



wwPDB EM Validation Summary Report ⓘ

Mar 27, 2026 – 08:01 PM UTC

PDB ID : 6QG5 / pdb_00006qg5
EMDB ID : EMD-4547
Title : Structure of eIF2B-eIF2 (phosphorylated at Ser51) complex (model C)
Authors : Llacer, J.L.; Gordiyenko, Y.; Ramakrishnan, V.
Deposited on : 2019-01-10
Resolution : 10.10 Å (reported)
Based on initial models : 5B04, 6FYX

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

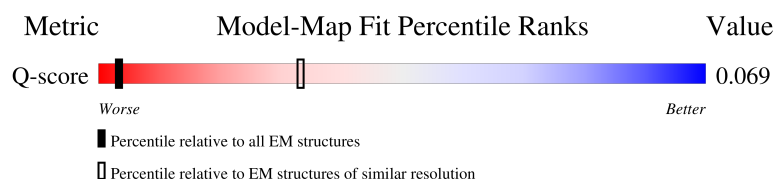
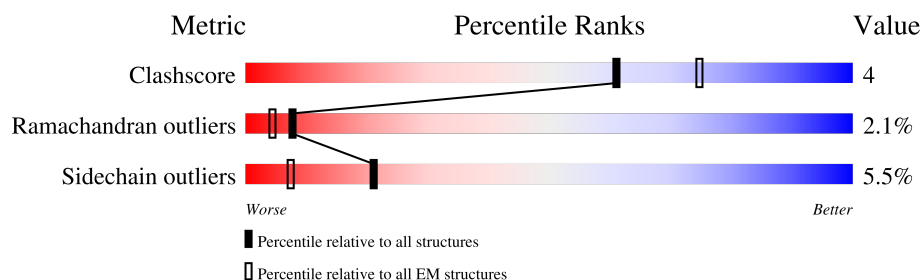
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 10.10 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	-
Q-score	-	25397	127 (9.60 - 10.60)

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	305	
1	B	305	
2	C	381	
2	D	381	

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Mol	Chain	Length	Quality of chain
3	E	578	
3	F	578	
4	G	651	
4	H	651	
5	I	712	
5	J	712	
6	K	304	
6	L	304	
7	M	527	
7	N	527	
8	O	285	
8	P	285	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 37875 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 Translation initiation factor eIF-2B subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	302	Total	C	N	O	S	0	0
			2351	1504	394	443	10		
1	B	302	Total	C	N	O	S	0	0
			2351	1504	394	443	10		

- Molecule 2 is a protein called Translation initiation factor eIF-2B subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	345	Total	C	N	O	S	0	0
			2665	1694	463	502	6		
2	D	345	Total	C	N	O	S	0	0
			2665	1694	463	502	6		

- Molecule 3 is a protein called Translation initiation factor eIF-2B subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	267	Total	C	N	O	S	0	0
			2164	1391	363	400	10		
3	F	267	Total	C	N	O	S	0	0
			2164	1391	363	400	10		

- Molecule 4 is a protein called Translation initiation factor eIF-2B subunit delta.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	355	Total	C	N	O	S	0	0
			2744	1738	474	521	11		
4	H	355	Total	C	N	O	S	0	0
			2744	1738	474	521	11		

- Molecule 5 is a protein called Translation initiation factor eIF-2B subunit epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	431	Total	C	N	O	S	0	0
			3406	2147	573	666	20		
5	J	431	Total	C	N	O	S	0	0
			3406	2147	573	666	20		

- Molecule 6 is a protein called Eukaryotic translation initiation factor 2 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	246	Total	C	N	O	P S	0	0
			1974	1259	324	382	1 8		
6	L	246	Total	C	N	O	P S	0	0
			1974	1259	324	382	1 8		

- Molecule 7 is a protein called Eukaryotic translation initiation factor 2 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	M	408	Total	C	N	O	S	0	0
			3044	1934	546	548	16		
7	N	408	Total	C	N	O	S	0	0
			3044	1934	546	548	16		

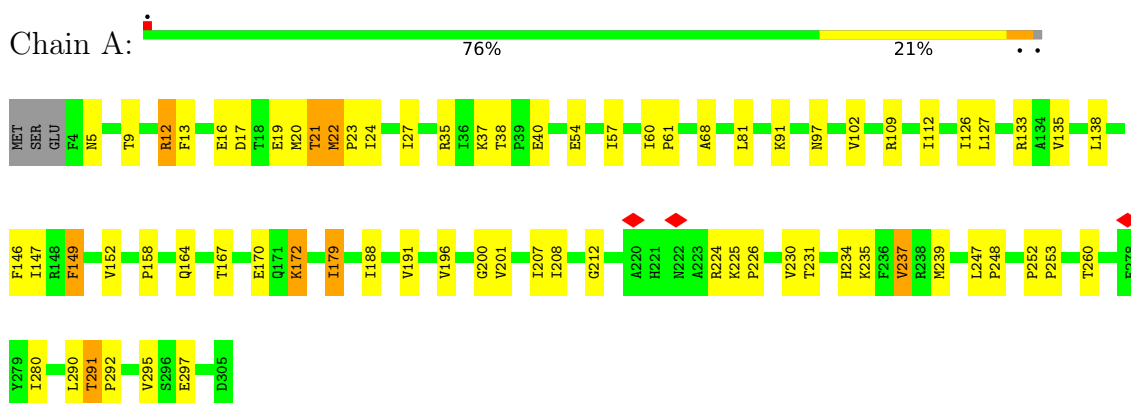
- Molecule 8 is a protein called Eukaryotic translation initiation factor 2 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	O	17	Total	C	N	O		0	0
			143	96	24	23			
8	P	128	Total	C	N	O	S	0	0
			1036	661	186	182	7		

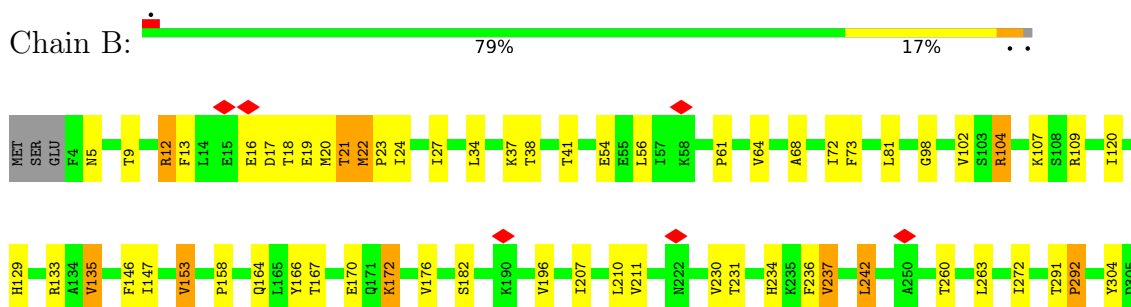
3 Residue-property plots

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.

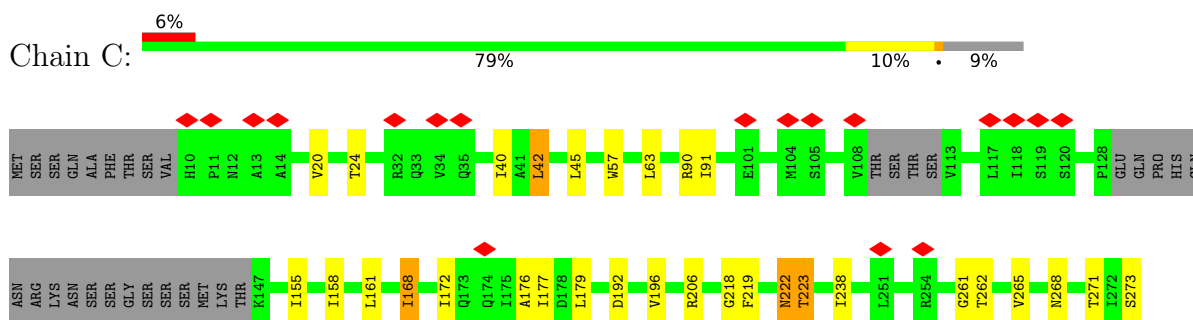
- Molecule 1: Translation initiation factor eIF-2B subunit alpha

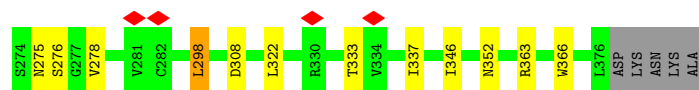


- Molecule 1: Translation initiation factor eIF-2B subunit alpha

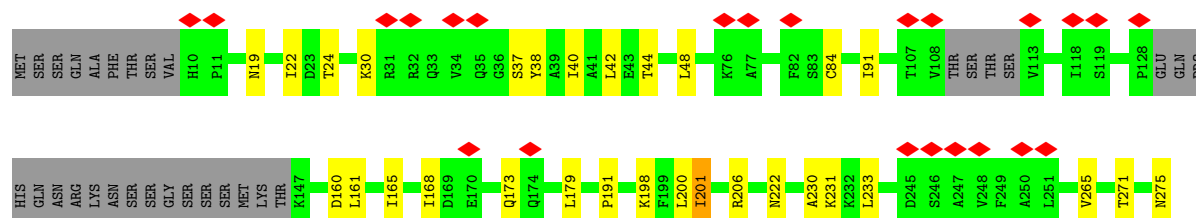
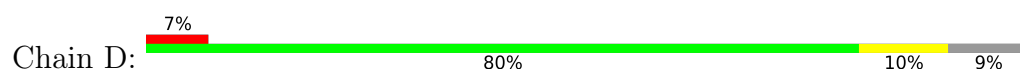


