



Full wwPDB EM Validation Report ⓘ

Jun 9, 2024 – 12:49 PM EDT

PDB ID : 8EXQ
EMDB ID : EMD-28659
Title : Cryo-EM structure of S. aureus BlaR1 with C1 symmetry
Authors : Worrall, L.J.; Alexander, J.A.N.; Vuckovic, M.; Strynadka, N.C.J.
Deposited on : 2022-10-25
Resolution : 4.90 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

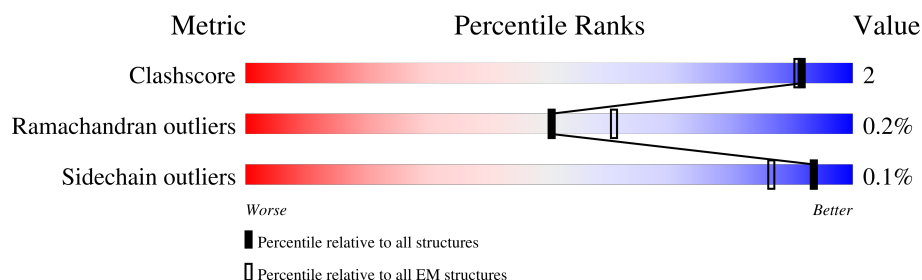
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.90 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	602	<div> <div>28%</div> <div>87%</div> <div>5%</div> <div>8%</div> </div>
1	B	602	<div> <div>23%</div> <div>86%</div> <div>6%</div> <div>8%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9304 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 Beta-lactam sensor/signal transducer BlaR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	554	Total	C	N	O	S	0	0
			4651	3056	767	809	19		
1	A	554	Total	C	N	O	S	0	0
			4651	3056	767	809	19		

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	586	GLU	-	expression tag	UNP Q00419
B	587	LEU	-	expression tag	UNP Q00419
B	588	ALA	-	expression tag	UNP Q00419
B	589	LEU	-	expression tag	UNP Q00419
B	590	VAL	-	expression tag	UNP Q00419
B	591	PRO	-	expression tag	UNP Q00419
B	592	ARG	-	expression tag	UNP Q00419
B	593	GLY	-	expression tag	UNP Q00419
B	594	SER	-	expression tag	UNP Q00419
B	595	SER	-	expression tag	UNP Q00419
B	596	ALA	-	expression tag	UNP Q00419
B	597	HIS	-	expression tag	UNP Q00419
B	598	HIS	-	expression tag	UNP Q00419
B	599	HIS	-	expression tag	UNP Q00419
B	600	HIS	-	expression tag	UNP Q00419
B	601	HIS	-	expression tag	UNP Q00419
B	602	HIS	-	expression tag	UNP Q00419
A	586	GLU	-	expression tag	UNP Q00419
A	587	LEU	-	expression tag	UNP Q00419
A	588	ALA	-	expression tag	UNP Q00419
A	589	LEU	-	expression tag	UNP Q00419
A	590	VAL	-	expression tag	UNP Q00419
A	591	PRO	-	expression tag	UNP Q00419
A	592	ARG	-	expression tag	UNP Q00419
A	593	GLY	-	expression tag	UNP Q00419
A	594	SER	-	expression tag	UNP Q00419

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Chain	Residue	Modelled	Actual	Comment	Reference
A	595	SER	-	expression tag	UNP Q00419
A	596	ALA	-	expression tag	UNP Q00419
A	597	HIS	-	expression tag	UNP Q00419
A	598	HIS	-	expression tag	UNP Q00419
A	599	HIS	-	expression tag	UNP Q00419
A	600	HIS	-	expression tag	UNP Q00419
A	601	HIS	-	expression tag	UNP Q00419
A	602	HIS	-	expression tag	UNP Q00419

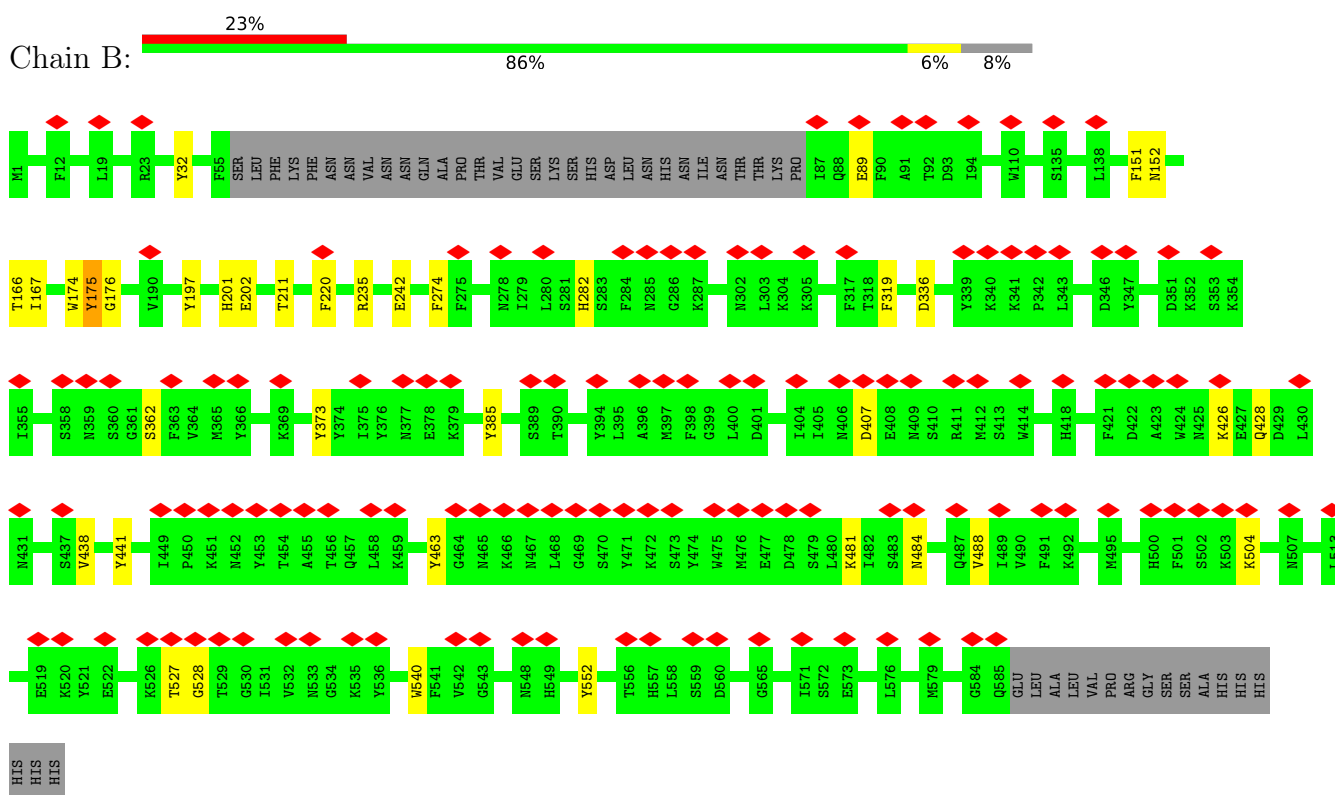
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
2	B	1	Total 1	Zn 1	0
2	A	1	Total 1	Zn 1	0

