



wwPDB EM Validation Summary Report ⓘ

Mar 15, 2026 – 07:18 AM UTC

PDB ID : 6RWK / pdb_00006rwk
EMDB ID : EMD-10040
Title : MxiD N0 N1 and MxiG C-terminal domains of the Shigella type 3 secretion system
Authors : Kamprad, A.; Lunelli, M.
Deposited on : 2019-06-05
Resolution : 3.86 Å(reported)
Based on initial model : 3GR5

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:

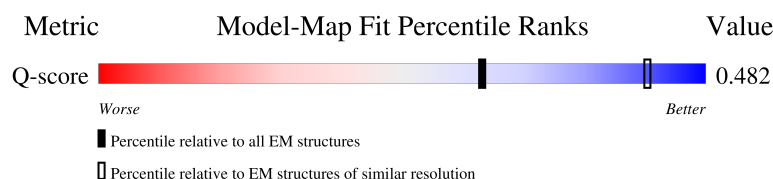
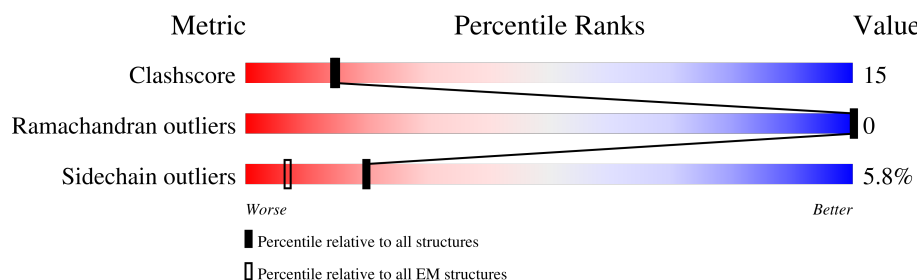
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.86 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.



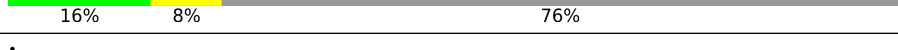
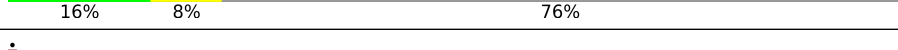
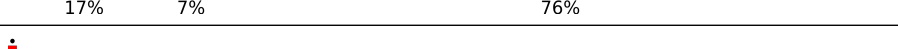
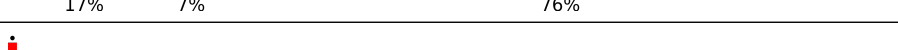
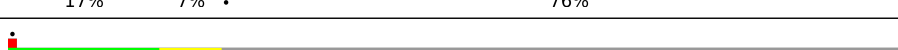
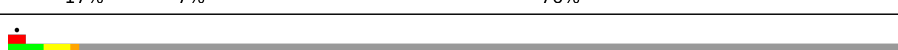
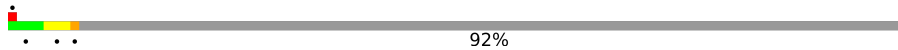
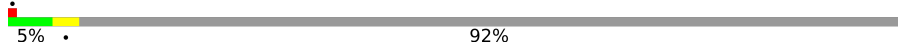
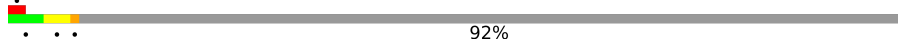
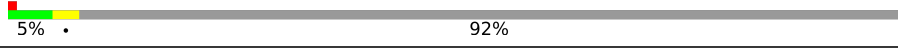
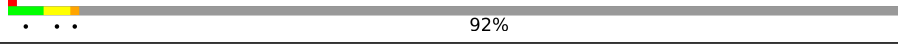
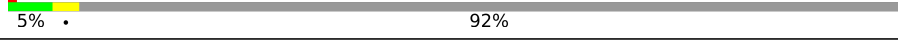
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8889 (3.36 - 4.35)

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	0	566	
1	1	566	
1	2	566	
1	3	566	

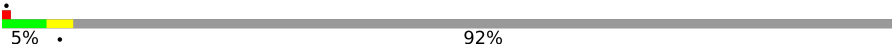
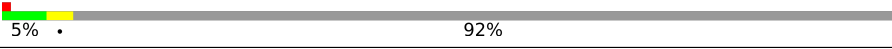
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Mol	Chain	Length	Quality of chain
1	4	566	 16% 8% 76%
1	5	566	 17% 7% 76%
1	6	566	 16% 8% 76%
1	7	566	 17% 7% 76%
1	8	566	 16% 8% 76%
1	9	566	 17% 7% 76%
1	X	566	 16% 8% 76%
1	Y	566	 16% 8% 76%
1	Z	566	 17% 7% 76%
1	x	566	 17% 7% 76%
1	y	566	 17% 7% 76%
1	z	566	 17% 7% 76%
2	A	371	 92%
2	B	371	 5% 92%
2	D	371	 92%
2	E	371	 5% 92%
2	G	371	 92%
2	H	371	 5% 92%
2	J	371	 92%
2	K	371	 5% 92%
2	M	371	 92%
2	N	371	 5% 92%
2	P	371	 92%
2	Q	371	 5% 92%
2	S	371	 92%

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Mol	Chain	Length	Quality of chain
2	T	371	 5% . 92%
2	U	371	 5% . . 92%
2	V	371	 5% . 92%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 21760 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.

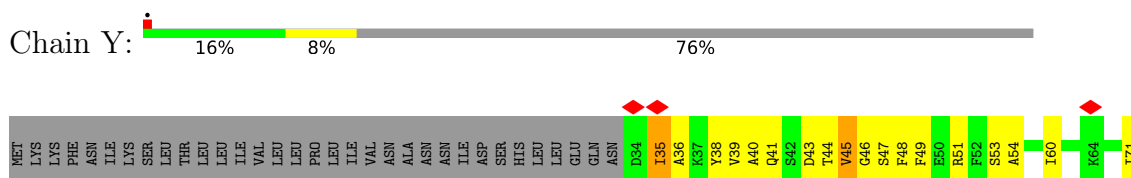
- Molecule 1 is a protein called Outer membrane protein MxiD.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	X	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	Y	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	Z	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	0	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	2	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	4	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	6	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	8	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	x	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	y	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	z	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	1	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	3	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	5	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	7	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		
1	9	138	Total	C	N	O	S	0	0
			1102	718	174	209	1		

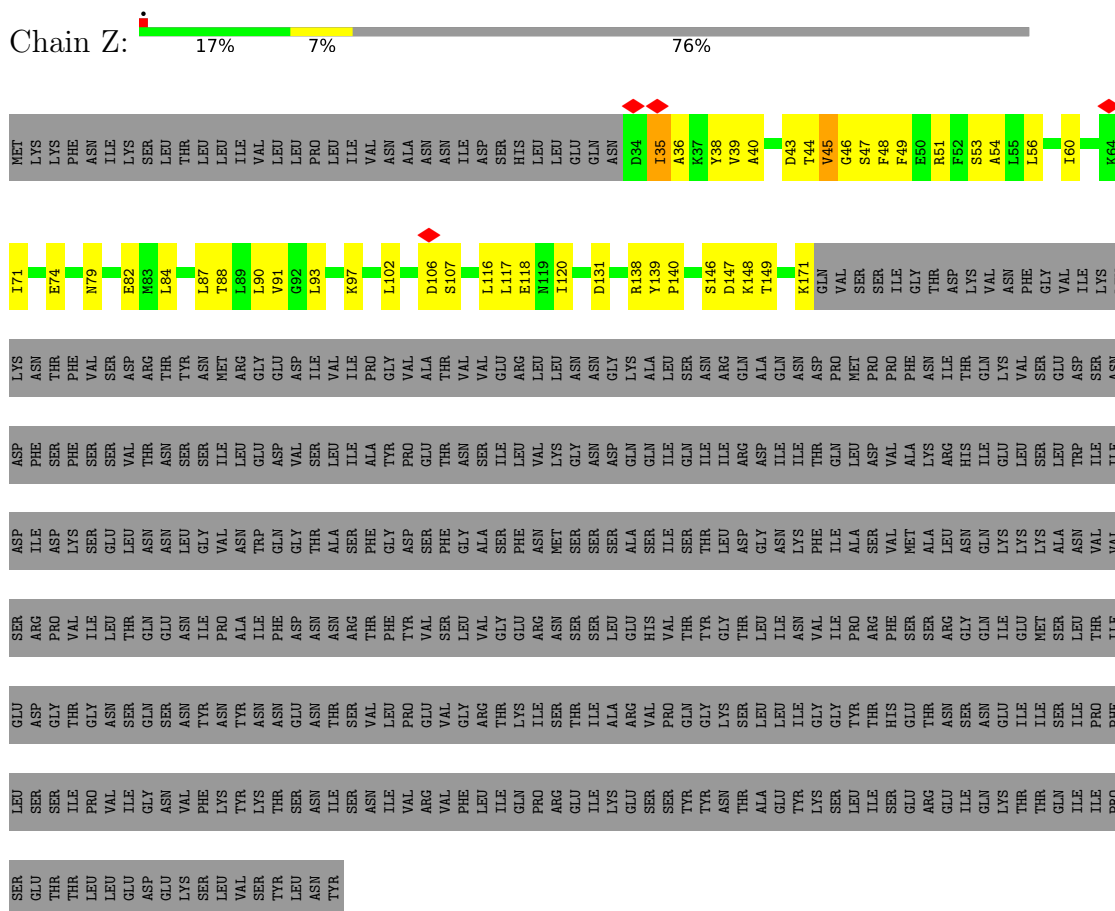
- Molecule 2 is a protein called Protein MxiG.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	D	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	G	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	J	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	M	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	P	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	S	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	U	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	B	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	E	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	H	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	K	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	N	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	Q	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	T	30	Total	C	N	O	S	0	0
			258	171	39	47	1		
2	V	30	Total	C	N	O	S	0	0
			258	171	39	47	1		

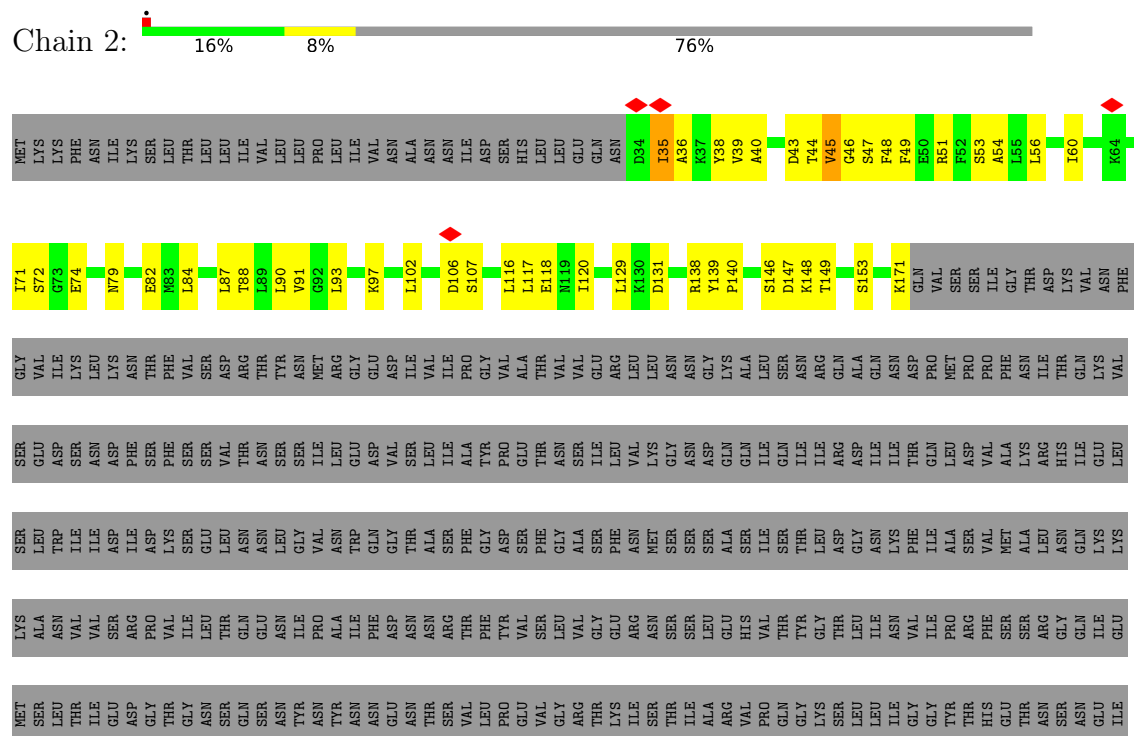
- Molecule 1: Outer membrane protein MxiD

