wwPDB EM Validation Summary Report

Nov 7, 2022 – 10:25 PM EST

PDB ID	:	6CXC
EMDB ID	:	EMD-7774
Title	:	3.9A Cryo-EM structure of murine antibody bound at a novel epitope of respiratory syncytial virus fusion protein
Authors	:	Xie, Q.; Wang, Z.; Chen, X.; Ni, F.; Ma, J.; Wang, Q.
Deposited on	:	2018-04-02
Resolution	:	3.90 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:

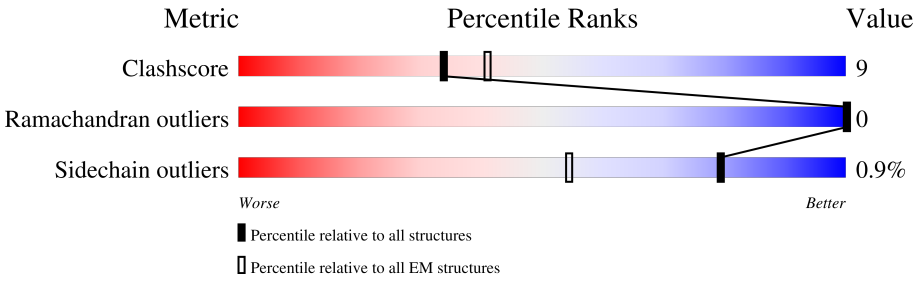
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (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 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



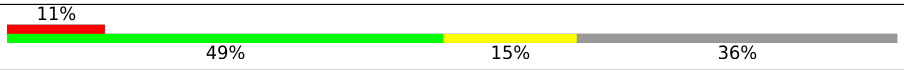
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	G	118	28% 67% 29%
1	I	118	28% 69% 26%
1	X	118	26% 67% 29%
2	J	122	20% 68% 20% 11%
2	K	122	23% 68% 20% 11%
2	Y	122	19% 70% 19% 11%
3	A	548	11% 87%
3	B	548	13% 49% 16% 35%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	C	548	
3	D	548	
3	E	548	
3	F	548	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 15196 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 R4.C6 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	X	114	Total	C	N	O	S	0	0
			872	552	147	169	4		
1	G	114	Total	C	N	O	S	0	0
			872	552	147	169	4		
1	I	114	Total	C	N	O	S	0	0
			872	552	147	169	4		

- Molecule 2 is a protein called R4.C6 Fab Light Chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Y	108	Total	C	N	O	S	0	0
			847	532	150	162	3		
2	J	108	Total	C	N	O	S	0	0
			847	532	150	162	3		
2	K	108	Total	C	N	O	S	0	0
			847	532	150	162	3		

- Molecule 3 is a protein called Fusion glycoprotein F0, Envelope glycoprotein chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	73	Total	C	N	O	S	0	0
			580	366	95	116	3		
3	B	358	Total	C	N	O	S	0	0
			2765	1744	458	545	18		
3	C	72	Total	C	N	O	S	0	0
			571	361	93	114	3		
3	D	352	Total	C	N	O	S	0	0
			2733	1725	452	538	18		
3	E	73	Total	C	N	O	S	0	0
			580	366	95	116	3		
3	F	351	Total	C	N	O	S	0	0
			2726	1720	451	537	18		

There are 138 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	102	ALA	PRO	conflict	UNP P03420
A	133	GLN	ARG	conflict	UNP P03420
A	135	GLN	ARG	conflict	UNP P03420
A	136	GLN	ARG	conflict	UNP P03420
A	379	VAL	ILE	conflict	UNP P03420
A	447	VAL	MET	conflict	UNP P03420
A	527	GLY	-	linker	UNP P03420
A	528	ALA	-	linker	UNP P03420
A	529	LEU	-	linker	UNP P03420
A	530	VAL	-	linker	UNP P03420
A	531	PRO	-	linker	UNP P03420
A	532	ARG	-	linker	UNP P03420
A	533	GLY	-	linker	UNP P03420
A	534	SER	-	linker	UNP P03420
A	535	PRO	-	linker	UNP P03420
A	536	GLY	-	linker	UNP P03420
A	537	SER	-	linker	UNP P03420
A	568	HIS	-	expression tag	UNP M1E1E4
A	569	HIS	-	expression tag	UNP M1E1E4
A	570	HIS	-	expression tag	UNP M1E1E4
A	571	HIS	-	expression tag	UNP M1E1E4
A	572	HIS	-	expression tag	UNP M1E1E4
A	573	HIS	-	expression tag	UNP M1E1E4
B	102	ALA	PRO	conflict	UNP P03420
B	133	GLN	ARG	conflict	UNP P03420
B	135	GLN	ARG	conflict	UNP P03420
B	136	GLN	ARG	conflict	UNP P03420
B	379	VAL	ILE	conflict	UNP P03420
B	447	VAL	MET	conflict	UNP P03420
B	527	GLY	-	linker	UNP P03420
B	528	ALA	-	linker	UNP P03420
B	529	LEU	-	linker	UNP P03420
B	530	VAL	-	linker	UNP P03420
B	531	PRO	-	linker	UNP P03420
B	532	ARG	-	linker	UNP P03420
B	533	GLY	-	linker	UNP P03420
B	534	SER	-	linker	UNP P03420
B	535	PRO	-	linker	UNP P03420
B	536	GLY	-	linker	UNP P03420
B	537	SER	-	linker	UNP P03420
B	568	HIS	-	expression tag	UNP M1E1E4
B	569	HIS	-	expression tag	UNP M1E1E4
B	570	HIS	-	expression tag	UNP M1E1E4

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	571	HIS	-	expression tag	UNP M1E1E4
B	572	HIS	-	expression tag	UNP M1E1E4
B	573	HIS	-	expression tag	UNP M1E1E4
C	102	ALA	PRO	conflict	UNP P03420
C	133	GLN	ARG	conflict	UNP P03420
C	135	GLN	ARG	conflict	UNP P03420
C	136	GLN	ARG	conflict	UNP P03420
C	379	VAL	ILE	conflict	UNP P03420
C	447	VAL	MET	conflict	UNP P03420
C	527	GLY	-	linker	UNP P03420
C	528	ALA	-	linker	UNP P03420
C	529	LEU	-	linker	UNP P03420
C	530	VAL	-	linker	UNP P03420
C	531	PRO	-	linker	UNP P03420
C	532	ARG	-	linker	UNP P03420
C	533	GLY	-	linker	UNP P03420
C	534	SER	-	linker	UNP P03420
C	535	PRO	-	linker	UNP P03420
C	536	GLY	-	linker	UNP P03420
C	537	SER	-	linker	UNP P03420
C	568	HIS	-	expression tag	UNP M1E1E4
C	569	HIS	-	expression tag	UNP M1E1E4
C	570	HIS	-	expression tag	UNP M1E1E4
C	571	HIS	-	expression tag	UNP M1E1E4
C	572	HIS	-	expression tag	UNP M1E1E4
C	573	HIS	-	expression tag	UNP M1E1E4
D	102	ALA	PRO	conflict	UNP P03420
D	133	GLN	ARG	conflict	UNP P03420
D	135	GLN	ARG	conflict	UNP P03420
D	136	GLN	ARG	conflict	UNP P03420
D	379	VAL	ILE	conflict	UNP P03420
D	447	VAL	MET	conflict	UNP P03420
D	527	GLY	-	linker	UNP P03420
D	528	ALA	-	linker	UNP P03420
D	529	LEU	-	linker	UNP P03420
D	530	VAL	-	linker	UNP P03420
D	531	PRO	-	linker	UNP P03420
D	532	ARG	-	linker	UNP P03420
D	533	GLY	-	linker	UNP P03420
D	534	SER	-	linker	UNP P03420
D	535	PRO	-	linker	UNP P03420
D	536	GLY	-	linker	UNP P03420

Continued on next page...

Continued from previous page...

