



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 05:02 PM UTC

PDB ID : 7SZ1 / pdb_00007sz1
EMDB ID : EMD-25559
Title : Cryo-EM structure of the extracellular module of the full-length EGFR L834R bound to EGF. "tips-separated" conformation
Authors : Huang, Y.; Ognjenovic, J.; Karandur, D.; Miller, K.; Merk, A.; Subramaniam, S.; Kuriyan, J.
Deposited on : 2021-11-25
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

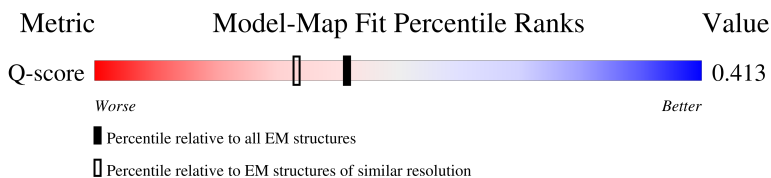
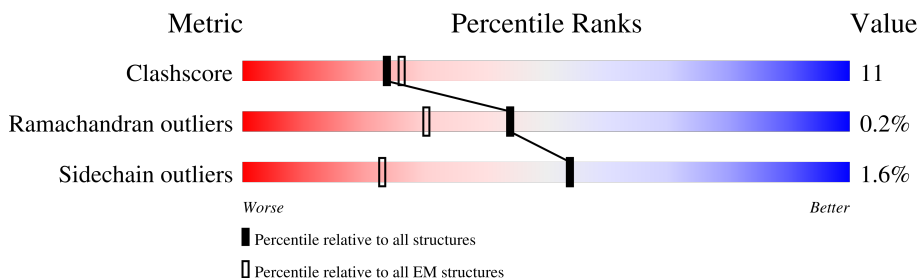
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	1210	
1	B	1210	
2	C	53	
2	D	53	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10216 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 Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	614	Total	C	N	O	S	0	0
			4723	2914	842	907	60		
1	B	614	Total	C	N	O	S	0	0
			4723	2914	842	907	60		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	ASN	ASP	conflict	UNP P00533
A	834	ARG	LEU	variant	UNP P00533
B	232	ASN	ASP	conflict	UNP P00533
B	834	ARG	LEU	variant	UNP P00533

- Molecule 2 is a protein called Epidermal growth factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	47	Total	C	N	O	S	0	0
			385	244	63	71	7		
2	D	47	Total	C	N	O	S	0	0
			385	244	63	71	7		

GLY	ASN	ALA
ALA	PRO	GLU
THR	TYR	TYR
THR	GLY	LEU
GLU	ASN	ARG
ASP	ASN	VAL
SER	THR	ALA
ILE	VAL	PRO
ASP	GLN	GLN
ASP	PRO	SER
THR	THR	SER
THR	CYS	PHE
LEU	VAL	PHE
PRO	ASN	VAL
VAL	SER	VAL
PRO	THR	SER
GLU	PHE	THR
TYR	ASP	ALA
ILE	SER	GLY
ASN	PRO	LEU
GLN	ALA	GLN
VAL	HIS	VAL
VAL	TRP	VAL
PRO	ALA	ALA
LYS	GLN	LYS
ARG	LYS	ARG
PRO	GLY	PRO
GLY	SER	ALA
GLN	HIS	GLN
VAL	ILE	VAL
GLN	SER	GLN
ASN	LEU	ASN
PRO	ASP	PRO
VAL	ASN	VAL
TYR	PRO	TYR
ASN	ASP	ASN
GLN	TYR	GLN
PRO	GLN	PRO
LEU	ASP	LEU
ASN	PHE	ASN
PRO	PHE	PRO
ALA	PRO	ALA
PRO	LYS	PRO
SER	GLU	SER
ARG	ALA	ARG
ASP	LYS	ASP
THR	ASN	THR
VAL	ALA	VAL
GLY	ASN	GLY