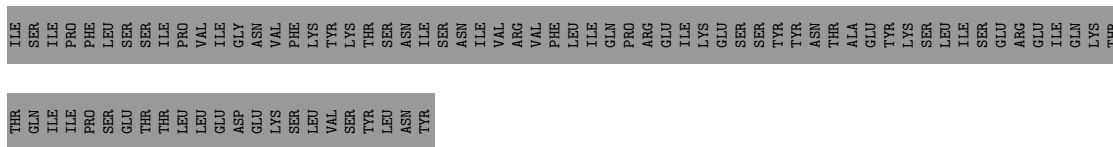


- Molecule 1: Outer membrane protein MxiD

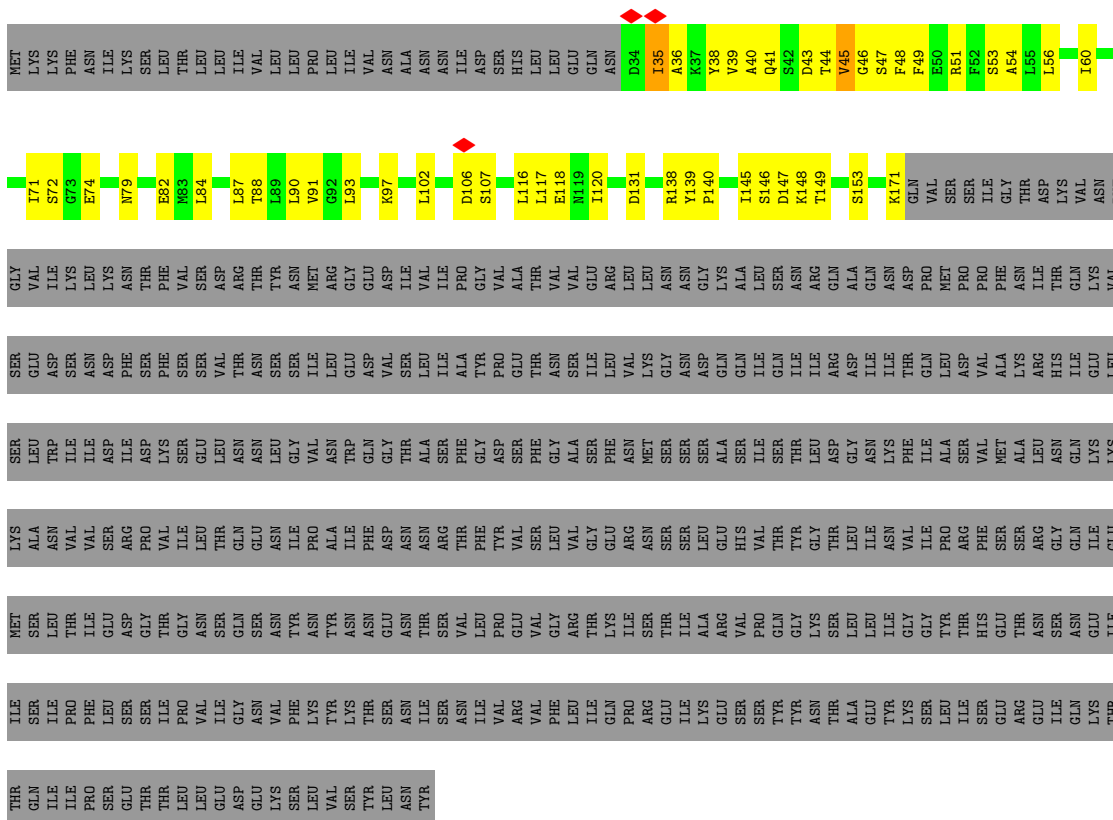


- Molecule 1: Outer membrane protein MxiD

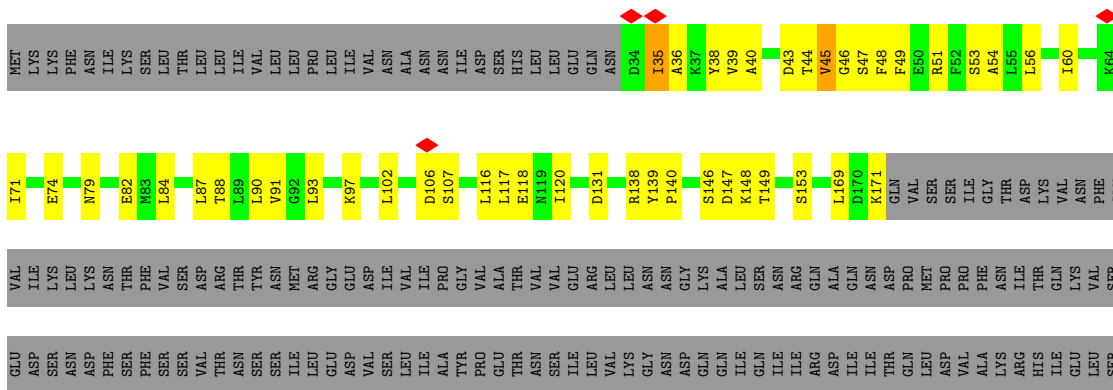




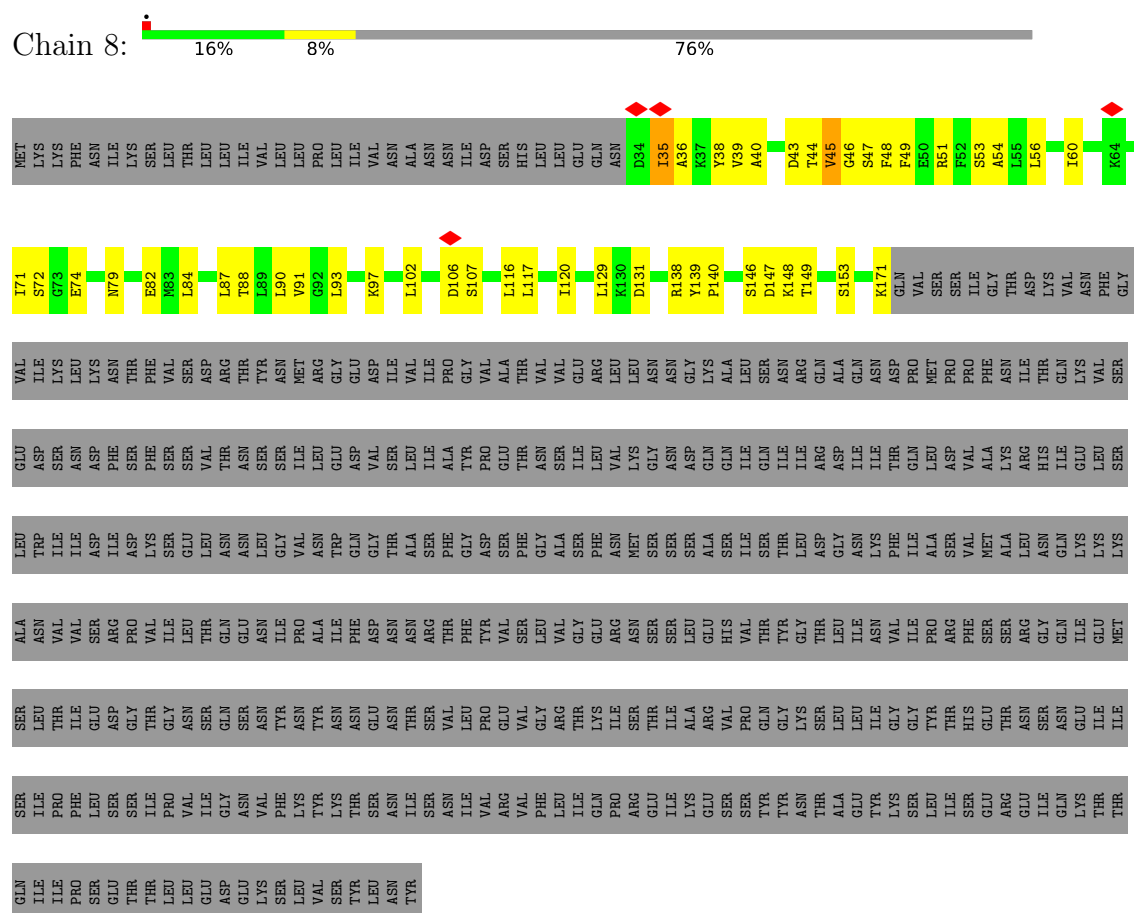
- Molecule 1: Outer membrane protein MxiD



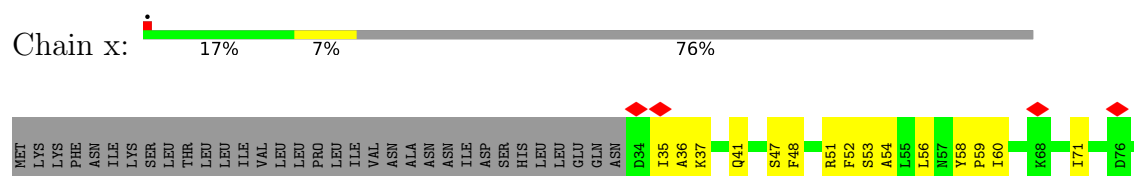
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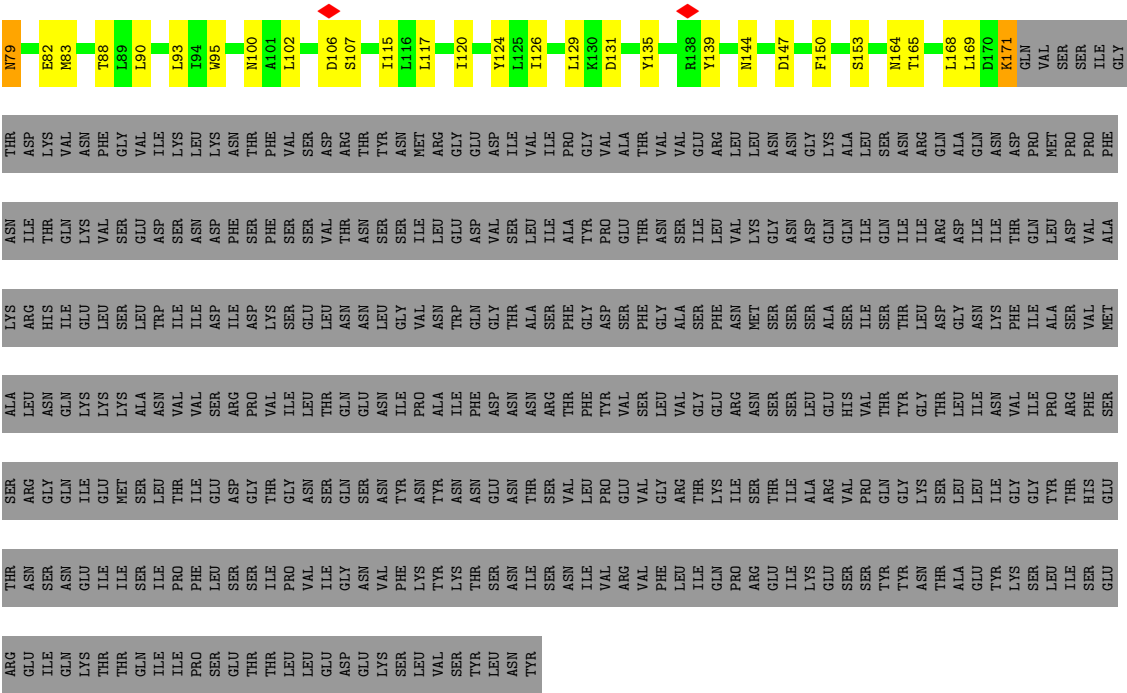


