



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 05:50 PM UTC

PDB ID : 7SZ0 / pdb_00007sz0
EMDB ID : EMD-25558
Title : Cryo-EM structure of the extracellular module of the full-length EGFR L834R bound to EGF. "tips-juxtaposed" conformation
Authors : Huang, Y.; Ognjenovic, J.; Karandur, D.; Miller, K.; Merk, A.; Subramaniam, S.; Kuriyan, J.
Deposited on : 2021-11-25
Resolution : 3.30 Å(reported)

This is a Full wwPDB EM Validation 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

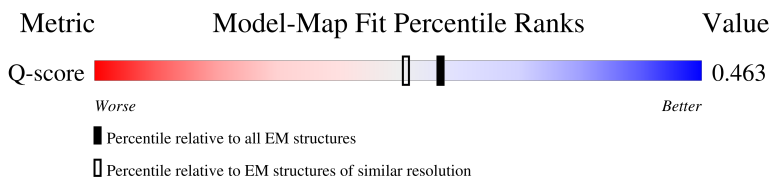
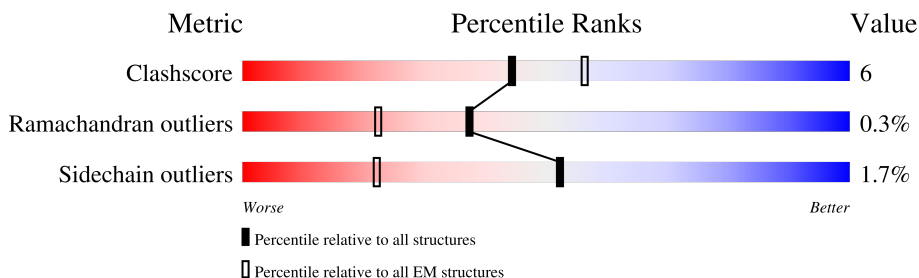
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	1	0
			4723	2914	842	907	60		
1	B	614	Total	C	N	O	S	1	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

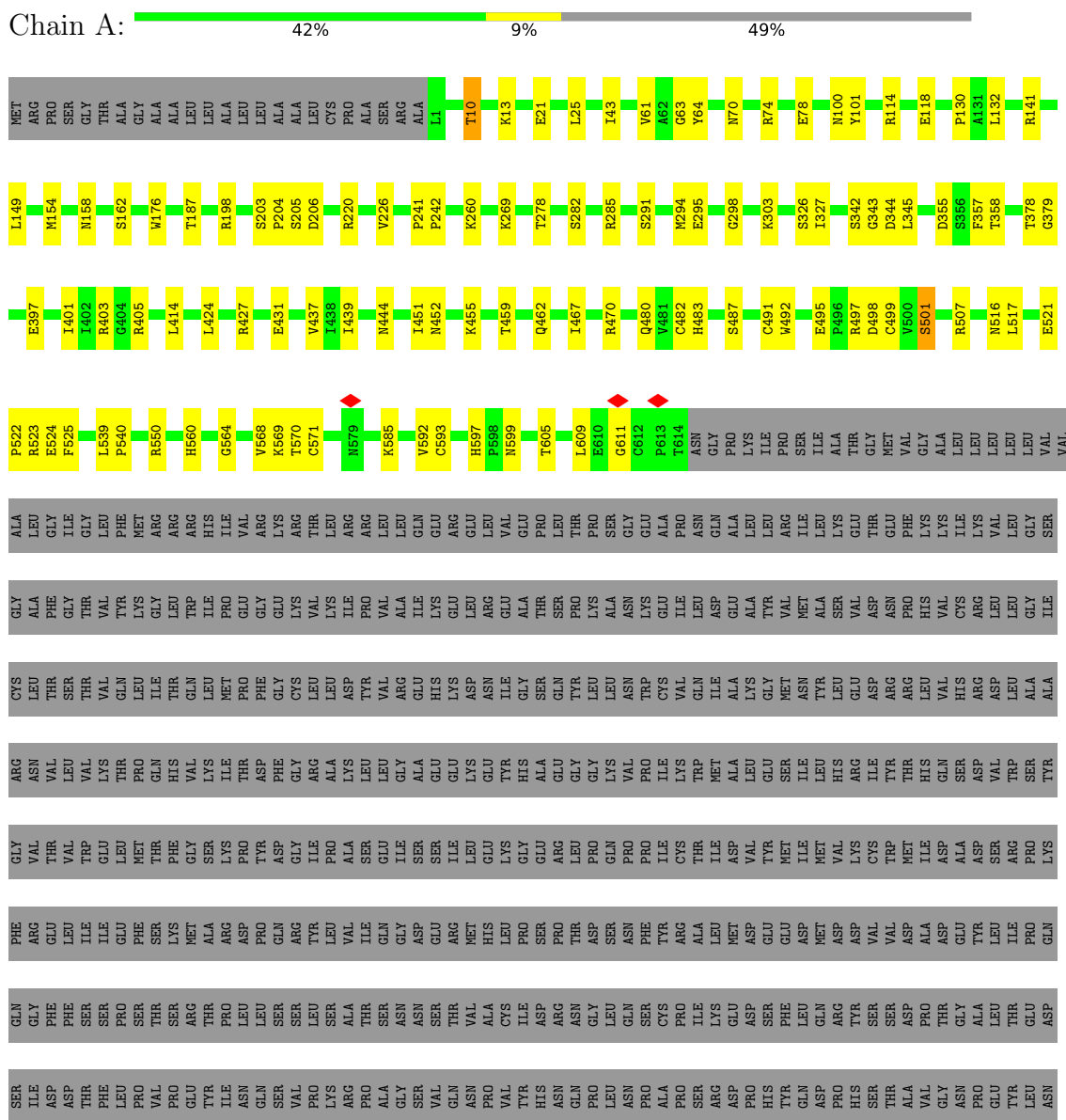
- Molecule 2 is a protein called Epidermal growth factor.

