



wwPDB EM Validation Summary Report ⓘ

Mar 17, 2026 – 04:04 PM UTC

PDB ID : 6SB5 / pdb_00006sb5
EMDB ID : EMD-10135
Title : CryoEM structure of murine perforin-2 ectodomain in a pore form
Authors : Ni, T.; Yu, X.; Gilbert, R.J.C.
Deposited on : 2019-07-18
Resolution : 5.00 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:

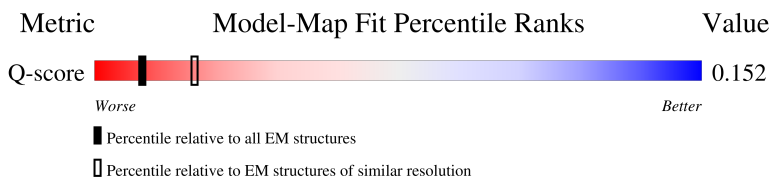
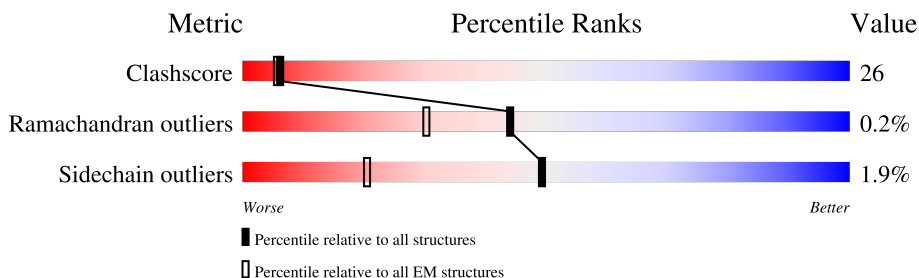
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 5.00 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	1057 (4.50 - 5.50)

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	646	16% 43% 39% 16%
1	B	646	16% 43% 39% 16%
1	C	646	16% 43% 39% 16%
1	D	646	16% 43% 39% 16%

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Mol	Chain	Length	Quality of chain
1	E	646	
1	F	646	
1	G	646	
1	H	646	
1	I	646	
1	J	646	
1	K	646	
1	L	646	
1	M	646	
1	N	646	
1	O	646	
1	P	646	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 67760 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 Macrophage-expressed gene 1 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	B	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	C	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	D	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	E	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	F	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	G	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	H	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	I	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	J	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	K	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	L	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	M	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	N	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	O	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		
1	P	543	Total	C	N	O	S	0	0
			4207	2668	701	809	29		

There are 208 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	GLU	-	expression tag	UNP A1L314
A	18	THR	-	expression tag	UNP A1L314
A	19	GLY	-	expression tag	UNP A1L314
A	653	GLY	-	expression tag	UNP A1L314
A	654	THR	-	expression tag	UNP A1L314
A	655	GLU	-	expression tag	UNP A1L314
A	656	THR	-	expression tag	UNP A1L314
A	657	SER	-	expression tag	UNP A1L314
A	658	GLN	-	expression tag	UNP A1L314
A	659	VAL	-	expression tag	UNP A1L314
A	660	ALA	-	expression tag	UNP A1L314
A	661	PRO	-	expression tag	UNP A1L314
A	662	ALA	-	expression tag	UNP A1L314
B	17	GLU	-	expression tag	UNP A1L314
B	18	THR	-	expression tag	UNP A1L314
B	19	GLY	-	expression tag	UNP A1L314
B	653	GLY	-	expression tag	UNP A1L314
B	654	THR	-	expression tag	UNP A1L314
B	655	GLU	-	expression tag	UNP A1L314
B	656	THR	-	expression tag	UNP A1L314
B	657	SER	-	expression tag	UNP A1L314
B	658	GLN	-	expression tag	UNP A1L314
B	659	VAL	-	expression tag	UNP A1L314
B	660	ALA	-	expression tag	UNP A1L314
B	661	PRO	-	expression tag	UNP A1L314
B	662	ALA	-	expression tag	UNP A1L314
C	17	GLU	-	expression tag	UNP A1L314
C	18	THR	-	expression tag	UNP A1L314
C	19	GLY	-	expression tag	UNP A1L314
C	653	GLY	-	expression tag	UNP A1L314
C	654	THR	-	expression tag	UNP A1L314
C	655	GLU	-	expression tag	UNP A1L314
C	656	THR	-	expression tag	UNP A1L314
C	657	SER	-	expression tag	UNP A1L314
C	658	GLN	-	expression tag	UNP A1L314
C	659	VAL	-	expression tag	UNP A1L314
C	660	ALA	-	expression tag	UNP A1L314
C	661	PRO	-	expression tag	UNP A1L314
C	662	ALA	-	expression tag	UNP A1L314
D	17	GLU	-	expression tag	UNP A1L314
D	18	THR	-	expression tag	UNP A1L314
D	19	GLY	-	expression tag	UNP A1L314
D	653	GLY	-	expression tag	UNP A1L314

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Chain	Residue	Modelled	Actual	Comment	Reference
D	654	THR	-	expression tag	UNP A1L314
D	655	GLU	-	expression tag	UNP A1L314
D	656	THR	-	expression tag	UNP A1L314
D	657	SER	-	expression tag	UNP A1L314
D	658	GLN	-	expression tag	UNP A1L314
D	659	VAL	-	expression tag	UNP A1L314
D	660	ALA	-	expression tag	UNP A1L314
D	661	PRO	-	expression tag	UNP A1L314
D	662	ALA	-	expression tag	UNP A1L314
E	17	GLU	-	expression tag	UNP A1L314
E	18	THR	-	expression tag	UNP A1L314
E	19	GLY	-	expression tag	UNP A1L314
E	653	GLY	-	expression tag	UNP A1L314
E	654	THR	-	expression tag	UNP A1L314
E	655	GLU	-	expression tag	UNP A1L314
E	656	THR	-	expression tag	UNP A1L314
E	657	SER	-	expression tag	UNP A1L314
E	658	GLN	-	expression tag	UNP A1L314
E	659	VAL	-	expression tag	UNP A1L314
E	660	ALA	-	expression tag	UNP A1L314
E	661	PRO	-	expression tag	UNP A1L314
E	662	ALA	-	expression tag	UNP A1L314
F	17	GLU	-	expression tag	UNP A1L314
F	18	THR	-	expression tag	UNP A1L314
F	19	GLY	-	expression tag	UNP A1L314
F	653	GLY	-	expression tag	UNP A1L314
F	654	THR	-	expression tag	UNP A1L314
F	655	GLU	-	expression tag	UNP A1L314
F	656	THR	-	expression tag	UNP A1L314
F	657	SER	-	expression tag	UNP A1L314
F	658	GLN	-	expression tag	UNP A1L314
F	659	VAL	-	expression tag	UNP A1L314
F	660	ALA	-	expression tag	UNP A1L314
F	661	PRO	-	expression tag	UNP A1L314
F	662	ALA	-	expression tag	UNP A1L314
G	17	GLU	-	expression tag	UNP A1L314
G	18	THR	-	expression tag	UNP A1L314
G	19	GLY	-	expression tag	UNP A1L314
G	653	GLY	-	expression tag	UNP A1L314
G	654	THR	-	expression tag	UNP A1L314
G	655	GLU	-	expression tag	UNP A1L314
G	656	THR	-	expression tag	UNP A1L314

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Chain	Residue	Modelled	Actual	Comment	Reference
G	657	SER	-	expression tag	UNP A1L314
G	658	GLN	-	expression tag	UNP A1L314
G	659	VAL	-	expression tag	UNP A1L314
G	660	ALA	-	expression tag	UNP A1L314
G	661	PRO	-	expression tag	UNP A1L314
G	662	ALA	-	expression tag	UNP A1L314
H	17	GLU	-	expression tag	UNP A1L314
H	18	THR	-	expression tag	UNP A1L314
H	19	GLY	-	expression tag	UNP A1L314
H	653	GLY	-	expression tag	UNP A1L314
H	654	THR	-	expression tag	UNP A1L314
H	655	GLU	-	expression tag	UNP A1L314
H	656	THR	-	expression tag	UNP A1L314
H	657	SER	-	expression tag	UNP A1L314
H	658	GLN	-	expression tag	UNP A1L314
H	659	VAL	-	expression tag	UNP A1L314
H	660	ALA	-	expression tag	UNP A1L314
H	661	PRO	-	expression tag	UNP A1L314
H	662	ALA	-	expression tag	UNP A1L314
I	17	GLU	-	expression tag	UNP A1L314
I	18	THR	-	expression tag	UNP A1L314
I	19	GLY	-	expression tag	UNP A1L314
I	653	GLY	-	expression tag	UNP A1L314
I	654	THR	-	expression tag	UNP A1L314
I	655	GLU	-	expression tag	UNP A1L314
I	656	THR	-	expression tag	UNP A1L314
I	657	SER	-	expression tag	UNP A1L314
I	658	GLN	-	expression tag	UNP A1L314
I	659	VAL	-	expression tag	UNP A1L314
I	660	ALA	-	expression tag	UNP A1L314
I	661	PRO	-	expression tag	UNP A1L314
I	662	ALA	-	expression tag	UNP A1L314
J	17	GLU	-	expression tag	UNP A1L314
J	18	THR	-	expression tag	UNP A1L314
J	19	GLY	-	expression tag	UNP A1L314
J	653	GLY	-	expression tag	UNP A1L314
J	654	THR	-	expression tag	UNP A1L314
J	655	GLU	-	expression tag	UNP A1L314
J	656	THR	-	expression tag	UNP A1L314
J	657	SER	-	expression tag	UNP A1L314
J	658	GLN	-	expression tag	UNP A1L314
J	659	VAL	-	expression tag	UNP A1L314

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Chain	Residue	Modelled	Actual	Comment	Reference
J	660	ALA	-	expression tag	UNP A1L314
J	661	PRO	-	expression tag	UNP A1L314
J	662	ALA	-	expression tag	UNP A1L314
K	17	GLU	-	expression tag	UNP A1L314
K	18	THR	-	expression tag	UNP A1L314
K	19	GLY	-	expression tag	UNP A1L314
K	653	GLY	-	expression tag	UNP A1L314
K	654	THR	-	expression tag	UNP A1L314
K	655	GLU	-	expression tag	UNP A1L314
K	656	THR	-	expression tag	UNP A1L314
K	657	SER	-	expression tag	UNP A1L314
K	658	GLN	-	expression tag	UNP A1L314
K	659	VAL	-	expression tag	UNP A1L314
K	660	ALA	-	expression tag	UNP A1L314
K	661	PRO	-	expression tag	UNP A1L314
K	662	ALA	-	expression tag	UNP A1L314
L	17	GLU	-	expression tag	UNP A1L314
L	18	THR	-	expression tag	UNP A1L314
L	19	GLY	-	expression tag	UNP A1L314
L	653	GLY	-	expression tag	UNP A1L314
L	654	THR	-	expression tag	UNP A1L314
L	655	GLU	-	expression tag	UNP A1L314
L	656	THR	-	expression tag	UNP A1L314
L	657	SER	-	expression tag	UNP A1L314
L	658	GLN	-	expression tag	UNP A1L314
L	659	VAL	-	expression tag	UNP A1L314
L	660	ALA	-	expression tag	UNP A1L314
L	661	PRO	-	expression tag	UNP A1L314
L	662	ALA	-	expression tag	UNP A1L314
M	17	GLU	-	expression tag	UNP A1L314
M	18	THR	-	expression tag	UNP A1L314
M	19	GLY	-	expression tag	UNP A1L314
M	653	GLY	-	expression tag	UNP A1L314
M	654	THR	-	expression tag	UNP A1L314
M	655	GLU	-	expression tag	UNP A1L314
M	656	THR	-	expression tag	UNP A1L314
M	657	SER	-	expression tag	UNP A1L314
M	658	GLN	-	expression tag	UNP A1L314
M	659	VAL	-	expression tag	UNP A1L314
M	660	ALA	-	expression tag	UNP A1L314
M	661	PRO	-	expression tag	UNP A1L314
M	662	ALA	-	expression tag	UNP A1L314

