



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 05:45 PM UTC

PDB ID : 8E6K / pdb_00008e6k
EMDB ID : EMD-27921
Title : 2H08 Fab in complex with influenza virus neuraminidase from A/Brevig Mission/1/1918 (H1N1)
Authors : Turner, H.L.; Ozorowski, G.; Ward, A.B.
Deposited on : 2022-08-22
Resolution : 3.10 Å(reported)
Based on initial model : 3BEQ

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

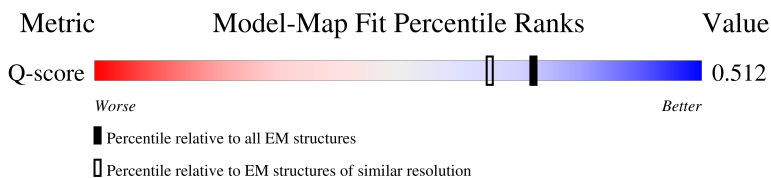
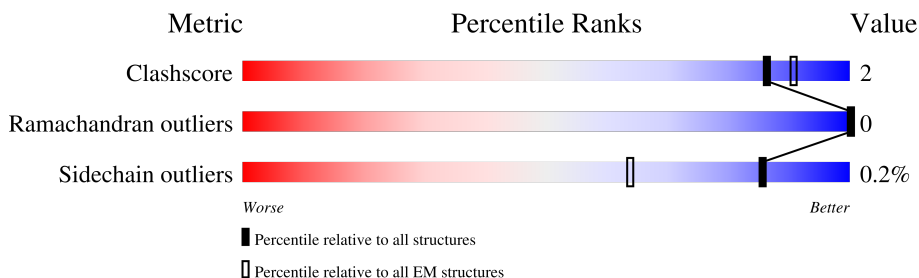
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14724 (2.60 - 3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	449	 80% 6% 14%
1	B	449	 80% 6% 14%
1	C	449	 81% 5% 14%
1	D	449	 81% 5% 14%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	I	215	46%5%50%
2	J	215	46%5%50%
2	K	215	46%.50%
2	L	215	46%5%50%
3	E	225	6%53%.46%
3	F	225	6%53%46%
3	G	225	6%53%.46%
3	H	225	6%53%46%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 18932 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 Neuraminidase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	385	Total 2963	C 1856	N 509	O 575	S 23	0	0
1	B	385	Total 2963	C 1856	N 509	O 575	S 23	0	0
1	C	385	Total 2963	C 1856	N 509	O 575	S 23	0	0
1	D	385	Total 2963	C 1856	N 509	O 575	S 23	0	0

