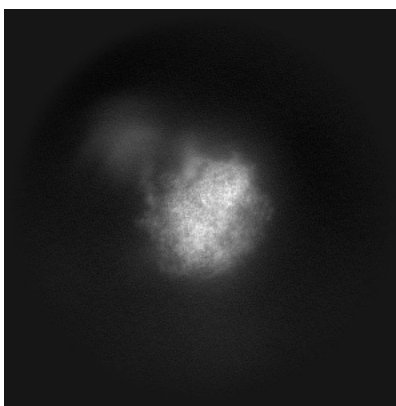
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

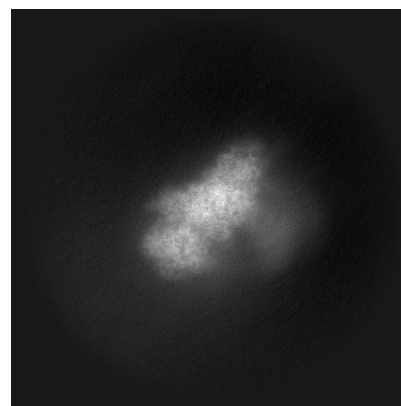
6.1.1 Primary map



X

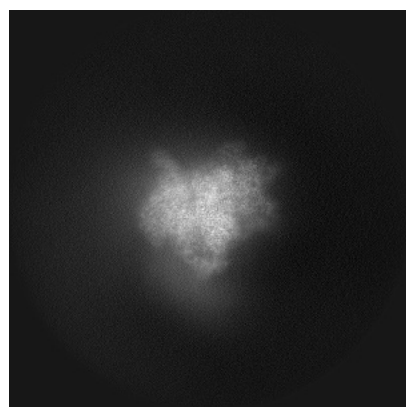


Y

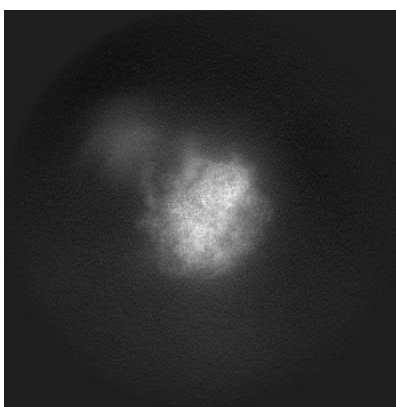


Z

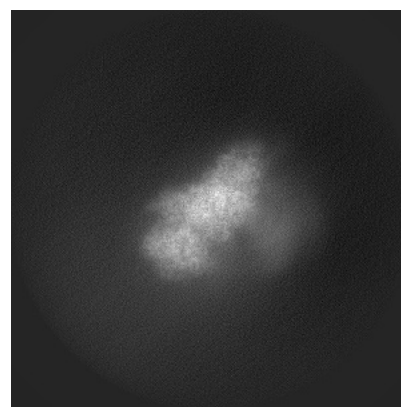
6.1.2 Raw map



X



Y

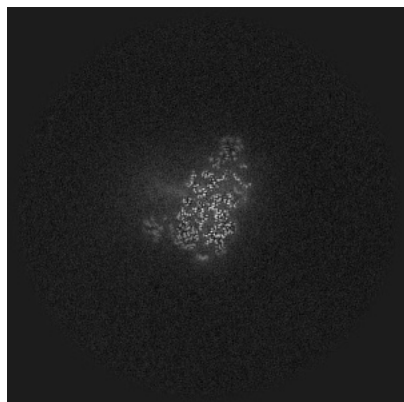


Z

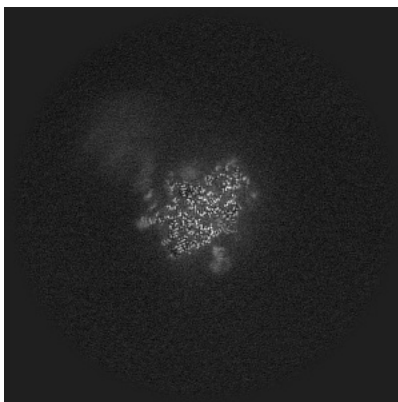
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

