



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 02:41 PM UTC

PDB ID : 6ZVT / pdb_00006zvt
EMDB ID : EMD-11470
Title : C13 symmetry: Bacterial Vipp1 and PspA are members of the ancient ESCRT-III membrane-remodeling superfamily.
Authors : Liu, J.W.; Tassinari, M.; Souza, D.P.; Naskar, S.; Noel, J.K.; Bohuszewicz, O.; Buck, M.; Williams, T.A.; Baum, B.; Low, H.H.
Deposited on : 2020-07-27
Resolution : 7.00 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:

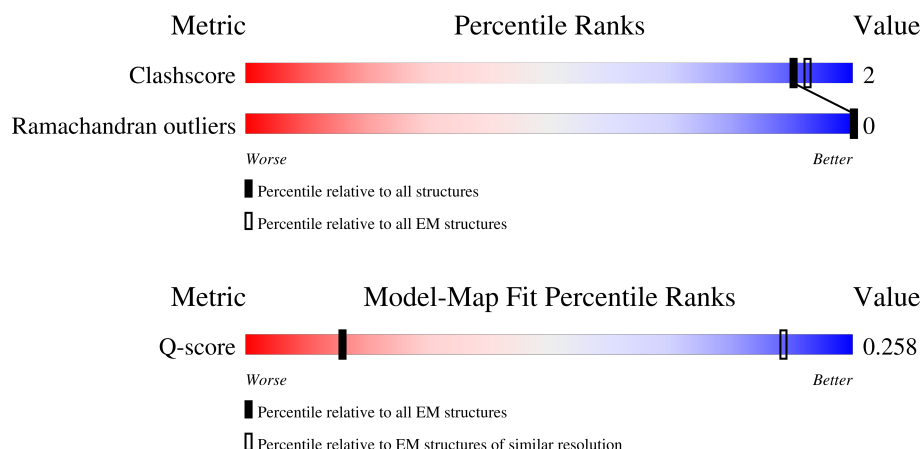
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

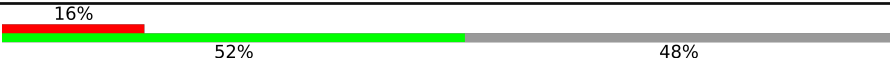
The reported resolution of this entry is 7.00 Å.

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.



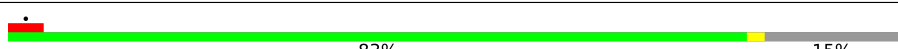
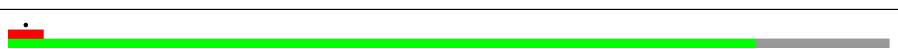
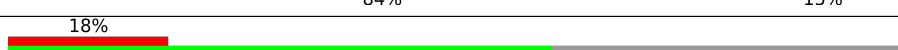
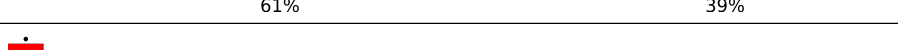
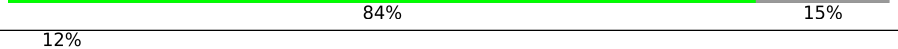
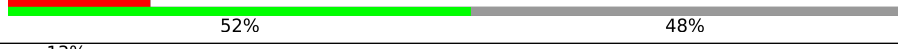
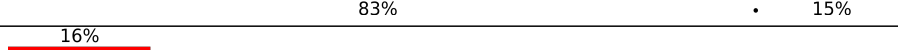
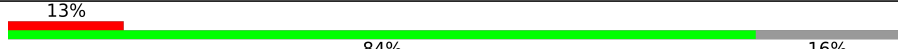
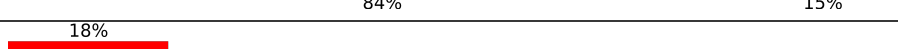
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Q-score	-	25397	483 (6.50 - 7.50)

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	258	
1	AA	258	
1	AB	258	
1	AC	258	
1	B	258	

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Mol	Chain	Length	Quality of chain
1	BA	258	
1	BB	258	
1	C	258	
1	CA	258	
1	CB	258	
1	D	258	
1	DA	258	
1	DB	258	
1	E	258	
1	EA	258	
1	EB	258	
1	F	258	
1	FA	258	
1	FB	258	
1	G	258	
1	GA	258	
1	GB	258	
1	H	258	
1	HA	258	
1	HB	258	
1	I	258	
1	IA	258	
1	IB	258	
1	J	258	
1	JA	258	

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Mol	Chain	Length	Quality of chain
1	JB	258	
1	K	258	
1	KA	258	
1	KB	258	
1	L	258	
1	LA	258	
1	LB	258	
1	M	258	
1	MA	258	
1	MB	258	
1	N	258	
1	NA	258	
1	NB	258	
1	O	258	
1	OA	258	
1	OB	258	
1	P	258	
1	PA	258	
1	PB	258	
1	Q	258	
1	QA	258	
1	QB	258	
1	R	258	
1	RA	258	
1	RB	258	

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Mol	Chain	Length	Quality of chain
1	S	258	
1	SA	258	
1	SB	258	
1	T	258	
1	TA	258	
1	TB	258	
1	UA	258	
1	UB	258	
1	V	258	
1	VA	258	
1	VB	258	
1	W	258	
1	WA	258	
1	WB	258	
1	X	258	
1	XA	258	
1	XB	258	
1	Y	258	
1	YA	258	
1	YB	258	
1	Z	258	
1	ZA	258	
1	ZB	258	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 75205 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 Vip1.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	133	Total 661	C 395	N 133	O 133	0	0
1	B	219	Total 1086	C 648	N 219	O 219	0	0
1	C	219	Total 1086	C 648	N 219	O 219	0	0
1	D	219	Total 1086	C 648	N 219	O 219	0	0
1	E	218	Total 1081	C 645	N 218	O 218	0	0
1	F	158	Total 785	C 469	N 158	O 158	0	0
1	G	133	Total 661	C 395	N 133	O 133	0	0
1	H	219	Total 1086	C 648	N 219	O 219	0	0
1	I	219	Total 1086	C 648	N 219	O 219	0	0
1	J	219	Total 1086	C 648	N 219	O 219	0	0
1	K	218	Total 1081	C 645	N 218	O 218	0	0
1	L	158	Total 785	C 469	N 158	O 158	0	0
1	M	133	Total 661	C 395	N 133	O 133	0	0
1	N	219	Total 1086	C 648	N 219	O 219	0	0
1	O	219	Total 1086	C 648	N 219	O 219	0	0
1	P	219	Total 1086	C 648	N 219	O 219	0	0
1	Q	218	Total 1081	C 645	N 218	O 218	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	R	158	Total 785	C 469	N 158	O 158	0	0
1	S	133	Total 661	C 395	N 133	O 133	0	0
1	T	219	Total 1086	C 648	N 219	O 219	0	0
1	V	219	Total 1086	C 648	N 219	O 219	0	0
1	W	219	Total 1086	C 648	N 219	O 219	0	0
1	X	218	Total 1081	C 645	N 218	O 218	0	0
1	Y	158	Total 785	C 469	N 158	O 158	0	0
1	Z	133	Total 661	C 395	N 133	O 133	0	0
1	AA	219	Total 1086	C 648	N 219	O 219	0	0
1	BA	219	Total 1086	C 648	N 219	O 219	0	0
1	CA	219	Total 1086	C 648	N 219	O 219	0	0
1	DA	218	Total 1081	C 645	N 218	O 218	0	0
1	EA	158	Total 785	C 469	N 158	O 158	0	0
1	FA	133	Total 661	C 395	N 133	O 133	0	0
1	GA	219	Total 1086	C 648	N 219	O 219	0	0
1	HA	219	Total 1086	C 648	N 219	O 219	0	0
1	IA	219	Total 1086	C 648	N 219	O 219	0	0
1	JA	218	Total 1081	C 645	N 218	O 218	0	0
1	KA	158	Total 785	C 469	N 158	O 158	0	0
1	LA	133	Total 661	C 395	N 133	O 133	0	0
1	MA	219	Total 1086	C 648	N 219	O 219	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	NA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	OA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	PA	218	Total	C	N	O	0	0
			1081	645	218	218		
1	QA	158	Total	C	N	O	0	0
			785	469	158	158		
1	RA	133	Total	C	N	O	0	0
			661	395	133	133		
1	SA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	TA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	UA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	VA	218	Total	C	N	O	0	0
			1081	645	218	218		
1	WA	158	Total	C	N	O	0	0
			785	469	158	158		
1	XA	133	Total	C	N	O	0	0
			661	395	133	133		
1	YA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	ZA	219	Total	C	N	O	0	0
			1086	648	219	219		
1	AB	219	Total	C	N	O	0	0
			1086	648	219	219		
1	BB	218	Total	C	N	O	0	0
			1081	645	218	218		
1	CB	158	Total	C	N	O	0	0
			785	469	158	158		
1	DB	133	Total	C	N	O	0	0
			661	395	133	133		
1	EB	219	Total	C	N	O	0	0
			1086	648	219	219		
1	FB	219	Total	C	N	O	0	0
			1086	648	219	219		
1	GB	219	Total	C	N	O	0	0
			1086	648	219	219		
1	HB	218	Total	C	N	O	0	0
			1081	645	218	218		

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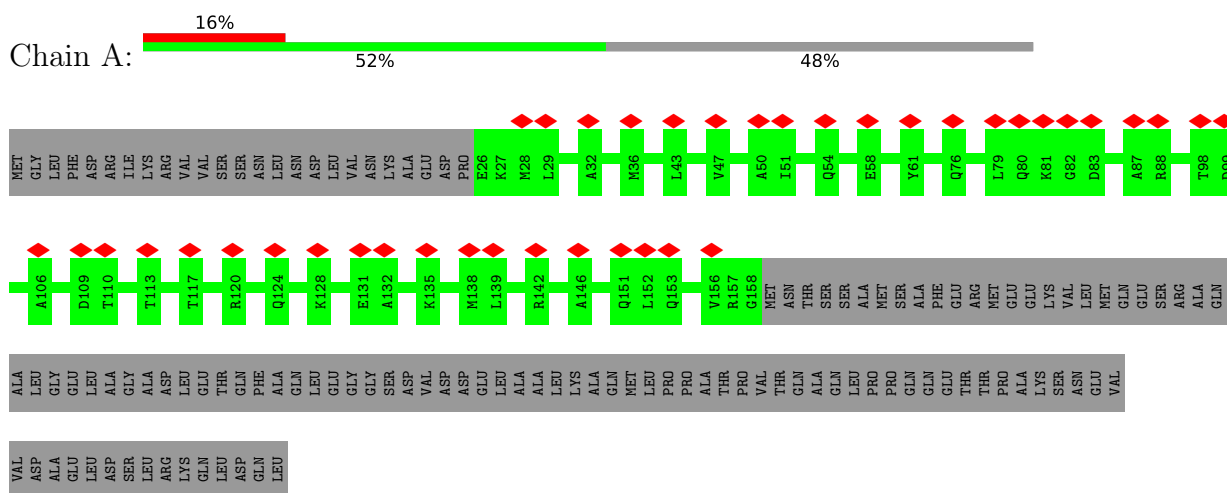
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Mol	Chain	Residues	Atoms				AltConf	Trace
1	IB	158	Total 785	C 469	N 158	O 158	0	0
1	JB	133	Total 661	C 395	N 133	O 133	0	0
1	KB	219	Total 1086	C 648	N 219	O 219	0	0
1	LB	219	Total 1086	C 648	N 219	O 219	0	0
1	MB	219	Total 1086	C 648	N 219	O 219	0	0
1	NB	218	Total 1081	C 645	N 218	O 218	0	0
1	OB	158	Total 785	C 469	N 158	O 158	0	0
1	PB	133	Total 661	C 395	N 133	O 133	0	0
1	QB	219	Total 1086	C 648	N 219	O 219	0	0
1	RB	219	Total 1086	C 648	N 219	O 219	0	0
1	SB	219	Total 1086	C 648	N 219	O 219	0	0
1	TB	218	Total 1081	C 645	N 218	O 218	0	0
1	UB	158	Total 785	C 469	N 158	O 158	0	0
1	VB	133	Total 661	C 395	N 133	O 133	0	0
1	WB	219	Total 1086	C 648	N 219	O 219	0	0
1	XB	219	Total 1086	C 648	N 219	O 219	0	0
1	YB	219	Total 1086	C 648	N 219	O 219	0	0
1	ZB	218	Total 1081	C 645	N 218	O 218	0	0
1	AC	158	Total 785	C 469	N 158	O 158	0	0

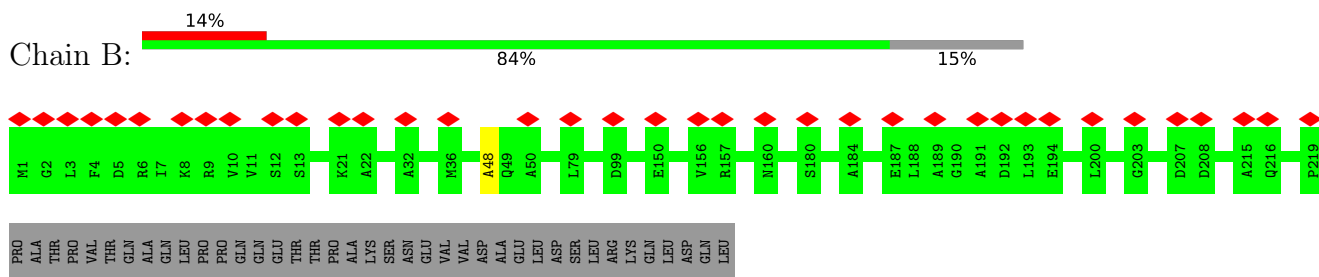
3 Residue-property plots [i](#)

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.