• Molecule 1: Epidermal growth factor receptor

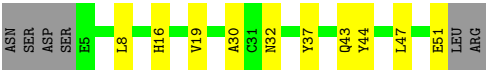
Chain B: 35% 15% 49%

MET	A62	C338	C446	I545	GLY	GLU	VAL	GLU	ASP	GLU	LYS
ARG	G63	D344	K454	T548	THR	THR	ASP	THR	ARG	THR	THR
PRO	Y64	L345	G549	G549	GLY	PHE	ASN	GLU	PRO	GLU	GLY
GLY	L66	H346	K465	R550	ALA	LYS	HIS	LYS	HIS	LYS	ALA
ASN	I67	P349	R470	P552	LEU	ILE	CYS	ILE	VAL	ILE	THR
THR	A68	D364	C482	N553	LEU	LYS	ARG	LYS	ARG	LYS	ASP
ALA	L80	E367	H483	N554	LEU	VAL	GLY	VAL	THR	VAL	ASP
GLN	I83	E376	L485	C555	VAL	SER	ALA	GLY	ALA	GLY	PRO
PRO	R84	I377	C486	I556	ALA	GLY	ARG	SER	ILE	THR	GLN
PHE	M87	T378	S487	D563	LEU	ALA	CYS	GLY	ALA	VAL	LEU
VAL	Y88	G379	P488	D564	LEU	PHE	ASN	ALA	GLY	THR	LEU
THR	R89	F380	E489	P565	GLY	THR	VAL	THR	LEU	THR	THR
PRO	V97	T250	C491	C567	GLY	VAL	LYS	VAL	ALA	THR	GLY
ASP	N100	Q252	P494	A572	PHE	TYR	PRO	GLN	ALA	PRO	PRO
SER	T106	K260	E495	A573	MET	LYS	ILE	ILE	CYS	THR	THR
ALA	R114	C267	P496	G574	ARG	GLY	GLN	GLY	ASP	THR	VAL
LYS	Q117	N274	D498	M575	THR	ILE	MET	ILE	LYS	PRO	ILE
GLN	E118	Y275	C500	M576	VAL	VAL	PRO	ARG	ALA	LEU	VAL
SER	T10	V276	S501	G577	ARG	GLY	THR	GLY	THR	ASP	GLY
HIS	S11	D279	R502	E578	LEU	GLY	VAL	VAL	VAL	PRO	GLY
GLN	N12	G281	R503	N579	LEU	VAL	LYS	VAL	GLY	THR	THR
VAL	K13	F126	V505	N580	ARG	LYS	LEU	VAL	ALA	LEU	LEU
LEU	L14	S127	S506	K585	LEU	ILE	ASP	ILE	LYS	ASP	ASP
ASN	T19	W140	G508	A589	LEU	VAL	TYR	VAL	LEU	VAL	VAL
PRO	D22	V144	A286	L595	GLY	GLY	ASN	ALA	GLY	GLY	GLY
TYR	H23	S145	C287	C596	GLU	ARG	GLY	ILE	ASN	GLY	ASN
GLN	S26	D147	D289	H597	LEU	GLY	ASP	ARG	ILE	LEU	GLN
LEU	Q28	F148	Y292	E602	VAL	VAL	ILE	GLY	LYS	GLY	TYR
ASN	R29	N151	E293	C604	GLY	THR	ALA	ALA	HIS	ALA	ALA
PRO	M30	M152	W294	T605	PRO	SER	GLN	GLY	ALA	SER	GLY
ALA	F31	C175	E295	G606	THR	PRO	ASN	LYS	ALA	THR	THR
PRO	N32	S174	V299	P607	GLY	LYS	GLY	VAL	ALA	VAL	VAL
SER	N33	C34	R300	G608	LEU	ALA	ASN	ASN	GLY	THR	THR
ASP	C34	E35	C301	V526	ALA	ILE	LYS	TRP	VAL	GLY	GLY
LYS	M40	N182	K302	C531	PRO	GLY	CYS	PRO	ILE	ILE	ALA
PRO	E42	Q184	K303	I532	THR	THR	VAL	GLY	LYS	THR	PRO
THR	T44	R198	C305	H535	ARG	VAL	GLY	GLY	ALA	VAL	ALA
SER	R48	G199	G313	P536	LEU	THR	ASN	ASN	GLY	THR	THR
THR	E60	R200	G315	E537	GLY	VAL	GLY	GLY	ALA	VAL	VAL
ALA	N210	H209	F335	C538	THR	MET	GLY	GLY	ALA	THR	THR
GLY	Q211	M444	L445	L539	ILE	ILE	PRO	PRO	THR	THR	THR
				P540	ALA	ALA	LYS	LYS	ALA	ALA	ALA
				A542	THR	THR	ILE	ILE	THR	THR	THR
				M543	THR	THR	ILE	ILE	THR	THR	THR
				N544	THR	THR	ILE	ILE	THR	THR	THR

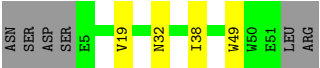
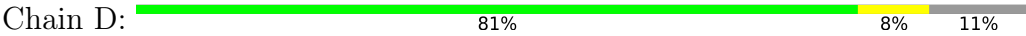
HIS
SER
THR
ALA
VAL
GLY
ASN
PRO
GLU
TYR
LEU
ASN
THR
VAL
GLN
PRO
SER
THR
CYS
VAL
ASN
PHE
ASP
SER
PRO
ALA
HIS
TRP
ALA
GLN
LYS
GLY
SER
HIS
GLN
ILE
SER
LEU
ASP
ASN
PRO
ASP
TYR
GLN
GLN
PHE
PHE
PRO
LYS
GLU
ALA
LYS
PRO
ASN
GLY
ILE
PHE
LYS

GLY
SER
THR
ALA
ASN
ALA
GLU
TYR
LEU
ARG
VAL
ALA
PRO
GLN
SER
SER
GLU
PHE
ILE
GLY
ALA

- Molecule 2: Epidermal growth factor



- Molecule 2: Epidermal growth factor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	100615	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.218	Depositor
Minimum map value	-0.483	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	345.408, 345.408, 345.408	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0794, 1.0794, 1.0794	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.21	0/4815	0.46	0/6514
1	B	0.32	0/4815	0.58	1/6514 (0.0%)
2	C	0.31	0/396	0.48	0/536
2	D	0.20	0/396	0.37	0/536
All	All	0.27	0/10422	0.51	1/14100 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	288	GLY	N-CA-C	9.08	118.47	110.21

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	4723	0	4556	98	0
1	B	4723	0	4556	118	0
2	C	385	0	344	5	0
2	D	385	0	344	3	0
All	All	10216	0	9800	218	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 11.

