



wwPDB EM Validation Summary Report ⓘ

Sep 24, 2026 – 01:14 PM EDT

PDB ID : 37BM / pdb_000037bm
EMDB ID : EMD-78039
Title : Bacillus subtilis GerAA:GerAB:GerAC, in glyco-diosgenin
Authors : Cofsky, J.C.; Kruse, A.C.
Deposited on : 2026-07-11
Resolution : 2.02 Å(reported)
Based on initial model : .

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:

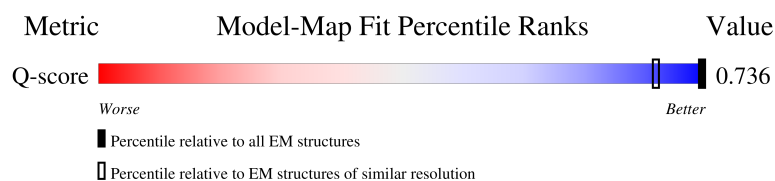
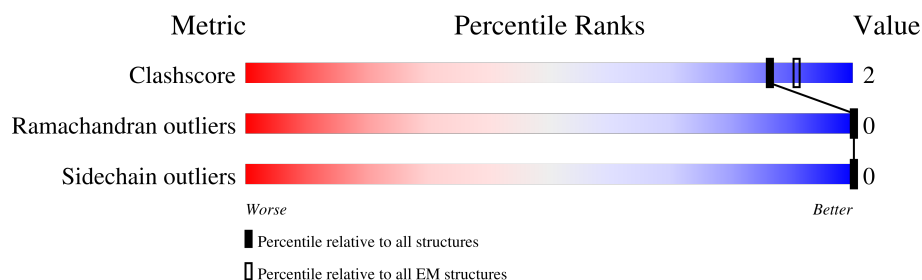
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 2.02 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.



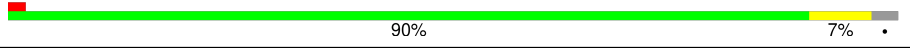
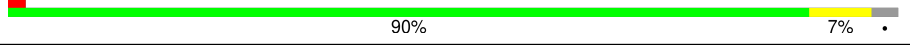
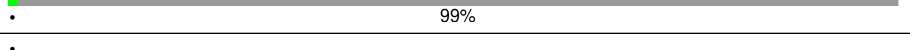
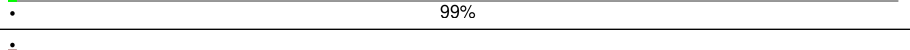
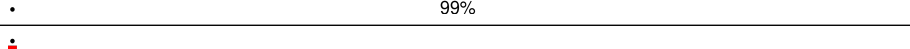
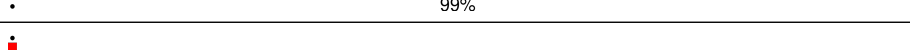
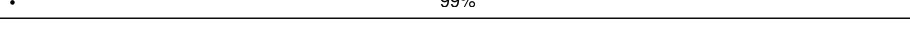
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	1728 (1.52 - 2.52)

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	505	86% 5% 9%
1	E	505	87% 5% 9%
1	I	505	87% 5% 9%
1	M	505	86% 6% 9%

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Mol	Chain	Length	Quality of chain
1	Q	505	 87%5%9%
2	B	365	 90%6%
2	F	365	 90%7%
2	J	365	 90%7%
2	N	365	 91%6%
2	R	365	 90%6%
3	C	356	 99%
3	G	356	 99%
3	K	356	 99%
3	O	356	 99%
3	S	356	 99%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 33660 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 Spore germination protein A1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	460	Total	C	N	O	S	10	0
			3695	2400	604	681	10		
1	E	460	Total	C	N	O	S	10	0
			3695	2400	604	681	10		
1	I	460	Total	C	N	O	S	10	0
			3695	2400	604	681	10		
1	M	460	Total	C	N	O	S	10	0
			3695	2400	604	681	10		
1	Q	460	Total	C	N	O	S	10	0
			3695	2400	604	681	10		

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	ASP	-	expression tag	UNP P07868
A	-21	TYR	-	expression tag	UNP P07868
A	-20	LYS	-	expression tag	UNP P07868
A	-19	ASP	-	expression tag	UNP P07868
A	-18	ASP	-	expression tag	UNP P07868
A	-17	ASP	-	expression tag	UNP P07868
A	-16	ASP	-	expression tag	UNP P07868
A	-15	LYS	-	expression tag	UNP P07868
A	-14	GLY	-	expression tag	UNP P07868
A	-13	SER	-	expression tag	UNP P07868
A	-12	LEU	-	expression tag	UNP P07868
A	-11	GLU	-	expression tag	UNP P07868
A	-10	VAL	-	expression tag	UNP P07868
A	-9	LEU	-	expression tag	UNP P07868
A	-8	PHE	-	expression tag	UNP P07868
A	-7	GLN	-	expression tag	UNP P07868
A	-6	GLY	-	expression tag	UNP P07868
A	-5	PRO	-	expression tag	UNP P07868
A	-4	GLY	-	expression tag	UNP P07868
A	-3	GLY	-	expression tag	UNP P07868

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP P07868
A	-1	GLY	-	expression tag	UNP P07868
A	0	SER	-	expression tag	UNP P07868
A	299	ALA	THR	conflict	UNP P07868
E	-22	ASP	-	expression tag	UNP P07868
E	-21	TYR	-	expression tag	UNP P07868
E	-20	LYS	-	expression tag	UNP P07868
E	-19	ASP	-	expression tag	UNP P07868
E	-18	ASP	-	expression tag	UNP P07868
E	-17	ASP	-	expression tag	UNP P07868
E	-16	ASP	-	expression tag	UNP P07868
E	-15	LYS	-	expression tag	UNP P07868
E	-14	GLY	-	expression tag	UNP P07868
E	-13	SER	-	expression tag	UNP P07868
E	-12	LEU	-	expression tag	UNP P07868
E	-11	GLU	-	expression tag	UNP P07868
E	-10	VAL	-	expression tag	UNP P07868
E	-9	LEU	-	expression tag	UNP P07868
E	-8	PHE	-	expression tag	UNP P07868
E	-7	GLN	-	expression tag	UNP P07868
E	-6	GLY	-	expression tag	UNP P07868
E	-5	PRO	-	expression tag	UNP P07868
E	-4	GLY	-	expression tag	UNP P07868
E	-3	GLY	-	expression tag	UNP P07868
E	-2	SER	-	expression tag	UNP P07868
E	-1	GLY	-	expression tag	UNP P07868
E	0	SER	-	expression tag	UNP P07868
E	299	ALA	THR	conflict	UNP P07868
I	-22	ASP	-	expression tag	UNP P07868
I	-21	TYR	-	expression tag	UNP P07868
I	-20	LYS	-	expression tag	UNP P07868
I	-19	ASP	-	expression tag	UNP P07868
I	-18	ASP	-	expression tag	UNP P07868
I	-17	ASP	-	expression tag	UNP P07868
I	-16	ASP	-	expression tag	UNP P07868
I	-15	LYS	-	expression tag	UNP P07868
I	-14	GLY	-	expression tag	UNP P07868
I	-13	SER	-	expression tag	UNP P07868
I	-12	LEU	-	expression tag	UNP P07868
I	-11	GLU	-	expression tag	UNP P07868
I	-10	VAL	-	expression tag	UNP P07868
I	-9	LEU	-	expression tag	UNP P07868