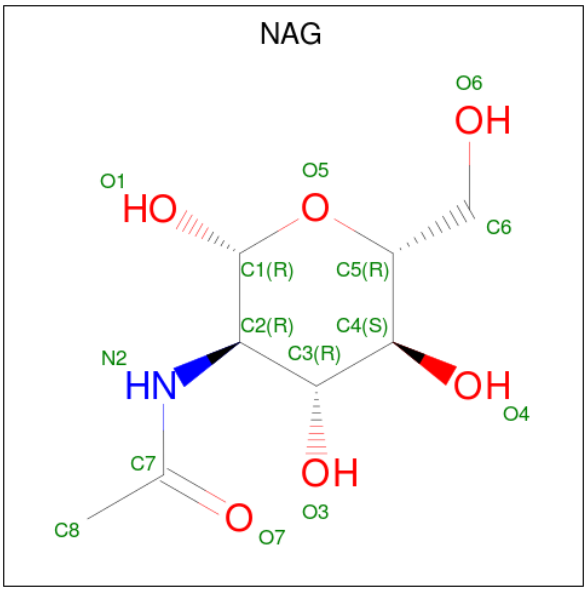
Chain	Residue	Modelled	Actual	Comment	Reference
D	537	SER	-	linker	UNP P03420
D	568	HIS	-	expression tag	UNP M1E1E4
D	569	HIS	-	expression tag	UNP M1E1E4
D	570	HIS	-	expression tag	UNP M1E1E4
D	571	HIS	-	expression tag	UNP M1E1E4
D	572	HIS	-	expression tag	UNP M1E1E4
D	573	HIS	-	expression tag	UNP M1E1E4
E	102	ALA	PRO	conflict	UNP P03420
E	133	GLN	ARG	conflict	UNP P03420
E	135	GLN	ARG	conflict	UNP P03420
E	136	GLN	ARG	conflict	UNP P03420
E	379	VAL	ILE	conflict	UNP P03420
E	447	VAL	MET	conflict	UNP P03420
E	527	GLY	-	linker	UNP P03420
E	528	ALA	-	linker	UNP P03420
E	529	LEU	-	linker	UNP P03420
E	530	VAL	-	linker	UNP P03420
E	531	PRO	-	linker	UNP P03420
E	532	ARG	-	linker	UNP P03420
E	533	GLY	-	linker	UNP P03420
E	534	SER	-	linker	UNP P03420
E	535	PRO	-	linker	UNP P03420
E	536	GLY	-	linker	UNP P03420
E	537	SER	-	linker	UNP P03420
E	568	HIS	-	expression tag	UNP M1E1E4
E	569	HIS	-	expression tag	UNP M1E1E4
E	570	HIS	-	expression tag	UNP M1E1E4
E	571	HIS	-	expression tag	UNP M1E1E4
E	572	HIS	-	expression tag	UNP M1E1E4
E	573	HIS	-	expression tag	UNP M1E1E4
F	102	ALA	PRO	conflict	UNP P03420
F	133	GLN	ARG	conflict	UNP P03420
F	135	GLN	ARG	conflict	UNP P03420
F	136	GLN	ARG	conflict	UNP P03420
F	379	VAL	ILE	conflict	UNP P03420
F	447	VAL	MET	conflict	UNP P03420
F	527	GLY	-	linker	UNP P03420
F	528	ALA	-	linker	UNP P03420
F	529	LEU	-	linker	UNP P03420
F	530	VAL	-	linker	UNP P03420
F	531	PRO	-	linker	UNP P03420
F	532	ARG	-	linker	UNP P03420

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	533	GLY	-	linker	UNP P03420
F	534	SER	-	linker	UNP P03420
F	535	PRO	-	linker	UNP P03420
F	536	GLY	-	linker	UNP P03420
F	537	SER	-	linker	UNP P03420
F	568	HIS	-	expression tag	UNP M1E1E4
F	569	HIS	-	expression tag	UNP M1E1E4
F	570	HIS	-	expression tag	UNP M1E1E4
F	571	HIS	-	expression tag	UNP M1E1E4
F	572	HIS	-	expression tag	UNP M1E1E4
F	573	HIS	-	expression tag	UNP M1E1E4

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	D	1	Total	C	N	O	0
			14	8	1	5	
4	E	1	Total	C	N	O	0
			14	8	1	5	

Continued on next page...

Continued from previous page...

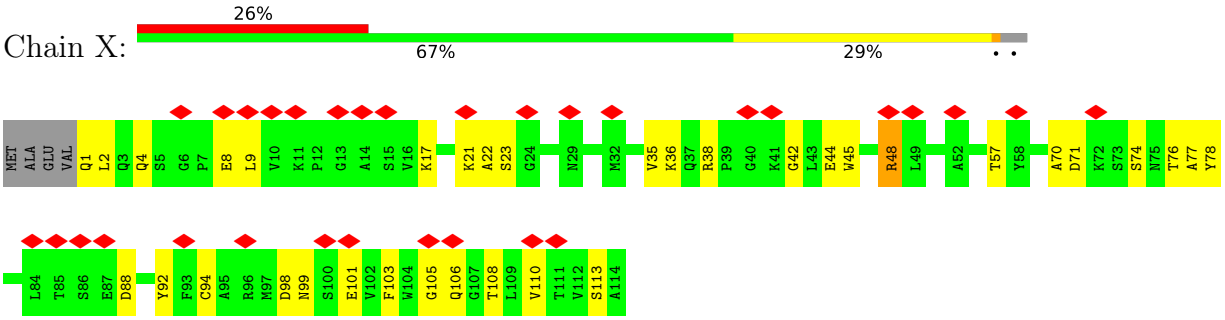
Mol	Chain	Residues	Atoms				AltConf
4	F	1	Total	C	N	O	0
			14	8	1	5	

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.

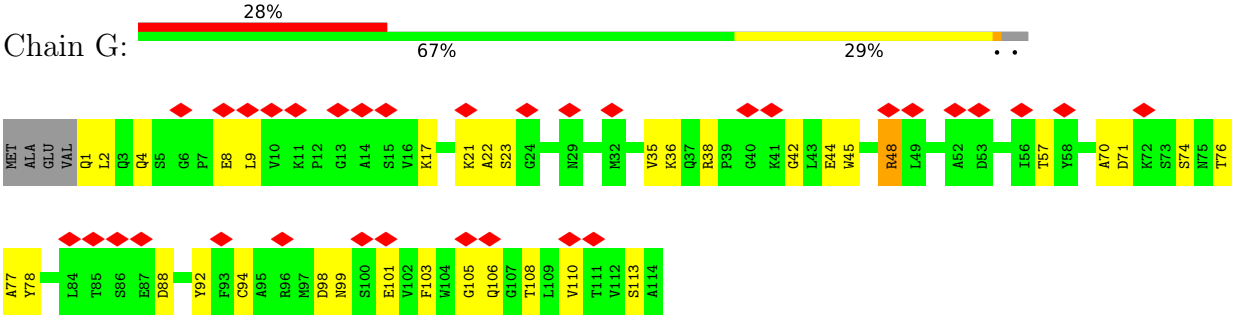
• Molecule 1: R4.C6 Fab Heavy Chain

Chain X:



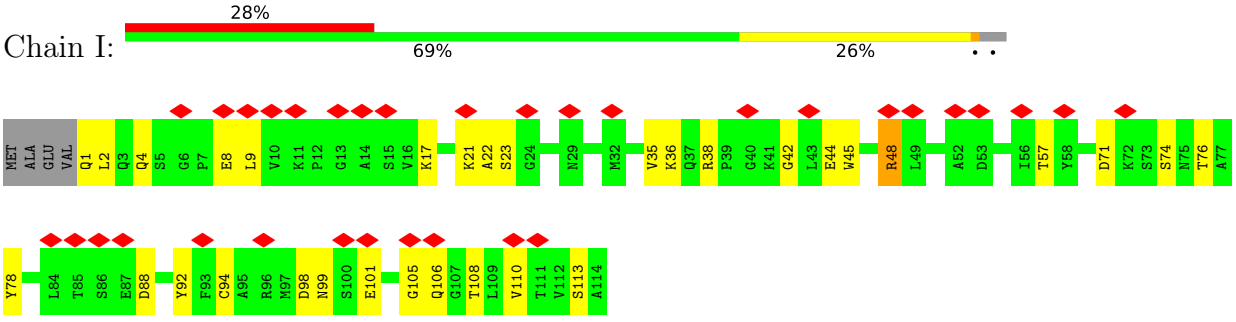
• Molecule 1: R4.C6 Fab Heavy Chain

Chain G:



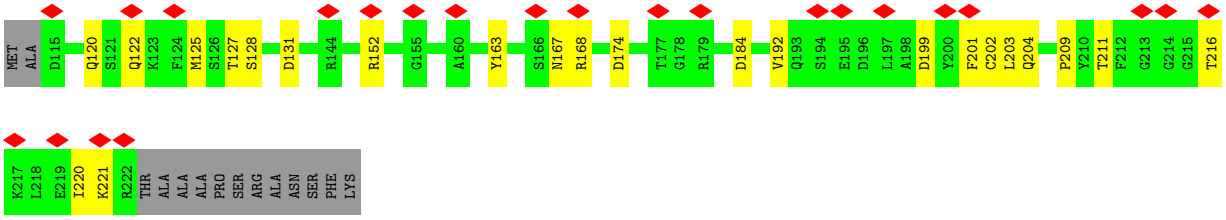
• Molecule 1: R4.C6 Fab Heavy Chain

Chain I:



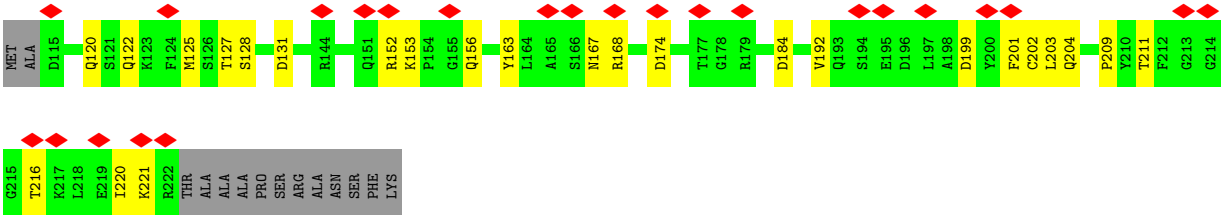
• Molecule 2: R4.C6 Fab Light Chain

Chain Y:



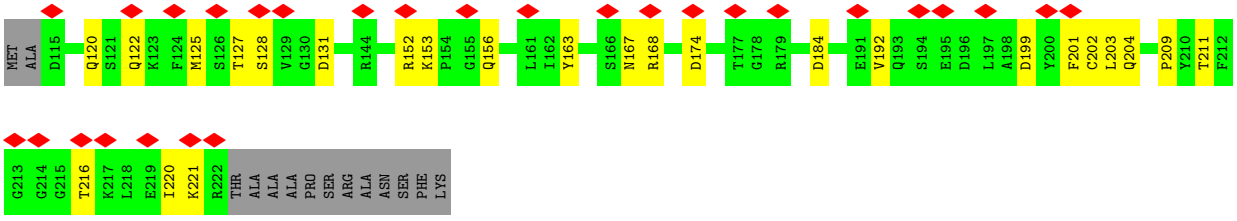
• Molecule 2: R4.C6 Fab Light Chain

Chain J:



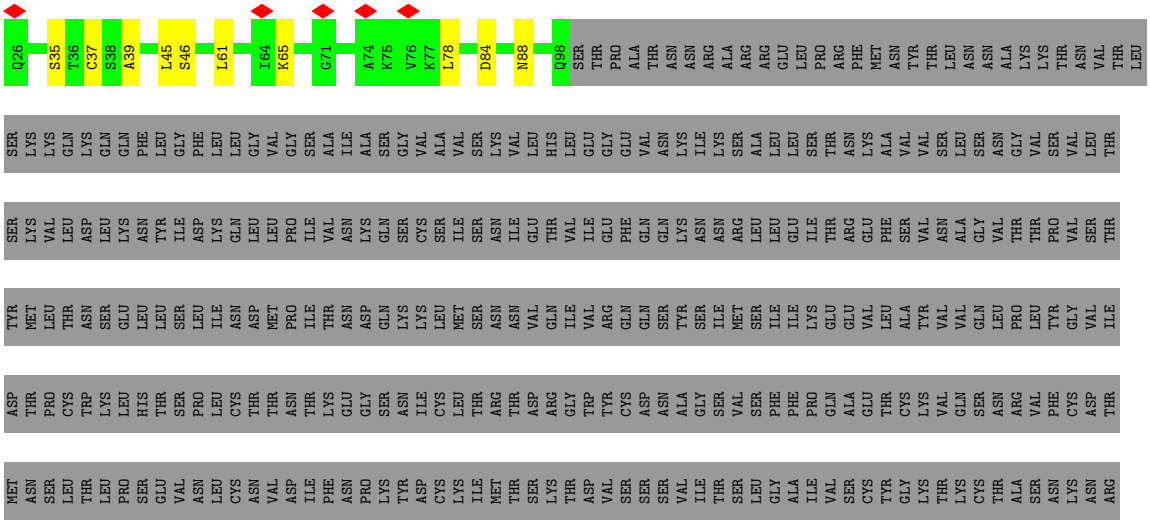
• Molecule 2: R4.C6 Fab Light Chain

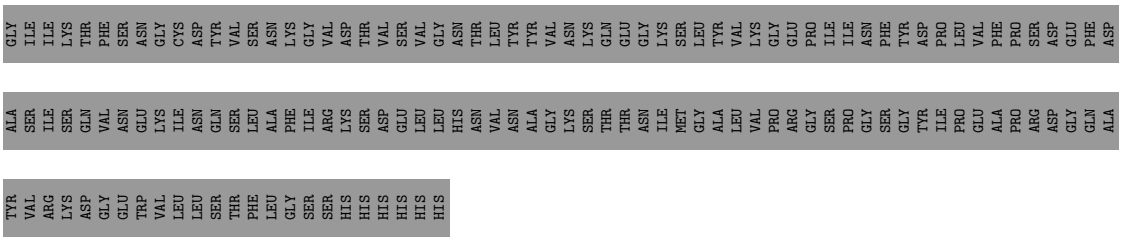
Chain K:



• Molecule 3: Fusion glycoprotein F0, Envelope glycoprotein chimera

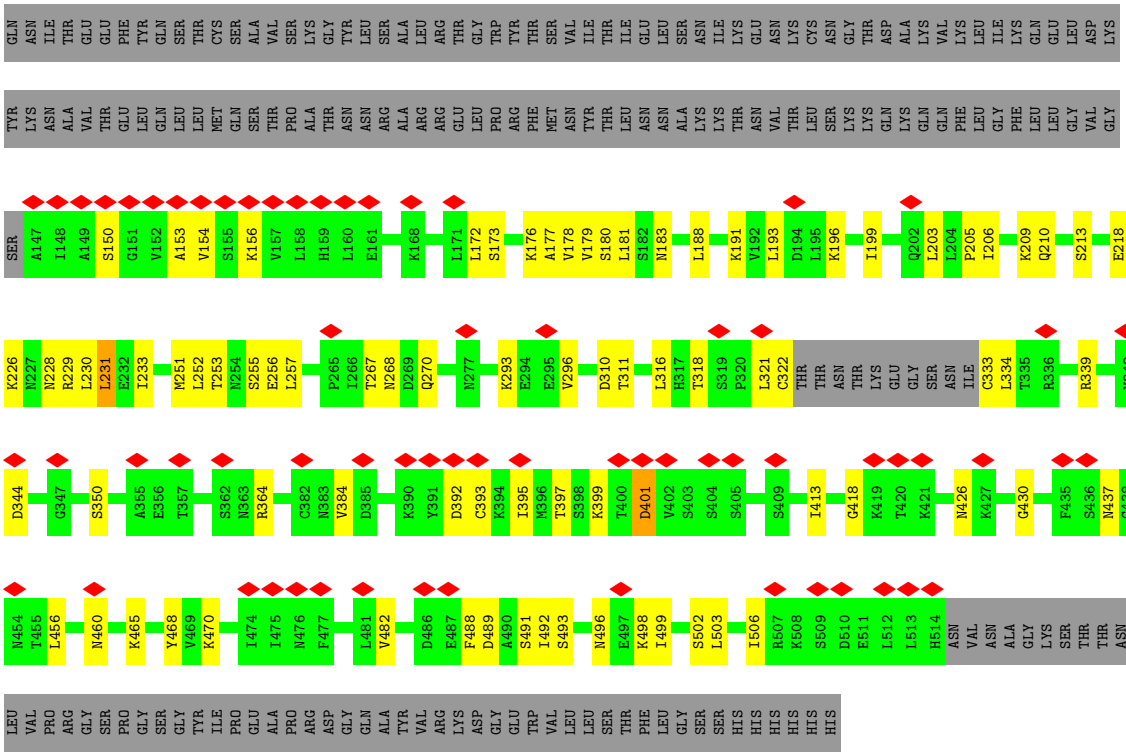
Chain A:





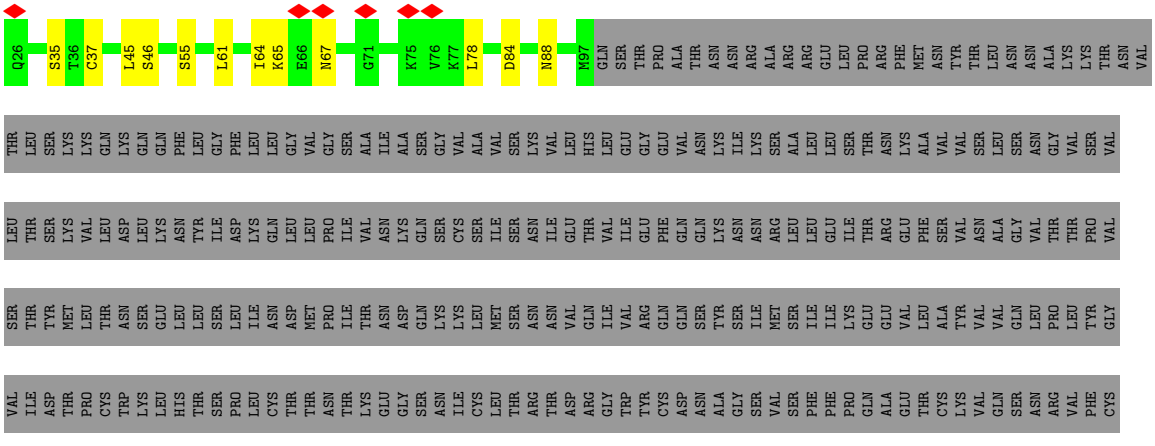
• Molecule 3: Fusion glycoprotein F0, Envelope glycoprotein chimera

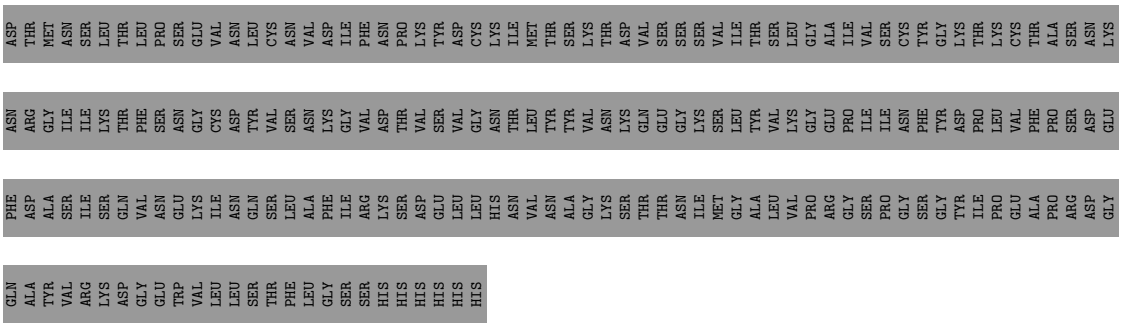
Chain B:



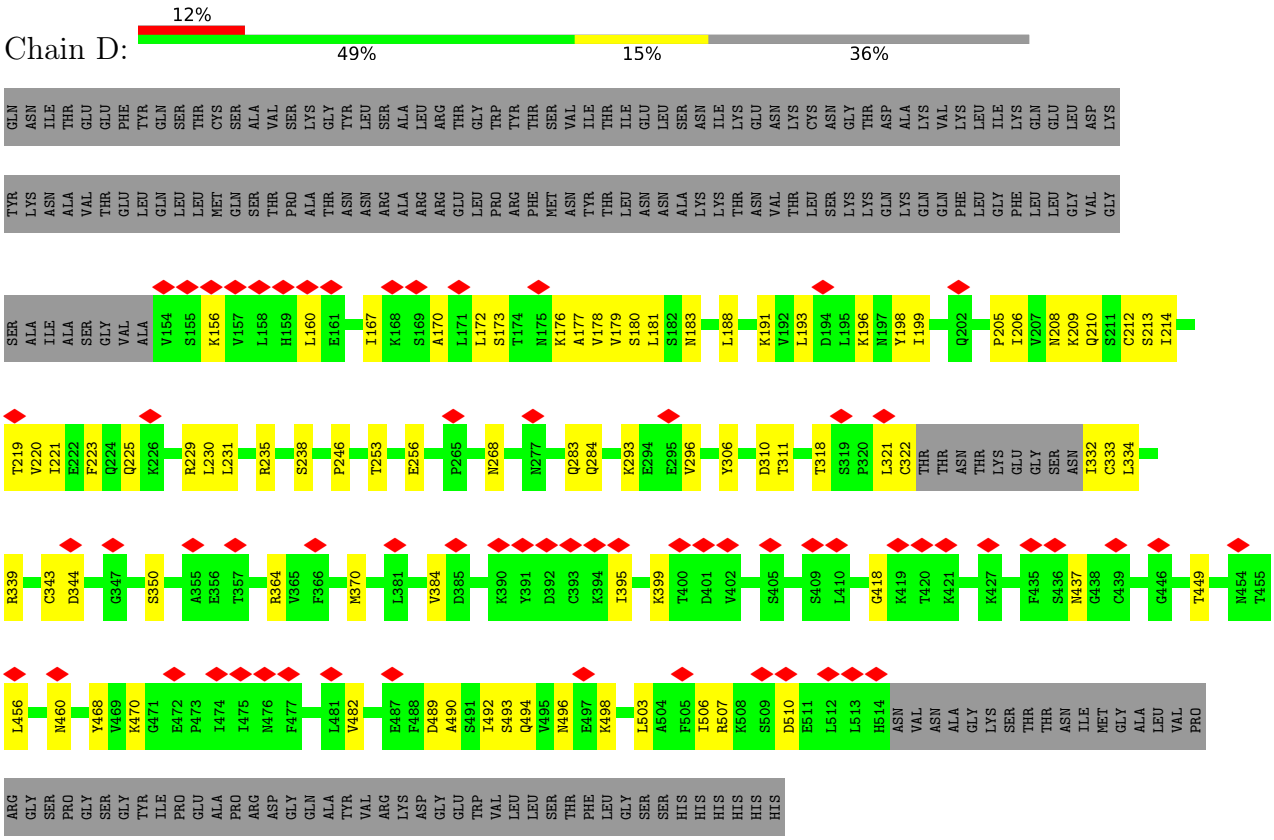
• Molecule 3: Fusion glycoprotein F0, Envelope glycoprotein chimera

Chain C:

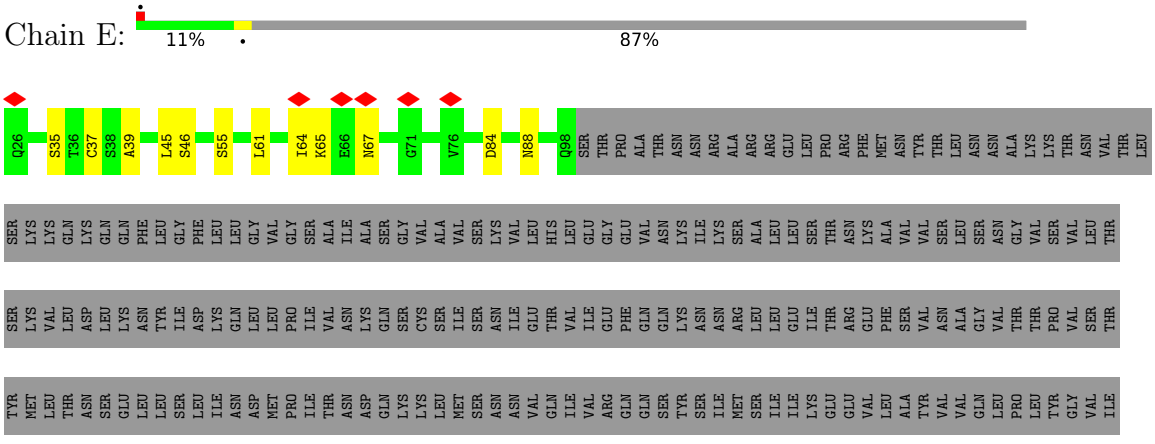


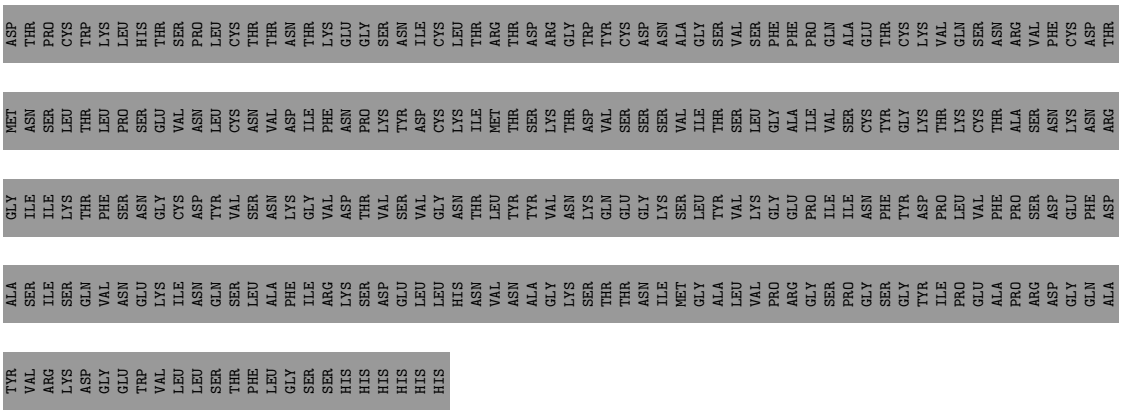


• Molecule 3: Fusion glycoprotein F0, Envelope glycoprotein chimera



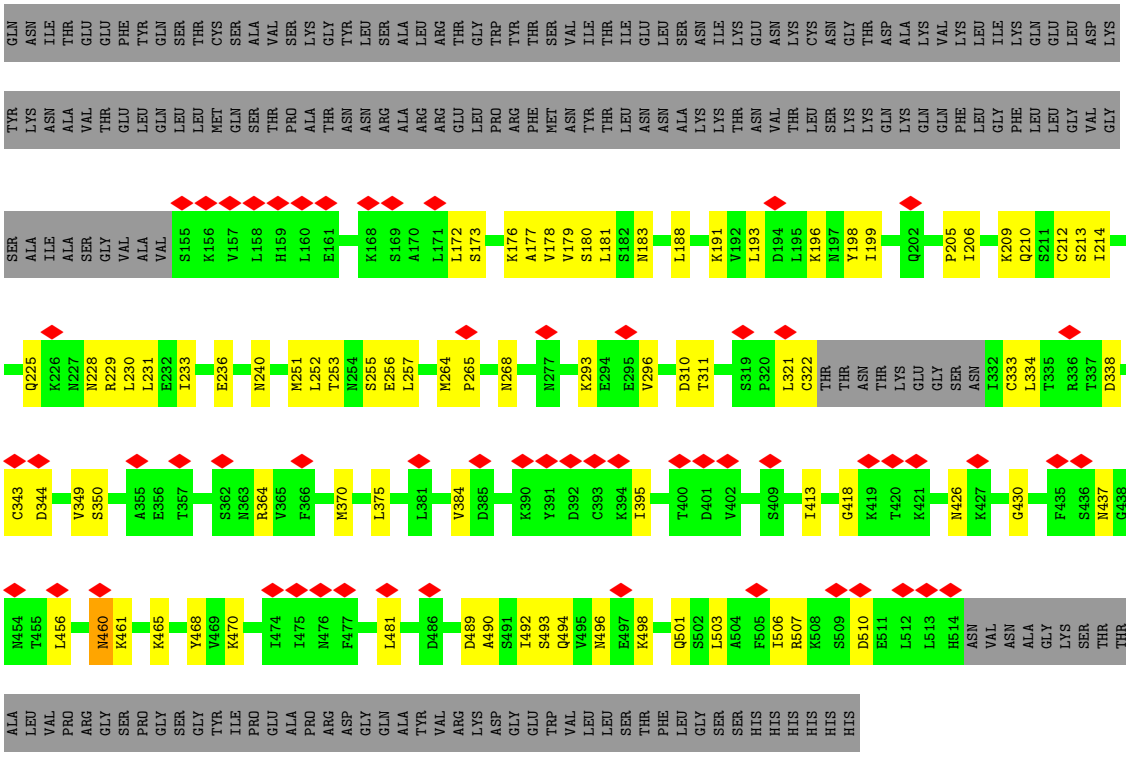
• Molecule 3: Fusion glycoprotein F0, Envelope glycoprotein chimera