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Chain	Residue	Modelled	Actual	Comment	Reference
N	17	GLU	-	expression tag	UNP A1L314
N	18	THR	-	expression tag	UNP A1L314
N	19	GLY	-	expression tag	UNP A1L314
N	653	GLY	-	expression tag	UNP A1L314
N	654	THR	-	expression tag	UNP A1L314
N	655	GLU	-	expression tag	UNP A1L314
N	656	THR	-	expression tag	UNP A1L314
N	657	SER	-	expression tag	UNP A1L314
N	658	GLN	-	expression tag	UNP A1L314
N	659	VAL	-	expression tag	UNP A1L314
N	660	ALA	-	expression tag	UNP A1L314
N	661	PRO	-	expression tag	UNP A1L314
N	662	ALA	-	expression tag	UNP A1L314
O	17	GLU	-	expression tag	UNP A1L314
O	18	THR	-	expression tag	UNP A1L314
O	19	GLY	-	expression tag	UNP A1L314
O	653	GLY	-	expression tag	UNP A1L314
O	654	THR	-	expression tag	UNP A1L314
O	655	GLU	-	expression tag	UNP A1L314
O	656	THR	-	expression tag	UNP A1L314
O	657	SER	-	expression tag	UNP A1L314
O	658	GLN	-	expression tag	UNP A1L314
O	659	VAL	-	expression tag	UNP A1L314
O	660	ALA	-	expression tag	UNP A1L314
O	661	PRO	-	expression tag	UNP A1L314
O	662	ALA	-	expression tag	UNP A1L314
P	17	GLU	-	expression tag	UNP A1L314
P	18	THR	-	expression tag	UNP A1L314
P	19	GLY	-	expression tag	UNP A1L314
P	653	GLY	-	expression tag	UNP A1L314
P	654	THR	-	expression tag	UNP A1L314
P	655	GLU	-	expression tag	UNP A1L314
P	656	THR	-	expression tag	UNP A1L314
P	657	SER	-	expression tag	UNP A1L314
P	658	GLN	-	expression tag	UNP A1L314
P	659	VAL	-	expression tag	UNP A1L314
P	660	ALA	-	expression tag	UNP A1L314
P	661	PRO	-	expression tag	UNP A1L314
P	662	ALA	-	expression tag	UNP A1L314

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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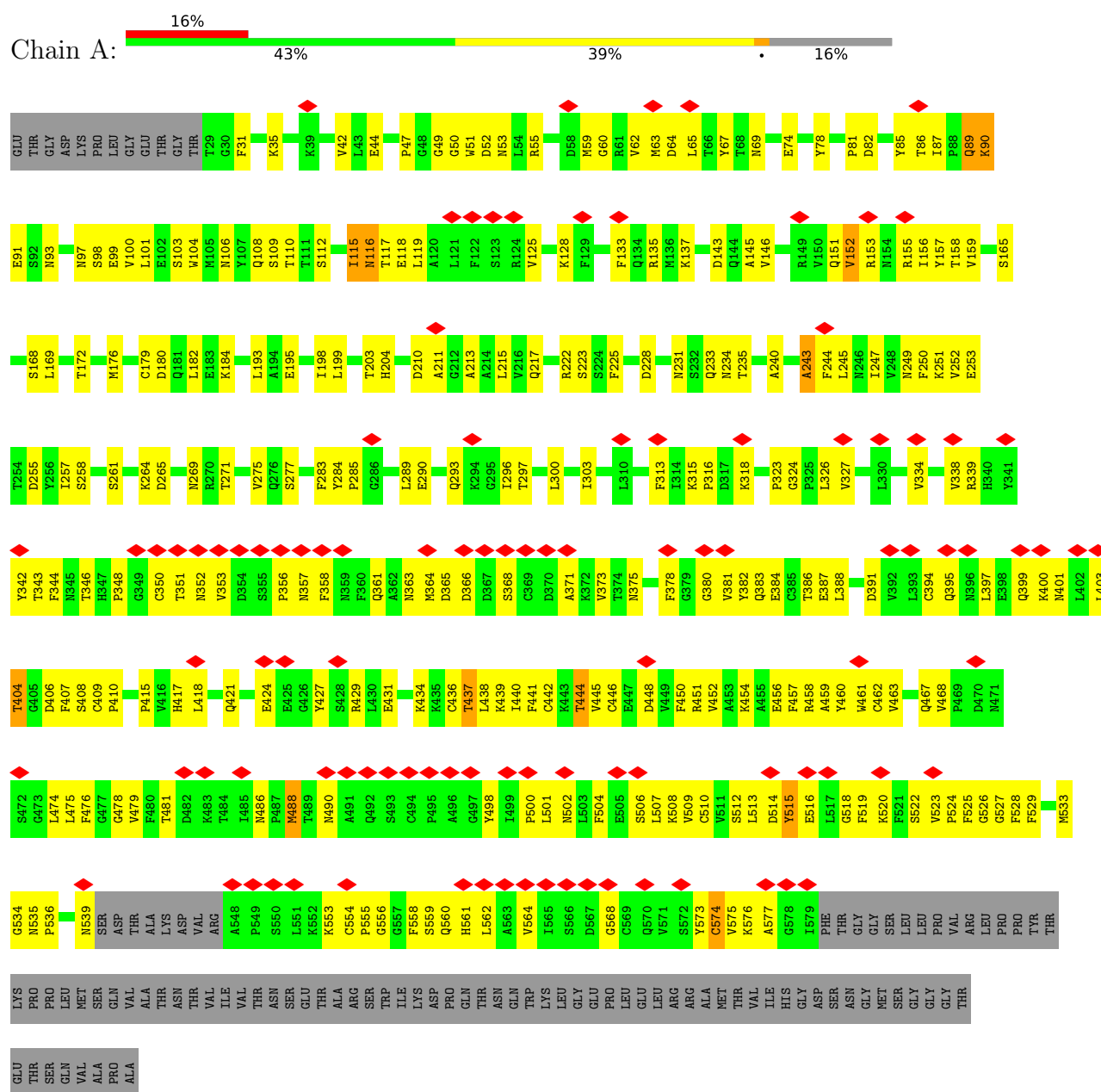
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Mol	Chain	Residues	Atoms				AltConf
2	H	1	Total	C	N	O	0
			14	8	1	5	
2	H	1	Total	C	N	O	0
			14	8	1	5	
2	I	1	Total	C	N	O	0
			14	8	1	5	
2	I	1	Total	C	N	O	0
			14	8	1	5	
2	J	1	Total	C	N	O	0
			14	8	1	5	
2	J	1	Total	C	N	O	0
			14	8	1	5	
2	K	1	Total	C	N	O	0
			14	8	1	5	
2	K	1	Total	C	N	O	0
			14	8	1	5	
2	L	1	Total	C	N	O	0
			14	8	1	5	
2	L	1	Total	C	N	O	0
			14	8	1	5	
2	M	1	Total	C	N	O	0
			14	8	1	5	
2	M	1	Total	C	N	O	0
			14	8	1	5	
2	N	1	Total	C	N	O	0
			14	8	1	5	
2	N	1	Total	C	N	O	0
			14	8	1	5	
2	O	1	Total	C	N	O	0
			14	8	1	5	
2	O	1	Total	C	N	O	0
			14	8	1	5	
2	P	1	Total	C	N	O	0
			14	8	1	5	
2	P	1	Total	C	N	O	0
			14	8	1	5	

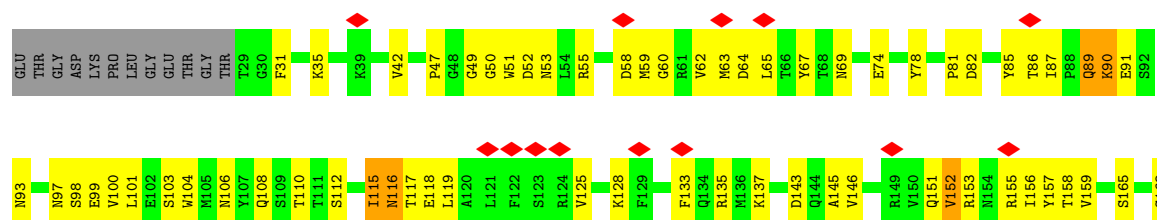
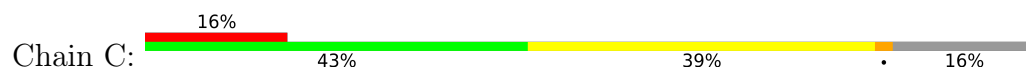
3 Residue-property plots [i](#)

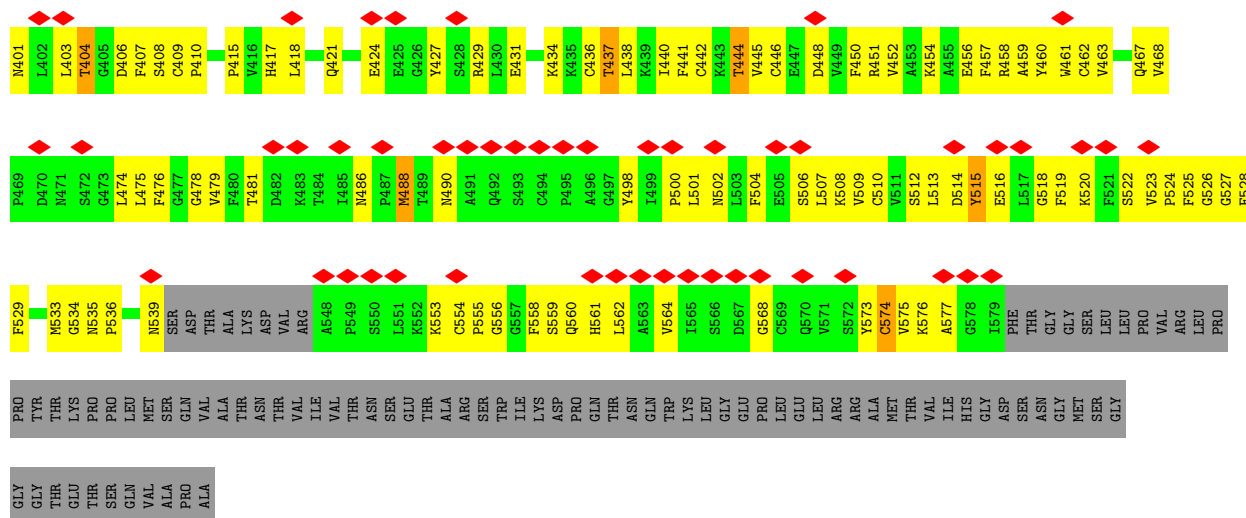
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Macrophage-expressed gene 1 protein

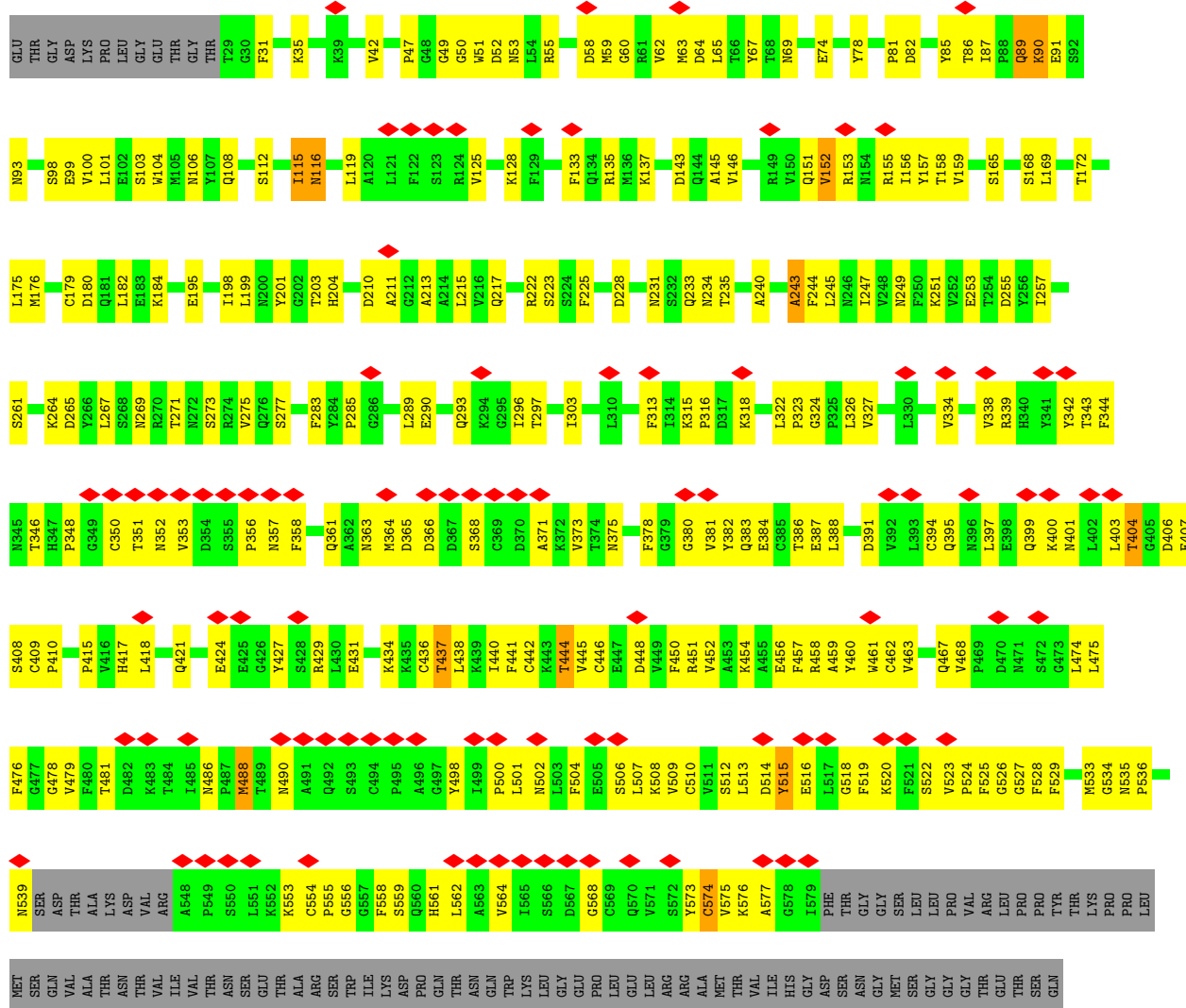


Chain B:

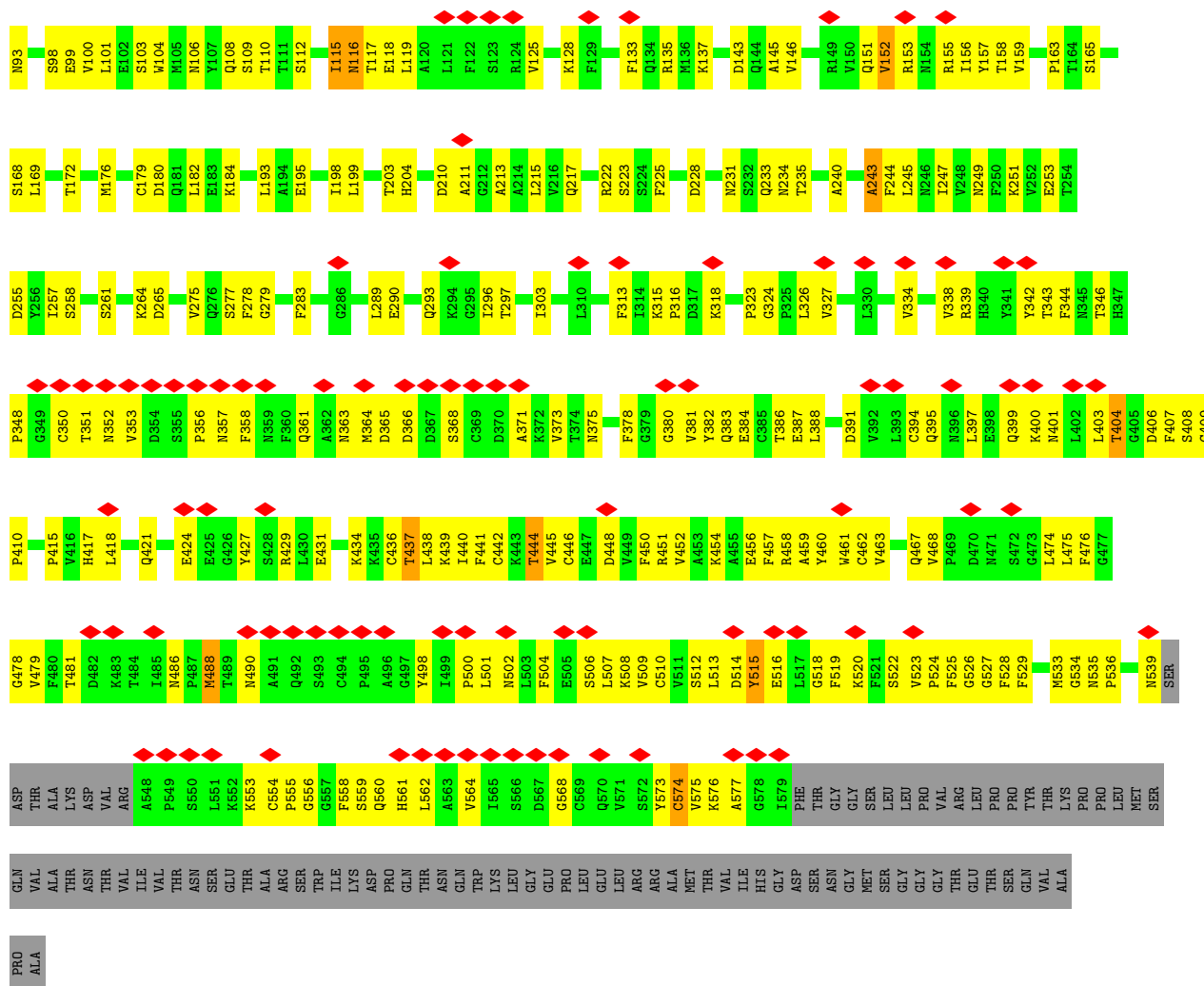




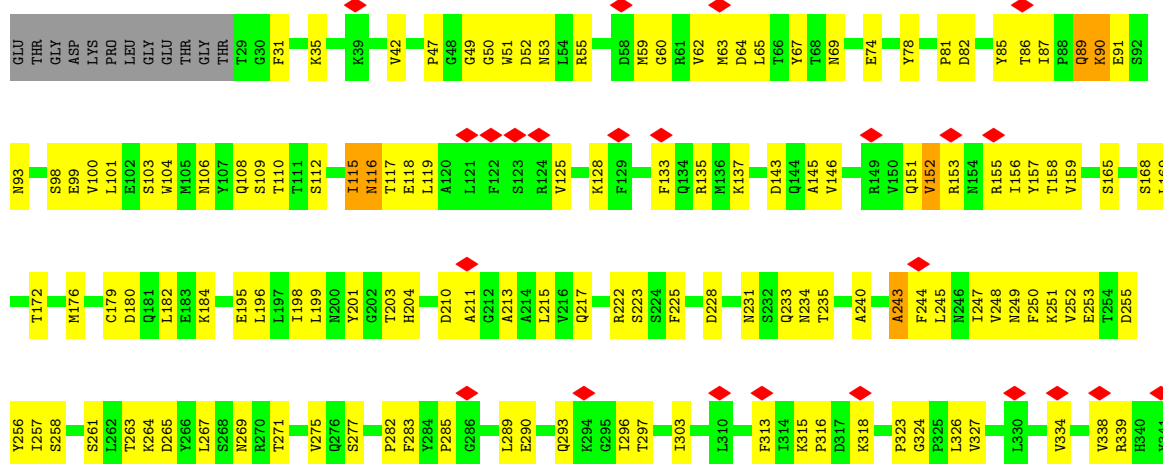
• Molecule 1: Macrophage-expressed gene 1 protein



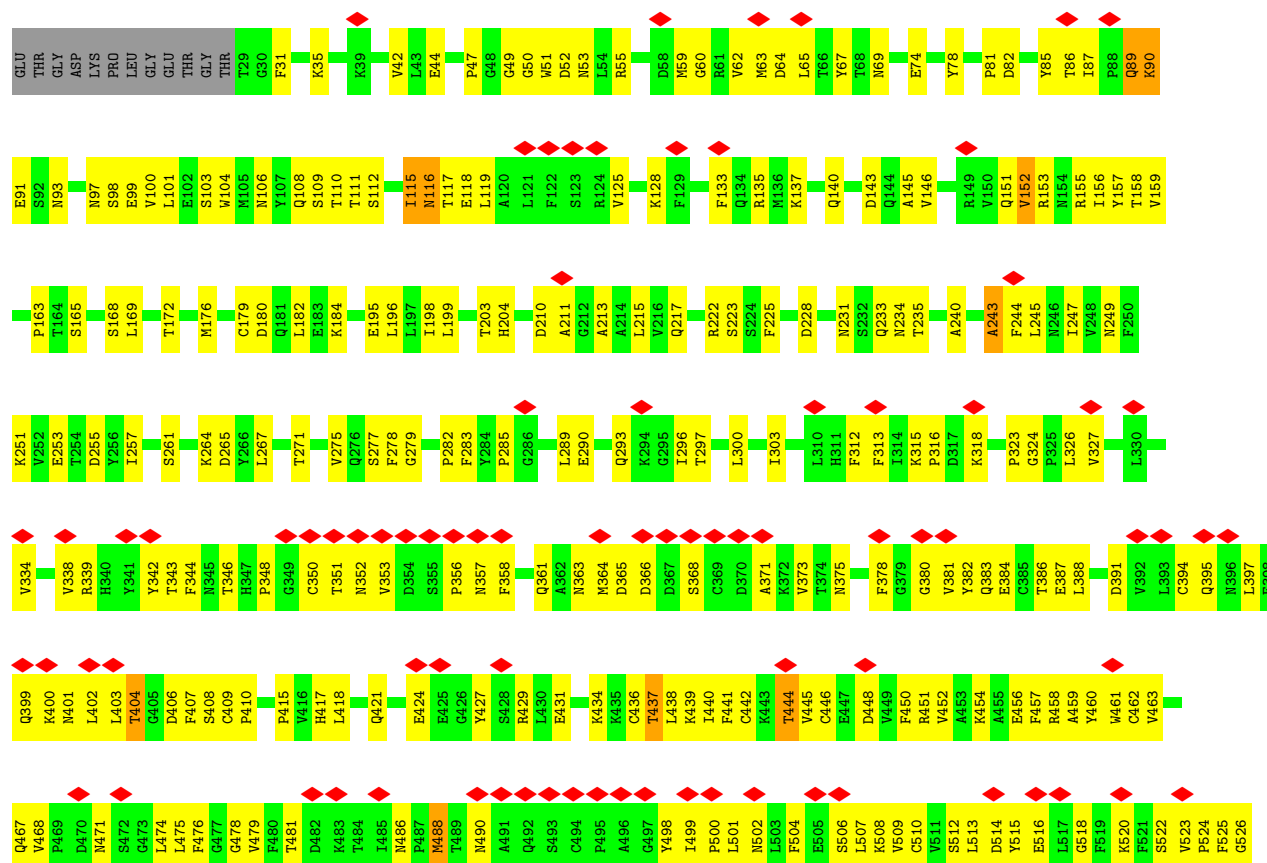
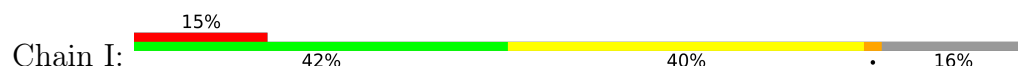
GLU	THR	GLY	ASP	LYS	PRO	LEU	GLY	GLU	THR	GLY	THR	T29	G30	F31	K35	K39	V42	P47	G48	G49	G50	W51	D52	N53	L54	R55	D58	M59	G60	R61	V62	M63	D64	L65	T66	V67	T68	N69	E74	Y78	P81	D82	Y85	T86	I87	P88	K89	K90	E91
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



• Molecule 1: Macrophage-expressed gene 1 protein

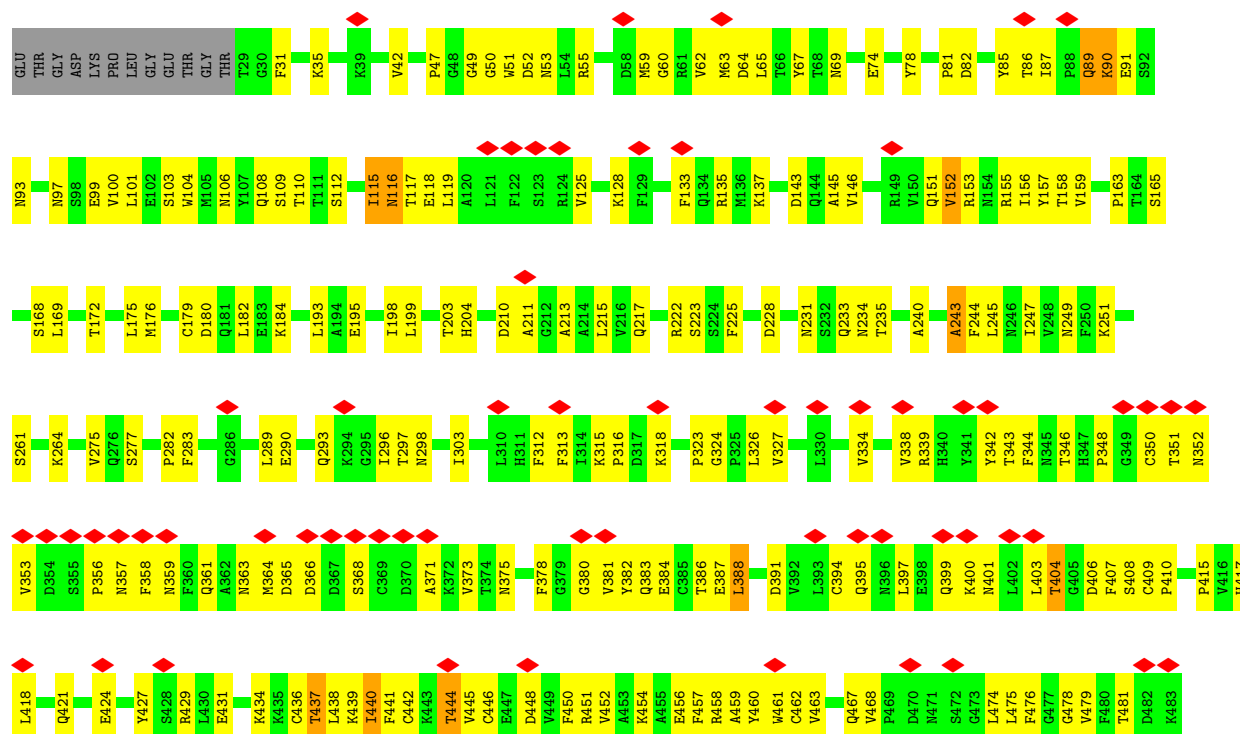
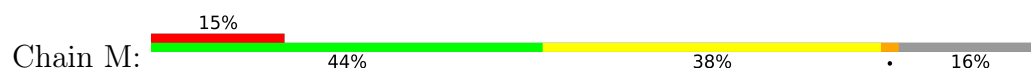


