Full wwPDB EM Validation Report ⓘ

Aug 4, 2025 – 10:45 AM EDT

PDB ID	:	9MQD / pdb_00009mqd
EMDB ID	:	EMD-48521
Title	:	Cryo-EM structure of hemagglutinin H5N1 in complex with Fab 310-12D03
Authors	:	Malla, T.N.; Tsybovsky, Y.; Zhou, T.
Deposited on	:	2025-01-02
Resolution	:	3.22 Å(reported)
Based on initial model	:	.

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:

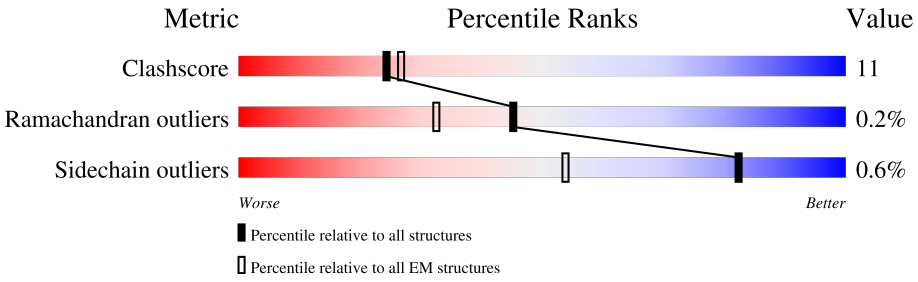
EMDB validation analysis	:	0.0.1.dev126
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.45.1

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 3.22 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.



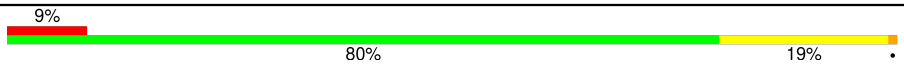
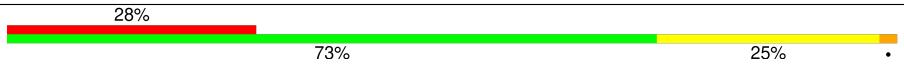
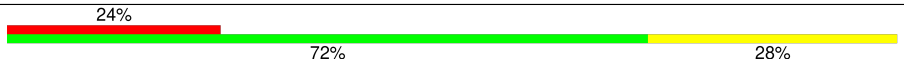
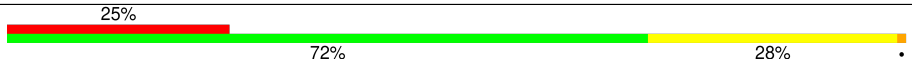
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	342	75% 17% • 8%
1	C	342	75% 17% • 8%
1	E	342	74% 18% 8%
2	B	227	20% 10% 70%
2	D	227	20% 9% 70%
2	F	227	19% 11% 70%
3	H	121	10% 69% 31%
3	I	121	11% 78% 21% •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	J	121	
4	L	109	
4	M	109	
4	N	109	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 14509 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 Hemagglutinin HA1 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	315	Total	C	N	O	S	0	0
			2495	1582	434	464	15		
1	C	316	Total	C	N	O	S	0	0
			2503	1588	435	465	15		
1	E	316	Total	C	N	O	S	0	0
			2503	1588	435	465	15		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	98	PHE	TYR	conflict	UNP A0AAX6NN08
A	199	ILE	THR	conflict	UNP A0AAX6NN08
C	98	PHE	TYR	conflict	UNP A0AAX6NN08
C	199	ILE	THR	conflict	UNP A0AAX6NN08
E	98	PHE	TYR	conflict	UNP A0AAX6NN08
E	199	ILE	THR	conflict	UNP A0AAX6NN08

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	68	Total	C	N	O	S	0	0
			577	361	101	112	3		
2	D	68	Total	C	N	O	S	0	0
			577	361	101	112	3		
2	F	68	Total	C	N	O	S	0	0
			577	361	101	112	3		

There are 156 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	174	SER	-	expression tag	UNP A0A5Q2MJY3
B	175	GLY	-	expression tag	UNP A0A5Q2MJY3
B	176	TYR	-	expression tag	UNP A0A5Q2MJY3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	177	ILE	-	expression tag	UNP A0A5Q2MJY3
B	178	PRO	-	expression tag	UNP A0A5Q2MJY3
B	179	GLU	-	expression tag	UNP A0A5Q2MJY3
B	180	ALA	-	expression tag	UNP A0A5Q2MJY3
B	181	PRO	-	expression tag	UNP A0A5Q2MJY3
B	182	ARG	-	expression tag	UNP A0A5Q2MJY3
B	183	ASP	-	expression tag	UNP A0A5Q2MJY3
B	184	GLY	-	expression tag	UNP A0A5Q2MJY3
B	185	GLN	-	expression tag	UNP A0A5Q2MJY3
B	186	ALA	-	expression tag	UNP A0A5Q2MJY3
B	187	TYR	-	expression tag	UNP A0A5Q2MJY3
B	188	VAL	-	expression tag	UNP A0A5Q2MJY3
B	189	ARG	-	expression tag	UNP A0A5Q2MJY3
B	190	LYS	-	expression tag	UNP A0A5Q2MJY3
B	191	ASP	-	expression tag	UNP A0A5Q2MJY3
B	192	GLY	-	expression tag	UNP A0A5Q2MJY3
B	193	GLU	-	expression tag	UNP A0A5Q2MJY3
B	194	TRP	-	expression tag	UNP A0A5Q2MJY3
B	195	VAL	-	expression tag	UNP A0A5Q2MJY3
B	196	LEU	-	expression tag	UNP A0A5Q2MJY3
B	197	LEU	-	expression tag	UNP A0A5Q2MJY3
B	198	SER	-	expression tag	UNP A0A5Q2MJY3
B	199	THR	-	expression tag	UNP A0A5Q2MJY3
B	200	PHE	-	expression tag	UNP A0A5Q2MJY3
B	201	LEU	-	expression tag	UNP A0A5Q2MJY3
B	202	GLY	-	expression tag	UNP A0A5Q2MJY3
B	203	SER	-	expression tag	UNP A0A5Q2MJY3
B	204	GLY	-	expression tag	UNP A0A5Q2MJY3
B	205	LEU	-	expression tag	UNP A0A5Q2MJY3
B	206	ASN	-	expression tag	UNP A0A5Q2MJY3
B	207	ASP	-	expression tag	UNP A0A5Q2MJY3
B	208	ILE	-	expression tag	UNP A0A5Q2MJY3
B	209	PHE	-	expression tag	UNP A0A5Q2MJY3
B	210	GLU	-	expression tag	UNP A0A5Q2MJY3
B	211	ALA	-	expression tag	UNP A0A5Q2MJY3
B	212	GLN	-	expression tag	UNP A0A5Q2MJY3
B	213	LYS	-	expression tag	UNP A0A5Q2MJY3
B	214	ILE	-	expression tag	UNP A0A5Q2MJY3
B	215	GLU	-	expression tag	UNP A0A5Q2MJY3
B	216	TRP	-	expression tag	UNP A0A5Q2MJY3
B	217	HIS	-	expression tag	UNP A0A5Q2MJY3
B	218	GLU	-	expression tag	UNP A0A5Q2MJY3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	219	GLY	-	expression tag	UNP A0A5Q2MJY3
B	220	HIS	-	expression tag	UNP A0A5Q2MJY3
B	221	HIS	-	expression tag	UNP A0A5Q2MJY3
B	222	HIS	-	expression tag	UNP A0A5Q2MJY3
B	223	HIS	-	expression tag	UNP A0A5Q2MJY3
B	224	HIS	-	expression tag	UNP A0A5Q2MJY3
B	225	HIS	-	expression tag	UNP A0A5Q2MJY3
D	174	SER	-	expression tag	UNP A0A5Q2MJY3
D	175	GLY	-	expression tag	UNP A0A5Q2MJY3
D	176	TYR	-	expression tag	UNP A0A5Q2MJY3
D	177	ILE	-	expression tag	UNP A0A5Q2MJY3
D	178	PRO	-	expression tag	UNP A0A5Q2MJY3
D	179	GLU	-	expression tag	UNP A0A5Q2MJY3
D	180	ALA	-	expression tag	UNP A0A5Q2MJY3
D	181	PRO	-	expression tag	UNP A0A5Q2MJY3
D	182	ARG	-	expression tag	UNP A0A5Q2MJY3
D	183	ASP	-	expression tag	UNP A0A5Q2MJY3
D	184	GLY	-	expression tag	UNP A0A5Q2MJY3
D	185	GLN	-	expression tag	UNP A0A5Q2MJY3
D	186	ALA	-	expression tag	UNP A0A5Q2MJY3
D	187	TYR	-	expression tag	UNP A0A5Q2MJY3
D	188	VAL	-	expression tag	UNP A0A5Q2MJY3
D	189	ARG	-	expression tag	UNP A0A5Q2MJY3
D	190	LYS	-	expression tag	UNP A0A5Q2MJY3
D	191	ASP	-	expression tag	UNP A0A5Q2MJY3
D	192	GLY	-	expression tag	UNP A0A5Q2MJY3
D	193	GLU	-	expression tag	UNP A0A5Q2MJY3
D	194	TRP	-	expression tag	UNP A0A5Q2MJY3
D	195	VAL	-	expression tag	UNP A0A5Q2MJY3
D	196	LEU	-	expression tag	UNP A0A5Q2MJY3
D	197	LEU	-	expression tag	UNP A0A5Q2MJY3
D	198	SER	-	expression tag	UNP A0A5Q2MJY3
D	199	THR	-	expression tag	UNP A0A5Q2MJY3
D	200	PHE	-	expression tag	UNP A0A5Q2MJY3
D	201	LEU	-	expression tag	UNP A0A5Q2MJY3
D	202	GLY	-	expression tag	UNP A0A5Q2MJY3
D	203	SER	-	expression tag	UNP A0A5Q2MJY3
D	204	GLY	-	expression tag	UNP A0A5Q2MJY3
D	205	LEU	-	expression tag	UNP A0A5Q2MJY3
D	206	ASN	-	expression tag	UNP A0A5Q2MJY3
D	207	ASP	-	expression tag	UNP A0A5Q2MJY3
D	208	ILE	-	expression tag	UNP A0A5Q2MJY3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	209	PHE	-	expression tag	UNP A0A5Q2MJY3
D	210	GLU	-	expression tag	UNP A0A5Q2MJY3
D	211	ALA	-	expression tag	UNP A0A5Q2MJY3
D	212	GLN	-	expression tag	UNP A0A5Q2MJY3
D	213	LYS	-	expression tag	UNP A0A5Q2MJY3
D	214	ILE	-	expression tag	UNP A0A5Q2MJY3
D	215	GLU	-	expression tag	UNP A0A5Q2MJY3
D	216	TRP	-	expression tag	UNP A0A5Q2MJY3
D	217	HIS	-	expression tag	UNP A0A5Q2MJY3
D	218	GLU	-	expression tag	UNP A0A5Q2MJY3
D	219	GLY	-	expression tag	UNP A0A5Q2MJY3
D	220	HIS	-	expression tag	UNP A0A5Q2MJY3
D	221	HIS	-	expression tag	UNP A0A5Q2MJY3
D	222	HIS	-	expression tag	UNP A0A5Q2MJY3
D	223	HIS	-	expression tag	UNP A0A5Q2MJY3
D	224	HIS	-	expression tag	UNP A0A5Q2MJY3
D	225	HIS	-	expression tag	UNP A0A5Q2MJY3
F	174	SER	-	expression tag	UNP A0A5Q2MJY3
F	175	GLY	-	expression tag	UNP A0A5Q2MJY3
F	176	TYR	-	expression tag	UNP A0A5Q2MJY3
F	177	ILE	-	expression tag	UNP A0A5Q2MJY3
F	178	PRO	-	expression tag	UNP A0A5Q2MJY3
F	179	GLU	-	expression tag	UNP A0A5Q2MJY3
F	180	ALA	-	expression tag	UNP A0A5Q2MJY3
F	181	PRO	-	expression tag	UNP A0A5Q2MJY3
F	182	ARG	-	expression tag	UNP A0A5Q2MJY3
F	183	ASP	-	expression tag	UNP A0A5Q2MJY3
F	184	GLY	-	expression tag	UNP A0A5Q2MJY3
F	185	GLN	-	expression tag	UNP A0A5Q2MJY3
F	186	ALA	-	expression tag	UNP A0A5Q2MJY3
F	187	TYR	-	expression tag	UNP A0A5Q2MJY3
F	188	VAL	-	expression tag	UNP A0A5Q2MJY3
F	189	ARG	-	expression tag	UNP A0A5Q2MJY3
F	190	LYS	-	expression tag	UNP A0A5Q2MJY3
F	191	ASP	-	expression tag	UNP A0A5Q2MJY3
F	192	GLY	-	expression tag	UNP A0A5Q2MJY3
F	193	GLU	-	expression tag	UNP A0A5Q2MJY3
F	194	TRP	-	expression tag	UNP A0A5Q2MJY3
F	195	VAL	-	expression tag	UNP A0A5Q2MJY3
F	196	LEU	-	expression tag	UNP A0A5Q2MJY3
F	197	LEU	-	expression tag	UNP A0A5Q2MJY3
F	198	SER	-	expression tag	UNP A0A5Q2MJY3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	199	THR	-	expression tag	UNP A0A5Q2MJY3
F	200	PHE	-	expression tag	UNP A0A5Q2MJY3
F	201	LEU	-	expression tag	UNP A0A5Q2MJY3
F	202	GLY	-	expression tag	UNP A0A5Q2MJY3
F	203	SER	-	expression tag	UNP A0A5Q2MJY3
F	204	GLY	-	expression tag	UNP A0A5Q2MJY3
F	205	LEU	-	expression tag	UNP A0A5Q2MJY3
F	206	ASN	-	expression tag	UNP A0A5Q2MJY3
F	207	ASP	-	expression tag	UNP A0A5Q2MJY3
F	208	ILE	-	expression tag	UNP A0A5Q2MJY3
F	209	PHE	-	expression tag	UNP A0A5Q2MJY3
F	210	GLU	-	expression tag	UNP A0A5Q2MJY3
F	211	ALA	-	expression tag	UNP A0A5Q2MJY3
F	212	GLN	-	expression tag	UNP A0A5Q2MJY3
F	213	LYS	-	expression tag	UNP A0A5Q2MJY3
F	214	ILE	-	expression tag	UNP A0A5Q2MJY3
F	215	GLU	-	expression tag	UNP A0A5Q2MJY3
F	216	TRP	-	expression tag	UNP A0A5Q2MJY3
F	217	HIS	-	expression tag	UNP A0A5Q2MJY3
F	218	GLU	-	expression tag	UNP A0A5Q2MJY3
F	219	GLY	-	expression tag	UNP A0A5Q2MJY3
F	220	HIS	-	expression tag	UNP A0A5Q2MJY3
F	221	HIS	-	expression tag	UNP A0A5Q2MJY3
F	222	HIS	-	expression tag	UNP A0A5Q2MJY3
F	223	HIS	-	expression tag	UNP A0A5Q2MJY3
F	224	HIS	-	expression tag	UNP A0A5Q2MJY3
F	225	HIS	-	expression tag	UNP A0A5Q2MJY3