- Molecule 1: Outer membrane protein MxiD

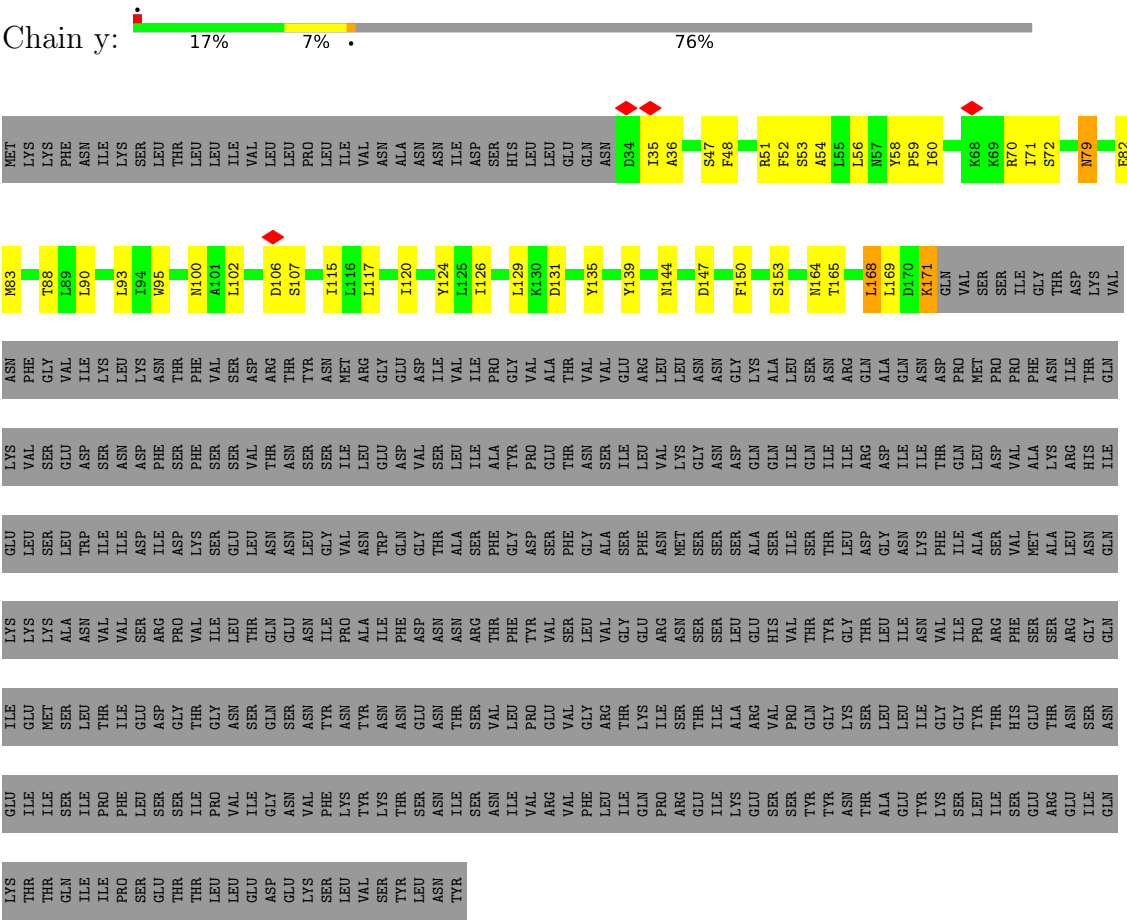


- Molecule 1: Outer membrane protein MxiD

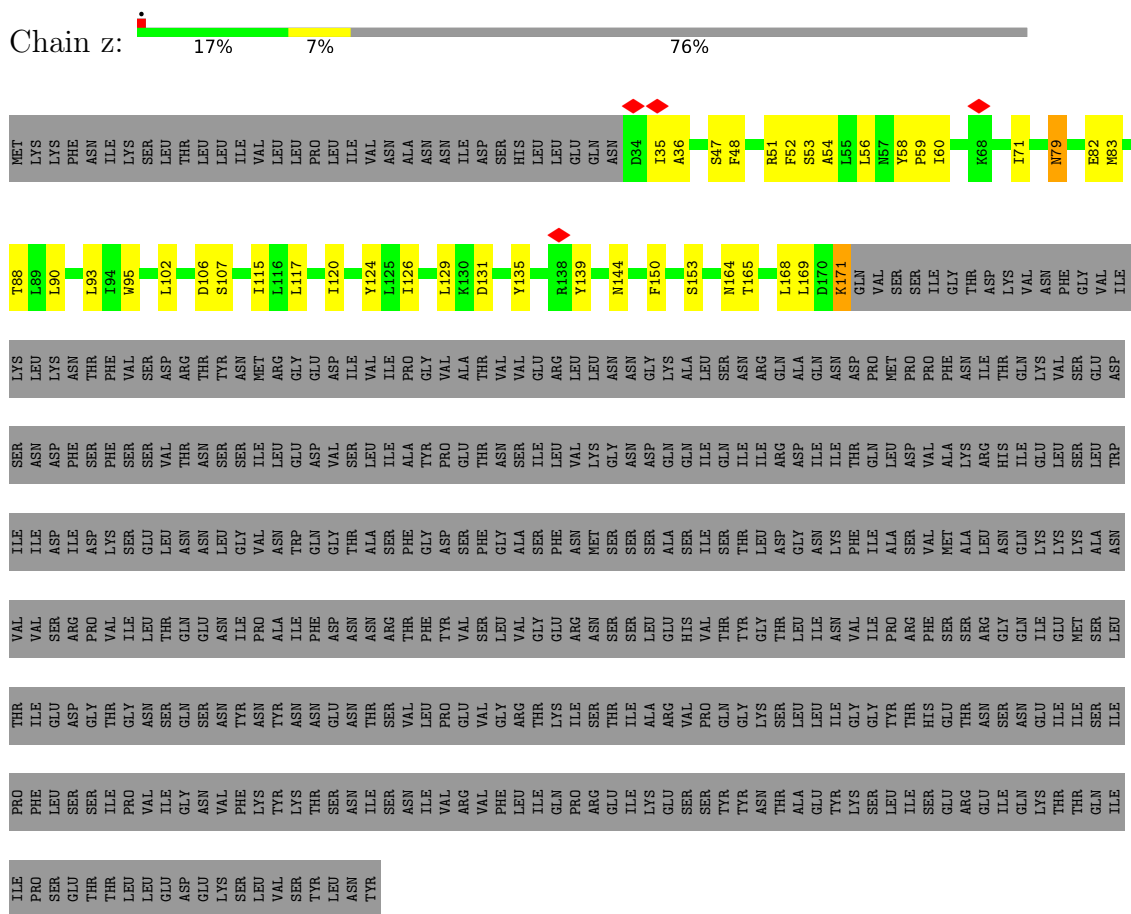




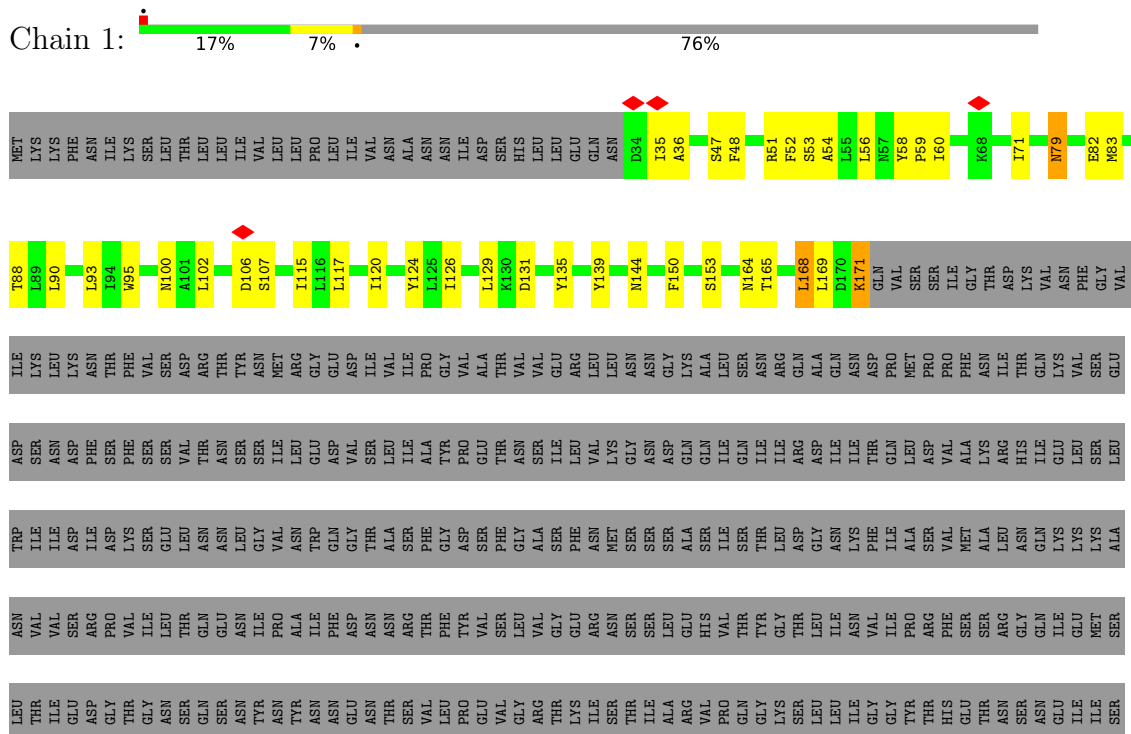
• Molecule 1: Outer membrane protein MxiD



• Molecule 1: Outer membrane protein MxiD



- Molecule 1: Outer membrane protein MxiD



ILE	PRO	PHE	LEU	SER	THR	ILE	PRO	VAL	GLY	ASN	VAL	PHE	VAL	ASN	THR	LYS	THR	SER	ASN	ILE	SER	ASN	ILE	VAL	ARG	ARG	GLN	PRO	ARG	GLU	ILE	LYS	GLY	SER	THR	TYR	ASN	TYR
ILE	PRO	SER	GLU	THR	THR	LEU	PRO	VAL	GLU	ASP	GLY	SER	VAL	LEU	ASN	LYS	THR	LEU	VAL	ASN	TYR																	

● Molecule 1: Outer membrane protein MxiD



GLU	ILE	ASN	ARG	GLY	ASN	LEU	HIS	THR	ASP	M83	MET
GLN	ASN	GLN	GLN	ILE	GLY	ASN	ILE	THR	LYS	T88	LYS
LYS	LYS	LYS	ILE	GLU	LYS	VAL	GLU	LYS	ASN	L90	PHE
THR	THR	ILE	GLU	SER	LYS	VAL	SER	VAL	PHE	L93	ASN
GLN	GLN	SER	THR	LEU	ALA	ASP	TRP	ASP	GLY	I94	LYS
ILE	ILE	ILE	LEU	ASN	ASN	LEU	ILE	SER	ILE	W95	SER
ILE	THR	PRO	THR	THR	VAL	VAL	ILE	ASN	LYS		LEU
PRO	PHE	LEU	GLY	ASP	SER	SER	ASP	ASP	LYS	M100	THR
SER	LEU	SER	ASP	ARG	THR	THR	ILE	PHE	THR	A101	LEU
GLU	GLU	ASN	GLY	PRO	ASN	ASN	ASP	SER	ASN	L102	LEU
THR	THR	SER	THR	VAL	VAL	THR	ILE	PHE	THR		VAL
THR	THR	PRO	GLY	GLY	ILE	SER	SER	SER	VAL	D106	LEU
LEU	LEU	VAL	VAL	ASN	LEU	GLU	GLU	SER	SER	S107	LEU
GLY	ILE	ILE	SER	SER	THR	THR	LEU	VAL	ASP		PRO
ASP	GLY	GLN	GLN	ASN	GLN	ASN	ASN	THR	ARG	I115	LEU
GLU	GLU	ASN	SER	ASN	GLU	SER	LEU	ASN	THR	L116	LEU
LYS	VAL	ASN	ASN	GLY	ASN	SER	GLY	SER	TYR	L117	PRO
LEU	LEU	TYR	TYR	VAL	PRO	ASN	VAL	ILE	MET		ASN
VAL	VAL	LYS	ASN	THR	ALA	LYS	THR	LEU	ARG	I120	ALA
SER	SER	LYS	ASN	ASN	ILE	ASN	TRP	GLY	GLY	S121	ASN
THR	THR	THR	ASN	PHE	PHE	THR	GLN	GLU	GLY	L122	ASN
LEU	LEU	SER	GLU	ASP	ASP	ASP	VAL	VAL	GLU	N123	ASN
ASN	ASN	ASN	ASN	ASN	ASN	ASN	THR	ASP	ASP	Y124	ILE
ILE	ILE	ILE	THR	THR	ASN	ASN	ALA	LEU	ILE	L125	SER
SER	SER	SER	SER	SER	ARG	ARG	SER	ILE	ILE	I126	HIS
ASN	ASN	ASN	VAL	VAL	THR	THR	PHE	ALA	PRO		LEU
ILE	ILE	ILE	LEU	LEU	PHE	PHE	GLY	TYR	GLY	L129	LEU
VAL	VAL	VAL	PRO	PRO	THR	THR	ASP	PRO	VAL	R130	GLU
GLU	GLU	VAL	GLU	VAL	VAL	VAL	SER	GLU	ALA	D131	GLN
PHE	PHE	THR	GLY	ARG	VAL	VAL	PHE	THR	THR		ASN
LEU	LEU	ILE	THR	THR	GLY	GLY	ALA	ASN	VAL	Y135	D34
GLN	GLN	ILE	LYS	THR	GLY	GLY	SER	ILE	GLY	R138	I35
PRO	PRO	PRO	ILE	ILE	GLU	GLU	PHE	LEU	ARG	Y139	A36
ARG	ARG	ASN	ILE	ILE	ARG	ARG	ASN	VAL	LEU		S47
SER	SER	SER	SER	SER	SER	SER	MET	LYS	LEU	M144	F48
GLU	GLU	GLU	THR	THR	SER	SER	THR	GLY	ASN	D147	R51
ILE	ILE	ILE	ILE	ALA	SER	SER	SER	ASN	ASN		F52
LYS	LYS	LYS	ALA	ARG	GLU	GLU	ALA	ASP	GLY	F150	S53
SER	SER	SER	VAL	VAL	HIS	THR	ILE	GLN	ALA	S153	A54
THR	THR	THR	PRO	GLN	VAL	VAL	ILE	GLN	LEU		L55
LYS	LYS	LYS	GLN	GLN	THR	THR	THR	GLN	SER		L56
TYR	TYR	TYR	GLY	TYR	THR	THR	THR	ILE	ASN	M164	N57
ASN	ASN	ASN	LYS	GLY	GLY	GLY	LEU	ILE	ARG	T165	Y58
THR	THR	THR	SER	SER	THR	THR	ASP	ARG	GLN		P59
ALA	ALA	ALA	LEU	LEU	LEU	LEU	GLY	ASP	ALA	L168	I60
GLY	GLY	GLY	LEU	LEU	ILE	ILE	ASN	ILE	GLN	L169	
TYR	TYR	TYR	LEU	LEU	ASN	ILE	LYS	ILE	ASN	D170	K68
LYS	LYS	LYS	GLY	GLY	VAL	VAL	PHE	THR	ASP	K171	
SER	SER	SER	GLY	GLY	ILE	ILE	ILE	GLN	ASN	GLN	I71
LEU	LEU	LEU	TYR	TYR	ILE	ILE	ALA	PRO	ASP	VAL	
ILE	ILE	ILE	THR	THR	THR	THR	ALA	LEU	MET	SER	D76
SER	SER	SER	HIS	HIS	PHE	PHE	VAL	VAL	PRO	SER	
GLU	GLU	GLU	THR	THR	SER	SER	VAL	ALA	ASP	ILE	N79
ARG	ARG	ARG	THR	THR	SER	SER	ALA	LYS	PHE	GLY	E82