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-8	PHE	-	expression tag	UNP P07868
I	-7	GLN	-	expression tag	UNP P07868
I	-6	GLY	-	expression tag	UNP P07868
I	-5	PRO	-	expression tag	UNP P07868
I	-4	GLY	-	expression tag	UNP P07868
I	-3	GLY	-	expression tag	UNP P07868
I	-2	SER	-	expression tag	UNP P07868
I	-1	GLY	-	expression tag	UNP P07868
I	0	SER	-	expression tag	UNP P07868
I	299	ALA	THR	conflict	UNP P07868
M	-22	ASP	-	expression tag	UNP P07868
M	-21	TYR	-	expression tag	UNP P07868
M	-20	LYS	-	expression tag	UNP P07868
M	-19	ASP	-	expression tag	UNP P07868
M	-18	ASP	-	expression tag	UNP P07868
M	-17	ASP	-	expression tag	UNP P07868
M	-16	ASP	-	expression tag	UNP P07868
M	-15	LYS	-	expression tag	UNP P07868
M	-14	GLY	-	expression tag	UNP P07868
M	-13	SER	-	expression tag	UNP P07868
M	-12	LEU	-	expression tag	UNP P07868
M	-11	GLU	-	expression tag	UNP P07868
M	-10	VAL	-	expression tag	UNP P07868
M	-9	LEU	-	expression tag	UNP P07868
M	-8	PHE	-	expression tag	UNP P07868
M	-7	GLN	-	expression tag	UNP P07868
M	-6	GLY	-	expression tag	UNP P07868
M	-5	PRO	-	expression tag	UNP P07868
M	-4	GLY	-	expression tag	UNP P07868
M	-3	GLY	-	expression tag	UNP P07868
M	-2	SER	-	expression tag	UNP P07868
M	-1	GLY	-	expression tag	UNP P07868
M	0	SER	-	expression tag	UNP P07868
M	299	ALA	THR	conflict	UNP P07868
Q	-22	ASP	-	expression tag	UNP P07868
Q	-21	TYR	-	expression tag	UNP P07868
Q	-20	LYS	-	expression tag	UNP P07868
Q	-19	ASP	-	expression tag	UNP P07868
Q	-18	ASP	-	expression tag	UNP P07868
Q	-17	ASP	-	expression tag	UNP P07868
Q	-16	ASP	-	expression tag	UNP P07868
Q	-15	LYS	-	expression tag	UNP P07868

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	-14	GLY	-	expression tag	UNP P07868
Q	-13	SER	-	expression tag	UNP P07868
Q	-12	LEU	-	expression tag	UNP P07868
Q	-11	GLU	-	expression tag	UNP P07868
Q	-10	VAL	-	expression tag	UNP P07868
Q	-9	LEU	-	expression tag	UNP P07868
Q	-8	PHE	-	expression tag	UNP P07868
Q	-7	GLN	-	expression tag	UNP P07868
Q	-6	GLY	-	expression tag	UNP P07868
Q	-5	PRO	-	expression tag	UNP P07868
Q	-4	GLY	-	expression tag	UNP P07868
Q	-3	GLY	-	expression tag	UNP P07868
Q	-2	SER	-	expression tag	UNP P07868
Q	-1	GLY	-	expression tag	UNP P07868
Q	0	SER	-	expression tag	UNP P07868
Q	299	ALA	THR	conflict	UNP P07868

- Molecule 2 is a protein called Spore germination protein A2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	353	Total	C	N	O	S	6	0
			2882	1968	426	473	15		
2	F	353	Total	C	N	O	S	6	0
			2882	1968	426	473	15		
2	J	353	Total	C	N	O	S	6	0
			2882	1968	426	473	15		
2	N	353	Total	C	N	O	S	6	0
			2882	1968	426	473	15		
2	R	353	Total	C	N	O	S	6	0
			2882	1968	426	473	15		

- Molecule 3 is a protein called Spore germination protein A3.

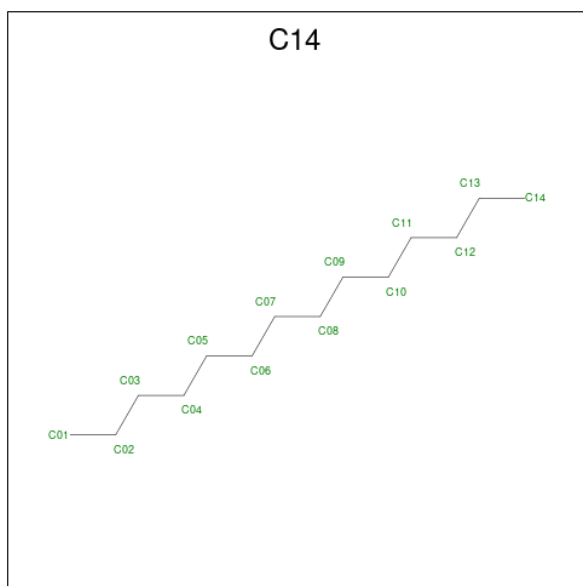
Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	5	Total	C	N	O	S	0	0
			43	26	6	10	1		
3	G	5	Total	C	N	O	S	0	0
			43	26	6	10	1		
3	K	5	Total	C	N	O	S	0	0
			43	26	6	10	1		
3	O	5	Total	C	N	O	S	0	0
			43	26	6	10	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	S	5	Total	C	N	O	S	0	0
			43	26	6	10	1		

- Molecule 4 is TETRADECANE (CCD ID: C14) (formula: C₁₄H₃₀).



Mol	Chain	Residues	Atoms		AltConf
4	A	1	Total	C	0
			14	14	
4	E	1	Total	C	0
			14	14	
4	I	1	Total	C	0
			14	14	
4	M	1	Total	C	0
			14	14	
4	Q	1	Total	C	0
			14	14	

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

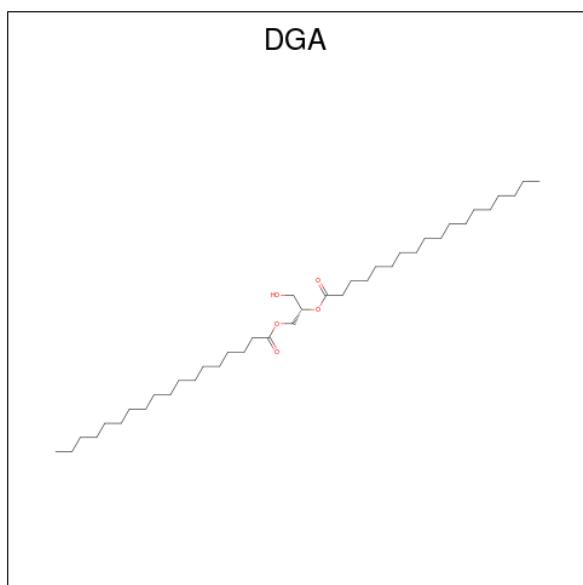
Mol	Chain	Residues	Atoms		AltConf
5	B	1	Total	Na	0
			1	1	
5	F	1	Total	Na	0
			1	1	
5	J	1	Total	Na	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
5	N	1	Total	Na	0
			1	1	
5	R	1	Total	Na	0
			1	1	

- Molecule 6 is DIACYL GLYCEROL (CCD ID: DGA) (formula: $C_{39}H_{76}O_5$).



Mol	Chain	Residues	Atoms			AltConf
6	C	1	Total	C	O	0
			11	7	4	
6	G	1	Total	C	O	0
			11	7	4	
6	K	1	Total	C	O	0
			11	7	4	
6	O	1	Total	C	O	0
			11	7	4	
6	S	1	Total	C	O	0
			11	7	4	

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		AltConf
7	A	58	Total	O	0
			58	58	
7	B	28	Total	O	0
			28	28	

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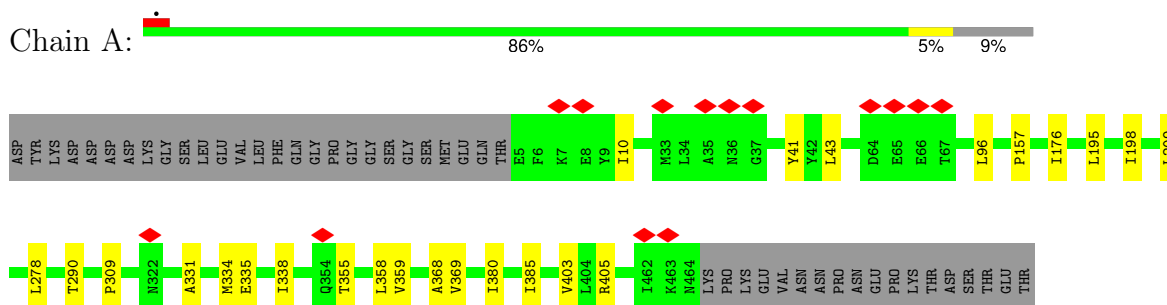
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Mol	Chain	Residues	Atoms		AltConf
7	E	59	Total 59	O 59	0
7	F	28	Total 28	O 28	0
7	I	57	Total 57	O 57	0
7	J	28	Total 28	O 28	0
7	M	58	Total 58	O 58	0
7	N	28	Total 28	O 28	0
7	Q	58	Total 58	O 58	0
7	R	28	Total 28	O 28	0

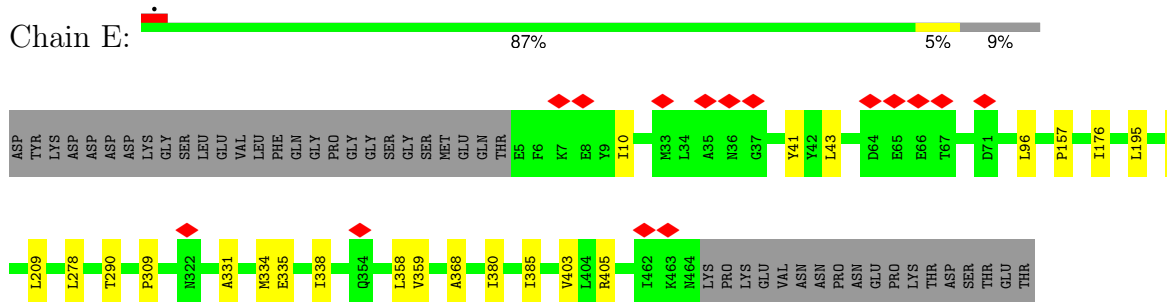
3 Residue-property plots [i](#)

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.

