



wwPDB EM Validation Summary Report ⓘ

Oct 19, 2024 – 07:35 PM EDT

PDB ID : 6O9Z
EMDB ID : EMD-0664
Title : Electron cryo-microscopy of the eukaryotic translation initiation factor 2B bound to eukaryotic translation initiation factor 2 from Homo sapiens
Authors : Nguyen, H.C.; Kenner, L.R.; Frost, A.S.
Deposited on : 2019-03-15
Resolution : 3.03 Å(reported)

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

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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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

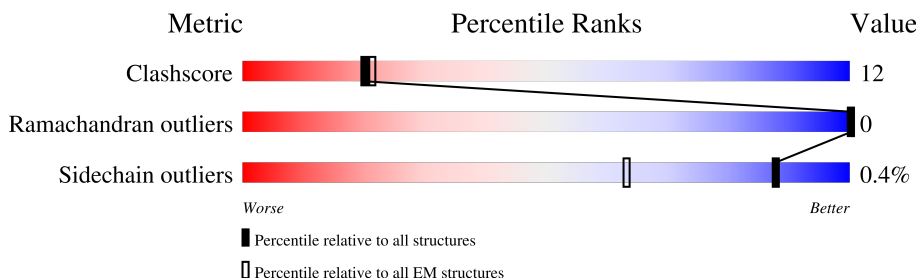
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.03 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	721	
1	B	721	
2	C	368	
2	D	368	
3	E	523	
3	F	523	
4	G	305	
4	H	305	

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Mol	Chain	Length	Quality of chain
5	I	452	
5	J	452	
6	L	323	
6	M	323	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 25788 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 epsilon.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	426	Total	C	N	O	S	0	0
			3172	2043	524	590	15		
1	B	426	Total	C	N	O	S	0	0
			3172	2043	524	590	15		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	587	VAL	ILE	conflict	UNP Q13144
B	587	VAL	ILE	conflict	UNP Q13144

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	317	Total	C	N	O	S	0	0
			2415	1558	394	448	15		
2	D	318	Total	C	N	O	S	0	0
			2425	1564	397	449	15		

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-16	MET	-	initiating methionine	UNP P49770
C	-15	HIS	-	expression tag	UNP P49770
C	-14	HIS	-	expression tag	UNP P49770
C	-13	HIS	-	expression tag	UNP P49770
C	-12	HIS	-	expression tag	UNP P49770
C	-11	HIS	-	expression tag	UNP P49770
C	-10	HIS	-	expression tag	UNP P49770
C	-9	GLY	-	expression tag	UNP P49770
C	-8	GLY	-	expression tag	UNP P49770
C	-7	GLY	-	expression tag	UNP P49770
C	-6	SER	-	expression tag	UNP P49770

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	GLU	-	expression tag	UNP P49770
C	-4	ASN	-	expression tag	UNP P49770
C	-3	LEU	-	expression tag	UNP P49770
C	-2	TYR	-	expression tag	UNP P49770
C	-1	PHE	-	expression tag	UNP P49770
C	0	GLN	-	expression tag	UNP P49770
C	1	SER	-	expression tag	UNP P49770
D	-16	MET	-	initiating methionine	UNP P49770
D	-15	HIS	-	expression tag	UNP P49770
D	-14	HIS	-	expression tag	UNP P49770
D	-13	HIS	-	expression tag	UNP P49770
D	-12	HIS	-	expression tag	UNP P49770
D	-11	HIS	-	expression tag	UNP P49770
D	-10	HIS	-	expression tag	UNP P49770
D	-9	GLY	-	expression tag	UNP P49770
D	-8	GLY	-	expression tag	UNP P49770
D	-7	GLY	-	expression tag	UNP P49770
D	-6	SER	-	expression tag	UNP P49770
D	-5	GLU	-	expression tag	UNP P49770
D	-4	ASN	-	expression tag	UNP P49770
D	-3	LEU	-	expression tag	UNP P49770
D	-2	TYR	-	expression tag	UNP P49770
D	-1	PHE	-	expression tag	UNP P49770
D	0	GLN	-	expression tag	UNP P49770
D	1	SER	-	expression tag	UNP P49770

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	353	Total	C	N	O	S	0	0
			2683	1733	443	493	14		
3	F	353	Total	C	N	O	S	0	0
			2683	1733	443	493	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	290	Total	C	N	O	S	0	0
			2080	1352	347	372	9		
4	H	290	Total	C	N	O	S	0	0
			2080	1352	347	372	9		

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

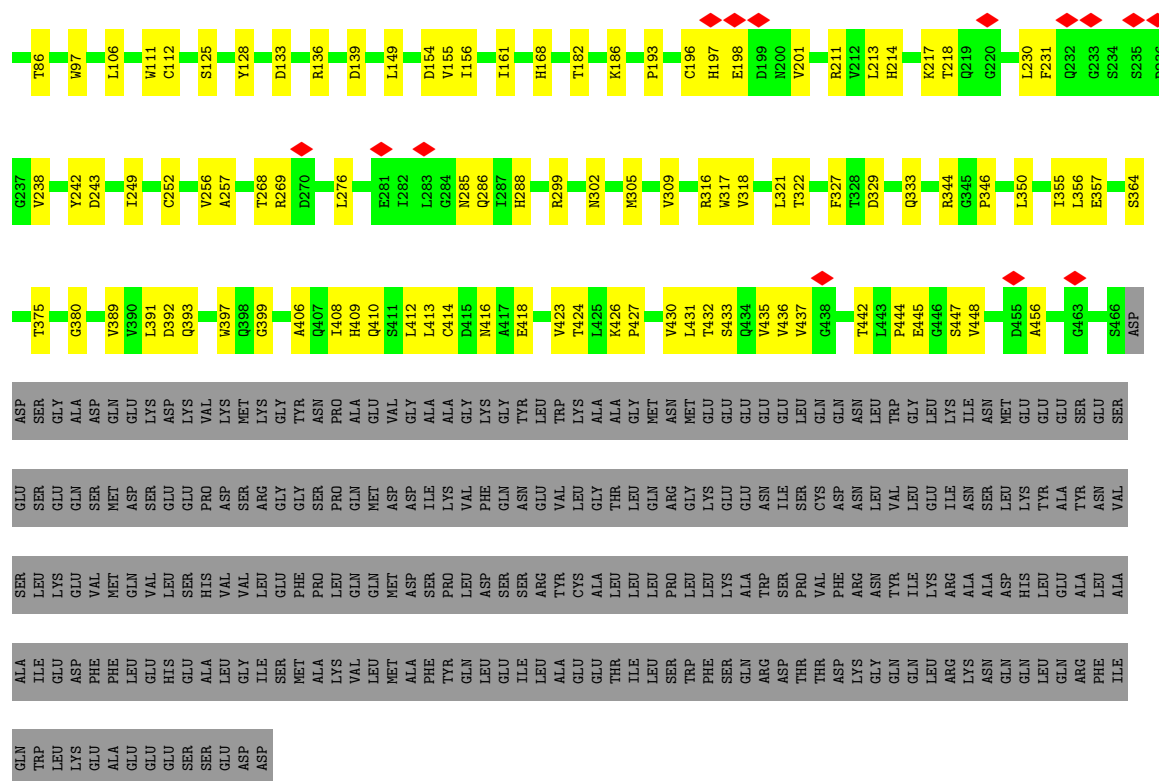
Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	240	Total	C	N	O	S	0	0
			1609	1050	266	285	8		
5	J	240	Total	C	N	O	S	0	0
			1609	1050	266	285	8		

