



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 05:11 AM UTC

PDB ID : 6W2S / pdb_00006w2s
EMDB ID : EMD-21529
Title : Structure of the Cricket Paralysis Virus 5-UTR IRES (CrPV 5-UTR-IRES)
bound to the small ribosomal subunit in the open state (Class 1)
Authors : Neupane, R.; Pisareva, V.; Rodriguez, C.F.; Pisarev, A.; Fernandez, I.S.
Deposited on : 2020-03-08
Resolution : 3.47 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:

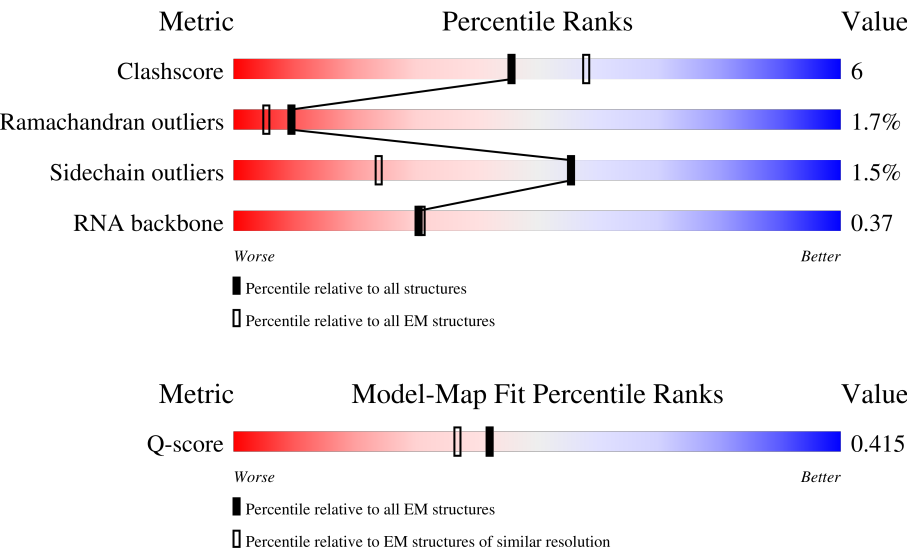
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.47 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.



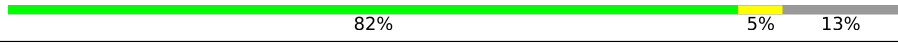
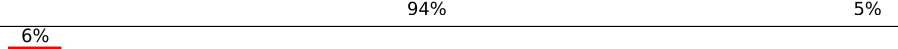
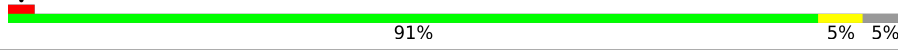
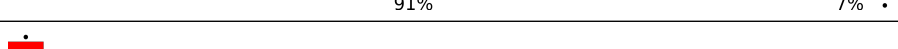
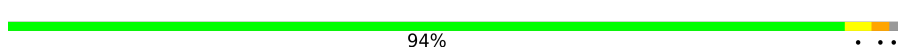
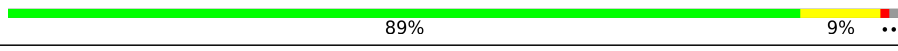
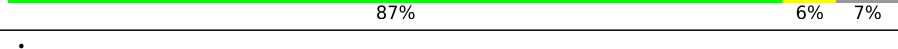
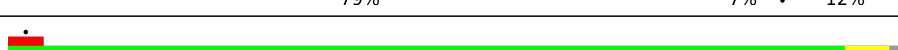
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13733 (2.97 - 3.97)

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	A	1697	
2	0	377	
3	B	295	

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Mol	Chain	Length	Quality of chain
4	C	264	
5	D	255	
6	F	263	
7	H	249	
8	I	194	
9	J	208	
10	K	194	
11	M	158	
12	O	151	
13	P	151	
14	W	83	
15	X	130	
16	Y	143	
17	Z	134	
18	b	115	
19	c	84	
20	f	133	
21	E	281	
22	G	204	
23	L	149	
24	N	132	
25	Q	145	
26	R	172	
27	S	135	
28	T	152	

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Mol	Chain	Length	Quality of chain
29	U	145	
30	V	119	
31	a	125	
32	d	69	
33	e	56	
34	g	156	
35	h	317	
36	1	1362	
37	2	913	
38	3	462	
39	4	364	
40	5	363	
41	6	218	
42	7	607	
43	8	374	

2 Entry composition

There are 45 unique types of molecules in this entry. The entry contains 106911 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1697	Total	C	N	O	P	0	0
			36229	16171	6507	11855	1696		

- Molecule 2 is a RNA chain called CrPV 5'-UTR IRES.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	339	Total	C	N	O	P	0	0
			7205	3222	1255	2389	339		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
0	569	U	C	conflict	GB 8895506
0	570	U	C	conflict	GB 8895506
0	571	U	A	conflict	GB 8895506
0	572	U	C	conflict	GB 8895506
0	574	U	C	conflict	GB 8895506
0	575	U	G	conflict	GB 8895506
0	729	G	-	expression tag	GB 8895506
0	730	G	-	expression tag	GB 8895506
0	731	A	-	expression tag	GB 8895506
0	732	U	-	expression tag	GB 8895506
0	733	C	-	expression tag	GB 8895506

- Molecule 3 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	217	Total	C	N	O	S	0	0
			1706	1084	296	318	8		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	114	THR	ALA	conflict	UNP G1TWL4
B	135	THR	MET	conflict	UNP G1TWL4
B	155	ARG	HIS	conflict	UNP G1TWL4
B	162	PRO	LEU	conflict	UNP G1TWL4

- Molecule 4 is a protein called eS1.

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

- Molecule 5 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	221	Total	C	N	O	S	0	0
			1717	1113	296	299	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	57	ASN	ASP	conflict	UNP G1SWM1
D	97	PHE	CYS	conflict	UNP G1SWM1
D	181	PRO	LEU	conflict	UNP G1SWM1
D	191	VAL	-	insertion	UNP G1SWM1

- Molecule 6 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	262	Total	C	N	O	S	0	0
			2072	1323	384	357	8		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	25	GLY	SER	conflict	UNP G1TK17
F	156	VAL	MET	conflict	UNP G1TK17

- Molecule 7 is a protein called eS6.

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

- Molecule 8 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 9 is a protein called eS8.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	47	ARG	GLY	conflict	UNP G1TJW1

- Molecule 10 is a protein called uS4.

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

- Molecule 11 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 12 is a protein called uS15.

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

- Molecule 13 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 14 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	W	83	Total	C	N	O	S	0	0
			634	390	116	123	5		

- Molecule 15 is a protein called uS8.

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

- Molecule 16 is a protein called uS12.

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

- Molecule 17 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Z	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 18 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	b	101	Total	C	N	O	S	0	0
			816	509	170	132	5		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	28	ARG	CYS	conflict	UNP G1TFE8

- Molecule 19 is a protein called eS27.

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

- Molecule 20 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	f	57	Total	C	N	O	S	0	0
			457	282	101	73	1		

- Molecule 21 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	E	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 22 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	G	191	Total	C	N	O	S	0	0
			1499	937	283	272	7		

- Molecule 23 is a protein called eS10.

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

- Molecule 24 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 25 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Q	115	Total	C	N	O	S	0	0
			956	610	176	163	7		

- Molecule 26 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 27 is a protein called eS17.

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

- Molecule 28 is a protein called uS13.

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

- Molecule 29 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 30 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 31 is a protein called eS25.

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

- Molecule 32 is a protein called eS28.

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

- Molecule 33 is a protein called eS29.

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

- Molecule 34 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 35 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	312	Total	C	N	O	S	0	0
			2429	1531	423	463	12		

- Molecule 36 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	1	534	Total	C	N	O	S	0	0
			4377	2770	778	808	21		

- Molecule 37 is a protein called Eukaryotic translation initiation factor 3 subunit C.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	2	547	Total	C	N	O	S	0	0
			4446	2791	785	837	33		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	671	GLU	VAL	conflict	UNP G1U971

- Molecule 38 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	3	419	Total	C	N	O	S	0	0
			3465	2220	586	639	20		

- Molecule 39 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	4	272	Total	C	N	O	S	0	0
			2111	1330	359	410	12		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	5	324	Total	C	N	O	S	0	0
			2624	1654	452	503	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
41	6	215	Total	C	N	O	S	0	0
			1737	1109	285	330	13		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
42	7	372	Total	C	N	O	S	0	0
			3109	2010	519	563	17		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
43	8	365	Total	C	N	O	S	0	0
			2918	1850	493	558	17		

- Molecule 44 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
44	A	1	Total	Mg	0
			1	1	

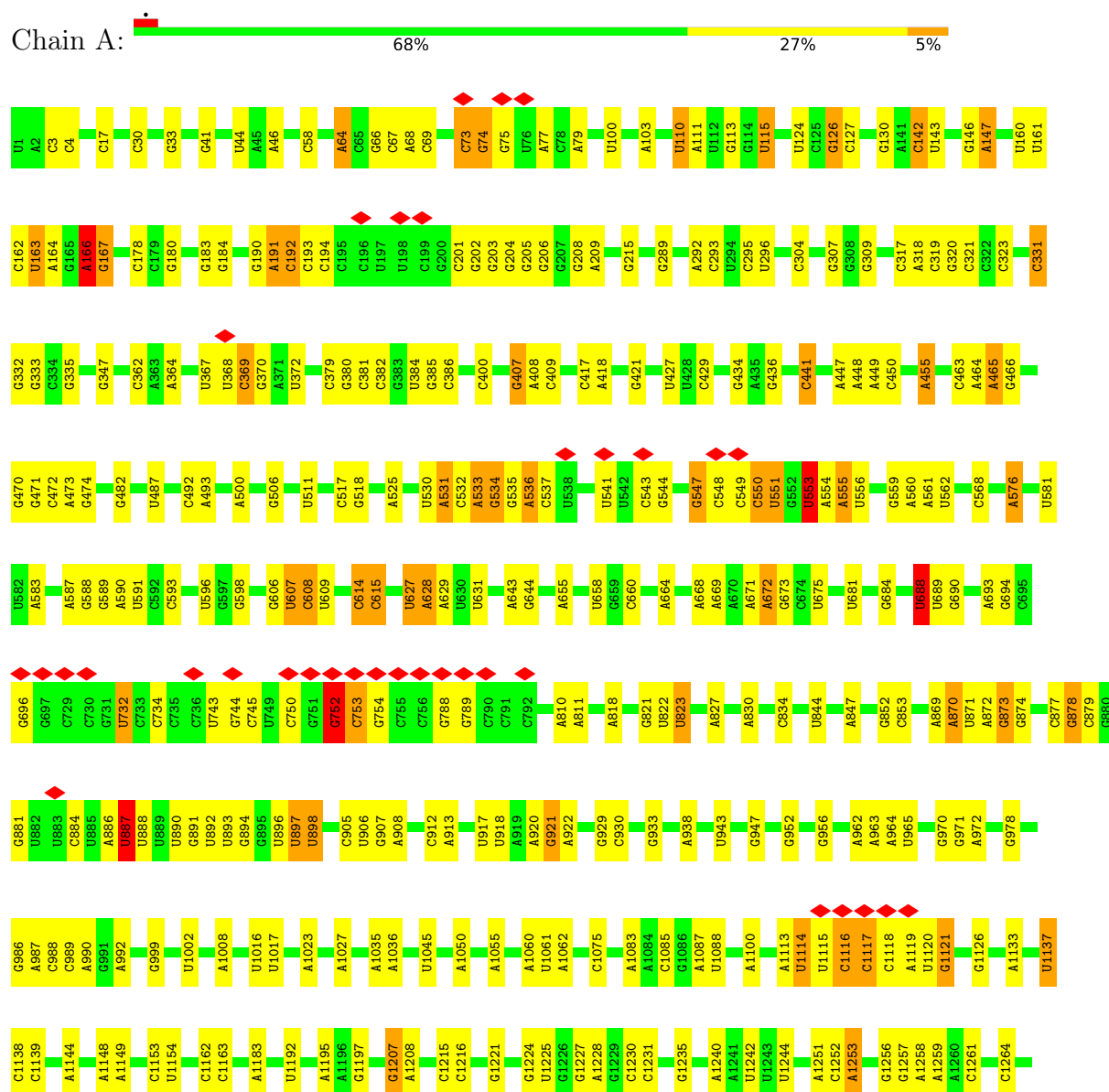
- Molecule 45 is ZINC ION (CCD ID: ZN) (formula: Zn).

