



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:35 PM UTC

PDB ID : 6W4S / pdb_00006w4s
EMDB ID : EMD-21539
Title : Structure of apo human ferroportin in lipid nanodisc
Authors : Billesboelle, C.B.; Azumaya, C.M.; Gonen, S.; Powers, A.; Kretsch, R.C.;
Schneider, S.; Arvedson, T.; Dror, R.O.; Cheng, Y.; Manglik, A.
Deposited on : 2020-03-11
Resolution : 3.20 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

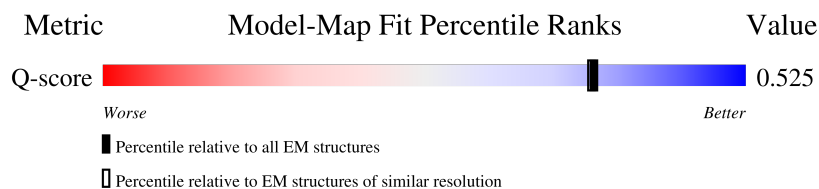
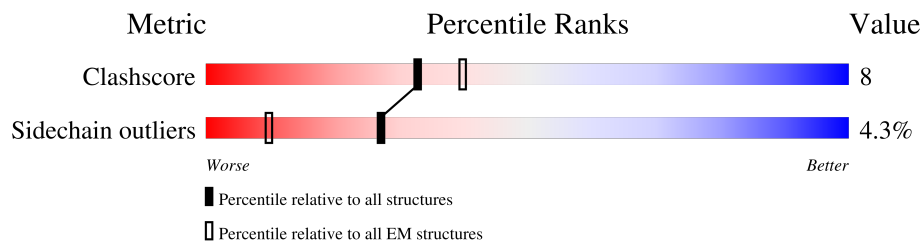
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	F	605	
2	H	220	
3	L	218	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4986 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 Solute carrier family 40 member 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	F	421	Total	C	N	O	S	0	0
			3216	2119	522	552	23		

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	572	GLY	-	expression tag	UNP Q9NP59
F	573	SER	-	expression tag	UNP Q9NP59
F	574	GLY	-	expression tag	UNP Q9NP59
F	575	LEU	-	expression tag	UNP Q9NP59
F	576	GLU	-	expression tag	UNP Q9NP59
F	577	VAL	-	expression tag	UNP Q9NP59
F	578	LEU	-	expression tag	UNP Q9NP59
F	579	PHE	-	expression tag	UNP Q9NP59
F	580	GLN	-	expression tag	UNP Q9NP59
F	581	GLY	-	expression tag	UNP Q9NP59
F	582	PRO	-	expression tag	UNP Q9NP59
F	583	GLY	-	expression tag	UNP Q9NP59
F	584	ALA	-	expression tag	UNP Q9NP59
F	585	ALA	-	expression tag	UNP Q9NP59
F	586	GLU	-	expression tag	UNP Q9NP59
F	587	ASP	-	expression tag	UNP Q9NP59
F	588	GLN	-	expression tag	UNP Q9NP59
F	589	VAL	-	expression tag	UNP Q9NP59
F	590	ASP	-	expression tag	UNP Q9NP59
F	591	PRO	-	expression tag	UNP Q9NP59
F	592	ARG	-	expression tag	UNP Q9NP59
F	593	LEU	-	expression tag	UNP Q9NP59
F	594	ILE	-	expression tag	UNP Q9NP59
F	595	ASP	-	expression tag	UNP Q9NP59
F	596	GLY	-	expression tag	UNP Q9NP59
F	597	LYS	-	expression tag	UNP Q9NP59
F	598	HIS	-	expression tag	UNP Q9NP59
F	599	HIS	-	expression tag	UNP Q9NP59

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Chain	Residue	Modelled	Actual	Comment	Reference
F	600	HIS	-	expression tag	UNP Q9NP59
F	601	HIS	-	expression tag	UNP Q9NP59
F	602	HIS	-	expression tag	UNP Q9NP59
F	603	HIS	-	expression tag	UNP Q9NP59
F	604	HIS	-	expression tag	UNP Q9NP59
F	605	HIS	-	expression tag	UNP Q9NP59

- Molecule 2 is a protein called Fab45D8 Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	118	Total	C	N	O	S	0	0
			926	587	149	187	3		

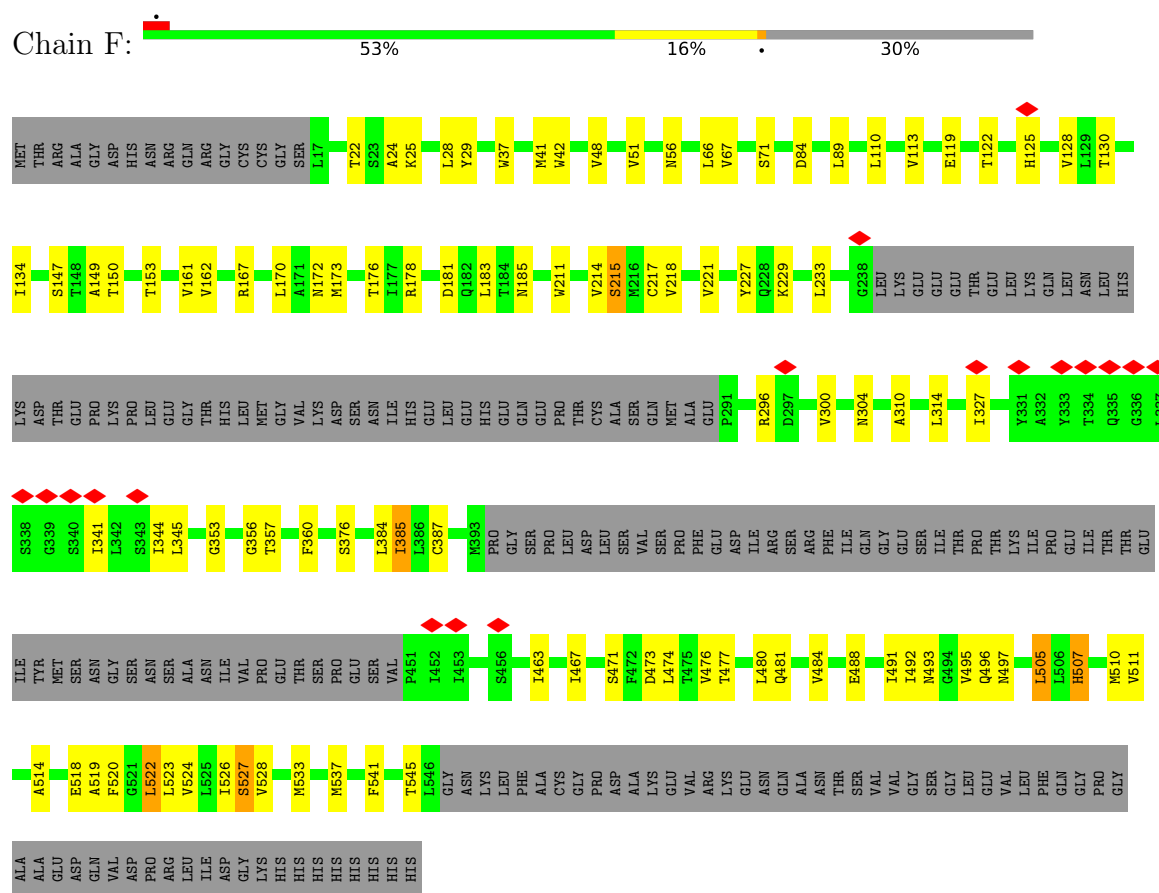
- Molecule 3 is a protein called Fab45D8 Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L	111	Total	C	N	O	S	0	0
			844	534	143	164	3		

