



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:21 AM UTC

PDB ID : 6MKS / pdb_00006mks
EMDB ID : EMD-9137
Title : Cryo-EM structure of NLRC4-CARD filament
Authors : Zheng, W.; Matyszewski, M.; Sohn, J.; Egelman, E.H.
Deposited on : 2018-09-26
Resolution : 3.40 Å(reported)
Based on initial model : 4IKM

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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

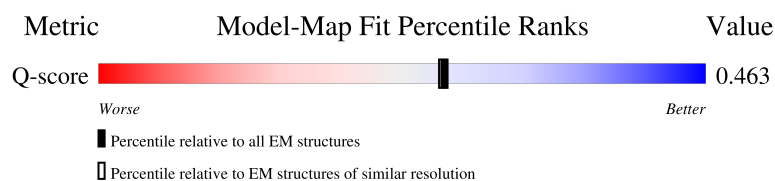
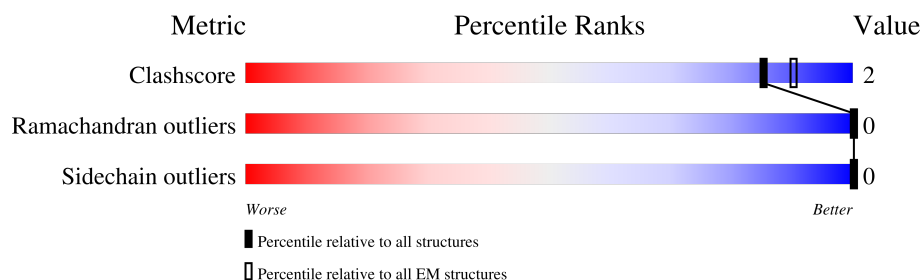
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

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	340	 25% 74%
1	B	340	 24% 74%
1	C	340	 25% 74%
1	D	340	 25% 74%

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Mol	Chain	Length	Quality of chain	
1	E	340		
1	F	340		
1	G	340		
1	H	340		
1	I	340		
1	J	340		
1	K	340		
1	L	340		
1	M	340		
1	N	340		
1	O	340		
1	P	340		
1	Q	340		
1	R	340		
1	S	340		
1	T	340		
1	U	340		
1	V	340		
1	W	340		
1	X	340		
1	Y	340		
1	Z	340		
1	a	340		
1	b	340		
1	c	340		

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Mol	Chain	Length	Quality of chain
1	d	340	25%74%
1	e	340	7%26%74%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 22754 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 Chimera protein of NLR family CARD domain-containing protein 4 and EGFP.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	B	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	C	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	D	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	E	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	F	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	G	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	H	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	I	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	J	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	K	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	L	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	M	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	N	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	O	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	P	90	Total	C	N	O	S	0	0
			734	468	126	133	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Q	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	R	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	S	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	T	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	U	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	V	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	W	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	X	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	Y	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	Z	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	a	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	b	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	c	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	d	90	Total	C	N	O	S	0	0
			734	468	126	133	7		
1	e	90	Total	C	N	O	S	0	0
			734	468	126	133	7		

There are 372 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q9NPP4
A	-1	THR	-	expression tag	UNP Q9NPP4
A	0	GLY	-	expression tag	UNP Q9NPP4
A	97	LYS	-	linker	UNP Q9NPP4
A	98	LEU	-	linker	UNP Q9NPP4
A	331	GLU	-	expression tag	UNP A0A1V0D974
A	332	HIS	-	expression tag	UNP A0A1V0D974
A	333	HIS	-	expression tag	UNP A0A1V0D974
A	334	HIS	-	expression tag	UNP A0A1V0D974

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Chain	Residue	Modelled	Actual	Comment	Reference
A	335	HIS	-	expression tag	UNP A0A1V0D974
A	336	HIS	-	expression tag	UNP A0A1V0D974
A	337	HIS	-	expression tag	UNP A0A1V0D974
B	-2	GLY	-	expression tag	UNP Q9NPP4
B	-1	THR	-	expression tag	UNP Q9NPP4
B	0	GLY	-	expression tag	UNP Q9NPP4
B	97	LYS	-	linker	UNP Q9NPP4
B	98	LEU	-	linker	UNP Q9NPP4
B	331	GLU	-	expression tag	UNP A0A1V0D974
B	332	HIS	-	expression tag	UNP A0A1V0D974
B	333	HIS	-	expression tag	UNP A0A1V0D974
B	334	HIS	-	expression tag	UNP A0A1V0D974
B	335	HIS	-	expression tag	UNP A0A1V0D974
B	336	HIS	-	expression tag	UNP A0A1V0D974
B	337	HIS	-	expression tag	UNP A0A1V0D974
C	-2	GLY	-	expression tag	UNP Q9NPP4
C	-1	THR	-	expression tag	UNP Q9NPP4
C	0	GLY	-	expression tag	UNP Q9NPP4
C	97	LYS	-	linker	UNP Q9NPP4
C	98	LEU	-	linker	UNP Q9NPP4
C	331	GLU	-	expression tag	UNP A0A1V0D974
C	332	HIS	-	expression tag	UNP A0A1V0D974
C	333	HIS	-	expression tag	UNP A0A1V0D974
C	334	HIS	-	expression tag	UNP A0A1V0D974
C	335	HIS	-	expression tag	UNP A0A1V0D974
C	336	HIS	-	expression tag	UNP A0A1V0D974
C	337	HIS	-	expression tag	UNP A0A1V0D974
D	-2	GLY	-	expression tag	UNP Q9NPP4
D	-1	THR	-	expression tag	UNP Q9NPP4
D	0	GLY	-	expression tag	UNP Q9NPP4
D	97	LYS	-	linker	UNP Q9NPP4
D	98	LEU	-	linker	UNP Q9NPP4
D	331	GLU	-	expression tag	UNP A0A1V0D974
D	332	HIS	-	expression tag	UNP A0A1V0D974
D	333	HIS	-	expression tag	UNP A0A1V0D974
D	334	HIS	-	expression tag	UNP A0A1V0D974
D	335	HIS	-	expression tag	UNP A0A1V0D974
D	336	HIS	-	expression tag	UNP A0A1V0D974
D	337	HIS	-	expression tag	UNP A0A1V0D974
E	-2	GLY	-	expression tag	UNP Q9NPP4
E	-1	THR	-	expression tag	UNP Q9NPP4
E	0	GLY	-	expression tag	UNP Q9NPP4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	97	LYS	-	linker	UNP Q9NPP4
E	98	LEU	-	linker	UNP Q9NPP4
E	331	GLU	-	expression tag	UNP A0A1V0D974
E	332	HIS	-	expression tag	UNP A0A1V0D974
E	333	HIS	-	expression tag	UNP A0A1V0D974
E	334	HIS	-	expression tag	UNP A0A1V0D974
E	335	HIS	-	expression tag	UNP A0A1V0D974
E	336	HIS	-	expression tag	UNP A0A1V0D974
E	337	HIS	-	expression tag	UNP A0A1V0D974
F	-2	GLY	-	expression tag	UNP Q9NPP4
F	-1	THR	-	expression tag	UNP Q9NPP4
F	0	GLY	-	expression tag	UNP Q9NPP4
F	97	LYS	-	linker	UNP Q9NPP4
F	98	LEU	-	linker	UNP Q9NPP4
F	331	GLU	-	expression tag	UNP A0A1V0D974
F	332	HIS	-	expression tag	UNP A0A1V0D974
F	333	HIS	-	expression tag	UNP A0A1V0D974
F	334	HIS	-	expression tag	UNP A0A1V0D974
F	335	HIS	-	expression tag	UNP A0A1V0D974
F	336	HIS	-	expression tag	UNP A0A1V0D974
F	337	HIS	-	expression tag	UNP A0A1V0D974
G	-2	GLY	-	expression tag	UNP Q9NPP4
G	-1	THR	-	expression tag	UNP Q9NPP4
G	0	GLY	-	expression tag	UNP Q9NPP4
G	97	LYS	-	linker	UNP Q9NPP4
G	98	LEU	-	linker	UNP Q9NPP4
G	331	GLU	-	expression tag	UNP A0A1V0D974
G	332	HIS	-	expression tag	UNP A0A1V0D974
G	333	HIS	-	expression tag	UNP A0A1V0D974
G	334	HIS	-	expression tag	UNP A0A1V0D974
G	335	HIS	-	expression tag	UNP A0A1V0D974
G	336	HIS	-	expression tag	UNP A0A1V0D974
G	337	HIS	-	expression tag	UNP A0A1V0D974
H	-2	GLY	-	expression tag	UNP Q9NPP4
H	-1	THR	-	expression tag	UNP Q9NPP4
H	0	GLY	-	expression tag	UNP Q9NPP4
H	97	LYS	-	linker	UNP Q9NPP4
H	98	LEU	-	linker	UNP Q9NPP4
H	331	GLU	-	expression tag	UNP A0A1V0D974
H	332	HIS	-	expression tag	UNP A0A1V0D974
H	333	HIS	-	expression tag	UNP A0A1V0D974
H	334	HIS	-	expression tag	UNP A0A1V0D974

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Chain	Residue	Modelled	Actual	Comment	Reference
H	335	HIS	-	expression tag	UNP A0A1V0D974
H	336	HIS	-	expression tag	UNP A0A1V0D974
H	337	HIS	-	expression tag	UNP A0A1V0D974
I	-2	GLY	-	expression tag	UNP Q9NPP4
I	-1	THR	-	expression tag	UNP Q9NPP4
I	0	GLY	-	expression tag	UNP Q9NPP4
I	97	LYS	-	linker	UNP Q9NPP4
I	98	LEU	-	linker	UNP Q9NPP4
I	331	GLU	-	expression tag	UNP A0A1V0D974
I	332	HIS	-	expression tag	UNP A0A1V0D974
I	333	HIS	-	expression tag	UNP A0A1V0D974
I	334	HIS	-	expression tag	UNP A0A1V0D974
I	335	HIS	-	expression tag	UNP A0A1V0D974
I	336	HIS	-	expression tag	UNP A0A1V0D974
I	337	HIS	-	expression tag	UNP A0A1V0D974
J	-2	GLY	-	expression tag	UNP Q9NPP4
J	-1	THR	-	expression tag	UNP Q9NPP4
J	0	GLY	-	expression tag	UNP Q9NPP4
J	97	LYS	-	linker	UNP Q9NPP4
J	98	LEU	-	linker	UNP Q9NPP4
J	331	GLU	-	expression tag	UNP A0A1V0D974
J	332	HIS	-	expression tag	UNP A0A1V0D974
J	333	HIS	-	expression tag	UNP A0A1V0D974
J	334	HIS	-	expression tag	UNP A0A1V0D974
J	335	HIS	-	expression tag	UNP A0A1V0D974
J	336	HIS	-	expression tag	UNP A0A1V0D974
J	337	HIS	-	expression tag	UNP A0A1V0D974
K	-2	GLY	-	expression tag	UNP Q9NPP4
K	-1	THR	-	expression tag	UNP Q9NPP4
K	0	GLY	-	expression tag	UNP Q9NPP4
K	97	LYS	-	linker	UNP Q9NPP4
K	98	LEU	-	linker	UNP Q9NPP4
K	331	GLU	-	expression tag	UNP A0A1V0D974
K	332	HIS	-	expression tag	UNP A0A1V0D974
K	333	HIS	-	expression tag	UNP A0A1V0D974
K	334	HIS	-	expression tag	UNP A0A1V0D974
K	335	HIS	-	expression tag	UNP A0A1V0D974
K	336	HIS	-	expression tag	UNP A0A1V0D974
K	337	HIS	-	expression tag	UNP A0A1V0D974
L	-2	GLY	-	expression tag	UNP Q9NPP4
L	-1	THR	-	expression tag	UNP Q9NPP4
L	0	GLY	-	expression tag	UNP Q9NPP4

