



Full wwPDB EM Validation Report ⓘ

Nov 15, 2022 – 12:15 AM EST

PDB ID : 6W4S
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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

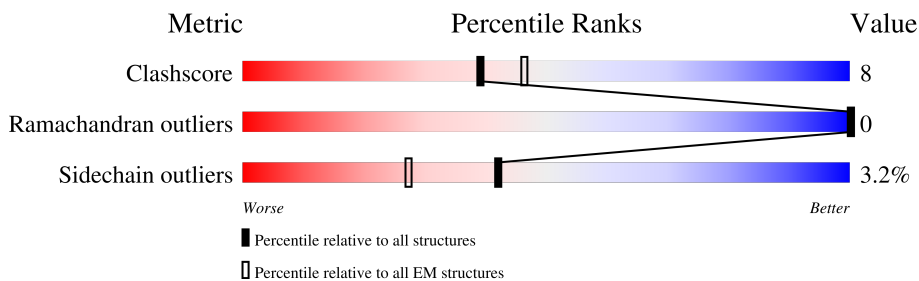
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 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)
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	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
			Total	C	N	O	S		
1	F	421	3216	2119	522	552	23	0	0

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.

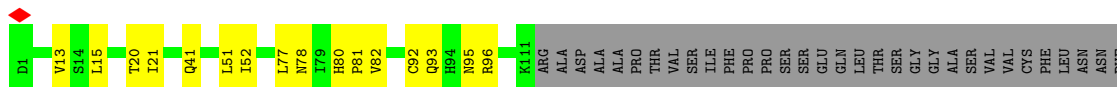
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	H	118	926	587	149	187	3	0	0

- Molecule 3 is a protein called Fab45D8 Light Chain.

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

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

● Molecule 3: Fab45D8 Light Chain



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

THR
SER
THR
THR
PRO
ILE
VAL
LYS
SER
PHE
ASN
ARG
ASN
GLU
CYS

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	4.0	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	0.28	0/3283	0.42	0/4471
2	H	0.34	0/951	0.49	0/1300
3	L	0.31	0/867	0.47	0/1181
All	All	0.30	0/5101	0.44	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	52	0
2	H	926	0	868	18	0
3	L	844	0	813	9	0
All	All	4986	0	5012	78	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 (78) 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
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
1:F:122:THR:OG1	3:L:96:ARG:O	2.18	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: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: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
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: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
2:H:19:SER:O	2:H:19:SER:OG	2.33	0.47
1:F:360:PHE:HB2	1:F:471:SER:HB2	1.96	0.46
2:H:117:SER:OG	2:H:118:SER:N	2.48	0.46
1:F:161:VAL:HG11	1:F:233:LEU:HD13	1.99	0.45
1:F:67:VAL:O	1:F:71:SER:OG	2.25	0.45
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
2:H:67:ILE:HD11	2:H:69:ILE:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
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](#)

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	F	415/605 (69%)	397 (96%)	18 (4%)	0	100	100
2	H	116/220 (53%)	107 (92%)	9 (8%)	0	100	100
3	L	109/218 (50%)	100 (92%)	9 (8%)	0	100	100
All	All	640/1043 (61%)	604 (94%)	36 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	345/511 (68%)	335 (97%)	10 (3%)	42	74
2	H	103/194 (53%)	97 (94%)	6 (6%)	20	55
3	L	91/191 (48%)	90 (99%)	1 (1%)	73	88
All	All	539/896 (60%)	522 (97%)	17 (3%)	42	71

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	42	TRP
1	F	114	PHE
1	F	124	TYR
1	F	215	SER
1	F	364	ARG

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Mol	Chain	Res	Type
1	F	473	ASP
1	F	507	HIS
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	92	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) 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	496	GLN
1	F	516	ASN
2	H	16	GLN
2	H	76	ASN
2	H	77	HIS
2	H	81	GLN
3	L	42	GLN
3	L	78	ASN

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 monosaccharides 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.