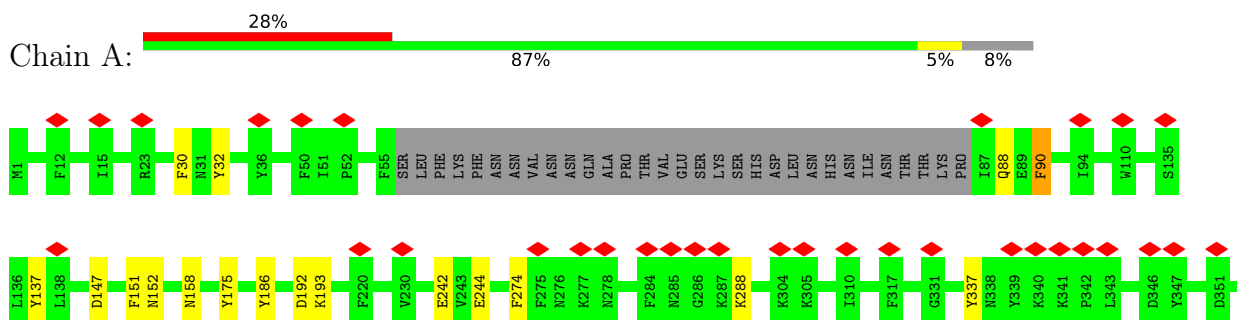
3 Residue-property plots

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: Beta-lactam sensor/signal transducer BlaR1



- Molecule 1: Beta-lactam sensor/signal transducer BlaR1



D560	G561	K562	I571	S572	E573	L576	K577	E578	M579	G580	V581	L582	N583	G584	Q585	GLU	LEU	LEU	ALA	LEU	VAL	PRO	ARG	GLY	SER	SER	ALA	HIS	HIS	HIS	HIS	HIS	HIS																							
F491	K492	M493	M498	M499	H500	F501	S502	K503	K504	A505	K506	N507	Q508	L509	S510	S511	S512	L513	L514	K520	Y521	E522	L523	Y524	G525	K526	T527	G528	T529	G530	I531	V532	N533	G534	K535	Y536	N537	N538	G539	G543	Y544	V545	I546	T547	N548	H549	D550	K551	Y552	Y553	F554	A555	T556	H557	L558	S559
K426	E427	M431	T432	A433	M434	Q435	M436	S437	Y438	M439	W440	Y441	I445	S446	D447	Q448	I449	P450	K451	M452	A455	T456	Q457	L458	K459	Q460	L461	M462	Y463	G464	M465	K466	M467	L468	G469	S470	Y471	K472	S473	Y474	W475	M476	E477	D478	S479	L480	K481	I482	S483	M484	L485	E486	Q487	V488	I489	V490
I355	S358	M359	S362	F363	V364	M365	Y366	S367	M368	K369	K370	Y373	Y374	E378	K379	R382	K383	R384	Y385	M388	S389	T390	Y391	K392	I393	Y394	L395	A396	M397	F398	G399	L400	D401	R402	H403	D407	E408	M409	S410	R411	M412	M415	H416	Y419	P420	F421	D422	A423	W424	M425						

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	23797	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)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.035	Depositor
Minimum map value	-0.607	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.045	Depositor
Recommended contour level	0.17	Depositor
Map size (Å)	231.0016, 231.0016, 231.0016	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.8047, 1.8047, 1.8047	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	1.02	7/4766 (0.1%)	0.95	9/6418 (0.1%)
1	B	1.04	7/4766 (0.1%)	0.94	11/6418 (0.2%)
All	All	1.03	14/9532 (0.1%)	0.94	20/12836 (0.2%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	552	TYR	CB-CG	-7.69	1.40	1.51
1	A	90	PHE	CB-CG	-7.28	1.39	1.51
1	A	30	PHE	CB-CG	-6.22	1.40	1.51
1	B	488	VAL	CB-CG2	-5.81	1.40	1.52
1	B	89	GLU	CD-OE1	-5.63	1.19	1.25
1	B	201	HIS	CB-CG	-5.52	1.40	1.50
1	A	186	TYR	CB-CG	-5.48	1.43	1.51
1	A	554	PHE	CB-CG	-5.44	1.42	1.51
1	B	319	PHE	CB-CG	-5.43	1.42	1.51
1	A	137	TYR	CB-CG	-5.27	1.43	1.51
1	A	244	GLU	CD-OE1	-5.17	1.20	1.25
1	B	242	GLU	CD-OE2	-5.13	1.20	1.25
1	B	202	GLU	CD-OE2	-5.11	1.20	1.25
1	A	242	GLU	CD-OE1	-5.06	1.20	1.25

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	385	TYR	CB-CG-CD1	-7.52	116.49	121.00
1	A	463	TYR	CB-CG-CD1	-7.38	116.57	121.00
1	B	385	TYR	CB-CG-CD1	-7.20	116.68	121.00
1	B	235	ARG	NE-CZ-NH2	-6.86	116.87	120.30
1	B	463	TYR	CB-CG-CD1	-6.34	117.20	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	463	TYR	CB-CG-CD2	6.31	124.79	121.00
1	B	235	ARG	NE-CZ-NH1	6.31	123.45	120.30
1	A	337	TYR	CB-CG-CD2	-6.03	117.38	121.00
1	A	552	TYR	CB-CG-CD1	-6.02	117.39	121.00
1	A	441	TYR	CB-CG-CD2	-6.01	117.39	121.00
1	A	463	TYR	CB-CG-CD2	5.95	124.57	121.00
1	A	32	TYR	CB-CG-CD2	-5.91	117.45	121.00
1	A	373	TYR	CB-CG-CD1	-5.70	117.58	121.00
1	B	220	PHE	CB-CG-CD2	-5.63	116.86	120.80
1	A	382	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	B	32	TYR	CB-CG-CD2	-5.50	117.70	121.00
1	B	552	TYR	CB-CG-CD2	-5.36	117.78	121.00
1	B	197	TYR	CB-CG-CD2	-5.35	117.79	121.00
1	B	540	TRP	CA-CB-CG	5.22	123.61	113.70
1	B	373	TYR	CB-CG-CD1	-5.07	117.96	121.00

There are no chirality outliers.

There are no planarity outliers.

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	4651	0	4747	12	0
1	B	4651	0	4747	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
All	All	9304	0	9494	29	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 2.