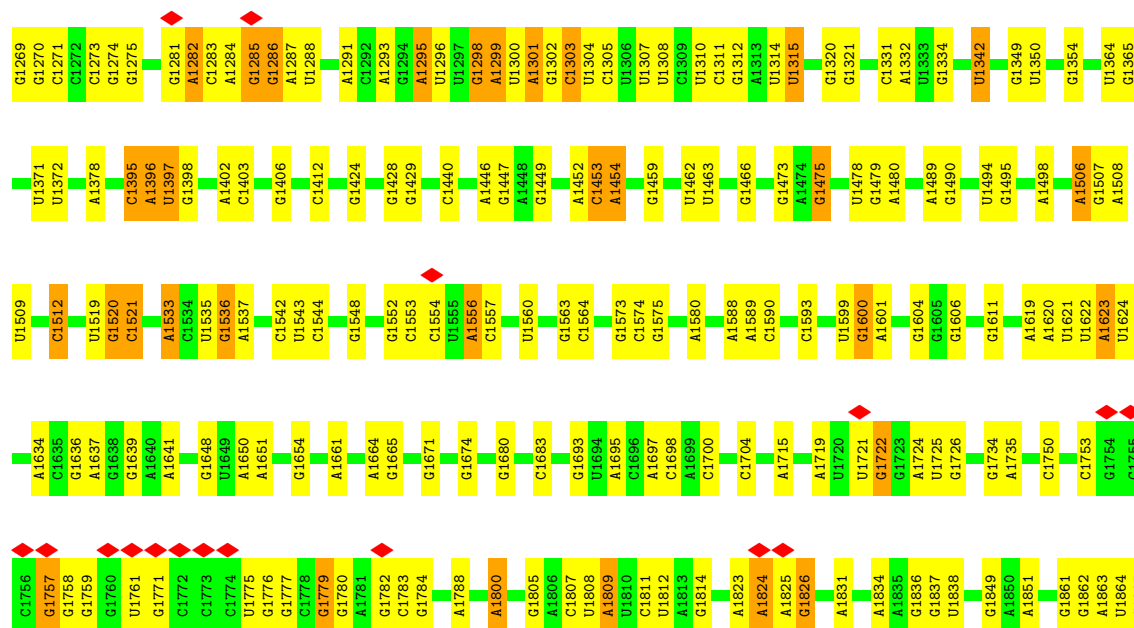
Mol	Chain	Residues	Atoms		AltConf
45	b	1	Total	Zn	0
			1	1	

3 Residue-property plots

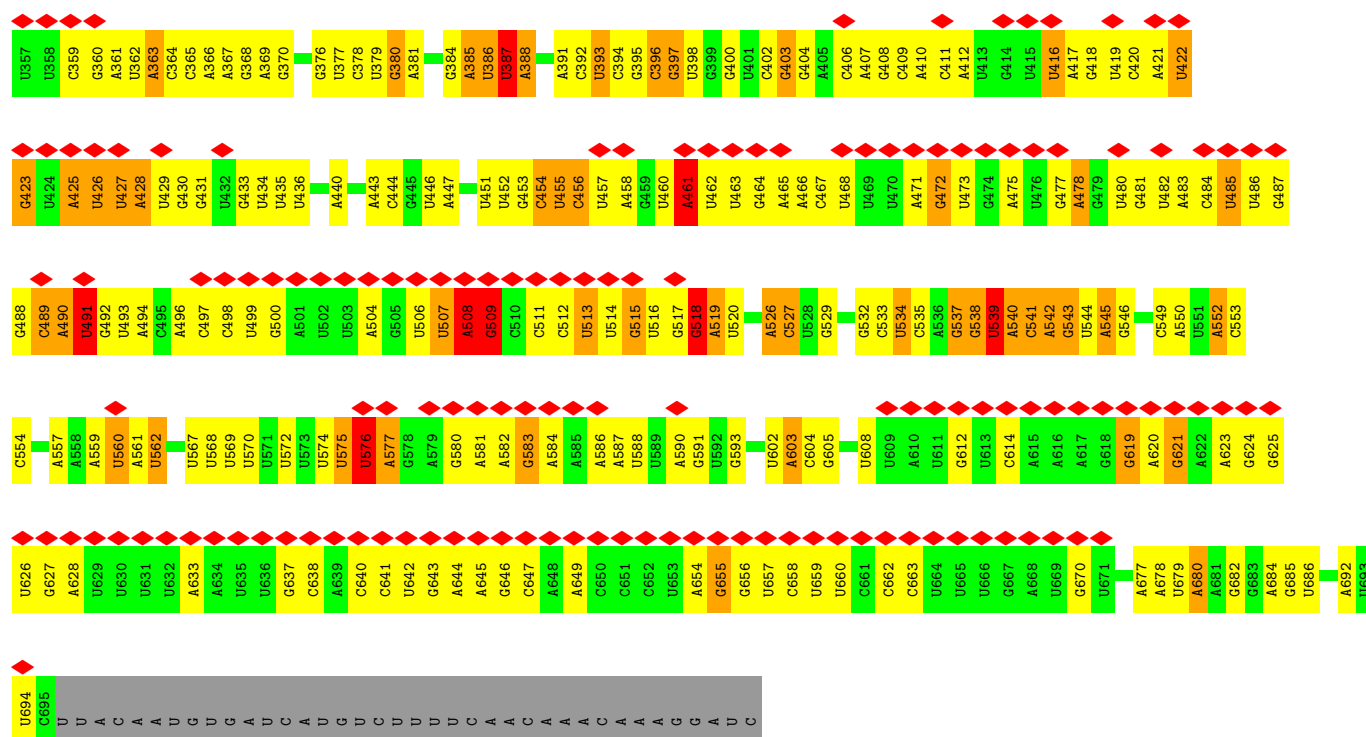
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 18S rRNA



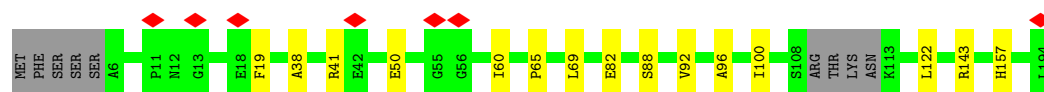


• Molecule 2: CrPV 5'-UTR IRES

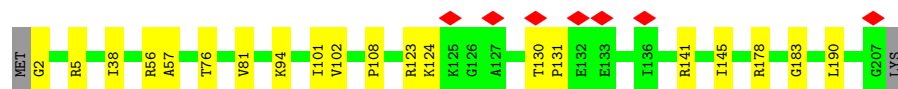
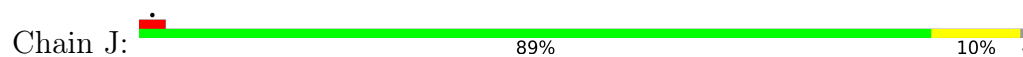


• Molecule 3: uS2

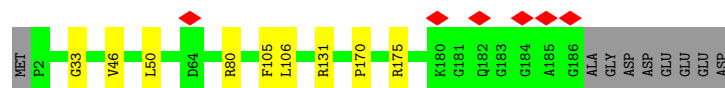




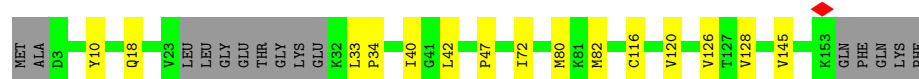
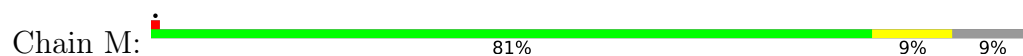
- Molecule 9: eS8



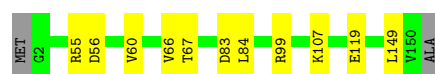
- Molecule 10: uS4



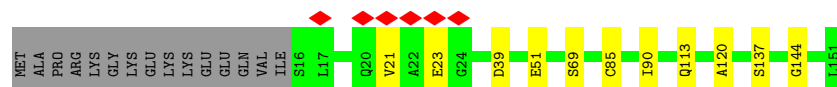
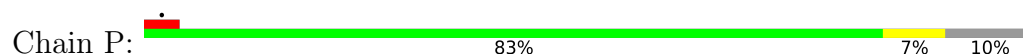
- Molecule 11: uS17



- Molecule 12: uS15



- Molecule 13: uS11



- Molecule 14: eS21

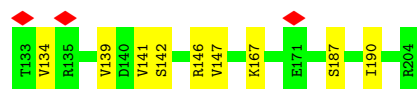
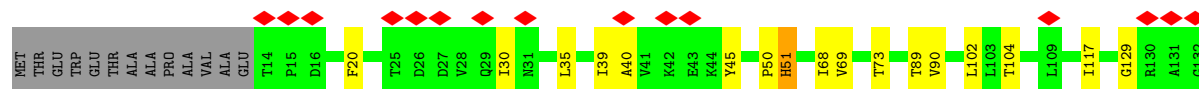
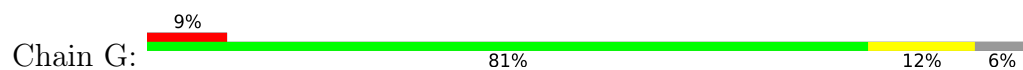


- Molecule 15: uS8

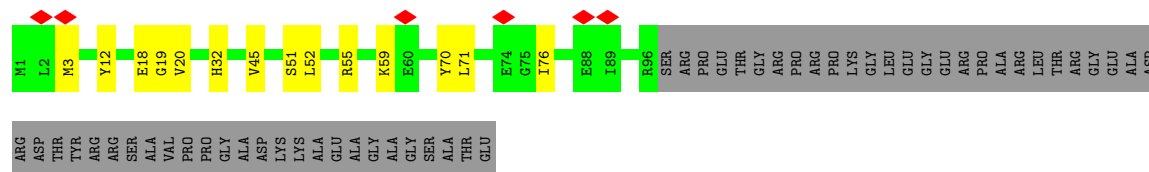




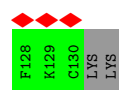
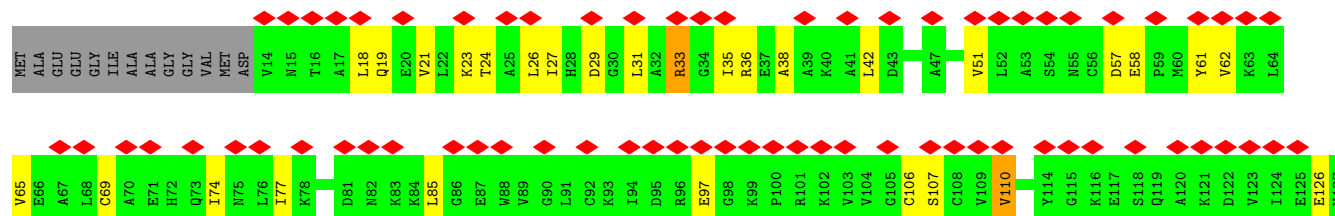
• Molecule 22: uS7



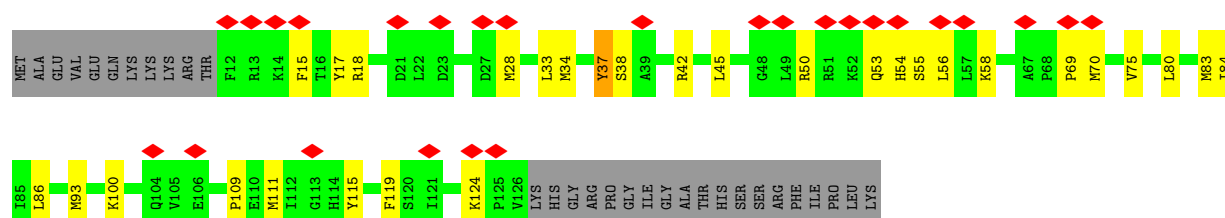
• Molecule 23: eS10



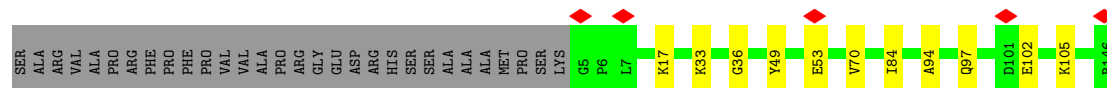
• Molecule 24: eS12



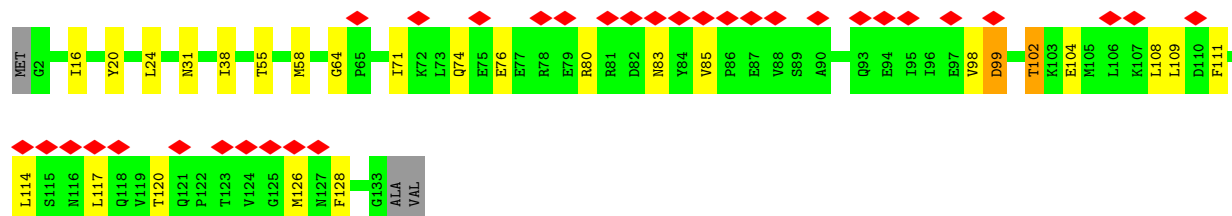
• Molecule 25: uS19



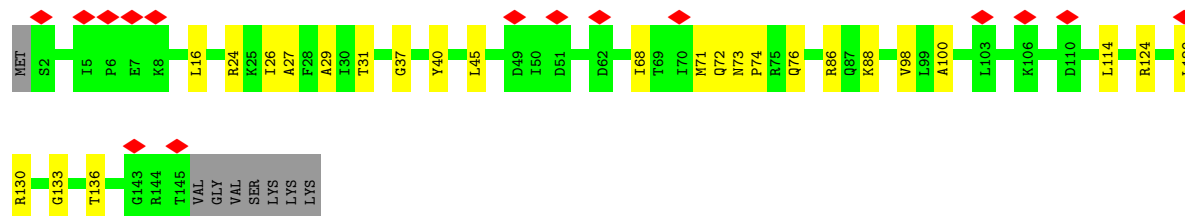
Chain R:



Chain S: 24% 79% 18%



Chain T: 10% 78% 16% 5%



Chain U:



Chain V: 5% 80% 16%

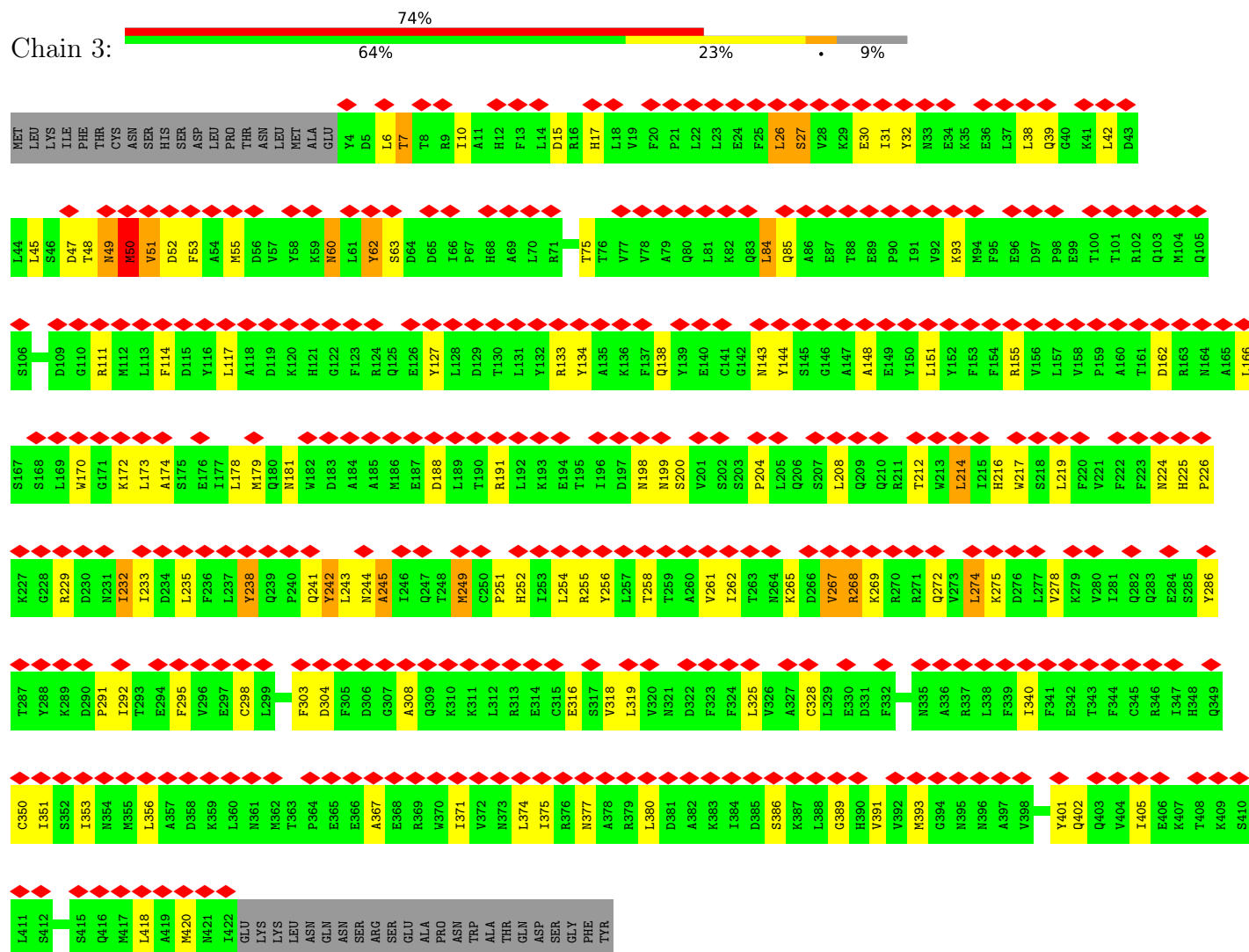


Chain a:

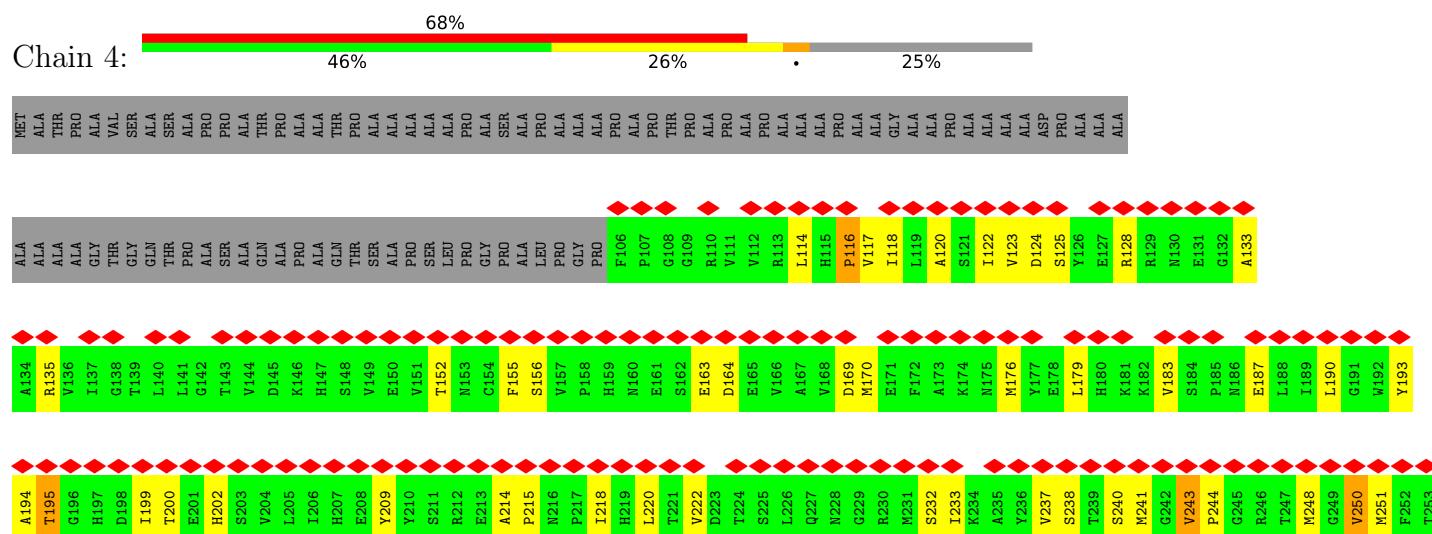
Chain 1:

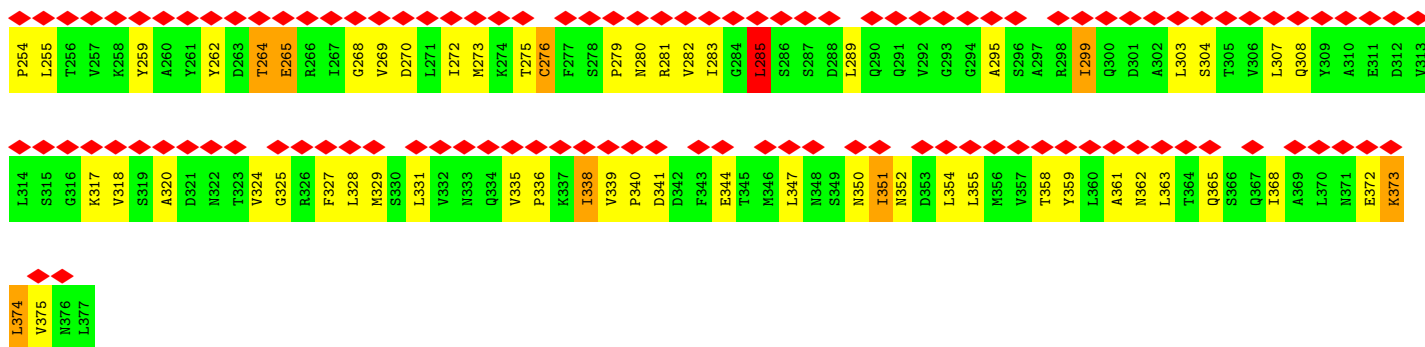


Chain 3:

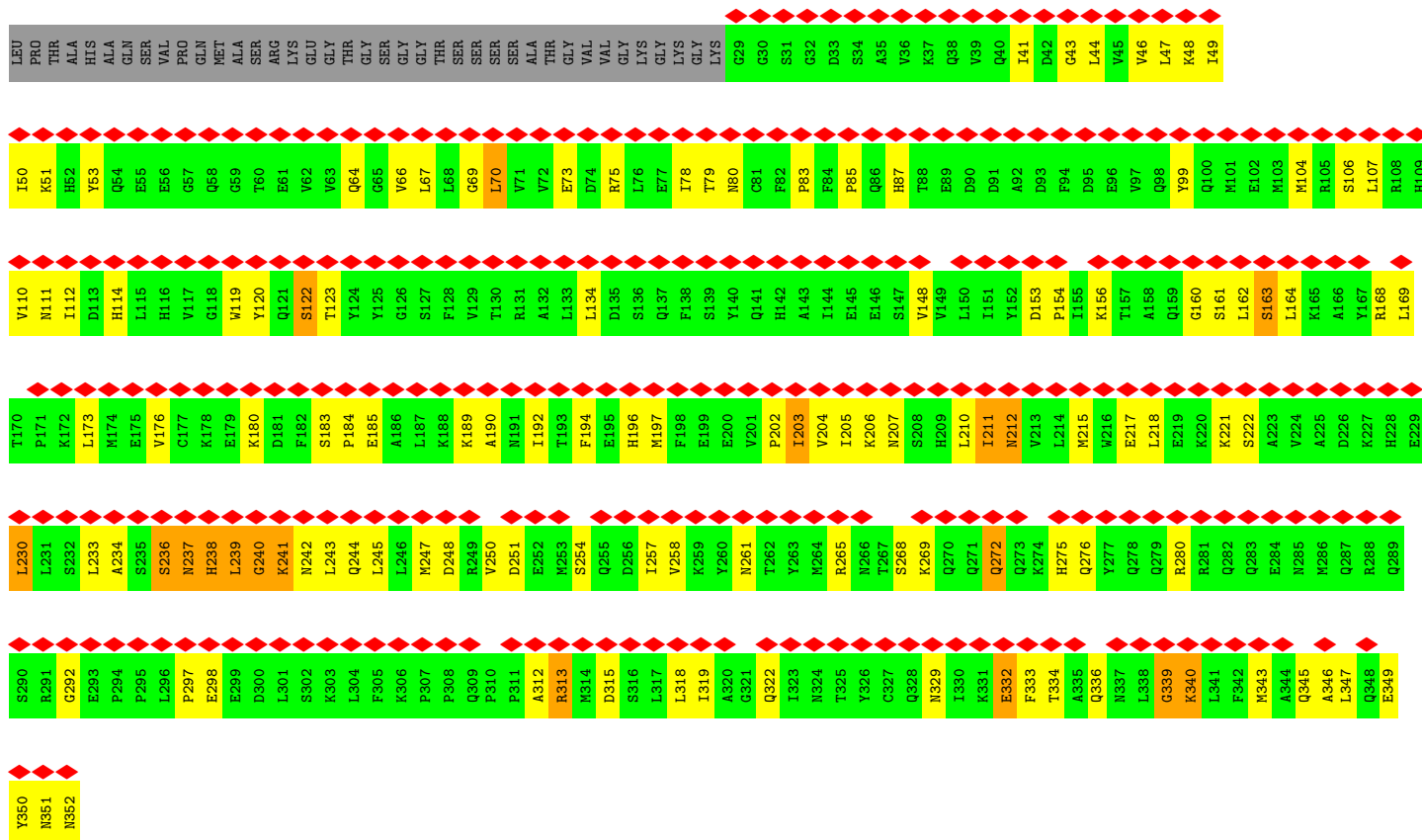
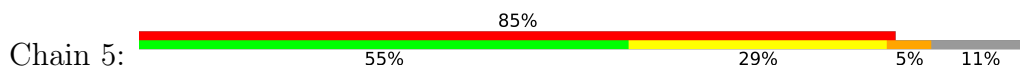


Chain 4:

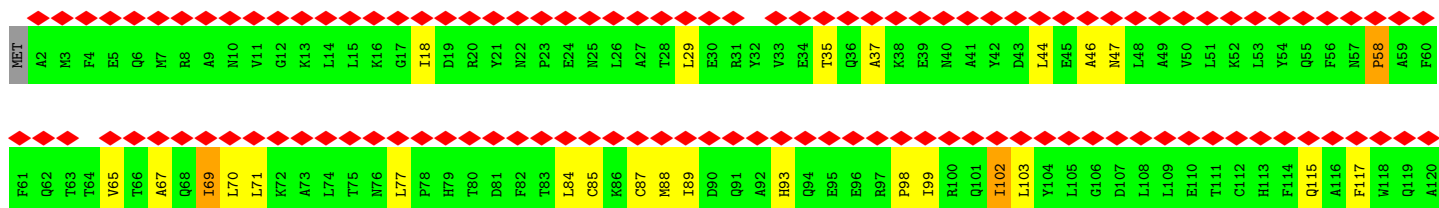
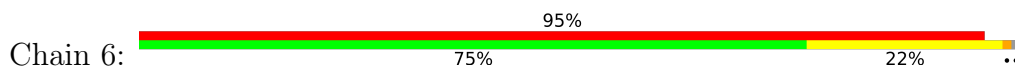




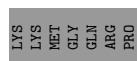
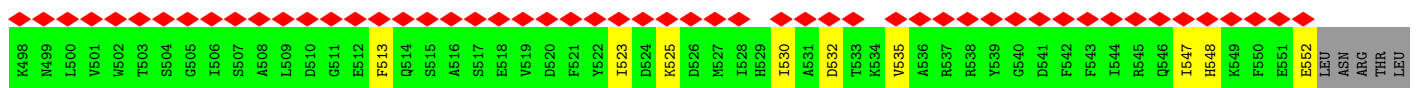
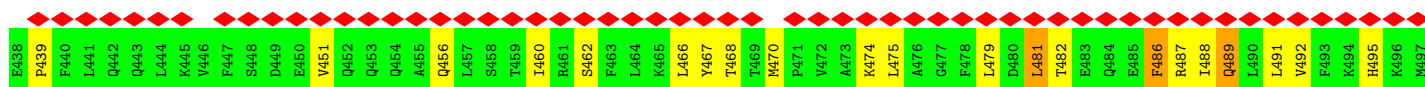
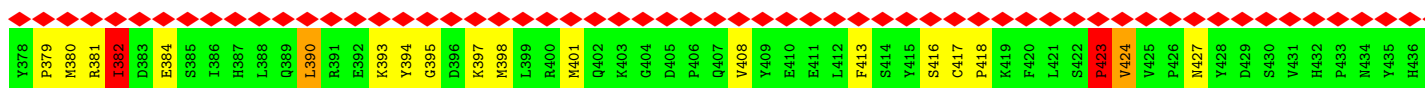
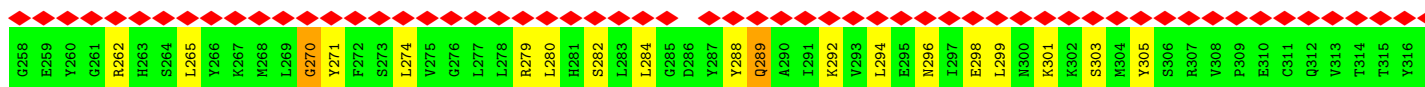
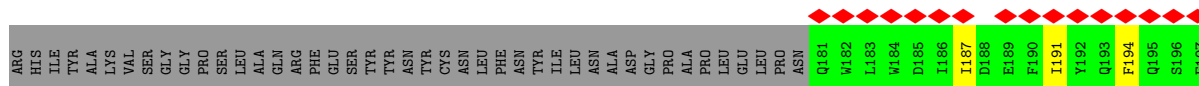
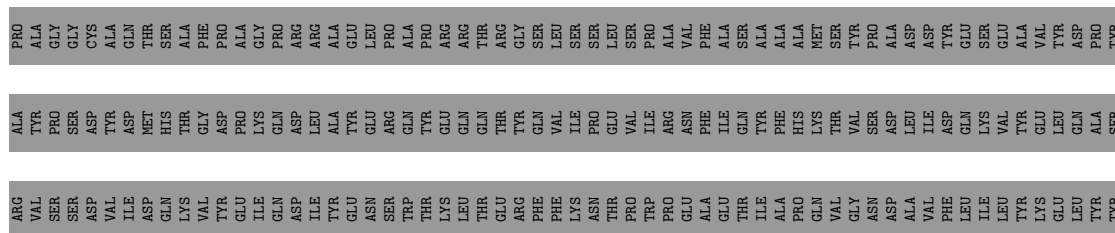
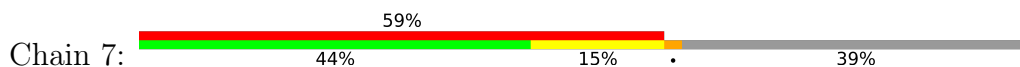
• Molecule 40: Eukaryotic translation initiation factor 3 subunit H



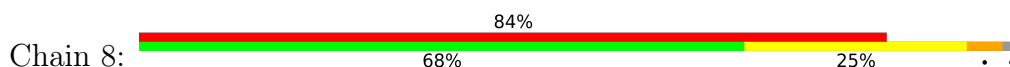
• Molecule 41: Eukaryotic translation initiation factor 3 subunit K



- Molecule 42: Eukaryotic translation initiation factor 3 subunit L



- Molecule 43: Eukaryotic translation initiation factor 3 subunit M





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	36100	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	56.90	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.154	Depositor
Minimum map value	-0.093	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.018	Depositor
Map size (Å)	424.2, 424.2, 424.2	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0605, 1.0605, 1.0605	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	A	0.37	0/40505	0.70	15/63112 (0.0%)
2	O	0.41	2/8053 (0.0%)	0.78	14/12543 (0.1%)
3	B	1.03	0/1743	1.48	2/2370 (0.1%)
4	C	1.06	0/1756	1.48	0/2350
5	D	1.05	0/1754	1.46	0/2370
6	F	1.05	0/2114	1.39	0/2843
7	H	1.05	0/1946	1.51	0/2590
8	I	1.06	0/1510	1.47	2/2022 (0.1%)
9	J	1.05	0/1715	1.45	0/2287
10	K	1.03	0/1550	1.55	0/2069
11	M	1.03	0/1195	1.31	0/1597
12	O	1.03	0/1226	1.57	0/1649
13	P	1.06	0/1029	1.46	1/1380 (0.1%)
14	W	1.08	0/641	1.55	0/858
15	X	1.04	0/1051	1.47	0/1406
16	Y	1.06	0/1116	1.45	0/1490
17	Z	1.04	0/1028	1.44	0/1366
18	b	1.05	0/830	1.43	0/1112
19	c	1.05	0/665	1.39	0/891
20	f	1.04	0/462	1.53	0/607
21	E	1.06	0/1796	1.50	0/2417
22	G	1.07	0/1521	1.61	0/2046
23	L	1.01	0/834	1.46	0/1125
24	N	1.07	0/918	1.52	2/1233 (0.2%)
25	Q	1.04	0/974	1.43	4/1301 (0.3%)
26	R	1.07	0/1146	1.49	0/1534
27	S	1.06	0/1082	1.55	0/1452
28	T	1.05	0/1208	1.52	0/1618
29	U	1.05	0/1115	1.56	0/1493
30	V	1.07	0/805	1.41	0/1081
31	a	1.08	0/604	1.53	0/810
32	d	1.09	0/490	1.35	1/656 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	1.02	0/470	1.34	0/623
34	g	1.06	0/567	1.38	0/753
35	h	1.08	0/2486	1.36	2/3384 (0.1%)
36	1	1.05	0/4460	1.54	0/6034
37	2	1.07	0/4522	1.52	4/6102 (0.1%)
38	3	1.06	0/3538	1.55	10/4786 (0.2%)
39	4	1.09	2/2149 (0.1%)	1.59	3/2920 (0.1%)
40	5	1.03	0/2674	1.53	5/3606 (0.1%)
41	6	1.13	3/1772 (0.2%)	1.53	1/2396 (0.0%)
42	7	1.10	6/3185 (0.2%)	1.55	7/4296 (0.2%)
43	8	1.10	1/2963 (0.0%)	1.60	2/3998 (0.1%)
All	All	0.84	14/113168 (0.0%)	1.20	75/162576 (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
16	Y	0	1
18	b	0	1
22	G	0	1
25	Q	0	1
27	S	0	1
36	1	0	4
37	2	0	4
38	3	0	6
39	4	0	3
40	5	0	6
42	7	0	3
43	8	0	4
All	All	0	35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	6	69	ILE	CG1-CD1	-13.66	0.98	1.51
42	7	187	ILE	CG1-CD1	-11.74	1.05	1.51
39	4	351	ILE	CG1-CD1	10.68	1.93	1.51
42	7	382	ILE	CG1-CD1	-9.25	1.15	1.51
42	7	240	ILE	CG1-CD1	-6.64	1.25	1.51

The worst 5 of 75 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
42	7	382	ILE	CB-CG1-CD1	12.87	140.82	113.80
42	7	240	ILE	CB-CG1-CD1	10.79	136.47	113.80
1	A	688	U	C2'-C3'-O3'	10.01	124.51	109.50
42	7	187	ILE	CB-CG1-CD1	9.74	134.25	113.80
2	0	387	U	C4'-C3'-O3'	7.99	121.39	109.40

There are no chirality outliers.

5 of 35 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
22	G	129	GLY	Peptide
25	Q	54	HIS	Peptide
27	S	64	GLY	Peptide
16	Y	61	GLN	Peptide
18	b	45	VAL	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	A	36229	0	18304	160	0
2	0	7205	0	3626	56	0
3	B	1706	0	1698	21	0
4	C	1729	0	1803	6	0
5	D	1717	0	1812	17	0
6	F	2072	0	2175	10	0
7	H	1923	0	2089	13	0
8	I	1488	0	1582	7	0
9	J	1686	0	1772	12	0
10	K	1525	0	1640	5	0
11	M	1175	0	1249	8	0
12	O	1202	0	1289	5	0
13	P	1016	0	1039	8	0
14	W	634	0	629	5	0
15	X	1034	0	1080	4	0
16	Y	1098	0	1167	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	Z	1011	0	1083	5	0
18	b	816	0	867	10	0
19	c	651	0	672	1	0
20	f	457	0	502	2	0
21	E	1768	0	1866	13	0
22	G	1499	0	1540	12	0
23	L	810	0	836	7	0
24	N	908	0	939	14	0
25	Q	956	0	1002	15	0
26	R	1128	0	1195	6	0
27	S	1068	0	1121	17	0
28	T	1190	0	1249	17	0
29	U	1097	0	1130	5	0
30	V	795	0	862	3	0
31	a	598	0	656	3	0
32	d	488	0	514	5	0
33	e	459	0	452	3	0
34	g	555	0	567	4	0
35	h	2429	0	2386	32	0
36	1	4377	0	4433	153	0
37	2	4446	0	4444	126	0
38	3	3465	0	3446	73	0
39	4	2111	0	2105	178	0
40	5	2624	0	2591	261	0
41	6	1737	0	1706	34	0
42	7	3109	0	3084	70	0
43	8	2918	0	2950	68	0
44	A	1	0	0	0	0
45	b	1	0	0	0	0
All	All	106911	0	87152	1184	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 1184 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)
5:D:127:PHE:CD1	5:D:141:LEU:HD21	1.26	1.61
5:D:127:PHE:CD1	5:D:141:LEU:CD2	1.95	1.50
36:1:523:LEU:HA	36:1:526:MET:SD	1.71	1.30
37:2:710:ILE:O	37:2:714:PHE:HD2	1.09	1.29

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:1:526:MET:HG2	40:5:236:SER:O	1.26	1.28

