



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 05:32 PM UTC

PDB ID : 6QG0 / pdb_00006qg0
EMDB ID : EMD-4543
Title : Structure of eIF2B-eIF2 (phosphorylated at Ser51) complex (model 1)
Authors : Llacer, J.L.; Gordiyenko, Y.; Ramakrishnan, V.
Deposited on : 2019-01-10
Resolution : 4.15 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:

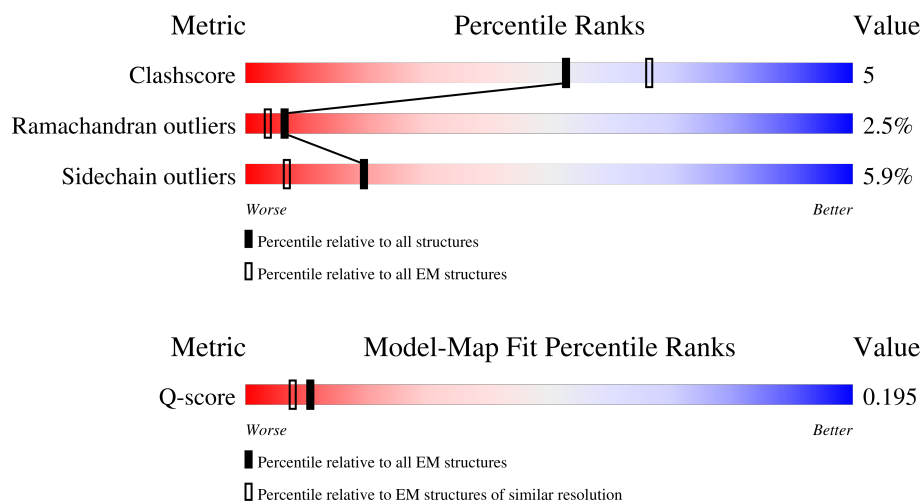
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 4.15 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	5475 (3.66 - 4.65)

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	37% 73% 22% . .
1	B	305	38% 72% 22% . .
2	C	381	19% 73% 16% . 9%
2	D	381	19% 73% 15% . 9%

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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 36980 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	D	345	Total	C	N	O	S	0	0
			2665	1694	463	502	6		
2	C	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	L	246	Total	C	N	O	P S	0	0
			1973	1259	324	381	1 8		
6	K	246	Total	C	N	O	P S	0	0
			1973	1259	324	381	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		

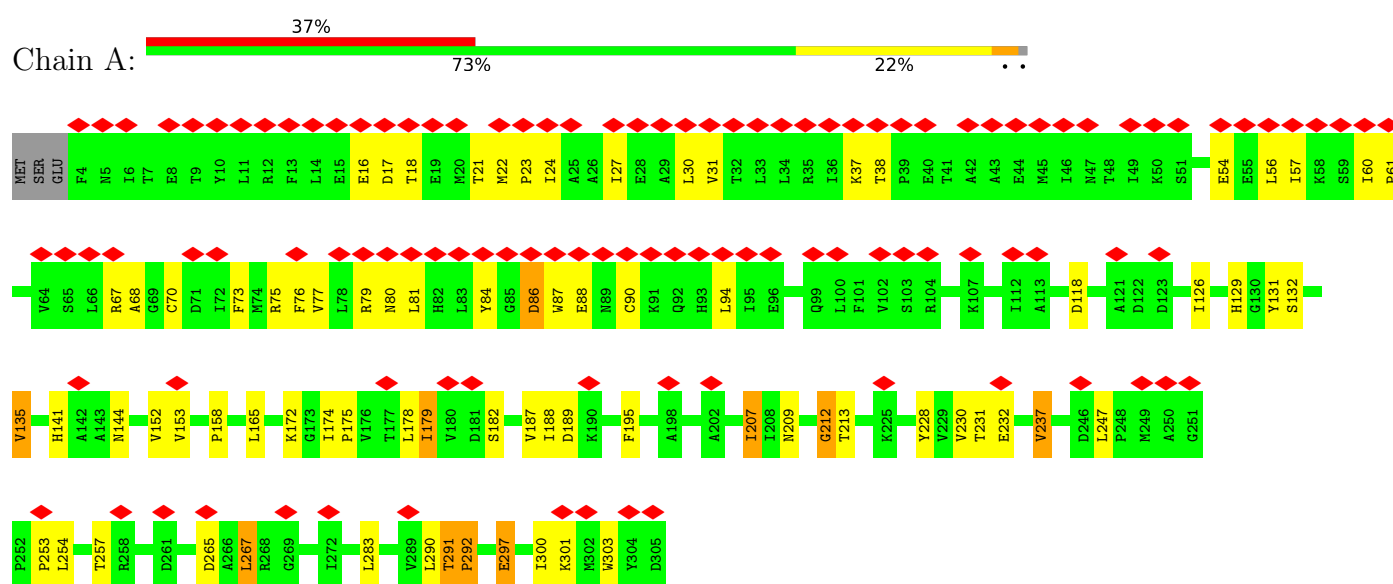
- Molecule 8 is a protein called Eukaryotic translation initiation factor 2 subunit beta.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	O	17	Total	C	N	O	0	0
			143	96	24	23		
8	P	17	Total	C	N	O	0	0
			143	96	24	23		

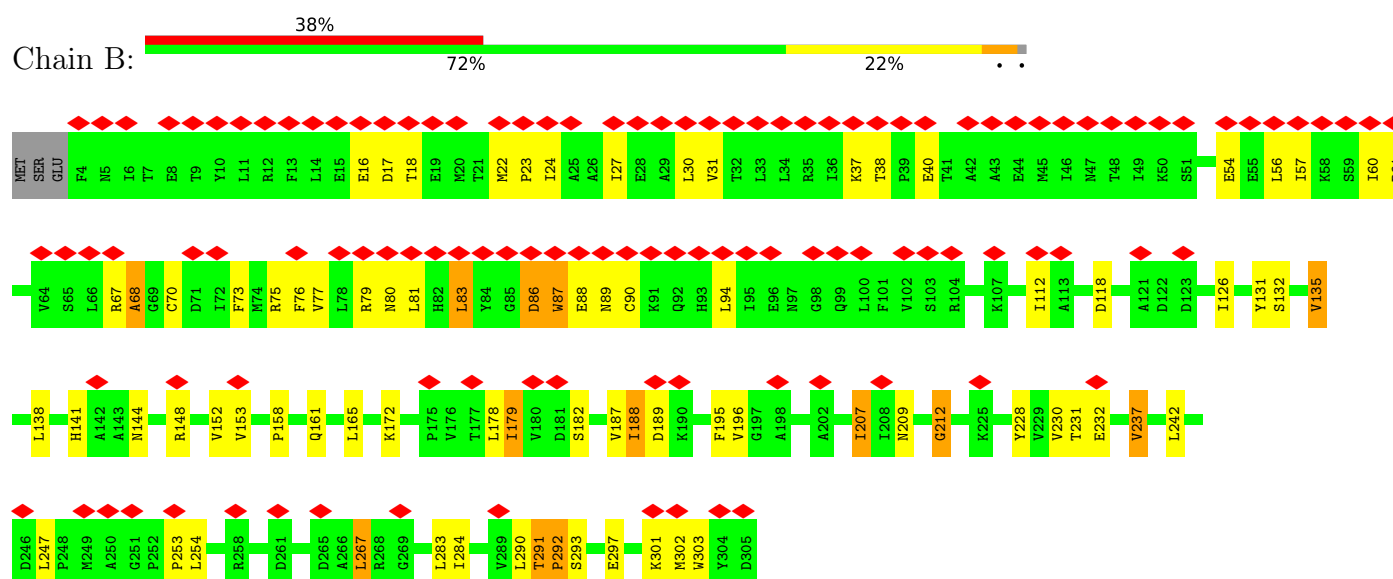
3 Residue-property plots

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.

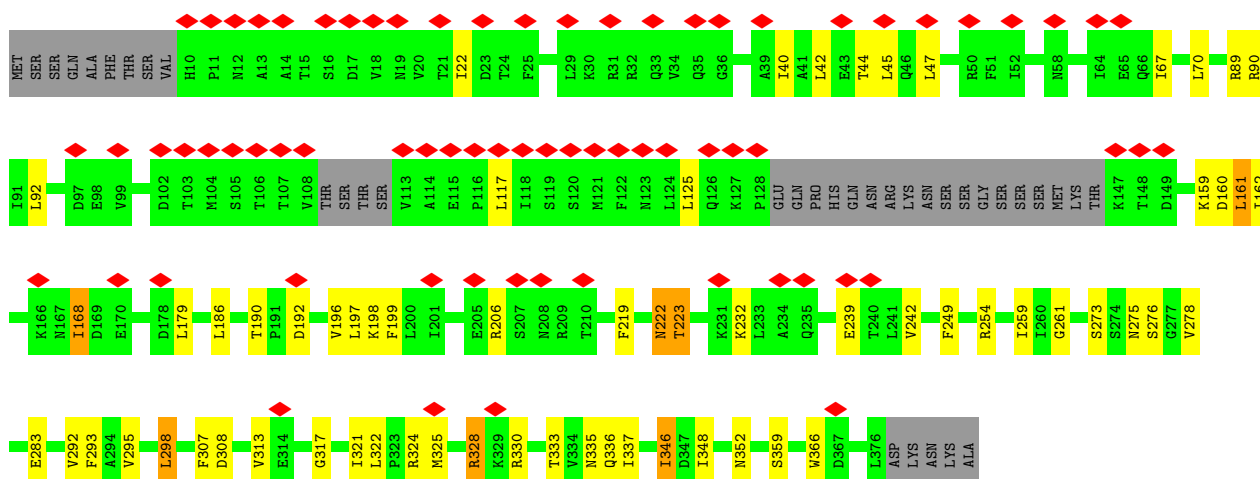
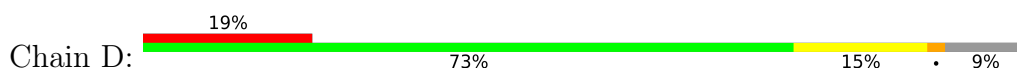
- Molecule 1: Translation initiation factor eIF-2B subunit alpha



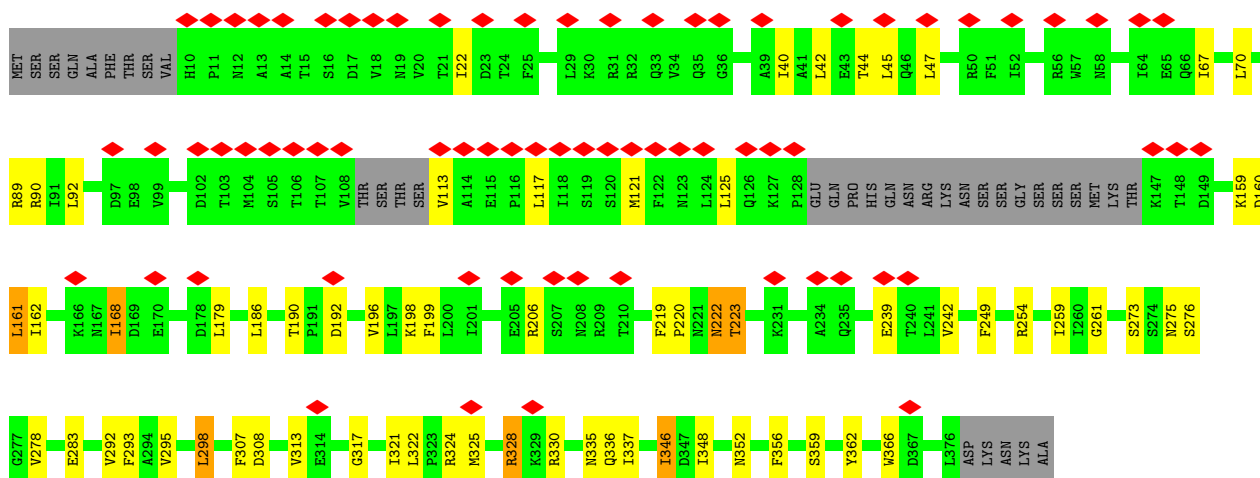
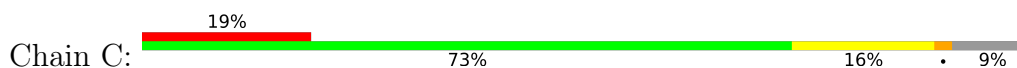
- Molecule 1: Translation initiation factor eIF-2B subunit alpha



