



wwPDB EM Validation Summary Report ⓘ

Oct 27, 2024 – 02:47 PM JST

PDB ID : 7D43
EMDB ID : EMD-30568
Title : eIF2B-eIF2(aP), aPg complex
Authors : Kashiwagi, K.; Ito, T.
Deposited on : 2020-09-22
Resolution : 4.30 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

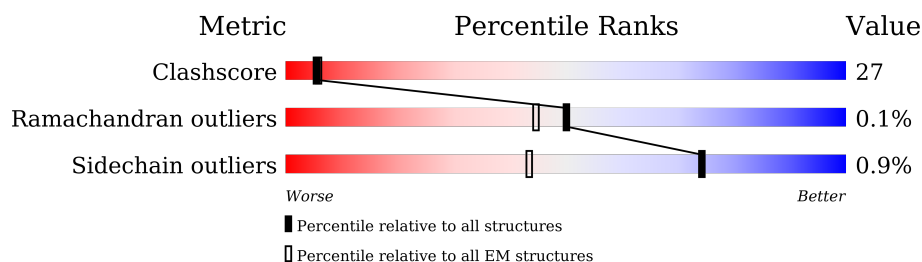
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.







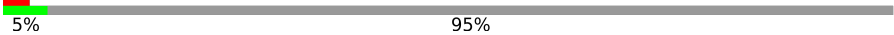

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	305	
1	B	305	
2	C	351	
2	D	351	
3	E	452	
3	F	452	
4	G	523	
4	H	523	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	I	721	 24%35%41%
5	J	721	 28%31%40%
6	K	315	 75%7%17%
6	L	315	 53%44%
7	M	333	 5%95%
8	P	472	 28%81%8%11%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 31009 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	293	Total	C	N	O	S	0	0
			2262	1449	377	424	12		
1	B	291	Total	C	N	O	S	0	0
			2249	1442	375	420	12		

- 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
			2476	1565	435	461	15		
2	D	324	Total	C	N	O	S	0	0
			2538	1605	445	473	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	344	Total	C	N	O	S	0	0
			2438	1546	424	453	15		
3	F	343	Total	C	N	O	S	0	0
			2430	1540	423	452	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	G	353	Total	C	N	O	S	0	0
			2750	1740	490	506	14		
4	H	353	Total	C	N	O	S	0	0
			2750	1740	490	506	14		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	427	Total	C	N	O	S	0	0
			3358	2115	591	637	15		
5	J	429	Total	C	N	O	S	0	0
			3371	2124	591	641	15		

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

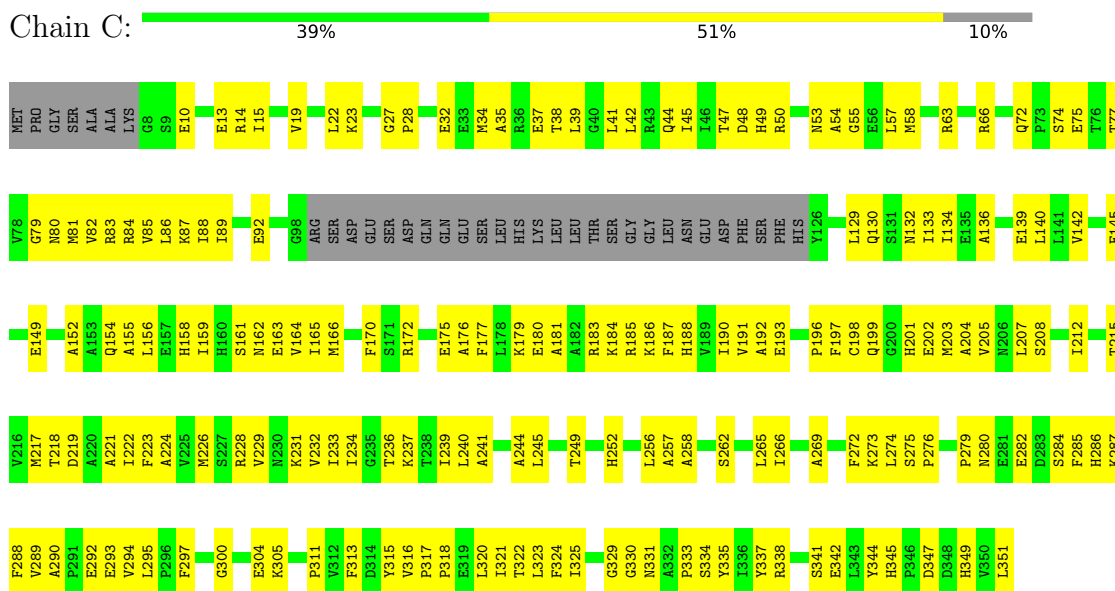
Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	260	Total	C	N	O	P	0	0
			1309	782	262	264	1		
6	L	176	Total	C	N	O	P	0	0
			889	529	179	180	1		

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

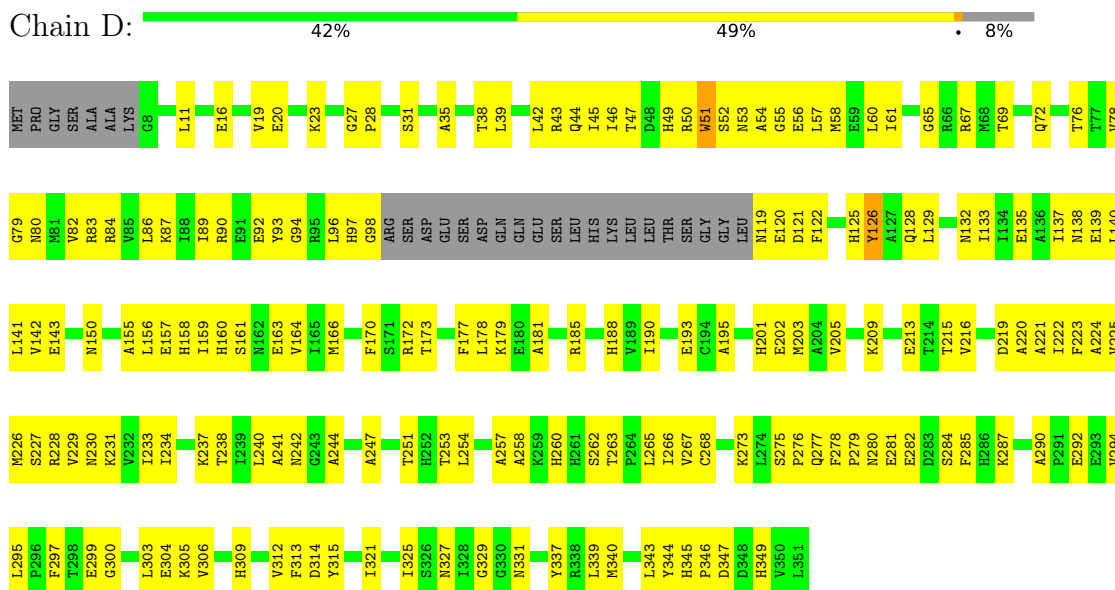
Mol	Chain	Residues	Atoms				AltConf	Trace
7	M	16	Total	C	N	O	0	0
			80	48	16	16		

- Molecule 8 is a protein called Eukaryotic translation initiation factor 2 subunit 3.