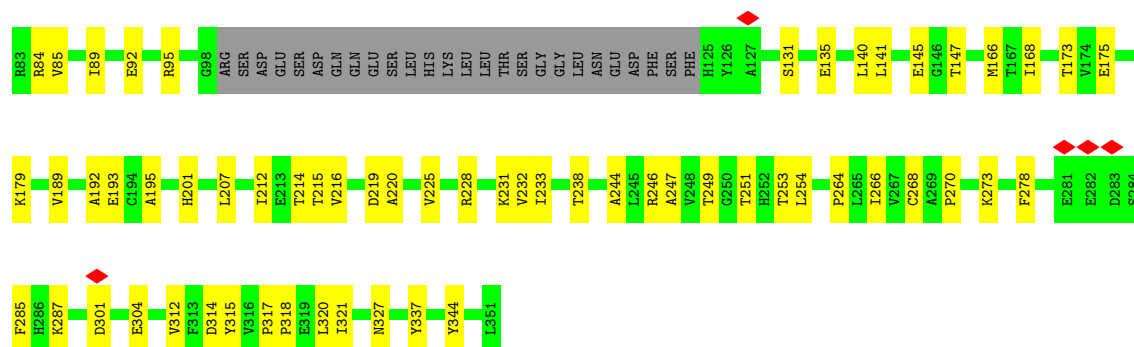
- Molecule 6 is a protein called Eukaryotic translation initiation factor 2 subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L	176	Total	C	N	O	P S	0	0
			930	553	192	183	1 1		
6	M	176	Total	C	N	O	P S	0	0
			930	553	192	183	1 1		

There are 18 discrepancies between the modelled and reference sequences:

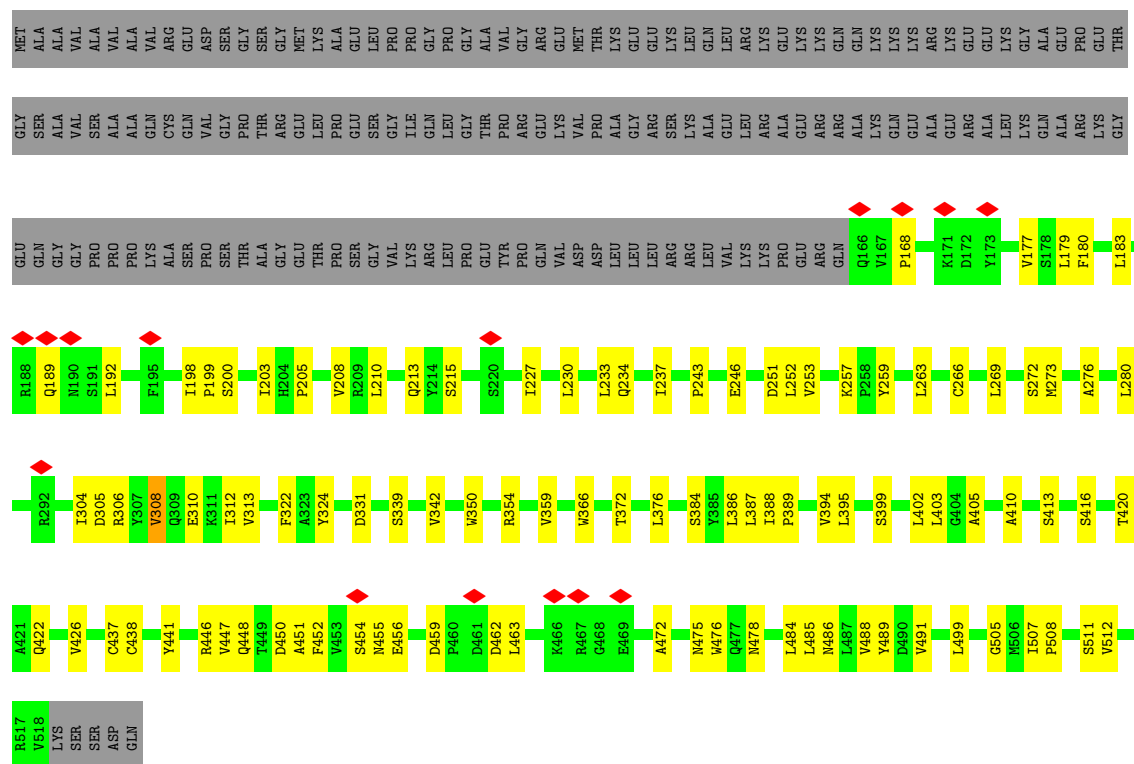
Chain	Residue	Modelled	Actual	Comment	Reference
L	-8	MET	-	initiating methionine	UNP P05198
L	-7	ASP	-	expression tag	UNP P05198
L	-6	TYR	-	expression tag	UNP P05198
L	-5	LYS	-	expression tag	UNP P05198
L	-4	ASP	-	expression tag	UNP P05198
L	-3	ASP	-	expression tag	UNP P05198
L	-2	ASP	-	expression tag	UNP P05198
L	-1	ASP	-	expression tag	UNP P05198
L	0	LYS	-	expression tag	UNP P05198
M	-8	MET	-	initiating methionine	UNP P05198
M	-7	ASP	-	expression tag	UNP P05198
M	-6	TYR	-	expression tag	UNP P05198
M	-5	LYS	-	expression tag	UNP P05198
M	-4	ASP	-	expression tag	UNP P05198
M	-3	ASP	-	expression tag	UNP P05198
M	-2	ASP	-	expression tag	UNP P05198
M	-1	ASP	-	expression tag	UNP P05198
M	0	LYS	-	expression tag	UNP P05198





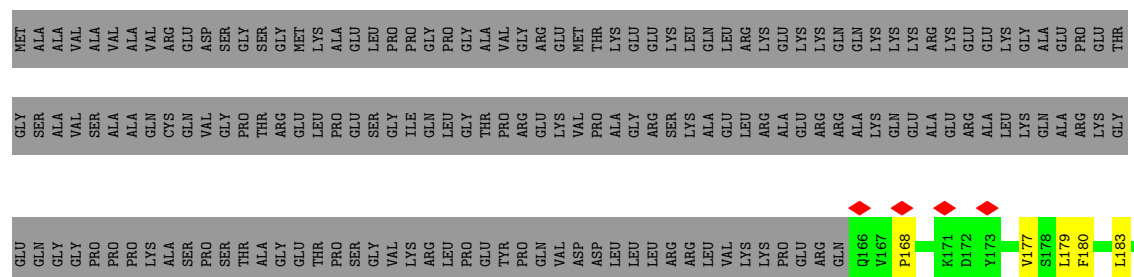
• Molecule 3: Translation initiation factor eIF-2B subunit delta

