



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 10:04 PM UTC

PDB ID : 7SZ7 / pdb_00007sz7
EMDB ID : EMD-25563
Title : Cryo-EM structure of the extracellular module of the full-length EGFR bound to TGF- α . "tips-juxtaposed" 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:

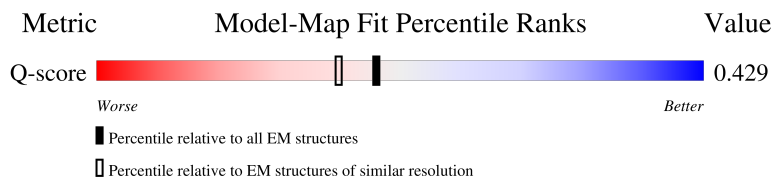
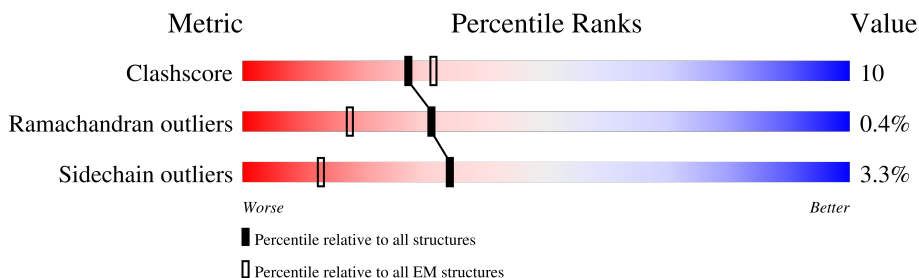
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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	50	
2	D	50	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10218 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 2 discrepancies between the modelled and reference sequences:

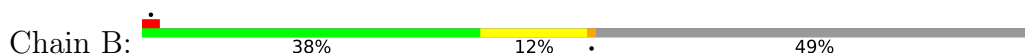
Chain	Residue	Modelled	Actual	Comment	Reference
A	232	ASN	ASP	conflict	UNP P00533
B	232	ASN	ASP	conflict	UNP P00533

- Molecule 2 is a protein called Transforming growth factor alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	50	Total	C	N	O	S	0	0
			386	239	70	71	6		
2	D	50	Total	C	N	O	S	0	0
			386	239	70	71	6		

GLN	ILE	SER	LEU	ASP	ASN	PRO	ASP	TYR	GLN	GLN	ASP	PHE	PHE	PRO	LYS	GLU	ALA	LYS	PRO	ASN	GLY	ILE	PHE	LYS	GLY	THR	ALA	GLU	ASN	ALA	GLU	TYR	LEU	ARG	VAL	ALA	ALA	PRO	GLN	SER	SER	GLU	PHE	ILE	GLY	ALA
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- Molecule 1: Epidermal growth factor receptor



MET	ARG	PRO	SER	GLY	THR	ALA	GLY	ALA	ALA	LEU	LEU	ALA	LEU	LEU	ALA	ALA	LEU	CYS	PRO	ALA	SER	ARG	ALA	L1	E2	N12	Q16	L17	L41	V46	L52	V65	T71	R74	A96	V97	L98	D102	K105	K109	E110	N128	A131	L132	C132
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M134	D142	I143	V144	S145	F148	M152	M158	H159	L160	G161	S162	G163	Q164	C170	C175	A176	G177	A178	M182	C183	L186	T187	Q194	R198	S203	D206	A213	V226	C227	R231	L243	Y261	V268	Y275	T278	D279	H280	Z281	2992
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R285
R286
E293
M294
R300
K303
G315
I318
S326
F335
C338
G343
D344
L348
D364
P365
G366
E367
K372
F380
P387
E388
R389
N390
T391
H394
E397
N398
R405
Q408
S413
L419
W420
I421
T422
S423
L424
P427

G435
 S440
 G441
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 K443
 I444
 L445
 T450
 F457
 T464
 R470
 G471
 E472
 I473
 S474
 C475
 T478
 G479
 Q480
 H483
 S487
 P488
 E489
 W492
 P496
 R497
 D498
 C499
 V500
 S501
 C502
 R503
 I504
 V505
 S506
 S507
 V512
 D513
 K514
 C515
 N516
 L517
 E521
 P522
 R523
 E524
 F525
 F526

Category	Item	Value
C500	C501	10
	C502	10
	C503	10
	C504	10
	C505	10
	C506	10
	C507	10
	C508	10
	C509	10
	C510	10
C550	C551	10
	C552	10
	C553	10
	C554	10
	C555	10
	C556	10
	C557	10
	C558	10
	C559	10
	C560	10
C600	C601	10
	C602	10
	C603	10
	C604	10
	C605	10
	C606	10
	C607	10
	C608	10
	C609	10
	C610	10