- Molecule 3 is a protein called Heavy chain of Fab 310-12D03.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	121	Total	C	N	O	S	0	0
			924	590	146	186	2		
3	I	121	Total	C	N	O	S	0	0
			924	590	146	186	2		
3	J	121	Total	C	N	O	S	0	0
			924	590	146	186	2		

- Molecule 4 is a protein called Light chain of Fab 310-12D03.

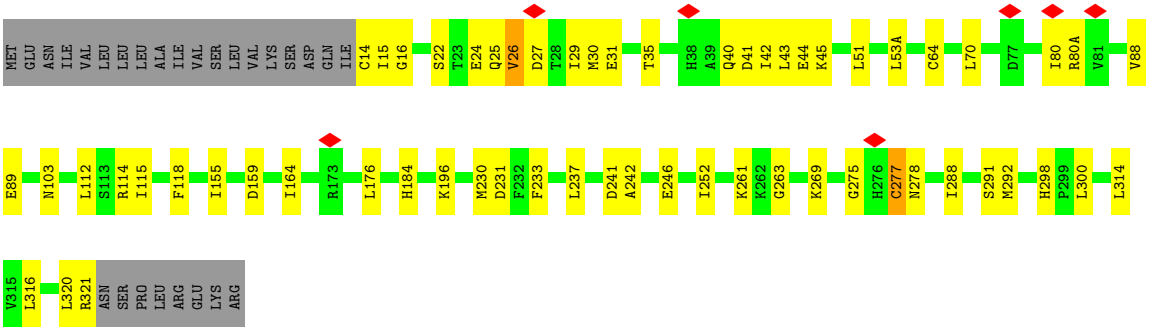
Mol	Chain	Residues	Atoms					AltConf	Trace
4	L	109	Total	C	N	O	S	0	0
			835	529	138	166	2		
4	M	109	Total	C	N	O	S	0	0
			835	529	138	166	2		
4	N	109	Total	C	N	O	S	0	0
			835	529	138	166	2		

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.

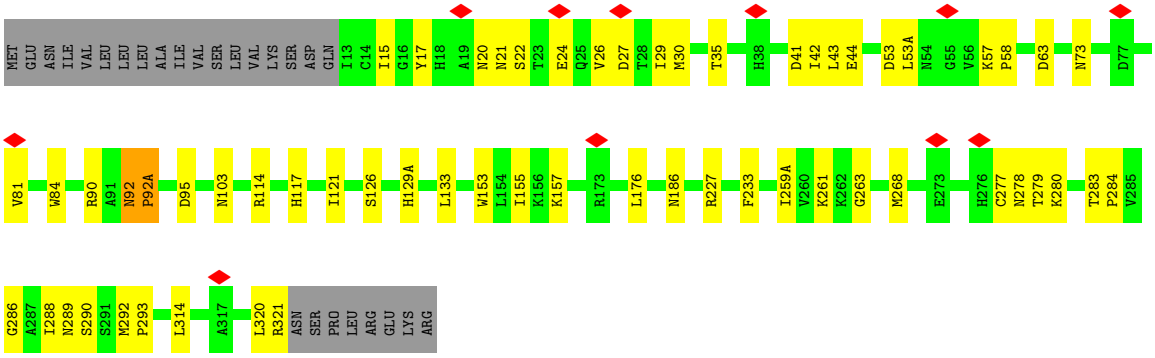
• Molecule 1: Hemagglutinin HA1 chain

Chain A:



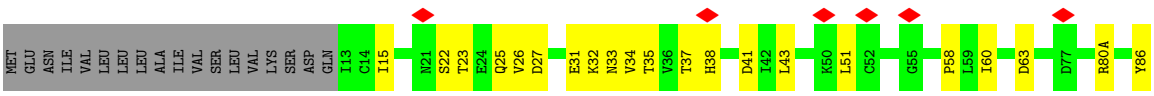
• Molecule 1: Hemagglutinin HA1 chain

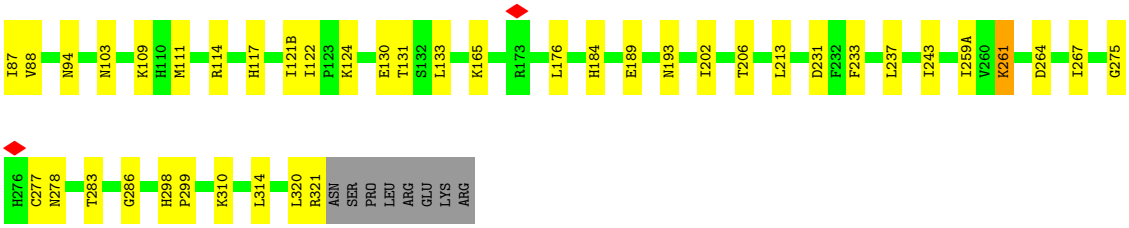
Chain C:



• Molecule 1: Hemagglutinin HA1 chain

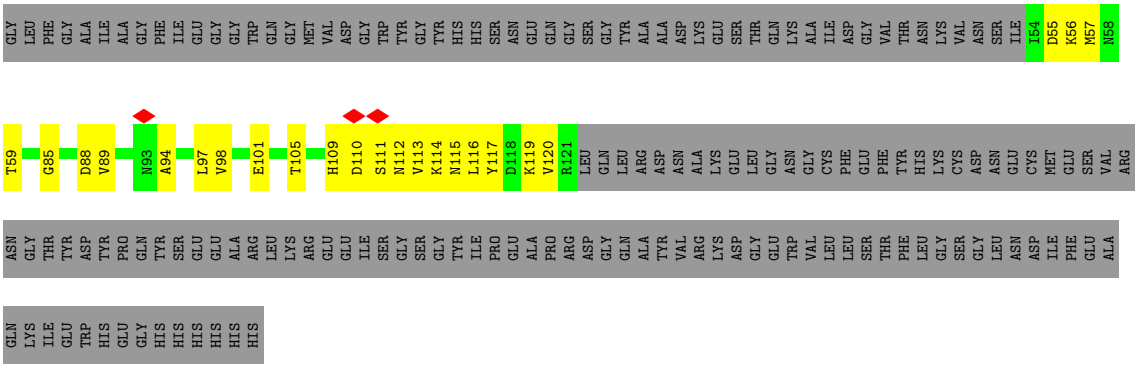
Chain E:





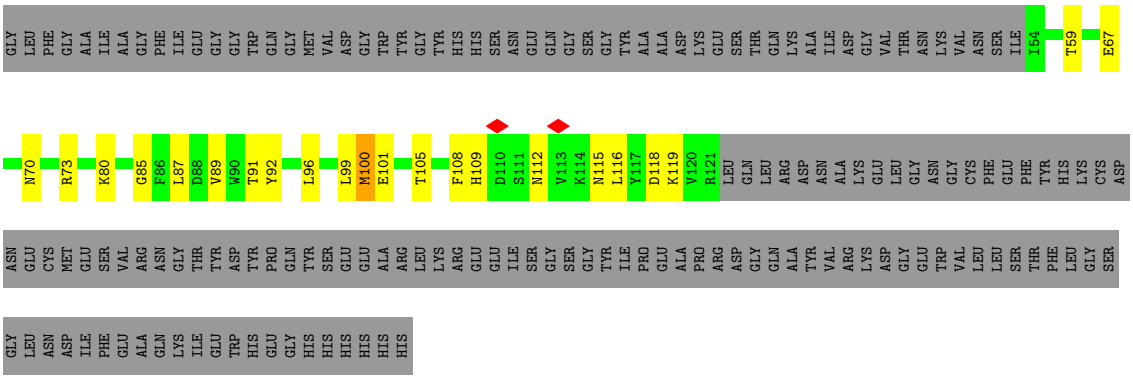
• Molecule 2: Hemagglutinin HA2 chain

Chain B:



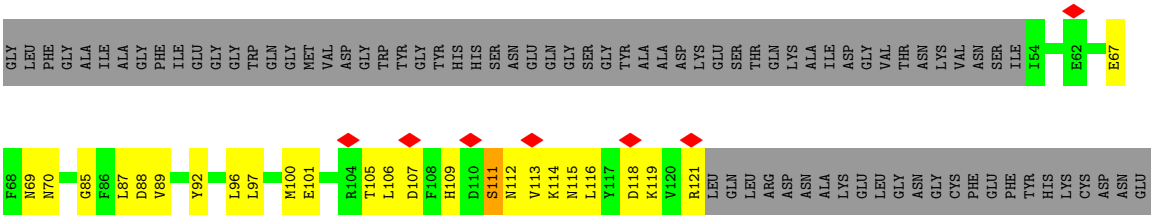
• Molecule 2: Hemagglutinin HA2 chain

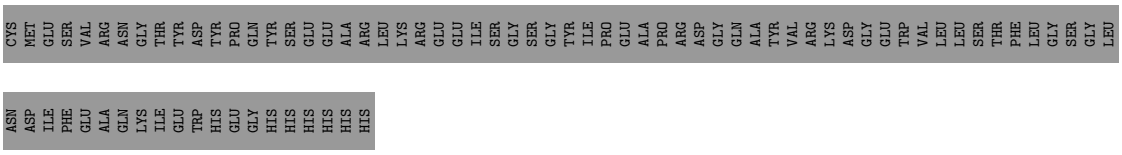
Chain D:



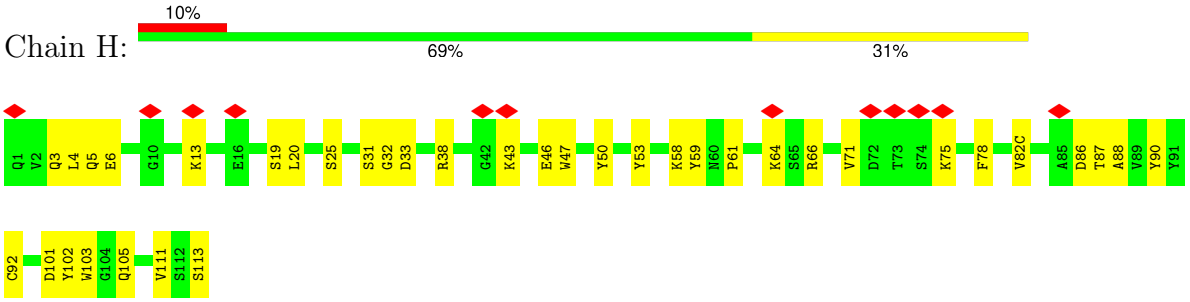
• Molecule 2: Hemagglutinin HA2 chain

Chain F:

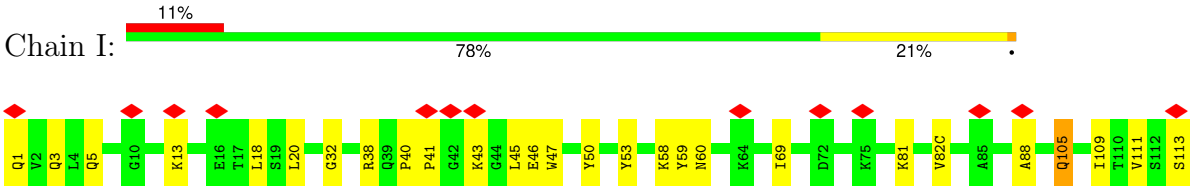




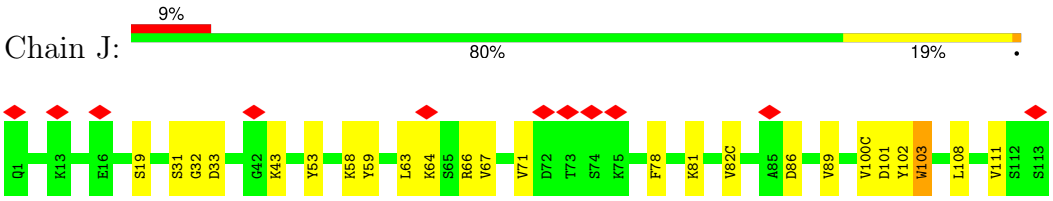
• Molecule 3: Heavy chain of Fab 310-12D03



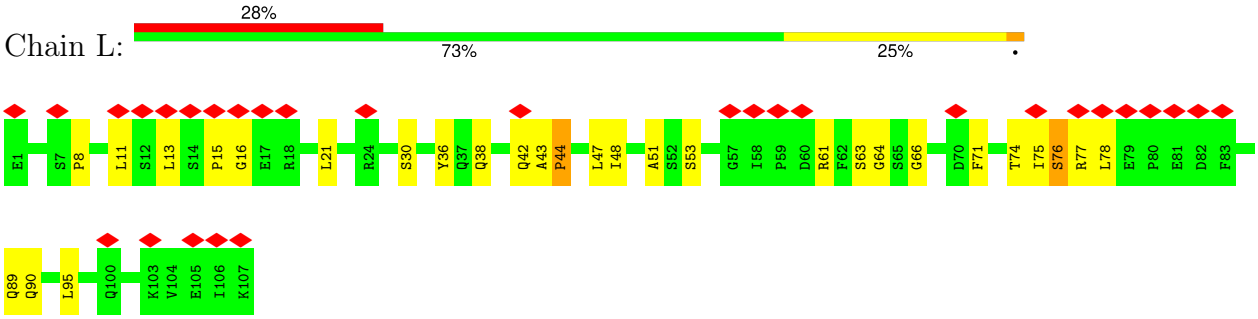
• Molecule 3: Heavy chain of Fab 310-12D03



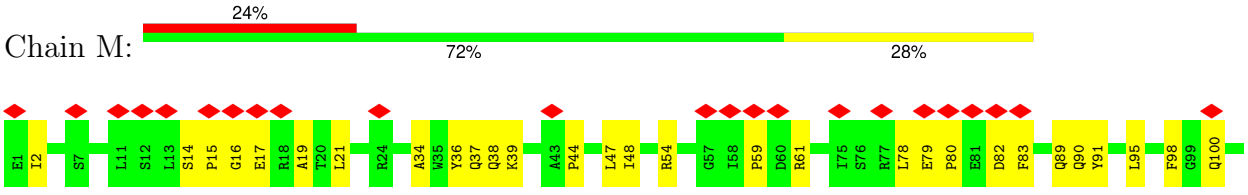
• Molecule 3: Heavy chain of Fab 310-12D03



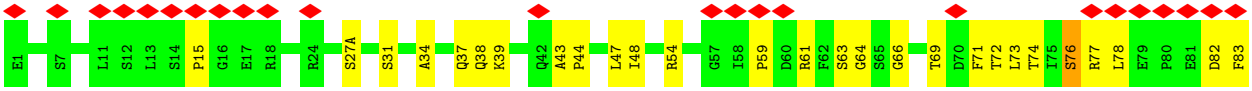
• Molecule 4: Light chain of Fab 310-12D03

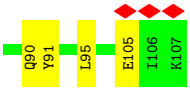


• Molecule 4: Light chain of Fab 310-12D03



• Molecule 4: Light chain of Fab 310-12D03





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1051276	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1900	Depositor
Magnification	Not provided	
Image detector	DIRECT ELECTRON APOLLO (4k x 4k)	Depositor
Maximum map value	2.551	Depositor
Minimum map value	-1.487	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.252	Depositor
Map size (Å)	400.0, 400.0, 400.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0, 1.0, 1.0	Depositor

5 Model quality

5.1 Standard geometry

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	0.17	0/2558	0.38	0/3476
1	C	0.18	0/2566	0.39	0/3487
1	E	0.17	0/2566	0.38	0/3487
2	B	0.18	0/585	0.44	0/785
2	D	0.17	0/585	0.42	0/785
2	F	0.17	0/585	0.44	0/785
3	H	0.16	0/947	0.36	0/1291
3	I	0.14	0/947	0.39	0/1291
3	J	0.16	0/947	0.41	0/1291
4	L	0.20	0/855	0.53	1/1159 (0.1%)
4	M	0.15	0/855	0.40	0/1159
4	N	0.14	0/855	0.38	0/1159
All	All	0.17	0/14851	0.40	1/20155 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	L	44	PRO	CA-N-CD	-5.74	103.96	112.00

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	2495	0	2453	44	0
1	C	2503	0	2466	43	0
1	E	2503	0	2464	44	0
2	B	577	0	558	21	0
2	D	577	0	558	23	0
2	F	577	0	558	24	0
3	H	924	0	897	23	0
3	I	924	0	897	18	0
3	J	924	0	897	19	0
4	L	835	0	813	20	0
4	M	835	0	813	20	0
4	N	835	0	813	25	0
All	All	14509	0	14187	302	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 11.