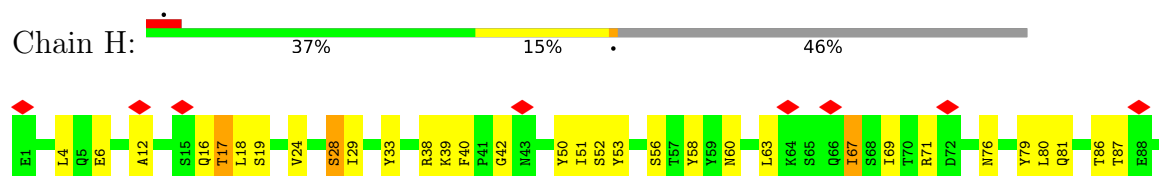
3 Residue-property plots

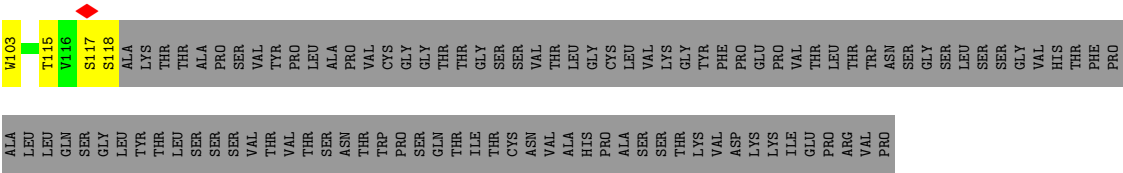
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Solute carrier family 40 member 1

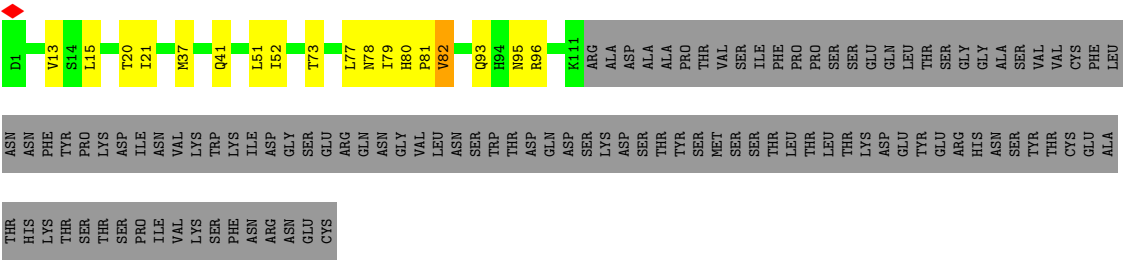


• Molecule 2: Fab45D8 Heavy Chain





● Molecule 3: Fab45D8 Light Chain



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	308366	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 ($e^-/\text{\AA}^2$)	60.0	Depositor
Minimum defocus (nm)	-8000	Depositor
Maximum defocus (nm)	-20000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	32.118	Depositor
Minimum map value	-19.696	Depositor
Average map value	-0.041	Depositor
Map value standard deviation	0.719	Depositor
Recommended contour level	4	Depositor
Map size (Å)	254.64, 254.64, 254.64	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8488, 0.8488, 0.8488	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	F	0.18	0/3283	0.34	0/4471
2	H	0.20	0/951	0.36	0/1300
3	L	0.19	0/867	0.36	0/1181
All	All	0.19	0/5101	0.35	0/6952

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	F	3216	0	3331	55	0
2	H	926	0	868	21	0
3	L	844	0	813	11	0
All	All	4986	0	5012	84	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 8.