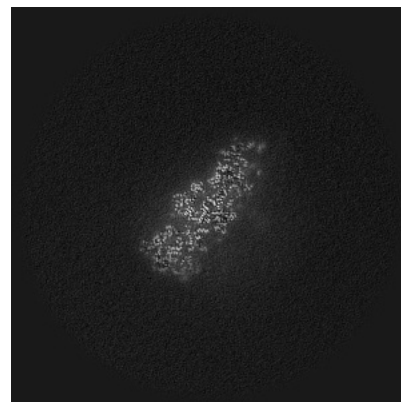
6.2.1 Primary map



X Index: 250

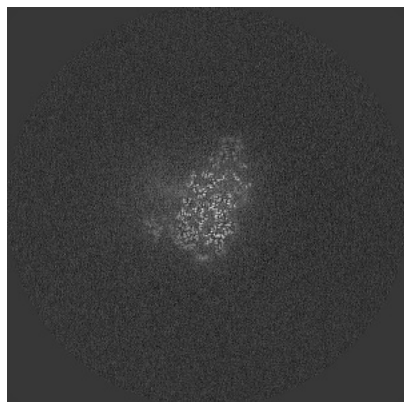


Y Index: 250

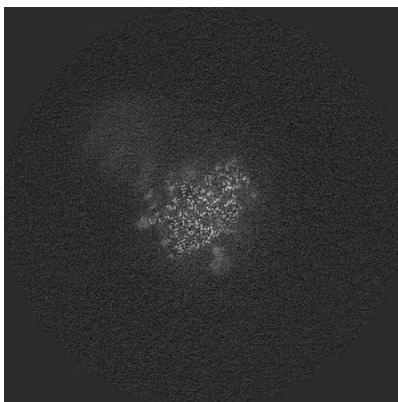


Z Index: 250

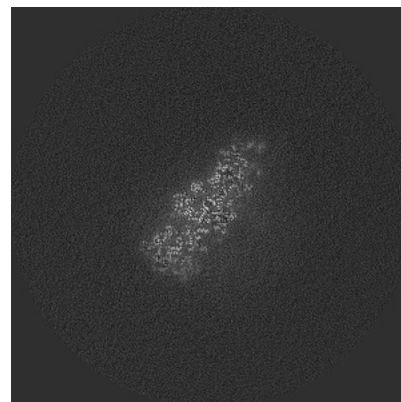
6.2.2 Raw map



X Index: 250



Y Index: 250

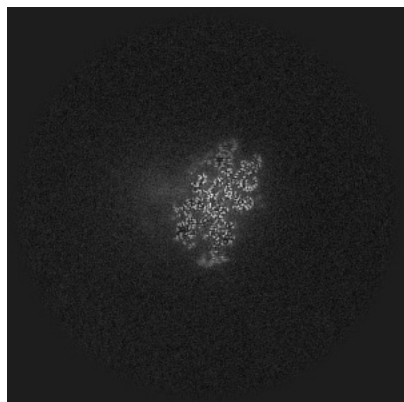


Z Index: 250

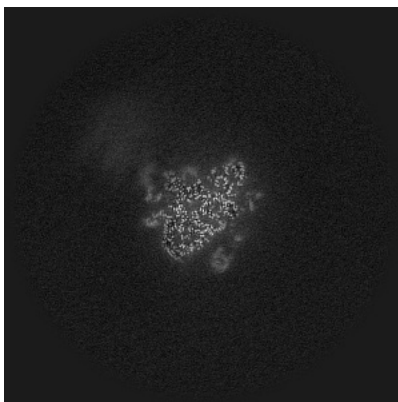
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

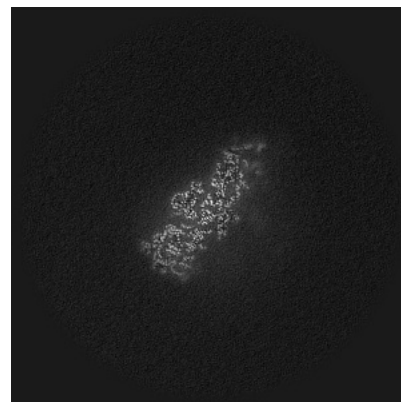
6.3.1 Primary map



X Index: 260

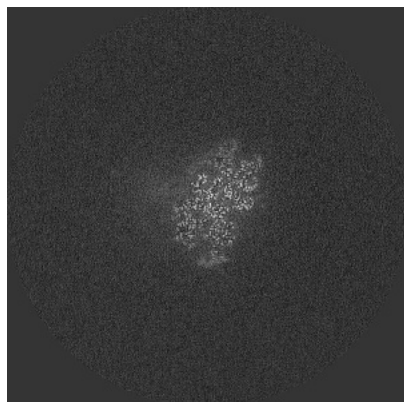


Y Index: 255

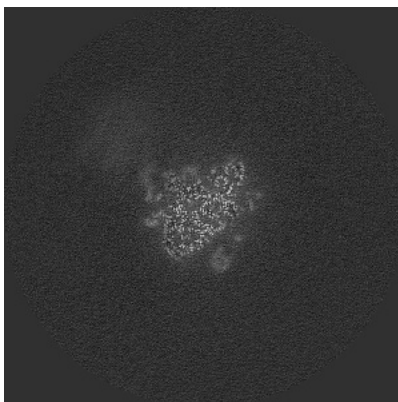


Z Index: 248

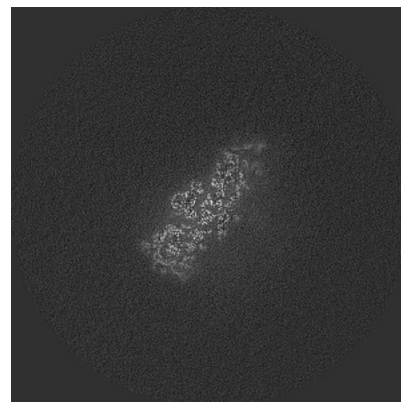
6.3.2 Raw map



X Index: 260



Y Index: 255

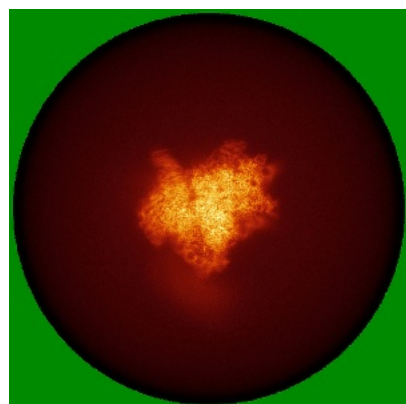


Z Index: 248

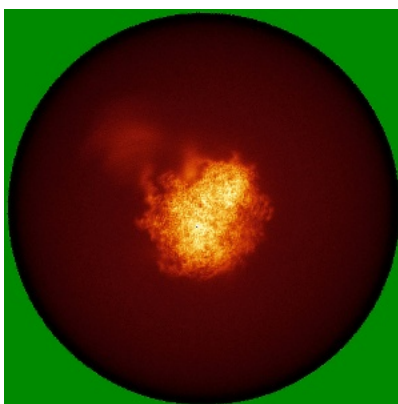
The images above show the largest variance slices of the map in three orthogonal directions.