The worst 5 of 218 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:521:GLU:HB3	1:B:522:PRO:HD3	1.57	0.86
1:B:67:ILE:O	1:B:100:ASN:ND2	2.20	0.74
1:A:82:ILE:HG21	1:A:226:VAL:HG11	1.72	0.71
1:A:403:ARG:O	1:A:433:SER:OG	2.09	0.70
1:A:438:ILE:HG22	1:A:465:LYS:HB3	1.73	0.70

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	612/1210 (51%)	535 (87%)	76 (12%)	1 (0%)	43	71
1	B	612/1210 (51%)	507 (83%)	104 (17%)	1 (0%)	43	71
2	C	45/53 (85%)	41 (91%)	4 (9%)	0	100	100
2	D	45/53 (85%)	38 (84%)	7 (16%)	0	100	100
All	All	1314/2526 (52%)	1121 (85%)	191 (14%)	2 (0%)	44	71

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	500	VAL
1	A	500	VAL

5.3.2 Protein sidechains [i](#)

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	536/1053 (51%)	533 (99%)	3 (1%)	78	80
1	B	536/1053 (51%)	522 (97%)	14 (3%)	40	61
2	C	41/47 (87%)	39 (95%)	2 (5%)	22	49
2	D	41/47 (87%)	41 (100%)	0	100	100
All	All	1154/2200 (52%)	1135 (98%)	19 (2%)	54	68

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	505	VAL
1	B	562	ILE
1	B	595	LEU
1	B	539	LEU
1	B	399	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	384	GLN
1	B	394	HIS
1	B	504	ASN
1	A	541	GLN
1	A	535	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [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.

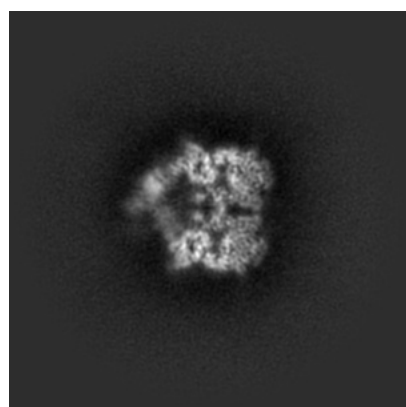
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25559. These allow visual inspection of the internal detail of the map and identification of artifacts.

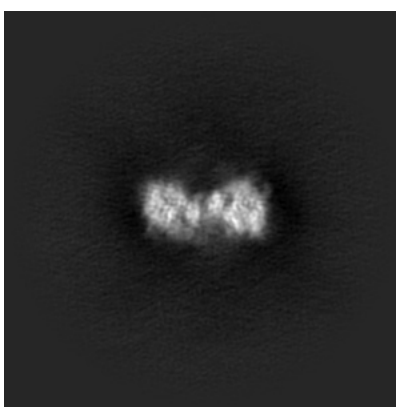
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

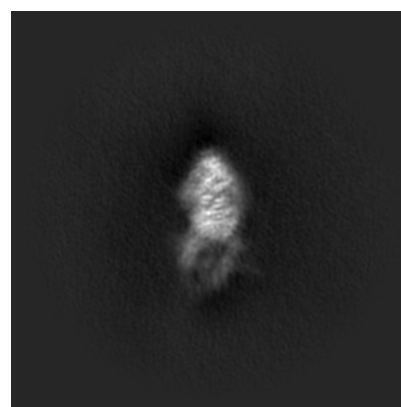
6.1.1 Primary map



X



Y

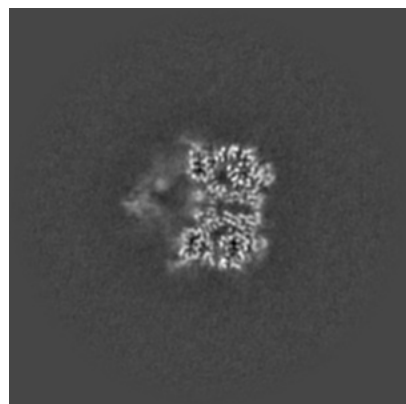


Z

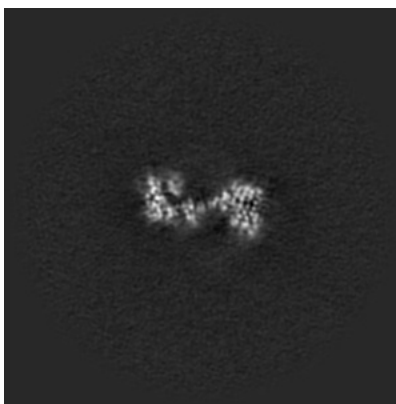
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

