



Full wwPDB EM Validation Report ⓘ

Mar 20, 2026 – 10:49 AM UTC

PDB ID : 6ZW6 / pdb_00006zw6
EMDB ID : EMD-11482
Title : C16 symmetry: Bacterial Vipp1 and PspA are members of the ancient ESCRT-III membrane-remodeling superfamily.
Authors : Liu, J.; 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 : 7.40 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 ⓘ 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:

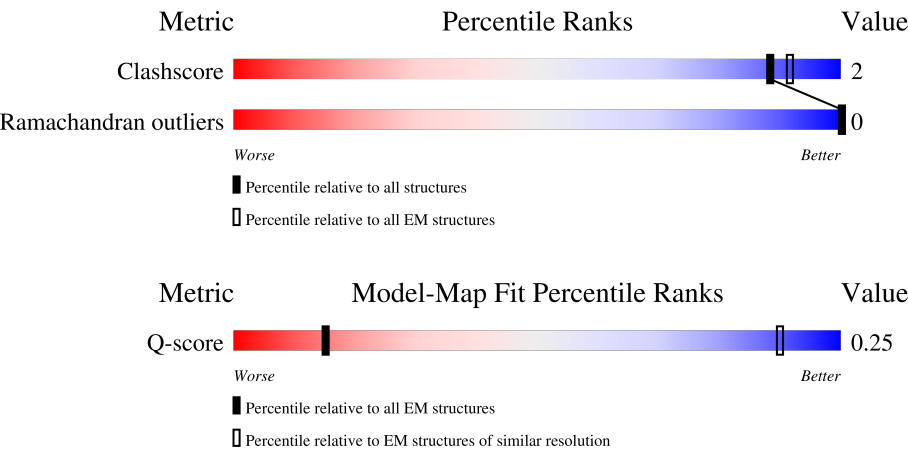
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 7.40 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	-
Q-score	-	25397	412 (6.90 - 7.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	258	21% 51% 48%
1	AA	258	83% 15%
1	AB	258	81% 15%
1	AC	258	21% 51% 48%
1	AD	258	10% 83% 16%

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Mol	Chain	Length	Quality of chain
1	B	258	
1	BA	258	
1	BB	258	
1	BC	258	
1	BD	258	
1	C	258	
1	CA	258	
1	CB	258	
1	CC	258	
1	CD	258	
1	D	258	
1	DA	258	
1	DB	258	
1	DC	258	
1	DD	258	
1	E	258	
1	EA	258	
1	EB	258	
1	EC	258	
1	ED	258	
1	F	258	
1	FA	258	
1	FB	258	
1	FC	258	
1	FD	258	

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Mol	Chain	Length	Quality of chain
1	G	258	
1	GA	258	
1	GB	258	
1	GC	258	
1	GD	258	
1	H	258	
1	HA	258	
1	HB	258	
1	HC	258	
1	HD	258	
1	I	258	
1	IA	258	
1	IB	258	
1	IC	258	
1	ID	258	
1	J	258	
1	JA	258	
1	JB	258	
1	JC	258	
1	K	258	
1	KA	258	
1	KB	258	
1	KC	258	
1	L	258	
1	LA	258	

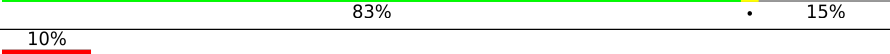
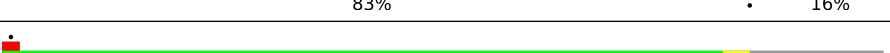
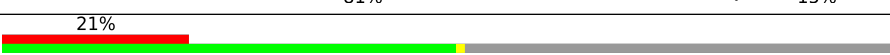
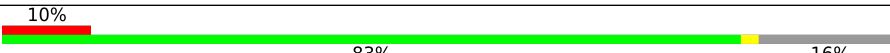
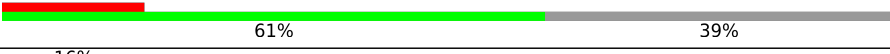
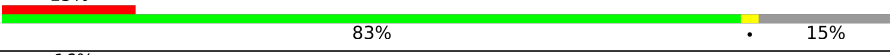
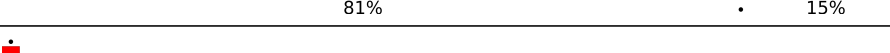
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Mol	Chain	Length	Quality of chain
1	LB	258	
1	LC	258	
1	M	258	
1	MA	258	
1	MB	258	
1	MC	258	
1	N	258	
1	NA	258	
1	NB	258	
1	NC	258	
1	O	258	
1	OA	258	
1	OB	258	
1	OC	258	
1	P	258	
1	PA	258	
1	PB	258	
1	PC	258	
1	Q	258	
1	QA	258	
1	QB	258	
1	QC	258	
1	R	258	
1	RA	258	
1	RB	258	

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Mol	Chain	Length	Quality of chain
1	RC	258	
1	S	258	
1	SA	258	
1	SB	258	
1	SC	258	
1	T	258	
1	TA	258	
1	TB	258	
1	TC	258	
1	UA	258	
1	UB	258	
1	UC	258	
1	V	258	
1	VA	258	
1	VB	258	
1	VC	258	
1	W	258	
1	WA	258	
1	WB	258	
1	WC	258	
1	X	258	
1	XA	258	
1	XB	258	
1	XC	258	
1	Y	258	

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Mol	Chain	Length	Quality of chain
1	YA	258	
1	YB	258	
1	YC	258	
1	Z	258	
1	ZA	258	
1	ZB	258	
1	ZC	258	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 109936 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 vipp1.

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	219	Total 1086	C 648	N 219	O 219	0	0
1	F	218	Total 1081	C 645	N 218	O 218	0	0
1	G	158	Total 785	C 469	N 158	O 158	0	0
1	H	133	Total 661	C 395	N 133	O 133	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	219	Total 1086	C 648	N 219	O 219	0	0
1	L	219	Total 1086	C 648	N 219	O 219	0	0
1	M	218	Total 1081	C 645	N 218	O 218	0	0
1	N	158	Total 785	C 469	N 158	O 158	0	0
1	O	133	Total 661	C 395	N 133	O 133	0	0
1	P	219	Total 1086	C 648	N 219	O 219	0	0
1	Q	219	Total 1086	C 648	N 219	O 219	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	R	219	Total 1086	C 648	N 219	O 219	0	0
1	S	219	Total 1086	C 648	N 219	O 219	0	0
1	T	218	Total 1081	C 645	N 218	O 218	0	0
1	V	158	Total 785	C 469	N 158	O 158	0	0
1	W	133	Total 661	C 395	N 133	O 133	0	0
1	X	219	Total 1086	C 648	N 219	O 219	0	0
1	Y	219	Total 1086	C 648	N 219	O 219	0	0
1	Z	219	Total 1086	C 648	N 219	O 219	0	0
1	AA	219	Total 1086	C 648	N 219	O 219	0	0
1	BA	218	Total 1081	C 645	N 218	O 218	0	0
1	CA	158	Total 785	C 469	N 158	O 158	0	0
1	DA	133	Total 661	C 395	N 133	O 133	0	0
1	EA	219	Total 1086	C 648	N 219	O 219	0	0
1	FA	219	Total 1086	C 648	N 219	O 219	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	218	Total 1081	C 645	N 218	O 218	0	0
1	JA	158	Total 785	C 469	N 158	O 158	0	0
1	KA	133	Total 661	C 395	N 133	O 133	0	0
1	LA	219	Total 1086	C 648	N 219	O 219	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 1086	C 648	N 219	O 219	0	0
1	OA	219	Total 1086	C 648	N 219	O 219	0	0
1	PA	218	Total 1081	C 645	N 218	O 218	0	0
1	QA	158	Total 785	C 469	N 158	O 158	0	0
1	RA	133	Total 661	C 395	N 133	O 133	0	0
1	SA	219	Total 1086	C 648	N 219	O 219	0	0
1	TA	219	Total 1086	C 648	N 219	O 219	0	0
1	UA	219	Total 1086	C 648	N 219	O 219	0	0
1	VA	219	Total 1086	C 648	N 219	O 219	0	0
1	WA	218	Total 1081	C 645	N 218	O 218	0	0
1	XA	158	Total 785	C 469	N 158	O 158	0	0
1	YA	133	Total 661	C 395	N 133	O 133	0	0
1	ZA	219	Total 1086	C 648	N 219	O 219	0	0
1	AB	219	Total 1086	C 648	N 219	O 219	0	0
1	BB	219	Total 1086	C 648	N 219	O 219	0	0
1	CB	219	Total 1086	C 648	N 219	O 219	0	0
1	DB	218	Total 1081	C 645	N 218	O 218	0	0
1	EB	158	Total 785	C 469	N 158	O 158	0	0
1	FB	133	Total 661	C 395	N 133	O 133	0	0
1	GB	219	Total 1086	C 648	N 219	O 219	0	0
1	HB	219	Total 1086	C 648	N 219	O 219	0	0

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

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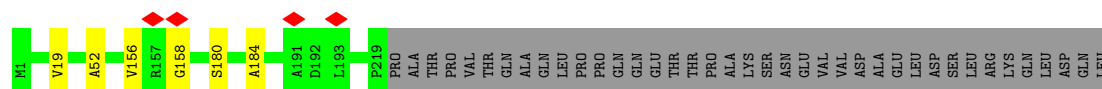
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Mol	Chain	Residues	Atoms				AltConf	Trace
1	DC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	EC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	FC	218	Total	C	N	O	0	0
			1081	645	218	218		
1	GC	158	Total	C	N	O	0	0
			785	469	158	158		
1	HC	133	Total	C	N	O	0	0
			661	395	133	133		
1	IC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	JC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	KC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	LC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	MC	218	Total	C	N	O	0	0
			1081	645	218	218		
1	NC	158	Total	C	N	O	0	0
			785	469	158	158		
1	OC	133	Total	C	N	O	0	0
			661	395	133	133		
1	PC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	QC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	RC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	SC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	TC	218	Total	C	N	O	0	0
			1081	645	218	218		
1	UC	158	Total	C	N	O	0	0
			785	469	158	158		
1	VC	133	Total	C	N	O	0	0
			661	395	133	133		
1	WC	219	Total	C	N	O	0	0
			1086	648	219	219		
1	XC	219	Total	C	N	O	0	0
			1086	648	219	219		

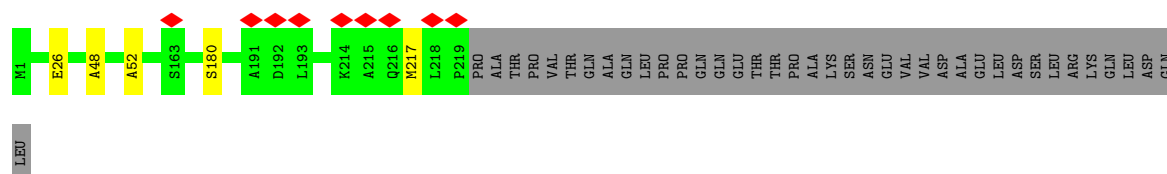
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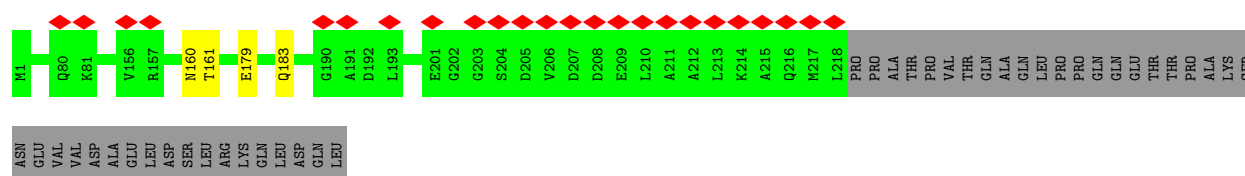
Mol	Chain	Residues	Atoms				AltConf	Trace
1	YC	219	Total 1086	C 648	N 219	O 219	0	0
1	ZC	219	Total 1086	C 648	N 219	O 219	0	0
1	AD	218	Total 1081	C 645	N 218	O 218	0	0
1	BD	158	Total 785	C 469	N 158	O 158	0	0
1	CD	133	Total 661	C 395	N 133	O 133	0	0
1	DD	219	Total 1086	C 648	N 219	O 219	0	0
1	ED	219	Total 1086	C 648	N 219	O 219	0	0
1	FD	219	Total 1086	C 648	N 219	O 219	0	0
1	GD	219	Total 1086	C 648	N 219	O 219	0	0
1	HD	218	Total 1081	C 645	N 218	O 218	0	0
1	ID	158	Total 785	C 469	N 158	O 158	0	0

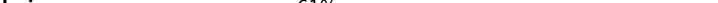


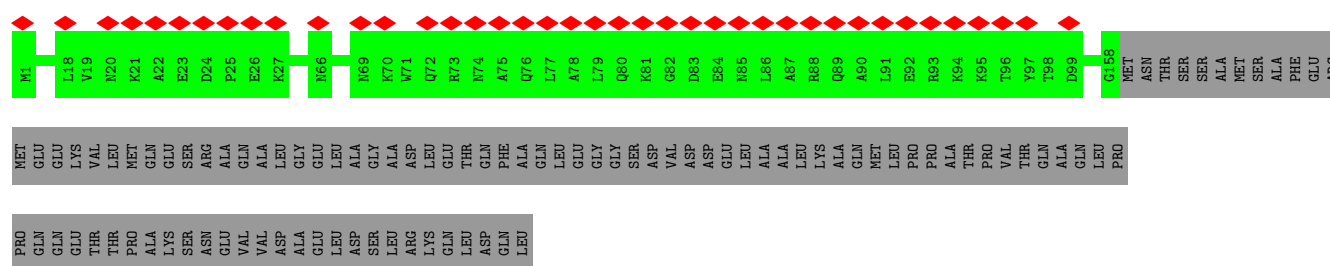
- Chain E:  83% 15%

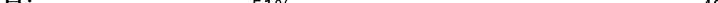


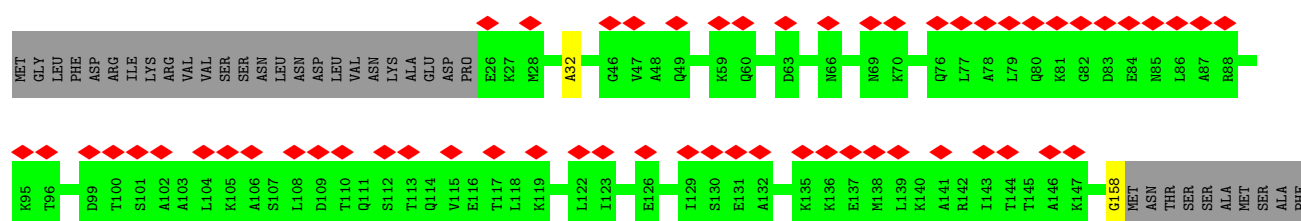
- Chain F:  9% 83% 16%



- Chain G: 



