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PDB ID	:	8XB8
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 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 (i) 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 (1)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $ELECTRON\ MICROSCOPY$

The reported resolution of this entry is 3.40 Å.

Ramachandran outliers

Sidechain outliers

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	Percentile Ran	ks Value
Ramachandran outliers		0
Sidechain outliers		0.8%
Worse		Better
Percenti	le relative to all structures	
Percenti	le relative to all EM structures	
	1	1
Metric	Whole archive	EM structures
IVIEUTIC	$(\# {\rm Entries})$	$(\# { m Entries})$

154571

154315

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 $\geq=3, 2, 1$ 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.

4023

3826

Mol	Chain	Length	Quality of chain					
1	0	137	72%	• 28%				
1	1	137	72%	• 28%				
1	2	137	72%	• 28%				
1	3	137	72%	• 28%				
1	4	137	72%	28%				
1	5	137	72%	28%				
1	6	137	72%	• 28%				
1	7	137	72%	28%				
1	А	137	72%	28%				



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Mol	Chain	Length	Quality of chain		
1	В	137	72%	•	28%
1	С	137	72%	•	28%
1	D	137	72%	·	28%
1	Е	137	72%		28%
1	F	137	72%		28%
1	G	137	71%	•	28%
1	Н	137	72%		28%
1	Ι	137	72%	•	28%
1	J	137	72%		28%
1	К	137	72%		28%
1	L	137	72%	•	28%
1	М	137	72%	•	28%
1	N	137	72%	•	28%
1	0	137	72%		28%
1	Р	137	71%	•	28%
1	Q	137	72%	•	28%
1	R	137	72%	•	28%
1	S	137	70%	•	28%
1	Т	137	72%		28%
1	U	137	72%		28%
1	V	137	72%	•	28%
1	W	137	72%		28%
1	X	137	72%	•	28%
1	Y	137	72%		28%
1	Z	137	70%	•	28%



Mol	Chain	Length	Quality of chain		
1	a	137	72%		28%
1	b	137	72%	•	28%
1	с	137	72%		28%
1	d	137	72%	•	28%
1	е	137	72%		28%
1	f	137	72%	·	28%
1	g	137	71%	•	28%
1	h	137	72%		28%
1	i	137	72%		28%
1	j	137	72%		28%
1	k	137	71%	•	28%
1	1	137	72%	•	28%
1	m	137	72%	•	28%
1	n	137	72%		28%
1	О	137	72%	•	28%
1	р	137	72%	•	28%
1	q	137	72%		28%
1	r	137	72%		28%
1	s	137	72%		28%
1	t	137	70%	•	28%
1	u	137	72%		28%
1	V	137	72%	•	28%
1	W	137	72%	•	28%
1	x	137	72%	•	28%
1	y	137	72%		28%
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Mol	Chain	Length	Quality of chain							
1	\mathbf{Z}	137	72%	• 28%						



2 Entry composition (i)

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.

Mol	Chain	Residues		At	oms			AltConf	Trace
1	٨	00	Total	С	Ν	0	S	0	0
1	А	99	840	545	140	150	5	0	0
1	D	00	Total	С	Ν	Ο	S	0	0
1	В	99	840	545	140	150	5	0	0
1	С	00	Total	С	Ν	0	S	0	0
1	U	99	840	545	140	150	5	0	0
1	D	99	Total	С	Ν	0	S	0	0
1	D	99	840	545	140	150	5	0	0
1	Ē	00	Total	С	Ν	0	S	0	0
1	Ε	99	840	545	140	150	5	0	0
1	F	00	Total	С	Ν	0	S	0	0
1	Г	99	840	545	140	150	5	0	0
1	C	00	Total	С	Ν	0	S	0	0
1	G	99	840	545	140	150	5	0	0
1	Н	00	Total	С	Ν	Ο	S	0	0
1	П	99	840	545	140	150	5		0
1	Ι	99	Total	С	Ν	0	S	0	0
1	1	99	840	545	140	150	5		
1	J	99	Total	С	Ν	0	S	0	
1	J	99	840	545	140	150	5	0	0
1	IZ.	00	Total	С	Ν	0	S	0	0
1	Κ	99	840	545	140	150	5	0	0
1	т	00	Total	С	Ν	0	S	0	0
1	L	99	840	545	140	150	5	0	0
1	М	99	Total	С	Ν	0	S	0	0
1	IVI	99	840	545	140	150	5	0	0
1	N	00	Total	С	Ν	0	S	0	0
1	Ν	99	840	545	140	150	5	0	0
1	0	00	Total	С	Ν	0	S	0	0
	Ο	99	840	545	140	150	5		0
1	Р	00	Total	С	Ν	0	S	0	0
1	Г	99	840	545	140	150	5		0
1	0	00	Total	С	Ν	0	S	0	0
1	Q	99	840	545	140	150	5	0	0

• Molecule 1 is a protein called A137R.



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Mol	Chain	Residues	0	At	oms			AltConf	Trace
1	р	00	Total	С	Ν	0	S	0	0
1	R	99	840	545	140	150	5	0	0
1	S	00	Total	С	Ν	0	S	0	0
1	S	99	840	545	140	150	5	0	0
1	Т	99	Total	С	Ν	0	S	0	0
1	1	99	840	545	140	150	5	0	0
1	U	99	Total	С	Ν	0	S	0	0
1	U	99	840	545	140	150	5	0	0
1	V	99	Total	С	Ν	Ο	S	0	0
T	v	33	840	545	140	150	5	0	0
1	W	99	Total	С	Ν	Ο	\mathbf{S}	0	0
T	**	55	840	545	140	150	5	0	0
1	Х	99	Total	С	Ν	Ο	\mathbf{S}	0	0
1		55	840	545	140	150	5	0	0
1	Y	99	Total	С	Ν	Ο	\mathbf{S}	0	0
1	1	55	840	545	140	150	5		
1	Z	99	Total	С	Ν	Ο	\mathbf{S}	0	0
T		00	840	545	140	150	5		
1	a	99	Total	С	Ν	Ο	\mathbf{S}	0	0
1	u	00	840	545	140	150	5		
1	b	99	Total	С	Ν	0	S	0	0
-	~		840	545	140	150	5	Ŭ	
1	с	99	Total	С	Ν	Ο	S	0	0
-			840	545	140	150	5	Ŭ	
1	d	99	Total	С	Ν	0	S	0	0
-			840	545	140	150	5	Ŭ	
1	е	99	Total	С	N	0	S	0	0
			840	545	140	150	5	-	_
1	f	99	Total	С	N	0	S	0	0
			840	545	140	150	5		
1	g	99	Total	C	N	0	S	0	0
	0		840	545	140	150	5		
1	h	99	Total	C	N	0	S	0	0
			840	545	140 N	150	5		
1	i	99	Total	C E 4 E	N 140	0 150	S E	0	0
			840 Tetal	545	140 N	150	5	0	
1	j	99	Total	C 545	N 140	O 150	S 5		0
			840 Total	545	140 N	$\frac{150}{0}$	$\frac{5}{S}$		
1	k	99	Total 840	C 545		O 150		0	0
				545 C	140 N	150 O	$\frac{5}{S}$		
1	1	99	Total 840					0	0
			840	545	140	150	$\frac{5}{\gamma_{ontin}}$		