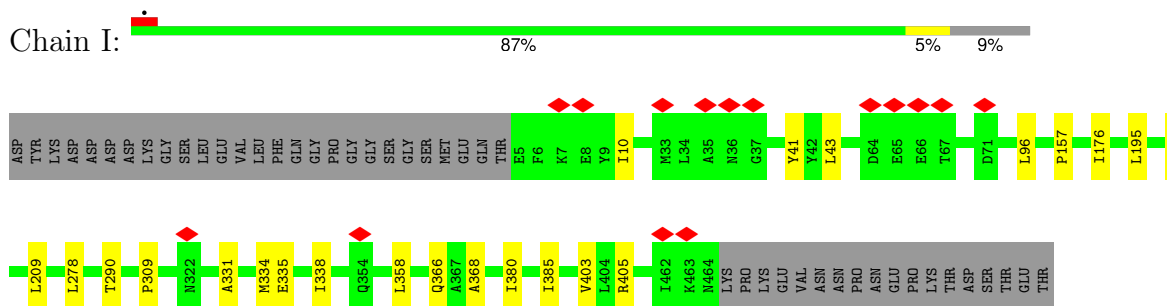
- Molecule 1: Spore germination protein A1



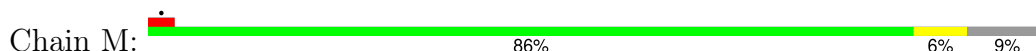
- Molecule 1: Spore germination protein A1

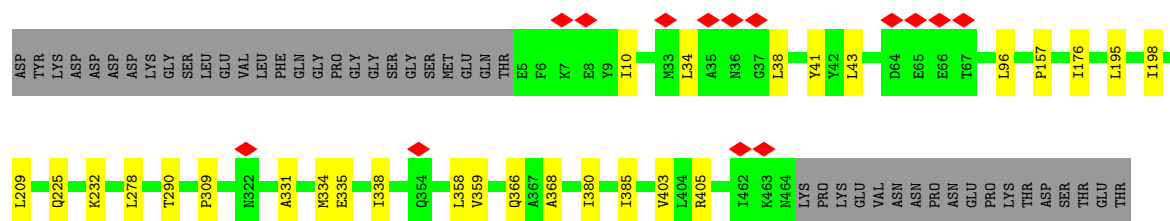


- Molecule 1: Spore germination protein A1

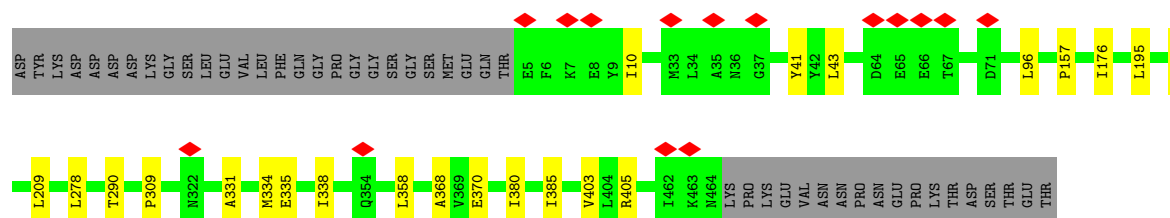
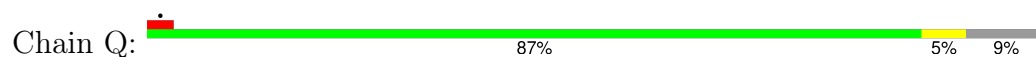


- Molecule 1: Spore germination protein A1

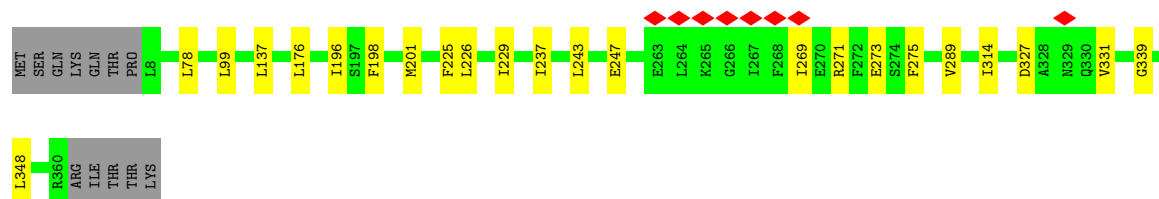




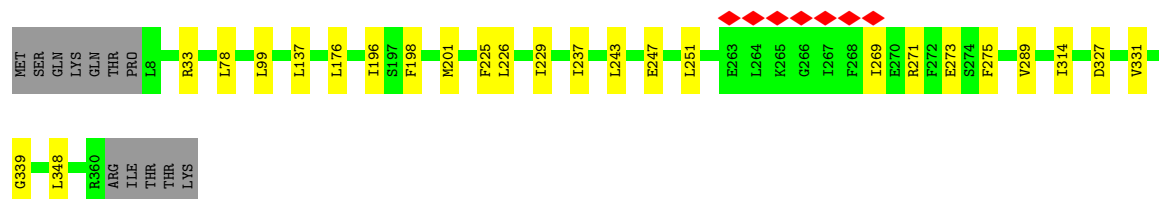
- Molecule 1: Spore germination protein A1



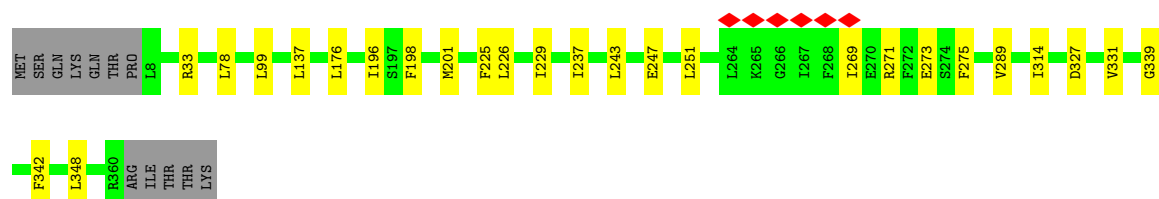
- Molecule 2: Spore germination protein A2



- Molecule 2: Spore germination protein A2



- Molecule 2: Spore germination protein A2



Chain N:

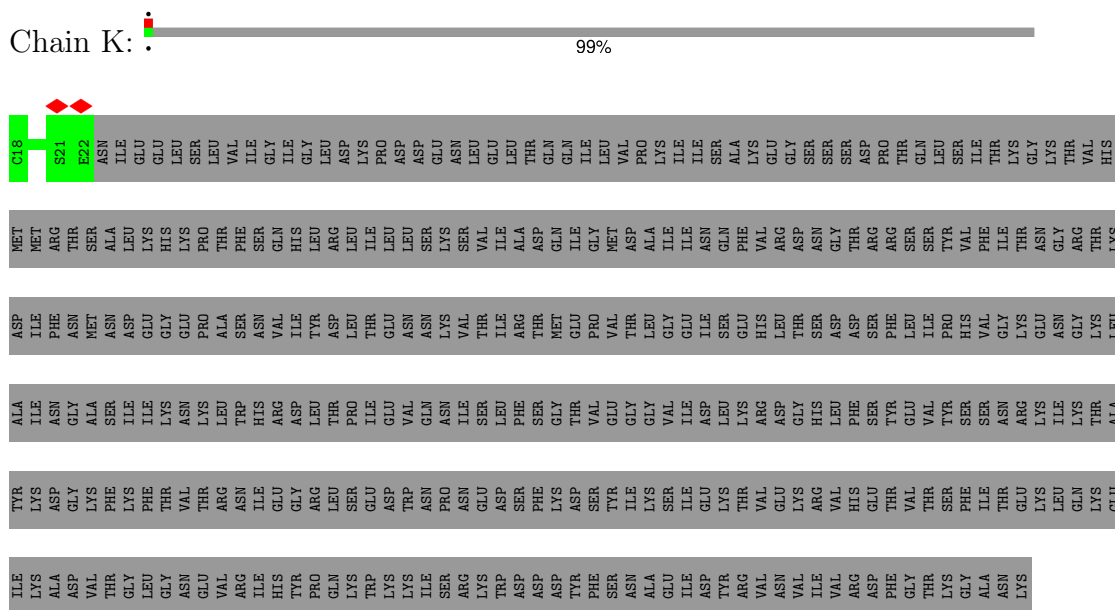
Chain R:

[illegible]

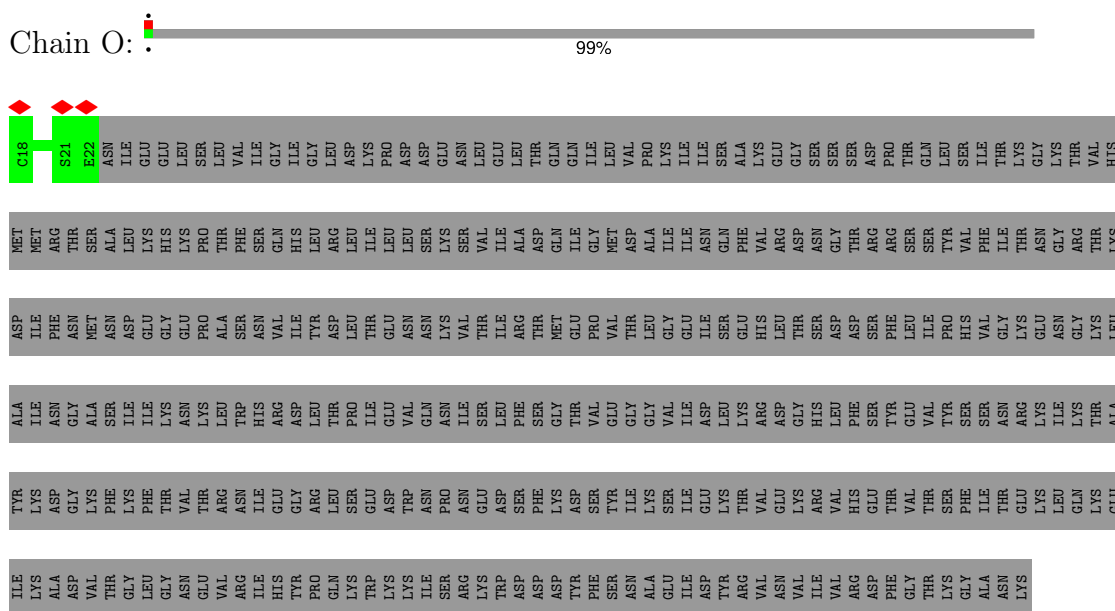
Chain G:

[illegible]

- Molecule 3: Spore germination protein A3



- Molecule 3: Spore germination protein A3



- Molecule 3: Spore germination protein A3

99%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C5	Depositor
Number of particles used	259371	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50.3	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	165000	Depositor
Image detector	TFS FALCON 4i (4k x 4k)	Depositor
Maximum map value	59.385	Depositor
Minimum map value	-41.300	Depositor
Average map value	0.006	Depositor
Map value standard deviation	1.254	Depositor
Recommended contour level	6	Depositor
Map size (Å)	331.52002, 331.52002, 331.52002	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.74000007, 0.74000007, 0.74000007	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, DGA, C14

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	0.10	0/3762	0.25	0/5097
1	E	0.10	0/3762	0.25	0/5097
1	I	0.11	0/3762	0.25	0/5097
1	M	0.12	0/3762	0.26	0/5097
1	Q	0.10	0/3762	0.25	0/5097
2	B	0.12	0/2959	0.27	0/4017
2	F	0.12	0/2959	0.27	0/4017
2	J	0.12	0/2959	0.27	0/4017
2	N	0.12	0/2959	0.27	0/4017
2	R	0.12	0/2959	0.27	0/4017
3	C	0.09	0/44	0.18	0/59
3	G	0.09	0/44	0.18	0/59
3	K	0.09	0/44	0.18	0/59
3	O	0.09	0/44	0.18	0/59
3	S	0.09	0/44	0.18	0/59
All	All	0.11	0/33825	0.26	0/45865

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

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	3695	0	3857	21	0
1	E	3695	0	3857	22	0
1	I	3695	0	3857	20	0
1	M	3695	0	3857	21	0
1	Q	3695	0	3857	18	0
2	B	2882	0	3035	14	0
2	F	2882	0	3035	15	0
2	J	2882	0	3035	16	0
2	N	2882	0	3035	13	0
2	R	2882	0	3035	14	0
3	C	43	0	28	0	0
3	G	43	0	28	0	0
3	K	43	0	28	0	0
3	O	43	0	28	0	0
3	S	43	0	28	0	0
4	A	14	0	30	1	0
4	E	14	0	30	1	0
4	I	14	0	30	1	0
4	M	14	0	30	1	0
4	Q	14	0	30	1	0
5	B	1	0	0	0	0
5	F	1	0	0	0	0
5	J	1	0	0	0	0
5	N	1	0	0	0	0
5	R	1	0	0	0	0
6	C	11	0	3	0	0
6	G	11	0	3	0	0
6	K	11	0	3	0	0
6	O	11	0	3	0	0
6	S	11	0	3	0	0
7	A	58	0	0	0	0
7	B	28	0	0	0	0
7	E	59	0	0	0	0
7	F	28	0	0	0	0
7	I	57	0	0	0	0
7	J	28	0	0	0	0
7	M	58	0	0	0	0
7	N	28	0	0	0	0
7	Q	58	0	0	0	0
7	R	28	0	0	0	0
All	All	33660	0	34765	144	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.

The worst 5 of 144 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:269:ILE:HD13	2:J:275:PHE:HZ	1.67	0.60
2:N:269:ILE:HD13	2:N:275:PHE:HZ	1.67	0.60
2:R:269:ILE:HD13	2:R:275:PHE:HZ	1.67	0.59
2:F:269:ILE:HD13	2:F:275:PHE:HZ	1.67	0.59
2:B:269:ILE:HD13	2:B:275:PHE:HZ	1.67	0.59

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	468/505 (93%)	466 (100%)	2 (0%)	0	100	100
1	E	468/505 (93%)	466 (100%)	2 (0%)	0	100	100
1	I	468/505 (93%)	466 (100%)	2 (0%)	0	100	100
1	M	468/505 (93%)	466 (100%)	2 (0%)	0	100	100
1	Q	468/505 (93%)	466 (100%)	2 (0%)	0	100	100
2	B	357/365 (98%)	352 (99%)	5 (1%)	0	100	100
2	F	357/365 (98%)	352 (99%)	5 (1%)	0	100	100
2	J	357/365 (98%)	352 (99%)	5 (1%)	0	100	100
2	N	357/365 (98%)	352 (99%)	5 (1%)	0	100	100
2	R	357/365 (98%)	352 (99%)	5 (1%)	0	100	100
3	C	3/356 (1%)	3 (100%)	0	0	100	100
3	G	3/356 (1%)	3 (100%)	0	0	100	100
3	K	3/356 (1%)	3 (100%)	0	0	100	100
3	O	3/356 (1%)	3 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	S	3/356 (1%)	3 (100%)	0	0	100	100
All	All	4140/6130 (68%)	4105 (99%)	35 (1%)	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	417/447 (93%)	417 (100%)	0	100	100
1	E	417/447 (93%)	417 (100%)	0	100	100
1	I	417/447 (93%)	417 (100%)	0	100	100
1	M	417/447 (93%)	417 (100%)	0	100	100
1	Q	417/447 (93%)	417 (100%)	0	100	100
2	B	317/323 (98%)	317 (100%)	0	100	100
2	F	317/323 (98%)	317 (100%)	0	100	100
2	J	317/323 (98%)	317 (100%)	0	100	100
2	N	317/323 (98%)	317 (100%)	0	100	100
2	R	317/323 (98%)	317 (100%)	0	100	100
3	C	5/323 (2%)	5 (100%)	0	100	100
3	G	5/323 (2%)	5 (100%)	0	100	100
3	K	5/323 (2%)	5 (100%)	0	100	100
3	O	5/323 (2%)	5 (100%)	0	100	100
3	S	5/323 (2%)	5 (100%)	0	100	100
All	All	3695/5465 (68%)	3695 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	M	216	ASN
1	Q	105	ASN
2	R	21	ASN
1	Q	216	ASN
2	N	21	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 5 are monoatomic - leaving 10 for Mogul analysis.