All (84) 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)
3:L:93:GLN:NE2	3:L:95:ASN:OD1	2.21	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:514:ALA:HB1	1:F:519:ALA:HB1	1.73	0.71
3:L:20:THR:OG1	3:L:78:ASN:ND2	2.29	0.65
2:H:28:SER:HA	2:H:76:ASN:HD21	1.63	0.64
1:F:178:ARG:HG3	1:F:474:LEU:HD11	1.80	0.64
1:F:181:ASP:O	1:F:185:ASN:ND2	2.29	0.62
1:F:122:THR:OG1	3:L:96:ARG:O	2.18	0.62
2:H:52:SER:HB3	2:H:56:SER:HB2	1.82	0.61
1:F:480:LEU:HD11	1:F:496:GLN:HE21	1.65	0.61
1:F:22:THR:O	1:F:229:LYS:NZ	2.33	0.60
2:H:16:GLN:HG2	2:H:17:THR:H	1.67	0.59
2:H:60:ASN:HB3	2:H:63:LEU:HG	1.85	0.59
2:H:12:ALA:HB2	2:H:18:LEU:HD21	1.84	0.58
1:F:519:ALA:O	1:F:523:LEU:HG	2.04	0.58
2:H:4:LEU:HD22	2:H:24:VAL:HG22	1.87	0.57
2:H:52:SER:OG	2:H:53:TYR:N	2.38	0.56
1:F:384:LEU:HA	1:F:387:CYS:HB2	1.88	0.56
1:F:353:GLY:O	1:F:357:THR:HG23	2.07	0.55
1:F:507:HIS:O	1:F:511:VAL:HG23	2.06	0.55
3:L:21:ILE:HD11	3:L:77:LEU:HD22	1.88	0.55
2:H:103:TRP:CD1	3:L:95:ASN:HD22	2.26	0.53
2:H:51:ILE:HD13	2:H:71:ARG:HB3	1.91	0.52
1:F:493:ASN:O	1:F:497:ASN:ND2	2.36	0.51
1:F:119:GLU:OE2	2:H:33:TYR:OH	2.26	0.49
1:F:533:MET:O	1:F:537:MET:HG3	2.12	0.49
1:F:66:LEU:HD22	1:F:505:LEU:HD12	1.94	0.49
1:F:314:LEU:HB2	1:F:476:VAL:HG11	1.95	0.48
2:H:6:GLU:N	2:H:6:GLU:OE1	2.47	0.48
1:F:524:VAL:O	1:F:528:VAL:HG23	2.13	0.47
2:H:39:LYS:NZ	2:H:42:GLY:O	2.44	0.47
1:F:125:HIS:O	1:F:128:VAL:HG12	2.14	0.47
1:F:214:VAL:O	1:F:218:VAL:HG23	2.15	0.47
1:F:345:LEU:HD22	1:F:463:ILE:HD11	1.95	0.47
2:H:18:LEU:O	2:H:81:GLN:HA	2.15	0.47
1:F:51:VAL:HA	1:F:56:ASN:H	1.79	0.47
1:F:518:GLU:H	1:F:518:GLU:CD	2.21	0.47
1:F:211:TRP:O	1:F:215:SER:HB3	2.14	0.47
1:F:172:ASN:O	1:F:176:THR:HG23	2.15	0.47
1:F:360:PHE:HB2	1:F:471:SER:HB2	1.96	0.46
1:F:161:VAL:HG11	1:F:233:LEU:HD13	1.99	0.45
2:H:117:SER:OG	2:H:118:SER:N	2.48	0.45
1:F:67:VAL:O	1:F:71:SER:OG	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:217:CYS:O	1:F:221:VAL:HG23	2.17	0.45
2:H:86:THR:HG22	2:H:87:THR:H	1.81	0.45
1:F:162:VAL:HG13	1:F:173:MET:HE1	1.98	0.45
2:H:67:ILE:HD11	2:H:69:ILE:HD11	1.99	0.45
1:F:25:LYS:HG2	1:F:29:TYR:CE2	2.52	0.44
1:F:522:LEU:O	1:F:526:ILE:HG13	2.18	0.44
1:F:376:SER:HB3	1:F:471:SER:OG	2.17	0.44
1:F:310:ALA:HB2	1:F:541:PHE:CD2	2.53	0.44
1:F:385:ILE:HD12	1:F:385:ILE:HA	1.77	0.44
1:F:523:LEU:O	1:F:527:SER:OG	2.30	0.44
3:L:13:VAL:HG11	3:L:82:VAL:HG11	1.98	0.44
3:L:52:ILE:HD12	3:L:77:LEU:HD12	2.00	0.44
1:F:296:ARG:O	1:F:300:VAL:HG23	2.18	0.43
1:F:170:LEU:HD11	1:F:481:GLN:NE2	2.32	0.43
1:F:480:LEU:HD11	1:F:496:GLN:NE2	2.33	0.43
1:F:488:GLU:O	1:F:492:ILE:HG12	2.18	0.43
2:H:29:ILE:HD12	2:H:71:ARG:HD2	2.01	0.43
3:L:15:LEU:HD12	3:L:15:LEU:H	1.84	0.43
2:H:38:ARG:NE	2:H:40:PHE:HE1	2.18	0.42
1:F:110:LEU:HA	1:F:113:VAL:HG12	2.01	0.42
2:H:19:SER:O	2:H:19:SER:OG	2.33	0.42
3:L:37:MET:HE2	3:L:37:MET:HB2	1.88	0.42
1:F:37:TRP:O	1:F:41:MET:HG3	2.19	0.42
3:L:41:GLN:HB2	3:L:51:LEU:HD11	2.02	0.42
1:F:48:VAL:HA	1:F:51:VAL:HG12	2.00	0.42
1:F:130:THR:O	1:F:134:ILE:HG23	2.20	0.42
1:F:341:ILE:HA	1:F:344:ILE:HG22	2.02	0.41
1:F:510:MET:SD	1:F:523:LEU:HD22	2.60	0.41
1:F:147:SER:HA	1:F:150:THR:HG22	2.03	0.41
1:F:520:PHE:O	1:F:524:VAL:HG23	2.20	0.41
2:H:50:TYR:CE2	2:H:58:TYR:HB3	2.56	0.41
1:F:149:ALA:O	1:F:153:THR:HG22	2.21	0.41
1:F:24:ALA:HB2	1:F:229:LYS:HG2	2.03	0.41
1:F:300:VAL:O	1:F:304:ASN:ND2	2.54	0.41
1:F:491:ILE:O	1:F:495:VAL:HG23	2.20	0.41
3:L:80:HIS:HA	3:L:81:PRO:HA	1.81	0.41
1:F:183:LEU:HD23	1:F:183:LEU:HA	1.93	0.40
1:F:356:GLY:HA2	1:F:467:ILE:HG23	2.02	0.40
1:F:84:ASP:OD1	1:F:491:ILE:N	2.54	0.40
2:H:86:THR:HG22	2:H:87:THR:N	2.36	0.40
1:F:89:LEU:HB2	1:F:227:TYR:CD1	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:150:THR:HA	1:F:153:THR:HG22	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	F	340/511 (66%)	326 (96%)	14 (4%)	27	60
2	H	103/194 (53%)	97 (94%)	6 (6%)	18	51
3	L	91/191 (48%)	88 (97%)	3 (3%)	33	65
All	All	534/896 (60%)	511 (96%)	23 (4%)	27	59