All (29) 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:211:THR:HG22	1:B:282:HIS:CD2	2.12	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:THR:CG2	1:B:282:HIS:CD2	2.61	0.83
1:B:211:THR:HG23	1:B:282:HIS:HD2	1.52	0.73
1:B:211:THR:HG23	1:B:282:HIS:CD2	2.30	0.65
1:A:175:TYR:CG	1:A:175:TYR:O	2.56	0.57
1:B:362:SER:OG	1:B:484:ASN:ND2	2.39	0.55
1:B:336:ASP:OD1	1:B:481:LYS:NZ	2.41	0.54
1:B:211:THR:CG2	1:B:282:HIS:HD2	2.07	0.53
1:B:152:ASN:N	1:B:152:ASN:OD1	2.41	0.51
1:A:421:PHE:HB2	1:A:424:TRP:CD1	2.49	0.48
1:B:166:THR:OG1	1:B:167:ILE:N	2.48	0.47
1:B:426:LYS:O	1:B:428:GLN:NE2	2.48	0.47
1:A:152:ASN:OD1	1:A:152:ASN:N	2.39	0.47
1:A:158:ASN:N	1:A:158:ASN:OD1	2.47	0.47
1:B:527:THR:OG1	1:B:528:GLY:N	2.49	0.46
1:A:407:ASP:OD1	1:A:407:ASP:N	2.48	0.45
1:A:438:VAL:HG12	1:A:441:TYR:H	1.81	0.45
1:B:151:PHE:CD1	1:B:151:PHE:C	2.90	0.44
1:B:175:TYR:O	1:B:175:TYR:CG	2.68	0.42
1:A:88:GLN:HB2	1:A:90:PHE:CE1	2.55	0.41
1:A:488:VAL:HG22	1:A:554:PHE:HA	2.01	0.41
1:A:424:TRP:CD1	1:A:438:VAL:HG22	2.56	0.41
1:B:407:ASP:OD2	1:B:504:LYS:NZ	2.44	0.41
1:A:192:ASP:CG	1:A:193:LYS:N	2.75	0.41
1:A:147:ASP:O	1:A:151:PHE:N	2.54	0.41
1:A:274:PHE:CD1	1:A:274:PHE:C	2.91	0.40
1:B:274:PHE:CD1	1:B:274:PHE:C	2.94	0.40
1:B:438:VAL:HG12	1:B:441:TYR:H	1.86	0.40
1:B:174:TRP:O	1:B:176:GLY:N	2.53	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	550/602 (91%)	536 (98%)	13 (2%)	1 (0%)	47	81
1	B	550/602 (91%)	534 (97%)	15 (3%)	1 (0%)	47	81
All	All	1100/1204 (91%)	1070 (97%)	28 (2%)	2 (0%)	50	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	175	TYR
1	A	474	TYR

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	518/562 (92%)	517 (100%)	1 (0%)	93	96
1	B	518/562 (92%)	518 (100%)	0	100	100
All	All	1036/1124 (92%)	1035 (100%)	1 (0%)	93	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	288	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	282	HIS
1	B	484	ASN
1	B	538	ASN
1	A	538	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

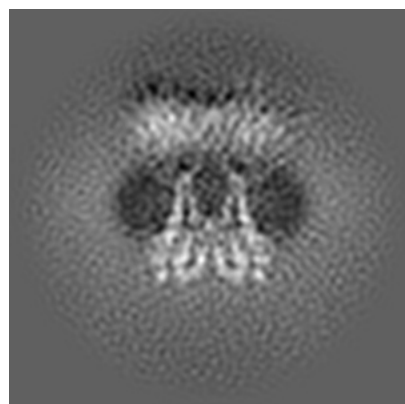
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-28659. These allow visual inspection of the internal detail of the map and identification of artifacts.

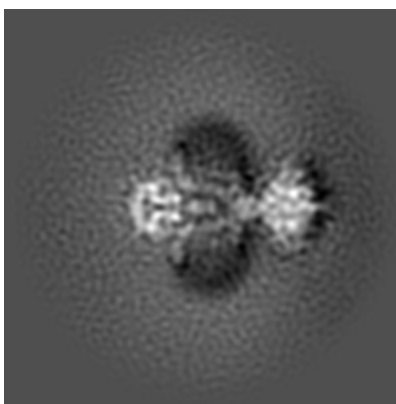
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

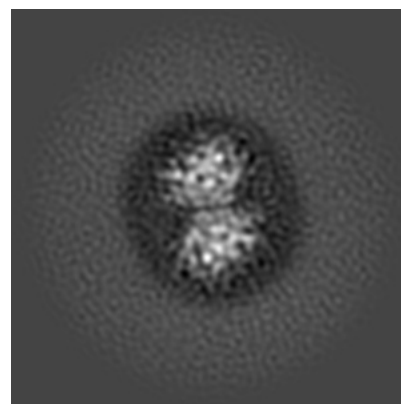
6.1.1 Primary map



X

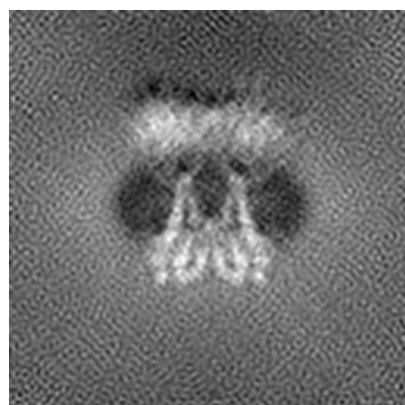


Y

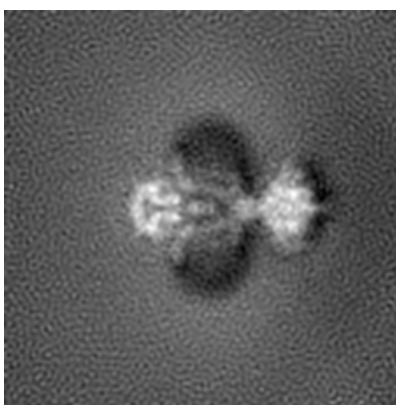


Z

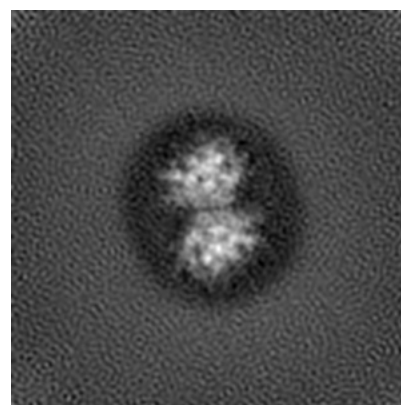
6.1.2 Raw map



X



Y

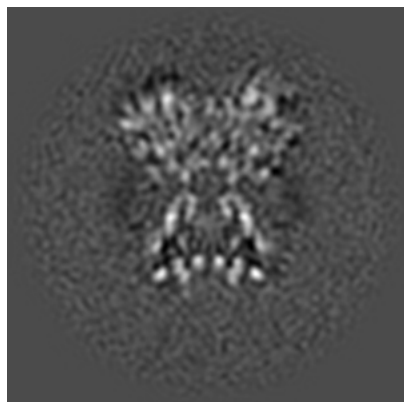


Z

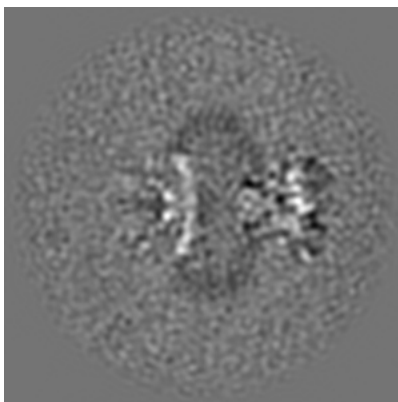
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