- Chain H:  22% 51% 48%



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

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

• Molecule 1: vipp1

Chain I: 13% 83% 15%

M1 G2 I3 F4 D5 R6 I7 K8 R9 V10 N16 A22 A32 A48 A52 G82 D83 E84 A157 A167 A174 V175 A189 G190 A191 D192 L193 E194 T195 Q196 F197 A198 S204 A215 Q216 M217 L218 P219 PRO ALA THR PRO VAL THR GLN GLN LEU

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

• Molecule 1: vipp1

Chain J: 81% 15%

H1 L18 A32 A48 A52 A146 T161 A167 S180 R181 Q183 A184 A191 D192 L193 E194 V206 P219 PRO ALA THR THR VAL THR GLN ALA GLN LEU LEU PRO PRO GLN GLN THR THR VAL THR GLN GLN LEU LEU ASP

SER LEU
ARG ARG
LYS LYS
GLN GLN
ASP ASP
GLN GLN
LEU LEU

• Molecule 1: vipp1

Chain K: 83% 15%

H1 V19 A52 V156 R157 G158 S180 A184 A191 D192 L193 P219 PRO THR VAL THR THR GLN ALA LYS SER ASN GLU VAL VAL ASP ALA GLU LEU LEU ASP SER LEU LEU ARG LYS GLN LEU LEU

• Molecule 1: vipp1

Chain L: 83% 15%

H1 E26 A48 A52 S163 S180 A191 D192 L193 K214 A215 Q216 M217 L218 P219 PRO ALA THR VAL THR THR GLN ALA GLN LEU LEU PRO PRO GLN GLN GLU GLU THR THR PRO PRO LYS SER ASN GLU VAL VAL ASP ALA GLU LEU LEU ASP SER LEU LEU ARG LYS GLN GLN ASP GLN

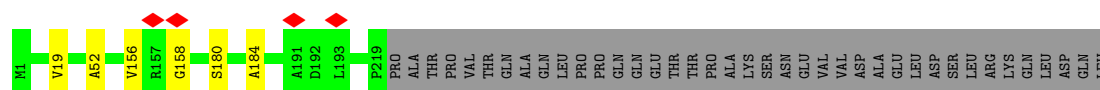
LEU

• Molecule 1: vipp1

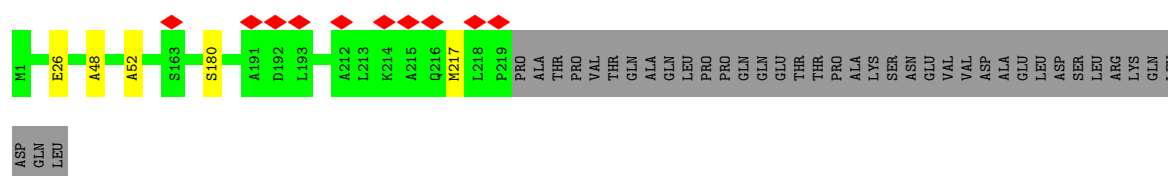
Chain M: 10% 83% 16%

H1 Q80 K81 V156 R157 T161 E179 Q183 G190 A191 D192 L193 E194 E201 G202 G203 S204 D205 V206 D207 D208 E209 L210 A211 A212 L213 K214 A215 Q216 M217 L218 PRO PRO ALA THR PRO PRO VAL THR THR GLN ALA SER LEU LEU PRO PRO GLN GLN GLU GLU THR THR PRO PRO ALA LYS

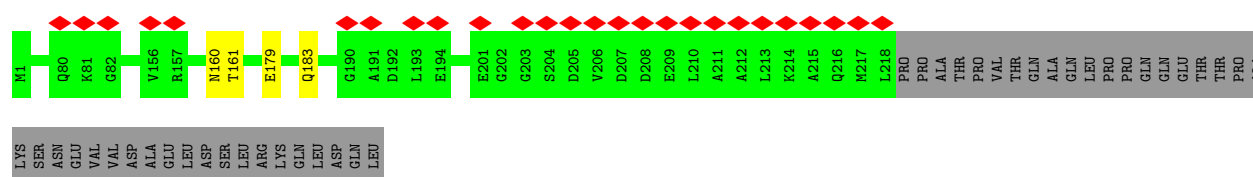
• Molecule 1: vipp1

Chain R:  83% 15%

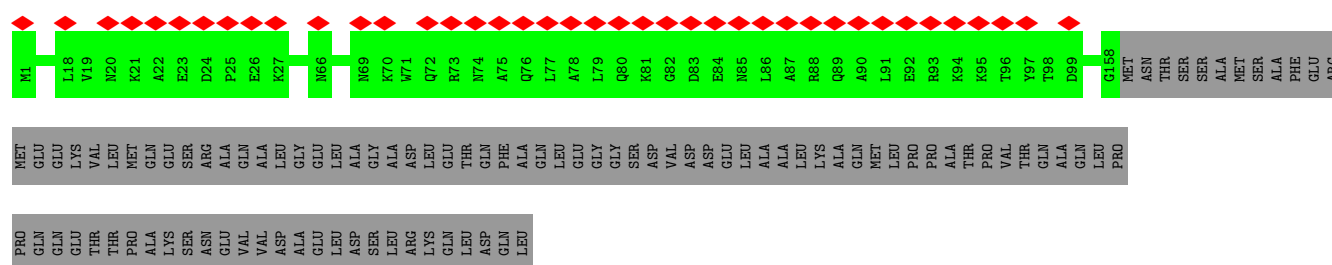
• Molecule 1: vipp1

Chain S:  83% 15%

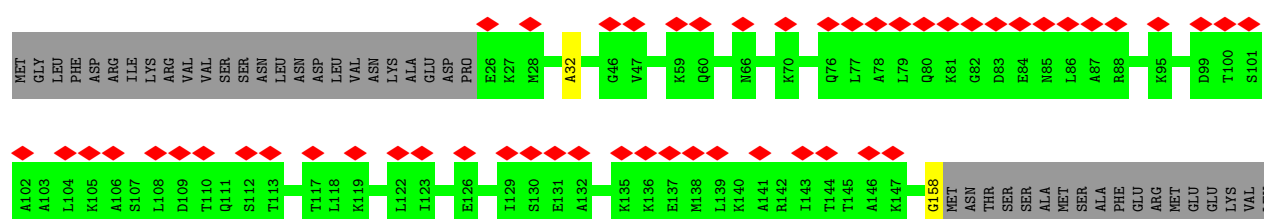
• Molecule 1: vipp1

Chain T:  10% 83% 16%

• Molecule 1: vipp1

Chain V:  16% 61% 39%

• Molecule 1: vipp1

Chain W:  21% 51% 48%

SER
ASN
GLU
VAL
VAL
ASP
ALA
GLU
LEU
ASP
SER
SER
LEU
ARG
LYS
GLN
LEU
ASP
GLN
LEU

• Molecule 1: vipp1



M1	L18	V19	N20	K21	A22	E23	D24	P25	E26	K27	N66	N69	K70	W71	Q72	R73	N74	A75	Q76	L77	A78	L79	Q80	K81	G82	D83	E84	N85	L86	A87	R88	Q89	A90	L91	E92	R93	K94	K95	T96	Y97	T98	D99	G158	MET	ASN	THR	SER	SER	ALA	MET	SER	ALA	PHE	GLU	ARG
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MET	GLU	GLU	LYS	VAL	LEU	MET	GLN	SER	ARG	ALA	ALA	GLN	ASP	GLY	ALA	ASP	GLY	PHE	ALA	GLN	LEU	LEU	GLY	GLY	ASP	VAL	ASP	ASP	GLU	LEU	ALA	ALA	ASP	LYS	ALA	GLN	PRO	PRO	THR	VAL	GLN	ALA	GLN	LEU	PRO
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PRO	GLN	GLN	GLU	THR	THR	PRO	ALA	LYS	SER	ASN	VAL	VAL	ASP	ALA	GLY	LEU	LEU	ASP	SER	GLY	ALA	ASP	GLY	GLY	ASP	VAL	ASP	ASP	GLU	LEU	ALA	ALA	ASP	LYS	GLN	LEU	ASP	GLN	LEU
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• Molecule 1: vipp1



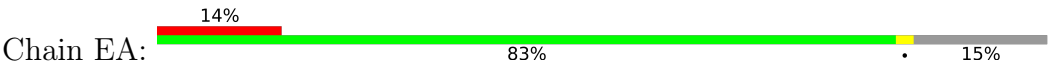
MET	GLY	LEU	PHE	ASP	ARG	ILE	LYS	ARG	VAL	SER	ASN	LEU	ASN	ASP	LEU	VAL	ASN	LYS	ALA	GLU	PRO	E26	K27	W28	A32	Q46	V47	A48	Q49	K59	Q60	N66	K70	Q76	L77	A78	L79	Q80	K81	G82	D83	E84	N85	L86	A87	R88	K95	D99
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T100	S101	A102	A103	L104	K105	A106	S107	L108	D109	Q110	Q111	S112	T113	T117	L118	K119	L122	I123	E126	I129	S130	E131	A132	K135	K136	E137	M138	L139	K140	A141	R142	I143	T144	T145	A146	K147	G158	MET	ASN	THR	SER	SER	ALA	MET	SER	PHE	GLU	ARG	MET	GLU	GLU	LYS
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VAL	LEU	MET	GLN	GLU	ARG	SER	ARG	ALA	GLN	LEU	GLY	GLY	ALA	ASP	LEU	GLU	LEU	THR	GLN	GLN	PHE	ALA	GLN	LEU	GLY	GLY	GLY	SER	ASP	VAL	ASP	GLU	LEU	ALA	ALA	LEU	ALA	GLN	GLN	LEU	PRO	PRO	GLN	GLN	GLU
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THR	THR	PRO	ALA	LYS	SER	ASN	GLU	VAL	VAL	ASP	ALA	GLY	LEU	ASP	ASN	LEU	ARG	LYS	GLN	ASP	GLN	LEU
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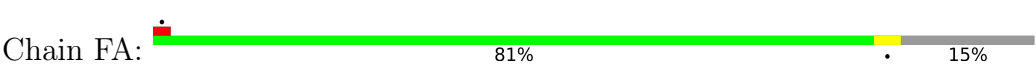
• Molecule 1: vipp1



M1	G2	L3	F4	D5	H6	I7	K8	R9	V10	N16	A22	A32	A48	A52	G82	E84	R157	A167	K174	V175	A189	G190	A191	D192	L193	E194	Q196	F197	A198	E201	S204	A211	A215	Q216	W217	L218	F219	PRO	ALA	ALA	THR	PRO	VAL	THR
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GLN	ALA	GLN	LEU	PRO	GLN	GLN	THR	THR	PRO	ALA	LYS	SER	ASN	GLU	VAL	VAL	ASP	ALA	GLU	LEU	ASP	SER	LEU	ARG	LYS	GLN	LEU	LEU	ASP	GLN	LEU
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• Molecule 1: vipp1

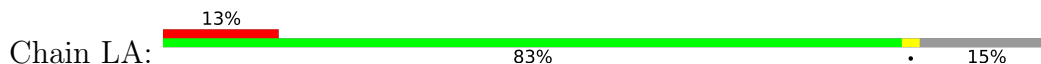


M1	L18	A32	A48	A52	A146	T161	A167	S180	A181	A182	Q183	A184	A191	D192	L193	E194	F219	PRO	ALA	THR	PRO	VAL	THR	GLN	GLN	LEU	PRO	PRO	GLN	GLU	THR	PRO	ALA	LYS	SER	ASN	GLU	VAL	VAL	ASP	ALA	GLU	LEU	ASP	SER	LEU
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ARG	LYS	GLN	LEU	ASP	GLN	LEU
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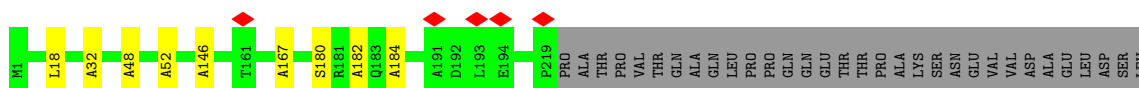
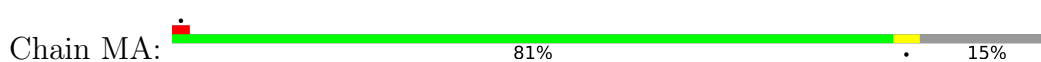
PRO GLN GLN GLU THR THR PRO PRO ALA LYS SER ASN GLU VAL VAL ASP ALA GLU LEU ASP SER LEU LEU ARG LYS GLN LEU LEU ASP GLN LEU

- Molecule 1: vippp1



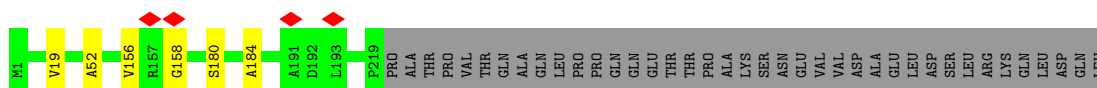
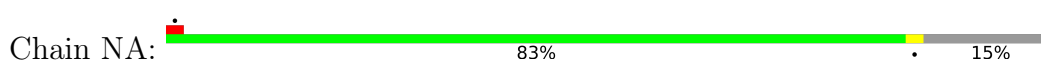
LEU	PRO	PRO	GLN	GLN	THR	THR	PRO	ALA	LYS	SER	ASN	GLU	VAL	VAL	ASP	ALA	GLU	GLU	LEU	ASP	SER	LEU	LEU	ARG	LYS	GLN	LEU	ASP	GLN	LEU	LEU
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- Molecule 1: vippp1

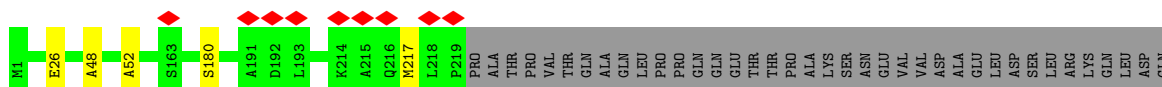
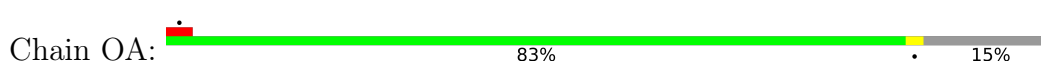


ARG
LYS
GLN
LEU
ASP
GLN
LEU

- Molecule 1: vippp1

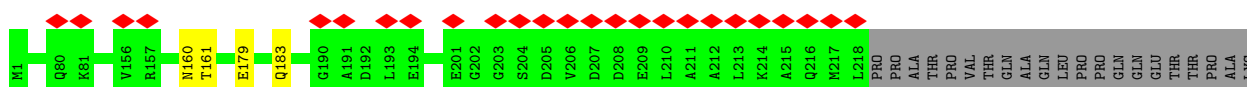
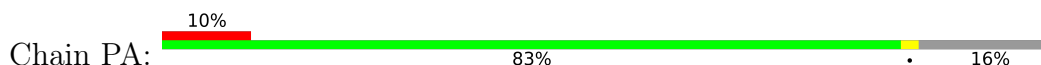