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	
3	B	215/295 (73%)	201 (94%)	13 (6%)	1 (0%)	24	58
4	C	211/264 (80%)	189 (90%)	21 (10%)	1 (0%)	24	58
5	D	219/255 (86%)	201 (92%)	17 (8%)	1 (0%)	24	58
6	F	260/263 (99%)	248 (95%)	12 (5%)	0	100	100
7	H	235/249 (94%)	216 (92%)	18 (8%)	1 (0%)	30	62
8	I	181/194 (93%)	160 (88%)	20 (11%)	1 (1%)	21	53
9	J	204/208 (98%)	188 (92%)	14 (7%)	2 (1%)	12	44
10	K	183/194 (94%)	170 (93%)	13 (7%)	0	100	100
11	M	139/158 (88%)	130 (94%)	9 (6%)	0	100	100
12	O	147/151 (97%)	137 (93%)	9 (6%)	1 (1%)	18	51
13	P	134/151 (89%)	120 (90%)	14 (10%)	0	100	100
14	W	81/83 (98%)	79 (98%)	2 (2%)	0	100	100
15	X	127/130 (98%)	119 (94%)	7 (6%)	1 (1%)	16	49
16	Y	139/143 (97%)	128 (92%)	7 (5%)	4 (3%)	3	26
17	Z	122/134 (91%)	115 (94%)	7 (6%)	0	100	100
18	b	99/115 (86%)	87 (88%)	10 (10%)	2 (2%)	6	32
19	c	81/84 (96%)	75 (93%)	5 (6%)	1 (1%)	10	41
20	f	55/133 (41%)	51 (93%)	4 (7%)	0	100	100
21	E	226/281 (80%)	209 (92%)	17 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	G	189/204 (93%)	165 (87%)	21 (11%)	3 (2%)	7	36
23	L	94/149 (63%)	83 (88%)	10 (11%)	1 (1%)	11	42
24	N	115/132 (87%)	96 (84%)	16 (14%)	3 (3%)	4	27
25	Q	113/145 (78%)	92 (81%)	17 (15%)	4 (4%)	3	22
26	R	140/172 (81%)	130 (93%)	9 (6%)	1 (1%)	18	51
27	S	130/135 (96%)	111 (85%)	17 (13%)	2 (2%)	8	37
28	T	142/152 (93%)	132 (93%)	8 (6%)	2 (1%)	9	38
29	U	139/145 (96%)	126 (91%)	12 (9%)	1 (1%)	18	51
30	V	98/119 (82%)	92 (94%)	6 (6%)	0	100	100
31	a	73/125 (58%)	67 (92%)	6 (8%)	0	100	100
32	d	60/69 (87%)	59 (98%)	1 (2%)	0	100	100
33	e	53/56 (95%)	49 (92%)	3 (6%)	1 (2%)	6	32
34	g	66/156 (42%)	54 (82%)	9 (14%)	3 (4%)	2	17
35	h	310/317 (98%)	274 (88%)	34 (11%)	2 (1%)	21	53
36	1	532/1362 (39%)	430 (81%)	85 (16%)	17 (3%)	3	24
37	2	543/913 (60%)	428 (79%)	105 (19%)	10 (2%)	6	33
38	3	417/462 (90%)	333 (80%)	67 (16%)	17 (4%)	2	19
39	4	270/364 (74%)	217 (80%)	45 (17%)	8 (3%)	3	25
40	5	320/363 (88%)	255 (80%)	54 (17%)	11 (3%)	3	23
41	6	213/218 (98%)	179 (84%)	31 (15%)	3 (1%)	9	38
42	7	370/607 (61%)	301 (81%)	57 (15%)	12 (3%)	3	24
43	8	363/374 (97%)	290 (80%)	61 (17%)	12 (3%)	3	23
All	All	7808/10224 (76%)	6786 (87%)	893 (11%)	129 (2%)	9	34

5 of 129 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	J	94	LYS
15	X	28	ARG
16	Y	61	GLN
22	G	134	VAL
24	N	57	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	
3	B	180/246 (73%)	177 (98%)	3 (2%)	53	69
4	C	194/231 (84%)	191 (98%)	3 (2%)	57	71
5	D	186/205 (91%)	184 (99%)	2 (1%)	65	74
6	F	223/224 (100%)	222 (100%)	1 (0%)	84	81
7	H	207/218 (95%)	203 (98%)	4 (2%)	50	67
8	I	165/174 (95%)	164 (99%)	1 (1%)	78	79
9	J	178/180 (99%)	177 (99%)	1 (1%)	78	79
10	K	161/168 (96%)	160 (99%)	1 (1%)	78	79
11	M	130/142 (92%)	129 (99%)	1 (1%)	73	76
12	O	130/131 (99%)	129 (99%)	1 (1%)	73	76
13	P	106/119 (89%)	106 (100%)	0	100	100
14	W	68/68 (100%)	67 (98%)	1 (2%)	57	71
15	X	112/113 (99%)	109 (97%)	3 (3%)	39	62
16	Y	113/114 (99%)	113 (100%)	0	100	100
17	Z	107/115 (93%)	106 (99%)	1 (1%)	70	75
18	b	89/99 (90%)	89 (100%)	0	100	100
19	c	75/76 (99%)	74 (99%)	1 (1%)	61	72
20	f	47/106 (44%)	47 (100%)	0	100	100
21	E	190/232 (82%)	189 (100%)	1 (0%)	81	80
22	G	158/170 (93%)	156 (99%)	2 (1%)	61	72
23	L	87/125 (70%)	86 (99%)	1 (1%)	65	74
24	N	99/108 (92%)	94 (95%)	5 (5%)	21	48
25	Q	105/130 (81%)	103 (98%)	2 (2%)	50	67
26	R	117/140 (84%)	117 (100%)	0	100	100
27	S	119/121 (98%)	118 (99%)	1 (1%)	73	76
28	T	125/132 (95%)	124 (99%)	1 (1%)	73	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	U	111/116 (96%)	110 (99%)	1 (1%)	70	75
30	V	92/107 (86%)	91 (99%)	1 (1%)	65	74
31	a	66/103 (64%)	66 (100%)	0	100	100
32	d	55/62 (89%)	54 (98%)	1 (2%)	51	69
33	e	48/49 (98%)	48 (100%)	0	100	100
34	g	61/140 (44%)	60 (98%)	1 (2%)	55	70
35	h	271/275 (98%)	265 (98%)	6 (2%)	45	65
36	1	490/1245 (39%)	480 (98%)	10 (2%)	48	66
37	2	494/812 (61%)	481 (97%)	13 (3%)	40	63
38	3	384/423 (91%)	375 (98%)	9 (2%)	44	64
39	4	239/282 (85%)	232 (97%)	7 (3%)	37	61
40	5	293/320 (92%)	287 (98%)	6 (2%)	48	66
41	6	190/193 (98%)	188 (99%)	2 (1%)	65	74
42	7	342/544 (63%)	337 (98%)	5 (2%)	57	71
43	8	327/335 (98%)	320 (98%)	7 (2%)	47	66
All	All	6934/8893 (78%)	6828 (98%)	106 (2%)	55	71

5 of 106 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	2	346	ASP
38	3	75	THR
43	8	75	GLU
37	2	462	THR
37	2	674	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 152 such sidechains are listed below:

Mol	Chain	Res	Type
39	4	350	ASN
42	7	489	GLN
40	5	64	GLN
40	5	351	ASN
43	8	355	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1683/1697 (99%)	409 (24%)	26 (1%)
2	0	338/377 (89%)	186 (55%)	20 (5%)
All	All	2021/2074 (97%)	595 (29%)	46 (2%)

5 of 595 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	3	C
1	A	4	C
1	A	17	C
1	A	33	G
1	A	41	G

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	0	406	C
2	0	485	U
2	0	416	U
2	0	456	C
2	0	508	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 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

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	15
40	5	1

The worst 5 of 16 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	697:G	O3'	729:C	P	18.10
1	A	834:C	O3'	841:G	P	17.97
1	A	130:G	O3'	141:A	P	17.73
1	A	756:C	O3'	788:G	P	15.69
1	A	323:C	O3'	329:G	P	15.54

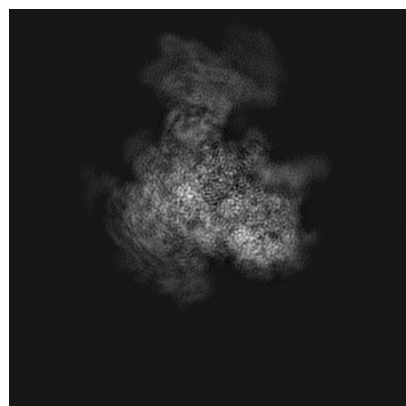
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21529. These allow visual inspection of the internal detail of the map and identification of artifacts.

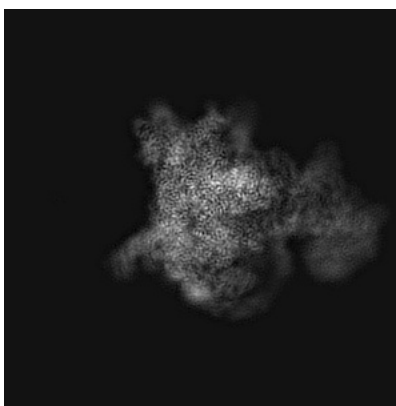
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

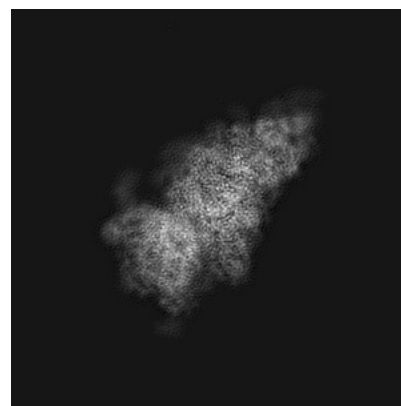
6.1.1 Primary map



X

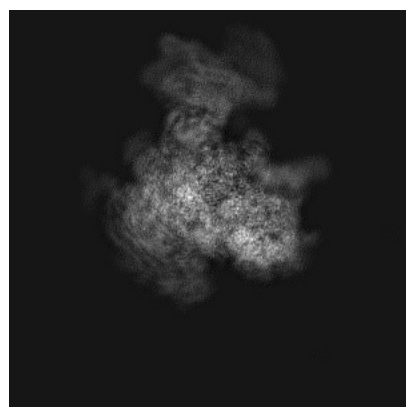


Y

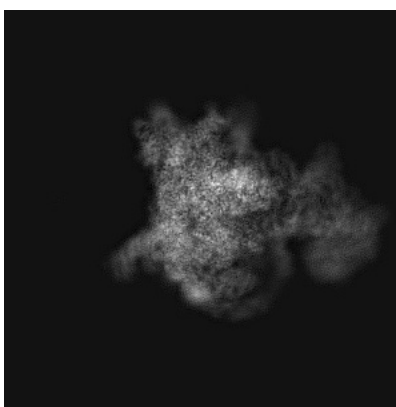


Z

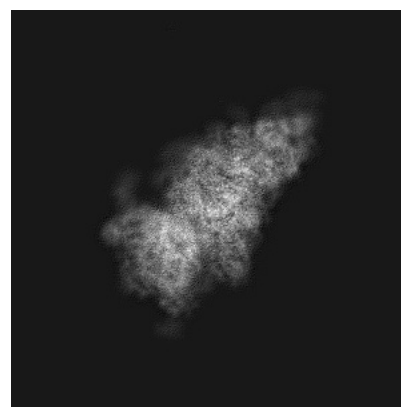
6.1.2 Raw map



X



Y

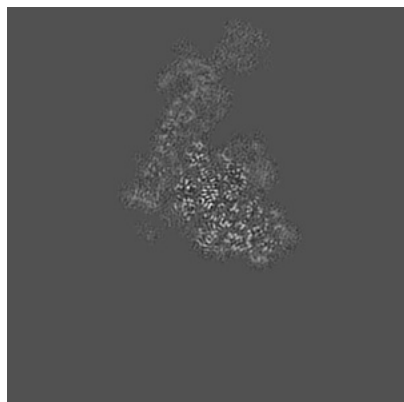


Z

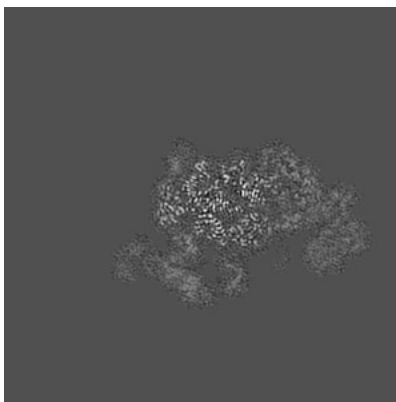
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

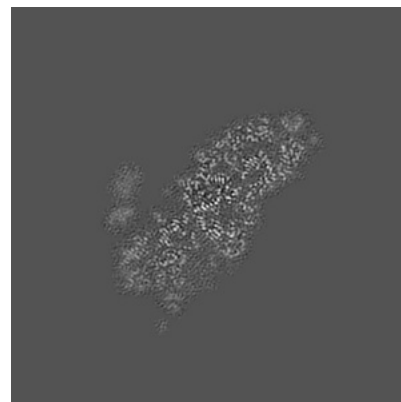
6.2.1 Primary map



X Index: 200

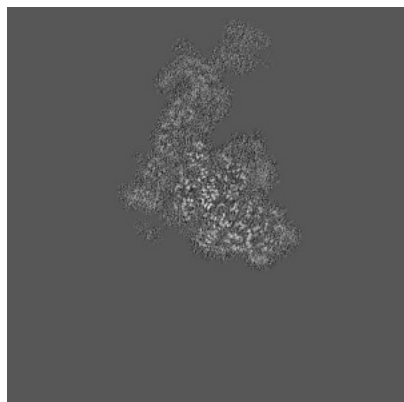


Y Index: 200

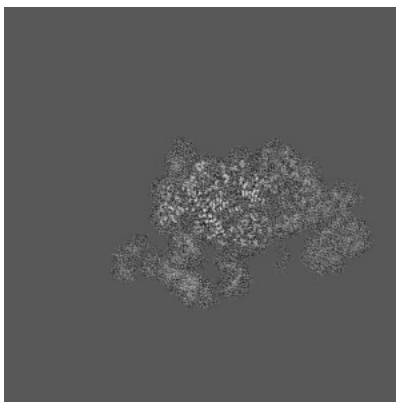


Z Index: 200

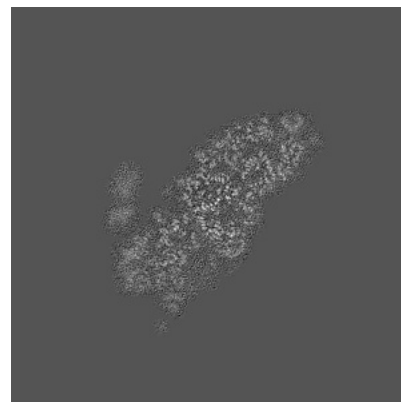
6.2.2 Raw map



X Index: 200



Y Index: 200

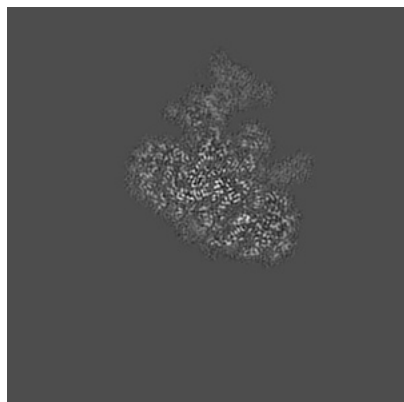


Z Index: 200

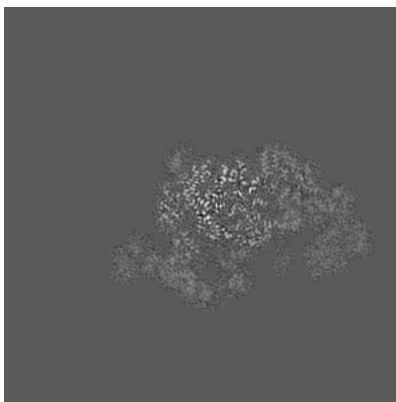
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