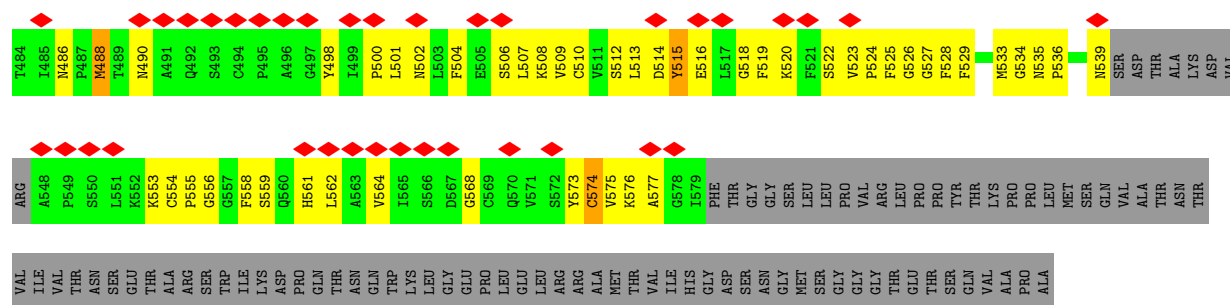
- Molecule 1: Macrophage-expressed gene 1 protein



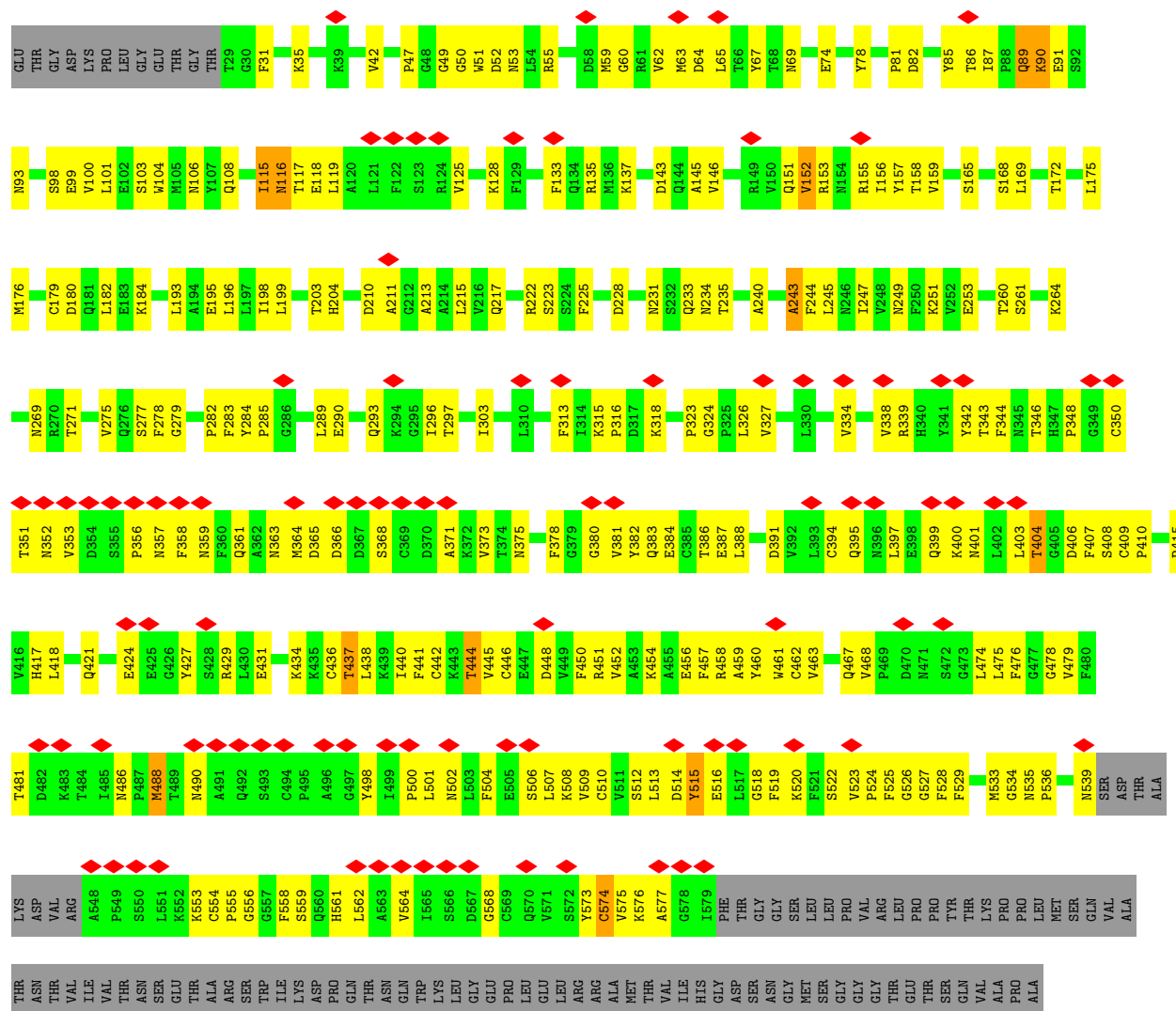
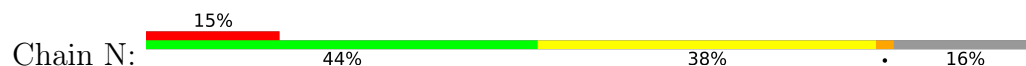


- Molecule 1: Macrophage-expressed gene 1 protein



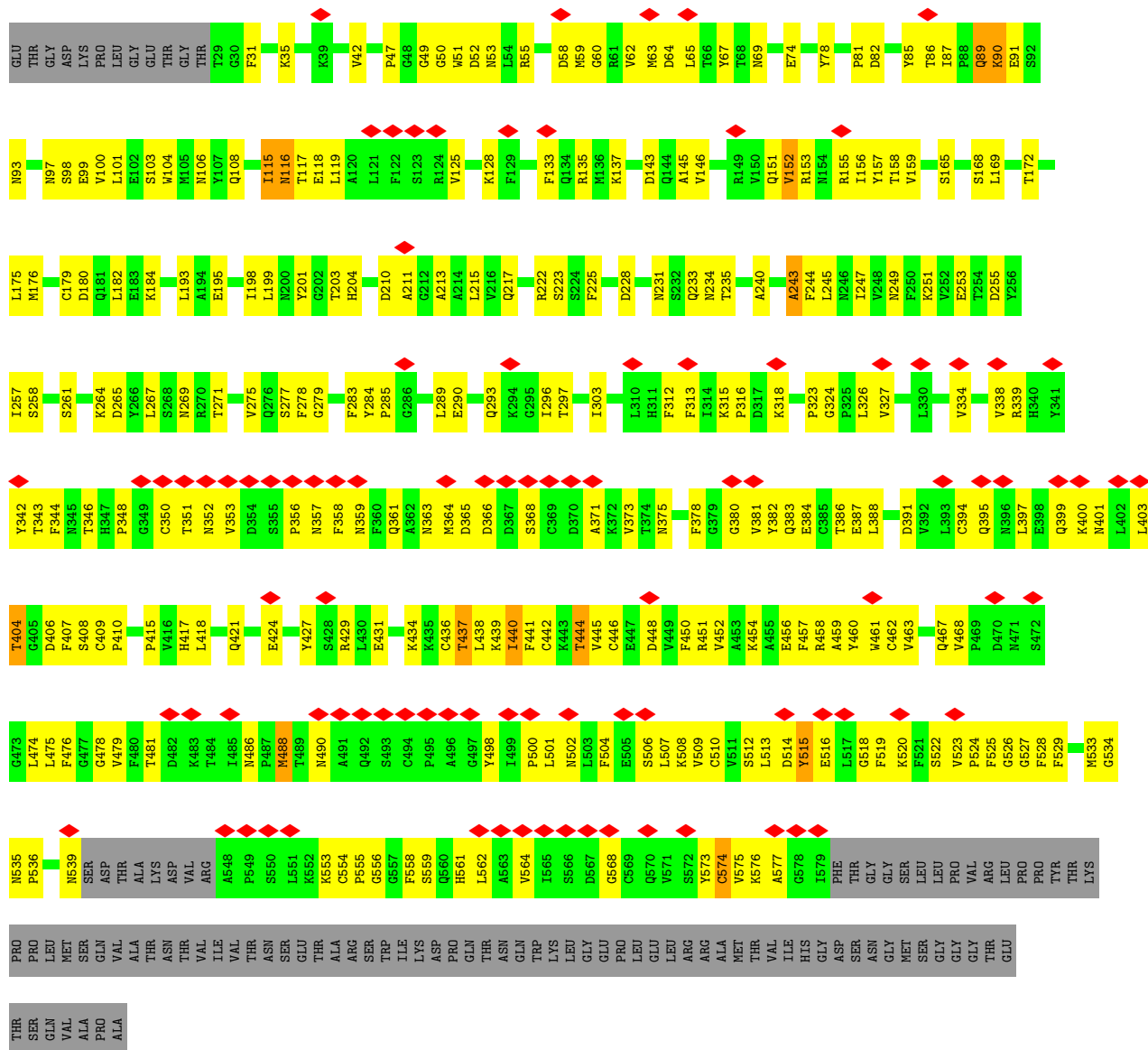


• Molecule 1: Macrophage-expressed gene 1 protein

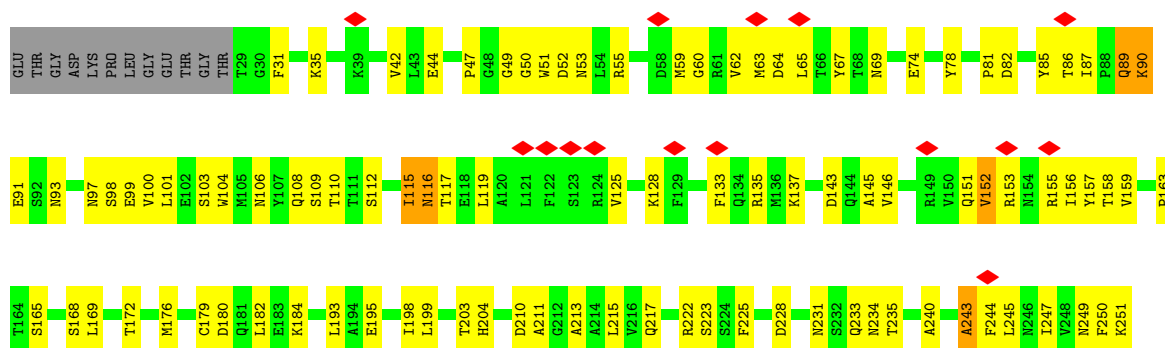


• Molecule 1: Macrophage-expressed gene 1 protein





● Molecule 1: Macrophage-expressed gene 1 protein





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C16	Depositor
Number of particles used	24936	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50, 50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k), FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.156	Depositor
Minimum map value	-0.050	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.048	Depositor
Map size (Å)	439.2, 439.2, 439.2	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.22, 1.22, 1.22	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	A	0.34	0/4295	0.51	0/5831
1	B	0.34	0/4295	0.51	0/5831
1	C	0.34	0/4295	0.51	0/5831
1	D	0.34	0/4295	0.52	0/5831
1	E	0.34	0/4295	0.52	0/5831
1	F	0.34	0/4295	0.52	0/5831
1	G	0.34	0/4295	0.51	0/5831
1	H	0.34	0/4295	0.51	0/5831
1	I	0.34	0/4295	0.52	0/5831
1	J	0.34	0/4295	0.51	0/5831
1	K	0.34	0/4295	0.51	0/5831
1	L	0.34	0/4295	0.52	0/5831
1	M	0.34	0/4295	0.51	0/5831
1	N	0.34	0/4295	0.51	0/5831
1	O	0.34	0/4295	0.51	0/5831
1	P	0.34	0/4295	0.52	0/5831
All	All	0.34	0/68720	0.51	0/93296

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6
1	B	0	6
1	C	0	6
1	D	0	6
1	E	0	6
1	F	0	6
1	G	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	6
1	I	0	6
1	J	0	6
1	K	0	6
1	L	0	6
1	M	0	6
1	N	0	6
1	O	0	6
1	P	0	6
All	All	0	96

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 96 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	115	ILE	Peptide
1	A	243	ALA	Peptide
1	A	69	ASN	Peptide
1	A	89	GLN	Peptide
1	A	90	LYS	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4207	0	4140	233	0
1	B	4207	0	4140	234	0
1	C	4207	0	4140	233	0
1	D	4207	0	4140	234	0
1	E	4207	0	4140	228	0
1	F	4207	0	4140	242	0
1	G	4207	0	4140	233	0
1	H	4207	0	4140	262	0
1	I	4207	0	4140	264	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	J	4207	0	4140	229	0
1	K	4207	0	4140	228	0
1	L	4207	0	4140	238	0
1	M	4207	0	4140	231	0
1	N	4207	0	4140	220	0
1	O	4207	0	4140	233	0
1	P	4207	0	4140	236	0
2	A	28	0	26	0	0
2	B	28	0	26	0	0
2	C	28	0	26	0	0
2	D	28	0	26	0	0
2	E	28	0	26	0	0
2	F	28	0	26	0	0
2	G	28	0	26	0	0
2	H	28	0	26	0	0
2	I	28	0	26	0	0
2	J	28	0	26	0	0
2	K	28	0	26	0	0
2	L	28	0	26	0	0
2	M	28	0	26	0	0
2	N	28	0	26	0	0
2	O	28	0	26	0	0
2	P	28	0	26	0	0
All	All	67760	0	66656	3475	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 26.