- Molecule 1: vippp1

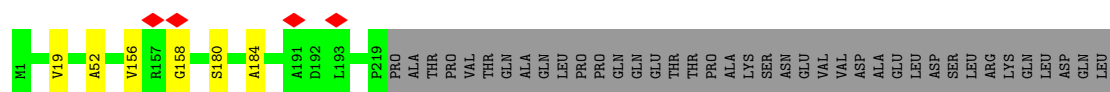


LEU

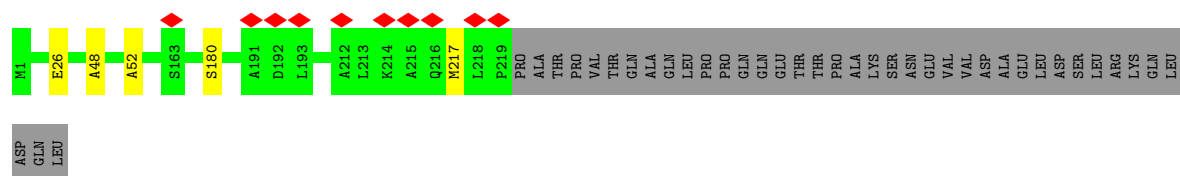
- Molecule 1: vippp1



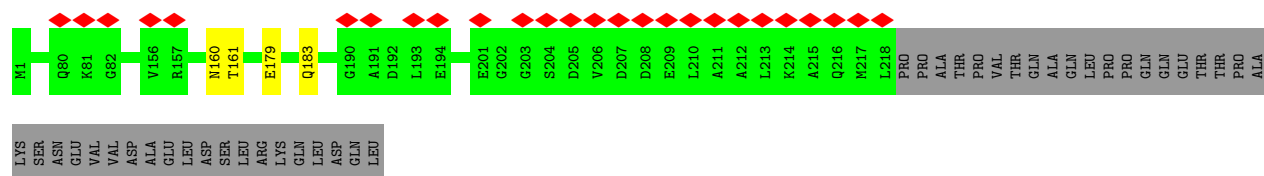
Chain UA: 83% 15%



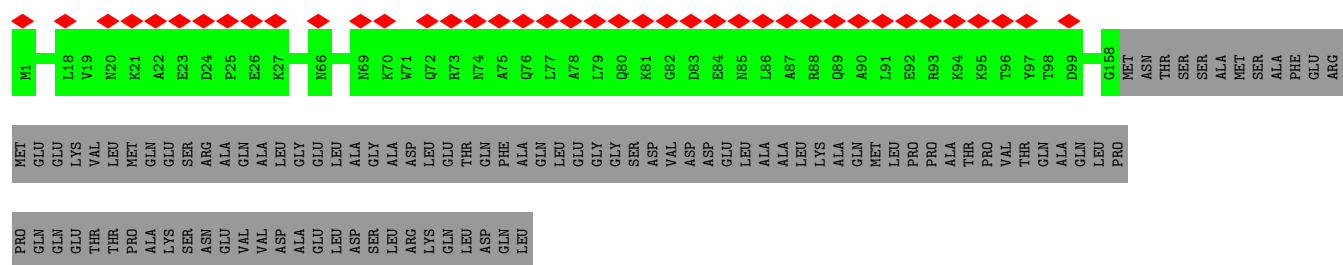
Chain VA: 83% 15%



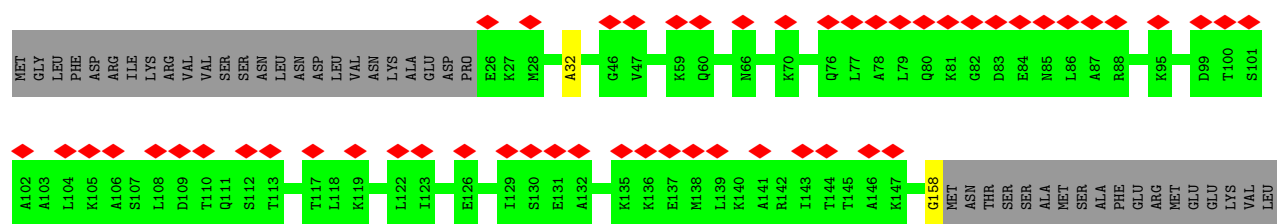
Chain WA:

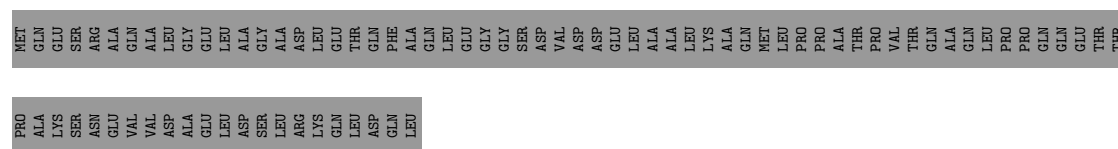


Chain XA:

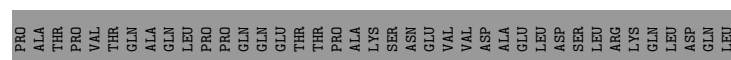
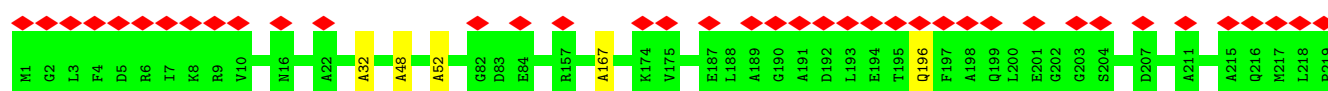
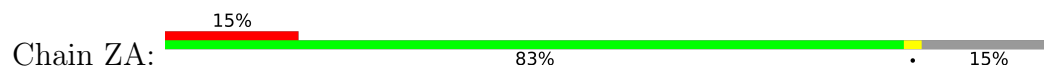


Chain YA:

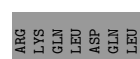
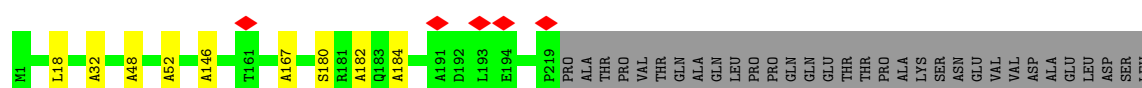
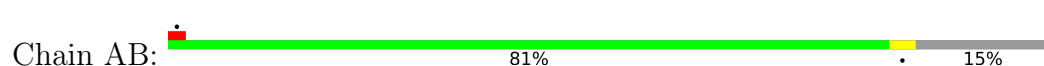




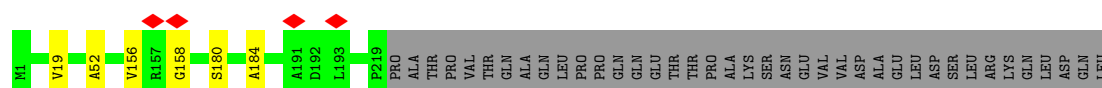
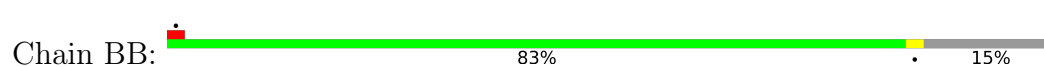
• Molecule 1: vipp1



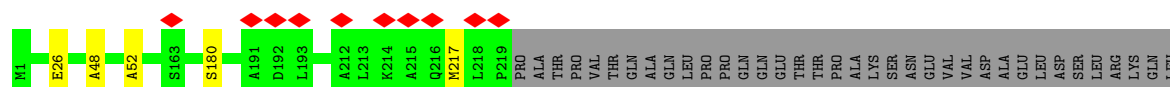
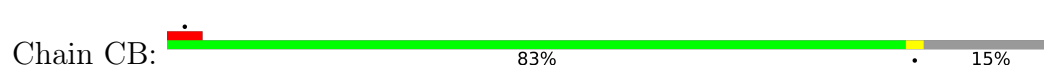
• Molecule 1: vipp1



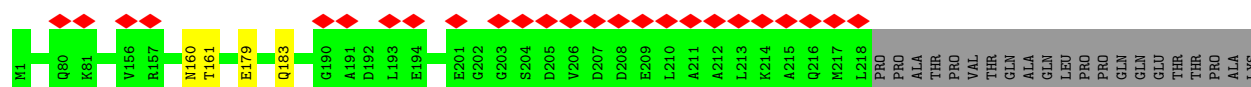
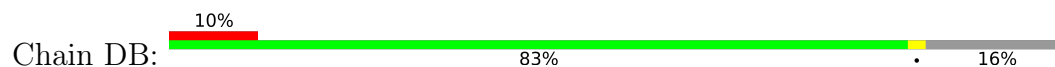
• Molecule 1: vipp1



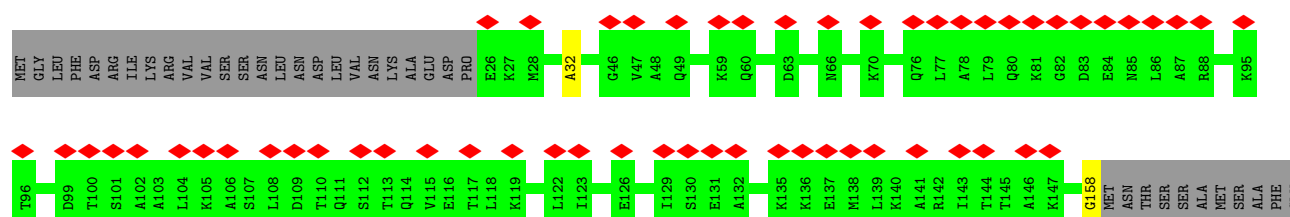
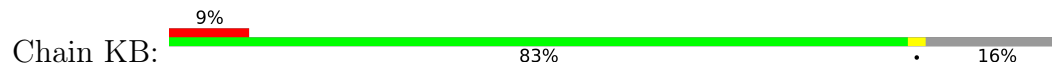
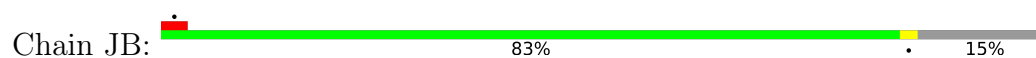
• Molecule 1: vipp1



• Molecule 1: vipp1

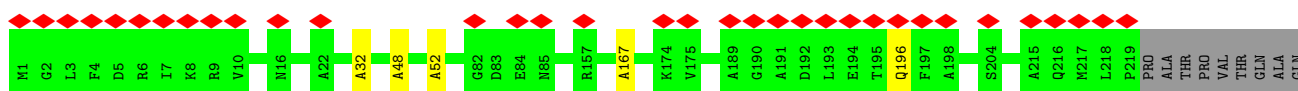
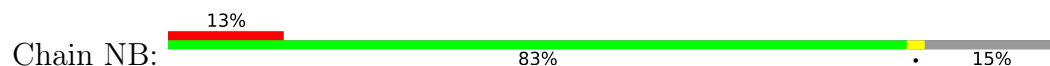


Chain IB: 83% 15%



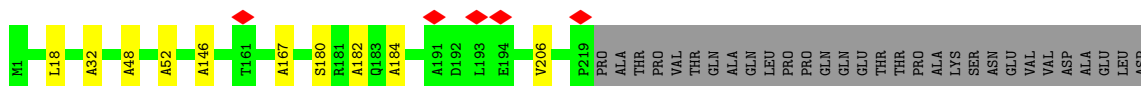
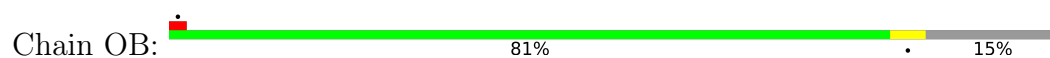
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- Molecule 1: vippp1



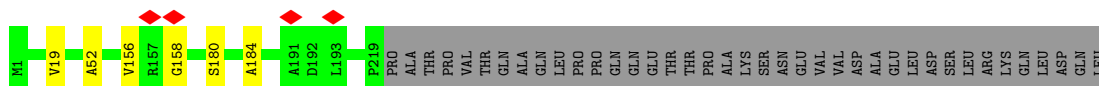
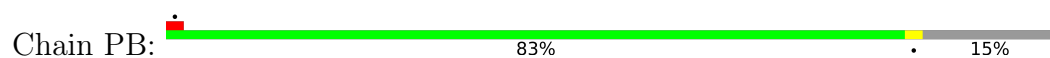
LEU PRO PRO GLN GLN THR THR PRO ALA LYS SER ASN GLU VAL VAL ASP ALA GLU LEU ASP SER LEU ARG LYS GLN LEU ASP GLN LEU

- Molecule 1: vippp1

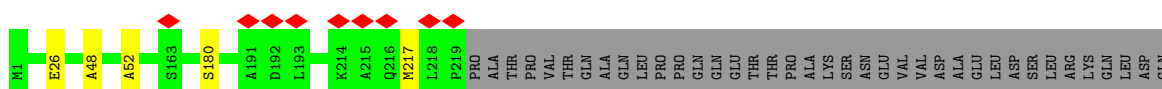
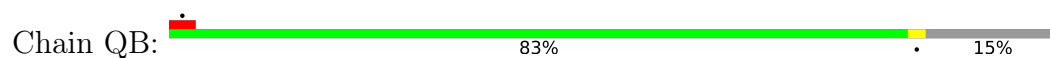


SER
LEU
ARG
LYS
GLN
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ASP
GLN
LEU

- Molecule 1: vippp1

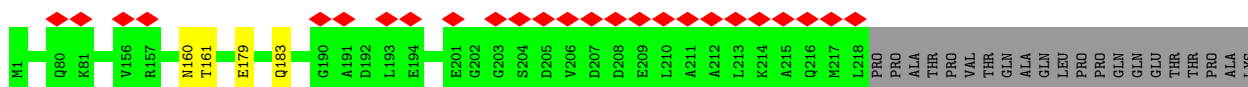
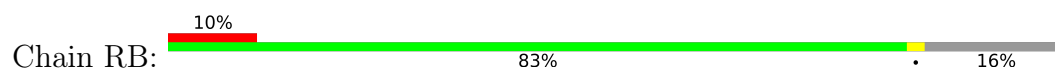