E610	G611	G612	P613	T614	ASN	GLY	GLY	PRO	PRO	LYS	ILE	PRO	SER	ILE	ALA	THR	GLY	MET	VAL	GLY	ALA	LEU	LEU	LEU	LEU	LEU	VAL	VAL	ALA	LEU	GLY	ILE	GLY	LEU	PHE	MET	ARG	ARG	ARG	ARG	HIS	ILE	VAL	ARG	LYS	ARG	THR	LEU	ARG	ARG	LEU	LEU	LEU	GLN	GLU	ARG	PRO	LEU	THR
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PRO	SER	GLY	GLU	ALA	GLU	PRO	ASN	GLN	ALA	ALA	LEU	LEU	LEU	ARG	ILE	LEU	LEU	GLU	GLU	PHE	LYS	ILE	ILE	ILE	LYS	VAL	VAL	LEU	GLY	SER	GLY	GLY	ALA	ALA	PHE	GLY	THR	VAL	TYR	LYS	GLY	LYS	LEU	THR	THR	ILE	PRO	PRO	GLU	GLY	GLU	VAL	VAL	PRO	VAL	ALA	ALA	ILE	LYS	ILE	LEU	LEU	ARG	GLU	GLU	THR	THR	SER	PRO
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LYS ASN ALA LYS GLU ILE LEU LEU ASP ASP GLU ALA TYR VAL MET ALA SER VAL ASP ASN PRO HIS VAL VAL CYS ARG LEU LEU GLY ILE LEU LEU THR SER THR VAL GLN VAL LEU ILE THR GLN LEU LEU MET PHE GLY CYS LEU LEU LEU ASP TYR VAL ARG GLU HIS LYS ASP ASN ILE GLY SER GLN TYR

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

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

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

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

- Molecule 2: Transforming growth factor alpha

Chain C:  70% 28% .



- Molecule 2: Transforming growth factor alpha

Chain D:  80% 18% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	126471	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	1.395	Depositor
Minimum map value	-0.513	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.027	Depositor
Recommended contour level	0.2	Depositor
Map size (Å)	431.75998, 431.75998, 431.75998	wwPDB
Map dimensions	400, 400, 400	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	0.24	0/4815	0.44	1/6514 (0.0%)
1	B	0.34	0/4815	0.57	2/6514 (0.0%)
2	C	0.39	0/397	0.64	1/538 (0.2%)
2	D	0.44	0/397	0.61	1/538 (0.2%)
All	All	0.31	0/10424	0.52	5/14104 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	169	SER	N-CA-C	-6.19	105.00	113.30
2	C	3	SER	CA-C-O	-6.04	114.15	120.55
2	D	4	HIS	N-CA-C	-5.67	105.11	113.61
1	B	128	ASN	CA-C-O	-5.48	115.48	121.84
1	B	450	THR	N-CA-C	-5.01	108.20	114.56

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	87	0
1	B	4723	0	4556	101	0
2	C	386	0	345	11	0
2	D	386	0	345	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	10218	0	9802	196	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 10.

The worst 5 of 196 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:A:602:TYR:HE1	1:A:612:CYS:SG	1.36	1.45
1:B:505:VAL:O	1:B:512:VAL:CG2	1.71	1.36
1:A:602:TYR:CE1	1:A:612:CYS:SG	2.24	1.30
1:B:505:VAL:O	1:B:512:VAL:HG23	1.22	1.16
1:B:505:VAL:HG11	1:B:531:CYS:SG	1.97	1.04

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%)	553 (90%)	58 (10%)	1 (0%)	43	71
1	B	612/1210 (51%)	535 (87%)	73 (12%)	4 (1%)	18	47
2	C	48/50 (96%)	41 (85%)	7 (15%)	0	100	100
2	D	48/50 (96%)	41 (85%)	7 (15%)	0	100	100
All	All	1320/2520 (52%)	1170 (89%)	145 (11%)	5 (0%)	31	59

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	504	ASN

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Mol	Chain	Res	Type
1	B	600	CYS
1	B	488	PRO
1	B	489	GLU
1	A	604	CYS

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	B	438/1053 (42%)	426 (97%)	12 (3%)	39	60
2	C	2/43 (5%)	1 (50%)	1 (50%)	0	0
2	D	43/43 (100%)	40 (93%)	3 (7%)	14	40
All	All	483/1139 (42%)	467 (97%)	16 (3%)	34	57

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	26	GLN
2	D	2	VAL
1	B	539	LEU
1	B	602	TYR
1	B	514	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	473	ASN
1	B	535	HIS
2	D	26	GLN
1	B	594	HIS
2	D	18	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

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.

