



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:29 PM UTC

PDB ID : 8XB8 / pdb_00008xb8
EMDB ID : EMD-38214
Title : The structure of ASFV A137R
Authors : Li, C.; Song, H.; Gao, G.F.
Deposited on : 2023-12-06
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
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

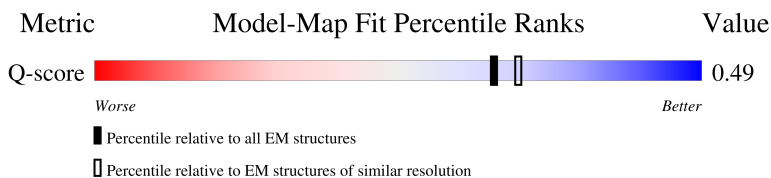
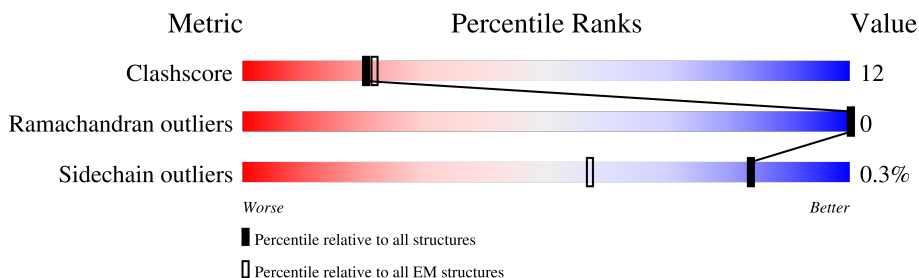
1 Overall quality at a glance

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.



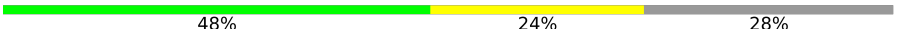
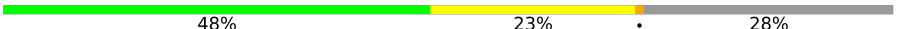
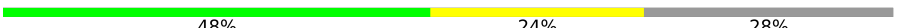
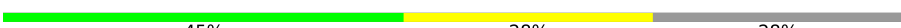
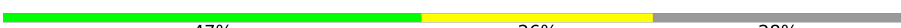
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	0	137	
1	1	137	
1	2	137	
1	3	137	

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Mol	Chain	Length	Quality of chain
1	4	137	
1	5	137	
1	6	137	
1	7	137	
1	A	137	
1	B	137	
1	C	137	
1	D	137	
1	E	137	
1	F	137	
1	G	137	
1	H	137	
1	I	137	
1	J	137	
1	K	137	
1	L	137	
1	M	137	
1	N	137	
1	O	137	
1	P	137	
1	Q	137	
1	R	137	
1	S	137	
1	T	137	
1	U	137	

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Mol	Chain	Length	Quality of chain		
1	V	137	49%	23%	28%
1	W	137	47%	26%	28%
1	X	137	45%	27%	28%
1	Y	137	49%	23%	28%
1	Z	137	51%	21%	28%
1	a	137	48%	24%	28%
1	b	137	47%	25%	28%
1	c	137	47%	25%	28%
1	d	137	50%	23%	28%
1	e	137	53%	18%	28%
1	f	137	48%	24%	28%
1	g	137	49%	23%	28%
1	h	137	45%	27%	28%
1	i	137	51%	21%	28%
1	j	137	49%	23%	28%
1	k	137	49%	23%	28%
1	l	137	50%	22%	28%
1	m	137	46%	26%	28%
1	n	137	48%	24%	28%
1	o	137	49%	23%	28%
1	p	137	49%	23%	28%
1	q	137	51%	21%	28%
1	r	137	47%	26%	28%
1	s	137	47%	26%	28%
1	t	137	50%	22%	28%

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Mol	Chain	Length	Quality of chain
1	u	137	 50% 22% 28%
1	v	137	 51% 21% 28%
1	w	137	 48% 24% 28%
1	x	137	 50% 23% 28%
1	y	137	 50% 22% 28%
1	z	137	 50% 23% 28%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 50400 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 A137R.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	B	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	C	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	D	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	E	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	F	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	G	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	H	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	I	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	J	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	K	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	L	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	M	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	N	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	O	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	P	99	Total	C	N	O	S	0	0
			840	545	140	150	5		
1	Q	99	Total	C	N	O	S	0	0
			840	545	140	150	5		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	S	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	T	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	U	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	V	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	W	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	X	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	Y	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	Z	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	a	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	b	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	c	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	d	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	e	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	f	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	g	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	h	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	i	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	j	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	k	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	l	99	Total 840	C 545	N 140	O 150	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	n	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	o	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	p	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	q	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	r	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	s	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	t	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	u	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	v	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	w	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	x	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	y	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	z	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	0	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	1	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	2	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	3	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	4	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	5	99	Total 840	C 545	N 140	O 150	S 5	0	0
1	6	99	Total 840	C 545	N 140	O 150	S 5	0	0

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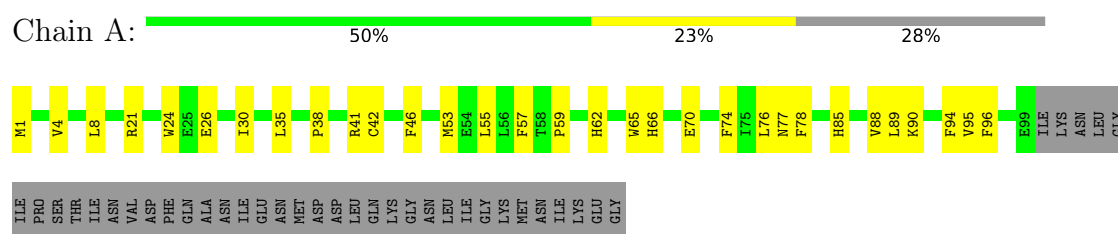
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	7	99	Total	C	N	O	S	0	0
			840	545	140	150	5		

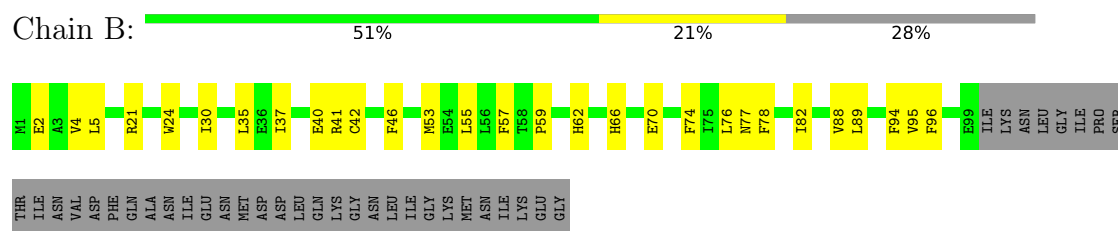
3 Residue-property plots

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.

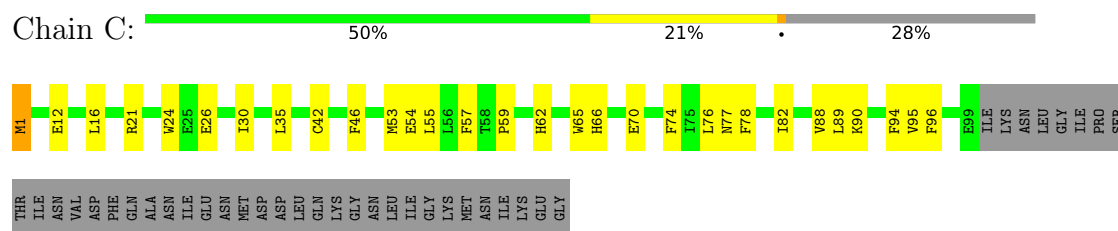
• Molecule 1: A137R



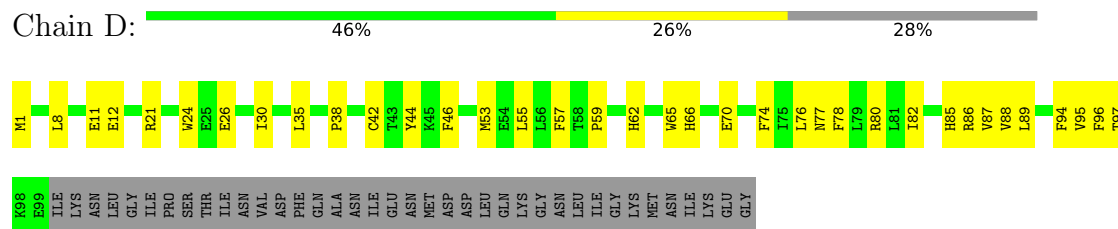
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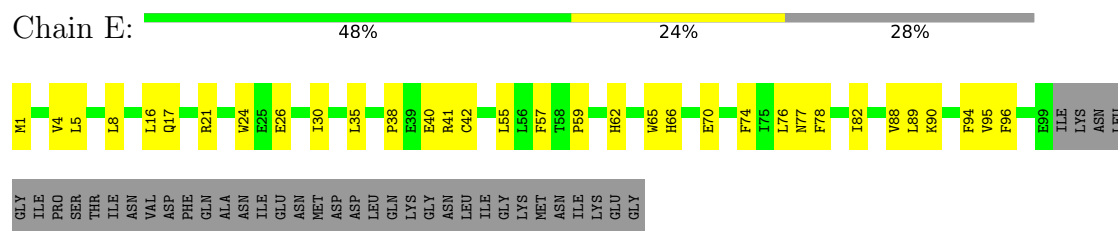
• Molecule 1: A137R