- Molecule 1: vippp1



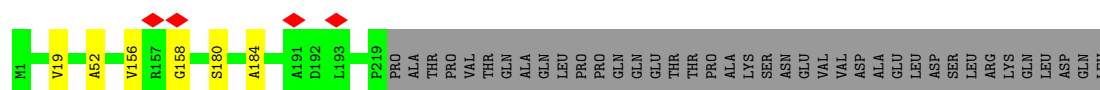
LEU

- Molecule 1: vippp1

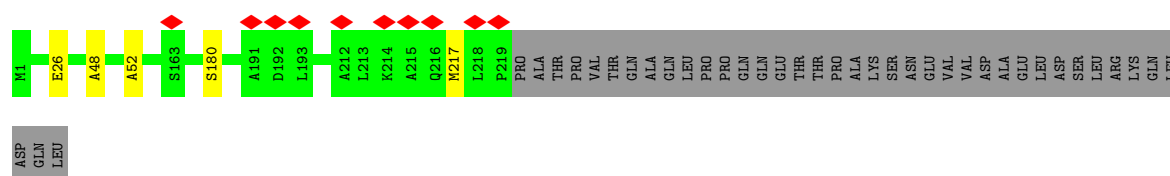




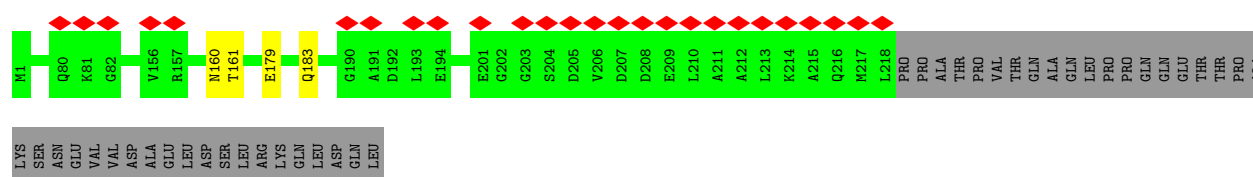
• Molecule 1: vipp1

Chain WB:  83% 15%

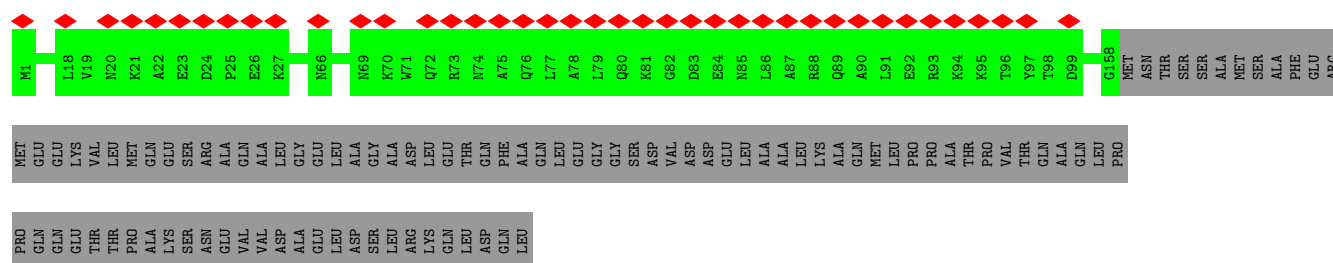
• Molecule 1: vipp1

Chain XB:  83% 15%

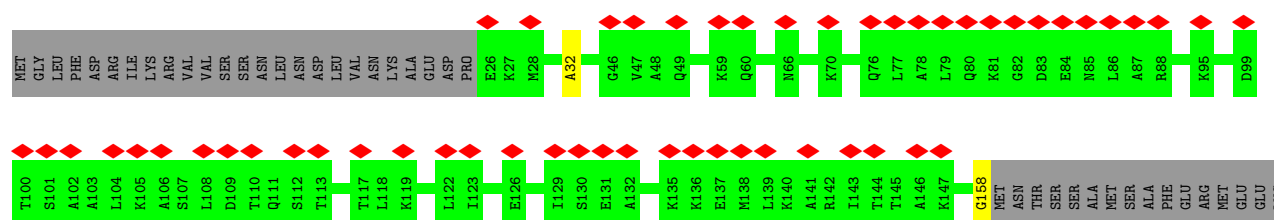
• Molecule 1: vipp1

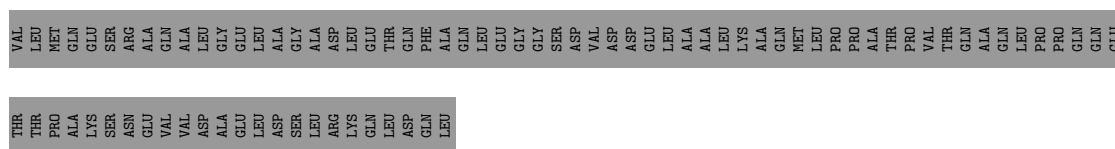
Chain YB:  10% 83% 16%

• Molecule 1: vipp1

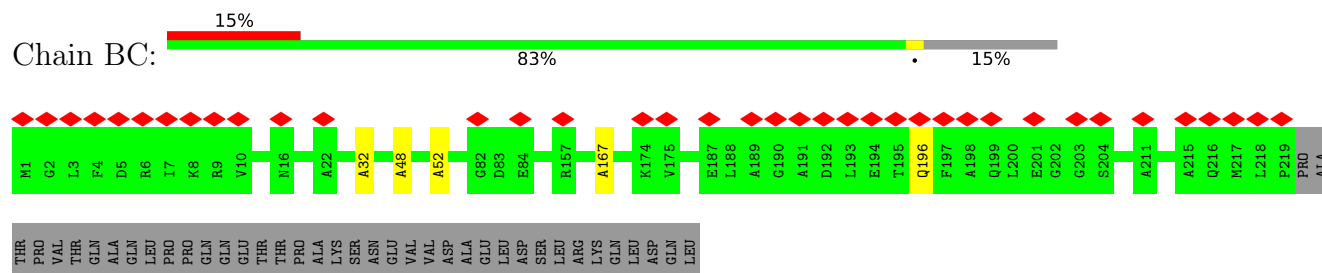
Chain ZB:  16% 61% 39%

• Molecule 1: vipp1

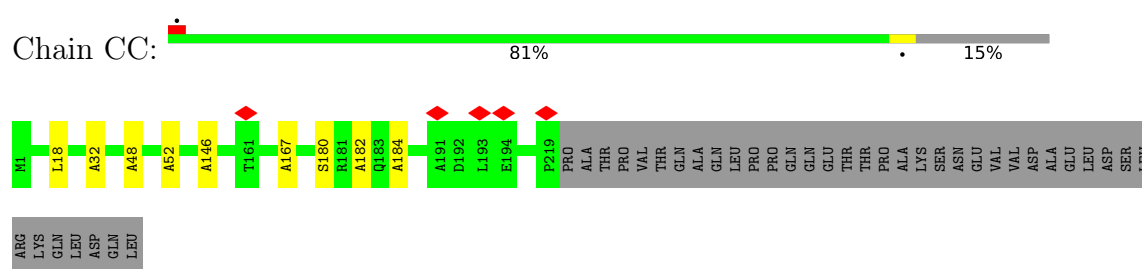
Chain AC:  21% 51% 48%



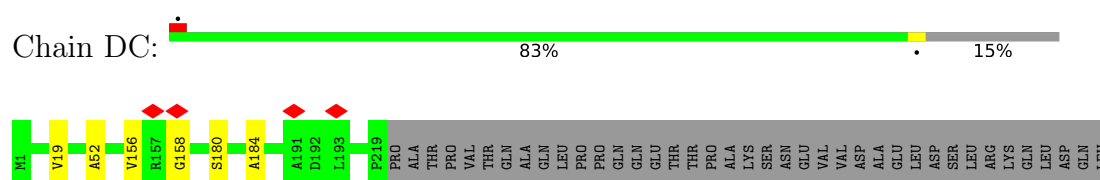
- Molecule 1: vippp1



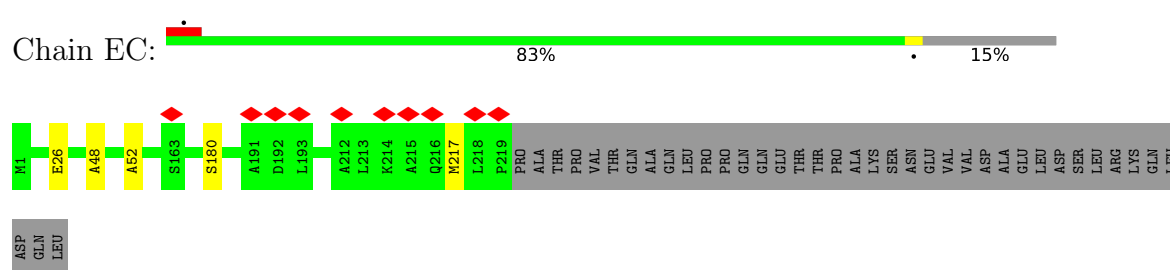
- Molecule 1: vippp1



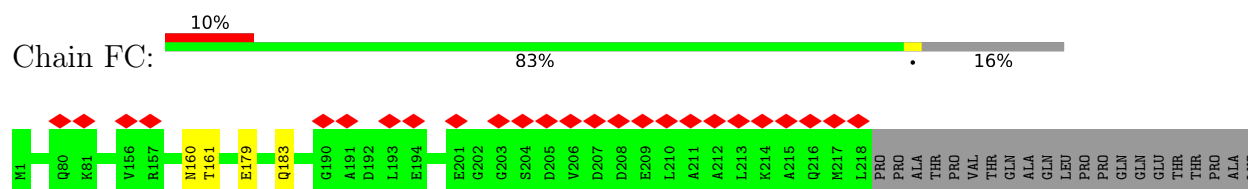
- Molecule 1: vippp1



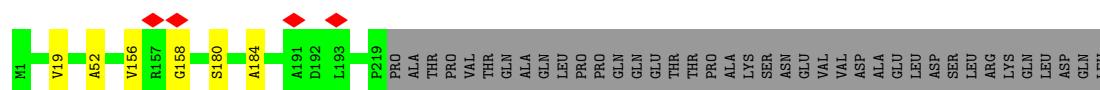
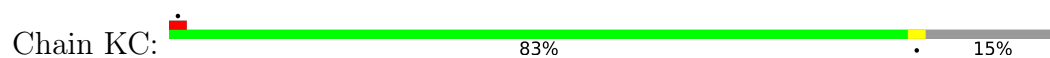
- Molecule 1: vippp1



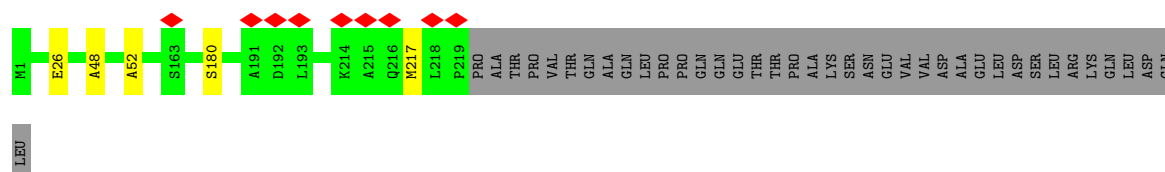
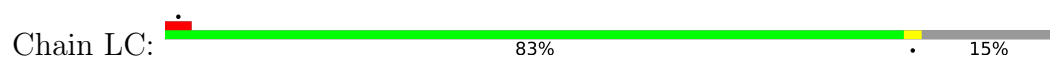
- Molecule 1: vippp1



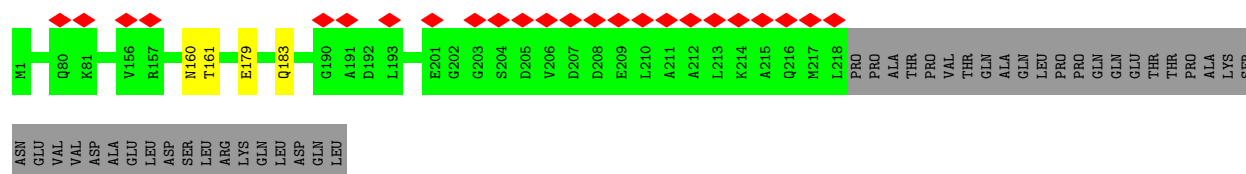
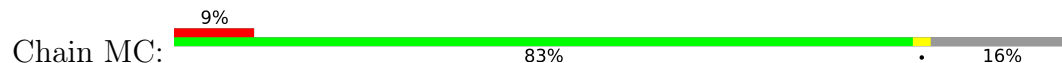
• Molecule 1: vipp1



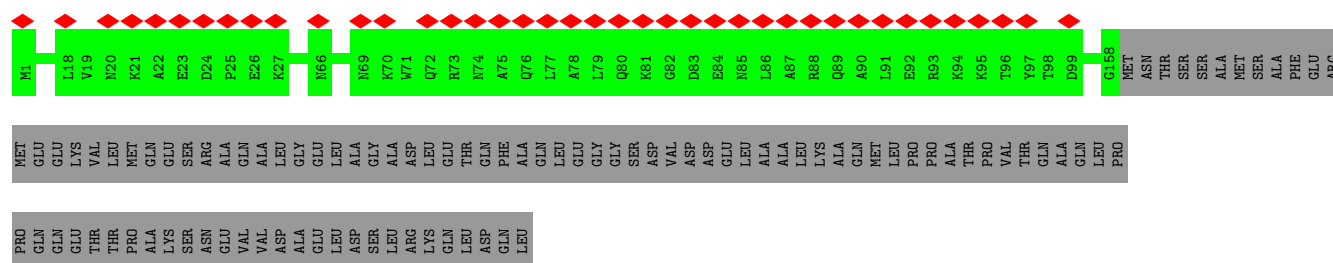
• Molecule 1: vipp1



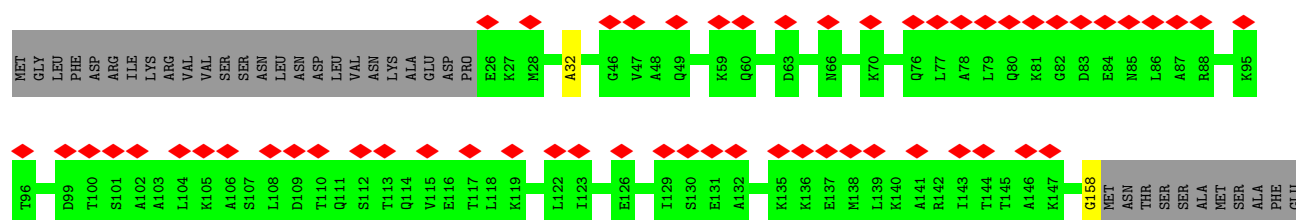
• Molecule 1: vipp1

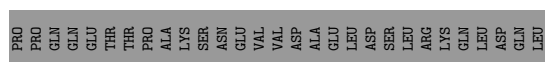


• Molecule 1: vipp1

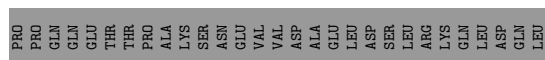
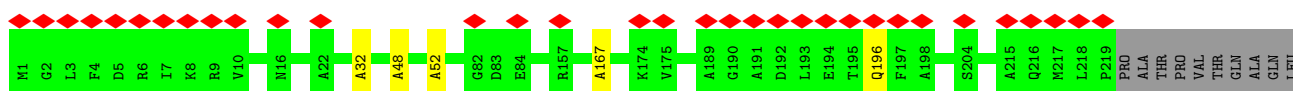