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		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Epidermal growth factor receptor



[illegible]

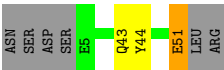
- Molecule 1: Epidermal growth factor receptor

Chain B: 41% 10% 49%

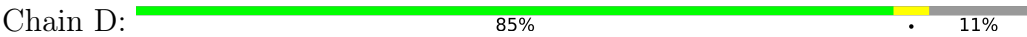
GLY	ILE	GLN	TYR	PHE	GLU	MET	SER	MET	VAL	ARG	SER	R507	K333	D102	MET
ILE	PHE	GLN	ASP	GLN	ASP	ILE	ILE	ASN	MET	ILE	ILE	V512	L345	A103	ARG
LYS	GLY	PRO	HIS	TYR	ASP	VAL	HIS	GLU	SER	LYS	GLY	C515	D364	K105	SER
SER	SER	SER	ILE	SER	VAL	CYS	ILE	ASP	VAL	THR	MET			R114	GLY
THR	THR	THR	TYR	SER	VAL	ASP	TYR	ARG	ASN	GLU	VAL	E521	E367		THR
ALA	ALA	ALA	ALA	ASP	MET	ASP	HIS	ARG	PRO	PHE	GLY	P522		L120	GLY
GLU	GLU	VAL	ILE	ILE	ILE	ALA	ILE	LEU	HIS	LYS	ALA	R523	K372		ALA
ASN	ASN	GLY	GLY	THR	ASP	VAL	GLN	VAL	VAL	LYS	LEU	E524		Q164	ALA
ALA	ALA	GLY	ASN	GLY	GLU	HIS	SER	HIS	CYS	ILE	LEU	F525	E376		LEU
GLU	GLU	PRO	GLU	ALA	TYR	ASP	ASP	ARG	ARG	VAL	LEU	V526	I377	S169	LEU
TYR	TYR	THR	THR	LEU	LEU	ASP	VAL	ASP	SER	LYS	LEU		T378	C170	LEU
LEU	LEU	THR	LEU	THR	ILE	PRO	TRP	LEU	GLY	GLY	VAL	C531	E388	N172	LEU
VAL	VAL	ASN	ASN	ASP	GLN	ALA	TYR	ALA	ILE	SER	VAL	I532		G173	ALA
ALA	ALA	THR	THR	SER	GLN	PHE	GLY	ARG	CYS	GLY	ALA	P540	D382	S174	ALA
PRO	PRO	VAL	VAL	VAL	GLY	ARG	VAL	ASN	LEU	ALA	LEU			C175	LEU
GLN	GLN	GLN	GLN	ASP	PHE	VAL	THR	VAL	THR	PHE	GLY	M543	N388	W176	CYS
SER	SER	PHE	ILE	LEU	GLY	VAL	TRP	LEU	SER	GLY	ILE	R550	R403	C183	ALA
SER	SER	ILE	ILE	THR	SER	VAL	GLU	VAL	VAL	VAL	LEU	G551	G404	Q184	SER
GLU	GLU	PHE	GLY	LEU	LYS	LYS	LEU	LYS	GLN	TYR	PHE	P552	R405		ARG
PHE	PHE	LEU	LEU	LEU	THR	THR	MET	PRO	LEU	LYS	MET			Q193	ALA
ILE	ILE	ASN	ASN	PRO	PRO	PRO	THR	ASN	LEU	GLY	ARG	I562	H409		ALA
GLY	GLY	SER	THR	GLN	GLN	GLN	THR	GLN	ILE	GLY	ARG	D563		P204	LI
ALA	ALA	THR	THR	LYS	HIS	HIS	PHE	LYS	THR	LEU	ARG	G564	L414	S205	N12
		ASP	GLY	VAL	VAL	VAL	GLY	VAL	GLN	TRP	ARG				K13
		ALA	SER	ALA	LYS	LEU	SER	LEU	LEU	ILE	HIS	P565		C212	L14
		ARG	LYS	ILE	ILE	ILE	LYS	ILE	MET	PRO	ILE	H566	N420		T15
		PRO	PRO	THR	THR	THR	PRO	THR	PRO	GLU	VAL	C567	I421		
		ASP	ASP	ASP	ASP	ASP	ASP	ASP	PHE	GLY	ARG		L424	V226	
		PRO	TYR	GLY	GLY	PHE	GLY	GLN	GLY	GLY	LYS	N579		C227	
		LEU	ILE	GLY	GLY	GLY	GLY	GLY	CYS	LYS	THR	N580	V437	R228	
		LEU	ILE	ILE	ILE	ILE	ILE	ALA	LEU	VAL	THR		I438		
		VAL	ALA	ALA	ALA	ALA	ALA	LYS	ASP	LYS	LEU	K585	I439	R231	
		ARG	ALA	LYS	TYR	TYR	ALA	LYS	TYR	ILE	ARG			F263	
		SER	SER	SER	SER	SER	GLY	GLY	GLY	PRO	ARG	A589	N444		
		SER	SER	SER	SER	GLY	ILE	GLY	VAL	VAL	LEU		L445	R273	V61
		ASN	ASN	ASN	ASN	GLY	ILE	GLY	ARG	ALA	LEU	C593	C446		A62
		SER	SER	SER	SER	GLU	GLY	GLU	HIS	ILE	GLN	H594	Y447	T278	G63
		THR	THR	THR	THR	GLY	ARG	GLY	LYS	LYS	GLU	L595			I67
		VAL	VAL	VAL	VAL	LYS	LEU	LYS	ASP	GLU	ARG	C596	G458	S282	N70

- Molecule 2: Epidermal growth factor

Chain C: 83% . . 11%



- Molecule 2: Epidermal growth factor



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	123670	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	1.305	Depositor
Minimum map value	-0.454	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.035	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	0.26	0/4806	0.45	0/6501
1	B	0.33	0/4806	0.56	0/6501
2	C	0.33	0/396	0.51	0/536
2	D	0.35	0/396	0.55	0/536
All	All	0.30	0/10404	0.51	0/14074

There are no bond length outliers.

There are no bond angle outliers.

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	60	0
1	B	4723	0	4556	71	0
2	C	385	0	344	2	0
2	D	385	0	344	1	0
All	All	10216	0	9800	129	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 6.