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	28	LEU
1	F	42	TRP
1	F	167	ARG
1	F	215	SER
1	F	327	ILE
1	F	385	ILE
1	F	473	ASP
1	F	477	THR
1	F	484	VAL
1	F	505	LEU
1	F	507	HIS

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Mol	Chain	Res	Type
1	F	522	LEU
1	F	527	SER
1	F	545	THR
2	H	17	THR
2	H	28	SER
2	H	67	ILE
2	H	79	TYR
2	H	80	LEU
2	H	115	THR
3	L	73	THR
3	L	79	ILE
3	L	82	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	86	ASN
1	F	99	GLN
1	F	141	ASN
1	F	174	ASN
1	F	304	ASN
1	F	481	GLN
1	F	483	ASN
1	F	496	GLN
1	F	516	ASN
2	H	5	GLN
2	H	16	GLN
2	H	76	ASN
2	H	77	HIS
2	H	81	GLN
2	H	83	ASN
2	H	98	GLN
3	L	17	GLN
3	L	42	GLN
3	L	78	ASN

5.3.3 RNA ⓘ

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.

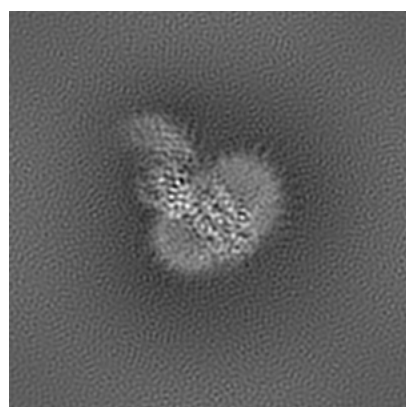
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21539. These allow visual inspection of the internal detail of the map and identification of artifacts.

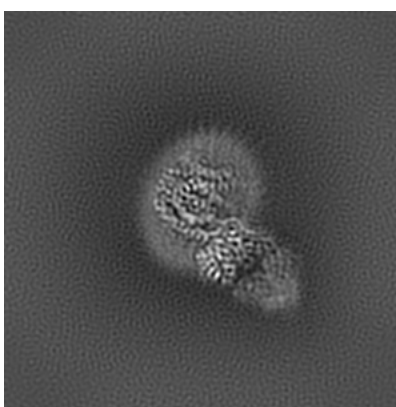
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

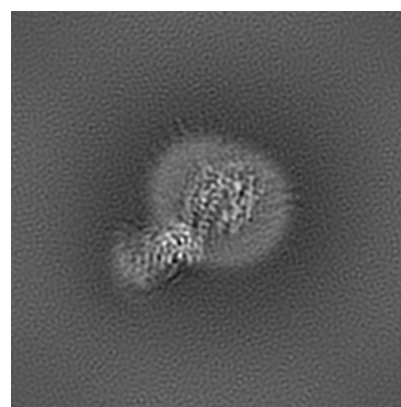
6.1.1 Primary map



X



Y

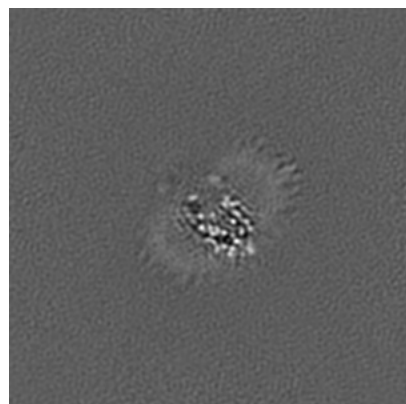


Z

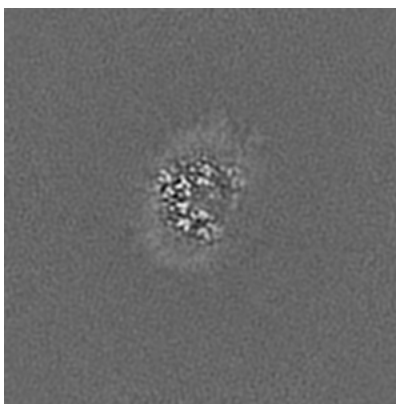
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

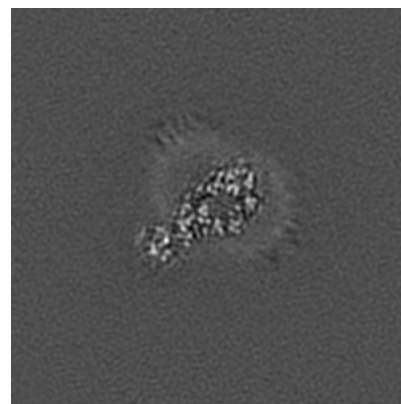
6.2.1 Primary map



X Index: 150



Y Index: 150

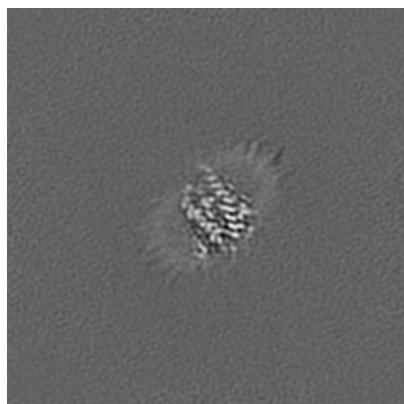


Z Index: 150

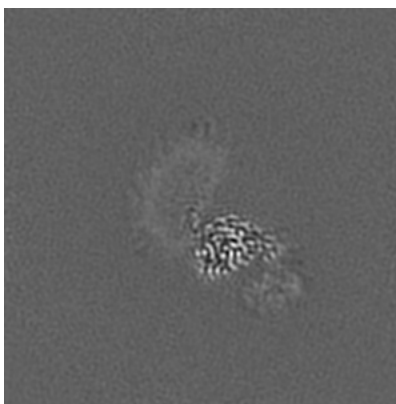
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