All (302) 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)
4:L:74:THR:HG22	4:L:76:SER:H	1.54	0.73
1:A:41:ASP:OD1	1:A:43:LEU:N	2.23	0.70
1:A:298:HIS:HE1	1:A:300:LEU:HG	1.55	0.69
1:E:109:LYS:HE3	1:E:267:ILE:HD12	1.74	0.69
2:D:105:THR:HG22	2:D:109:HIS:CE1	2.28	0.68
1:E:206:THR:HG22	1:E:243:ILE:HG13	1.75	0.68
1:A:16:GLY:HA2	2:B:113:VAL:HG21	1.76	0.67
1:C:186:ASN:ND2	1:C:227:ARG:O	2.27	0.67
2:B:116:LEU:HD23	2:B:119:LYS:HE2	1.76	0.67
2:B:101:GLU:O	2:B:105:THR:OG1	2.11	0.66
1:C:133:LEU:HB2	1:C:155:ILE:HD11	1.78	0.66
1:E:121(B):ILE:HG13	1:E:122:ILE:HG12	1.78	0.65
2:F:116:LEU:HA	2:F:119:LYS:HG2	1.78	0.65
1:C:92:ASN:HD22	1:C:92:ASN:C	2.05	0.65
2:D:101:GLU:O	2:D:105:THR:OG1	2.13	0.65
1:C:92:ASN:O	1:C:92:ASN:ND2	2.22	0.65
2:B:57:MET:HE3	2:F:92:TYR:HA	1.79	0.64
2:F:85:GLY:O	2:F:89:VAL:HG23	1.98	0.63
1:C:43:LEU:HD22	1:C:314:LEU:HD23	1.80	0.63
3:J:31:SER:OG	3:J:33:ASP:OD1	2.16	0.63
1:A:70:LEU:HD11	1:A:112:LEU:HD21	1.80	0.62
2:B:85:GLY:O	2:B:89:VAL:HG23	1.98	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:103:TRP:HZ3	4:N:44:PRO:HD2	1.62	0.62
4:M:61:ARG:NH2	4:M:82:ASP:OD2	2.32	0.62
2:D:85:GLY:O	2:D:89:VAL:HG23	2.00	0.62
1:E:202:ILE:HD11	1:E:213:LEU:HD12	1.81	0.62
3:J:32:GLY:HA2	3:J:53:TYR:HB2	1.82	0.62
1:A:261:LYS:NZ	1:A:263:GLY:O	2.27	0.61
1:E:15:ILE:HD11	2:F:116:LEU:HD12	1.81	0.61
2:F:112:ASN:O	2:F:116:LEU:HG	2.01	0.61
3:I:38:ARG:HH11	3:I:40:PRO:HG3	1.66	0.61
1:A:51:LEU:O	1:A:275:GLY:N	2.34	0.61
3:I:1:GLN:OE1	3:I:3:GLN:NE2	2.33	0.61
3:H:46:GLU:HG2	3:H:47:TRP:H	1.65	0.60
3:I:32:GLY:HA2	3:I:53:TYR:HB2	1.83	0.60
4:M:79:GLU:HG2	4:M:80:PRO:HD2	1.82	0.60
2:B:111:SER:O	2:B:115:ASN:ND2	2.34	0.60
4:L:42:GLN:HG2	4:L:43:ALA:H	1.67	0.60
4:N:74:THR:HG22	4:N:76:SER:H	1.67	0.60
1:A:292:MET:SD	1:A:292:MET:N	2.75	0.59
3:J:101:ASP:OD1	3:J:101:ASP:N	2.35	0.59
1:E:27:ASP:OD1	1:E:27:ASP:N	2.35	0.59
2:B:112:ASN:HA	2:B:115:ASN:HD21	1.67	0.59
3:I:5:GLN:OE1	3:I:105:GLN:NE2	2.36	0.59
2:D:92:TYR:HE1	2:D:96:LEU:HD22	1.67	0.59
3:H:82(C):VAL:HG21	3:H:111:VAL:HG11	1.83	0.59
3:J:59:TYR:HB2	3:J:64:LYS:HD3	1.84	0.59
3:J:66:ARG:NH1	3:J:86:ASP:OD2	2.26	0.59
3:I:46:GLU:HG2	3:I:47:TRP:H	1.68	0.58
1:E:87:ILE:HB	1:E:267:ILE:HG23	1.85	0.58
3:H:58:LYS:HB3	4:L:95:LEU:HD11	1.84	0.58
2:F:106:LEU:HA	2:F:109:HIS:HB2	1.85	0.58
1:E:310:LYS:O	1:E:310:LYS:HG2	2.03	0.58
1:A:298:HIS:CE1	1:A:300:LEU:HG	2.38	0.57
4:L:15:PRO:HA	4:L:78:LEU:HB3	1.85	0.57
3:H:101:ASP:OD1	3:H:101:ASP:N	2.36	0.57
4:N:66:GLY:HA3	4:N:71:PHE:HA	1.85	0.57
2:D:115:ASN:O	2:D:119:LYS:HG2	2.04	0.57
2:F:96:LEU:O	2:F:100:MET:HG3	2.05	0.57
1:E:111:MET:O	1:E:261:LYS:NZ	2.36	0.57
3:I:47:TRP:HE3	3:I:60:ASN:HD22	1.52	0.57
4:N:63:SER:OG	4:N:64:GLY:N	2.38	0.57
1:A:31:GLU:N	1:A:31:GLU:OE1	2.37	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:38:ARG:HB2	3:H:88:ALA:HB1	1.87	0.56
1:C:283:THR:OG1	1:C:286:GLY:O	2.21	0.56
1:E:25:GLN:HE21	1:E:35:THR:HG22	1.69	0.56
2:F:107:ASP:O	2:F:111:SER:OG	2.23	0.56
1:E:51:LEU:O	1:E:275:GLY:N	2.36	0.56
2:F:112:ASN:HA	2:F:115:ASN:ND2	2.20	0.56
1:C:42:ILE:HA	1:C:292:MET:HG2	1.87	0.55
2:D:112:ASN:O	2:D:116:LEU:HG	2.06	0.55
2:F:67:GLU:N	2:F:67:GLU:OE2	2.40	0.55
3:I:13:LYS:NZ	3:I:113:SER:O	2.36	0.55
4:M:36:TYR:OH	4:M:89:GLN:OE1	2.10	0.55
1:A:41:ASP:OD1	1:A:42:ILE:N	2.40	0.54
3:H:31:SER:OG	3:H:33:ASP:OD1	2.17	0.54
1:E:130:GLU:OE2	4:N:31:SER:OG	2.20	0.54
4:L:76:SER:OG	4:L:77:ARG:N	2.37	0.54
1:E:31:GLU:OE2	1:E:33:ASN:N	2.41	0.54
2:D:96:LEU:HD12	2:D:99:LEU:HD12	1.88	0.54
4:N:76:SER:OG	4:N:77:ARG:N	2.30	0.54
1:A:14:CYS:SG	1:A:15:ILE:N	2.81	0.54
1:C:29:ILE:HB	2:D:99:LEU:HB3	1.90	0.54
3:H:3:GLN:OE1	3:H:25:SER:OG	2.27	0.53
3:H:5:GLN:OE1	3:H:6:GLU:N	2.41	0.53
4:N:15:PRO:HA	4:N:78:LEU:HB3	1.90	0.53
1:E:26:VAL:HG22	1:E:27:ASP:H	1.74	0.53
1:E:31:GLU:OE2	1:E:34:VAL:HG13	2.08	0.53
2:D:115:ASN:HA	2:D:118:ASP:OD2	2.09	0.52
3:I:58:LYS:HD2	4:M:95:LEU:HD21	1.89	0.52
4:M:15:PRO:HA	4:M:78:LEU:HB3	1.91	0.52
1:A:80:ILE:HG12	1:A:80(A):ARG:HG2	1.91	0.52
1:E:60:ILE:HD13	1:E:88:VAL:HB	1.91	0.52
4:M:37:GLN:HB2	4:M:47:LEU:HD11	1.90	0.52
1:A:184:HIS:NE2	1:A:231:ASP:OD2	2.43	0.52
2:B:94:ALA:O	2:B:98:VAL:HG12	2.10	0.52
1:C:279:THR:OG1	1:C:280:LYS:N	2.41	0.52
3:I:20:LEU:HD21	3:I:109:ILE:HD11	1.90	0.52
1:E:277:CYS:SG	1:E:278:ASN:N	2.84	0.51
3:J:82(C):VAL:HG11	3:J:111:VAL:HG11	1.91	0.51
4:N:83:PHE:HD1	4:N:105:GLU:HA	1.74	0.51
1:C:277:CYS:SG	1:C:278:ASN:N	2.84	0.51
4:L:38:GLN:HG3	4:L:44:PRO:HG3	1.91	0.51
2:B:56:LYS:HB3	2:B:57:MET:SD	2.50	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:38:ARG:NH2	3:H:87:THR:O	2.42	0.51
3:I:46:GLU:HG2	3:I:47:TRP:N	2.26	0.51
4:M:14:SER:OG	4:M:17:GLU:OE2	2.25	0.51
1:C:103:ASN:HD22	1:C:233:PHE:HE1	1.59	0.51
2:B:55:ASP:OD1	2:B:55:ASP:N	2.37	0.51
1:A:103:ASN:HD22	1:A:233:PHE:HE1	1.56	0.51
2:F:105:THR:HG22	2:F:109:HIS:CE1	2.46	0.51
1:E:320:LEU:HD23	1:E:321:ARG:N	2.25	0.50
1:C:29:ILE:HG23	1:C:30:MET:HG3	1.94	0.50
1:A:114:ARG:HG3	1:A:114:ARG:O	2.11	0.50
3:H:32:GLY:HA2	3:H:53:TYR:HB2	1.92	0.50
1:A:27:ASP:OD1	1:A:27:ASP:N	2.44	0.50
1:C:22:SER:OG	1:C:24:GLU:OE1	2.29	0.50
3:J:71:VAL:HG23	3:J:78:PHE:HB3	1.92	0.50
3:J:102:TYR:C	3:J:103:TRP:HD1	2.20	0.50
1:A:159:ASP:O	1:A:196:LYS:HE2	2.12	0.50
2:D:105:THR:HG22	2:D:109:HIS:HE1	1.74	0.50
2:F:97:LEU:O	2:F:101:GLU:HB2	2.11	0.50
1:A:51:LEU:HD11	1:A:88:VAL:HG21	1.94	0.50
1:A:241:ASP:OD1	1:A:242:ALA:N	2.44	0.50
3:J:103:TRP:CZ3	4:N:44:PRO:HD2	2.46	0.50
3:I:18:LEU:HD21	3:I:109:ILE:HD13	1.94	0.50
4:N:54:ARG:NH1	4:N:59:PRO:O	2.45	0.50
1:C:15:ILE:HD11	2:D:116:LEU:HD12	1.93	0.49
1:C:268:MET:HE2	1:C:284:PRO:HD3	1.93	0.49
2:D:109:HIS:HA	2:D:112:ASN:HD21	1.76	0.49
1:C:121:ILE:HD11	1:C:176:LEU:HD21	1.95	0.49
2:D:115:ASN:OD1	2:D:116:LEU:N	2.45	0.49
1:C:73:ASN:ND2	1:C:95:ASP:O	2.46	0.49
4:L:90:GLN:CD	4:L:90:GLN:O	2.55	0.49
1:A:26:VAL:HG12	1:A:27:ASP:H	1.76	0.48
1:A:277:CYS:SG	1:A:278:ASN:N	2.86	0.48
4:M:34:ALA:HB2	4:M:91:TYR:HE2	1.77	0.48
1:A:25:GLN:NE2	1:A:35:THR:HG22	2.29	0.48
1:E:114:ARG:O	1:E:114:ARG:HG3	2.12	0.48
1:E:117:HIS:O	1:E:259(A):ILE:HA	2.13	0.48
2:F:115:ASN:HA	2:F:118:ASP:OD2	2.14	0.48
4:M:90:GLN:CD	4:M:90:GLN:O	2.57	0.48
1:A:291:SER:OG	1:A:292:MET:SD	2.72	0.48
4:L:66:GLY:HA3	4:L:71:PHE:HA	1.94	0.48
1:A:15:ILE:HG21	2:B:117:TYR:CD1	2.49	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:26:VAL:HG22	1:C:27:ASP:H	1.77	0.48
3:J:89:VAL:HG13	3:J:108:LEU:HD22	1.95	0.48
1:A:44:GLU:CD	1:A:288:ILE:HG12	2.39	0.48
1:E:22:SER:OG	1:E:23:THR:N	2.46	0.48
3:H:59:TYR:HB2	3:H:64:LYS:HE3	1.95	0.48
3:H:88:ALA:HB3	3:H:90:TYR:CE2	2.49	0.48
1:E:264:ASP:N	1:E:264:ASP:OD1	2.46	0.48
1:E:103:ASN:HD22	1:E:233:PHE:HE1	1.62	0.47
1:A:316:LEU:HB3	2:B:98:VAL:HG23	1.96	0.47
1:C:44:GLU:OE1	1:C:290:SER:OG	2.32	0.47
1:E:43:LEU:HB2	1:E:314:LEU:HB2	1.96	0.47
1:E:298:HIS:ND1	1:E:299:PRO:HD2	2.30	0.47
4:N:27(A):SER:HA	4:N:69:THR:HG22	1.96	0.47
4:L:63:SER:OG	4:L:64:GLY:N	2.45	0.47
4:M:16:GLY:H	4:M:78:LEU:HB3	1.79	0.47
2:D:108:PHE:O	2:D:112:ASN:ND2	2.47	0.47
3:I:40:PRO:HB2	3:I:43:LYS:HB2	1.96	0.47
1:A:298:HIS:HE1	1:A:300:LEU:CG	2.26	0.47
1:A:320:LEU:HD12	1:A:321:ARG:H	1.78	0.47
2:D:112:ASN:HA	2:D:115:ASN:ND2	2.30	0.47
1:E:320:LEU:HD23	1:E:321:ARG:HB3	1.97	0.47
3:I:41:PRO:HD3	3:I:88:ALA:HA	1.95	0.47
4:N:34:ALA:HB2	4:N:91:TYR:HE1	1.79	0.47
4:N:47:LEU:O	4:N:48:ILE:HD13	2.15	0.47
1:A:176:LEU:HB2	1:A:237:LEU:HD21	1.97	0.47
2:B:117:TYR:O	2:B:120:VAL:HG22	2.14	0.47
1:C:63:ASP:N	1:C:63:ASP:OD1	2.48	0.47
4:M:89:GLN:HG2	4:M:90:GLN:N	2.29	0.47
3:H:19:SER:C	3:H:20:LEU:HD23	2.40	0.47
1:A:42:ILE:HG22	1:A:292:MET:HE3	1.96	0.46
1:A:176:LEU:HB2	1:A:237:LEU:CD2	2.45	0.46
1:E:25:GLN:NE2	1:E:35:THR:HG22	2.30	0.46
2:B:113:VAL:HA	2:B:116:LEU:HD12	1.98	0.46
3:I:82(C):VAL:HG21	3:I:111:VAL:HG11	1.98	0.46
1:A:115:ILE:HG21	1:A:118:PHE:HD1	1.79	0.46
3:J:100(C):VAL:HG23	3:J:103:TRP:NE1	2.31	0.46
2:B:105:THR:HG22	2:B:109:HIS:NE2	2.30	0.46
1:C:126:SER:O	1:C:126:SER:OG	2.32	0.46
2:F:112:ASN:HA	2:F:115:ASN:CG	2.40	0.46
3:J:81:LYS:HA	3:J:81:LYS:HD3	1.82	0.46
1:C:289:ASN:OD1	1:C:289:ASN:N	2.48	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:36:TYR:HE2	4:L:89:GLN:HB2	1.81	0.46
1:E:41:ASP:OD1	1:E:41:ASP:N	2.48	0.46
1:C:117:HIS:O	1:C:259(A):ILE:HA	2.16	0.46
1:E:184:HIS:NE2	1:E:231:ASP:OD2	2.49	0.46
4:L:42:GLN:HG2	4:L:43:ALA:N	2.30	0.46
1:E:15:ILE:HD13	2:F:113:VAL:O	2.16	0.45
1:A:22:SER:OG	1:A:24:GLU:OE1	2.32	0.45
1:E:176:LEU:HB2	1:E:237:LEU:HD21	1.98	0.45
4:N:90:GLN:O	4:N:90:GLN:CD	2.59	0.45
1:C:92:ASN:C	1:C:92:ASN:ND2	2.72	0.45
1:C:288:ILE:HG13	1:C:289:ASN:N	2.32	0.45
2:B:114:LYS:HD3	2:B:114:LYS:HA	1.71	0.45
1:C:114:ARG:HG2	1:C:263:GLY:HA3	1.99	0.45
4:L:8:PRO:HG2	4:L:21:LEU:HA	1.99	0.45
1:C:20:ASN:OD1	1:C:21:ASN:N	2.50	0.45
3:H:47:TRP:HZ2	3:H:50:TYR:CD2	2.35	0.45
1:E:63:ASP:O	1:E:94:ASN:ND2	2.47	0.45
4:N:38:GLN:HG3	4:N:44:PRO:HG3	1.99	0.45
2:F:114:LYS:HD2	2:F:114:LYS:HA	1.69	0.44
3:J:63:LEU:O	3:J:67:VAL:HG23	2.17	0.44
1:A:230:MET:HE2	1:A:252:ILE:HD11	1.98	0.44
1:C:27:ASP:OD1	1:C:27:ASP:N	2.50	0.44
1:C:320:LEU:HD12	1:C:321:ARG:H	1.82	0.44
1:E:189:GLU:OE2	1:E:193:ASN:ND2	2.50	0.44
2:D:67:GLU:N	2:D:67:GLU:OE1	2.51	0.44
2:D:70:ASN:O	2:D:73:ARG:NH1	2.48	0.44
4:M:83:PHE:HD1	4:M:104:VAL:HG13	1.83	0.44
1:A:43:LEU:O	1:A:45:LYS:NZ	2.45	0.44
1:C:53:ASP:OD1	1:C:53(A):LEU:N	2.51	0.44
2:D:96:LEU:HD21	2:F:97:LEU:HD11	2.00	0.44
2:D:112:ASN:HA	2:D:115:ASN:CG	2.43	0.44
2:F:118:ASP:O	2:F:121:ARG:HD2	2.17	0.44
3:H:61:PRO:HA	3:H:64:LYS:HD2	1.99	0.44
3:J:19:SER:HB2	3:J:81:LYS:HE3	1.99	0.44
4:N:38:GLN:HB2	4:N:44:PRO:HG3	2.00	0.44
2:B:97:LEU:O	2:B:101:GLU:HB2	2.18	0.43
1:E:124:LYS:HZ2	1:E:131:THR:HG1	1.60	0.43
2:F:101:GLU:O	2:F:105:THR:OG1	2.16	0.43
4:M:2:ILE:N	4:M:2:ILE:HD12	2.33	0.43
1:C:153:TRP:CD1	1:C:153:TRP:C	2.96	0.43
1:A:41:ASP:OD2	1:A:45:LYS:NZ	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:25:GLN:HA	1:E:34:VAL:O	2.18	0.43
1:E:310:LYS:HE3	2:F:87:LEU:HD21	2.00	0.43
3:I:47:TRP:HZ2	3:I:50:TYR:CD2	2.36	0.43
2:D:80:LYS:HE2	2:D:80:LYS:HB3	1.90	0.43
1:C:53(A):LEU:HD23	1:C:53(A):LEU:HA	1.83	0.43
1:E:130:GLU:HG2	1:E:133:LEU:HG	2.00	0.43
3:H:43:LYS:HB3	3:H:43:LYS:HE3	1.68	0.43
4:L:11:LEU:HD12	4:L:13:LEU:HD21	1.99	0.43
2:B:110:ASP:O	2:B:113:VAL:HG12	2.18	0.43
3:H:102:TYR:C	3:H:103:TRP:HD1	2.26	0.43
3:H:103:TRP:CZ3	4:L:44:PRO:HD2	2.54	0.42
1:A:35:THR:O	1:A:35:THR:OG1	2.37	0.42
2:D:87:LEU:O	2:D:91:THR:HG22	2.18	0.42
1:C:129(A):HIS:HA	1:C:157:LYS:HB2	2.00	0.42
4:N:95:LEU:HD12	4:N:95:LEU:HA	1.85	0.42
1:A:43:LEU:HD13	1:A:314:LEU:HD12	2.01	0.42
1:C:35:THR:O	1:C:35:THR:OG1	2.29	0.42
1:C:81:VAL:HB	1:C:84:TRP:CZ3	2.55	0.42
2:F:115:ASN:OD1	2:F:116:LEU:N	2.53	0.42
3:I:45:LEU:HD12	4:M:98:PHE:CE2	2.55	0.42
3:J:43:LYS:HB3	3:J:43:LYS:HE3	1.82	0.42
1:A:53(A):LEU:HD23	1:A:53(A):LEU:HA	1.82	0.42
4:M:47:LEU:O	4:M:48:ILE:HD13	2.18	0.42
1:A:89:GLU:O	1:A:269:LYS:HA	2.20	0.42
3:H:66:ARG:NH1	3:H:86:ASP:OD2	2.53	0.42
4:N:76:SER:HG	4:N:77:ARG:H	1.64	0.42
4:M:38:GLN:HG3	4:M:44:PRO:HG3	2.02	0.42
1:E:165:LYS:HE2	1:E:165:LYS:HB2	1.71	0.42
4:L:75:ILE:O	4:L:77:ARG:N	2.53	0.42
4:M:100:GLN:H	4:M:100:GLN:HG3	1.75	0.42
4:N:37:GLN:O	4:N:44:PRO:HA	2.19	0.42
1:A:40:GLN:HG2	1:A:41:ASP:H	1.85	0.41
1:A:316:LEU:H	1:A:316:LEU:HD23	1.84	0.41
1:C:17:TYR:O	1:C:17:TYR:CD1	2.72	0.41
1:C:42:ILE:HB	1:C:293:PRO:HD2	2.02	0.41
1:E:176:LEU:HB2	1:E:237:LEU:CD2	2.50	0.41
4:M:39:LYS:HB3	4:M:39:LYS:HE3	1.68	0.41
2:B:59:THR:HG22	2:F:88:ASP:OD2	2.20	0.41
2:B:88:ASP:CG	2:D:59:THR:HG22	2.45	0.41
1:C:41:ASP:CG	1:C:43:LEU:H	2.27	0.41
1:C:90:ARG:O	1:C:92(A):PRO:HG3	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:61:ARG:H	4:L:61:ARG:HG2	1.60	0.41
4:N:72:THR:OG1	4:N:73:LEU:N	2.54	0.41
1:C:57:LYS:HG2	1:C:58:PRO:HD2	2.03	0.41
3:I:59:TYR:HE2	3:I:69:ILE:HD12	1.86	0.41
3:J:58:LYS:HB3	4:N:95:LEU:HD11	2.03	0.41
3:J:103:TRP:CH2	4:N:44:PRO:HB2	2.56	0.41
4:L:16:GLY:H	4:L:78:LEU:HB3	1.85	0.41
2:B:112:ASN:HA	2:B:115:ASN:ND2	2.32	0.41
2:D:96:LEU:O	2:D:100:MET:HG3	2.20	0.41
1:E:283:THR:HB	1:E:286:GLY:O	2.21	0.41
4:M:54:ARG:NH1	4:M:59:PRO:O	2.54	0.41
3:H:4:LEU:HD13	3:H:92:CYS:HB3	2.02	0.41
3:I:81:LYS:HE2	3:I:81:LYS:HB2	1.83	0.41
4:L:30:SER:HB3	4:L:51:ALA:HB2	2.03	0.41
4:L:47:LEU:O	4:L:48:ILE:HD13	2.20	0.41
1:A:29:ILE:HG23	1:A:30:MET:HG3	2.02	0.41
1:C:261:LYS:HB3	1:C:261:LYS:HE3	1.86	0.41
1:E:32:LYS:HA	1:E:32:LYS:HD2	1.87	0.41
1:E:58:PRO:HB3	1:E:86:TYR:CE1	2.56	0.41
2:F:121:ARG:NH1	2:F:121:ARG:HA	2.35	0.41
3:H:13:LYS:NZ	3:H:113:SER:O	2.38	0.41
4:M:19:ALA:HB1	4:M:21:LEU:HD23	2.03	0.41
1:C:81:VAL:HB	1:C:84:TRP:HZ3	1.86	0.41
1:C:133:LEU:HB2	1:C:155:ILE:CD1	2.49	0.41
3:H:75:LYS:H	3:H:75:LYS:HG2	1.74	0.41
1:E:80(A):ARG:HD2	1:E:80(A):ARG:HA	1.76	0.40
4:N:39:LYS:HE3	4:N:39:LYS:HB3	1.94	0.40
2:F:69:ASN:OD1	2:F:70:ASN:N	2.48	0.40
3:H:71:VAL:HG23	3:H:78:PHE:HB3	2.02	0.40
4:L:48:ILE:HG23	4:L:53:SER:H	1.86	0.40
3:J:103:TRP:CE3	4:N:43:ALA:HB1	2.56	0.40
1:A:164:ILE:O	1:A:246:GLU:HA	2.21	0.40
1:E:37:THR:C	1:E:38:HIS:ND1	2.80	0.40
4:N:61:ARG:NH2	4:N:82:ASP:OD2	2.54	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	313/342 (92%)	278 (89%)	35 (11%)	0	100 100
1	C	314/342 (92%)	278 (88%)	36 (12%)	0	100 100
1	E	314/342 (92%)	279 (89%)	34 (11%)	1 (0%)	37 68
2	B	66/227 (29%)	64 (97%)	2 (3%)	0	100 100
2	D	66/227 (29%)	64 (97%)	2 (3%)	0	100 100
2	F	66/227 (29%)	62 (94%)	3 (4%)	1 (2%)	8 37
3	H	119/121 (98%)	110 (92%)	9 (8%)	0	100 100
3	I	119/121 (98%)	108 (91%)	11 (9%)	0	100 100
3	J	119/121 (98%)	110 (92%)	9 (8%)	0	100 100
4	L	107/109 (98%)	99 (92%)	7 (6%)	1 (1%)	14 48
4	M	107/109 (98%)	101 (94%)	6 (6%)	0	100 100
4	N	107/109 (98%)	94 (88%)	12 (11%)	1 (1%)	14 48
All	All	1817/2397 (76%)	1647 (91%)	166 (9%)	4 (0%)	45 74