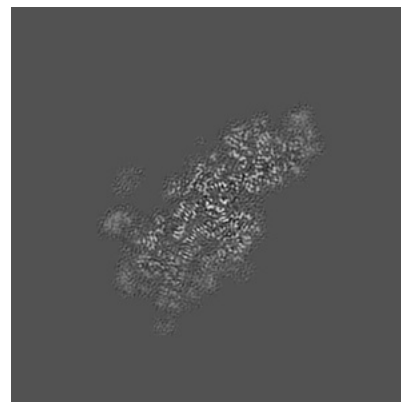
6.3.1 Primary map



X Index: 225

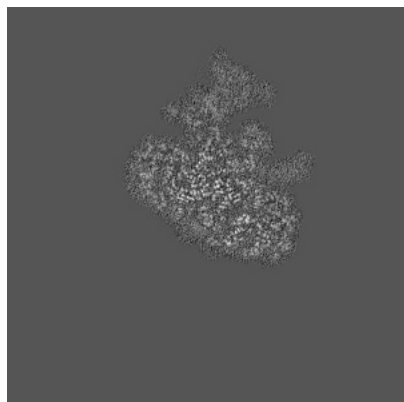


Y Index: 197

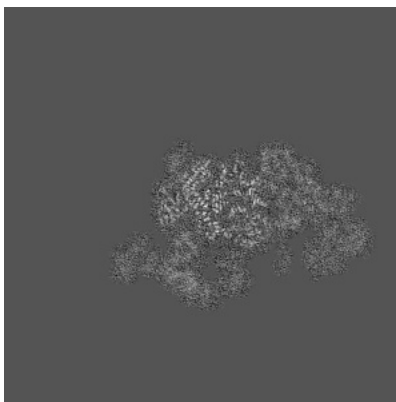


Z Index: 209

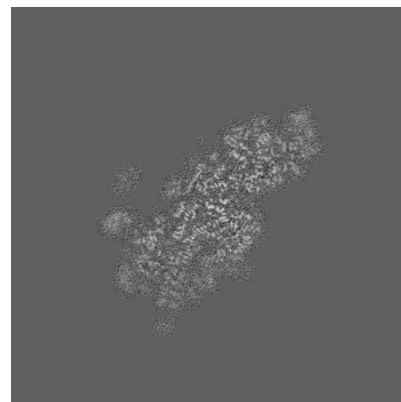
6.3.2 Raw map



X Index: 225



Y Index: 198

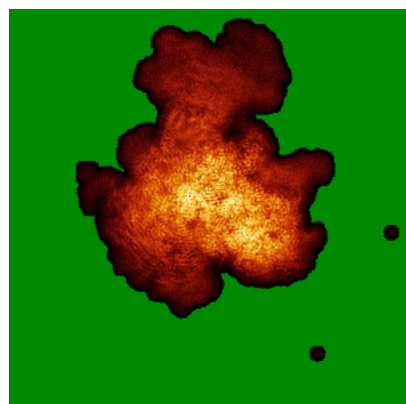


Z Index: 209

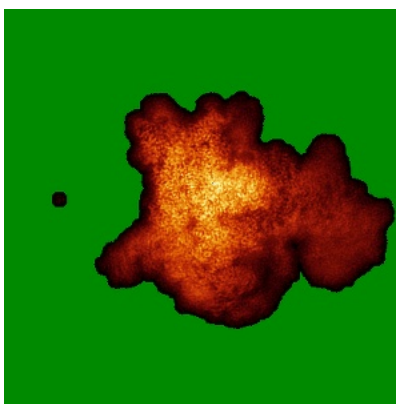
The images above show the largest variance slices of the map in three orthogonal directions.

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

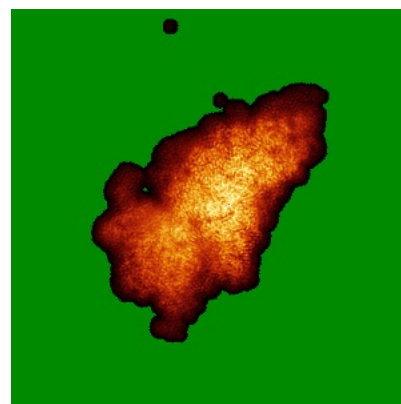
6.4.1 Primary map



X

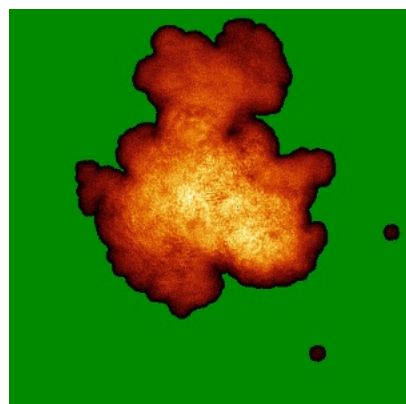


Y

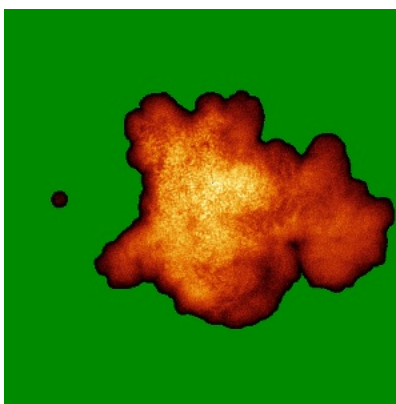


Z

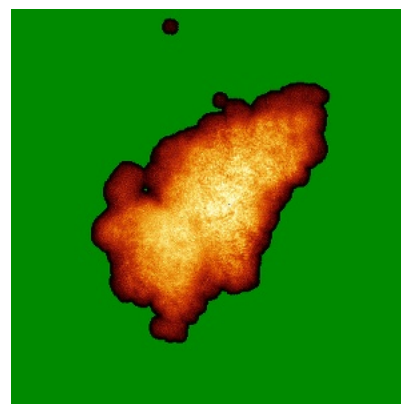
6.4.2 Raw map



X



Y

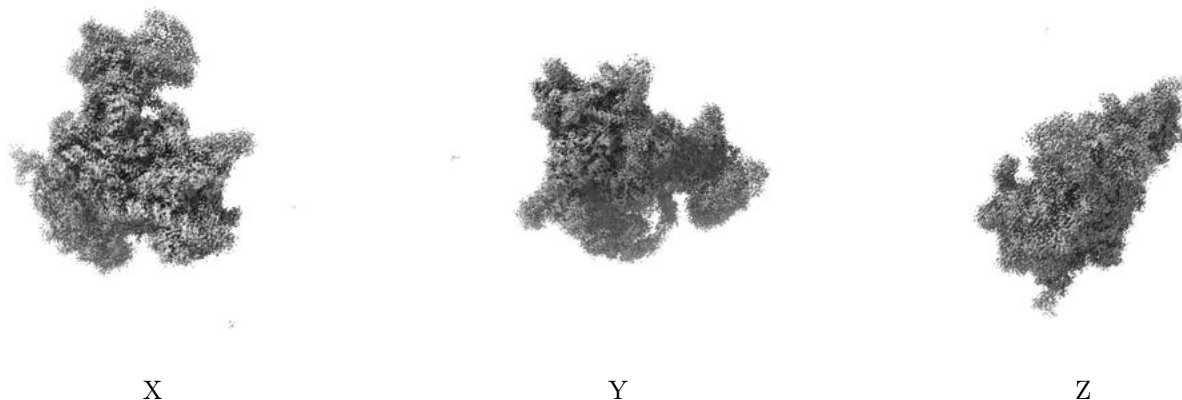


Z

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.

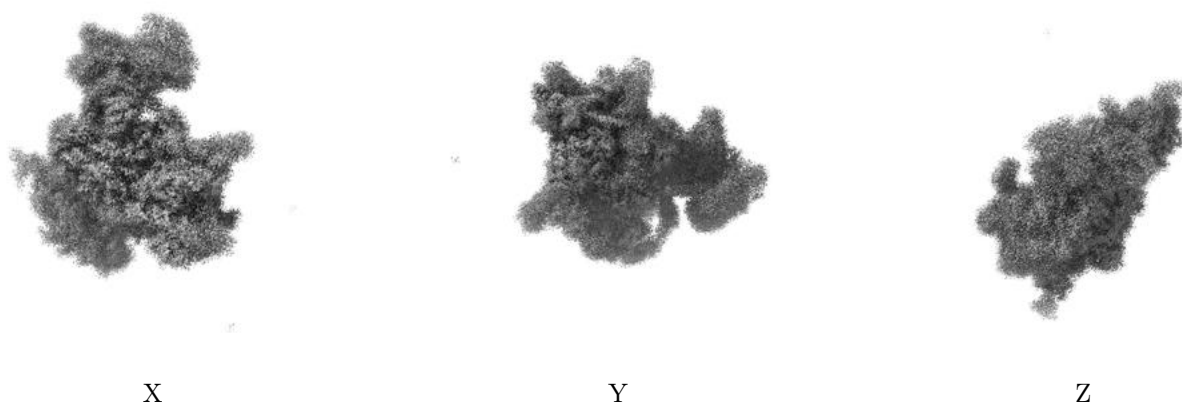
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.018. 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.

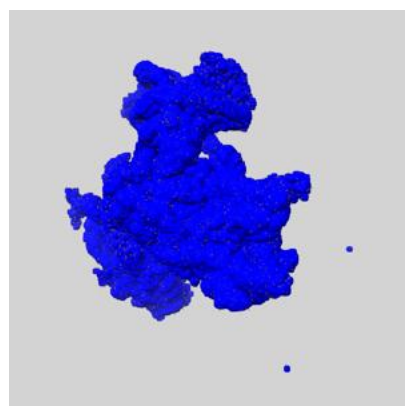
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

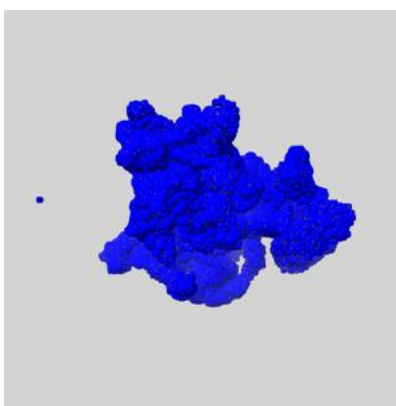
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

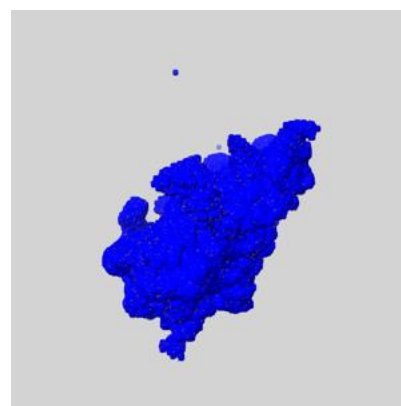
6.6.1 emd_21529_msk_1.map [i](#)