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

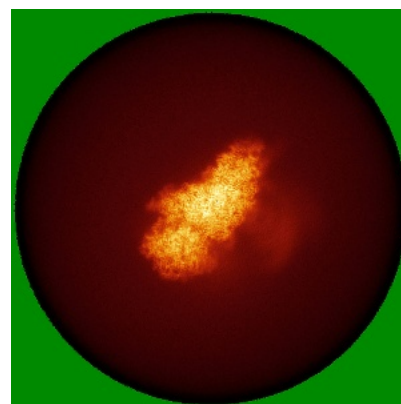
6.4.1 Primary map



X

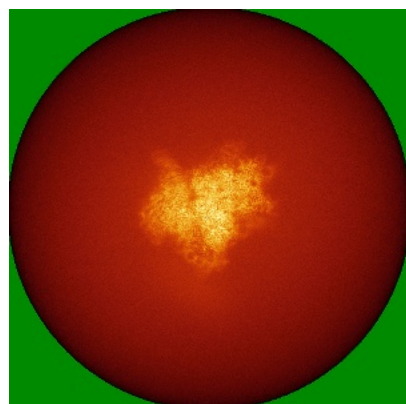


Y

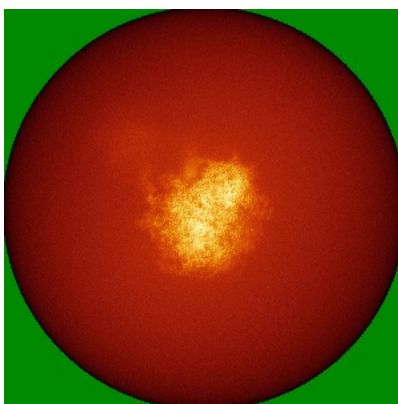


Z

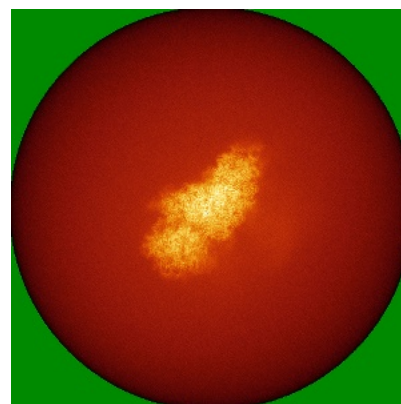
6.4.2 Raw map



X



Y

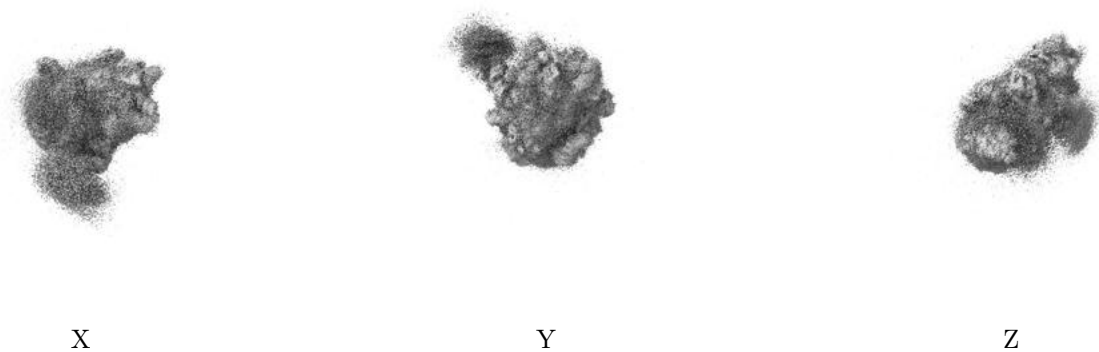


Z

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.

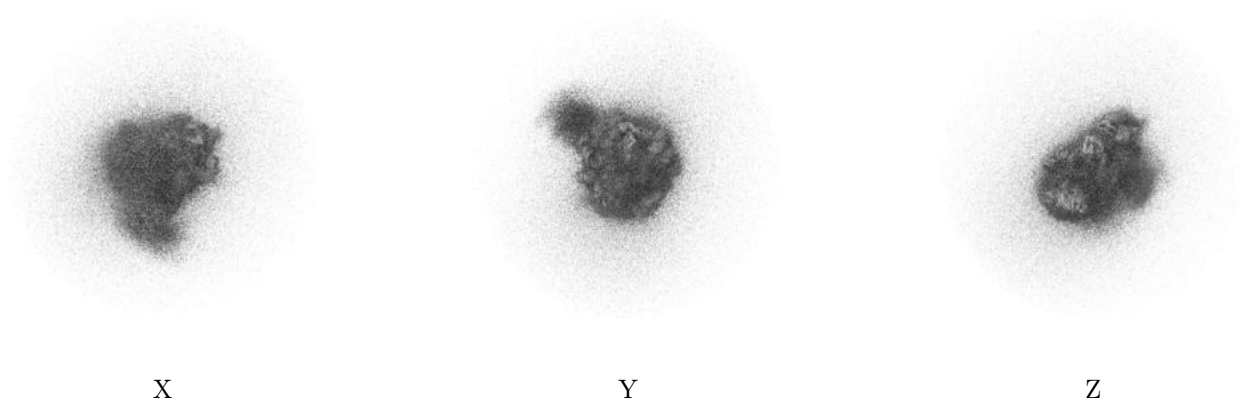
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.011. 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.