- Molecule 2: Translation initiation factor eIF-2B subunit beta

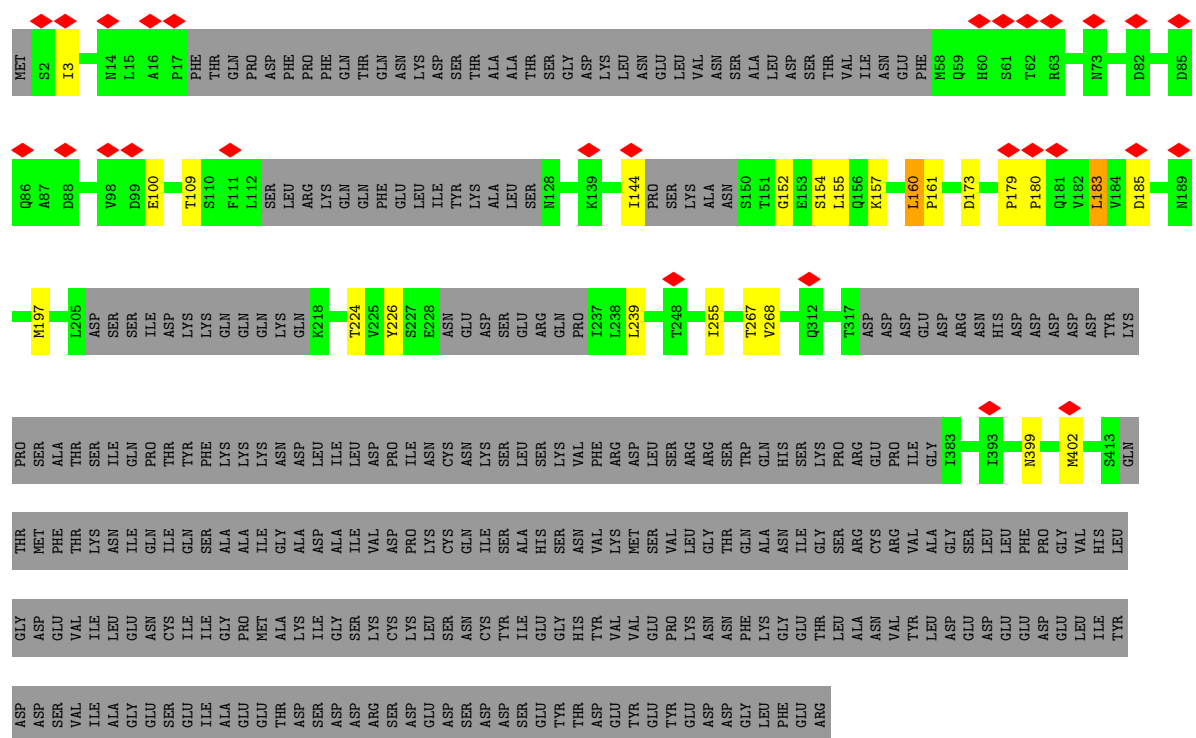
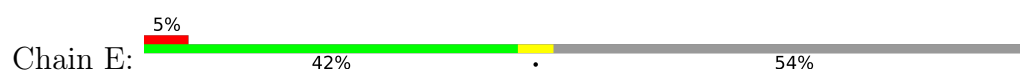




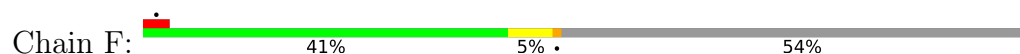
- Molecule 2: Translation initiation factor eIF-2B subunit beta