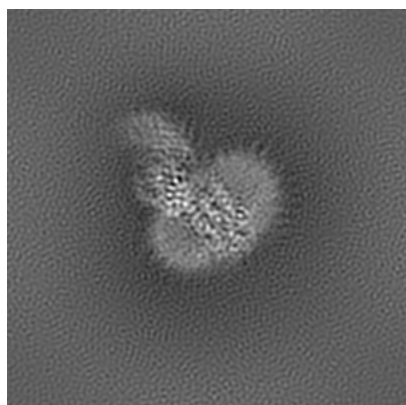
6 Map visualisation [i](#)

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.

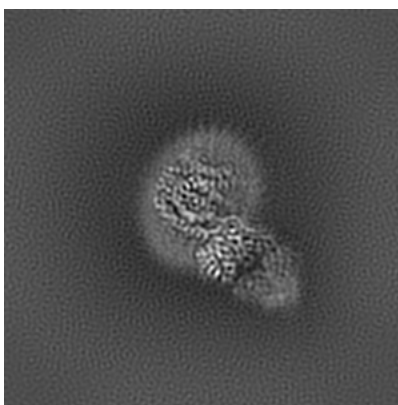
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

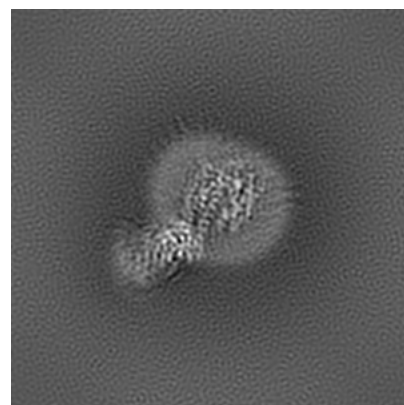
6.1.1 Primary map



X



Y

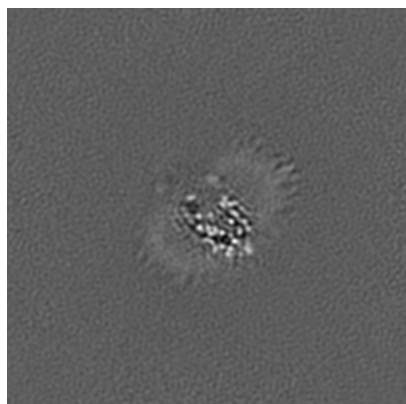


Z

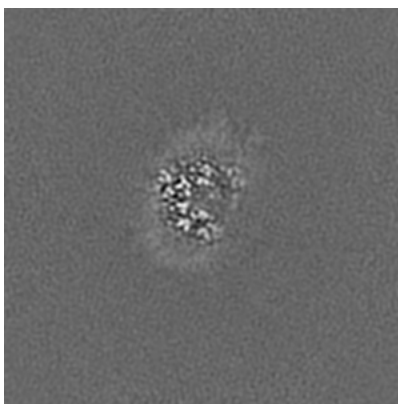
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