X



Y

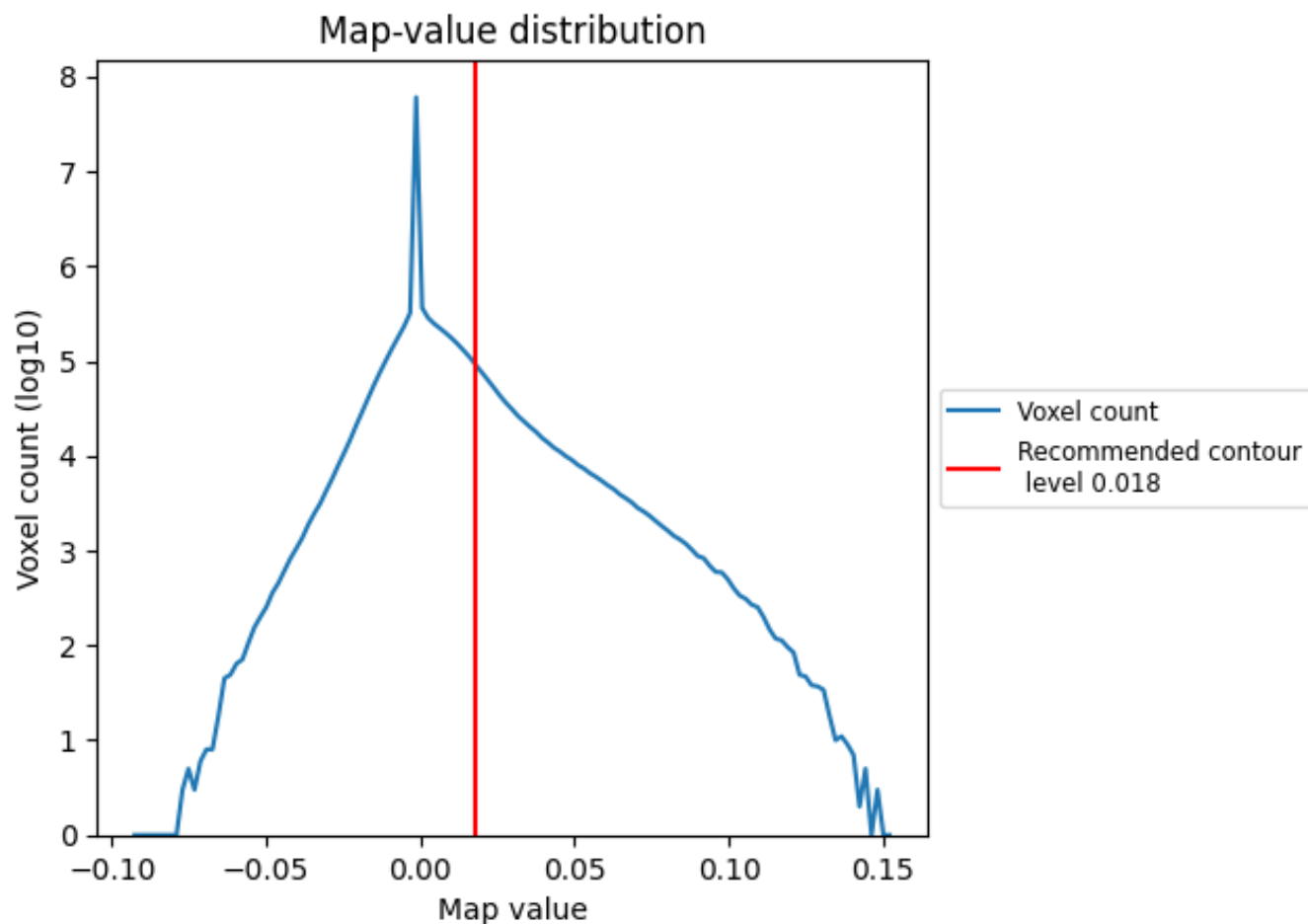


Z

7 Map analysis [i](#)

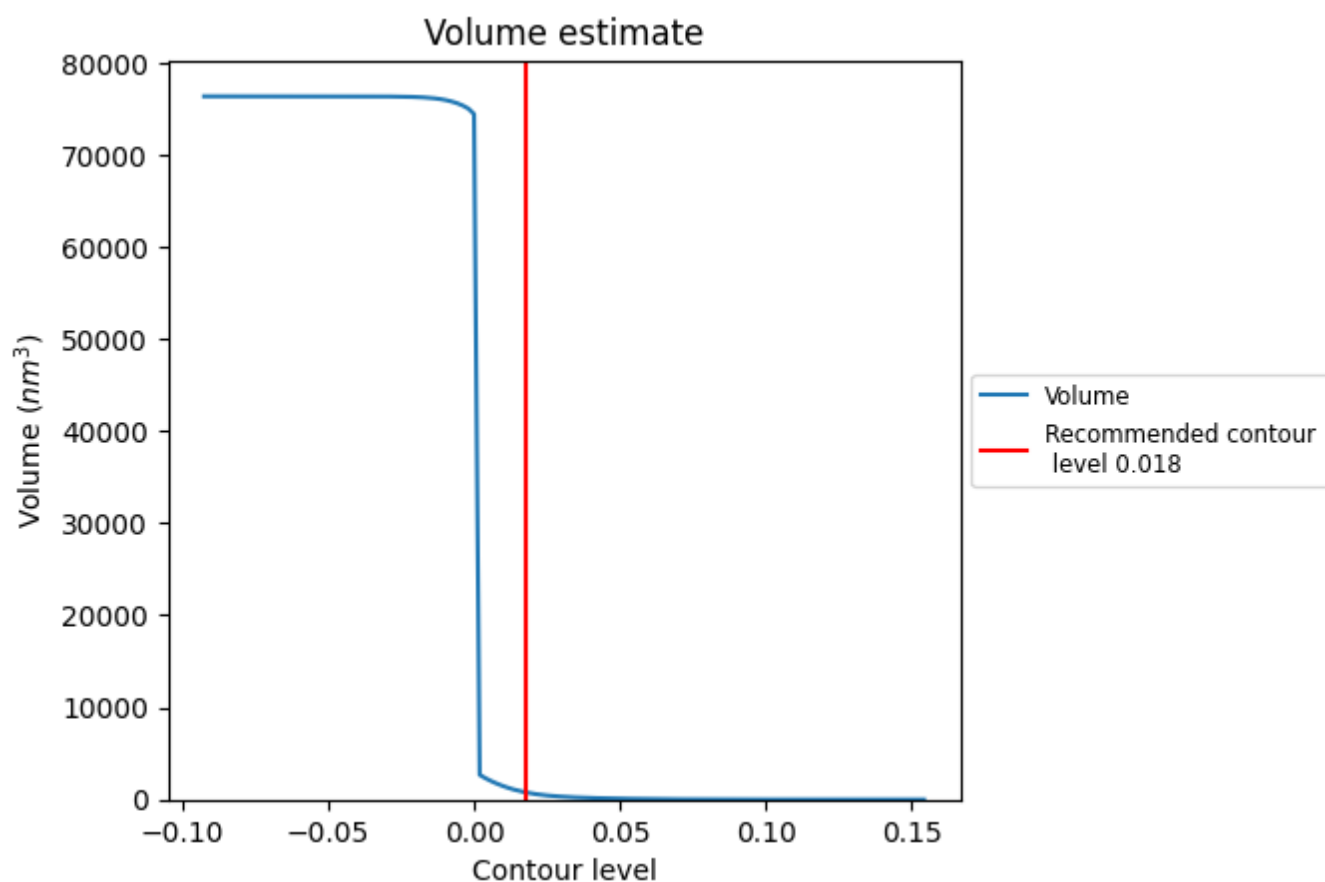
This section contains the results of statistical analysis of the map.

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.

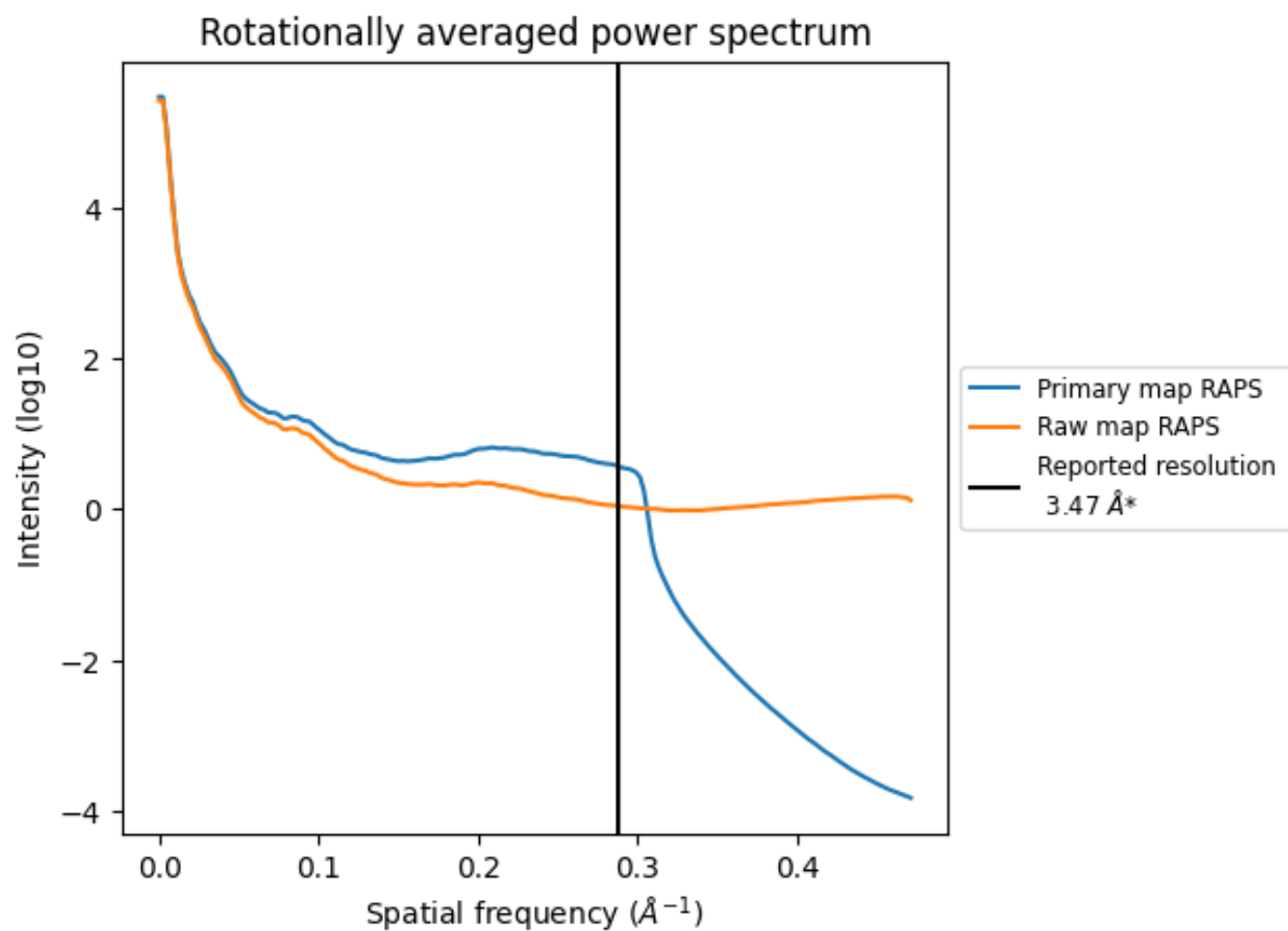
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 758 nm³; this corresponds to an approximate mass of 685 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 ⓘ