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	$\# Z > 2$
6	DGA	S	401	3	10,10,43	0.24	0	12,12,45	0.28	0
4	C14	A	501	-	13,13,13	0.23	0	12,12,12	0.16	0
6	DGA	K	401	3	10,10,43	0.24	0	12,12,45	0.28	0
4	C14	E	501	-	13,13,13	0.23	0	12,12,12	0.16	0
6	DGA	O	401	3	10,10,43	0.24	0	12,12,45	0.28	0
4	C14	Q	501	-	13,13,13	0.23	0	12,12,12	0.16	0
4	C14	M	501	-	13,13,13	0.23	0	12,12,12	0.16	0
6	DGA	G	401	3	10,10,43	0.25	0	12,12,45	0.28	0
4	C14	I	501	-	13,13,13	0.24	0	12,12,12	0.16	0
6	DGA	C	401	3	10,10,43	0.25	0	12,12,45	0.28	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
6	DGA	S	401	3	-	0/9/9/45	-
4	C14	A	501	-	-	4/11/11/11	-
6	DGA	K	401	3	-	0/9/9/45	-
4	C14	E	501	-	-	4/11/11/11	-
6	DGA	O	401	3	-	0/9/9/45	-
4	C14	Q	501	-	-	4/11/11/11	-
4	C14	M	501	-	-	4/11/11/11	-
6	DGA	G	401	3	-	0/9/9/45	-
4	C14	I	501	-	-	4/11/11/11	-
6	DGA	C	401	3	-	0/9/9/45	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	C14	C07-C08-C09-C10
4	E	501	C14	C07-C08-C09-C10
4	I	501	C14	C07-C08-C09-C10
4	M	501	C14	C07-C08-C09-C10
4	Q	501	C14	C07-C08-C09-C10

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	501	C14	1	0
4	E	501	C14	1	0
4	Q	501	C14	1	0
4	M	501	C14	1	0
4	I	501	C14	1	0

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.

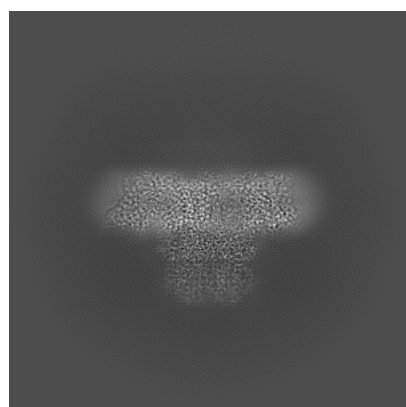
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-78039. These allow visual inspection of the internal detail of the map and identification of artifacts.

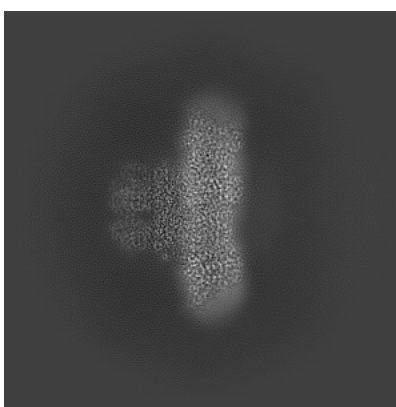
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

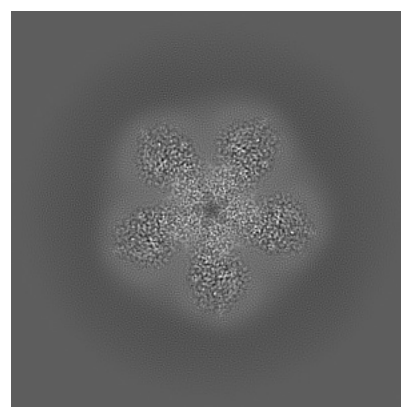
6.1.1 Primary map



X



Y

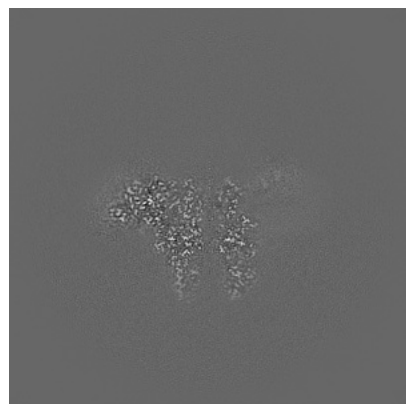


Z

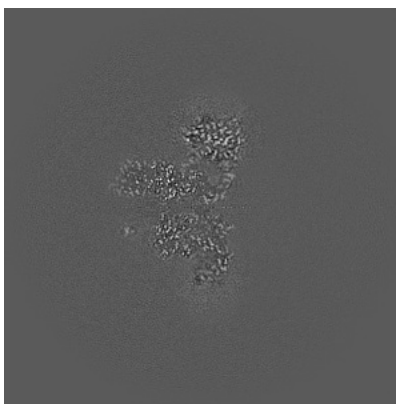
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

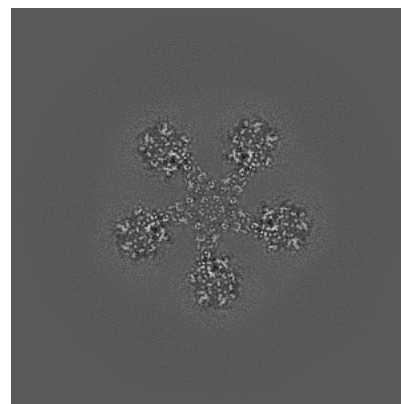
6.2.1 Primary map



X Index: 224



Y Index: 224

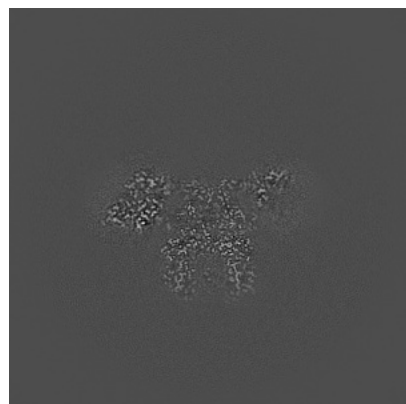


Z Index: 224

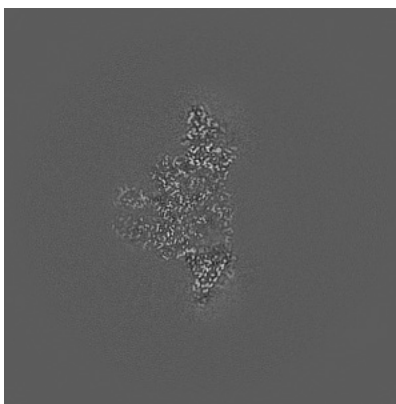
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

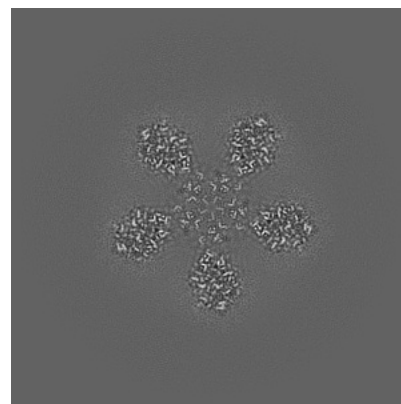
6.3.1 Primary map



X Index: 238



Y Index: 205

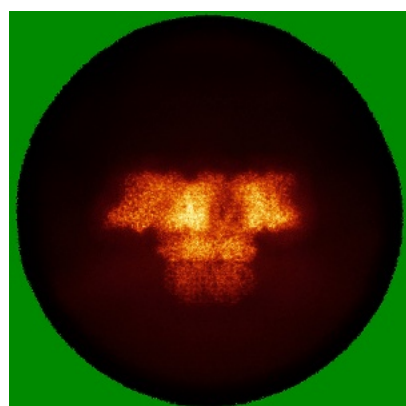


Z Index: 218

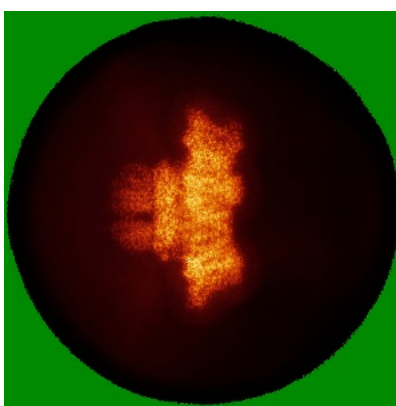
The images above show the largest variance slices of the map in three orthogonal directions.