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Chain	Residue	Modelled	Actual	Comment	Reference
L	97	LYS	-	linker	UNP Q9NPP4
L	98	LEU	-	linker	UNP Q9NPP4
L	331	GLU	-	expression tag	UNP A0A1V0D974
L	332	HIS	-	expression tag	UNP A0A1V0D974
L	333	HIS	-	expression tag	UNP A0A1V0D974
L	334	HIS	-	expression tag	UNP A0A1V0D974
L	335	HIS	-	expression tag	UNP A0A1V0D974
L	336	HIS	-	expression tag	UNP A0A1V0D974
L	337	HIS	-	expression tag	UNP A0A1V0D974
M	-2	GLY	-	expression tag	UNP Q9NPP4
M	-1	THR	-	expression tag	UNP Q9NPP4
M	0	GLY	-	expression tag	UNP Q9NPP4
M	97	LYS	-	linker	UNP Q9NPP4
M	98	LEU	-	linker	UNP Q9NPP4
M	331	GLU	-	expression tag	UNP A0A1V0D974
M	332	HIS	-	expression tag	UNP A0A1V0D974
M	333	HIS	-	expression tag	UNP A0A1V0D974
M	334	HIS	-	expression tag	UNP A0A1V0D974
M	335	HIS	-	expression tag	UNP A0A1V0D974
M	336	HIS	-	expression tag	UNP A0A1V0D974
M	337	HIS	-	expression tag	UNP A0A1V0D974
N	-2	GLY	-	expression tag	UNP Q9NPP4
N	-1	THR	-	expression tag	UNP Q9NPP4
N	0	GLY	-	expression tag	UNP Q9NPP4
N	97	LYS	-	linker	UNP Q9NPP4
N	98	LEU	-	linker	UNP Q9NPP4
N	331	GLU	-	expression tag	UNP A0A1V0D974
N	332	HIS	-	expression tag	UNP A0A1V0D974
N	333	HIS	-	expression tag	UNP A0A1V0D974
N	334	HIS	-	expression tag	UNP A0A1V0D974
N	335	HIS	-	expression tag	UNP A0A1V0D974
N	336	HIS	-	expression tag	UNP A0A1V0D974
N	337	HIS	-	expression tag	UNP A0A1V0D974
O	-2	GLY	-	expression tag	UNP Q9NPP4
O	-1	THR	-	expression tag	UNP Q9NPP4
O	0	GLY	-	expression tag	UNP Q9NPP4
O	97	LYS	-	linker	UNP Q9NPP4
O	98	LEU	-	linker	UNP Q9NPP4
O	331	GLU	-	expression tag	UNP A0A1V0D974
O	332	HIS	-	expression tag	UNP A0A1V0D974
O	333	HIS	-	expression tag	UNP A0A1V0D974
O	334	HIS	-	expression tag	UNP A0A1V0D974

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Chain	Residue	Modelled	Actual	Comment	Reference
O	335	HIS	-	expression tag	UNP A0A1V0D974
O	336	HIS	-	expression tag	UNP A0A1V0D974
O	337	HIS	-	expression tag	UNP A0A1V0D974
P	-2	GLY	-	expression tag	UNP Q9NPP4
P	-1	THR	-	expression tag	UNP Q9NPP4
P	0	GLY	-	expression tag	UNP Q9NPP4
P	97	LYS	-	linker	UNP Q9NPP4
P	98	LEU	-	linker	UNP Q9NPP4
P	331	GLU	-	expression tag	UNP A0A1V0D974
P	332	HIS	-	expression tag	UNP A0A1V0D974
P	333	HIS	-	expression tag	UNP A0A1V0D974
P	334	HIS	-	expression tag	UNP A0A1V0D974
P	335	HIS	-	expression tag	UNP A0A1V0D974
P	336	HIS	-	expression tag	UNP A0A1V0D974
P	337	HIS	-	expression tag	UNP A0A1V0D974
Q	-2	GLY	-	expression tag	UNP Q9NPP4
Q	-1	THR	-	expression tag	UNP Q9NPP4
Q	0	GLY	-	expression tag	UNP Q9NPP4
Q	97	LYS	-	linker	UNP Q9NPP4
Q	98	LEU	-	linker	UNP Q9NPP4
Q	331	GLU	-	expression tag	UNP A0A1V0D974
Q	332	HIS	-	expression tag	UNP A0A1V0D974
Q	333	HIS	-	expression tag	UNP A0A1V0D974
Q	334	HIS	-	expression tag	UNP A0A1V0D974
Q	335	HIS	-	expression tag	UNP A0A1V0D974
Q	336	HIS	-	expression tag	UNP A0A1V0D974
Q	337	HIS	-	expression tag	UNP A0A1V0D974
R	-2	GLY	-	expression tag	UNP Q9NPP4
R	-1	THR	-	expression tag	UNP Q9NPP4
R	0	GLY	-	expression tag	UNP Q9NPP4
R	97	LYS	-	linker	UNP Q9NPP4
R	98	LEU	-	linker	UNP Q9NPP4
R	331	GLU	-	expression tag	UNP A0A1V0D974
R	332	HIS	-	expression tag	UNP A0A1V0D974
R	333	HIS	-	expression tag	UNP A0A1V0D974
R	334	HIS	-	expression tag	UNP A0A1V0D974
R	335	HIS	-	expression tag	UNP A0A1V0D974
R	336	HIS	-	expression tag	UNP A0A1V0D974
R	337	HIS	-	expression tag	UNP A0A1V0D974
S	-2	GLY	-	expression tag	UNP Q9NPP4
S	-1	THR	-	expression tag	UNP Q9NPP4
S	0	GLY	-	expression tag	UNP Q9NPP4

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Chain	Residue	Modelled	Actual	Comment	Reference
S	97	LYS	-	linker	UNP Q9NPP4
S	98	LEU	-	linker	UNP Q9NPP4
S	331	GLU	-	expression tag	UNP A0A1V0D974
S	332	HIS	-	expression tag	UNP A0A1V0D974
S	333	HIS	-	expression tag	UNP A0A1V0D974
S	334	HIS	-	expression tag	UNP A0A1V0D974
S	335	HIS	-	expression tag	UNP A0A1V0D974
S	336	HIS	-	expression tag	UNP A0A1V0D974
S	337	HIS	-	expression tag	UNP A0A1V0D974
T	-2	GLY	-	expression tag	UNP Q9NPP4
T	-1	THR	-	expression tag	UNP Q9NPP4
T	0	GLY	-	expression tag	UNP Q9NPP4
T	97	LYS	-	linker	UNP Q9NPP4
T	98	LEU	-	linker	UNP Q9NPP4
T	331	GLU	-	expression tag	UNP A0A1V0D974
T	332	HIS	-	expression tag	UNP A0A1V0D974
T	333	HIS	-	expression tag	UNP A0A1V0D974
T	334	HIS	-	expression tag	UNP A0A1V0D974
T	335	HIS	-	expression tag	UNP A0A1V0D974
T	336	HIS	-	expression tag	UNP A0A1V0D974
T	337	HIS	-	expression tag	UNP A0A1V0D974
U	-2	GLY	-	expression tag	UNP Q9NPP4
U	-1	THR	-	expression tag	UNP Q9NPP4
U	0	GLY	-	expression tag	UNP Q9NPP4
U	97	LYS	-	linker	UNP Q9NPP4
U	98	LEU	-	linker	UNP Q9NPP4
U	331	GLU	-	expression tag	UNP A0A1V0D974
U	332	HIS	-	expression tag	UNP A0A1V0D974
U	333	HIS	-	expression tag	UNP A0A1V0D974
U	334	HIS	-	expression tag	UNP A0A1V0D974
U	335	HIS	-	expression tag	UNP A0A1V0D974
U	336	HIS	-	expression tag	UNP A0A1V0D974
U	337	HIS	-	expression tag	UNP A0A1V0D974
V	-2	GLY	-	expression tag	UNP Q9NPP4
V	-1	THR	-	expression tag	UNP Q9NPP4
V	0	GLY	-	expression tag	UNP Q9NPP4
V	97	LYS	-	linker	UNP Q9NPP4
V	98	LEU	-	linker	UNP Q9NPP4
V	331	GLU	-	expression tag	UNP A0A1V0D974
V	332	HIS	-	expression tag	UNP A0A1V0D974
V	333	HIS	-	expression tag	UNP A0A1V0D974
V	334	HIS	-	expression tag	UNP A0A1V0D974

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Chain	Residue	Modelled	Actual	Comment	Reference
V	335	HIS	-	expression tag	UNP A0A1V0D974
V	336	HIS	-	expression tag	UNP A0A1V0D974
V	337	HIS	-	expression tag	UNP A0A1V0D974
W	-2	GLY	-	expression tag	UNP Q9NPP4
W	-1	THR	-	expression tag	UNP Q9NPP4
W	0	GLY	-	expression tag	UNP Q9NPP4
W	97	LYS	-	linker	UNP Q9NPP4
W	98	LEU	-	linker	UNP Q9NPP4
W	331	GLU	-	expression tag	UNP A0A1V0D974
W	332	HIS	-	expression tag	UNP A0A1V0D974
W	333	HIS	-	expression tag	UNP A0A1V0D974
W	334	HIS	-	expression tag	UNP A0A1V0D974
W	335	HIS	-	expression tag	UNP A0A1V0D974
W	336	HIS	-	expression tag	UNP A0A1V0D974
W	337	HIS	-	expression tag	UNP A0A1V0D974
X	-2	GLY	-	expression tag	UNP Q9NPP4
X	-1	THR	-	expression tag	UNP Q9NPP4
X	0	GLY	-	expression tag	UNP Q9NPP4
X	97	LYS	-	linker	UNP Q9NPP4
X	98	LEU	-	linker	UNP Q9NPP4
X	331	GLU	-	expression tag	UNP A0A1V0D974
X	332	HIS	-	expression tag	UNP A0A1V0D974
X	333	HIS	-	expression tag	UNP A0A1V0D974
X	334	HIS	-	expression tag	UNP A0A1V0D974
X	335	HIS	-	expression tag	UNP A0A1V0D974
X	336	HIS	-	expression tag	UNP A0A1V0D974
X	337	HIS	-	expression tag	UNP A0A1V0D974
Y	-2	GLY	-	expression tag	UNP Q9NPP4
Y	-1	THR	-	expression tag	UNP Q9NPP4
Y	0	GLY	-	expression tag	UNP Q9NPP4
Y	97	LYS	-	linker	UNP Q9NPP4
Y	98	LEU	-	linker	UNP Q9NPP4
Y	331	GLU	-	expression tag	UNP A0A1V0D974
Y	332	HIS	-	expression tag	UNP A0A1V0D974
Y	333	HIS	-	expression tag	UNP A0A1V0D974
Y	334	HIS	-	expression tag	UNP A0A1V0D974
Y	335	HIS	-	expression tag	UNP A0A1V0D974
Y	336	HIS	-	expression tag	UNP A0A1V0D974
Y	337	HIS	-	expression tag	UNP A0A1V0D974
Z	-2	GLY	-	expression tag	UNP Q9NPP4
Z	-1	THR	-	expression tag	UNP Q9NPP4
Z	0	GLY	-	expression tag	UNP Q9NPP4