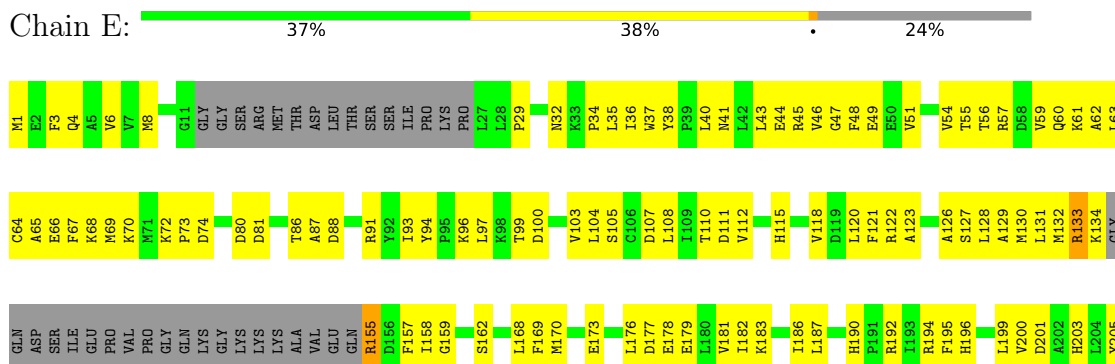
Mol	Chain	Residues	Atoms				AltConf	Trace
8	P	421	Total	C	N	O	0	0
			2109	1267	421	421		



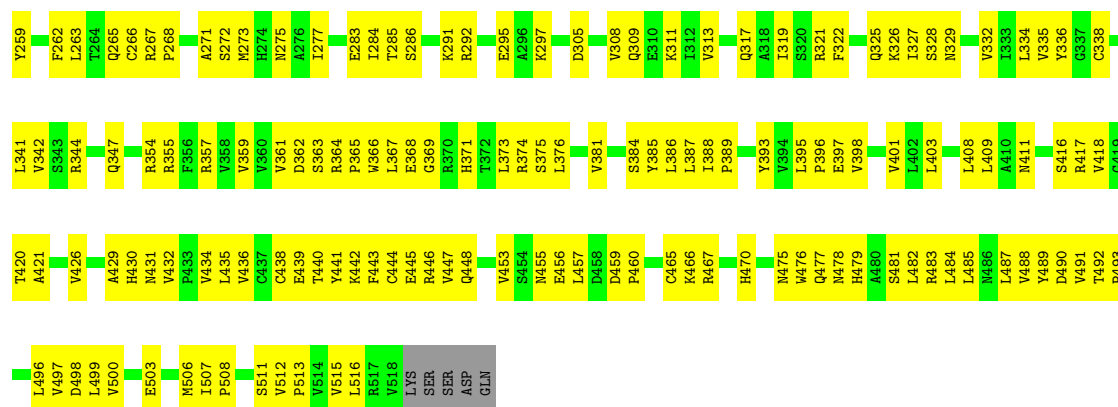
- Molecule 2: Translation initiation factor eIF-2B subunit beta



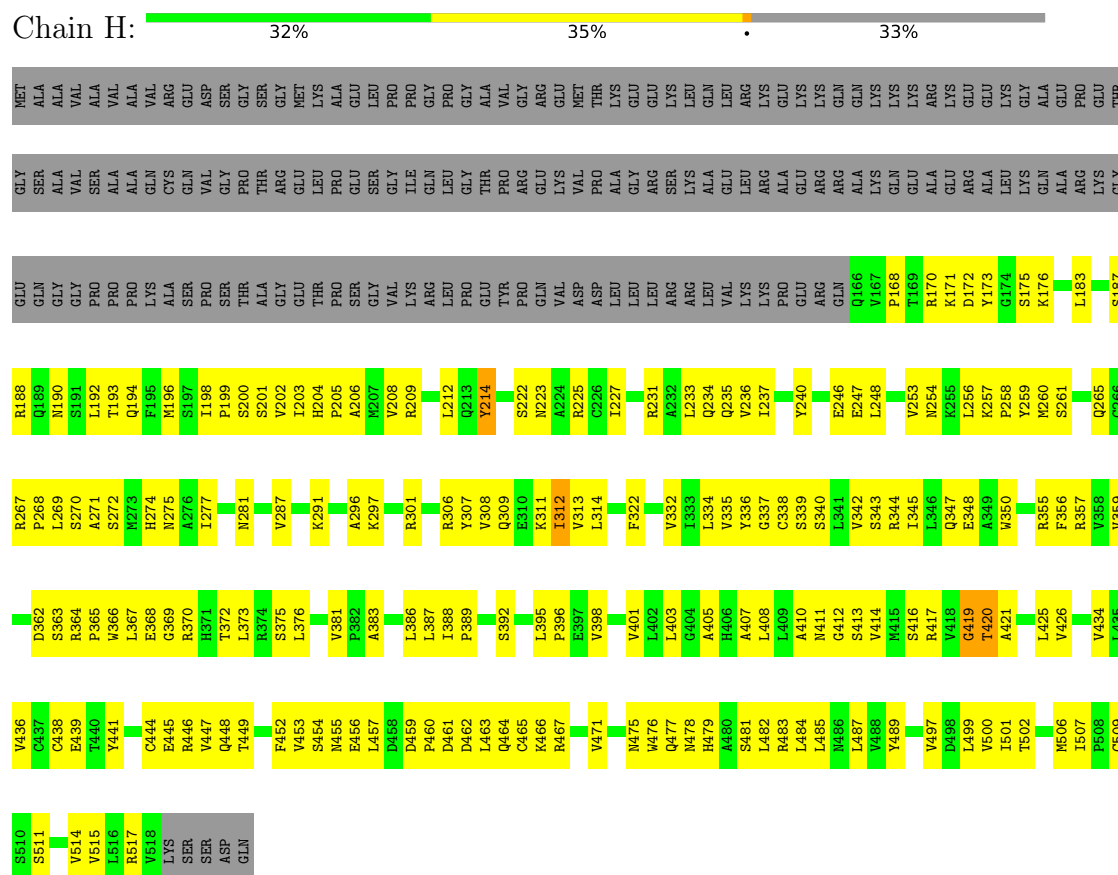
- Molecule 3: Translation initiation factor eIF-2B subunit gamma