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Mol	Chain	Residues		At	oms			AltConf	Trace
1		00	Total	С	Ν	0	S	0	0
1	m	99	840	545	140	150	5	0	0
1		00	Total	С	Ν	Ο	S	0	0
1	n	99	840	545	140	150	5	0	0
1		00	Total	С	Ν	0	S	0	0
1	Ο	99	840	545	140	150	5	0	0
1	5	99	Total	С	Ν	0	S	0	0
1	р	99	840	545	140	150	5	0	0
1	a	99	Total	С	Ν	0	S	0	0
T	q	99	840	545	140	150	5	0	0
1	r	99	Total	С	Ν	0	S	0	0
T	r	99	840	545	140	150	5	0	0
1	g	99	Total	С	Ν	Ο	S	0	0
T	\mathbf{S}	99	840	545	140	150	5	0	0
1	t	99	Total	С	Ν	0	S	0	0
T	U	99	840	545	140	150	5	0	U
1	11	99	Total	С	Ν	0	S	0	0
T	u	99	840	545	140	150	5		0
1		99	Total	С	Ν	Ο	S	0	0
T	V	99	840	545	140	150	5		0
1	117	99	Total	С	Ν	Ο	S	0	0
T	W	99	840	545	140	150	5		
1	v	99	Total	С	Ν	Ο	\mathbf{S}	0	0
T	х	99	840	545	140	150	5	0	0
1	37	99	Total	С	Ν	Ο	S	0	0
T	У	99	840	545	140	150	5	0	0
1	Z	99	Total	С	Ν	Ο	S	0	0
T	Z	33	840	545	140	150	5	0	0
1	0	99	Total	С	Ν	Ο	S	0	0
T	0	55	840	545	140	150	5	0	0
1	1	99	Total	С	Ν	Ο	\mathbf{S}	0	0
T	1	55	840	545	140	150	5	0	0
1	2	99	Total	С	Ν	Ο	\mathbf{S}	0	0
T		55	840	545	140	150	5	0	0
1	3	99	Total	С	Ν	Ο	\mathbf{S}	0	0
Ŧ	0		840	545	140	150	5		
1	4	99	Total	С	Ν	Ο	\mathbf{S}	0	0
<u> </u>	*		840	545	140	150	5		
1	5	99	Total	С	Ν	Ο	\mathbf{S}	0	0
*	5		840	545	140	150	5		
1	6	99	Total	С	Ν	Ο	S	0	0
*	0		840	545	140	150	5		



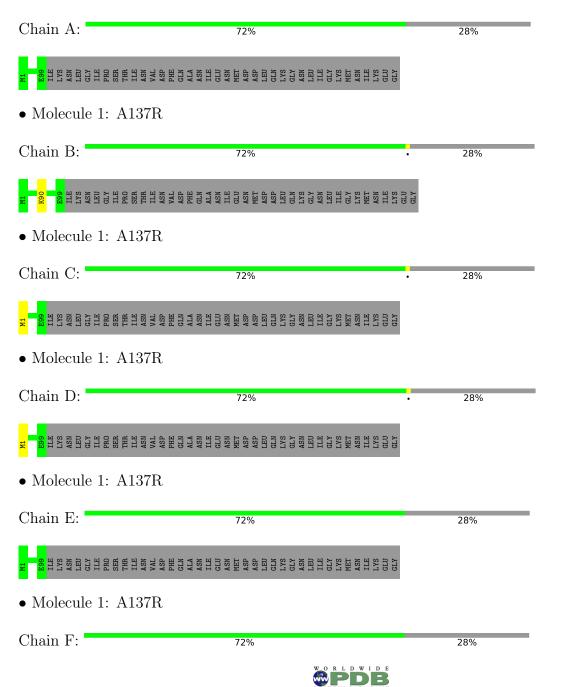
Mol	Chain	Residues		At	oms			AltConf	Trace
1	7	99	Total 840	C 545	N 140	0 150	${f S}{5}$	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: A137R



MI E59 LTEE LTEE LEU ASN ASN THR THR THR THR ASP PRE PHE PHE PHE CLA	11.5.1 ASN MET ASP ASP ASP ASP CLV GLV ASP CLV ASN ASN ASN ASN ASN ASN ASN ASN ASN ASN	
• Molecule 1: A137R		
Chain G:	71% .	28%
MI K28 K28 K28 K28 K28 K28 K28 K28 K28 K28	PHE PHE CLM ASN ASN ASN ASN ASN ASN ASN ASN CLM CLM CLM CLM CLM CLM CLM CLM CLM CLM	
• Molecule 1: A137R		
Chain H:	72%	28%
MI EE9 E29 ASN ASN ALN THE THE THE ASN ASP ASP ALA ALA ALA	ALM ALM ALM ALM ALM ALM ALM ALM ALM ALM	
• Molecule 1: A137R		
Chain I:	72% •	28%
MI E80 LLVS ASN ASN ASN THR THR ASN ASN ASN ASN ASN ALA	11.5 11.6 11.6 11.6 11.6 11.6 11.7 11.6 11.1 11.6 11.1 11.6 11.7 11.1 11.6 11.7 11.1 11.6 11.7 11.7	
• Molecule 1: A137R		
Chain J:	72%	28%
M1 E89 LLYS LLYS ASN ASN LLE LLE LLE LLE LLE ASP ASP CLN ASP ALA ALA	ALM ALM ALU ALU ALM ALM ALM ALM ALM ALM ALM ALM ALM ALM	
• Molecule 1: A137R		
Chain K:	72%	28%
M1 EB9 EB9 ASN ASN ALEU LLFU LLFU LLFU ASN ASN ASP ASP ALA	ALSN ALSN ALSN ALSN ALSP ALSP ALSP ALSN ALSN ALSN ALSN ALSN ALSN ALSN ALSN	
• Molecule 1: A137R		
Chain L:	72%	28%
M1 K90 K90 LLEU LLEU LLEU ALSU ALSU ALSU ALSU ALSU ALSU ALSU ALS	ALM ALM ALL CLLE CLLE ALM MET ALM ALF ALM ALM ALM ALM ALM ALM ALM ALL ALM ALL ALM ALL	
• Molecule 1: A137R		
Chain M:	72%	28%