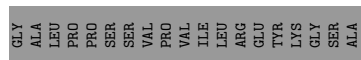


- Molecule 3: Translation initiation factor eIF-2B subunit gamma

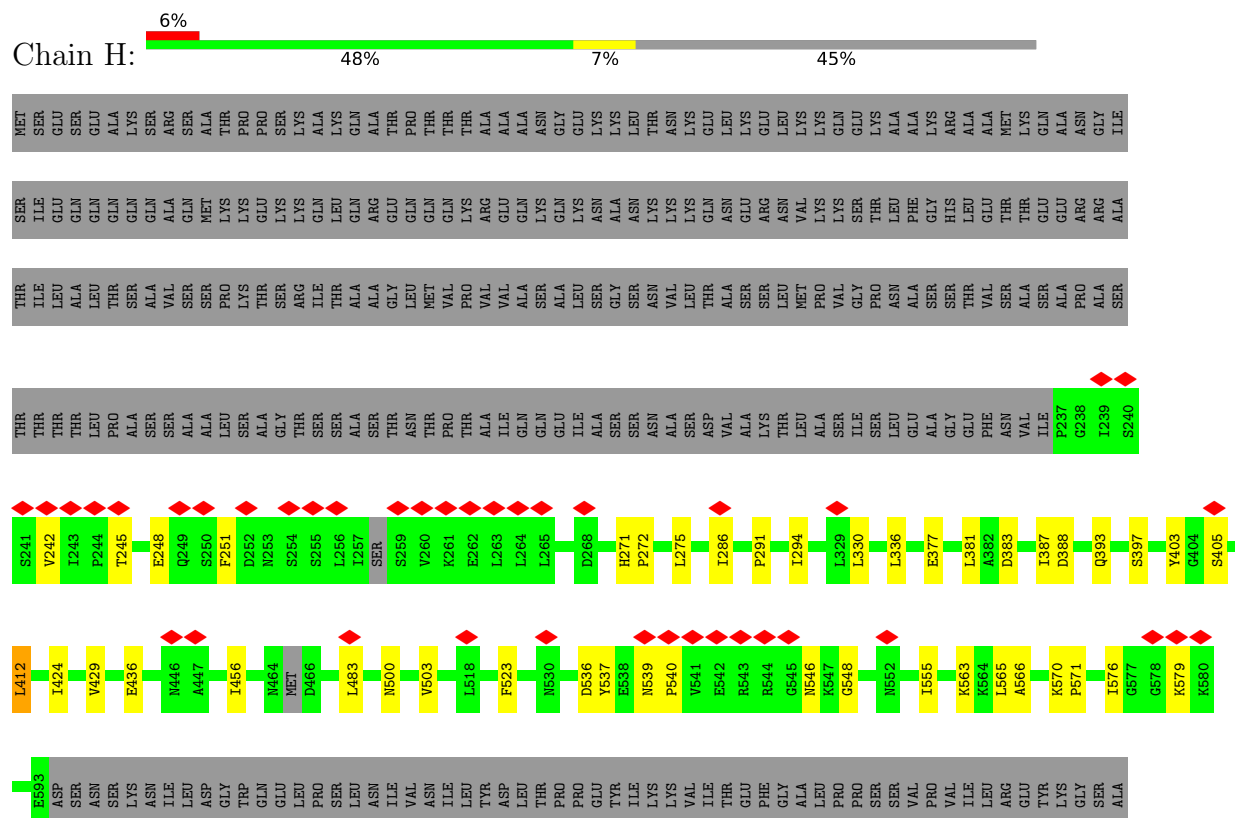


- Molecule 3: Translation initiation factor eIF-2B subunit gamma

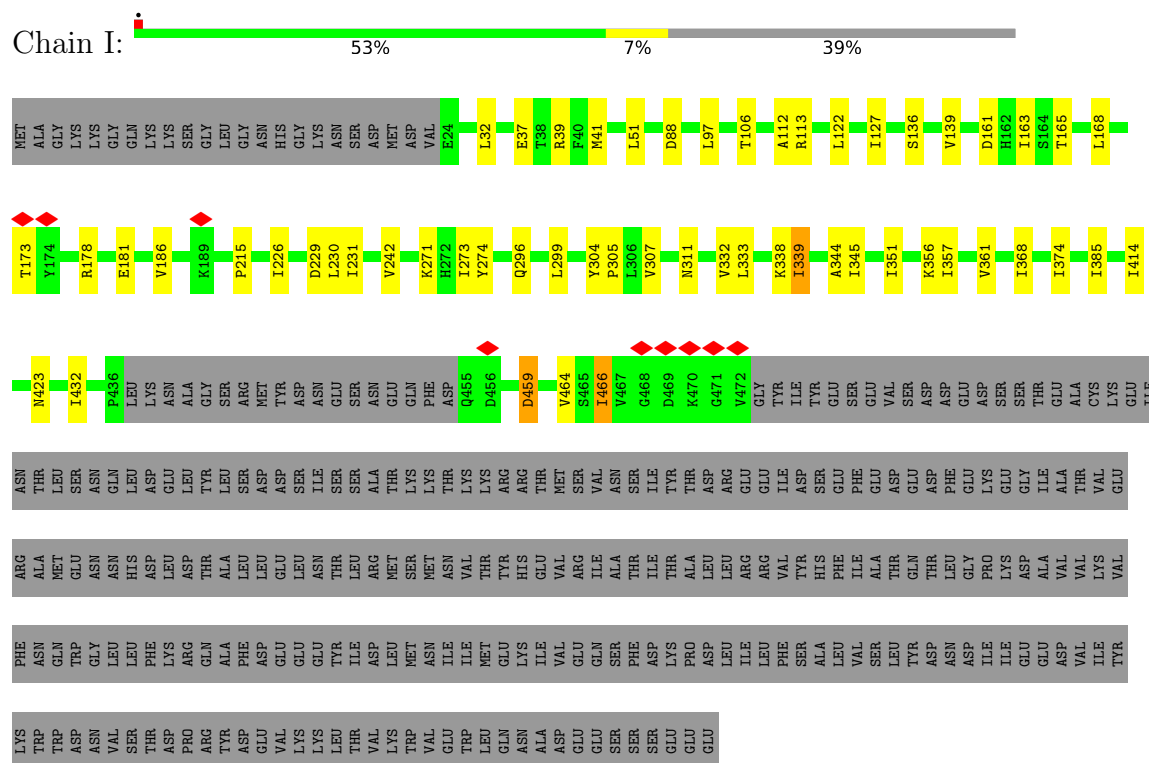




- Molecule 4: Translation initiation factor eIF-2B subunit delta



- Molecule 5: Translation initiation factor eIF-2B subunit epsilon



- Molecule 5: Translation initiation factor eIF-2B subunit epsilon

LEU
LEU
GLU
SER
SER
LYS
GLY
LEU
ASP
ASN
SER
SER
ASP
SER
GLU
ASP
ASP
GLU

• Molecule 7: Eukaryotic translation initiation factor 2 subunit gamma

Chain M:  14% 69% 9% 23%

MET SER ASP LEU LYS GLN GLN GLU PRO ILE ILE ILE ASN GLY ASP ASN LEU GLU ASP PRO VAL GLY GLU ASP PRO ILE VAL GLU THR THR VAL ALA ALA GLN THR GLN GLU THR F128 LYS ASP ALA ASP LYS PRO LYS LYS VAL ALA PHE THR GLY LEU GLU GLU ASP GLY THR

GLU GLU GLU LYS ARG LYS LYS GLU PHE GLU GLY GLY GLY LEU PRO GLN GLN PRO VAL ASN GLY I94 Q98 R127 F128 LYS ASP ALA ASP LYS PRO LYS LYS VAL G141 Y142 K149 C150 Q151 E152 PRO THR CYS PRO PRO

ASP CYS TYR ARG F164 K168 I169 I170 I171 P172 K173 C174 Q175 R176 P177 C178 G179 P180 G181 R182 Y183 K184 A209 L215 L216 E237 I238 M239 K240 H243 V244 I245 I246 K268 R271 Q272 T273 I274 A275 D276 I291 M295 V299 K300 T301 I302 R307

M310 I311 P312 P313 R319 V337 G345 G350 I353 R356 D363 K365 I368 E383 P392 I396 G399 V402 L406 C407 R408 A409 D410 R411 V416 Y427 I430 E431 I432 F435 L436 L437 R438 R439 K444 THR ASP GLN K449

Q450 A451 K452 V461 L462 M463 V464 M465 I466 G467 A470 T471 G472 A473 R474 V475 T488 S489 P490 A491 C492 T493 E494 I495 E497 K498 I499 R503 R504 I505 E506 K507 H508 W509 R510 T516 I517 F518 K519 GLY THR THR THR LEU PRO ILE ALA

• Molecule 7: Eukaryotic translation initiation factor 2 subunit gamma

Chain N:  6% 62% 13% 23%

MET SER ASP LEU LYS GLN GLN GLU PRO SER ILE ILE ILE ASN GLY ASP ASN LEU GLU PRO VAL ASN GLY GLU ASP PRO ILE VAL GLU THR THR VAL ALA ALA GLN THR GLN GLU THR R118 Q124 T125 V126 R127 F128 LYS ASP L132 E133 R134 M135 I136 E152 PRO THR CYS

GLU GLU GLU LYS ARG LYS LYS GLU PHE GLU GLU GLY GLY GLY LEU PRO GLU GLN PRO LEU ASN ASP PHE SER LYS LEU ASN PRO THR VAL SER ALA I94 I101 K113 S114 R118 Q124 T125 V126 R127 F128 LYS ASP L132 E133 R134 M135 I136 E152 PRO THR CYS

PRO GLU PRO ASP CYS TYR ARG S163 R176 P177 G178 V189 G196 H197 L200 M204 V210 L215 Q226 P227 I245 I246 L247 V251 R255 I302 P305 P306 R307 D308 F309 M310 I311 S312 P313 R314 L315 I316 I330 E331 D332 L333 V337 I342

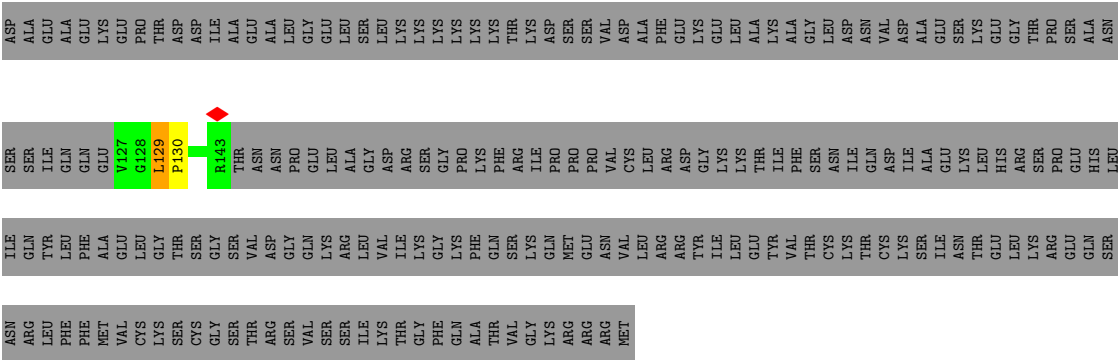
L343 N344 G345 V346 L349 I353 E354 I355 R356 P357 G358 I359 K362 D363 ASP K365 I368 K371 E383 G399 D403 L406 C407 R408 A409 D410 R411 L412 Q415 V416 V417 K420 G421 H422 L423 P424 N425 I426 I427 T428 D429 I430 D332 E431 I432 V443 K444 THR ASP

GLY GLN K449 Q450 I466 T469 L485 Q486 L487 T488 S489 P490 A491 C492 T493 E494 E497 K498 I499 I505 E506 K507 H508 A515 T516 I517 K518 K519 GLY THR THR LEU GLU PRO ILE ALA

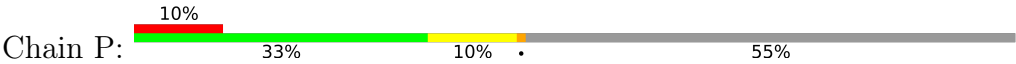
• Molecule 8: Eukaryotic translation initiation factor 2 subunit beta

Chain O:  5% 94%

MET SER SER ASP LEU ALA ALA GLU LEU GLY PHE ASP PRO ALA LEU LYS LYS LYS THR LYS LYS VAL ILE PRO ASP ASP PHE ASP ALA ALA VAL ASN GLY GLY GLY ASP ASP LEU PHE ALA GLY LEU LYS LYS LYS LYS LYS SER SER SER VAL ALA



● Molecule 8: Eukaryotic translation initiation factor 2 subunit beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	23909	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.126	Depositor
Minimum map value	-0.044	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	375.2, 375.2, 375.2	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.34, 1.34, 1.34	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SEP

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	0.53	0/2395	0.94	0/3251
1	B	0.53	0/2395	0.93	0/3251
2	C	0.58	0/2714	1.02	0/3693
2	D	0.56	0/2714	0.99	1/3693 (0.0%)
3	E	0.56	0/2209	0.90	1/2989 (0.0%)
3	F	0.56	0/2209	0.92	0/2989
4	G	0.55	0/2781	0.97	1/3747 (0.0%)
4	H	0.55	0/2781	0.98	0/3747
5	I	0.57	1/3468 (0.0%)	0.91	0/4704
5	J	0.58	0/3468	0.91	2/4704 (0.0%)
6	K	0.55	0/1989	0.96	2/2675 (0.1%)
6	L	0.55	0/1989	0.96	1/2675 (0.0%)
7	M	0.57	0/3087	0.90	2/4173 (0.0%)
7	N	0.56	0/3087	0.88	3/4173 (0.1%)
8	O	0.56	0/146	0.97	0/196
8	P	0.50	0/1051	0.83	0/1402
All	All	0.56	1/38483 (0.0%)	0.94	13/52062 (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
7	N	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	242	VAL	CA-CB	5.03	1.56	1.54

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	M	300	LYS	N-CA-C	6.85	118.44	110.97
7	N	489	SER	CA-C-N	6.53	128.00	119.84
7	N	489	SER	C-N-CA	6.53	128.00	119.84
7	M	356	ARG	N-CA-C	6.34	120.84	112.35
6	K	254	VAL	N-CA-C	6.01	116.67	110.36