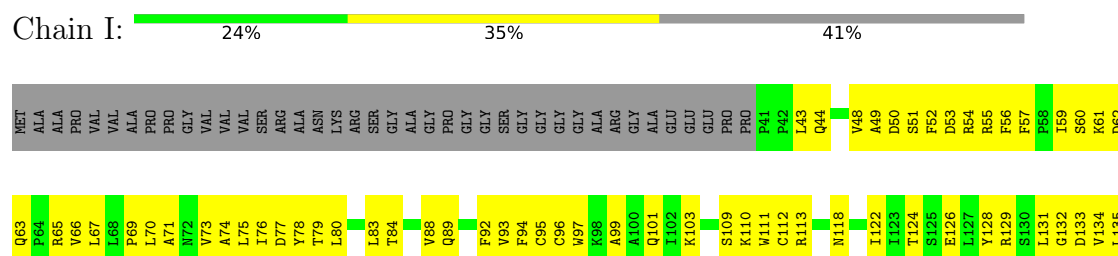




• Molecule 4: Translation initiation factor eIF-2B subunit delta

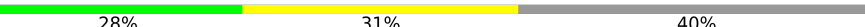


• Molecule 5: Translation initiation factor eIF-2B subunit epsilon



LEU	SER	PRO	TRP	PHE	SER	GLN	ALA	TRP	ARG	GLN	MET	T432	S364	R274	T208	R136
PRO	TRP	LEU	GLY	LEU	LEU	LYS	GLU	GLU	ARG	ASN	GLU	S433	I368	L277	N210	V138
PHE	LEU	LEU	LEU	LEU	LYS	GLU	GLU	GLU	GLY	GLU	GLU	V435	G369	L277	R211	D139
SER	GLN	ALA	GLU	ALA	GLU	GLU	GLU	GLU	GLU	GLU	GLU	N440	C372	E281	L213	L143
ARG	TRP	ASP	ILE	TRP	ASN	GLU	GLU	GLU	GLU	GLU	GLU	I441	T375		H214	V144
ASP	SER	SER	ILE	SER	ILE	GLU	GLU	GLU	GLU	GLU	GLU	T442	T375		F215	V144
THR	THR	PRO	SER	PRO	CYS	LEU	SER	LEU	SER	LEU	LEU	L443	N376	Q286	Q216	S146
THR	THR	VAL	SER	VAL	CYS	LEU	SER	LEU	GLN	GLN	GLN	P444	S377	T287	K217	D147
ASP	PHE	ASP	ASP	PHE	ASP	ASN	ASP	ASN	GLN	ASN	ASN	E445	V378	H288	T218	F148
LYS	ARG	ASN	ASN	ARG	ASN	ASN	ASN	ASN	ASN	ASN	ASN	G446	I379	M289	Q219	L149
GLY	ASN	TRP	VAL	GLN	VAL	TRP	VAL	VAL	LEU	LEU	LEU	S447	G380	H290	G220	L150
GLN	GLN	TYR	GLN	ILE	LEU	GLY	LEU	LEU	GLY	GLY	GLY	V448	P381		L221	V151
LEU	LEU	LYS	LYS	ARG	GLU	LEU	GLU	GLU	GLU	GLU	GLU	I449		Y296	R222	G153
ARG	ARG	ARG	ILE	ARG	ILE	LYS	LYS	LYS	LYS	LYS	LYS	S450	H384	Q297	R223	D154
LYS	ALA	ALA	ASN	ALA	ASN	ILE	ASN	ASN	ASN	ILE	ILE	L451		R299	F226	V155
ASN	ASN	ALA	SER	ALA	SER	ASN	SER	SER	SER	ASN	ASN	H452	D387	R299	P227	I156
GLN	GLN	ASP	ASP	ASP	LEU	LEU	LEU	LEU	LEU	LEU	LEU	P453	N388	V300	L228	S157
GLN	GLN	HIS	HIS	HIS	LYS	LYS	LYS	LYS	LYS	GLU	GLU	P454	V390	S301	S229	
LEU	LEU	LEU	LEU	LEU	TYR	TYR	TYR	TYR	TYR	GLU	GLU	E460	L391	Y306	L230	I161
GLU	GLU	GLU	GLU	GLU	ALA	ALA	ALA	ALA	ALA	GLU	GLU			S307	F231	
ARG	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	ALA	GLU	SER	E464	T394	A308		A164
PHE	PHE	LEU	ALA	ALA	ASN	GLU	ASN	ASN	GLU	GLU	GLU		Y395	V309	D236	L165
GLU	ILE	ALA	ALA	ALA	ILE	LEU	ILE	ILE	SER	GLU	SER	D467	L396	C310	G237	E166
GLN	GLN	ALA	ALA	ALA	SER	GLU	SER	GLU	GLU	GLU	GLU	ASP	W397		E167	E167
TRP	TRP	ILE	ILE	ILE	LEU	LEU	LEU	LEU	SER	SER	SER		Q398	I314	E239	H168
LEU	LEU	GLU	GLU	GLU	LYS	LYS	LYS	LYS	GLY	GLY	GLY	GLY	G399	R315	V240	
LYS	LYS	ASP	GLU	GLU	GLU	GLN	GLU	GLU	GLN	GLN	GLN	ALA	V400	R316	R241	
GLU	GLU	ASP	ASP	ASP	GLU	GLU	GLU	GLU	GLU	GLU	SER	ALA	R401		Y242	R171
PHE	PHE	GLU	PHE	PHE	VAL	VAL	VAL	VAL	SER	SER	SER	MET		P323	K172	
ALA	ALA	LEU	LEU	LEU	GLU	GLN	GLN	GLN	GLN	GLN	GLN	GLN	A404	E324	R173	
GLU	GLU	GLU	GLU	GLU	VAL	VAL	VAL	VAL	SER	SER	SER	LYS	G405		L243	K173
GLU	GLU	GLU	GLU	GLU	VAL	VAL	VAL	VAL	SER	SER	SER	LYS	A405		L244	L174
HIS	HIS	GLU	GLU	GLU	VAL	VAL	VAL	VAL	GLU	GLU	GLU	LYS	A406		L245	E175
GLU	GLU	GLU	GLU	GLU	SER	SER	SER	SER	GLU	GLU	GLU	ASP	A407		D246	K176
SER	SER	ALA	ALA	ALA	LEU	LEU	LEU	LEU	GLU	GLU	GLU	PRO	Q407		C247	N177
SER	SER	LEU	LEU	LEU	ALA	HIS	HIS	HIS	ALA	ALA	ALA	VAL	T408		H248	V178
ASP	ASP	GLU	GLU	GLU	VAL	VAL	VAL	VAL	VAL	VAL	VAL	ASP	H409		L249	
ASP	ASP	ILE	ILE	ILE	VAL	VAL	VAL	VAL	SER	SER	SER	MET	Q410		S179	
ASP	ASP	ILE	ILE	ILE	VAL	VAL	VAL	VAL	GLY	GLY	GLY	ARG	S411		V180	M181
ASP	ASP	GLU	GLU	GLU	GLU	GLU	GLU	GLU	GLY	GLY	GLY	GLY	L412		T182	
ASP	ASP	MET	MET	MET	PHE	PHE	PHE	PHE	GLY	GLY	GLY	TYR	L413		S253	
ALA	ALA	ALA	ALA	ALA	PRO	PRO	PRO	PRO	ALA	ALA	ALA	ASN	C414		F185	
LYS	LYS	LYS	LYS	LYS	LEU	LEU	LEU	LEU	SER	SER	SER	PRO	D415		K186	
VAL	VAL	VAL	VAL	VAL	GLN	GLN	GLN	GLN	GLN	GLN	GLN	PRO	N416		Q254	
LEU	LEU	LEU	LEU	LEU	GLM	GLM	GLM	GLM	GLU	GLU	GLU	ALA	A417		V256	
MET	MET	MET	MET	MET	MET	MET	MET	MET	GLU	GLU	GLU	VAL	GLU		A257	S188
ALA	ALA	ALA	ALA	ALA	ASP	ASP	ASP	ASP	ASP	ASP	ASP	VAL	E418		Q258	S189
ALA	ALA	ALA	ALA	ALA	ASP	ASP	ASP	ASP	ILE	ILE	ILE	GLY	V419		L259	
PHE	PHE	TYR	TYR	TYR	SER	SER	SER	SER	LYS	LYS	LYS	ALA	R420		F260	H192
TYR	TYR	GLN	GLN	GLN	PRO	PRO	PRO	PRO	VAL	VAL	VAL	GLY	G353		T261	P193
GLN	GLN	LEU	LEU	LEU	GLN	GLN	GLN	GLN	VAL	VAL	VAL	GLY	R422		D262	T194
ILE	ILE	GLU	GLU	GLU	ASP	ASP	ASP	ASP	PHE	PHE	PHE	GLY	V423		N263	R195
GLU	GLU	GLU	GLU	GLU	SER	SER	SER	SER	GLN	GLN	GLN	GLY	L355			
ILE	ILE	SER	SER	SER	SER	SER	SER	SER	ASN	ASN	ASN	TYR	T424			
LEU	LEU	ARG	ARG	ARG	GLU	GLU	GLU	GLU	GLU	GLU	GLU	LEU	L425		Y266	N200
ALA	ALA	TRP	TRP	TRP	ALA	ALA	ALA	ALA	VAL	VAL	VAL	TRP	P427		R269	V203
GLU	GLU	GLU	GLU	GLU	VAL	VAL	VAL	VAL	GLY	GLY	GLY	GLY	R428		D270	A204
GLU	GLU	GLU	GLU	GLU	CYS	CYS	CYS	CYS	LYS	LYS	LYS	ALA	S429		D271	V205
THR	THR	THR	THR	THR	ALA	ALA	ALA	ALA	LEU	LEU	LEU	ALA	V430		F272	D206
THR	THR	THR	THR	THR	LEU	LEU	LEU	LEU	THR	THR	THR	GLY	L431		V273	S207