There are 244 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	ALA	-	expression tag	UNP Q9IGQ6
A	22	ASP	-	expression tag	UNP Q9IGQ6
A	23	PRO	-	expression tag	UNP Q9IGQ6
A	24	HIS	-	expression tag	UNP Q9IGQ6
A	25	HIS	-	expression tag	UNP Q9IGQ6
A	26	HIS	-	expression tag	UNP Q9IGQ6
A	27	HIS	-	expression tag	UNP Q9IGQ6
A	28	HIS	-	expression tag	UNP Q9IGQ6
A	29	HIS	-	expression tag	UNP Q9IGQ6
A	30	SER	-	expression tag	UNP Q9IGQ6
A	31	SER	-	expression tag	UNP Q9IGQ6
A	32	SER	-	expression tag	UNP Q9IGQ6
A	33	ASP	-	expression tag	UNP Q9IGQ6
A	34	TYR	-	expression tag	UNP Q9IGQ6
A	35	SER	-	expression tag	UNP Q9IGQ6
A	36	ASP	-	expression tag	UNP Q9IGQ6
A	37	LEU	-	expression tag	UNP Q9IGQ6
A	38	GLN	-	expression tag	UNP Q9IGQ6
A	39	ARG	-	expression tag	UNP Q9IGQ6
A	40	VAL	-	expression tag	UNP Q9IGQ6
A	41	LYS	-	expression tag	UNP Q9IGQ6
A	42	GLN	-	expression tag	UNP Q9IGQ6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	43	GLU	-	expression tag	UNP Q9IGQ6
A	44	LEU	-	expression tag	UNP Q9IGQ6
A	45	LEU	-	expression tag	UNP Q9IGQ6
A	46	GLU	-	expression tag	UNP Q9IGQ6
A	47	GLU	-	expression tag	UNP Q9IGQ6
A	48	VAL	-	expression tag	UNP Q9IGQ6
A	49	LYS	-	expression tag	UNP Q9IGQ6
A	50	LYS	-	expression tag	UNP Q9IGQ6
A	51	GLU	-	expression tag	UNP Q9IGQ6
A	52	LEU	-	expression tag	UNP Q9IGQ6
A	53	GLN	-	expression tag	UNP Q9IGQ6
A	54	LYS	-	expression tag	UNP Q9IGQ6
A	55	VAL	-	expression tag	UNP Q9IGQ6
A	56	LYS	-	expression tag	UNP Q9IGQ6
A	57	GLU	-	expression tag	UNP Q9IGQ6
A	58	GLU	-	expression tag	UNP Q9IGQ6
A	59	ILE	-	expression tag	UNP Q9IGQ6
A	60	ILE	-	expression tag	UNP Q9IGQ6
A	61	GLU	-	expression tag	UNP Q9IGQ6
A	62	ALA	-	expression tag	UNP Q9IGQ6
A	63	PHE	-	expression tag	UNP Q9IGQ6
A	64	VAL	-	expression tag	UNP Q9IGQ6
A	65	GLN	-	expression tag	UNP Q9IGQ6
A	66	GLU	-	expression tag	UNP Q9IGQ6
A	67	LEU	-	expression tag	UNP Q9IGQ6
A	68	ARG	-	expression tag	UNP Q9IGQ6
A	69	LYS	-	expression tag	UNP Q9IGQ6
A	70	ARG	-	expression tag	UNP Q9IGQ6
A	71	GLY	-	expression tag	UNP Q9IGQ6
A	72	SER	-	expression tag	UNP Q9IGQ6
A	73	LEU	-	expression tag	UNP Q9IGQ6
A	74	VAL	-	expression tag	UNP Q9IGQ6
A	75	PRO	-	expression tag	UNP Q9IGQ6
A	76	ARG	-	expression tag	UNP Q9IGQ6
A	77	GLY	-	expression tag	UNP Q9IGQ6
A	78	SER	-	expression tag	UNP Q9IGQ6
A	79	PRO	-	expression tag	UNP Q9IGQ6
A	80	SER	-	expression tag	UNP Q9IGQ6
A	81	ARG	-	expression tag	UNP Q9IGQ6
B	21	ALA	-	expression tag	UNP Q9IGQ6
B	22	ASP	-	expression tag	UNP Q9IGQ6
B	23	PRO	-	expression tag	UNP Q9IGQ6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	24	HIS	-	expression tag	UNP Q9IGQ6
B	25	HIS	-	expression tag	UNP Q9IGQ6
B	26	HIS	-	expression tag	UNP Q9IGQ6
B	27	HIS	-	expression tag	UNP Q9IGQ6
B	28	HIS	-	expression tag	UNP Q9IGQ6
B	29	HIS	-	expression tag	UNP Q9IGQ6
B	30	SER	-	expression tag	UNP Q9IGQ6
B	31	SER	-	expression tag	UNP Q9IGQ6
B	32	SER	-	expression tag	UNP Q9IGQ6
B	33	ASP	-	expression tag	UNP Q9IGQ6
B	34	TYR	-	expression tag	UNP Q9IGQ6
B	35	SER	-	expression tag	UNP Q9IGQ6
B	36	ASP	-	expression tag	UNP Q9IGQ6
B	37	LEU	-	expression tag	UNP Q9IGQ6
B	38	GLN	-	expression tag	UNP Q9IGQ6
B	39	ARG	-	expression tag	UNP Q9IGQ6
B	40	VAL	-	expression tag	UNP Q9IGQ6
B	41	LYS	-	expression tag	UNP Q9IGQ6
B	42	GLN	-	expression tag	UNP Q9IGQ6
B	43	GLU	-	expression tag	UNP Q9IGQ6
B	44	LEU	-	expression tag	UNP Q9IGQ6
B	45	LEU	-	expression tag	UNP Q9IGQ6
B	46	GLU	-	expression tag	UNP Q9IGQ6
B	47	GLU	-	expression tag	UNP Q9IGQ6
B	48	VAL	-	expression tag	UNP Q9IGQ6
B	49	LYS	-	expression tag	UNP Q9IGQ6
B	50	LYS	-	expression tag	UNP Q9IGQ6
B	51	GLU	-	expression tag	UNP Q9IGQ6
B	52	LEU	-	expression tag	UNP Q9IGQ6
B	53	GLN	-	expression tag	UNP Q9IGQ6
B	54	LYS	-	expression tag	UNP Q9IGQ6
B	55	VAL	-	expression tag	UNP Q9IGQ6
B	56	LYS	-	expression tag	UNP Q9IGQ6
B	57	GLU	-	expression tag	UNP Q9IGQ6
B	58	GLU	-	expression tag	UNP Q9IGQ6
B	59	ILE	-	expression tag	UNP Q9IGQ6
B	60	ILE	-	expression tag	UNP Q9IGQ6
B	61	GLU	-	expression tag	UNP Q9IGQ6
B	62	ALA	-	expression tag	UNP Q9IGQ6
B	63	PHE	-	expression tag	UNP Q9IGQ6
B	64	VAL	-	expression tag	UNP Q9IGQ6
B	65	GLN	-	expression tag	UNP Q9IGQ6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	66	GLU	-	expression tag	UNP Q9IGQ6
B	67	LEU	-	expression tag	UNP Q9IGQ6
B	68	ARG	-	expression tag	UNP Q9IGQ6
B	69	LYS	-	expression tag	UNP Q9IGQ6
B	70	ARG	-	expression tag	UNP Q9IGQ6
B	71	GLY	-	expression tag	UNP Q9IGQ6
B	72	SER	-	expression tag	UNP Q9IGQ6
B	73	LEU	-	expression tag	UNP Q9IGQ6
B	74	VAL	-	expression tag	UNP Q9IGQ6
B	75	PRO	-	expression tag	UNP Q9IGQ6
B	76	ARG	-	expression tag	UNP Q9IGQ6
B	77	GLY	-	expression tag	UNP Q9IGQ6
B	78	SER	-	expression tag	UNP Q9IGQ6
B	79	PRO	-	expression tag	UNP Q9IGQ6
B	80	SER	-	expression tag	UNP Q9IGQ6
B	81	ARG	-	expression tag	UNP Q9IGQ6
C	21	ALA	-	expression tag	UNP Q9IGQ6
C	22	ASP	-	expression tag	UNP Q9IGQ6
C	23	PRO	-	expression tag	UNP Q9IGQ6
C	24	HIS	-	expression tag	UNP Q9IGQ6
C	25	HIS	-	expression tag	UNP Q9IGQ6
C	26	HIS	-	expression tag	UNP Q9IGQ6
C	27	HIS	-	expression tag	UNP Q9IGQ6
C	28	HIS	-	expression tag	UNP Q9IGQ6
C	29	HIS	-	expression tag	UNP Q9IGQ6
C	30	SER	-	expression tag	UNP Q9IGQ6
C	31	SER	-	expression tag	UNP Q9IGQ6
C	32	SER	-	expression tag	UNP Q9IGQ6
C	33	ASP	-	expression tag	UNP Q9IGQ6
C	34	TYR	-	expression tag	UNP Q9IGQ6
C	35	SER	-	expression tag	UNP Q9IGQ6
C	36	ASP	-	expression tag	UNP Q9IGQ6
C	37	LEU	-	expression tag	UNP Q9IGQ6
C	38	GLN	-	expression tag	UNP Q9IGQ6
C	39	ARG	-	expression tag	UNP Q9IGQ6
C	40	VAL	-	expression tag	UNP Q9IGQ6
C	41	LYS	-	expression tag	UNP Q9IGQ6
C	42	GLN	-	expression tag	UNP Q9IGQ6
C	43	GLU	-	expression tag	UNP Q9IGQ6
C	44	LEU	-	expression tag	UNP Q9IGQ6
C	45	LEU	-	expression tag	UNP Q9IGQ6
C	46	GLU	-	expression tag	UNP Q9IGQ6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	47	GLU	-	expression tag	UNP Q9IGQ6
C	48	VAL	-	expression tag	UNP Q9IGQ6
C	49	LYS	-	expression tag	UNP Q9IGQ6
C	50	LYS	-	expression tag	UNP Q9IGQ6
C	51	GLU	-	expression tag	UNP Q9IGQ6
C	52	LEU	-	expression tag	UNP Q9IGQ6
C	53	GLN	-	expression tag	UNP Q9IGQ6
C	54	LYS	-	expression tag	UNP Q9IGQ6
C	55	VAL	-	expression tag	UNP Q9IGQ6
C	56	LYS	-	expression tag	UNP Q9IGQ6
C	57	GLU	-	expression tag	UNP Q9IGQ6
C	58	GLU	-	expression tag	UNP Q9IGQ6
C	59	ILE	-	expression tag	UNP Q9IGQ6
C	60	ILE	-	expression tag	UNP Q9IGQ6
C	61	GLU	-	expression tag	UNP Q9IGQ6
C	62	ALA	-	expression tag	UNP Q9IGQ6
C	63	PHE	-	expression tag	UNP Q9IGQ6
C	64	VAL	-	expression tag	UNP Q9IGQ6
C	65	GLN	-	expression tag	UNP Q9IGQ6
C	66	GLU	-	expression tag	UNP Q9IGQ6
C	67	LEU	-	expression tag	UNP Q9IGQ6
C	68	ARG	-	expression tag	UNP Q9IGQ6
C	69	LYS	-	expression tag	UNP Q9IGQ6
C	70	ARG	-	expression tag	UNP Q9IGQ6
C	71	GLY	-	expression tag	UNP Q9IGQ6
C	72	SER	-	expression tag	UNP Q9IGQ6
C	73	LEU	-	expression tag	UNP Q9IGQ6
C	74	VAL	-	expression tag	UNP Q9IGQ6
C	75	PRO	-	expression tag	UNP Q9IGQ6
C	76	ARG	-	expression tag	UNP Q9IGQ6
C	77	GLY	-	expression tag	UNP Q9IGQ6
C	78	SER	-	expression tag	UNP Q9IGQ6
C	79	PRO	-	expression tag	UNP Q9IGQ6
C	80	SER	-	expression tag	UNP Q9IGQ6
C	81	ARG	-	expression tag	UNP Q9IGQ6
D	21	ALA	-	expression tag	UNP Q9IGQ6
D	22	ASP	-	expression tag	UNP Q9IGQ6
D	23	PRO	-	expression tag	UNP Q9IGQ6
D	24	HIS	-	expression tag	UNP Q9IGQ6
D	25	HIS	-	expression tag	UNP Q9IGQ6
D	26	HIS	-	expression tag	UNP Q9IGQ6
D	27	HIS	-	expression tag	UNP Q9IGQ6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	28	HIS	-	expression tag	UNP Q9IGQ6
D	29	HIS	-	expression tag	UNP Q9IGQ6
D	30	SER	-	expression tag	UNP Q9IGQ6
D	31	SER	-	expression tag	UNP Q9IGQ6
D	32	SER	-	expression tag	UNP Q9IGQ6
D	33	ASP	-	expression tag	UNP Q9IGQ6
D	34	TYR	-	expression tag	UNP Q9IGQ6
D	35	SER	-	expression tag	UNP Q9IGQ6
D	36	ASP	-	expression tag	UNP Q9IGQ6
D	37	LEU	-	expression tag	UNP Q9IGQ6
D	38	GLN	-	expression tag	UNP Q9IGQ6
D	39	ARG	-	expression tag	UNP Q9IGQ6
D	40	VAL	-	expression tag	UNP Q9IGQ6
D	41	LYS	-	expression tag	UNP Q9IGQ6
D	42	GLN	-	expression tag	UNP Q9IGQ6
D	43	GLU	-	expression tag	UNP Q9IGQ6
D	44	LEU	-	expression tag	UNP Q9IGQ6
D	45	LEU	-	expression tag	UNP Q9IGQ6
D	46	GLU	-	expression tag	UNP Q9IGQ6
D	47	GLU	-	expression tag	UNP Q9IGQ6
D	48	VAL	-	expression tag	UNP Q9IGQ6
D	49	LYS	-	expression tag	UNP Q9IGQ6
D	50	LYS	-	expression tag	UNP Q9IGQ6
D	51	GLU	-	expression tag	UNP Q9IGQ6
D	52	LEU	-	expression tag	UNP Q9IGQ6
D	53	GLN	-	expression tag	UNP Q9IGQ6
D	54	LYS	-	expression tag	UNP Q9IGQ6
D	55	VAL	-	expression tag	UNP Q9IGQ6
D	56	LYS	-	expression tag	UNP Q9IGQ6
D	57	GLU	-	expression tag	UNP Q9IGQ6
D	58	GLU	-	expression tag	UNP Q9IGQ6
D	59	ILE	-	expression tag	UNP Q9IGQ6
D	60	ILE	-	expression tag	UNP Q9IGQ6
D	61	GLU	-	expression tag	UNP Q9IGQ6
D	62	ALA	-	expression tag	UNP Q9IGQ6
D	63	PHE	-	expression tag	UNP Q9IGQ6
D	64	VAL	-	expression tag	UNP Q9IGQ6
D	65	GLN	-	expression tag	UNP Q9IGQ6
D	66	GLU	-	expression tag	UNP Q9IGQ6
D	67	LEU	-	expression tag	UNP Q9IGQ6
D	68	ARG	-	expression tag	UNP Q9IGQ6
D	69	LYS	-	expression tag	UNP Q9IGQ6

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	70	ARG	-	expression tag	UNP Q9IGQ6
D	71	GLY	-	expression tag	UNP Q9IGQ6
D	72	SER	-	expression tag	UNP Q9IGQ6
D	73	LEU	-	expression tag	UNP Q9IGQ6
D	74	VAL	-	expression tag	UNP Q9IGQ6
D	75	PRO	-	expression tag	UNP Q9IGQ6
D	76	ARG	-	expression tag	UNP Q9IGQ6
D	77	GLY	-	expression tag	UNP Q9IGQ6
D	78	SER	-	expression tag	UNP Q9IGQ6
D	79	PRO	-	expression tag	UNP Q9IGQ6
D	80	SER	-	expression tag	UNP Q9IGQ6
D	81	ARG	-	expression tag	UNP Q9IGQ6

- Molecule 2 is a protein called 2H08 fragment antigen binding light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	108	Total	C	N	O	S	0	0
			828	522	137	166	3		
2	I	108	Total	C	N	O	S	0	0
			828	522	137	166	3		
2	J	108	Total	C	N	O	S	0	0
			828	522	137	166	3		
2	K	108	Total	C	N	O	S	0	0
			828	522	137	166	3		

- Molecule 3 is a protein called 2H08 fragment antigen binding heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	121	Total	C	N	O	S	0	0
			928	591	153	180	4		
3	E	121	Total	C	N	O	S	0	0
			928	591	153	180	4		
3	F	121	Total	C	N	O	S	0	0
			928	591	153	180	4		
3	G	121	Total	C	N	O	S	0	0
			928	591	153	180	4		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



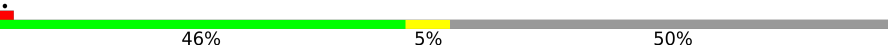
Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	N	O	0
			14	8	1	5	
4	B	1	Total	C	N	O	0
			14	8	1	5	
4	C	1	Total	C	N	O	0
			14	8	1	5	
4	D	1	Total	C	N	O	0
			14	8	1	5	

Chain D:  81% 5% 14%

ALA ASP PRO HIS HIS HIS HIS SER SER ASP LEU GLN ARG VAL LYS GLN GLU LEU LEU GLU VAL LYS LYS GLU LEU VAL LYS VAL LYS GLU ILE ALA PHE VAL GLN LEU ARG LYS ARG GLY SER LEU VAL ARG GLY PRO SER