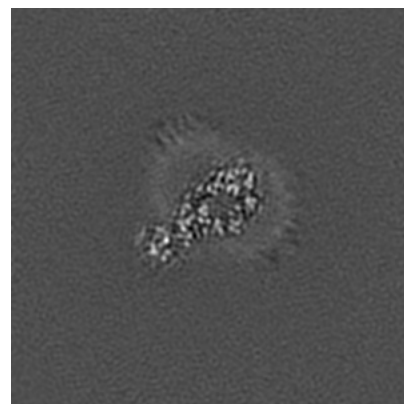
6.2.1 Primary map



X Index: 150



Y Index: 150

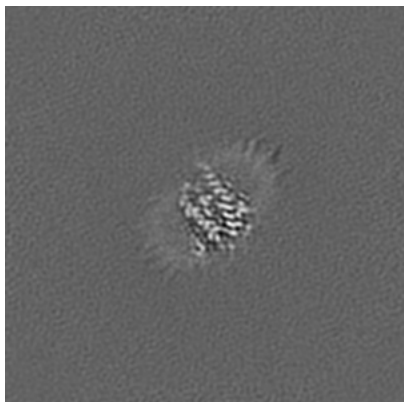


Z Index: 150

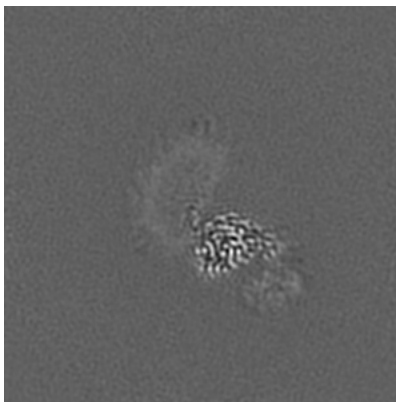
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

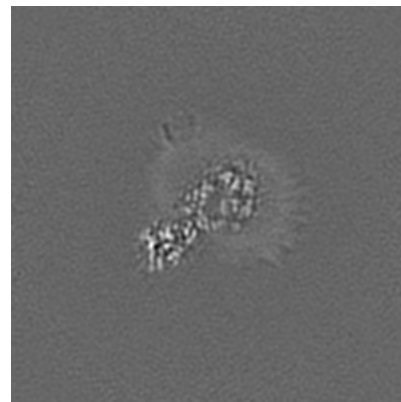
6.3.1 Primary map



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 surface views [i](#)

6.4.1 Primary map



X



Y



Z

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.