The worst 5 of 3475 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:59:MET:O	1:D:85:TYR:OH	1.92	0.86
1:H:253:GLU:H	1:I:115:ILE:HG22	1.42	0.85
1:E:59:MET:O	1:F:85:TYR:OH	1.95	0.85
1:G:427:TYR:H	1:G:429:ARG:HH21	1.25	0.84
1:H:427:TYR:H	1:H:429:ARG:HH21	1.25	0.84

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	539/646 (83%)	443 (82%)	95 (18%)	1 (0%)	43	77
1	B	539/646 (83%)	442 (82%)	96 (18%)	1 (0%)	43	77
1	C	539/646 (83%)	444 (82%)	94 (17%)	1 (0%)	43	77
1	D	539/646 (83%)	444 (82%)	94 (17%)	1 (0%)	43	77
1	E	539/646 (83%)	443 (82%)	95 (18%)	1 (0%)	43	77
1	F	539/646 (83%)	443 (82%)	95 (18%)	1 (0%)	43	77
1	G	539/646 (83%)	442 (82%)	96 (18%)	1 (0%)	43	77
1	H	539/646 (83%)	443 (82%)	95 (18%)	1 (0%)	43	77
1	I	539/646 (83%)	443 (82%)	95 (18%)	1 (0%)	43	77
1	J	539/646 (83%)	443 (82%)	95 (18%)	1 (0%)	43	77
1	K	539/646 (83%)	443 (82%)	95 (18%)	1 (0%)	43	77
1	L	539/646 (83%)	442 (82%)	96 (18%)	1 (0%)	43	77
1	M	539/646 (83%)	443 (82%)	95 (18%)	1 (0%)	43	77
1	N	539/646 (83%)	442 (82%)	96 (18%)	1 (0%)	43	77
1	O	539/646 (83%)	443 (82%)	95 (18%)	1 (0%)	43	77
1	P	539/646 (83%)	442 (82%)	96 (18%)	1 (0%)	43	77
All	All	8624/10336 (83%)	7085 (82%)	1523 (18%)	16 (0%)	44	77

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	116	ASN
1	B	116	ASN
1	C	116	ASN
1	D	116	ASN
1	E	116	ASN

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	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	B	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	C	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	D	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	E	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	F	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	G	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	H	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	I	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	J	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	K	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	L	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	M	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	N	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	O	475/564 (84%)	466 (98%)	9 (2%)	50	66
1	P	475/564 (84%)	466 (98%)	9 (2%)	50	66
All	All	7600/9024 (84%)	7456 (98%)	144 (2%)	49	66

5 of 144 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	488	MET
1	P	574	CYS
1	N	388	LEU
1	O	437	THR
1	F	404	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 111 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	217	GLN
1	P	359	ASN
1	K	144	GLN
1	P	293	GLN
1	O	220	HIS

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](#)

32 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	$\# Z > 2$
2	NAG	F	702	1	14,14,15	0.21	0	17,19,21	0.59	0
2	NAG	P	701	1	14,14,15	0.45	0	17,19,21	0.43	0
2	NAG	A	702	1	14,14,15	0.18	0	17,19,21	0.57	0
2	NAG	A	701	1	14,14,15	0.45	0	17,19,21	0.43	0
2	NAG	C	702	1	14,14,15	0.18	0	17,19,21	0.58	0
2	NAG	E	702	1	14,14,15	0.19	0	17,19,21	0.57	0
2	NAG	B	702	1	14,14,15	0.18	0	17,19,21	0.58	0
2	NAG	M	701	1	14,14,15	0.45	0	17,19,21	0.43	0
2	NAG	C	701	1	14,14,15	0.45	0	17,19,21	0.42	0
2	NAG	M	702	1	14,14,15	0.18	0	17,19,21	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	I	701	1	14,14,15	0.46	0	17,19,21	0.42	0
2	NAG	D	701	1	14,14,15	0.45	0	17,19,21	0.43	0
2	NAG	D	702	1	14,14,15	0.20	0	17,19,21	0.57	0
2	NAG	H	701	1	14,14,15	0.45	0	17,19,21	0.43	0
2	NAG	P	702	1	14,14,15	0.19	0	17,19,21	0.57	0
2	NAG	N	702	1	14,14,15	0.17	0	17,19,21	0.57	0
2	NAG	K	701	1	14,14,15	0.43	0	17,19,21	0.43	0
2	NAG	L	701	1	14,14,15	0.45	0	17,19,21	0.42	0
2	NAG	F	701	1	14,14,15	0.44	0	17,19,21	0.43	0
2	NAG	H	702	1	14,14,15	0.19	0	17,19,21	0.59	0
2	NAG	O	702	1	14,14,15	0.18	0	17,19,21	0.58	0
2	NAG	L	702	1	14,14,15	0.19	0	17,19,21	0.58	0
2	NAG	N	701	1	14,14,15	0.45	0	17,19,21	0.42	0
2	NAG	I	702	1	14,14,15	0.18	0	17,19,21	0.57	0
2	NAG	B	701	1	14,14,15	0.43	0	17,19,21	0.42	0
2	NAG	J	701	1	14,14,15	0.44	0	17,19,21	0.42	0
2	NAG	K	702	1	14,14,15	0.20	0	17,19,21	0.57	0
2	NAG	E	701	1	14,14,15	0.46	0	17,19,21	0.43	0
2	NAG	J	702	1	14,14,15	0.18	0	17,19,21	0.57	0
2	NAG	O	701	1	14,14,15	0.44	0	17,19,21	0.42	0
2	NAG	G	701	1	14,14,15	0.44	0	17,19,21	0.42	0
2	NAG	G	702	1	14,14,15	0.21	0	17,19,21	0.57	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
2	NAG	F	702	1	-	2/6/23/26	0/1/1/1
2	NAG	P	701	1	-	2/6/23/26	0/1/1/1
2	NAG	A	702	1	-	2/6/23/26	0/1/1/1
2	NAG	A	701	1	-	2/6/23/26	0/1/1/1
2	NAG	C	702	1	-	2/6/23/26	0/1/1/1
2	NAG	E	702	1	-	2/6/23/26	0/1/1/1
2	NAG	B	702	1	-	2/6/23/26	0/1/1/1
2	NAG	M	701	1	-	2/6/23/26	0/1/1/1
2	NAG	C	701	1	-	2/6/23/26	0/1/1/1
2	NAG	M	702	1	-	2/6/23/26	0/1/1/1
2	NAG	I	701	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	701	1	-	2/6/23/26	0/1/1/1
2	NAG	D	702	1	-	2/6/23/26	0/1/1/1
2	NAG	H	701	1	-	2/6/23/26	0/1/1/1
2	NAG	P	702	1	-	2/6/23/26	0/1/1/1
2	NAG	N	702	1	-	2/6/23/26	0/1/1/1
2	NAG	K	701	1	-	2/6/23/26	0/1/1/1
2	NAG	L	701	1	-	2/6/23/26	0/1/1/1
2	NAG	F	701	1	-	2/6/23/26	0/1/1/1
2	NAG	H	702	1	-	2/6/23/26	0/1/1/1
2	NAG	O	702	1	-	2/6/23/26	0/1/1/1
2	NAG	L	702	1	-	2/6/23/26	0/1/1/1
2	NAG	N	701	1	-	2/6/23/26	0/1/1/1
2	NAG	I	702	1	-	2/6/23/26	0/1/1/1
2	NAG	B	701	1	-	2/6/23/26	0/1/1/1
2	NAG	J	701	1	-	2/6/23/26	0/1/1/1
2	NAG	K	702	1	-	2/6/23/26	0/1/1/1
2	NAG	E	701	1	-	2/6/23/26	0/1/1/1
2	NAG	J	702	1	-	2/6/23/26	0/1/1/1
2	NAG	O	701	1	-	2/6/23/26	0/1/1/1
2	NAG	G	701	1	-	2/6/23/26	0/1/1/1
2	NAG	G	702	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.

5 of 64 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	NAG	C1-C2-N2-C7
2	A	702	NAG	C1-C2-N2-C7
2	B	701	NAG	C1-C2-N2-C7
2	B	702	NAG	C1-C2-N2-C7
2	C	701	NAG	C1-C2-N2-C7

There are no ring outliers.

No monomer is involved in short contacts.

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.

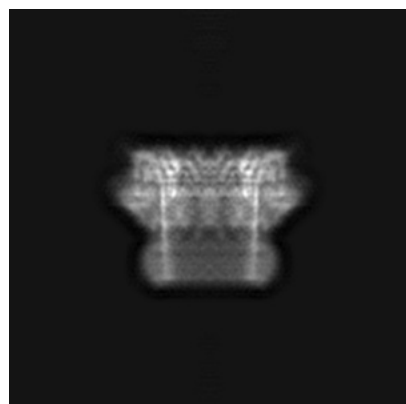
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10135. These allow visual inspection of the internal detail of the map and identification of artifacts.

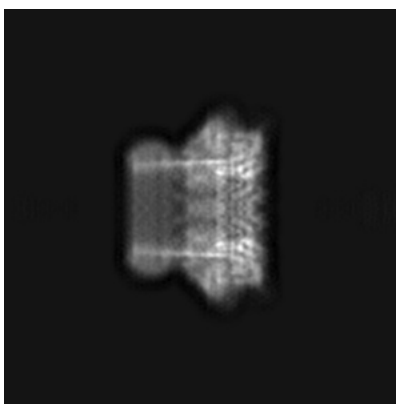
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

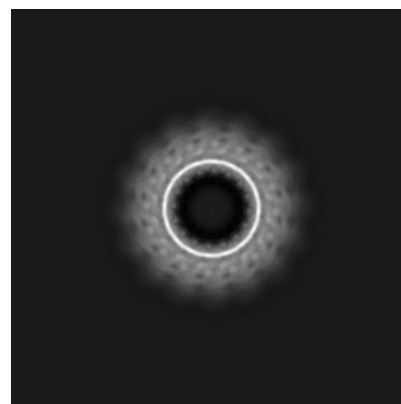
6.1.1 Primary map



X

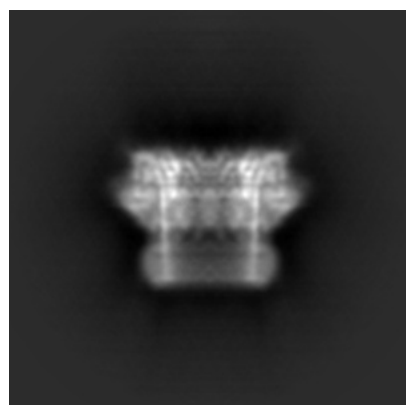


Y

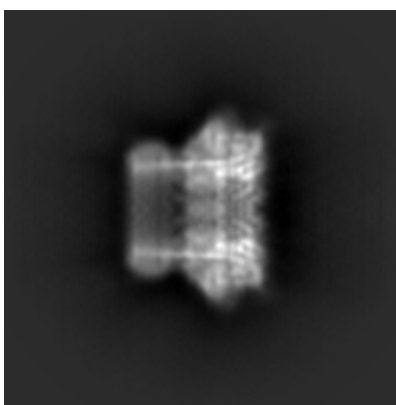


Z

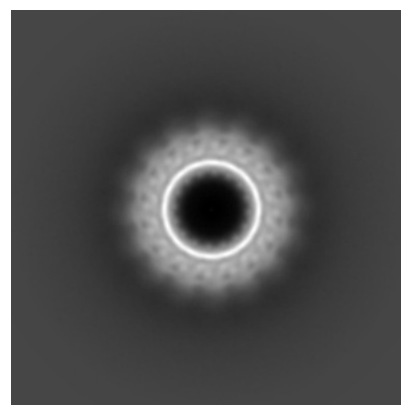
6.1.2 Raw map



X



Y

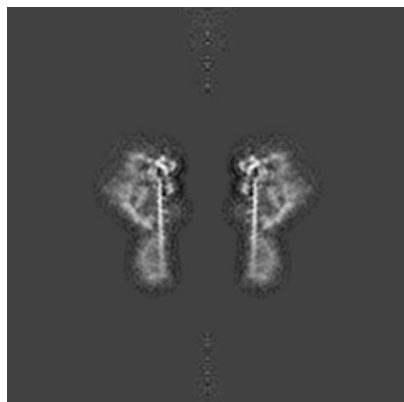


Z

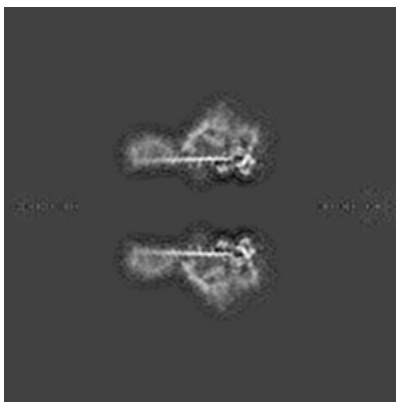
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