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	N	423	LEU	Peptide

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	A	2351	0	2367	45	0
1	B	2351	0	2367	56	0
2	C	2665	0	2626	14	0
2	D	2665	0	2626	12	0
3	E	2164	0	2154	9	0
3	F	2164	0	2154	11	0
4	G	2744	0	2819	18	0
4	H	2744	0	2819	15	0
5	I	3406	0	3359	20	0
5	J	3406	0	3359	27	0
6	K	1974	0	2020	13	0
6	L	1974	0	2020	24	0
7	M	3044	0	3126	23	0
7	N	3044	0	3126	71	0
8	O	143	0	148	1	0
8	P	1036	0	1080	18	0
All	All	37875	0	38170	337	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 337 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)
1:B:20:MET:SD	1:B:102:VAL:HG13	1.27	1.70
7:N:312:SER:HB2	7:N:422:HIS:CE1	1.47	1.49
1:B:20:MET:SD	1:B:102:VAL:CG1	2.22	1.27
7:N:314:ARG:HH21	7:N:423:LEU:C	1.47	1.23
1:A:20:MET:SD	1:A:102:VAL:CG1	2.34	1.16

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	A	300/305 (98%)	254 (85%)	39 (13%)	7 (2%)	5	28
1	B	300/305 (98%)	256 (85%)	35 (12%)	9 (3%)	3	23
2	C	339/381 (89%)	308 (91%)	28 (8%)	3 (1%)	14	51
2	D	339/381 (89%)	309 (91%)	25 (7%)	5 (2%)	8	40
3	E	253/578 (44%)	217 (86%)	34 (13%)	2 (1%)	16	54
3	F	253/578 (44%)	211 (83%)	37 (15%)	5 (2%)	6	31
4	G	349/651 (54%)	303 (87%)	35 (10%)	11 (3%)	3	21
4	H	349/651 (54%)	302 (86%)	36 (10%)	11 (3%)	3	21
5	I	427/712 (60%)	379 (89%)	41 (10%)	7 (2%)	7	38
5	J	427/712 (60%)	365 (86%)	45 (10%)	17 (4%)	2	18
6	K	237/304 (78%)	208 (88%)	27 (11%)	2 (1%)	16	54
6	L	237/304 (78%)	211 (89%)	25 (10%)	1 (0%)	30	67
7	M	398/527 (76%)	345 (87%)	48 (12%)	5 (1%)	9	42
7	N	398/527 (76%)	330 (83%)	55 (14%)	13 (3%)	3	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	O	15/285 (5%)	13 (87%)	1 (7%)	1 (7%)	1	12
8	P	120/285 (42%)	100 (83%)	18 (15%)	2 (2%)	7	36
All	All	4741/7486 (63%)	4111 (87%)	529 (11%)	101 (2%)	8	30

5 of 101 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	61	PRO
3	E	100	GLU
3	F	100	GLU
4	G	487	ALA
4	H	536	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	A	257/265 (97%)	234 (91%)	23 (9%)	9	28
1	B	257/265 (97%)	240 (93%)	17 (7%)	15	37
2	C	286/338 (85%)	266 (93%)	20 (7%)	14	35
2	D	286/338 (85%)	270 (94%)	16 (6%)	19	40
3	E	249/529 (47%)	243 (98%)	6 (2%)	43	64
3	F	249/529 (47%)	241 (97%)	8 (3%)	34	56
4	G	305/561 (54%)	295 (97%)	10 (3%)	33	55
4	H	305/561 (54%)	295 (97%)	10 (3%)	33	55
5	I	389/649 (60%)	372 (96%)	17 (4%)	25	47
5	J	389/649 (60%)	372 (96%)	17 (4%)	25	47
6	K	219/273 (80%)	198 (90%)	21 (10%)	8	25
6	L	219/273 (80%)	198 (90%)	21 (10%)	8	25
7	M	319/449 (71%)	309 (97%)	10 (3%)	35	56
7	N	319/449 (71%)	298 (93%)	21 (7%)	15	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	O	16/246 (6%)	16 (100%)	0	100	100
8	P	119/246 (48%)	106 (89%)	13 (11%)	6	21
All	All	4183/6620 (63%)	3953 (94%)	230 (6%)	21	41

5 of 230 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	I	113	ARG
8	P	174	PHE
5	J	467	VAL
8	P	170	LYS
7	N	309	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 105 such sidechains are listed below:

Mol	Chain	Res	Type
5	I	73	HIS
5	J	387	ASN
7	N	422	HIS
5	I	87	ASN
5	I	423	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	SEP	L	52	6	8,9,10	0.66	0	7,12,14	1.23	1 (14%)
6	SEP	K	52	6	8,9,10	0.66	0	7,12,14	1.18	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	SEP	L	52	6	-	2/6/8/10	-
6	SEP	K	52	6	-	2/6/8/10	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	52	SEP	OG-CB-CA	2.01	110.11	108.14

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	K	52	SEP	N-CA-CB-OG
6	K	52	SEP	C-CA-CB-OG
6	L	52	SEP	N-CA-CB-OG
6	L	52	SEP	C-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

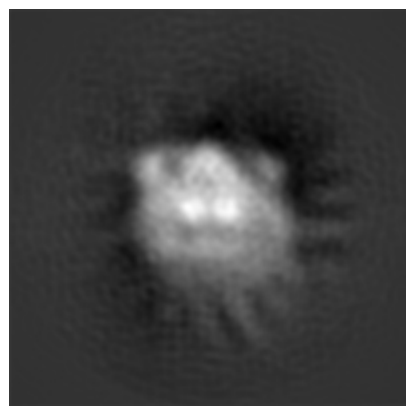
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4547. These allow visual inspection of the internal detail of the map and identification of artifacts.

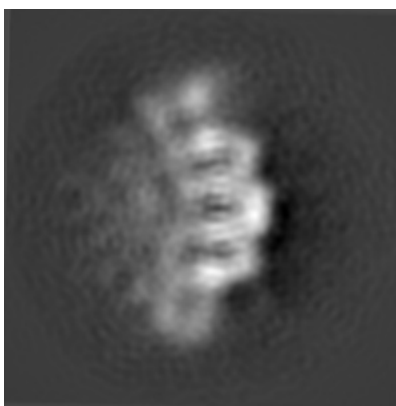
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

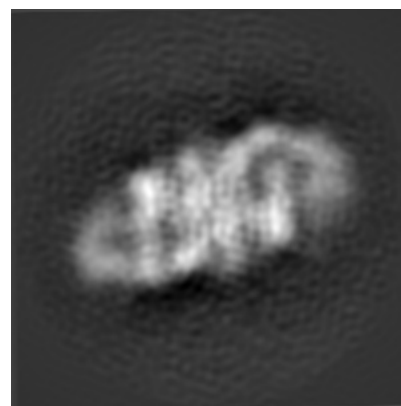
6.1.1 Primary map



X

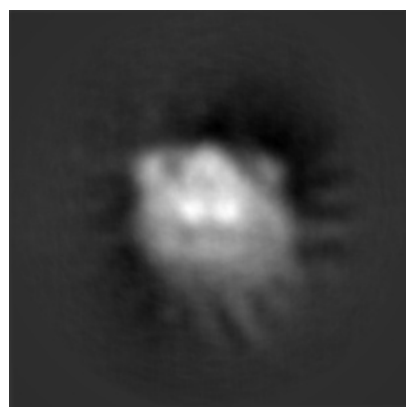


Y

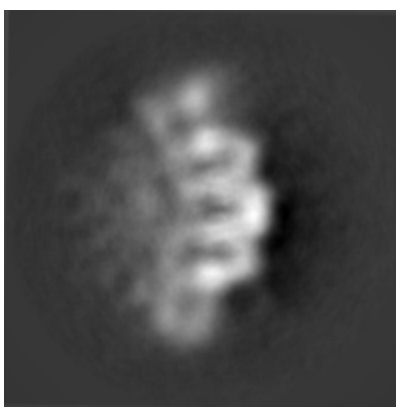


Z

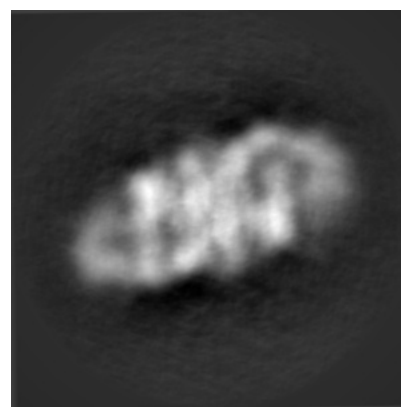
6.1.2 Raw map



X



Y

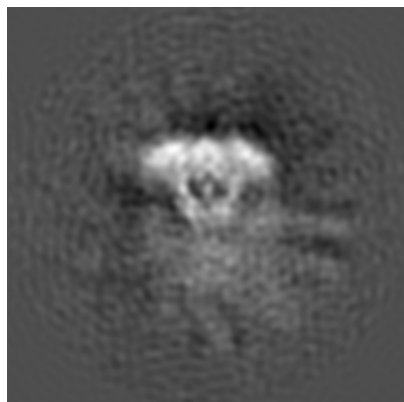


Z

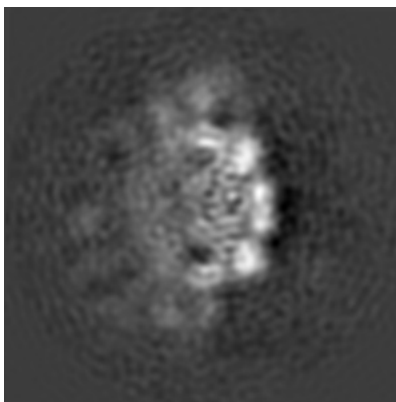
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