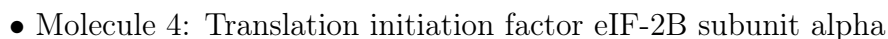
Chain E: 48% 20% 33%



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

Chain F: 48% 19% 33%





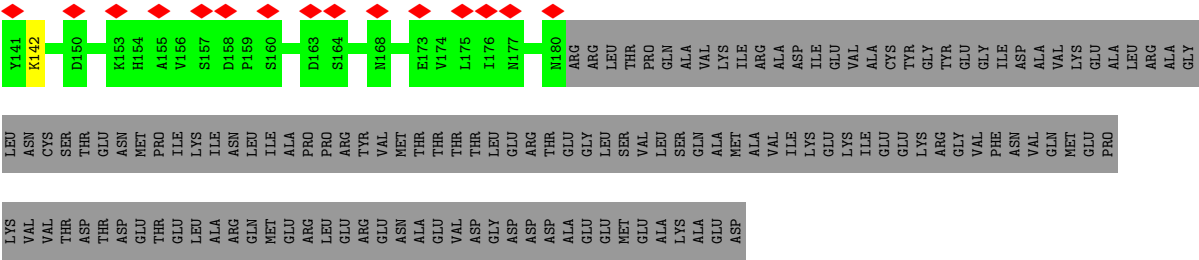
THR	L160	Y1
LEU	G161	K4
LYS	L162	E5
VAL	A165	Y9
ALA		
GLN	P174	M20
THR		A21
GLY	V178	V24
ASP	L179	A25
LYS		A26
LEU	I186	I27
E286	R187	R28
W272	E188	T29
V273		V63
D274	L192	S67
Y275	V193	L71
	I194	L78
	V195	L81
L283		K38
L284	V201	I92
F285	E202	R96
T286	N203	F100
D287		L101
V290	I207	I104
A295	N208	C115
V296	K209	L126
	I210	T127
	G211	H128
		S131
	Q214	V134
D298	V217	V137
E299		S149
L300	P225	V150
I301	F226	Y151
	Y227	V152
	V228	
S297	V229	S155
	A230	Q166
	E231	P167
	S232	L168
		A169
	V236	
	R237	
	L238	
	F239	
	P240	
	L241	
	N242	
	Q243	
	Q244	
	D245	
	F250	
	K251	
	Y252	
	L253	
	F254	
	L255	
	ALA	
	L258	
	ASP	

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

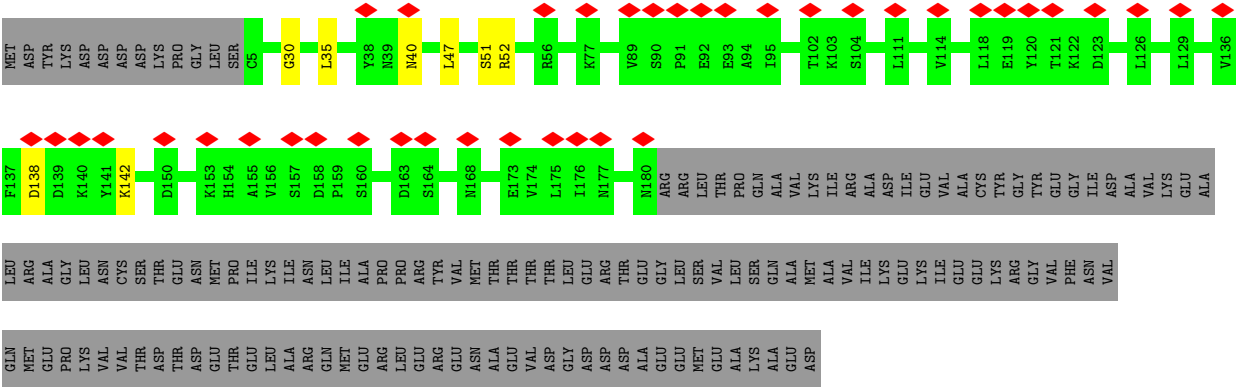
LYS	K162	M1
VAL	A165	K4
ALA	GLN	E5
THR	P174	Y9
GLY	V178	M20
GLN	L179	A21
ASP	I186	V24
LEU	M187	A25
LYS	E188	A26
E268	D191	I27
W272	I192	I28
V273	V193	T29
D274	I194	V63
Y275	V195	S67
L283	V201	L78
L284	E202	L81
P285	N203	K88
T286	I207	I92
D287	N208	R96
V290	K209	F100
A295	I210	L101
V296	I211	I104
S297	G211	C115
D298	Q214	L126
D299	V217	T127
L300	F226	H128
L301	Y227	S131
L305	V228	V134
	A230	V137
	E231	S149
	S232	V150
	V236	V151
	R237	V152
	L238	S155
	F239	Q156
	P240	P157
	L241	D158
	N242	L159
	Q243	ASP
	Q244	THR
	D245	L160
	F250	G161
	E251	
	Y252	
	LYS	
	ALA	
	ASP	
	THR	
	LEU	

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

Figure 1: Schematic representation of the 175 amino acid residues of the protein. The protein is shown as a horizontal bar divided into segments representing different regions. The segments are color-coded: yellow for the N-terminal region (residues 1-10), green for the first alpha-helix (residues 11-20), grey for the first beta-sheet (residues 21-30), yellow for the second alpha-helix (residues 31-40), green for the second beta-sheet (residues 41-50), yellow for the third alpha-helix (residues 51-60), green for the third beta-sheet (residues 61-70), yellow for the fourth alpha-helix (residues 71-80), green for the fourth beta-sheet (residues 81-90), yellow for the fifth alpha-helix (residues 91-100), green for the fifth beta-sheet (residues 101-110), yellow for the sixth alpha-helix (residues 111-120), green for the sixth beta-sheet (residues 121-130), yellow for the seventh alpha-helix (residues 131-140), green for the seventh beta-sheet (residues 141-150), yellow for the eighth alpha-helix (residues 151-160), green for the eighth beta-sheet (residues 161-170), and yellow for the C-terminal region (residues 171-175). Red diamonds indicate the positions of the 175 amino acid residues. The residues are labeled with their three-letter codes: M1, A5, V6, W7, M8, G11, GLY, GLY, SER, ARG, MET, THR, ASP, LEU, THR, SER, SER, ILE, PRO, LYS, PRO, LEU, L28, P29, V30, G31, N32, K33, P34, L35, L36, K37, V38, P39, L40, N41, L42, L43, E44, R45, F48, I52, V53, R57, D58, V59, D60, K61, A65, R69, K72.



● Molecule 6: Eukaryotic translation initiation factor 2 subunit 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34014	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 ($e^-/\text{\AA}^2$)	80	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	14.365	Depositor
Minimum map value	-8.686	Depositor
Average map value	-0.011	Depositor
Map value standard deviation	0.787	Depositor
Recommended contour level	1.9	Depositor
Map size (Å)	289.344, 289.344, 289.344	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82199997, 0.82199997, 0.82199997	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	0.42	0/3236	0.57	0/4403
1	B	0.42	0/3236	0.57	0/4403
2	C	0.43	0/2460	0.57	0/3318
2	D	0.42	0/2471	0.56	0/3333
3	E	0.44	0/2732	0.61	0/3699
3	F	0.44	0/2732	0.61	0/3699
4	G	0.47	0/2114	0.60	1/2867 (0.0%)
4	H	0.47	0/2114	0.60	1/2867 (0.0%)
5	I	0.34	0/1630	0.57	0/2219
5	J	0.34	0/1630	0.57	0/2219
6	L	0.26	0/918	0.44	0/1268
6	M	0.26	0/918	0.44	0/1268
All	All	0.41	0/26191	0.57	2/35563 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	284	LEU	CA-CB-CG	5.01	126.83	115.30
4	H	284	LEU	CA-CB-CG	5.01	126.83	115.30

There are no chirality outliers.