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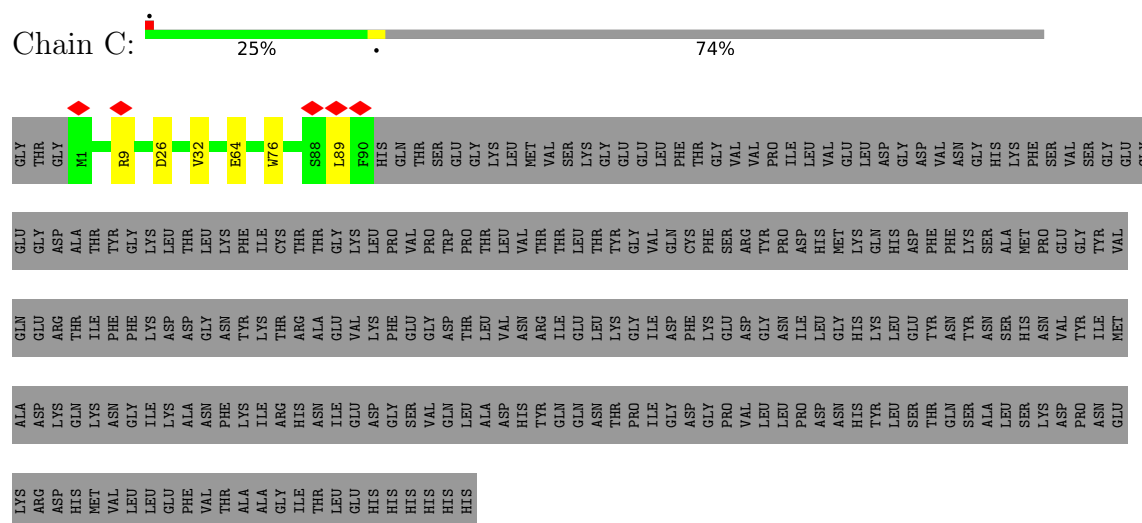
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Chain	Residue	Modelled	Actual	Comment	Reference
Z	97	LYS	-	linker	UNP Q9NPP4
Z	98	LEU	-	linker	UNP Q9NPP4
Z	331	GLU	-	expression tag	UNP A0A1V0D974
Z	332	HIS	-	expression tag	UNP A0A1V0D974
Z	333	HIS	-	expression tag	UNP A0A1V0D974
Z	334	HIS	-	expression tag	UNP A0A1V0D974
Z	335	HIS	-	expression tag	UNP A0A1V0D974
Z	336	HIS	-	expression tag	UNP A0A1V0D974
Z	337	HIS	-	expression tag	UNP A0A1V0D974
a	-2	GLY	-	expression tag	UNP Q9NPP4
a	-1	THR	-	expression tag	UNP Q9NPP4
a	0	GLY	-	expression tag	UNP Q9NPP4
a	97	LYS	-	linker	UNP Q9NPP4
a	98	LEU	-	linker	UNP Q9NPP4
a	331	GLU	-	expression tag	UNP A0A1V0D974
a	332	HIS	-	expression tag	UNP A0A1V0D974
a	333	HIS	-	expression tag	UNP A0A1V0D974
a	334	HIS	-	expression tag	UNP A0A1V0D974
a	335	HIS	-	expression tag	UNP A0A1V0D974
a	336	HIS	-	expression tag	UNP A0A1V0D974
a	337	HIS	-	expression tag	UNP A0A1V0D974
b	-2	GLY	-	expression tag	UNP Q9NPP4
b	-1	THR	-	expression tag	UNP Q9NPP4
b	0	GLY	-	expression tag	UNP Q9NPP4
b	97	LYS	-	linker	UNP Q9NPP4
b	98	LEU	-	linker	UNP Q9NPP4
b	331	GLU	-	expression tag	UNP A0A1V0D974
b	332	HIS	-	expression tag	UNP A0A1V0D974
b	333	HIS	-	expression tag	UNP A0A1V0D974
b	334	HIS	-	expression tag	UNP A0A1V0D974
b	335	HIS	-	expression tag	UNP A0A1V0D974
b	336	HIS	-	expression tag	UNP A0A1V0D974
b	337	HIS	-	expression tag	UNP A0A1V0D974
c	-2	GLY	-	expression tag	UNP Q9NPP4
c	-1	THR	-	expression tag	UNP Q9NPP4
c	0	GLY	-	expression tag	UNP Q9NPP4
c	97	LYS	-	linker	UNP Q9NPP4
c	98	LEU	-	linker	UNP Q9NPP4
c	331	GLU	-	expression tag	UNP A0A1V0D974
c	332	HIS	-	expression tag	UNP A0A1V0D974
c	333	HIS	-	expression tag	UNP A0A1V0D974
c	334	HIS	-	expression tag	UNP A0A1V0D974

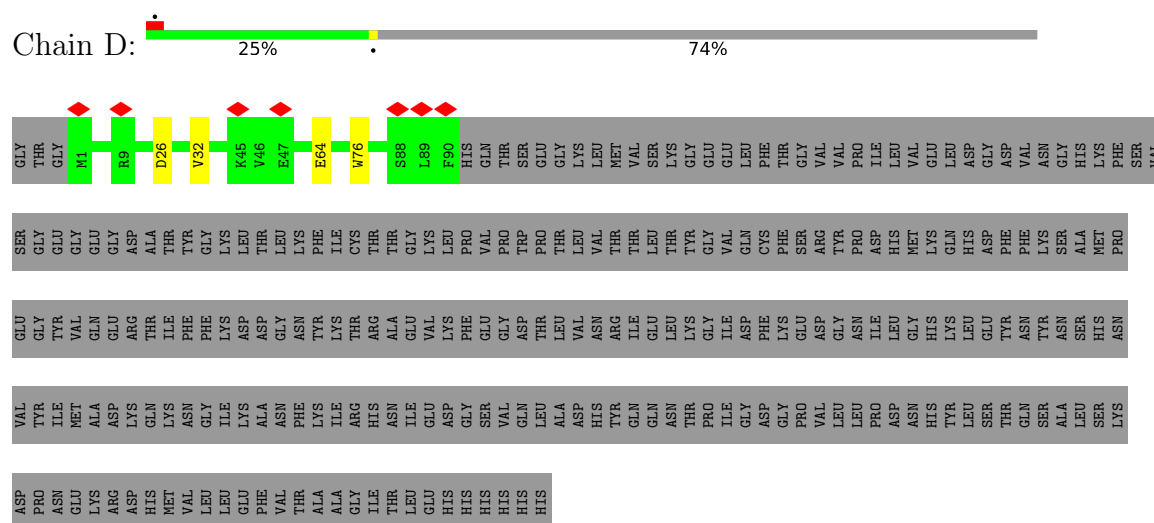
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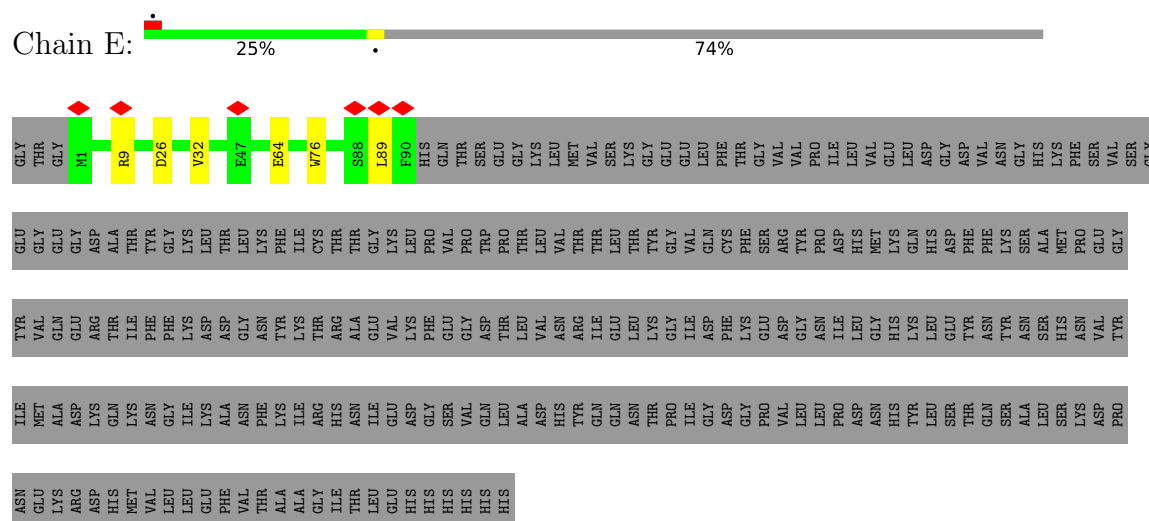
Chain	Residue	Modelled	Actual	Comment	Reference
c	335	HIS	-	expression tag	UNP A0A1V0D974
c	336	HIS	-	expression tag	UNP A0A1V0D974
c	337	HIS	-	expression tag	UNP A0A1V0D974
d	-2	GLY	-	expression tag	UNP Q9NPP4
d	-1	THR	-	expression tag	UNP Q9NPP4
d	0	GLY	-	expression tag	UNP Q9NPP4
d	97	LYS	-	linker	UNP Q9NPP4
d	98	LEU	-	linker	UNP Q9NPP4
d	331	GLU	-	expression tag	UNP A0A1V0D974
d	332	HIS	-	expression tag	UNP A0A1V0D974
d	333	HIS	-	expression tag	UNP A0A1V0D974
d	334	HIS	-	expression tag	UNP A0A1V0D974
d	335	HIS	-	expression tag	UNP A0A1V0D974
d	336	HIS	-	expression tag	UNP A0A1V0D974
d	337	HIS	-	expression tag	UNP A0A1V0D974
e	-2	GLY	-	expression tag	UNP Q9NPP4
e	-1	THR	-	expression tag	UNP Q9NPP4
e	0	GLY	-	expression tag	UNP Q9NPP4
e	97	LYS	-	linker	UNP Q9NPP4
e	98	LEU	-	linker	UNP Q9NPP4
e	331	GLU	-	expression tag	UNP A0A1V0D974
e	332	HIS	-	expression tag	UNP A0A1V0D974
e	333	HIS	-	expression tag	UNP A0A1V0D974
e	334	HIS	-	expression tag	UNP A0A1V0D974
e	335	HIS	-	expression tag	UNP A0A1V0D974
e	336	HIS	-	expression tag	UNP A0A1V0D974
e	337	HIS	-	expression tag	UNP A0A1V0D974



- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP



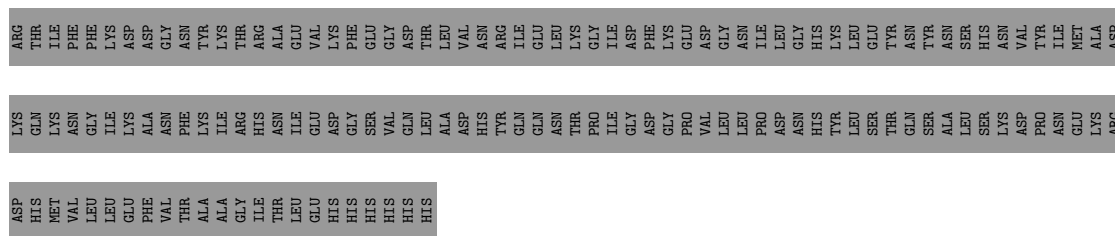
- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP



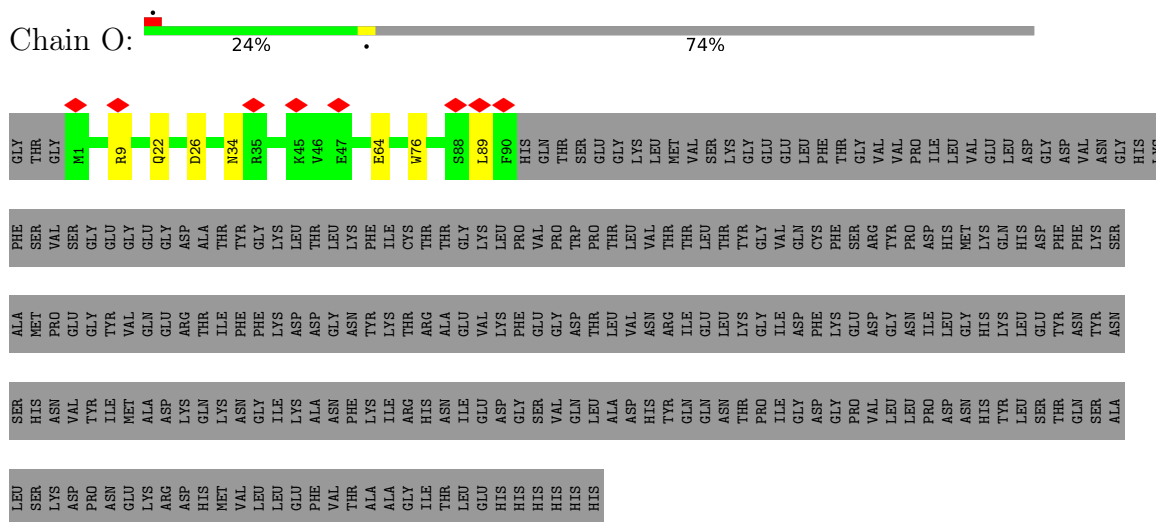
- [illegible]