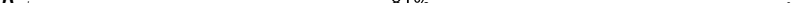
• Molecule 1: vipp1

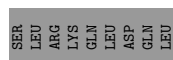
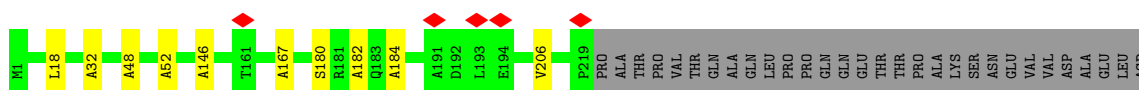




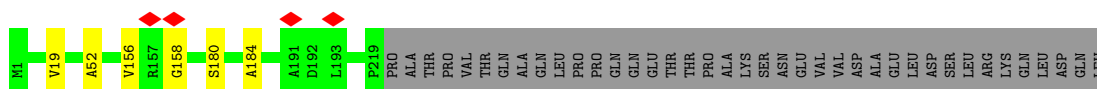
Chain PC:  13% 83% 15%



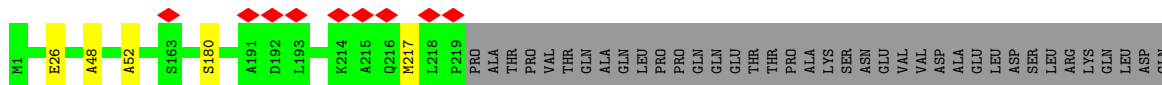
Chain QC:  81% 15%



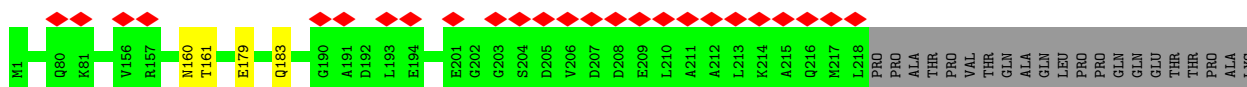
Chain RC:  83% 15%



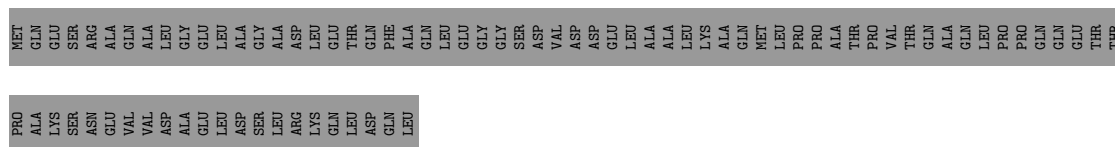
Chain SC:  83% 15%



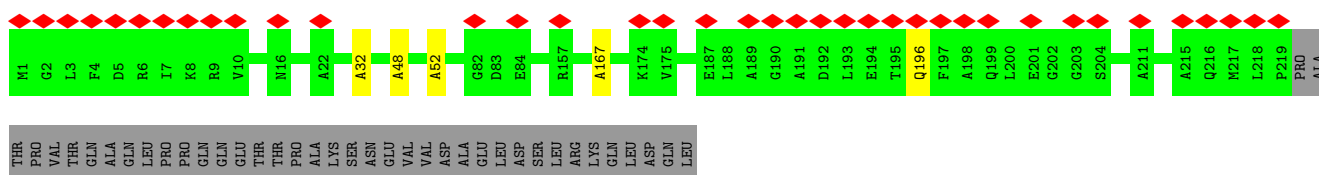
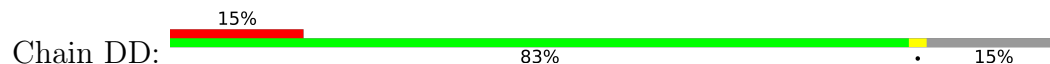
Chain TC: 



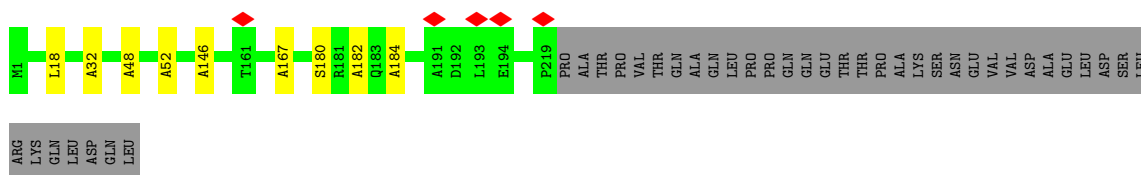
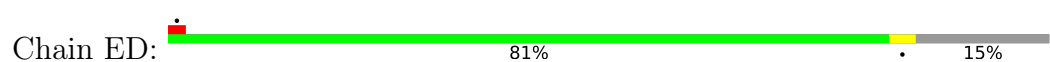




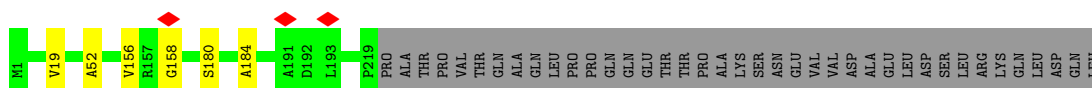
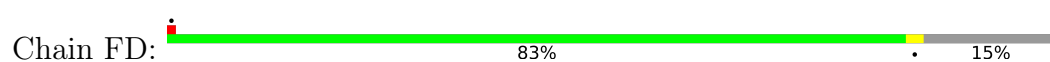
• Molecule 1: vipp1



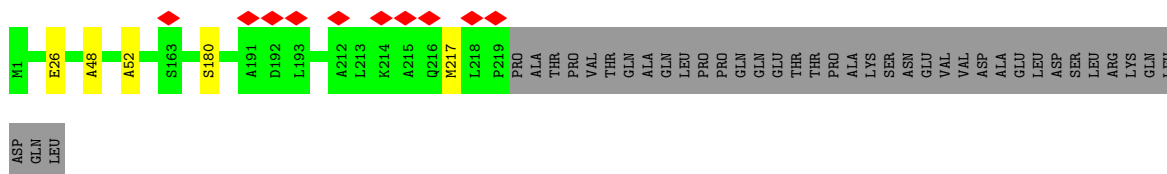
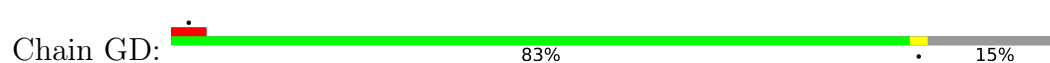
• Molecule 1: vipp1



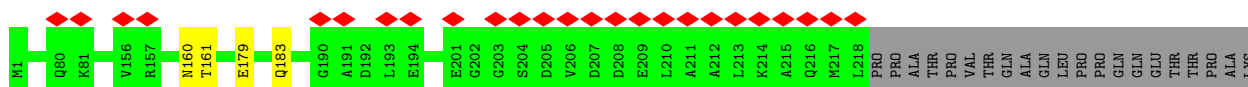
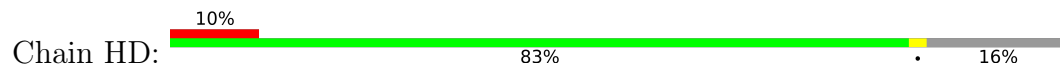
• Molecule 1: vipp1



• Molecule 1: vipp1

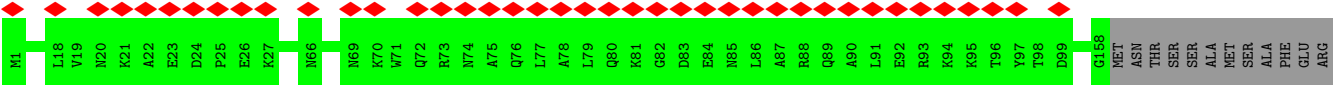


• Molecule 1: vipp1



SER
ASN
GLU
VAL
VAL
ASP
ALA
GLU
LEU
ASP
SER
SER
LEU
ARG
LYS
GLN
LEU
ASP
GLN
LEU

● Molecule 1: vippl



MET
GLU
GLU
LYS
VAL
LEU
MET
GLN
GLU
SER
SER
ARG
ALA
GLN
ALA
LEU
GLY
GLU
LEU
LEU
ALA
GLY
LEU
ALA
GLY
LEU
ALA
ASP
LEU
GLY
GLY
SER
ASP
VAL
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ASP
ASP
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ALA
ALA
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LYS
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MET
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ASP
SER
LEU
ARG
LYS
GLN
LEU
LEU
GLN
ASP
GLN
LEU

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7017	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	0.036	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.014	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	0.34	0/660	0.89	0/920
1	AA	0.36	0/1085	0.89	2/1512 (0.1%)
1	AB	0.36	0/1085	0.91	1/1512 (0.1%)
1	AC	0.34	0/660	0.89	0/920
1	AD	0.36	0/1080	0.95	0/1505
1	B	0.35	0/1085	0.93	1/1512 (0.1%)
1	BA	0.36	0/1080	0.95	0/1505
1	BB	0.37	0/1085	0.98	3/1512 (0.2%)
1	BC	0.35	0/1085	0.93	1/1512 (0.1%)
1	BD	0.35	0/784	0.92	0/1093
1	C	0.35	0/1085	0.91	1/1512 (0.1%)
1	CA	0.35	0/784	0.92	0/1093
1	CB	0.36	0/1085	0.89	2/1512 (0.1%)
1	CC	0.36	0/1085	0.91	1/1512 (0.1%)
1	CD	0.34	0/660	0.89	0/920
1	D	0.37	0/1085	0.98	3/1512 (0.2%)
1	DA	0.34	0/660	0.89	0/920
1	DB	0.36	0/1080	0.95	0/1505
1	DC	0.37	0/1085	0.98	3/1512 (0.2%)
1	DD	0.36	0/1085	0.93	1/1512 (0.1%)
1	E	0.36	0/1085	0.89	2/1512 (0.1%)
1	EA	0.35	0/1085	0.93	1/1512 (0.1%)
1	EB	0.35	0/784	0.92	0/1093
1	EC	0.36	0/1085	0.89	2/1512 (0.1%)
1	ED	0.36	0/1085	0.91	1/1512 (0.1%)
1	F	0.36	0/1080	0.95	0/1505
1	FA	0.35	0/1085	0.91	1/1512 (0.1%)
1	FB	0.34	0/660	0.89	0/920
1	FC	0.36	0/1080	0.95	0/1505
1	FD	0.37	0/1085	0.98	3/1512 (0.2%)
1	G	0.35	0/784	0.92	0/1093
1	GA	0.37	0/1085	0.98	3/1512 (0.2%)
1	GB	0.35	0/1085	0.93	1/1512 (0.1%)
1	GC	0.35	0/784	0.92	0/1093

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	GD	0.36	0/1085	0.89	2/1512 (0.1%)
1	H	0.34	0/660	0.89	0/920
1	HA	0.36	0/1085	0.89	2/1512 (0.1%)
1	HB	0.35	0/1085	0.91	1/1512 (0.1%)
1	HC	0.34	0/660	0.89	0/920
1	HD	0.36	0/1080	0.95	0/1505
1	I	0.35	0/1085	0.93	1/1512 (0.1%)
1	IA	0.36	0/1080	0.95	0/1505
1	IB	0.37	0/1085	0.98	3/1512 (0.2%)
1	IC	0.35	0/1085	0.93	1/1512 (0.1%)
1	ID	0.35	0/784	0.92	0/1093
1	J	0.36	0/1085	0.91	2/1512 (0.1%)
1	JA	0.35	0/784	0.92	0/1093
1	JB	0.36	0/1085	0.89	2/1512 (0.1%)
1	JC	0.35	0/1085	0.91	1/1512 (0.1%)
1	K	0.37	0/1085	0.98	3/1512 (0.2%)
1	KA	0.34	0/660	0.89	0/920
1	KB	0.36	0/1080	0.95	0/1505
1	KC	0.37	0/1085	0.98	3/1512 (0.2%)
1	L	0.36	0/1085	0.89	2/1512 (0.1%)
1	LA	0.36	0/1085	0.93	1/1512 (0.1%)
1	LB	0.35	0/784	0.92	0/1093
1	LC	0.36	0/1085	0.89	2/1512 (0.1%)
1	M	0.37	0/1080	0.95	0/1505
1	MA	0.36	0/1085	0.91	1/1512 (0.1%)
1	MB	0.34	0/660	0.89	0/920
1	MC	0.36	0/1080	0.95	0/1505
1	N	0.35	0/784	0.92	0/1093
1	NA	0.37	0/1085	0.98	3/1512 (0.2%)
1	NB	0.36	0/1085	0.93	1/1512 (0.1%)
1	NC	0.35	0/784	0.92	0/1093
1	O	0.34	0/660	0.89	0/920
1	OA	0.36	0/1085	0.89	2/1512 (0.1%)
1	OB	0.36	0/1085	0.91	2/1512 (0.1%)
1	OC	0.34	0/660	0.89	0/920
1	P	0.35	0/1085	0.93	1/1512 (0.1%)
1	PA	0.37	0/1080	0.95	0/1505
1	PB	0.37	0/1085	0.98	3/1512 (0.2%)
1	PC	0.36	0/1085	0.93	1/1512 (0.1%)
1	Q	0.36	0/1085	0.91	1/1512 (0.1%)
1	QA	0.35	0/784	0.92	0/1093
1	QB	0.36	0/1085	0.89	2/1512 (0.1%)
1	QC	0.36	0/1085	0.91	2/1512 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	R	0.37	0/1085	0.98	3/1512 (0.2%)
1	RA	0.34	0/660	0.89	0/920
1	RB	0.36	0/1080	0.95	0/1505
1	RC	0.37	0/1085	0.98	3/1512 (0.2%)
1	S	0.36	0/1085	0.89	2/1512 (0.1%)
1	SA	0.35	0/1085	0.93	1/1512 (0.1%)
1	SB	0.35	0/784	0.92	0/1093
1	SC	0.36	0/1085	0.89	2/1512 (0.1%)
1	T	0.36	0/1080	0.95	0/1505
1	TA	0.35	0/1085	0.91	1/1512 (0.1%)
1	TB	0.34	0/660	0.89	0/920
1	TC	0.36	0/1080	0.95	0/1505
1	UA	0.37	0/1085	0.98	3/1512 (0.2%)
1	UB	0.35	0/1085	0.93	1/1512 (0.1%)
1	UC	0.35	0/784	0.92	0/1093
1	V	0.35	0/784	0.93	0/1093
1	VA	0.36	0/1085	0.89	2/1512 (0.1%)
1	VB	0.35	0/1085	0.91	2/1512 (0.1%)
1	VC	0.34	0/660	0.89	0/920
1	W	0.34	0/660	0.89	0/920
1	WA	0.36	0/1080	0.95	0/1505
1	WB	0.37	0/1085	0.98	3/1512 (0.2%)
1	WC	0.35	0/1085	0.93	1/1512 (0.1%)
1	X	0.36	0/1085	0.93	1/1512 (0.1%)
1	XA	0.34	0/784	0.92	0/1093
1	XB	0.36	0/1085	0.89	2/1512 (0.1%)
1	XC	0.36	0/1085	0.91	2/1512 (0.1%)
1	Y	0.36	0/1085	0.91	1/1512 (0.1%)
1	YA	0.34	0/660	0.89	0/920
1	YB	0.36	0/1080	0.95	0/1505
1	YC	0.37	0/1085	0.98	3/1512 (0.2%)
1	Z	0.37	0/1085	0.98	3/1512 (0.2%)
1	ZA	0.35	0/1085	0.93	1/1512 (0.1%)
1	ZB	0.35	0/784	0.92	0/1093
1	ZC	0.36	0/1085	0.89	2/1512 (0.1%)
All	All	0.36	0/109824	0.93	117/153056 (0.1%)

There are no bond length outliers.