• Molecule 3: Fusion glycoprotein F0, Envelope glycoprotein chimera

Chain F:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C3	Depositor
Number of particles used	543639	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL 3200FSC	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.079	Depositor
Minimum map value	-0.039	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0232	Depositor
Map size (Å)	321.1776, 321.1776, 321.1776	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2546, 1.2546, 1.2546	Depositor

5 Model quality

5.1 Standard geometry

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

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	G	0.35	0/893	0.58	0/1209
1	I	0.35	0/893	0.58	0/1209
1	X	0.35	0/893	0.58	0/1209
2	J	0.34	0/865	0.54	0/1170
2	K	0.34	0/865	0.54	0/1170
2	Y	0.34	0/865	0.54	0/1170
3	A	0.34	0/586	0.61	0/789
3	B	0.37	0/2805	0.58	1/3803 (0.0%)
3	C	0.34	0/577	0.61	0/777
3	D	0.37	0/2773	0.55	0/3759
3	E	0.34	0/586	0.61	0/789
3	F	0.37	0/2766	0.55	0/3749
All	All	0.36	0/15367	0.57	1/20803 (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
3	B	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	231	LEU	CA-CB-CG	-5.08	103.61	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	218	GLU	Peptide
3	B	401	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	G	872	0	844	19	0
1	I	872	0	844	17	0
1	X	872	0	844	18	0
2	J	847	0	835	16	0
2	K	847	0	835	16	0
2	Y	847	0	835	15	0
3	A	580	0	588	8	0
3	B	2765	0	2798	61	0
3	C	571	0	579	10	0
3	D	2733	0	2766	59	0
3	E	580	0	587	10	0
3	F	2726	0	2757	60	0
4	A	14	0	13	0	0
4	B	14	0	13	0	0
4	C	14	0	13	0	0
4	D	14	0	13	0	0
4	E	14	0	13	0	0
4	F	14	0	13	0	0
All	All	15196	0	15190	272	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 9.

The worst 5 of 272 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)
2:J:163:TYR:HB3	2:J:167:ASN:HB2	1.70	0.73
2:K:163:TYR:HB3	2:K:167:ASN:HB2	1.70	0.73
2:Y:163:TYR:HB3	2:Y:167:ASN:HB2	1.70	0.72
1:I:8:GLU:HB3	1:I:110:VAL:HG22	1.76	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:8:GLU:HB3	1:G:110:VAL:HG22	1.76	0.68

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	G	112/118 (95%)	103 (92%)	9 (8%)	0	100	100
1	I	112/118 (95%)	103 (92%)	9 (8%)	0	100	100
1	X	112/118 (95%)	103 (92%)	9 (8%)	0	100	100
2	J	106/122 (87%)	99 (93%)	7 (7%)	0	100	100
2	K	106/122 (87%)	99 (93%)	7 (7%)	0	100	100
2	Y	106/122 (87%)	99 (93%)	7 (7%)	0	100	100
3	A	71/548 (13%)	65 (92%)	6 (8%)	0	100	100
3	B	354/548 (65%)	332 (94%)	22 (6%)	0	100	100
3	C	70/548 (13%)	65 (93%)	5 (7%)	0	100	100
3	D	348/548 (64%)	332 (95%)	16 (5%)	0	100	100
3	E	71/548 (13%)	64 (90%)	7 (10%)	0	100	100
3	F	347/548 (63%)	333 (96%)	14 (4%)	0	100	100
All	All	1915/4008 (48%)	1797 (94%)	118 (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	G	93/96 (97%)	91 (98%)	2 (2%)	52	71
1	I	93/96 (97%)	91 (98%)	2 (2%)	52	71
1	X	93/96 (97%)	91 (98%)	2 (2%)	52	71
2	J	94/103 (91%)	94 (100%)	0	100	100
2	K	94/103 (91%)	94 (100%)	0	100	100
2	Y	94/103 (91%)	94 (100%)	0	100	100
3	A	66/494 (13%)	65 (98%)	1 (2%)	65	80
3	B	329/494 (67%)	326 (99%)	3 (1%)	78	87
3	C	65/494 (13%)	64 (98%)	1 (2%)	65	80
3	D	327/494 (66%)	325 (99%)	2 (1%)	86	91
3	E	66/494 (13%)	65 (98%)	1 (2%)	65	80
3	F	326/494 (66%)	324 (99%)	2 (1%)	86	91
All	All	1740/3561 (49%)	1724 (99%)	16 (1%)	79	87

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	268	ASN
3	E	65	LYS
3	B	268	ASN
3	D	460	ASN
3	B	226	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	460	ASN
3	F	460	ASN
3	F	227	ASN
2	K	169	HIS
3	D	227	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)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	NAG	F	800	-	14,14,15	0.46	0	17,19,21	0.40	0
4	NAG	C	601	3	14,14,15	0.52	0	17,19,21	0.46	0
4	NAG	A	601	3	14,14,15	0.53	0	17,19,21	0.51	0
4	NAG	B	800	-	14,14,15	0.46	0	17,19,21	0.97	1 (5%)
4	NAG	E	601	3	14,14,15	0.49	0	17,19,21	0.47	0
4	NAG	D	800	-	14,14,15	0.26	0	17,19,21	0.46	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	F	800	-	-	2/6/23/26	0/1/1/1
4	NAG	C	601	3	-	2/6/23/26	0/1/1/1
4	NAG	A	601	3	-	2/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	800	-	-	3/6/23/26	0/1/1/1
4	NAG	E	601	3	-	2/6/23/26	0/1/1/1
4	NAG	D	800	-	-	0/6/23/26	0/1/1/1

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	B	800	NAG	C2-N2-C7	3.08	127.28	122.90

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	601	NAG	O5-C5-C6-O6
4	A	601	NAG	O5-C5-C6-O6
4	C	601	NAG	O5-C5-C6-O6
4	B	800	NAG	C4-C5-C6-O6
4	B	800	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

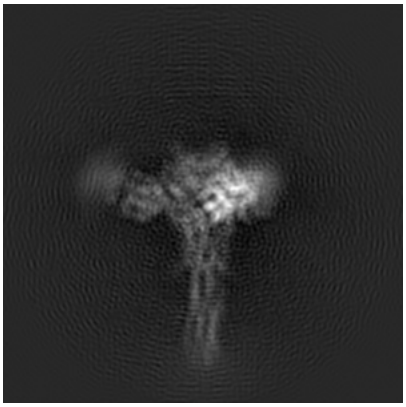
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-7774. These allow visual inspection of the internal detail of the map and identification of artifacts.

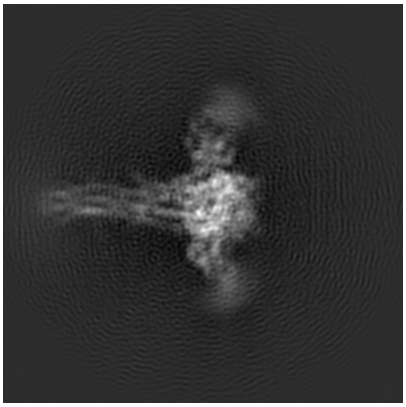
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

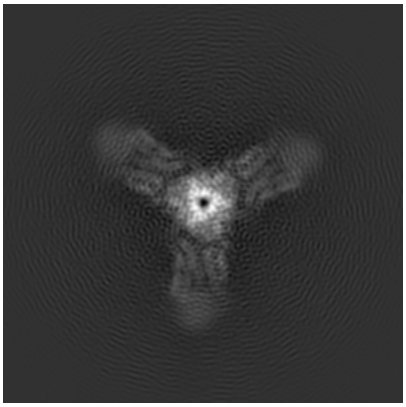
6.1.1 Primary map



X



Y

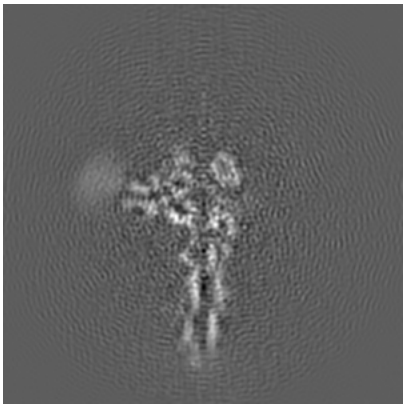


Z

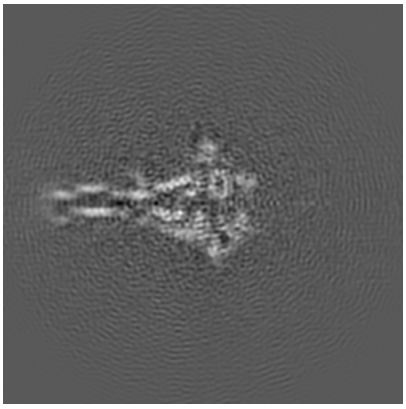
The images above show the map projected in three orthogonal directions.