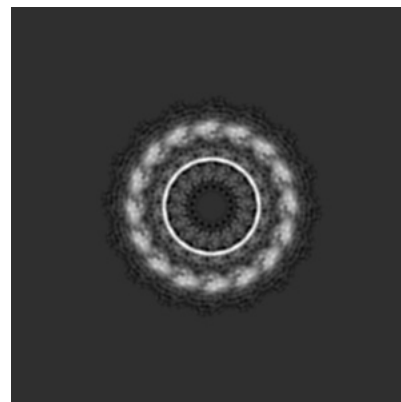
6.2.1 Primary map



X Index: 180

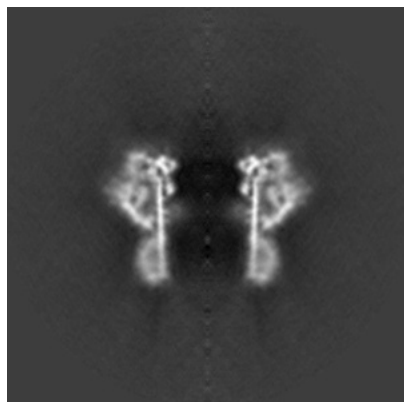


Y Index: 180

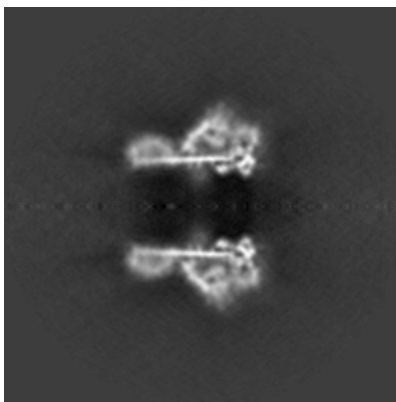


Z Index: 180

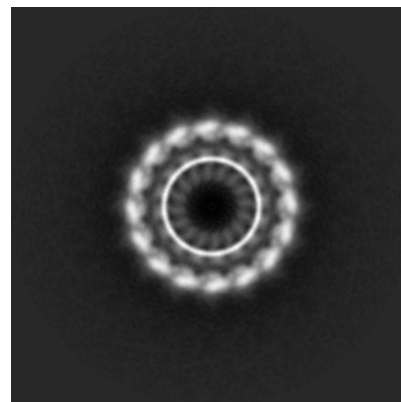
6.2.2 Raw map



X Index: 180



Y Index: 180

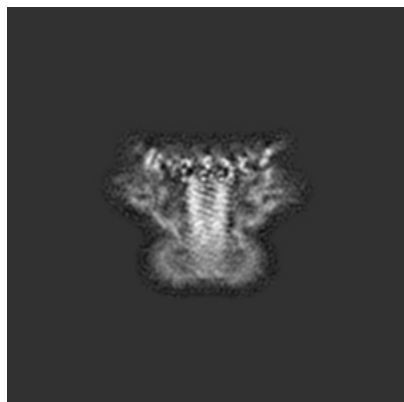


Z Index: 180

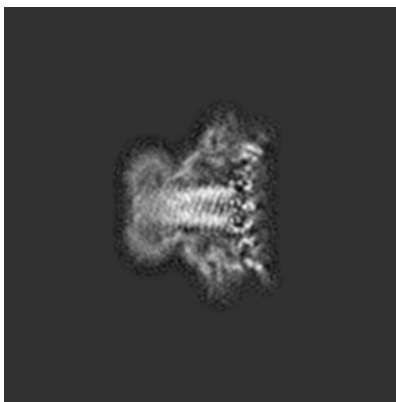
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

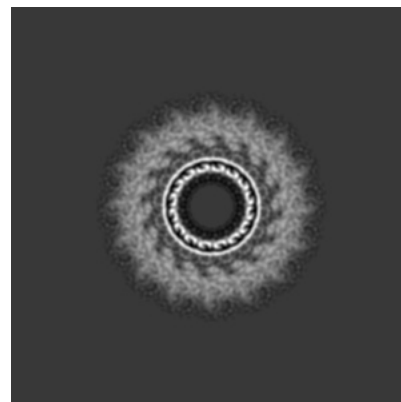
6.3.1 Primary map



X Index: 221

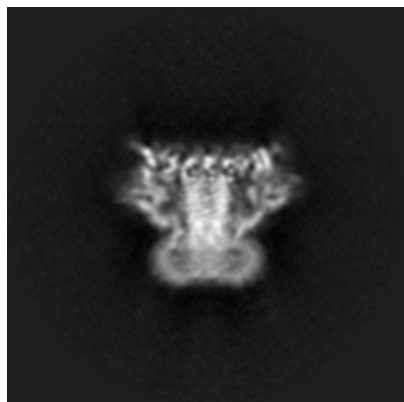


Y Index: 221

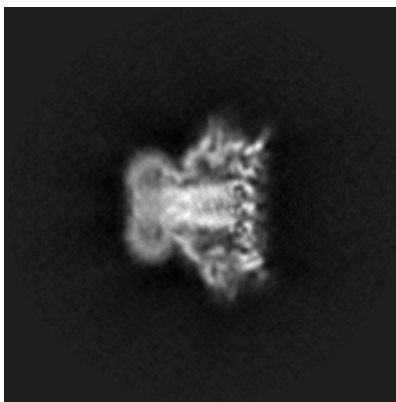


Z Index: 193

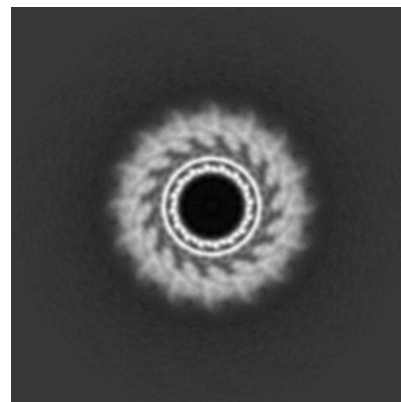
6.3.2 Raw map



X Index: 139



Y Index: 139

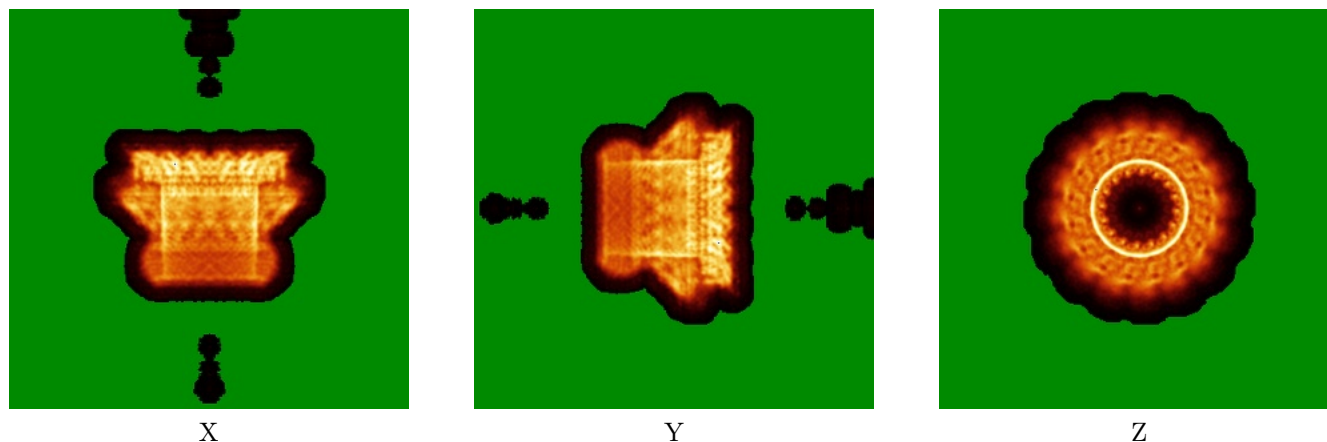


Z Index: 193

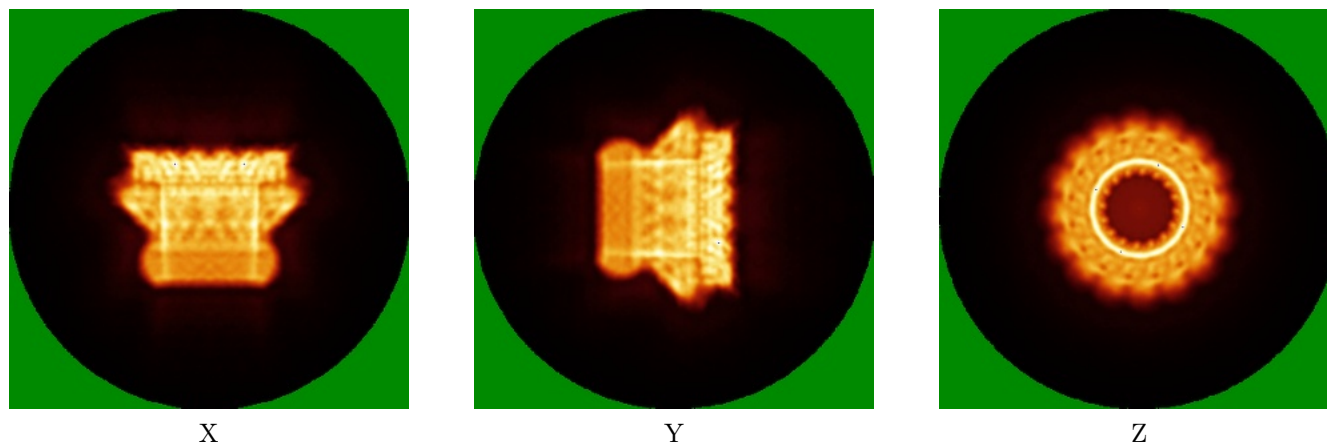
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



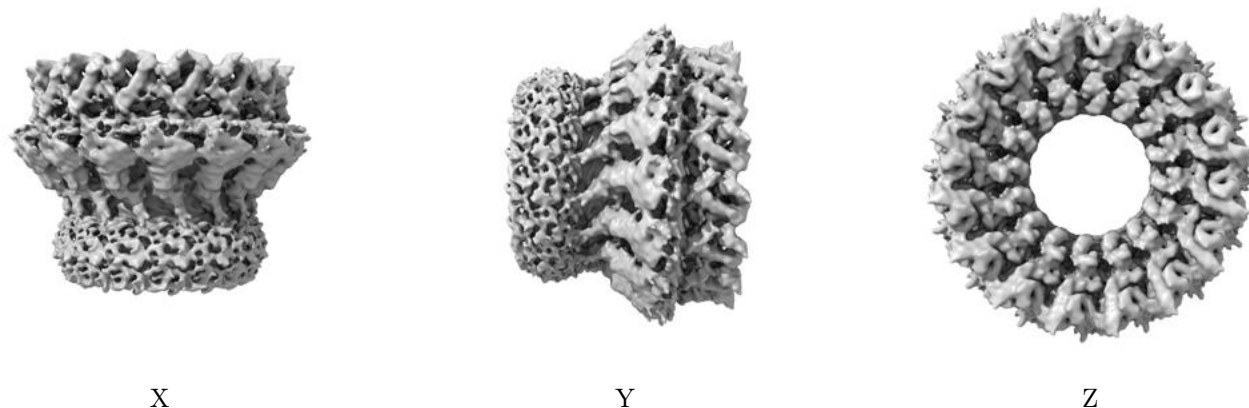
6.4.2 Raw map



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 0.048. 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.