All (117) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	UA	158	GLY	N-CA-C	6.22	120.19	112.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	YC	158	GLY	N-CA-C	6.22	120.19	112.73
1	PB	158	GLY	N-CA-C	6.20	120.17	112.73
1	D	158	GLY	N-CA-C	6.20	120.17	112.73
1	GA	158	GLY	N-CA-C	6.20	120.17	112.73
1	NA	158	GLY	N-CA-C	6.20	120.17	112.73
1	IB	158	GLY	N-CA-C	6.20	120.17	112.73
1	KC	158	GLY	N-CA-C	6.20	120.17	112.73
1	RC	158	GLY	N-CA-C	6.20	120.17	112.73
1	R	158	GLY	N-CA-C	6.19	120.16	112.73
1	Z	158	GLY	N-CA-C	6.18	120.15	112.73
1	BB	158	GLY	N-CA-C	6.18	120.15	112.73
1	WB	158	GLY	N-CA-C	6.18	120.15	112.73
1	DC	158	GLY	N-CA-C	6.18	120.15	112.73
1	FD	158	GLY	N-CA-C	6.18	120.15	112.73
1	K	158	GLY	N-CA-C	6.17	120.13	112.73
1	K	156	VAL	N-CA-C	5.82	116.00	110.53
1	NA	156	VAL	N-CA-C	5.82	116.00	110.53
1	R	156	VAL	N-CA-C	5.81	116.00	110.53
1	BB	156	VAL	N-CA-C	5.81	115.99	110.53
1	DC	156	VAL	N-CA-C	5.81	115.99	110.53
1	PB	156	VAL	N-CA-C	5.80	115.99	110.53
1	RC	156	VAL	N-CA-C	5.80	115.99	110.53
1	D	156	VAL	N-CA-C	5.80	115.98	110.53
1	GA	156	VAL	N-CA-C	5.80	115.98	110.53
1	IB	156	VAL	N-CA-C	5.80	115.98	110.53
1	WB	156	VAL	N-CA-C	5.80	115.98	110.53
1	KC	156	VAL	N-CA-C	5.80	115.98	110.53
1	Z	156	VAL	N-CA-C	5.79	115.98	110.53
1	FD	156	VAL	N-CA-C	5.79	115.98	110.53
1	UA	156	VAL	N-CA-C	5.78	115.96	110.53
1	YC	156	VAL	N-CA-C	5.78	115.96	110.53
1	WC	196	GLN	N-CA-C	5.76	117.24	111.07
1	SA	196	GLN	N-CA-C	5.74	117.21	111.07
1	UB	196	GLN	N-CA-C	5.74	117.21	111.07
1	X	196	GLN	N-CA-C	5.73	117.20	111.07
1	DD	196	GLN	N-CA-C	5.73	117.20	111.07
1	B	196	GLN	N-CA-C	5.72	117.19	111.07
1	EA	196	GLN	N-CA-C	5.72	117.19	111.07
1	GB	196	GLN	N-CA-C	5.72	117.19	111.07
1	IC	196	GLN	N-CA-C	5.72	117.19	111.07
1	PC	196	GLN	N-CA-C	5.72	117.19	111.07
1	ZA	196	GLN	N-CA-C	5.71	117.18	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BC	196	GLN	N-CA-C	5.71	117.18	111.07
1	NB	196	GLN	N-CA-C	5.71	117.18	111.07
1	I	196	GLN	N-CA-C	5.71	117.18	111.07
1	LA	196	GLN	N-CA-C	5.71	117.18	111.07
1	P	196	GLN	N-CA-C	5.70	117.16	111.07
1	CB	26	GLU	N-CA-C	5.66	117.12	111.07
1	QB	26	GLU	N-CA-C	5.65	117.12	111.07
1	AA	26	GLU	N-CA-C	5.65	117.11	111.07
1	XB	26	GLU	N-CA-C	5.65	117.11	111.07
1	GD	26	GLU	N-CA-C	5.65	117.11	111.07
1	E	26	GLU	N-CA-C	5.63	117.10	111.07
1	HA	26	GLU	N-CA-C	5.63	117.10	111.07
1	JB	26	GLU	N-CA-C	5.63	117.10	111.07
1	LC	26	GLU	N-CA-C	5.63	117.10	111.07
1	EC	26	GLU	N-CA-C	5.63	117.09	111.07
1	L	26	GLU	N-CA-C	5.62	117.08	111.07
1	OA	26	GLU	N-CA-C	5.62	117.08	111.07
1	SC	26	GLU	N-CA-C	5.62	117.08	111.07
1	S	26	GLU	N-CA-C	5.62	117.08	111.07
1	VA	26	GLU	N-CA-C	5.62	117.08	111.07
1	ZC	26	GLU	N-CA-C	5.62	117.08	111.07
1	NA	19	VAL	N-CA-C	5.60	116.33	110.62
1	Z	19	VAL	N-CA-C	5.57	116.30	110.62
1	FD	19	VAL	N-CA-C	5.57	116.30	110.62
1	K	19	VAL	N-CA-C	5.56	116.30	110.62
1	PB	19	VAL	N-CA-C	5.56	116.29	110.62
1	RC	19	VAL	N-CA-C	5.56	116.29	110.62
1	WB	19	VAL	N-CA-C	5.56	116.29	110.62
1	YC	19	VAL	N-CA-C	5.56	116.29	110.62
1	D	19	VAL	N-CA-C	5.55	116.28	110.62
1	GA	19	VAL	N-CA-C	5.55	116.28	110.62
1	IB	19	VAL	N-CA-C	5.55	116.28	110.62
1	KC	19	VAL	N-CA-C	5.55	116.28	110.62
1	BB	19	VAL	N-CA-C	5.53	116.26	110.62
1	DC	19	VAL	N-CA-C	5.53	116.26	110.62
1	R	19	VAL	N-CA-C	5.53	116.26	110.62
1	UA	19	VAL	N-CA-C	5.53	116.26	110.62
1	S	217	MET	N-CA-C	5.37	117.13	111.28
1	AA	217	MET	N-CA-C	5.33	117.09	111.28
1	GD	217	MET	N-CA-C	5.33	117.09	111.28
1	L	217	MET	N-CA-C	5.33	117.08	111.28
1	OA	217	MET	N-CA-C	5.33	117.08	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	QB	217	MET	N-CA-C	5.33	117.08	111.28
1	E	217	MET	N-CA-C	5.32	117.08	111.28
1	HA	217	MET	N-CA-C	5.32	117.08	111.28
1	JB	217	MET	N-CA-C	5.32	117.08	111.28
1	LC	217	MET	N-CA-C	5.32	117.08	111.28
1	VA	217	MET	N-CA-C	5.31	117.06	111.28
1	XB	217	MET	N-CA-C	5.31	117.06	111.28
1	SC	217	MET	N-CA-C	5.31	117.06	111.28
1	ZC	217	MET	N-CA-C	5.31	117.06	111.28
1	CB	217	MET	N-CA-C	5.30	117.06	111.28
1	EC	217	MET	N-CA-C	5.30	117.06	111.28
1	J	18	LEU	N-CA-C	5.15	116.89	111.28
1	TA	18	LEU	N-CA-C	5.11	116.85	111.28
1	XC	18	LEU	N-CA-C	5.11	116.85	111.28
1	Q	18	LEU	N-CA-C	5.11	116.85	111.28
1	MA	18	LEU	N-CA-C	5.10	116.84	111.28
1	QC	18	LEU	N-CA-C	5.10	116.84	111.28
1	OB	18	LEU	N-CA-C	5.09	116.83	111.28
1	C	18	LEU	N-CA-C	5.09	116.83	111.28
1	FA	18	LEU	N-CA-C	5.09	116.83	111.28
1	HB	18	LEU	N-CA-C	5.09	116.83	111.28
1	JC	18	LEU	N-CA-C	5.09	116.83	111.28
1	Y	18	LEU	N-CA-C	5.07	116.81	111.28
1	AB	18	LEU	N-CA-C	5.07	116.81	111.28
1	CC	18	LEU	N-CA-C	5.07	116.81	111.28
1	ED	18	LEU	N-CA-C	5.07	116.81	111.28
1	VB	18	LEU	N-CA-C	5.05	116.79	111.28
1	J	206	VAL	N-CA-C	5.01	115.73	110.62
1	VB	206	VAL	N-CA-C	5.01	115.73	110.62
1	XC	206	VAL	N-CA-C	5.01	115.73	110.62
1	OB	206	VAL	N-CA-C	5.00	115.72	110.62
1	QC	206	VAL	N-CA-C	5.00	115.72	110.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	661	0	320	6	0
1	AA	1086	0	531	6	0
1	AB	1086	0	531	10	0
1	AC	661	0	320	6	0
1	AD	1081	0	530	4	0
1	B	1086	0	531	6	0
1	BA	1081	0	530	5	0
1	BB	1086	0	531	5	0
1	BC	1086	0	531	6	0
1	BD	785	0	376	0	0
1	C	1086	0	531	10	0
1	CA	785	0	376	0	0
1	CB	1086	0	531	6	0
1	CC	1086	0	531	10	0
1	CD	661	0	320	6	0
1	D	1086	0	531	5	0
1	DA	661	0	320	6	0
1	DB	1081	0	530	4	0
1	DC	1086	0	531	5	0
1	DD	1086	0	531	6	0
1	E	1086	0	531	6	0
1	EA	1086	0	531	6	0
1	EB	785	0	376	0	0
1	EC	1086	0	531	6	0
1	ED	1086	0	531	10	0
1	F	1081	0	530	4	0
1	FA	1086	0	531	10	0
1	FB	661	0	320	6	0
1	FC	1081	0	530	4	0
1	FD	1086	0	531	5	0
1	G	785	0	376	0	0
1	GA	1086	0	531	5	0
1	GB	1086	0	531	6	0
1	GC	785	0	376	0	0
1	GD	1086	0	531	6	0
1	H	661	0	320	6	0
1	HA	1086	0	531	6	0
1	HB	1086	0	531	10	0
1	HC	661	0	320	6	0
1	HD	1081	0	530	4	0
1	I	1086	0	531	6	0
1	IA	1081	0	530	4	0
1	IB	1086	0	531	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	IC	1086	0	531	6	0
1	ID	785	0	376	0	0
1	J	1086	0	531	10	0
1	JA	785	0	376	0	0
1	JB	1086	0	531	6	0
1	JC	1086	0	531	10	0
1	K	1086	0	531	5	0
1	KA	661	0	320	6	0
1	KB	1081	0	530	5	0
1	KC	1086	0	531	5	0
1	L	1086	0	531	6	0
1	LA	1086	0	531	6	0
1	LB	785	0	376	0	0
1	LC	1086	0	531	6	0
1	M	1081	0	530	4	0
1	MA	1086	0	531	10	0
1	MB	661	0	320	6	0
1	MC	1081	0	530	4	0
1	N	785	0	376	0	0
1	NA	1086	0	531	5	0
1	NB	1086	0	531	6	0
1	NC	785	0	376	0	0
1	O	661	0	320	6	0
1	OA	1086	0	531	7	0
1	OB	1086	0	531	10	0
1	OC	661	0	320	6	0
1	P	1086	0	531	6	0
1	PA	1081	0	530	4	0
1	PB	1086	0	531	5	0
1	PC	1086	0	531	6	0
1	Q	1086	0	531	10	0
1	QA	785	0	376	0	0
1	QB	1086	0	531	6	0
1	QC	1086	0	531	10	0
1	R	1086	0	531	5	0
1	RA	661	0	320	6	0
1	RB	1081	0	530	4	0
1	RC	1086	0	531	5	0
1	S	1086	0	531	6	0
1	SA	1086	0	531	6	0
1	SB	785	0	376	0	0
1	SC	1086	0	531	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	T	1081	0	530	4	0
1	TA	1086	0	531	10	0
1	TB	661	0	320	6	0
1	TC	1081	0	530	4	0
1	UA	1086	0	531	5	0
1	UB	1086	0	531	6	0
1	UC	785	0	376	0	0
1	V	785	0	376	0	0
1	VA	1086	0	531	6	0
1	VB	1086	0	531	10	0
1	VC	661	0	320	6	0
1	W	661	0	320	6	0
1	WA	1081	0	530	4	0
1	WB	1086	0	531	5	0
1	WC	1086	0	531	6	0
1	X	1086	0	531	6	0
1	XA	785	0	376	0	0
1	XB	1086	0	531	7	0
1	XC	1086	0	531	10	0
1	Y	1086	0	531	10	0
1	YA	661	0	320	6	0
1	YB	1081	0	530	4	0
1	YC	1086	0	531	5	0
1	Z	1086	0	531	5	0
1	ZA	1086	0	531	6	0
1	ZB	785	0	376	0	0
1	ZC	1086	0	531	6	0
All	All	109936	0	53600	306	0