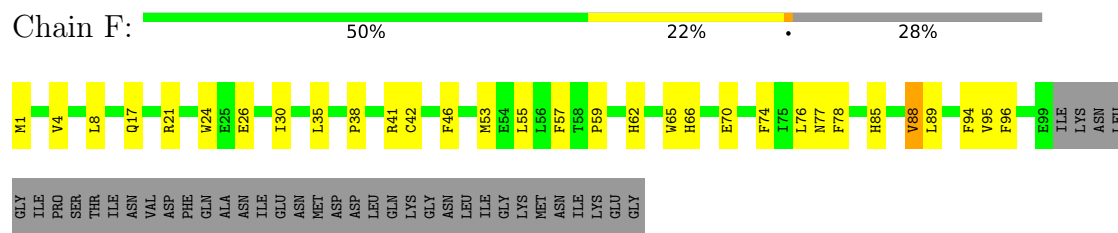
• Molecule 1: A137R



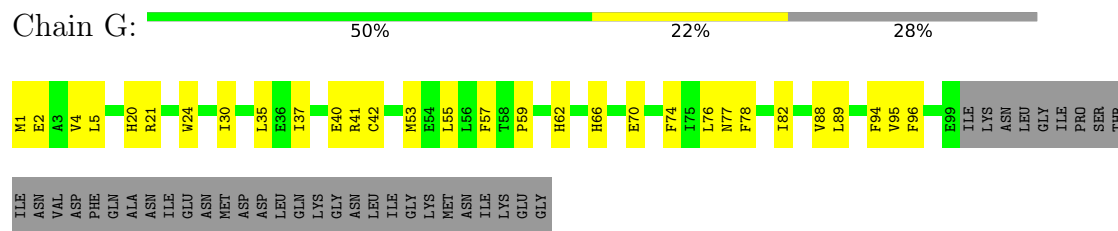
● Molecule 1: A137R



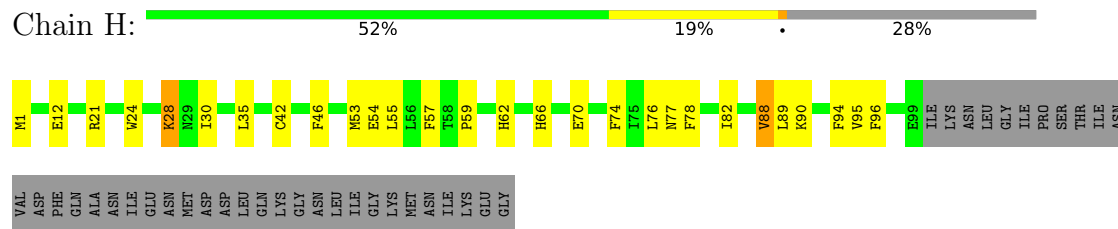
● Molecule 1: A137R



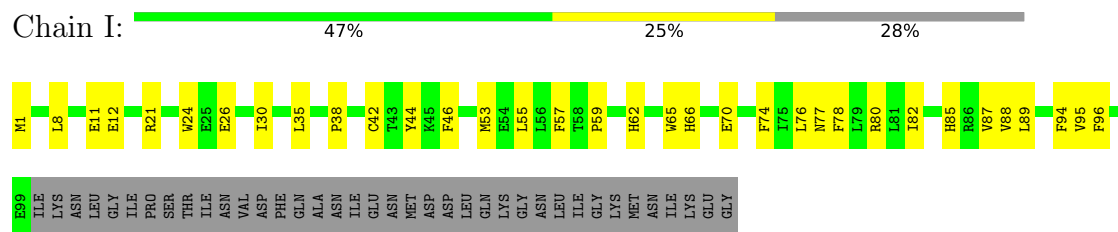
● Molecule 1: A137R



● Molecule 1: A137R

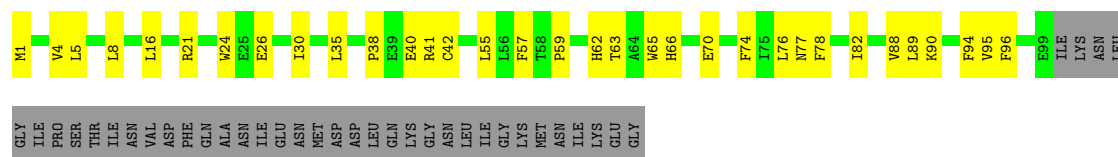


● Molecule 1: A137R

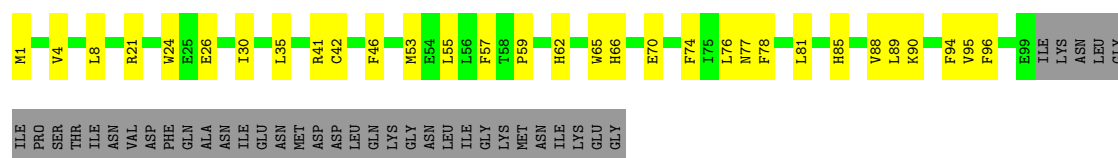


● Molecule 1: A137R

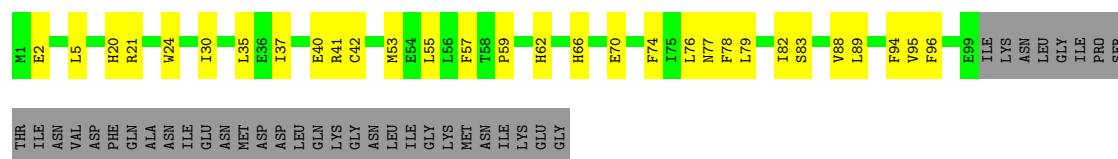




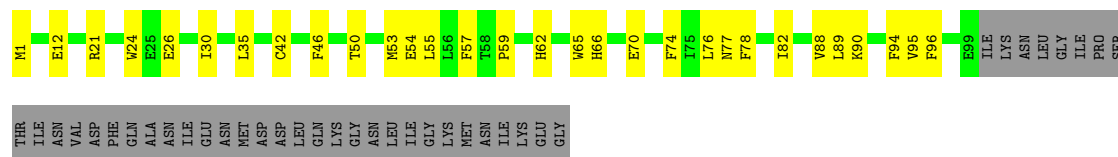
- Molecule 1: A137R



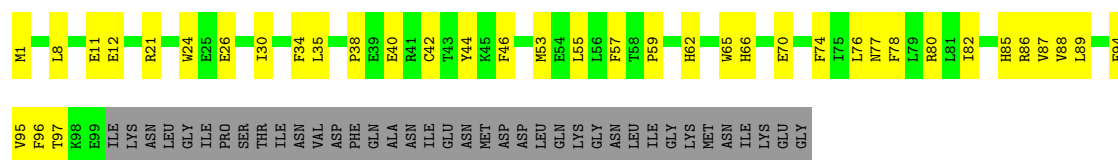
- Molecule 1: A137R



- Molecule 1: A137R



- Molecule 1: A137R



- Molecule 1: A137R



SER THR ILE ASN VAL ASP PHE GLN ALA ASN ILE GLU ASN MET ASP ASP LEU GLN LYS GLY

• Molecule 1: A137R

Chain P: 47% 26% 28%

M1 V4 L8 E12 R21 W24 E25 E26 I30 L35 Y44 K45 F46 M53 E54 L55 L56 F57 T58 P59 H62 W65 H66 E70 F74 I75 L76 N77 F78 L79 R80 L81 I82 V87 V88 L89 K90 T93 F94 V95 F96 E99 ILE LYS

ASN LEU GLY ILE PRO SER THR ILE VAL ASP PHE GLN MET ASP LEU ALA ILE ILE ASN MET ASP LEU GLN LYS MET ASN ILE LYS GLY

• Molecule 1: A137R

Chain Q: 51% 21% 28%

M1 Q17 R21 W24 I30 L35 E36 I37 E40 R41 C42 M53 E54 L55 L56 F57 T58 P59 H62 H66 E70 F74 I75 L76 N77 F78 I82 V88 L89 T93 F94 V95 F96 E99 ILE LYS ASN LEU GLY ILE PRO SER THR ILE ASN

VAL ASP PHE GLN ALA ASN ILE GLU MET ASP PHE GLN MET ASP LEU GLN LYS ILE ILE GLY ASN ILE GLY

• Molecule 1: A137R

Chain R: 47% 25% 28%

M1 E12 R21 W24 E25 E26 I30 L35 E36 I37 P38 E39 R41 C42 F46 M53 E54 L55 L56 F57 T58 P59 H62 W65 H66 E70 F74 I75 L76 N77 F78 L79 R80 L81 I82 V87 V88 L89 F94 V95 F96 E99 ILE LYS ASN

LEU GLY ILE PRO SER THR ILE ASN VAL ASP PHE GLN ALA ASN ILE GLU MET ASP PHE GLN LYS MET ASP LEU GLN LYS ILE ILE GLY LYS ILE GLY

• Molecule 1: A137R

Chain S: 47% 26% 28%

M1 E2 A3 V4 E11 E12 L16 R21 W24 I30 L35 E36 I37 P38 C42 F46 M53 E54 L55 L56 F57 T58 P59 H62 W65 H66 E70 F74 I75 L76 N77 F78 I82 R85 R86 V87 V88 L89 F94 V95 F96 T97 K98 E99 ILE

LYS ASN LEU GLY ILE PRO SER THR ILE VAL ASP PHE GLN ALA ASN ILE GLU MET ASP PHE GLN LYS MET ASP LEU GLN LYS ILE ILE GLY

• Molecule 1: A137R

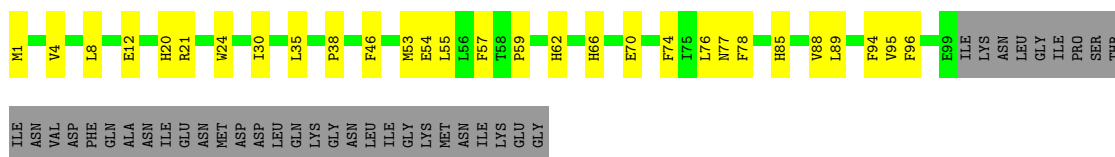
Chain T: 47% 25% 28%

M1 V4 L5 L8 D9 R21 W24 E25 E26 I30 F34 M35 P38 E39 E40 R41 C42 M53 E54 L55 L56 F57 T58 P59 H62 W65 H66 E70 F74 I75 L76 N77 F78 I82 V88 L89 K90 F94 V95 F96 E99 ILE LYS ASN

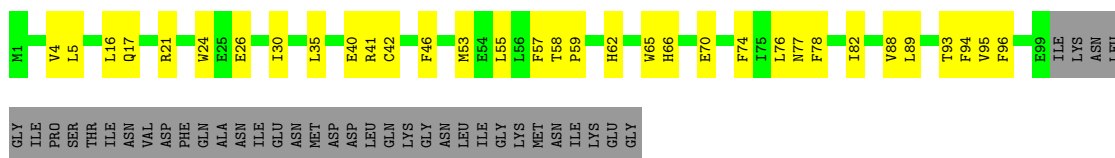
LEU GLY ILE PRO SER THR ILE VAL ASP PHE GLN ALA ASN ILE GLU MET ASP PHE GLN LYS MET ASP LEU GLN LYS ILE ILE GLY

• Molecule 1: A137R

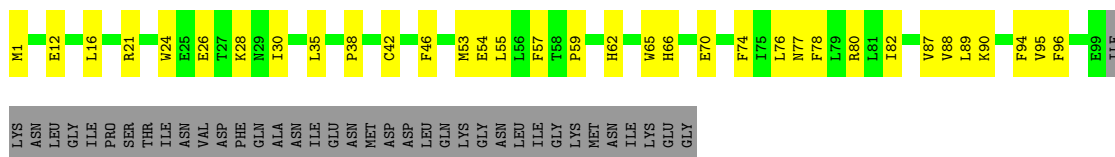




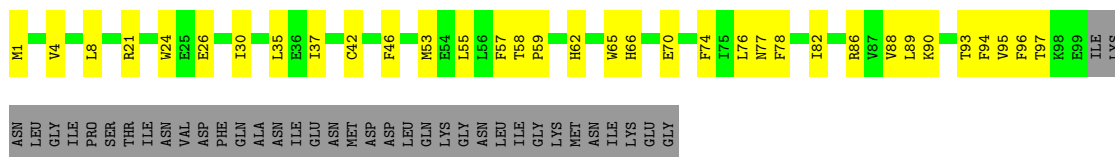
- Molecule 1: A137R



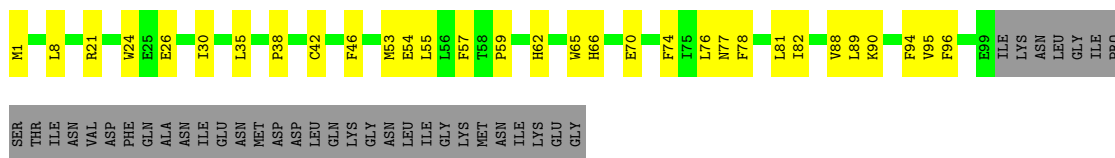
- Molecule 1: A137R



- Molecule 1: A137R



- Molecule 1: A137R

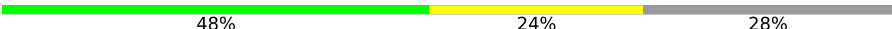


- Molecule 1: A137R



PHE
GLN
ALA
ASN
ILE
GLU
ASN
MET
ASP
ASP
LEU
GLN
LYS
GLY
ASN
LEU
ILE
GLY
LYS
MET
ASN
ASN
LYS
GLU
GLY

- Molecule 1: A137R

Chain f:  48% 24% 28%

M1 Q17 R21 W24 E25 E26 I30 L35 P38 E39 E40 R41 C42 F46 M53 E54 E55 L56 F57 T58 P59 H62 W65 H66 E70 F74 I75 L76 N77 F78 I82 V88 L89 T93 F94 V95 F96 E99 ILE LYS ASN LEU GLY ILE

