wwPDB EM Validation Summary Report

Nov 16, 2022 – 12:52 PM JST

PDB ID	:	6LXW
EMDB ID	:	EMD-30008
Title	:	Cryo-EM structure of human secretory immunoglobulin A in complex with the N-terminal domain of SpsA
Authors	:	Wang, Y.; Wang, G.; Li, Y.; Xiao, J.
Deposited on	:	2020-02-12
Resolution	:	3.27 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

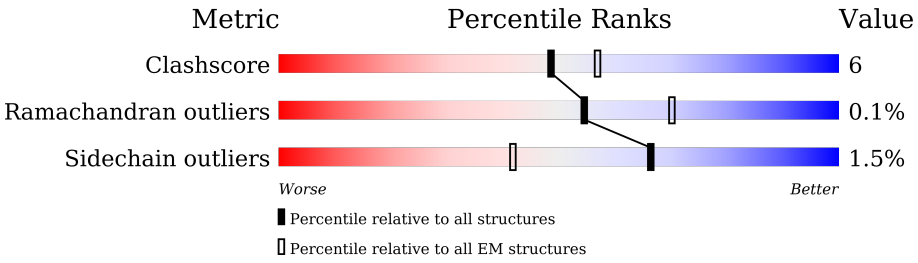
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.27 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 <=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	291	63% 14% 23%
1	B	291	60% 15% 25%
1	C	291	8% 63% 12% 24%
1	D	291	67% 11% 21%
2	J	167	68% 8% 23%
3	P	573	72% 16% 10%
4	S	317	17% 81%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 12299 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 Interleukin-2,Immunoglobulin heavy constant alpha 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	225	Total	C	N	O	S	0	0
			1707	1076	291	330	10		
1	B	218	Total	C	N	O	S	0	0
			1660	1048	286	317	9		
1	C	221	Total	C	N	O	S	0	0
			1682	1062	290	321	9		
1	D	229	Total	C	N	O	S	0	0
			1740	1097	298	335	10		

There are 152 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	203	ARG	-	linker	UNP P60568
A	204	ILE	-	linker	UNP P60568
A	205	HIS	-	linker	UNP P60568
A	206	MET	-	linker	UNP P60568
A	207	SER	-	linker	UNP P60568
A	208	ALA	-	linker	UNP P60568
A	209	TRP	-	linker	UNP P60568
A	210	SER	-	linker	UNP P60568
A	211	HIS	-	linker	UNP P60568
A	212	PRO	-	linker	UNP P60568
A	213	GLN	-	linker	UNP P60568
A	214	PHE	-	linker	UNP P60568
A	215	GLU	-	linker	UNP P60568
A	216	LYS	-	linker	UNP P60568
A	217	GLY	-	linker	UNP P60568
A	218	GLY	-	linker	UNP P60568
A	219	GLY	-	linker	UNP P60568
A	220	SER	-	linker	UNP P60568
A	221	GLY	-	linker	UNP P60568
A	222	GLY	-	linker	UNP P60568
A	223	GLY	-	linker	UNP P60568
A	224	SER	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
A	225	GLY	-	linker	UNP P60568
A	226	GLY	-	linker	UNP P60568
A	227	SER	-	linker	UNP P60568
A	228	ALA	-	linker	UNP P60568
A	229	TRP	-	linker	UNP P60568
A	230	SER	-	linker	UNP P60568
A	231	HIS	-	linker	UNP P60568
A	232	PRO	-	linker	UNP P60568
A	233	GLN	-	linker	UNP P60568
A	234	PHE	-	linker	UNP P60568
A	235	GLU	-	linker	UNP P60568
A	236	LYS	-	linker	UNP P60568
A	237	ILE	-	linker	UNP P60568
A	238	ASP	-	linker	UNP P60568
A	239	THR	-	linker	UNP P60568
A	240	THR	-	linker	UNP P60568
B	203	ARG	-	linker	UNP P60568
B	204	ILE	-	linker	UNP P60568
B	205	HIS	-	linker	UNP P60568
B	206	MET	-	linker	UNP P60568
B	207	SER	-	linker	UNP P60568
B	208	ALA	-	linker	UNP P60568
B	209	TRP	-	linker	UNP P60568
B	210	SER	-	linker	UNP P60568
B	211	HIS	-	linker	UNP P60568
B	212	PRO	-	linker	UNP P60568
B	213	GLN	-	linker	UNP P60568
B	214	PHE	-	linker	UNP P60568
B	215	GLU	-	linker	UNP P60568
B	216	LYS	-	linker	UNP P60568
B	217	GLY	-	linker	UNP P60568
B	218	GLY	-	linker	UNP P60568
B	219	GLY	-	linker	UNP P60568
B	220	SER	-	linker	UNP P60568
B	221	GLY	-	linker	UNP P60568
B	222	GLY	-	linker	UNP P60568
B	223	GLY	-	linker	UNP P60568
B	224	SER	-	linker	UNP P60568
B	225	GLY	-	linker	UNP P60568
B	226	GLY	-	linker	UNP P60568
B	227	SER	-	linker	UNP P60568
B	228	ALA	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
B	229	TRP	-	linker	UNP P60568
B	230	SER	-	linker	UNP P60568
B	231	HIS	-	linker	UNP P60568
B	232	PRO	-	linker	UNP P60568
B	233	GLN	-	linker	UNP P60568
B	234	PHE	-	linker	UNP P60568
B	235	GLU	-	linker	UNP P60568
B	236	LYS	-	linker	UNP P60568
B	237	ILE	-	linker	UNP P60568
B	238	ASP	-	linker	UNP P60568
B	239	THR	-	linker	UNP P60568
B	240	THR	-	linker	UNP P60568
C	203	ARG	-	linker	UNP P60568
C	204	ILE	-	linker	UNP P60568
C	205	HIS	-	linker	UNP P60568
C	206	MET	-	linker	UNP P60568
C	207	SER	-	linker	UNP P60568
C	208	ALA	-	linker	UNP P60568
C	209	TRP	-	linker	UNP P60568
C	210	SER	-	linker	UNP P60568
C	211	HIS	-	linker	UNP P60568
C	212	PRO	-	linker	UNP P60568
C	213	GLN	-	linker	UNP P60568
C	214	PHE	-	linker	UNP P60568
C	215	GLU	-	linker	UNP P60568
C	216	LYS	-	linker	UNP P60568
C	217	GLY	-	linker	UNP P60568
C	218	GLY	-	linker	UNP P60568
C	219	GLY	-	linker	UNP P60568
C	220	SER	-	linker	UNP P60568
C	221	GLY	-	linker	UNP P60568
C	222	GLY	-	linker	UNP P60568
C	223	GLY	-	linker	UNP P60568
C	224	SER	-	linker	UNP P60568
C	225	GLY	-	linker	UNP P60568
C	226	GLY	-	linker	UNP P60568
C	227	SER	-	linker	UNP P60568
C	228	ALA	-	linker	UNP P60568
C	229	TRP	-	linker	UNP P60568
C	230	SER	-	linker	UNP P60568
C	231	HIS	-	linker	UNP P60568
C	232	PRO	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
C	233	GLN	-	linker	UNP P60568
C	234	PHE	-	linker	UNP P60568
C	235	GLU	-	linker	UNP P60568
C	236	LYS	-	linker	UNP P60568
C	237	ILE	-	linker	UNP P60568
C	238	ASP	-	linker	UNP P60568
C	239	THR	-	linker	UNP P60568
C	240	THR	-	linker	UNP P60568
D	203	ARG	-	linker	UNP P60568
D	204	ILE	-	linker	UNP P60568
D	205	HIS	-	linker	UNP P60568
D	206	MET	-	linker	UNP P60568
D	207	SER	-	linker	UNP P60568
D	208	ALA	-	linker	UNP P60568
D	209	TRP	-	linker	UNP P60568
D	210	SER	-	linker	UNP P60568
D	211	HIS	-	linker	UNP P60568
D	212	PRO	-	linker	UNP P60568
D	213	GLN	-	linker	UNP P60568
D	214	PHE	-	linker	UNP P60568
D	215	GLU	-	linker	UNP P60568
D	216	LYS	-	linker	UNP P60568
D	217	GLY	-	linker	UNP P60568
D	218	GLY	-	linker	UNP P60568
D	219	GLY	-	linker	UNP P60568
D	220	SER	-	linker	UNP P60568
D	221	GLY	-	linker	UNP P60568
D	222	GLY	-	linker	UNP P60568
D	223	GLY	-	linker	UNP P60568
D	224	SER	-	linker	UNP P60568
D	225	GLY	-	linker	UNP P60568
D	226	GLY	-	linker	UNP P60568
D	227	SER	-	linker	UNP P60568
D	228	ALA	-	linker	UNP P60568
D	229	TRP	-	linker	UNP P60568
D	230	SER	-	linker	UNP P60568
D	231	HIS	-	linker	UNP P60568
D	232	PRO	-	linker	UNP P60568
D	233	GLN	-	linker	UNP P60568
D	234	PHE	-	linker	UNP P60568
D	235	GLU	-	linker	UNP P60568
D	236	LYS	-	linker	UNP P60568