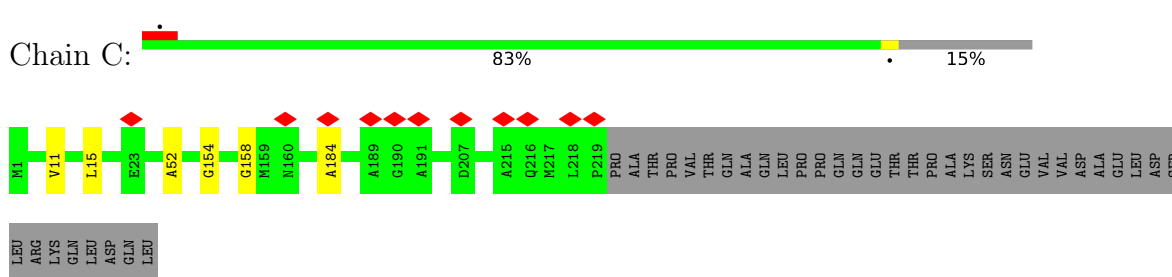
• Molecule 1: Vipp1



• Molecule 1: Vipp1



• Molecule 1: Vipp1

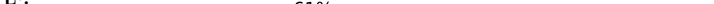


• Molecule 1: Vipp1

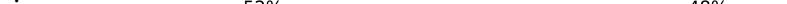
Element	Concentration (ppm)	Limit (ppm)	Compliance
Mn	10	100	Yes
Pb	10	100	Yes
Cr	10	100	Yes
Cu	10	100	Yes
Co	10	100	Yes
Fe	10	100	Yes
Si	10	100	Yes
Al	10	100	Yes
Ca	10	100	Yes
Mg	10	100	Yes
K	10	100	Yes
Na	10	100	Yes
Cl	10	100	Yes
S	10	100	Yes
O	10	100	Yes
H	10	100	Yes
N	10	100	Yes
C	10	100	Yes
F	10	100	Yes
B	10	100	Yes
I	10	100	Yes
Br	10	100	Yes
J	10	100	Yes
Ar	10	100	Yes
Kr	10	100	Yes
Xe	10	100	Yes
Rn	10	100	Yes
Fr	10	100	Yes
Ra	10	100	Yes
Ac	10	100	Yes
Th	10	100	Yes
Pa	10	100	Yes
U	10	100	Yes
Np	10	100	Yes
Pu	10	100	Yes
Am	10	100	Yes
Cm	10	100	Yes
Bk	10	100	Yes
Cf	10	100	Yes
Es	10	100	Yes
Fm	10	100	Yes
Md	10	100	Yes
No	10	100	Yes
Lr	10	100	Yes
Lu	10	100	Yes
Hf	10	100	Yes
Ta	10	100	Yes
W	10	100	Yes
Re	10	100	Yes
Os	10	100	Yes
Ir	10	100	Yes
Pt	10	100	Yes
Au	10	100	Yes
Hg	10	100	Yes
Tl	10	100	Yes
Pb	10	100	Yes
Bi	10	100	Yes
Po	10	100	Yes
At	10	100	Yes
Rn	10	100	Yes
Fr	10	100	Yes
Ra	10	100	Yes
Ac	10	100	Yes
Th	10	100	Yes
Pa	10	100	Yes
U	10	100	Yes
Np	10	100	Yes
Pu	10	100	Yes
Am	10	100	Yes
Cm	10	100	Yes
Bk	10	100	Yes
Cf	10	100	Yes
Es	10	100	Yes
Fm	10	100	Yes
Md	10	100	Yes
No	10	100	Yes
Lr	10	100	Yes
Lu	10	100	Yes
Hf	10	100	Yes
Ta	10	100	Yes
W	10	100	Yes
Re	10	100	Yes
Os	10	100	Yes
Ir	10	100	Yes
Pt	10	100	Yes
Au	10	100	Yes
Hg	10	100	Yes
Tl	10	100	Yes
Pb	10	100	Yes
Bi	10	100	Yes
Po	10	100	Yes
At	10	100	Yes
Rn	10	100	Yes
Fr	10	100	Yes
Ra	10	100	Yes
Ac	10	100	Yes
Th	10	100	Yes
Pa	10	100	Yes
U	10	100	Yes
Np	10	100	Yes
Pu	10	100	Yes
Am	10	100	Yes
Cm	10	100	Yes
Bk	10	100	Yes
Cf	10	100	Yes
Es	10	100	Yes
Fm	10	1	

- Chain E: 

MI	MI6	K21	A22	M28	L139	A146	Q153	G154	M155	V156	R157	NI60	E179	A189	G190	A191	D192	L193	G202	G203	S204	D205	V206	D207	D208	E209	L210	A211	A212	L213	K214	A215	Q216	M217	L218	PRO	PRO	ALA	THR	PRO	VAL	THR	GLN	ALA	GLN	LEU	PRO	PRO	GLN
GLN	GLU	THR	THR	PRO	ALA	LYS	SER	ASN	GLU	VAL	VAL	ASP	ALA	GLU	LEU	ASP	SER	SER	LYS	GLN	GLN	LEU	ASP	GLN	LEU	GLN	ASP	GLN	LEU	GLN	LEU	ASP	GLN	LEU	PRO	PRO	ALA	THR	PRO	VAL	THR	GLN	ALA	GLN	LEU	PRO	PRO	GLN	

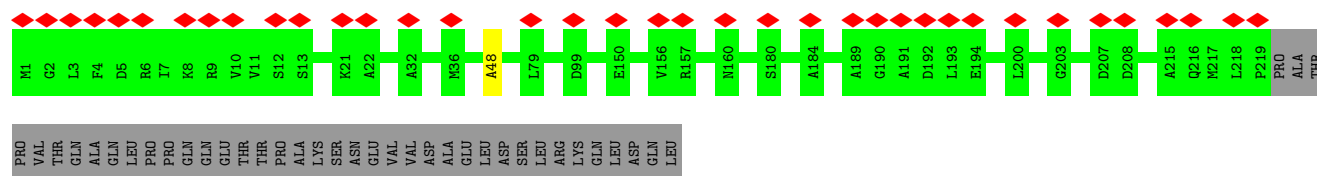
- Chain F:  18% 61% 39%

Protein	Residue	Residue Type	Protein	Residue	Residue Type
LEU	R142	Arginine	LEU	R1	Arginine
ALA	A146	Alanine	ALA	R9	Arginine
LEU	E150	Glutamic acid	LEU	K21	Lysine
GLN	R157	Arginine	ALA	A22	Alanine
MET	G158	Glycine	MET	E23	Glutamic acid
PRO	MET	Methionine	LEU	D24	Aspartic acid
ALA	THR	Threonine	PRO	P25	Proline
THR	THR	Threonine	PRO	E26	Glutamic acid
PRO	SER	Serine	VAL	K27	Lysine
VAL	SER	Serine	VAL	M28	Methionine
THR	ALA	Alanine	THR	Q31	Glutamine
GLN	MET	Methionine	GLN	A32	Alanine
ALA	SER	Serine	ALA	E35	Glutamic acid
GLN	ALA	Alanine	LEU	PHE	Phenylalanine
LEU	GLU	Glutamic acid	PRO	GLU	Glutamic acid
PRO	ARG	Arginine	PRO	ARG	Arginine
GLN	MET	Methionine	GLN	MET	Methionine
GLN	GLU	Glutamic acid	GLN	GLU	Glutamic acid
GLU	GLU	Glutamic acid	GLU	A53	Alanine
THR	LYS	Lysine	THR	E67	Glutamic acid
THR	VAL	Valine	THR	I68	Isoleucine
PRO	LEU	Leucine	PRO	N69	Asparagine
ALA	MET	Methionine	ALA	K70	Lysine
LYS	GLN	Glutamine	LYS	GLU	Glutamic acid
SER	GLU	Glutamic acid	SER	SER	Serine
ASN	ARG	Arginine	ASN	W71	Tryptophan
GLU	ARG	Arginine	GLU	Q72	Glutamine
VAL	ALA	Alanine	VAL	R73	Arginine
ASP	GLN	Glutamine	VAL	N74	Asparagine
ALA	ALA	Alanine	ASP	A75	Alanine
GLU	LEU	Leucine	ALA	Q76	Glutamine
LEU	GLU	Glutamic acid	GLU	L77	Leucine
LEU	GLU	Glutamic acid	LEU	A78	Alanine
ASP	ALA	Alanine	SER	L79	Serine
LEU	GLY	Glycine	LEU	Q80	Glutamine
ARG	ALA	Alanine	ARG	K81	Lysine
LYS	ASP	Asparagine	LYS	G82	Lysine
GLN	LEU	Leucine	GLN	D83	Aspartic acid
LEU	GLU	Glutamic acid	LEU	F84	Phenylalanine
ASP	THR	Threonine	ASP	N85	Asparagine
GLN	GLN	Glutamine	GLN	L86	Leucine
LEU	PHE	Phenylalanine	LEU	A87	Alanine
LEU	ALA	Alanine	LEU	R88	Arginine
GLN	GLN	Glutamine	GLU	Q89	Glutamine
LEU	GLY	Glycine	LEU	A90	Alanine
LEU	GLY	Glycine	LEU	L91	Leucine
ASP	SER	Serine	ASP	E92	Glutamic acid
GLU	VAL	Valine	GLU	R93	Arginine
GLU	ASP	Asparagine	GLU	K94	Lysine
GLU	GLU	Glutamic acid	GLU	K95	Lysine
				T96	Threonine
				D99	Aspartic acid
				K128	Lysine
				A132	Alanine
				I136	Isoleucine

- Chain G: 

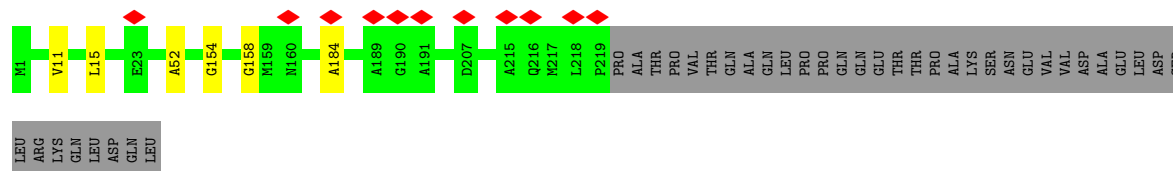
[illegible]