There are no planarity outliers.

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	3172	0	3018	68	0
1	B	3172	0	3018	69	0
2	C	2415	0	2390	62	0
2	D	2425	0	2397	60	0
3	E	2683	0	2685	83	0
3	F	2683	0	2685	82	0
4	G	2080	0	2010	69	0
4	H	2080	0	2010	69	0
5	I	1609	0	1377	39	0
5	J	1609	0	1377	39	0
6	L	930	0	484	4	0
6	M	930	0	484	5	0
All	All	25788	0	23935	599	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 12.

The worst 5 of 599 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)
4:H:210:ILE:H	4:H:210:ILE:HD12	1.42	0.84
4:G:210:ILE:HD12	4:G:210:ILE:H	1.42	0.83
3:E:199:PRO:HG3	5:I:48:PHE:H	1.44	0.82
3:F:199:PRO:HG3	5:J:48:PHE:H	1.47	0.80
2:C:253:THR:HG21	3:F:422:GLN:HE21	1.48	0.79

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	424/721 (59%)	402 (95%)	22 (5%)	0	100	100
1	B	424/721 (59%)	402 (95%)	22 (5%)	0	100	100
2	C	313/368 (85%)	305 (97%)	8 (3%)	0	100	100
2	D	314/368 (85%)	301 (96%)	13 (4%)	0	100	100
3	E	351/523 (67%)	342 (97%)	9 (3%)	0	100	100
3	F	351/523 (67%)	342 (97%)	9 (3%)	0	100	100
4	G	286/305 (94%)	269 (94%)	17 (6%)	0	100	100
4	H	286/305 (94%)	270 (94%)	16 (6%)	0	100	100
5	I	232/452 (51%)	223 (96%)	9 (4%)	0	100	100
5	J	232/452 (51%)	223 (96%)	9 (4%)	0	100	100
6	L	173/323 (54%)	165 (95%)	8 (5%)	0	100	100
6	M	173/323 (54%)	165 (95%)	8 (5%)	0	100	100
All	All	3559/5384 (66%)	3409 (96%)	150 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	347/626 (55%)	346 (100%)	1 (0%)	91	95
1	B	347/626 (55%)	346 (100%)	1 (0%)	91	95
2	C	265/312 (85%)	265 (100%)	0	100	100
2	D	266/312 (85%)	266 (100%)	0	100	100
3	E	307/444 (69%)	306 (100%)	1 (0%)	91	95
3	F	307/444 (69%)	306 (100%)	1 (0%)	91	95
4	G	199/260 (76%)	198 (100%)	1 (0%)	86	93
4	H	199/260 (76%)	198 (100%)	1 (0%)	86	93
5	I	127/398 (32%)	125 (98%)	2 (2%)	58	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	J	127/398 (32%)	125 (98%)	2 (2%)	58	79
6	L	12/287 (4%)	12 (100%)	0	100	100
6	M	12/287 (4%)	12 (100%)	0	100	100
All	All	2515/4654 (54%)	2505 (100%)	10 (0%)	88	94

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	I	162	SER
5	J	76	VAL
5	J	162	SER
3	F	308	VAL
4	G	4	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	281	ASN
4	G	214	GLN
4	H	214	GLN
4	H	156	GLN
2	D	154	GLN

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	M	51	6	8,9,10	1.55	1 (12%)	7,12,14	1.40	1 (14%)
6	SEP	L	51	6	8,9,10	1.55	1 (12%)	7,12,14	1.37	1 (14%)

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	M	51	6	-	1/6/8/10	-
6	SEP	L	51	6	-	1/6/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	L	51	SEP	P-O1P	3.38	1.61	1.50
6	M	51	SEP	P-O1P	3.35	1.60	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	M	51	SEP	OG-CB-CA	3.17	111.23	108.14
6	L	51	SEP	OG-CB-CA	3.11	111.17	108.14

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	L	51	SEP	N-CA-CB-OG
6	M	51	SEP	N-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.

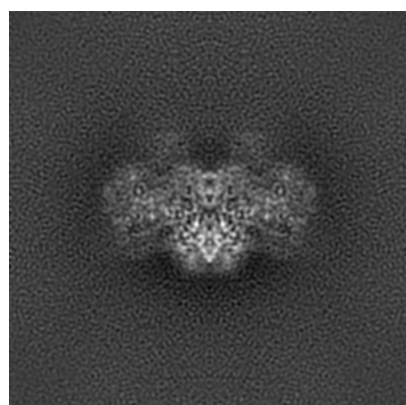
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0664. These allow visual inspection of the internal detail of the map and identification of artifacts.

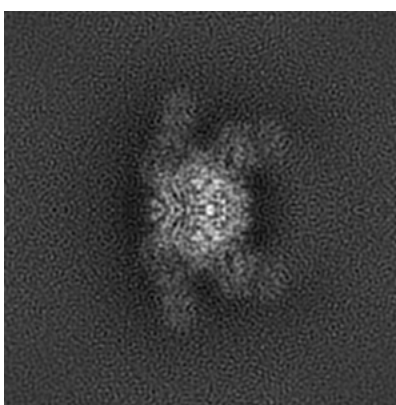
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

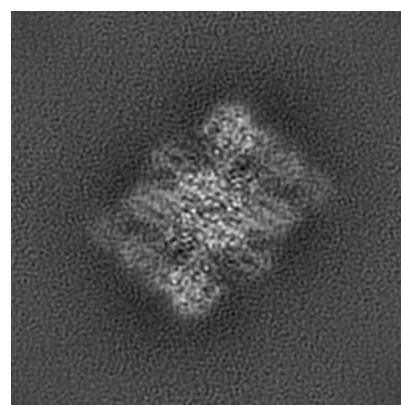
6.1.1 Primary map



X



Y

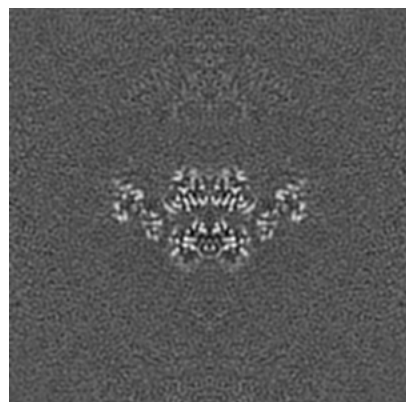


Z

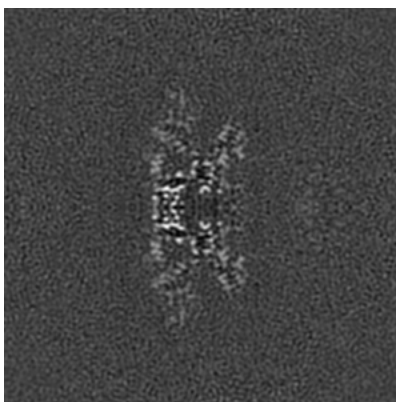
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