● Molecule 1: Outer membrane protein MxiD



GLU	ASP	SER	ASN	ASP	PHE	SER	PHE	SER	SER	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
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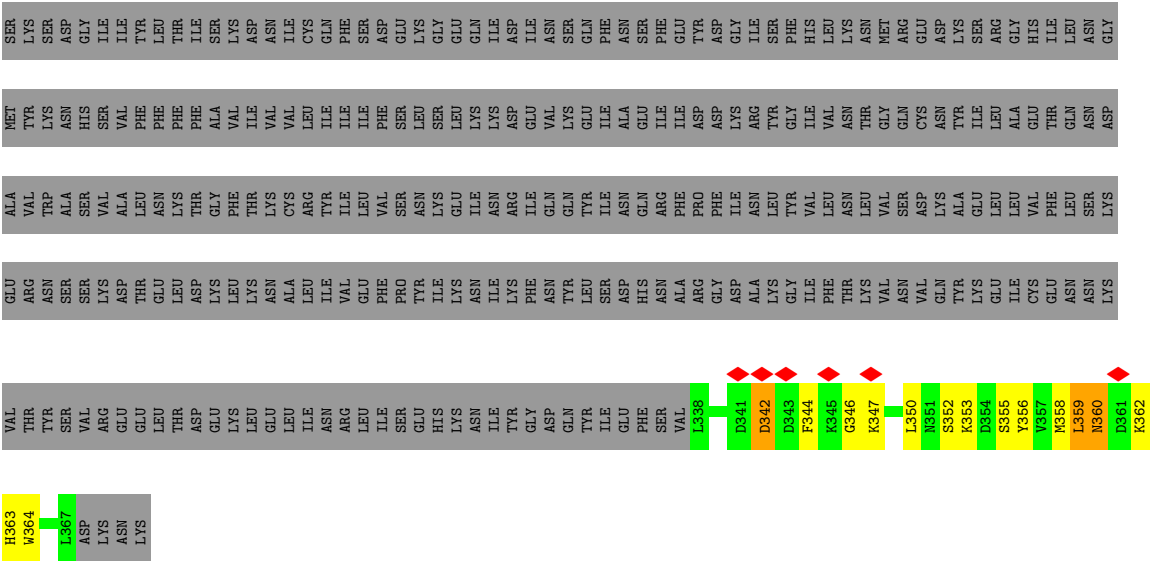
• Molecule 2: Protein MxiG

Chain A:				92%																																										
MET	SER	GLU	ALA	ASN	LYS	ASN	SER	ASN	LEU	ALA	PRO	PHE	ARG	LEU	LEU	VAL	GLY	THR	ASN	GLY	VAL	GLY	ASP	PHE	PRO	LEU	ASN	GLY	THR	LEU	GLU	PHE	GLY	ASN	ASN	PHE	PRO	GLU	ASN	GLY	THR	ILE	GLY	THR	ASN	GLY
SER	LYS	SER	ASP	GLY	ASN	ILE	THR	THR	ASN	ILE	THR	ILE	LYS	ASP	THR	CYS	PHE	SER	ASN	GLY	GLY	GLN	ILE	GLY	GLN	ASN	ILE	PHE	THR	ASN	LEU	THR	ASN	GLY	GLY	ASP	LYS	THR	ASN	GLY	THR	ASN	GLY	THR	ASN	GLY
MET	TYR	LYS	ASN	HIS	VAL	SER	PHE	ALA	VAL	VAL	ILE	ILE	THR	ILE	ILE	THR	ASN	PHE	ASP	LEU	GLY	LYS	ILE	GLY	LYS	ASN	ILE	GLY	GLY	VAL	VAL	THR	ASN	GLY	ASN	ASN	ASN	THR	ILE	LEU	ASN	GLY	THR	ASN	GLY	
ALA	VAL	TRP	ALA	SER	VAL	ALA	LEU	ASN	THR	THR	GLY	PHE	THR	LYS	LEU	CYS	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR
GLU	ARG	ASN	SER	SER	LYS	ASP	THR	THR	GLU	THR	ASP	LYS	LEU	LYS	ALA	ASN	VAL	GLY	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	THR	
VAL	THR	SER	VAL	ARG	GLY	GLU	GLU	LEU	THR	THR	GLU	LEU	ASN	ARG	THR	ILE	ASN	ARG	LEU	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	ILE	

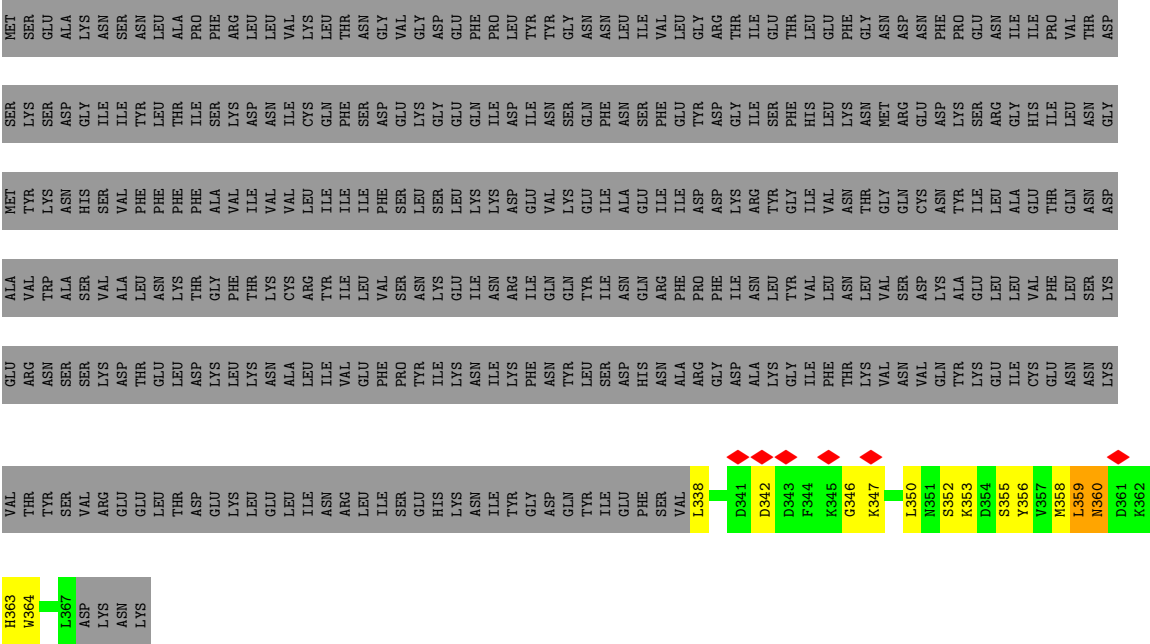
H363	W364	L367	ASP	ASN	LYS
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• Molecule 2: Protein MxiG

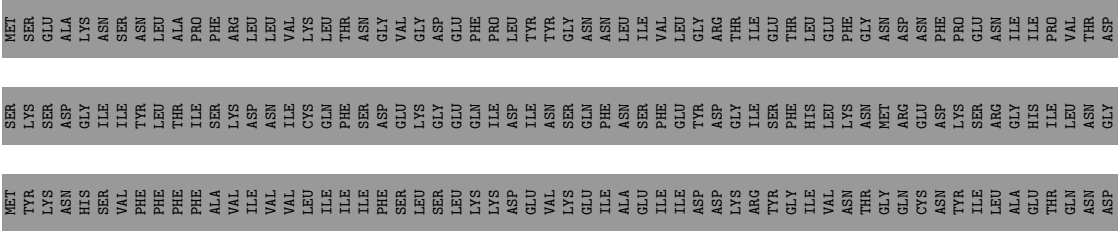
Chain D:				92%																																				
MET	SER	GLU	ALA	LYS	ASN	SER	ASN	LEU	THR	PHE	ARG	LEU	GLU	GLU	LEU	ILE	ASN	THR	THR	ASN	GLY	THR	VAL	GLY	GLY	ASP	GLY	THR	ASN	ASN	ASN	PHE	PRO	GLU	ILE	ILE	PRO	VAL	THR	ASP