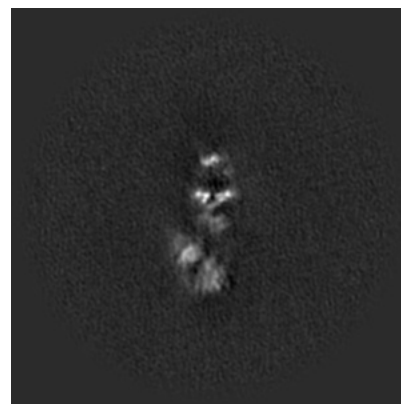
6.2.1 Primary map



X Index: 160



Y Index: 160

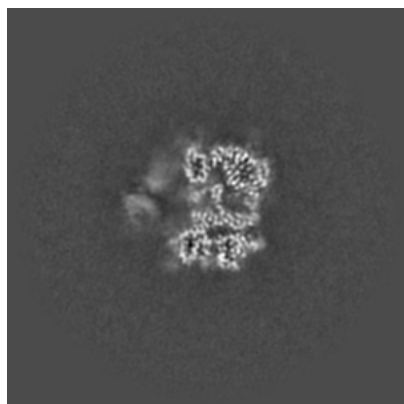


Z Index: 160

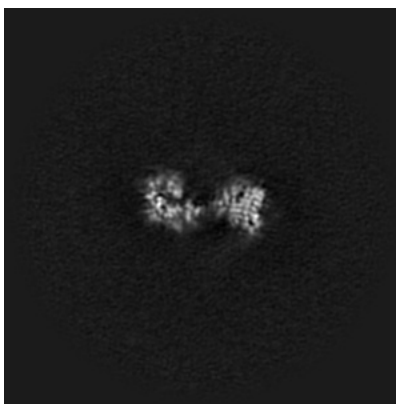
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

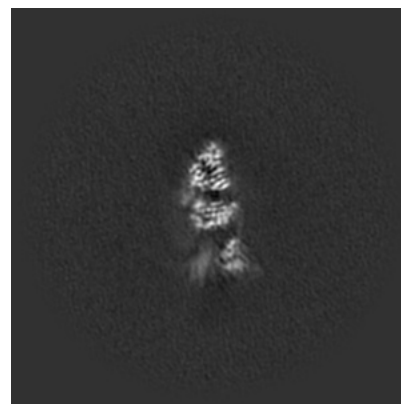
6.3.1 Primary map



X Index: 157



Y Index: 158

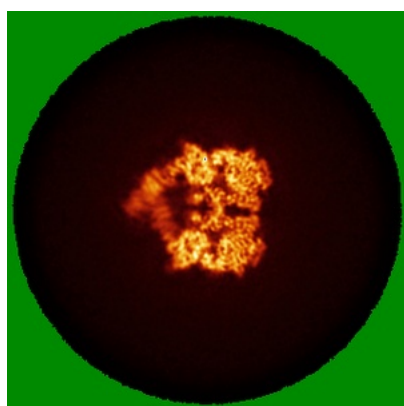


Z Index: 185

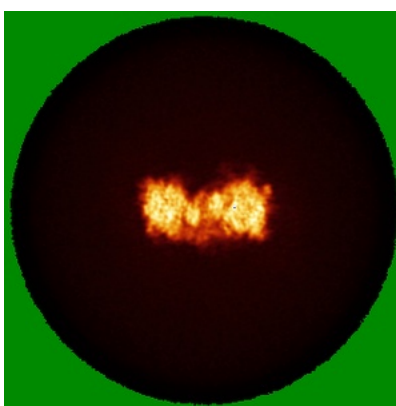
The images above show the largest variance slices of the map in three orthogonal directions.