- Chain H:  14% 84% 15%



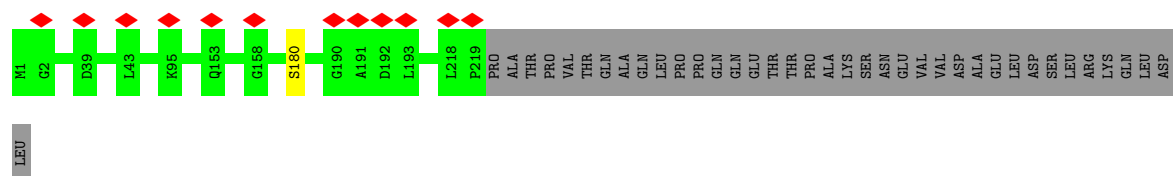
• Molecule 1: Vipp1

Chain I: 83% 15%



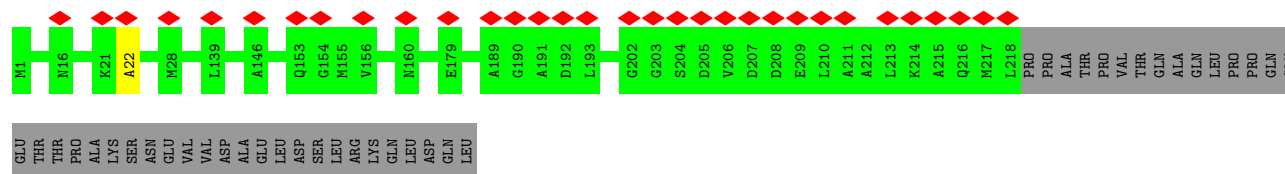
• Molecule 1: Vipp1

Chain J: 84% 15%



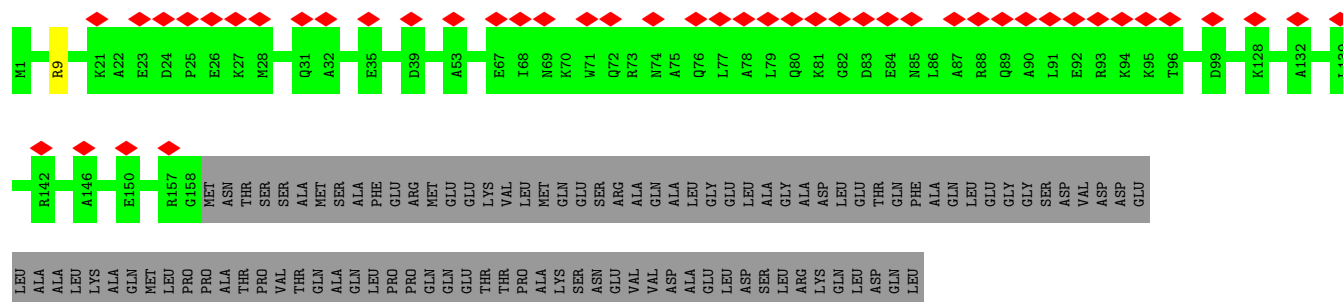
• Molecule 1: Vipp1

Chain K: 84% 16%

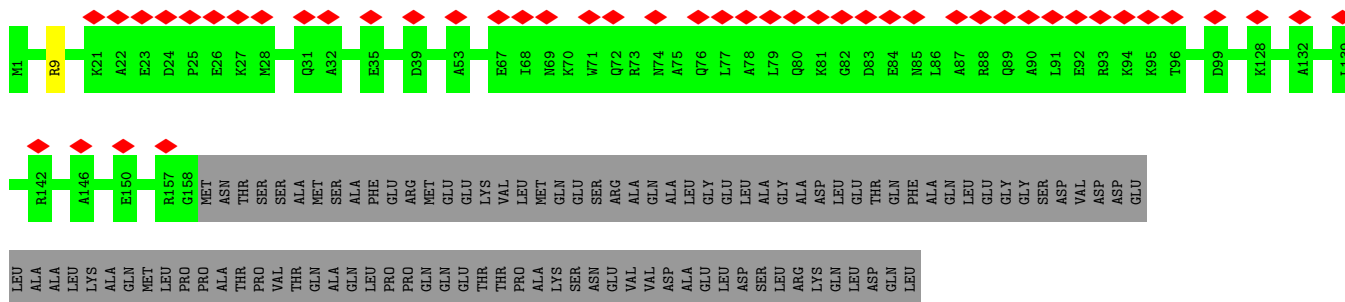


• Molecule 1: Vipp1

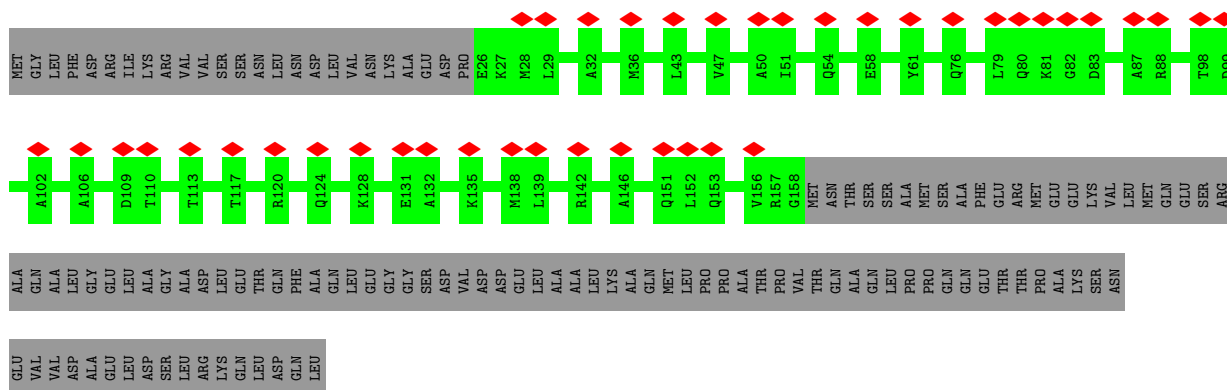
Chain L: 61% 39%



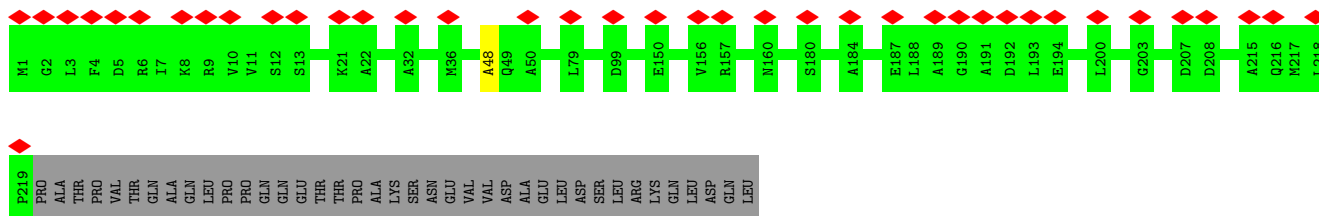
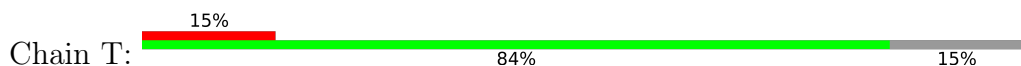
- Molecule 1: Vippp1



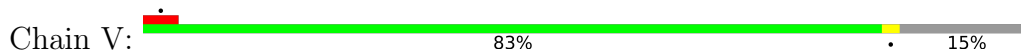
- Molecule 1: Vippp1

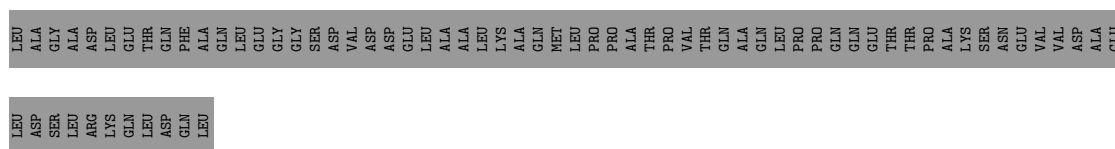


- Molecule 1: Vippp1

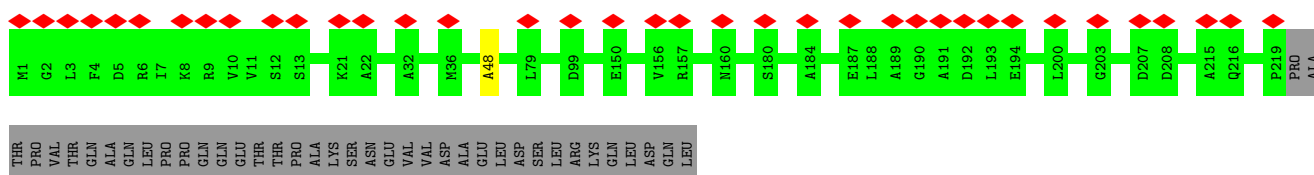
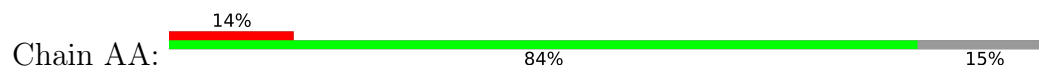


- Molecule 1: Vippp1

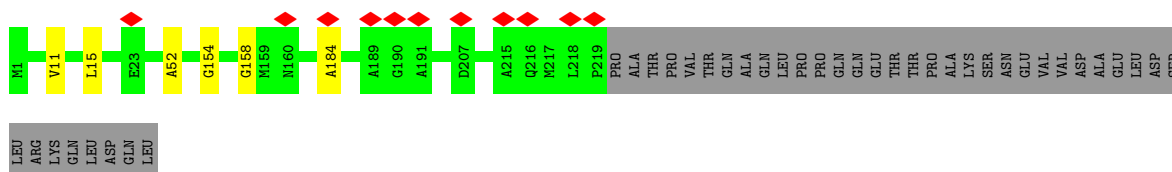
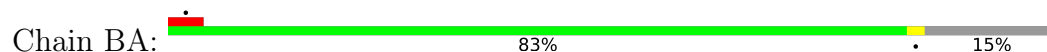




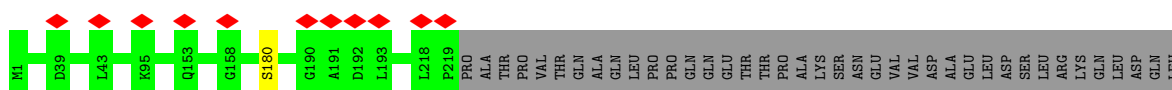
• Molecule 1: Vipp1



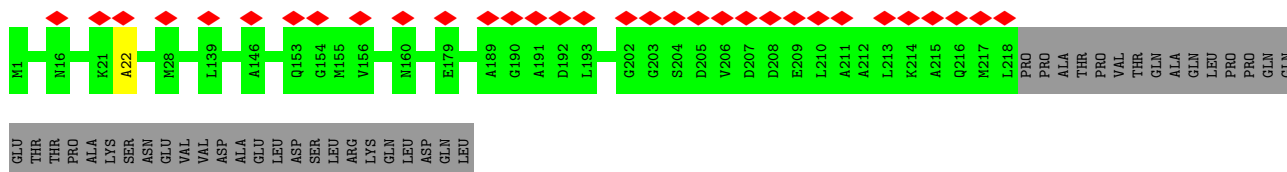
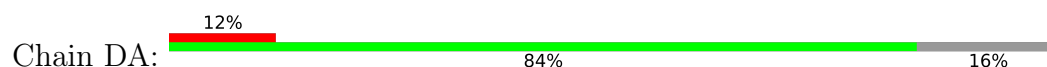
• Molecule 1: Vipp1



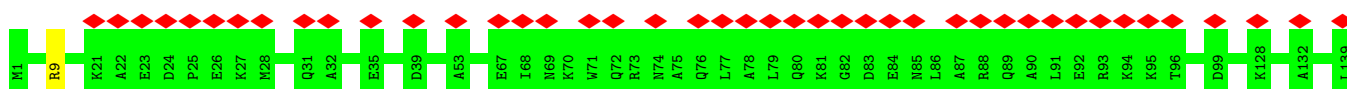
• Molecule 1: Vipp1



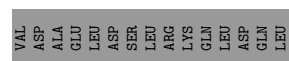
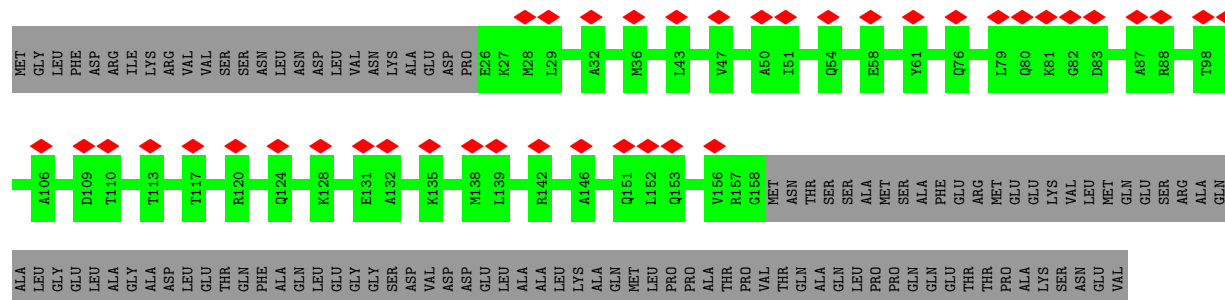
• Molecule 1: Vipp1