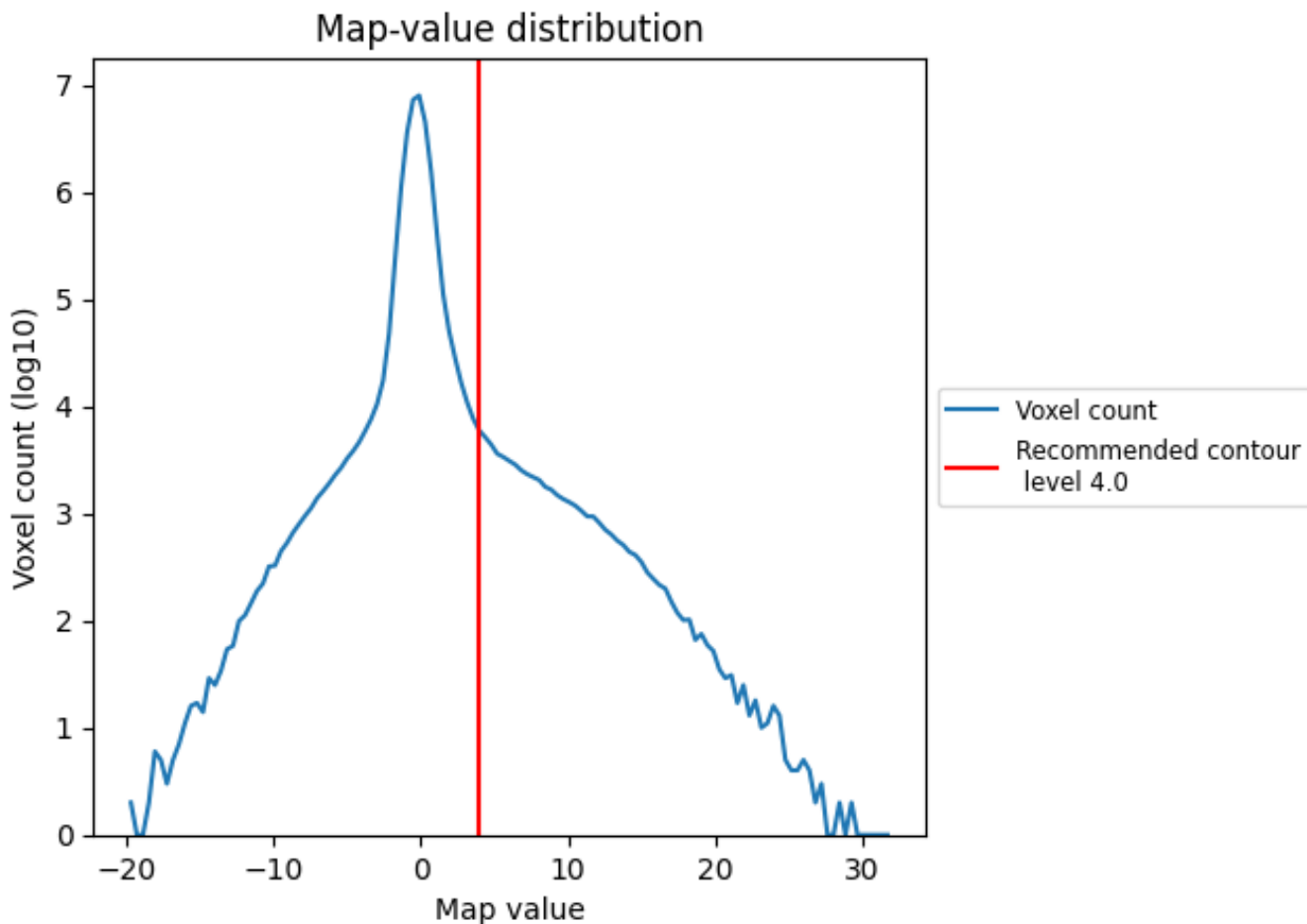
6.5 Mask visualisation

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

7 Map analysis [i](#)

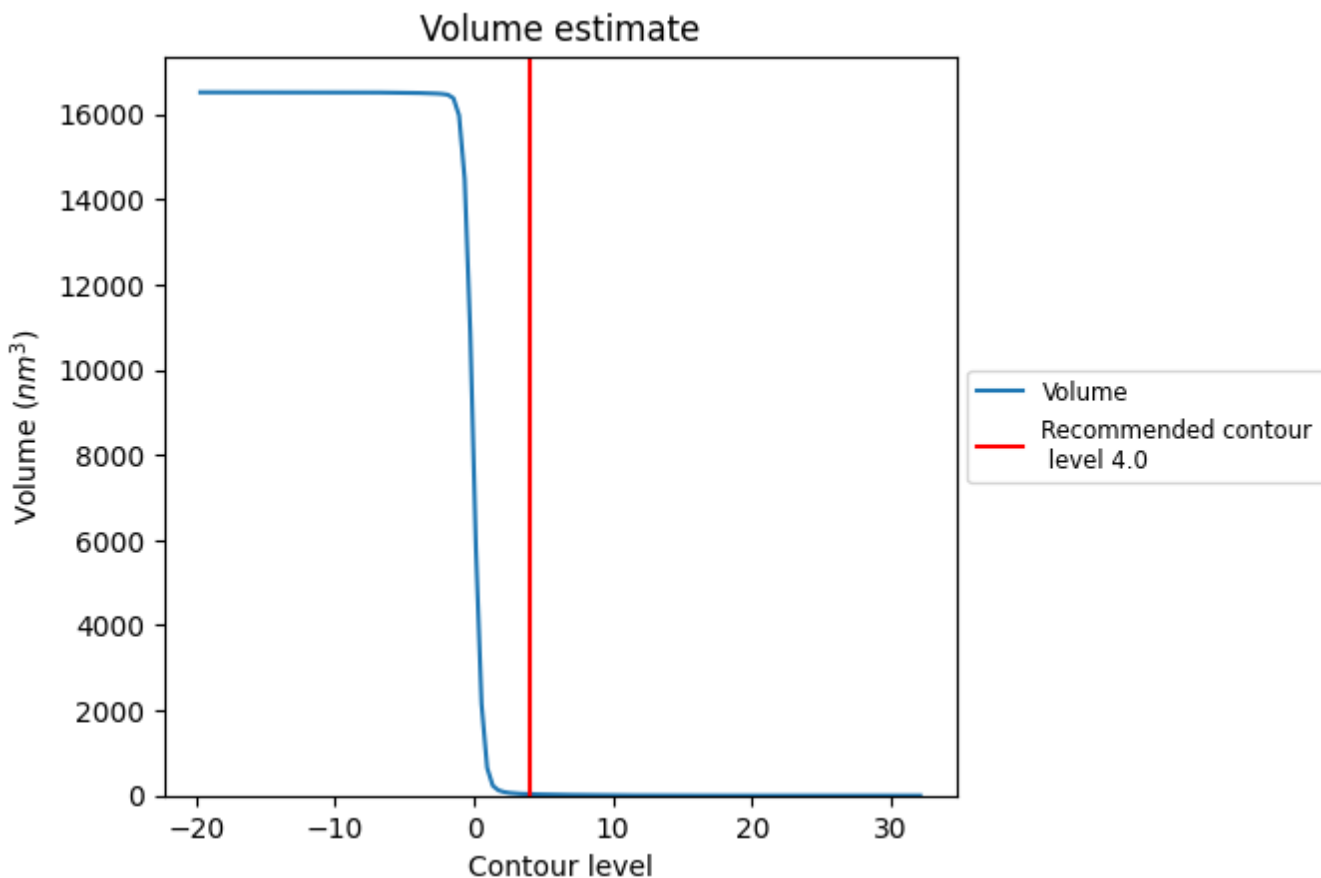
This section contains the results of statistical analysis of the map.