- Chain G:**
-
- | Position | Amino Acid(s) |
|----------|---------------|
| M1 | MET |
| R9 | ARG |
| D26 | ASP |
| N34 | ASN |
| K45 | LYS |
| V46 | VAL |
| E47 | GLU |
| E64 | GLY |
| W76 | TRP |
| S88 | SER |
| L89 | LEU |
| F90 | PHE |

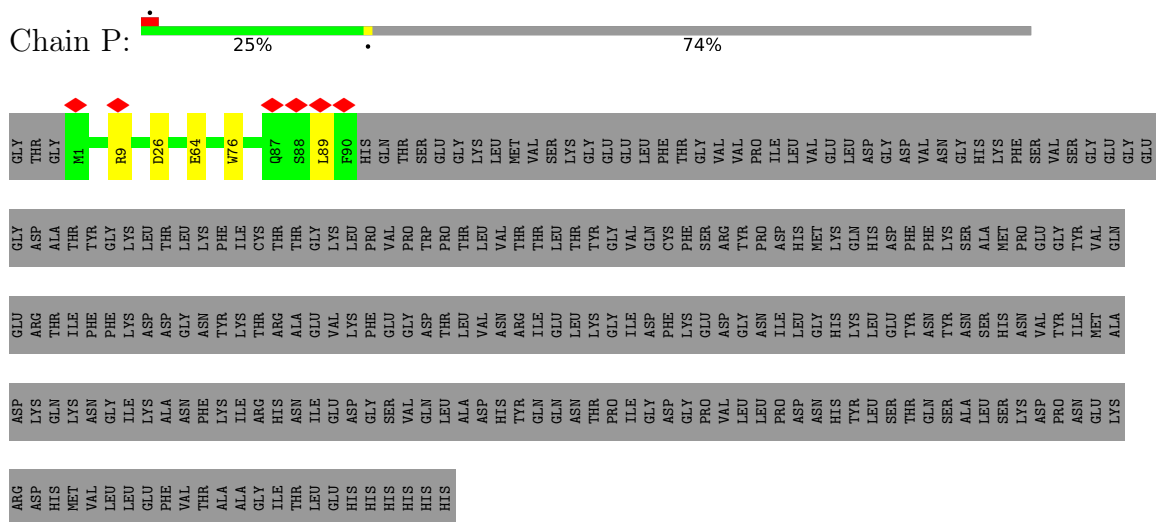
- [illegible]



- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP



- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP

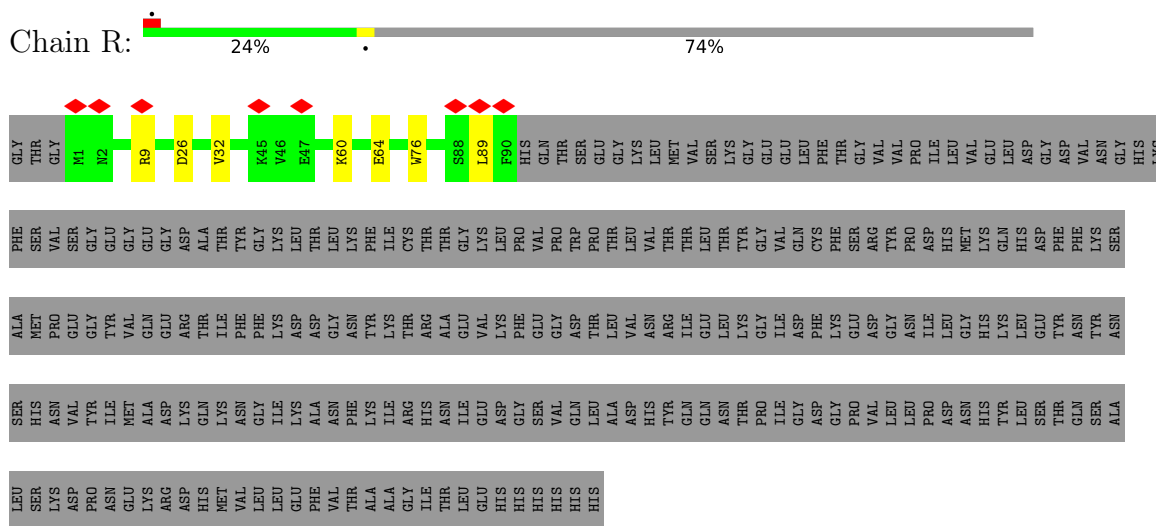


- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP

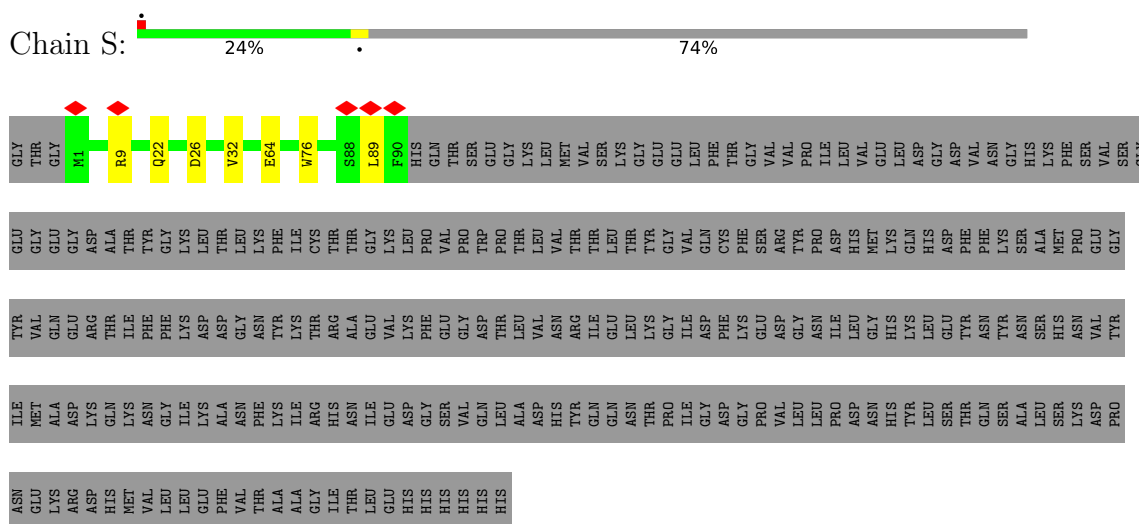


ASP	PRO	VAL	GLU	SER
ASN	TYR	GLY	GLY	GLU
GLU	ILE	VAL	VAL	GLY
LYS	MET	ALA	GLN	GLU
ARG	ASP	ASP	GLU	GLY
HIS	LYS	ARG	ARG	ASP
MET	GLN	THR	THR	ALA
VAL	LYS	ILE	ILE	THR
VAL	ASN	PHE	PHE	TYR
LEU	GLY	GLY	PHE	GLY
LEU	ILE	LYS	LYS	LYS
GLU	LYS	ASP	ASP	LEU
PHE	ALA	ASP	ASP	THR
VAL	ASN	GLY	GLY	LEU
THR	PHE	ASN	ASN	LYS
ALA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

- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP

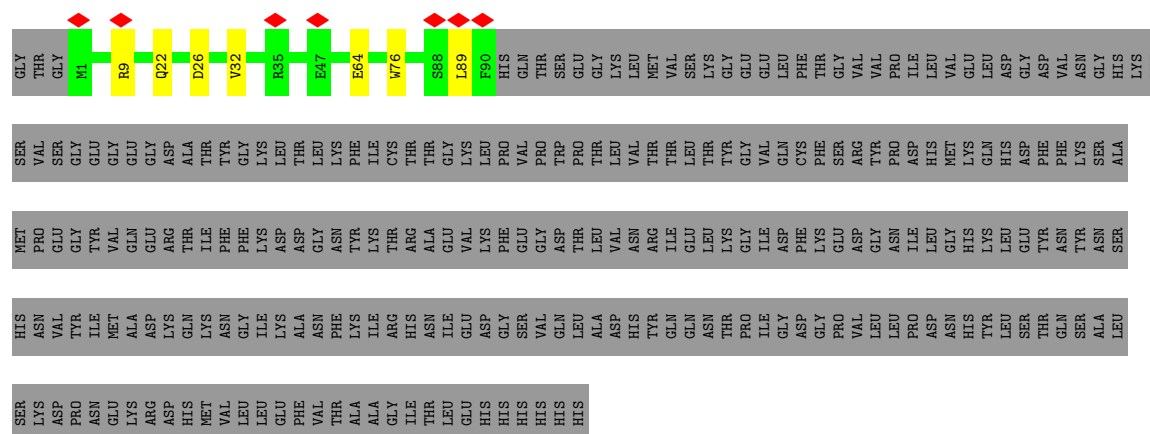


- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP

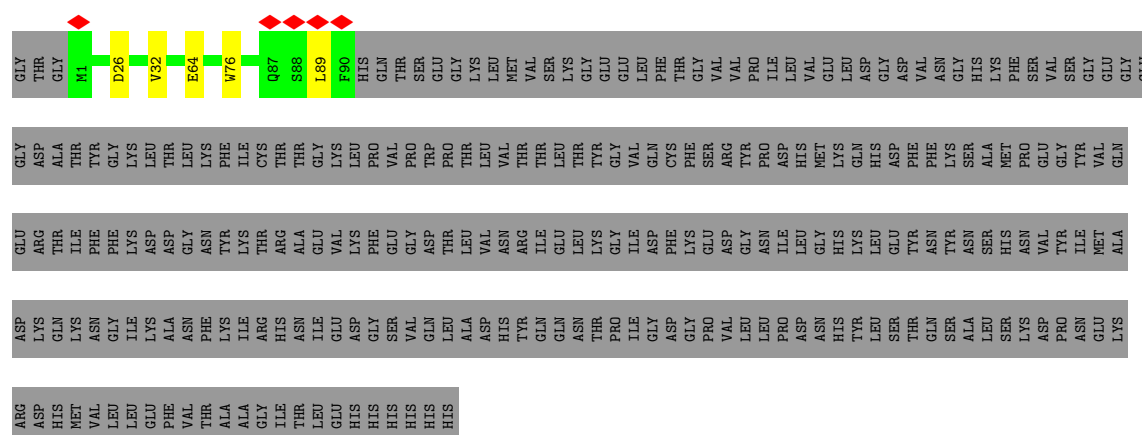


- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP

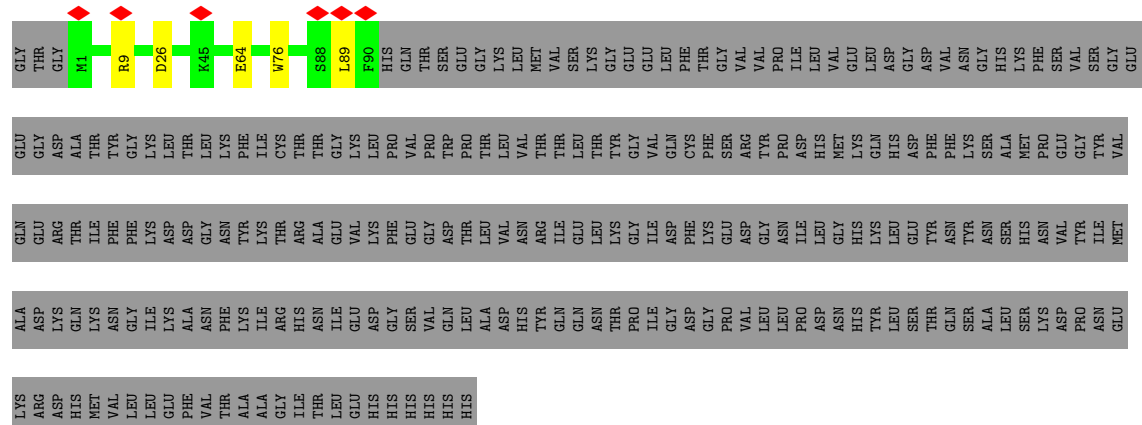




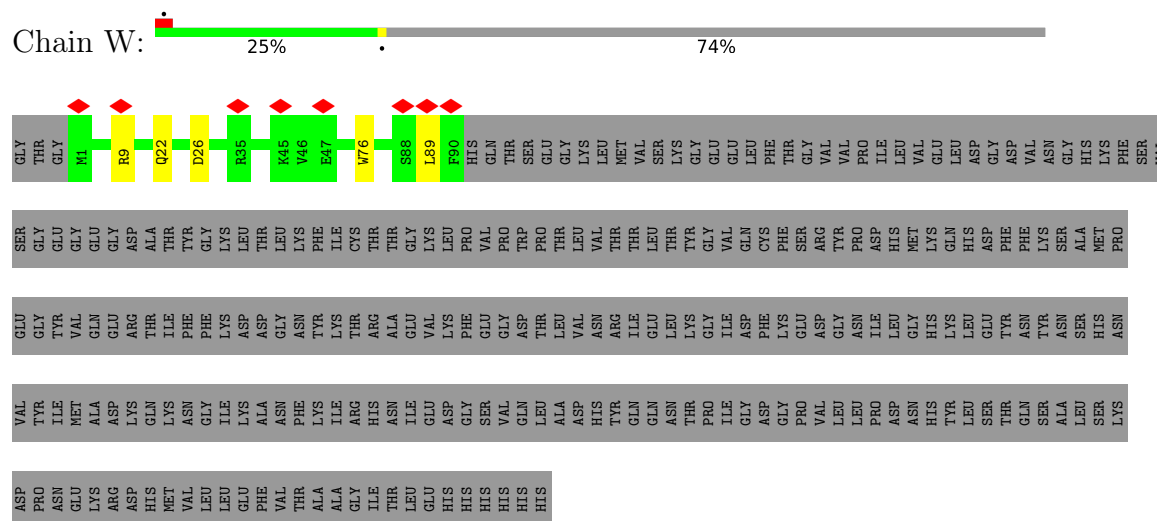
- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP



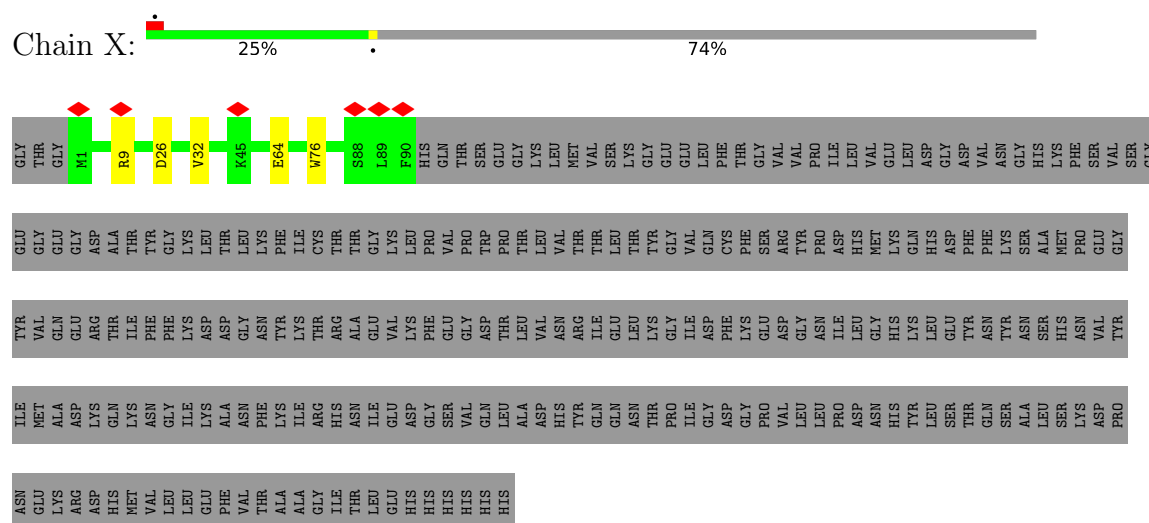
- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP



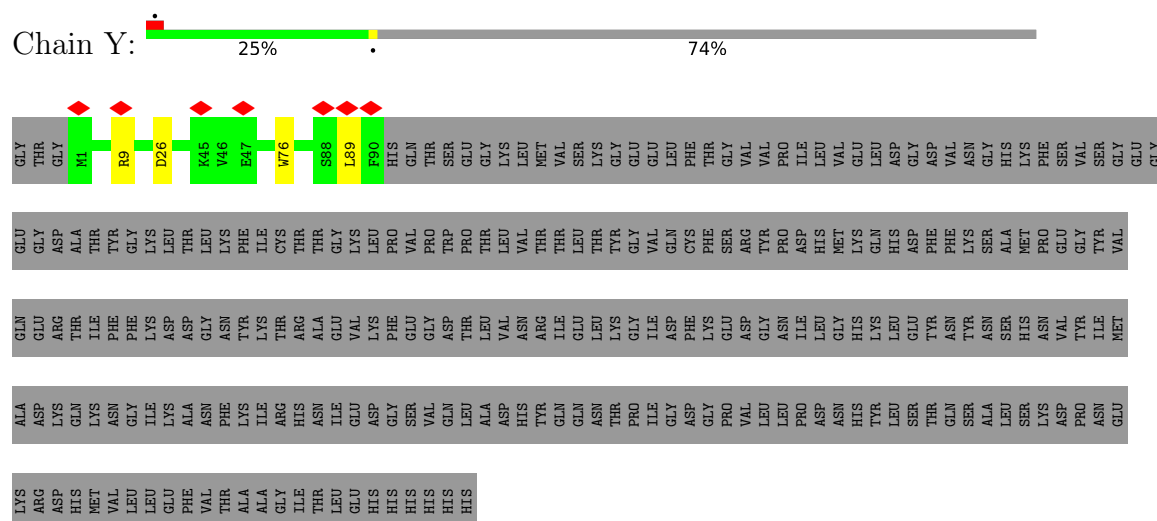
- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP



- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP



- Molecule 1: Chimera protein of NLR family CARD domain-containing protein 4 and EGFP



- Chain Z: 

- Chain a:  26% 74%
- | Position | Residue | Category |
|----------|---------|----------|
| 1 | GLY | Grey |
| 2 | THR | Grey |
| 3 | GLY | Grey |
| 4 | M1 | Green |
| 5 | THR | Grey |
| 6 | GLY | Grey |
| 7 | R9 | Green |
| 8 | LYS | Grey |
| 9 | LEU | Grey |
| 10 | THR | Grey |
| 11 | D26 | Yellow |
| 12 | LEU | Grey |
| 13 | K45 | Green |
| 14 | LYS | Grey |
| 15 | PHE | Grey |
| 16 | ILE | Grey |
| 17 | W76 | Yellow |
| 18 | CYS | Grey |
| 19 | THR | Grey |
| 20 | Q87 | Green |
| 21 | THR | Grey |
| 22 | S88 | Green |
| 23 | GLY | Grey |
| 24 | L89 | Yellow |
| 25 | F90 | Green |
| 26 | LEU | Grey |
| 27 | PRO | Grey |
| 28 | GLN | Grey |
| 29 | THR | Grey |
| 30 | TRP | Grey |
| 31 | SER | Grey |
| 32 | GLU | Grey |
| 33 | GLY | Grey |
| 34 | LYS | Grey |
| 35 | VAL | Grey |
| 36 | THR | Grey |
| 37 | LEU | Grey |
| 38 | SER | Grey |
| 39 | LYS | Grey |
| 40 | GLY | Grey |
| 41 | GLU | Grey |
| 42 | GLU | Grey |
| 43 | LEU | Grey |
| 44 | PHE | Grey |
| 45 | THR | Grey |
| 46 | CYS | Grey |
| 47 | PHE | Grey |
| 48 | SER | Grey |
| 49 | ARG | Grey |
| 50 | VAL | Grey |
| 51 | TYR | Grey |
| 52 | PRO | Grey |
| 53 | PRO | Grey |
| 54 | ASP | Grey |
| 55 | ILE | Grey |
| 56 | HIS | Grey |
| 57 | LEU | Grey |
| 58 | MET | Grey |
| 59 | VAL | Grey |
| 60 | GLY | Grey |
| 61 | GLN | Grey |

[illegible]

[illegible]

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=100.6°, rise=5.0 Å, axial sym=C1	Depositor
Number of segments used	299537	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	42	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.001	Depositor
Minimum map value	-0.000	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.00032	Depositor
Map size (Å)	168.96, 168.96, 168.96	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.50	0/745	0.57	0/1000
1	B	0.50	0/745	0.57	0/1000
1	C	0.50	0/745	0.57	0/1000
1	D	0.51	0/745	0.57	0/1000
1	E	0.51	0/745	0.57	0/1000
1	F	0.50	0/745	0.57	0/1000
1	G	0.51	0/745	0.57	0/1000
1	H	0.50	0/745	0.57	0/1000
1	I	0.51	0/745	0.57	0/1000
1	J	0.51	0/745	0.57	0/1000
1	K	0.51	0/745	0.57	0/1000
1	L	0.51	0/745	0.57	0/1000
1	M	0.51	0/745	0.57	0/1000
1	N	0.50	0/745	0.57	0/1000
1	O	0.50	0/745	0.57	0/1000
1	P	0.51	0/745	0.57	0/1000
1	Q	0.50	0/745	0.57	0/1000
1	R	0.51	0/745	0.57	0/1000
1	S	0.51	0/745	0.57	0/1000
1	T	0.50	0/745	0.57	0/1000
1	U	0.51	0/745	0.57	0/1000
1	V	0.50	0/745	0.57	0/1000
1	W	0.51	0/745	0.57	0/1000
1	X	0.50	0/745	0.57	0/1000
1	Y	0.50	0/745	0.57	0/1000
1	Z	0.50	0/745	0.57	0/1000
1	a	0.50	0/745	0.57	0/1000
1	b	0.51	0/745	0.57	0/1000
1	c	0.51	0/745	0.57	0/1000
1	d	0.51	0/745	0.57	0/1000
1	e	0.50	0/745	0.57	0/1000
All	All	0.50	0/23095	0.57	0/31000