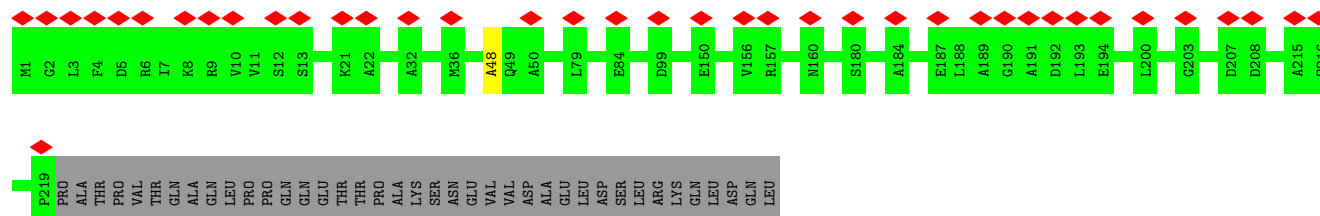
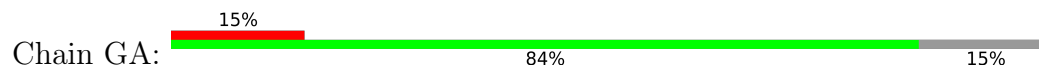
• Molecule 1: Vipp1



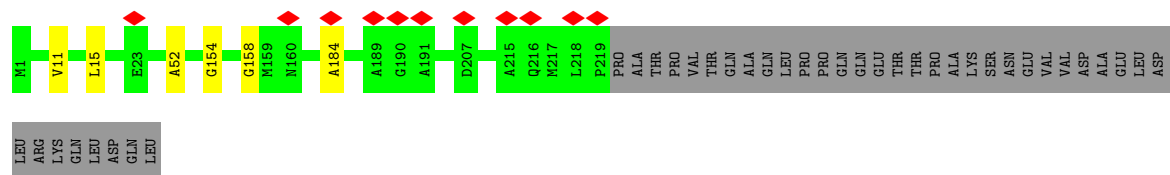
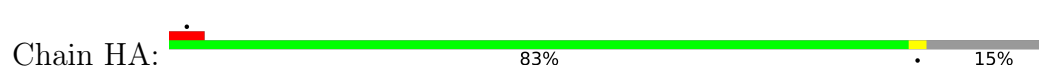
- Molecule 1: Vippp1



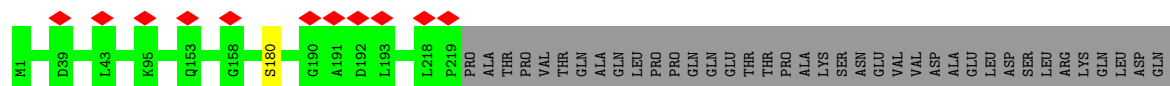
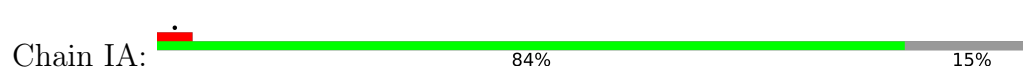
- Molecule 1: Vippp1



- Molecule 1: Vippp1



- Molecule 1: Vippp1



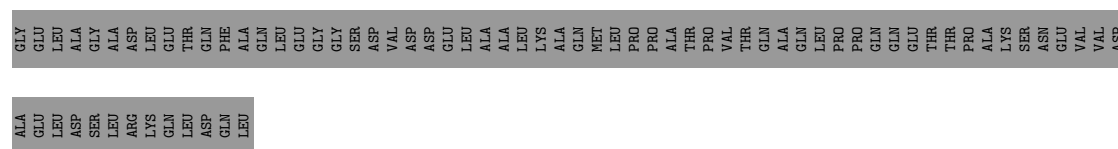
Sequence logo for the 10th position. The y-axis represents information content in bits (0.00 to 0.25). The x-axis lists amino acids. The top row (0.20-0.25 bits) includes MT, V11, L15, E23, A52, G154, G158, M159, N160, A184, A189, G190, A191, D207, A215, Q216, P219, and PRO. The bottom row (0.00-0.05 bits) includes ARG, LYS, GLN, LEU, ASP, GLN, and LEU. Red diamonds indicate positions with high information content.

-
- Sequence logo for the 1000bp upstream region of the human POU3F1 gene. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis shows positions from -1000 to +1000. The sequence is displayed below the plot, with positions -1000 to -1 marked with red diamonds indicating high conservation. The sequence is: M1, D39, L43, K95, Q153, G158, S180, G190, A191, D192, L193, L218, P219, P219, A1A, A1A, THR, THR, PRO, PRO, VAL, VAL, THR, THR, GLN, GLN, ALA, ALA, GLN, GLN, LEU, LEU, PRO, PRO, PRO, PRO, GLN, GLN, GLN, GLU, GLU, THR, THR, THR, THR, PRO, PRO, ALA, LYS, SER, SER, ASN, ASN, GLU, GLU, VAL, VAL, VAL, ASP, ALA, GLU, GLU, LEU, LEU, ASP, SER, ARG, ARG, LYS, LYS, GLN, GLN, LEU, LEU, ASP, ASP, GLN, GLN.

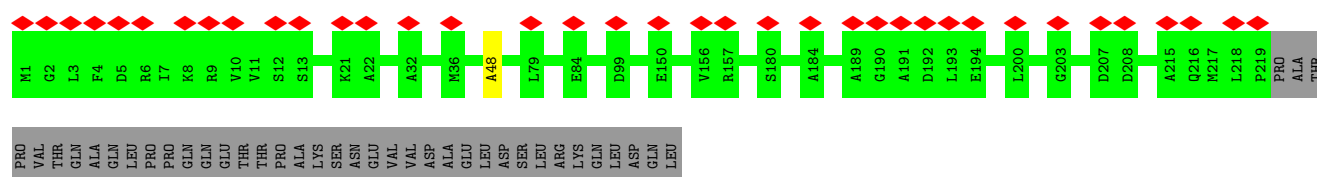
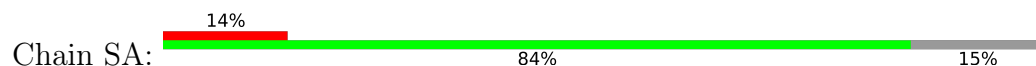
- [illegible]

- [illegible]

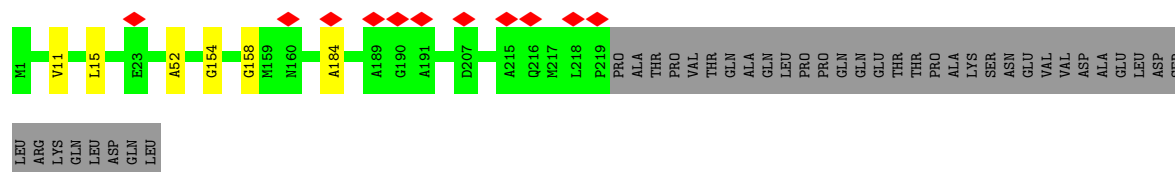
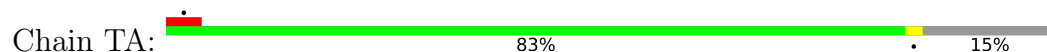
- [illegible]



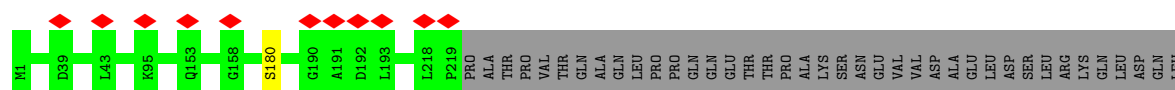
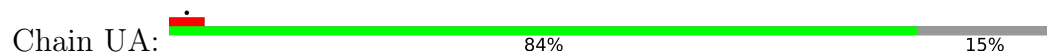
• Molecule 1: Vipp1



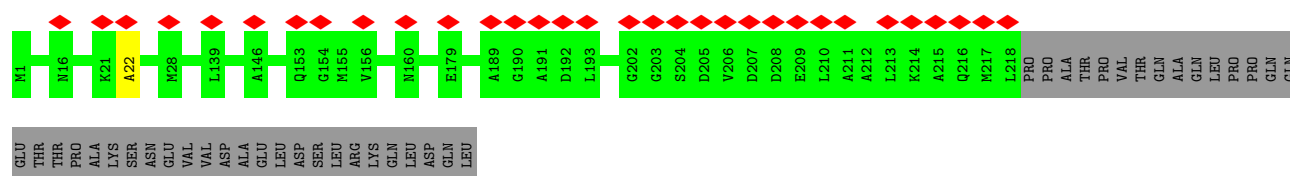
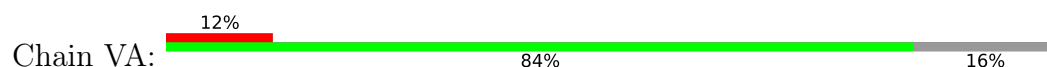
• Molecule 1: Vipp1



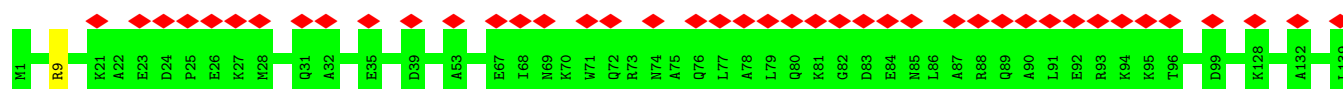
• Molecule 1: Vipp1



• Molecule 1: Vipp1

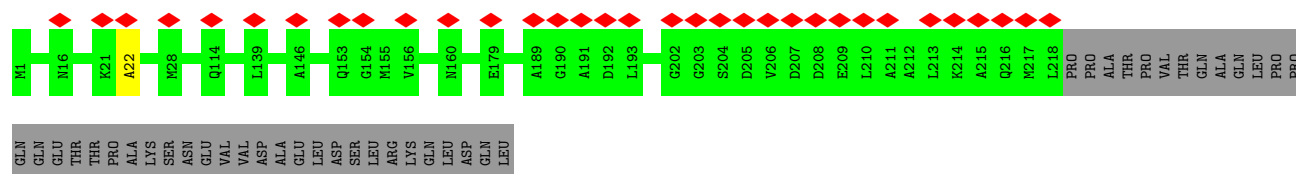


• Molecule 1: Vipp1



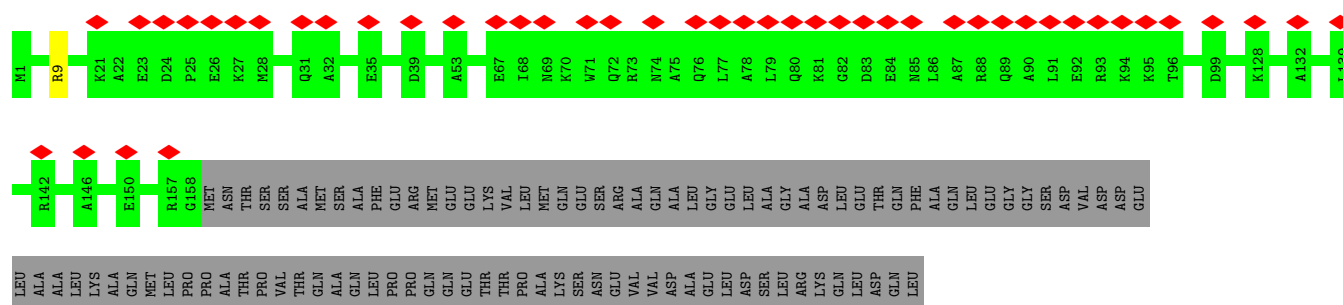
- Molecule 1: Vipp1

Chain BB: 