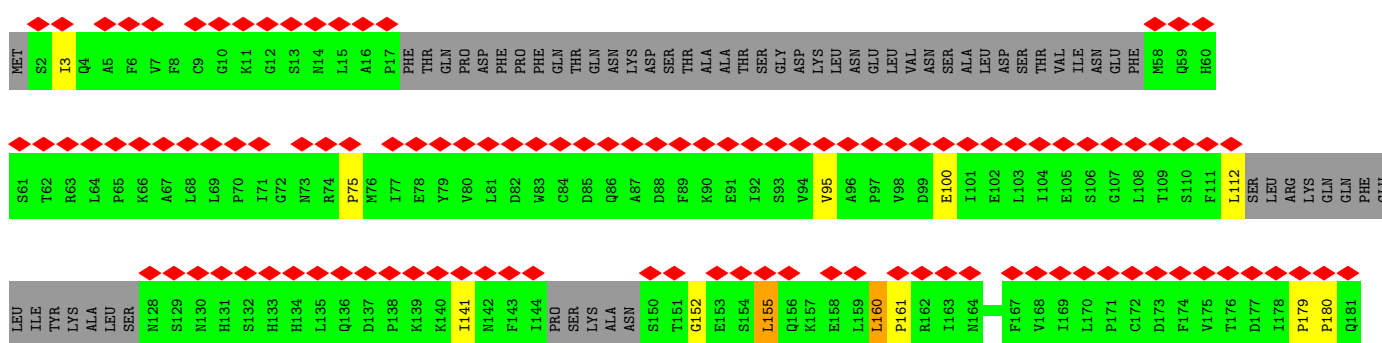
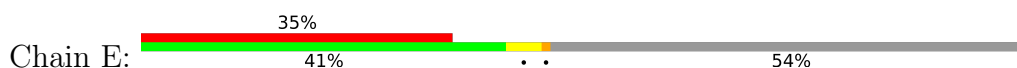
- Molecule 2: Translation initiation factor eIF-2B subunit beta



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



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



[illegible]

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



MET	SER	GLU	SER	GLU	ALA	LYS	SER	ARG	ALA	THR	PRO	PRO	SER	LYS	LYS	GLN	THR	THR	THR	THR	ALA	ALA	ALA	ASN	GLY	GLY	LYS	LYS	ASN	LYS	GLU	LEU	LEU	LYS	GLN	GLU	LYS	LYS	ALA	ALA	LYS	ARG	ALA	ALA	ALA	MET	LYS	GLN	ALA	ALA	ASN	GLY	THR
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SER	ILE	GLU	GLN	GLN	GLN	GLN	ALA	ALA	MET	LYS	LYS	LYS	GLN	LEU	GLN	ARG	GLU	GLN	GLN	LYS	ARG	GLU	GLN	GLN	LYS	GLN	LYS	ASN	ASN	ASN	LYS	LYS	LYS	GLN	ASN	ASN	GLU	ARG	ASN	VAL	LYS	LYS	LYS	SER	SER	THR	THR	LEU	LEU	PHE	GLY	HIS	LYS	LEU	LEU	GLU	THR	THR	GLU	GLU	ARG	ARG	ALA
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THR	ILE	LEU	LEU	LEU	THR	THR	ALA	ALA	VAL	SER	SER	SER	PRO	PRO	LYS	THR	SER	SER	ARG	ILE	THR	ALA	ALA	ALA	LEU	GLY	MET	VAL	VAL	PRO	PRO	VAL	VAL	ALA	ALA	ALA	ALA	ALA	LEU	SER	SER	GLY	ASN	ASN	VAL	VAL	LEU	LEU	THR	THR	ALA	ALA	SER	SER	SER	THR	THR	VAL	SER	SER	ALA	ALA	PRO	PRO	ALA	ALA	ALA	THR
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[illegible]

S241	V242	T243	T244	T245	V246	L247	E248	Q249	S250	N253	S254	S255	L256	T257	SER	S259	V260	K261	E262	L263	L264	L265	N266	K267	D268	L269	L276	S279	Y284	K285	L286	V287	K288	S289	T290	P291	K292	C293	T294	A295	I302	D306	K311	G312	R317	S324	D328	K332
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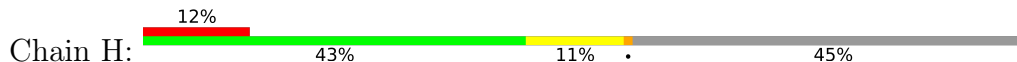
A333	A340	A341	A342	A345	A346	A347	A348	A351	A361	Q373	E377	A382	D383	Q384	L385	L386	L387	D388	S397	T398	V401	V408	L409	T410	F411	L412	L413	L414	H415	H416	I424	T427	V428	V429	D430	S431	F435	M440	M452	L455	L456	L459
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D460	T461	L462	F463	M464	ME1	D466	L472	L478	F482	L483	A487	M494	R498	I501	P502	V505	E508	K511	V516	Q517	V521	T522	F523	N524	F525	L526	A527	D528	P529	N530	D531	L532	V533	D536	E537	E538	N539	P540	V541	R543	R544	G545	N546	K547	V549
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AS49	AS50	AS51	AS52	AS53	AS54	AS55	AS56	AS57	AS58	AS59	AS60	AS61	AS62	AS63	AS64	AS65	AS66	AS67	AS68	AS69	AS70	AS71	AS72	AS73	AS74	AS75	AS76	AS77	AS78	AS79	AS80	AS81	AS82	AS83	AS84	AS85	AS86	AS87	AS88	AS89	AS90	AS91	AS92	AS93	AS94	AS95	AS96	AS97	AS98	AS99	AS100
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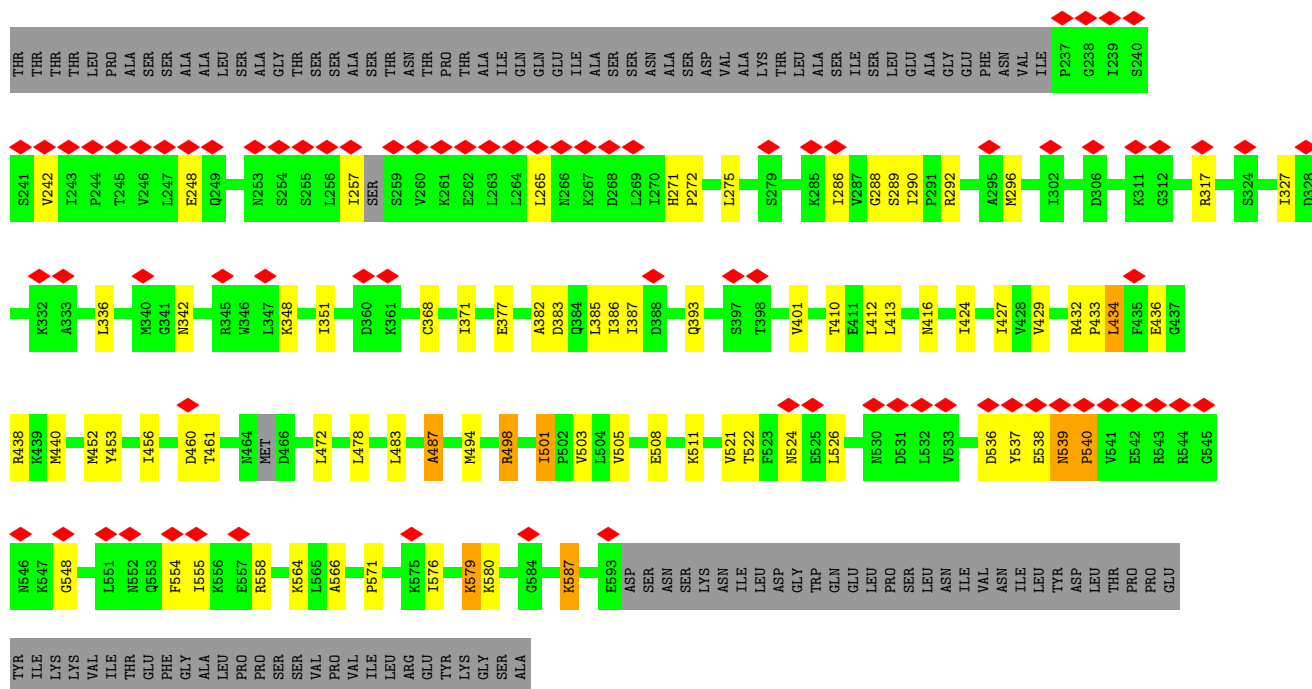
- Molecule 4: Translation initiation factor eIF-2B subunit delta