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	734	0	748	6	0
1	B	734	0	748	7	0
1	C	734	0	748	5	0
1	D	734	0	748	4	0
1	E	734	0	748	7	0
1	F	734	0	748	4	0
1	G	734	0	748	7	0
1	H	734	0	748	7	0
1	I	734	0	748	6	0
1	J	734	0	748	8	0
1	K	734	0	748	7	0
1	L	734	0	748	5	0
1	M	734	0	748	7	0
1	N	734	0	748	5	0
1	O	734	0	748	7	0
1	P	734	0	748	6	0
1	Q	734	0	748	6	0
1	R	734	0	748	7	0
1	S	734	0	748	8	0
1	T	734	0	748	7	0
1	U	734	0	748	6	0
1	V	734	0	748	5	0
1	W	734	0	748	5	0
1	X	734	0	748	5	0
1	Y	734	0	748	4	0
1	Z	734	0	748	3	0
1	a	734	0	748	4	0
1	b	734	0	748	3	0
1	c	734	0	748	4	0
1	d	734	0	748	4	0
1	e	734	0	748	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	22754	0	23188	101	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (101) 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:U:26:ASP:OD2	1:U:76:TRP:NE1	2.37	0.58
1:G:26:ASP:OD2	1:G:76:TRP:NE1	2.37	0.58
1:E:26:ASP:OD2	1:E:76:TRP:NE1	2.37	0.57
1:H:26:ASP:OD2	1:H:76:TRP:NE1	2.37	0.57
1:S:26:ASP:OD2	1:S:76:TRP:NE1	2.37	0.57
1:P:26:ASP:OD2	1:P:76:TRP:NE1	2.37	0.57
1:d:26:ASP:OD2	1:d:76:TRP:NE1	2.37	0.57
1:R:26:ASP:OD2	1:R:76:TRP:NE1	2.37	0.57
1:B:26:ASP:OD2	1:B:76:TRP:NE1	2.37	0.57
1:M:26:ASP:OD2	1:M:76:TRP:NE1	2.37	0.57
1:V:26:ASP:OD2	1:V:76:TRP:NE1	2.37	0.57
1:T:89:LEU:N	1:b:64:GLU:OE1	2.38	0.57
1:a:26:ASP:OD2	1:a:76:TRP:NE1	2.37	0.57
1:D:26:ASP:OD2	1:D:76:TRP:NE1	2.37	0.57
1:c:26:ASP:OD2	1:c:76:TRP:NE1	2.37	0.56
1:K:26:ASP:OD2	1:K:76:TRP:NE1	2.37	0.56
1:O:26:ASP:OD2	1:O:76:TRP:NE1	2.37	0.56
1:Y:26:ASP:OD2	1:Y:76:TRP:NE1	2.37	0.56
1:U:64:GLU:OE1	1:c:89:LEU:N	2.38	0.56
1:A:26:ASP:OD2	1:A:76:TRP:NE1	2.37	0.56
1:N:26:ASP:OD2	1:N:76:TRP:NE1	2.37	0.56
1:A:89:LEU:N	1:H:64:GLU:OE1	2.38	0.56
1:b:26:ASP:OD2	1:b:76:TRP:NE1	2.37	0.56
1:Z:26:ASP:OD2	1:Z:76:TRP:NE1	2.37	0.55
1:W:26:ASP:OD2	1:W:76:TRP:NE1	2.37	0.55
1:L:26:ASP:OD2	1:L:76:TRP:NE1	2.37	0.55
1:C:26:ASP:OD2	1:C:76:TRP:NE1	2.37	0.55
1:Q:26:ASP:OD2	1:Q:76:TRP:NE1	2.37	0.55
1:T:26:ASP:OD2	1:T:76:TRP:NE1	2.37	0.55
1:e:26:ASP:OD2	1:e:76:TRP:NE1	2.37	0.55
1:I:26:ASP:OD2	1:I:76:TRP:NE1	2.37	0.55
1:X:26:ASP:OD2	1:X:76:TRP:NE1	2.37	0.55
1:F:26:ASP:OD2	1:F:76:TRP:NE1	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:26:ASP:OD2	1:J:76:TRP:NE1	2.37	0.54
1:S:9:ARG:NE	1:Y:26:ASP:OD1	2.41	0.54
1:D:64:GLU:OE1	1:E:89:LEU:N	2.40	0.53
1:P:89:LEU:N	1:X:64:GLU:OE1	2.41	0.52
1:J:89:LEU:N	1:R:64:GLU:OE1	2.42	0.52
1:Q:64:GLU:OE1	1:Y:89:LEU:N	2.43	0.52
1:S:32:VAL:CG1	1:a:89:LEU:HD11	2.41	0.51
1:T:22:GLN:NE2	1:b:34:ASN:OD1	2.42	0.51
1:D:26:ASP:OD1	1:J:9:ARG:NE	2.44	0.50
1:C:64:GLU:OE1	1:K:89:LEU:N	2.44	0.50
1:V:89:LEU:N	1:d:64:GLU:OE1	2.43	0.50
1:G:34:ASN:OD1	1:O:22:GLN:NE2	2.44	0.50
1:O:64:GLU:OE1	1:W:89:LEU:N	2.45	0.49
1:Y:9:ARG:NE	1:e:26:ASP:OD1	2.45	0.49
1:T:26:ASP:OD1	1:Z:9:ARG:NE	2.45	0.49
1:C:89:LEU:N	1:F:64:GLU:OE1	2.46	0.49
1:C:9:ARG:NE	1:I:26:ASP:OD1	2.46	0.48
1:L:26:ASP:OD1	1:R:9:ARG:NE	2.46	0.48
1:M:9:ARG:NE	1:S:26:ASP:OD1	2.47	0.48
1:R:89:LEU:N	1:Z:64:GLU:OE1	2.47	0.48
1:E:64:GLU:OE1	1:M:89:LEU:N	2.46	0.47
1:N:26:ASP:OD1	1:T:9:ARG:NE	2.47	0.47
1:K:64:GLU:OE1	1:S:89:LEU:N	2.47	0.47
1:X:26:ASP:OD1	1:d:9:ARG:NE	2.47	0.46
1:C:32:VAL:CG1	1:K:89:LEU:HD11	2.45	0.46
1:I:64:GLU:OE1	1:Q:89:LEU:N	2.49	0.46
1:L:89:LEU:N	1:T:64:GLU:OE1	2.47	0.46
1:G:9:ARG:NE	1:M:26:ASP:OD1	2.48	0.46
1:P:26:ASP:OD1	1:V:9:ARG:NE	2.48	0.46
1:K:9:ARG:NE	1:Q:26:ASP:OD1	2.48	0.46
1:J:89:LEU:HD11	1:R:32:VAL:CG1	2.45	0.46
1:K:34:ASN:OD1	1:S:22:GLN:NE2	2.49	0.46
1:R:26:ASP:OD1	1:X:9:ARG:NE	2.49	0.46
1:I:9:ARG:NE	1:O:26:ASP:OD1	2.49	0.45
1:Q:9:ARG:NE	1:W:26:ASP:OD1	2.49	0.45
1:B:9:ARG:NE	1:E:26:ASP:OD1	2.50	0.45
1:U:32:VAL:CG1	1:c:89:LEU:HD11	2.46	0.44
1:E:9:ARG:NE	1:K:26:ASP:OD1	2.50	0.44
1:M:64:GLU:OE1	1:U:89:LEU:N	2.49	0.44
1:E:32:VAL:CG1	1:M:89:LEU:HD11	2.47	0.44
1:W:9:ARG:NE	1:c:26:ASP:OD1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:ASP:OD1	1:H:9:ARG:NE	2.51	0.44
1:B:89:LEU:N	1:J:64:GLU:OE1	2.50	0.43
1:I:34:ASN:OD1	1:Q:22:GLN:NE2	2.50	0.43
1:N:89:LEU:N	1:V:64:GLU:OE1	2.51	0.43
1:S:64:GLU:OE1	1:a:89:LEU:N	2.50	0.43
1:B:32:VAL:CG1	1:G:89:LEU:HD11	2.48	0.43
1:D:32:VAL:CG1	1:E:89:LEU:HD11	2.49	0.43
1:F:89:LEU:N	1:N:64:GLU:OE1	2.52	0.43
1:J:26:ASP:OD1	1:P:9:ARG:NE	2.52	0.43
1:S:32:VAL:HG12	1:a:89:LEU:HD11	2.01	0.43
1:H:26:ASP:OD1	1:N:9:ARG:NE	2.52	0.42
1:O:34:ASN:OD1	1:W:22:GLN:NE2	2.52	0.42
1:B:22:GLN:NE2	1:J:34:ASN:OD1	2.50	0.42
1:A:9:ARG:NE	1:G:26:ASP:OD1	2.52	0.42
1:O:9:ARG:NE	1:U:26:ASP:OD1	2.52	0.42
1:V:89:LEU:HD11	1:d:32:VAL:CG1	2.50	0.42
1:B:64:GLU:OE1	1:G:89:LEU:N	2.52	0.42
1:F:26:ASP:OD1	1:L:9:ARG:NE	2.53	0.42
1:A:64:GLU:OE1	1:I:89:LEU:N	2.51	0.41
1:M:32:VAL:CG1	1:U:89:LEU:HD11	2.50	0.41
1:L:89:LEU:HD11	1:T:32:VAL:CG1	2.50	0.41
1:H:89:LEU:N	1:P:64:GLU:OE1	2.53	0.41
1:P:89:LEU:HD11	1:X:32:VAL:CG1	2.50	0.41
1:G:64:GLU:OE1	1:O:89:LEU:N	2.52	0.41
1:A:89:LEU:HD11	1:H:32:VAL:CG1	2.51	0.41
1:J:47:GLU:OE2	1:R:60:LYS:NZ	2.50	0.41
1:A:22:GLN:NE2	1:H:34:ASN:OD1	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	B	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	C	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	D	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	E	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	F	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	G	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	H	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	I	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	J	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	K	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	L	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	M	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	N	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	O	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	P	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	Q	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	R	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	S	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	T	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	U	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	V	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	W	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	X	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	Y	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	Z	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	a	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	b	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	c	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	d	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
1	e	88/340 (26%)	87 (99%)	1 (1%)	0	100	100
All	All	2728/10540 (26%)	2697 (99%)	31 (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	83/300 (28%)	83 (100%)	0	100	100
1	B	83/300 (28%)	83 (100%)	0	100	100
1	C	83/300 (28%)	83 (100%)	0	100	100
1	D	83/300 (28%)	83 (100%)	0	100	100
1	E	83/300 (28%)	83 (100%)	0	100	100
1	F	83/300 (28%)	83 (100%)	0	100	100
1	G	83/300 (28%)	83 (100%)	0	100	100
1	H	83/300 (28%)	83 (100%)	0	100	100
1	I	83/300 (28%)	83 (100%)	0	100	100
1	J	83/300 (28%)	83 (100%)	0	100	100
1	K	83/300 (28%)	83 (100%)	0	100	100
1	L	83/300 (28%)	83 (100%)	0	100	100
1	M	83/300 (28%)	83 (100%)	0	100	100
1	N	83/300 (28%)	83 (100%)	0	100	100
1	O	83/300 (28%)	83 (100%)	0	100	100
1	P	83/300 (28%)	83 (100%)	0	100	100
1	Q	83/300 (28%)	83 (100%)	0	100	100
1	R	83/300 (28%)	83 (100%)	0	100	100
1	S	83/300 (28%)	83 (100%)	0	100	100
1	T	83/300 (28%)	83 (100%)	0	100	100
1	U	83/300 (28%)	83 (100%)	0	100	100
1	V	83/300 (28%)	83 (100%)	0	100	100
1	W	83/300 (28%)	83 (100%)	0	100	100
1	X	83/300 (28%)	83 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Y	83/300 (28%)	83 (100%)	0	100	100
1	Z	83/300 (28%)	83 (100%)	0	100	100
1	a	83/300 (28%)	83 (100%)	0	100	100
1	b	83/300 (28%)	83 (100%)	0	100	100
1	c	83/300 (28%)	83 (100%)	0	100	100
1	d	83/300 (28%)	83 (100%)	0	100	100
1	e	83/300 (28%)	83 (100%)	0	100	100
All	All	2573/9300 (28%)	2573 (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. All (45) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	HIS
1	B	39	ASN
1	B	56	HIS
1	C	39	ASN
1	C	56	HIS
1	D	56	HIS
1	E	39	ASN
1	E	56	HIS
1	F	39	ASN
1	F	56	HIS
1	G	39	ASN
1	G	56	HIS
1	I	39	ASN
1	I	56	HIS
1	J	56	HIS
1	K	39	ASN
1	K	56	HIS
1	L	39	ASN
1	L	56	HIS
1	M	39	ASN
1	M	56	HIS
1	N	56	HIS
1	P	56	HIS
1	Q	56	HIS
1	R	56	HIS

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Mol	Chain	Res	Type
1	S	56	HIS
1	T	39	ASN
1	T	56	HIS
1	V	39	ASN
1	V	56	HIS
1	W	56	HIS
1	X	39	ASN
1	X	56	HIS
1	Y	34	ASN
1	Y	56	HIS
1	a	34	ASN
1	a	39	ASN
1	a	56	HIS
1	b	39	ASN
1	b	56	HIS
1	c	34	ASN
1	c	39	ASN
1	d	39	ASN
1	d	56	HIS
1	e	34	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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

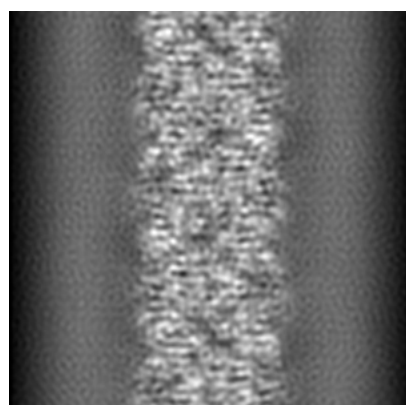
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9137. These allow visual inspection of the internal detail of the map and identification of artifacts.