M1 EES ASN CLEU LLE CLEU CLEU CLEU ASN ASN ASN ASN ASN ASN ASN ASN ASN ASN	ASN ASP ASP ASP ASP CLV CLV CLV CLV ASN CLV ASN ASN CLV ASN ASN CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	
• Molecule 1: A137R		
Chain N:	72% ·	28%
M1 EE C C C C C C C C C C C C C C C C C C	ASN MET ASP ASP ASP CLEU CLEU CLYS ASN CLY ASN ASN ASN CLY CLY CLY CLY CLY CLY CLY CLY	
• Molecule 1: A137R		
Chain O:	72%	28%
M Egg LIYS LIYS LIYS CLIY CLIY CLIY ASN ALA ALA ALA ALA ALA ALA ALA ALA ALA AL	ASN ASP ASP ASP ASP ASP CLU CLV ASU CLV ASU CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	
• Molecule 1: A137R		
Chain P:	71% •	28%
M1 K90 K90 K90 K90 LEU LEU LEU LEU ASN ASP ASP ASP ASP ASP ASP ASP ASP ASA ASP ASP	ILE GLU ASN ASP ASP ASP ASP CLN CLN CLN CLN CLN CLN CLN CLN CLN CLN	
• Molecule 1: A137R		
Chain Q:	72% ·	28%
M1 K90 E89 E89 E89 CLEU CLEU CLEU CLEU ASN ASP PHE PHE PHE ASP ASS ASS ASS ASS ASS ASS ASS ASS ASS	ILE ILE ASN MET ASP ASP ASP CLU CLEU CLEU CLEU CLEU CLEU CLEU CLEU	
• Molecule 1: A137R		
Chain R:	72% ·	28%
M1 1689 1788 1788 1788 1788 1788 1788 1788 17	ASN MET ASP ASP ASP ASP CLU GLU GLY ASN ASN CLY GLU GLY GLY GLY	
• Molecule 1: A137R		
Chain S:	70% ·	28%
MI K14 K14 K14 K90 LEU LEU LEU LEU ASN ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	ALA ALA ASN ASN ASN ASP ASP ASP ASP ASP CLV CLN CLN CLN CLN CLN CLN CLN CLN CLN CLN	
• Molecule 1: A137R		
Chain T:	72%	28%



M1 E99 LLYS LLYS LEU CLEU CLEU SERO SERO	THR THR ASP VAEN VAEN VAEN VAEN ASP PHE GLU ASN ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	
• Molecule 1: .	A137R	
Chain U:	72%	28%
M1 E99 LYS ASN LEU ILE PR0 SER	THR THR VAS VAS VAS VAS VAS ASP THR THR ASP THR ASP THR ASP THR ASP THR ASP THR ASP CUV CVS CUV CVS CUV CVS CUV CVS CUV CVS CUV CVS CUV CVS CUV CVS CVS CVS CVS CVS CVS CVS CVS CVS CV	
• Molecule 1:	A137R	
Chain V:	72%	28%
M1 K90 LLE LLYS ASN ASN CLY CLY	PARD TILE TILE SER ASN ASN ASN ASN ASN ASN ASN ASN ASN ASN	
• Molecule 1: .	A137R	
Chain W:	72%	28%
M1 11E 11E 11F ASN GLY GLY FRO SER SER	JERR VAL VAL VAL VAL VAL ASP PHE CLN ASP ASN ASN ASP CLU ASP CLU ASN ASN CLU ASN ASN CLU ASN ASN CLU ASN CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	
• Molecule 1: .	A137R	
Chain X:	72% ·	28%
M1 LLF LLYS ASN GLY FLEU FLEU FLEU SER SER	THR THR THR VAL VAL ASP THE CHE CHE CHE CHE CHE CHE CHE CLN ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	
• Molecule 1: .	A137R	
Chain Y:	72%	28%
M1 11E 11E 11F ASN GLY GLY FRO SER SER	JERR VAL VAL VAL VAL VAL ASP PHE CLN ASP ASN ASN ASP CLU ASP CLU ASN ASN CLU ASN ASN CLU ASN ASN CLU ASN CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	
• Molecule 1: .	A137R	
Chain Z:	70% .	28%
M1 M53 K90 LILE LILE LILE	LIN LIN LIEU LIEU PRO PRO PRO PRO PRO PRO PRO ASN ASN ASN ASN ASN ASN ASN ASN ASN ASN	GLY
• Molecule 1: .	A137R	_
Chain a:	72%	28%



MI ESS LILE LILE LILE LILE LILE ASN VAL ASN ASN ALA ALA ALA ALA ALA ALA ALA ALA ALA CLU	ASN ASP ASP ASP ASP CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	
• Molecule 1: A137R		
Chain b:	72% .	28%
M1 E99 LILE LVS LVS LLE LVS CLE CLE VAL ASN ASN ASN ASN ASN ALA ALA ALA ALA ALA ALA CLU	ASN MET ASP ASP ASP ASP CLN GLN GLN GLN GLN ASN MET ASN CLY GLV GLV GLV GLV	
• Molecule 1: A137R		
Chain c:	72%	28%
M1 E59 LTE LTE LTE LTE ASN CLE ASN ASP ASP ALA ALA ALA ALA ALA ALA ALU CLU	ASN MET ASP ASP ASP ASP GLV GLV GLY ASN MET ASN ASN ASN CLY GLY GLY GLY	
• Molecule 1: A137R		
Chain d:	72% ·	28%
M1 M53 M53 M53 M53 M53 M53 ASN ASN ASN ASN ASN	CLE CLE ASP ASP ASP ASP ASP CLV CLV CLV CLV ASN ASN ASN ASN CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	
• Molecule 1: A137R		
Chain e:	72%	28%
M E99 LTS LTS LTS LTS LTS LTS LTS TTE TTE ASN ASP ASP ASP ASP ASP ASN ASA ASN ASI ASN ASI ASN ASI ASN ASI ASN ASI ASI ASI ASI ASI ASI ASI ASI ASI ASI	MET ASP ASP ASP ASP LEU CLY GLY ASN MET ASN MET ASN CLY GLY GLU GLU	
• Molecule 1: A137R		
Chain f:	72% •	28%
M1 M53 M53 M53 M53 M53 LEU LEU LEU LEU CLA ASN ASN ASN ASN	CLE CLE ASP ASP ASP ASP CLV CLV CLV CLV CLV ASN ASN ASN CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	
• Molecule 1: A137R		
Chain g:	71% •	28%
M K90 LLEU LLEU LLEU LLEU LLEU LLEU LLEU LLE	11.E GLU ASN ASP ASP ASP ASP CLU CLU CLU CLU CLU ASN CLY ASN CLY ASN CLY CLY CLY CLY CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	
• Molecule 1: A137R		
Chain h:	72%	28%