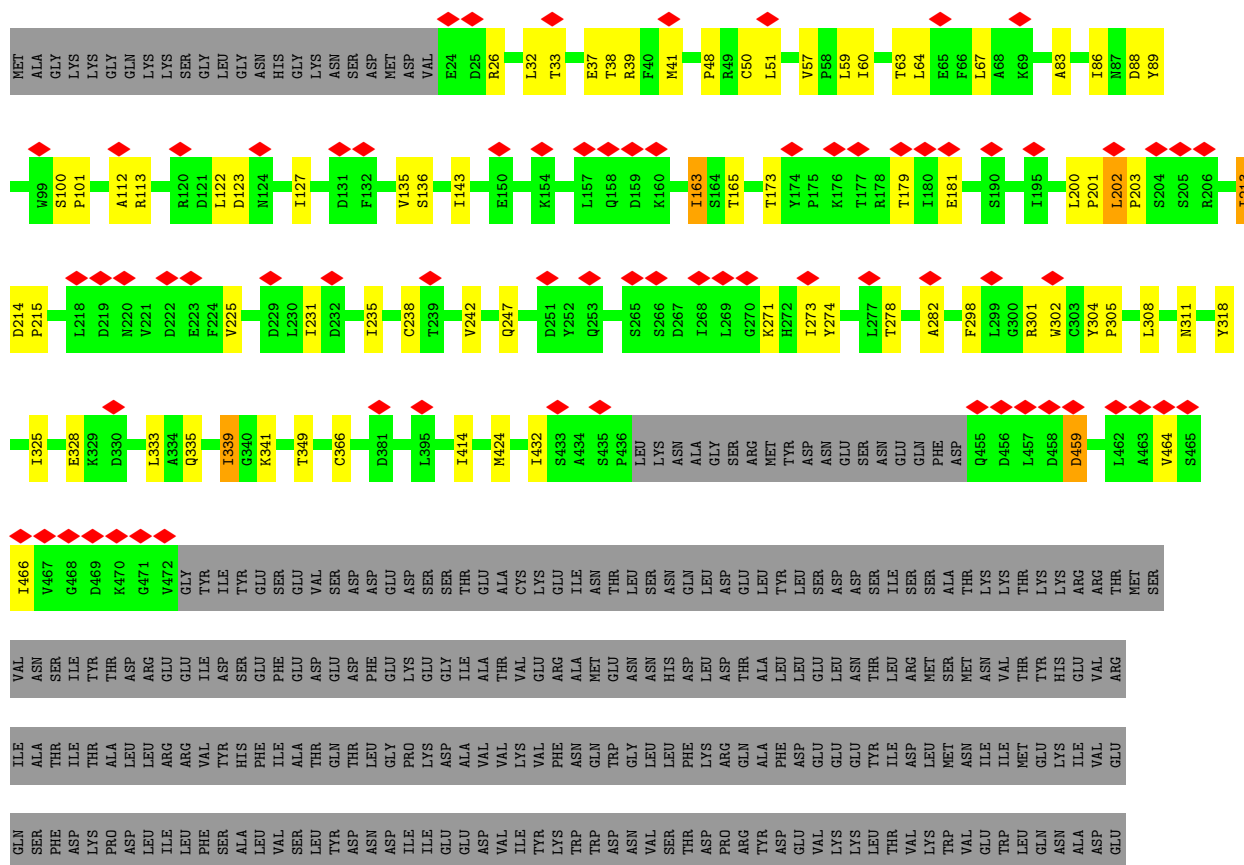
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SER	ILE	GLU	GLN	GLN	GLN	GLN	ALA	ALA	MET	LYS	LYS	GLU	LYS	GLN	LEU	GLN	ARG	GLU	GLN	GLN	GLN	LYS	LYS	GLU	GLN	GLN	GLN	LYS	LYS	ASN	ASN	ALA	ALA	LYS	LYS	LYS	GLN	GLN	GLN	ASN	ASN	ARG	GLU	GLU	ASN	ASN	VAL	LEU	PHE	GLY	HIS	LYS	LYS	LYS	LEU	LEU	GLU	GLU	THR	THR	THR	GLU	GLU	ARG	ARG	ALA
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THR	ILE	LEU	ALA	ALA	THR	SER	ALA	SER	SER	PRO	PRO	LYS	THR	SER	SER	ILE	ARG	THR	ALA	ALA	GLY	LEU	MET	VAL	VAL	VAL	VAL	ALA	ALA	ALA	ALA	LEU	SER	GLY	SER	SER	ASN	VAL	VAL	LEU	LEU	THR	ALA	ALA	SER	SER	SER	SER	THR	THR	VAL	SER	ALA	ALA	SER	PRO	PRO	ALA	ALA	ALA	SER
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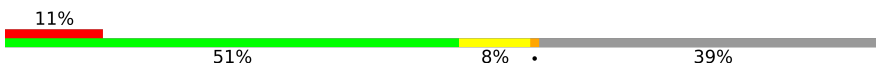


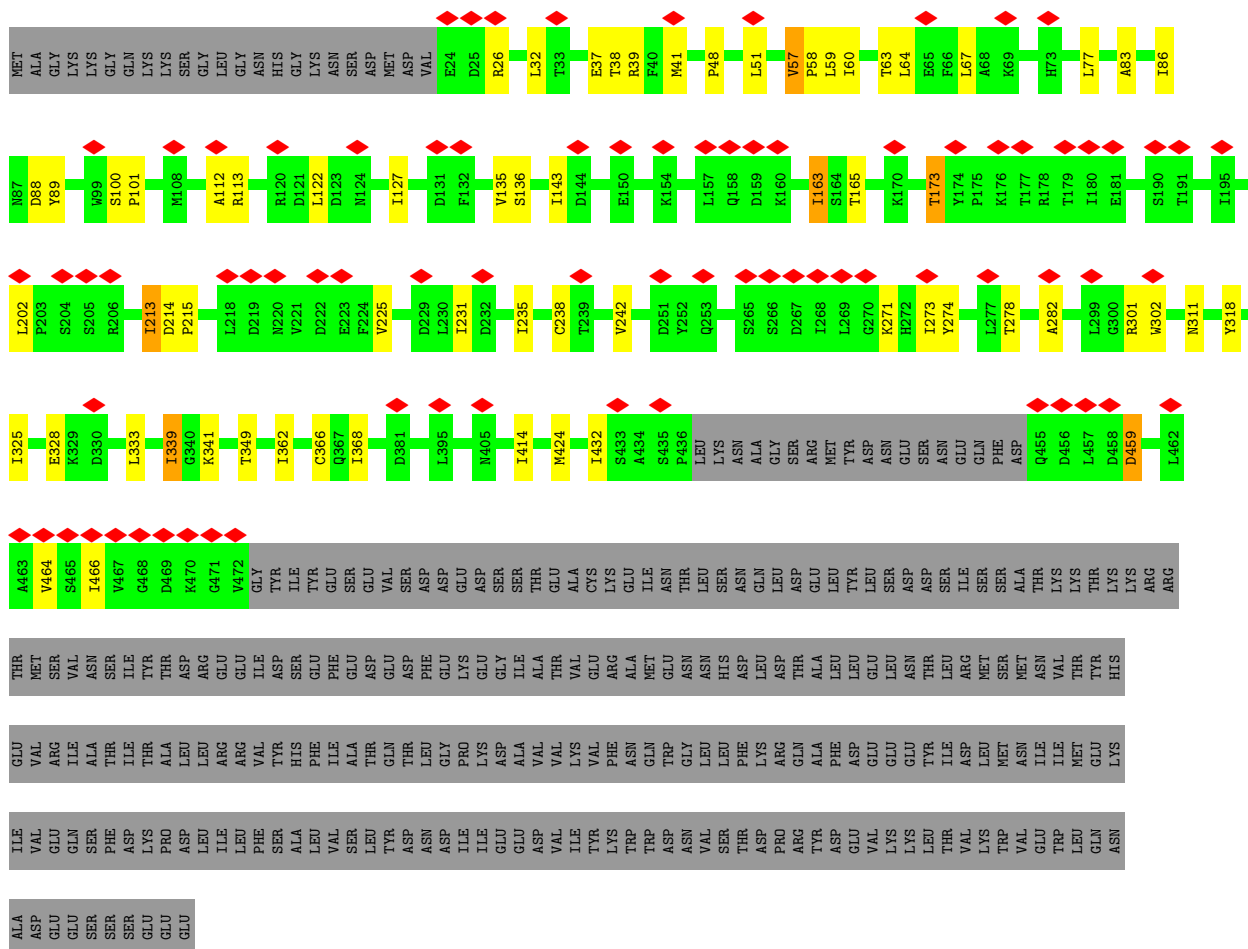
• Molecule 5: Translation initiation factor eIF-2B subunit epsilon



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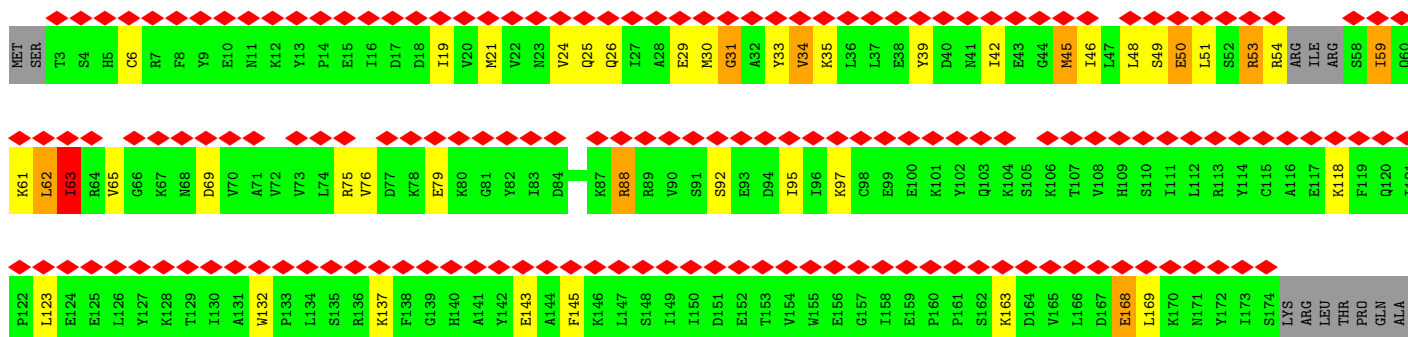
• Molecule 5: Translation initiation factor eIF-2B subunit epsilon

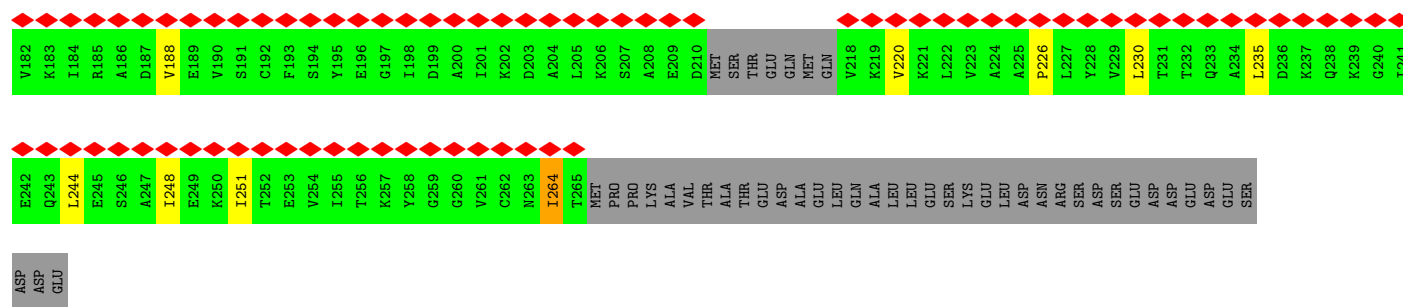
Chain J: 



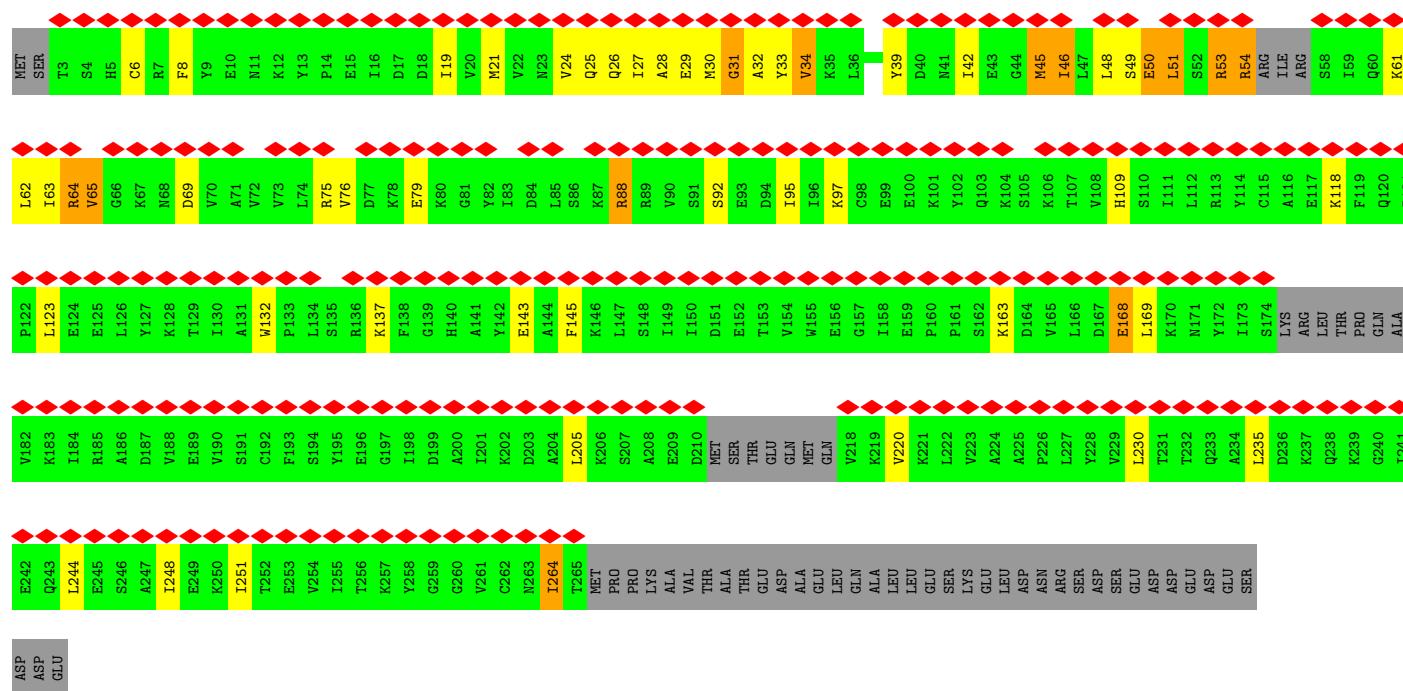
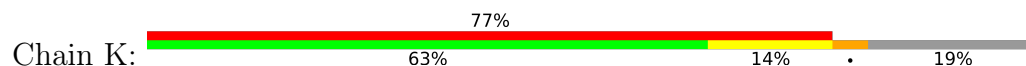
• Molecule 6: Eukaryotic translation initiation factor 2 subunit alpha