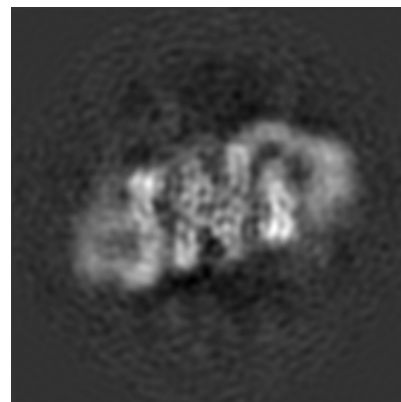
6.2.1 Primary map



X Index: 140

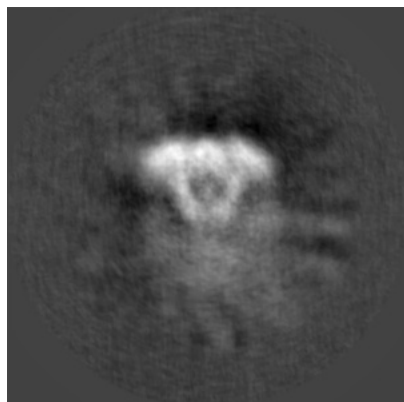


Y Index: 140

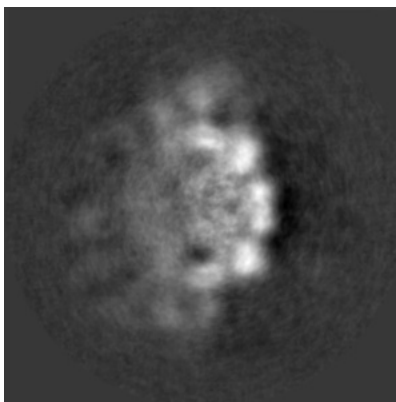


Z Index: 140

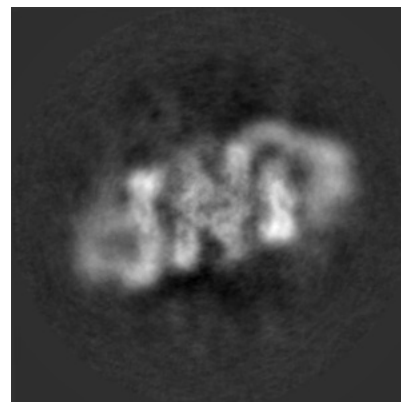
6.2.2 Raw map



X Index: 140



Y Index: 140

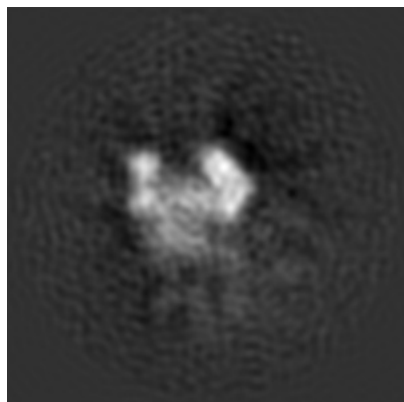


Z Index: 140

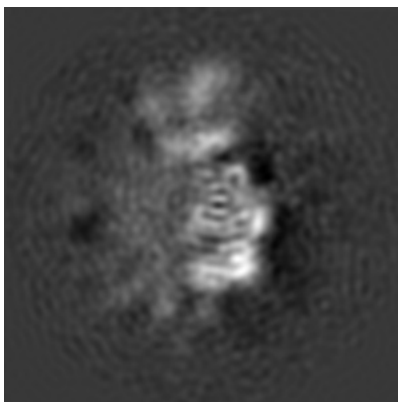
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

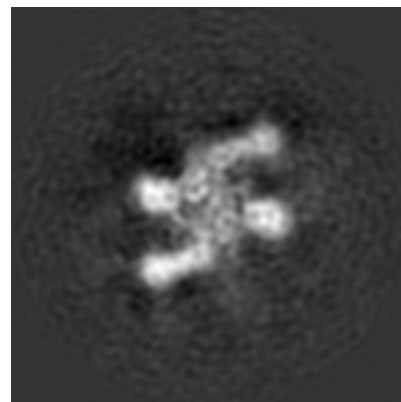
6.3.1 Primary map



X Index: 96

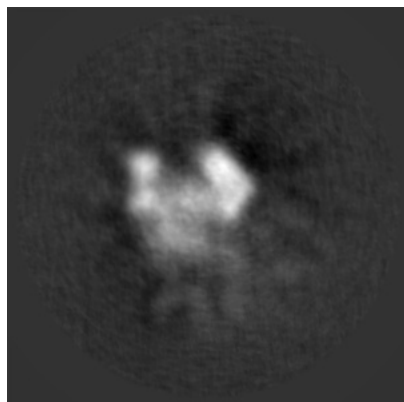


Y Index: 152

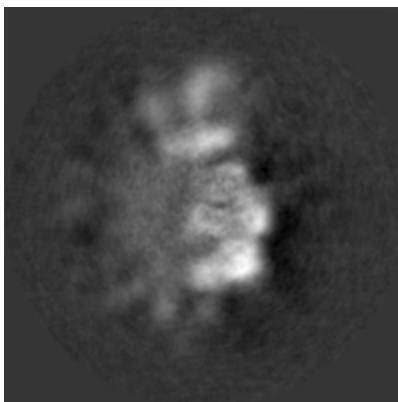


Z Index: 169

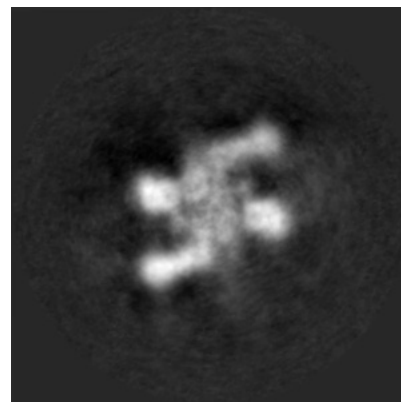
6.3.2 Raw map



X Index: 96



Y Index: 150

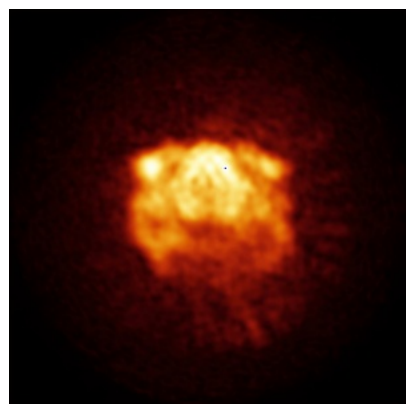


Z Index: 168

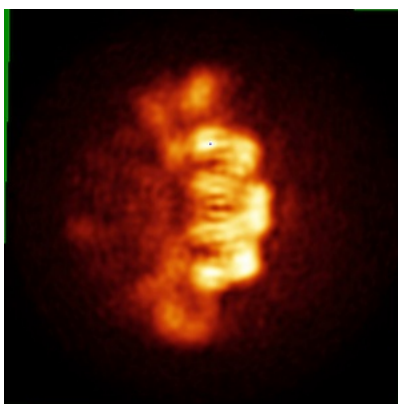
The images above show the largest variance slices of the map in three orthogonal directions.

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

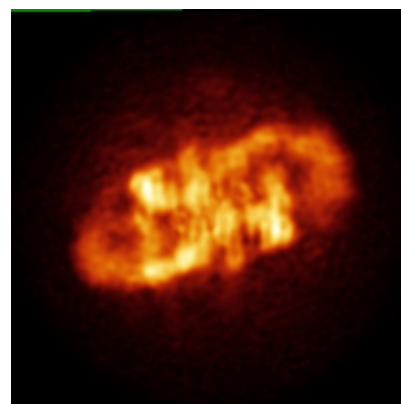
6.4.1 Primary map



X

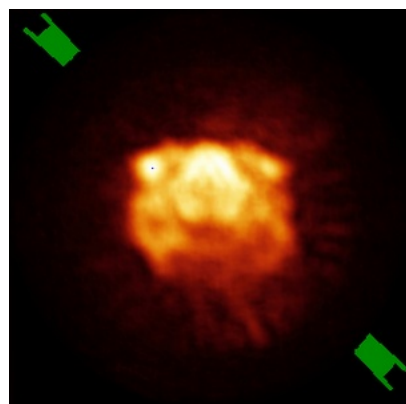


Y

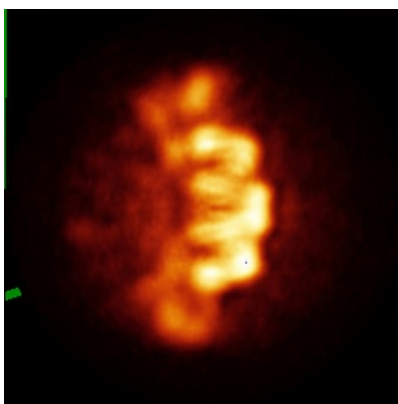


Z

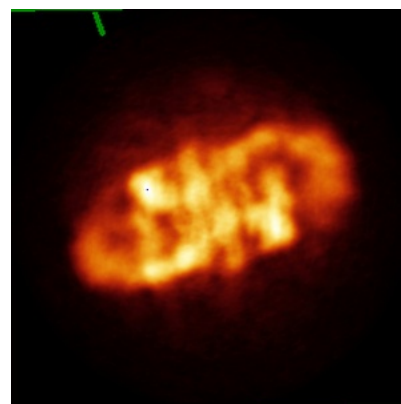
6.4.2 Raw map



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.