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	111	SER
4	L	76	SER
4	N	76	SER
1	E	261	LYS

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	279/305 (92%)	275 (99%)	4 (1%)	62 80
1	C	280/305 (92%)	278 (99%)	2 (1%)	81 90
1	E	280/305 (92%)	280 (100%)	0	100 100
2	B	64/192 (33%)	64 (100%)	0	100 100
2	D	64/192 (33%)	63 (98%)	1 (2%)	58 78
2	F	64/192 (33%)	64 (100%)	0	100 100
3	H	103/103 (100%)	102 (99%)	1 (1%)	73 86
3	I	103/103 (100%)	102 (99%)	1 (1%)	73 86
3	J	103/103 (100%)	102 (99%)	1 (1%)	73 86
4	L	91/91 (100%)	91 (100%)	0	100 100
4	M	91/91 (100%)	91 (100%)	0	100 100
4	N	91/91 (100%)	91 (100%)	0	100 100
All	All	1613/2073 (78%)	1603 (99%)	10 (1%)	82 91

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	VAL
1	A	64	CYS
1	A	155	ILE
1	A	277	CYS
1	C	92	ASN
1	C	92(A)	PRO
2	D	100	MET
3	H	105	GLN
3	I	105	GLN
3	J	103	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	ASN
1	A	150	ASN
1	A	172	ASN
2	B	102	ASN
2	B	115	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	116	ASN
1	C	121(A)	GLN
1	C	129	ASN
1	C	172	ASN
1	C	186	ASN
1	C	296	ASN
2	D	79	ASN
1	E	18	HIS
1	E	47	HIS
1	E	172	ASN
1	E	197	ASN
1	E	276	HIS
3	H	39	GLN
3	I	60	ASN
3	I	77	GLN
4	N	6	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

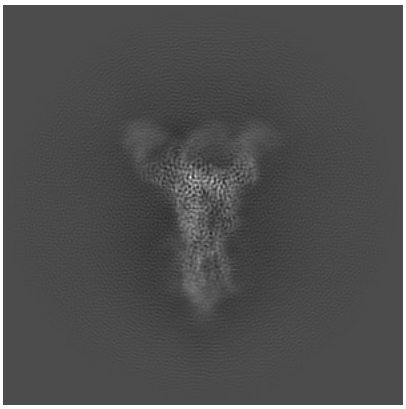
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-48521. These allow visual inspection of the internal detail of the map and identification of artifacts.

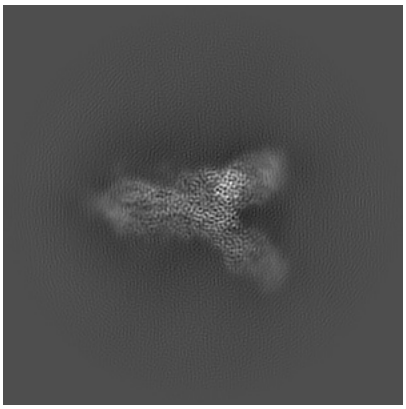
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