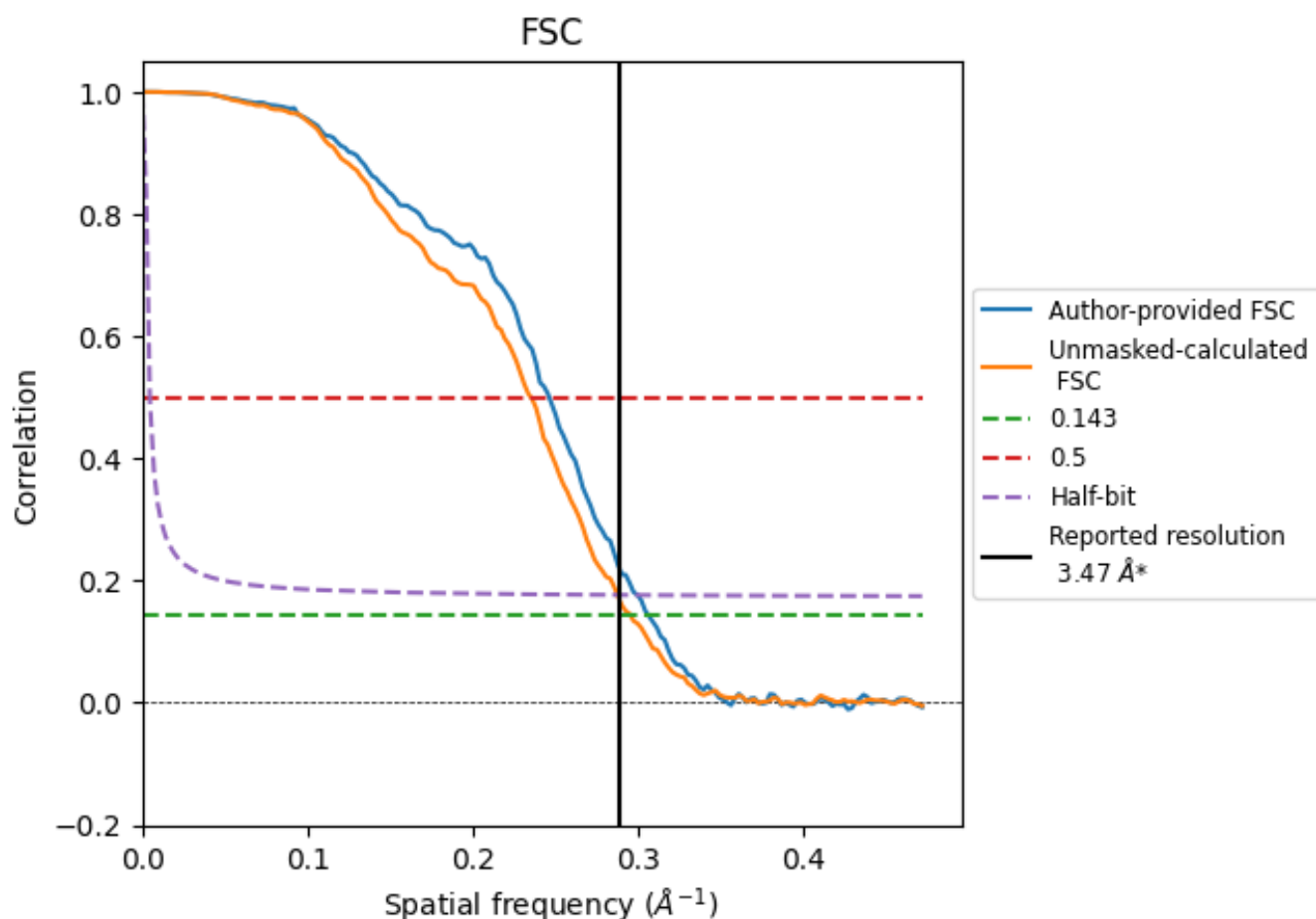


*Reported resolution corresponds to spatial frequency of $0.288 \text{ \AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.288 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

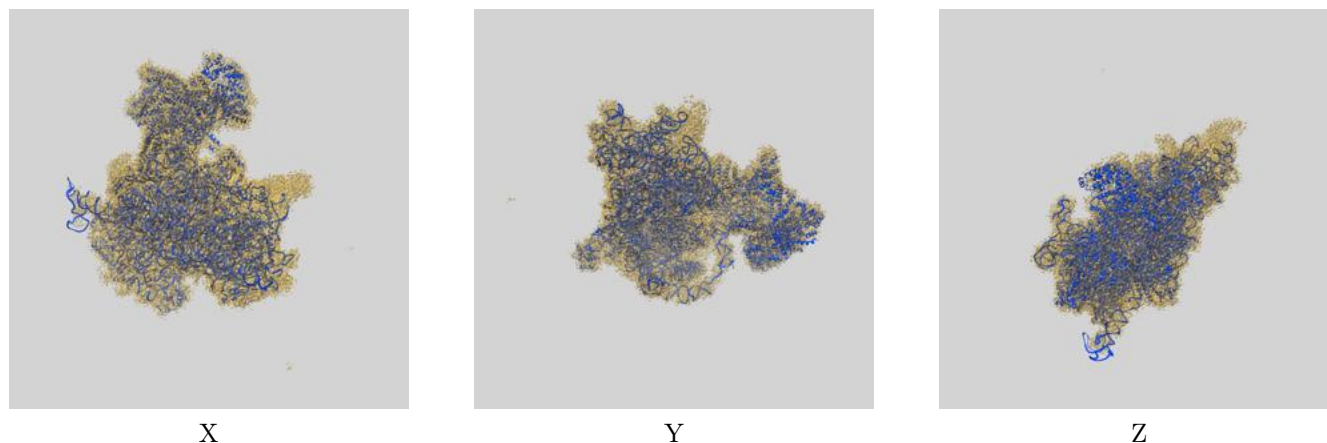
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.47	-	-
Author-provided FSC curve	3.27	4.06	3.34
Unmasked-calculated*	3.39	4.26	3.48

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

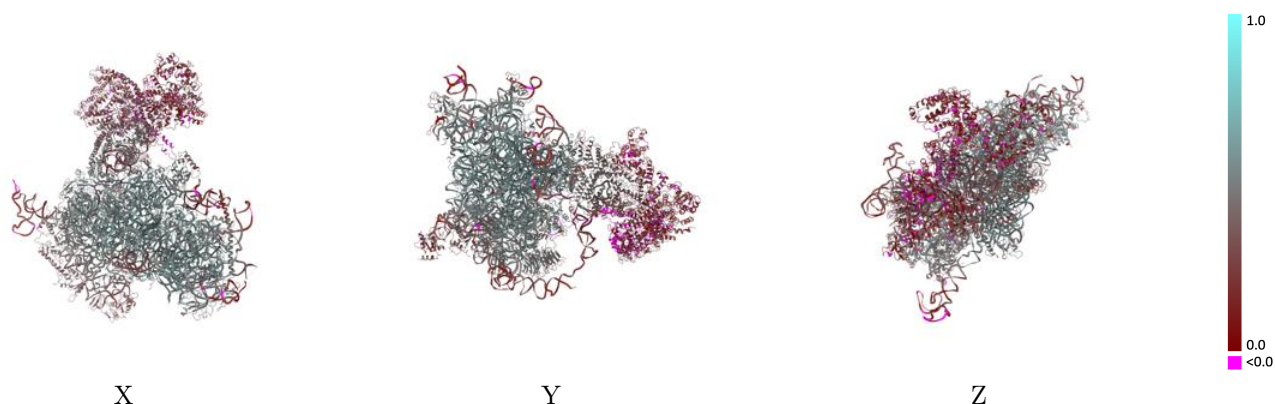
This section contains information regarding the fit between EMDB map EMD-21529 and PDB model 6W2S. Per-residue inclusion information can be found in section 3 on page 13.

9.1 Map-model overlay [i](#)



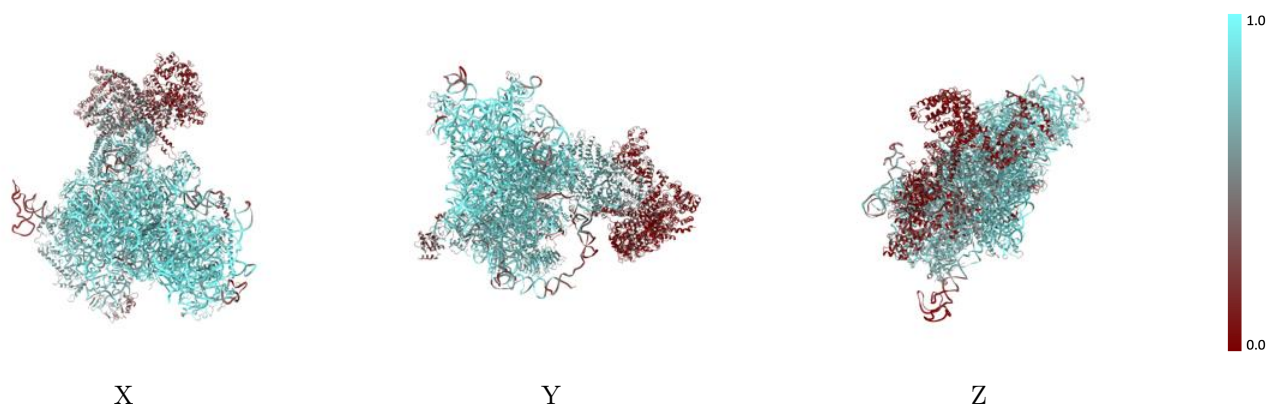
The images above show the 3D surface view of the map at the recommended contour level 0.018 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



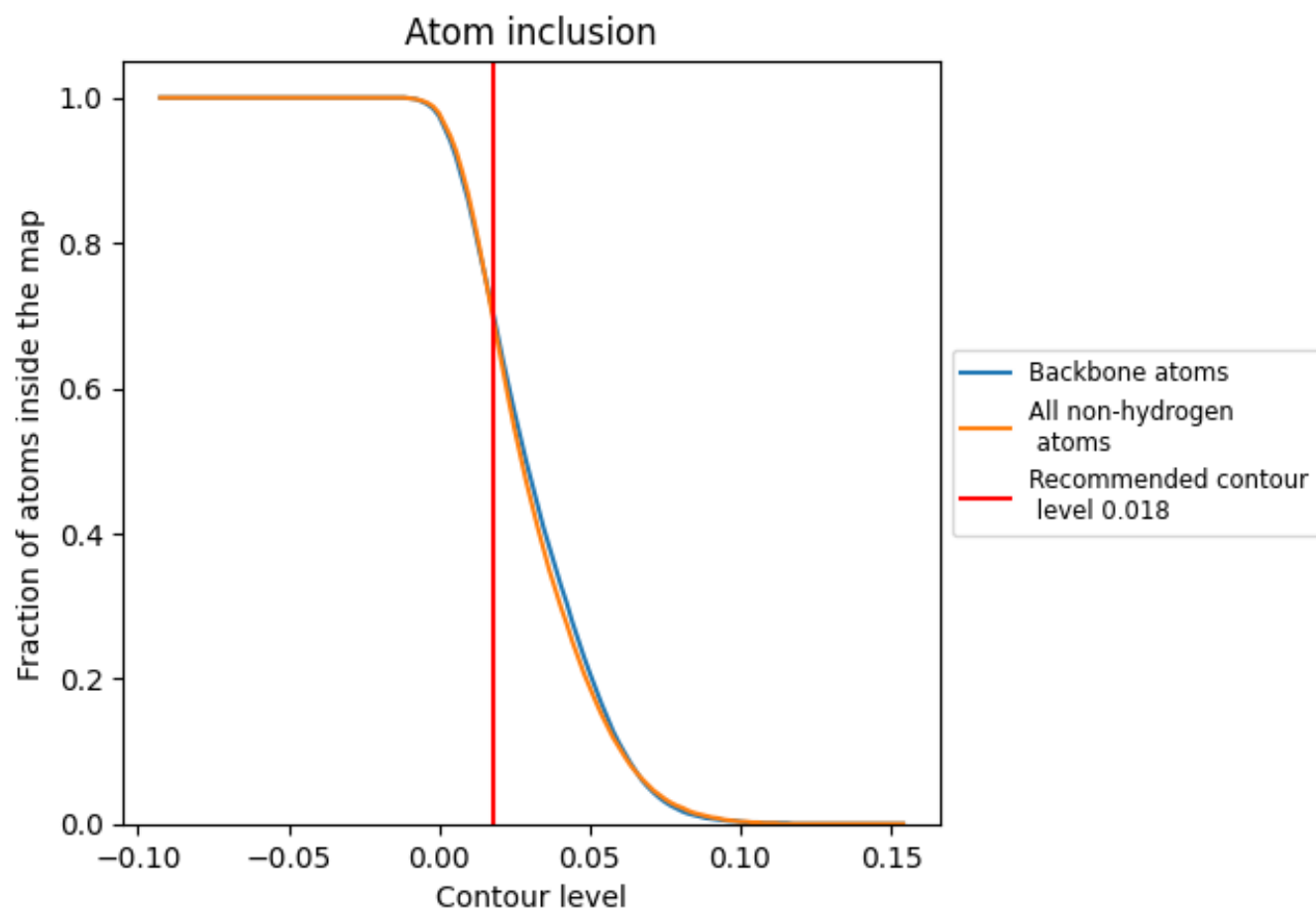
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.018).

9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 69% 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 (0.018) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6930	 0.4150
0	 0.5050	 0.2600
1	 0.5660	 0.3510
2	 0.5910	 0.3680
3	 0.2170	 0.2080
4	 0.1820	 0.2000
5	 0.1130	 0.0170
6	 0.1010	 0.2130
7	 0.0900	 0.1990
8	 0.1990	 0.2230
A	 0.9030	 0.4920
B	 0.8470	 0.5350
C	 0.8270	 0.5230
D	 0.8700	 0.5460
E	 0.7560	 0.4730
F	 0.8630	 0.5440
G	 0.7100	 0.4560
H	 0.7680	 0.4610
I	 0.7800	 0.4770
J	 0.8420	 0.5090
K	 0.8560	 0.5340
L	 0.6890	 0.3860
M	 0.8800	 0.5510
N	 0.3510	 0.2660
O	 0.8660	 0.5370
P	 0.8220	 0.5250
Q	 0.5890	 0.3520
R	 0.7800	 0.4900
S	 0.6170	 0.4090
T	 0.6500	 0.3970
U	 0.7770	 0.4520
V	 0.7730	 0.4750
W	 0.8820	 0.5410
X	 0.9030	 0.5660
Y	 0.8870	 0.5530



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Z	 0.8530	 0.5190
a	 0.6230	 0.4040
b	 0.8300	 0.5350
c	 0.8310	 0.5280
d	 0.6790	 0.4590
e	 0.8460	 0.4960
f	 0.7770	 0.4890
g	 0.4560	 0.3000
h	 0.7320	 0.4350