MI ESS LEE LEV LEV LEV CLY LEV CLY ASN ASN ASN ASN ASN ASN ASN ASN ASN ASN	ASN MET ASP ASP ASP ASP CLN LFS GLY CLN CLN ASN MET ASN ASN CLY CLY CLY CLY CLY CLY CLY CLY CLU CLY CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	
• Molecule 1: A137R		
Chain i:	72%	28%
MI E99 LLYS ASN ASN ASN TTR TTR TTR ASN ASN ASN ASN ASN ASN ASN ASN TTL ASN ASN ASN ASN ASN ASN ASN ASN ASN ASN	ASIN MET ASP ASP ASP CLIN CLIN CLIN CLIN CLIN CLIN CLIN CLIN	
• Molecule 1: A137R		
Chain j:	72%	28%
M1 1112 1112 1112 1112 1112 1112 1112 1	ASP MET ASP ASP ASP ASP CLY GLY CLY CLY ASN LYS CLY ASN CLY CLY CLY CLY CLY CLY CLY CLY CLY CLY	
• Molecule 1: A137R		
Chain k:	71% .	28%
M1 D9 K90 LLYS LLYS LLYS SER LLYS CLY LLUE LLEU LLEU LLEU LLEU LLEU ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	od.n 11.E 11.E 11.E 11.E 11.E 11.E 11.E 11	
• Molecule 1: A137R		
Chain l:	72% .	28%
M1 EB9 LLYS ASN ASN ASN ASN ASN ASN ASN ASN ASN AS	ASN MET ASP ASP ASP CLN CLN CLN CLN CLN CLN CLN CLN CLN CLN	
• Molecule 1: A137R		
Chain m:	72%	28%
MI E 20 E	AGN MET ASP ASP ASP ASP CLY CLU CLU CLY ASN ASN ASN ASN ASN ASN CLY STL ASN ASN CLY CLY CLY CLY CLY CLY CLY CLY CLY CLY	
• Molecule 1: A137R		
Chain n:	72%	28%
M1 E59 LYS LYS LYS LYS LYS LYS ASN ASN ASN ASN ASN ASN ASN ASN ASN AS	ASU MET ASP ASP ASP CLN CLU CLV CLV CLV ASN CLV ASN TLE CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	
• Molecule 1: A137R		
Chain o:	72% ·	28%



MI ES9 LYS LYS LYS LYS CLY CLY CLY CLY CLY CLY CLY CLY CLY CLY	ASP PHE GLN ALA ALA ALA ALA ALA ASP CLU CLU CLU CLU CLU CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	
• Molecule 1: A137F	3	
Chain p:	72% •	28%
M K90 L1/E L1/E L1/E L1/E L1/E L1/E L1/E L1/E	ASN VAL ASP ASS ASS ASS ASS ASS ASS ASS ASS ASS	
• Molecule 1: A137H	3	
Chain q:	72%	28%
M1 E99 LYE LYE LYE ASN 01F TLE TLE TLE THR THR THR YAL	ASP PHE GIN ALA ALA ALA ALA ALA ALA ASN ASN ASP CLU ASP CLU ASP CLU CLU CLV ASP CLU CLV CLV CLV CLV CLV CLV CLV CLV CLV CLV	
• Molecule 1: A137	3	
Chain r:	72%	28%
M1 E99 LTE LTE LTE LEU GLY TLE TLE ASN VSL	ASP PHE GLN ALA ALA ALA ALA ASN ASP ASN ASP CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	
• Molecule 1: A137F	3	
Chain s:	72%	28%
M1 E99 LTLE LTLE LTLE LTLE CLEU GLEV CLEU TLE TLE TLE ASN VASN	ASP PHE GLN ALA ALA ALA ASN ASN ASP CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	
• Molecule 1: A137F	3	
Chain t:	70% •	28%
M1 K28 M53 M53 M53 M53 M53 K90 A53 A53 A54 A54 A54 A54 A54 A54 A54 A54 A54 A54	PRO SER THR ASP VASI ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	411
• Molecule 1: A137I	3	
Chain u:	72%	28%
M1 E99 LLE LLE LLEU LLEU GLFU GLFV GLFY TLE FRO SER ASN VAL	ASP PHE GLN GLN AIA ASN ASN ASN ASN ASN CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	
• Molecule 1: A137	3	
Chain v:	72%	28%



M1 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2 M2	
• Molecule 1: A137R	
Chain w: 72%	• 28%
M1 K90 K90 LEU CLEU CLEU CLEU CLEU CLEU CLEU CLEU	GLY
• Molecule 1: A137R	
Chain x: 72%	• 28%
M M M M M M M M M M M M M M M M M M M	ATD BTU
• Molecule 1: A137R	
Chain y: 72%	28%
M1 E99 11.5 11.5 11.5 11.6 11.8 11.8 11.8 11.8 11.8 11.8 11.8	
• Molecule 1: A137R	
Chain z: 72%	• 28%
	• 28%
M1 M1 M5 M5 M5 M5 M5 M5 M5 M5 M5 M5 M5 M5 M5	
 ※ 8日25日26日25日26日10555100日1555500日3555500日3555500日3555500日3555500日3555500日35555500日35555500000000	GLY
2 2 <th2< th=""> <th2< th=""> <th2< th=""> <th2< th=""></th2<></th2<></th2<></th2<>	• 28%
W S B H S	• 28%
2 2	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Image: Construction of the second	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0