Chain L: 

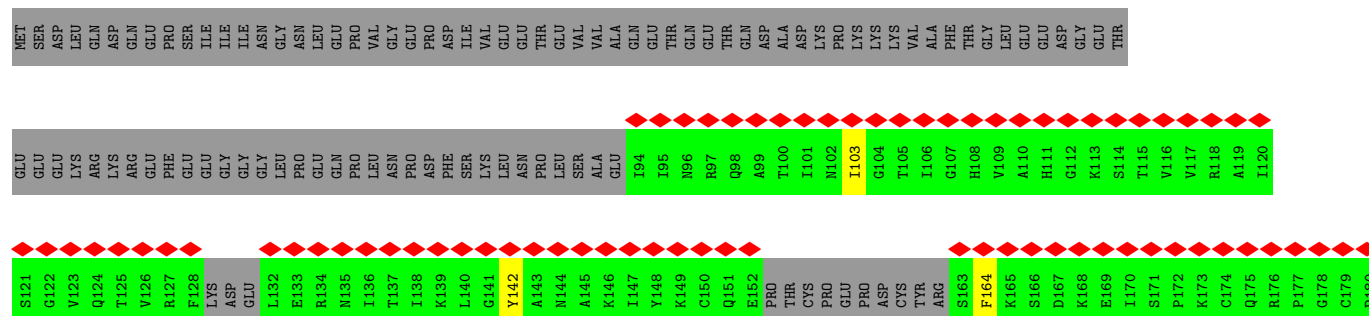
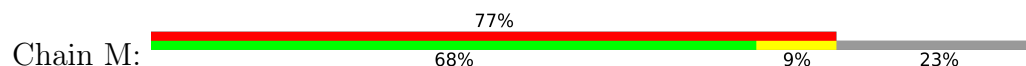




• Molecule 6: Eukaryotic translation initiation factor 2 subunit alpha

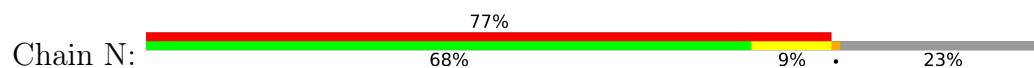


• Molecule 7: Eukaryotic translation initiation factor 2 subunit gamma

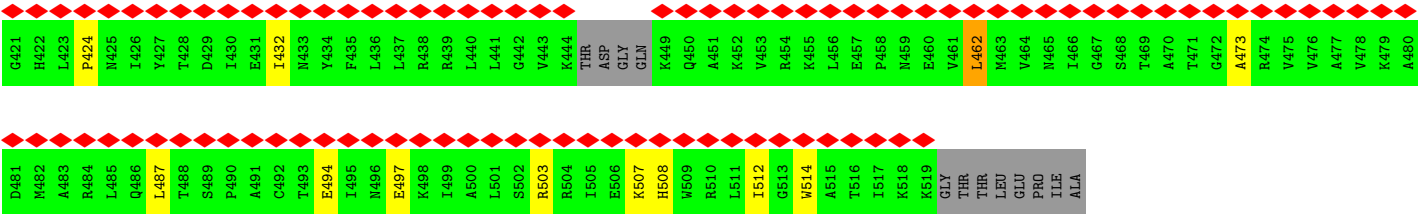


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G421	H422	A423	P424	M425	I426	Y427	T428	D429	I430	E431	I432	M433	Y434	F435	L436	L437	R438	R439	L440	L441	C442	V443	K444	THR	ASP	GLY	GLN	K449	Q450	A451	K452	V453	R454	K455	L456	E457	P458	M459	E460	V461	L462	M463	V464	M465	I466	G467	S468	T469	A470	T471	G472	A473	R474	V475	V476	A477	V478	K479	A480
T361	K362	D363	ASP	K365	G366	K367	I368	Q369	C370	M371	P372	I373	F374	S375	N376	I377	V378	S379	L380	F381	A382	E383	Q384	N385	D386	L387	K388	F389	A390	V391	P392	G393	G394	L395	I396	G397	V398	G399	T400	K401	V402	D403	P404	T405	L406	C407	R408	A409	D410	R411	L412	V413	Q414	V415	V416	V417	C418	A419	K420
T301	I302	P303	V304	P305	P306	R307	D308	F309	M310	I311	S312	P313	R314	L315	I316	V317	I318	R319	S320	F321	D322	Q323	N324	K325	P326	G327	A328	E329	I330	E331	D332	L333	K334	G335	G336	V337	A338	G339	C340	S341	I342	L343	N344	T405	L406	F347	K348	A409	N290	D351	D292	A293	V294	N295	E296	F297	C358	I359	V360
L241	K242	H243	V244	I245	I246	L247	Q248	N249	K250	V251	D252	L253	M254	R255	E256	E257	S258	A259	L260	E261	H262	Q263	K264	S265	I266	L267	K268	F269	I270	R271	G272	T273	I274	A275	D276	G277	A278	P279	I280	N281	P282	L283	S284	A285	Q286	L287	K288	Y289	N290	I291	D292	L233	A234	A235	I236	E237	I238	M239	K240
G181	R182	Y183	K184	L185	V186	R187	H188	V189	S190	F191	V192	D193	C194	P195	G196	H197	D198	I199	L200	M201	S202	T203	M204	L205	S206	G207	A208	A209	V210	M211	D212	A213	A214	L215	L216	L217	I218	A219	G220	N221	E222	S223	C224	P225	Q226	P227	Q228	T229	S230	E231	H232	L233	A234	A235	I236	E237	I238	M239	K240

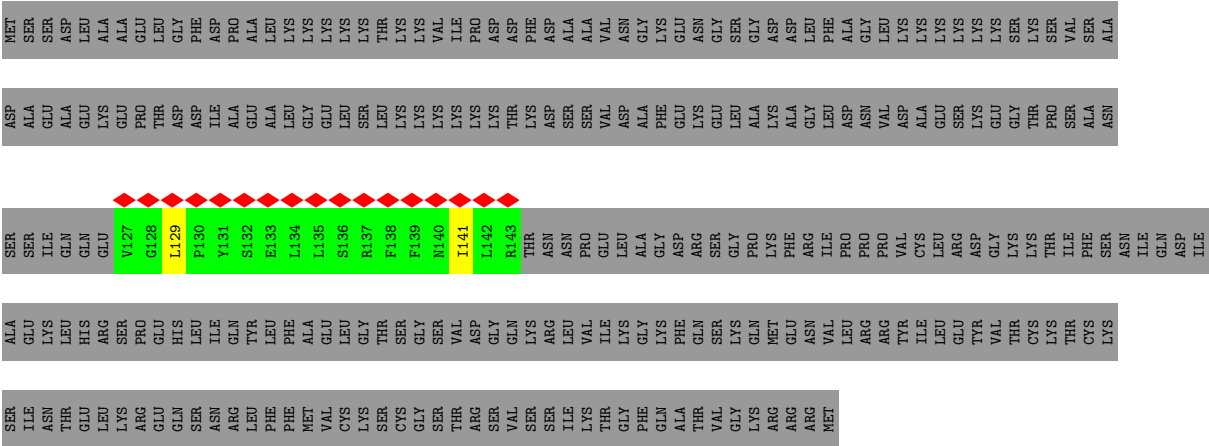
• Molecule 7: Eukaryotic translation initiation factor 2 subunit gamma



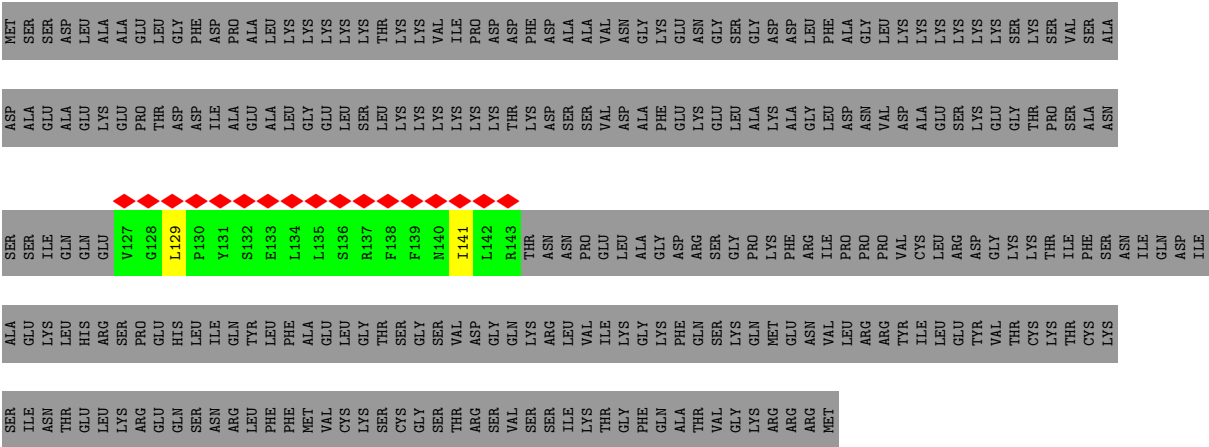
MET	SER	ASP	LEU	GLN	ASP	GLN	GLU	PRO	SER	ILE	ILE	ILE	ASN	GLY	ASN	GLU	PRO	VAL	GLY	GLU	VAL	THR	GLU	GLN	THR	GLU	GLN	GLN	GLN	ASP	ALA	ASP	LYS	PRO	LYS	LYS	VAL	ALA	PHE	THR	GLY	LEU	GLU	ASP	GLY	GLU	THR	