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Chain	Residue	Modelled	Actual	Comment	Reference
D	237	ILE	-	linker	UNP P60568
D	238	ASP	-	linker	UNP P60568
D	239	THR	-	linker	UNP P60568
D	240	THR	-	linker	UNP P60568

- Molecule 2 is a protein called Immunoglobulin J chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	J	128	Total	C	N	O	S	0	0
			1016	626	177	204	9		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	137	HIS	-	expression tag	UNP P01591
J	138	HIS	-	expression tag	UNP P01591
J	139	HIS	-	expression tag	UNP P01591
J	140	HIS	-	expression tag	UNP P01591
J	141	HIS	-	expression tag	UNP P01591
J	142	HIS	-	expression tag	UNP P01591
J	143	HIS	-	expression tag	UNP P01591
J	144	HIS	-	expression tag	UNP P01591

- Molecule 3 is a protein called Polymeric immunoglobulin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	P	513	Total	C	N	O	S	0	0
			3988	2519	693	756	20		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	548	HIS	-	expression tag	UNP P01833
P	549	HIS	-	expression tag	UNP P01833
P	550	HIS	-	expression tag	UNP P01833
P	551	HIS	-	expression tag	UNP P01833
P	552	HIS	-	expression tag	UNP P01833
P	553	HIS	-	expression tag	UNP P01833
P	554	HIS	-	expression tag	UNP P01833
P	555	HIS	-	expression tag	UNP P01833

- Molecule 4 is a protein called SigA binding protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
4	S	61	Total	C	N	O	0	0
			506	312	83	111		

There are 30 discrepancies between the modelled and reference sequences:

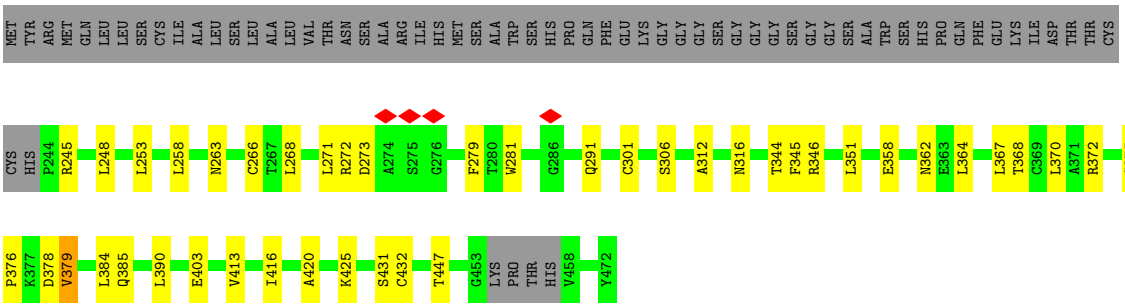
Chain	Residue	Modelled	Actual	Comment	Reference
S	8	MET	-	initiating methionine	UNP O33753
S	9	GLY	-	expression tag	UNP O33753
S	10	SER	-	expression tag	UNP O33753
S	11	HIS	-	expression tag	UNP O33753
S	12	HIS	-	expression tag	UNP O33753
S	13	HIS	-	expression tag	UNP O33753
S	14	HIS	-	expression tag	UNP O33753
S	15	HIS	-	expression tag	UNP O33753
S	16	HIS	-	expression tag	UNP O33753
S	17	HIS	-	expression tag	UNP O33753
S	18	HIS	-	expression tag	UNP O33753
S	19	GLY	-	expression tag	UNP O33753
S	20	SER	-	expression tag	UNP O33753
S	21	ASP	-	expression tag	UNP O33753
S	22	TYR	-	expression tag	UNP O33753
S	23	ASP	-	expression tag	UNP O33753
S	24	ILE	-	expression tag	UNP O33753
S	25	PRO	-	expression tag	UNP O33753
S	26	THR	-	expression tag	UNP O33753
S	27	THR	-	expression tag	UNP O33753
S	28	GLU	-	expression tag	UNP O33753
S	29	ASN	-	expression tag	UNP O33753
S	30	LEU	-	expression tag	UNP O33753
S	31	TYR	-	expression tag	UNP O33753
S	32	PHE	-	expression tag	UNP O33753
S	33	GLN	-	expression tag	UNP O33753
S	34	GLY	-	expression tag	UNP O33753
S	35	SER	-	expression tag	UNP O33753
S	36	GLU	-	expression tag	UNP O33753
S	37	PHE	-	expression tag	UNP O33753

3 Residue-property plots (i)

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.

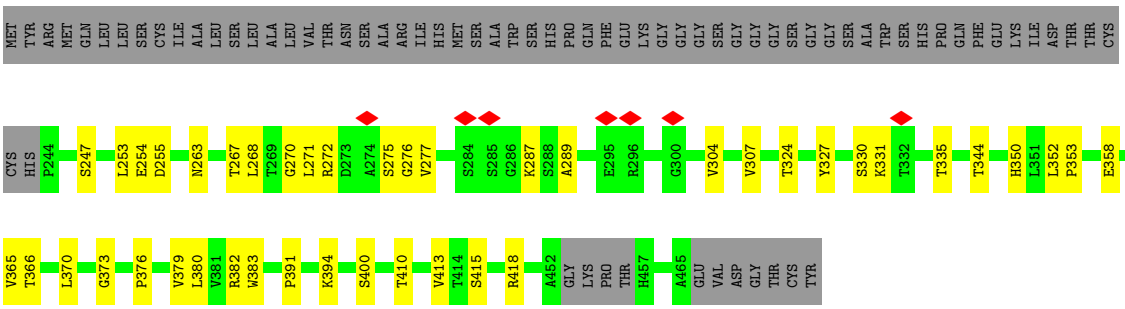
• Molecule 1: Interleukin-2,Immunoglobulin heavy constant alpha 1

Chain A:



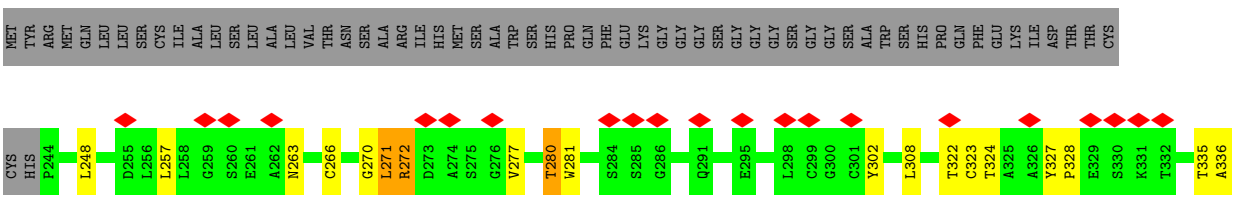
• Molecule 1: Interleukin-2,Immunoglobulin heavy constant alpha 1

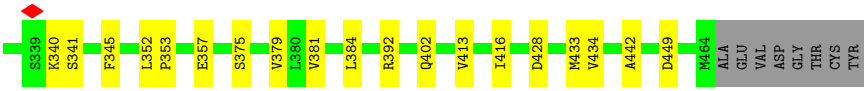
Chain B:



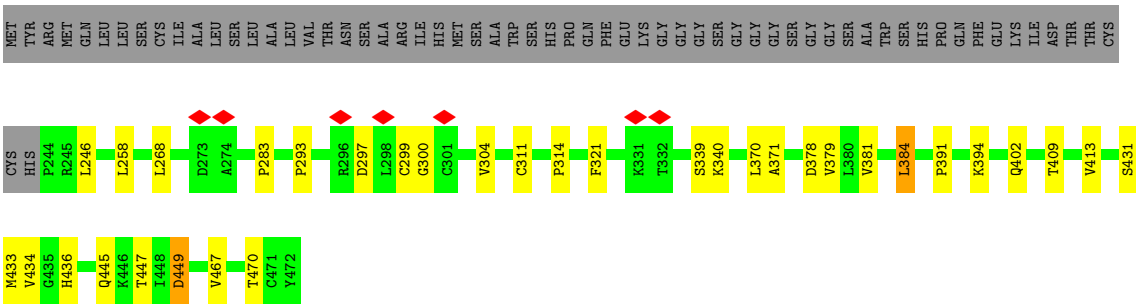
• Molecule 1: Interleukin-2,Immunoglobulin heavy constant alpha 1

Chain C:

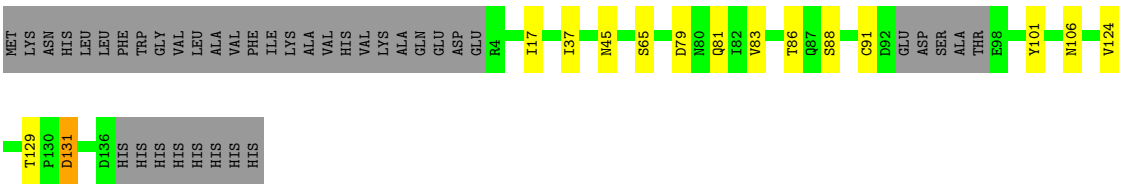




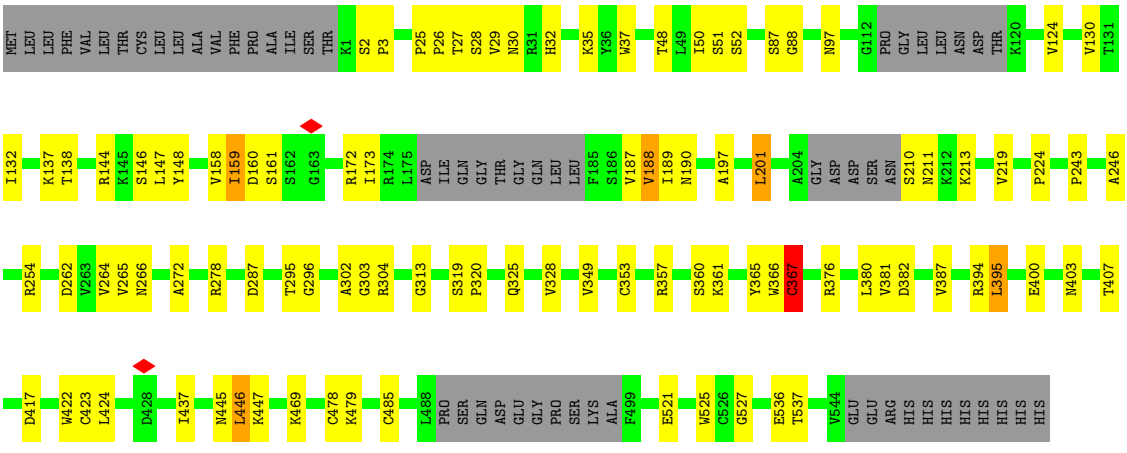
• Molecule 1: Interleukin-2,Immunoglobulin heavy constant alpha 1



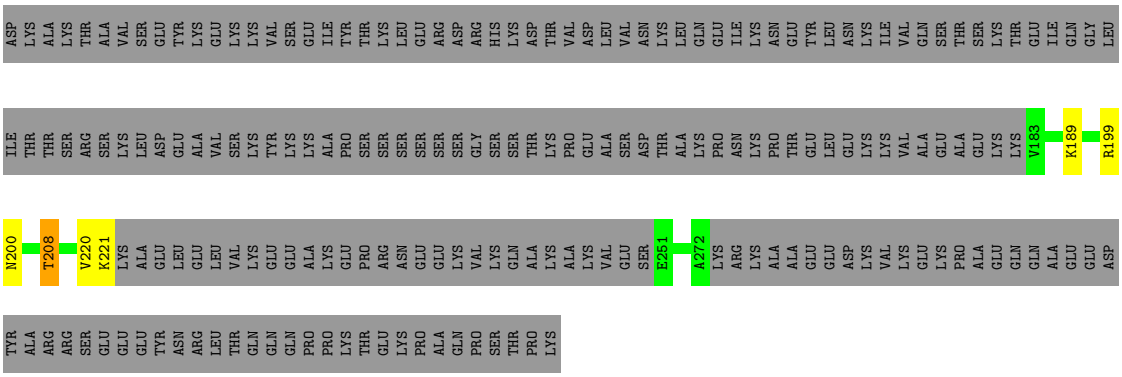
• Molecule 2: Immunoglobulin J chain



• Molecule 3: Polymeric immunoglobulin receptor



• Molecule 4: SigA binding protein


ASP LYS ALA LYS THR ALA VAL SER GLU TYR LYS GLU LYS LYS VAL SER GLU ILE TYR THR LYS LEU GLU ARG ASP ARG HIS LYS ASP THR VAL ASP LEU VAL ASN LYS LEU GLN GLU GLU ILE LYS ASN GLU TYR LEU ASN LYS ILE VAL GLN SER THR SER LYS THR GLU ILE GLN GLY LEU
ILE THR THR SER ARG SER LYS LEU ASP GLU ALA VAL SER LYS TYR LYS LYS ALA PRO SER SER SER SER SER SER GLY SER SER THR LYS PRO GLU ALA SER ASP THR ALA LYS PRO ASN LYS PRO THR GLU LEU GLU LYS LYS VAL ALA GLU ALA GLU LYS LYS V183 K189 R199
N200 T208 V220 K221 LYS ALA GLU LEU GLU LEU VAL LYS GLU GLU ALA LYS GLU PRO ARG ASN GLU GLU LYS VAL LYS GLN ALA LYS ALA LYS VAL GLU SER E251 A272 LYS ARG LYS ALA ALA GLU GLU ASP LYS VAL LYS GLU LYS PRO ALA GLU GLN GLN ALA GLU GLU ASP
TYR ALA ARG ARG SER GLU GLU GLU TYR ASN ARG LEU THR GLN GLN GLN PRO PRO LYS THR GLU LYS PRO ALA GLN PRO SER THR PRO LYS