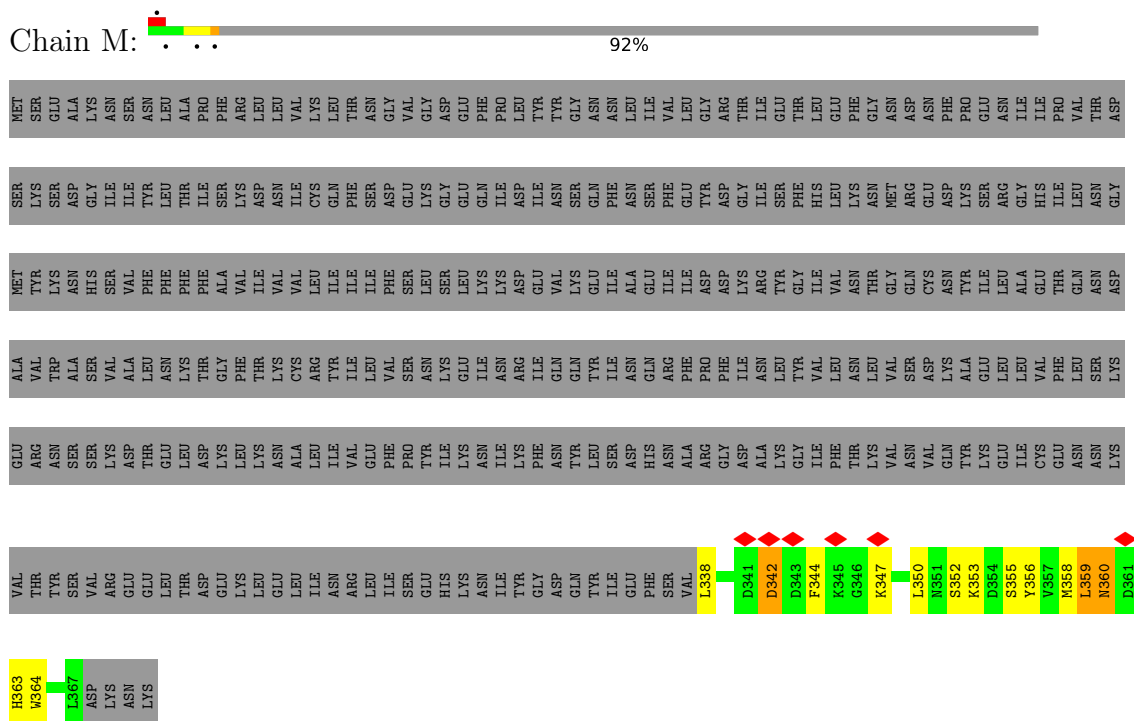
● Molecule 2: Protein MxiG



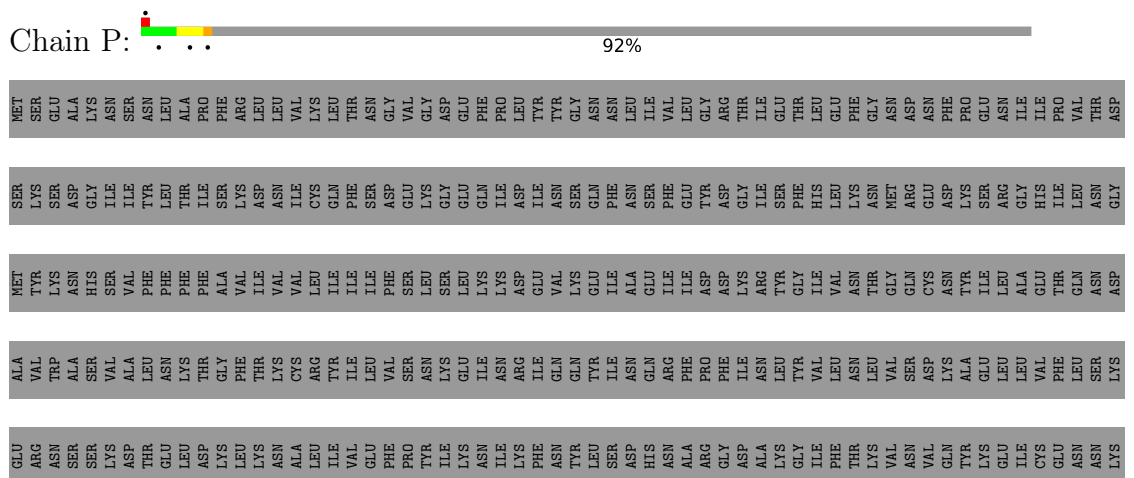
● Molecule 2: Protein MxiG

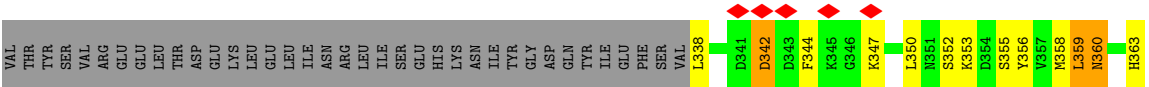


- Molecule 2: Protein MxiG

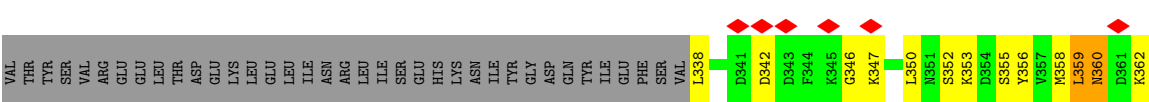
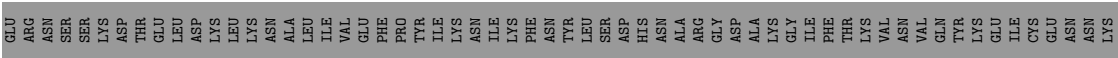
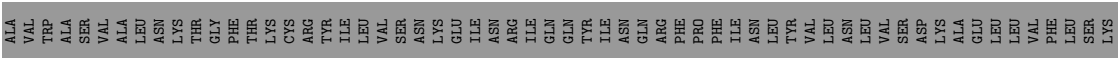
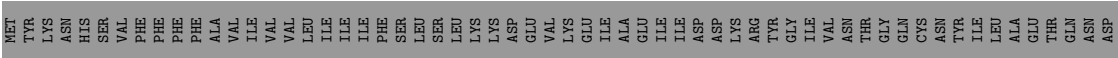
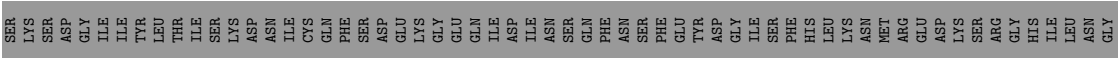
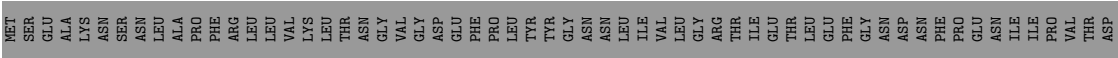


- Molecule 2: Protein MxiG

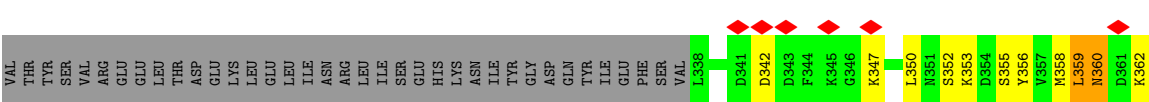
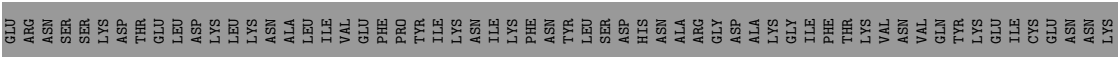
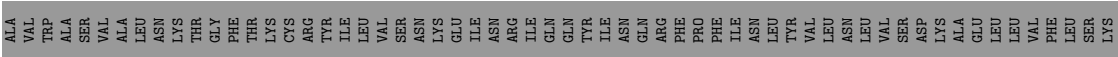
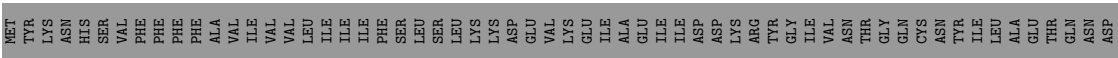
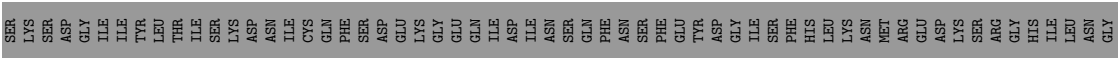
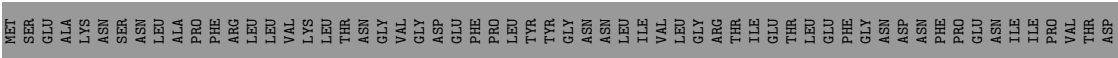




● Molecule 2: Protein MxiG



● Molecule 2: Protein MxiG



L367	ASP
	LYS
	ASN
	LYS

W364	L367	ASP
		LYS
		ASN
		LYS

MET	SER	GLU	ALA	LYS	ASN	SER	ASN	LEU	ALA	PRO	PHE	ARG	LEU	LEU	VAL	LYS	LEU	THR	ASN	GLY	VAL	VAL	GLY	ASP	GLU	GLU	PHE	PRO	TYR	TYR	GLY	ASN	ASN	LEU	ILE	VAL	LEU	GLY	PHE	GLY	ARG	THR	ILE	GLU	THR	GLU	LEU	GLU	PHE	PRO	GLU	ASN	ILE	ILE	PRO	VAL	THR	STD
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 2: Protein MxiG



F364 F365 F366 L367 ASP LYS ASN ASN LYS	VAL	GLU	ALA	MET	SER	MET
	THR	ASN	VAL	TYR	LYS	TYR
	TRP	ARG	TRP	LYS	SER	GLY
	SER	ASN	SER	ASN	ASP	ALA
	SER	SER	SER	HIS	GLY	ASN
	LYS	LYS	VAL	SER	ILE	ASN
	ASP	ASP	ALA	VAL	ILE	SER
	GLU	THR	LEU	PHE	TYR	ASN
	GLU	GLU	ASN	PHE	LEU	LEU
	THR	LEU	ASN	PHE	THR	ALA
ASP	ASP	THR	PHE	ILE	ALA	
GLU	LYS	THR	ALA	SER	PRO	
LYS	LEU	PHE	VAL	LYS	ARG	
LEU	LYS	THR	ILE	ASP	LEU	
GLU	ASN	LYS	VAL	ASN	LEU	
LEU	ALA	CYS	VAL	ILE	VAL	
ILE	LEU	ARG	LYS	CYS	VAL	
ASN	ILE	THR	ILE	GLN	LEU	
ARG	VAL	ILE	ILE	PHE	THR	
LEU	GLU	LEU	ILE	SER	ASN	
ILE	PRO	VAL	ILE	ASP	GLY	
SER	PRO	SER	SER	GLU	VAL	
GLU	TYR	ASN	LYS	LYS	GLY	
HIS	ILE	ASN	SER	GLY	ASP	
LYS	LYS	GLU	LEU	GLU	PHE	
ASN	ASN	ILE	LYS	GLN	THR	
ILE	ILE	ASN	LYS	ILE	PRO	
THR	LYS	ARG	ASP	ASP	LEU	
GLY	PHE	ILE	GLU	SER	LEU	
ASN	ASN	ARG	ILE	PHE	ILE	
GLN	TYR	GLN	VAL	ASN	VAL	
TYR	LEU	TYR	ILE	GLN	GLY	
ILE	SER	ILE	ILE	PHE	GLY	
ASP	ASP	ASN	ALA	ASN	THR	
HIS	HIS	GLN	GLU	SER	ILE	
VAL	VAL	ARG	ILE	LEU	THR	
L338	L338	ASP	ILE	GLY	ARG	
L339	L339	GLY	ILE	LYS	ILE	
I340	I340	ALA	ASN	ARG	THR	
D341	D341	LYS	LEU	TYR	GLU	
D342	D342	GLY	TYR	GLY	THR	
D343	D343	ILE	VAL	ILE	LEU	
F344	F344	PHE	LEU	VAL	GLU	
K345	K345	THR	ASN	LYS	PHE	
		LYS	LEU	ASN	GLY	
		VAL	VAL	THR	ASN	
L350	L350	ASN	GLN	MET	ASN	
N351	N351	ASN	SER	ARG	ASP	
S352	S352	VAL	CYS	GLU	ASP	
K353	K353	GLN	LYS	ASN	PHE	
D354	D354	TYR	ALA	TYR	PRO	
S355	S355	LYS	GLU	SER	GLU	
Y356	Y356	GLU	LEU	ARG	ASN	
Y357	Y357	ILE	LEU	GLY	ILE	
M358	M358	CYS	VAL	GLU	ILE	
L359	L359	GLU	PHE	THR	ILE	
N360	N360	ASN	LEU	GLN	VAL	
D361	D361	ASN	SER	ASN	THR	
K362	K362	LYS	LYS	ASP	ASP	

- Molecule 2: Protein MxiG

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C8	Depositor
Number of particles used	72298	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1.5	Depositor
Maximum defocus (nm)	4	Depositor
Magnification	101179	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.471	Depositor
Minimum map value	-0.240	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	664.1712, 664.1712, 664.1712	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38369, 1.38369, 1.38369	Depositor

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.33	0/1124	0.44	0/1525
1	1	0.33	0/1124	0.41	0/1525
1	2	0.33	0/1124	0.44	0/1525
1	3	0.33	0/1124	0.42	0/1525
1	4	0.33	0/1124	0.44	0/1525
1	5	0.33	0/1124	0.41	0/1525
1	6	0.33	0/1124	0.44	0/1525
1	7	0.33	0/1124	0.41	0/1525
1	8	0.33	0/1124	0.44	0/1525
1	9	0.33	0/1124	0.42	0/1525
1	X	0.33	0/1124	0.44	0/1525
1	Y	0.33	0/1124	0.44	0/1525
1	Z	0.33	0/1124	0.44	0/1525
1	x	0.33	0/1124	0.41	0/1525
1	y	0.33	0/1124	0.41	0/1525
1	z	0.33	0/1124	0.41	0/1525
2	A	0.30	0/265	0.52	0/355
2	B	0.30	0/265	0.40	0/355
2	D	0.30	0/265	0.53	0/355
2	E	0.29	0/265	0.40	0/355
2	G	0.30	0/265	0.53	0/355
2	H	0.30	0/265	0.40	0/355
2	J	0.30	0/265	0.53	0/355
2	K	0.30	0/265	0.40	0/355
2	M	0.30	0/265	0.53	0/355
2	N	0.30	0/265	0.40	0/355
2	P	0.30	0/265	0.52	0/355
2	Q	0.30	0/265	0.40	0/355
2	S	0.30	0/265	0.53	0/355
2	T	0.29	0/265	0.40	0/355
2	U	0.30	0/265	0.53	0/355
2	V	0.30	0/265	0.40	0/355
All	All	0.33	0/22224	0.44	0/30080

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	0	1102	0	1118	35	0
1	1	1102	0	1118	26	0
1	2	1102	0	1118	37	0
1	3	1102	0	1118	31	0
1	4	1102	0	1118	40	0
1	5	1102	0	1118	29	0
1	6	1102	0	1118	37	0
1	7	1102	0	1118	32	0
1	8	1102	0	1118	37	0
1	9	1102	0	1118	31	0
1	X	1102	0	1118	37	0
1	Y	1102	0	1118	37	0
1	Z	1102	0	1118	33	0
1	x	1102	0	1118	32	0
1	y	1102	0	1118	32	0
1	z	1102	0	1118	27	0
2	A	258	0	247	18	0
2	B	258	0	247	12	0
2	D	258	0	247	19	0
2	E	258	0	247	13	0
2	G	258	0	247	17	0
2	H	258	0	247	11	0
2	J	258	0	247	17	0
2	K	258	0	247	11	0
2	M	258	0	247	16	0
2	N	258	0	247	9	0
2	P	258	0	247	17	0
2	Q	258	0	247	12	0
2	S	258	0	247	16	0
2	T	258	0	247	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	U	258	0	247	17	0
2	V	258	0	247	12	0
All	All	21760	0	21840	656	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 15.