ARG SER V83 I94 E128 D142 S160 R172 H178 T194 I211 T212 D213 T214 T239 T240 Y252 D293 Y316 R327 C336 G339 G345 T365 D379 G382 D387 S388 D416 R419 I437 I468 ASP LYS

- Molecule 2: 2H08 fragment antigen binding light chain

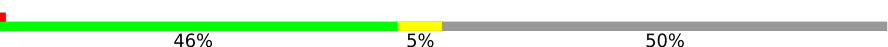
Chain L:  46% 5% 50%

D1 Q6 G16 D17 R18 R24 L33 T51 R56 G57 D70 S76 S77 L78 Q100 I106 K107 ARG THR VAL ALA ALA TYR PRO LEU SER PHE ILE PHE PRO PRO SER ASP GLN LYS LEU THR ALA VAL VAL CYS LEU LEU ASN ASN PHE TYR

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

LEU SER SER PRO VAL THR LYS SER PHE ARG ASN GLY CYS

- Molecule 2: 2H08 fragment antigen binding light chain

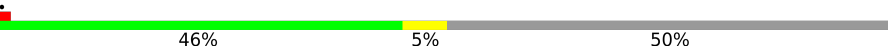
Chain I:  46% 5% 50%

D1 Q6 G16 D17 R18 R24 L33 T51 R56 G57 D70 S76 S77 L78 Q100 I106 K107 ARG THR VAL ALA ALA TYR PRO LEU SER VAL PHE THR LEU PRO LEU SER LYS ALA ASP GLN LYS LEU SER LYS HIS GLY THR VAL TYR SER ALA VAL CYS GLU VAL THR LEU THR HIS GLN GLY

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

LEU SER SER PRO VAL THR LYS SER PHE ARG ASN GLY CYS

- Molecule 2: 2H08 fragment antigen binding light chain

Chain J:  46% 5% 50%

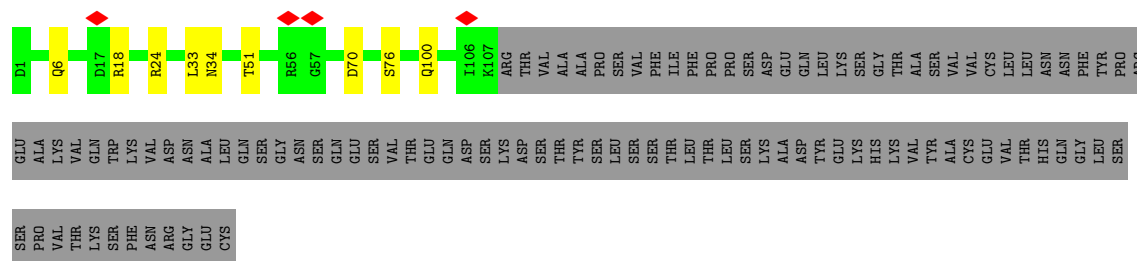
D1 Q6 G16 D17 R18 R24 L33 T51 R56 G57 D70 S76 S77 L78 Q100 I106 K107 ARG THR VAL ALA ALA TYR PRO LEU SER VAL PHE THR LEU PRO LEU SER LYS ALA ASP GLN LYS LEU SER LYS HIS GLY THR VAL TYR SER ALA VAL CYS GLU VAL THR LEU THR HIS GLN GLY

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

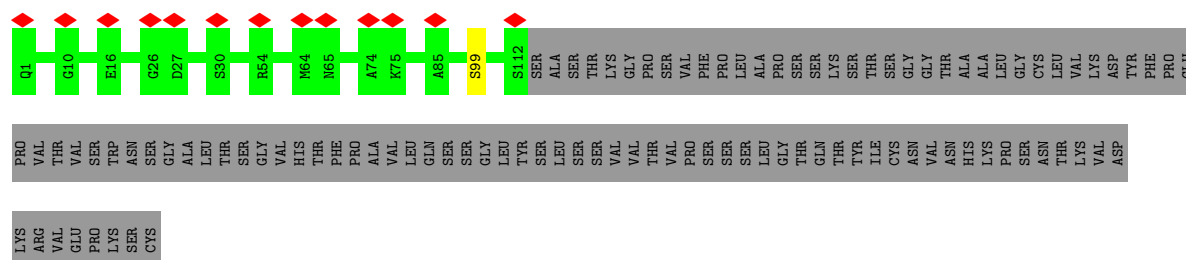
LEU SER SER PRO VAL THR LYS SER PHE ARG ASN GLY CYS

- Molecule 2: 2H08 fragment antigen binding light chain

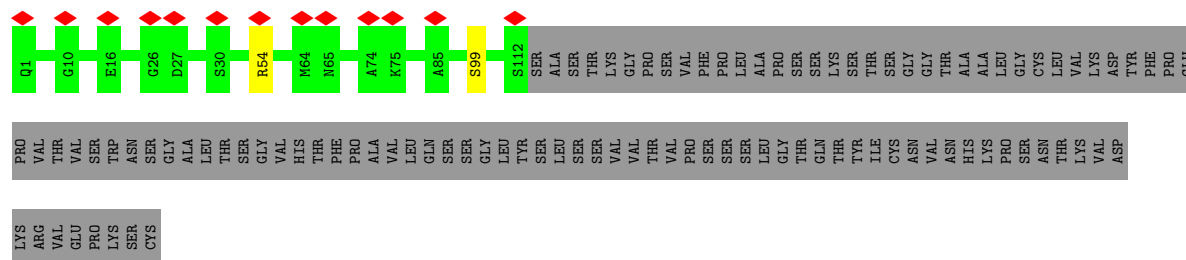
Chain K:  46% 5% 50%



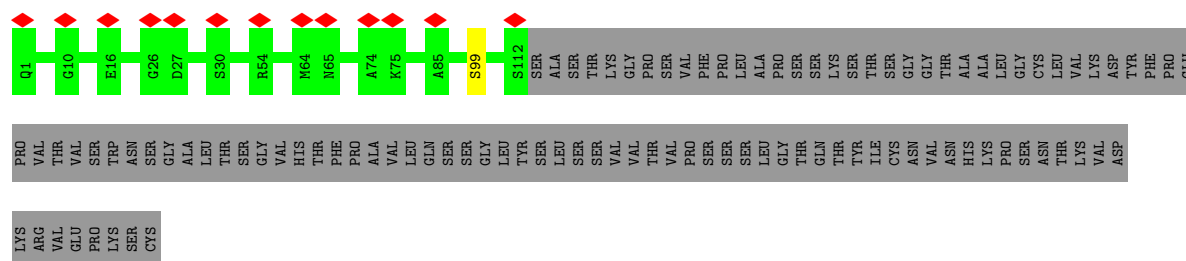
- Molecule 3: 2H08 fragment antigen binding heavy chain



- Molecule 3: 2H08 fragment antigen binding heavy chain

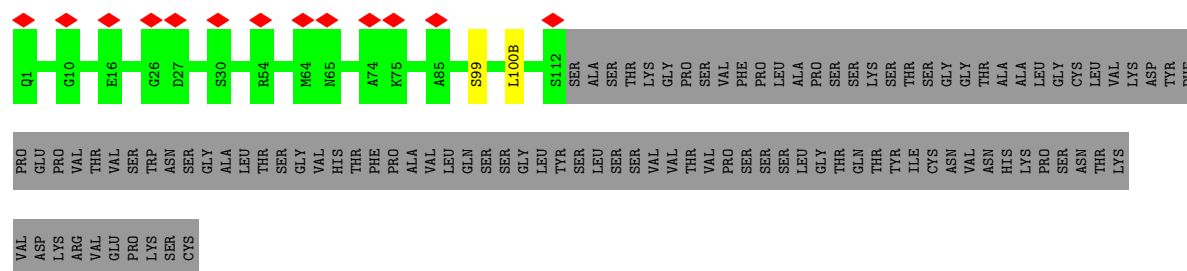


- Molecule 3: 2H08 fragment antigen binding heavy chain



- Molecule 3: 2H08 fragment antigen binding heavy chain





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C4	Depositor
Number of particles used	45771	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	33.5	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	190000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.655	Depositor
Minimum map value	-0.408	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	304.5, 304.5, 304.5	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.725, 0.725, 0.725	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	A	0.27	0/3044	0.65	0/4138
1	B	0.27	0/3044	0.65	0/4138
1	C	0.27	0/3044	0.65	0/4138
1	D	0.27	0/3044	0.65	0/4138
2	I	0.32	0/847	0.63	0/1150
2	J	0.32	0/847	0.63	0/1150
2	K	0.32	0/847	0.63	0/1150
2	L	0.32	0/847	0.63	0/1150
3	E	0.28	0/953	0.64	0/1303
3	F	0.28	0/953	0.64	0/1303
3	G	0.28	0/953	0.64	0/1303
3	H	0.28	0/953	0.64	0/1303
All	All	0.28	0/19376	0.65	0/26364

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2963	0	2785	15	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2963	0	2785	17	0
1	C	2963	0	2785	14	0
1	D	2963	0	2785	14	0
2	I	828	0	812	5	0
2	J	828	0	812	5	0
2	K	828	0	812	5	0
2	L	828	0	812	5	0
3	E	928	0	899	2	0
3	F	928	0	899	1	0
3	G	928	0	899	2	0
3	H	928	0	899	1	0
4	A	14	0	13	1	0
4	B	14	0	13	1	0
4	C	14	0	13	1	0
4	D	14	0	13	1	0
All	All	18932	0	18036	76	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 2.