All (129) 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	0.85
1:B:505:VAL:HG23	1:B:512:VAL:HG23	1.62	0.81
1:A:585:LYS:HB3	1:A:593:CYS:HB3	1.63	0.79
1:B:175:CYS:HA	1:B:183:CYS:HA	1.70	0.72
1:A:118:GLU:OE1	1:A:198:ARG:NH2	2.24	0.71
1:B:523:ARG:NH1	1:B:540:PRO:HB3	2.05	0.70
1:A:74[B]:ARG:NH2	1:A:78:GLU:OE2	2.25	0.69
1:A:327:ILE:HD11	1:A:345:LEU:HD22	1.74	0.67
1:A:132:LEU:O	1:A:158:ASN:ND2	2.27	0.67
1:B:102:ASP:OD1	1:B:103:ALA:N	2.28	0.66
1:A:571:CYS:HB3	1:A:585:LYS:HD2	1.78	0.65
1:B:227:CYS:SG	1:B:231:ARG:NH1	2.69	0.65
1:B:364:ASP:HB3	1:B:367:GLU:HG3	1.80	0.64
1:A:452:ASN:O	1:A:455:LYS:NZ	2.31	0.64
1:B:378:THR:HA	1:B:403:ARG:HB2	1.81	0.62
1:B:523:ARG:HD2	1:B:540:PRO:HA	1.79	0.62
1:A:285:ARG:O	1:A:405:ARG:NH1	2.32	0.62
1:A:43:ILE:O	1:A:70:ASN:ND2	2.26	0.61
1:A:397:GLU:OE2	1:A:427:ARG:NH1	2.33	0.61
1:B:273:ARG:NH1	1:B:458:GLY:O	2.33	0.61
1:B:285:ARG:O	1:B:405:ARG:NH1	2.33	0.60
1:A:203:SER:OG	1:A:206:ASP:OD2	2.18	0.60
1:B:376:GLU:OE1	1:B:403:ARG:NH1	2.35	0.60
1:B:74[B]:ARG:NH2	1:B:78:GLU:OE2	2.36	0.59
1:A:444:ASN:HA	1:A:470:ARG:HB2	1.83	0.59
1:B:604:CYS:CB	1:B:612:CYS:HB3	2.32	0.59
1:A:459:THR:HB	1:A:462:GLN:HE21	1.66	0.58
1:A:220:ARG:NH1	1:B:193:GLN:O	2.37	0.58
1:B:552:PRO:HB2	1:B:567:CYS:H	1.69	0.58
1:B:532:ILE:HG21	1:B:550:ARG:HG2	1.86	0.57
1:B:597:HIS:HB2	1:B:608:GLY:HA2	1.85	0.57
1:B:330:THR:O	1:B:333:LYS:NZ	2.38	0.57
1:B:12:ASN:HB3	1:B:15:THR:HB	1.86	0.57
1:A:101:TYR:HB3	1:A:130:PRO:HD2	1.87	0.56
1:B:114:ARG:HA	1:B:176:TRP:CD1	2.42	0.55
1:B:515:CYS:SG	1:B:526:VAL:HG22	2.47	0.55
1:A:424:LEU:HD11	1:A:439:ILE:HD13	1.88	0.55
1:A:605:THR:OG1	1:A:611:GLY:O	2.25	0.54
1:B:212:CYS:O	1:B:228:ARG:NH1	2.38	0.54
1:B:372:LYS:O	1:B:398:ASN:ND2	2.34	0.54
1:A:294:MET:HE3	1:A:303:LYS:HD3	1.90	0.53
1:B:563:ASP:HA	1:B:593:CYS:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:ASN:HD22	1:B:75:ILE:HD11	1.74	0.53
1:B:543:MET:HA	1:B:543:MET:HE2	1.90	0.52
1:B:326:SER:OG	1:B:327:ILE:N	2.41	0.51
1:B:604:CYS:HB3	1:B:612:CYS:HB3	1.93	0.50
1:B:278:THR:OG1	1:B:282:SER:OG	2.23	0.50
1:A:560:HIS:ND1	1:A:569:LYS:HG2	2.27	0.50
1:A:507:ARG:NH1	1:A:524:GLU:OE2	2.45	0.50
1:A:539:LEU:HD12	1:A:540:PRO:HD2	1.93	0.50
1:B:447:TYR:OH	1:B:480:GLN:NE2	2.45	0.49
1:B:475:CYS:HB2	1:B:480:GLN:HB2	1.94	0.49
1:A:495:GLU:OE1	1:A:497:ARG:NE	2.45	0.49
1:A:487:SER:OG	1:A:501:SER:HB3	2.13	0.49
1:A:521:GLU:HG2	1:A:522:PRO:HD2	1.94	0.49
1:B:444:ASN:HA	1:B:470:ARG:HB2	1.95	0.49
1:B:82:ILE:HD11	1:B:120:LEU:HG	1.95	0.48
1:B:421:ILE:HG13	1:B:445:LEU:HD12	1.95	0.48
1:B:507:ARG:HD3	1:B:531:CYS:HB2	1.95	0.48
1:A:355:ASP:OD2	1:A:358:THR:OG1	2.30	0.48
1:A:61:VAL:HG12	1:A:63:GLY:H	1.78	0.48
1:A:414:LEU:HB3	1:A:437:VAL:HG22	1.96	0.48
1:B:438:ILE:HD12	1:B:465:LYS:HE3	1.95	0.48
1:B:585:LYS:HG2	1:B:595:LEU:HA	1.94	0.48
1:A:525:PHE:HZ	1:A:550:ARG:HD3	1.80	0.47
1:A:378:THR:HA	1:A:403:ARG:HB2	1.96	0.47
1:A:154:MET:HE2	1:A:154:MET:HB3	1.80	0.47
1:B:525:PHE:CE1	1:B:532:ILE:HB	2.49	0.47
1:A:326:SER:OG	1:A:327:ILE:N	2.48	0.47
1:A:205:SER:HB2	1:B:204:PRO:HB2	1.97	0.46
1:A:278:THR:HG1	1:A:282:SER:HG	1.63	0.46
1:A:599:ASN:HB2	1:A:609:LEU:HD21	1.97	0.46
1:B:14:LEU:HD23	1:B:14:LEU:HA	1.81	0.46
1:B:295:GLU:OE1	1:B:296:GLU:N	2.49	0.46
1:B:409:HIS:HB3	2:D:48:LYS:HE3	1.97	0.46
1:A:260:LYS:HE2	1:A:269:LYS:HE3	1.96	0.46
1:B:502:CYS:SG	1:B:506:SER:HB3	2.55	0.46
1:B:67:ILE:HG22	1:B:100:ASN:HD21	1.80	0.46
1:A:162:SER:O	1:A:162:SER:OG	2.30	0.45
1:A:13:LYS:HD3	1:A:64:TYR:OH	2.17	0.45
1:A:467:ILE:HD11	2:C:51:GLU:HB3	1.98	0.45
1:B:43:ILE:HG22	1:B:70:ASN:HD21	1.82	0.45
1:A:427:ARG:NH2	1:A:498:ASP:OD1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:43:GLN:HG2	2:C:44:TYR:N	2.31	0.45
1:B:392:ASP:N	1:B:392:ASP:OD1	2.48	0.45
1:A:427:ARG:HA	1:A:492:TRP:CD1	2.52	0.45
1:A:523:ARG:HG2	1:A:540:PRO:HB3	1.99	0.44
1:B:532:ILE:HD12	1:B:532:ILE:N	2.32	0.44
1:B:609:LEU:C	1:B:611:GLY:H	2.26	0.44
1:B:388:GLU:OE1	1:B:420:ASN:ND2	2.46	0.44
1:A:357:PHE:HD2	1:A:358:THR:HG23	1.82	0.44
1:A:401:ILE:HG12	1:A:431:GLU:HB2	2.00	0.44
1:A:295:GLU:OE2	1:A:298:GLY:N	2.41	0.44
1:B:164:GLN:OE1	1:B:164:GLN:N	2.39	0.44
1:A:204:PRO:HB2	1:B:205:SER:HB2	2.00	0.44
1:B:61:VAL:HG12	1:B:63:GLY:H	1.83	0.44
1:B:174:SER:O	1:B:184:GLN:N	2.51	0.43
1:B:424:LEU:HD11	1:B:439:ILE:HD13	1.99	0.43
1:B:444:ASN:OD1	1:B:444:ASN:N	2.50	0.43
1:A:114:ARG:HA	1:A:176:TRP:CD1	2.53	0.43
1:A:597:HIS:HB3	1:A:599:ASN:HD22	1.83	0.43
1:A:491:CYS:HA	1:A:499:CYS:HA	1.99	0.43
1:B:263:PHE:HD1	1:B:283:CYS:HB2	1.82	0.43
1:B:564:GLY:HA3	1:B:565:PRO:HD2	1.83	0.43
1:B:294:MET:N	1:B:301:LYS:O	2.50	0.43
1:A:344:ASP:N	1:A:344:ASP:OD1	2.52	0.43
1:B:105:LYS:HE2	1:B:105:LYS:HB2	1.84	0.43
1:B:175:CYS:HA	1:B:183:CYS:CA	2.44	0.43
1:B:51:ASP:OD1	1:B:53:SER:OG	2.21	0.42
1:B:293:GLU:OE1	1:B:300:ARG:NH2	2.49	0.42
1:A:564:GLY:H	1:A:592:VAL:HG23	1.84	0.42
1:A:342:SER:O	1:A:342:SER:OG	2.37	0.42
1:A:343:GLY:O	1:A:379:GLY:HA3	2.20	0.42
1:B:521:GLU:CB	1:B:522:PRO:HD3	2.37	0.42
1:A:451:ILE:HD13	1:A:491:CYS:H	1.85	0.42
1:A:187:THR:OG1	1:A:198:ARG:NH1	2.51	0.41
1:B:414:LEU:HB3	1:B:437:VAL:HG23	2.02	0.41
1:B:84:ARG:HA	1:B:120:LEU:HB2	2.01	0.41
1:A:21:GLU:O	1:A:25:LEU:HD23	2.21	0.41
1:B:52:LEU:HD12	1:B:72:VAL:HG11	2.03	0.41
1:B:293:GLU:HB3	1:B:300:ARG:HH21	1.85	0.41
1:A:70:ASN:OD1	1:A:100:ASN:ND2	2.53	0.41
1:A:568:VAL:HG12	1:A:570:THR:H	1.86	0.41
1:A:241:PRO:HA	1:A:242:PRO:HD3	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:SER:OG	1:A:303:LYS:O	2.39	0.41
1:B:82:ILE:HG21	1:B:226:VAL:HG11	2.03	0.41
1:B:171:PRO:O	1:B:172:ASN:C	2.63	0.41
1:B:345:LEU:HD23	1:B:345:LEU:HA	1.93	0.40
1:A:141:ARG:HB3	1:A:149:LEU:HD11	2.03	0.40