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

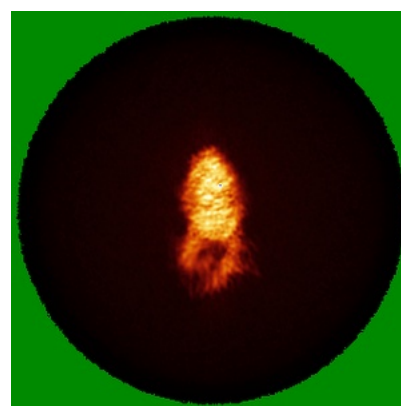
6.4.1 Primary map



X



Y

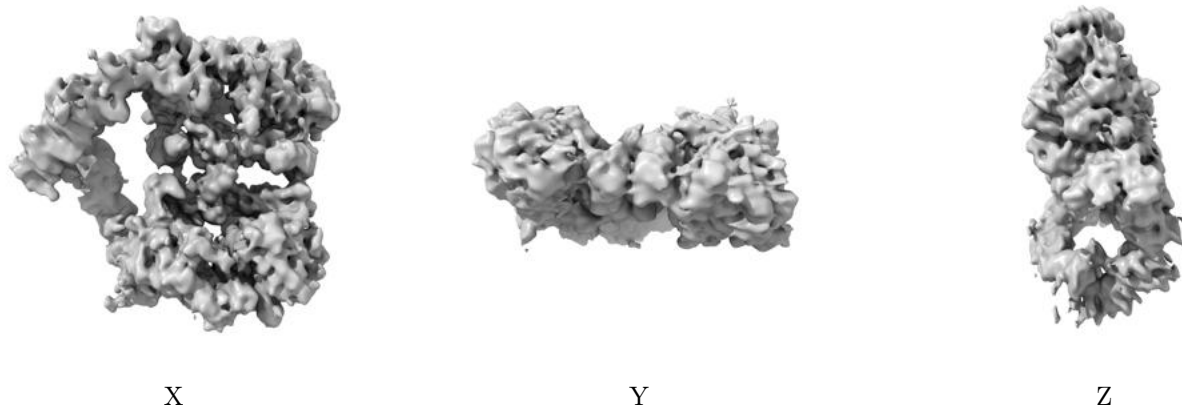


Z

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

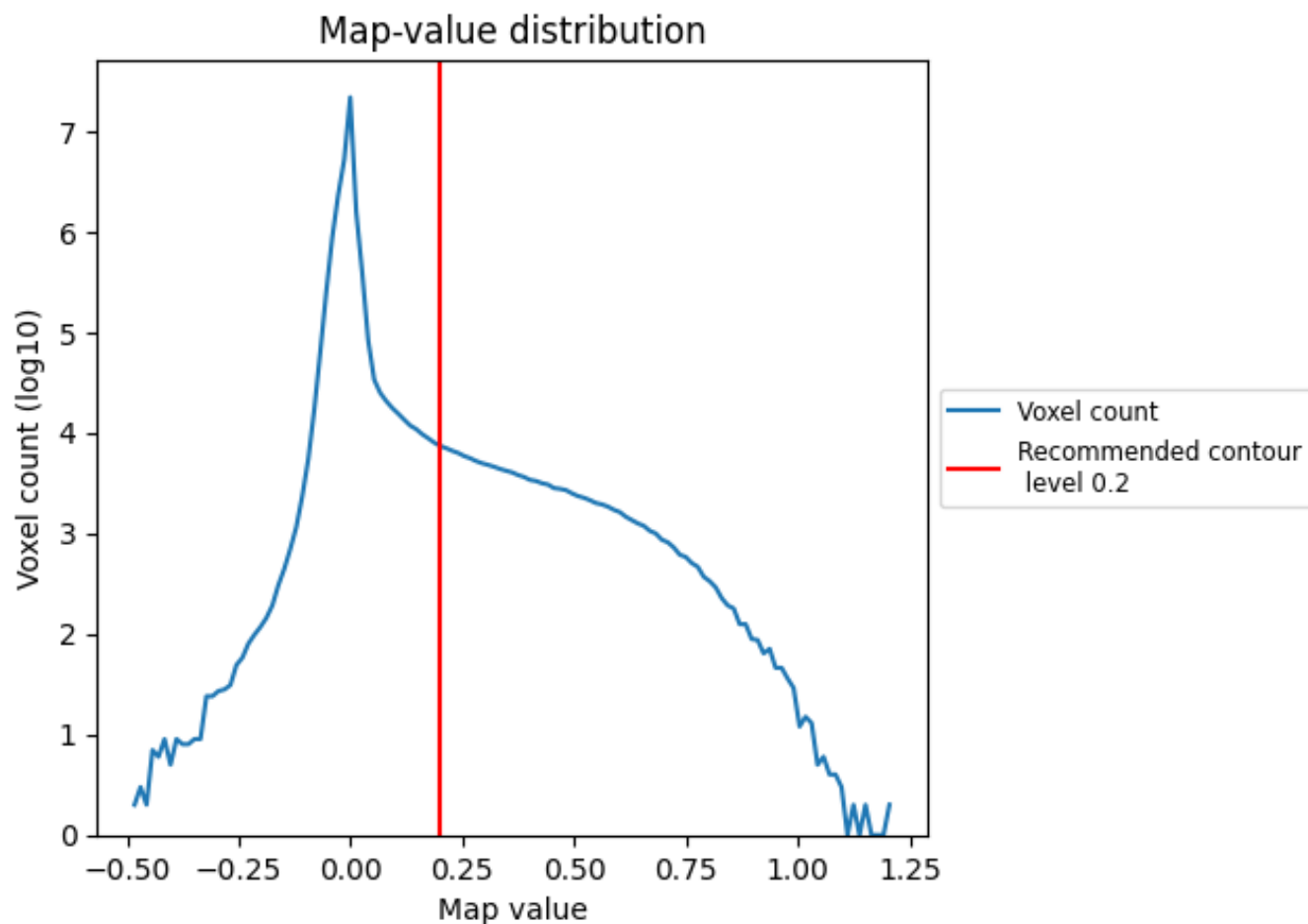
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