All (76) 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:I:6:GLN:O	2:I:100:GLN:NE2	2.26	0.69
2:L:6:GLN:O	2:L:100:GLN:NE2	2.26	0.69
2:J:6:GLN:O	2:J:100:GLN:NE2	2.26	0.69
2:K:6:GLN:O	2:K:100:GLN:NE2	2.26	0.69
1:D:437:ILE:HG21	4:D:501:NAG:H82	1.78	0.65
1:C:437:ILE:HG21	4:C:501:NAG:H82	1.78	0.64
1:A:437:ILE:HG21	4:A:501:NAG:H82	1.78	0.64
1:C:293:ASP:OD2	1:C:316:TYR:OH	2.17	0.63
1:C:142:ASP:N	1:C:142:ASP:OD1	2.32	0.63
1:B:437:ILE:HG21	4:B:501:NAG:H82	1.78	0.63
1:D:293:ASP:OD2	1:D:316:TYR:OH	2.17	0.63
1:B:293:ASP:OD2	1:B:316:TYR:OH	2.17	0.62
1:B:142:ASP:N	1:B:142:ASP:OD1	2.32	0.62
1:A:293:ASP:OD2	1:A:316:TYR:OH	2.17	0.62
1:D:142:ASP:N	1:D:142:ASP:OD1	2.32	0.61
1:A:142:ASP:N	1:A:142:ASP:OD1	2.32	0.61
1:C:419:ARG:NH1	1:D:211:ILE:O	2.37	0.57
1:A:419:ARG:NH1	1:B:211:ILE:O	2.37	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:387:ASP:OD1	1:C:388:SER:N	2.39	0.56
1:D:387:ASP:OD1	1:D:388:SER:N	2.39	0.56
1:A:387:ASP:OD1	1:A:388:SER:N	2.39	0.55
1:B:387:ASP:OD1	1:B:388:SER:N	2.39	0.55
2:L:24:ARG:NE	2:L:70:ASP:OD1	2.40	0.54
1:B:419:ARG:NH1	1:C:211:ILE:O	2.37	0.54
2:J:24:ARG:NE	2:J:70:ASP:OD1	2.40	0.54
1:A:211:ILE:O	1:D:419:ARG:NH1	2.37	0.54
2:K:24:ARG:NE	2:K:70:ASP:OD1	2.40	0.54
2:I:24:ARG:NE	2:I:70:ASP:OD1	2.40	0.54
1:C:327:ARG:NH1	1:C:365:THR:O	2.48	0.47
1:D:160:SER:O	1:D:172:ARG:N	2.48	0.47
1:D:327:ARG:NH1	1:D:365:THR:O	2.48	0.47
1:A:327:ARG:NH1	1:A:365:THR:O	2.48	0.47
1:C:160:SER:O	1:C:172:ARG:N	2.48	0.46
1:D:379:ASP:OD1	1:D:382:GLY:N	2.48	0.46
1:C:178:TRP:N	1:C:194:ILE:O	2.48	0.46
1:A:160:SER:O	1:A:172:ARG:N	2.48	0.46
1:A:379:ASP:OD1	1:A:382:GLY:N	2.48	0.46
1:B:379:ASP:OD1	1:B:382:GLY:N	2.48	0.46
1:C:379:ASP:OD1	1:C:382:GLY:N	2.48	0.46
1:D:94:ILE:O	3:G:99:SER:OG	2.34	0.46
1:B:327:ARG:NH1	1:B:365:THR:O	2.48	0.46
1:A:94:ILE:O	3:H:99:SER:OG	2.34	0.46
1:B:94:ILE:O	3:E:99:SER:OG	2.34	0.46
1:B:160:SER:O	1:B:172:ARG:N	2.48	0.46
1:C:94:ILE:O	3:F:99:SER:OG	2.34	0.45
1:B:178:TRP:N	1:B:194:ILE:O	2.48	0.45
2:J:18:ARG:HG3	2:J:76:SER:HA	1.99	0.45
2:J:33:LEU:O	2:J:51:THR:N	2.50	0.45
2:K:18:ARG:HG3	2:K:76:SER:HA	1.99	0.44
2:L:18:ARG:HG3	2:L:76:SER:HA	1.99	0.44
1:C:102:LYS:NZ	1:C:459:PRO:O	2.51	0.44
2:J:16:GLY:N	2:J:78:LEU:O	2.47	0.44
1:C:239:THR:OG1	1:C:240:ILE:N	2.51	0.44
1:D:178:TRP:N	1:D:194:ILE:O	2.48	0.44
1:A:239:THR:OG1	1:A:240:ILE:N	2.51	0.43
1:B:239:THR:OG1	1:B:240:ILE:N	2.51	0.43
1:B:316:TYR:HB2	1:B:336:CYS:O	2.18	0.43
1:A:316:TYR:HB2	1:A:336:CYS:O	2.18	0.43
1:A:366:LYS:NZ	1:A:396:ASP:OD1	2.47	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:33:LEU:O	2:L:51:THR:N	2.50	0.43
2:I:18:ARG:HG3	2:I:76:SER:HA	1.99	0.43
2:K:33:LEU:O	2:K:51:THR:N	2.50	0.43
2:I:16:GLY:N	2:I:78:LEU:O	2.47	0.43
1:D:239:THR:OG1	1:D:240:ILE:N	2.51	0.43
1:A:178:TRP:N	1:A:194:ILE:O	2.48	0.43
1:C:316:TYR:HB2	1:C:336:CYS:O	2.18	0.43
1:D:213:ASP:OD1	1:D:214:THR:N	2.50	0.43
1:B:213:ASP:OD1	1:B:214:THR:N	2.50	0.42
1:D:316:TYR:HB2	1:D:336:CYS:O	2.18	0.42
1:B:366:LYS:NZ	1:B:396:ASP:OD1	2.47	0.42
2:L:16:GLY:N	2:L:78:LEU:O	2.47	0.41
2:I:33:LEU:O	2:I:51:THR:N	2.50	0.41
1:A:102:LYS:NZ	1:A:459:PRO:O	2.51	0.41
1:B:102:LYS:NZ	1:B:459:PRO:O	2.51	0.41
1:B:385:GLU:HG2	3:E:54:ARG:HE	1.87	0.40
2:K:34:ASN:ND2	3:G:100(B):LEU:O	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	383/449 (85%)	366 (96%)	17 (4%)	0	100	100
1	B	383/449 (85%)	366 (96%)	17 (4%)	0	100	100
1	C	383/449 (85%)	366 (96%)	17 (4%)	0	100	100
1	D	383/449 (85%)	366 (96%)	17 (4%)	0	100	100
2	I	106/215 (49%)	103 (97%)	3 (3%)	0	100	100
2	J	106/215 (49%)	103 (97%)	3 (3%)	0	100	100
2	K	106/215 (49%)	103 (97%)	3 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	L	106/215 (49%)	103 (97%)	3 (3%)	0	100	100
3	E	119/225 (53%)	117 (98%)	2 (2%)	0	100	100
3	F	119/225 (53%)	117 (98%)	2 (2%)	0	100	100
3	G	119/225 (53%)	117 (98%)	2 (2%)	0	100	100
3	H	119/225 (53%)	117 (98%)	2 (2%)	0	100	100
All	All	2432/3556 (68%)	2344 (96%)	88 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	330/390 (85%)	329 (100%)	1 (0%)	86	87
1	B	330/390 (85%)	329 (100%)	1 (0%)	86	87
1	C	330/390 (85%)	329 (100%)	1 (0%)	86	87
1	D	330/390 (85%)	329 (100%)	1 (0%)	86	87
2	I	94/190 (50%)	94 (100%)	0	100	100
2	J	94/190 (50%)	94 (100%)	0	100	100
2	K	94/190 (50%)	94 (100%)	0	100	100
2	L	94/190 (50%)	94 (100%)	0	100	100
3	E	104/194 (54%)	104 (100%)	0	100	100
3	F	104/194 (54%)	104 (100%)	0	100	100
3	G	104/194 (54%)	104 (100%)	0	100	100
3	H	104/194 (54%)	104 (100%)	0	100	100
All	All	2112/3096 (68%)	2108 (100%)	4 (0%)	85	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	252	TYR
1	B	252	TYR
1	C	252	TYR
1	D	252	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	274	HIS
2	L	37	GLN
2	L	55	GLN
1	B	274	HIS
2	I	37	GLN
1	C	274	HIS
2	J	37	GLN
2	J	55	GLN
1	D	274	HIS
2	K	37	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	A	501	1	14,14,15	0.39	0	17,19,21	0.48	0
4	NAG	B	501	1	14,14,15	0.39	0	17,19,21	0.48	0
4	NAG	C	501	1	14,14,15	0.39	0	17,19,21	0.48	0
4	NAG	D	501	1	14,14,15	0.39	0	17,19,21	0.48	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	A	501	1	-	2/6/23/26	0/1/1/1
4	NAG	B	501	1	-	2/6/23/26	0/1/1/1
4	NAG	C	501	1	-	2/6/23/26	0/1/1/1
4	NAG	D	501	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	NAG	C8-C7-N2-C2
4	B	501	NAG	C8-C7-N2-C2
4	C	501	NAG	C8-C7-N2-C2
4	D	501	NAG	C8-C7-N2-C2
4	A	501	NAG	O7-C7-N2-C2
4	B	501	NAG	O7-C7-N2-C2
4	C	501	NAG	O7-C7-N2-C2
4	D	501	NAG	O7-C7-N2-C2

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	NAG	1	0
4	B	501	NAG	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	501	NAG	1	0
4	D	501	NAG	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

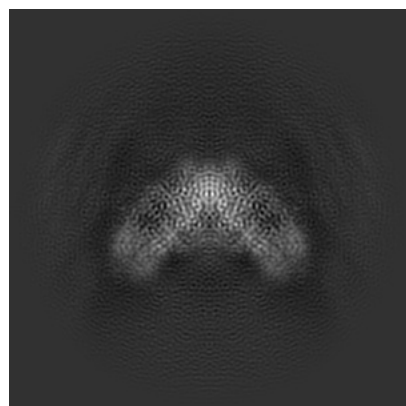
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-27921. These allow visual inspection of the internal detail of the map and identification of artifacts.