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

All (306) 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:MA:184:ALA:CB	1:ZA:48:ALA:HB1	1.85	1.06
1:TA:184:ALA:CB	1:GB:48:ALA:HB1	1.85	1.06
1:JC:184:ALA:CB	1:WC:48:ALA:HB1	1.85	1.06
1:I:48:ALA:HB1	1:ED:184:ALA:CB	1.85	1.05
1:Q:184:ALA:CB	1:EA:48:ALA:HB1	1.85	1.05
1:CC:184:ALA:CB	1:PC:48:ALA:HB1	1.85	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:QC:184:ALA:CB	1:DD:48:ALA:HB1	1.85	1.05
1:B:48:ALA:HB1	1:XC:184:ALA:CB	1.85	1.05
1:AB:184:ALA:CB	1:NB:48:ALA:HB1	1.85	1.05
1:C:184:ALA:CB	1:P:48:ALA:HB1	1.85	1.05
1:J:184:ALA:CB	1:X:48:ALA:HB1	1.85	1.05
1:VB:184:ALA:CB	1:IC:48:ALA:HB1	1.85	1.05
1:Y:184:ALA:CB	1:LA:48:ALA:HB1	1.85	1.05
1:OB:184:ALA:CB	1:BC:48:ALA:HB1	1.85	1.05
1:FA:184:ALA:CB	1:SA:48:ALA:HB1	1.85	1.04
1:HB:184:ALA:CB	1:UB:48:ALA:HB1	1.85	1.04
1:Y:184:ALA:HB1	1:LA:48:ALA:HB1	1.00	1.00
1:FA:184:ALA:HB1	1:SA:48:ALA:HB1	1.00	1.00
1:FA:184:ALA:HB1	1:SA:48:ALA:CB	1.92	0.99
1:JC:184:ALA:HB1	1:WC:48:ALA:CB	1.92	0.99
1:MA:184:ALA:HB1	1:ZA:48:ALA:CB	1.92	0.99
1:CC:184:ALA:HB1	1:PC:48:ALA:CB	1.92	0.99
1:Y:184:ALA:HB1	1:LA:48:ALA:CB	1.92	0.99
1:QC:184:ALA:HB1	1:DD:48:ALA:CB	1.92	0.99
1:B:48:ALA:CB	1:XC:184:ALA:HB1	1.92	0.99
1:I:48:ALA:CB	1:ED:184:ALA:HB1	1.92	0.99
1:Q:184:ALA:HB1	1:EA:48:ALA:HB1	1.00	0.99
1:VB:184:ALA:HB1	1:IC:48:ALA:CB	1.92	0.99
1:OB:184:ALA:HB1	1:BC:48:ALA:CB	1.92	0.99
1:MA:184:ALA:HB1	1:ZA:48:ALA:HB1	1.00	0.98
1:VB:184:ALA:HB1	1:IC:48:ALA:HB1	1.00	0.98
1:I:48:ALA:HB1	1:ED:184:ALA:HB1	1.00	0.98
1:C:184:ALA:HB1	1:P:48:ALA:CB	1.92	0.98
1:C:184:ALA:HB1	1:P:48:ALA:HB1	1.00	0.98
1:OB:184:ALA:HB1	1:BC:48:ALA:HB1	1.00	0.98
1:QC:184:ALA:HB1	1:DD:48:ALA:HB1	1.01	0.98
1:J:184:ALA:HB1	1:X:48:ALA:CB	1.92	0.98
1:HB:184:ALA:HB1	1:UB:48:ALA:CB	1.92	0.98
1:Q:184:ALA:HB1	1:EA:48:ALA:CB	1.92	0.98
1:CC:184:ALA:HB1	1:PC:48:ALA:HB1	1.00	0.98
1:JC:184:ALA:HB1	1:WC:48:ALA:HB1	1.00	0.98
1:AB:184:ALA:HB1	1:NB:48:ALA:HB1	1.00	0.98
1:HB:184:ALA:HB1	1:UB:48:ALA:HB1	1.00	0.97
1:TA:184:ALA:HB1	1:GB:48:ALA:CB	1.92	0.97
1:B:48:ALA:HB1	1:XC:184:ALA:HB1	1.00	0.97
1:AB:184:ALA:HB1	1:NB:48:ALA:CB	1.92	0.97
1:J:184:ALA:HB1	1:X:48:ALA:HB1	1.00	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:TA:184:ALA:HB1	1:GB:48:ALA:HB1	1.00	0.96
1:WA:179:GLU:CB	1:JB:52:ALA:HB1	2.01	0.91
1:DB:179:GLU:CB	1:QB:52:ALA:HB1	2.01	0.91
1:PA:179:GLU:CB	1:CB:52:ALA:HB1	2.01	0.91
1:KB:179:GLU:CB	1:XB:52:ALA:HB1	2.01	0.91
1:BA:179:GLU:CB	1:OA:52:ALA:HB1	2.00	0.91
1:IA:179:GLU:CB	1:VA:52:ALA:HB1	2.01	0.91
1:RB:179:GLU:CB	1:EC:52:ALA:HB1	2.01	0.91
1:YB:179:GLU:CB	1:LC:52:ALA:HB1	2.01	0.91
1:T:179:GLU:CB	1:HA:52:ALA:HB1	2.01	0.91
1:FC:179:GLU:CB	1:SC:52:ALA:HB1	2.01	0.91
1:MC:179:GLU:CB	1:ZC:52:ALA:HB1	2.01	0.91
1:F:179:GLU:CB	1:S:52:ALA:HB1	2.01	0.91
1:M:179:GLU:CB	1:AA:52:ALA:HB1	2.01	0.91
1:E:52:ALA:HB1	1:AD:179:GLU:CB	2.01	0.91
1:L:52:ALA:HB1	1:HD:179:GLU:CB	2.01	0.91
1:TC:179:GLU:CB	1:GD:52:ALA:HB1	2.01	0.91
1:WB:180:SER:CB	1:JC:52:ALA:HB1	2.05	0.87
1:IB:180:SER:CB	1:VB:52:ALA:HB1	2.05	0.86
1:NA:180:SER:CB	1:AB:52:ALA:HB1	2.05	0.86
1:UA:180:SER:CB	1:HB:52:ALA:HB1	2.05	0.86
1:RC:180:SER:CB	1:ED:52:ALA:HB1	2.05	0.86
1:KC:180:SER:CB	1:XC:52:ALA:HB1	2.05	0.86
1:BB:180:SER:CB	1:OB:52:ALA:HB1	2.05	0.86
1:PB:180:SER:CB	1:CC:52:ALA:HB1	2.05	0.86
1:Z:180:SER:CB	1:MA:52:ALA:HB1	2.05	0.86
1:D:180:SER:CB	1:Q:52:ALA:HB1	2.05	0.86
1:DC:180:SER:CB	1:QC:52:ALA:HB1	2.06	0.85
1:R:180:SER:CB	1:FA:52:ALA:HB1	2.05	0.85
1:LC:180:SER:CB	1:YC:52:ALA:CB	2.55	0.85
1:C:52:ALA:HB1	1:YC:180:SER:CB	2.05	0.85
1:J:52:ALA:HB1	1:FD:180:SER:CB	2.05	0.85
1:XB:180:SER:CB	1:KC:52:ALA:CB	2.54	0.85
1:EC:180:SER:CB	1:RC:52:ALA:CB	2.55	0.85
1:GA:180:SER:CB	1:TA:52:ALA:HB1	2.05	0.85
1:SC:180:SER:CB	1:FD:52:ALA:CB	2.54	0.85
1:AA:180:SER:CB	1:NA:52:ALA:CB	2.54	0.85
1:L:180:SER:CB	1:Z:52:ALA:CB	2.55	0.85
1:S:180:SER:CB	1:GA:52:ALA:CB	2.55	0.85
1:HA:180:SER:CB	1:UA:52:ALA:CB	2.55	0.85
1:CB:180:SER:CB	1:PB:52:ALA:CB	2.54	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:VA:180:SER:CB	1:IB:52:ALA:CB	2.54	0.84
1:JB:180:SER:CB	1:WB:52:ALA:CB	2.55	0.84
1:E:180:SER:CB	1:R:52:ALA:CB	2.54	0.84
1:OA:180:SER:CB	1:BB:52:ALA:CB	2.55	0.84
1:K:180:SER:CB	1:Y:52:ALA:HB1	2.05	0.84
1:QB:180:SER:CB	1:DC:52:ALA:CB	2.55	0.84
1:D:52:ALA:CB	1:ZC:180:SER:CB	2.55	0.83
1:K:52:ALA:CB	1:GD:180:SER:CB	2.55	0.83
1:AA:180:SER:CB	1:NA:52:ALA:HB1	2.10	0.81
1:VA:180:SER:CB	1:IB:52:ALA:HB1	2.10	0.81
1:OA:180:SER:CB	1:BB:52:ALA:HB1	2.11	0.81
1:HA:180:SER:CB	1:UA:52:ALA:HB1	2.10	0.81
1:CB:180:SER:CB	1:PB:52:ALA:HB1	2.10	0.81
1:KC:184:ALA:HB1	1:XC:48:ALA:HB1	1.63	0.81
1:S:180:SER:CB	1:GA:52:ALA:HB1	2.11	0.81
1:JB:180:SER:CB	1:WB:52:ALA:HB1	2.11	0.81
1:J:48:ALA:HB1	1:FD:184:ALA:HB1	1.63	0.81
1:RC:184:ALA:HB1	1:ED:48:ALA:HB1	1.64	0.80
1:E:180:SER:CB	1:R:52:ALA:HB1	2.11	0.80
1:L:180:SER:CB	1:Z:52:ALA:HB1	2.10	0.80
1:DC:184:ALA:HB1	1:QC:48:ALA:HB1	1.64	0.80
1:C:48:ALA:HB1	1:YC:184:ALA:HB1	1.64	0.80
1:XB:180:SER:CB	1:KC:52:ALA:HB1	2.10	0.80
1:D:52:ALA:HB1	1:ZC:180:SER:CB	2.10	0.80
1:PB:184:ALA:HB1	1:CC:48:ALA:HB1	1.63	0.80
1:QB:180:SER:CB	1:DC:52:ALA:HB1	2.11	0.80
1:D:184:ALA:HB1	1:Q:48:ALA:HB1	1.63	0.80
1:SC:180:SER:CB	1:FD:52:ALA:HB1	2.10	0.80
1:T:183:GLN:CB	1:HA:48:ALA:HB1	2.12	0.80
1:WB:184:ALA:HB1	1:JC:48:ALA:HB1	1.64	0.80
1:EC:180:SER:CB	1:RC:52:ALA:HB1	2.11	0.80
1:K:52:ALA:HB1	1:GD:180:SER:CB	2.11	0.80
1:K:184:ALA:HB1	1:Y:48:ALA:HB1	1.64	0.80
1:M:183:GLN:CB	1:AA:48:ALA:HB1	2.12	0.80
1:BA:183:GLN:CB	1:OA:48:ALA:HB1	2.12	0.80
1:F:183:GLN:CB	1:S:48:ALA:HB1	2.12	0.79
1:LC:180:SER:CB	1:YC:52:ALA:HB1	2.11	0.79
1:TC:183:GLN:CB	1:GD:48:ALA:HB1	2.12	0.79
1:L:48:ALA:HB1	1:HD:183:GLN:CB	2.12	0.79
1:IA:183:GLN:CB	1:VA:48:ALA:HB1	2.12	0.79
1:IB:184:ALA:HB1	1:VB:48:ALA:HB1	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:KB:183:GLN:CB	1:XB:48:ALA:HB1	2.12	0.79
1:RB:183:GLN:CB	1:EC:48:ALA:HB1	2.12	0.79
1:PA:183:GLN:CB	1:CB:48:ALA:HB1	2.12	0.79
1:MC:183:GLN:CB	1:ZC:48:ALA:HB1	2.12	0.79
1:R:184:ALA:HB1	1:FA:48:ALA:HB1	1.63	0.79
1:WA:183:GLN:CB	1:JB:48:ALA:HB1	2.12	0.79
1:YB:183:GLN:CB	1:LC:48:ALA:HB1	2.12	0.79
1:NA:184:ALA:HB1	1:AB:48:ALA:HB1	1.63	0.79
1:FC:183:GLN:CB	1:SC:48:ALA:HB1	2.12	0.79
1:E:48:ALA:HB1	1:AD:183:GLN:CB	2.12	0.78
1:DB:183:GLN:CB	1:QB:48:ALA:HB1	2.12	0.78
1:Z:184:ALA:HB1	1:MA:48:ALA:HB1	1.64	0.78
1:UA:184:ALA:HB1	1:HB:48:ALA:HB1	1.63	0.78
1:GA:184:ALA:HB1	1:TA:48:ALA:HB1	1.64	0.78
1:BB:184:ALA:HB1	1:OB:48:ALA:HB1	1.64	0.78
1:SC:180:SER:CB	1:FD:52:ALA:HB2	2.17	0.74
1:QB:180:SER:CB	1:DC:52:ALA:HB2	2.17	0.74
1:LC:180:SER:CB	1:YC:52:ALA:HB2	2.18	0.74
1:CB:180:SER:CB	1:PB:52:ALA:HB2	2.18	0.74
1:D:52:ALA:HB2	1:ZC:180:SER:CB	2.18	0.74
1:EC:180:SER:CB	1:RC:52:ALA:HB2	2.18	0.74
1:AA:180:SER:CB	1:NA:52:ALA:HB2	2.17	0.73
1:E:180:SER:CB	1:R:52:ALA:HB2	2.17	0.73
1:K:52:ALA:HB2	1:GD:180:SER:CB	2.18	0.73
1:JB:180:SER:CB	1:WB:52:ALA:HB2	2.18	0.73
1:HA:180:SER:CB	1:UA:52:ALA:HB2	2.18	0.73
1:VA:180:SER:CB	1:IB:52:ALA:HB2	2.17	0.73
1:XB:180:SER:CB	1:KC:52:ALA:HB2	2.17	0.73
1:L:180:SER:CB	1:Z:52:ALA:HB2	2.18	0.73
1:S:180:SER:CB	1:GA:52:ALA:HB2	2.18	0.73
1:OA:180:SER:CB	1:BB:52:ALA:HB2	2.18	0.73
1:WA:179:GLU:CB	1:JB:52:ALA:CB	2.69	0.70
1:MC:179:GLU:CB	1:ZC:52:ALA:CB	2.69	0.70
1:DB:179:GLU:CB	1:QB:52:ALA:CB	2.70	0.70
1:BA:179:GLU:CB	1:OA:52:ALA:CB	2.69	0.70
1:TC:179:GLU:CB	1:GD:52:ALA:CB	2.69	0.70
1:KB:179:GLU:CB	1:XB:52:ALA:CB	2.70	0.70
1:RB:179:GLU:CB	1:EC:52:ALA:CB	2.69	0.70
1:PA:179:GLU:CB	1:CB:52:ALA:CB	2.70	0.70
1:F:179:GLU:CB	1:S:52:ALA:CB	2.69	0.70
1:T:179:GLU:CB	1:HA:52:ALA:CB	2.70	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:FC:179:GLU:CB	1:SC:52:ALA:CB	2.70	0.70
1:L:52:ALA:CB	1:HD:179:GLU:CB	2.70	0.69
1:IA:179:GLU:CB	1:VA:52:ALA:CB	2.70	0.69
1:YB:179:GLU:CB	1:LC:52:ALA:CB	2.69	0.69
1:M:179:GLU:CB	1:AA:52:ALA:CB	2.70	0.68
1:E:52:ALA:CB	1:AD:179:GLU:CB	2.70	0.68
1:X:167:ALA:HB2	1:EA:32:ALA:HB2	1.76	0.68
1:GB:167:ALA:HB2	1:NB:32:ALA:HB2	1.76	0.68
1:UB:167:ALA:HB2	1:BC:32:ALA:HB2	1.76	0.68
1:SA:167:ALA:HB2	1:ZA:32:ALA:HB2	1.76	0.68
1:I:167:ALA:HB2	1:P:32:ALA:HB2	1.76	0.67
1:EA:167:ALA:HB2	1:LA:32:ALA:HB2	1.76	0.67
1:WC:167:ALA:HB2	1:DD:32:ALA:HB2	1.76	0.67
1:B:167:ALA:HB2	1:I:32:ALA:HB2	1.76	0.67
1:BC:167:ALA:HB2	1:IC:32:ALA:HB2	1.76	0.67
1:LA:167:ALA:HB2	1:SA:32:ALA:HB2	1.76	0.67
1:PC:167:ALA:HB2	1:WC:32:ALA:HB2	1.76	0.67
1:ZA:167:ALA:HB2	1:GB:32:ALA:HB2	1.76	0.66
1:IC:167:ALA:HB2	1:PC:32:ALA:HB2	1.76	0.66
1:NB:167:ALA:HB2	1:UB:32:ALA:HB2	1.76	0.66
1:P:167:ALA:HB2	1:X:32:ALA:HB2	1.76	0.65
1:B:32:ALA:HB2	1:DD:167:ALA:HB2	1.76	0.65
1:Y:180:SER:CB	1:LA:52:ALA:HB1	2.31	0.61
1:C:180:SER:CB	1:P:52:ALA:HB1	2.31	0.61
1:I:52:ALA:HB1	1:ED:180:SER:CB	2.31	0.61
1:FA:180:SER:CB	1:SA:52:ALA:HB1	2.31	0.61
1:QC:180:SER:CB	1:DD:52:ALA:HB1	2.31	0.61
1:TA:180:SER:CB	1:GB:52:ALA:HB1	2.31	0.61
1:B:52:ALA:HB1	1:XC:180:SER:CB	2.31	0.61
1:J:180:SER:CB	1:X:52:ALA:HB1	2.31	0.61
1:Q:180:SER:CB	1:EA:52:ALA:HB1	2.31	0.61
1:AB:180:SER:CB	1:NB:52:ALA:HB1	2.31	0.61
1:MA:180:SER:CB	1:ZA:52:ALA:HB1	2.31	0.60
1:JC:180:SER:CB	1:WC:52:ALA:HB1	2.31	0.60
1:OB:180:SER:CB	1:BC:52:ALA:HB1	2.31	0.60
1:VB:180:SER:CB	1:IC:52:ALA:HB1	2.31	0.60
1:CC:180:SER:CB	1:PC:52:ALA:HB1	2.31	0.60
1:HB:180:SER:CB	1:UB:52:ALA:HB1	2.31	0.60
1:RA:158:GLY:HA3	1:YA:32:ALA:HB1	1.88	0.56
1:FB:158:GLY:HA3	1:MB:32:ALA:HB1	1.88	0.56
1:TB:158:GLY:HA3	1:AC:32:ALA:HB1	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:ALA:HB1	1:CD:158:GLY:HA3	1.88	0.55
1:H:158:GLY:HA3	1:O:32:ALA:HB1	1.88	0.55
1:W:158:GLY:HA3	1:DA:32:ALA:HB1	1.89	0.55
1:DA:158:GLY:HA3	1:KA:32:ALA:HB1	1.88	0.55
1:OC:158:GLY:HA3	1:VC:32:ALA:HB1	1.89	0.55
1:VC:158:GLY:HA3	1:CD:32:ALA:HB1	1.89	0.55
1:O:158:GLY:HA3	1:W:32:ALA:HB1	1.89	0.55
1:HC:158:GLY:HA3	1:OC:32:ALA:HB1	1.89	0.55
1:KA:158:GLY:HA3	1:RA:32:ALA:HB1	1.89	0.55
1:YA:158:GLY:HA3	1:FB:32:ALA:HB1	1.89	0.55
1:A:158:GLY:HA3	1:H:32:ALA:HB1	1.89	0.54
1:AC:158:GLY:HA3	1:HC:32:ALA:HB1	1.89	0.54
1:MB:158:GLY:HA3	1:TB:32:ALA:HB1	1.90	0.54
1:DA:158:GLY:HA3	1:KA:32:ALA:CB	2.40	0.52
1:OC:158:GLY:HA3	1:VC:32:ALA:CB	2.39	0.52
1:RA:158:GLY:HA3	1:YA:32:ALA:CB	2.39	0.52
1:Q:167:ALA:HB1	1:Y:32:ALA:HB2	1.91	0.52
1:TB:158:GLY:HA3	1:AC:32:ALA:CB	2.40	0.52
1:A:32:ALA:CB	1:CD:158:GLY:HA3	2.40	0.52
1:FB:158:GLY:HA3	1:MB:32:ALA:CB	2.40	0.52
1:MA:167:ALA:HB1	1:TA:32:ALA:HB2	1.91	0.52
1:O:158:GLY:HA3	1:W:32:ALA:CB	2.40	0.52
1:Y:167:ALA:HB1	1:FA:32:ALA:HB2	1.92	0.52
1:TA:167:ALA:HB1	1:AB:32:ALA:HB2	1.92	0.52
1:CC:167:ALA:HB1	1:JC:32:ALA:HB2	1.91	0.52
1:HC:158:GLY:HA3	1:OC:32:ALA:CB	2.40	0.52
1:JC:167:ALA:HB1	1:QC:32:ALA:HB2	1.91	0.52
1:QC:167:ALA:HB1	1:XC:32:ALA:HB2	1.91	0.52
1:A:158:GLY:HA3	1:H:32:ALA:CB	2.40	0.51
1:AC:158:GLY:HA3	1:HC:32:ALA:CB	2.40	0.51
1:VC:158:GLY:HA3	1:CD:32:ALA:CB	2.41	0.51
1:J:167:ALA:HB1	1:Q:32:ALA:HB2	1.92	0.51
1:H:158:GLY:HA3	1:O:32:ALA:CB	2.40	0.51
1:FA:167:ALA:HB1	1:MA:32:ALA:HB2	1.91	0.51
1:OB:167:ALA:HB1	1:VB:32:ALA:HB2	1.91	0.51
1:MB:158:GLY:HA3	1:TB:32:ALA:CB	2.40	0.51
1:AB:167:ALA:HB1	1:HB:32:ALA:HB2	1.91	0.51
1:C:32:ALA:HB2	1:ED:167:ALA:HB1	1.92	0.51
1:YA:158:GLY:HA3	1:FB:32:ALA:CB	2.41	0.51
1:HB:167:ALA:HB1	1:OB:32:ALA:HB2	1.92	0.51
1:XC:167:ALA:HB1	1:ED:32:ALA:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:167:ALA:HB1	1:J:32:ALA:HB2	1.91	0.51
1:KA:158:GLY:HA3	1:RA:32:ALA:CB	2.41	0.51
1:VB:167:ALA:HB1	1:CC:32:ALA:HB2	1.92	0.51
1:W:158:GLY:HA3	1:DA:32:ALA:CB	2.40	0.51
1:MA:182:ALA:HB2	1:TA:146:ALA:HB1	1.96	0.48
1:C:182:ALA:HB2	1:J:146:ALA:HB1	1.96	0.48
1:Q:182:ALA:HB2	1:Y:146:ALA:HB1	1.96	0.48
1:YB:160:ASN:O	1:YB:161:THR:C	2.57	0.47
1:KB:160:ASN:O	1:KB:161:THR:C	2.57	0.47
1:MC:160:ASN:O	1:MC:161:THR:C	2.57	0.47
1:HD:160:ASN:O	1:HD:161:THR:C	2.57	0.47
1:Y:182:ALA:HB2	1:FA:146:ALA:HB1	1.97	0.47
1:TC:160:ASN:O	1:TC:161:THR:C	2.57	0.47
1:C:146:ALA:HB1	1:ED:182:ALA:HB2	1.97	0.47
1:FC:160:ASN:O	1:FC:161:THR:C	2.57	0.47
1:JC:182:ALA:HB2	1:QC:146:ALA:HB1	1.96	0.47
1:PA:160:ASN:O	1:PA:161:THR:C	2.57	0.47
1:T:160:ASN:O	1:T:161:THR:C	2.57	0.47
1:AB:182:ALA:HB2	1:HB:146:ALA:HB1	1.96	0.47
1:XC:182:ALA:HB2	1:ED:146:ALA:HB1	1.96	0.46
1:RB:160:ASN:O	1:RB:161:THR:C	2.57	0.46
1:QC:182:ALA:HB2	1:XC:146:ALA:HB1	1.97	0.46
1:WA:160:ASN:O	1:WA:161:THR:C	2.57	0.46
1:F:160:ASN:O	1:F:161:THR:C	2.57	0.46
1:OB:182:ALA:HB2	1:VB:146:ALA:HB1	1.96	0.46
1:J:182:ALA:HB2	1:Q:146:ALA:HB1	1.97	0.46
1:BA:160:ASN:O	1:BA:161:THR:C	2.57	0.46
1:HB:182:ALA:HB2	1:OB:146:ALA:HB1	1.97	0.46
1:CC:182:ALA:HB2	1:JC:146:ALA:HB1	1.96	0.46
1:FA:182:ALA:HB2	1:MA:146:ALA:HB1	1.97	0.46
1:IA:160:ASN:O	1:IA:161:THR:C	2.57	0.46
1:VB:182:ALA:HB2	1:CC:146:ALA:HB1	1.97	0.46
1:TA:182:ALA:HB2	1:AB:146:ALA:HB1	1.97	0.45
1:AD:160:ASN:O	1:AD:161:THR:C	2.57	0.45
1:M:160:ASN:O	1:M:161:THR:C	2.57	0.45
1:DB:160:ASN:O	1:DB:161:THR:C	2.57	0.45
1:RA:158:GLY:CA	1:YA:32:ALA:HB2	2.50	0.42
1:OC:158:GLY:CA	1:VC:32:ALA:HB2	2.50	0.42
1:TB:158:GLY:CA	1:AC:32:ALA:HB2	2.50	0.42
1:H:158:GLY:CA	1:O:32:ALA:HB2	2.50	0.41
1:O:158:GLY:CA	1:W:32:ALA:HB2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:158:GLY:CA	1:HC:32:ALA:HB2	2.50	0.41
1:FB:158:GLY:CA	1:MB:32:ALA:HB2	2.50	0.41
1:MB:158:GLY:CA	1:TB:32:ALA:HB2	2.50	0.41
1:HC:158:GLY:CA	1:OC:32:ALA:HB2	2.51	0.41
1:A:158:GLY:CA	1:H:32:ALA:HB2	2.51	0.41
1:DA:158:GLY:CA	1:KA:32:ALA:HB2	2.50	0.41
1:KB:183:GLN:CB	1:XB:48:ALA:CB	2.94	0.41
1:BA:183:GLN:CB	1:OA:48:ALA:CB	2.94	0.41
1:W:158:GLY:CA	1:DA:32:ALA:HB2	2.51	0.41
1:A:32:ALA:HB2	1:CD:158:GLY:CA	2.50	0.41
1:KA:158:GLY:CA	1:RA:32:ALA:HB2	2.51	0.41
1:YA:158:GLY:CA	1:FB:32:ALA:HB2	2.51	0.41
1:VC:158:GLY:CA	1:CD:32:ALA:HB2	2.51	0.40