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%)	546 (89%)	65 (11%)	1 (0%)	43	71
1	B	612/1210 (51%)	538 (88%)	71 (12%)	3 (0%)	24	55
2	C	45/53 (85%)	40 (89%)	5 (11%)	0	100	100
2	D	45/53 (85%)	40 (89%)	5 (11%)	0	100	100
All	All	1314/2526 (52%)	1164 (89%)	146 (11%)	4 (0%)	37	65

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	92	SER
1	B	613	PRO
1	A	10	THR
1	B	171	PRO

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	535/1053 (51%)	527 (98%)	8 (2%)	57	72
1	B	535/1053 (51%)	525 (98%)	10 (2%)	50	68
2	C	41/47 (87%)	40 (98%)	1 (2%)	43	65
2	D	41/47 (87%)	40 (98%)	1 (2%)	43	65
All	All	1152/2200 (52%)	1132 (98%)	20 (2%)	52	71

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	THR
1	A	226	VAL
1	A	480	GLN
1	A	482	CYS
1	A	483	HIS
1	A	501	SER
1	A	516	ASN
1	A	517	LEU
2	C	51	GLU
1	B	169	SER
1	B	172	ASN
1	B	183	CYS
1	B	485	LEU
1	B	500	VAL
1	B	501	SER
1	B	515	CYS
1	B	562	ILE
1	B	595	LEU
1	B	596	CYS
2	D	14	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	33	ASN
1	A	40	ASN
1	A	70	ASN
1	A	100	ASN

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Mol	Chain	Res	Type
1	A	128	ASN
1	A	134	ASN
1	A	159	HIS
1	A	193	GLN
1	A	209	HIS
1	A	211	GLN
1	A	252	GLN
1	A	334	HIS
1	A	394	HIS
1	A	408	GLN
1	A	462	GLN
1	A	597	HIS
1	A	599	ASN
1	B	23	HIS
1	B	70	ASN
1	B	134	ASN
1	B	139	GLN
1	B	182	ASN
1	B	209	HIS
1	B	210	ASN
1	B	247	ASN
1	B	252	GLN
1	B	409	HIS
1	B	480	GLN
1	B	554	ASN
1	B	594	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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

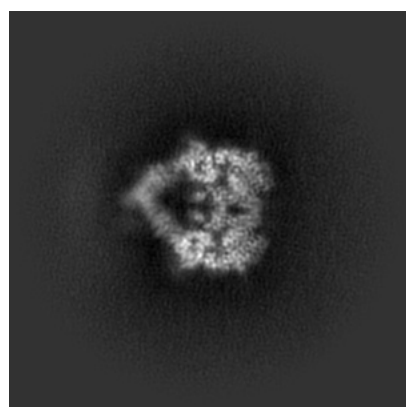
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25558. These allow visual inspection of the internal detail of the map and identification of artifacts.