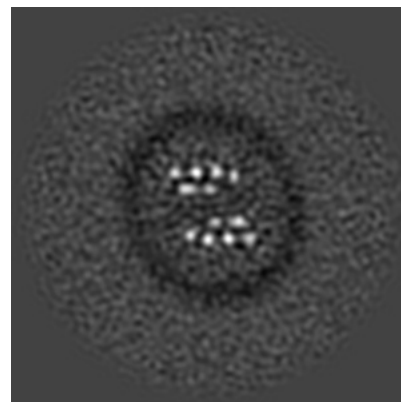
6.2.1 Primary map



X Index: 64

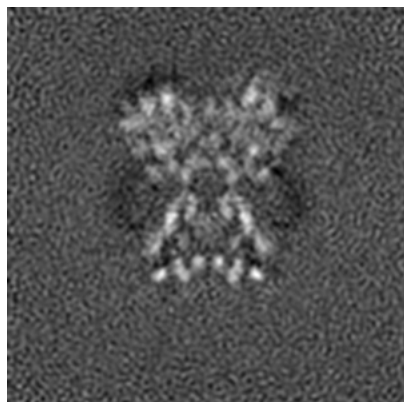


Y Index: 64

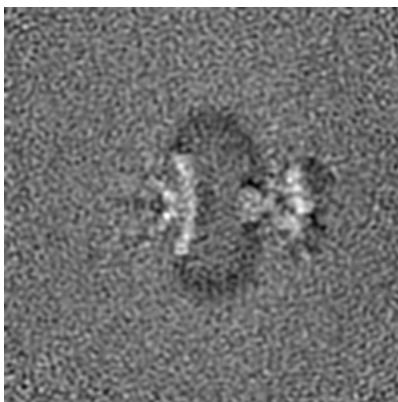


Z Index: 64

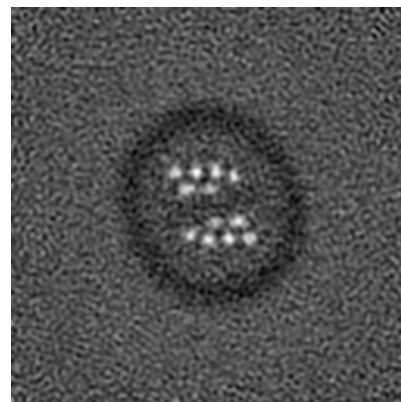
6.2.2 Raw map



X Index: 64



Y Index: 64

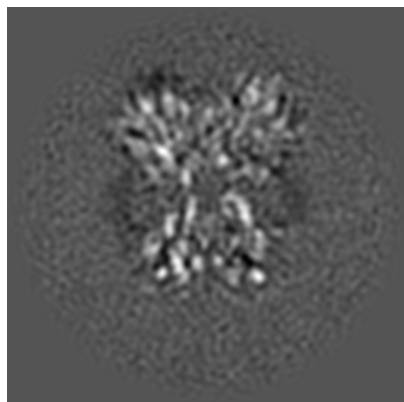


Z Index: 64

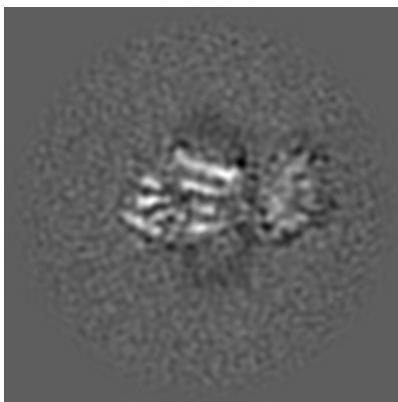
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

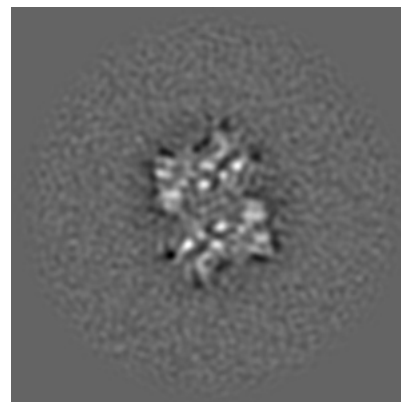
6.3.1 Primary map



X Index: 65

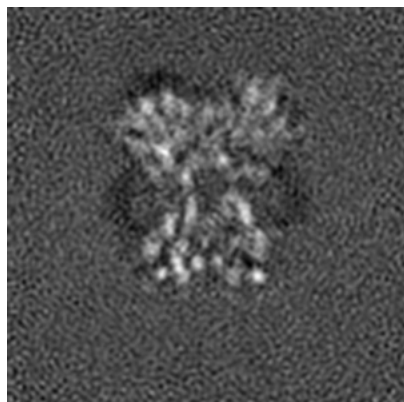


Y Index: 54

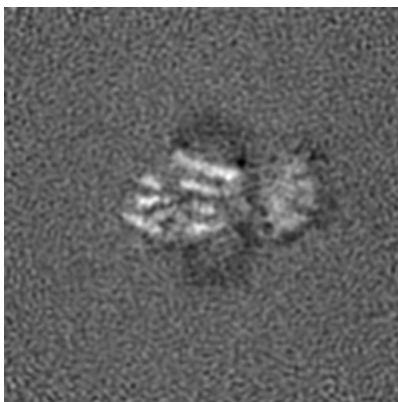


Z Index: 56

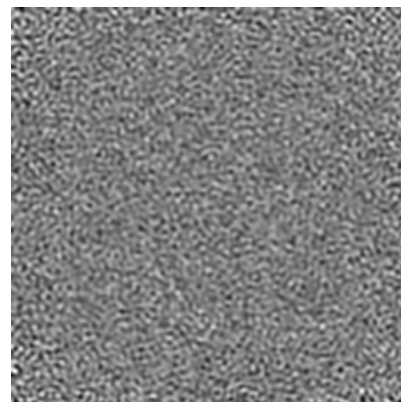
6.3.2 Raw map



X Index: 65



Y Index: 54

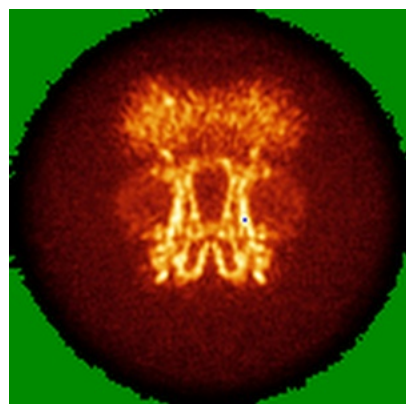


Z Index: 0

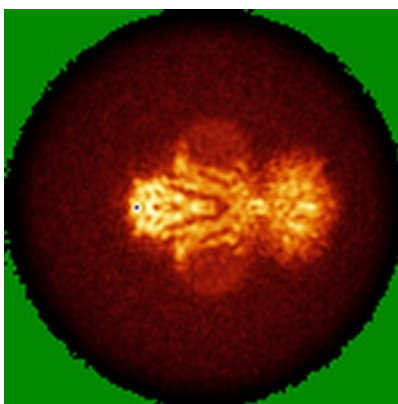
The images above show the largest variance slices of the map in three orthogonal directions.