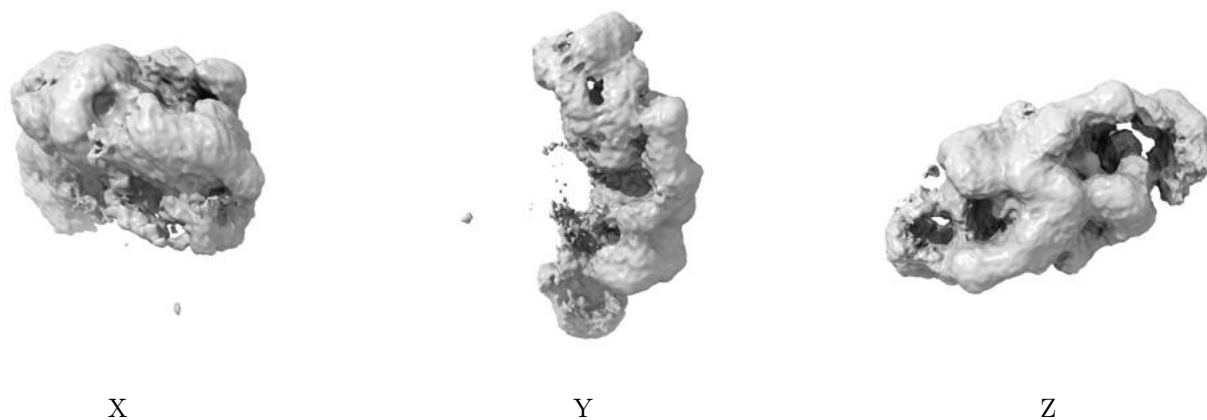
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. 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.

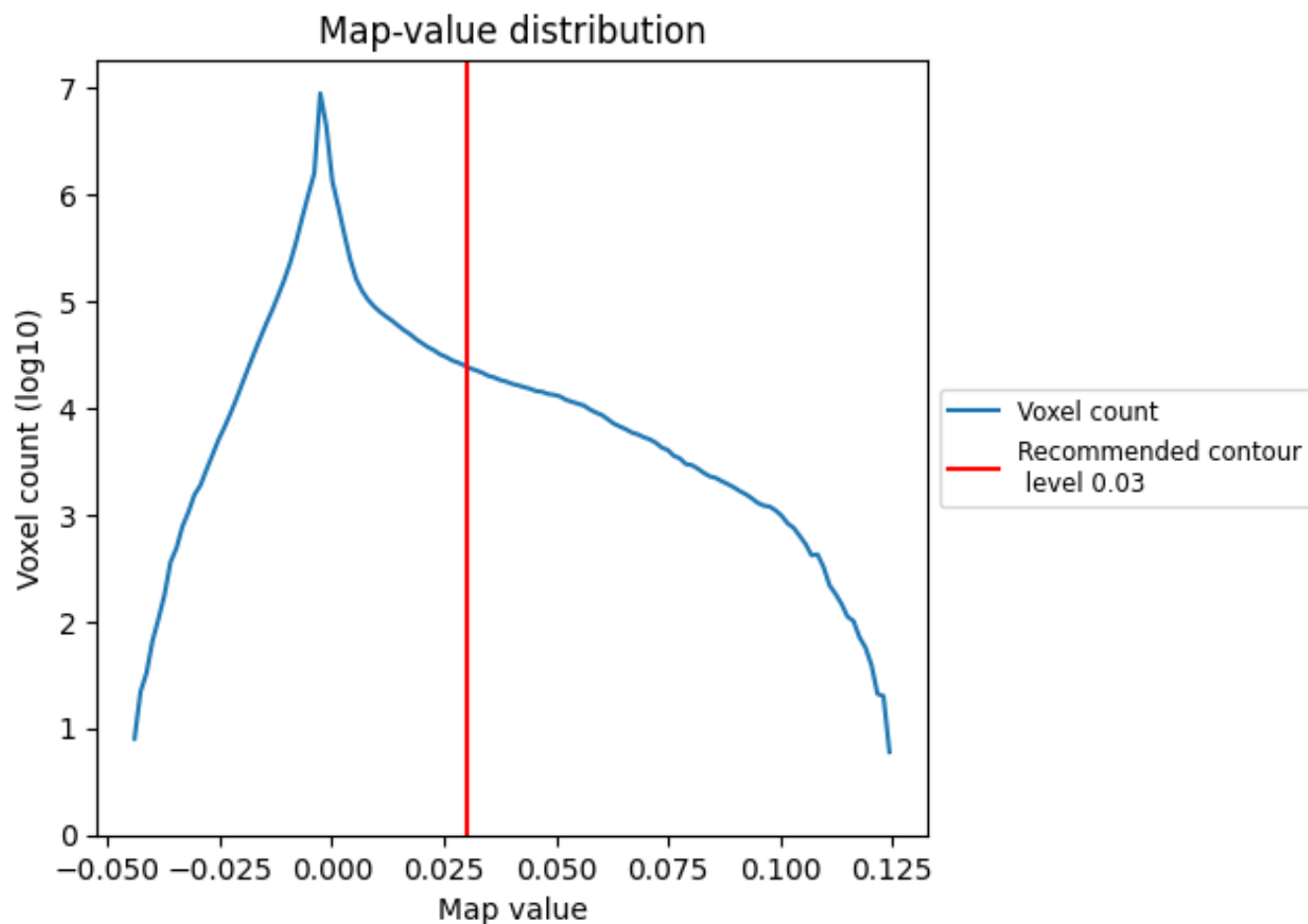
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

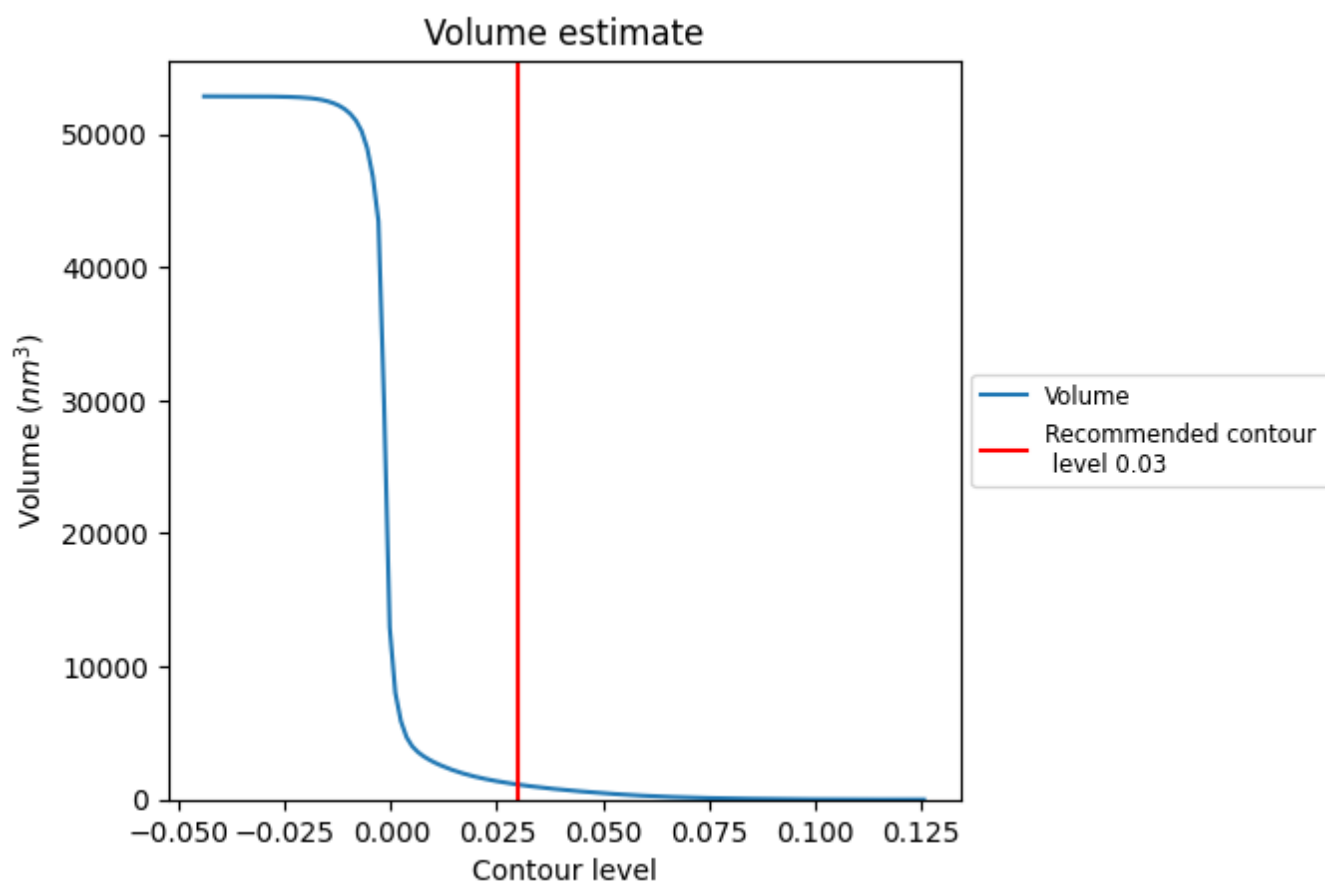
This section contains the results of statistical analysis of the map.