The worst 5 of 656 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:X:47:SER:OG	1:X:51:ARG:NH1	2.18	0.76
1:Y:47:SER:OG	1:Y:51:ARG:NH1	2.18	0.76
1:Z:47:SER:OG	1:Z:51:ARG:NH1	2.18	0.76
1:8:47:SER:OG	1:8:51:ARG:NH1	2.18	0.76
1:6:47:SER:OG	1:6:51:ARG:NH1	2.18	0.76

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	0	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	1	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	2	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	3	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	4	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	5	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	6	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	7	136/566 (24%)	121 (89%)	15 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	8	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	9	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	X	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	Y	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	Z	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	x	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	y	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
1	z	136/566 (24%)	121 (89%)	15 (11%)	0	100	100
2	A	28/371 (8%)	21 (75%)	7 (25%)	0	100	100
2	B	28/371 (8%)	25 (89%)	3 (11%)	0	100	100
2	D	28/371 (8%)	21 (75%)	7 (25%)	0	100	100
2	E	28/371 (8%)	25 (89%)	3 (11%)	0	100	100
2	G	28/371 (8%)	21 (75%)	7 (25%)	0	100	100
2	H	28/371 (8%)	25 (89%)	3 (11%)	0	100	100
2	J	28/371 (8%)	21 (75%)	7 (25%)	0	100	100
2	K	28/371 (8%)	25 (89%)	3 (11%)	0	100	100
2	M	28/371 (8%)	21 (75%)	7 (25%)	0	100	100
2	N	28/371 (8%)	25 (89%)	3 (11%)	0	100	100
2	P	28/371 (8%)	21 (75%)	7 (25%)	0	100	100
2	Q	28/371 (8%)	25 (89%)	3 (11%)	0	100	100
2	S	28/371 (8%)	21 (75%)	7 (25%)	0	100	100
2	T	28/371 (8%)	25 (89%)	3 (11%)	0	100	100
2	U	28/371 (8%)	21 (75%)	7 (25%)	0	100	100
2	V	28/371 (8%)	25 (89%)	3 (11%)	0	100	100
All	All	2624/14992 (18%)	2304 (88%)	320 (12%)	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	0	121/513 (24%)	116 (96%)	5 (4%)	27	51
1	1	121/513 (24%)	112 (93%)	9 (7%)	13	39
1	2	121/513 (24%)	116 (96%)	5 (4%)	27	51
1	3	121/513 (24%)	113 (93%)	8 (7%)	15	42
1	4	121/513 (24%)	116 (96%)	5 (4%)	27	51
1	5	121/513 (24%)	113 (93%)	8 (7%)	15	42
1	6	121/513 (24%)	116 (96%)	5 (4%)	27	51
1	7	121/513 (24%)	112 (93%)	9 (7%)	13	39
1	8	121/513 (24%)	116 (96%)	5 (4%)	27	51
1	9	121/513 (24%)	113 (93%)	8 (7%)	15	42
1	X	121/513 (24%)	115 (95%)	6 (5%)	22	47
1	Y	121/513 (24%)	116 (96%)	5 (4%)	27	51
1	Z	121/513 (24%)	116 (96%)	5 (4%)	27	51
1	x	121/513 (24%)	113 (93%)	8 (7%)	15	42
1	y	121/513 (24%)	112 (93%)	9 (7%)	13	39
1	z	121/513 (24%)	113 (93%)	8 (7%)	15	42
2	A	29/342 (8%)	26 (90%)	3 (10%)	7	26
2	B	29/342 (8%)	28 (97%)	1 (3%)	32	56
2	D	29/342 (8%)	26 (90%)	3 (10%)	7	26
2	E	29/342 (8%)	28 (97%)	1 (3%)	32	56
2	G	29/342 (8%)	26 (90%)	3 (10%)	7	26
2	H	29/342 (8%)	28 (97%)	1 (3%)	32	56
2	J	29/342 (8%)	26 (90%)	3 (10%)	7	26
2	K	29/342 (8%)	28 (97%)	1 (3%)	32	56
2	M	29/342 (8%)	26 (90%)	3 (10%)	7	26
2	N	29/342 (8%)	28 (97%)	1 (3%)	32	56
2	P	29/342 (8%)	26 (90%)	3 (10%)	7	26
2	Q	29/342 (8%)	28 (97%)	1 (3%)	32	56
2	S	29/342 (8%)	26 (90%)	3 (10%)	7	26
2	T	29/342 (8%)	28 (97%)	1 (3%)	32	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	U	29/342 (8%)	26 (90%)	3 (10%)	7	26
2	V	29/342 (8%)	28 (97%)	1 (3%)	32	56
All	All	2400/13680 (18%)	2260 (94%)	140 (6%)	20	45

5 of 140 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	359	LEU
2	J	360	ASN
2	U	359	LEU
1	x	171	LYS
1	x	165	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 52 such sidechains are listed below:

Mol	Chain	Res	Type
1	3	100	ASN
1	7	144	ASN
2	Q	351	ASN
1	3	144	ASN
1	5	144	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](#)

There are no ligands in this entry.

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.

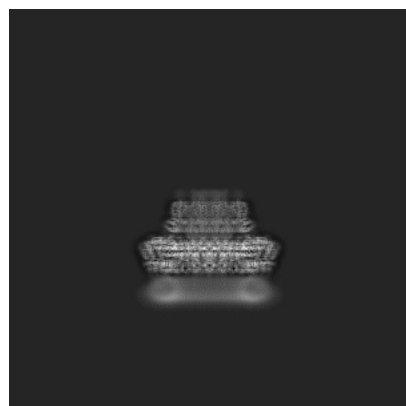
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10040. 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](#)

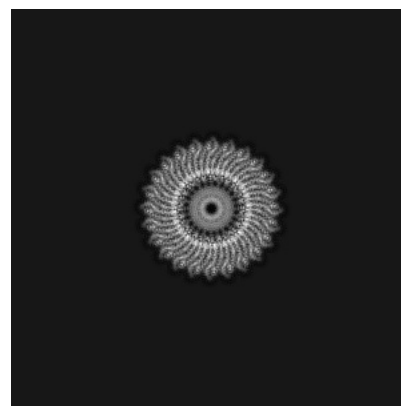
6.1.1 Primary map



X

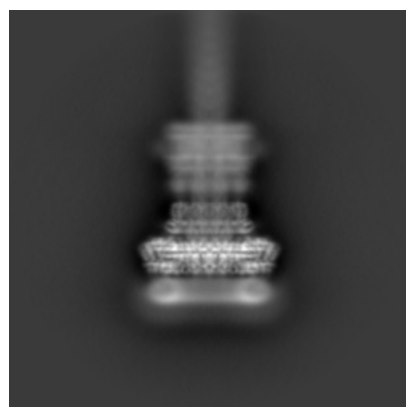


Y



Z

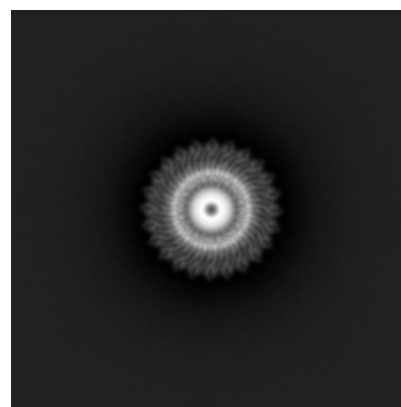
6.1.2 Raw map



X



Y



Z

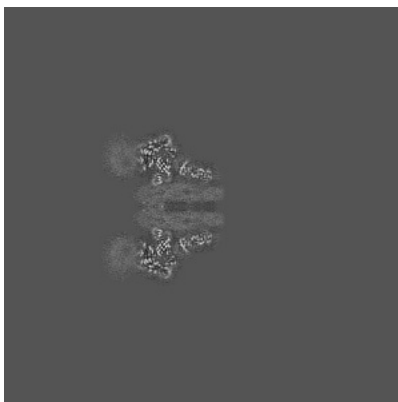
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

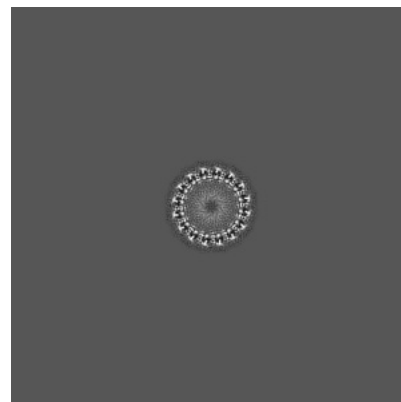
6.2.1 Primary map



X Index: 240

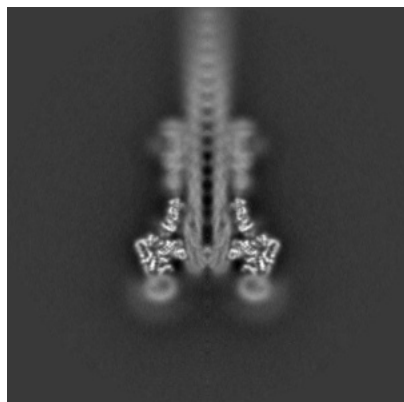


Y Index: 240

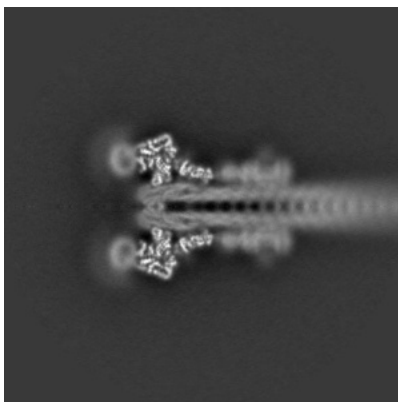


Z Index: 240

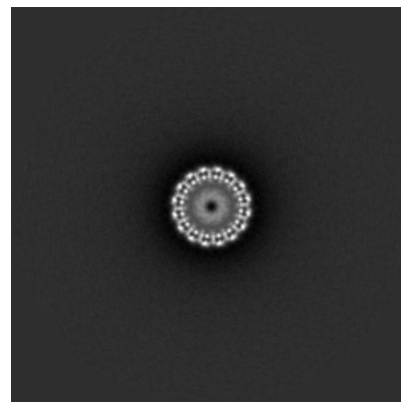
6.2.2 Raw map



X Index: 240



Y Index: 240



Z Index: 240

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

6.3 Largest variance slices [i](#)

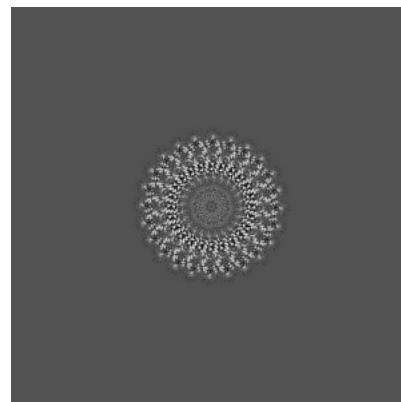
6.3.1 Primary map



X Index: 279

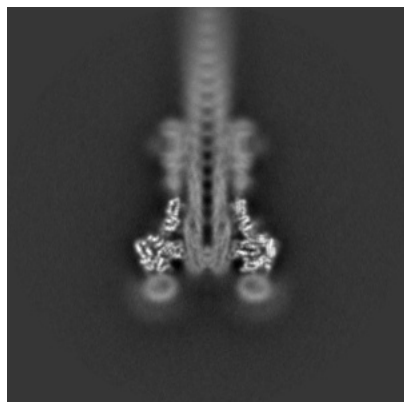


Y Index: 201

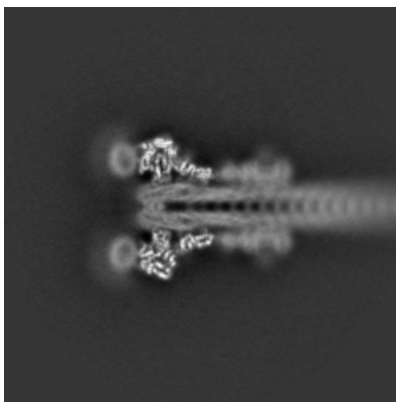


Z Index: 192

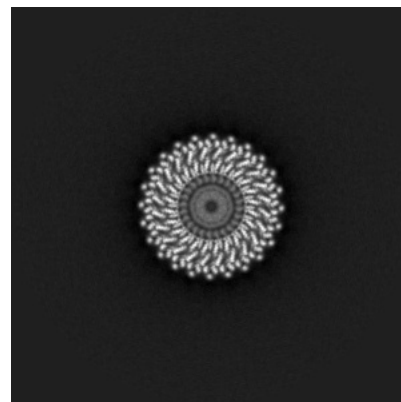
6.3.2 Raw map



X Index: 237



Y Index: 243

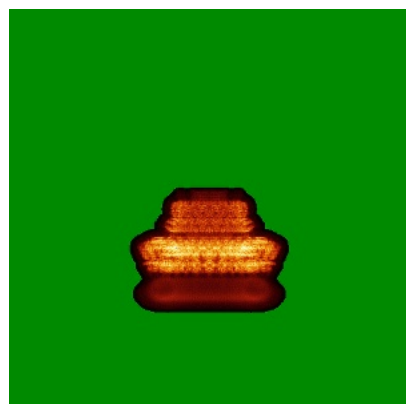


Z Index: 193

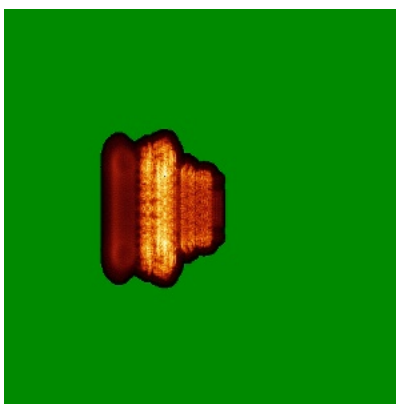
The images above show the largest variance slices of the map in three orthogonal directions.