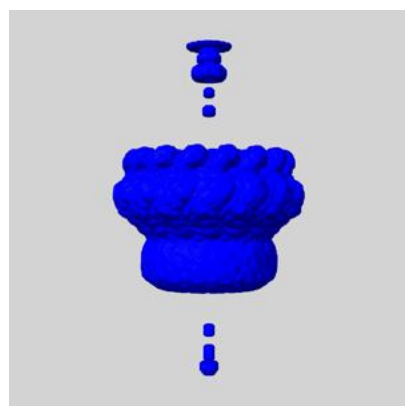
6.6 Mask visualisation [i](#)

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

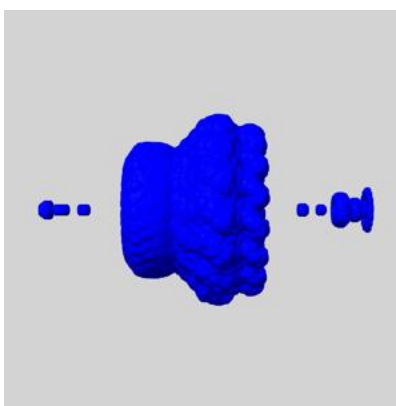
A mask typically either:

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

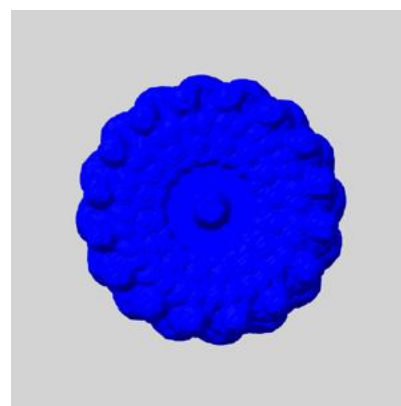
6.6.1 emd_10135_msk_1.map [i](#)



X



Y

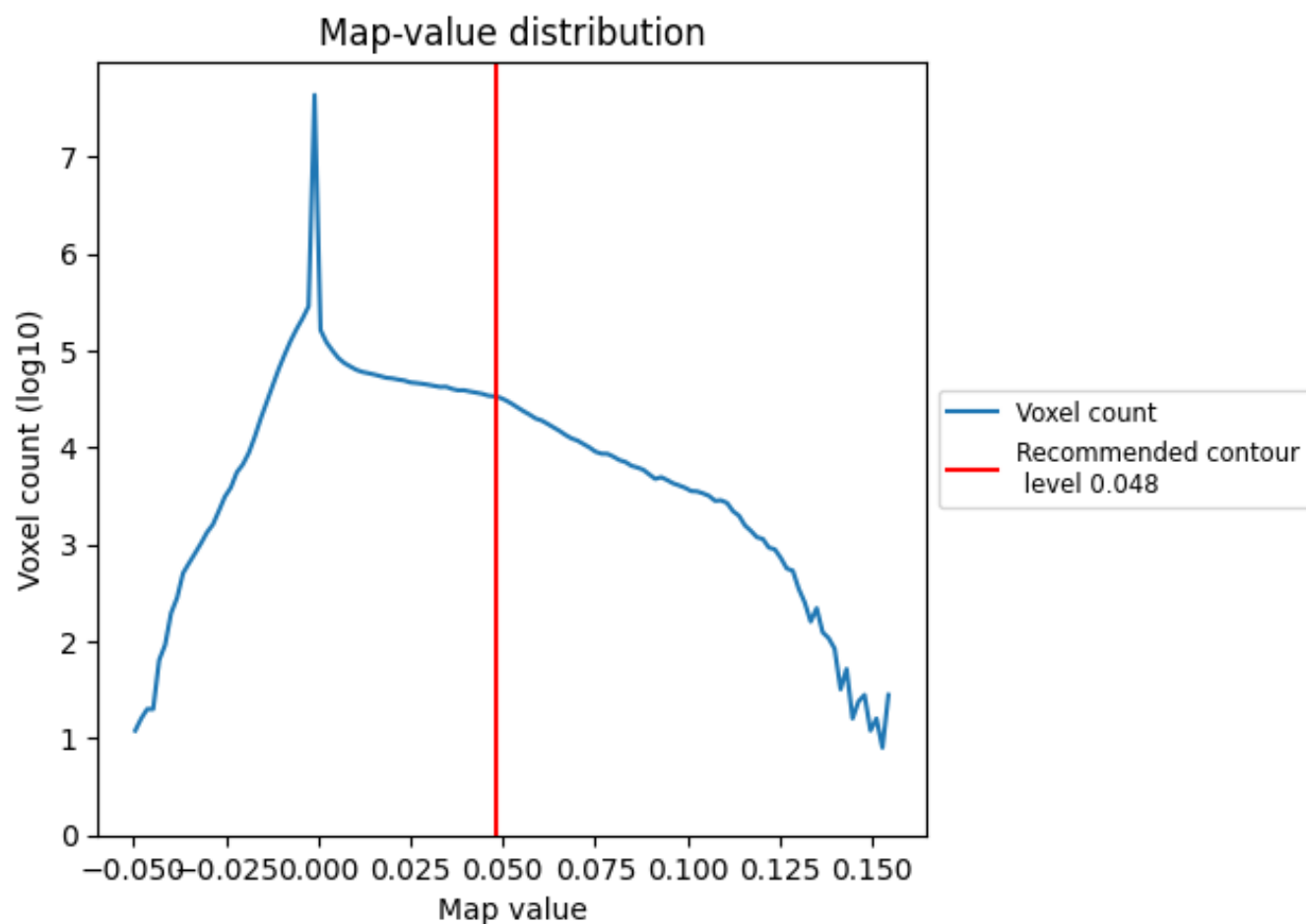


Z

7 Map analysis [i](#)

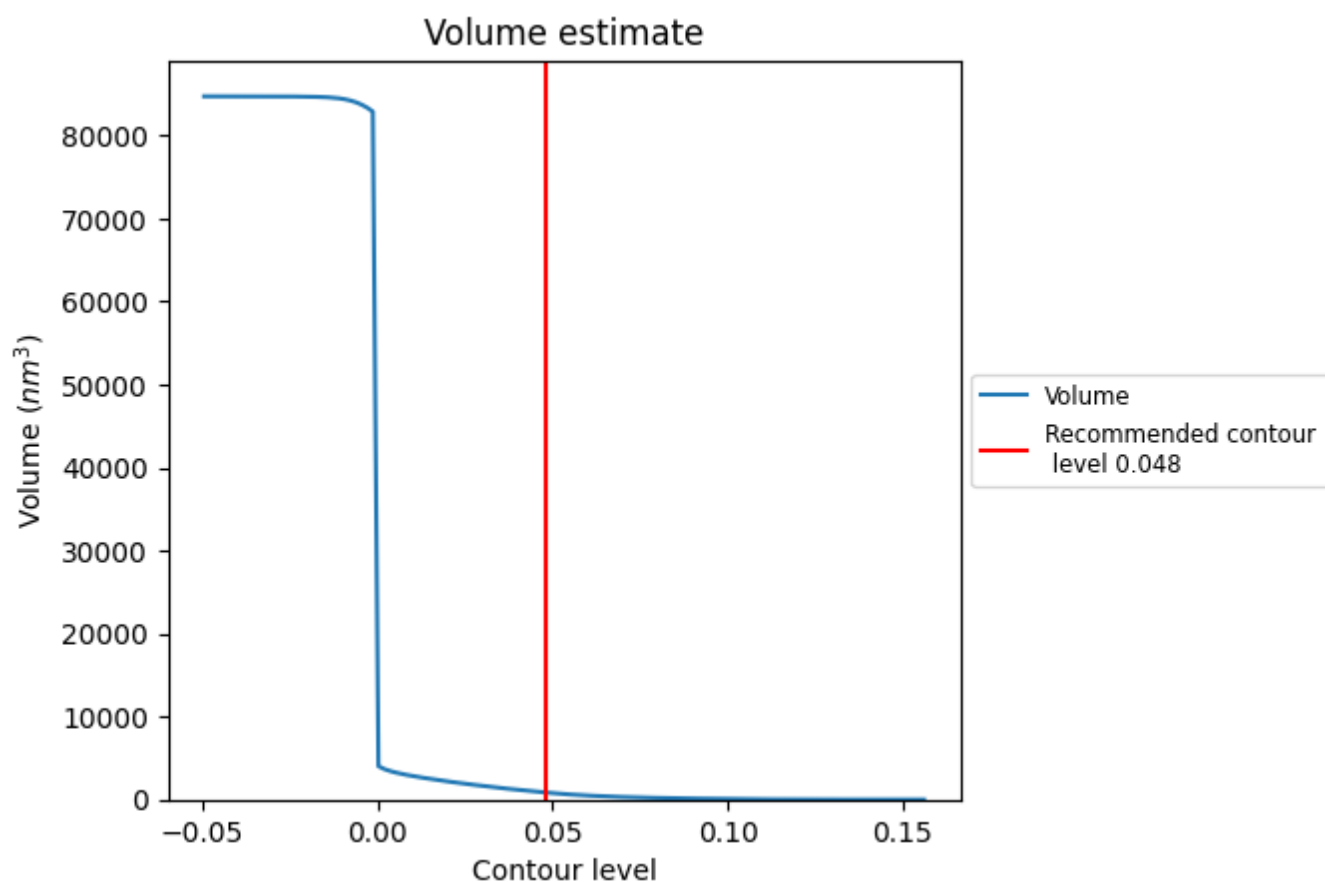
This section contains the results of statistical analysis of the map.

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.

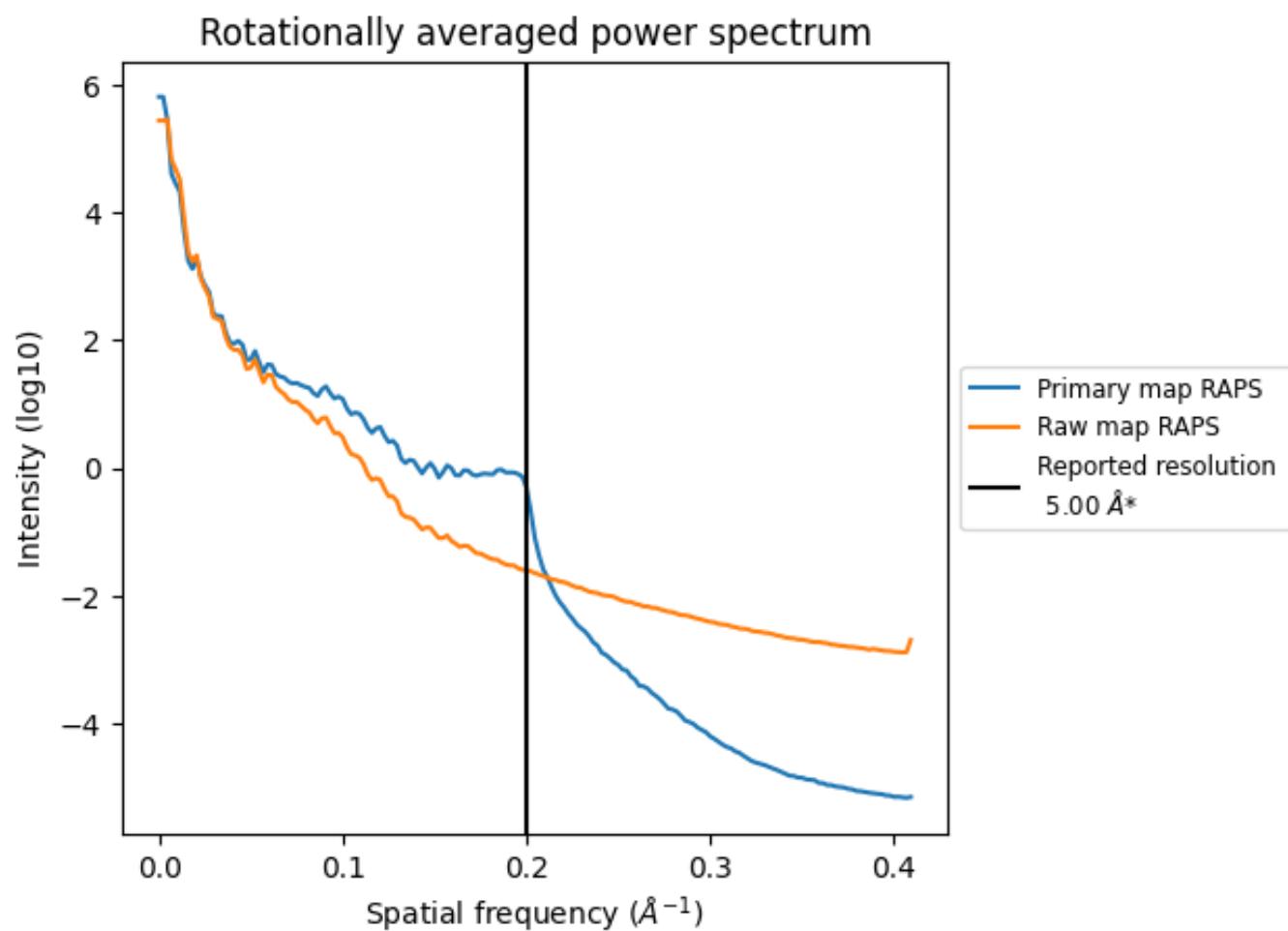
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 853 nm³; this corresponds to an approximate mass of 771 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 ⓘ