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	280791	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 ($e^-/Å^2$)	59.74	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.119	Depositor
Minimum map value	-0.086	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.00863	Depositor
Map size (Å)	264.96, 264.96, 264.96	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.82799995, 0.82799995, 0.82799995	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	0.67	0/1747	0.72	1/2384 (0.0%)
1	B	0.58	0/1700	0.69	0/2320
1	C	0.54	1/1724 (0.1%)	0.67	1/2354 (0.0%)
1	D	0.64	0/1783	0.70	1/2435 (0.0%)
2	J	0.66	0/1030	0.72	1/1401 (0.1%)
3	P	0.77	2/4073 (0.0%)	0.71	4/5526 (0.1%)
4	S	0.54	0/508	0.59	0/676
All	All	0.67	3/12565 (0.0%)	0.70	8/17096 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	J	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	P	367	CYS	CB-SG	-6.35	1.71	1.82
3	P	265	VAL	CB-CG2	-6.15	1.40	1.52
1	C	402	GLN	C-N	-5.80	1.20	1.34

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	J	131	ASP	CB-CG-OD1	8.56	126.00	118.30
3	P	446	LEU	CA-CB-CG	6.71	130.72	115.30
1	C	271	LEU	CA-CB-CG	6.65	130.60	115.30
3	P	201	LEU	CA-CB-CG	6.38	129.97	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	384	LEU	CB-CG-CD2	-5.68	101.33	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	273	ASP	Peptide
2	J	79	ASP	Peptide

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	1707	0	1688	25	0
1	B	1660	0	1650	27	0
1	C	1682	0	1676	22	0
1	D	1740	0	1722	17	0
2	J	1016	0	999	8	0
3	P	3988	0	3905	59	0
4	S	506	0	504	5	0
All	All	12299	0	12144	151	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.

The worst 5 of 151 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:C:263:ASN:HA	1:C:308:LEU:O	1.74	0.88
1:B:383:TRP:HE1	1:B:415:SER:HG	1.30	0.80
1:B:277:VAL:HG11	1:B:304:VAL:HG21	1.77	0.67
3:P:224:PRO:HG3	3:P:304:ARG:HH22	1.62	0.63
1:B:324:THR:HG23	1:B:335:THR:HG22	1.80	0.63

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	221/291 (76%)	184 (83%)	37 (17%)	0	100 100
1	B	214/291 (74%)	183 (86%)	31 (14%)	0	100 100
1	C	219/291 (75%)	190 (87%)	29 (13%)	0	100 100
1	D	227/291 (78%)	196 (86%)	31 (14%)	0	100 100
2	J	124/167 (74%)	102 (82%)	22 (18%)	0	100 100
3	P	503/573 (88%)	449 (89%)	53 (10%)	1 (0%)	47 77
4	S	57/317 (18%)	53 (93%)	3 (5%)	1 (2%)	8 36
All	All	1565/2221 (70%)	1357 (87%)	206 (13%)	2 (0%)	54 82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	S	208	THR
3	P	161	SER

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	191/244 (78%)	188 (98%)	3 (2%)	62 79
1	B	186/244 (76%)	186 (100%)	0	100 100
1	C	189/244 (78%)	186 (98%)	3 (2%)	62 79
1	D	195/244 (80%)	190 (97%)	5 (3%)	46 71

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	J	121/155 (78%)	118 (98%)	3 (2%)	47 72
3	P	438/490 (89%)	432 (99%)	6 (1%)	67 82
4	S	55/283 (19%)	55 (100%)	0	100 100
All	All	1375/1904 (72%)	1355 (98%)	20 (2%)	66 81

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	P	138	THR
3	P	262	ASP
3	P	367	CYS
3	P	366	TRP
1	D	378	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
3	P	32	HIS
3	P	111	GLN
4	S	193	GLN
3	P	481	ASN
1	D	402	GLN

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

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.

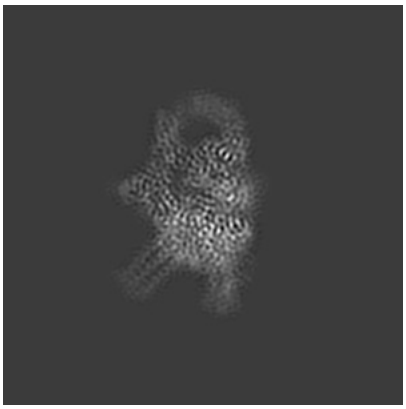
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-30008. 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.

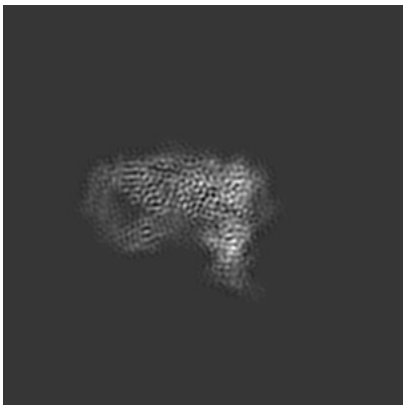
6.1 Orthogonal projections

6.1.1 Primary map



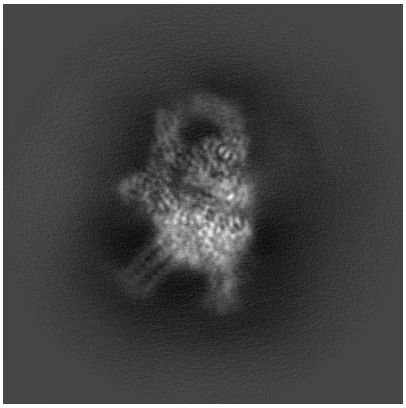
X

Y

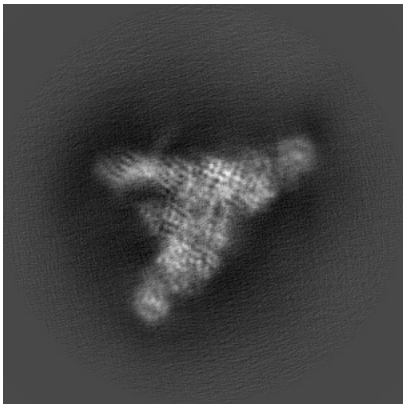


Z

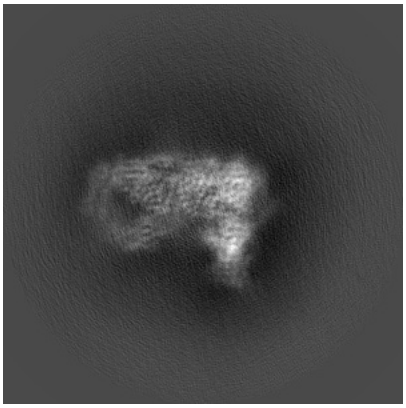
6.1.2 Raw map



X



Y



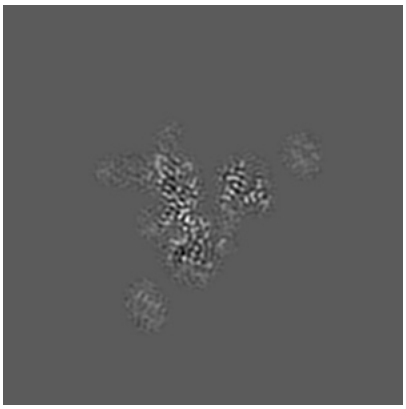
Z

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

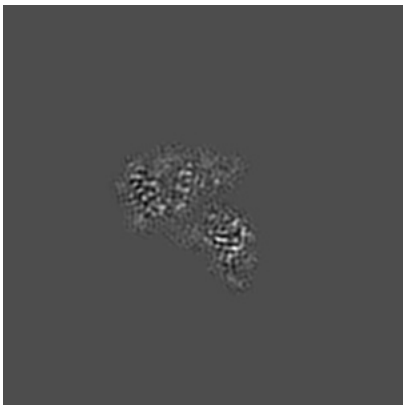
6.2 Central slices (i)