PRO
SER
THR
ILE
ASN
VAL
ASP
PHE
GLN
ALA
ASN
ILE
GLU
ASN
MET
ASP
ASP
LEU
GLN
LYS
GLY
ASN
LEU
ILE
GLY
LYS
MET
ASN
ILE
LYS
LYS
GLU
GLY

- Molecule 1: A137R

Chain g:  49% 23% 28%

M1 V4 E12 R21 W24 E25 E26 I30 L35 E36 I37 P38 F39 E40 C42 M53 E54 L55 L56 F57 T58 P59 H62 W65 H66 E70 F74 I75 L76 N77 F78 I82 V88 L89 F94 V95 F96 E99 ILE LYS ASN LEU GLY ILE

PRO
SER
THR
ILE
ASN
VAL
ASP
PHE
GLN
ALA
ASN
ILE
GLU
ASN
MET
ASP
ASP
LEU
GLN
LYS
GLY
ASN
LEU
ILE
GLY
LYS
MET
ASN
ILE
LYS
LYS
GLU
GLY

- Molecule 1: A137R

Chain h:  45% 27% 28%

M1 V4 E12 R21 W24 E25 E26 I30 L35 P38 R41 C42 F46 M53 E54 L55 L56 F57 T58 P59 H62 W65 H66 E70 F74 I75 L76 N77 F78 I82 V88 L89 R86 V87 V88 K90 T93 F94 V95 F96 K98

E99 ILE LYS ASN LEU GLY ILE PRO SER THR ILE ASN VAL ASP PHE GLN ALA ASN ILE GLU ASN MET ASP ASP LEU GLN LYS GLY ASN LEU ILE GLY LYS MET ASN ILE LYS GLU GLY

- Molecule 1: A137R

Chain i:  51% 21% 28%

M1 V4 L5 L8 R21 W24 E25 E26 I30 L35 P38 C42 L55 L56 F57 T58 P59 H62 I75 L76 N77 F78 I82 R86 V87 V88 L89 K90 F94 V95 F96 T97 K98 E99 ILE LYS ASN LEU GLY ILE PRO SER THR

ILE ASN VAL ASP PHE GLN ALA ASN ILE GLU ASN MET ASP ASP LEU GLN LYS GLY ASN LEU ILE GLY LYS MET ASN ILE LYS GLY

- Molecule 1: A137R

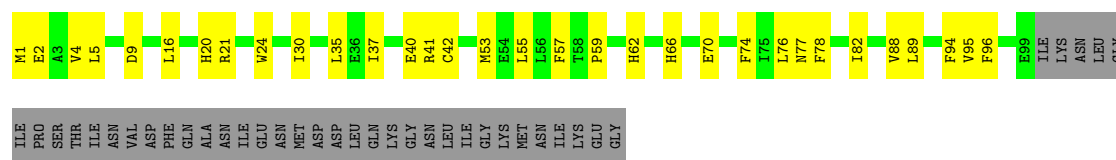
Chain j:  49% 23% 28%

M1 E2 A3 V4 L8 R21 W24 E25 E26 I30 L35 P38 R41 C42 F46 M53 E54 L55 L56 F57 T58 P59 H62 W65 H66 E70 F74 I75 L76 N77 F78 I82 V88 L89 H85 V88 L89 F94 V95 F96 E99 ILE LYS ASN

LEU GLY ILE PRO SER THR ILE ASN VAL ASP PHE GLN ALA ASN ILE GLU ASN MET ASP ASP LEU GLN LYS MET ASN ILE LYS GLY

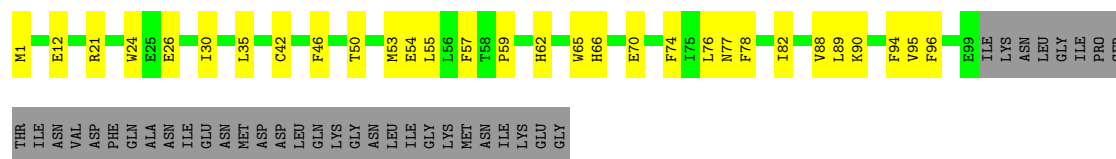
- Molecule 1: A137R

Chain k:  49% 23% 28%



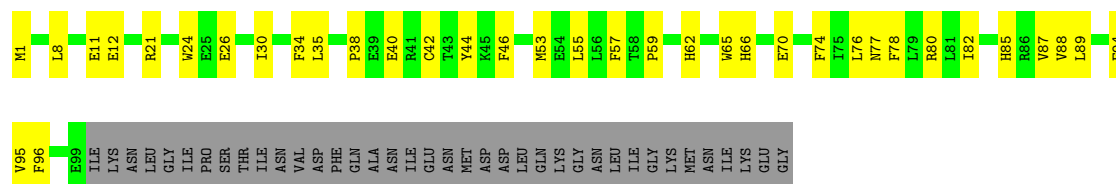
• Molecule 1: A137R

Chain l:  50% 22% 28%



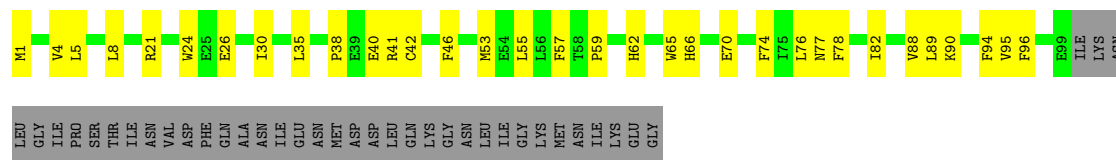
• Molecule 1: A137R

Chain m:  46% 26% 28%



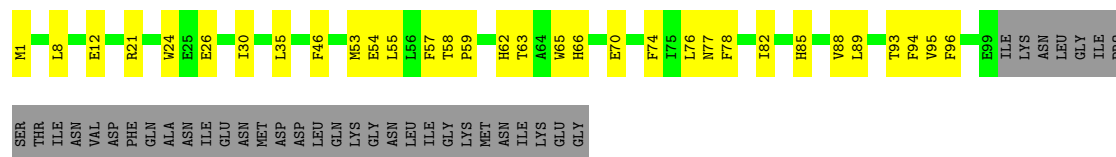
• Molecule 1: A137R

Chain n:  48% 24% 28%



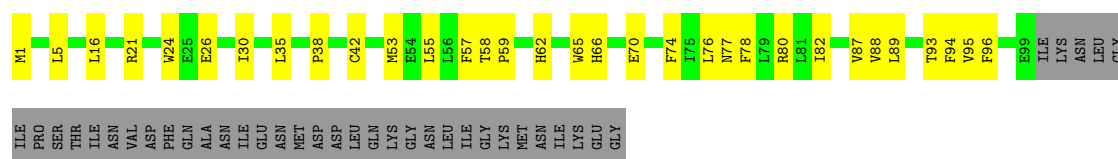
• Molecule 1: A137R

Chain o:  49% 23% 28%

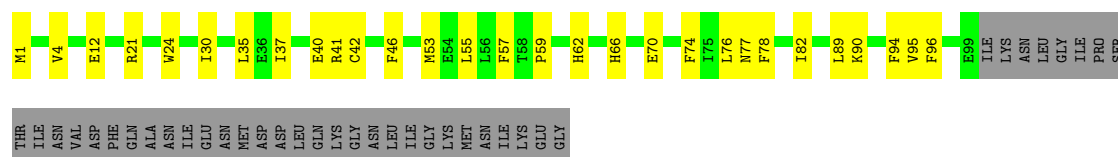


• Molecule 1: A137R

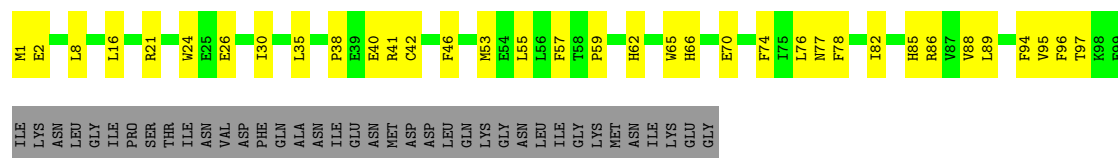
Chain p:  49% 23% 28%



● Molecule 1: A137R



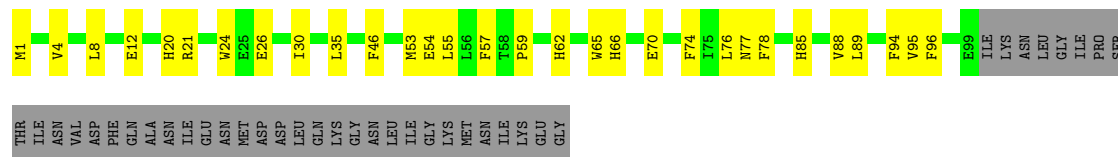
● Molecule 1: A137R



● Molecule 1: A137R



● Molecule 1: A137R



● Molecule 1: A137R



THR
ILE
ASN
VAL
ASP
PHE
GLN
ALA
ASN
GLU
ILE
ASN
MET
ASP
ASP
LEU
GLN
LYS
GLY
ASN
LEU
ILE
GLY
LYS
MET
ASN
ILE
LYS
GLU
GLY

- Molecule 1: A137R

Chain v:  51% 21% 28%

M1 E12 L16 R21 W24 I30 L35 P38 C42 F46 M53 E54 L55 L56 L57 T58 P59 H62 H66 E70 F74 I75 L76 N77 F78 I82 V88 L89 K90 F94 V95 F96 E99 ILE LYS ASN LEU GLY ILE PRO SER THR

ILE
ASN
VAL
ASP
PHE
GLN
ALA
ASN
GLU
ILE
ASN
MET
ASP
ASP
LEU
GLN
LYS
GLY
ASN
LEU
ILE
GLY
LYS
MET
ILE
LYS
GLU
GLY

- Molecule 1: A137R

Chain w:  48% 24% 28%

M1 V4 L8 L16 R21 W24 I30 L35 E36 E37 I37 C42 F46 T50 M53 E54 L55 L56 L57 T58 P59 H62 H66 E70 F74 I75 L76 N77 F78 I82 R86 V87 V88 L89 T93 F94 V95 F96 T97 K98 E99 ILE LYS

ASN
LEU
GLY
ILE
PRO
SER
THR
ILE
ASN
VAL
PHE
GLN
ALA
ASN
ILE
GLU
ASN
MET
ASP
ASP
LEU
GLN
LYS
GLY
ASN
LEU
ILE
LYS
GLU
GLY

- Molecule 1: A137R

Chain x:  50% 23% 28%

M1 L8 R21 W24 E25 E26 I30 L35 P38 C42 F46 T50 M53 E54 L55 L56 L57 T58 P59 H62 W65 H66 E70 F74 I75 L76 N77 F78 I82 V88 L89 K90 F94 V95 F96 E99 ILE LYS ASN LEU GLY ILE

PRO
SER
THR
ILE
ASN
VAL
ASP
PHE
GLN
ALA
ASN
ILE
GLU
ASN
MET
ASP
ASP
LEU
GLN
LYS
GLY
ASN
LEU
ILE
GLY
LYS
MET
ASN
ILE
LYS
GLU
GLY

- Molecule 1: A137R

Chain y:  50% 22% 28%

M1 V4 L8 Q17 R21 W24 E25 E26 I30 L35 Y44 F45 F46 M53 E54 L55 L56 L57 T58 P59 H62 T63 H66 E70 F74 I75 L76 N77 F78 I82 V88 L89 K90 F94 V95 F96 E99 ILE LYS ASN LEU GLY ILE