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

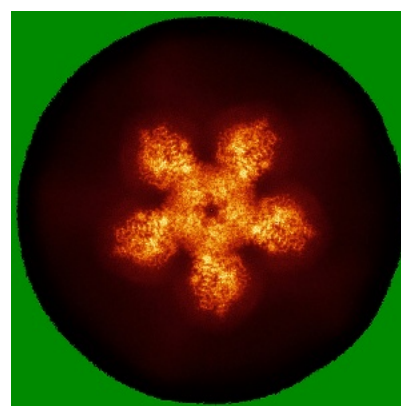
6.4.1 Primary map



X



Y

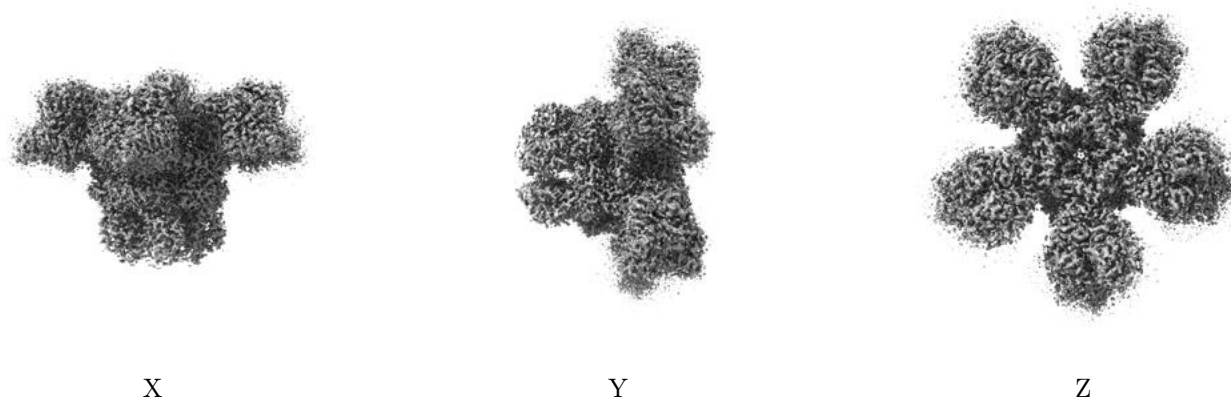


Z

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

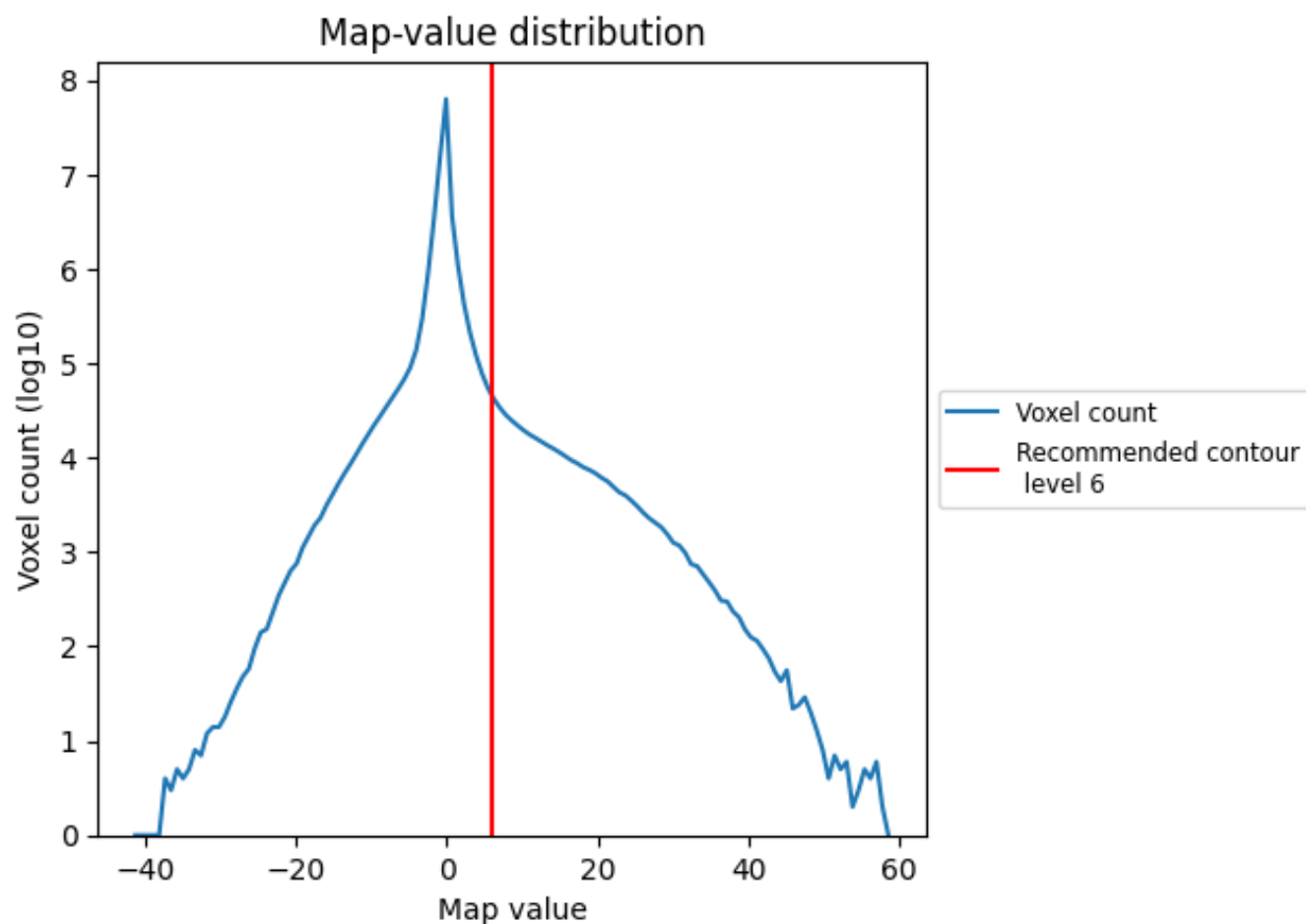
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