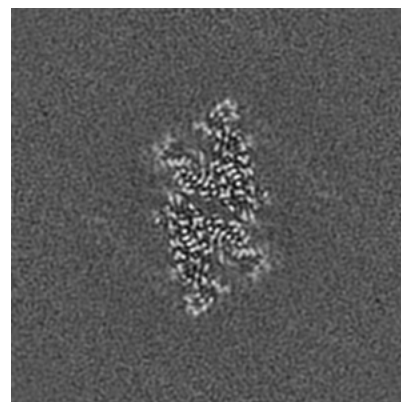
6.2.1 Primary map



X Index: 176



Y Index: 176

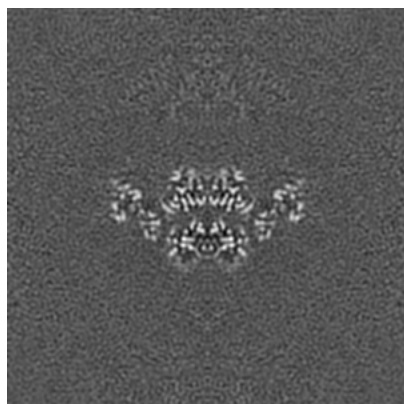


Z Index: 176

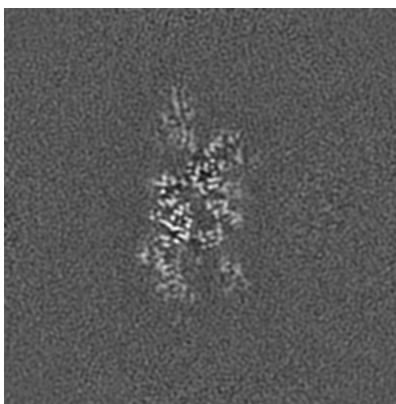
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

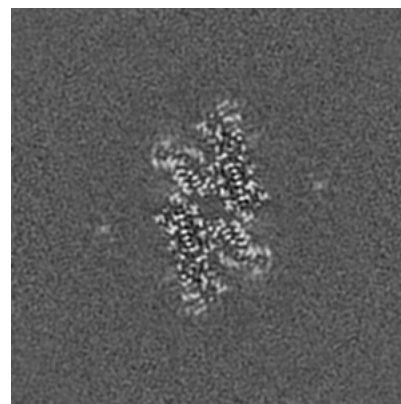
6.3.1 Primary map



X Index: 176



Y Index: 181

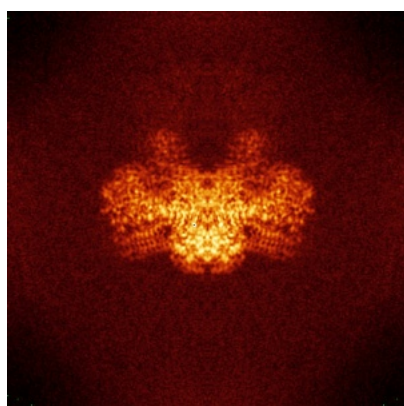


Z Index: 174

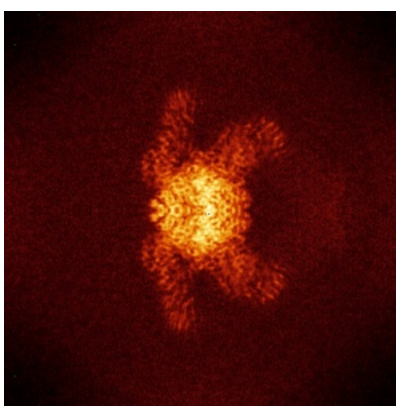
The images above show the largest variance slices of the map in three orthogonal directions.

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

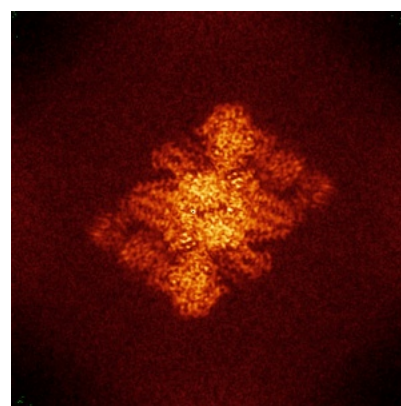
6.4.1 Primary map



X



Y

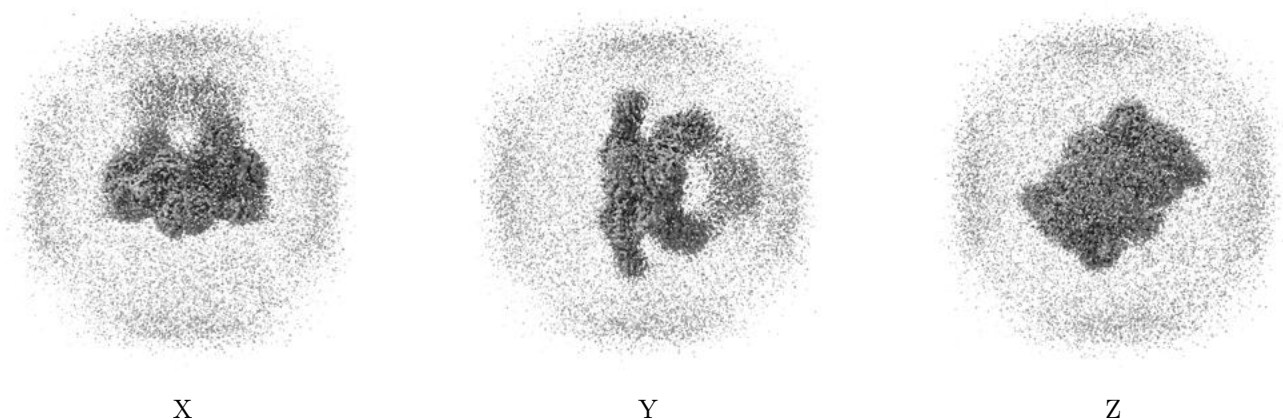


Z

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 1.9. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