M1 11 11 11 11 11 11 11 11 11 11 11 11 1	ASP PHE GLA ASN ALA ASN ASN ASN ASP ASP ASP CLU ASP CLU ASP CLN ASP CLN ASP CLN ASP CLN ASP CLN ASP ASP ASN ASN ASN ASN ASN ASN ASN ASN ASN ASN	CTV CTV
• Molecule 1: A137	R	
Chain 3:	72%	• 28%
M1 E99 ILE LV CLEU CLEU CLEU CLEU CLEU CLEU CLEU TLE FRO SER TLE ASN VAL	ASP PHE ALA ALA ASN ASN CLU CLU ASN ASP CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	LYS GLY GLY
• Molecule 1: A137	R	
Chain 4:	72%	28%
H E99 LLE LLY LLE LLU CLFU CLFU CLFU CLFU CLFU CLFA CLFA FRO SER ASI VASI	ASP PHE PHE GHL ALA ALA ASN ASN ASN ASN ASN ASP CLU CLU CLU CLU CLU CLU CLU CLU CLU CLU	CTV CLV CLV
• Molecule 1: A137	R	
Chain 5:	72%	28%
	72% 72% 8H4 8H4 8H4 8H5 8H5 8H5 8H5 8H5 8H5 8H5 8H5 8H5 8H5	28%
	ASP PHE CLA ASP ASN ASN ASN ASP ASP CLU ASP CLU CLEU CLEU CLEU CLEU CLEU CLEU CLEU	28%
MI E99 LYS LYS LYS LEU GIY THE THE THE SER YAL	ASP PHE CLA ASP ASN ASN ASN ASP ASP CLU ASP CLU CLEU CLEU CLEU CLEU CLEU CLEU CLEU	28% 28%
E BHHEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	ASP ASP ASP ASP ASP ASP ASP ASP ASP ASP	• 28%
E BHHEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE	R 72% 811 811 811 811 811 811 811 811 811 81	• 28%
• Molecule 1: A1371 Chain 6: •	R 72% 811 811 811 811 811 811 811 811 811 81	• 28%



4 Experimental information (i)

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 $(^{\circ})$	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
WIOI	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5
1	0	0.26	0/862	0.48	0/1162
1	1	0.26	0/862	0.46	0/1162
1	2	0.26	0/862	0.46	0/1162
1	3	0.26	0/862	0.46	0/1162
1	4	0.26	0/862	0.44	0/1162
1	5	0.26	0/862	0.46	0/1162
1	6	0.26	0/862	0.46	0/1162
1	7	0.26	0/862	0.44	0/1162
1	А	0.26	0/862	0.47	0/1162
1	В	0.26	0/862	0.45	0/1162
1	С	0.26	0/862	0.46	0/1162
1	D	0.26	0/862	0.46	0/1162
1	Е	0.26	0/862	0.45	0/1162
1	F	0.26	0/862	0.47	0/1162
1	G	0.26	0/862	0.45	0/1162
1	Н	0.26	0/862	0.46	0/1162
1	Ι	0.26	0/862	0.46	0/1162
1	J	0.26	0/862	0.45	0/1162
1	Κ	0.26	0/862	0.47	0/1162
1	L	0.26	0/862	0.45	0/1162
1	М	0.26	0/862	0.45	0/1162
1	Ν	0.26	0/862	0.46	0/1162
1	0	0.26	0/862	0.45	0/1162
1	Р	0.26	0/862	0.46	0/1162
1	Q	0.26	0/862	0.45	0/1162
1	R	0.26	0/862	0.46	0/1162
1	S	0.26	0/862	0.45	0/1162
1	Т	0.26	0/862	0.46	0/1162
1	U	0.26	0/862	0.46	0/1162
1	V	0.26	0/862	0.44	0/1162
1	W	0.26	0/862	0.46	0/1162
1	Х	0.26	0/862	0.47	0/1162
1	Y	0.26	0/862	0.45	0/1162
1	Ζ	0.26	0/862	0.46	0/1162



Mol	Chain	Bond	lengths	Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	a	0.26	0/862	0.45	0/1162	
1	b	0.26	0/862	0.45	0/1162	
1	с	0.26	0/862	0.46	0/1162	
1	d	0.26	0/862	0.45	0/1162	
1	е	0.26	0/862	0.47	0/1162	
1	f	0.26	0/862	0.45	0/1162	
1	g	0.27	0/862	0.49	0/1162	
1	h	0.26	0/862	0.46	0/1162	
1	i	0.26	0/862	0.45	0/1162	
1	j	0.26	0/862	0.46	0/1162	
1	k	0.27	0/862	0.46	0/1162	
1	1	0.26	0/862	0.46	0/1162	
1	m	0.26	0/862	0.46	0/1162	
1	n	0.26	0/862	0.45	0/1162	
1	0	0.26	0/862	0.46	0/1162	
1	р	0.26	0/862	0.44	0/1162	
1	q	0.26	0/862	0.46	0/1162	
1	r	0.26	0/862	0.46	0/1162	
1	s	0.26	0/862	0.45	0/1162	
1	t	0.26	0/862	0.46	0/1162	
1	u	0.26	0/862	0.45	0/1162	
1	V	0.26	0/862	0.46	0/1162	
1	W	0.26	0/862	0.46	0/1162	
1	Х	0.26	0/862	0.45	0/1162	
1	у	0.26	0/862	0.47	0/1162	
1	Z	0.26	0/862	0.45	0/1162	
All	All	0.26	0/51720	0.46	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)

Due to software issues we are unable to calculate clashes - this section is therefore empty.



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	Perce	ntiles
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	А	97/137~(71%)	95 (98%)	2 (2%)	0	100	100
1	В	97/137~(71%)	97 (100%)	0	0	100	100
1	С	97/137~(71%)	94 (97%)	3 (3%)	0	100	100
1	D	97/137~(71%)	95 (98%)	2 (2%)	0	100	100
1	Е	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	Н	97/137~(71%)	95 (98%)	2 (2%)	0	100	100
1	Ι	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	М	97/137~(71%)	95 (98%)	2 (2%)	0	100	100
1	Ν	97/137~(71%)	95 (98%)	2 (2%)	0	100	100
1	О	97/137~(71%)	94 (97%)	3 (3%)	0	100	100
1	Р	97/137~(71%)	94 (97%)	3 (3%)	0	100	100
1	Q	97/137~(71%)	96 (99%)	1 (1%)	0	100	100



Mol	Chain	n previous page Analysed	Favoured	Allowed	Outliers	Perce	ntiles
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	Т	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
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	с	97/137~(71%)	96 (99%)	1 (1%)	0	100	100
1	d	97/137~(71%)	95 (98%)	2 (2%)	0	100	100
1	е	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	1	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	0	97/137~(71%)	94 (97%)	3(3%)	0	100	100
1	р	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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	ntiles
1	W	97/137~(71%)	96~(99%)	1 (1%)	0	100	100
1	х	97/137~(71%)	95~(98%)	2(2%)	0	100	100
1	У	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 (i)