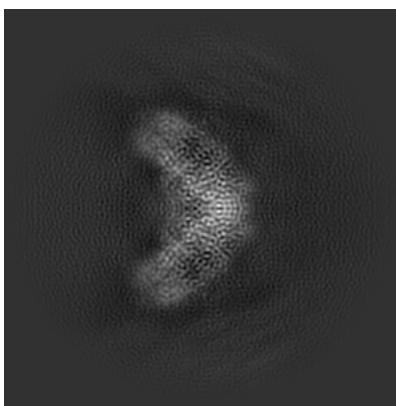
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

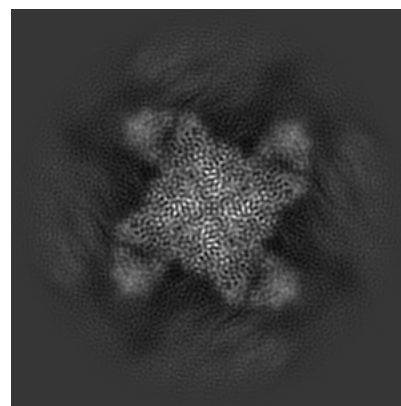
6.1.1 Primary map



X

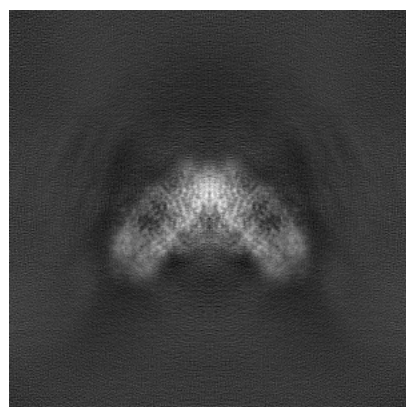


Y

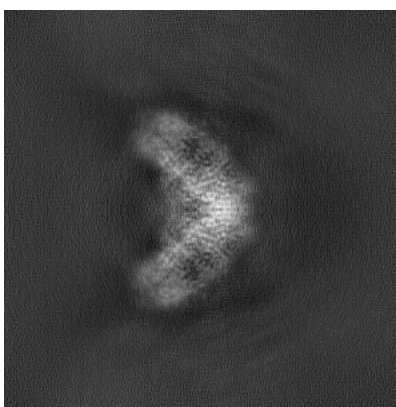


Z

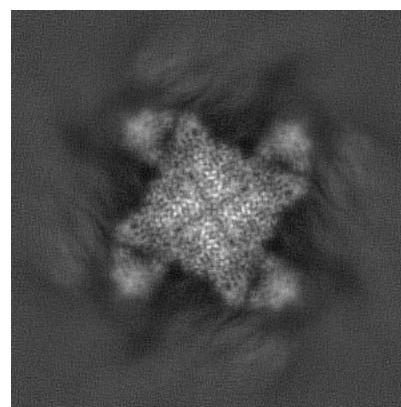
6.1.2 Raw map



X



Y

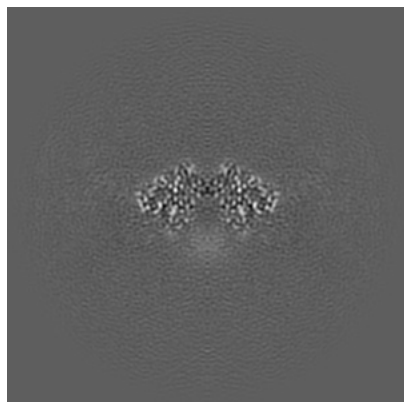


Z

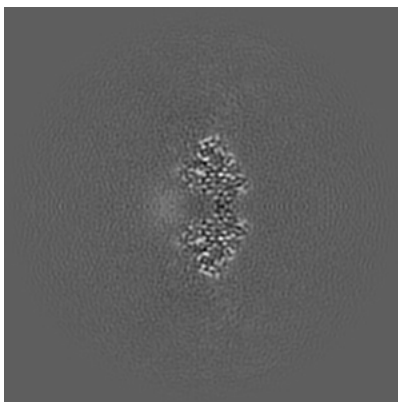
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

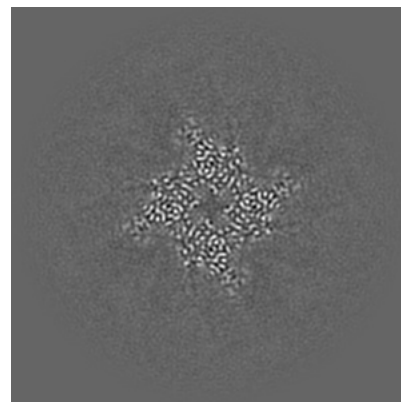
6.2.1 Primary map



X Index: 210

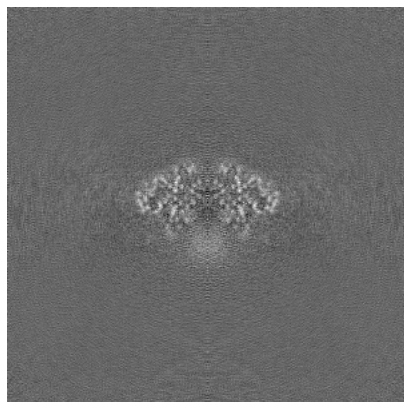


Y Index: 210

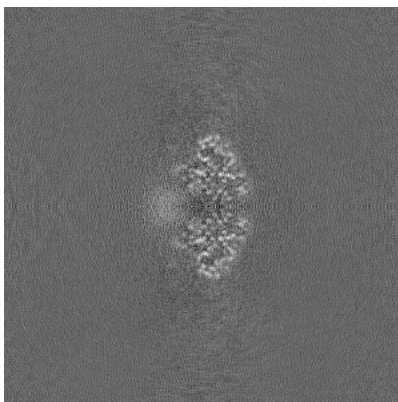


Z Index: 210

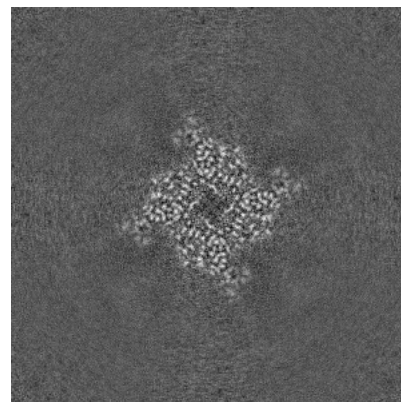
6.2.2 Raw map



X Index: 210



Y Index: 210

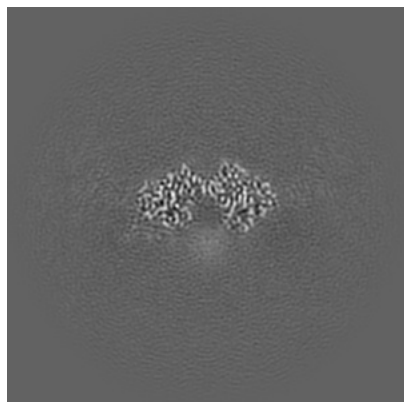


Z Index: 210

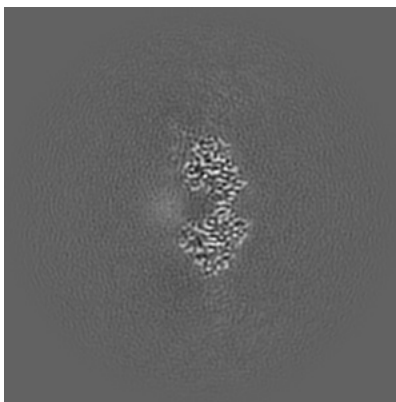
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

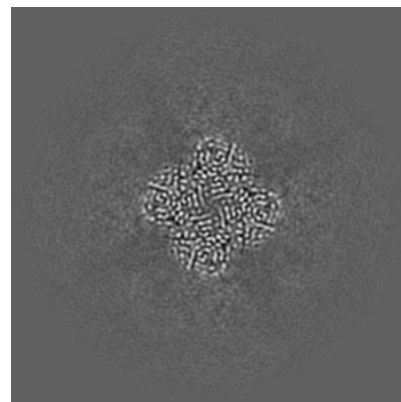
6.3.1 Primary map



X Index: 213

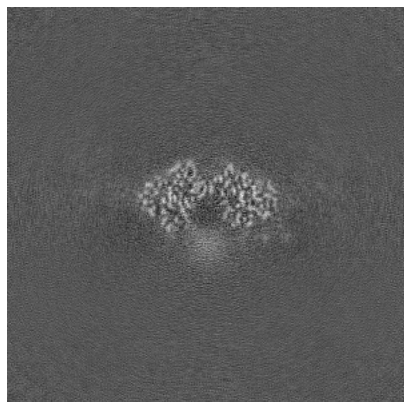


Y Index: 213

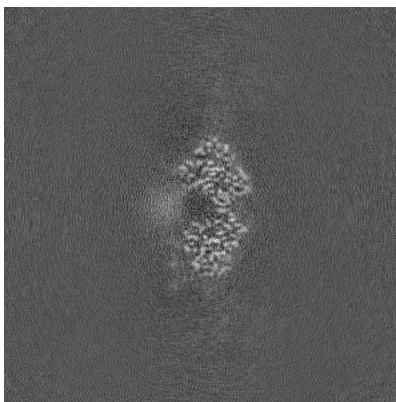


Z Index: 218

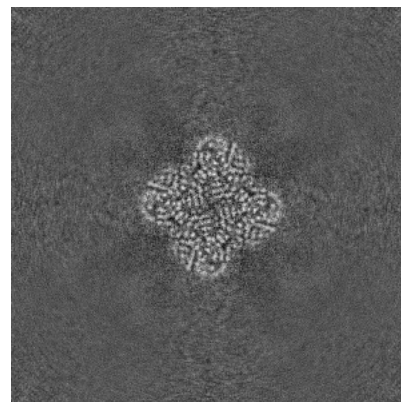
6.3.2 Raw map



X Index: 207



Y Index: 207

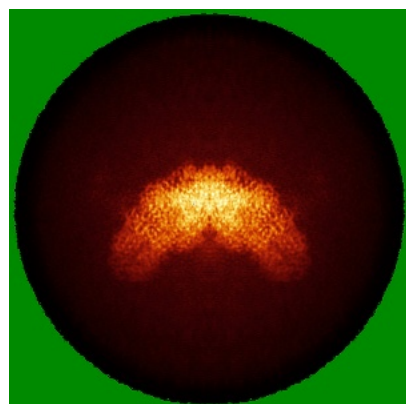


Z Index: 218

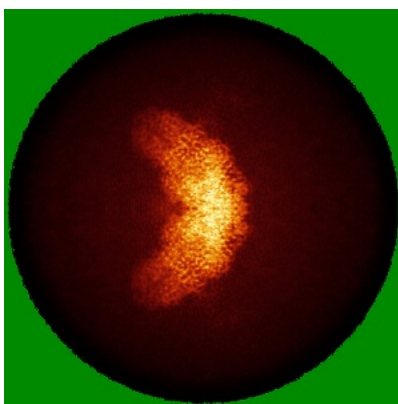
The images above show the largest variance slices of the map in three orthogonal directions.