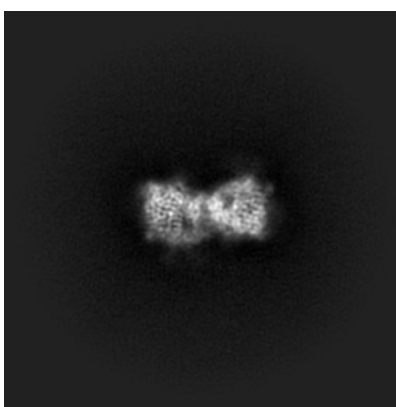
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

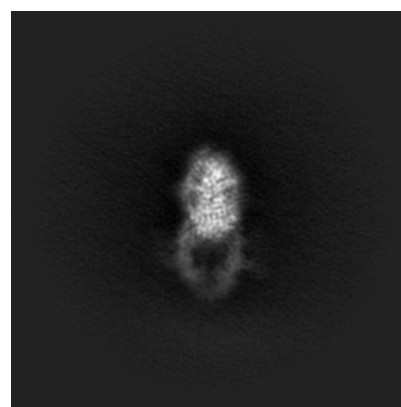
6.1.1 Primary map



X



Y

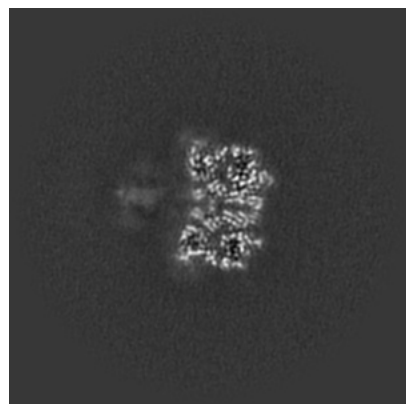


Z

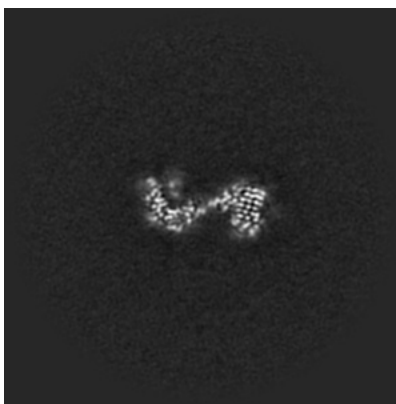
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 160



Y Index: 160

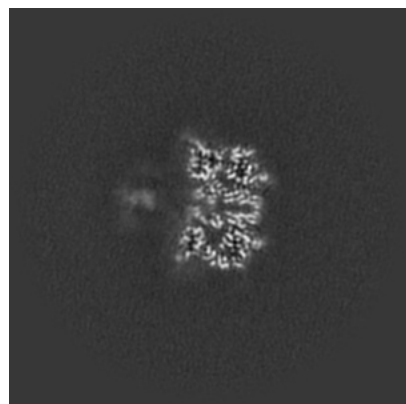


Z Index: 160

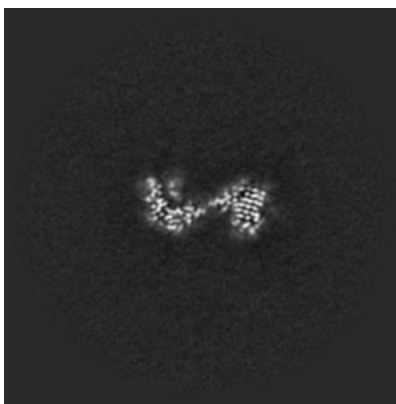
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

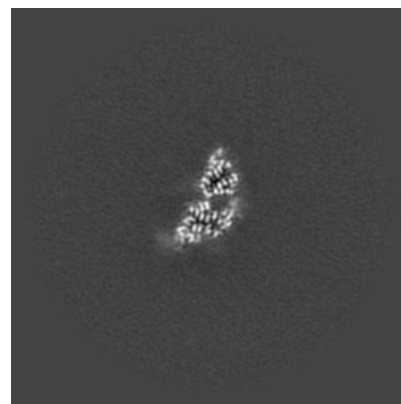
6.3.1 Primary map



X Index: 162



Y Index: 159

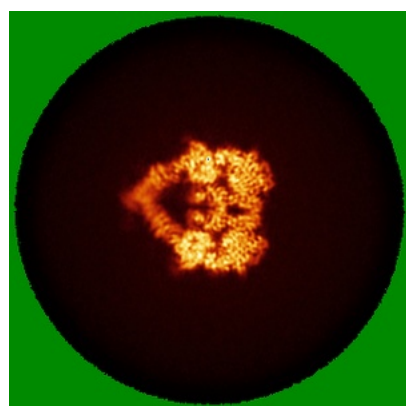


Z Index: 132

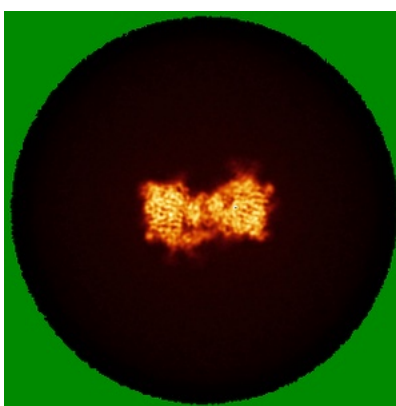
The images above show the largest variance slices of the map in three orthogonal directions.

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

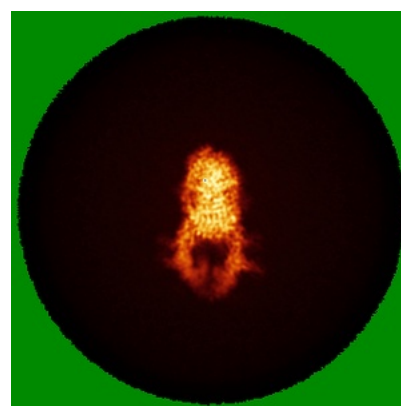
6.4.1 Primary map



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

This section was not generated.