• Molecule 8: Eukaryotic translation initiation factor 2 subunit beta



• Molecule 8: Eukaryotic translation initiation factor 2 subunit beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	131663	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 ($e^-/\text{\AA}^2$)	21	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	0.579	Depositor
Minimum map value	-0.341	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	375.2, 375.2, 375.2	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.65	0/2395	1.01	2/3251 (0.1%)
1	B	0.68	2/2395 (0.1%)	1.01	2/3251 (0.1%)
2	C	0.56	0/2714	1.01	0/3693
2	D	0.56	0/2714	1.00	0/3693
3	E	0.61	0/2209	0.90	0/2989
3	F	0.61	0/2209	0.90	0/2989
4	G	0.60	0/2781	1.02	0/3747
4	H	0.60	0/2781	1.03	1/3747 (0.0%)
5	I	0.55	0/3468	0.93	3/4704 (0.1%)
5	J	0.56	0/3468	0.93	2/4704 (0.0%)
6	K	0.66	0/1988	0.98	0/2674
6	L	0.66	0/1988	0.96	0/2674
7	M	0.67	0/3087	0.90	1/4173 (0.0%)
7	N	0.67	0/3087	0.90	1/4173 (0.0%)
8	O	0.61	0/146	0.93	0/196
8	P	0.61	0/146	0.92	0/196
All	All	0.61	2/37576 (0.0%)	0.96	12/50854 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	89	ASN	N-CA	6.61	1.54	1.46
1	B	68	ALA	C-N	-5.66	1.25	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	N	356	ARG	N-CA-C	6.75	121.39	112.35
7	M	356	ARG	N-CA-C	6.74	121.39	112.35
4	H	501	ILE	N-CA-C	6.21	114.80	109.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	207	ILE	N-CA-C	5.29	116.34	108.46
1	B	207	ILE	N-CA-C	5.24	116.27	108.46

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	A	2351	0	2365	47	0
1	B	2351	0	2365	55	0
2	C	2665	0	2626	40	0
2	D	2665	0	2626	34	0
3	E	2164	0	2154	12	0
3	F	2164	0	2154	10	0
4	G	2744	0	2819	37	0
4	H	2744	0	2819	39	0
5	I	3406	0	3359	31	0
5	J	3406	0	3359	26	0
6	K	1973	0	2016	40	0
6	L	1973	0	2014	50	0
7	M	3044	0	3126	18	0
7	N	3044	0	3126	17	0
8	O	143	0	148	0	0
8	P	143	0	148	0	0
All	All	36980	0	37224	396	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 396 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)
6:L:25:GLN:OE1	6:L:35:LYS:HE2	1.34	1.21
6:L:25:GLN:OE1	6:L:35:LYS:CE	1.98	1.11

Continued on next page...

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:L:26:GLN:HG2	6:L:33:TYR:N	1.34	1.10
1:A:31:VAL:HG22	1:A:73:PHE:CE2	1.89	1.06
1:B:81:LEU:HG	1:B:90:CYS:SG	1.95	1.05

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%)	260 (87%)	28 (9%)	12 (4%)	2	19
1	B	300/305 (98%)	261 (87%)	26 (9%)	13 (4%)	2	18
2	C	339/381 (89%)	302 (89%)	31 (9%)	6 (2%)	6	33
2	D	339/381 (89%)	302 (89%)	31 (9%)	6 (2%)	6	33
3	E	253/578 (44%)	218 (86%)	30 (12%)	5 (2%)	6	31
3	F	253/578 (44%)	222 (88%)	26 (10%)	5 (2%)	6	31
4	G	349/651 (54%)	298 (85%)	41 (12%)	10 (3%)	3	24
4	H	349/651 (54%)	300 (86%)	35 (10%)	14 (4%)	2	19
5	I	427/712 (60%)	388 (91%)	31 (7%)	8 (2%)	6	32
5	J	427/712 (60%)	387 (91%)	32 (8%)	8 (2%)	6	32
6	K	237/304 (78%)	199 (84%)	30 (13%)	8 (3%)	3	21
6	L	237/304 (78%)	199 (84%)	29 (12%)	9 (4%)	2	20
7	M	398/527 (76%)	347 (87%)	47 (12%)	4 (1%)	12	46
7	N	398/527 (76%)	351 (88%)	43 (11%)	4 (1%)	12	46
8	O	15/285 (5%)	12 (80%)	2 (13%)	1 (7%)	1	12
8	P	15/285 (5%)	12 (80%)	2 (13%)	1 (7%)	1	12
All	All	4636/7486 (62%)	4058 (88%)	464 (10%)	114 (2%)	6	27

5 of 114 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	292	PRO
1	B	158	PRO
1	B	292	PRO
4	H	487	ALA
5	I	202	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	257/265 (97%)	236 (92%)	21 (8%)	10	31
1	B	257/265 (97%)	236 (92%)	21 (8%)	10	31
2	C	286/338 (85%)	266 (93%)	20 (7%)	14	37
2	D	286/338 (85%)	266 (93%)	20 (7%)	14	37
3	E	249/529 (47%)	243 (98%)	6 (2%)	43	63
3	F	249/529 (47%)	242 (97%)	7 (3%)	38	59
4	G	305/561 (54%)	293 (96%)	12 (4%)	28	50
4	H	305/561 (54%)	288 (94%)	17 (6%)	19	42
5	I	389/649 (60%)	371 (95%)	18 (5%)	24	46
5	J	389/649 (60%)	370 (95%)	19 (5%)	22	45
6	K	218/273 (80%)	192 (88%)	26 (12%)	5	19
6	L	218/273 (80%)	193 (88%)	25 (12%)	5	20
7	M	319/449 (71%)	306 (96%)	13 (4%)	27	49
7	N	319/449 (71%)	305 (96%)	14 (4%)	25	48
8	O	16/246 (6%)	15 (94%)	1 (6%)	16	39
8	P	16/246 (6%)	15 (94%)	1 (6%)	16	39
All	All	4078/6620 (62%)	3837 (94%)	241 (6%)	19	41

5 of 241 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	I	213	ILE
2	C	22	ILE
6	L	42	ILE
6	K	251	ILE
2	C	328	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 89 such sidechains are listed below:

Mol	Chain	Res	Type
7	M	144	ASN
7	N	508	HIS
7	M	226	GLN
7	N	98	GLN
6	K	60	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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	0.81	0	7,12,14	1.14	0
6	SEP	K	52	6	8,9,10	0.89	0	7,12,14	1.24	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	-	6/6/8/10	-
6	SEP	K	52	6	-	6/6/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	52	SEP	C-CA-CB-OG
6	L	52	SEP	CA-CB-OG-P
6	L	52	SEP	CB-OG-P-O2P
6	L	52	SEP	CB-OG-P-O3P
6	K	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.

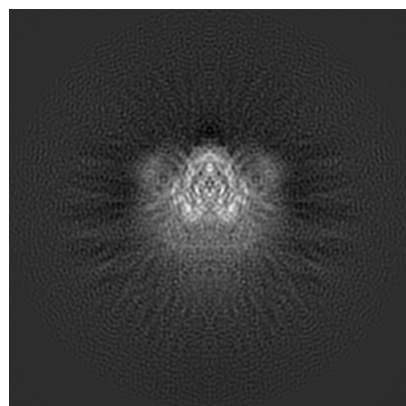
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4543. These allow visual inspection of the internal detail of the map and identification of artifacts.

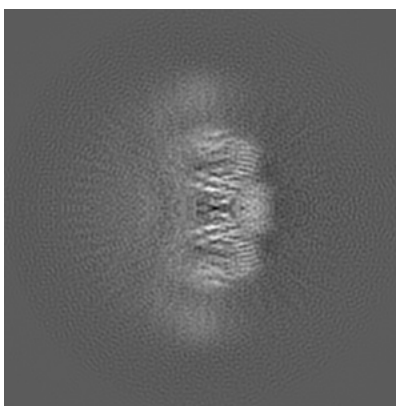
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

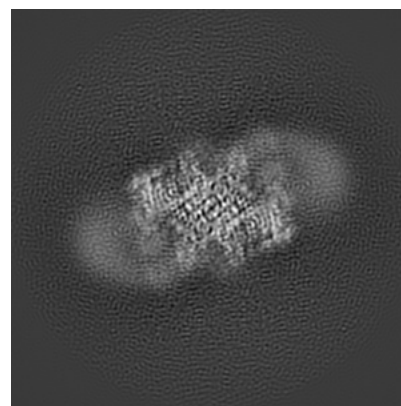
6.1.1 Primary map



X

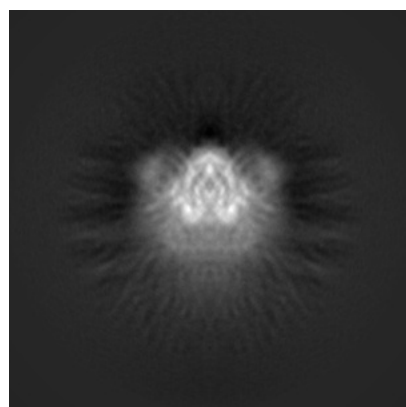


Y

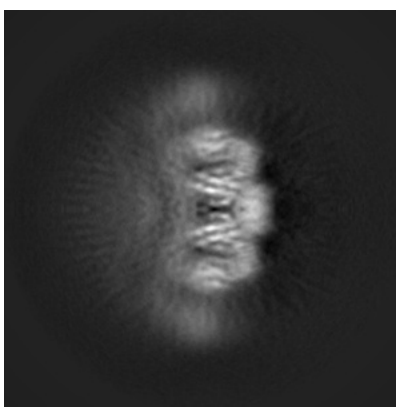


Z

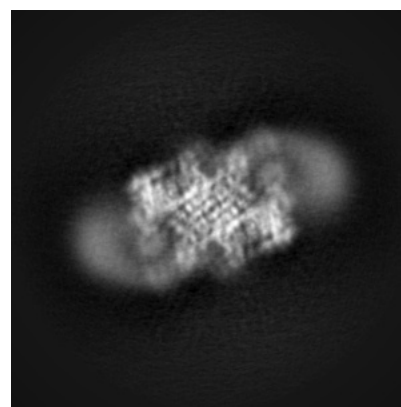
6.1.2 Raw map



X



Y

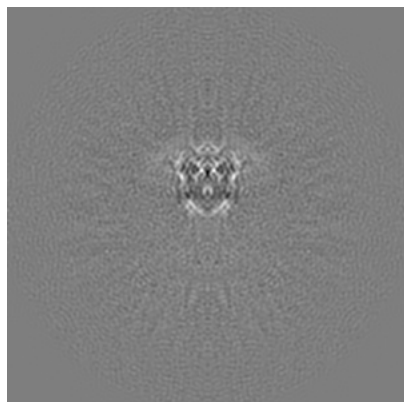


Z

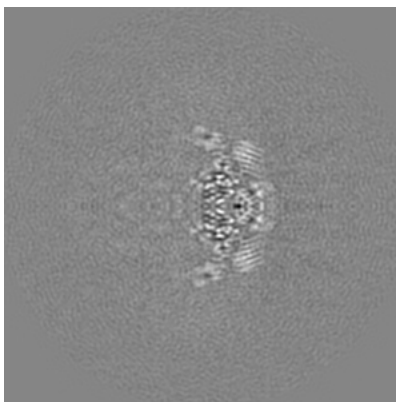
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