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

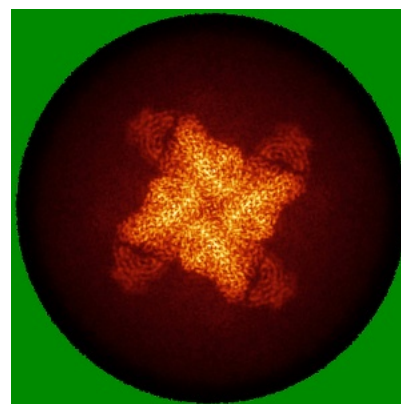
6.4.1 Primary map



X

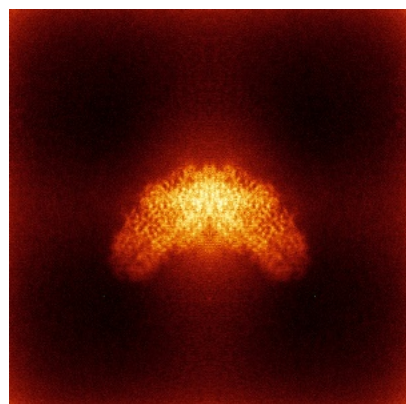


Y

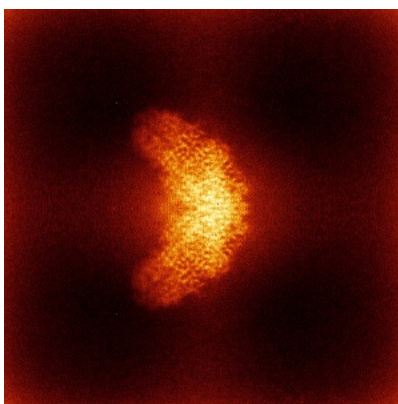


Z

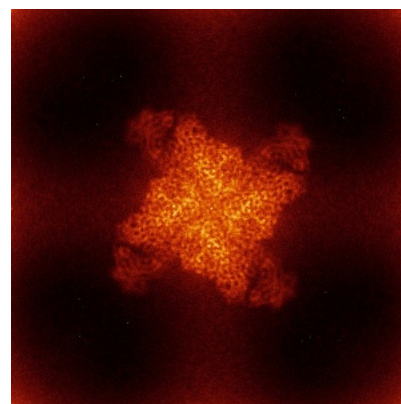
6.4.2 Raw map



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.

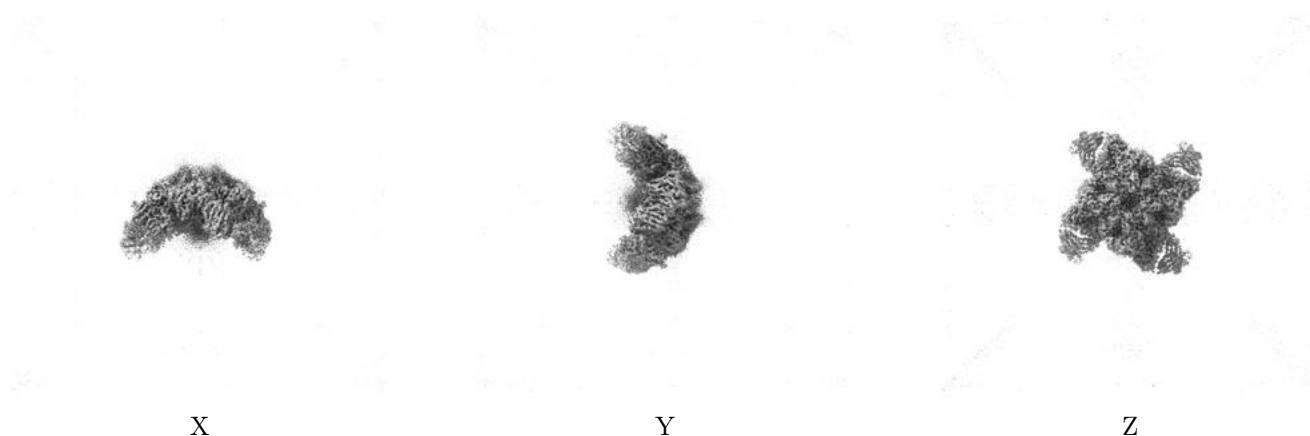
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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



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.

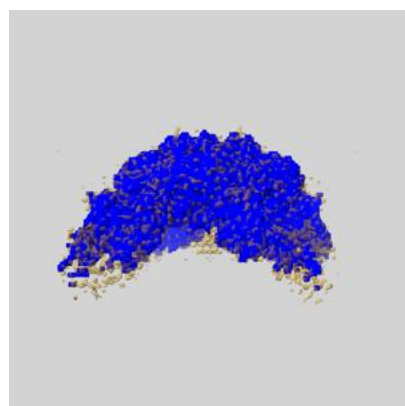
6.6 Mask visualisation [i](#)

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

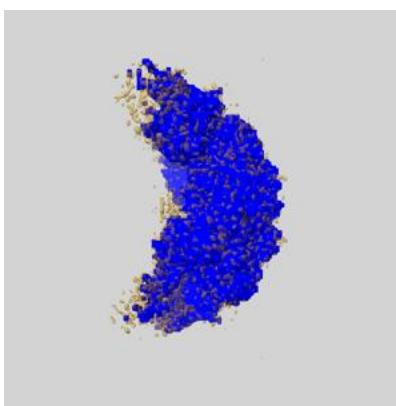
A mask typically either:

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

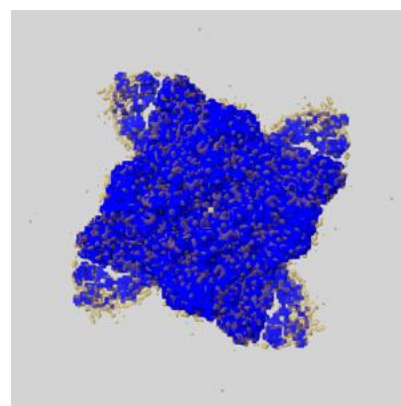
6.6.1 emd_27921_msk_1.map [i](#)