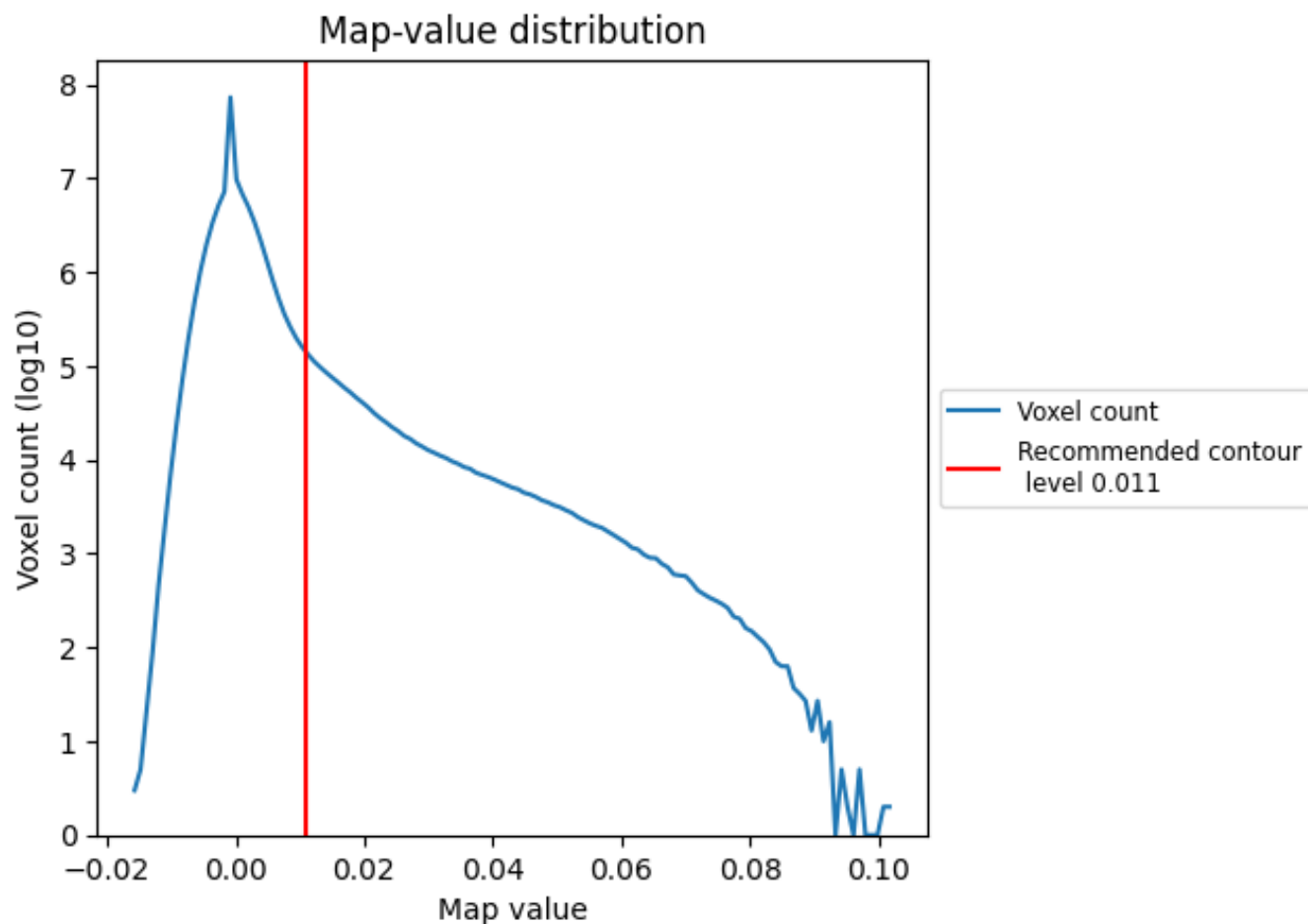
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