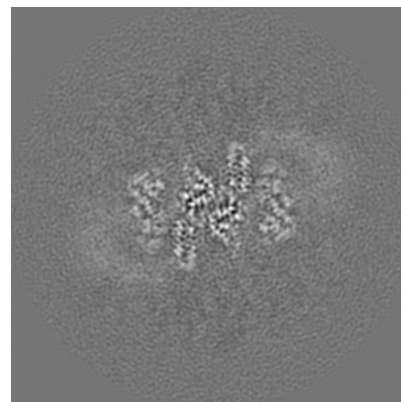
6.2.1 Primary map



X Index: 140

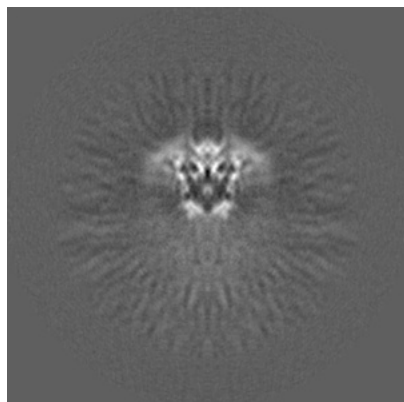


Y Index: 140

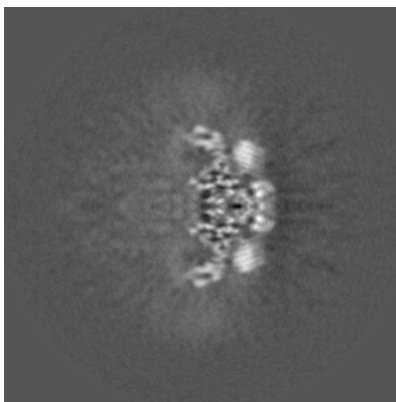


Z Index: 140

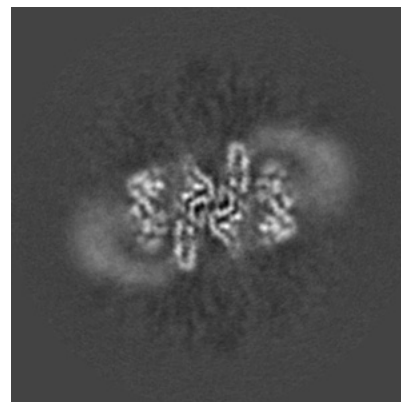
6.2.2 Raw map



X Index: 140



Y Index: 140

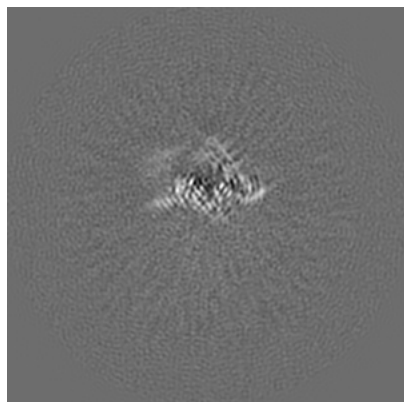


Z Index: 140

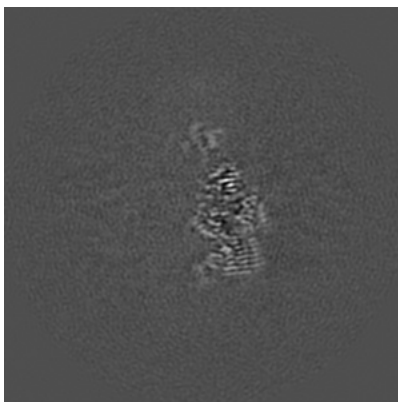
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

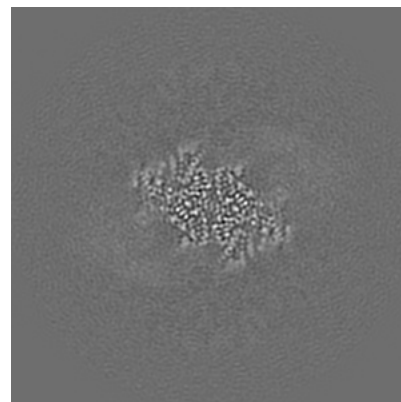
6.3.1 Primary map



X Index: 127

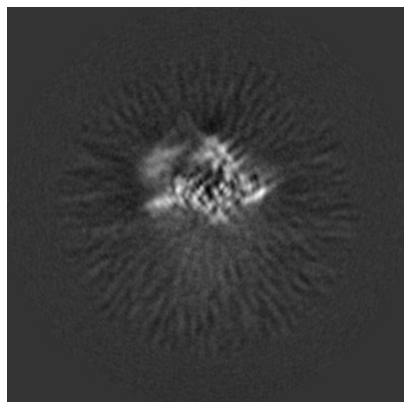


Y Index: 147

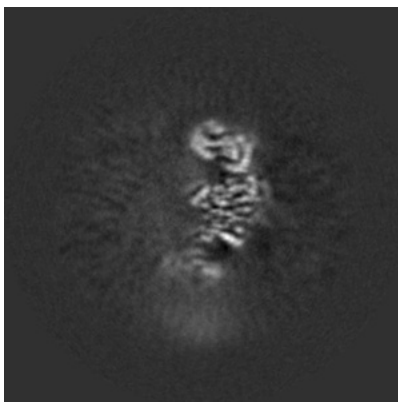


Z Index: 153

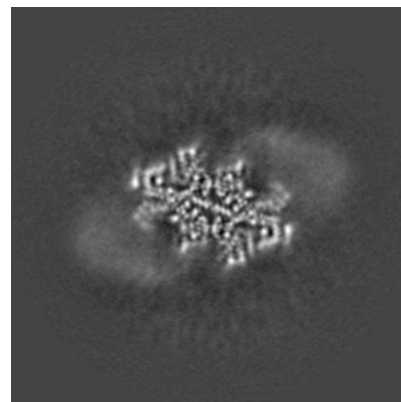
6.3.2 Raw map



X Index: 127



Y Index: 126

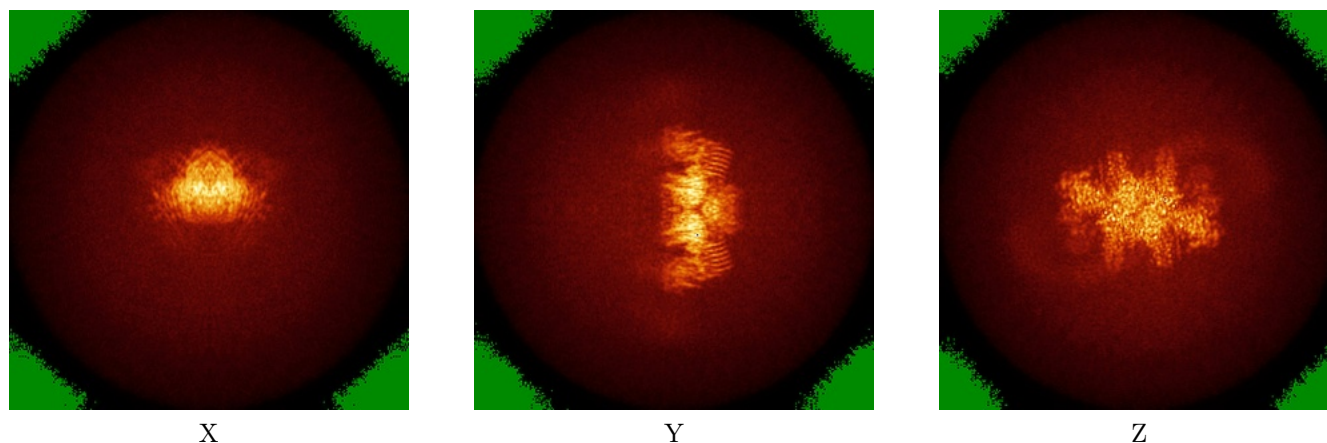


Z Index: 151

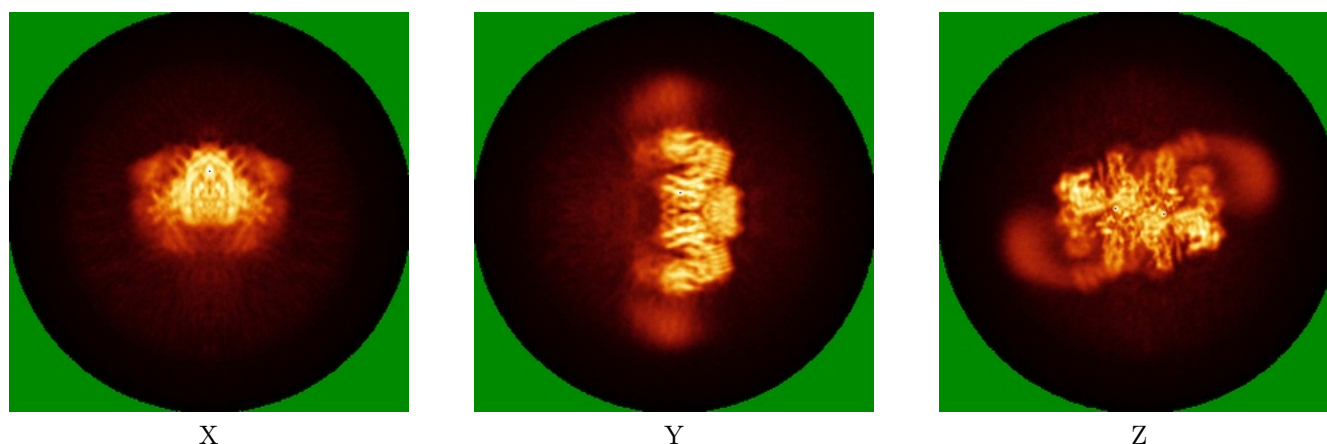
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

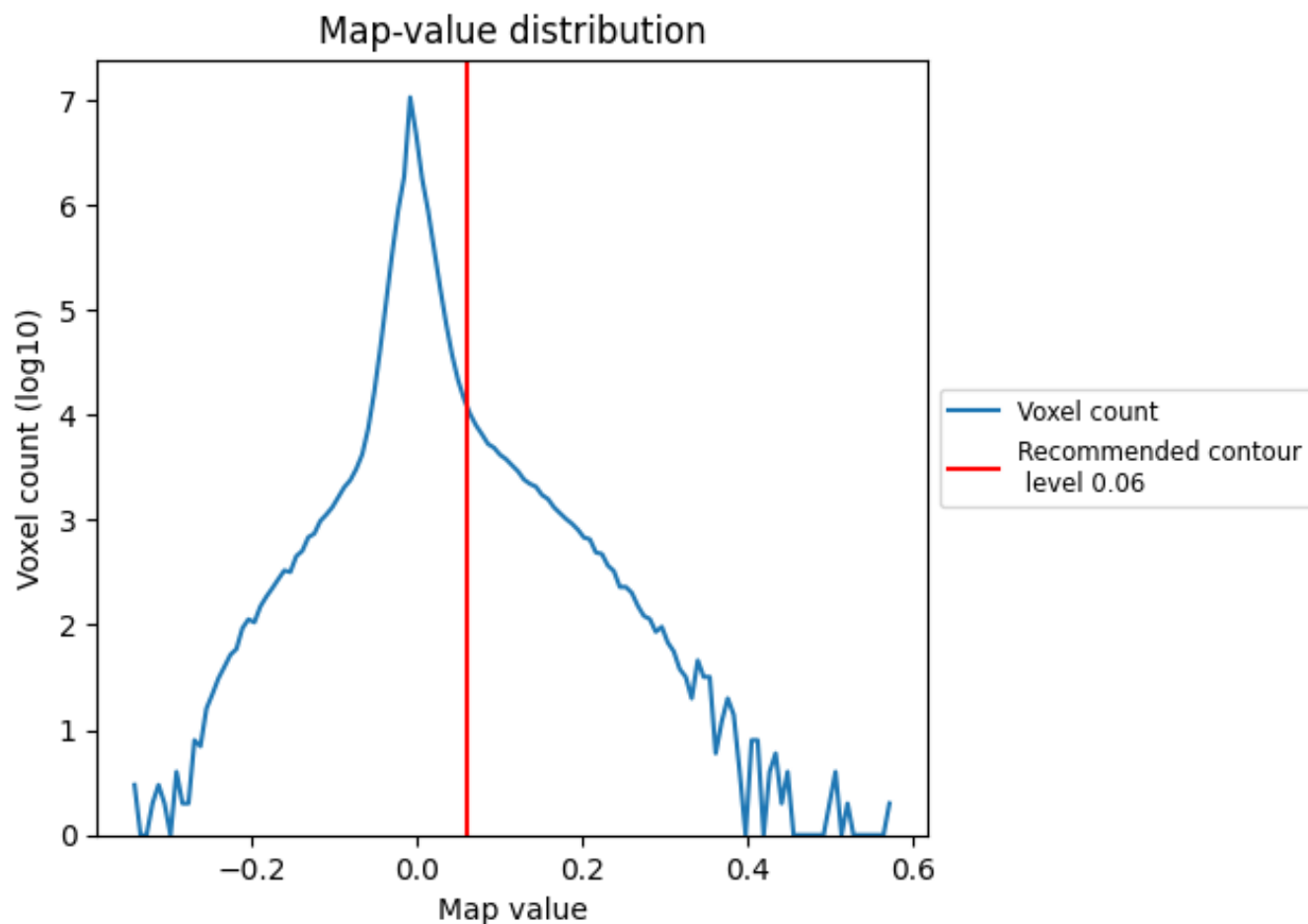
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