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

Chain J:  28% 31% 40%

MET	ALA	PRO	VAL	ALA	PRO	PRO	GLY	VAL	VAL	VAL	SER	ARG	ALA	ASN	LYS	ARG	ARG	GLY	GLY	GLY	GLY	GLY	GLY	GLY	ALA	ALA	GLU	GLU	GLU	PRO	GLU	P40	L43	Q44	A45	V46	V48	A49	D50	S51	R54	R55	F56	F57	P58	I59	S60	K61	D62	
Q63	P64	R65	V66	L67	L68	P69	L70	A71	G153	D154	V155	I156	S157	N158	I159	A164	L165	H168	R169	L170	R171	R172	K173	L174	E175	K176	N177	V178	S179	V180	M181	I182	M183	I184	F185	K186	S189	H192	P193	T194	R195	N200	V203	A204	R211	V212	L213	H214	F215	R223
E239	V240	R241	Y242	D243	L244	L245	D246	C247	H248	I249	S250	Q255	V256	A257	L259	F260	T261	D262	N263	F264	Q267	T268	R269	F272	G275	L276	L277	N278	N279	E280	E281	I282	L283	G284	N285	Q286	I287	L288	H289	H290	V291	T292								
A293	G297	V306	Y306	V309	C310	R316	Q317	V318	Y319	P320	P323	E324	A325	N326	F327	I328	D329	Q333	S334	C335	T336	H337	S338	R339	Y343	R344	G345	V348	G351	L356	E357	V360	I368	F373	L374	P377	V378	I379	G380											
H384	I385	V389	V390	T394	Y395	W397	Q398	G399	V400	R401	I408	L412	L413	C414	A417	K420	E421	R422	V423	T424	L425	K426	P427	R428	S429	V430	L431	T432	V435	P439	R440	I441	T442	L443	P444	E445	G446	S447	V448	I449	S450	H451	H452	A456	E457	E458	D459	E460		

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	66721	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.102	Depositor
Minimum map value	-0.045	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0125	Depositor
Map size (\AA)	441.0, 441.0, 441.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.47, 1.47, 1.47	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	0.37	0/2296	0.54	0/3099
1	B	0.39	0/2283	0.52	0/3081
2	C	0.39	0/2522	0.52	0/3411
2	D	0.37	0/2587	0.52	0/3498
3	E	0.31	0/2472	0.54	0/3357
3	F	0.31	0/2464	0.53	0/3346
4	G	0.40	0/2802	0.55	0/3809
4	H	0.41	0/2802	0.53	0/3809
5	I	0.38	0/3427	0.56	0/4662
5	J	0.37	0/3441	0.55	0/4682
6	K	0.25	0/1301	0.46	0/1812
6	L	0.24	0/879	0.44	0/1224
7	M	0.21	0/79	0.45	0/109
8	P	0.30	0/2129	0.56	1/2973 (0.0%)
All	All	0.36	0/31484	0.53	1/42872 (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
2	D	0	1
3	E	0	1
4	H	0	1
6	K	0	1
8	P	0	2
All	All	0	6

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	P	94	PRO	N-CA-C	5.85	127.30	112.10

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	126	TYR	Peptide
3	E	290	TRP	Peptide
4	H	419	GLY	Peptide
6	K	223	MET	Peptide
8	P	94	PRO	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	2262	0	2333	128	0
1	B	2249	0	2324	124	0
2	C	2476	0	2493	149	0
2	D	2538	0	2538	164	0
3	E	2438	0	2208	175	0
3	F	2430	0	2197	148	0
4	G	2750	0	2811	178	0
4	H	2750	0	2811	175	0
5	I	3358	0	3325	233	0
5	J	3371	0	3332	207	0
6	K	1309	0	612	14	0
6	L	889	0	401	7	0
7	M	80	0	31	0	0
8	P	2109	0	1073	24	0
All	All	31009	0	28489	1626	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 27.

The worst 5 of 1626 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:G:364:ARG:HH22	4:G:465:CYS:HA	1.25	0.97
6:K:35:LEU:O	6:K:40:ASN:HA	1.71	0.91
3:F:156:ASP:HA	3:F:171:ALA:O	1.71	0.89
3:E:212:VAL:O	3:E:216:MET:HB2	1.72	0.89
5:J:56:PHE:HB3	5:J:59:ILE:HB	1.55	0.88

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	289/305 (95%)	238 (82%)	51 (18%)	0	100	100
1	B	287/305 (94%)	239 (83%)	48 (17%)	0	100	100
2	C	313/351 (89%)	267 (85%)	46 (15%)	0	100	100
2	D	320/351 (91%)	275 (86%)	45 (14%)	0	100	100
3	E	334/452 (74%)	255 (76%)	79 (24%)	0	100	100
3	F	333/452 (74%)	251 (75%)	82 (25%)	0	100	100
4	G	351/523 (67%)	300 (86%)	51 (14%)	0	100	100
4	H	351/523 (67%)	299 (85%)	51 (14%)	1 (0%)	37	72
5	I	425/721 (59%)	348 (82%)	77 (18%)	0	100	100
5	J	427/721 (59%)	346 (81%)	81 (19%)	0	100	100
6	K	255/315 (81%)	208 (82%)	46 (18%)	1 (0%)	30	67
6	L	173/315 (55%)	148 (86%)	25 (14%)	0	100	100
7	M	14/333 (4%)	13 (93%)	1 (7%)	0	100	100
8	P	419/472 (89%)	316 (75%)	101 (24%)	2 (0%)	25	63
All	All	4291/6139 (70%)	3503 (82%)	784 (18%)	4 (0%)	50	83

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	P	278	VAL
8	P	94	PRO
6	K	60	LYS
4	H	460	PRO