6.2 Central slices

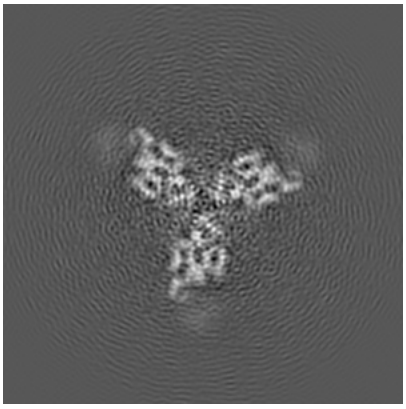
6.2.1 Primary map



X Index: 128



Y Index: 128

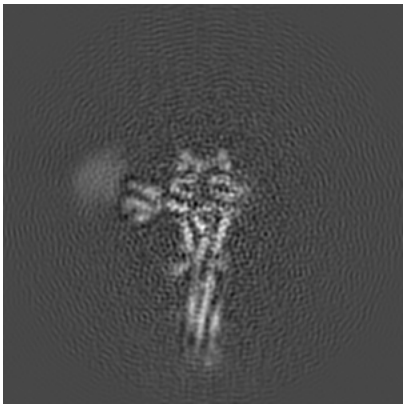


Z Index: 128

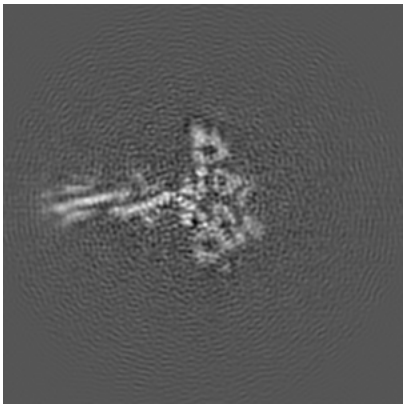
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

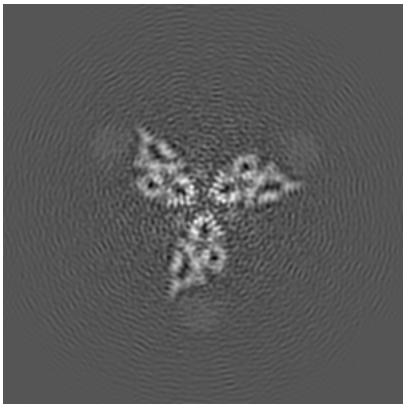
6.3.1 Primary map



X Index: 122



Y Index: 133



Z Index: 126

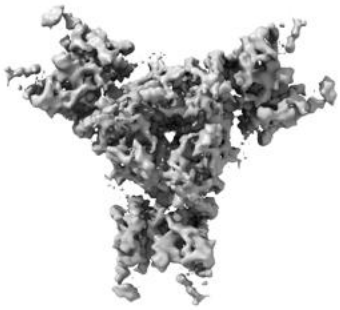
The images above show the largest variance slices of the map in three orthogonal directions.

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 0.0232. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

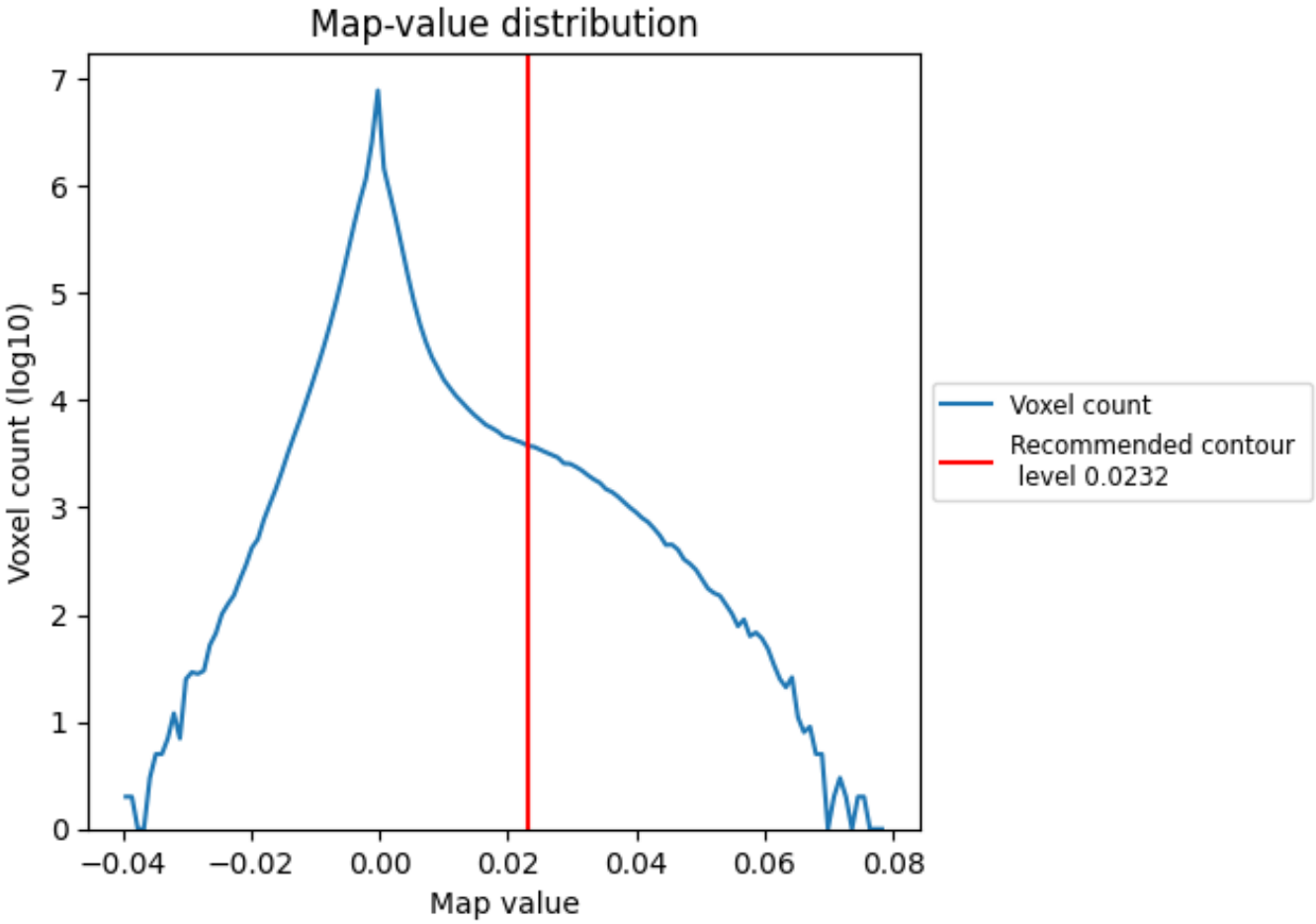
6.5 Mask visualisation (i)

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

7 Map analysis

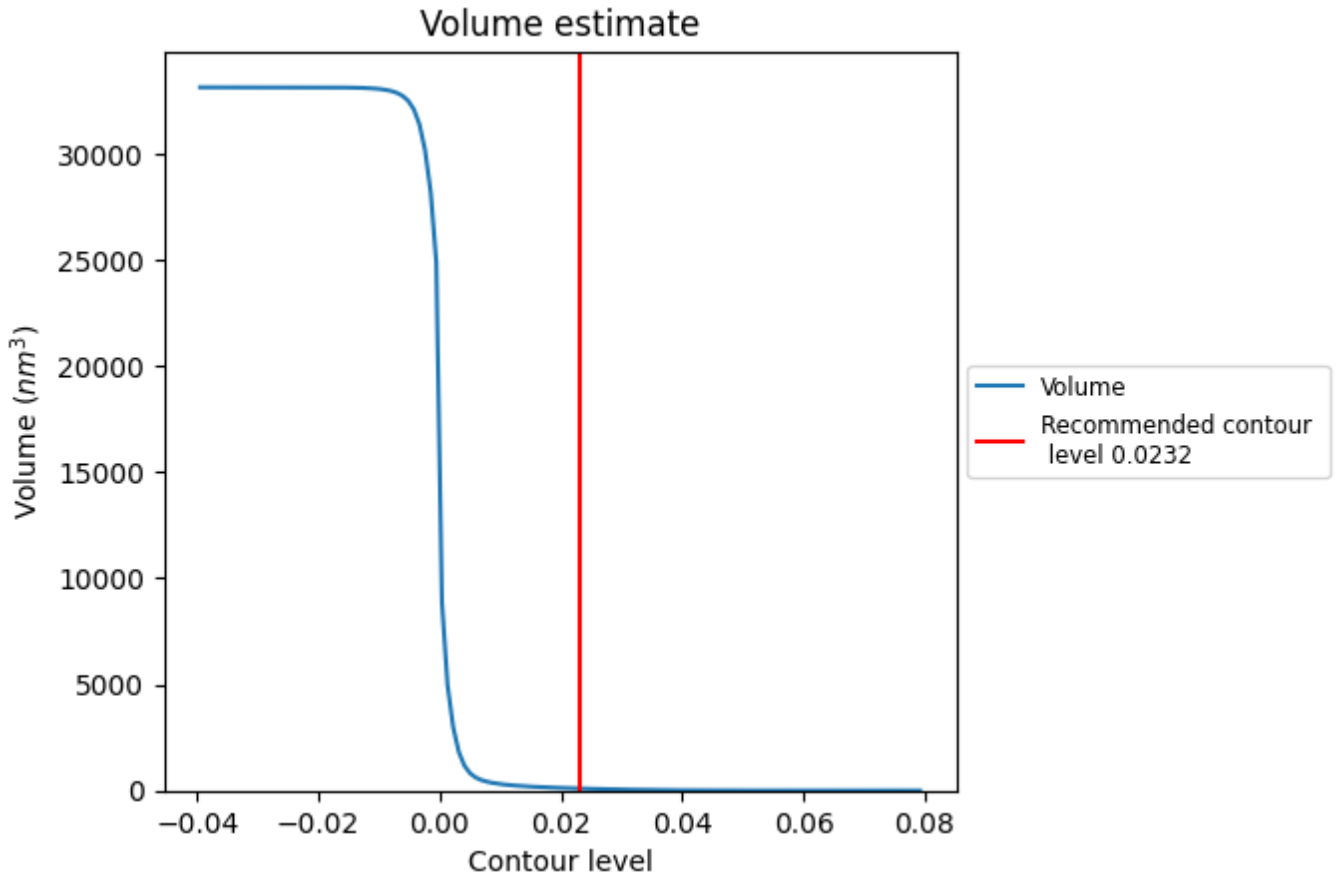
This section contains the results of statistical analysis of the map.