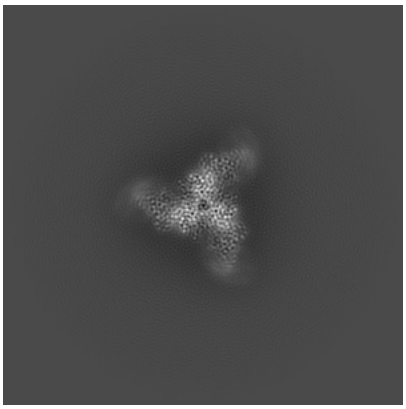
6.1.1 Primary map



X

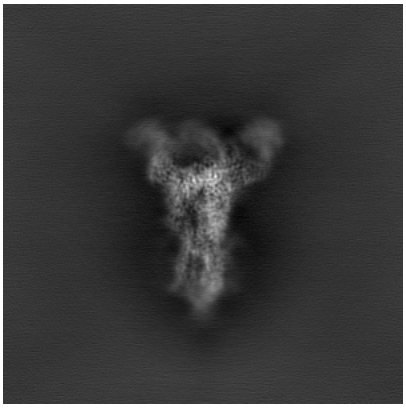


Y

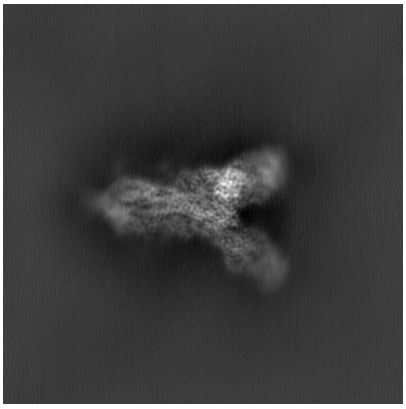


Z

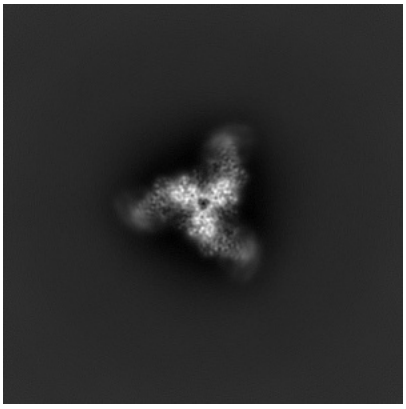
6.1.2 Raw map



X



Y

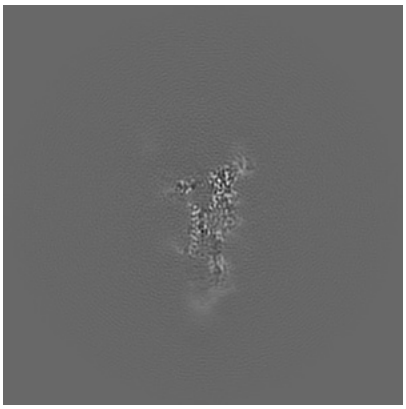


Z

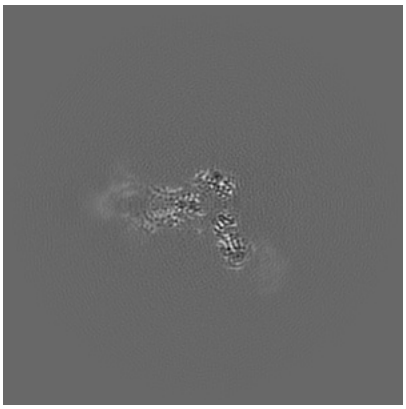
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

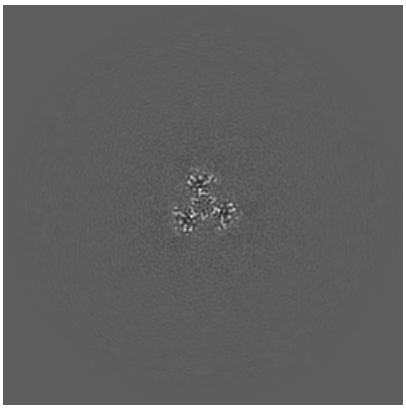
6.2.1 Primary map



X Index: 200

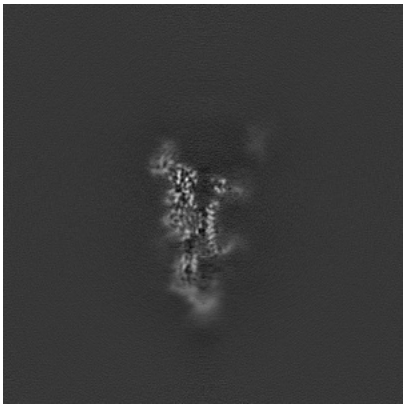


Y Index: 200

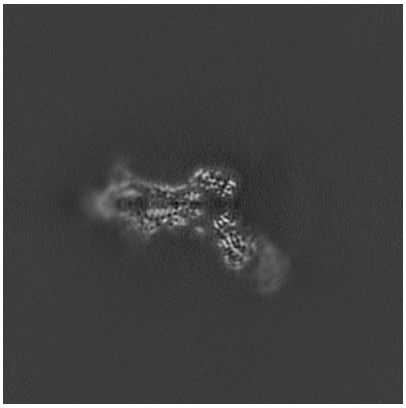


Z Index: 200

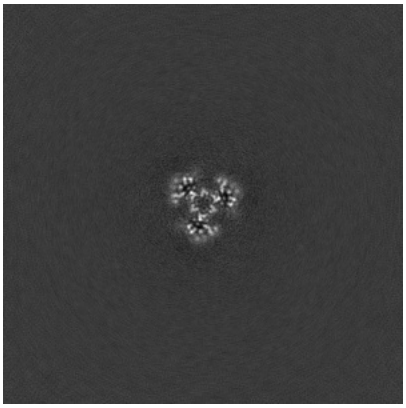
6.2.2 Raw map



X Index: 200



Y Index: 200

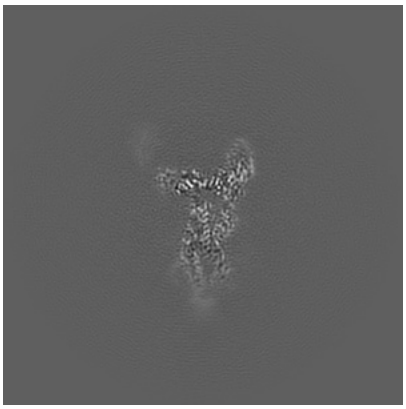


Z Index: 200

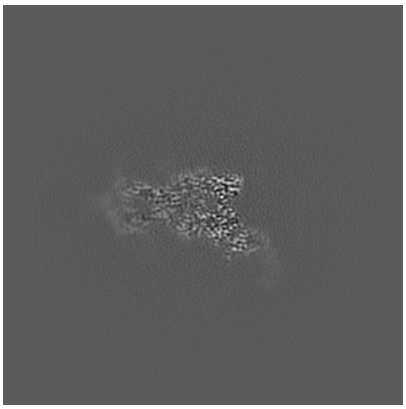
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

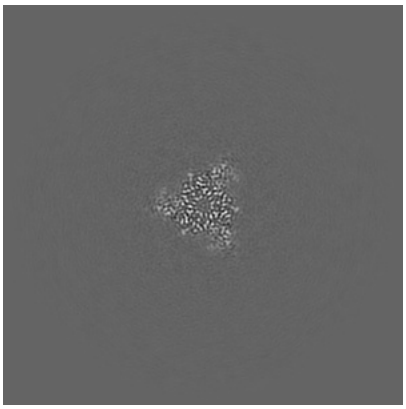
6.3.1 Primary map



X Index: 208

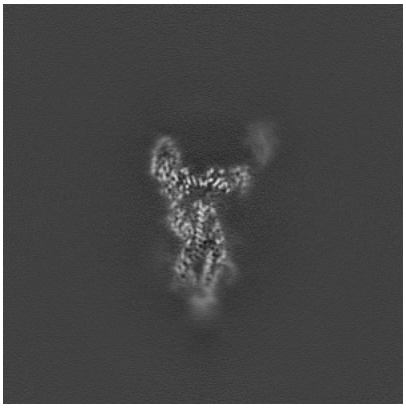


Y Index: 188

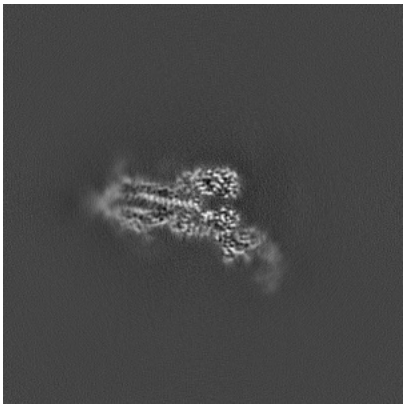


Z Index: 219

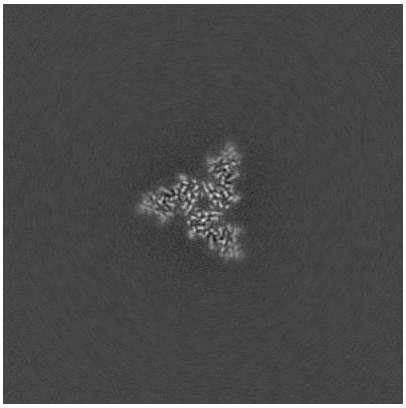
6.3.2 Raw map



X Index: 208



Y Index: 206

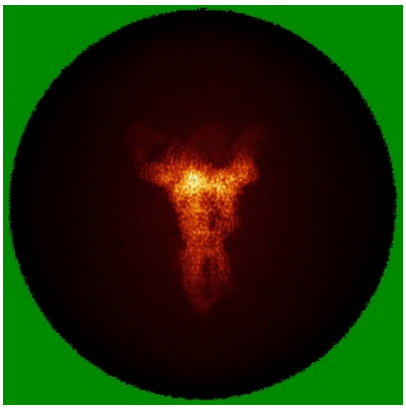


Z Index: 224

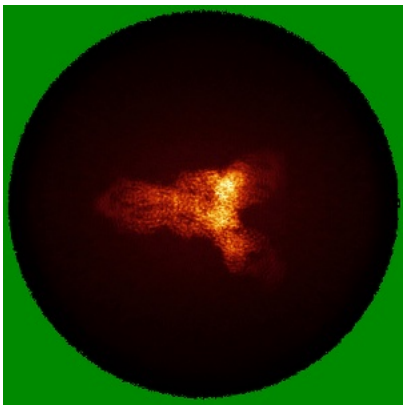
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

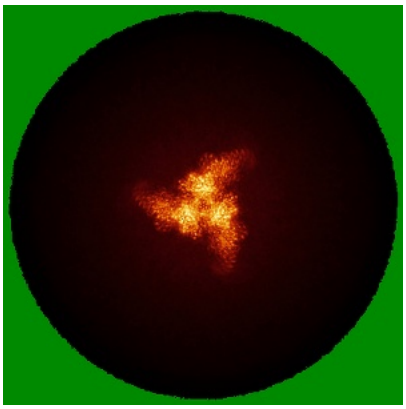
6.4.1 Primary map



X

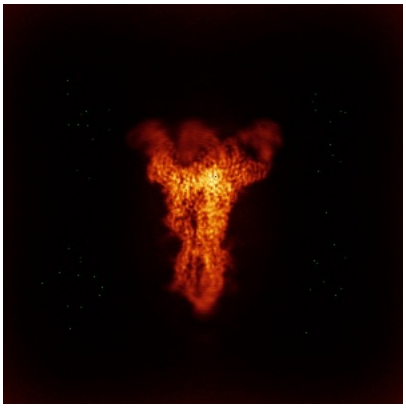


Y

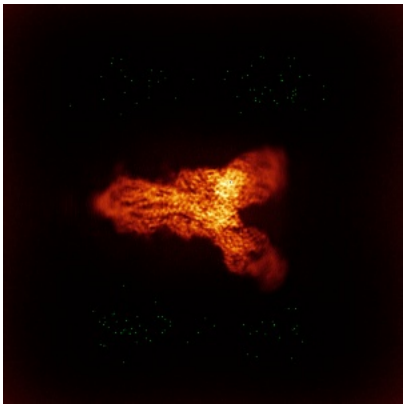


Z

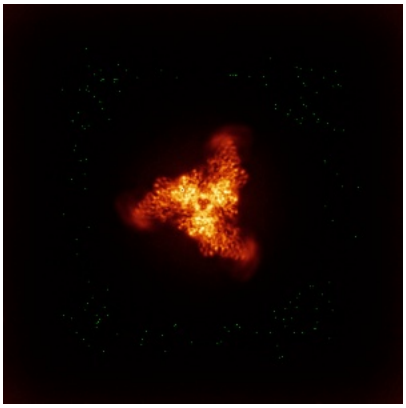
6.4.2 Raw map



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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.252. 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

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.