PRO
SER
THR
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ASN
VAL
ASP
PHE
GLN
ALA
ASN
ILE
GLU
ASN
MET
ASP
ASP
LEU
GLN
LYS
GLY
ASN
LEU
ILE
GLY
LYS
MET
ASN
ILE
LYS
GLU
GLY

- Molecule 1: A137R

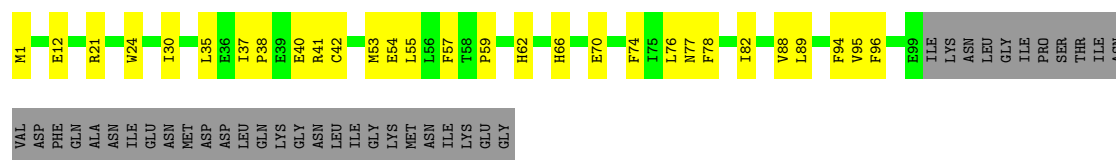
Chain z:  50% 23% 28%

M1 E2 R21 W24 I30 L35 E40 R41 C42 F46 T50 M53 E54 L55 L56 L57 T58 P59 H62 H66 E70 F74 I75 L76 N77 F78 I82 V88 L89 T93 F94 V95 F96 E99 ILE LYS ASN LEU GLY ILE PRO SER THR ILE

ASN
VAL
ASP
PHE
GLN
ALA
ASN
ILE
GLU
MET
ASP
ASP
LEU
GLN
LYS
GLY
ASN
LEU
ILE
GLY
LYS
MET
ASN
ILE
LYS
GLU
GLY

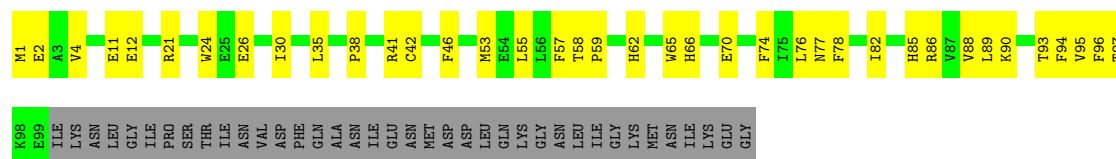
- Molecule 1: A137R

Chain 0:  51% 21% 28%



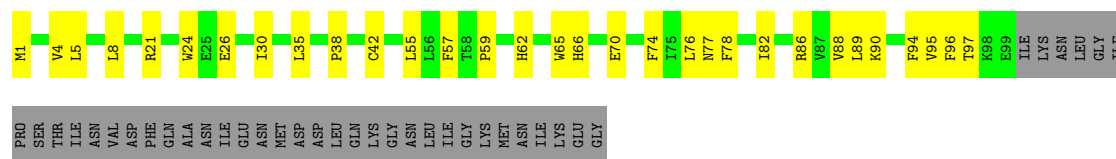
• Molecule 1: A137R

Chain 1:  45% 28% 28%



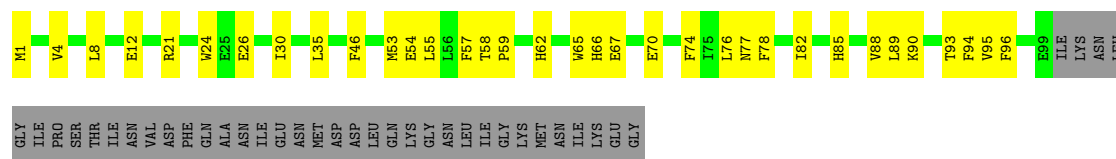
• Molecule 1: A137R

Chain 2:  50% 23% 28%



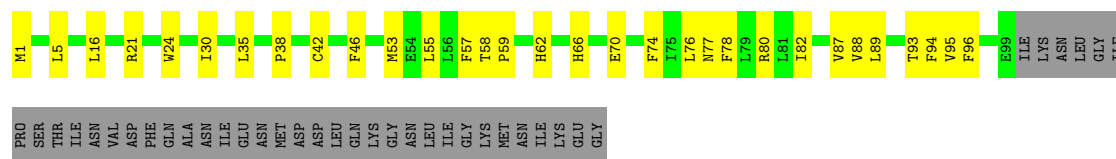
• Molecule 1: A137R

Chain 3:  47% 25% 28%



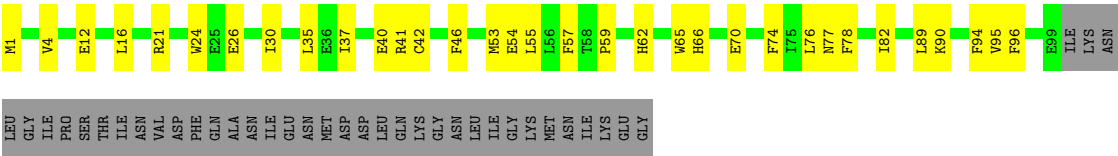
• Molecule 1: A137R

Chain 4:  50% 23% 28%

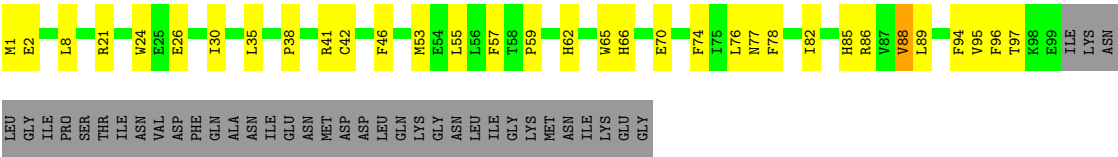


• Molecule 1: A137R

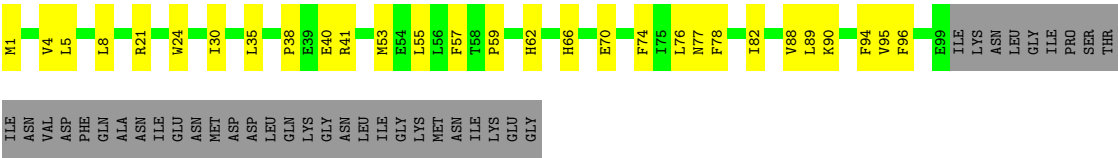
Chain 5:  48% 24% 28%



• Molecule 1: A137R



• Molecule 1: A137R



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	130876	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.132	Depositor
Minimum map value	-0.085	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	374.4, 374.4, 374.4	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	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	0	0.15	0/862	0.33	0/1162
1	1	0.14	0/862	0.29	0/1162
1	2	0.14	0/862	0.28	0/1162
1	3	0.14	0/862	0.28	0/1162
1	4	0.14	0/862	0.28	0/1162
1	5	0.14	0/862	0.31	0/1162
1	6	0.14	0/862	0.31	0/1162
1	7	0.14	0/862	0.28	0/1162
1	A	0.14	0/862	0.31	0/1162
1	B	0.14	0/862	0.29	0/1162
1	C	0.15	0/862	0.30	0/1162
1	D	0.14	0/862	0.30	0/1162
1	E	0.14	0/862	0.28	0/1162
1	F	0.14	0/862	0.31	0/1162
1	G	0.14	0/862	0.29	0/1162
1	H	0.14	0/862	0.29	0/1162
1	I	0.14	0/862	0.30	0/1162
1	J	0.14	0/862	0.28	0/1162
1	K	0.14	0/862	0.30	0/1162
1	L	0.14	0/862	0.29	0/1162
1	M	0.14	0/862	0.29	0/1162
1	N	0.14	0/862	0.30	0/1162
1	O	0.14	0/862	0.28	0/1162
1	P	0.14	0/862	0.30	0/1162
1	Q	0.14	0/862	0.29	0/1162
1	R	0.15	0/862	0.31	0/1162
1	S	0.14	0/862	0.30	0/1162
1	T	0.14	0/862	0.29	0/1162
1	U	0.14	0/862	0.28	0/1162
1	V	0.14	0/862	0.28	0/1162
1	W	0.14	0/862	0.31	0/1162
1	X	0.15	0/862	0.33	0/1162
1	Y	0.14	0/862	0.29	0/1162
1	Z	0.14	0/862	0.29	0/1162

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.14	0/862	0.28	0/1162
1	b	0.14	0/862	0.29	0/1162
1	c	0.15	0/862	0.30	0/1162
1	d	0.14	0/862	0.27	0/1162
1	e	0.14	0/862	0.29	0/1162
1	f	0.14	0/862	0.27	0/1162
1	g	0.15	0/862	0.33	0/1162
1	h	0.14	0/862	0.29	0/1162
1	i	0.14	0/862	0.28	0/1162
1	j	0.14	0/862	0.30	0/1162
1	k	0.17	0/862	0.32	0/1162
1	l	0.14	0/862	0.29	0/1162
1	m	0.14	0/862	0.30	0/1162
1	n	0.14	0/862	0.28	0/1162
1	o	0.14	0/862	0.28	0/1162
1	p	0.14	0/862	0.27	0/1162
1	q	0.14	0/862	0.30	0/1162
1	r	0.14	0/862	0.31	0/1162
1	s	0.14	0/862	0.30	0/1162
1	t	0.14	0/862	0.29	0/1162
1	u	0.14	0/862	0.27	0/1162
1	v	0.14	0/862	0.29	0/1162
1	w	0.15	0/862	0.31	0/1162
1	x	0.14	0/862	0.27	0/1162
1	y	0.14	0/862	0.30	0/1162
1	z	0.13	0/862	0.27	0/1162
All	All	0.14	0/51720	0.29	0/69720

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	840	0	832	27	0
1	1	840	0	832	33	0
1	2	840	0	832	27	0
1	3	840	0	832	26	0
1	4	840	0	832	25	0
1	5	840	0	832	28	0
1	6	840	0	832	32	0
1	7	840	0	832	27	0
1	A	840	0	832	26	0
1	B	840	0	832	25	0
1	C	840	0	832	28	0
1	D	840	0	832	29	0
1	E	840	0	832	26	0
1	F	840	0	832	25	0
1	G	840	0	832	26	0
1	H	840	0	832	26	0
1	I	840	0	832	28	0
1	J	840	0	832	26	0
1	K	840	0	832	26	0
1	L	840	0	832	24	0
1	M	840	0	832	26	0
1	N	840	0	832	31	0
1	O	840	0	832	25	0
1	P	840	0	832	26	0
1	Q	840	0	832	23	0
1	R	840	0	832	28	0
1	S	840	0	832	31	0
1	T	840	0	832	32	0
1	U	840	0	832	27	0
1	V	840	0	832	25	0
1	W	840	0	832	30	0
1	X	840	0	832	34	0
1	Y	840	0	832	27	0
1	Z	840	0	832	24	0
1	a	840	0	832	28	0
1	b	840	0	832	26	0
1	c	840	0	832	30	0
1	d	840	0	832	29	0
1	e	840	0	832	21	0
1	f	840	0	832	27	0
1	g	840	0	832	29	0
1	h	840	0	832	32	0
1	i	840	0	832	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	j	840	0	832	27	0
1	k	840	0	832	26	0
1	l	840	0	832	27	0
1	m	840	0	832	31	0
1	n	840	0	832	26	0
1	o	840	0	832	25	0
1	p	840	0	832	25	0
1	q	840	0	832	24	0
1	r	840	0	832	33	0
1	s	840	0	832	32	0
1	t	840	0	832	24	0
1	u	840	0	832	23	0
1	v	840	0	832	25	0
1	w	840	0	832	28	0
1	x	840	0	832	28	0
1	y	840	0	832	26	0
1	z	840	0	832	24	0
All	All	50400	0	49920	1224	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 12.