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.

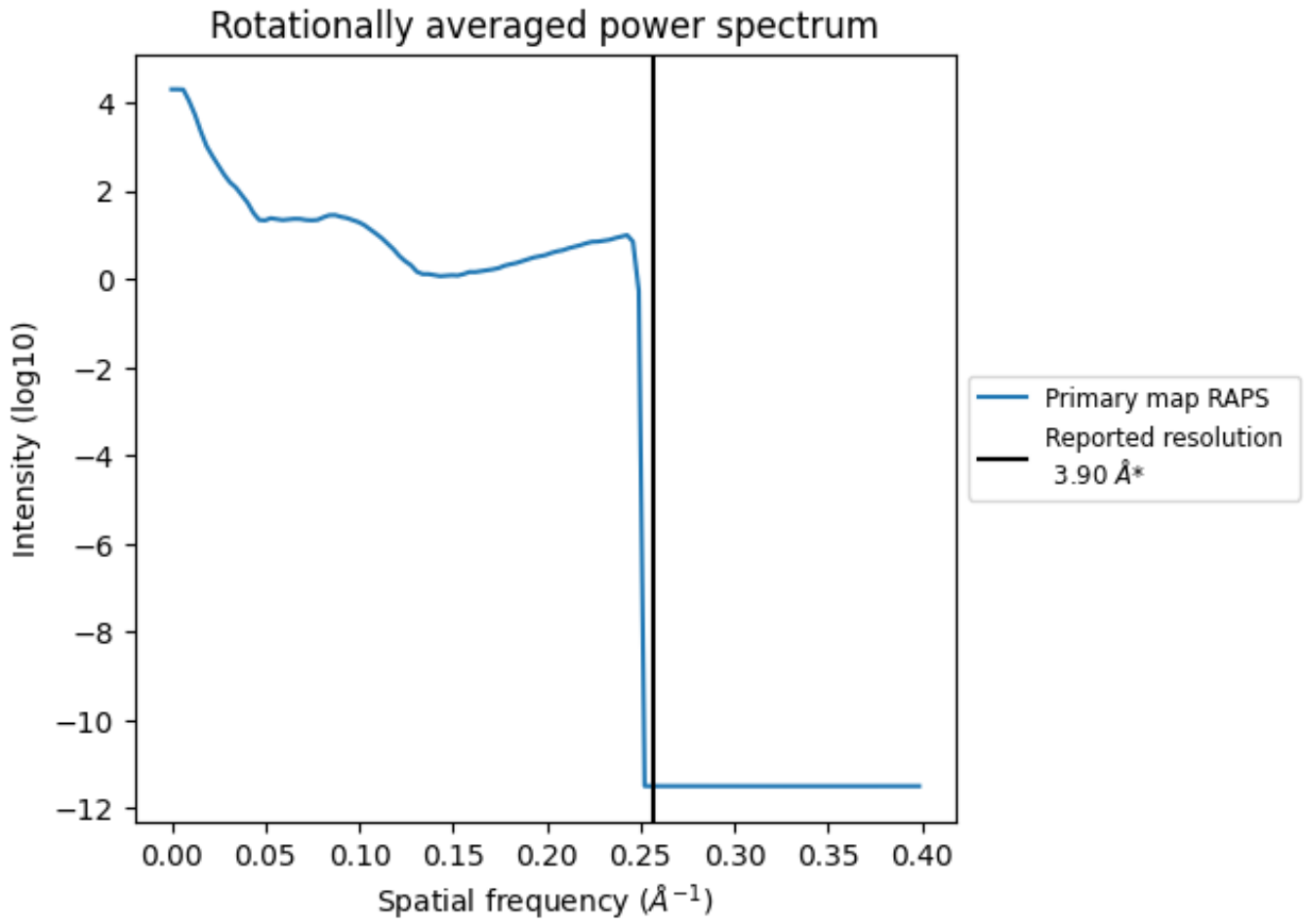
7.2 Volume estimate (i)



The volume at the recommended contour level is 96 nm^3; this corresponds to an approximate mass of 87 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)

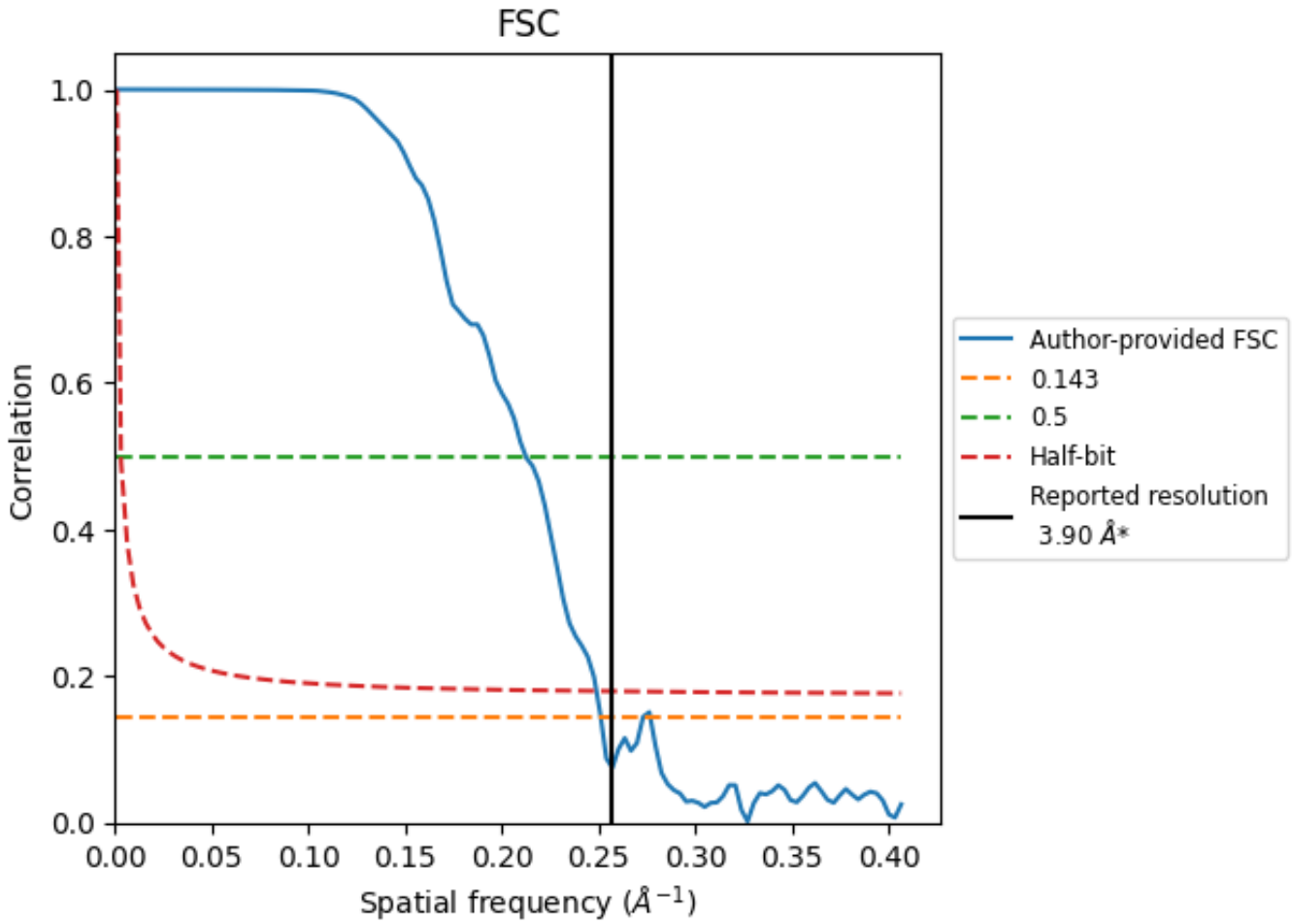


*Reported resolution corresponds to spatial frequency of 0.256 Å^{-1}

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 0.256 Å^{-1}

8.2 Resolution estimates (i)

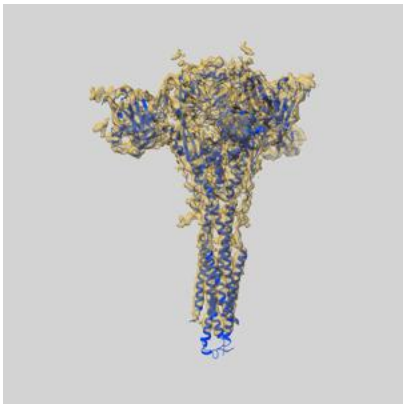
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.98	4.71	4.02
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

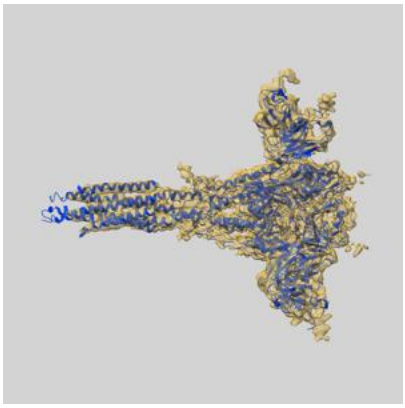
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-7774 and PDB model 6CXC. Per-residue inclusion information can be found in section 3 on page 10.