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

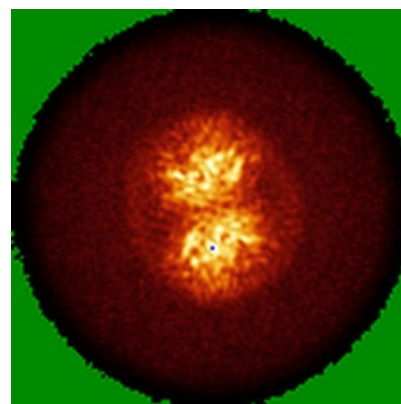
6.4.1 Primary map



X

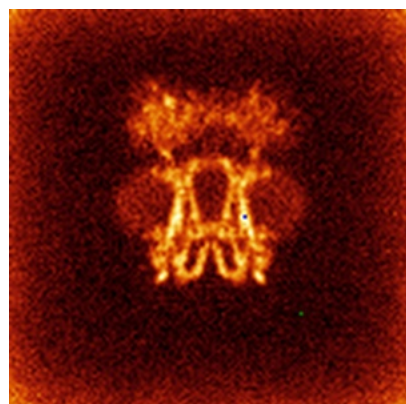


Y

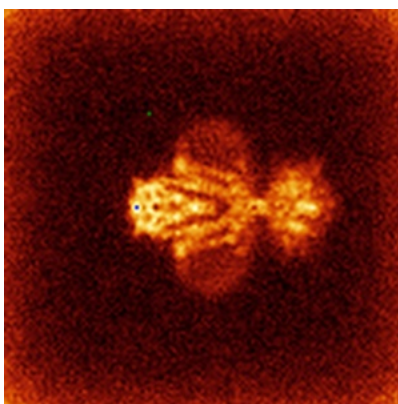


Z

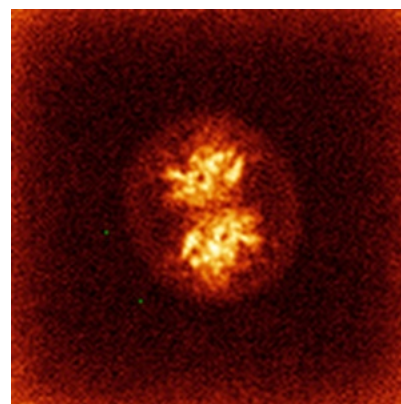
6.4.2 Raw map



X



Y

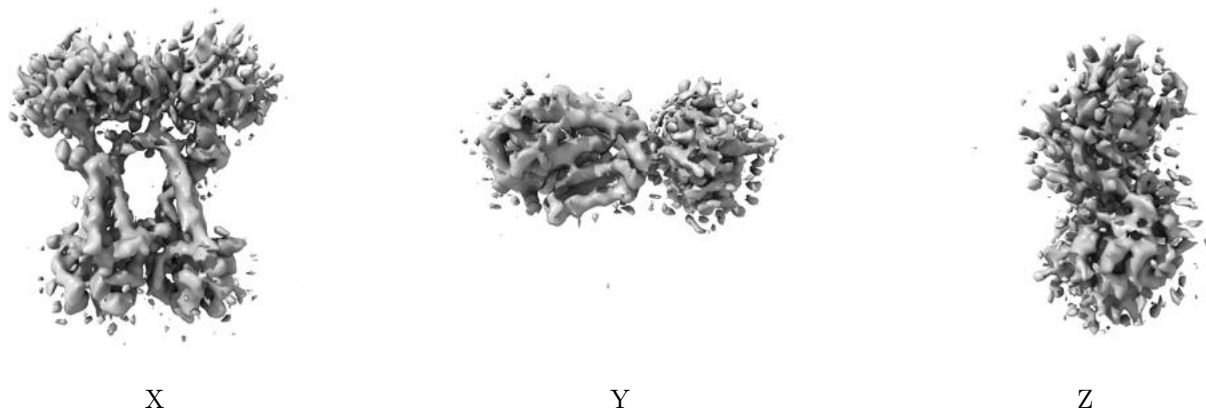


Z

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.

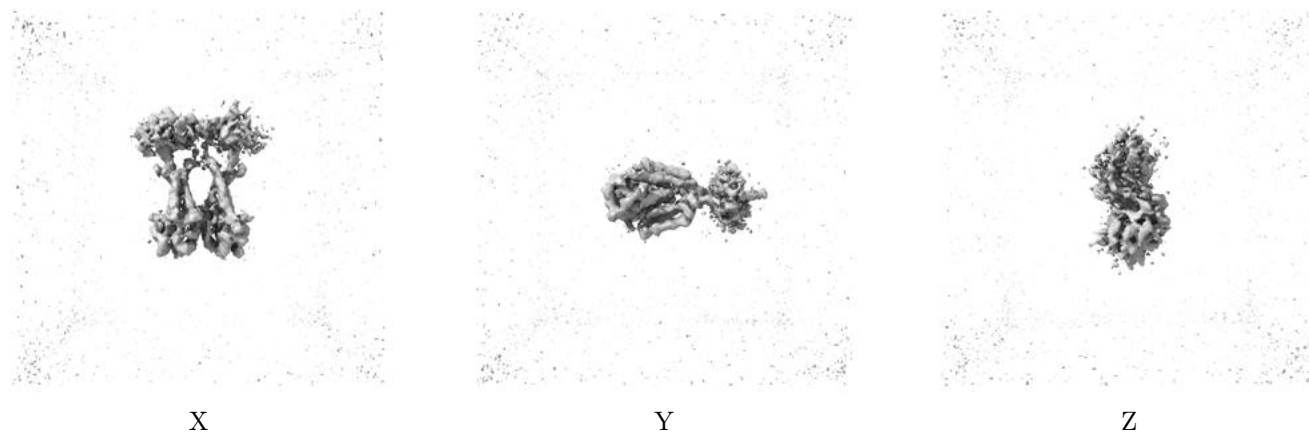
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.17. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

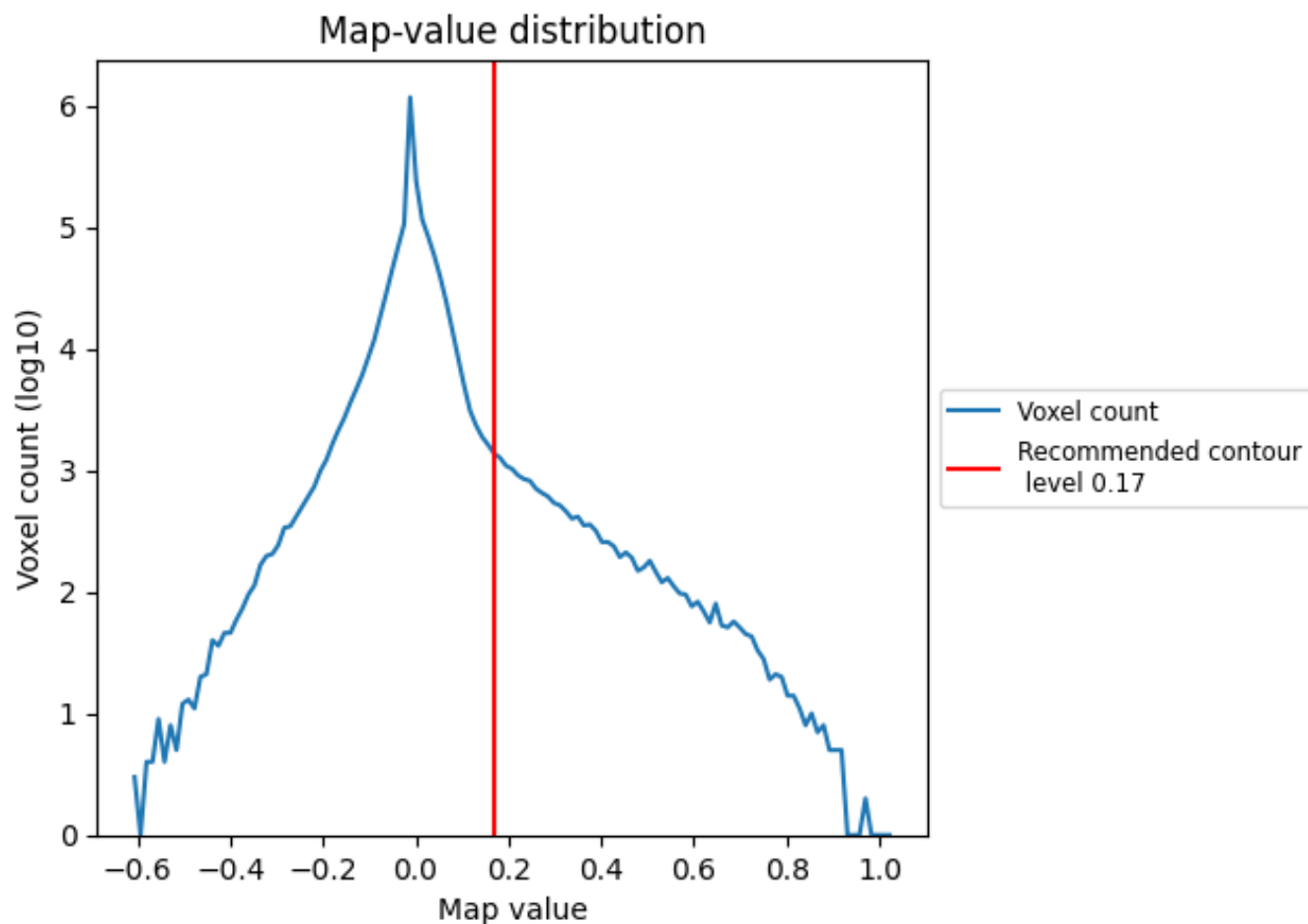
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