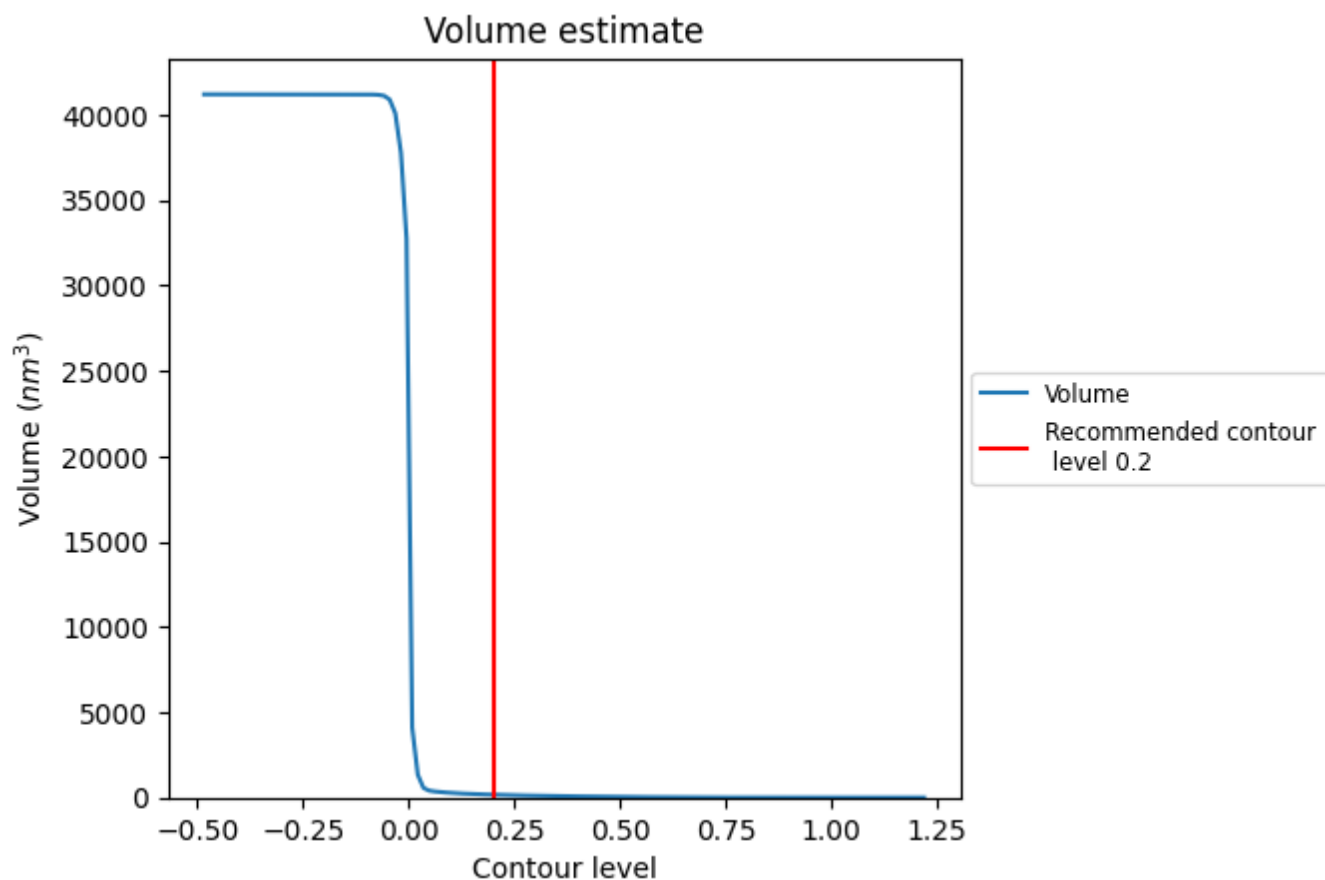
This section contains the results of statistical analysis of the map.

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.

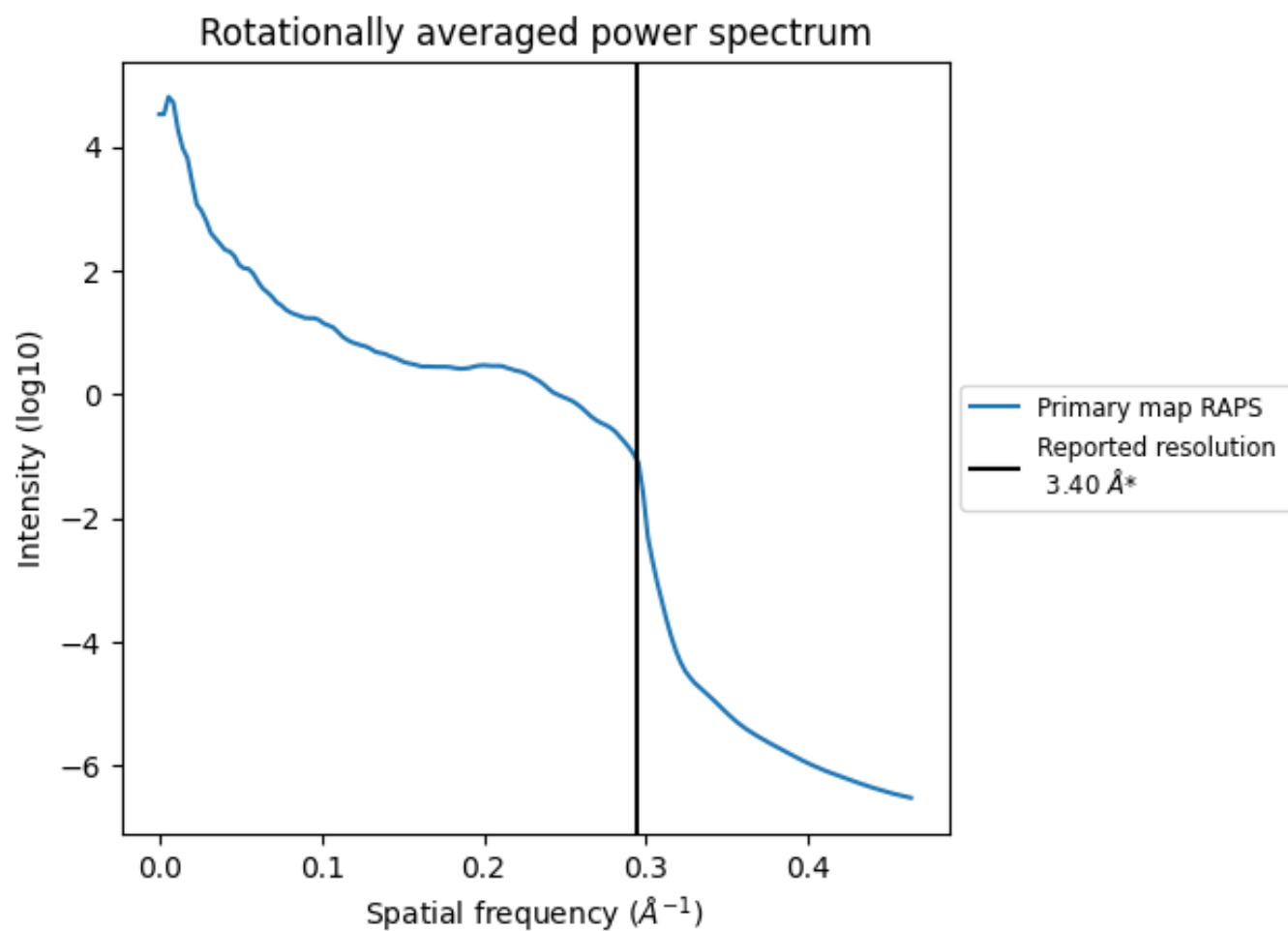
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 167 nm³; this corresponds to an approximate mass of 150 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 0.294 Å⁻¹