- Molecule 1: Vipp1

Chain CB: 



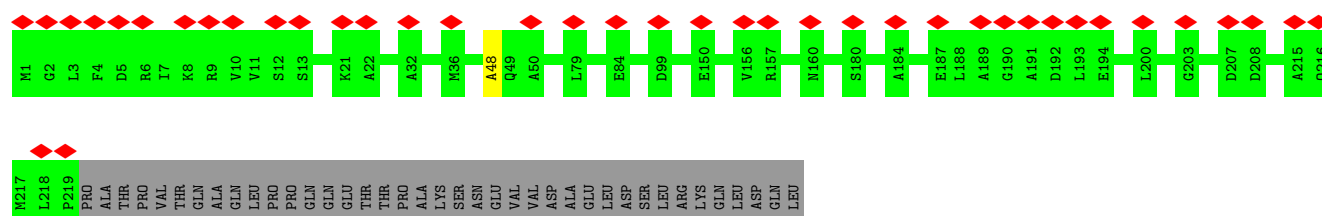
- Molecule 1: Vipp1

Chain DB: 



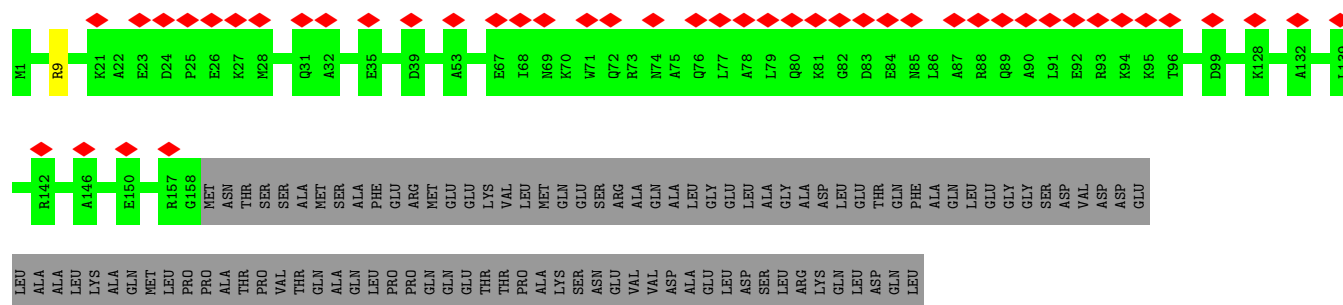
- Molecule 1: Vipp1

Chain EB: 

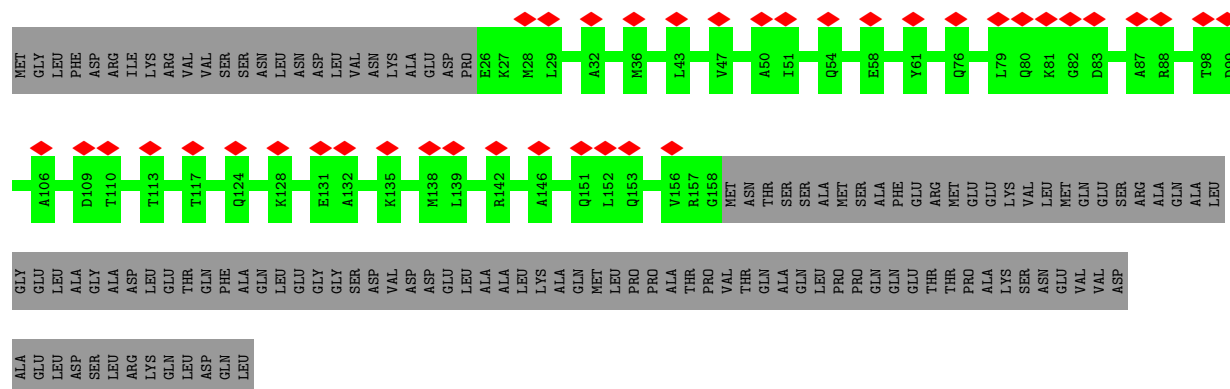


MET	GLY	LEU	PHE	ASP	ARG	ILE	LYS	ARG	VAL	VAL	SER	SER	ASN	LEU	ASP	ASP	LEU	VAL	ASN	LYS	ALA	GLU	ASP	PRO	E26	K27	M28	L29	A32	M36	L43	V47	A50	I51	Q54	E58	Y61	Q76	L79	Q80	K81	G82	D83	A87	R88	T98
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

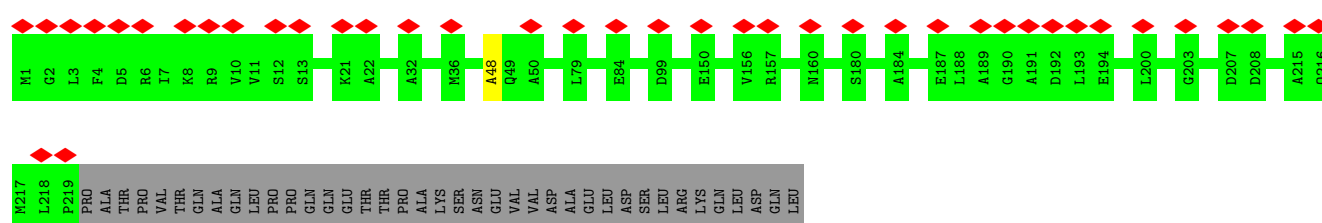
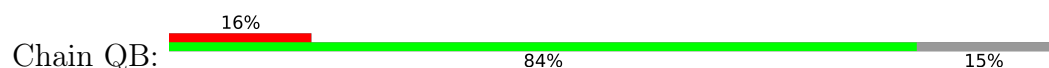
• Molecule 1: Vipp1



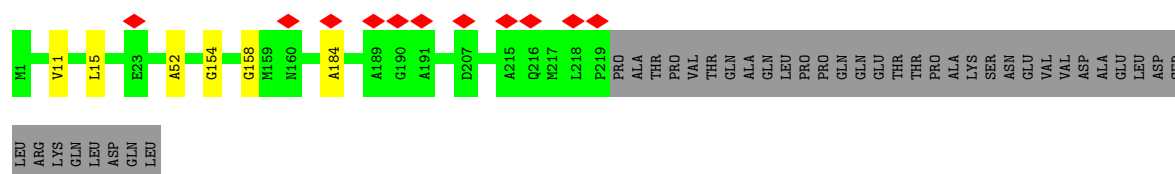
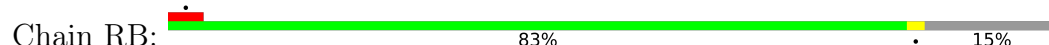
• Molecule 1: Vipp1

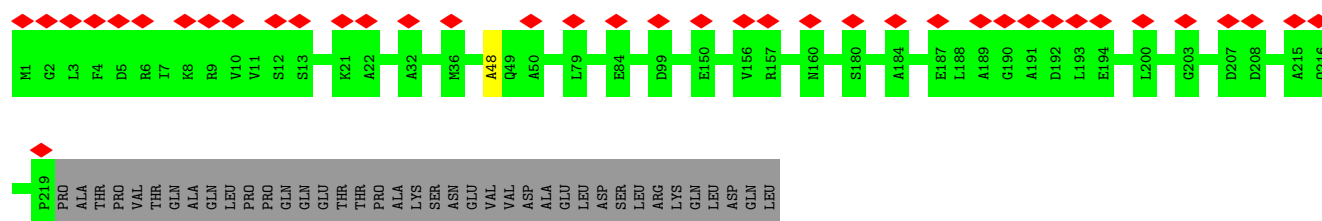
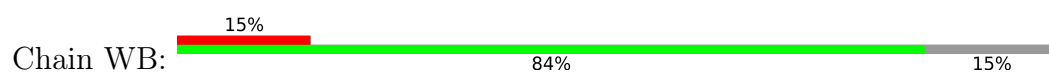


• Molecule 1: Vipp1

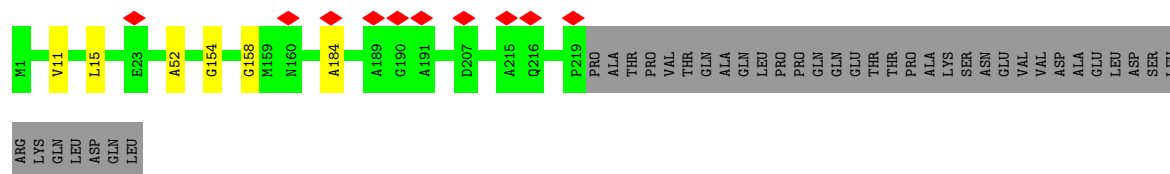
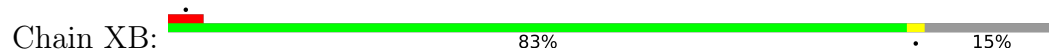


• Molecule 1: Vipp1

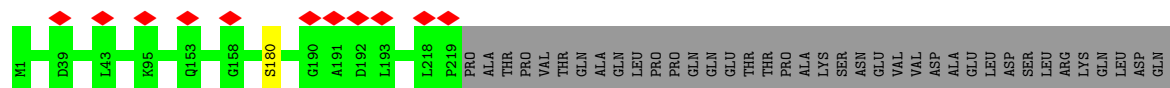
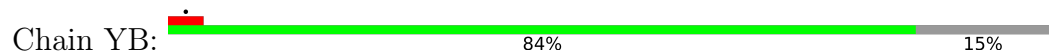




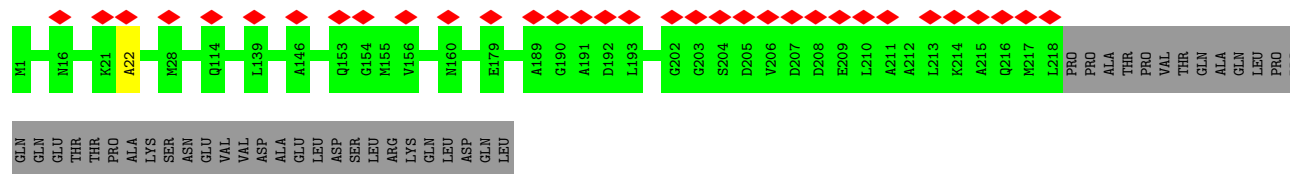
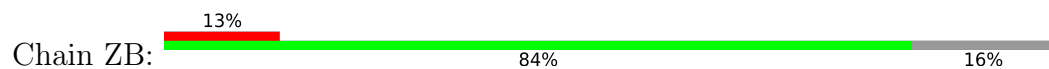
- Molecule 1: Vipp1