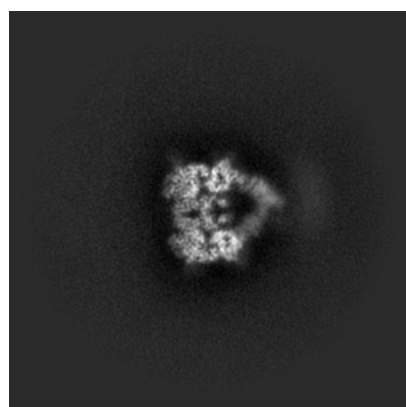
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25563. These allow visual inspection of the internal detail of the map and identification of artifacts.

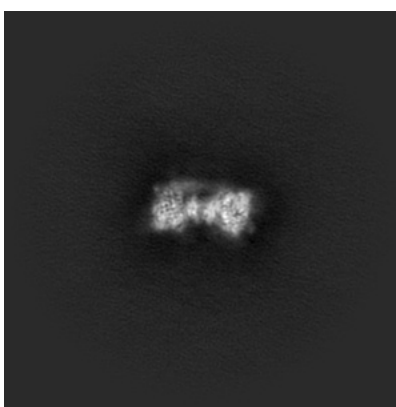
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

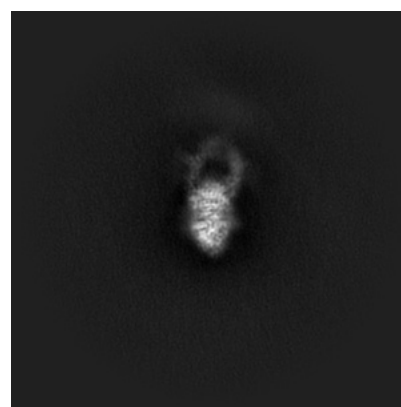
6.1.1 Primary map



X



Y

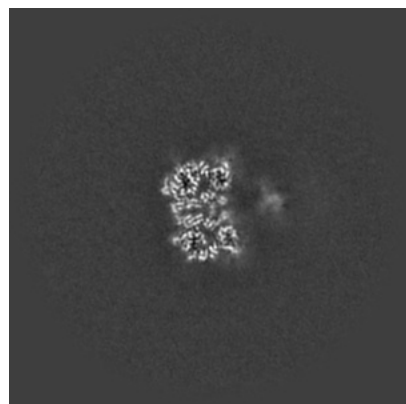


Z

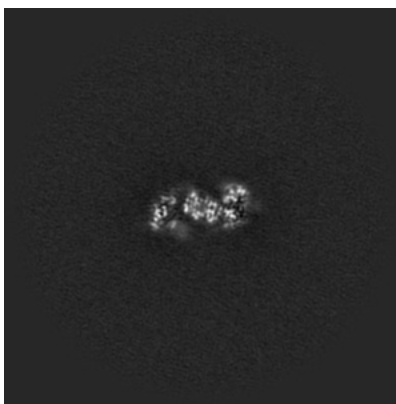
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

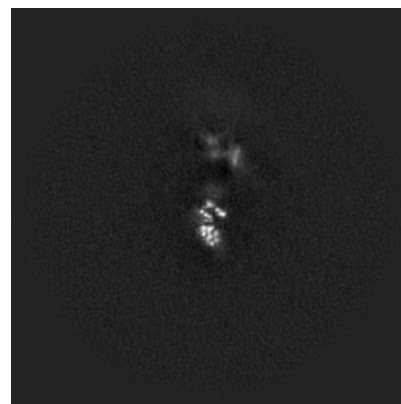
6.2.1 Primary map



X Index: 200



Y Index: 200

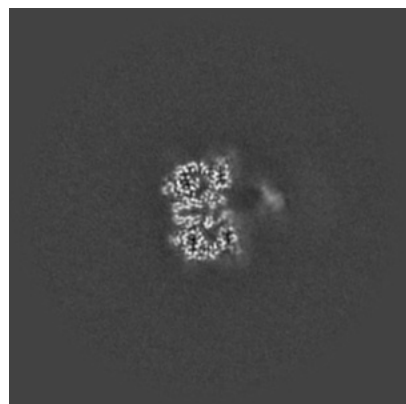


Z Index: 200

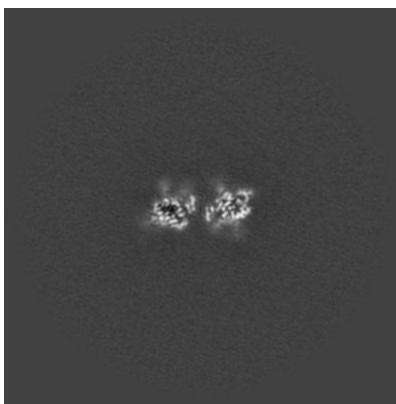
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 198