The worst 5 of 1224 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:S:82:ILE:HG13	1:T:1:MET:HE2	1.60	0.81
1:I:82:ILE:HG13	1:J:1:MET:HE2	1.63	0.81
1:D:82:ILE:HG13	1:E:1:MET:HE2	1.63	0.81
1:m:82:ILE:HG13	1:n:1:MET:HE2	1.63	0.79
1:N:82:ILE:HG13	1:O:1:MET:HE2	1.63	0.79

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	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	1	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	2	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	3	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	4	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	5	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	6	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	7	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	A	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	B	97/137 (71%)	97 (100%)	0	0	100	100
1	C	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	D	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	E	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	F	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	G	97/137 (71%)	97 (100%)	0	0	100	100
1	H	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	I	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	J	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	K	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	L	97/137 (71%)	97 (100%)	0	0	100	100
1	M	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	N	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	O	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	P	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	Q	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	R	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	S	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	T	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	U	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	V	97/137 (71%)	94 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	W	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	X	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	Y	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	Z	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	a	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	b	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	c	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	d	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	e	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	f	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	g	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	h	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	i	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	j	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	k	97/137 (71%)	97 (100%)	0	0	100	100
1	l	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	m	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	n	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	o	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	p	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	q	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	r	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	s	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	t	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	u	97/137 (71%)	94 (97%)	3 (3%)	0	100	100
1	v	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	w	97/137 (71%)	96 (99%)	1 (1%)	0	100	100
1	x	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	y	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
1	z	97/137 (71%)	95 (98%)	2 (2%)	0	100	100
All	All	5820/8220 (71%)	5705 (98%)	115 (2%)	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	93/126 (74%)	93 (100%)	0	100	100
1	1	93/126 (74%)	93 (100%)	0	100	100
1	2	93/126 (74%)	93 (100%)	0	100	100
1	3	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	4	93/126 (74%)	93 (100%)	0	100	100
1	5	93/126 (74%)	93 (100%)	0	100	100
1	6	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	7	93/126 (74%)	93 (100%)	0	100	100
1	A	93/126 (74%)	93 (100%)	0	100	100
1	B	93/126 (74%)	93 (100%)	0	100	100
1	C	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	D	93/126 (74%)	93 (100%)	0	100	100
1	E	93/126 (74%)	93 (100%)	0	100	100
1	F	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	G	93/126 (74%)	93 (100%)	0	100	100
1	H	93/126 (74%)	91 (98%)	2 (2%)	45	63
1	I	93/126 (74%)	93 (100%)	0	100	100
1	J	93/126 (74%)	93 (100%)	0	100	100
1	K	93/126 (74%)	93 (100%)	0	100	100
1	L	93/126 (74%)	93 (100%)	0	100	100
1	M	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	N	93/126 (74%)	93 (100%)	0	100	100
1	O	93/126 (74%)	93 (100%)	0	100	100
1	P	93/126 (74%)	93 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Q	93/126 (74%)	93 (100%)	0	100	100
1	R	93/126 (74%)	93 (100%)	0	100	100
1	S	93/126 (74%)	93 (100%)	0	100	100
1	T	93/126 (74%)	93 (100%)	0	100	100
1	U	93/126 (74%)	93 (100%)	0	100	100
1	V	93/126 (74%)	93 (100%)	0	100	100
1	W	93/126 (74%)	93 (100%)	0	100	100
1	X	93/126 (74%)	93 (100%)	0	100	100
1	Y	93/126 (74%)	93 (100%)	0	100	100
1	Z	93/126 (74%)	93 (100%)	0	100	100
1	a	93/126 (74%)	93 (100%)	0	100	100
1	b	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	c	93/126 (74%)	93 (100%)	0	100	100
1	d	93/126 (74%)	93 (100%)	0	100	100
1	e	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	f	93/126 (74%)	93 (100%)	0	100	100
1	g	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	h	93/126 (74%)	93 (100%)	0	100	100
1	i	93/126 (74%)	93 (100%)	0	100	100
1	j	93/126 (74%)	93 (100%)	0	100	100
1	k	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	l	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	m	93/126 (74%)	93 (100%)	0	100	100
1	n	93/126 (74%)	93 (100%)	0	100	100
1	o	93/126 (74%)	93 (100%)	0	100	100
1	p	93/126 (74%)	93 (100%)	0	100	100
1	q	93/126 (74%)	93 (100%)	0	100	100
1	r	93/126 (74%)	93 (100%)	0	100	100
1	s	93/126 (74%)	93 (100%)	0	100	100
1	t	93/126 (74%)	93 (100%)	0	100	100
1	u	93/126 (74%)	91 (98%)	2 (2%)	45	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	v	93/126 (74%)	93 (100%)	0	100	100
1	w	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	x	93/126 (74%)	92 (99%)	1 (1%)	65	74
1	y	93/126 (74%)	93 (100%)	0	100	100
1	z	93/126 (74%)	92 (99%)	1 (1%)	65	74
All	All	5580/7560 (74%)	5563 (100%)	17 (0%)	84	84

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	z	50	THR
1	6	88	VAL
1	g	1	MET
1	k	9	ASP
1	l	50	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	62	HIS
1	b	85	HIS
1	s	47	ASN
1	v	85	HIS
1	3	85	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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.

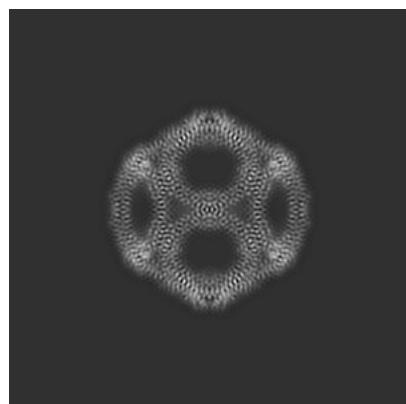
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-38214. These allow visual inspection of the internal detail of the map and identification of artifacts.

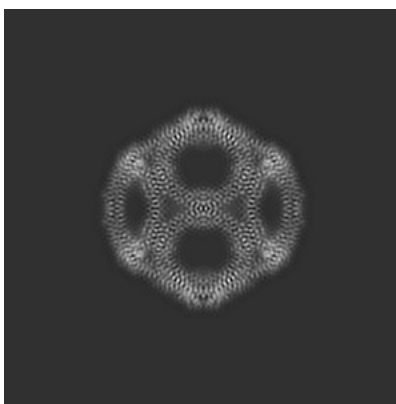
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

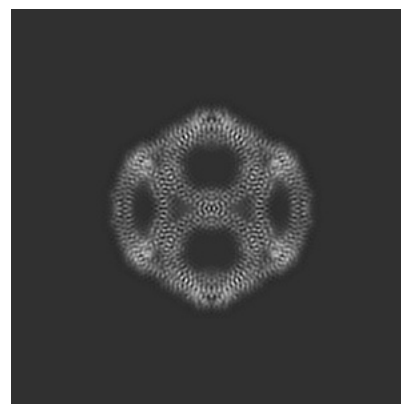
6.1.1 Primary map



X

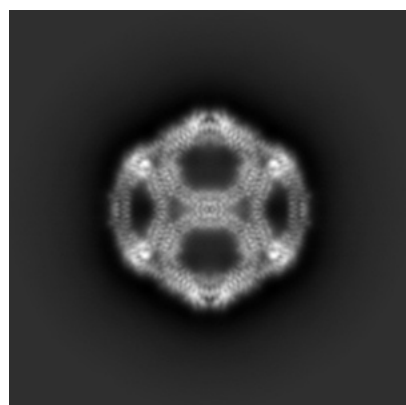


Y

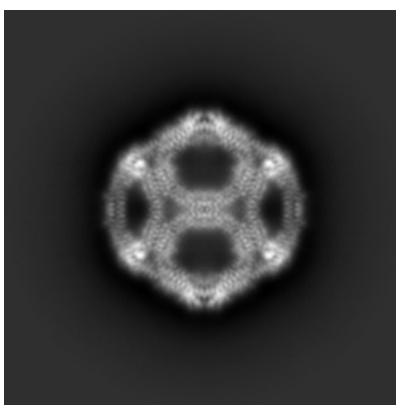


Z

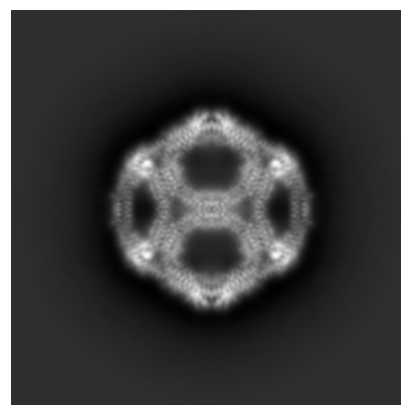
6.1.2 Raw map



X



Y

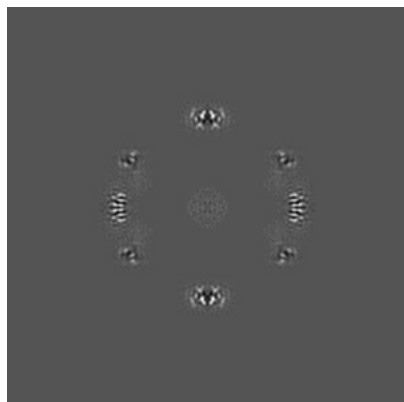


Z

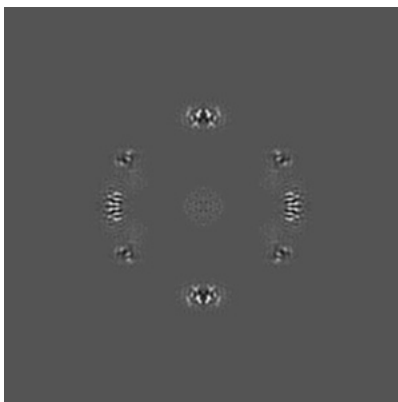
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