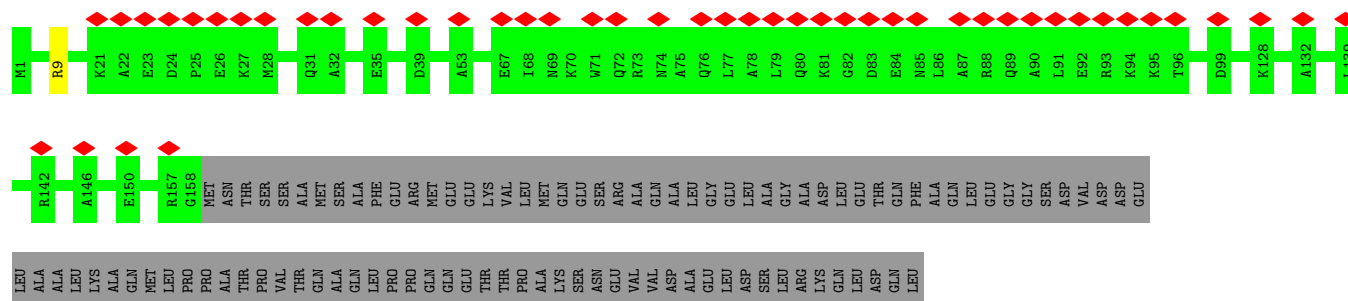
- Molecule 1: Vipp1



- Molecule 1: Vipp1



- Molecule 1: Vipp1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6920	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.5	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	0.055	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0187	Depositor
Map size ($\text{\AA}$)	467.04, 467.04, 467.04	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.39, 1.39, 1.39	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.33	0/660	0.85	0/920
1	AA	0.33	0/1085	0.84	0/1512
1	AB	0.36	0/1085	0.93	0/1512
1	AC	0.35	0/784	0.94	0/1093
1	B	0.33	0/1085	0.84	0/1512
1	BA	0.35	0/1085	0.86	0/1512
1	BB	0.36	0/1080	0.93	0/1505
1	C	0.35	0/1085	0.86	0/1512
1	CA	0.35	0/1085	0.93	0/1512
1	CB	0.35	0/784	0.94	0/1093
1	D	0.35	0/1085	0.93	0/1512
1	DA	0.36	0/1080	0.93	0/1505
1	DB	0.33	0/660	0.85	0/920
1	E	0.36	0/1080	0.93	0/1505
1	EA	0.35	0/784	0.94	0/1093
1	EB	0.33	0/1085	0.84	0/1512
1	F	0.35	0/784	0.94	0/1093
1	FA	0.33	0/660	0.85	0/920
1	FB	0.35	0/1085	0.86	0/1512
1	G	0.33	0/660	0.85	0/920
1	GA	0.33	0/1085	0.84	0/1512
1	GB	0.35	0/1085	0.93	0/1512
1	H	0.33	0/1085	0.84	0/1512
1	HA	0.35	0/1085	0.86	0/1512
1	HB	0.36	0/1080	0.93	0/1505
1	I	0.36	0/1085	0.86	0/1512
1	IA	0.36	0/1085	0.93	0/1512
1	IB	0.35	0/784	0.94	0/1093
1	J	0.36	0/1085	0.93	0/1512
1	JA	0.36	0/1080	0.93	0/1505
1	JB	0.33	0/660	0.85	0/920
1	K	0.36	0/1080	0.93	0/1505
1	KA	0.35	0/784	0.94	0/1093
1	KB	0.33	0/1085	0.84	0/1512

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	L	0.35	0/784	0.94	0/1093
1	LA	0.33	0/660	0.85	0/920
1	LB	0.36	0/1085	0.86	0/1512
1	M	0.33	0/660	0.85	0/920
1	MA	0.33	0/1085	0.84	0/1512
1	MB	0.35	0/1085	0.93	0/1512
1	N	0.33	0/1085	0.84	0/1512
1	NA	0.35	0/1085	0.86	0/1512
1	NB	0.36	0/1080	0.93	0/1505
1	O	0.36	0/1085	0.86	0/1512
1	OA	0.35	0/1085	0.93	0/1512
1	OB	0.35	0/784	0.94	0/1093
1	P	0.36	0/1085	0.93	0/1512
1	PA	0.36	0/1080	0.93	0/1505
1	PB	0.33	0/660	0.85	0/920
1	Q	0.36	0/1080	0.93	0/1505
1	QA	0.35	0/784	0.94	0/1093
1	QB	0.33	0/1085	0.84	0/1512
1	R	0.35	0/784	0.94	0/1093
1	RA	0.33	0/660	0.85	0/920
1	RB	0.36	0/1085	0.86	0/1512
1	S	0.33	0/660	0.85	0/920
1	SA	0.33	0/1085	0.84	0/1512
1	SB	0.35	0/1085	0.93	0/1512
1	T	0.33	0/1085	0.84	0/1512
1	TA	0.35	0/1085	0.86	0/1512
1	TB	0.36	0/1080	0.93	0/1505
1	UA	0.35	0/1085	0.93	0/1512
1	UB	0.35	0/784	0.94	0/1093
1	V	0.36	0/1085	0.86	0/1512
1	VA	0.36	0/1080	0.93	0/1505
1	VB	0.33	0/660	0.85	0/920
1	W	0.35	0/1085	0.93	0/1512
1	WA	0.35	0/784	0.94	0/1093
1	WB	0.33	0/1085	0.84	0/1512
1	X	0.36	0/1080	0.93	0/1505
1	XA	0.33	0/660	0.85	0/920
1	XB	0.35	0/1085	0.86	0/1512
1	Y	0.35	0/784	0.94	0/1093
1	YA	0.33	0/1085	0.84	0/1512
1	YB	0.36	0/1085	0.93	0/1512
1	Z	0.33	0/660	0.85	0/920
1	ZA	0.35	0/1085	0.86	0/1512

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	ZB	0.36	0/1080	0.93	0/1505
All	All	0.35	0/75127	0.89	0/104702

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	A	661	0	320	0	0
1	AA	1086	0	531	1	0
1	AB	1086	0	531	3	0
1	AC	785	0	376	2	0
1	B	1086	0	531	1	0
1	BA	1086	0	531	12	0
1	BB	1081	0	530	2	0
1	C	1086	0	531	13	0
1	CA	1086	0	531	3	0
1	CB	785	0	376	2	0
1	D	1086	0	531	3	0
1	DA	1081	0	530	2	0
1	DB	661	0	320	0	0
1	E	1081	0	530	2	0
1	EA	785	0	376	2	0
1	EB	1086	0	531	1	0
1	F	785	0	376	2	0
1	FA	661	0	320	0	0
1	FB	1086	0	531	13	0
1	G	661	0	320	0	0
1	GA	1086	0	531	1	0
1	GB	1086	0	531	3	0
1	H	1086	0	531	1	0
1	HA	1086	0	531	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	HB	1081	0	530	2	0
1	I	1086	0	531	13	0
1	IA	1086	0	531	3	0
1	IB	785	0	376	2	0
1	J	1086	0	531	3	0
1	JA	1081	0	530	2	0
1	JB	661	0	320	0	0
1	K	1081	0	530	2	0
1	KA	785	0	376	2	0
1	KB	1086	0	531	1	0
1	L	785	0	376	2	0
1	LA	661	0	320	0	0
1	LB	1086	0	531	13	0
1	M	661	0	320	0	0
1	MA	1086	0	531	1	0
1	MB	1086	0	531	3	0
1	N	1086	0	531	1	0
1	NA	1086	0	531	12	0
1	NB	1081	0	530	2	0
1	O	1086	0	531	13	0
1	OA	1086	0	531	3	0
1	OB	785	0	376	2	0
1	P	1086	0	531	3	0
1	PA	1081	0	530	2	0
1	PB	661	0	320	0	0
1	Q	1081	0	530	2	0
1	QA	785	0	376	2	0
1	QB	1086	0	531	1	0
1	R	785	0	376	2	0
1	RA	661	0	320	0	0
1	RB	1086	0	531	13	0
1	S	661	0	320	0	0
1	SA	1086	0	531	1	0
1	SB	1086	0	531	3	0
1	T	1086	0	531	1	0
1	TA	1086	0	531	12	0
1	TB	1081	0	530	2	0
1	UA	1086	0	531	3	0
1	UB	785	0	376	2	0
1	V	1086	0	531	12	0
1	VA	1081	0	530	2	0
1	VB	661	0	320	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	W	1086	0	531	3	0
1	WA	785	0	376	2	0
1	WB	1086	0	531	1	0
1	X	1081	0	530	2	0
1	XA	661	0	320	0	0
1	XB	1086	0	531	13	0
1	Y	785	0	376	2	0
1	YA	1086	0	531	1	0
1	YB	1086	0	531	3	0
1	Z	661	0	320	0	0
1	ZA	1086	0	531	13	0
1	ZB	1081	0	530	2	0
All	All	75205	0	36647	190	0

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

The worst 5 of 190 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:BA:154:GLY:O	1:BA:158:GLY:CA	2.11	0.98
1:XB:154:GLY:O	1:XB:158:GLY:CA	2.11	0.98
1:HA:154:GLY:O	1:HA:158:GLY:CA	2.11	0.98
1:C:154:GLY:O	1:C:158:GLY:CA	2.11	0.98
1:RB:154:GLY:O	1:RB:158:GLY:CA	2.12	0.98

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	AA	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	AB	217/258 (84%)	217 (100%)	0	0	100	100
1	AC	156/258 (60%)	156 (100%)	0	0	100	100
1	B	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	BA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	BB	216/258 (84%)	216 (100%)	0	0	100	100
1	C	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	CA	217/258 (84%)	217 (100%)	0	0	100	100
1	CB	156/258 (60%)	156 (100%)	0	0	100	100
1	D	217/258 (84%)	217 (100%)	0	0	100	100
1	DA	216/258 (84%)	216 (100%)	0	0	100	100
1	DB	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	E	216/258 (84%)	216 (100%)	0	0	100	100
1	EA	156/258 (60%)	156 (100%)	0	0	100	100
1	EB	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	F	156/258 (60%)	156 (100%)	0	0	100	100
1	FA	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	FB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	G	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	GA	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	GB	217/258 (84%)	217 (100%)	0	0	100	100
1	H	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	HA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	HB	216/258 (84%)	216 (100%)	0	0	100	100
1	I	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	IA	217/258 (84%)	217 (100%)	0	0	100	100
1	IB	156/258 (60%)	156 (100%)	0	0	100	100
1	J	217/258 (84%)	217 (100%)	0	0	100	100
1	JA	216/258 (84%)	216 (100%)	0	0	100	100
1	JB	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	K	216/258 (84%)	216 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	KA	156/258 (60%)	156 (100%)	0	0	100	100
1	KB	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	L	156/258 (60%)	156 (100%)	0	0	100	100
1	LA	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	LB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	M	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	MA	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	MB	217/258 (84%)	217 (100%)	0	0	100	100
1	N	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	NA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	NB	216/258 (84%)	216 (100%)	0	0	100	100
1	O	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	OA	217/258 (84%)	217 (100%)	0	0	100	100
1	OB	156/258 (60%)	156 (100%)	0	0	100	100
1	P	217/258 (84%)	217 (100%)	0	0	100	100
1	PA	216/258 (84%)	216 (100%)	0	0	100	100
1	PB	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	Q	216/258 (84%)	216 (100%)	0	0	100	100
1	QA	156/258 (60%)	156 (100%)	0	0	100	100
1	QB	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	R	156/258 (60%)	156 (100%)	0	0	100	100
1	RA	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	RB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	S	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	SA	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	SB	217/258 (84%)	217 (100%)	0	0	100	100
1	T	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	TA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	TB	216/258 (84%)	216 (100%)	0	0	100	100
1	UA	217/258 (84%)	217 (100%)	0	0	100	100
1	UB	156/258 (60%)	156 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	V	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	VA	216/258 (84%)	216 (100%)	0	0	100	100
1	VB	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	W	217/258 (84%)	217 (100%)	0	0	100	100
1	WA	156/258 (60%)	156 (100%)	0	0	100	100
1	WB	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	X	216/258 (84%)	216 (100%)	0	0	100	100
1	XA	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	XB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	Y	156/258 (60%)	156 (100%)	0	0	100	100
1	YA	217/258 (84%)	210 (97%)	7 (3%)	0	100	100
1	YB	217/258 (84%)	217 (100%)	0	0	100	100
1	Z	131/258 (51%)	129 (98%)	2 (2%)	0	100	100
1	ZA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	ZB	216/258 (84%)	216 (100%)	0	0	100	100
All	All	15002/20124 (74%)	14872 (99%)	130 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

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.

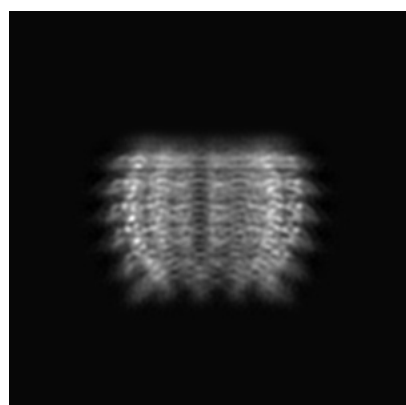
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11470. These allow visual inspection of the internal detail of the map and identification of artifacts.