X



Y

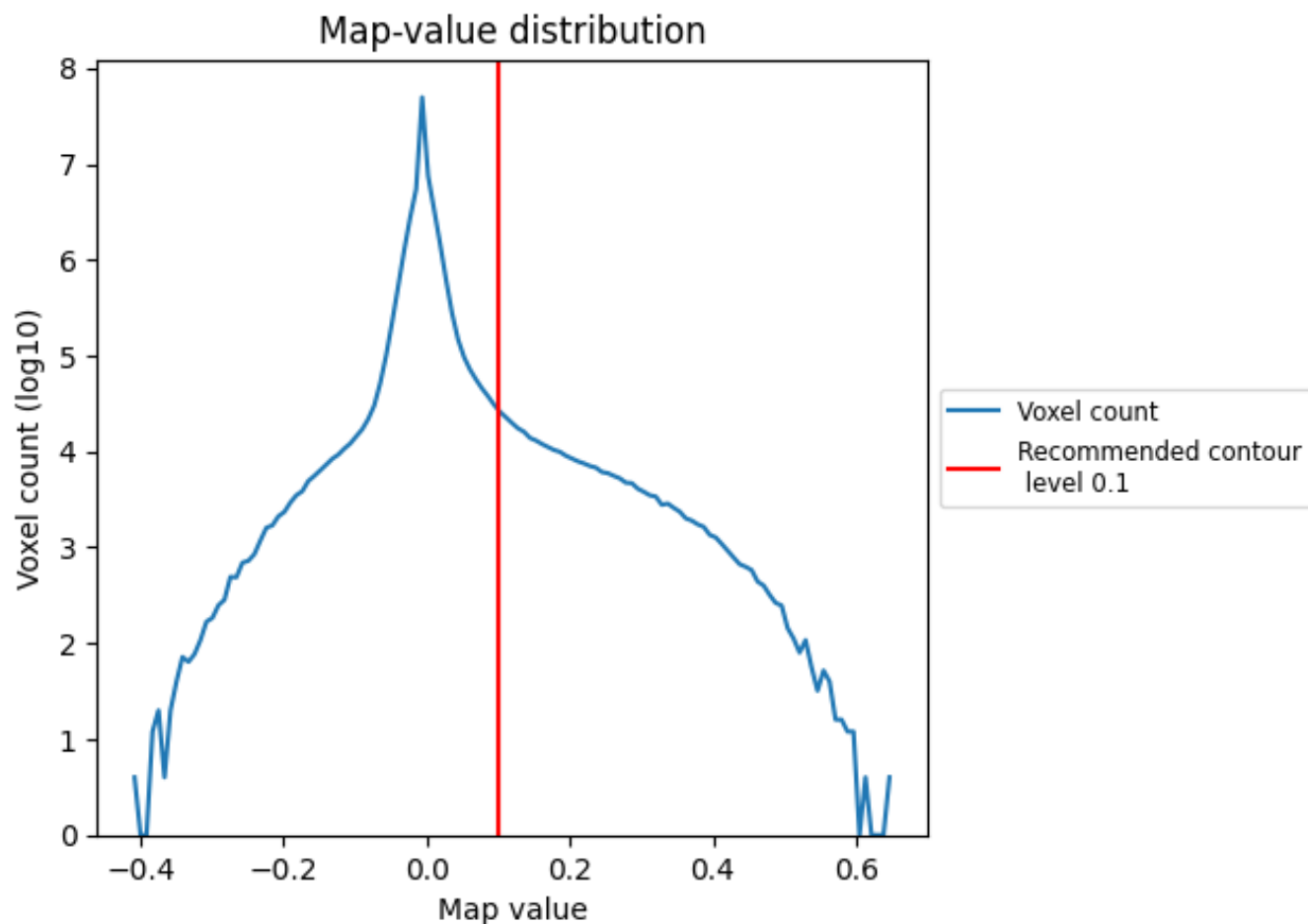


Z

7 Map analysis [i](#)

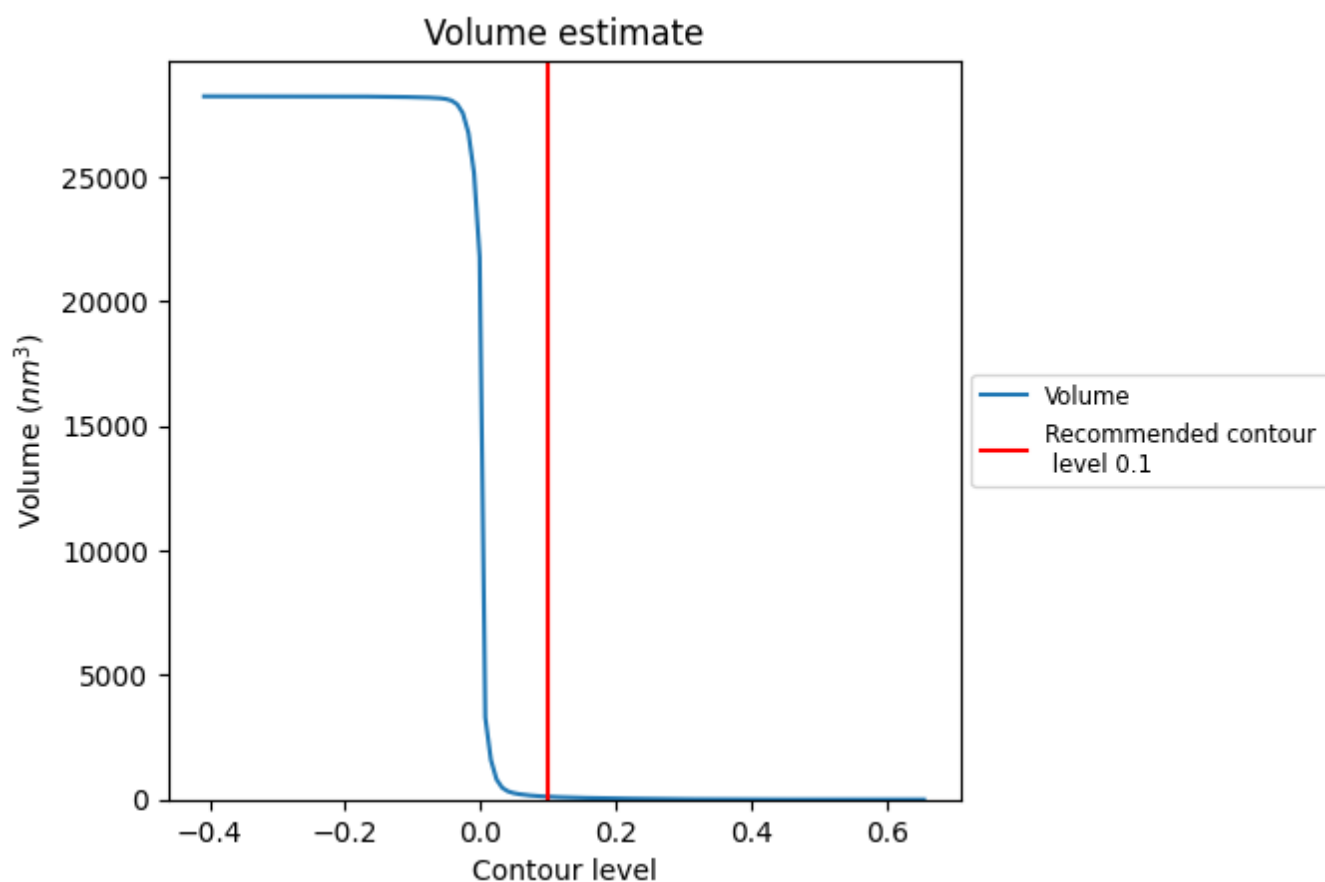
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

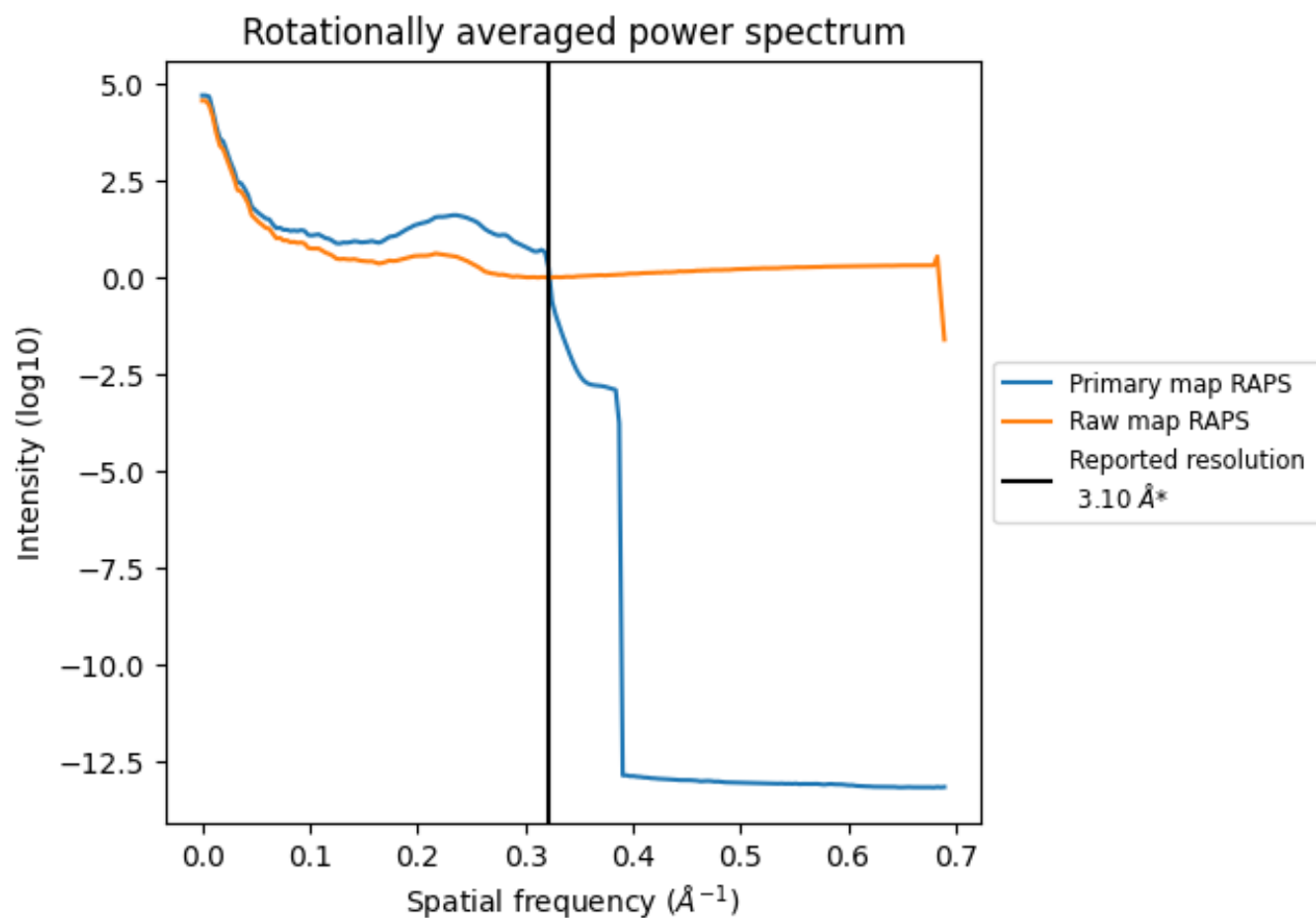
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 115 nm³; this corresponds to an approximate mass of 104 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