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	248/260 (95%)	244 (98%)	4 (2%)	58	74
1	B	247/260 (95%)	245 (99%)	2 (1%)	79	85
2	C	269/298 (90%)	269 (100%)	0	100	100
2	D	276/298 (93%)	272 (99%)	4 (1%)	62	76
3	E	215/398 (54%)	212 (99%)	3 (1%)	62	76
3	F	214/398 (54%)	212 (99%)	2 (1%)	75	83
4	G	309/444 (70%)	309 (100%)	0	100	100
4	H	309/444 (70%)	305 (99%)	4 (1%)	65	77
5	I	381/626 (61%)	379 (100%)	2 (0%)	86	90
5	J	383/626 (61%)	379 (99%)	4 (1%)	73	82
6	K	6/279 (2%)	6 (100%)	0	100	100
6	L	3/279 (1%)	3 (100%)	0	100	100
8	P	21/397 (5%)	21 (100%)	0	100	100
All	All	2881/5007 (58%)	2856 (99%)	25 (1%)	74	83

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	133	ARG
4	H	312	ILE
5	J	230	LEU
4	H	306	ARG
4	H	420	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
5	I	105	HIS
5	J	255	GLN
5	I	200	ASN
5	J	72	ASN
5	J	388	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	K	51	6	8,9,10	1.55	1 (12%)	8,12,14	1.48	2 (25%)
6	SEP	L	51	6	8,9,10	1.51	1 (12%)	8,12,14	1.57	1 (12%)

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	K	51	6	-	2/5/8/10	-
6	SEP	L	51	6	-	5/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	K	51	SEP	P-O1P	3.39	1.61	1.50
6	L	51	SEP	P-O1P	3.25	1.61	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	L	51	SEP	OG-CB-CA	3.29	111.34	108.14
6	K	51	SEP	P-OG-CB	-2.63	111.05	118.30
6	K	51	SEP	OG-CB-CA	2.54	110.62	108.14

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	K	51	SEP	CA-CB-OG-P
6	L	51	SEP	N-CA-CB-OG
6	L	51	SEP	CA-CB-OG-P
6	L	51	SEP	CB-OG-P-O2P
6	K	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.

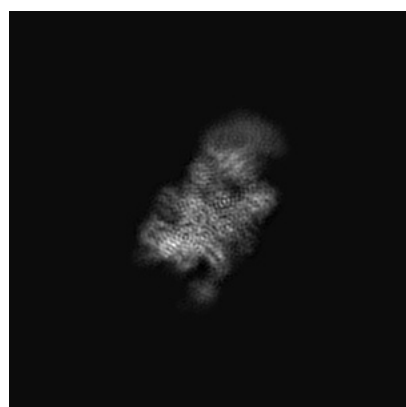
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30568. These allow visual inspection of the internal detail of the map and identification of artifacts.

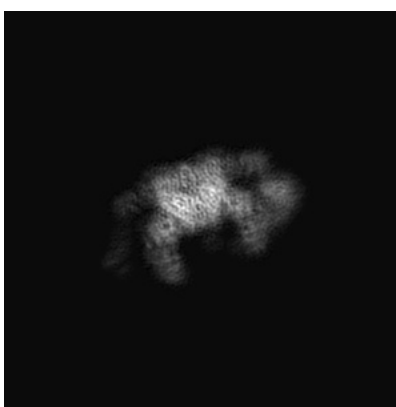
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

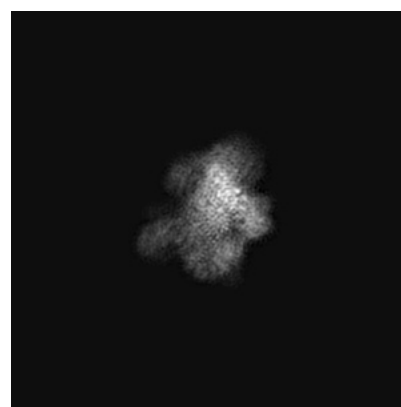
6.1.1 Primary map



X



Y

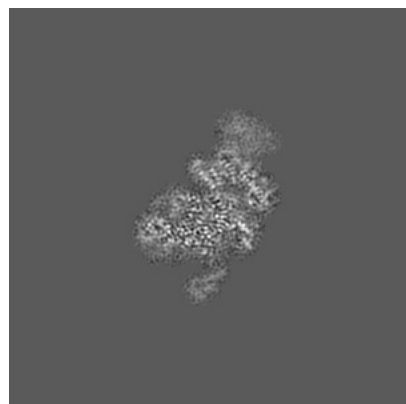


Z

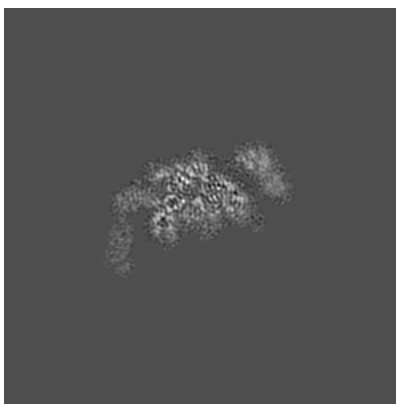
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

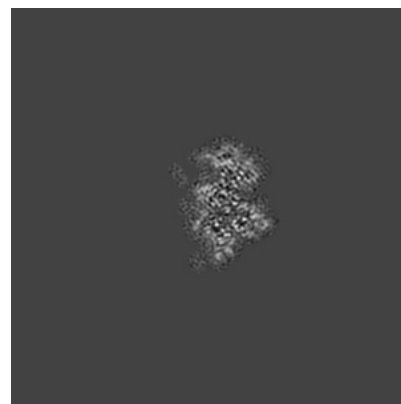
6.2.1 Primary map



X Index: 150



Y Index: 150

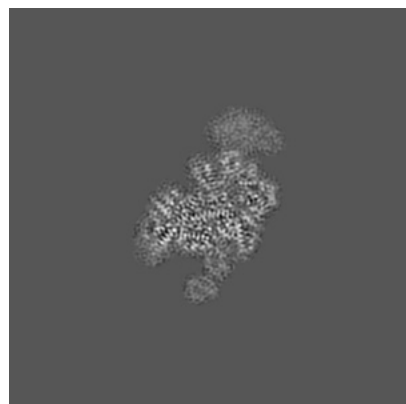


Z Index: 150

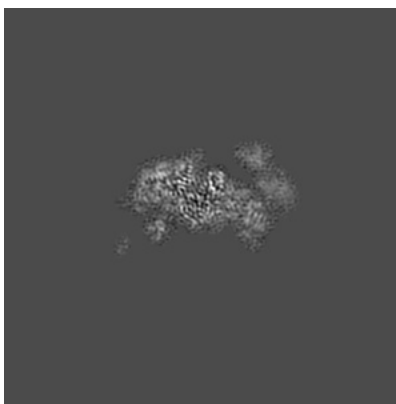
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