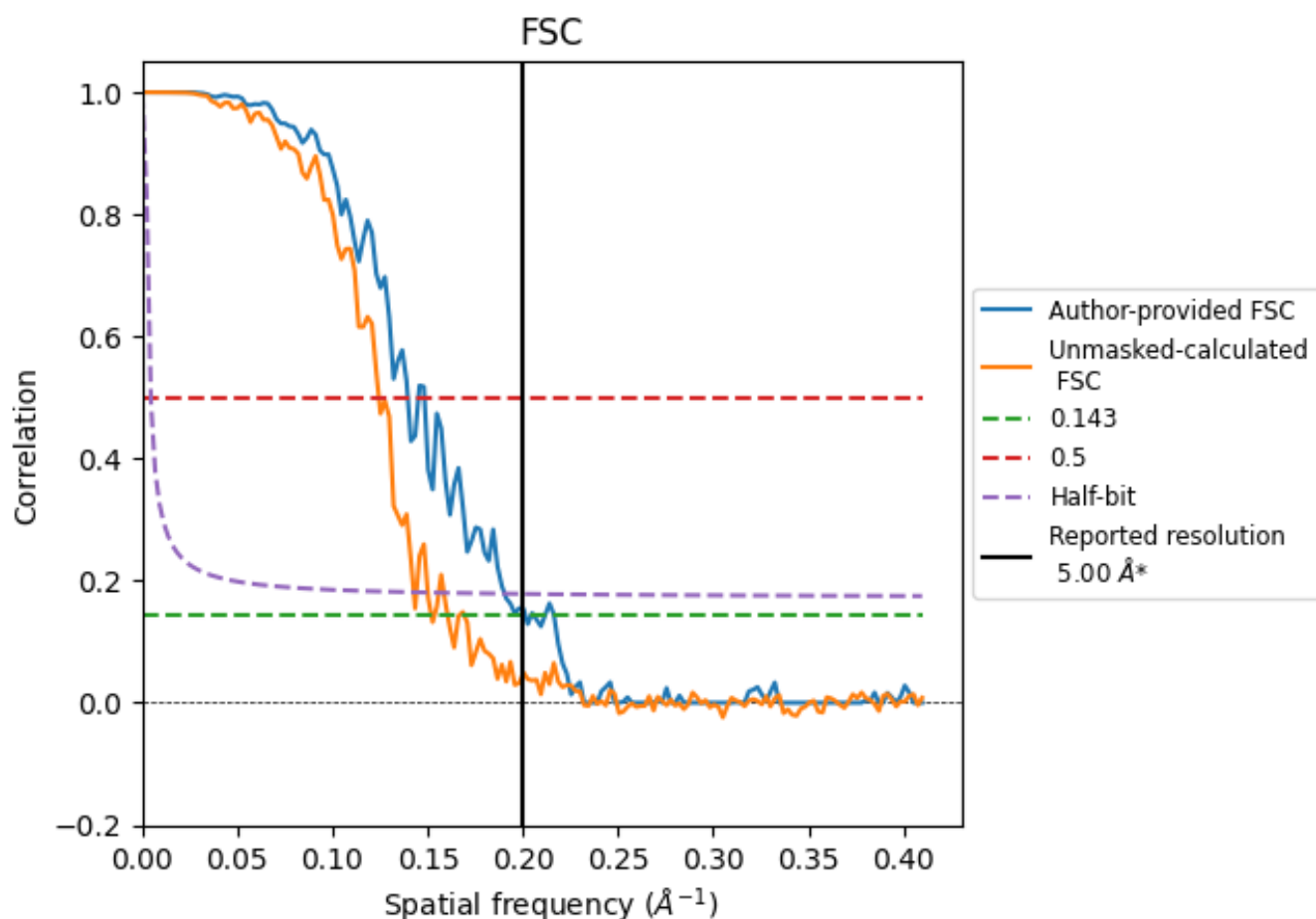


*Reported resolution corresponds to spatial frequency of 0.200 $\text{\AA}^{-1}$

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 0.200 Å⁻¹

8.2 Resolution estimates [i](#)

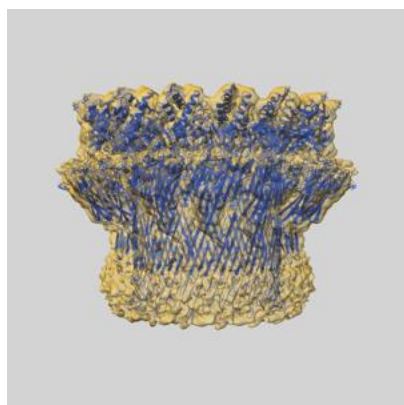
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.00	-	-
Author-provided FSC curve	4.97	7.17	5.25
Unmasked-calculated*	6.58	8.05	7.01

*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 6.58 differs from the reported value 5.0 by more than 10 %

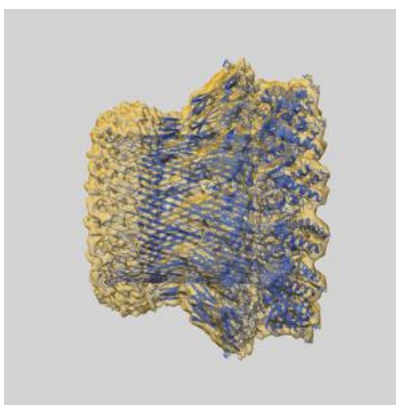
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10135 and PDB model 6SB5. Per-residue inclusion information can be found in section [3](#) on page [12](#).

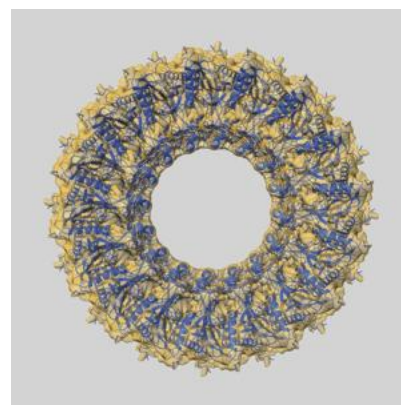
9.1 Map-model overlay [i](#)



X



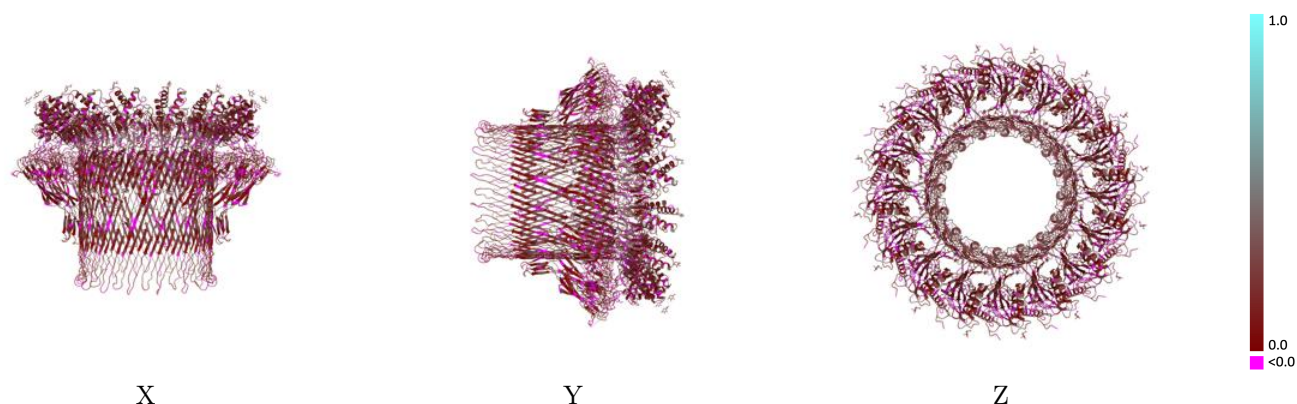
Y



Z

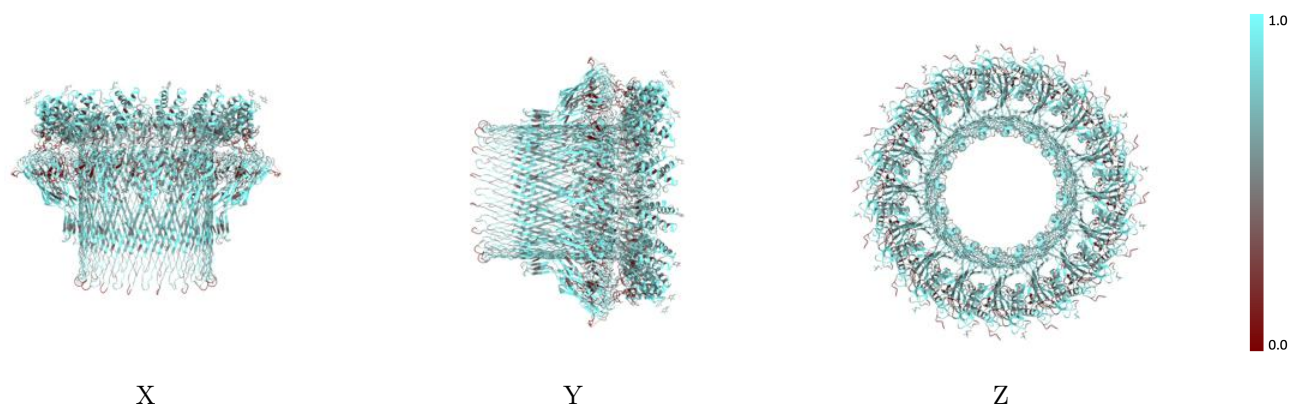
The images above show the 3D surface view of the map at the recommended contour level 0.048 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



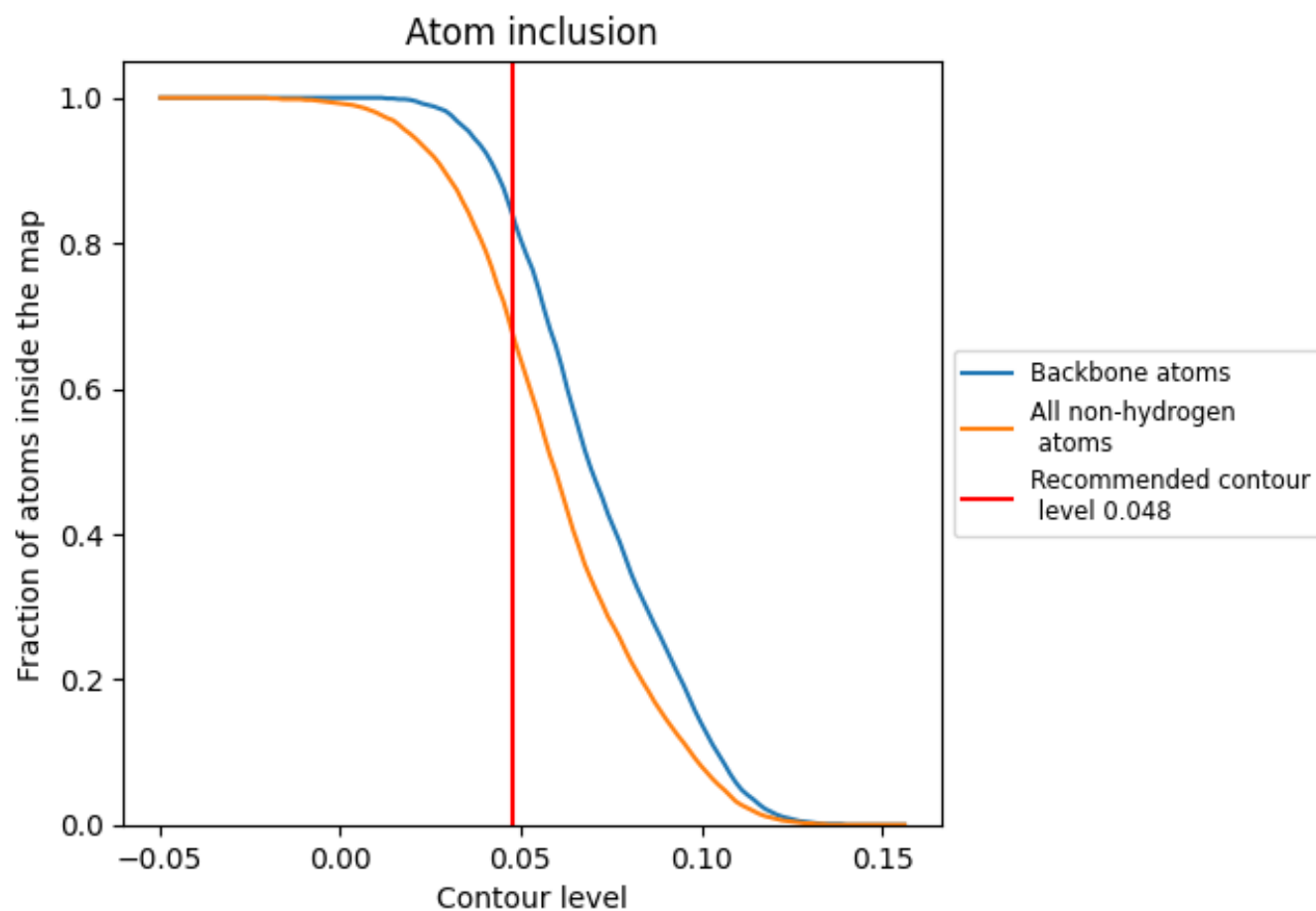
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.048).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 67% 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 (0.048) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6730	0.1520
A	0.6730	0.1530
B	0.6700	0.1520
C	0.6690	0.1500
D	0.6690	0.1500
E	0.6700	0.1530
F	0.6680	0.1470
G	0.6680	0.1500
H	0.6730	0.1520
I	0.6760	0.1500
J	0.6720	0.1490
K	0.6740	0.1520
L	0.6710	0.1500
M	0.6740	0.1520
N	0.6760	0.1570
O	0.6790	0.1570
P	0.6780	0.1550

1.0

0.0

<0.0