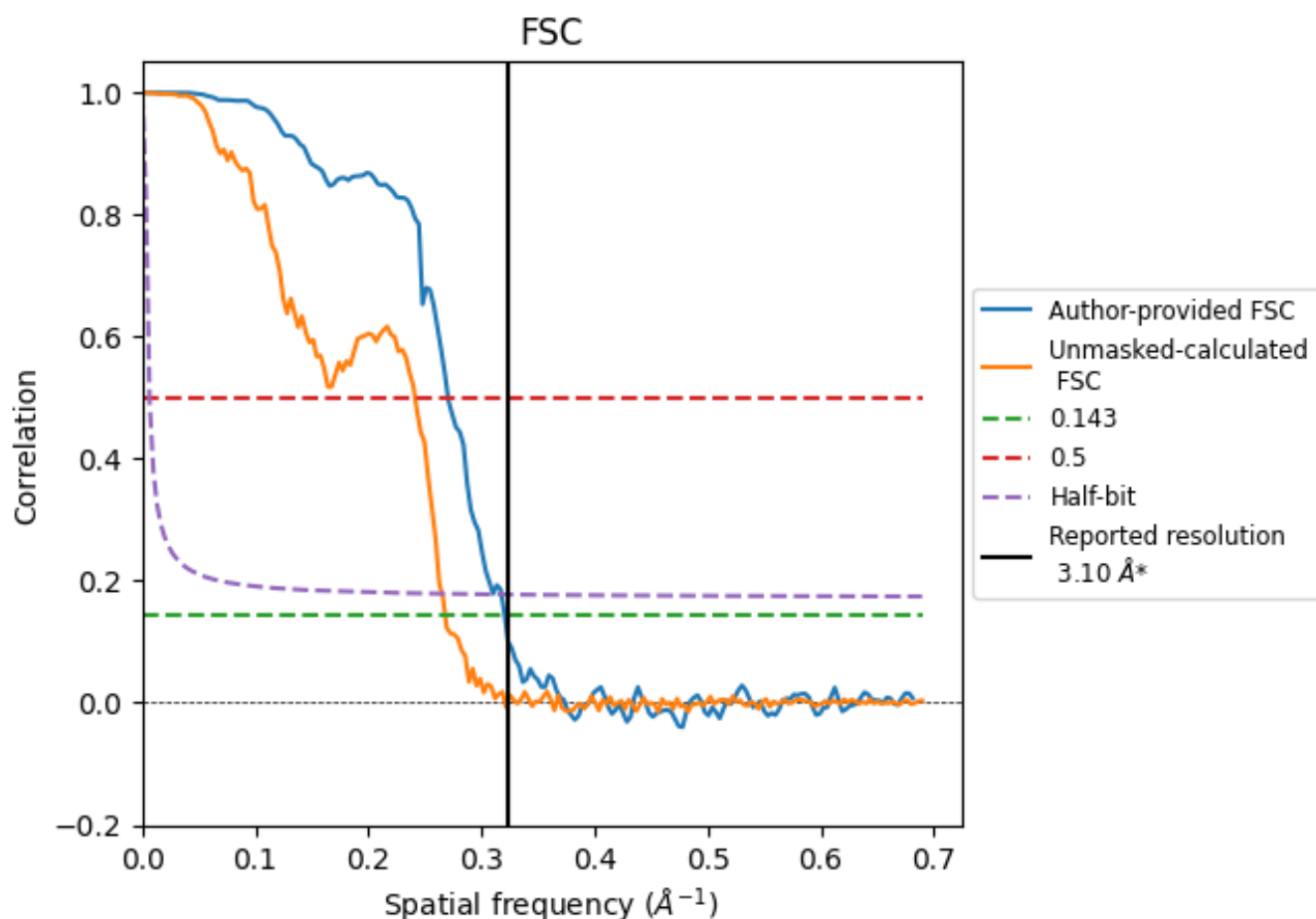


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.70	3.15
Unmasked-calculated*	3.73	4.14	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 3.73 differs from the reported value 3.1 by more than 10 %

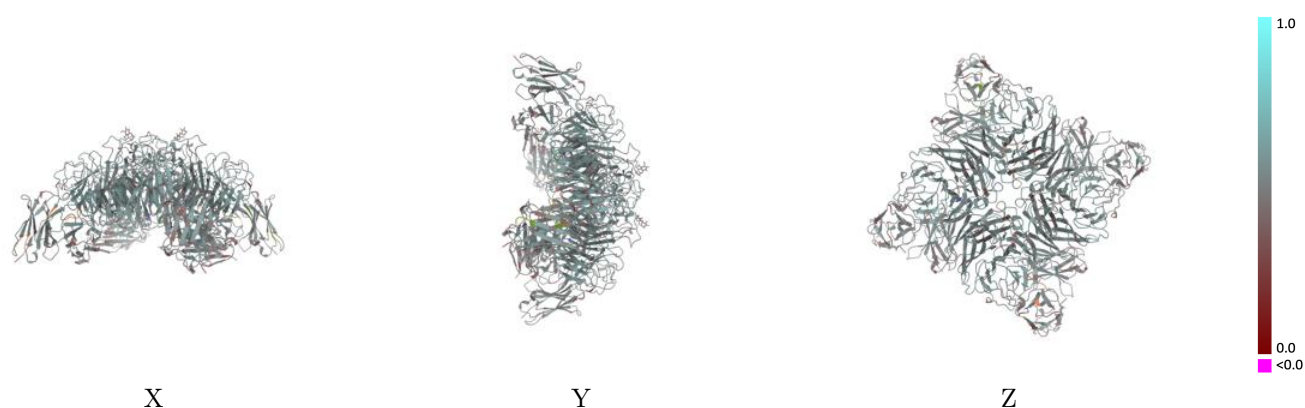
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-27921 and PDB model 8E6K. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)

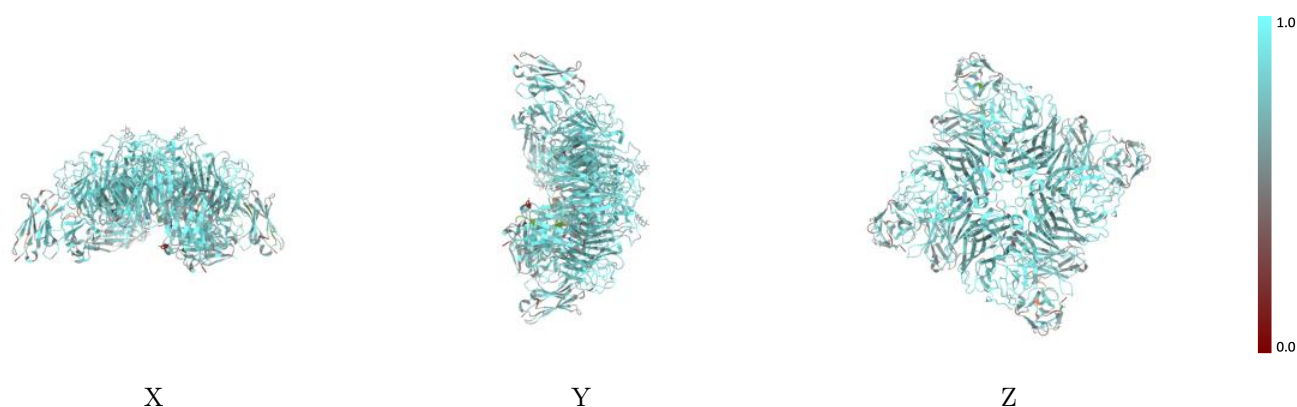
This section was not generated.

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



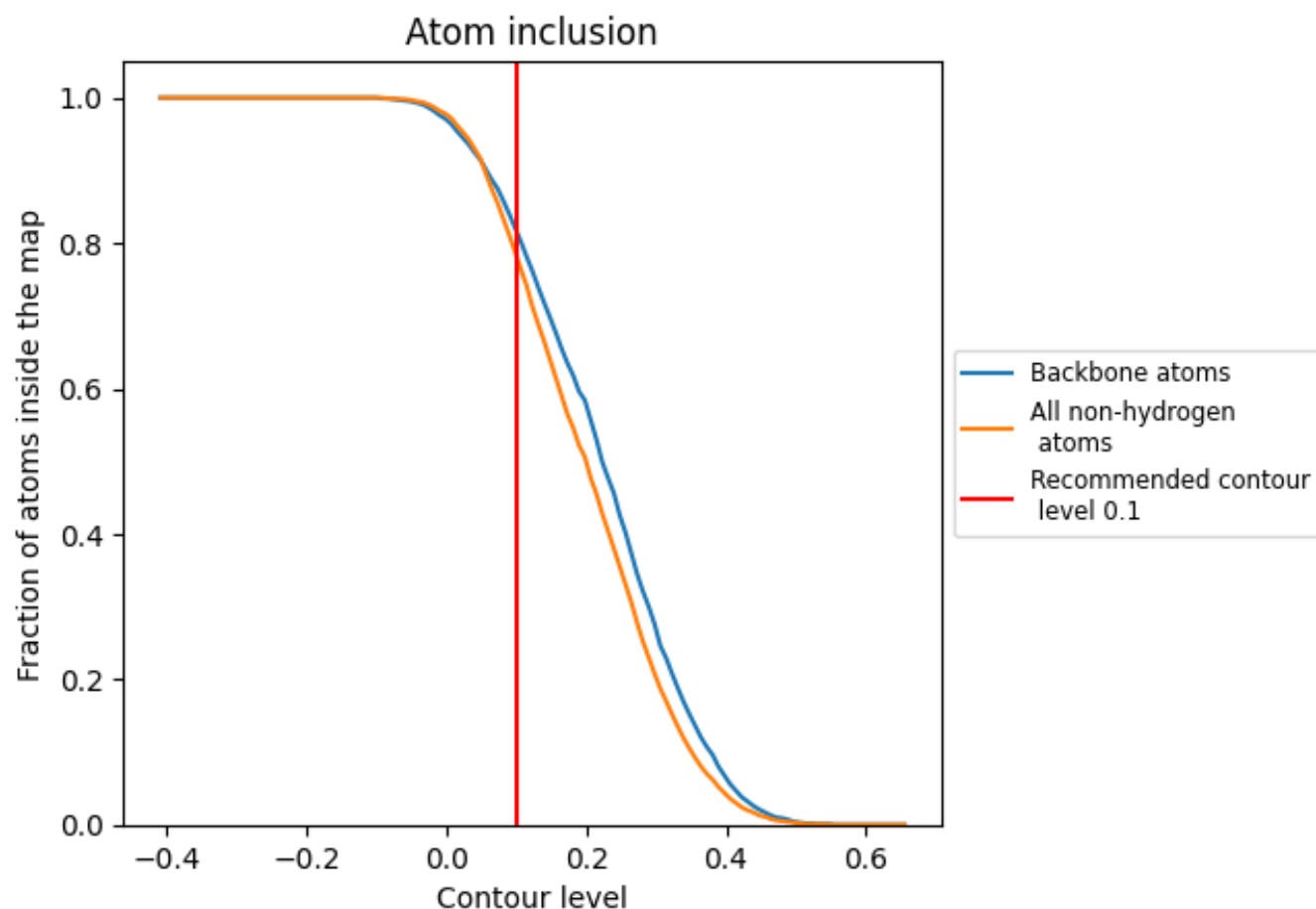
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 78% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7840	0.5120
A	0.8250	0.5320
B	0.8250	0.5320
C	0.8250	0.5300
D	0.8250	0.5300
E	0.6910	0.4760
F	0.6910	0.4780
G	0.6910	0.4780
H	0.6910	0.4770
I	0.7410	0.4850
J	0.7410	0.4870
K	0.7410	0.4860
L	0.7410	0.4860