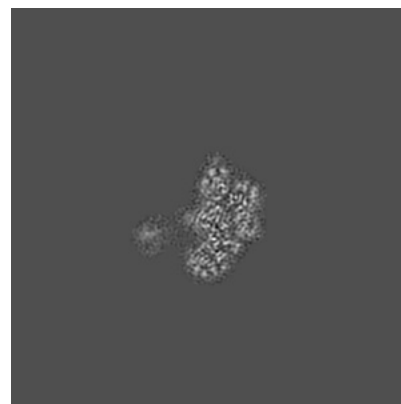
6.3.1 Primary map



X Index: 155



Y Index: 158

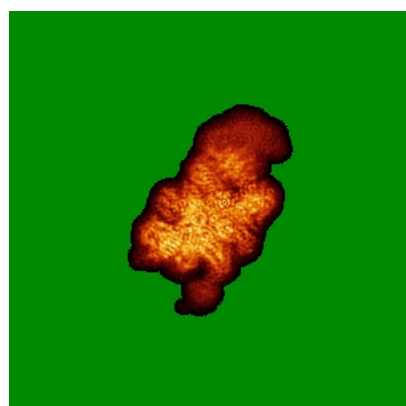


Z Index: 134

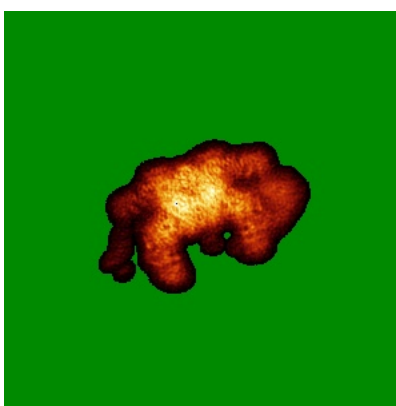
The images above show the largest variance slices of the map in three orthogonal directions.

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

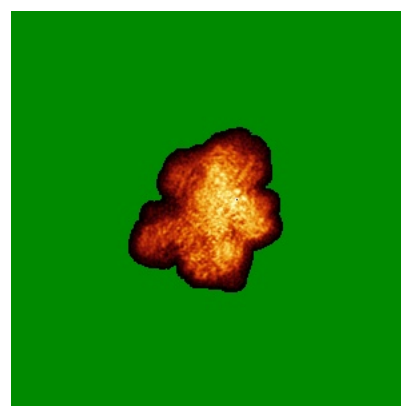
6.4.1 Primary map



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 0.0125. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

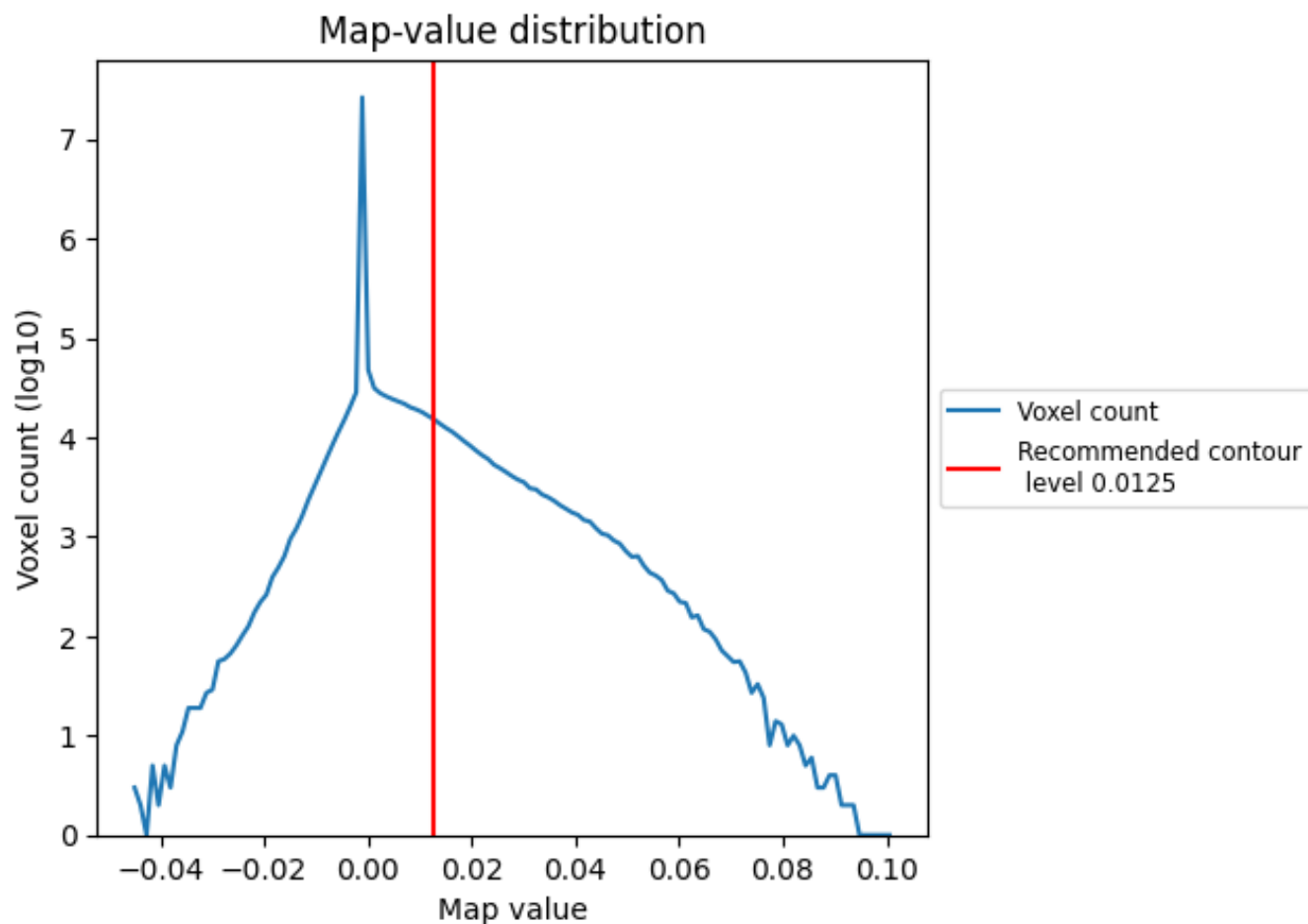
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