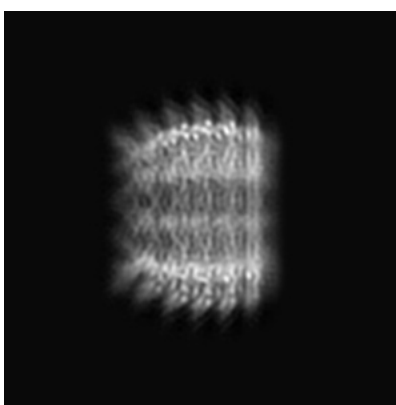
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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: 168



Y Index: 168



Z Index: 168

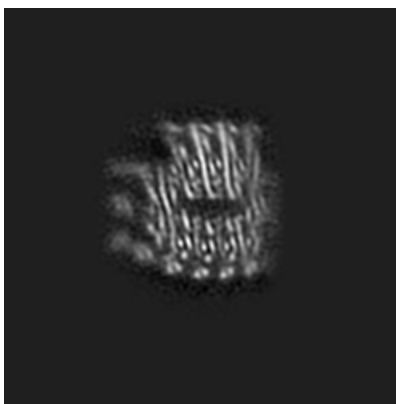
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 232



Y Index: 105

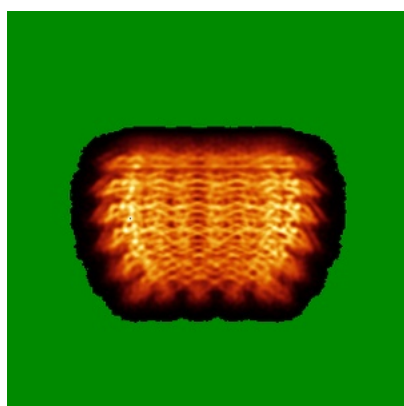


Z Index: 171

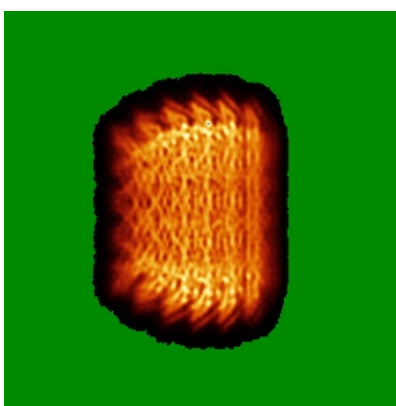
The images above show the largest variance slices of the map in three orthogonal directions.

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

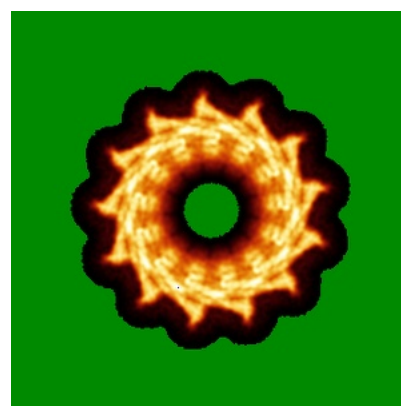
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0187. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

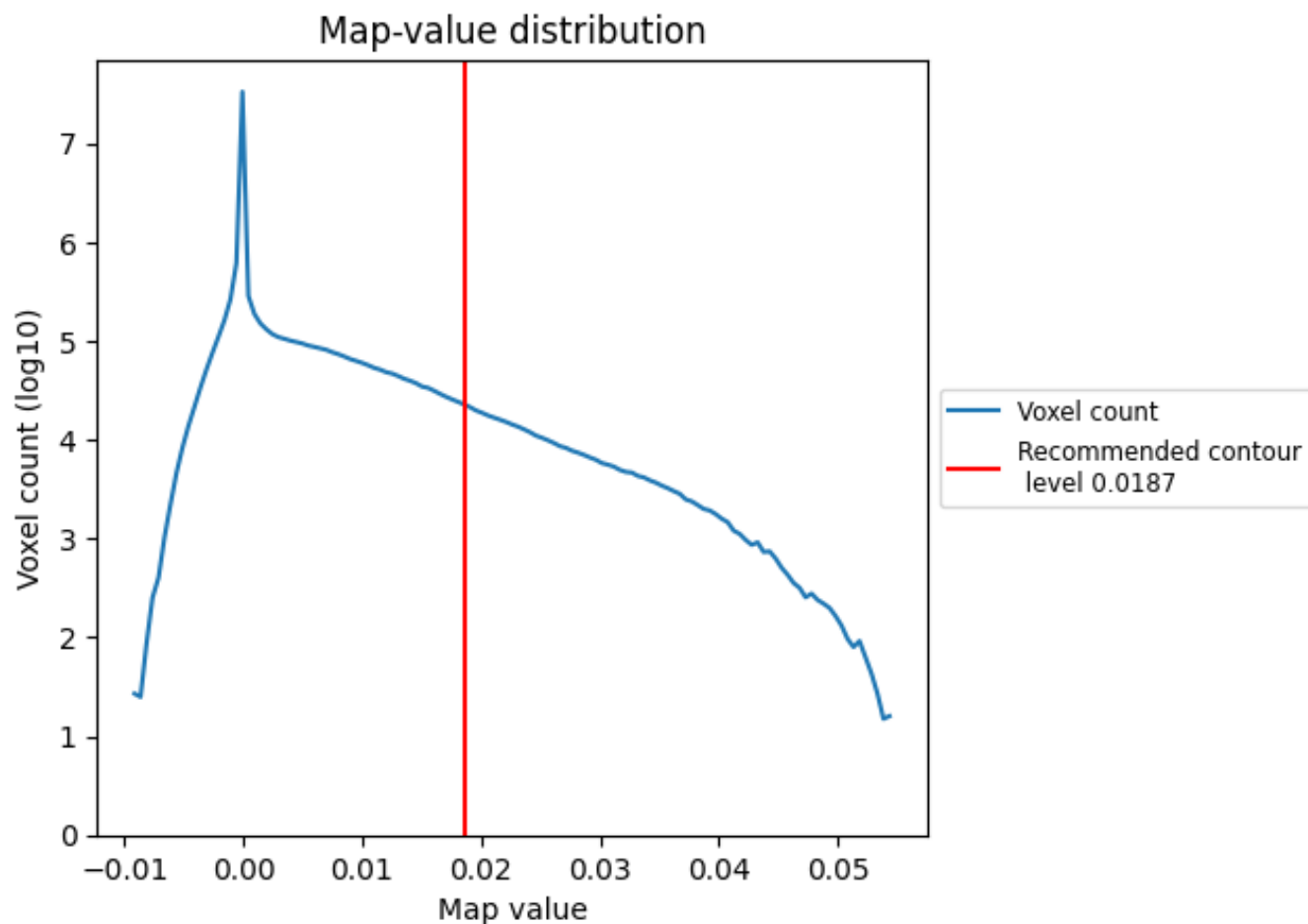
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

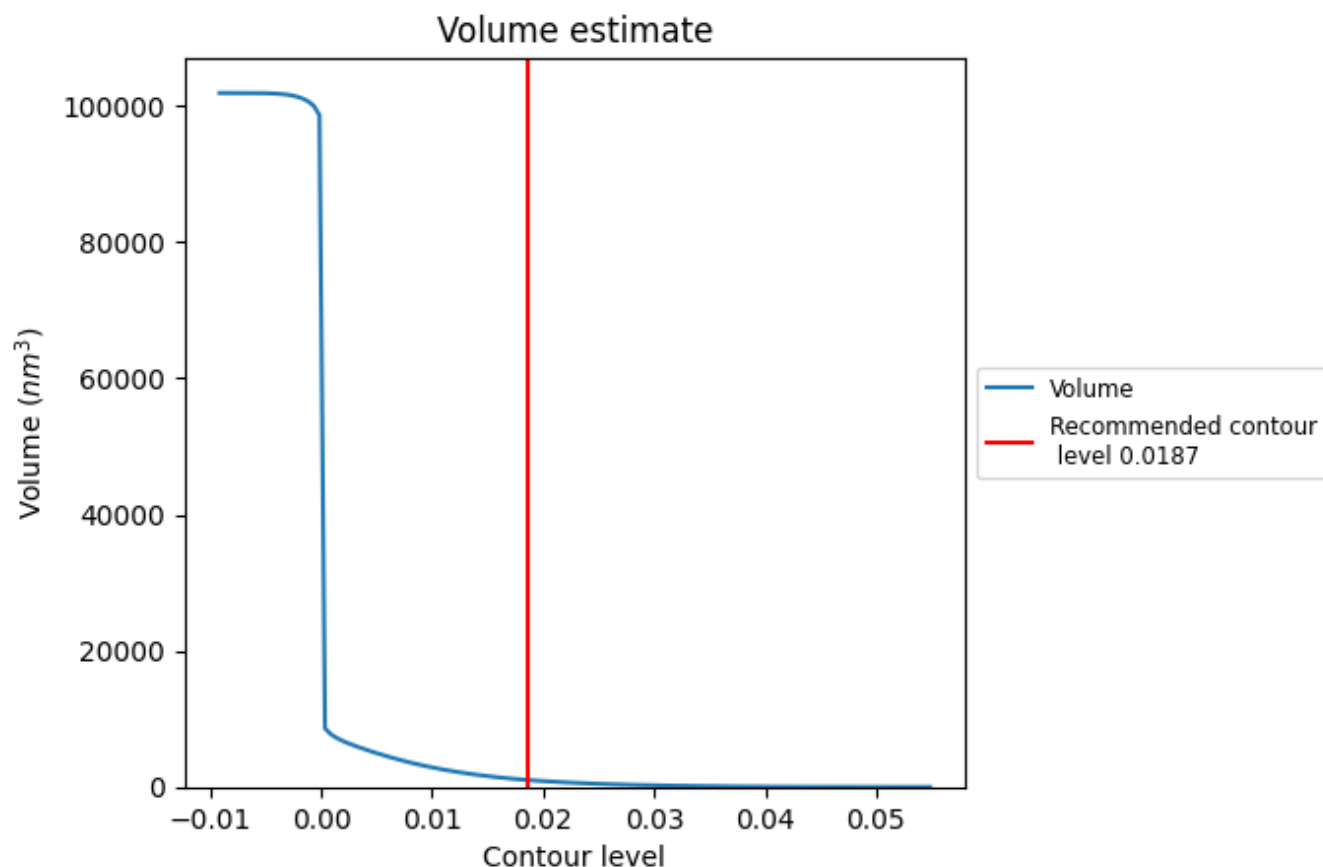
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

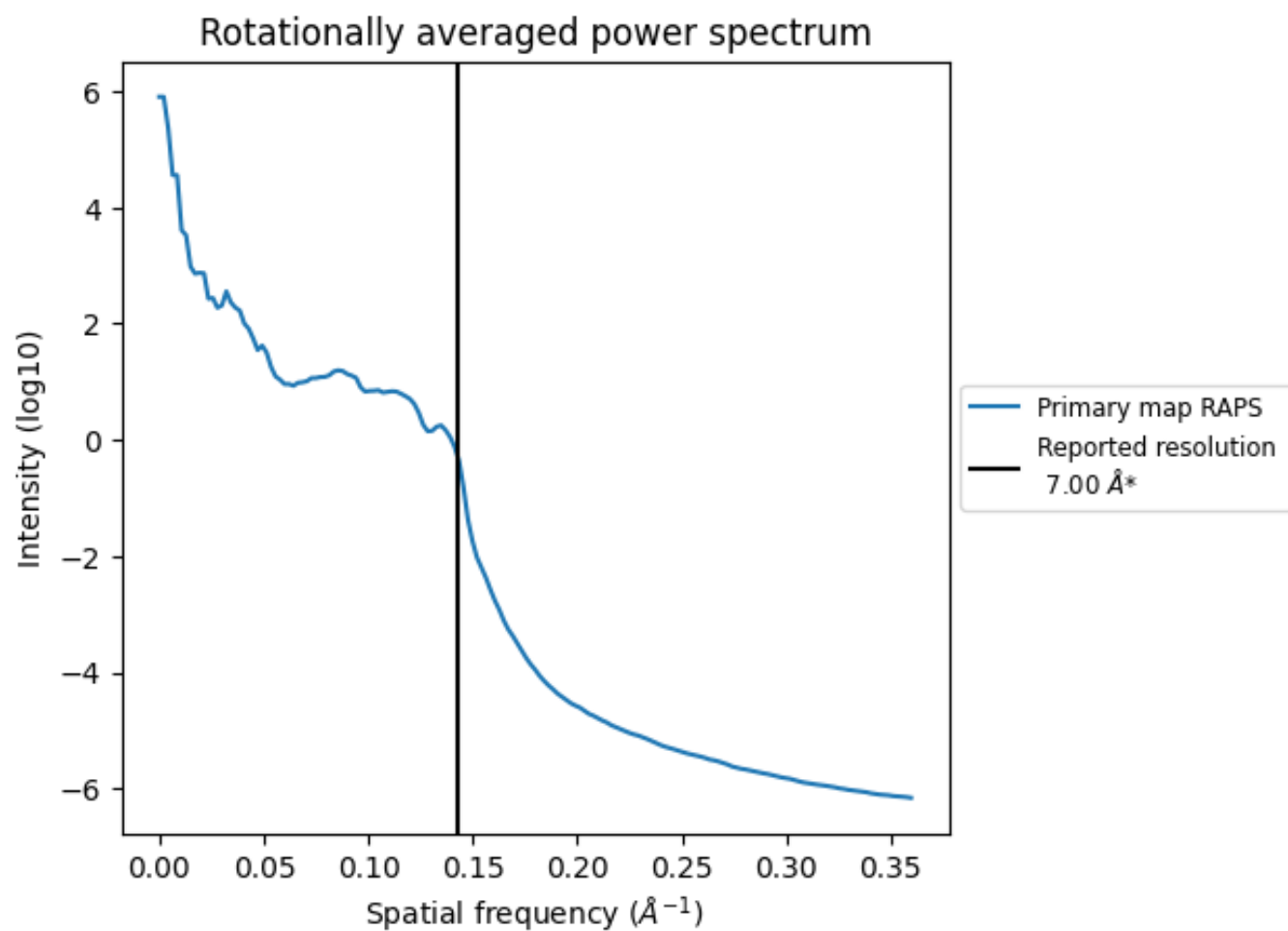
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1006 nm³; this corresponds to an approximate mass of 909 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 0.143 Å⁻¹