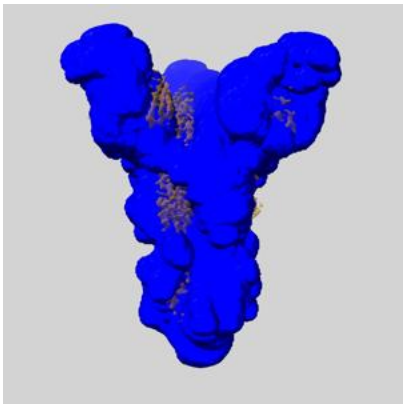
6.6 Mask visualisation (i)

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

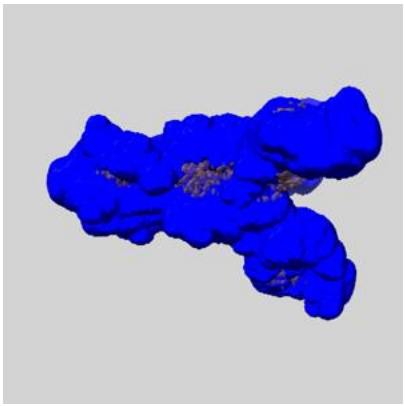
A mask typically either:

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

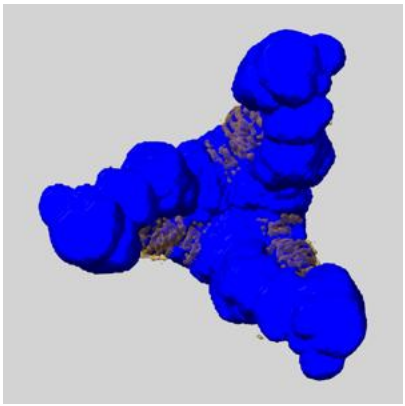
6.6.1 emd_48521_msk_1.map (i)



X



Y

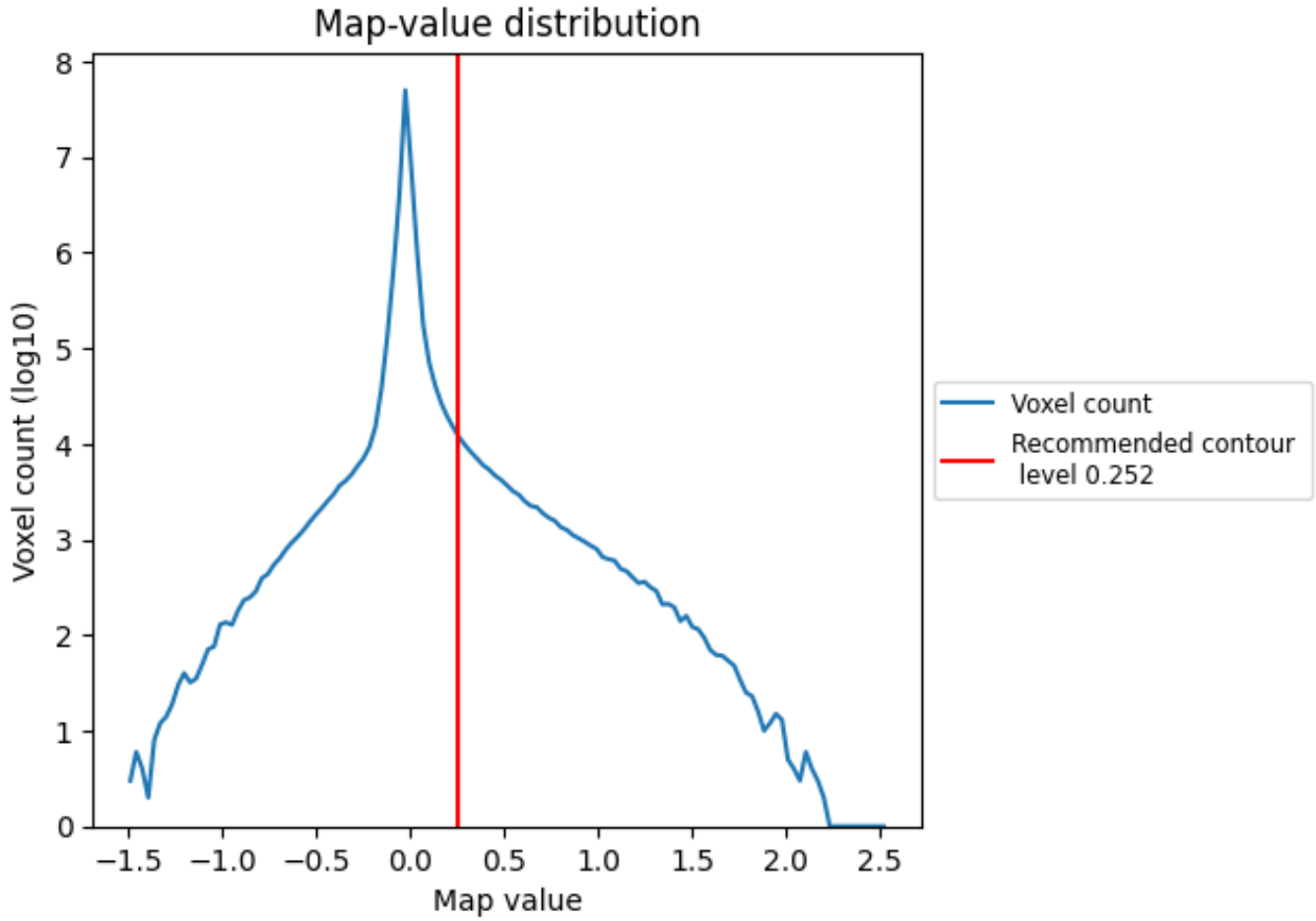


Z

7 Map analysis

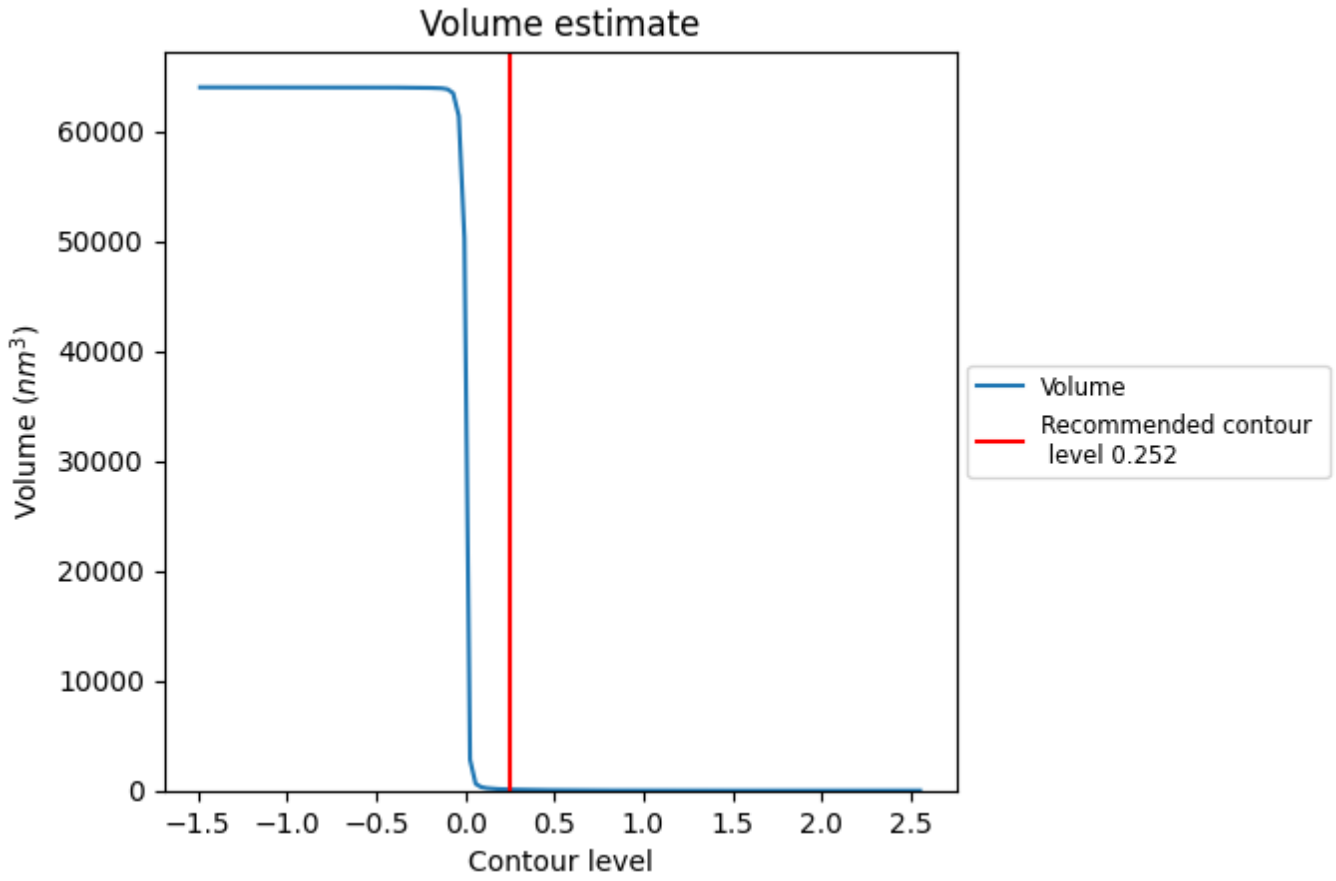
This section contains the results of statistical analysis of the map.

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.

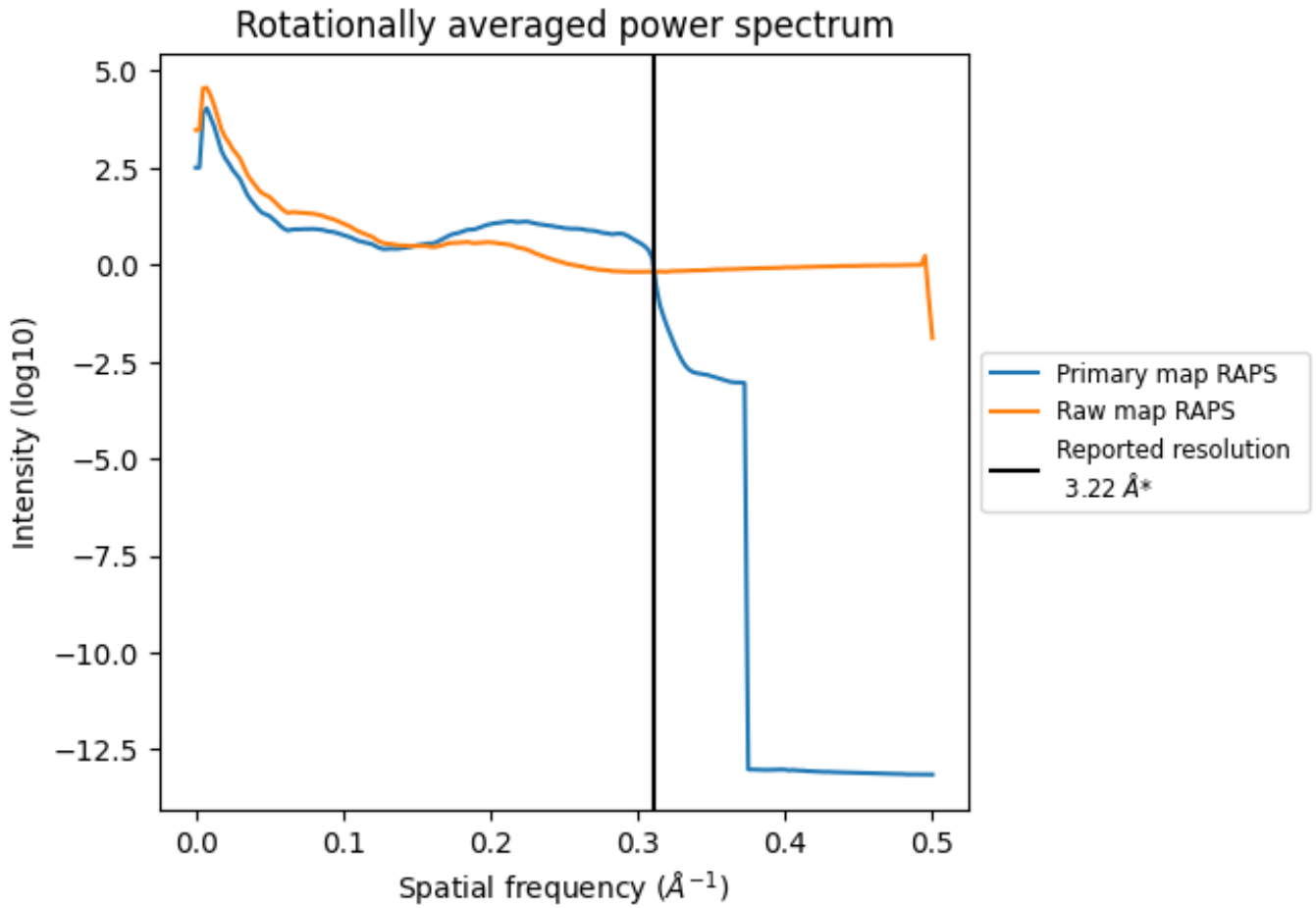
7.2 Volume estimate (i)



The volume at the recommended contour level is 97 nm^3; this corresponds to an approximate mass of 88 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)