6.2.1 Primary map

X Index: 160

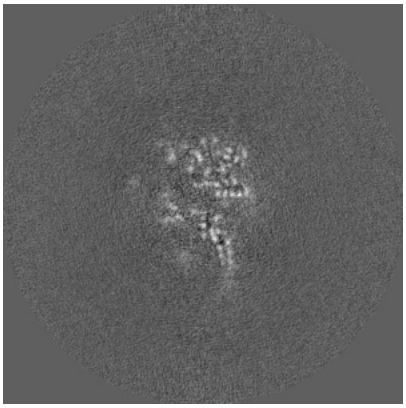


Y Index: 160

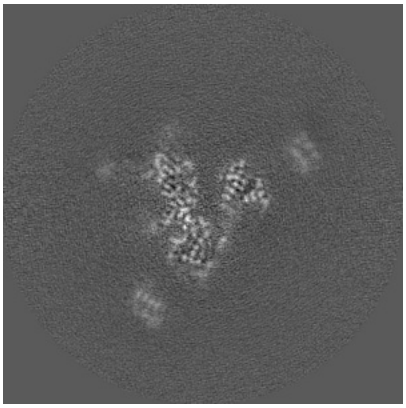


Z Index: 160

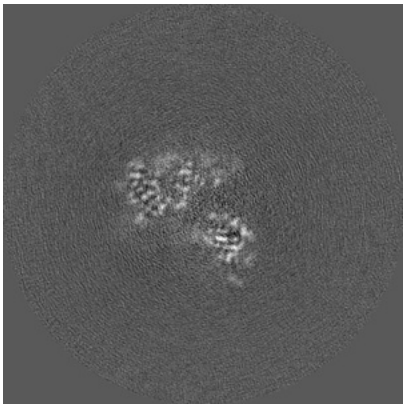
6.2.2 Raw map



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)

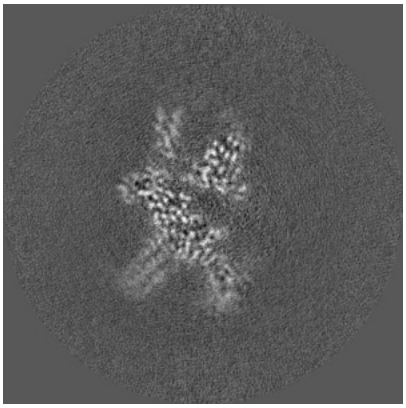
6.3.1 Primary map

X Index: 181

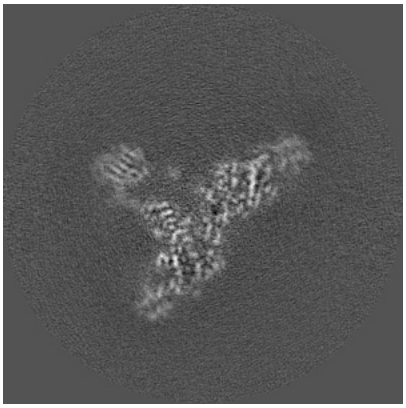
Y Index: 179

Z Index: 138

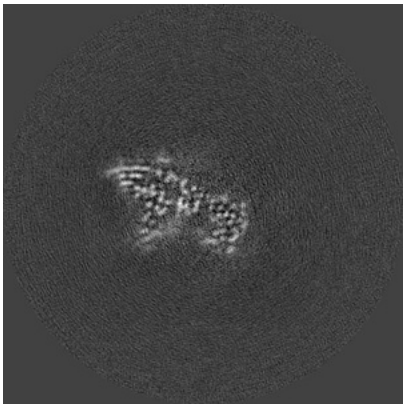
6.3.2 Raw map



X Index: 182



Y Index: 179



Z Index: 145

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 0.00863. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map

X Y Z

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.

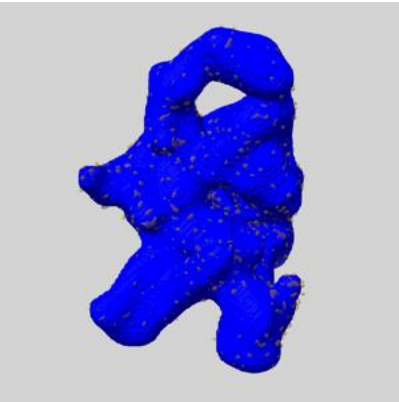
6.5 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

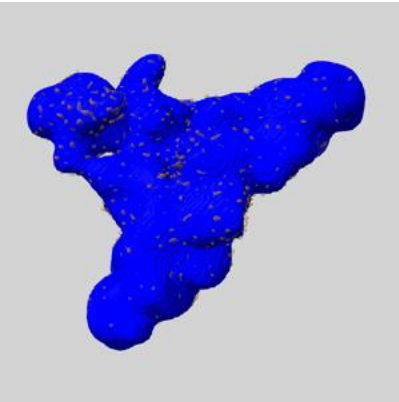
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

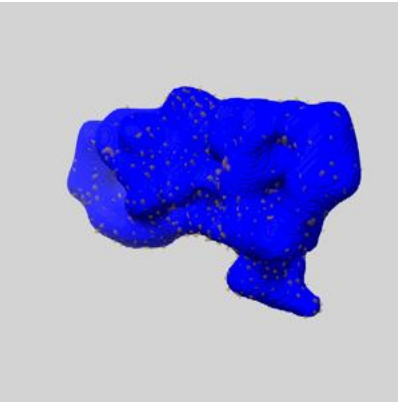
6.5.1 emd_30008_msk_1.map (i)