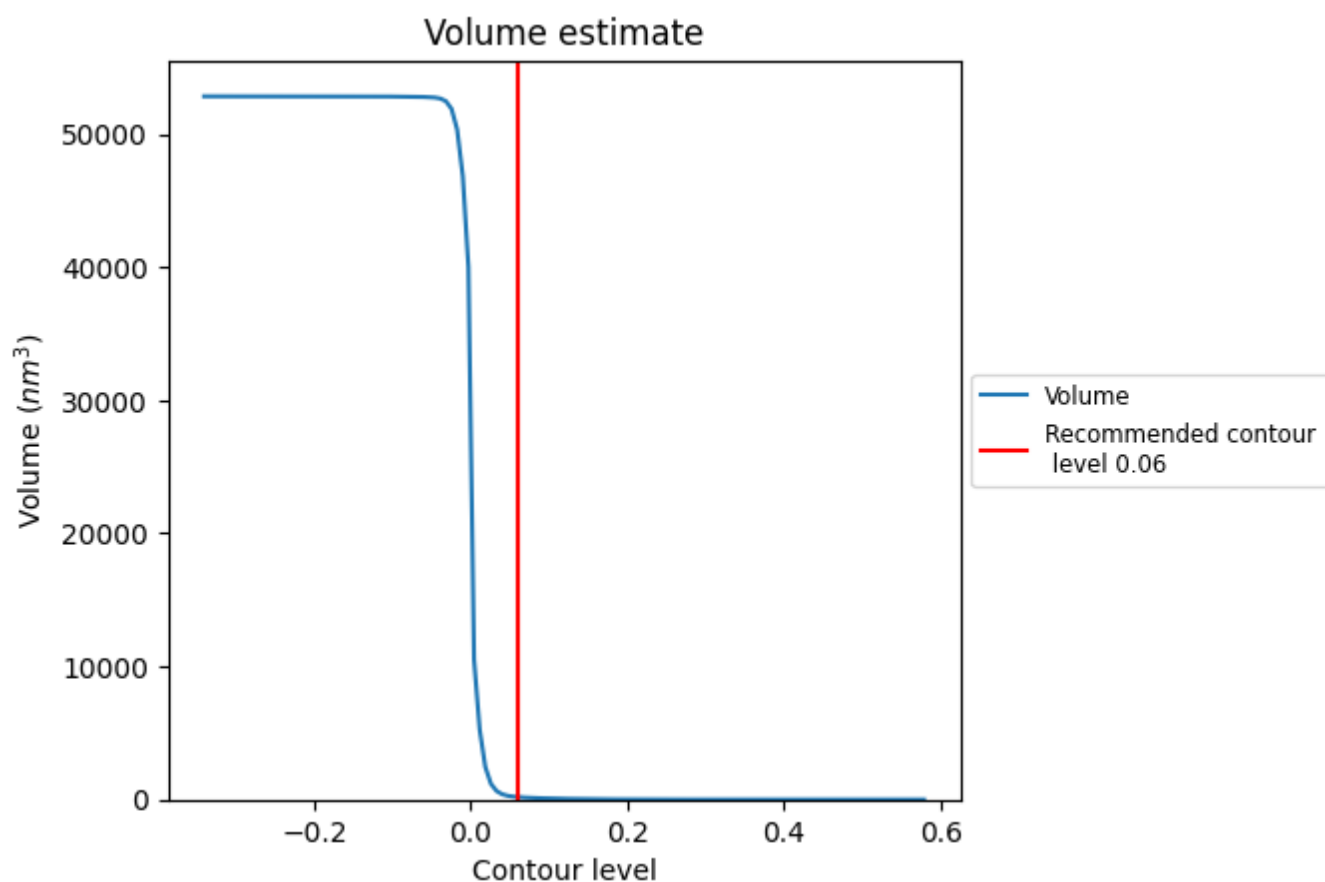
This section contains the results of statistical analysis of the map.

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.

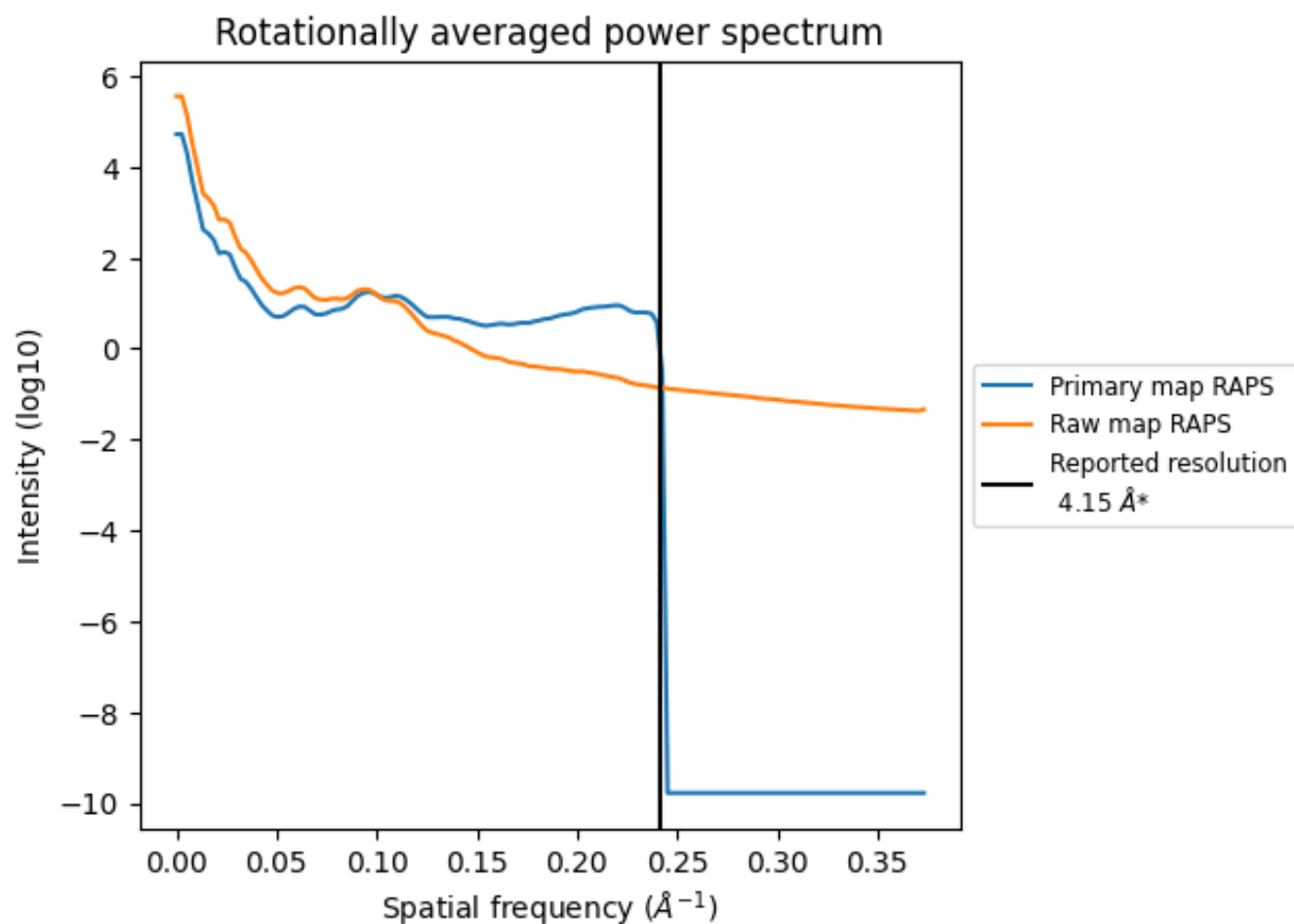
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 189 nm^3 ; this corresponds to an approximate mass of 170 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 ⓘ