Y Index: 184

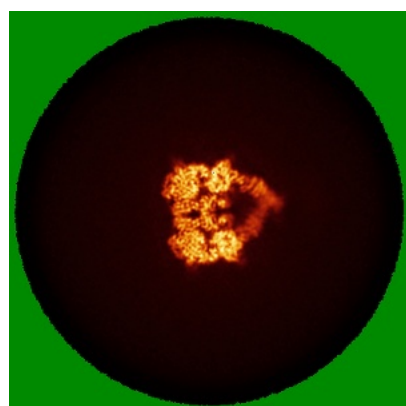


Z Index: 169

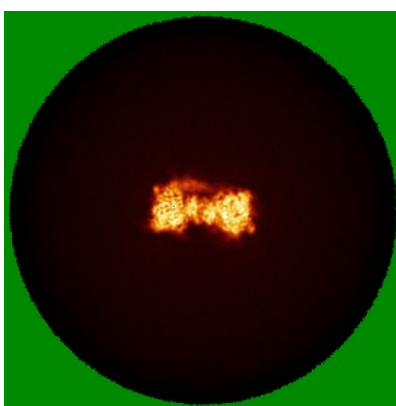
The images above show the largest variance slices of the map in three orthogonal directions.

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

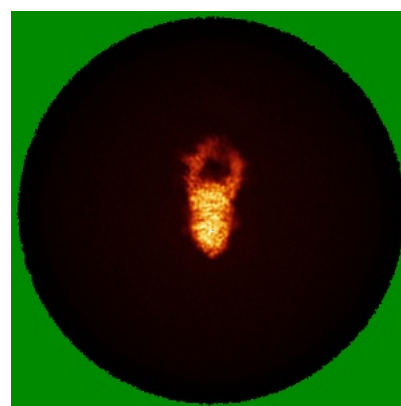
6.4.1 Primary map



X



Y

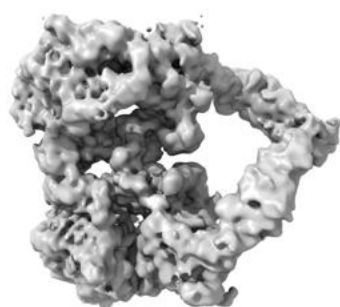


Z

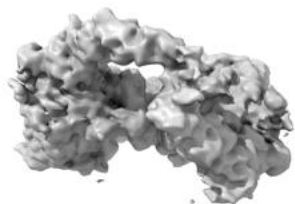
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

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.

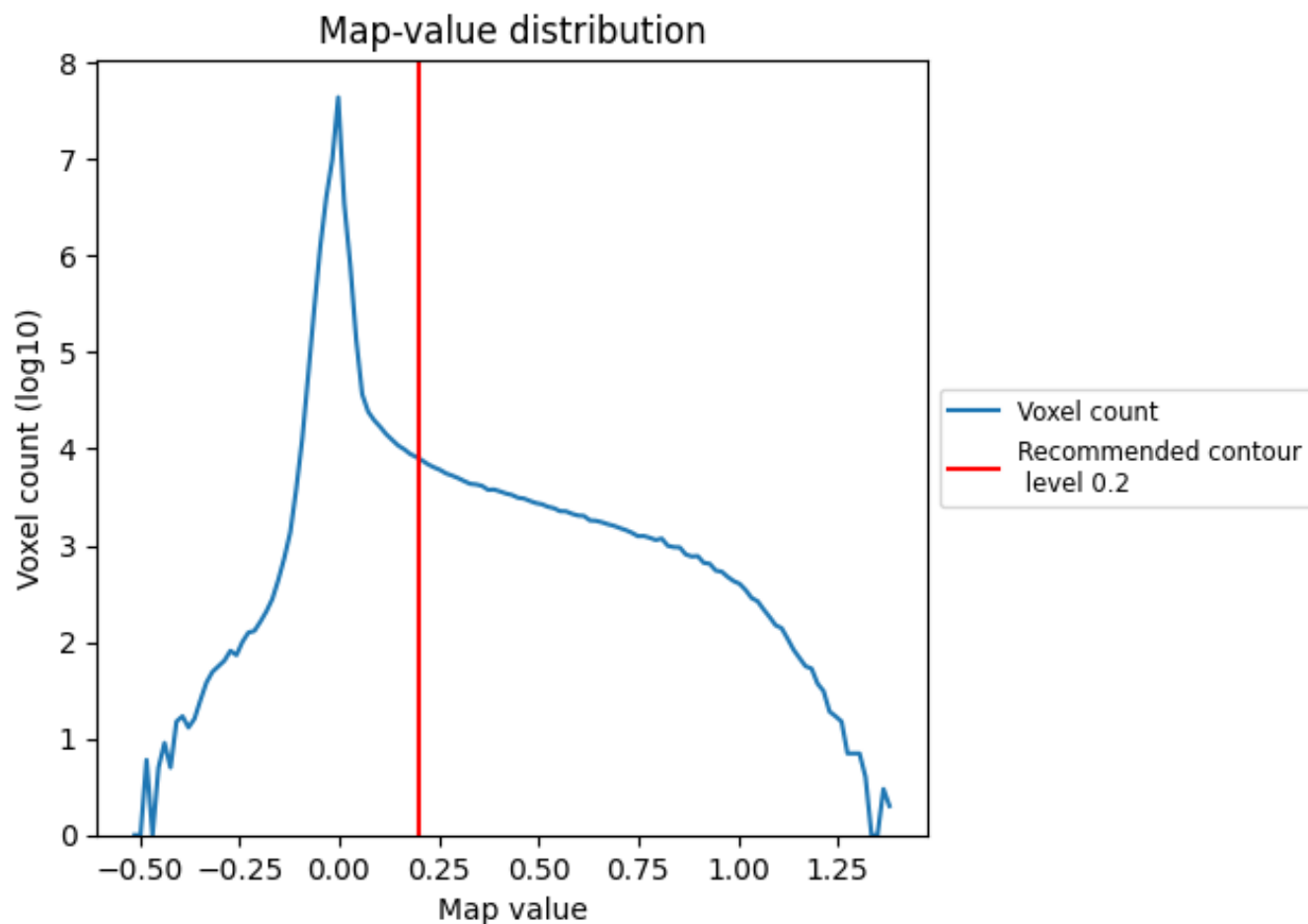
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