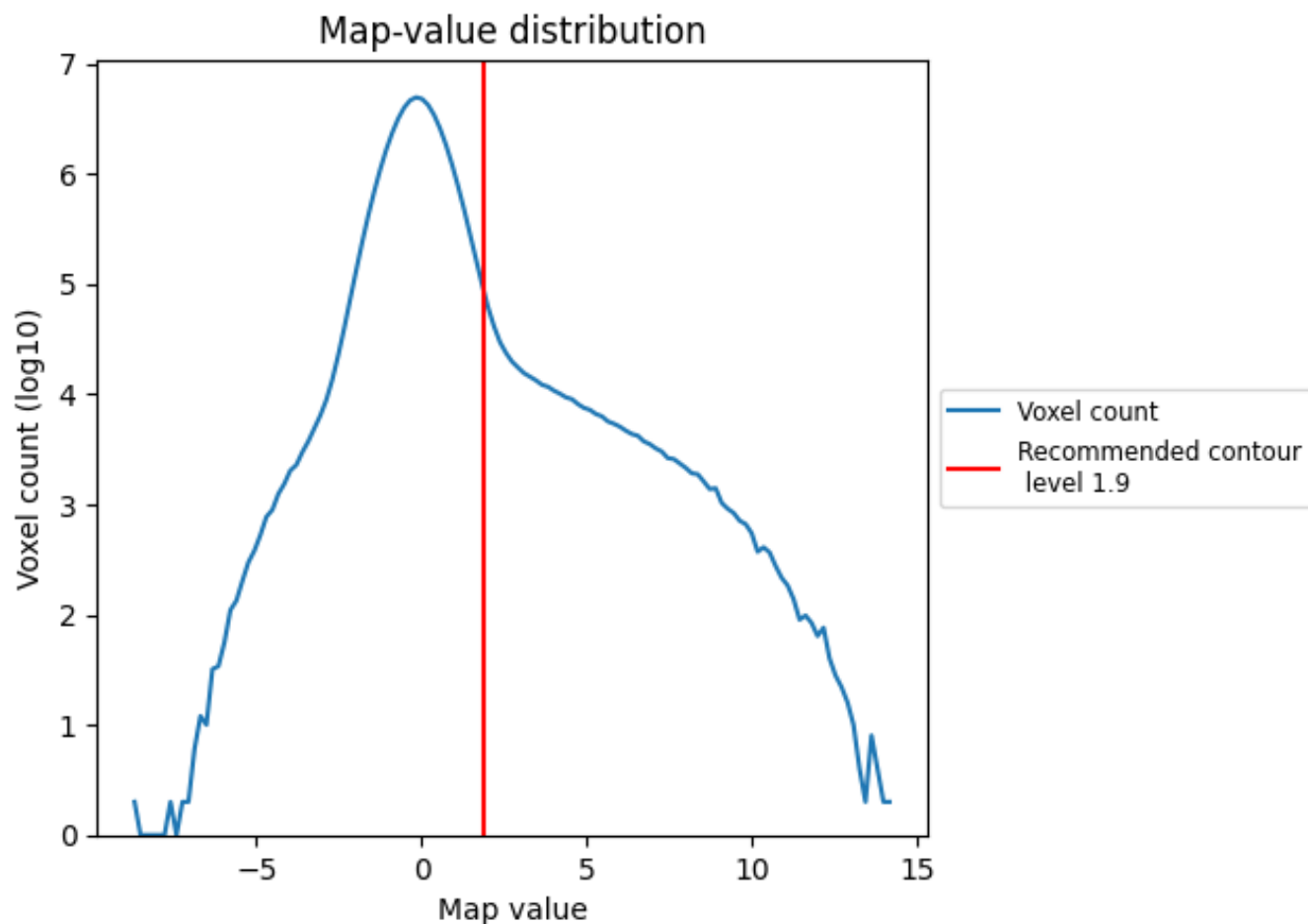
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

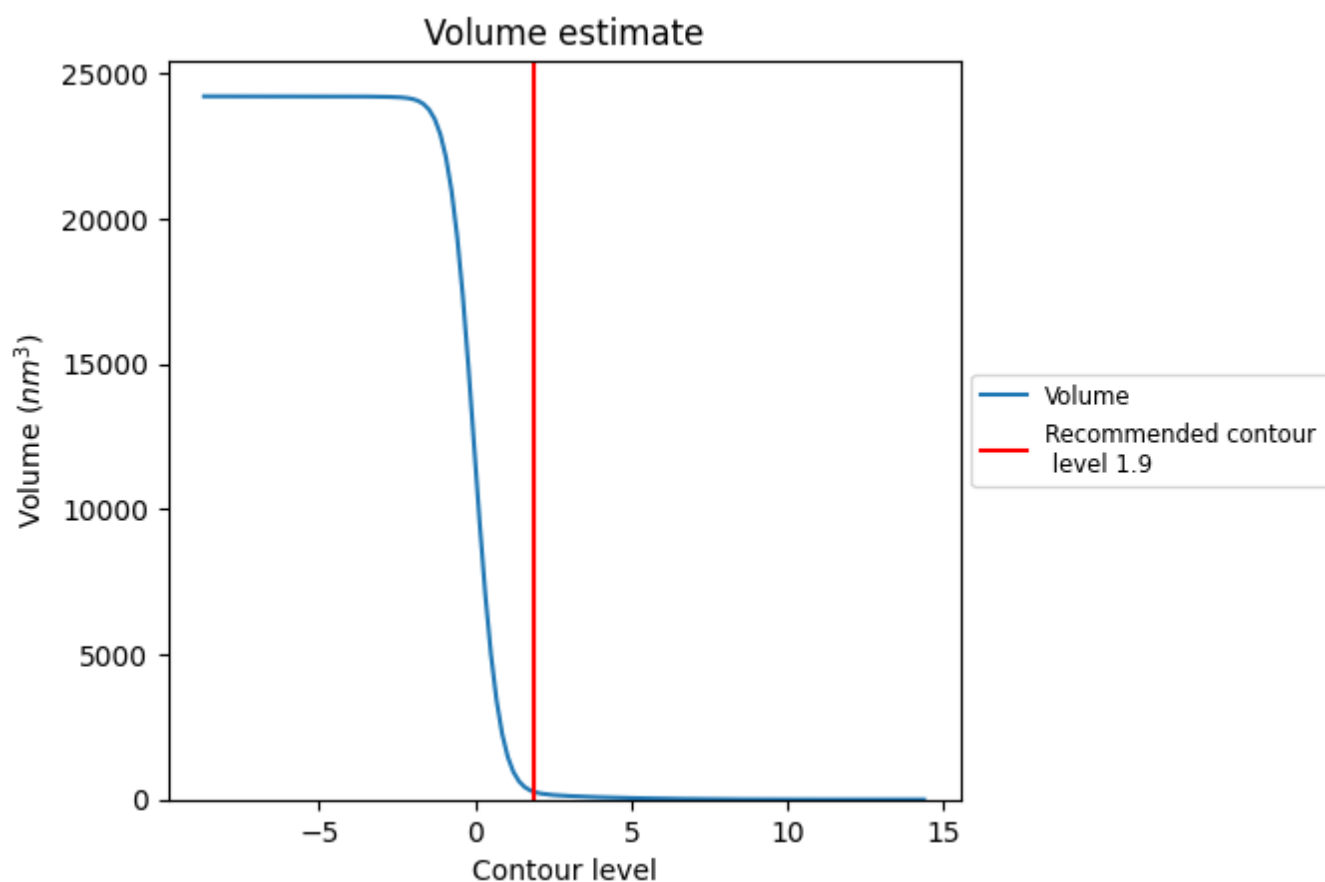
This section contains the results of statistical analysis of the map.

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.