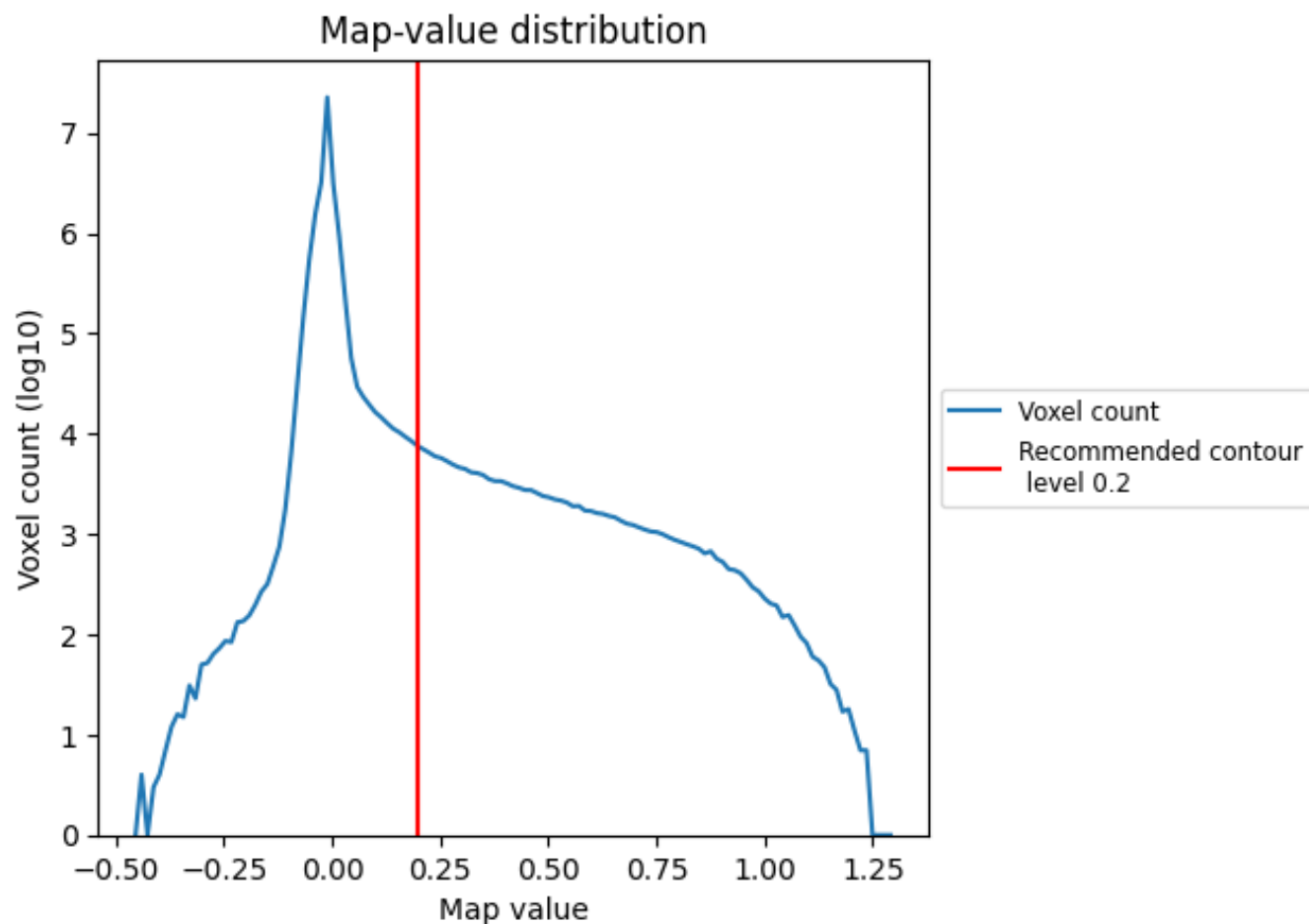
6.6 Mask visualisation

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

7 Map analysis [i](#)

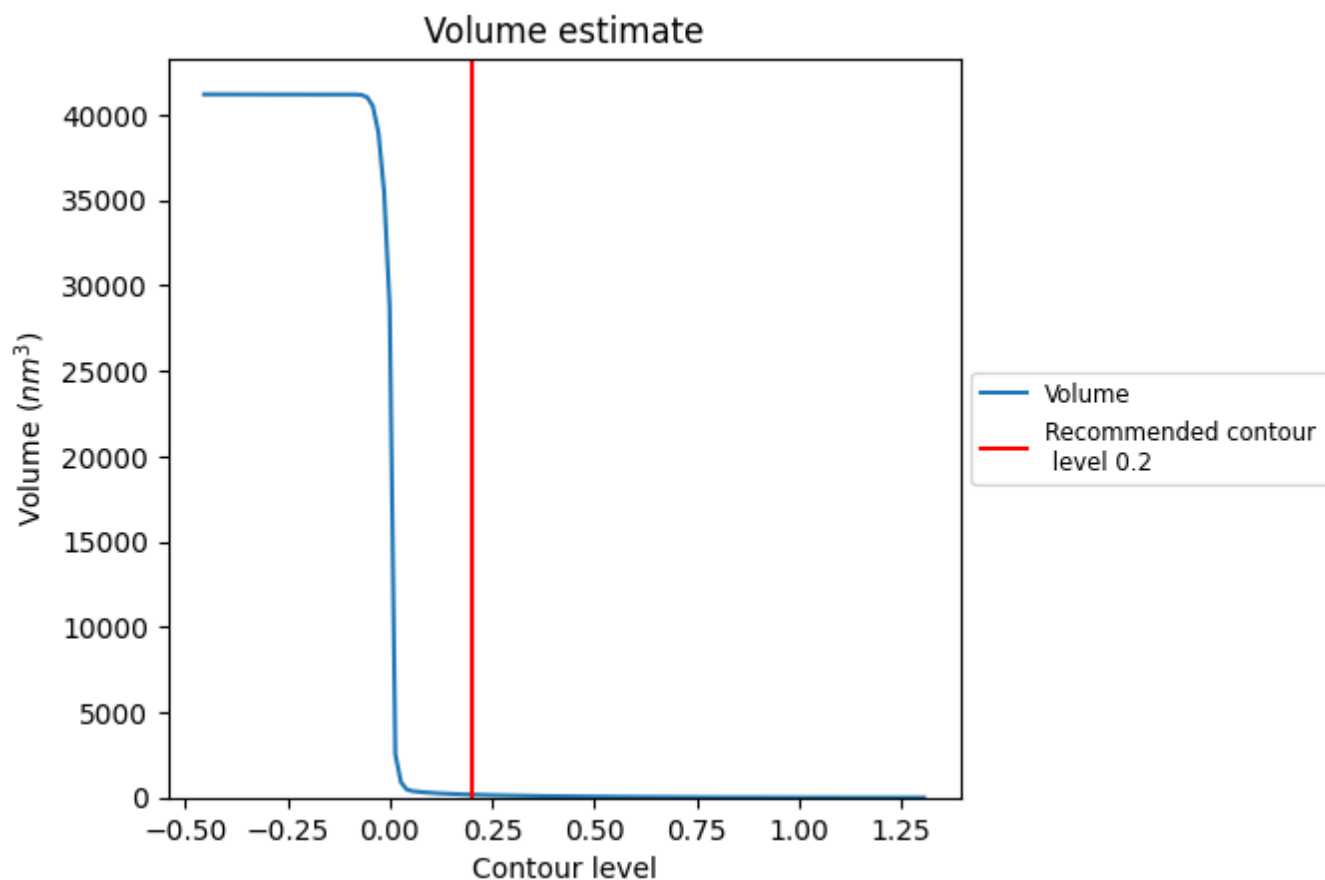
This section contains the results of statistical analysis of the map.