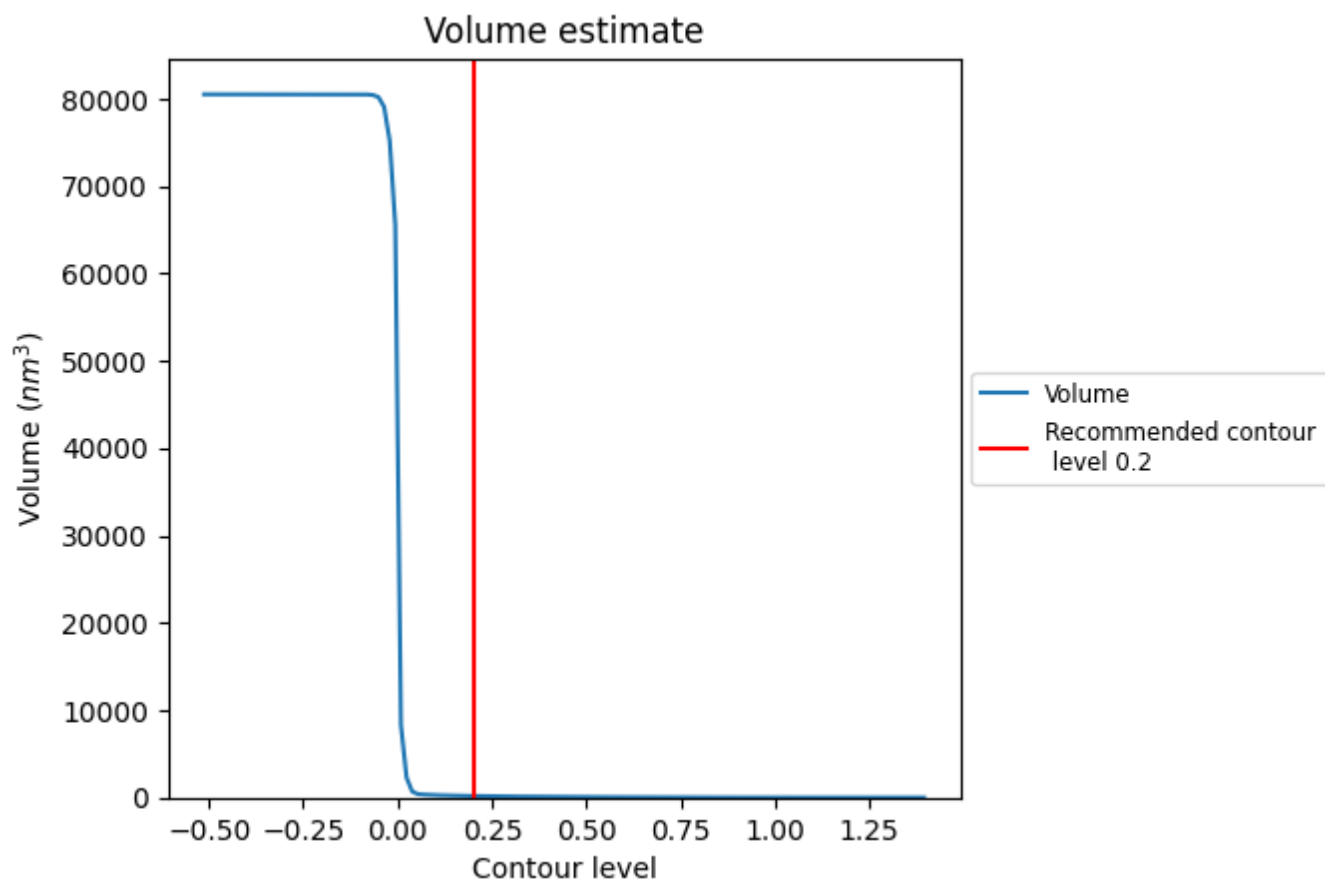
This section contains the results of statistical analysis of the map.