X



Y

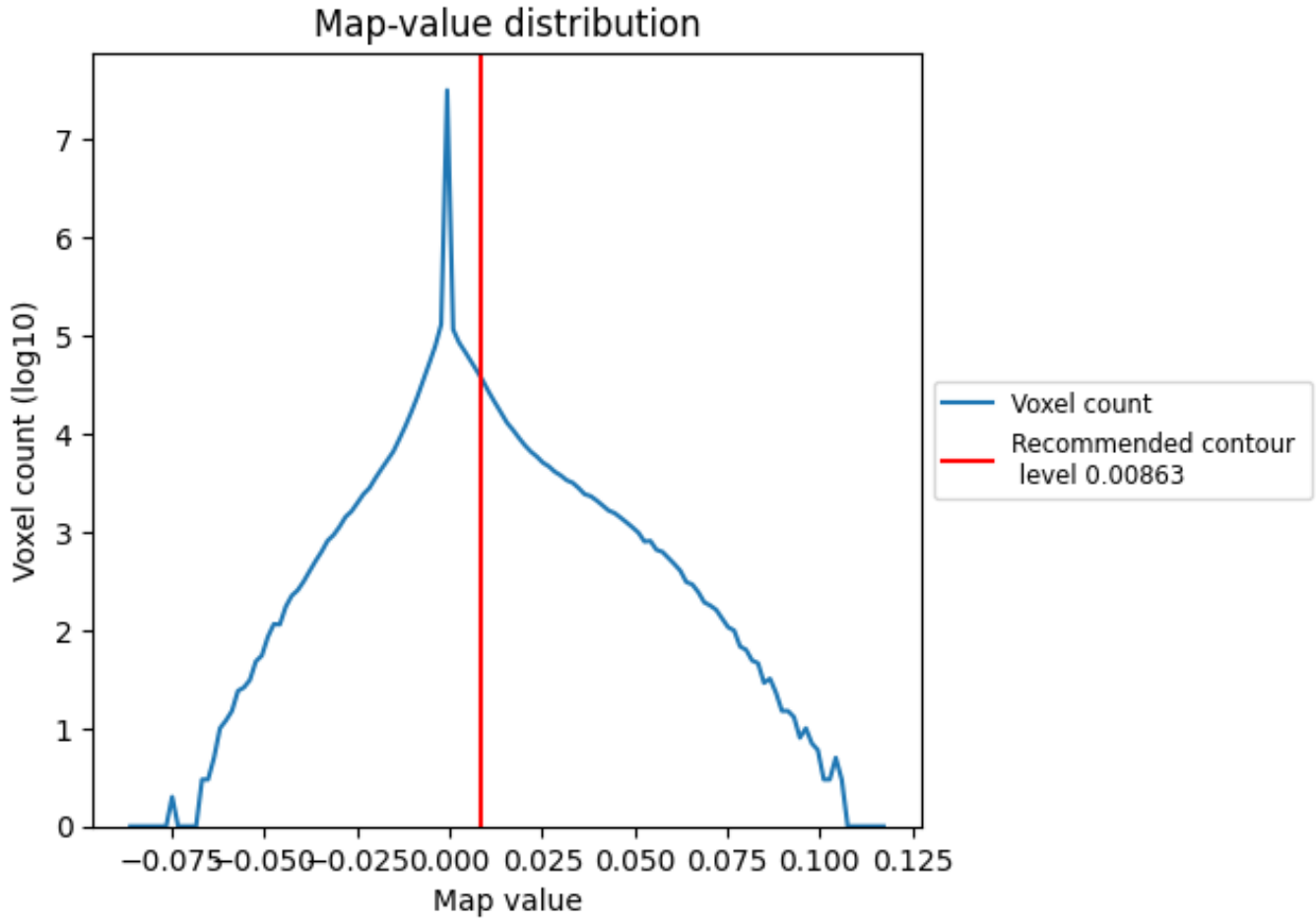


Z

7 Map analysis

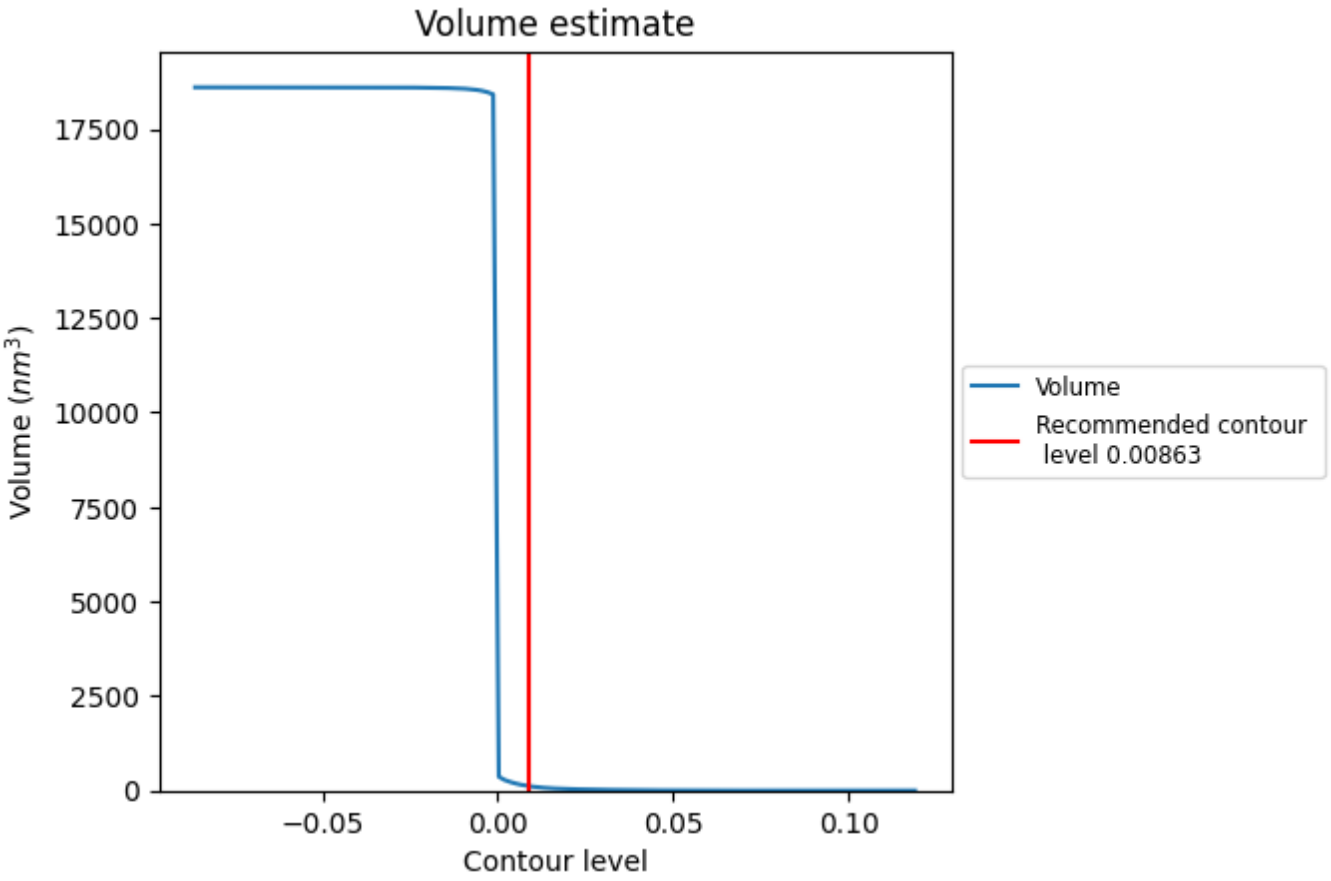
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