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.

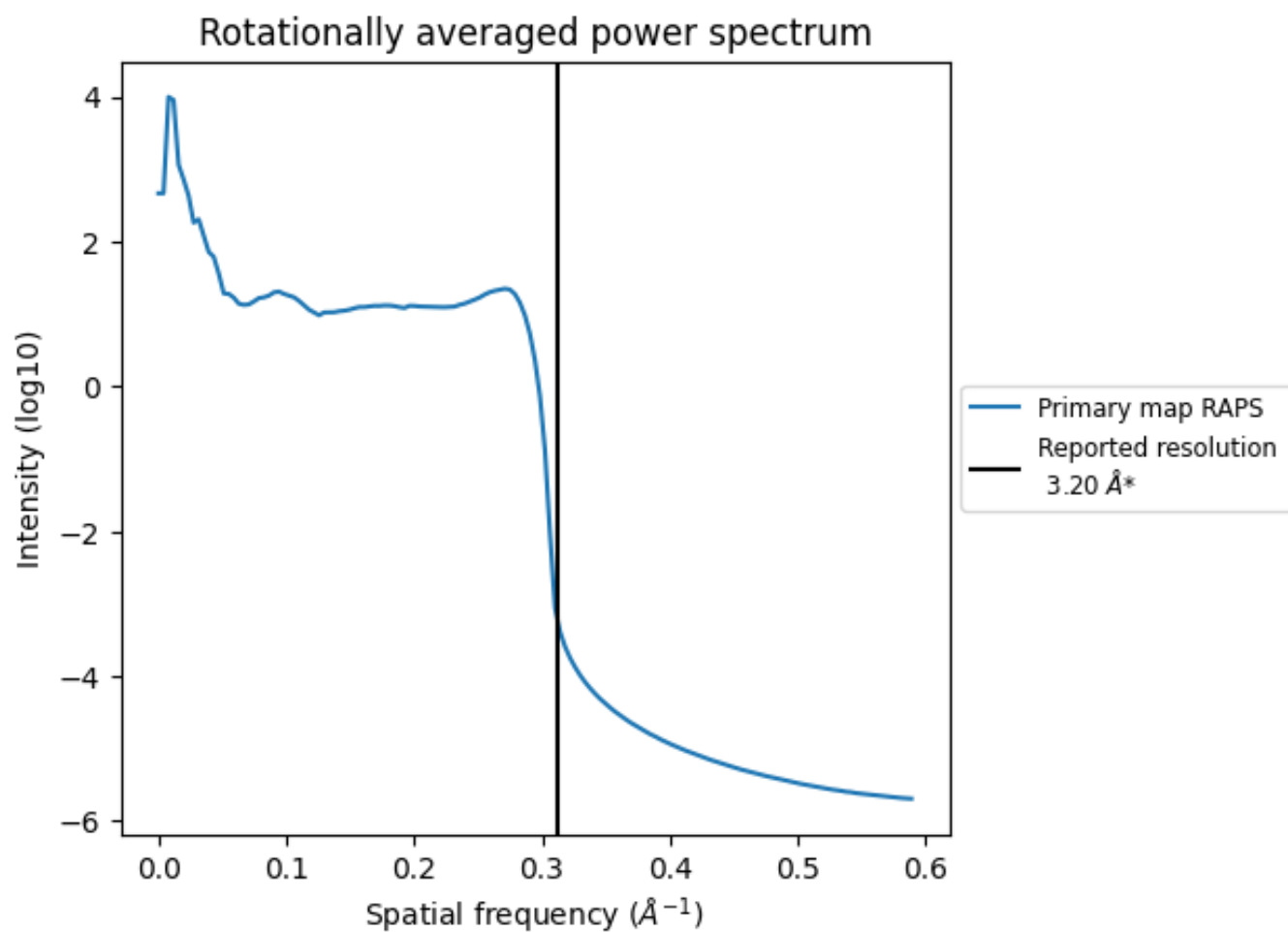
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 34 nm³; 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.312\AA^{-1}