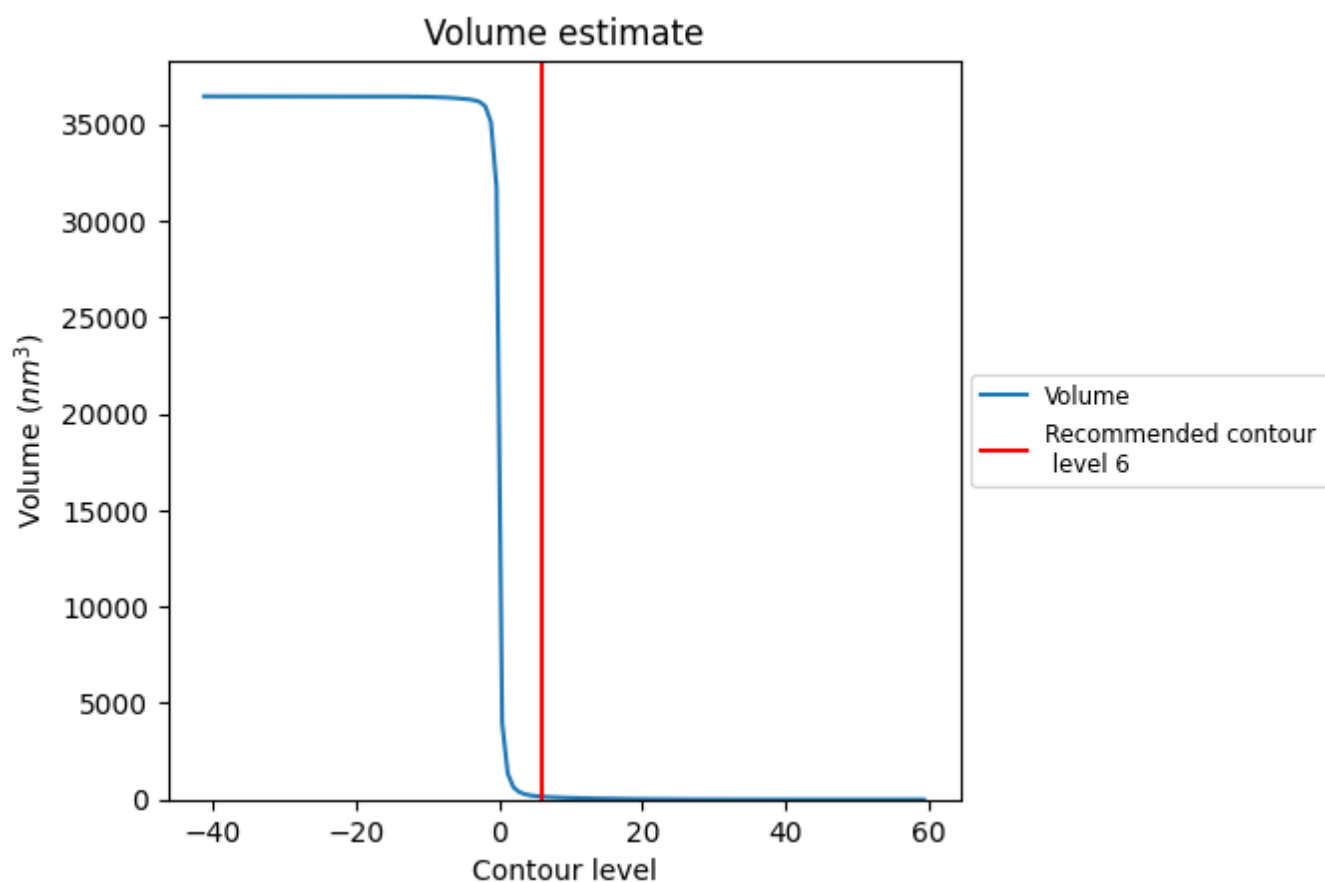
This section contains the results of statistical analysis of the map.

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.

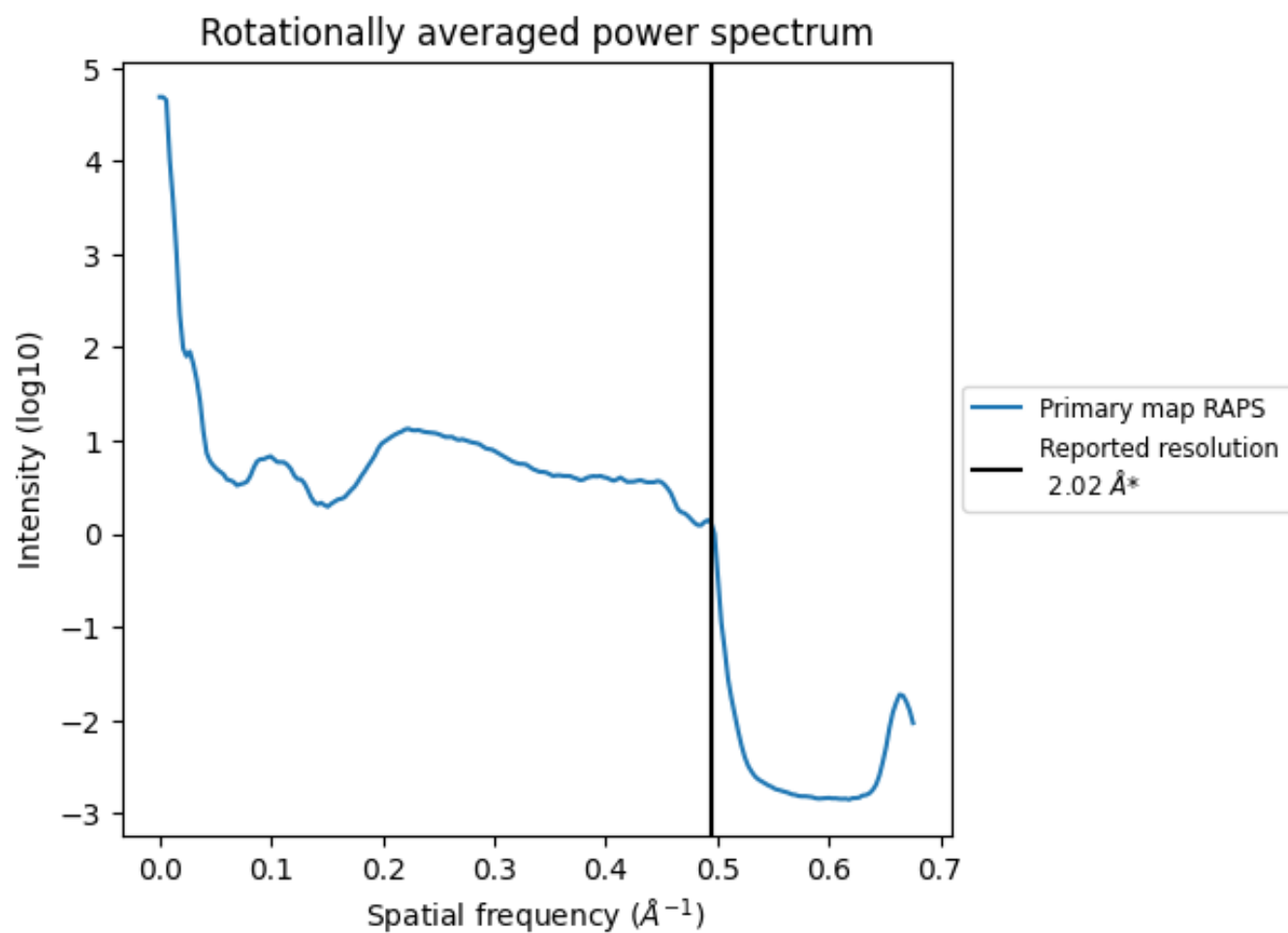
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 151 nm³; this corresponds to an approximate mass of 137 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 0.495 Å⁻¹

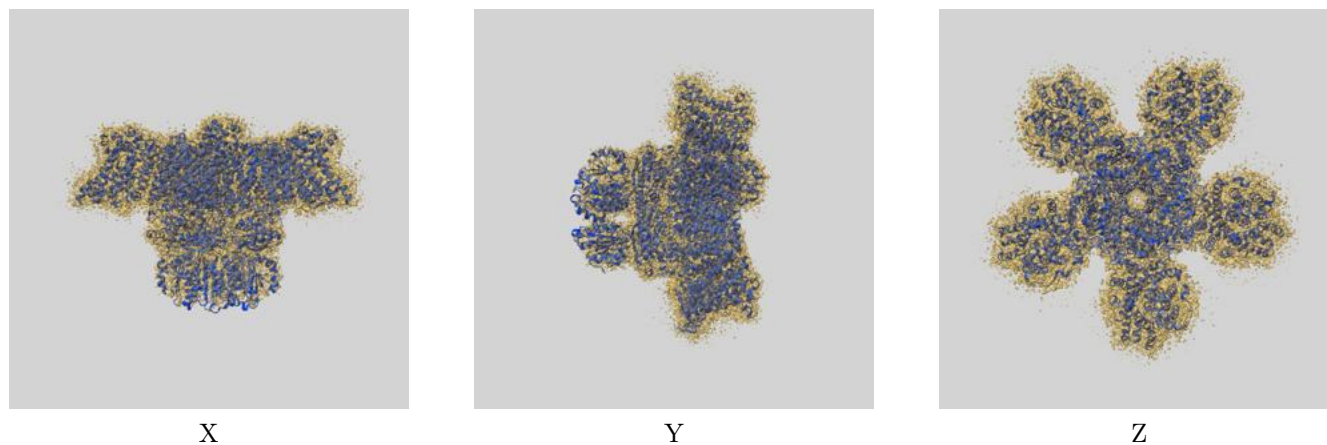
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