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

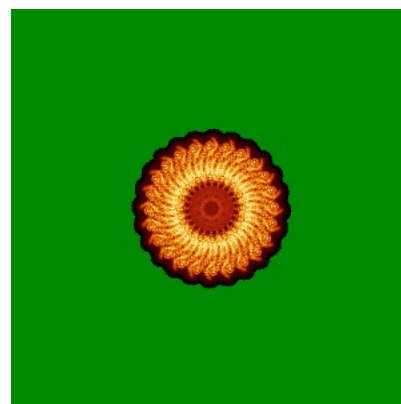
6.4.1 Primary map



X

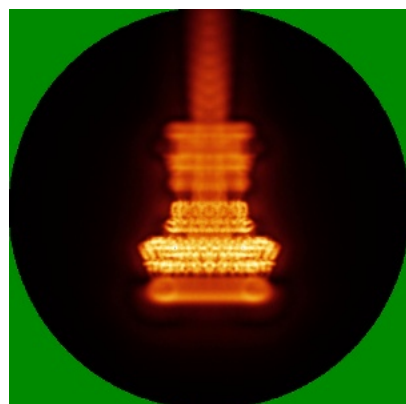


Y

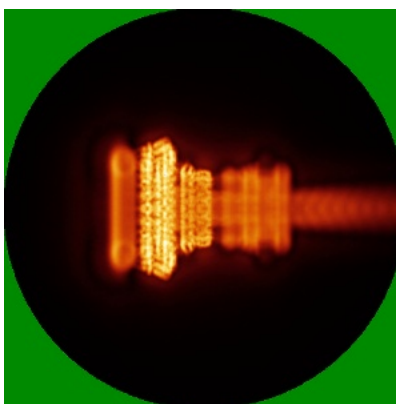


Z

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](#)

This section was not generated.

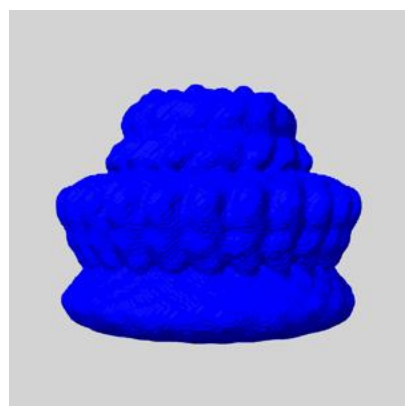
6.6 Mask visualisation [i](#)

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

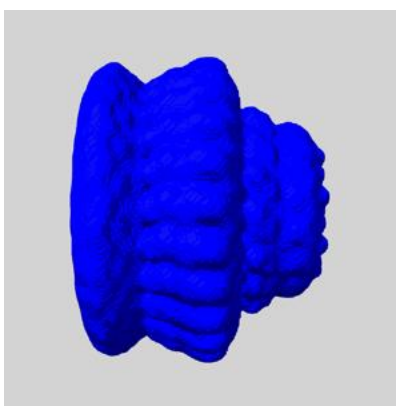
A mask typically either:

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

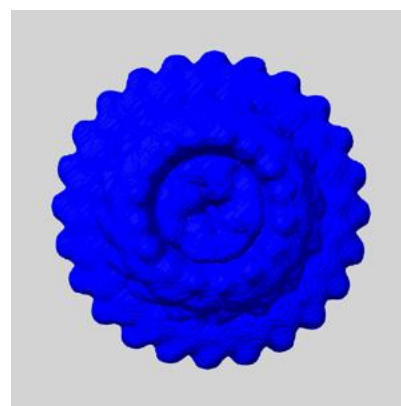
6.6.1 emd_10040_msk_1.map [i](#)



X



Y

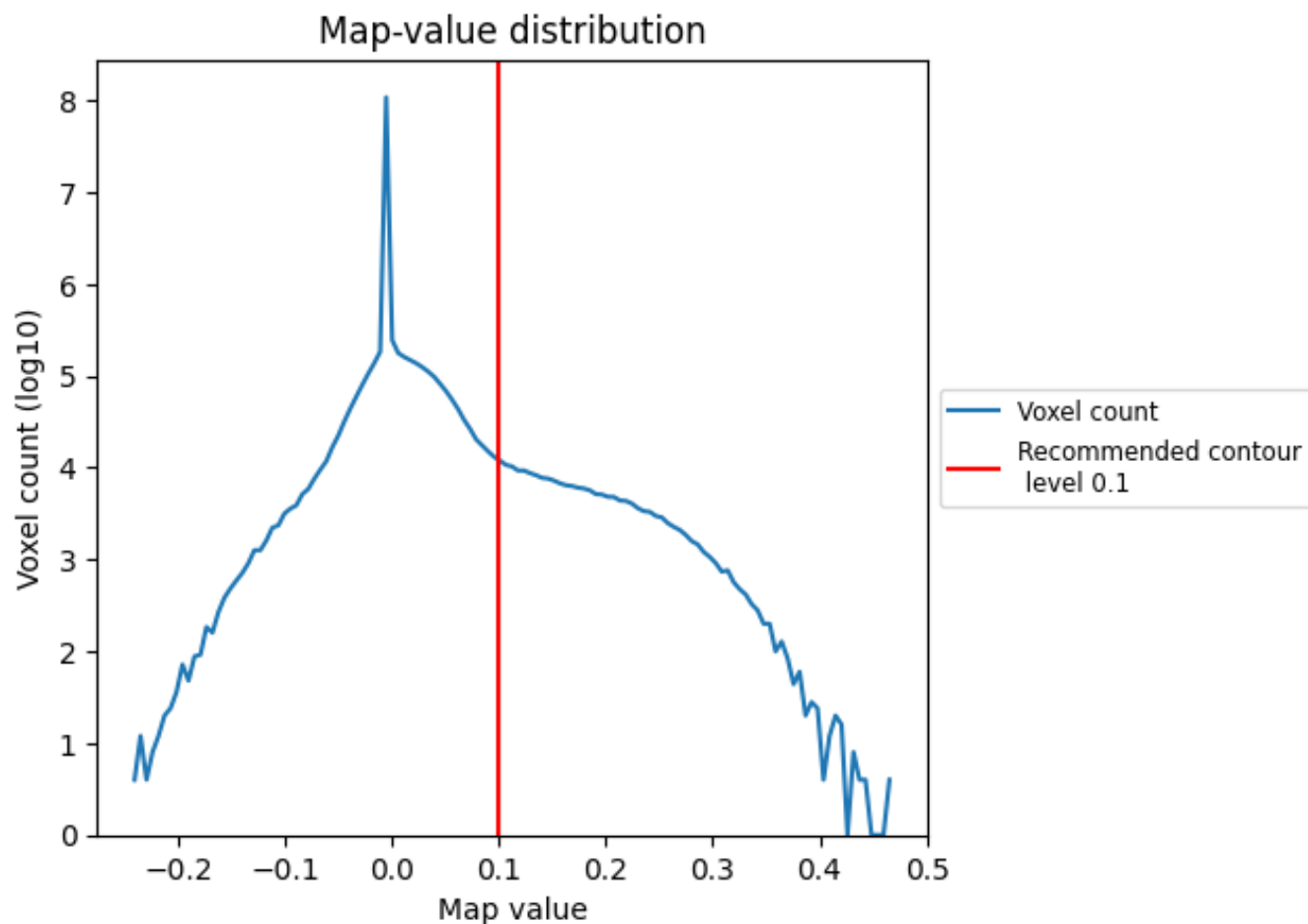


Z

7 Map analysis [i](#)

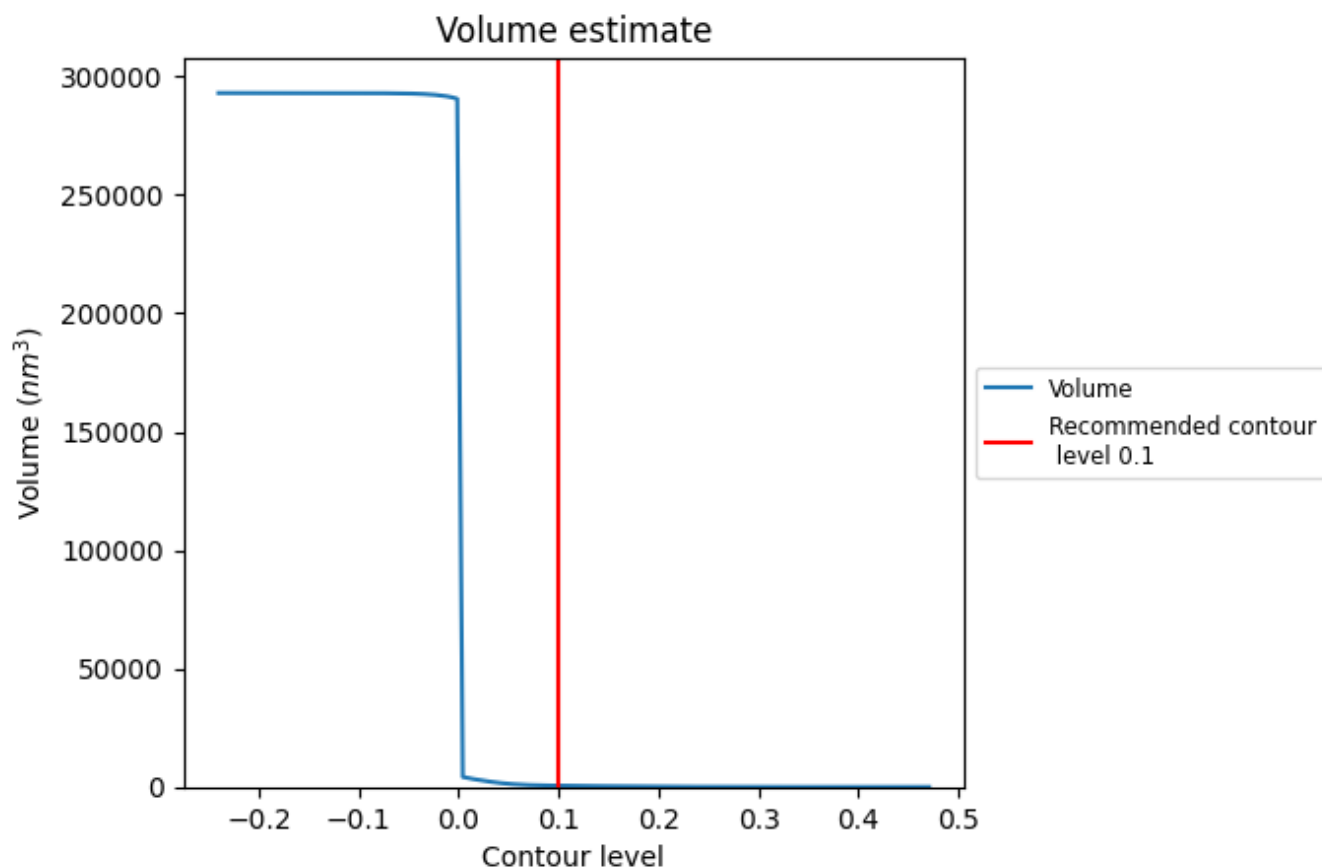
This section contains the results of statistical analysis of the map.

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.