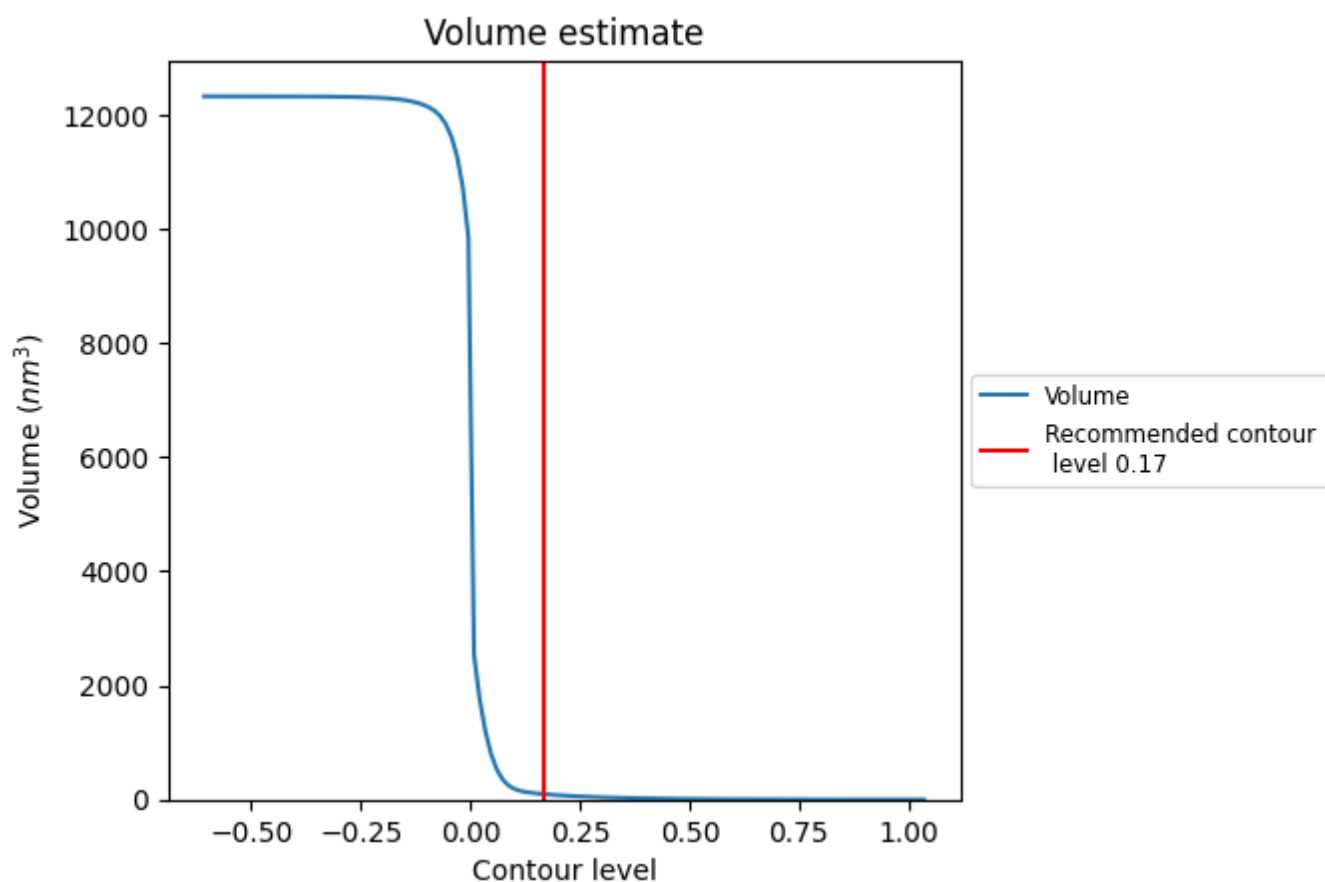
This section contains the results of statistical analysis of the map.

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.

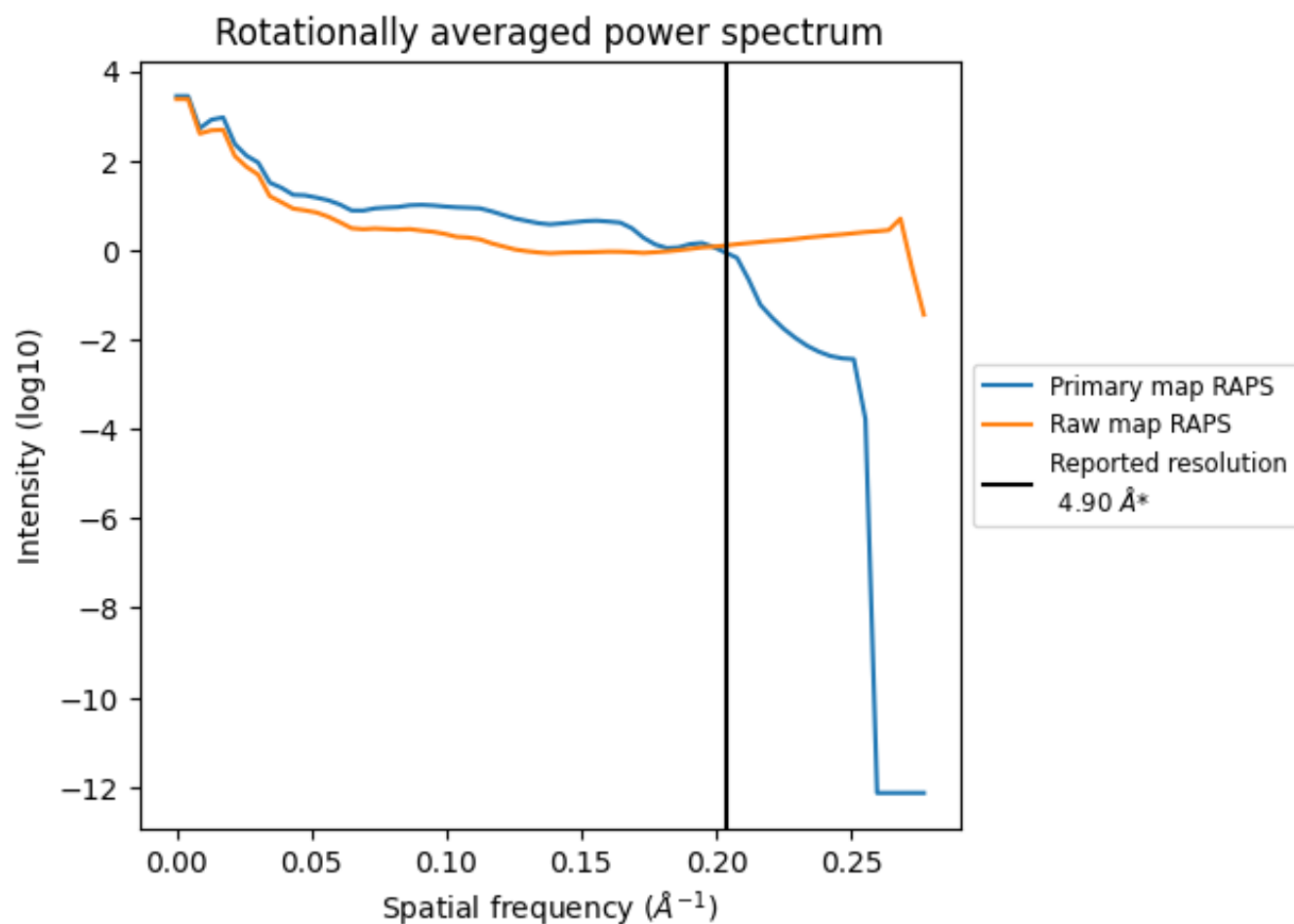
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 94 nm³; this corresponds to an approximate mass of 85 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 ⓘ