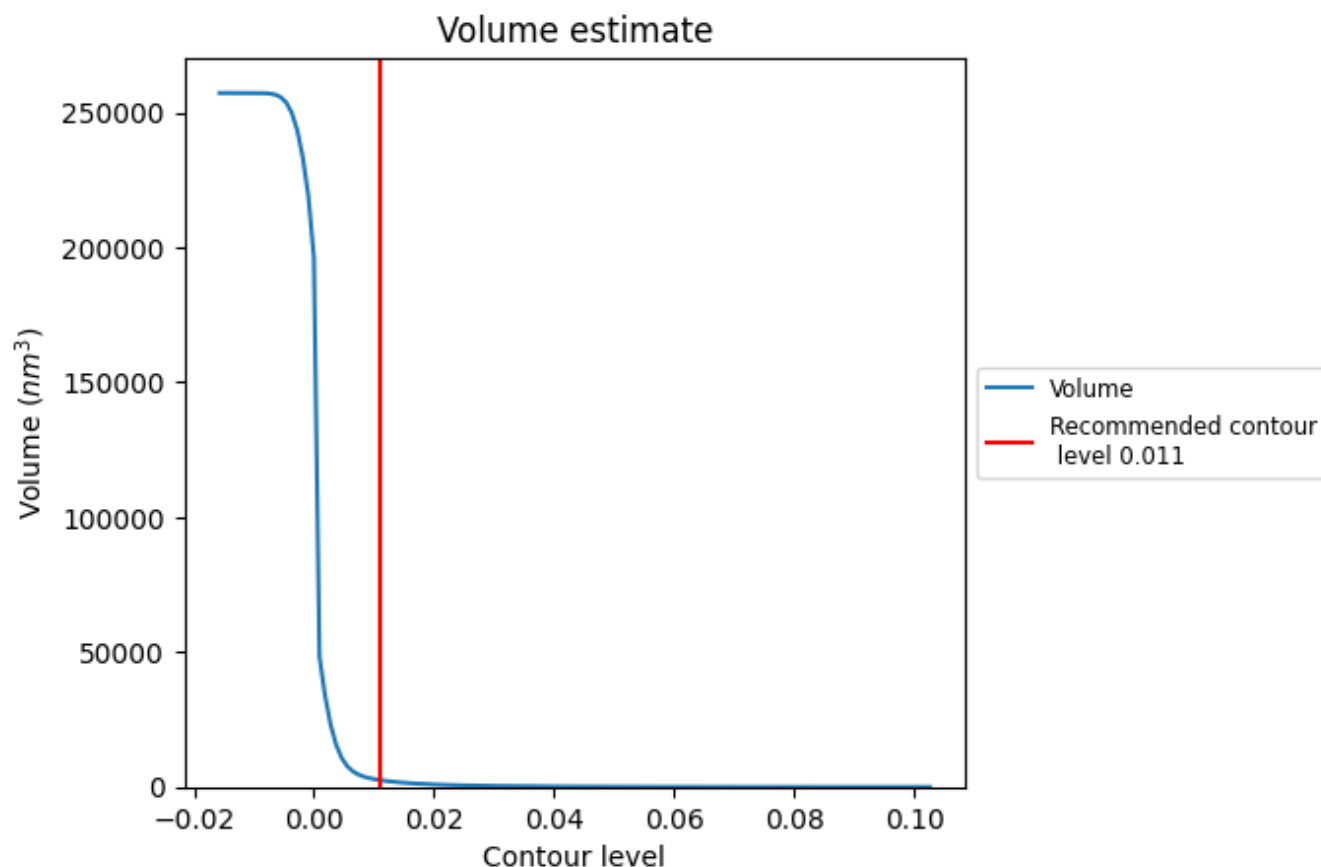
This section contains the results of statistical analysis of the map.

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.

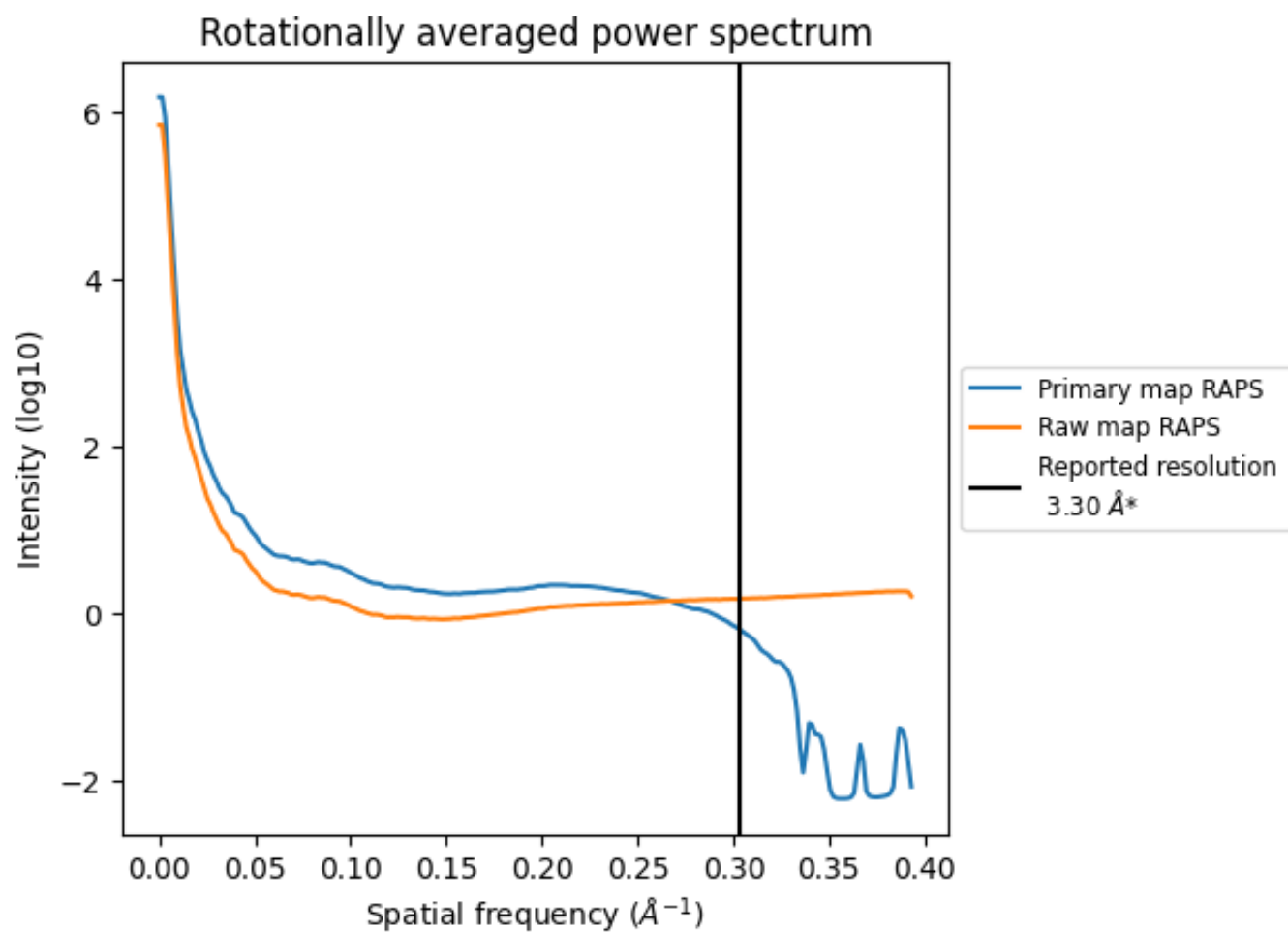
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2536 nm^3 ; this corresponds to an approximate mass of 2291 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 ⓘ