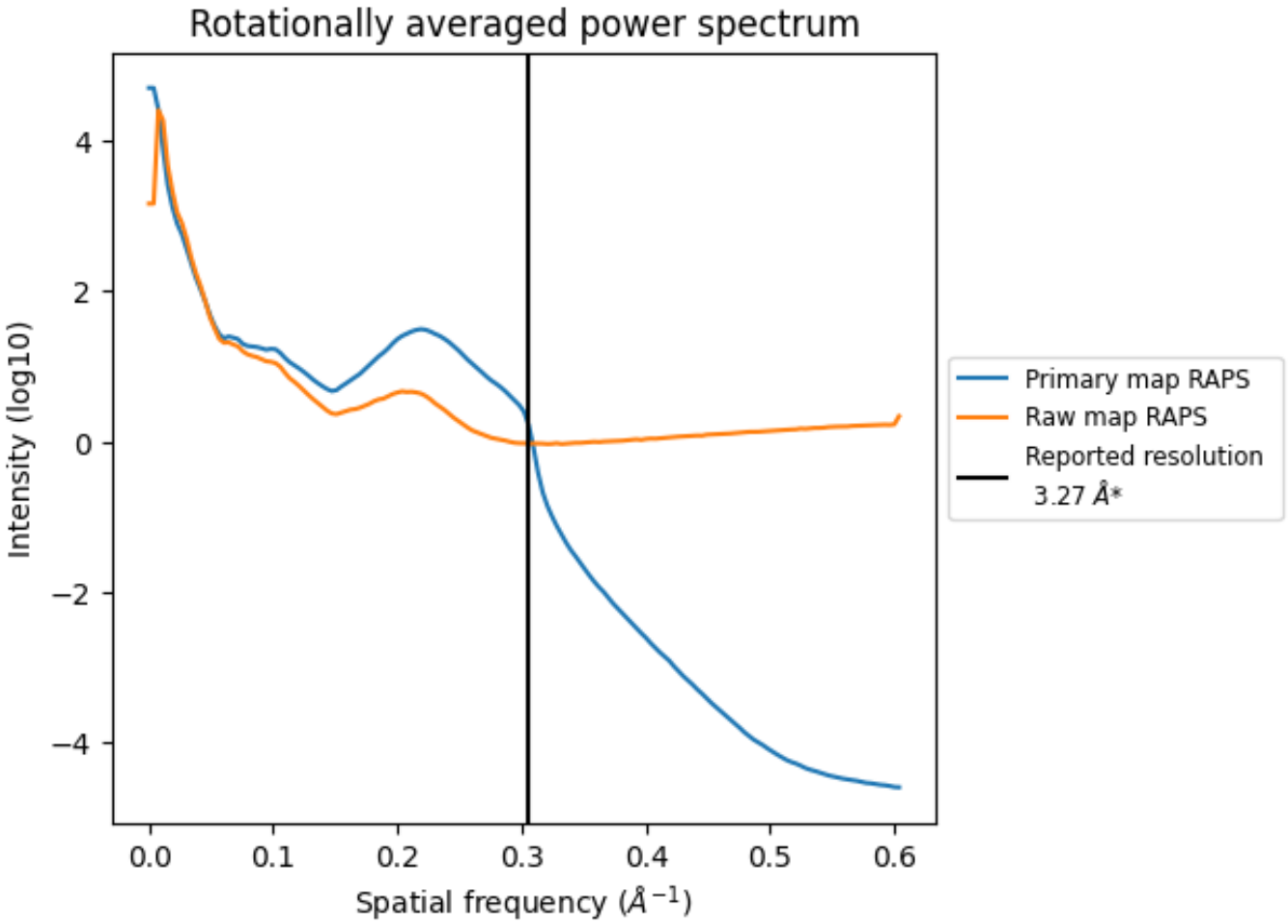
7.2 Volume estimate (i)



The volume at the recommended contour level is 121 nm^3; this corresponds to an approximate mass of 109 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)

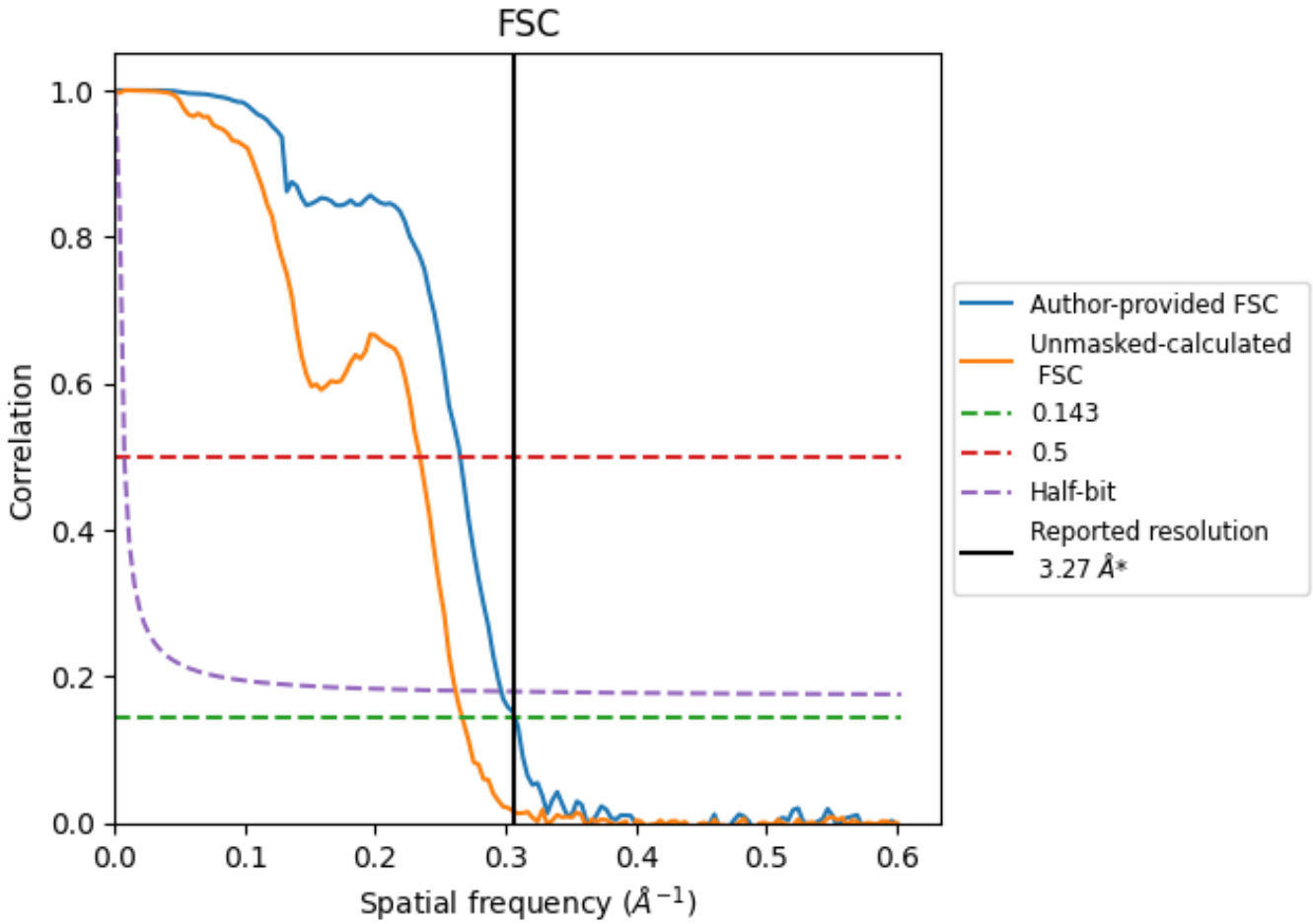


*Reported resolution corresponds to spatial frequency of 0.306 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.306 Å^{-1}

8.2 Resolution estimates (i)

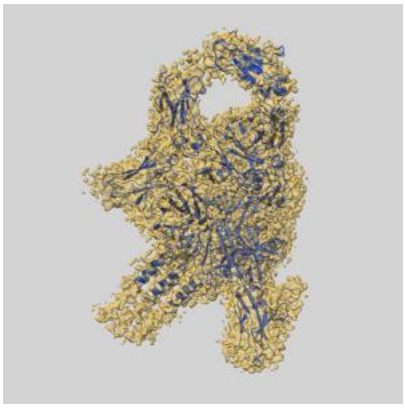
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.27	-	-
Author-provided FSC curve	3.25	3.77	3.37
Unmasked-calculated*	3.75	4.27	3.82

*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 3.75 differs from the reported value 3.27 by more than 10 %

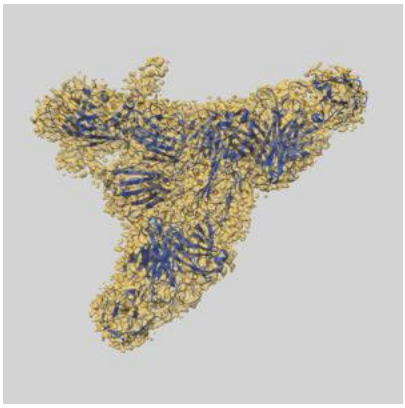
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-30008 and PDB model 6LXW. Per-residue inclusion information can be found in section 3 on page 9.