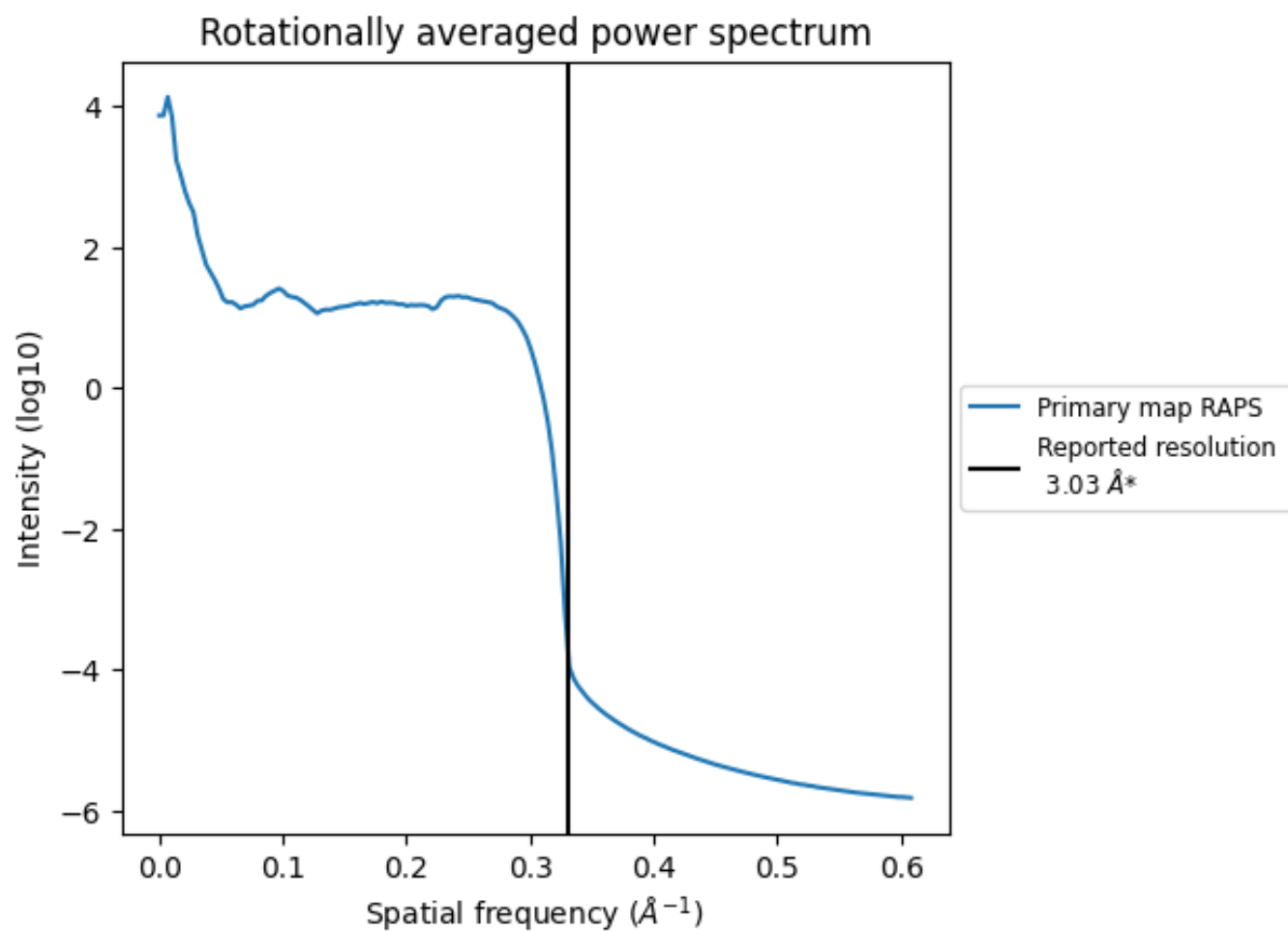
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 261 nm³; this corresponds to an approximate mass of 236 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 0.330 Å⁻¹

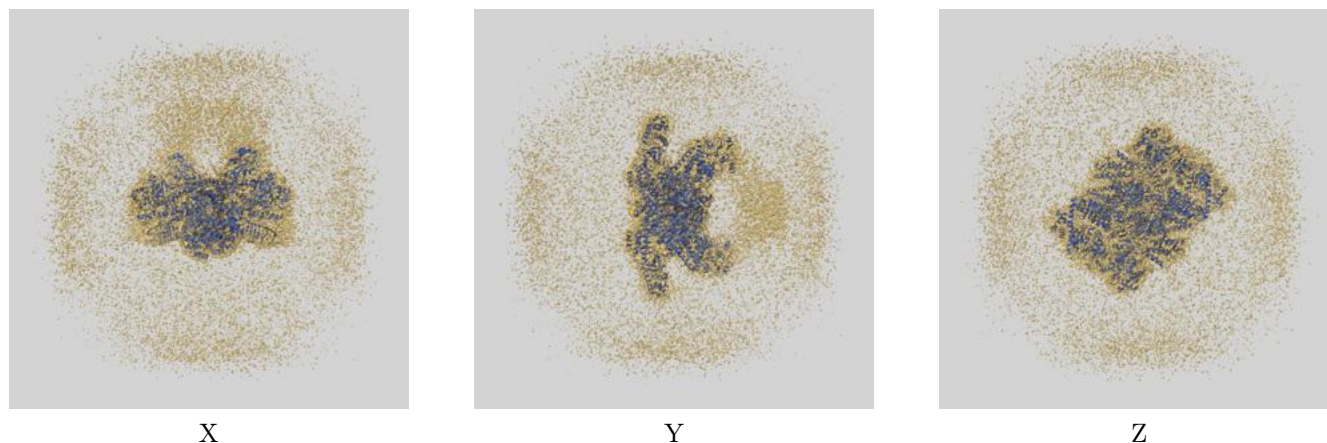
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

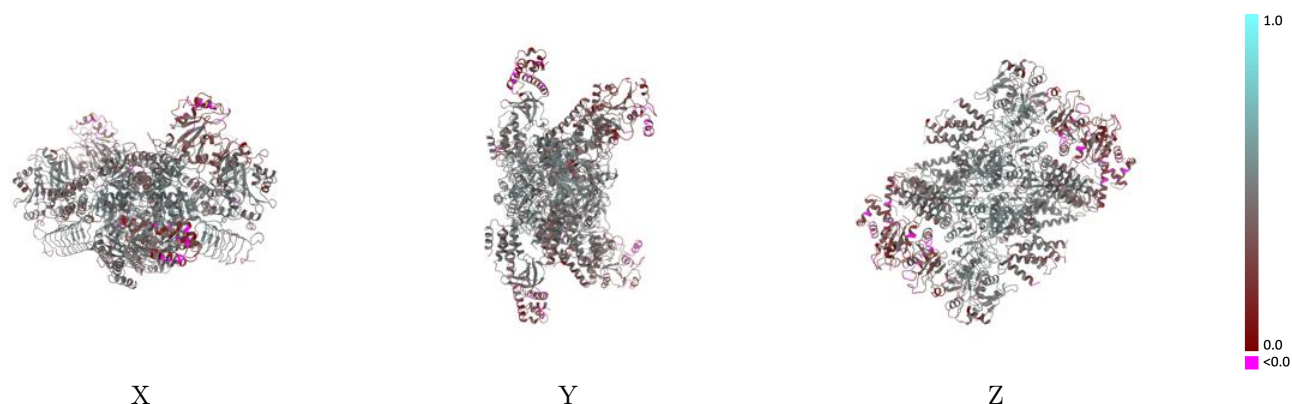
This section contains information regarding the fit between EMDB map EMD-0664 and PDB model 6O9Z. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