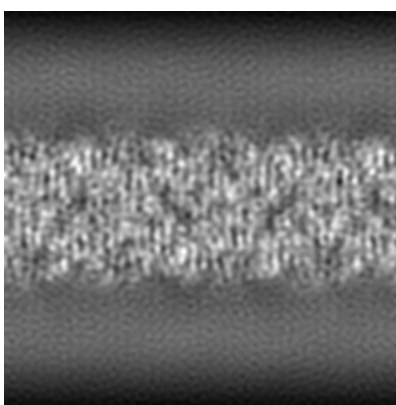
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

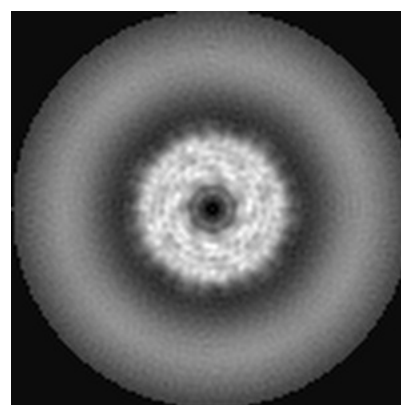
6.1.1 Primary map



X



Y

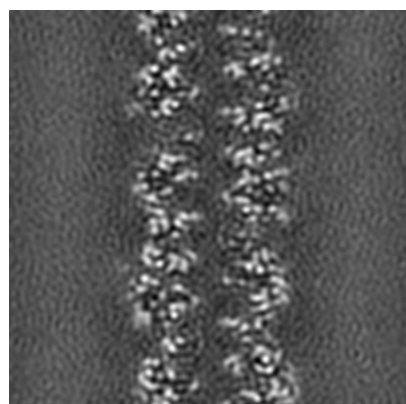


Z

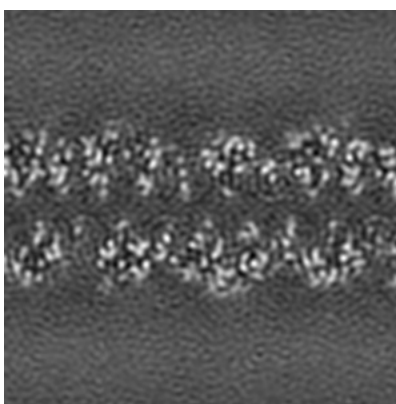
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

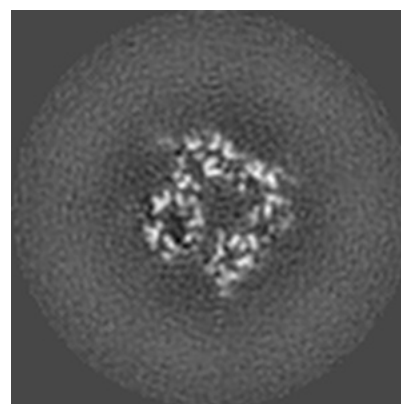
6.2.1 Primary map



X Index: 64



Y Index: 64

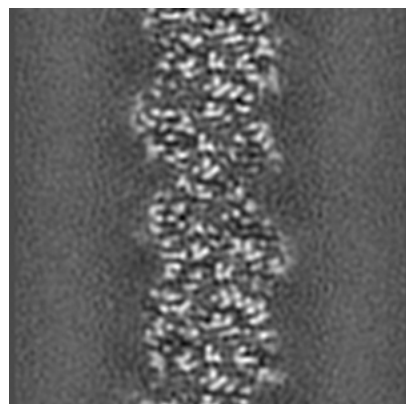


Z Index: 64

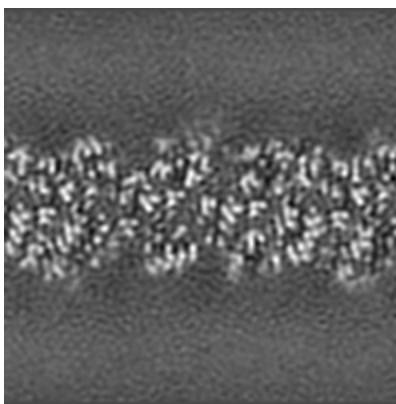
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

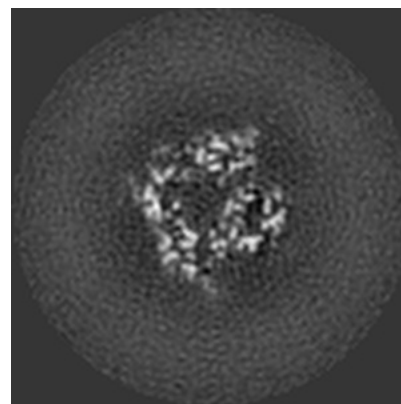
6.3.1 Primary map



X Index: 76



Y Index: 76

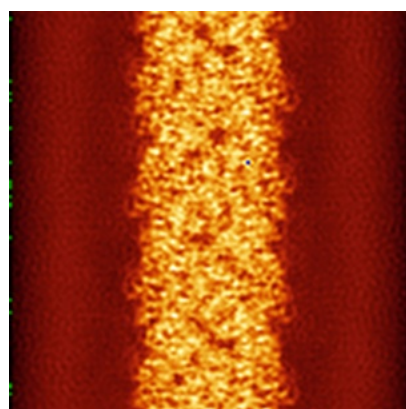


Z Index: 45

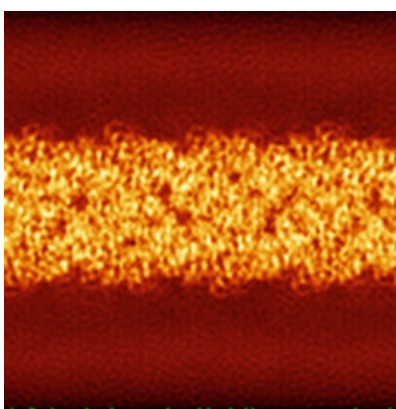
The images above show the largest variance slices of the map in three orthogonal directions.

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

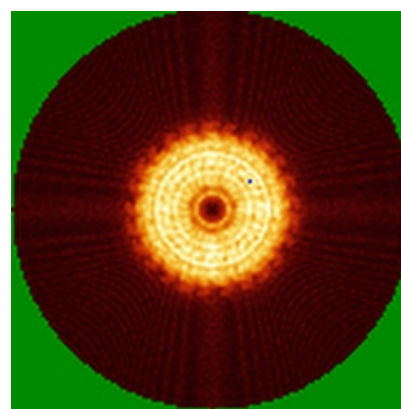
6.4.1 Primary map



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

This section was not generated.

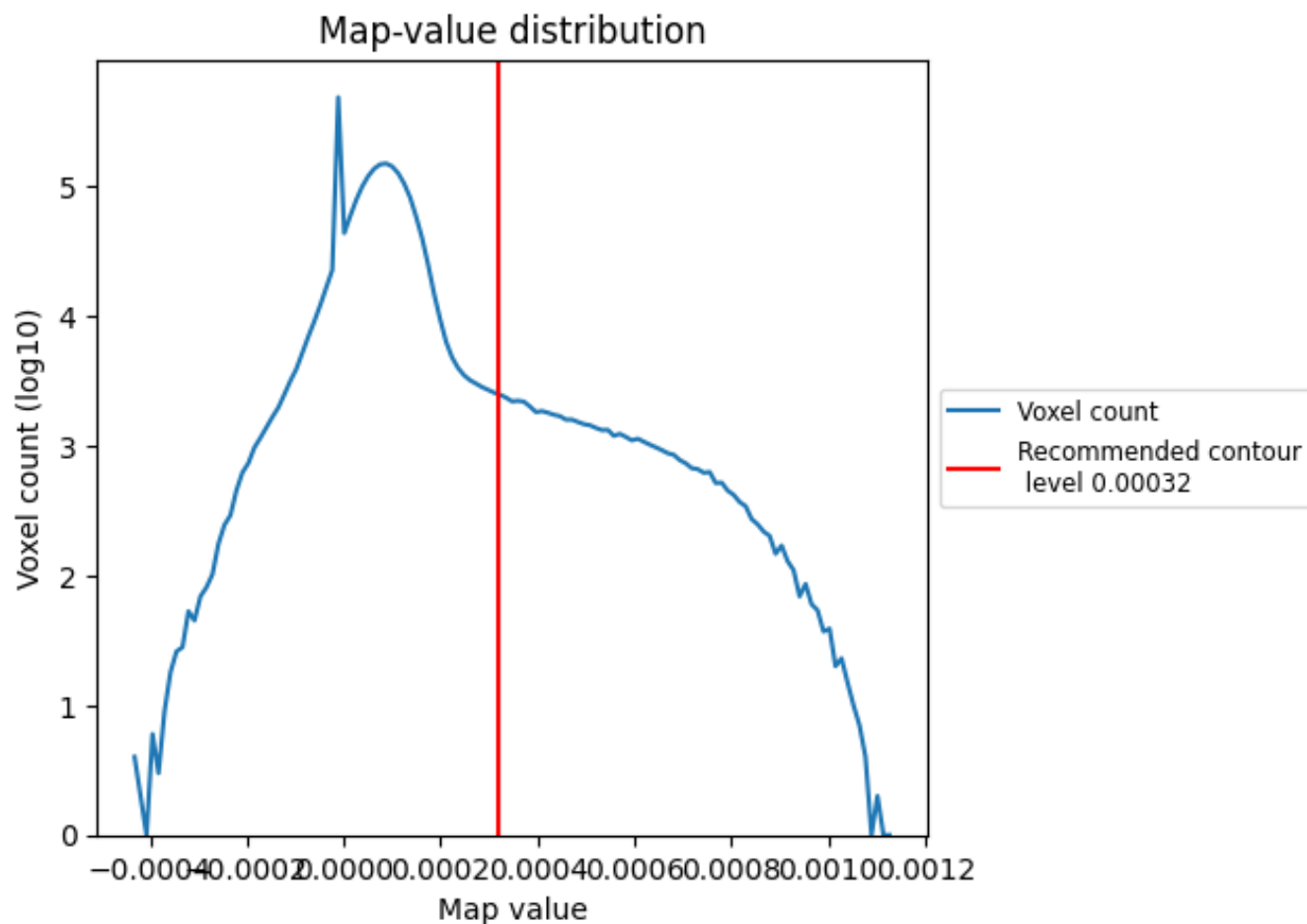
6.6 Mask visualisation

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

7 Map analysis [i](#)

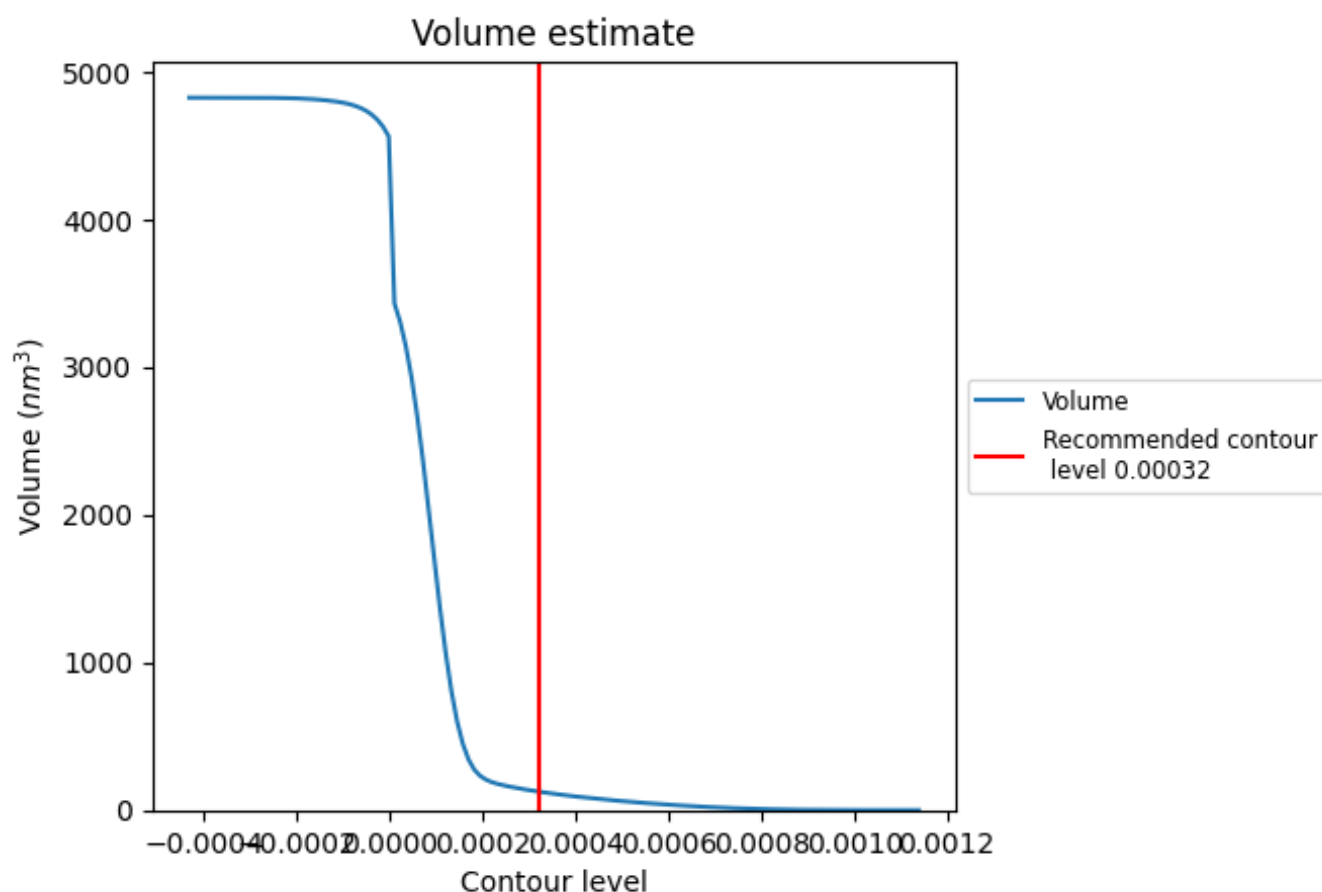
This section contains the results of statistical analysis of the map.