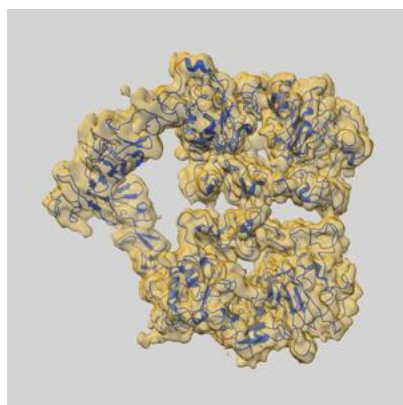
8 Fourier-Shell correlation

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

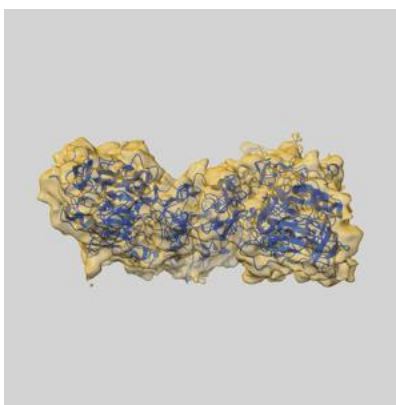
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25559 and PDB model 7SZ1. Per-residue inclusion information can be found in [section 3](#) on [page 4](#).

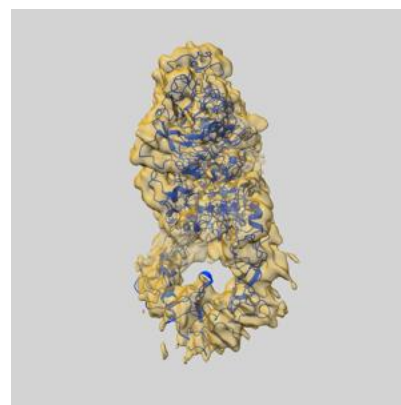
9.1 Map-model overlay [i](#)