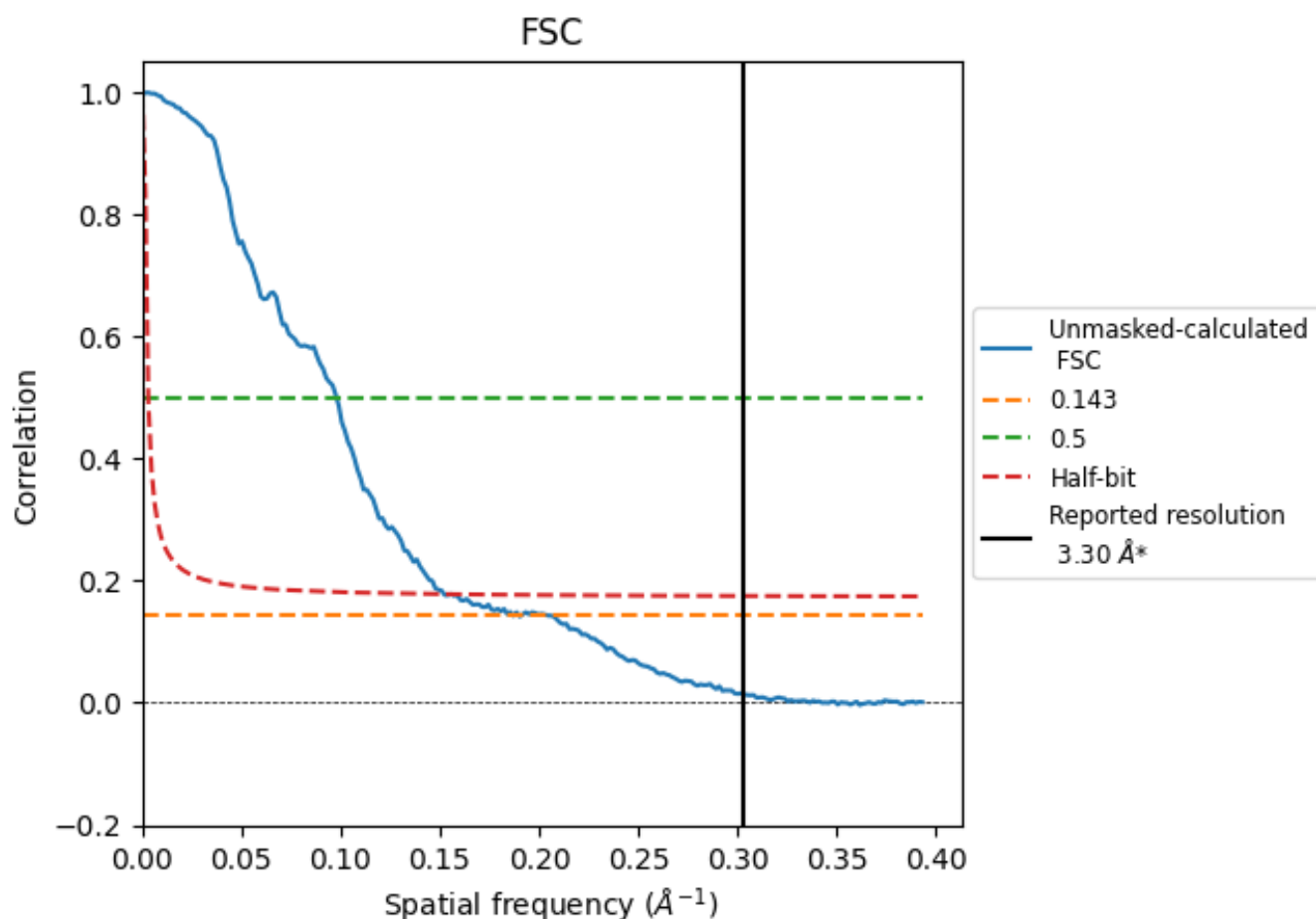


*Reported resolution corresponds to spatial frequency of 0.303 \AA^{-1}

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 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