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.

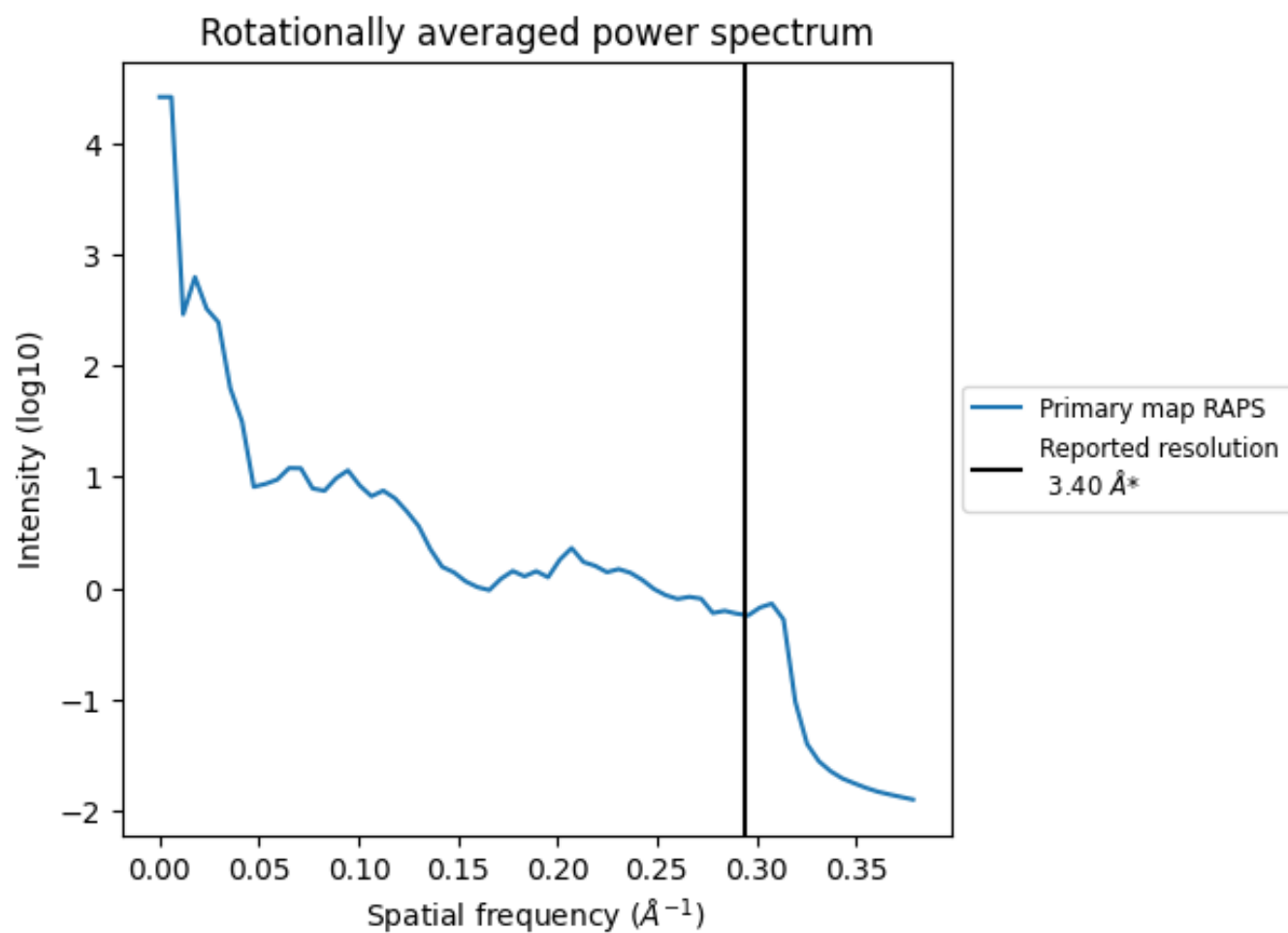
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 126 nm^3 ; this corresponds to an approximate mass of 114 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 0.294 Å⁻¹

8 Fourier-Shell correlation

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

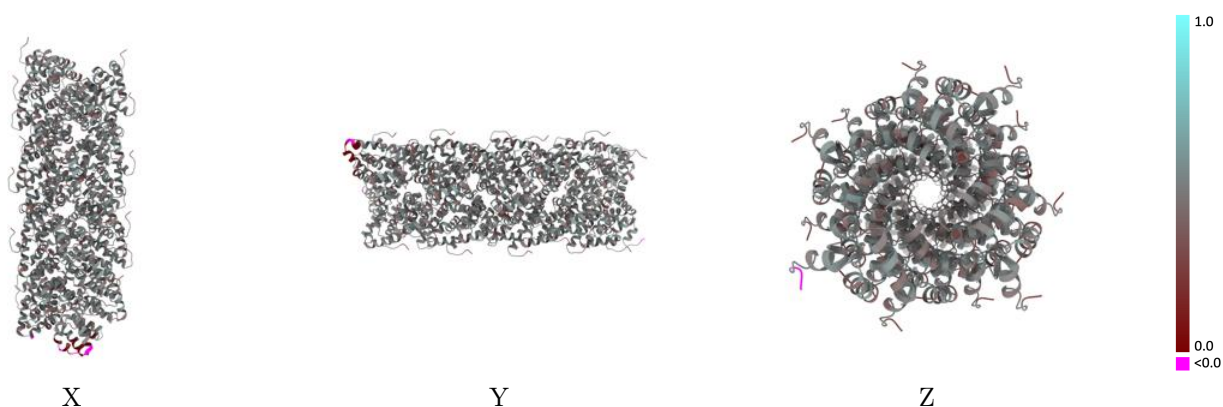
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9137 and PDB model 6MKS. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)

This section was not generated.

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

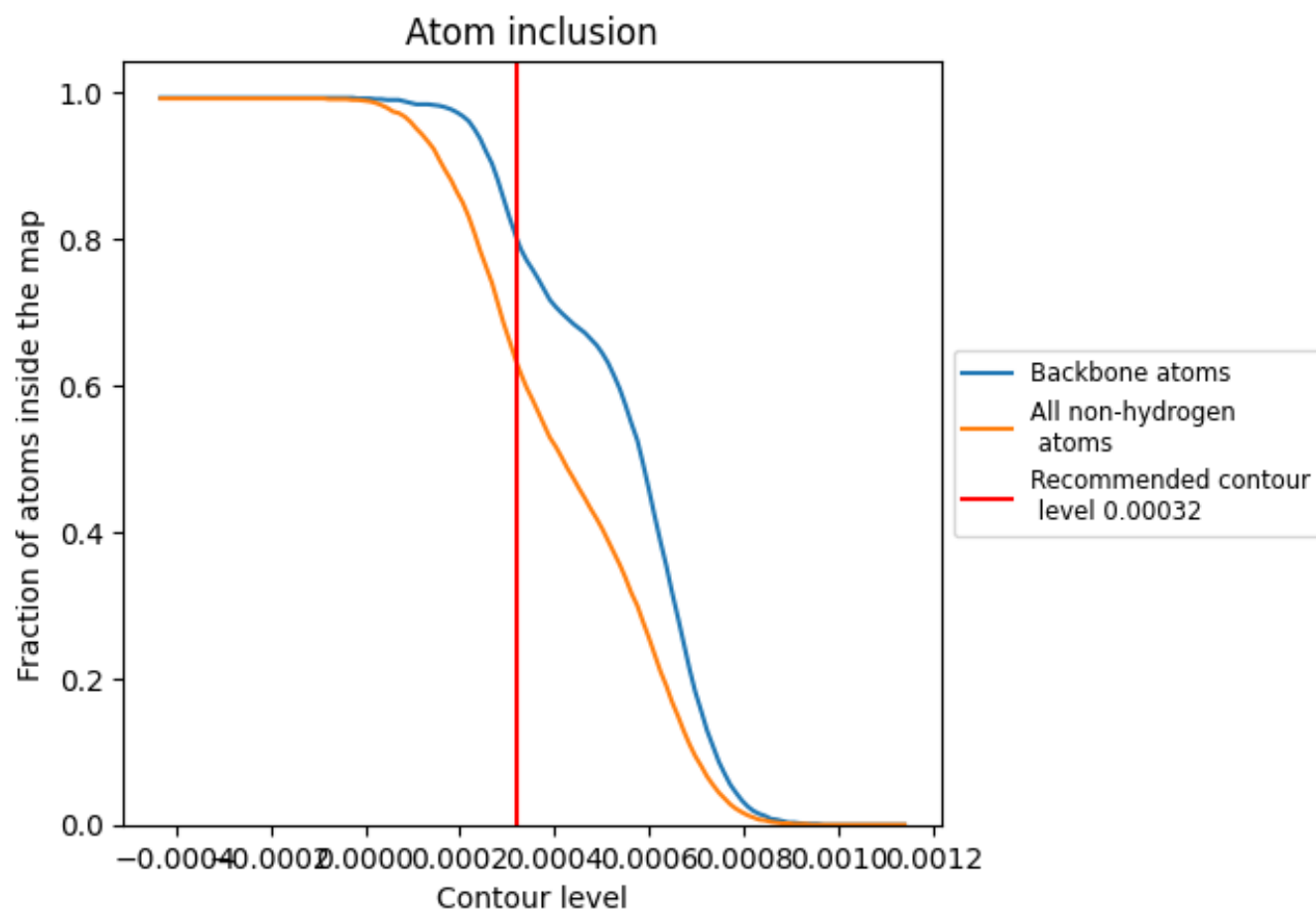


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 63% 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 (0.00032) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6310	 0.4630
A	 0.6310	 0.4700
B	 0.6400	 0.4680
C	 0.6320	 0.4650
D	 0.6500	 0.4650
E	 0.6380	 0.4640
F	 0.6330	 0.4640
G	 0.6390	 0.4690
H	 0.6270	 0.4690
I	 0.6290	 0.4710
J	 0.6380	 0.4690
K	 0.6320	 0.4670
L	 0.6420	 0.4670
M	 0.6380	 0.4650
N	 0.6350	 0.4650
O	 0.6400	 0.4690
P	 0.6360	 0.4640
Q	 0.6250	 0.4710
R	 0.6290	 0.4680
S	 0.6280	 0.4600
T	 0.6380	 0.4650
U	 0.6430	 0.4620
V	 0.6280	 0.4670
W	 0.6290	 0.4700
X	 0.6310	 0.4690
Y	 0.6280	 0.4680
Z	 0.6400	 0.4690
a	 0.6310	 0.4630
b	 0.6360	 0.4650
c	 0.6200	 0.4520
d	 0.6330	 0.4550
e	 0.5310	 0.3630