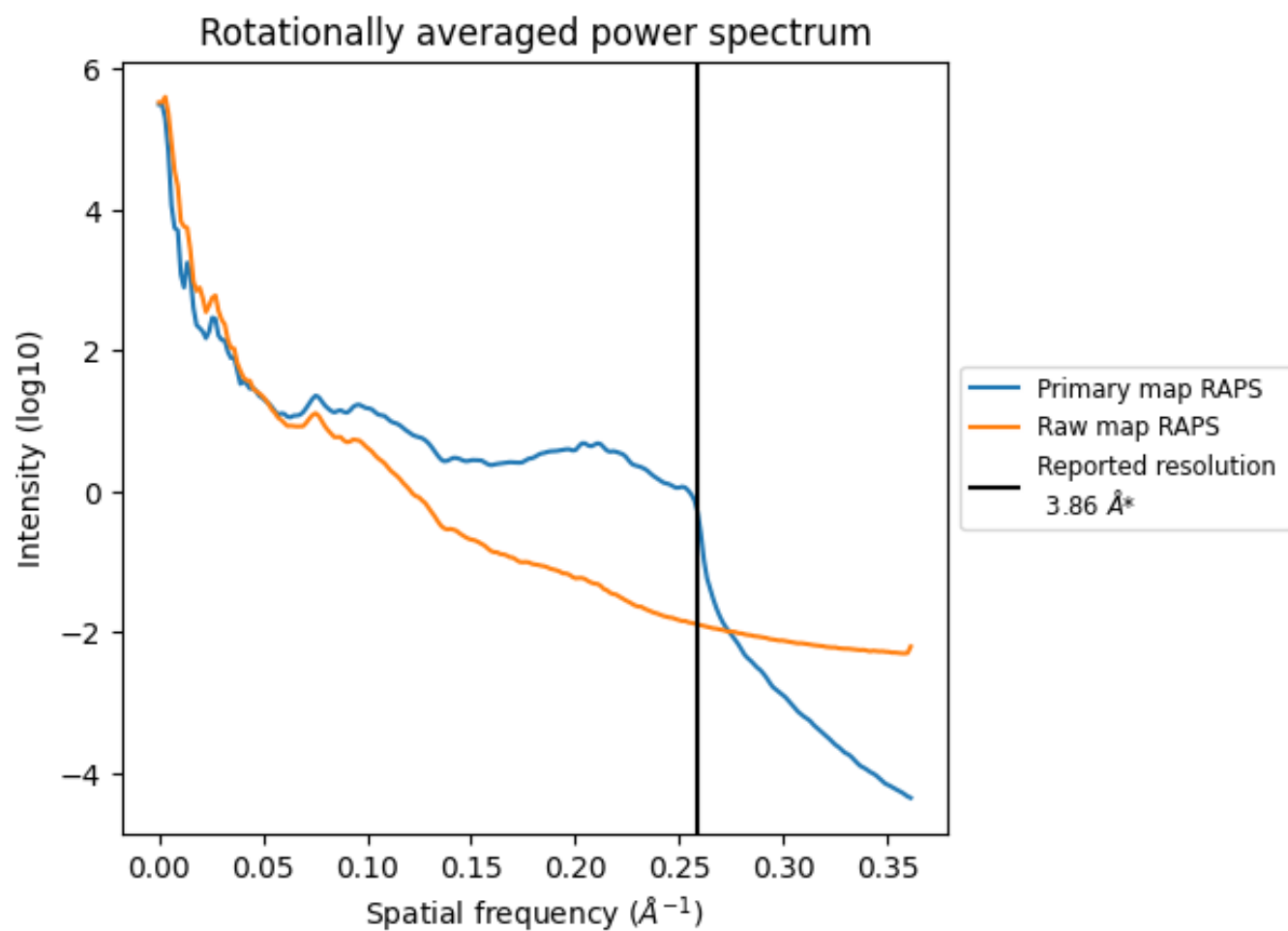
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 529 nm³; this corresponds to an approximate mass of 478 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 ⓘ

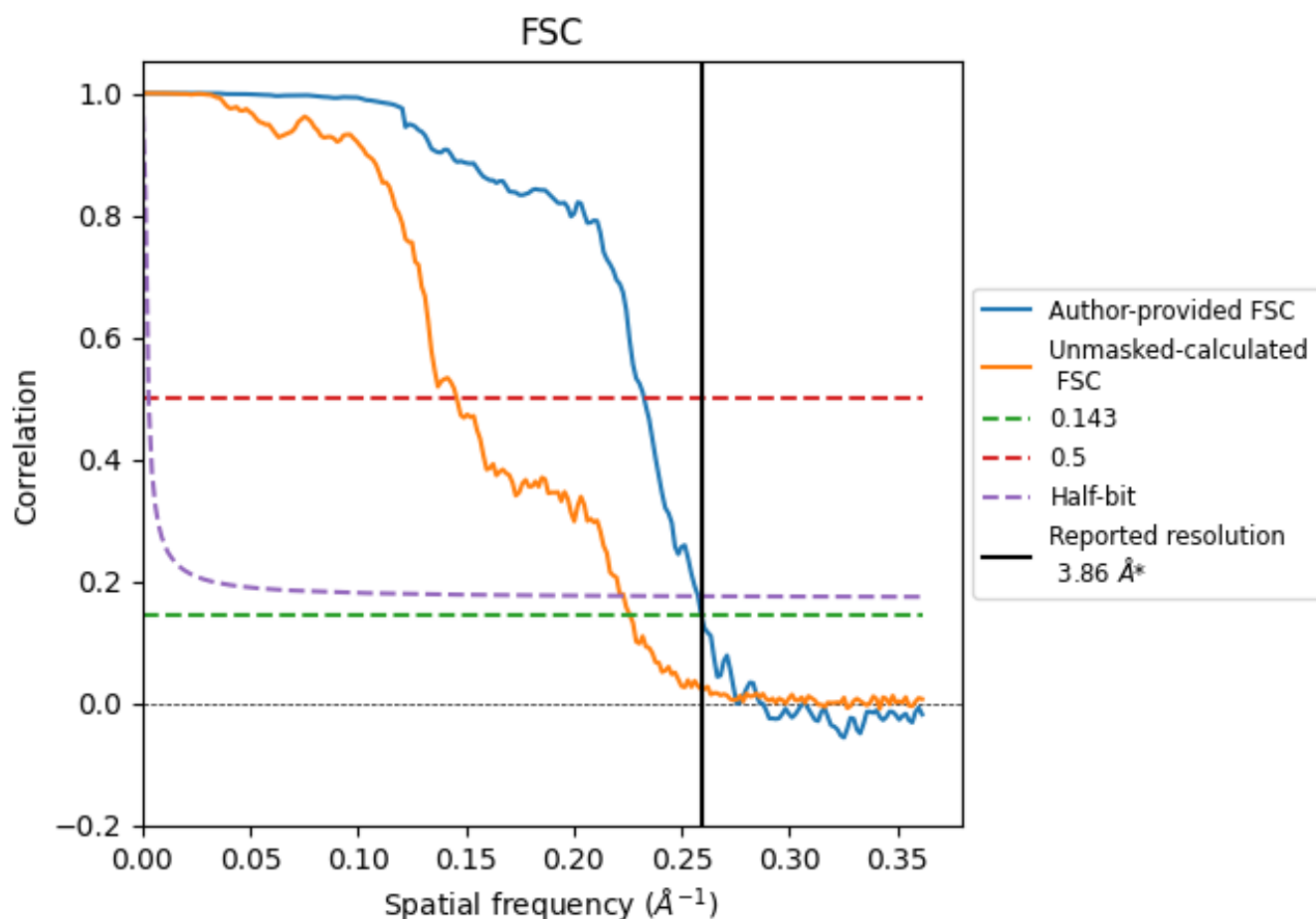


*Reported resolution corresponds to spatial frequency of 0.259 Å⁻¹

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 0.259 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.86	-	-
Author-provided FSC curve	3.86	4.30	3.88
Unmasked-calculated*	4.42	6.86	4.48

*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 4.42 differs from the reported value 3.86 by more than 10 %

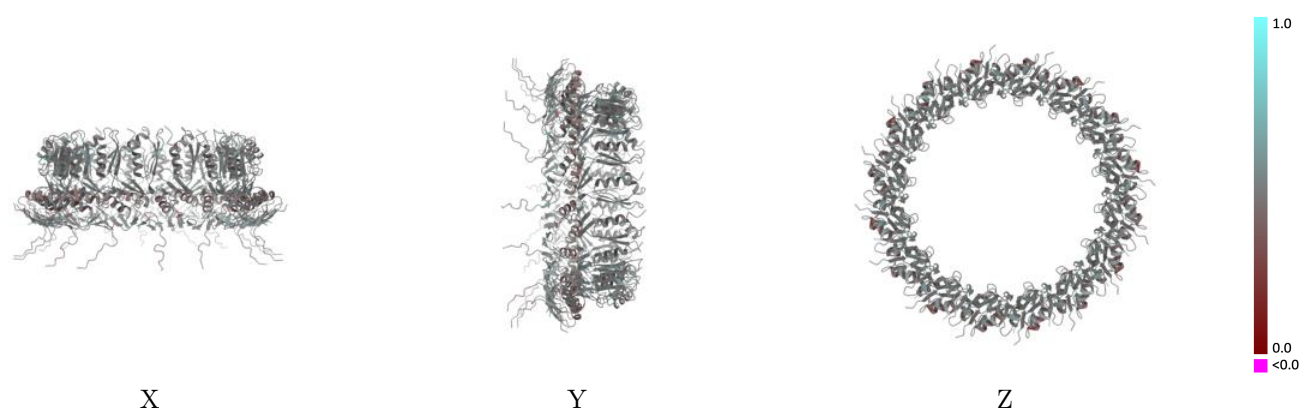
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10040 and PDB model 6RWK. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

This section was not generated.

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

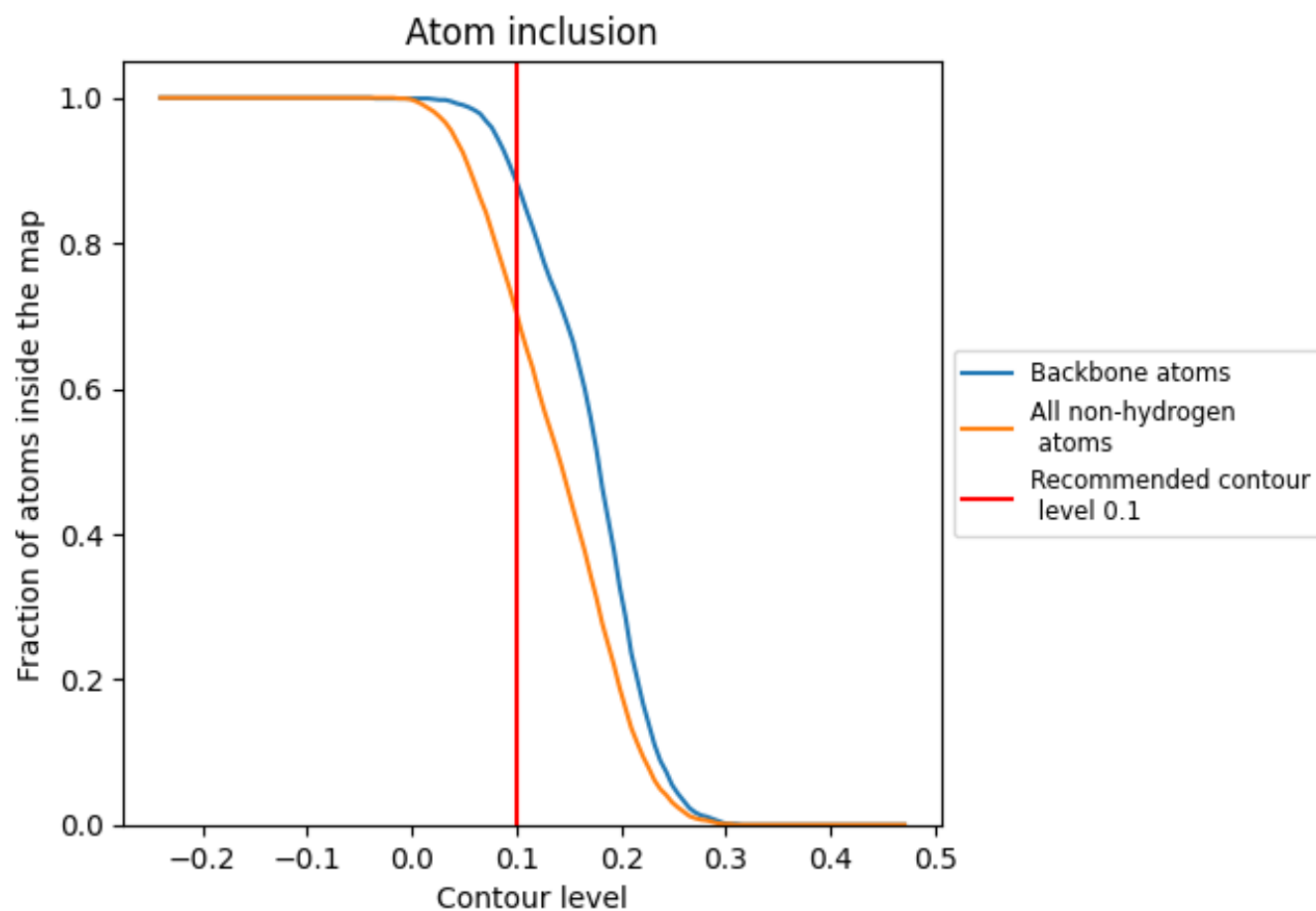


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 70% 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	 0.7040	 0.4820
0	 0.7060	 0.4780
1	 0.7300	 0.4860
2	 0.7110	 0.4790
3	 0.7160	 0.4840
4	 0.7050	 0.4790
5	 0.7290	 0.4880
6	 0.7100	 0.4810
7	 0.7140	 0.4850
8	 0.7050	 0.4820
9	 0.7300	 0.4870
A	 0.6550	 0.4750
B	 0.6630	 0.4890
D	 0.6550	 0.4780
E	 0.6510	 0.4830
G	 0.6470	 0.4750
H	 0.6670	 0.4890
J	 0.6350	 0.4750
K	 0.6550	 0.4860
M	 0.6590	 0.4750
N	 0.6590	 0.4900
P	 0.6550	 0.4720
Q	 0.6430	 0.4870
S	 0.6510	 0.4760
T	 0.6590	 0.4840
U	 0.6550	 0.4720
V	 0.6470	 0.4810
X	 0.7120	 0.4800
Y	 0.7080	 0.4800
Z	 0.7110	 0.4790
x	 0.7170	 0.4830
y	 0.7290	 0.4880
z	 0.7190	 0.4840