In the following table, the Percentiles column shows the percent side chain 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	Perce	ntiles
1	0	93/126~(74%)	92~(99%)	1 (1%)	73	86
1	1	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	2	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	3	93/126~(74%)	92 (99%)	1 (1%)	73	86
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%)	73	86
1	7	93/126~(74%)	93 (100%)	0	100	100
1	А	93/126~(74%)	93 (100%)	0	100	100
1	В	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	С	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	D	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	Ε	93/126~(74%)	93 (100%)	0	100	100
1	F	93/126~(74%)	93 (100%)	0	100	100
1	G	93/126~(74%)	91 (98%)	2(2%)	52	75
1	Н	93/126~(74%)	93 (100%)	0	100	100
1	Ι	93/126~(74%)	92 (99%)	1 (1%)	73	86



Mol	Chain	Analysed	Rotameric	Outliers	Perce	ntiles
1	J	93/126~(74%)	93~(100%)	0	100	100
1	Κ	93/126~(74%)	93 (100%)	0	100	100
1	L	93/126~(74%)	92~(99%)	1 (1%)	73	86
1	М	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	Ν	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	Ο	93/126~(74%)	93 (100%)	0	100	100
1	Р	93/126~(74%)	91 (98%)	2(2%)	52	75
1	Q	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	R	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	S	93/126~(74%)	90 (97%)	3 (3%)	39	67
1	Т	93/126 (74%)	93 (100%)	0	100	100
1	U	93/126~(74%)	93 (100%)	0	100	100
1	V	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	W	93/126~(74%)	93 (100%)	0	100	100
1	Х	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	Y	93/126~(74%)	93 (100%)	0	100	100
1	Ζ	93/126~(74%)	90 (97%)	3(3%)	39	67
1	a	93/126~(74%)	93 (100%)	0	100	100
1	b	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	с	93/126~(74%)	93 (100%)	0	100	100
1	d	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	е	93/126~(74%)	93 (100%)	0	100	100
1	f	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	g	93/126~(74%)	91 (98%)	2(2%)	52	75
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%)	91 (98%)	2 (2%)	52	75
1	1	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	m	93/126~(74%)	92 (99%)	1 (1%)	73	86
1	n	93/126~(74%)	93 (100%)	0	100	100



Mol	Chain	Analysed	Rotameric	Outliers	Perce	entiles
1	О	93/126~(74%)	92~(99%)	1 (1%)	73	86
1	р	93/126~(74%)	92~(99%)	1 (1%)	73	86
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%)	90~(97%)	3~(3%)	39	67
1	u	93/126~(74%)	93~(100%)	0	100	100
1	v	93/126~(74%)	92~(99%)	1 (1%)	73	86
1	W	93/126~(74%)	92~(99%)	1 (1%)	73	86
1	х	93/126~(74%)	92~(99%)	1 (1%)	73	86
1	У	93/126~(74%)	93 (100%)	0	100	100
1	Z	93/126~(74%)	92~(99%)	1 (1%)	73	86
All	All	5580/7560~(74%)	5536 (99%)	44 (1%)	82	91

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	В	90	LYS
1	С	1	MET
1	C D G	1	MET
1	G	28	LYS
1	G	90	LYS
1	Ι	1	MET
1	L	90	LYS
1	М	1	MET
1	Ν	1	MET
1	N P P	1	MET
1	Р	90	LYS
1	Q R	90	LYS
1	R	1	MET
1	S	1	MET
1	S	14	LYS
1	S	90	LYS
1	V	90	LYS
1	Х	1	MET
1	Ζ	28	LYS
1	Ζ	53	MET
1	Z	90	LYS



Mol	Chain	Res	Type
1	b	1	MET
1	d	53	MET
1	f	53	MET
1	g	1	MET
1	g	90	LYS
1	k	9	ASP
1	k	90	LYS
1	1	1	MET
1	m	1	MET
1	0	1	MET
1	р	90	LYS
1	t	28	LYS
1	\mathbf{t}	53	MET
1	t	90	LYS
1	V	1	MET
1	W	90	LYS
1	Х	53	MET
1	Z	53	MET
1	0	90	LYS
1	1	1	MET
1	2	1	MET
1	3	1	MET
1	6	1	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides 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.



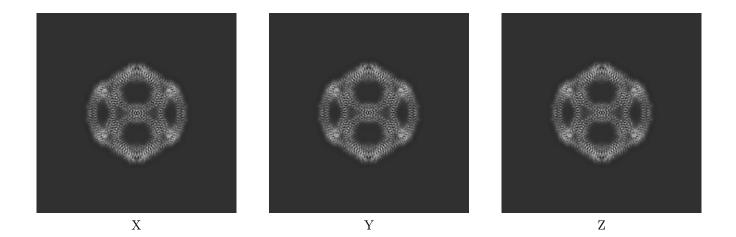
6 Map visualisation (i)

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.

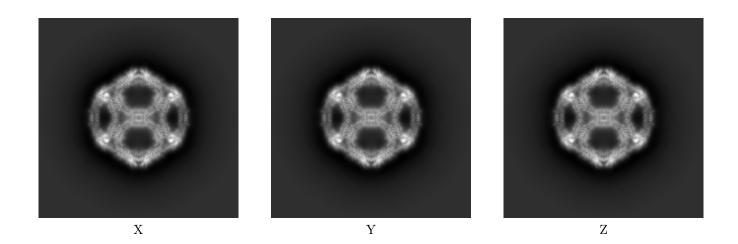
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

6.1.1 Primary map



6.1.2 Raw map

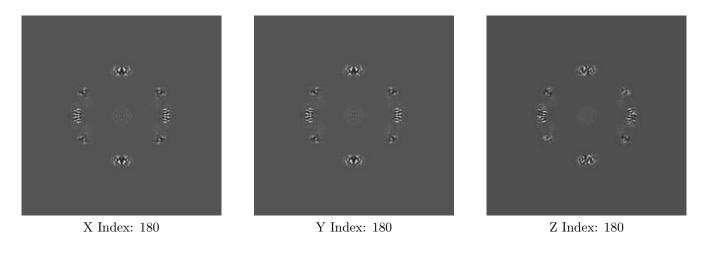


The images above show the map projected in three orthogonal directions.