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.

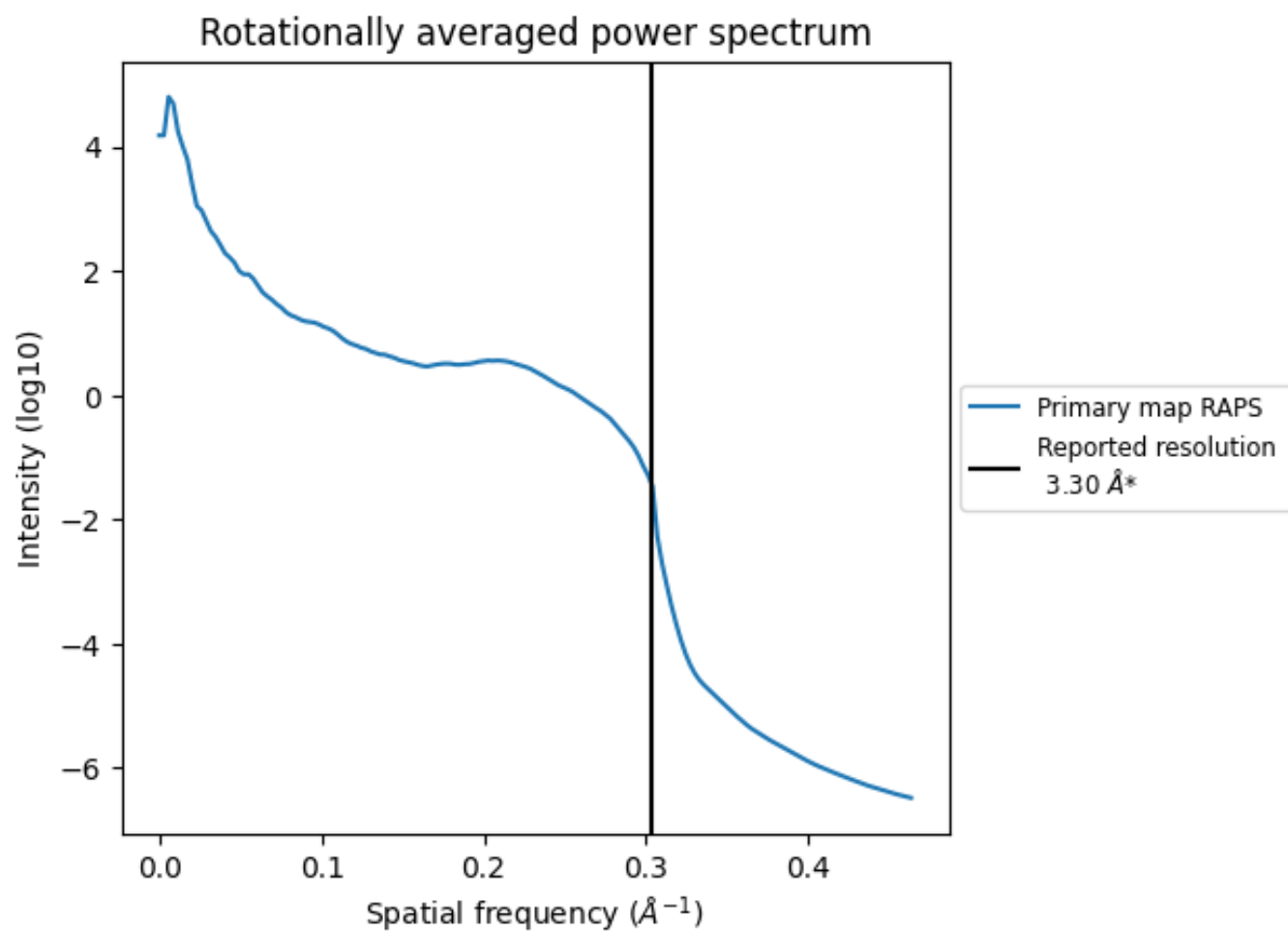
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 170 nm^3 ; this corresponds to an approximate mass of 153 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 0.303 Å⁻¹

8 Fourier-Shell correlation

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

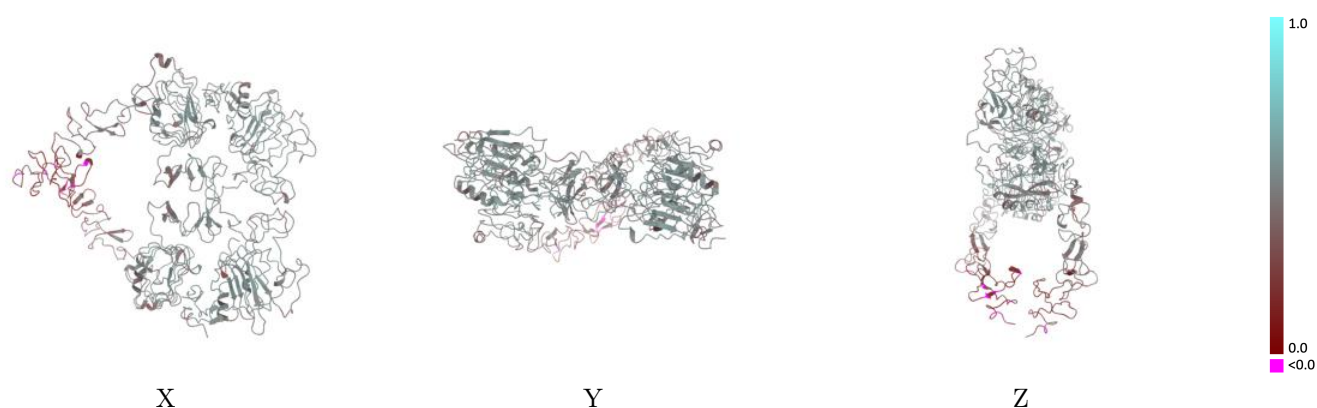
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25558 and PDB model 7SZ0. Per-residue inclusion information can be found in section 3 on page 4.