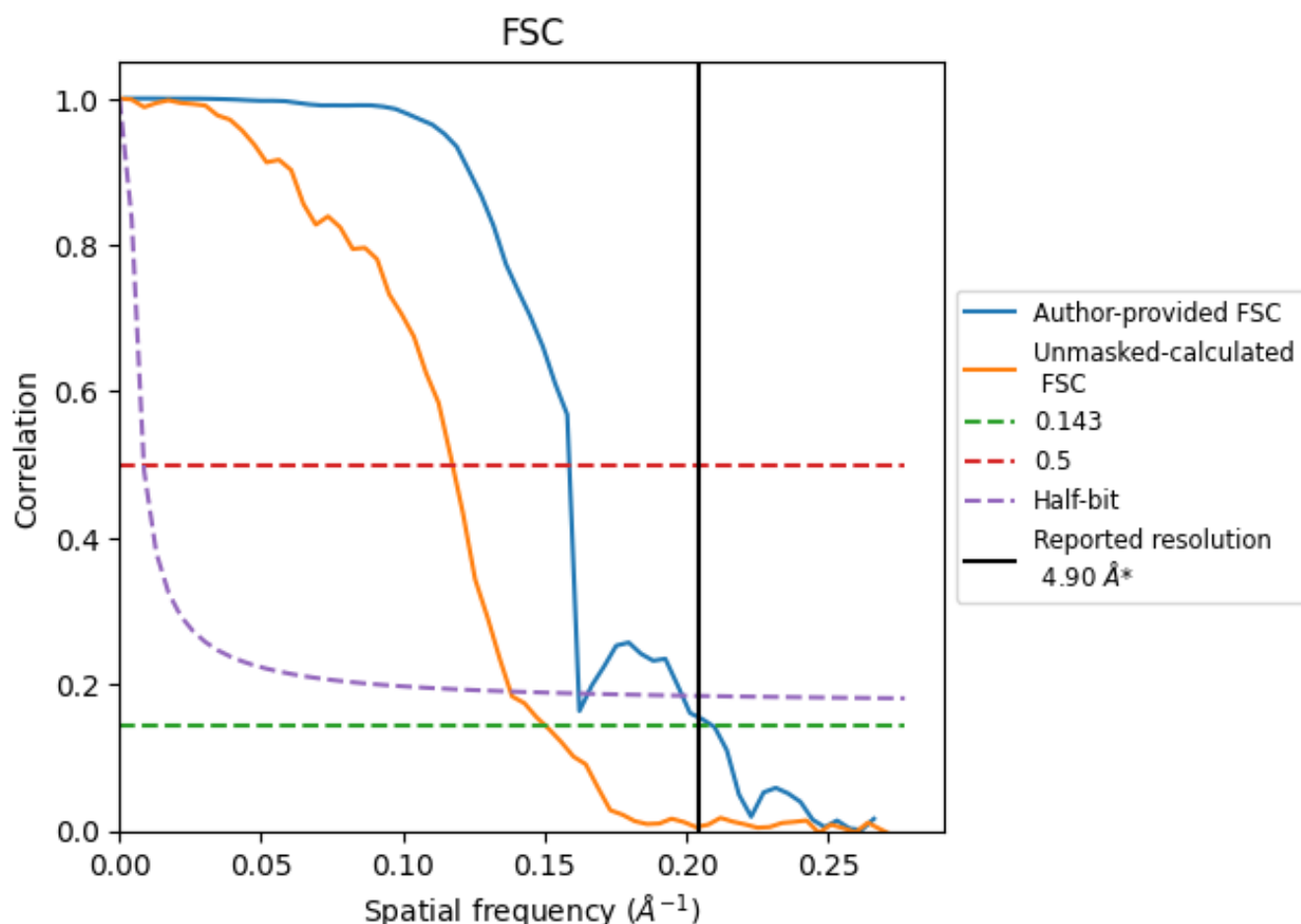


*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.204 Å⁻¹

8.2 Resolution estimates [i](#)

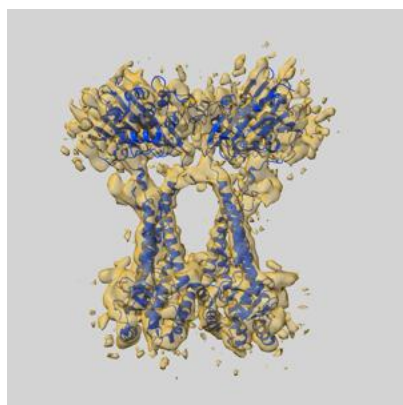
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.90	-	-
Author-provided FSC curve	4.78	6.30	6.17
Unmasked-calculated*	6.65	8.51	7.25

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.65 differs from the reported value 4.9 by more than 10 %

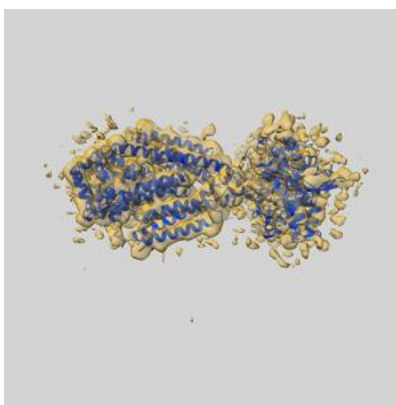
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-28659 and PDB model 8EXQ. Per-residue inclusion information can be found in section 3 on page 5.