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.

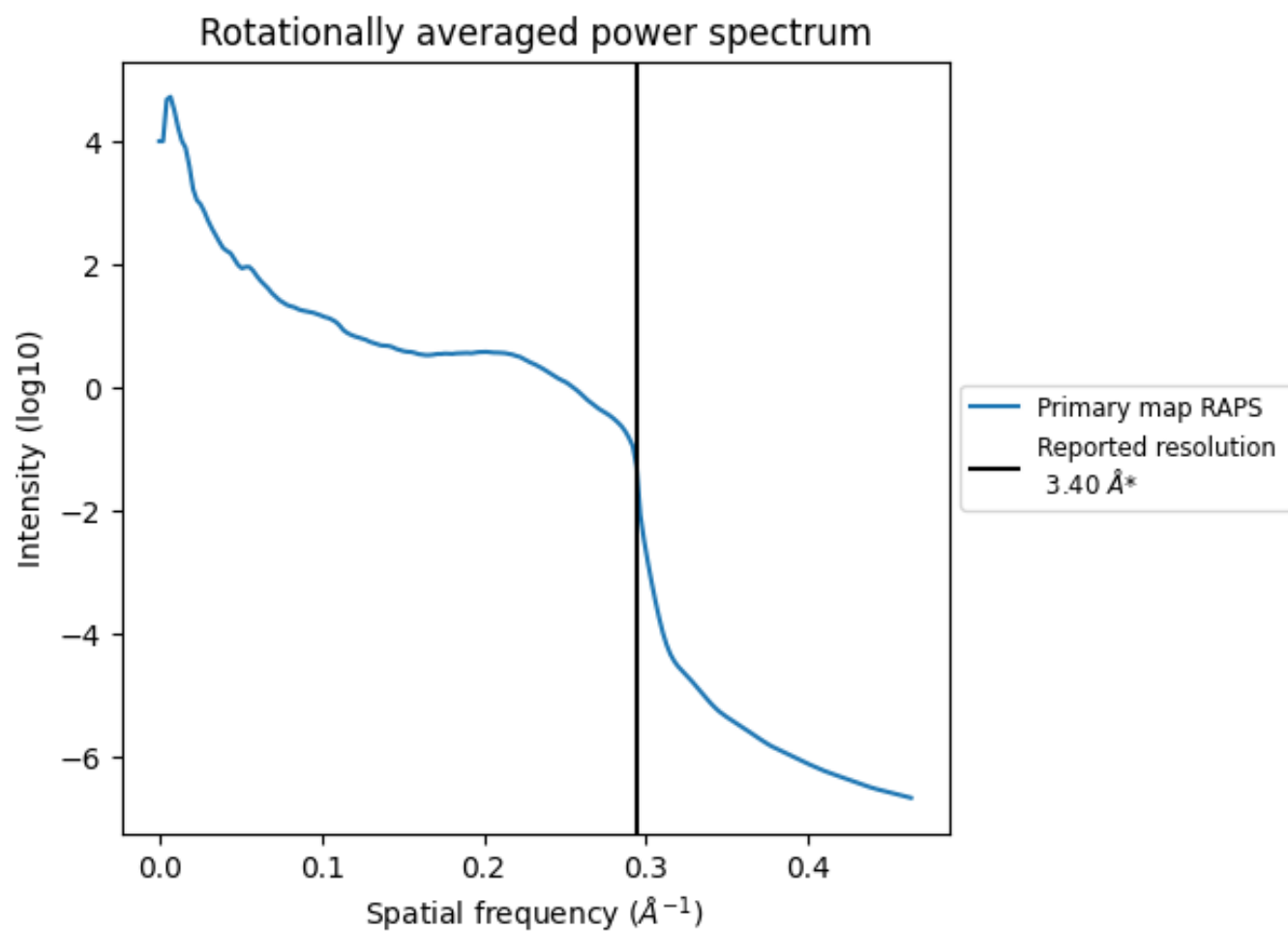
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 180 nm³; this corresponds to an approximate mass of 162 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