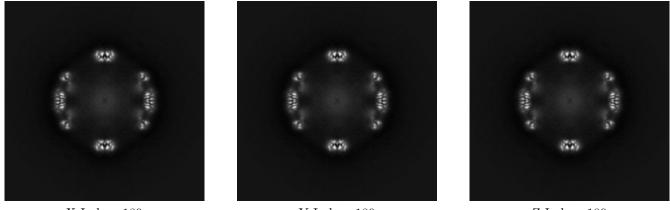


6.2 Central slices (i)

6.2.1 Primary map



6.2.2 Raw map



X Index: 180

Y Index: 180

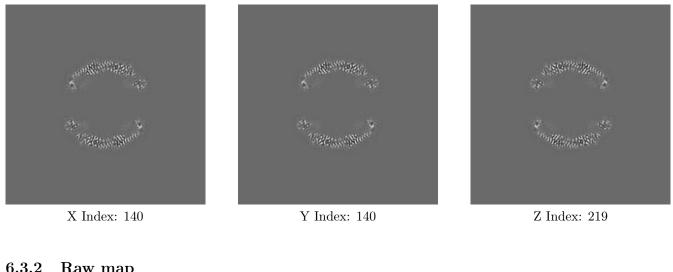


The images above show central slices of the map in three orthogonal directions.

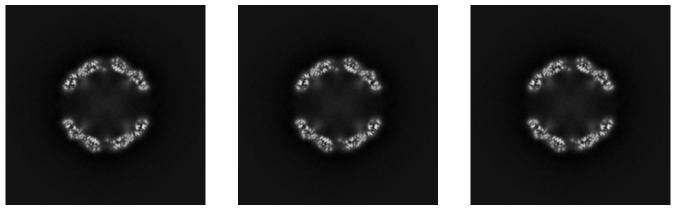


6.3 Largest variance slices (i)

Primary map 6.3.1



Raw map 6.3.2



X Index: 147

Y Index: 147

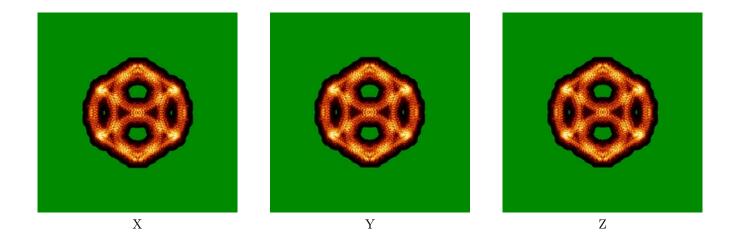


The images above show the largest variance slices of the map in three orthogonal directions.

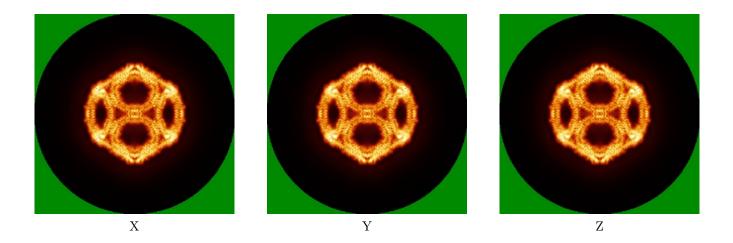


6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map



6.4.2 Raw map

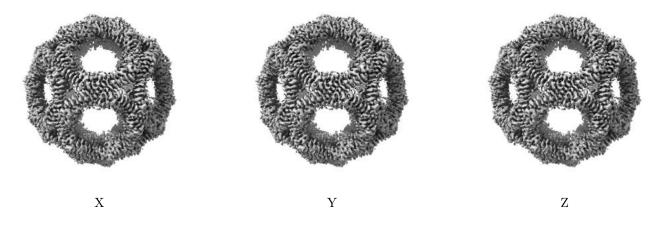


The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.



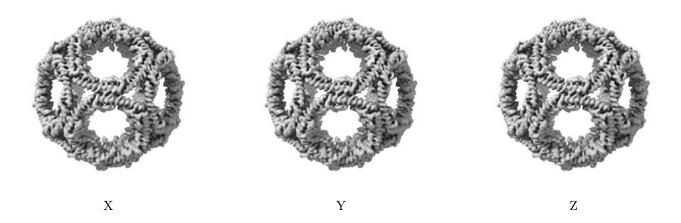
6.5 Orthogonal surface views (i)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

6.6 Mask visualisation (i)

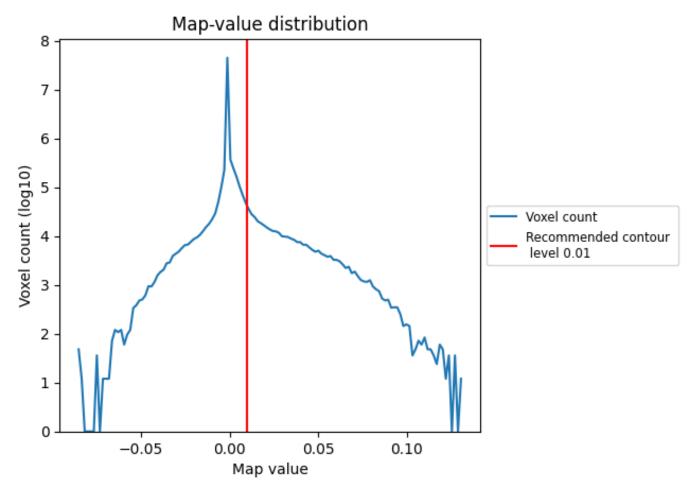
This section was not generated. No masks/segmentation were deposited.



7 Map analysis (i)

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

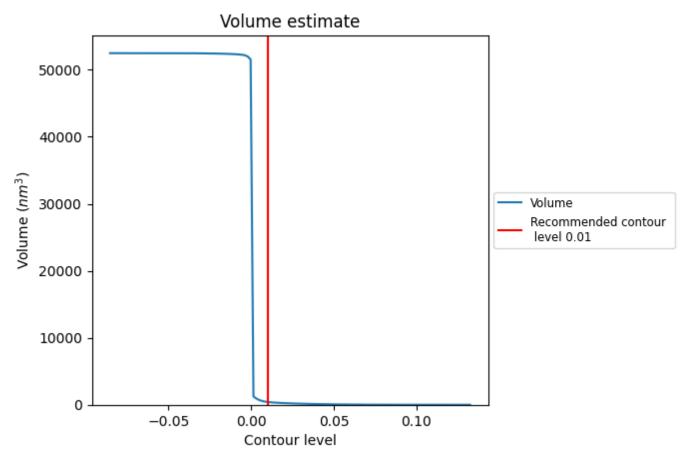
7.1 Map-value distribution (i)



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)

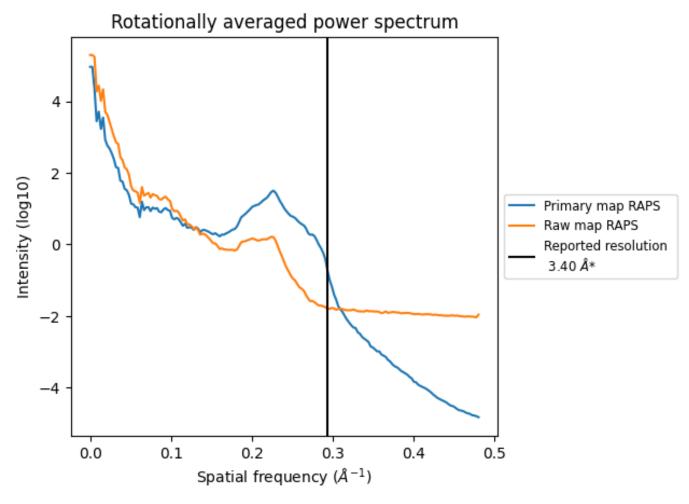


The volume at the recommended contour level is 420 $\rm nm^3;$ this corresponds to an approximate mass of 379 kDa.