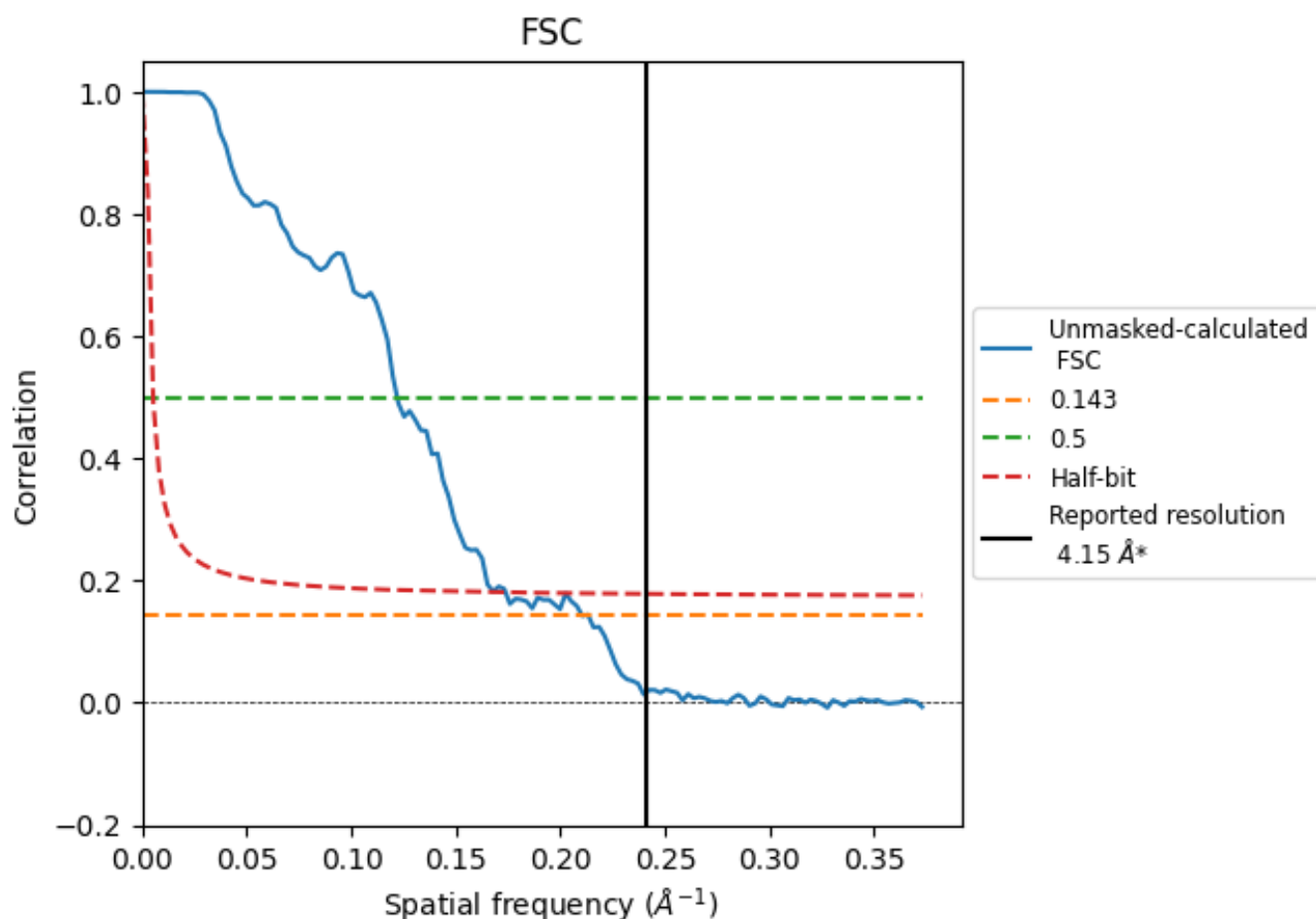


*Reported resolution corresponds to spatial frequency of 0.241 Å⁻¹

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 0.241 Å⁻¹

8.2 Resolution estimates [i](#)

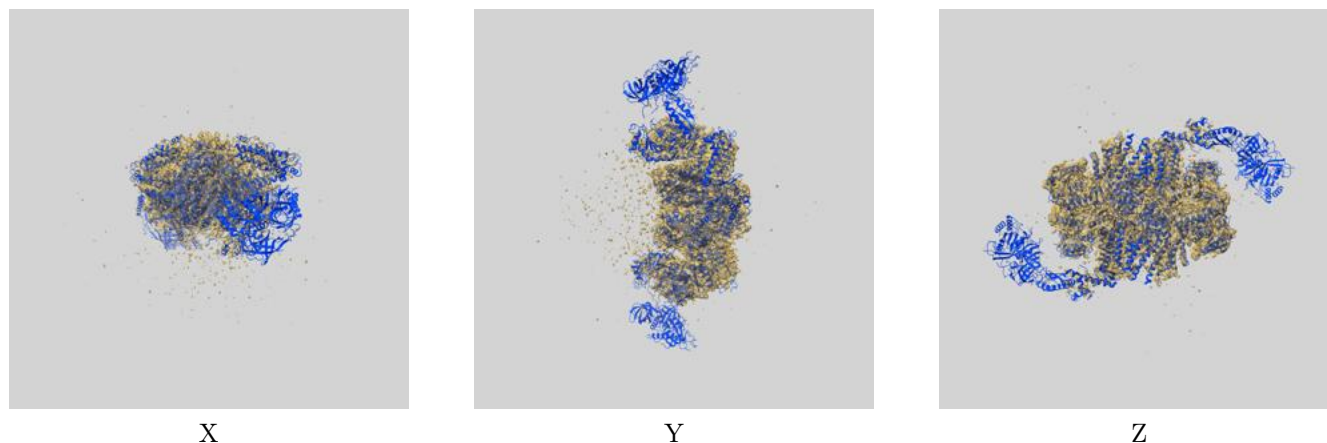
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.15	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.75	8.20	5.75

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.75 differs from the reported value 4.15 by more than 10 %

9 Map-model fit [i](#)

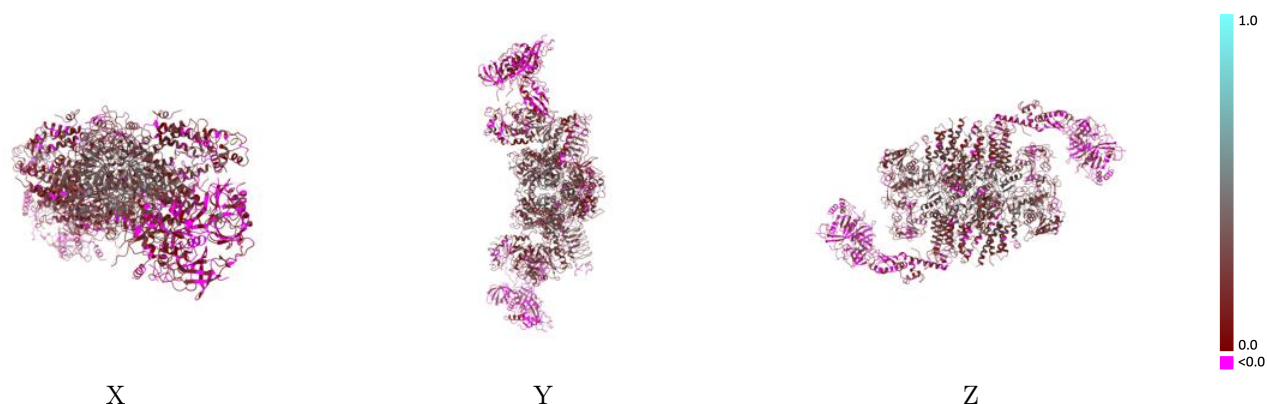
This section contains information regarding the fit between EMDB map EMD-4543 and PDB model 6QG0. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



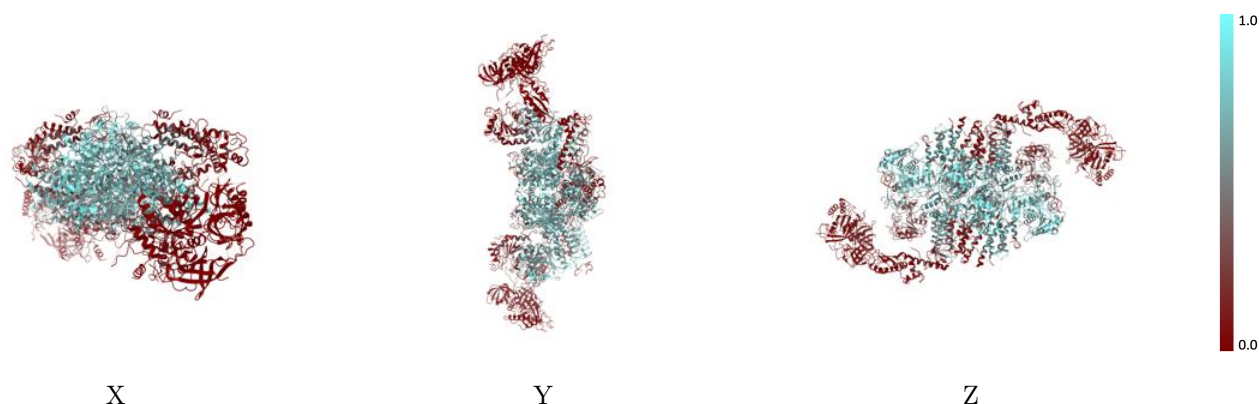
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



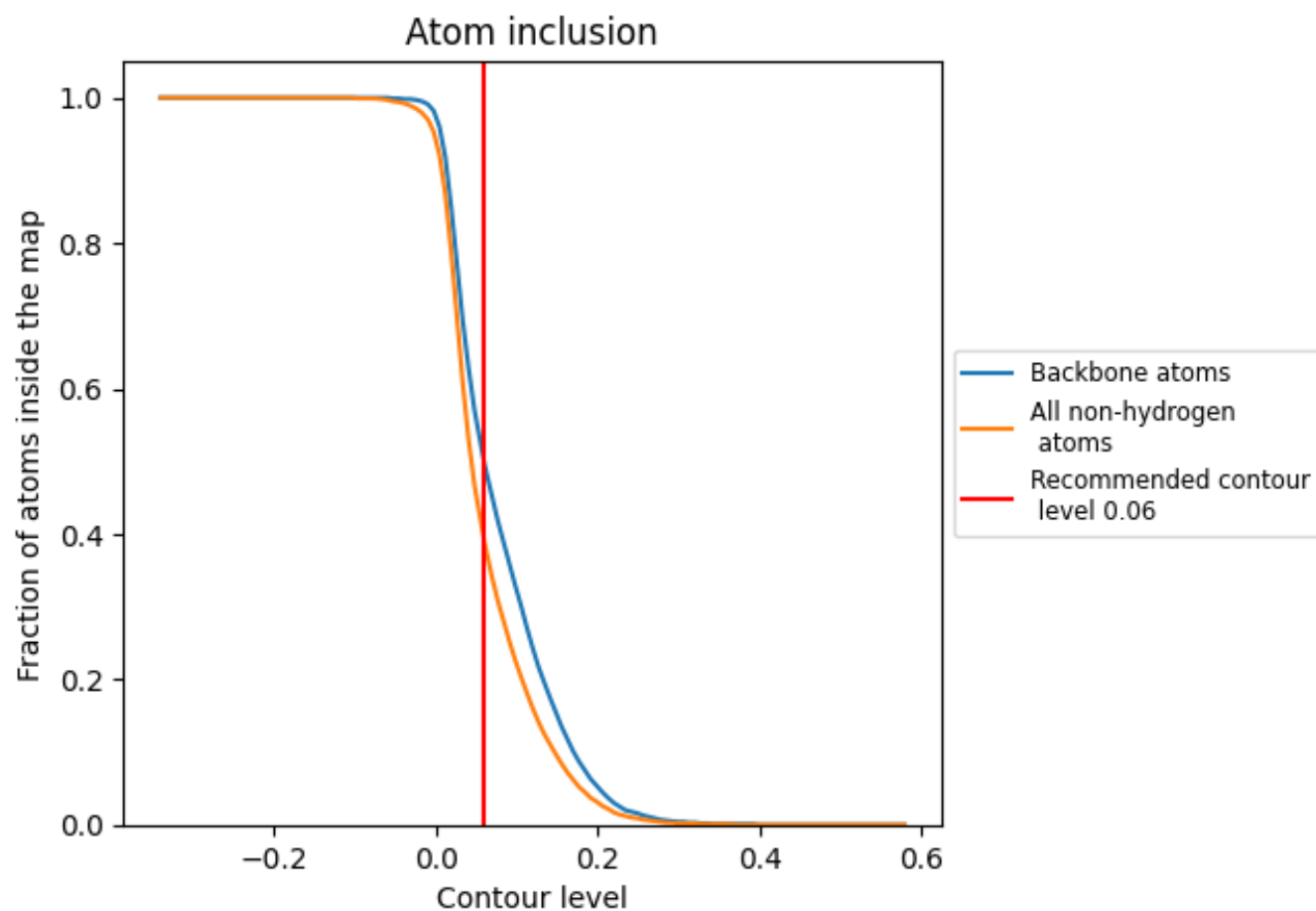
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).

9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 39% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3870	 0.1950
A	 0.4840	 0.2220
B	 0.4870	 0.2170
C	 0.6190	 0.2960
D	 0.6180	 0.2930
E	 0.2190	 0.1470
F	 0.2220	 0.1510
G	 0.5890	 0.2820
H	 0.5900	 0.2900
I	 0.6360	 0.2680
J	 0.6360	 0.2700
K	 0.0560	 0.1120
L	 0.0580	 0.1090
M	 0.0000	 0.0240
N	 0.0010	 0.0230
O	 0.0000	 0.0020
P	 0.0000	 -0.0320