9.1 Map-model overlay [i](#)

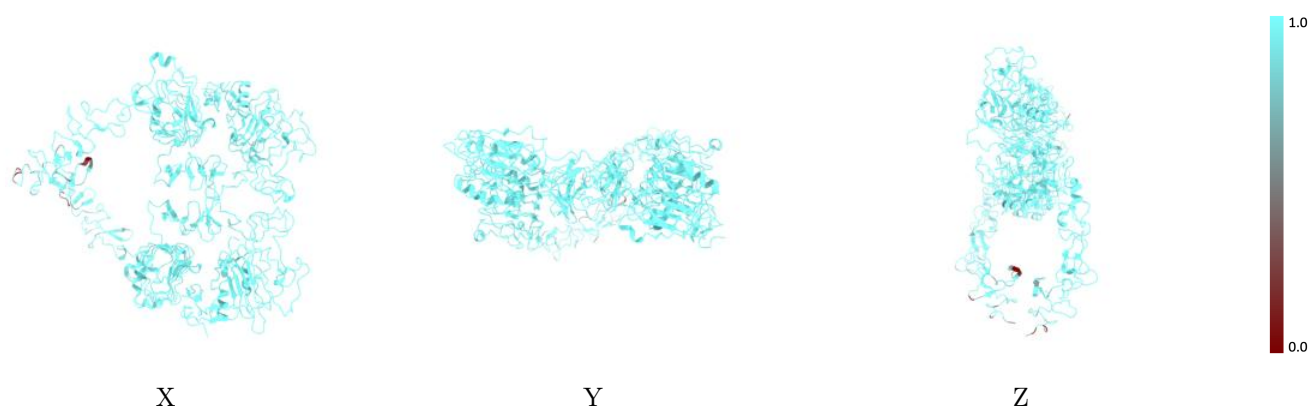
This section was not generated.

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



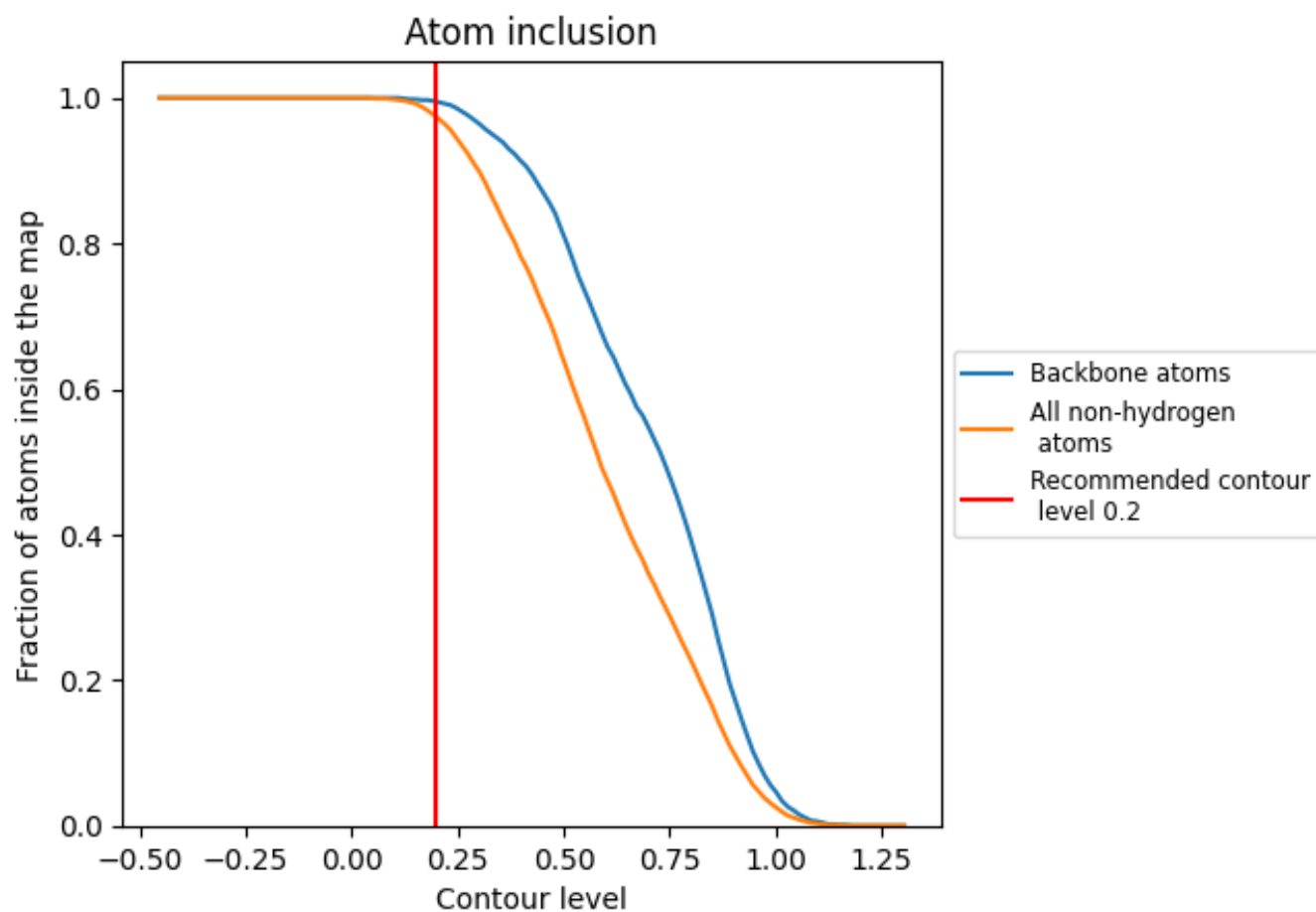
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 100% of all backbone atoms, 97% 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	0.9740	0.4630
A	0.9770	0.4680
B	0.9700	0.4530
C	0.9870	0.4910
D	0.9870	0.5000