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 (i)



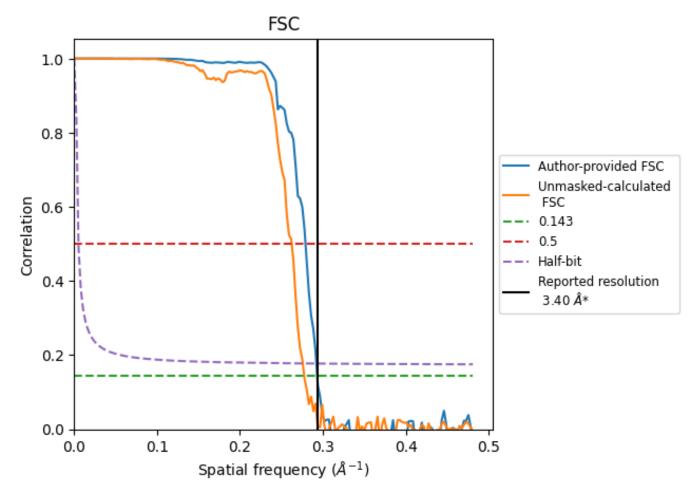
*Reported resolution corresponds to spatial frequency of 0.294 $\mathrm{\AA^{-1}}$



8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.294 $\mathrm{\AA^{-1}}$



8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
Resolution estimate (A)	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	

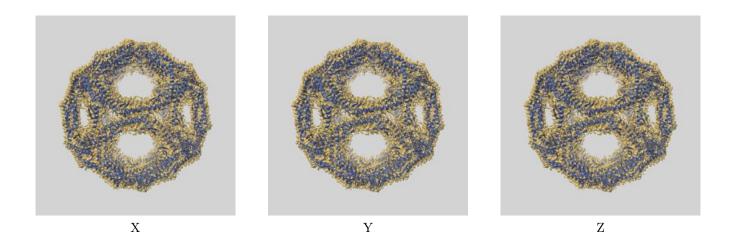
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



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.

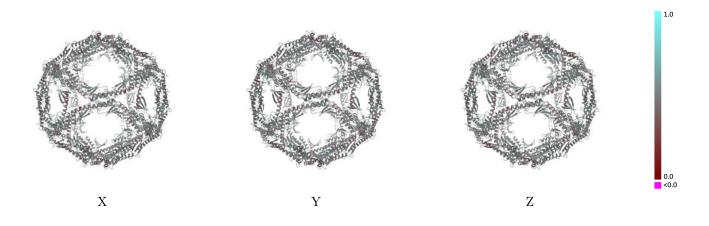
9.1 Map-model overlay (i)



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.

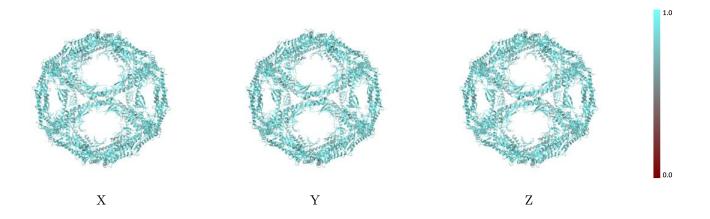


9.2 Q-score mapped to coordinate model (i)



The images above show the model with each residue coloured according 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.

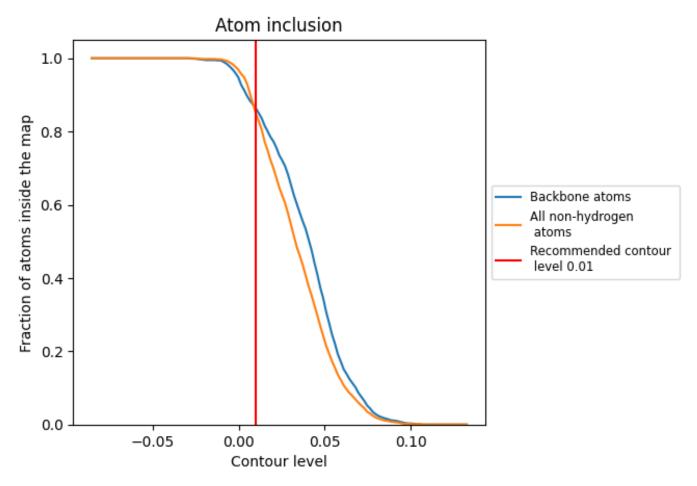
9.3 Atom inclusion mapped to coordinate model (i)



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 (i)

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
А	0.8450	0.4900
В	0.8520	0.4930
С	0.8490	0.4920
D	0.8490	0.4890
Е	0.8510	0.4940
F	0.8440	0.4860
G	0.8520	0.4910
Н	0.8490	0.4920
Ι	0.8500	0.4890
J	0.8520	0.4930
K	0.8440	0.4930
L	0.8520	0.4890
М	0.8490	0.4900
Ν	0.8490	0.4890
О	0.8510	0.4940
Р	0.8460	0.4850
Q	0.8490	0.4900
R	0.8460	0.4860
S	0.8570	0.4900
Т	0.8480	0.4850
U	0.8490	0.4870
V	0.8500	0.4910
W	0.8490	0.4890
Х	0.8520	0.4890
Y	0.8510	0.4900
Z	0.8440	0.4910

0.0 <0.0

1.0



Chain	Atom inclusion	Q-score
a	0.8510	0.4880
b	0.8490	0.4890
С	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
1	0.8490	0.4870
m	0.8490	0.4890
n	0.8510	0.4940
0	0.8510	0.4870
р	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
У	0.8480	0.4860
Z	0.8480	0.4930