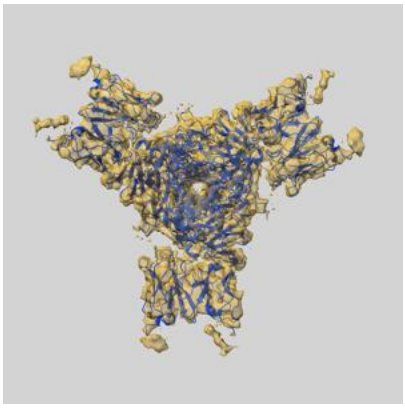
9.1 Map-model overlay



X



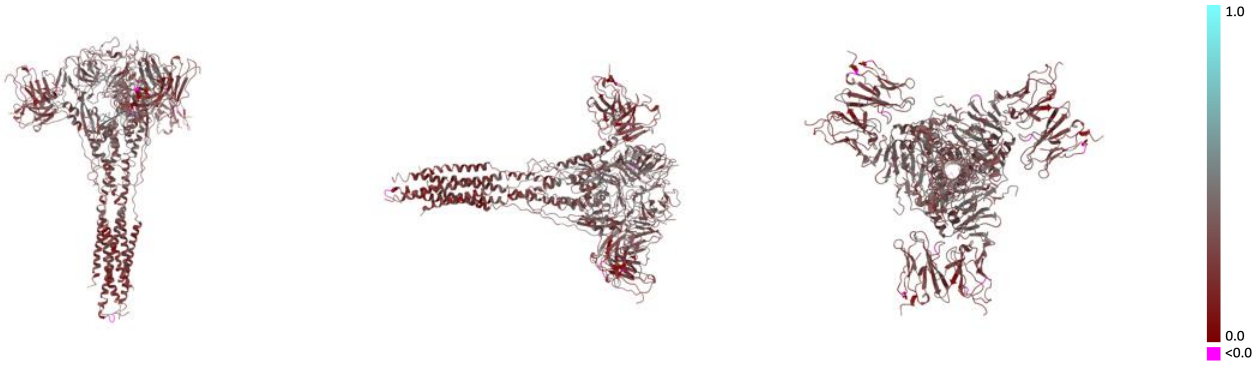
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0232 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.

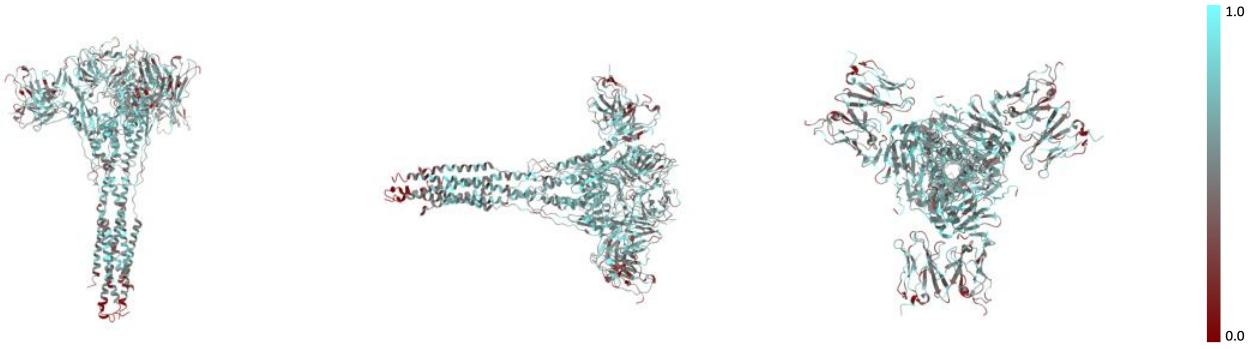
9.2 Q-score mapped to coordinate model (i)



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.

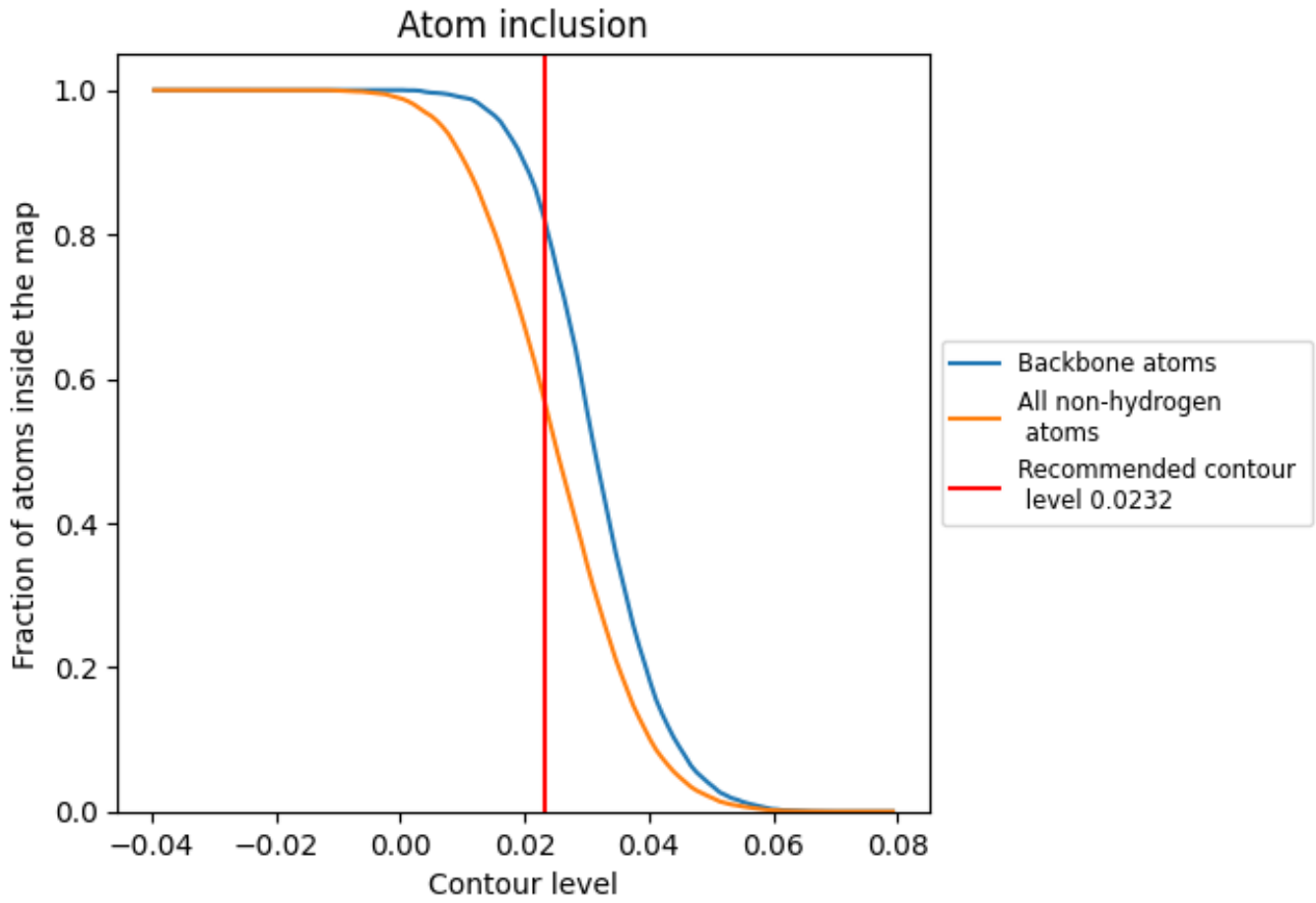
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.0232).

9.4 Atom inclusion (i)



At the recommended contour level, 82% of all backbone atoms, 57% 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 (0.0232) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5695	0.3080
A	0.6405	0.3630
B	0.5717	0.3210
C	0.6401	0.3680
D	0.5799	0.3250
E	0.6337	0.3670
F	0.5836	0.3240
G	0.5256	0.2620
I	0.5256	0.2630
J	0.5357	0.2670
K	0.5284	0.2620
X	0.5373	0.2590
Y	0.5357	0.2700