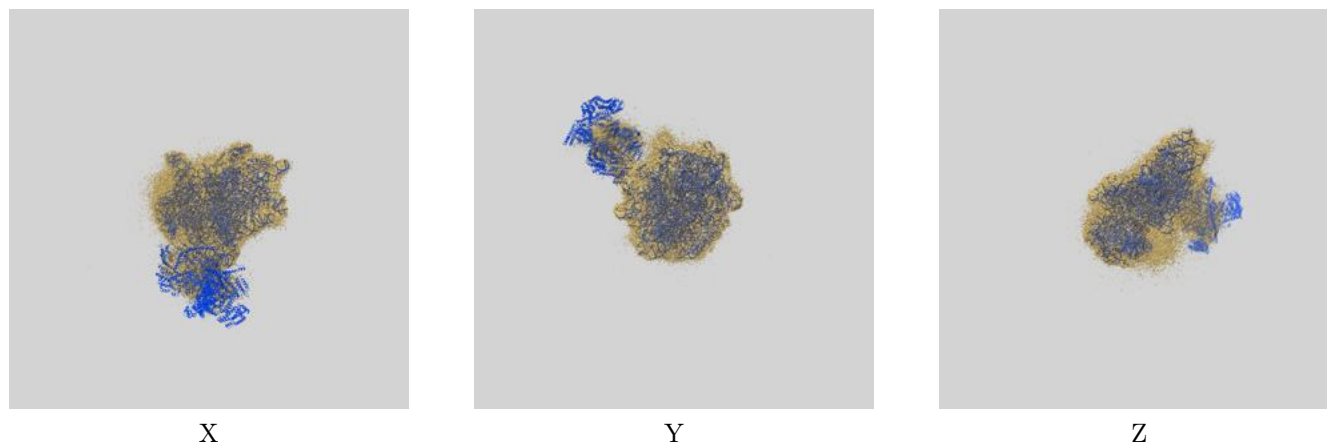
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.35	10.21	6.57

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.35 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

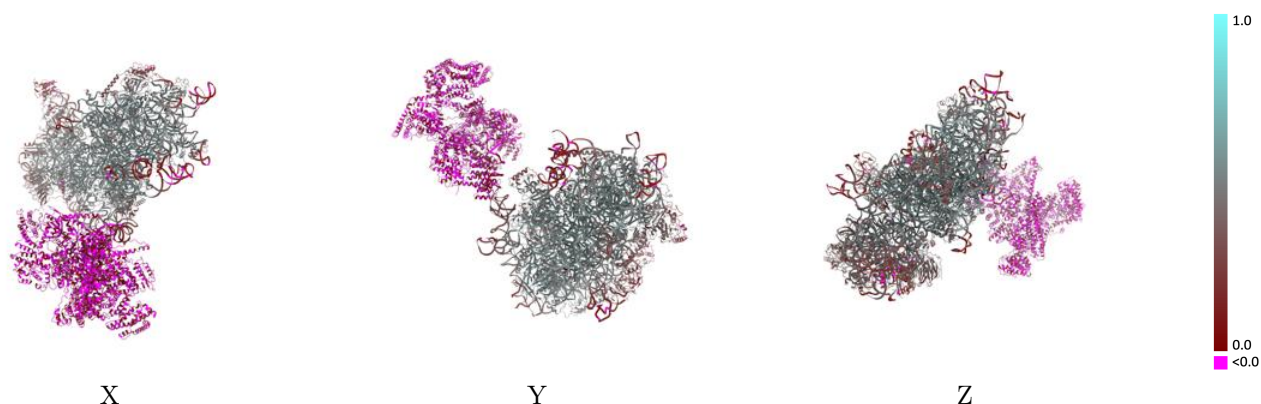
This section contains information regarding the fit between EMDB map EMD-62454 and PDB model 9KN6. Per-residue inclusion information can be found in section [3](#) on page [13](#).

9.1 Map-model overlay [i](#)



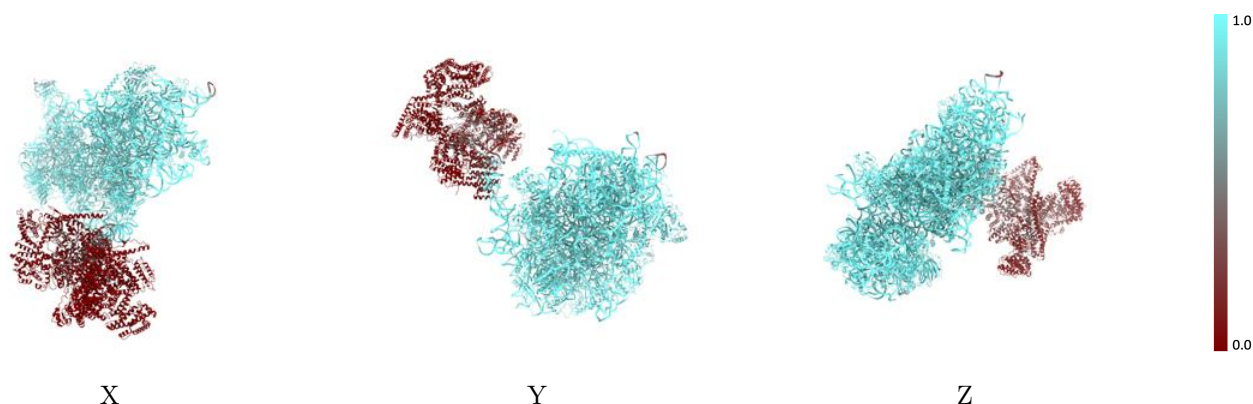
The images above show the 3D surface view of the map at the recommended contour level 0.011 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