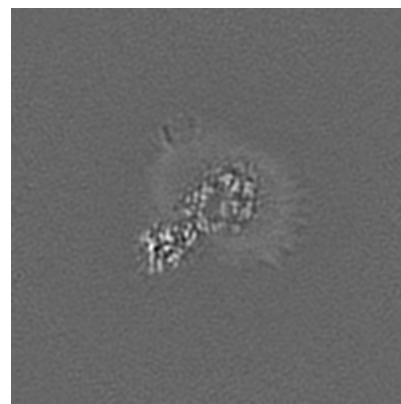
6.3.1 Primary map



X Index: 168



Y Index: 126

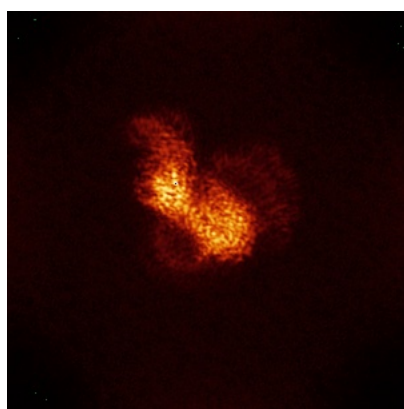


Z Index: 155

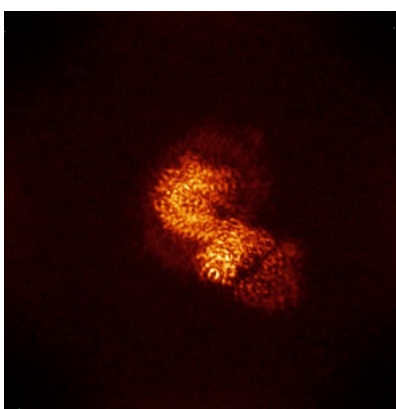
The images above show the largest variance slices of the map in three orthogonal directions.

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

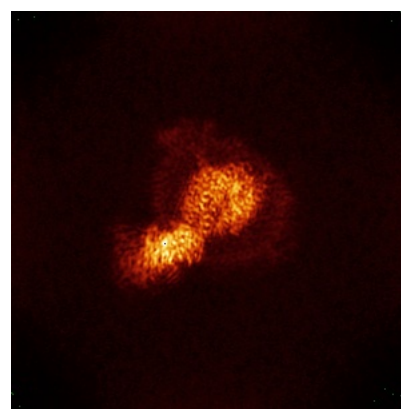
6.4.1 Primary map



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

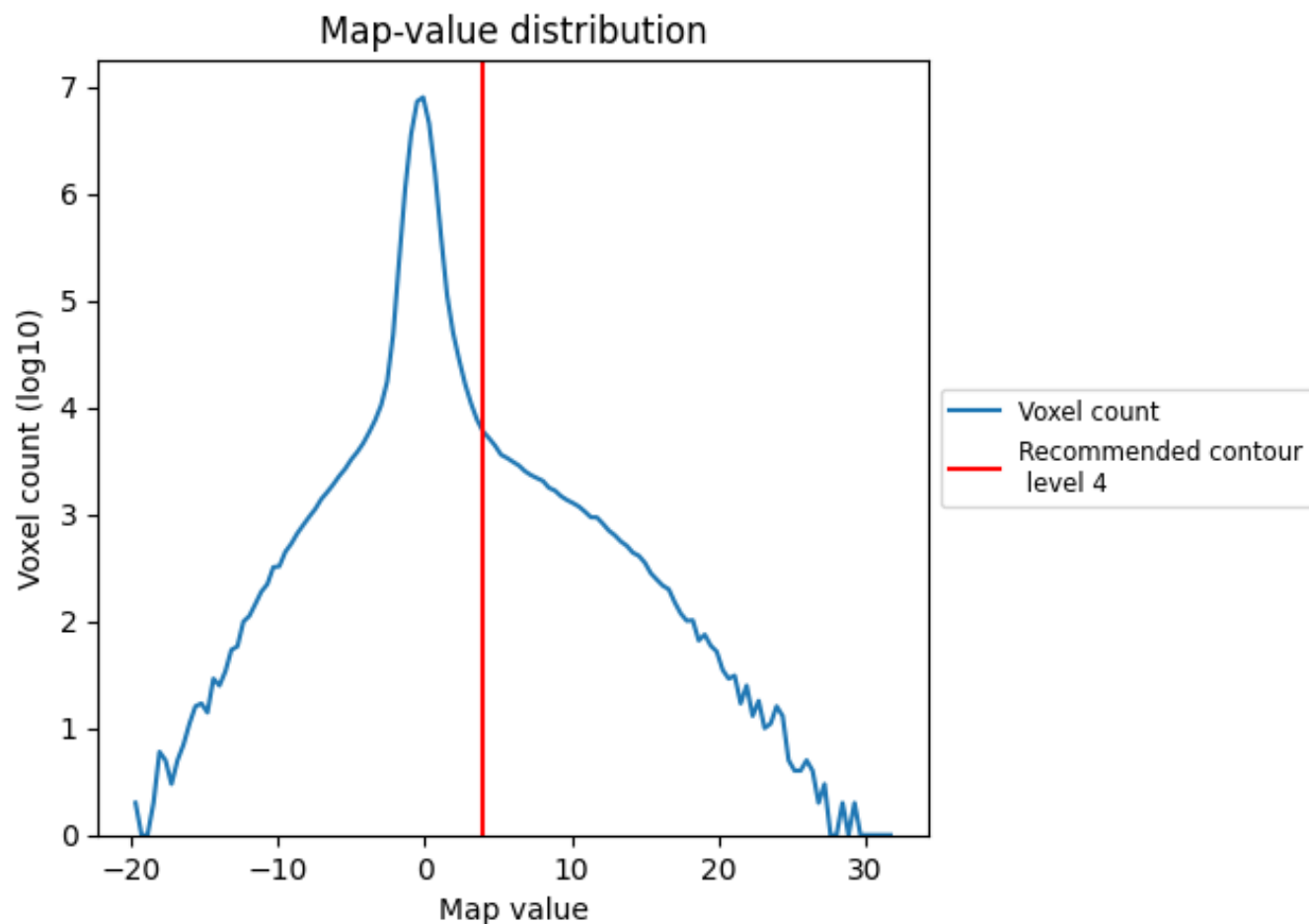
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