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.

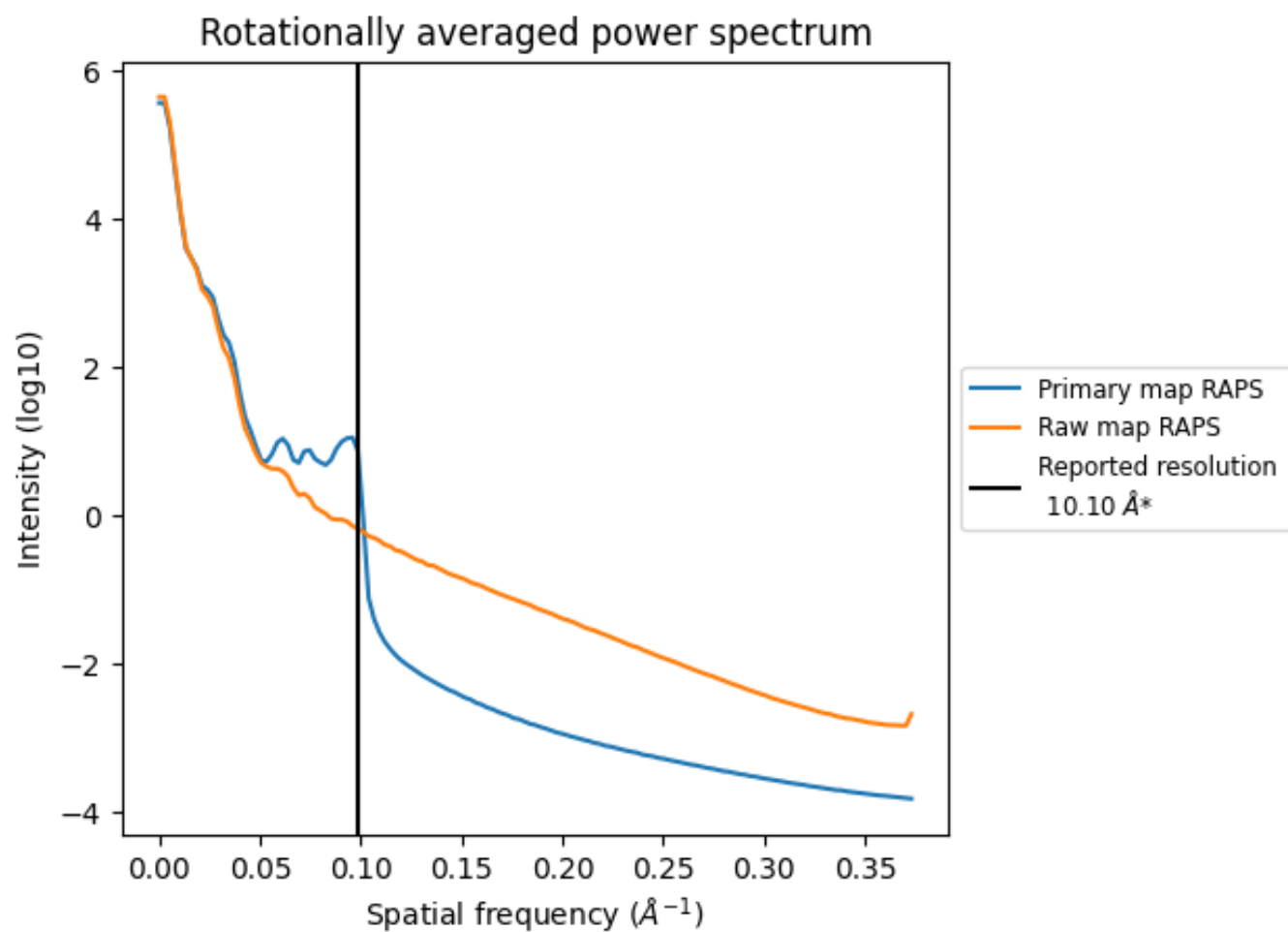
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1127 nm³; this corresponds to an approximate mass of 1018 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 ⓘ

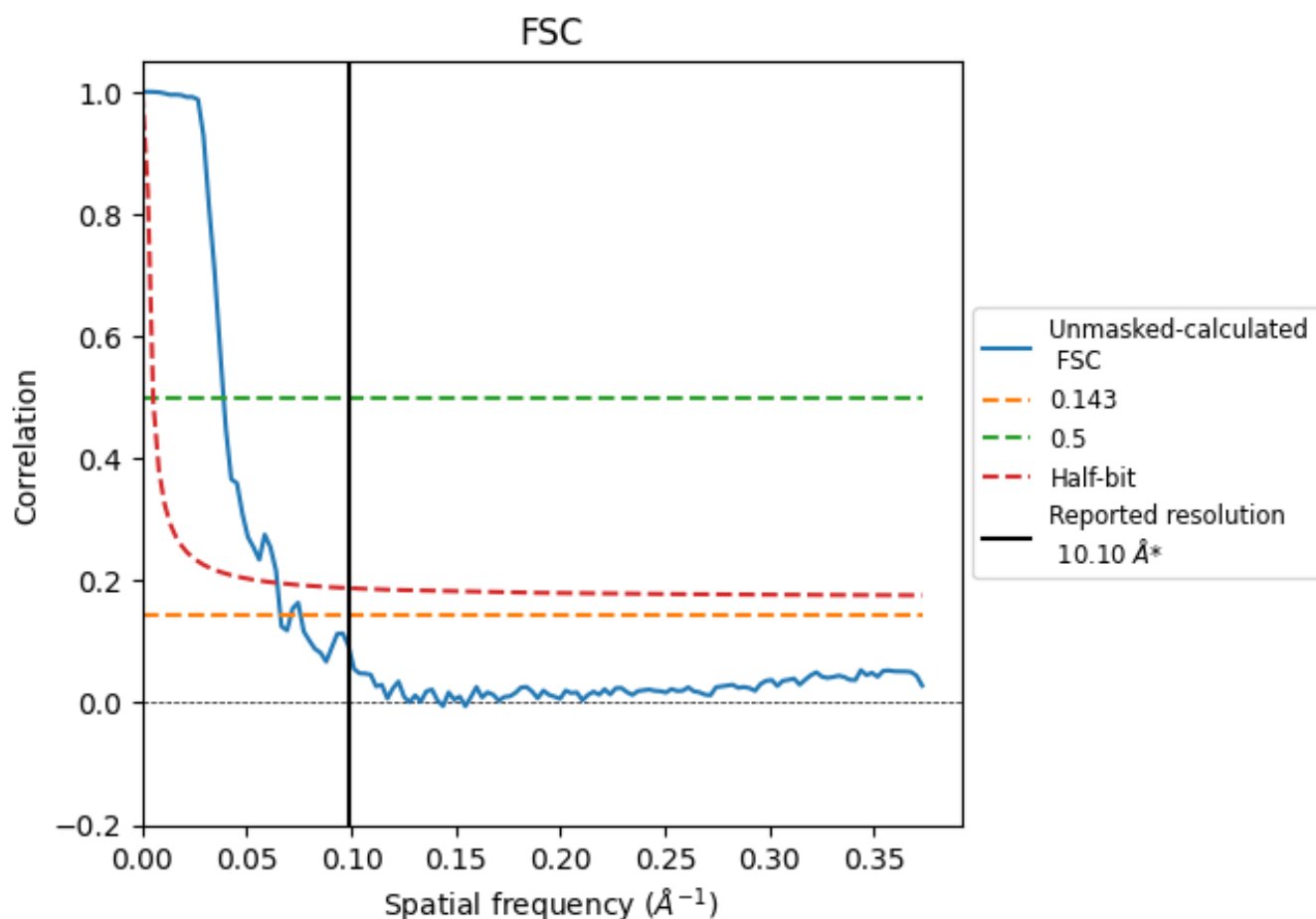


*Reported resolution corresponds to spatial frequency of 0.099 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.099 Å⁻¹

8.2 Resolution estimates [i](#)

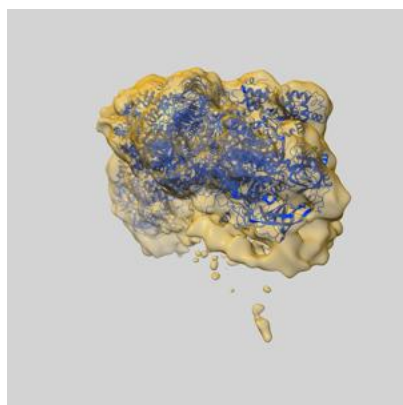
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	10.10	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	15.13	25.71	15.48

*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 15.13 differs from the reported value 10.1 by more than 10 %

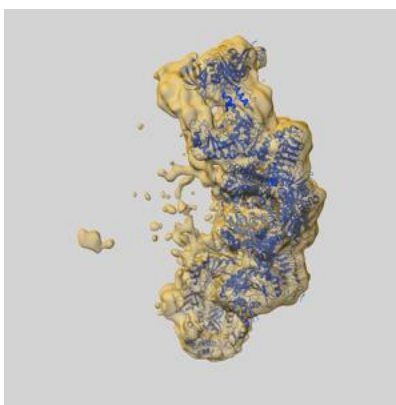
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4547 and PDB model 6QG5. Per-residue inclusion information can be found in section 3 on page 6.