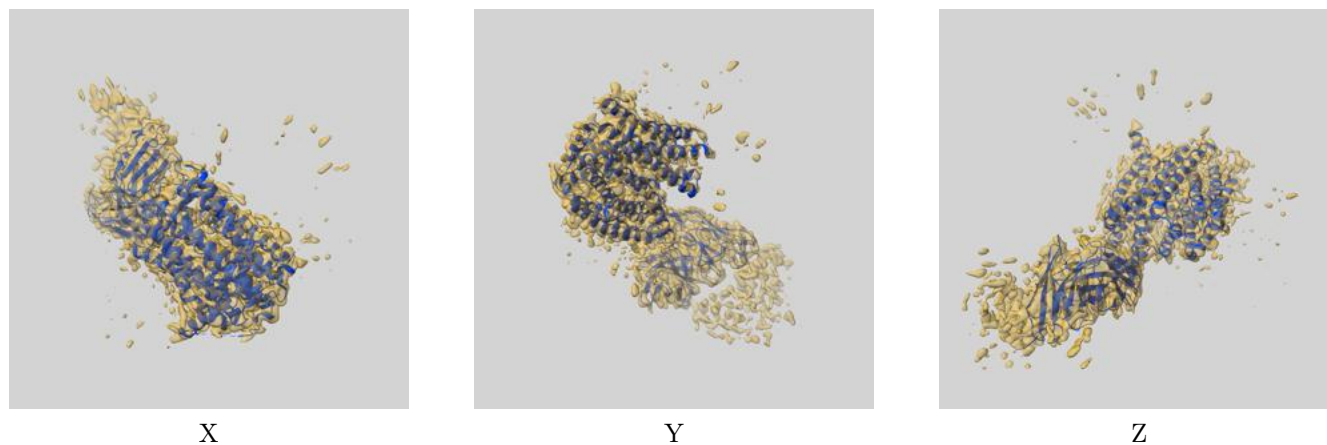
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