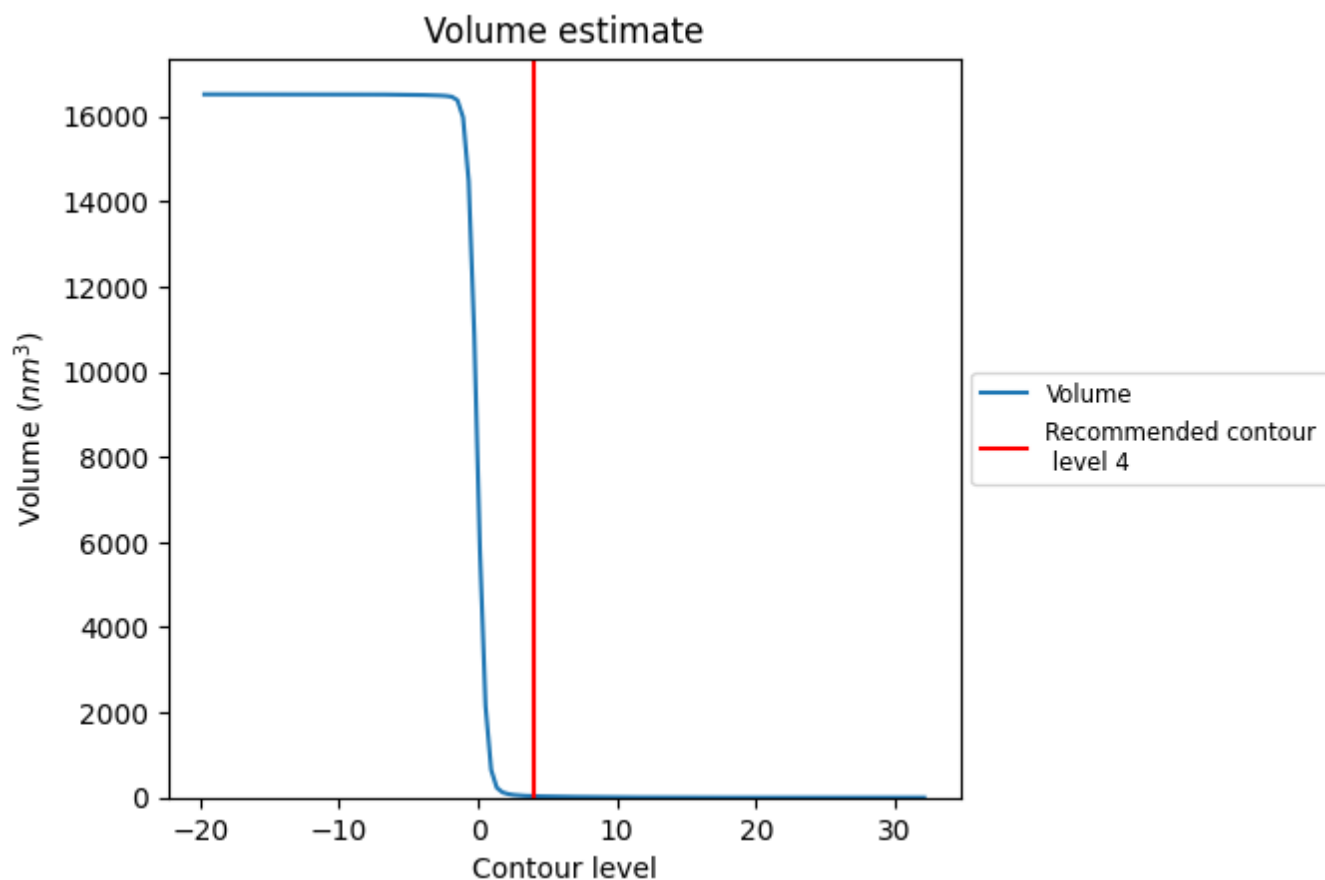
This section contains the results of statistical analysis of the map.

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.