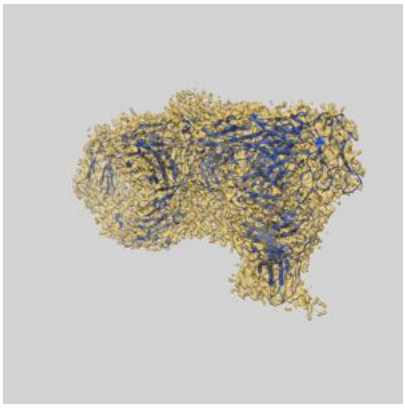
9.1 Map-model overlay



X



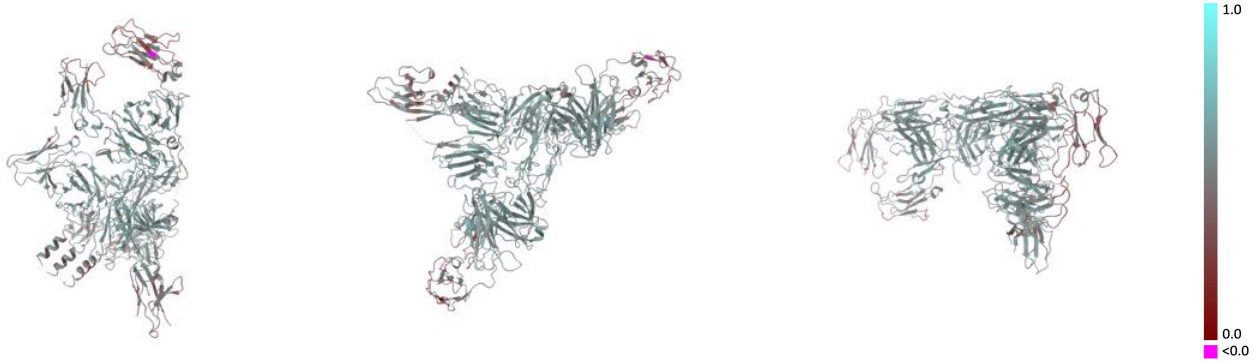
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00863 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.

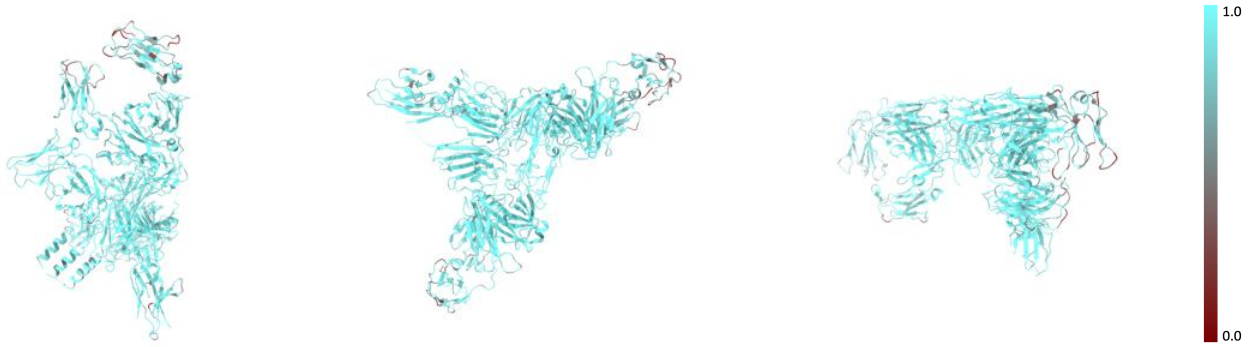
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

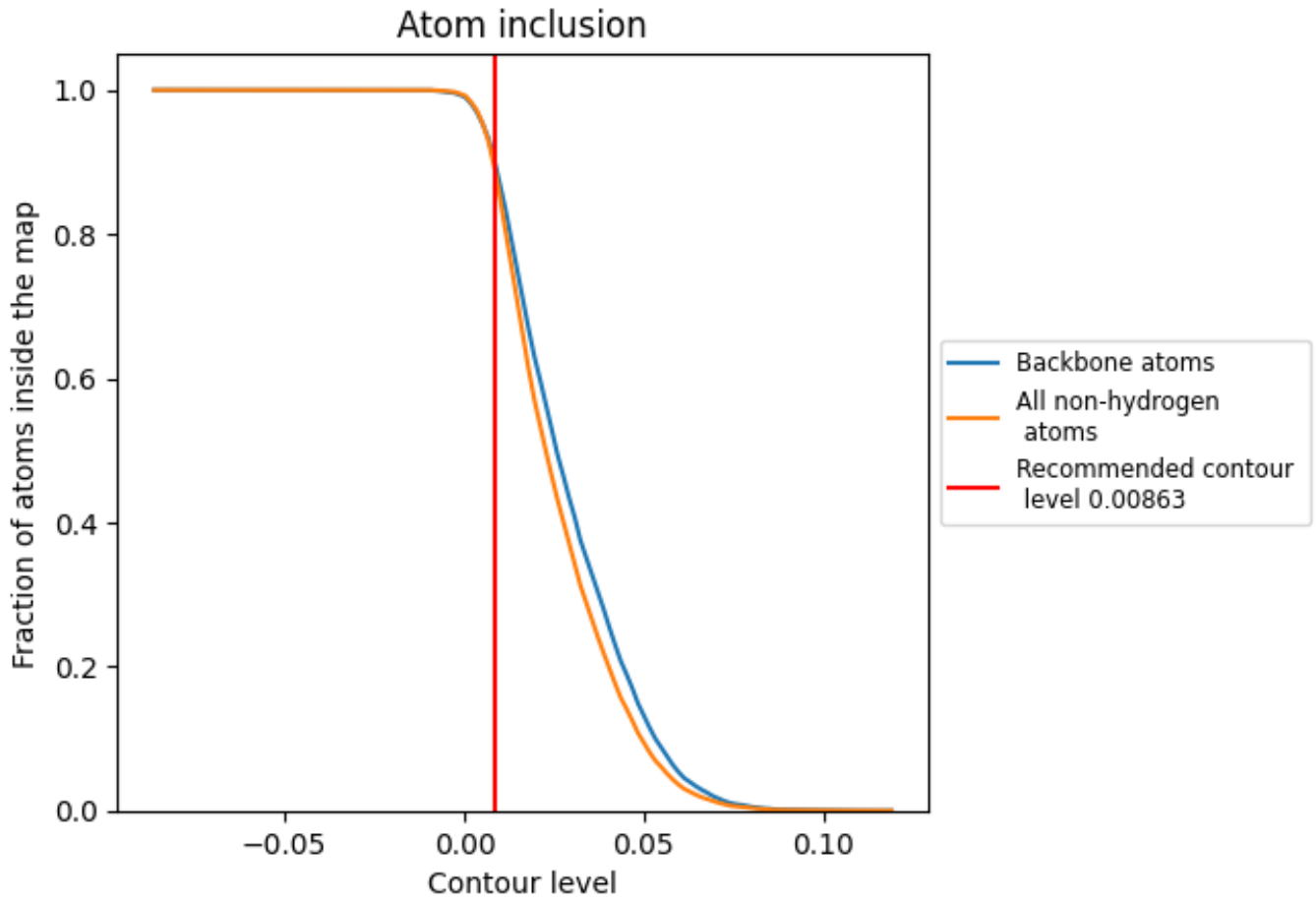
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.00863).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 89% 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 (0.00863) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8877	0.5130
A	0.9087	0.5110
B	0.8632	0.4870
C	0.7930	0.4710
D	0.8841	0.5210
J	0.9384	0.5450
P	0.9211	0.5350
S	0.8612	0.4840