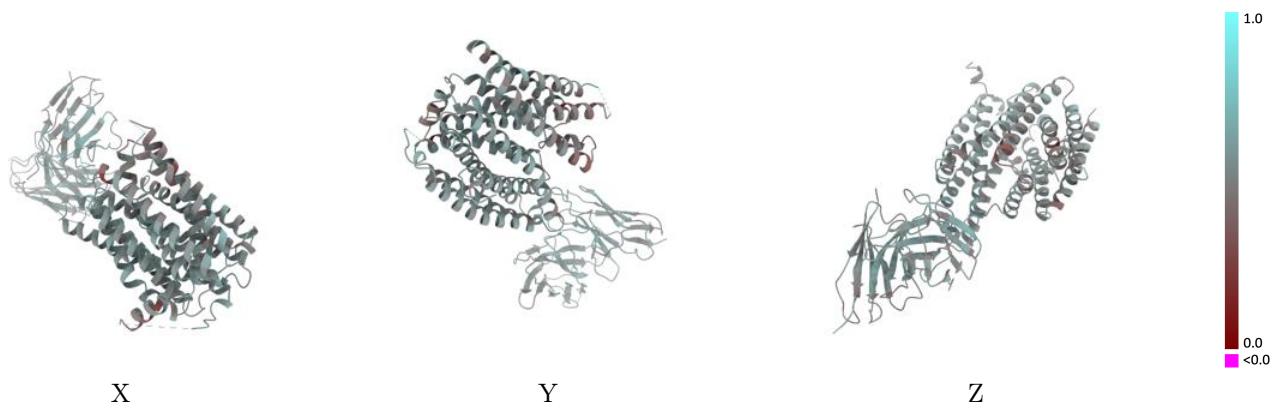
This section contains information regarding the fit between EMDB map EMD-21539 and PDB model 6W4S. Per-residue inclusion information can be found in section 3 on page 5.

9.1 Map-model overlay [i](#)



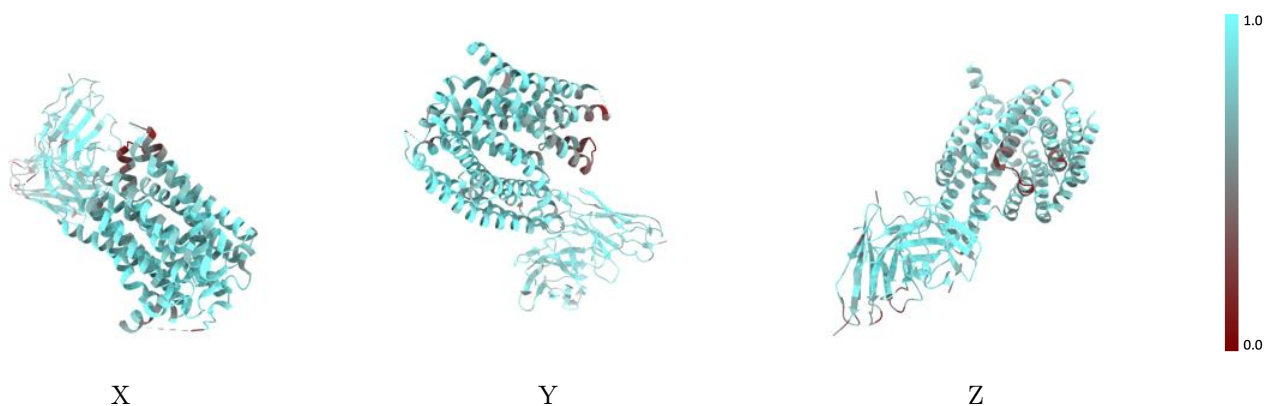
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