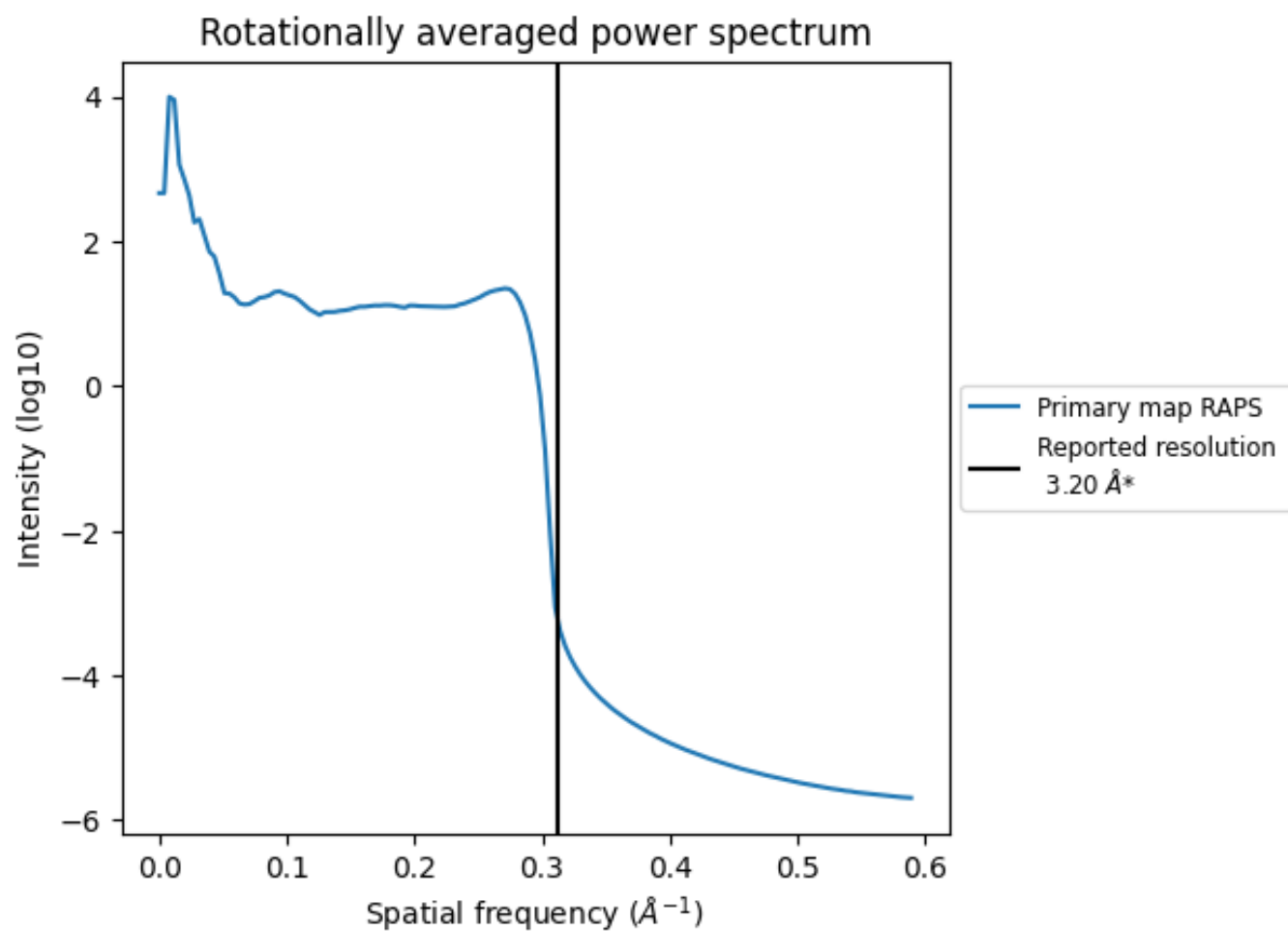
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 34 nm^3 ; this corresponds to an approximate mass of 30 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 0.312 Å⁻¹

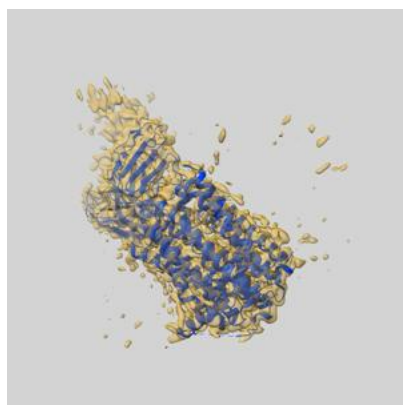
8 Fourier-Shell correlation

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

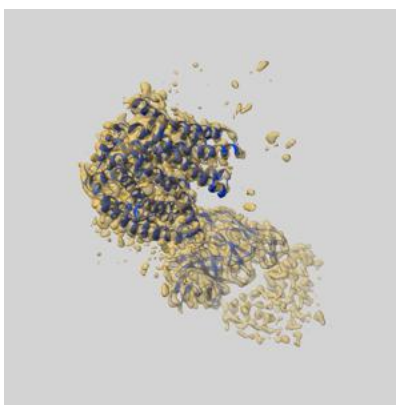
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21539 and PDB model 6W4S. Per-residue inclusion information can be found in section 3 on page 5.

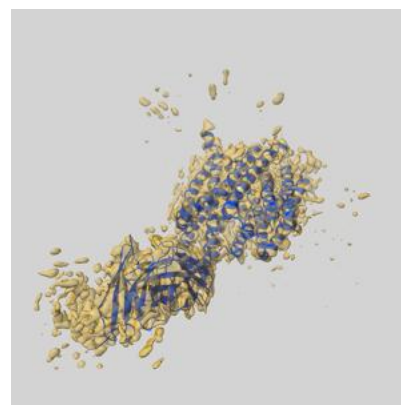
9.1 Map-model overlay [i](#)