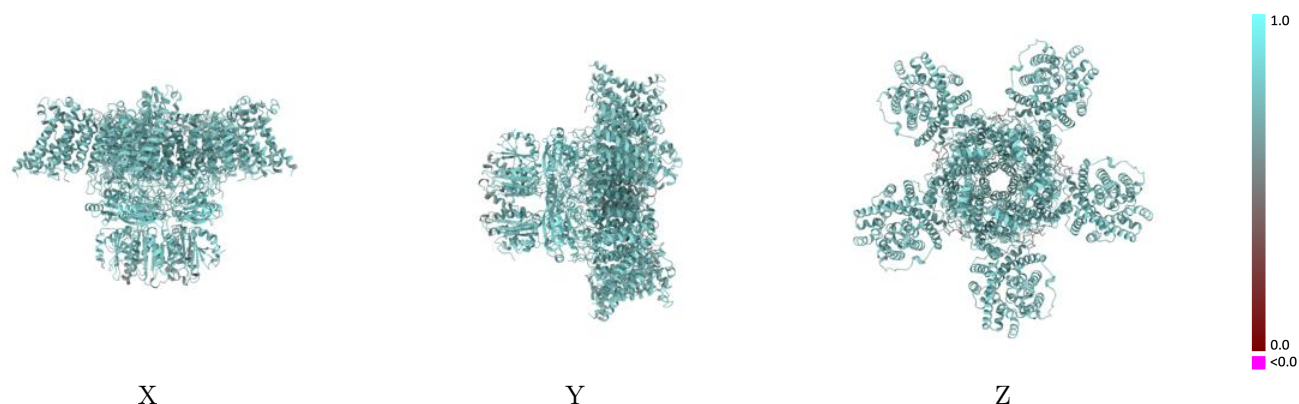
This section contains information regarding the fit between EMDB map EMD-78039 and PDB model 37BM. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)



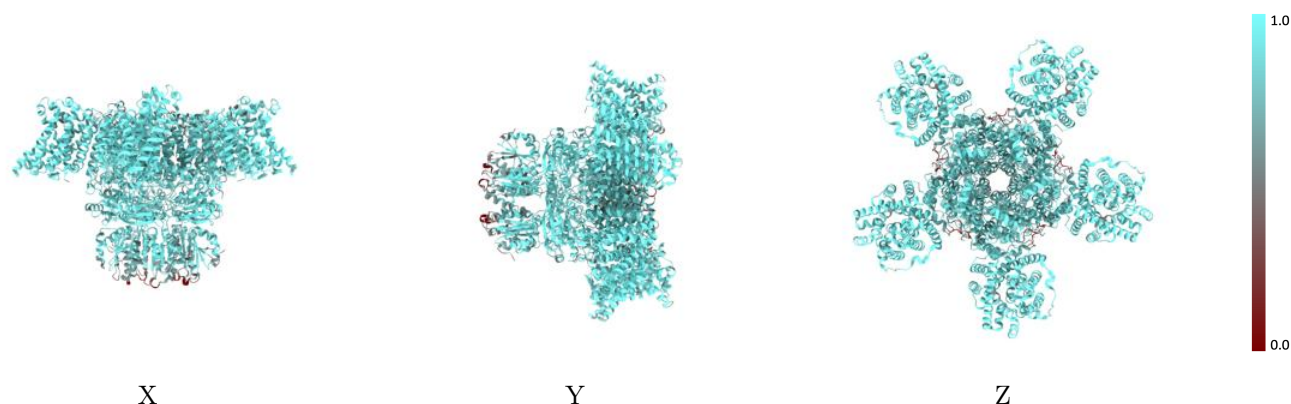
The images above show the 3D surface view of the map at the recommended contour level 6.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



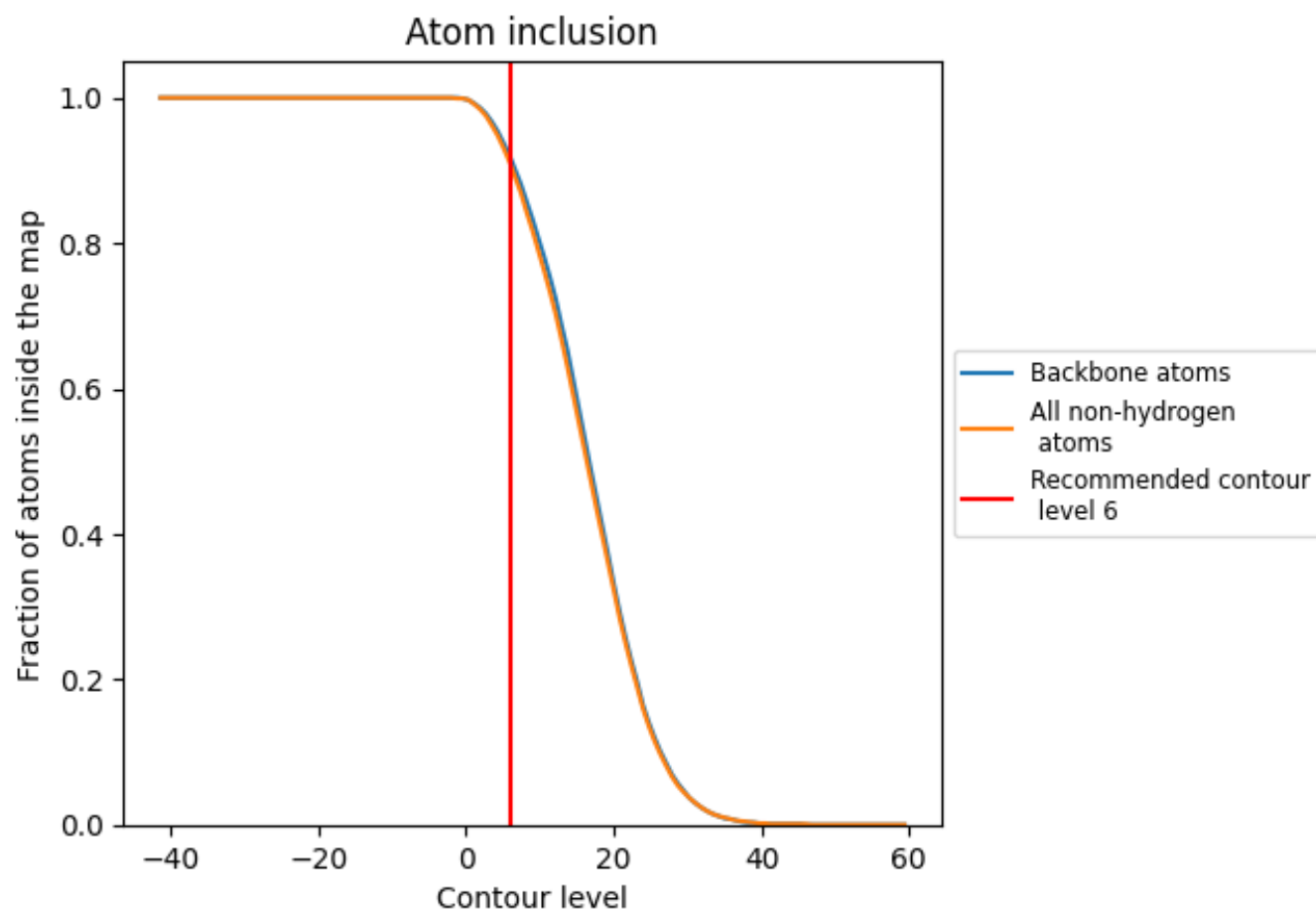
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 91% 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 (6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9100	0.7360
A	0.9030	0.7620
B	0.9410	0.7090
C	0.3960	0.6010
E	0.8960	0.7590
F	0.9390	0.7080
G	0.3770	0.5950
I	0.9000	0.7590
J	0.9390	0.7070
K	0.3770	0.6070
M	0.8990	0.7600
N	0.9370	0.7070
O	0.3770	0.6100
Q	0.8990	0.7610
R	0.9380	0.7080
S	0.3960	0.6040

1.0
0.0
<0.0