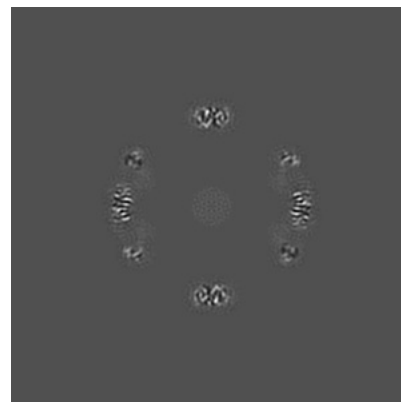
6.2.1 Primary map



X Index: 180

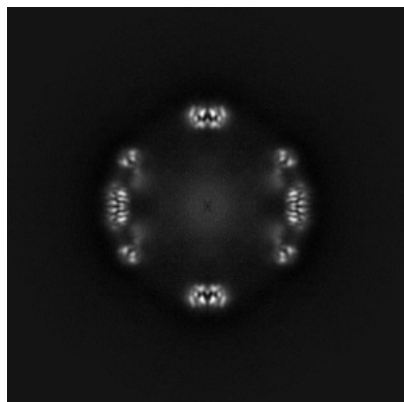


Y Index: 180

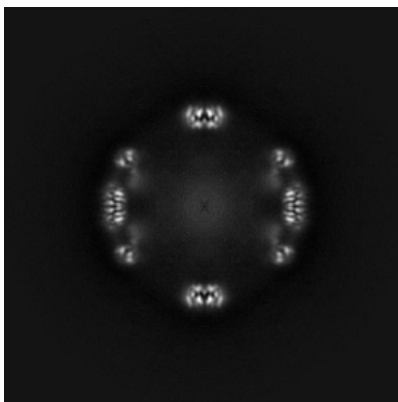


Z Index: 180

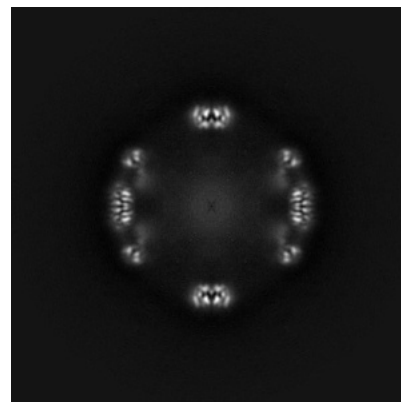
6.2.2 Raw map



X Index: 180



Y Index: 180

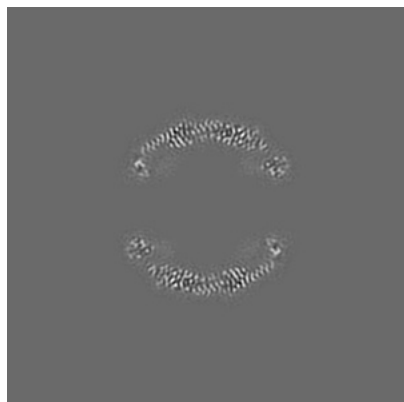


Z Index: 180

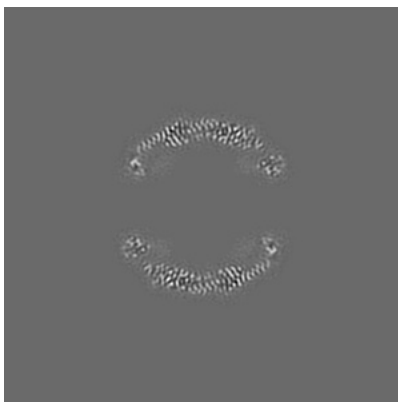
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

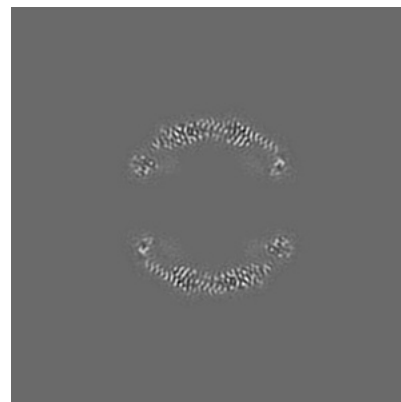
6.3.1 Primary map



X Index: 140

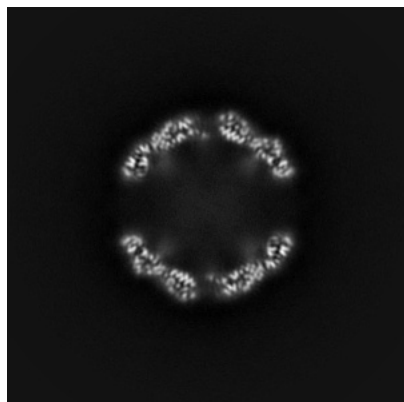


Y Index: 140

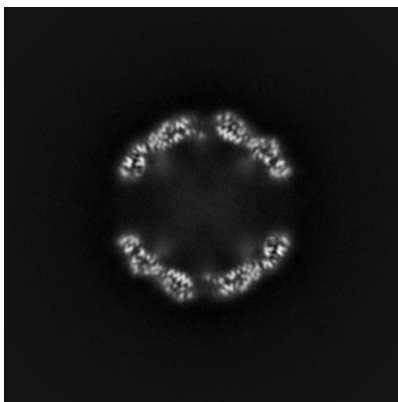


Z Index: 219

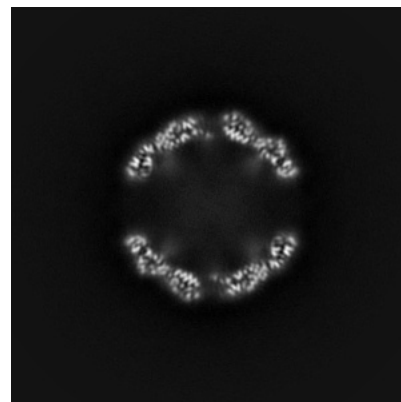
6.3.2 Raw map



X Index: 147



Y Index: 147

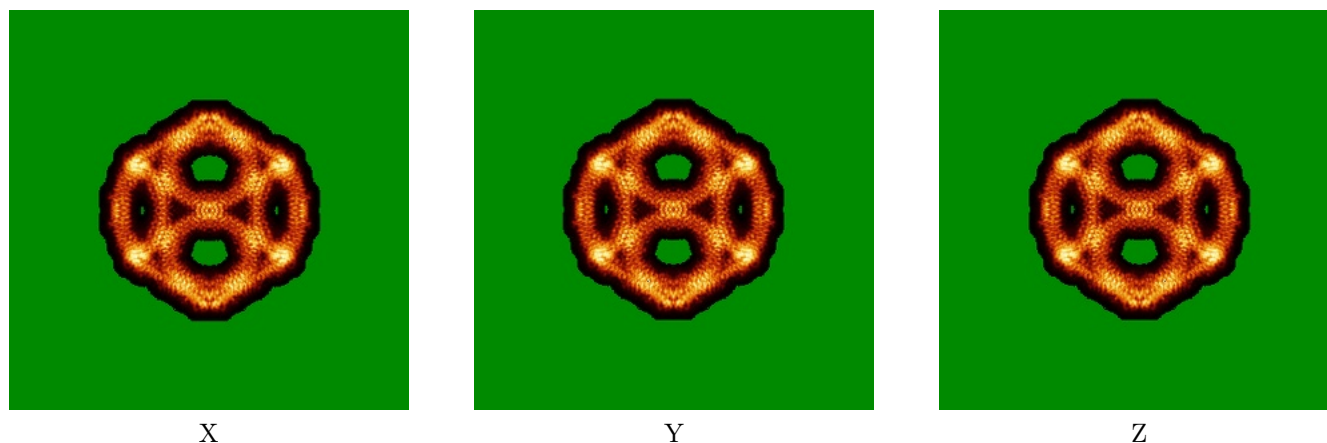


Z Index: 147

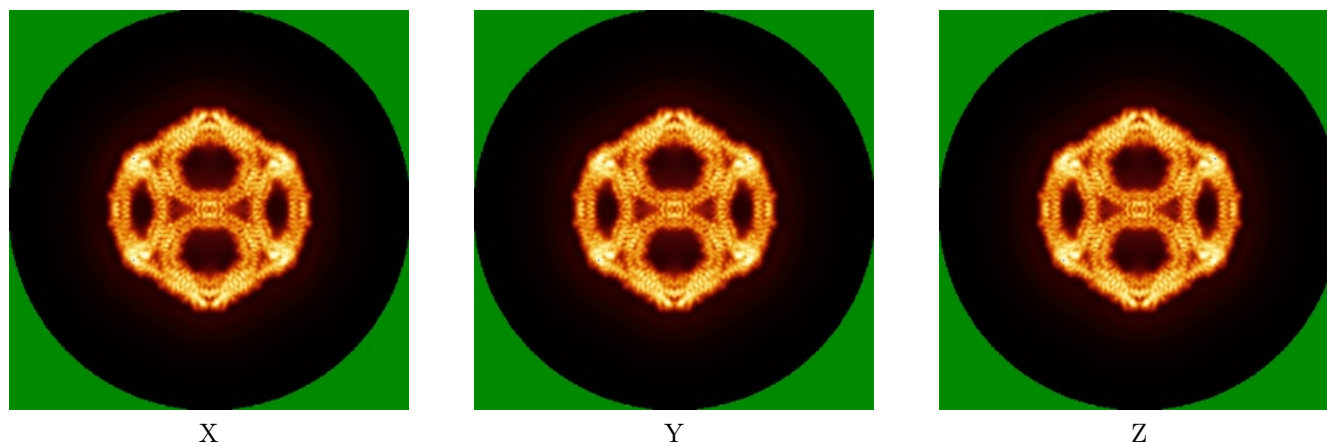
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

This section was not generated.

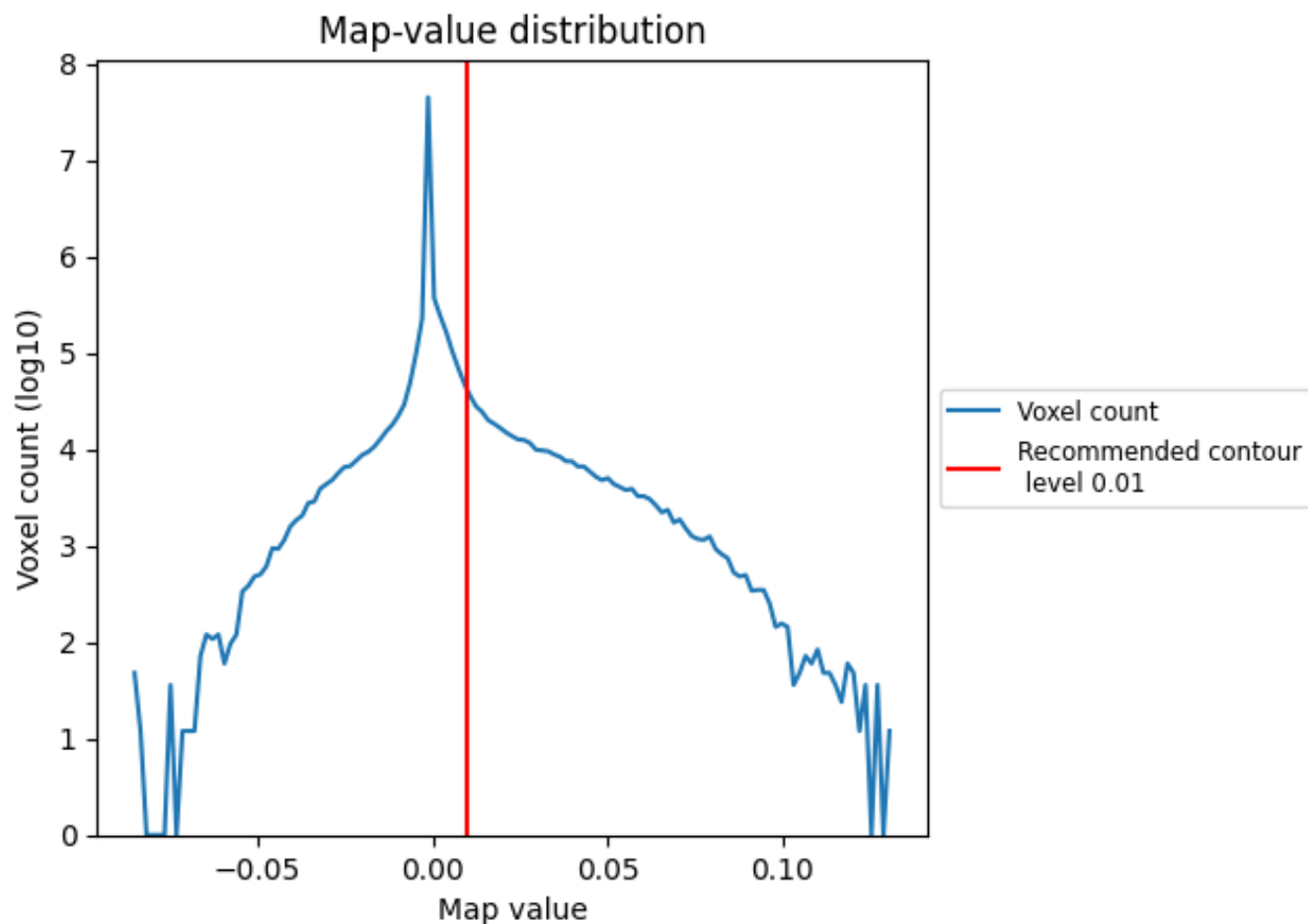
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