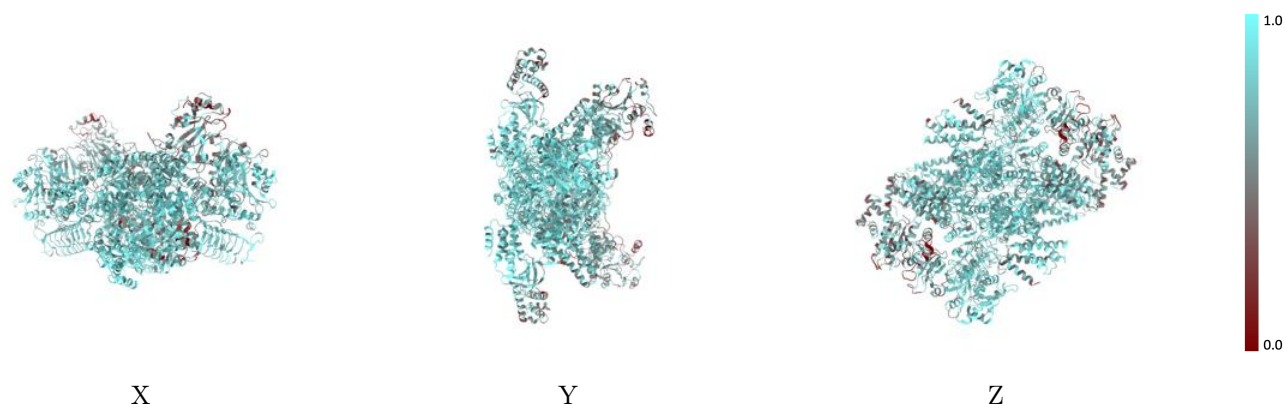
The images above show the 3D surface view of the map at the recommended contour level 1.9 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



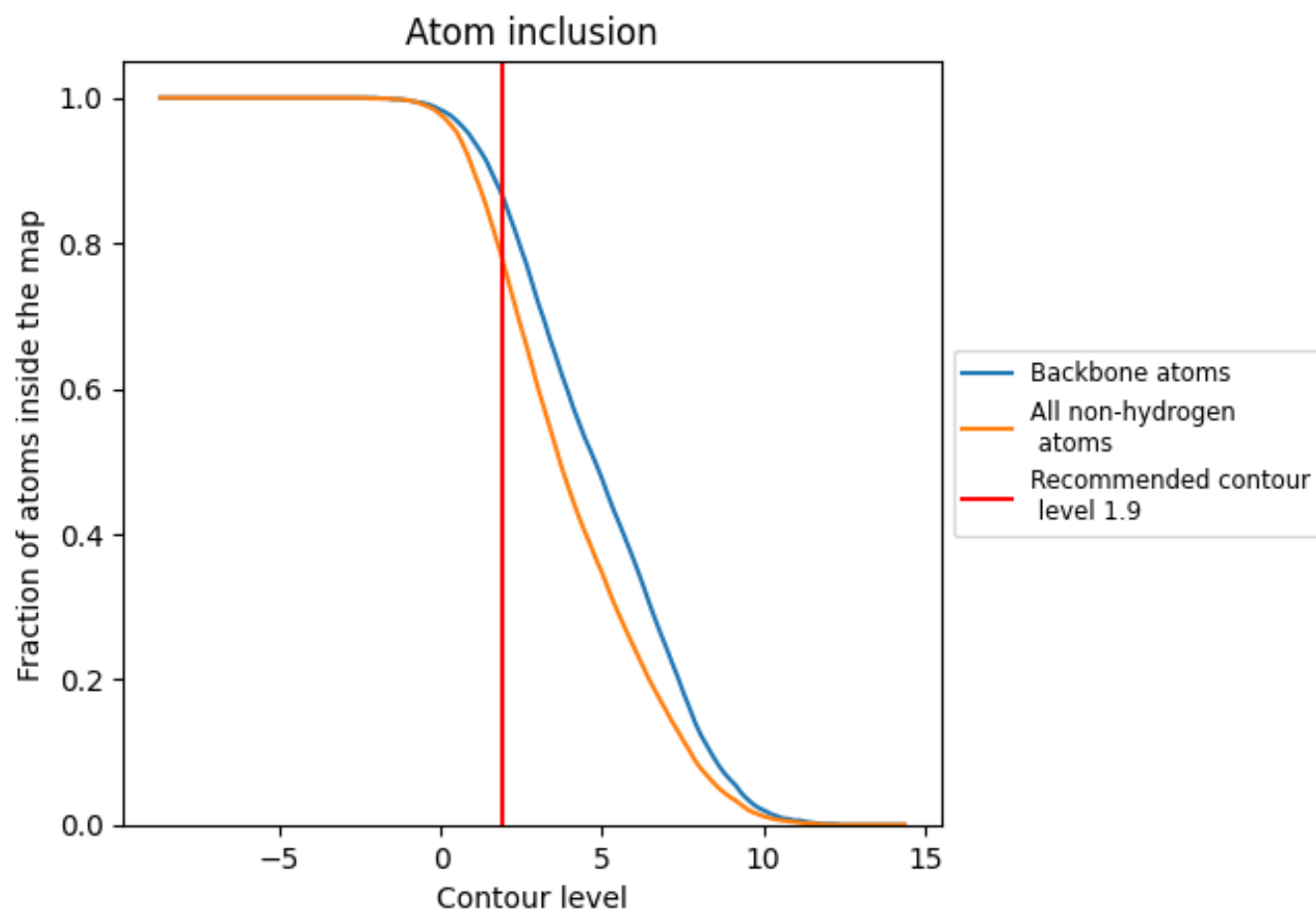
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.9).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 78% 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 (1.9) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.7790</div>	<div><div></div>0.4410</div>
A	<div><div></div>0.8180</div>	<div><div></div>0.4580</div>
B	<div><div></div>0.8150</div>	<div><div></div>0.4580</div>
C	<div><div></div>0.8030</div>	<div><div></div>0.4650</div>
D	<div><div></div>0.8010</div>	<div><div></div>0.4660</div>
E	<div><div></div>0.7770</div>	<div><div></div>0.4720</div>
F	<div><div></div>0.7770</div>	<div><div></div>0.4720</div>
G	<div><div></div>0.8900</div>	<div><div></div>0.4930</div>
H	<div><div></div>0.8890</div>	<div><div></div>0.4910</div>
I	<div><div></div>0.5890</div>	<div><div></div>0.3140</div>
J	<div><div></div>0.5870</div>	<div><div></div>0.3110</div>
L	<div><div></div>0.6770</div>	<div><div></div>0.3330</div>
M	<div><div></div>0.6770</div>	<div><div></div>0.3330</div>

1.0

0.0

<0.0