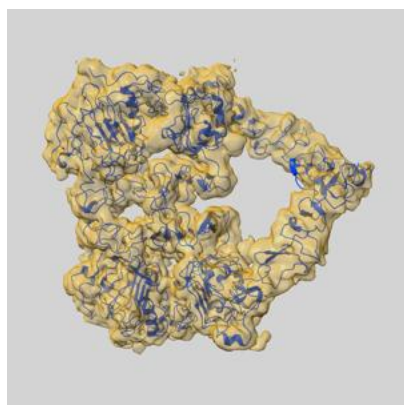
8 Fourier-Shell correlation

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

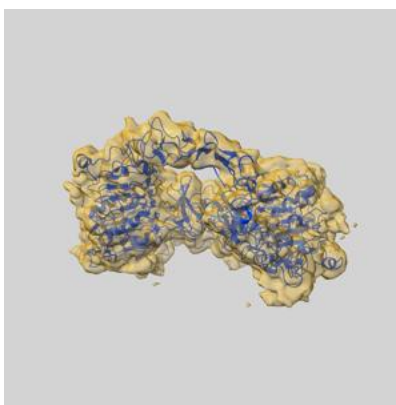
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25563 and PDB model 7SZ7. Per-residue inclusion information can be found in section [3](#) on page [4](#).

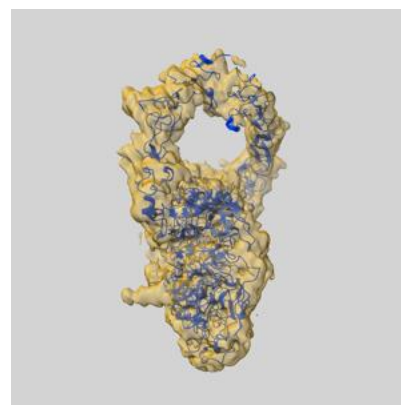
9.1 Map-model overlay [i](#)



X



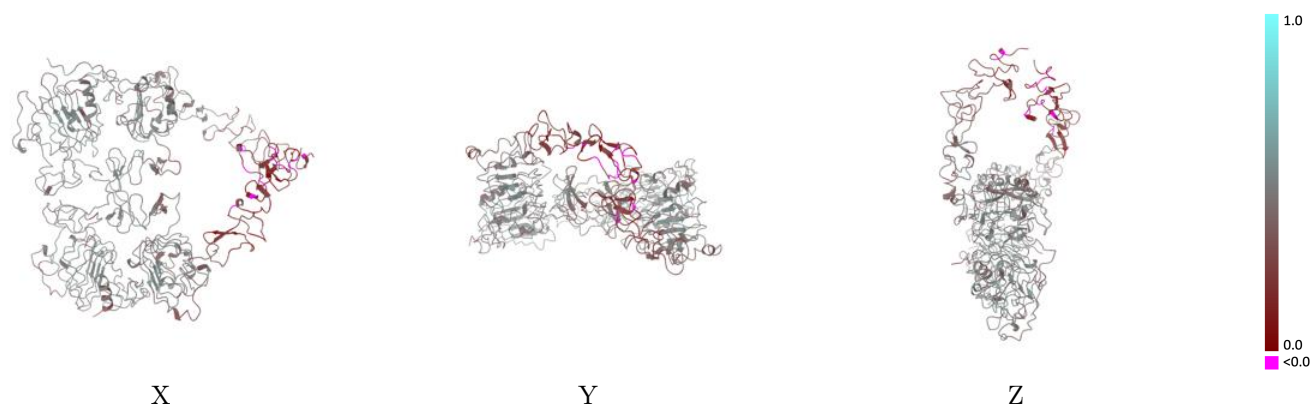
Y



Z

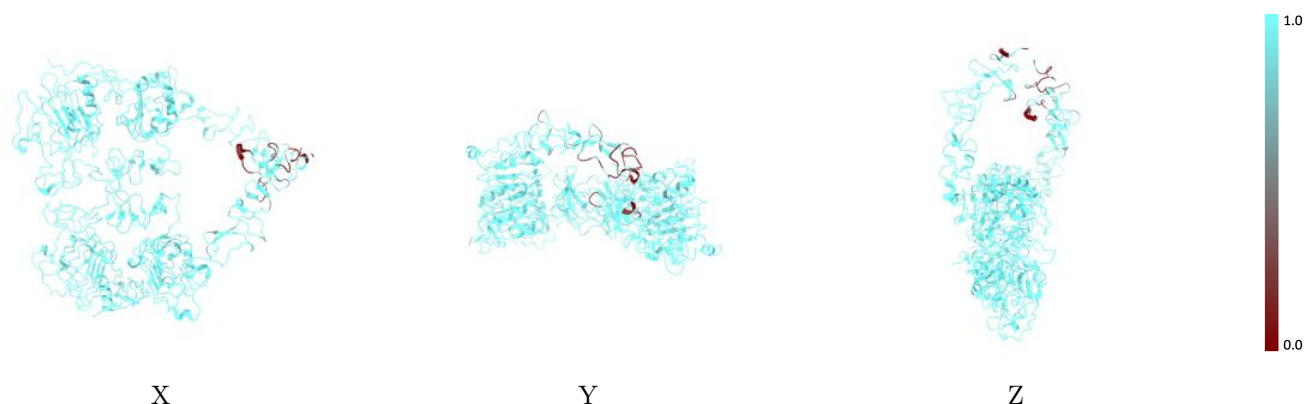
The images above show the 3D surface view of the map at the recommended contour level 0.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