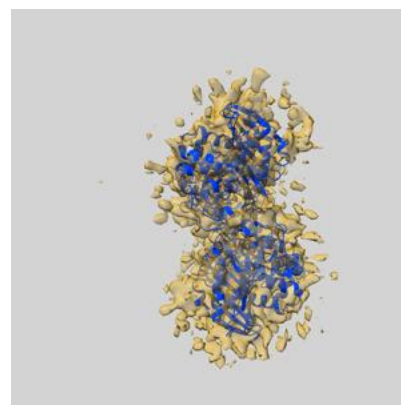
9.1 Map-model overlay [i](#)



X



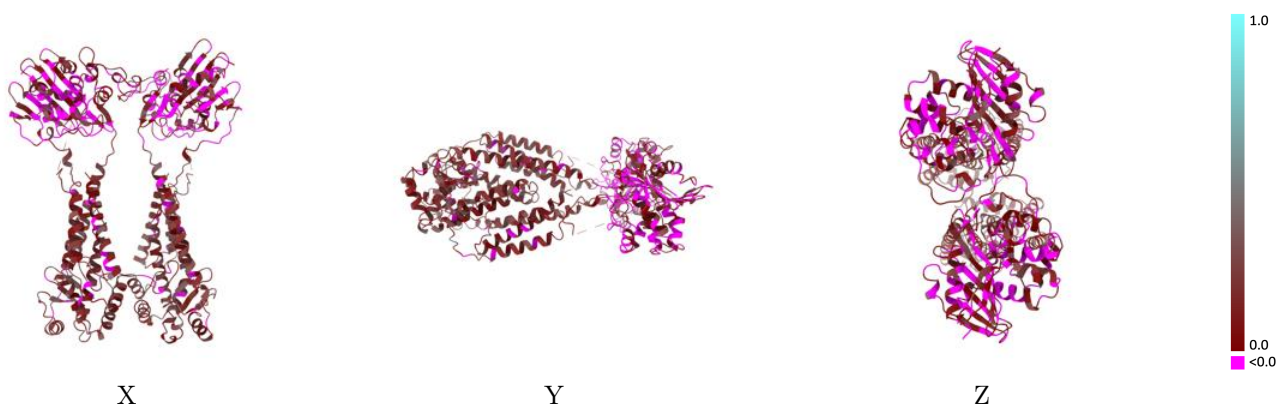
Y



Z

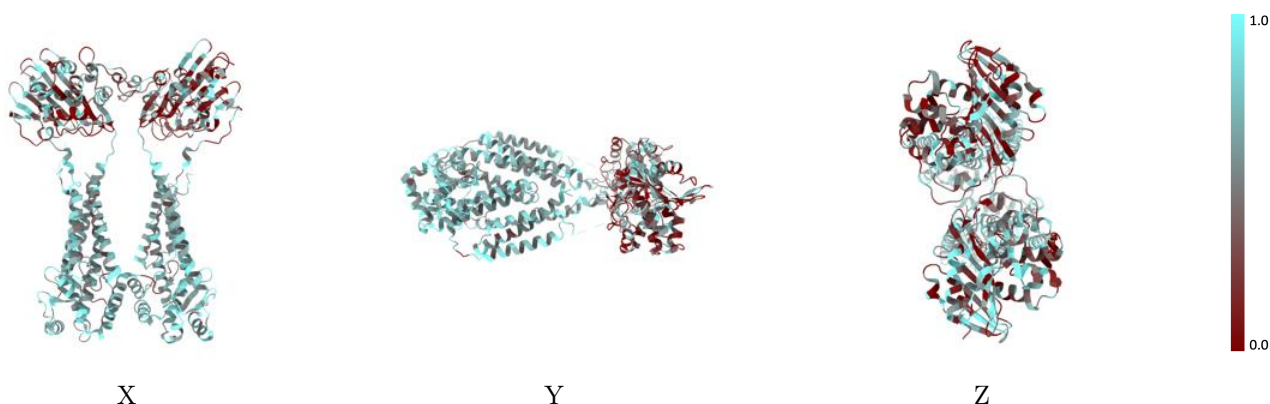
The images above show the 3D surface view of the map at the recommended contour level 0.17 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



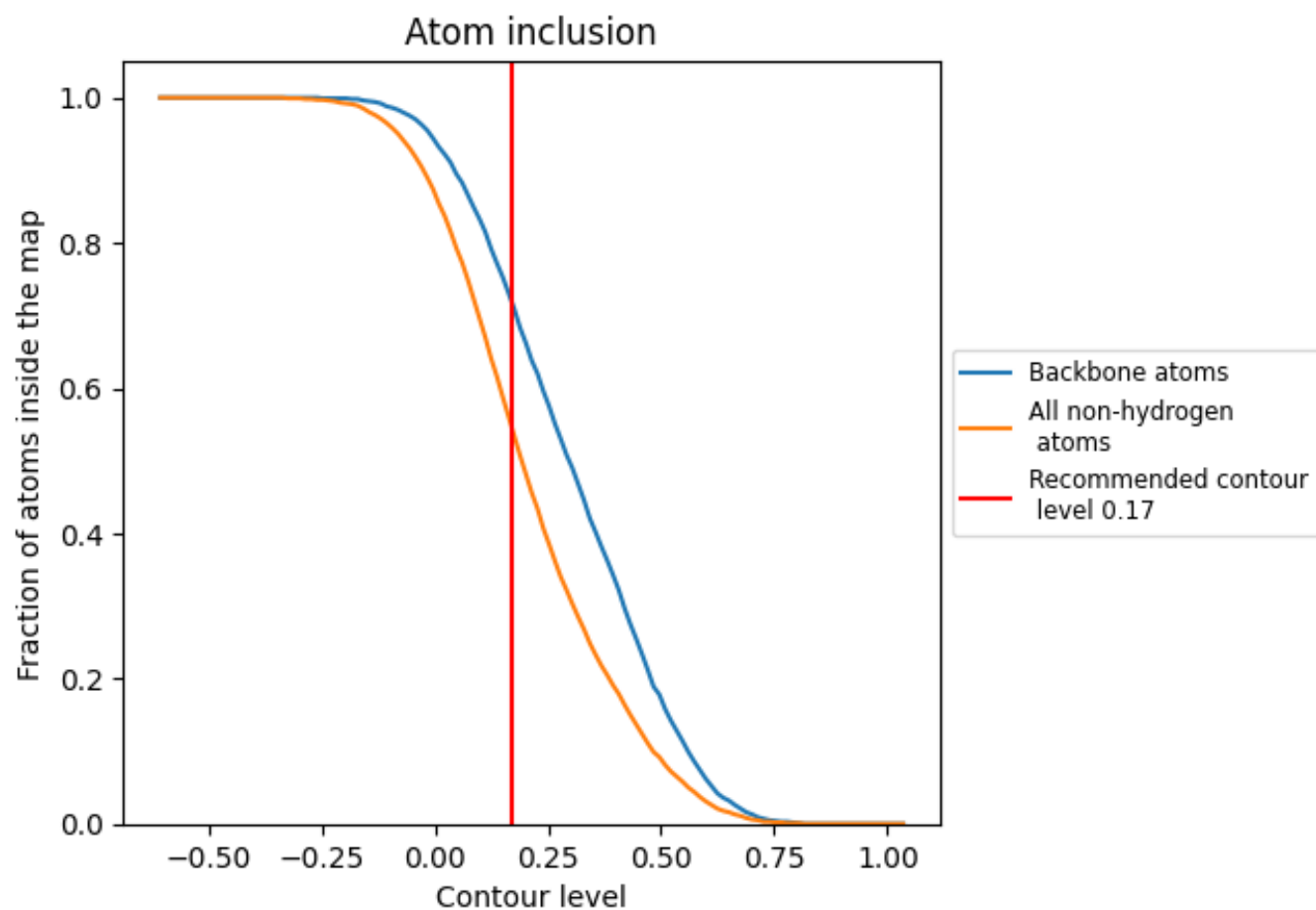
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.17).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 55% 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 (0.17) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.5460	<div></div> 0.1220
A	<div></div> 0.5230	<div></div> 0.1230
B	<div></div> 0.5690	<div></div> 0.1210