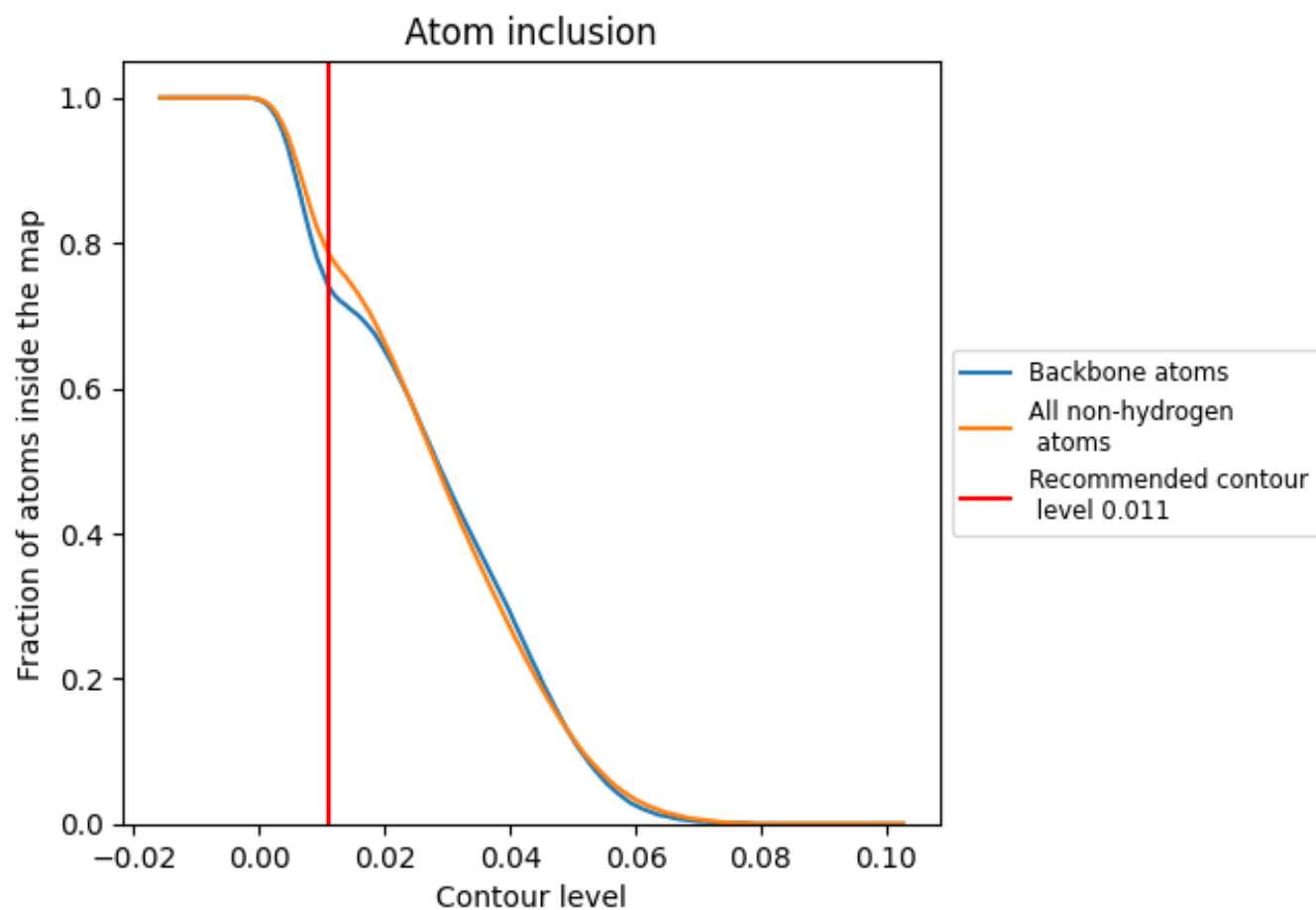
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.011).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 74% of all backbone atoms, 79% 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 (0.011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7870	 0.3500
1A	 0.9900	 0.4410
3a	 0.1570	 0.0020
3c	 0.0930	 -0.0030
3d	 0.0270	 -0.0250
3e	 0.0200	 -0.0010
3f	 0.1090	 0.0040
3h	 0.1570	 -0.0020
3k	 0.0070	 0.0190
3l	 0.0110	 0.0050
3m	 0.0220	 0.0060
5B	 0.9480	 0.3550
Ln	 1.0000	 0.5100
S2	 0.9930	 0.4690
SA	 0.9970	 0.5080
SB	 0.9890	 0.5170
SC	 0.9990	 0.5310
SD	 0.9990	 0.4530
SE	 0.9980	 0.5250
SF	 0.9970	 0.5110
SG	 0.9780	 0.4420
SH	 0.9830	 0.4420
SI	 0.9800	 0.4850
SJ	 0.9980	 0.5190
SK	 0.9920	 0.3710
SL	 0.9870	 0.5100
SN	 1.0000	 0.5160
SO	 0.9980	 0.5260
SP	 0.9650	 0.3710
SQ	 0.9980	 0.4680
SR	 0.9960	 0.4510
SS	 0.9860	 0.4350
ST	 0.9850	 0.4160
SU	 0.9910	 0.4250
SV	 0.9980	 0.5180



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Chain	Atom inclusion	Q-score
SW	 0.9990	 0.5430
SX	 1.0000	 0.5390
SY	 0.9970	 0.4970
SZ	 0.9860	 0.4530
Sa	 1.0000	 0.5310
Sb	 0.9980	 0.4990
Sc	 1.0000	 0.5130
Sd	 1.0000	 0.4750
Se	 1.0000	 0.4750
Sf	 0.8300	 0.1640
Sg	 0.9800	 0.3610
sh	 0.9020	 0.2190
zy	 0.9820	 0.2600
zz	 0.9210	 0.3100