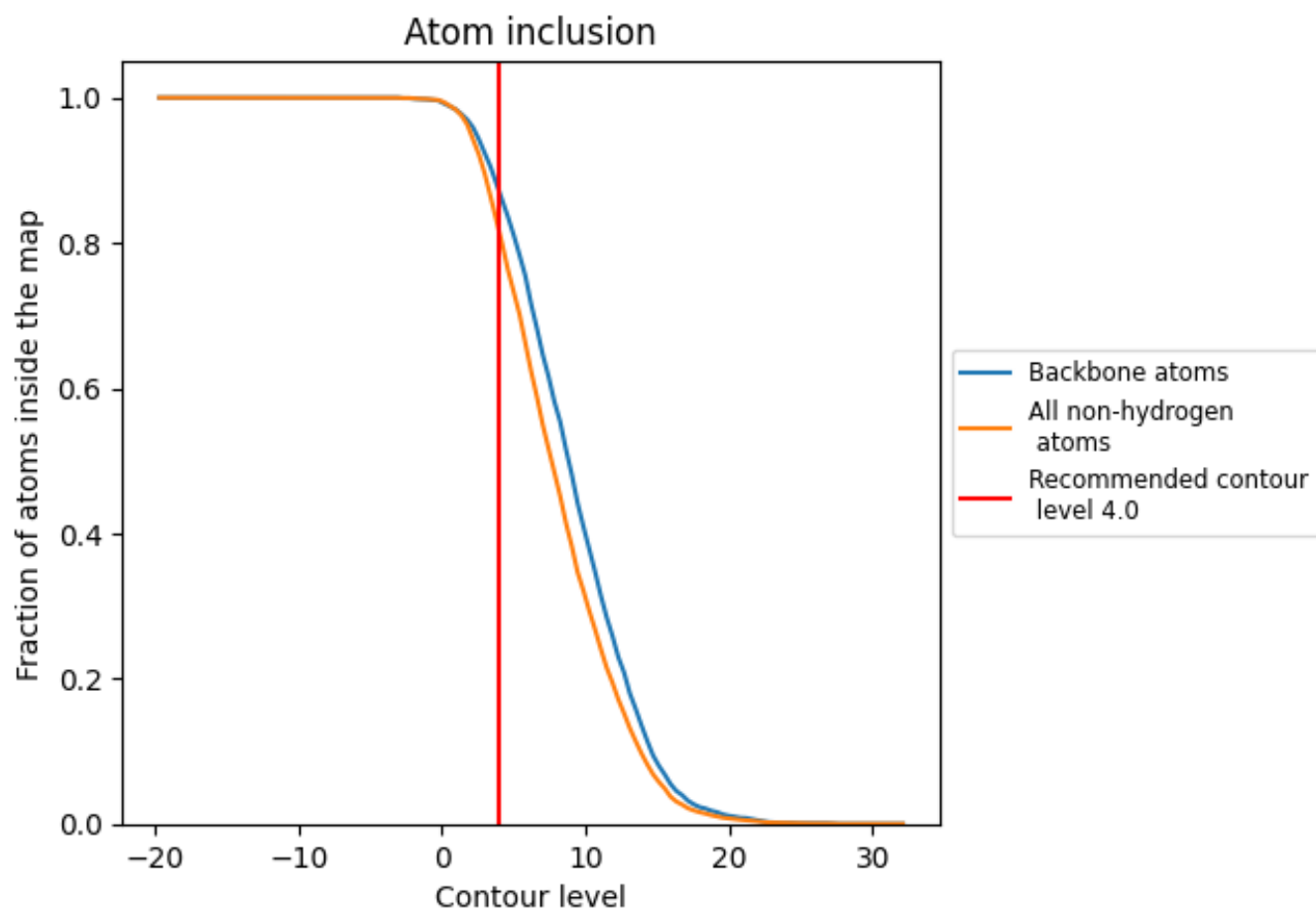
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.0).









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 [i](#)

The table lists the average atom inclusion at the recommended contour level (4.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8134	 0.5250
F	 0.8126	 0.5230
H	 0.7856	 0.5220
L	 0.8466	 0.5380