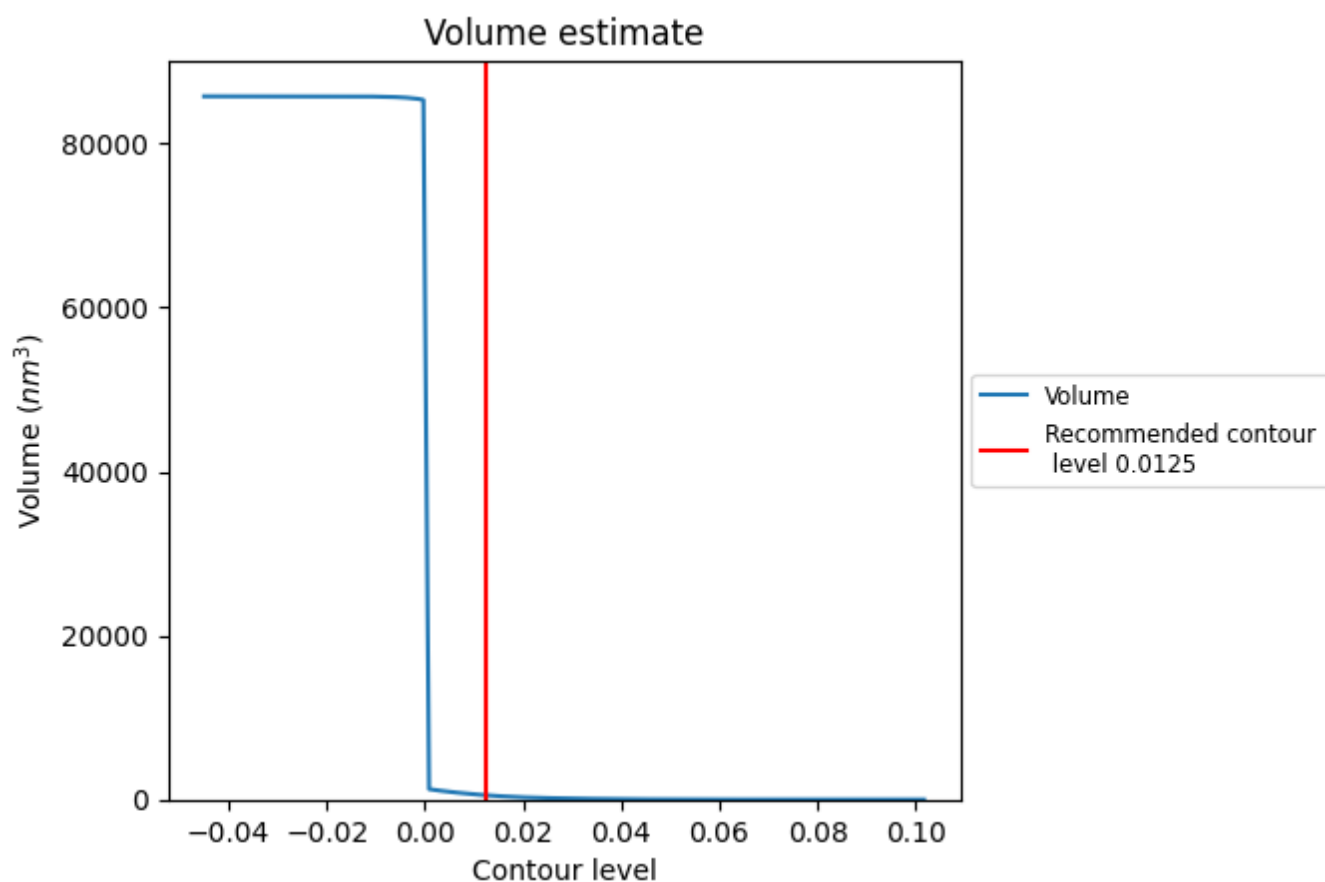
This section contains the results of statistical analysis of the map.

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.

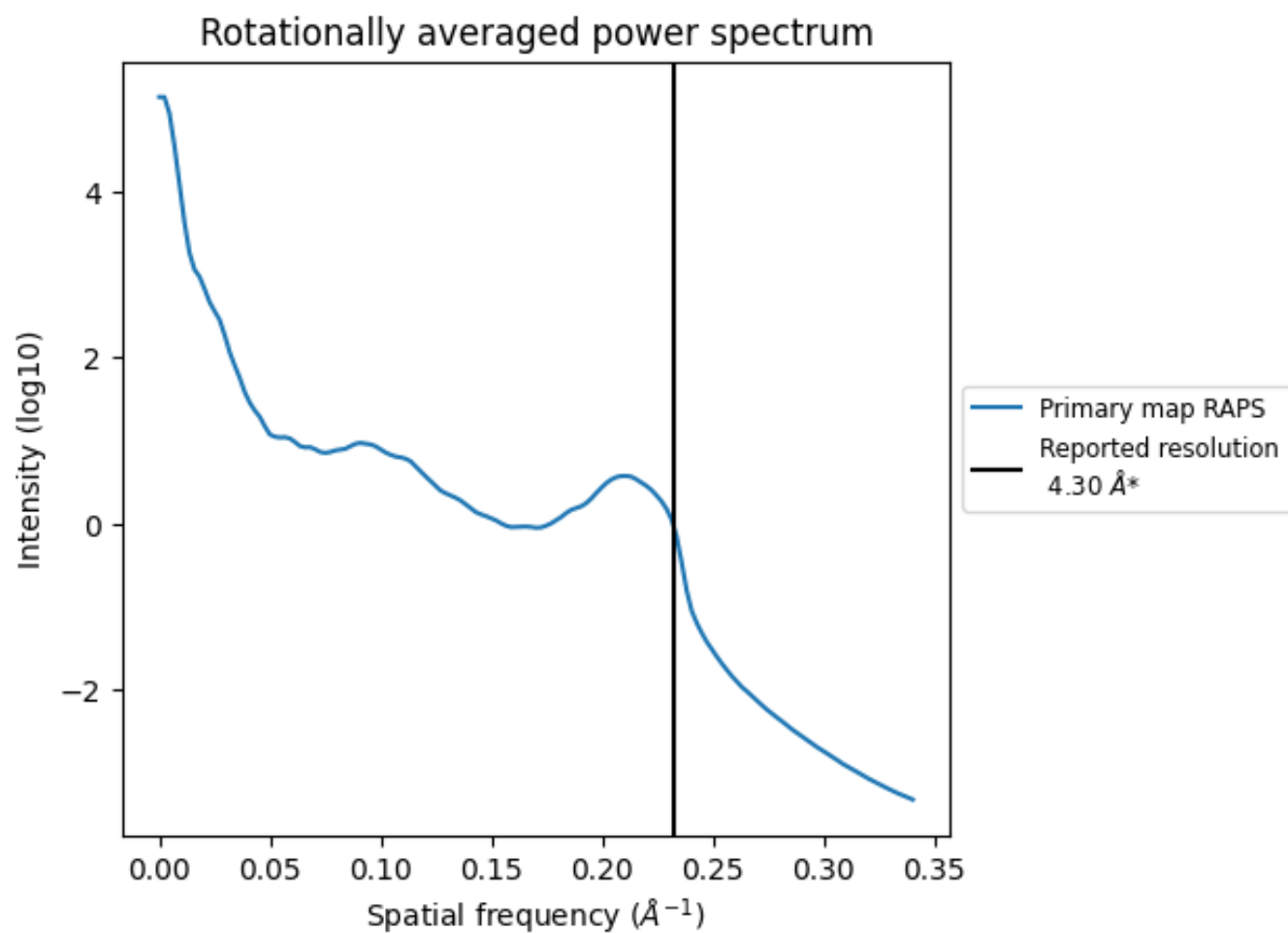
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 525 nm³; this corresponds to an approximate mass of 475 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 0.233 Å⁻¹