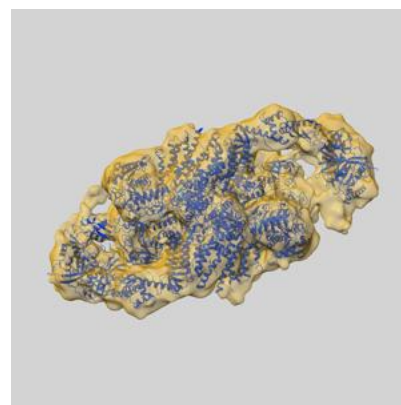
9.1 Map-model overlay [i](#)



X



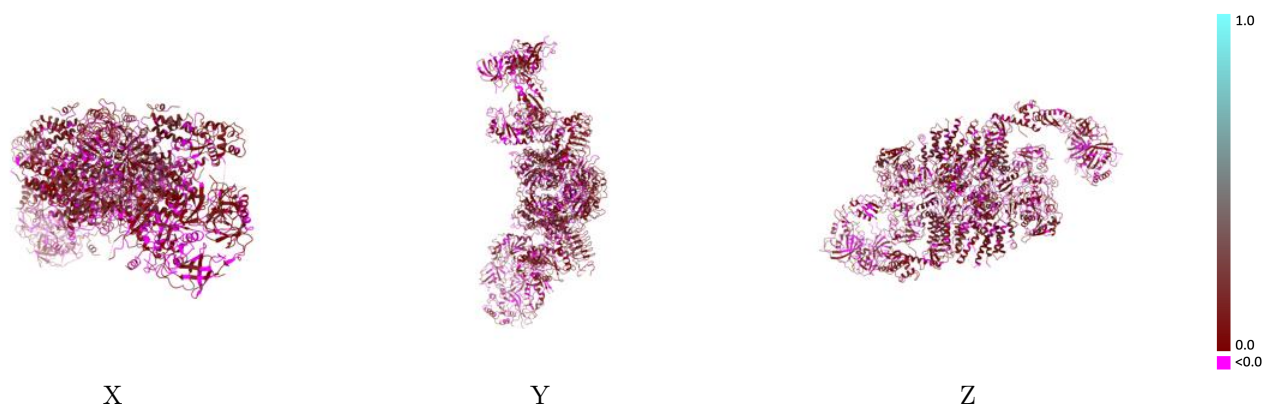
Y



Z

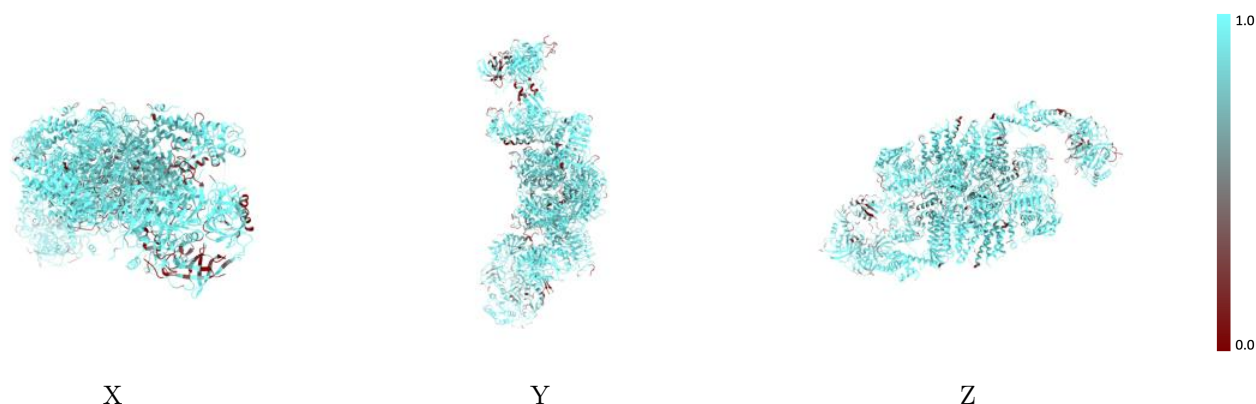
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



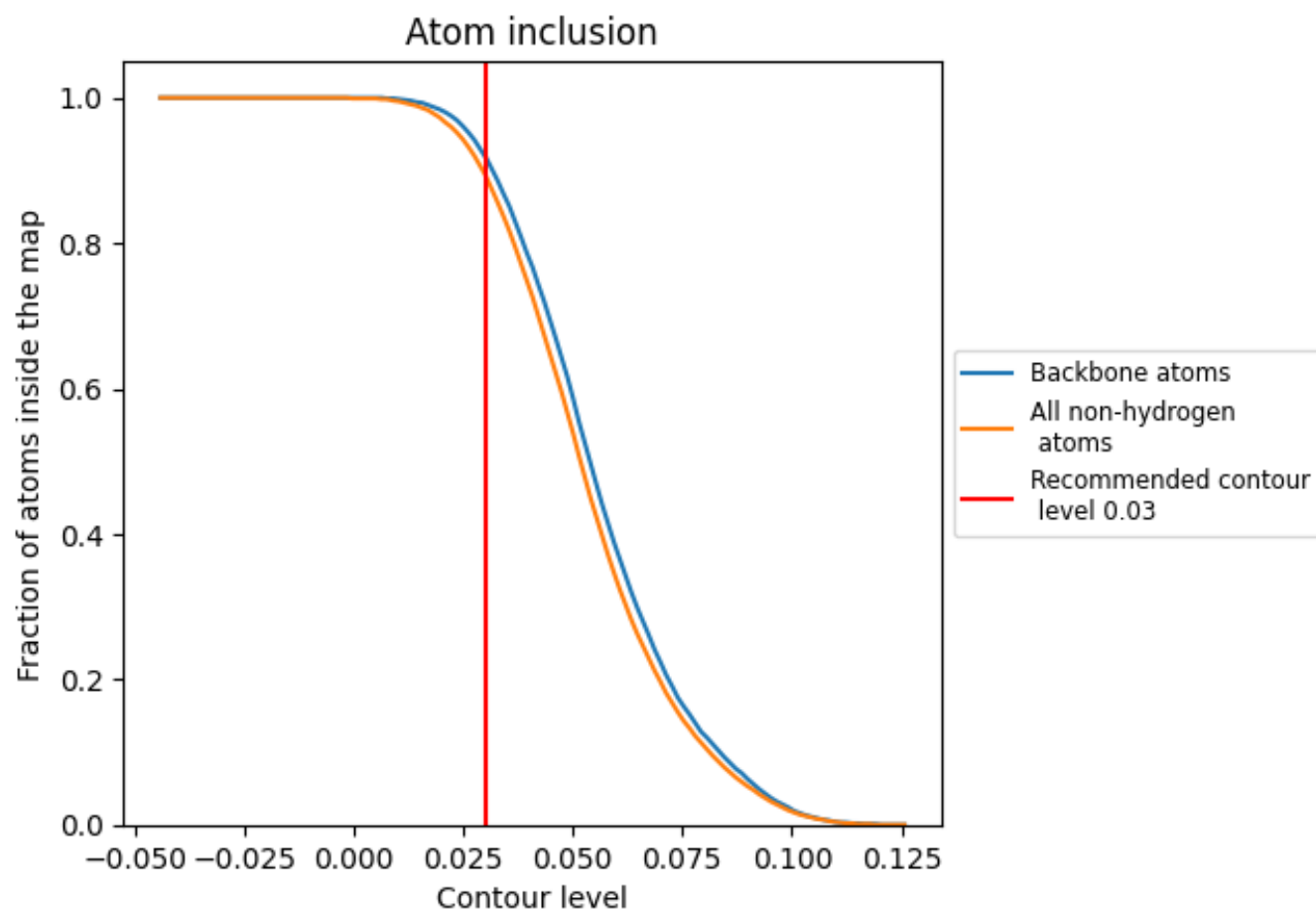
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 89% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8940	 0.0690
A	 0.9750	 0.0770
B	 0.9600	 0.0810
C	 0.9020	 0.0750
D	 0.8880	 0.0740
E	 0.8670	 0.0430
F	 0.9120	 0.0500
G	 0.8500	 0.0880
H	 0.8390	 0.0890
I	 0.9590	 0.0820
J	 0.9620	 0.0820
K	 0.8280	 0.0670
L	 0.9840	 0.0760
M	 0.7870	 0.0350
N	 0.8860	 0.0430
O	 0.9130	 0.0540
P	 0.6850	 0.0590