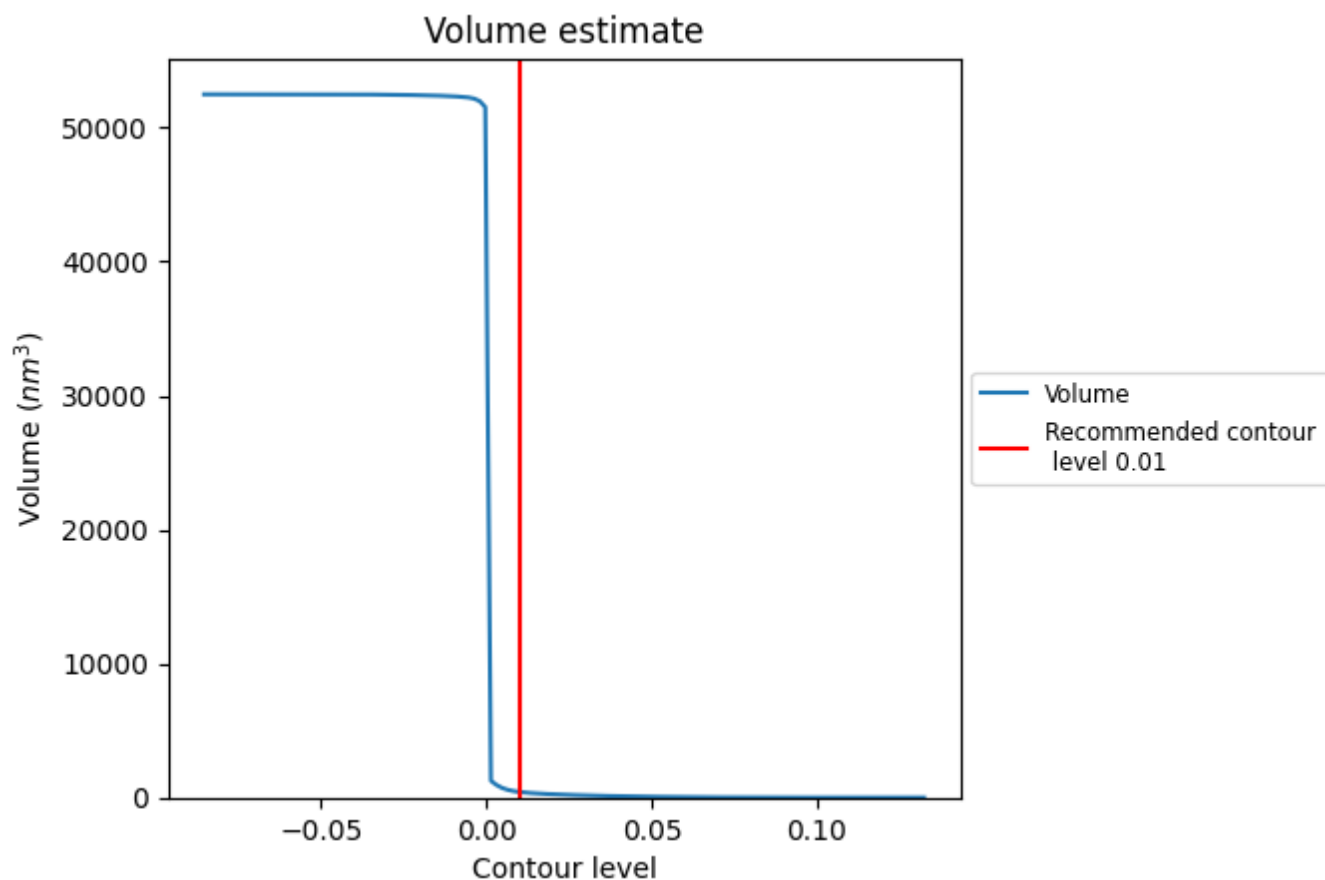
This section contains the results of statistical analysis of the map.

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.

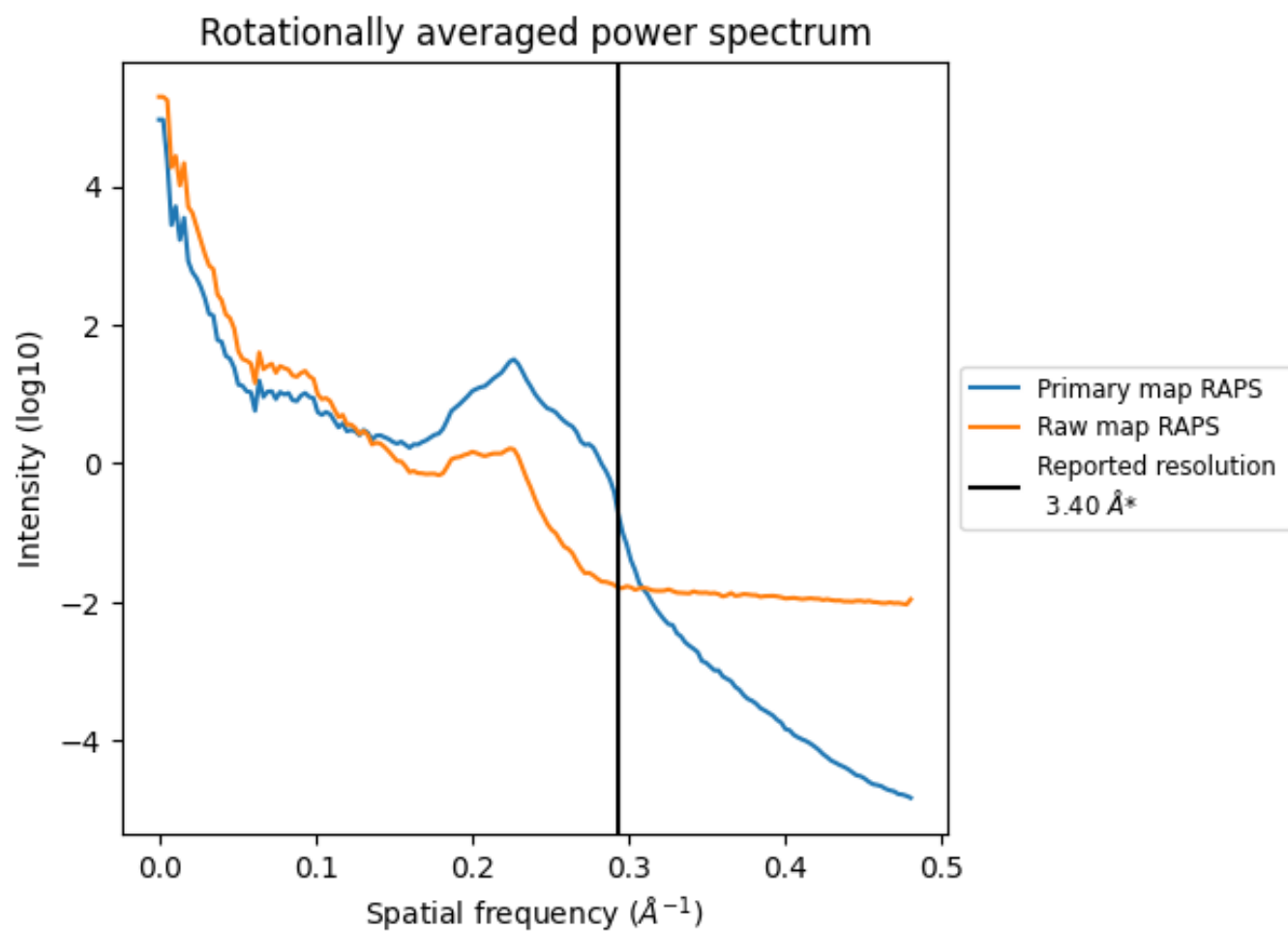
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 420 nm^3 ; this corresponds to an approximate mass of 379 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 ⓘ

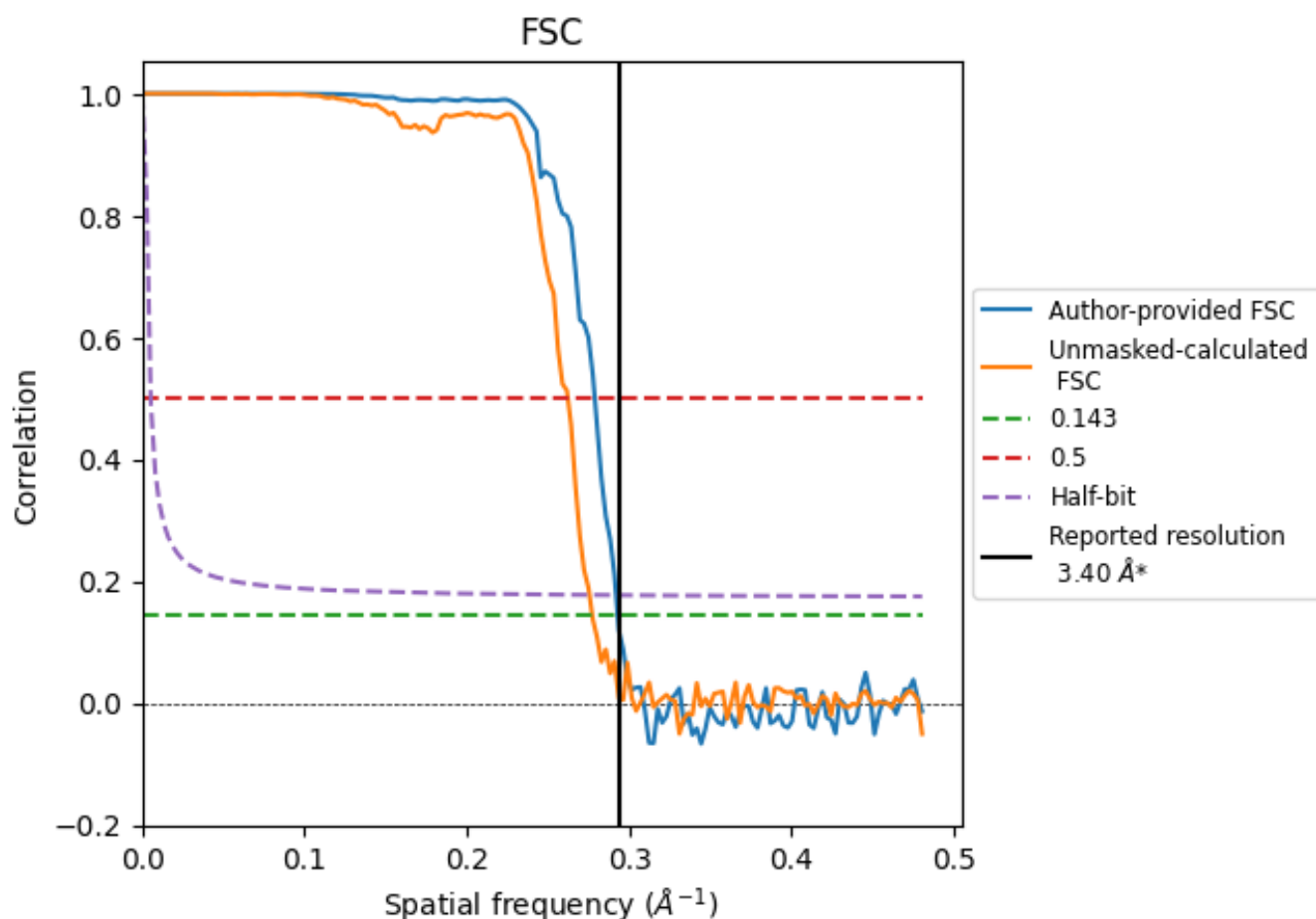


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [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 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