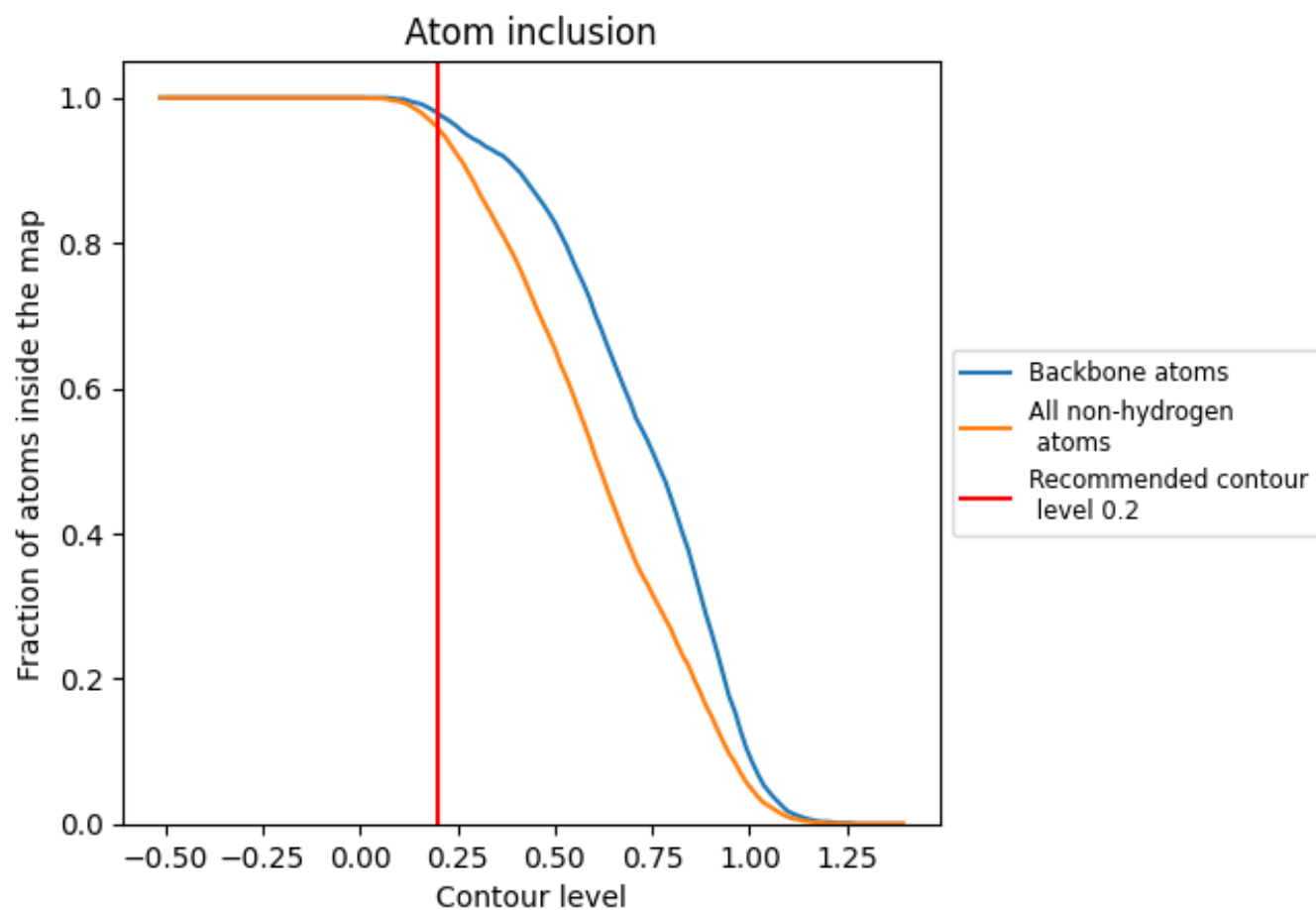
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 96% 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	0.9590	0.4290
A	0.9740	0.4410
B	0.9410	0.4140
C	0.9790	0.4620
D	0.9710	0.4400