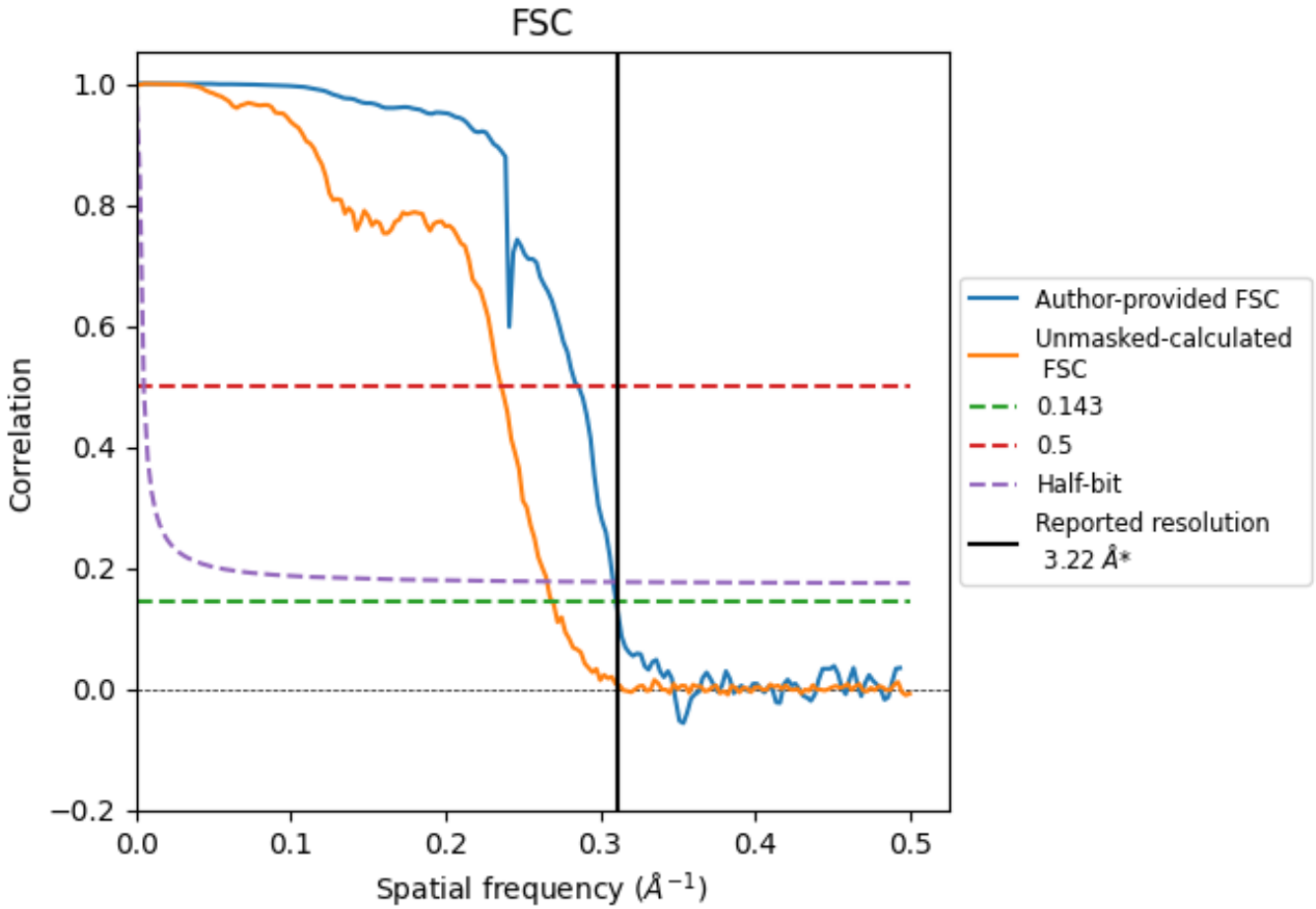


*Reported resolution corresponds to spatial frequency of 0.311 $Å^{-1}$

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 0.311 Å^{-1}

8.2 Resolution estimates (i)

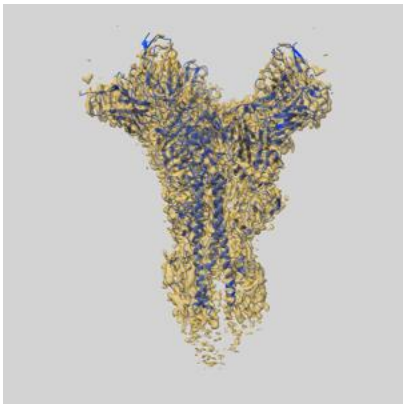
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.22	-	-
Author-provided FSC curve	3.22	3.50	3.24
Unmasked-calculated*	3.71	4.24	3.77

*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 3.71 differs from the reported value 3.22 by more than 10 %

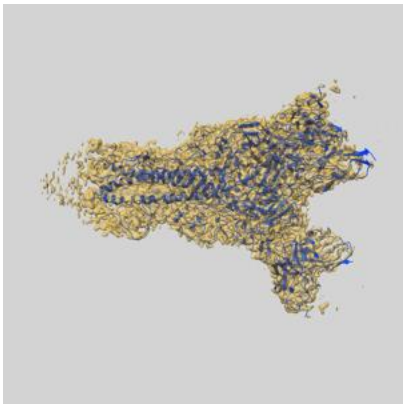
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-48521 and PDB model 9MQD. Per-residue inclusion information can be found in section 3 on page 10.

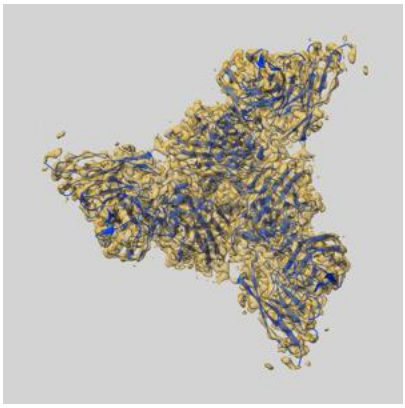
9.1 Map-model overlay



X



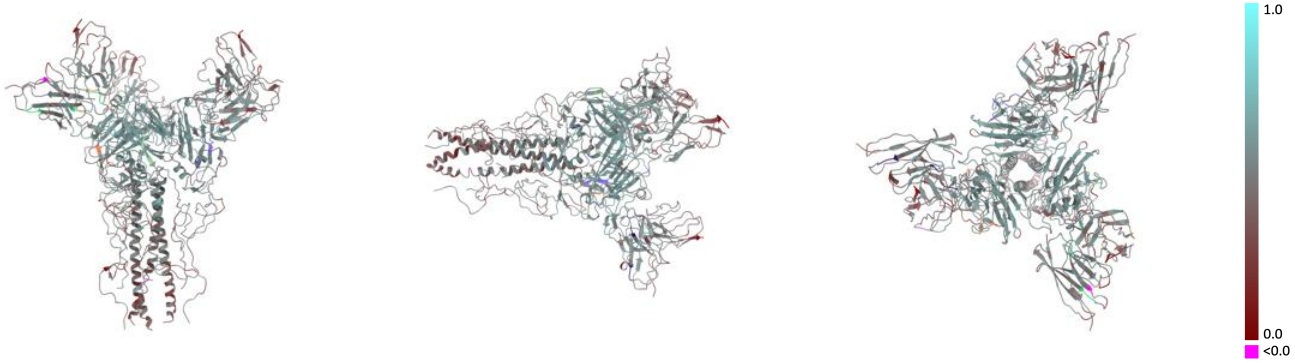
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.252 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.

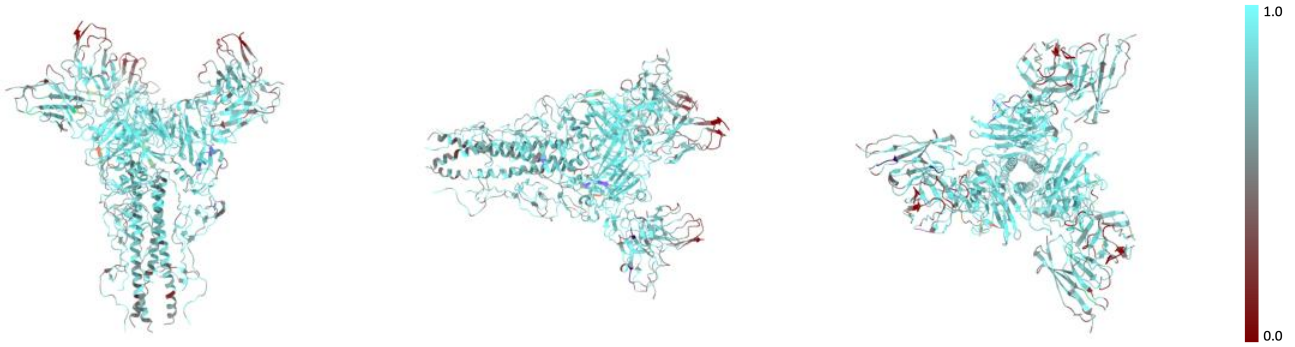
9.2 Q-score mapped to coordinate model (i)



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.

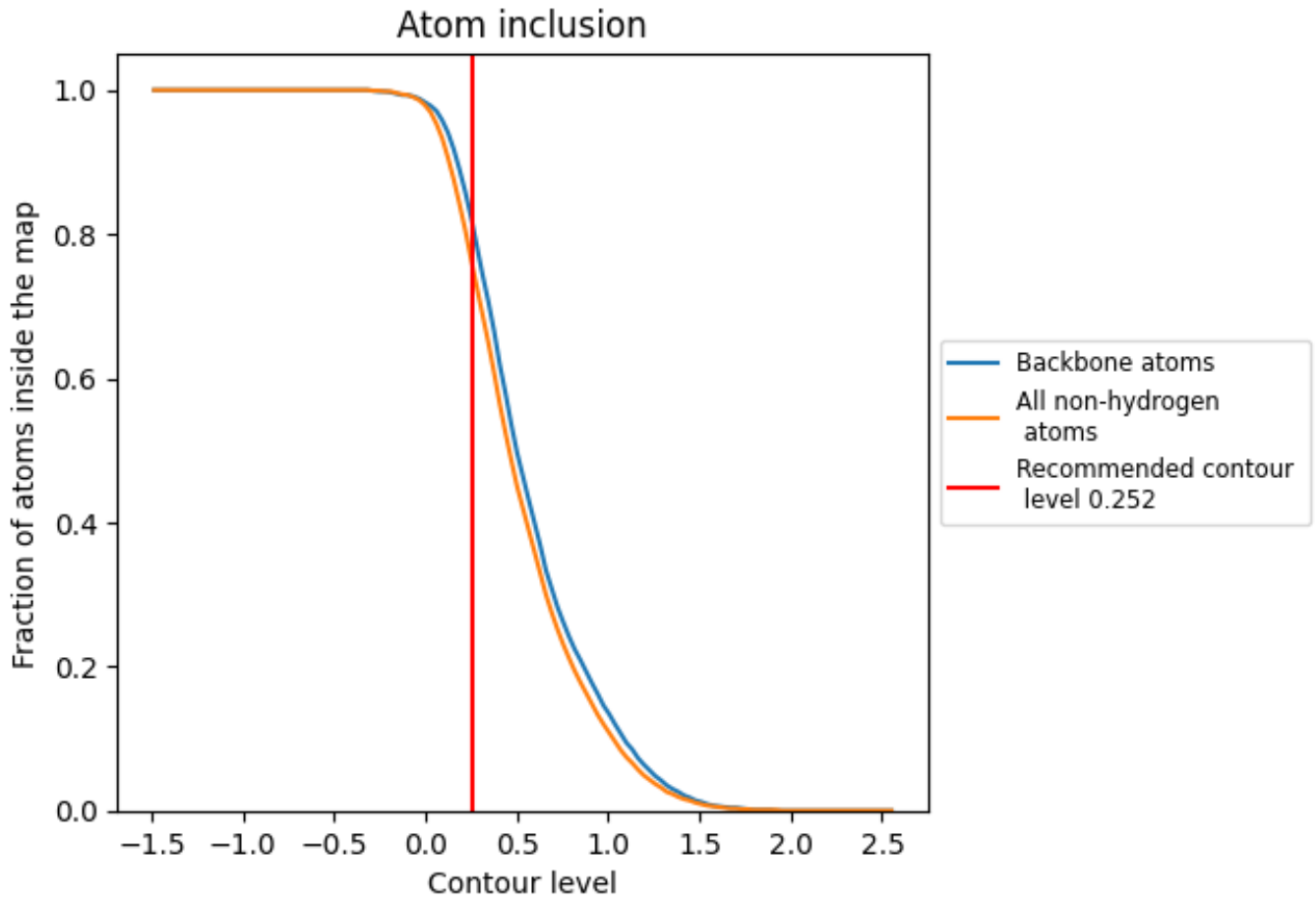
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.252).

9.4 Atom inclusion (i)



At the recommended contour level, 82% of all backbone atoms, 76% 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 (0.252) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7610	0.4870
A	0.8360	0.5170
B	0.7270	0.4420
C	0.8320	0.5120
D	0.7200	0.4250
E	0.8300	0.5160
F	0.7230	0.4400
H	0.7380	0.4780
I	0.7390	0.4780
J	0.7350	0.4870
L	0.5960	0.4460
M	0.5990	0.4440
N	0.6030	0.4440