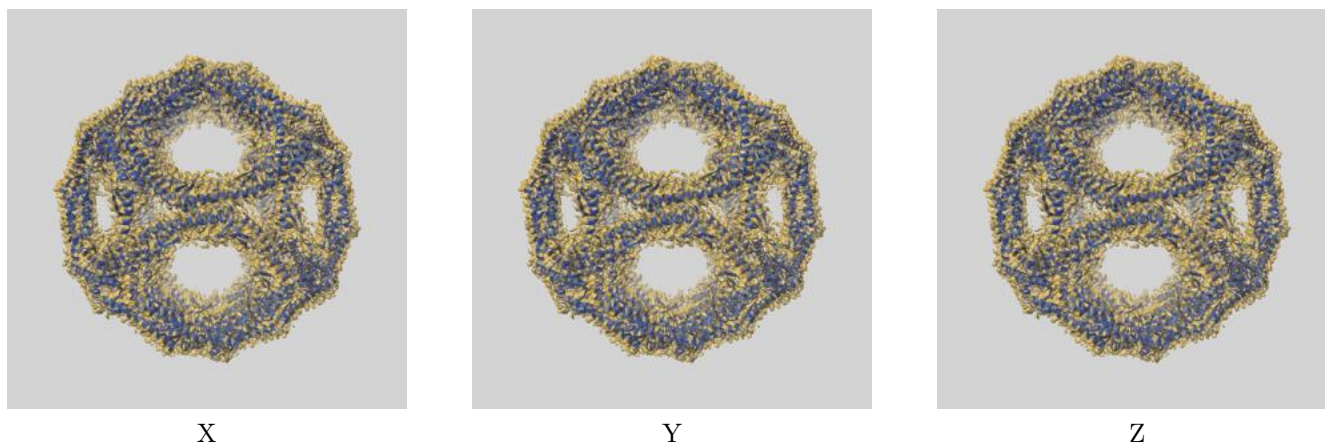
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.41	3.58	3.42
Unmasked-calculated*	3.60	3.81	3.63

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

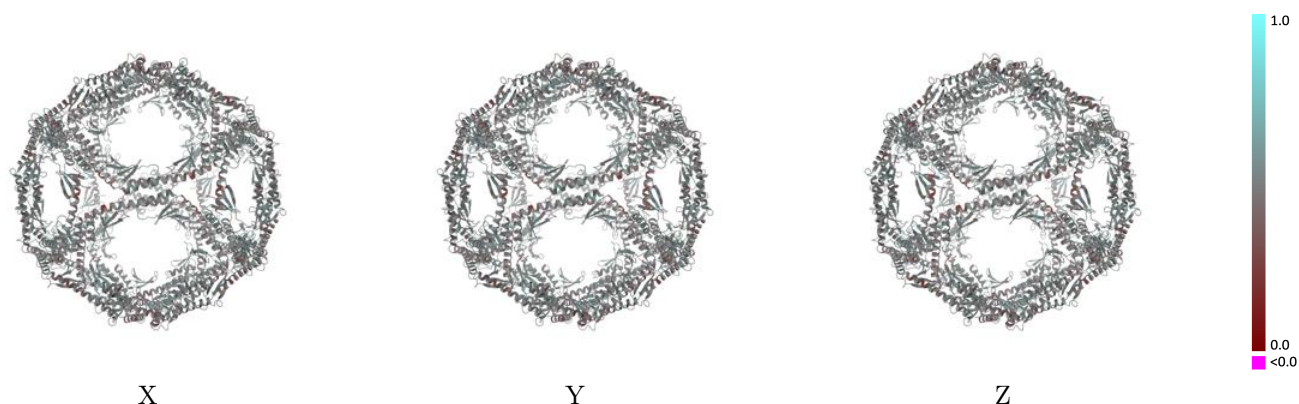
This section contains information regarding the fit between EMDB map EMD-38214 and PDB model 8XB8. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



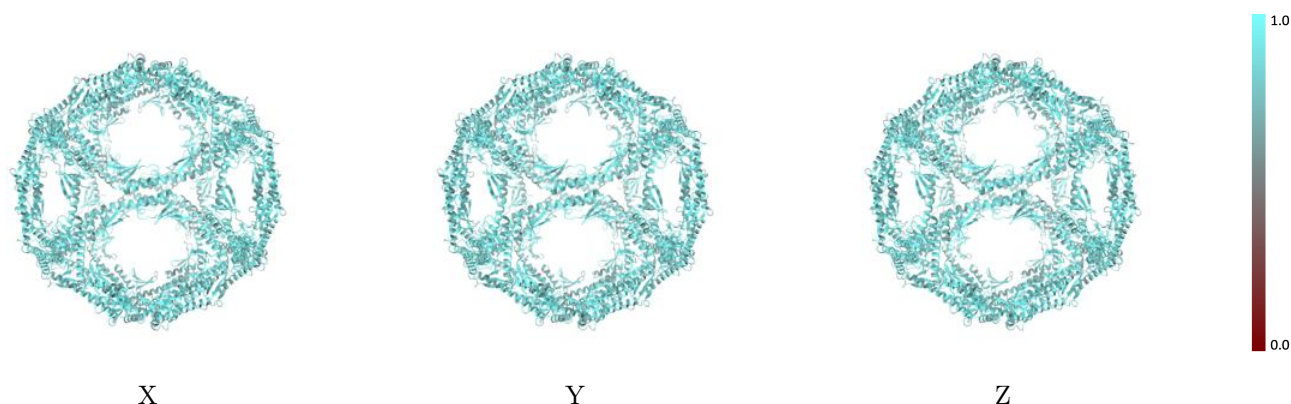
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



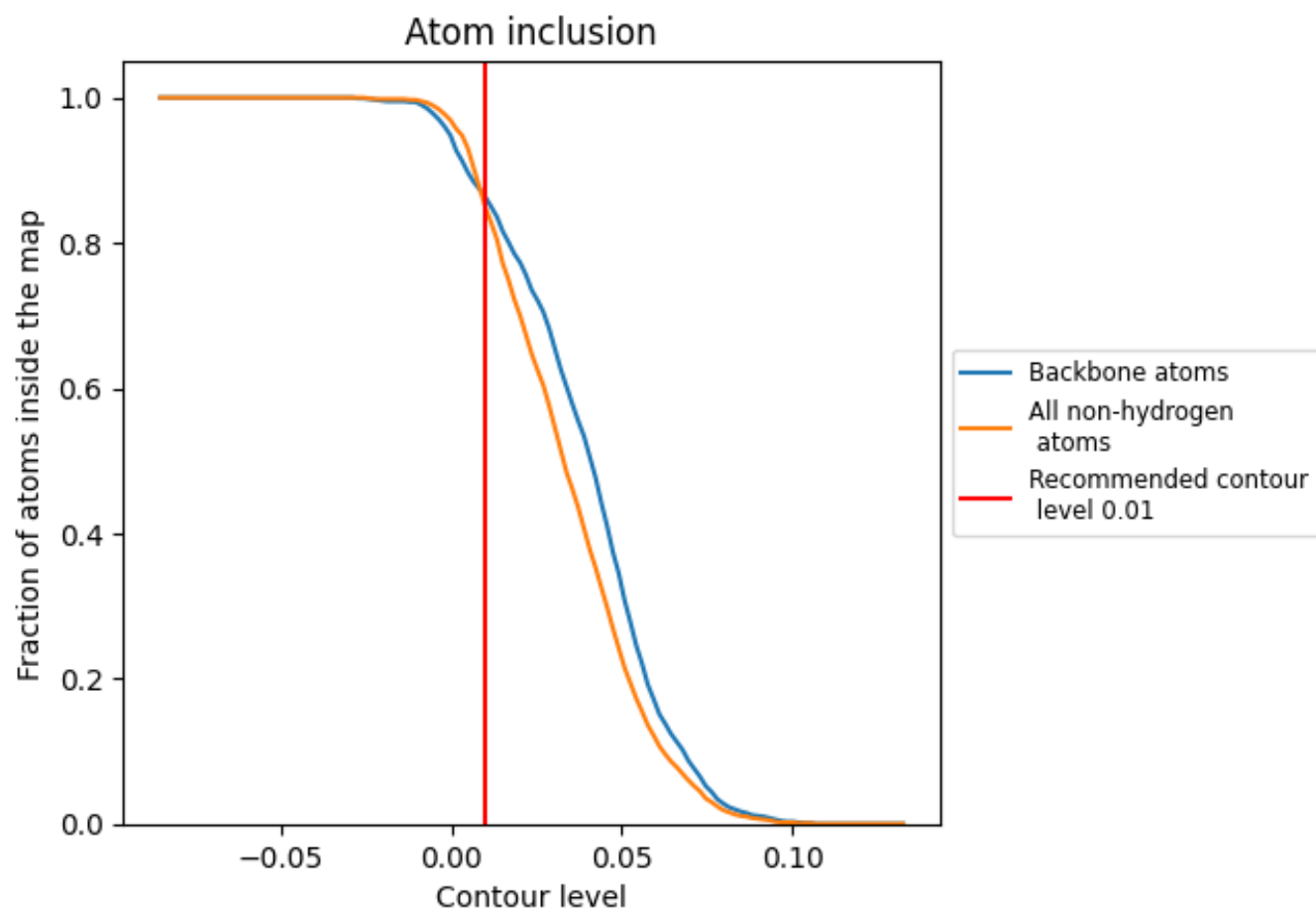
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 85% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8490	 0.4900
0	 0.8500	 0.4890
1	 0.8510	 0.4860
2	 0.8490	 0.4900
3	 0.8540	 0.4880
4	 0.8500	 0.4920
5	 0.8490	 0.4930
6	 0.8500	 0.4940
7	 0.8520	 0.4910
A	 0.8450	 0.4900
B	 0.8520	 0.4930
C	 0.8490	 0.4920
D	 0.8490	 0.4890
E	 0.8510	 0.4940
F	 0.8440	 0.4860
G	 0.8520	 0.4910
H	 0.8490	 0.4920
I	 0.8500	 0.4890
J	 0.8520	 0.4930
K	 0.8440	 0.4930
L	 0.8520	 0.4890
M	 0.8490	 0.4900
N	 0.8490	 0.4890
O	 0.8510	 0.4940
P	 0.8460	 0.4850
Q	 0.8490	 0.4900
R	 0.8460	 0.4860
S	 0.8570	 0.4900
T	 0.8480	 0.4850
U	 0.8490	 0.4870
V	 0.8500	 0.4910
W	 0.8490	 0.4890
X	 0.8520	 0.4890
Y	 0.8510	 0.4900
Z	 0.8440	 0.4910



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Chain	Atom inclusion	Q-score
a	 0.8510	 0.4880
b	 0.8490	 0.4890
c	 0.8560	 0.4930
d	 0.8430	 0.4930
e	 0.8480	 0.4880
f	 0.8480	 0.4890
g	 0.8500	 0.4920
h	 0.8510	 0.4890
i	 0.8490	 0.4930
j	 0.8430	 0.4890
k	 0.8540	 0.4880
l	 0.8490	 0.4870
m	 0.8490	 0.4890
n	 0.8510	 0.4940
o	 0.8510	 0.4870
p	 0.8500	 0.4930
q	 0.8480	 0.4870
r	 0.8520	 0.4890
s	 0.8500	 0.4930
t	 0.8460	 0.4900
u	 0.8540	 0.4910
v	 0.8490	 0.4860
w	 0.8550	 0.4930
x	 0.8410	 0.4910
y	 0.8480	 0.4860
z	 0.8480	 0.4930