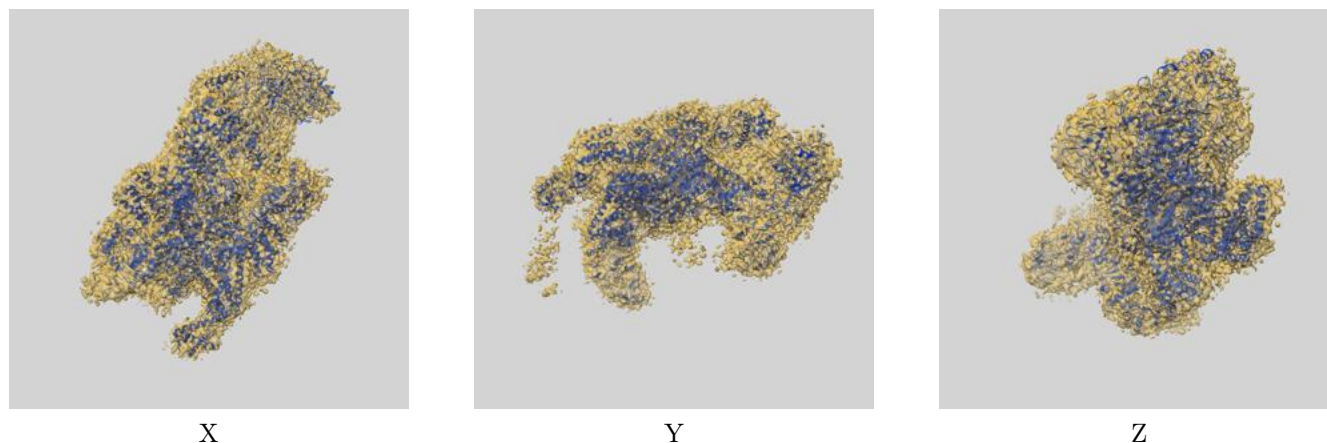
8 Fourier-Shell correlation

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-30568 and PDB model 7D43. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



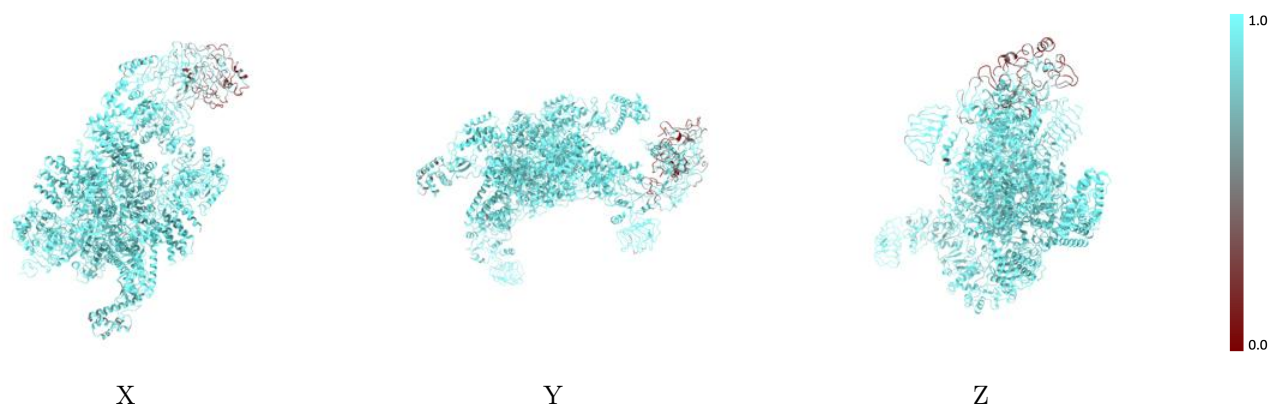
The images above show the 3D surface view of the map at the recommended contour level 0.0125 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



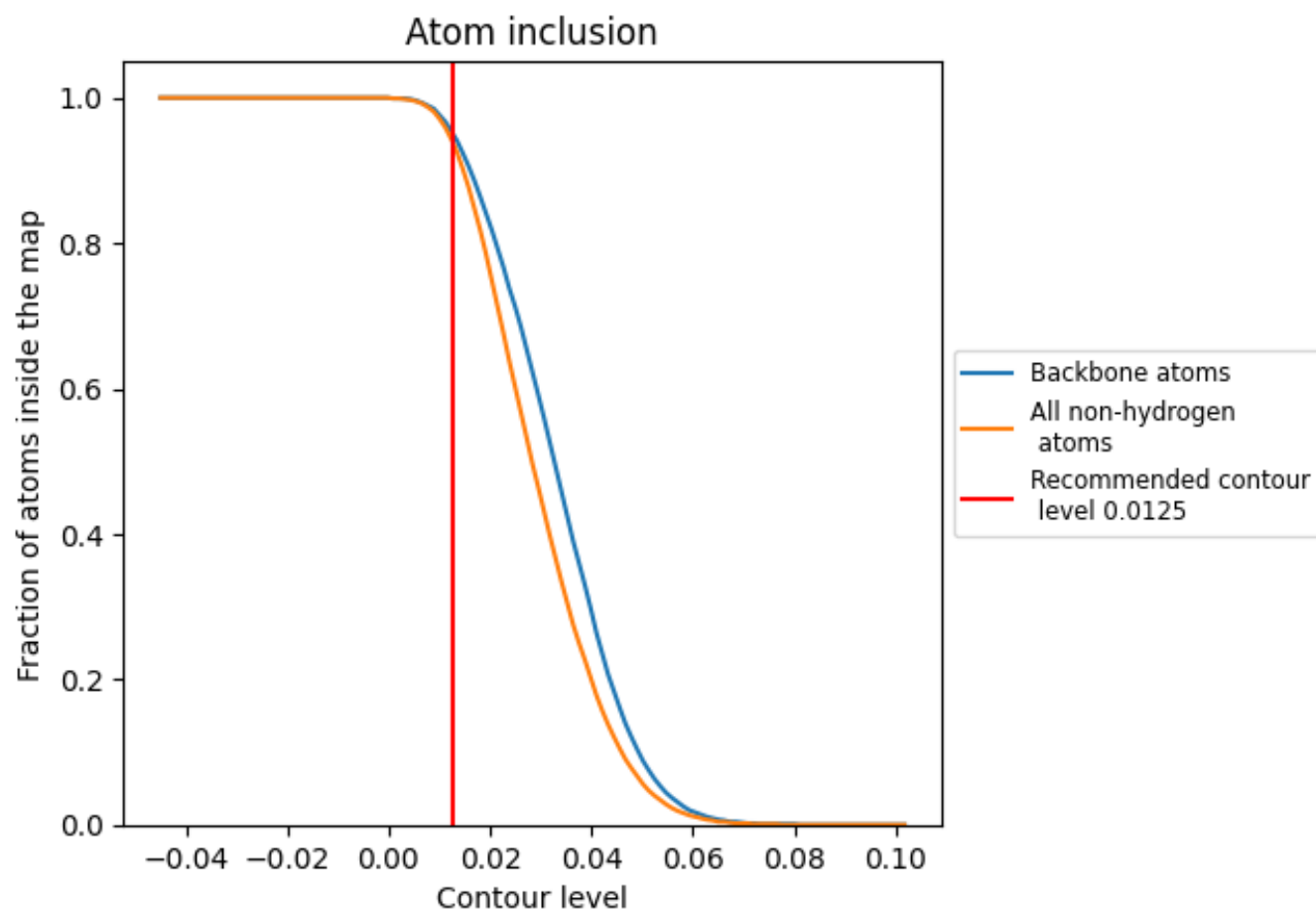
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0125).































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% 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 (0.0125) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9410	 0.3850
A	 0.9750	 0.4160
B	 0.9770	 0.4110
C	 0.9680	 0.4230
D	 0.9690	 0.4250
E	 0.9540	 0.3370
F	 0.9600	 0.3340
G	 0.9650	 0.4100
H	 0.9660	 0.4230
I	 0.9640	 0.4030
J	 0.9750	 0.4030
K	 0.9680	 0.3230
L	 0.8570	 0.3500
M	 0.3750	 0.3070
P	 0.6540	 0.2620