X



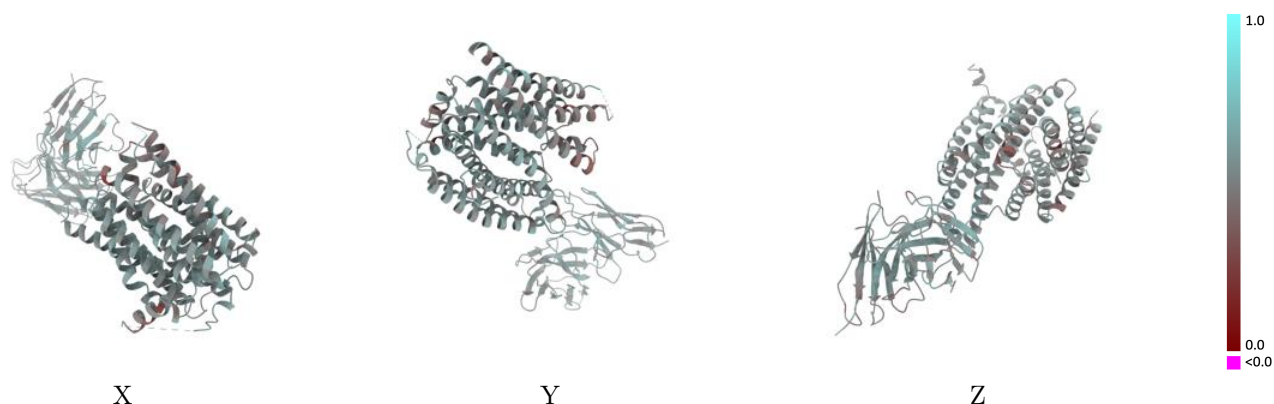
Y



Z

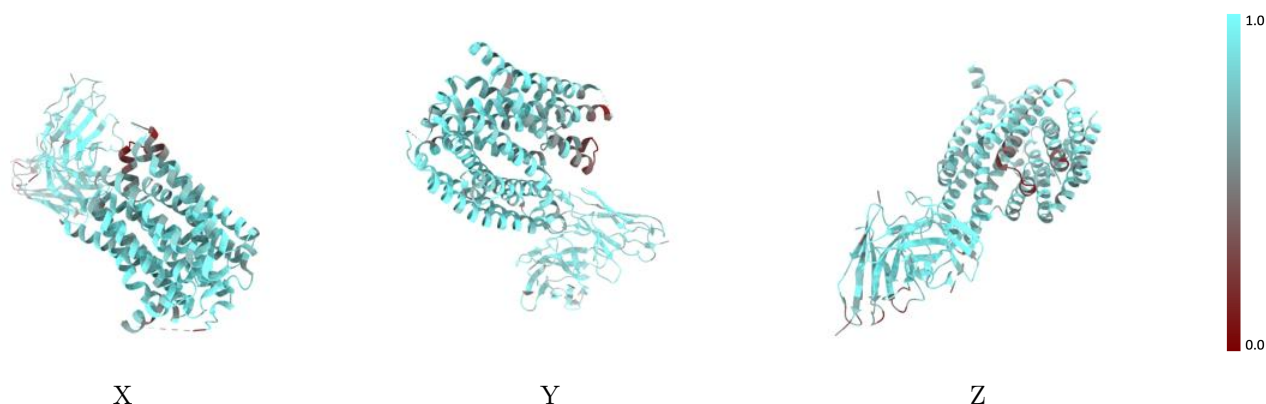
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



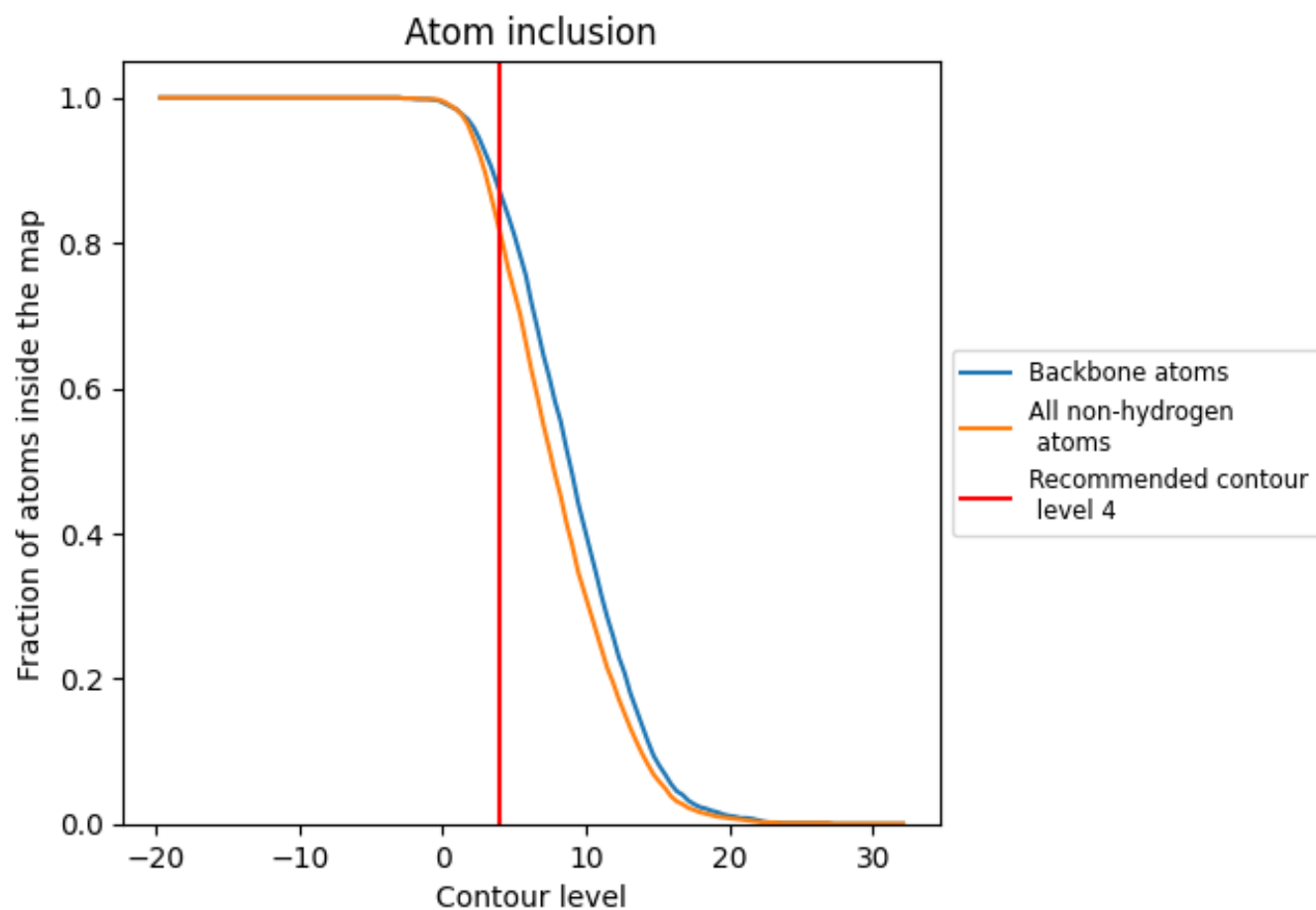
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 81% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8130	0.5250
F	0.8130	0.5230
H	0.7860	0.5220
L	0.8470	0.5380