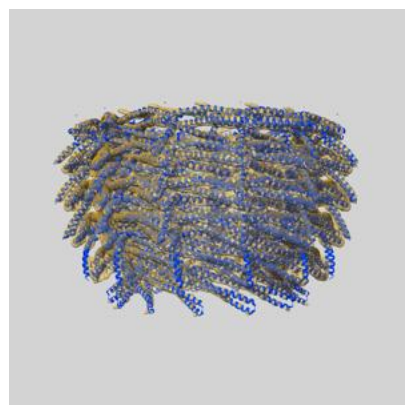
8 Fourier-Shell correlation

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

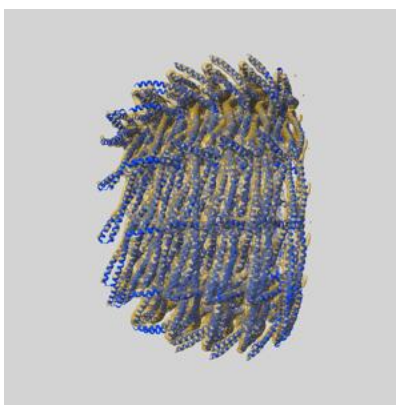
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11470 and PDB model 6ZVT. Per-residue inclusion information can be found in section [3](#) on page [10](#).

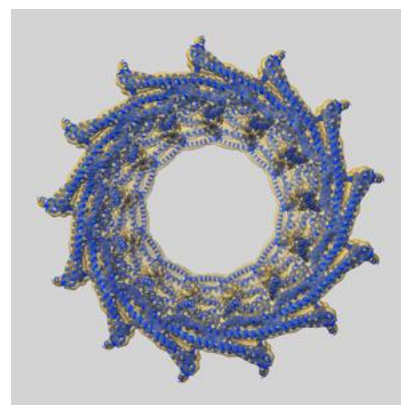
9.1 Map-model overlay [i](#)



X



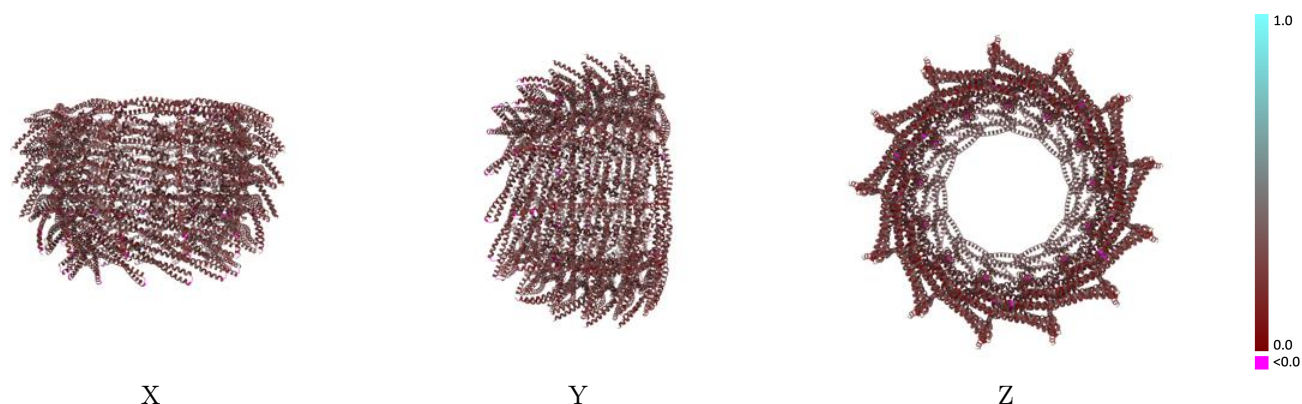
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0187 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](#)

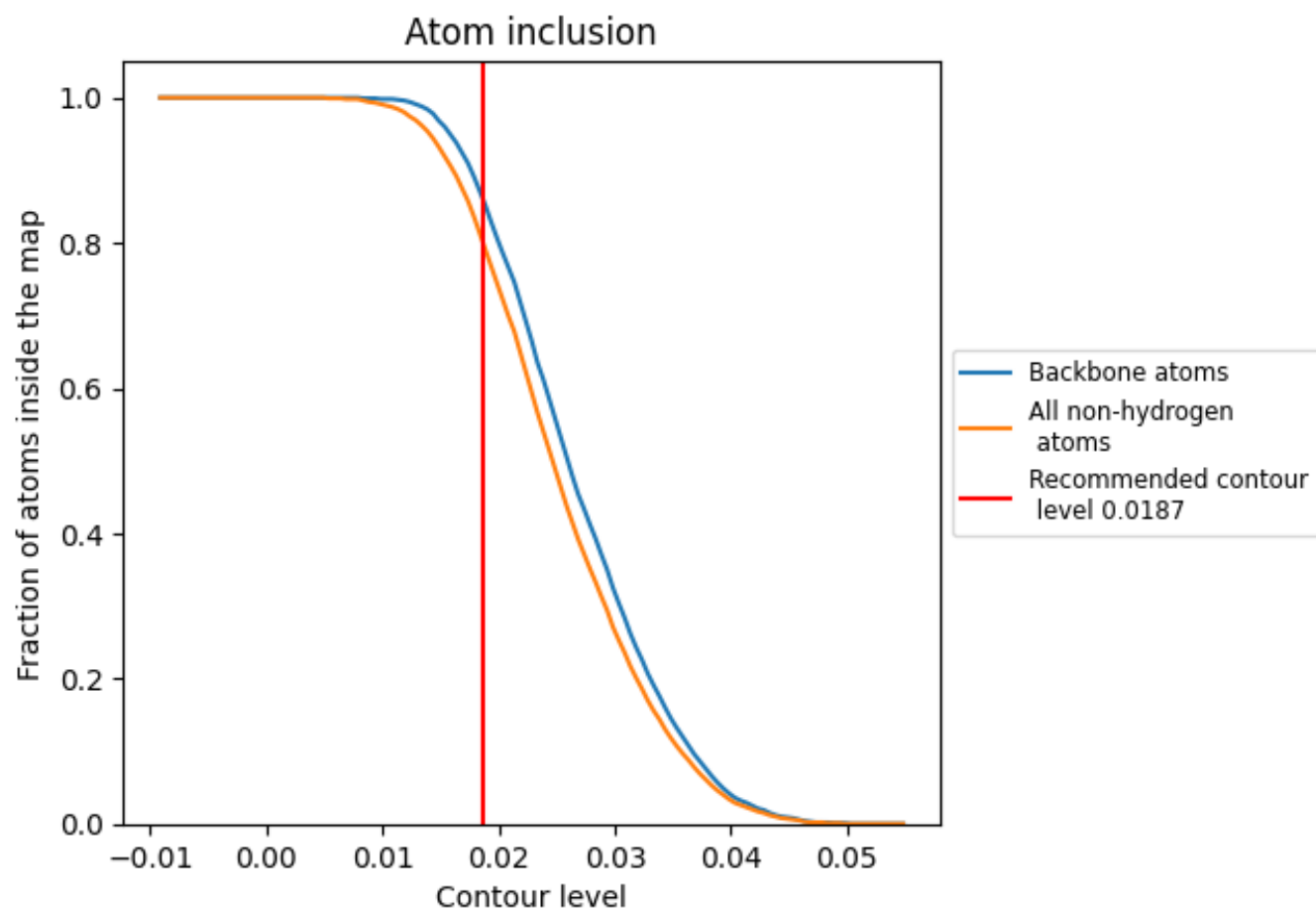


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 80% 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 (0.0187) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7980	 0.2580
A	 0.6960	 0.2520
AA	 0.7820	 0.2520
AB	 0.8840	 0.2690
AC	 0.6660	 0.2560
B	 0.7840	 0.2520
BA	 0.8840	 0.2620
BB	 0.7960	 0.2550
C	 0.8880	 0.2640
CA	 0.8830	 0.2660
CB	 0.6710	 0.2560
D	 0.8870	 0.2690
DA	 0.7970	 0.2560
DB	 0.6900	 0.2530
E	 0.8010	 0.2560
EA	 0.6700	 0.2560
EB	 0.7800	 0.2550
F	 0.6690	 0.2560
FA	 0.6930	 0.2550
FB	 0.8830	 0.2630
G	 0.6960	 0.2540
GA	 0.7790	 0.2530
GB	 0.8830	 0.2680
H	 0.7840	 0.2520
HA	 0.8850	 0.2630
HB	 0.7960	 0.2550
I	 0.8840	 0.2630
IA	 0.8850	 0.2670
IB	 0.6700	 0.2560
J	 0.8840	 0.2650
JA	 0.7960	 0.2580
JB	 0.6940	 0.2520
K	 0.7960	 0.2550
KA	 0.6690	 0.2540
KB	 0.7810	 0.2500



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Chain	Atom inclusion	Q-score
L	 0.6730	 0.2540
LA	 0.6930	 0.2550
LB	 0.8850	 0.2630
M	 0.6940	 0.2530
MA	 0.7840	 0.2540
MB	 0.8820	 0.2660
N	 0.7820	 0.2500
NA	 0.8840	 0.2650
NB	 0.7960	 0.2540
O	 0.8860	 0.2620
OA	 0.8840	 0.2700
OB	 0.6730	 0.2560
P	 0.8800	 0.2680
PA	 0.8010	 0.2570
PB	 0.6960	 0.2520
Q	 0.7970	 0.2570
QA	 0.6710	 0.2560
QB	 0.7800	 0.2520
R	 0.6730	 0.2550
RA	 0.6960	 0.2510
RB	 0.8840	 0.2640
S	 0.6930	 0.2540
SA	 0.7860	 0.2540
SB	 0.8830	 0.2670
T	 0.7810	 0.2520
TA	 0.8850	 0.2650
TB	 0.7960	 0.2550
UA	 0.8850	 0.2690
UB	 0.6690	 0.2550
V	 0.8820	 0.2640
VA	 0.8010	 0.2570
VB	 0.6910	 0.2530
W	 0.8820	 0.2660
WA	 0.6730	 0.2550
WB	 0.7800	 0.2520
X	 0.7990	 0.2570
XA	 0.6940	 0.2540
XB	 0.8850	 0.2620
Y	 0.6750	 0.2550
YA	 0.7790	 0.2540
YB	 0.8830	 0.2660
Z	 0.6970	 0.2530

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Chain	Atom inclusion	Q-score
ZA	 0.8830	 0.2660
ZB	 0.8000	 0.2550