X



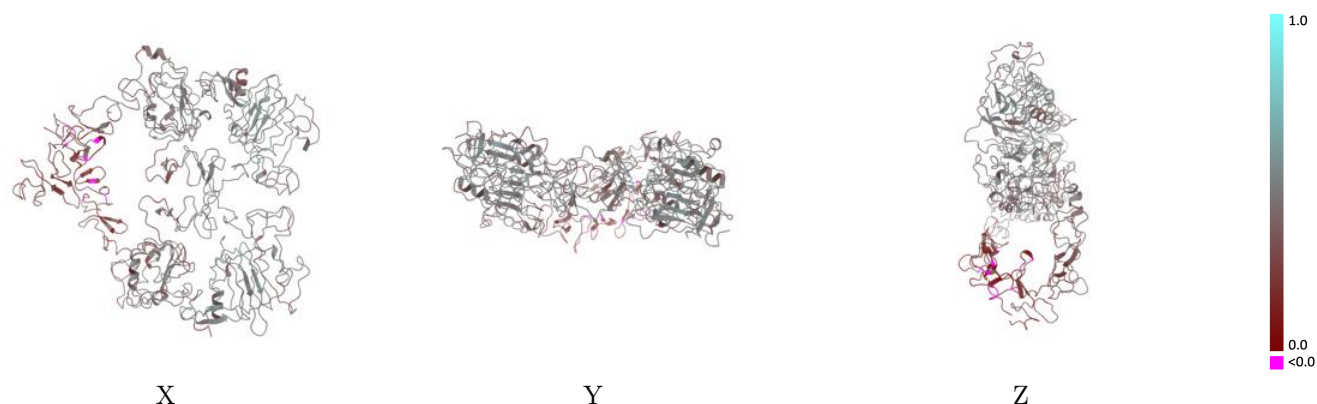
Y



Z

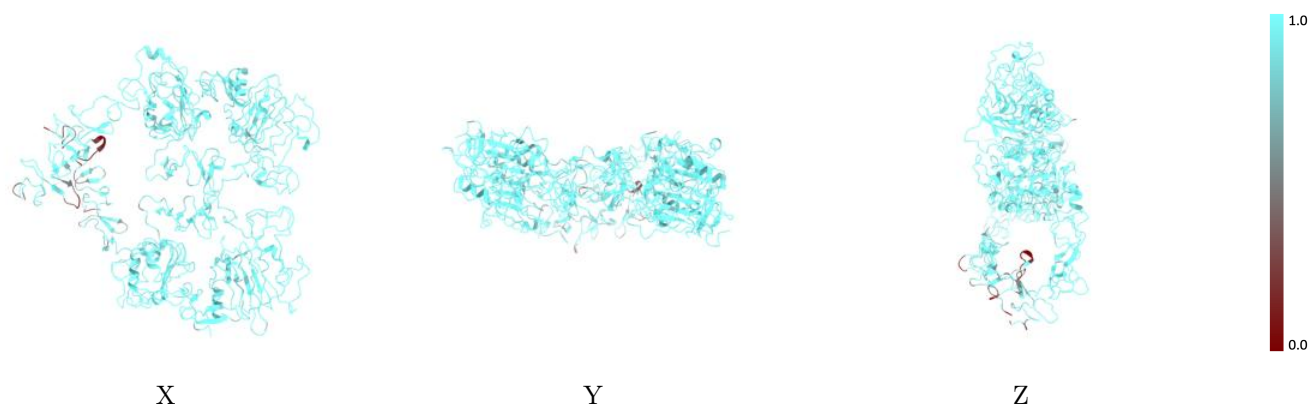
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



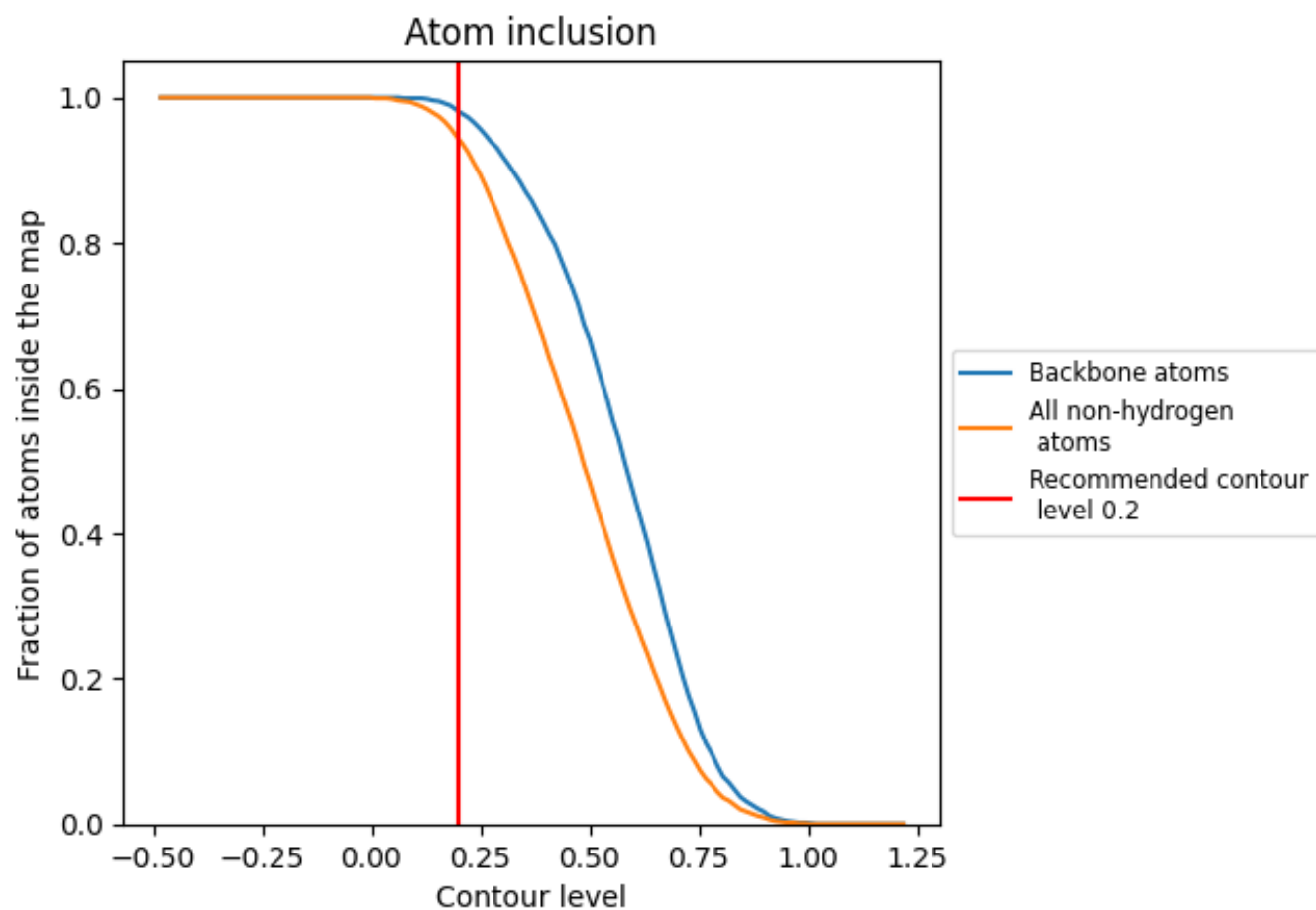
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% 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 (0.2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9430	0.4130
A	0.9550	0.4290
B	0.9270	0.3910
C	0.9730	0.4470
D	0.9630	0.4520