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%)	131 (100%)	0	0	100	100
1	AA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	AB	217/258 (84%)	217 (100%)	0	0	100	100
1	AC	131/258 (51%)	131 (100%)	0	0	100	100
1	AD	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	B	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	BA	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	BB	217/258 (84%)	217 (100%)	0	0	100	100
1	BC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	BD	156/258 (60%)	156 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	217/258 (84%)	217 (100%)	0	0	100	100
1	CA	156/258 (60%)	156 (100%)	0	0	100	100
1	CB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	CC	217/258 (84%)	217 (100%)	0	0	100	100
1	CD	131/258 (51%)	131 (100%)	0	0	100	100
1	D	217/258 (84%)	217 (100%)	0	0	100	100
1	DA	131/258 (51%)	131 (100%)	0	0	100	100
1	DB	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	DC	217/258 (84%)	217 (100%)	0	0	100	100
1	DD	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	E	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	EA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	EB	156/258 (60%)	156 (100%)	0	0	100	100
1	EC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	ED	217/258 (84%)	217 (100%)	0	0	100	100
1	F	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	FA	217/258 (84%)	217 (100%)	0	0	100	100
1	FB	131/258 (51%)	131 (100%)	0	0	100	100
1	FC	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	FD	217/258 (84%)	217 (100%)	0	0	100	100
1	G	156/258 (60%)	156 (100%)	0	0	100	100
1	GA	217/258 (84%)	217 (100%)	0	0	100	100
1	GB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	GC	156/258 (60%)	156 (100%)	0	0	100	100
1	GD	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	H	131/258 (51%)	131 (100%)	0	0	100	100
1	HA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	HB	217/258 (84%)	217 (100%)	0	0	100	100
1	HC	131/258 (51%)	131 (100%)	0	0	100	100
1	HD	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	I	217/258 (84%)	216 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	IA	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	IB	217/258 (84%)	217 (100%)	0	0	100	100
1	IC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	ID	156/258 (60%)	156 (100%)	0	0	100	100
1	J	217/258 (84%)	217 (100%)	0	0	100	100
1	JA	156/258 (60%)	156 (100%)	0	0	100	100
1	JB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	JC	217/258 (84%)	217 (100%)	0	0	100	100
1	K	217/258 (84%)	217 (100%)	0	0	100	100
1	KA	131/258 (51%)	131 (100%)	0	0	100	100
1	KB	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	KC	217/258 (84%)	217 (100%)	0	0	100	100
1	L	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	LA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	LB	156/258 (60%)	156 (100%)	0	0	100	100
1	LC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	M	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	MA	217/258 (84%)	217 (100%)	0	0	100	100
1	MB	131/258 (51%)	131 (100%)	0	0	100	100
1	MC	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	N	156/258 (60%)	156 (100%)	0	0	100	100
1	NA	217/258 (84%)	217 (100%)	0	0	100	100
1	NB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	NC	156/258 (60%)	156 (100%)	0	0	100	100
1	O	131/258 (51%)	131 (100%)	0	0	100	100
1	OA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	OB	217/258 (84%)	217 (100%)	0	0	100	100
1	OC	131/258 (51%)	131 (100%)	0	0	100	100
1	P	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	PA	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	PB	217/258 (84%)	217 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	PC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	Q	217/258 (84%)	217 (100%)	0	0	100	100
1	QA	156/258 (60%)	156 (100%)	0	0	100	100
1	QB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	QC	217/258 (84%)	217 (100%)	0	0	100	100
1	R	217/258 (84%)	217 (100%)	0	0	100	100
1	RA	131/258 (51%)	131 (100%)	0	0	100	100
1	RB	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	RC	217/258 (84%)	217 (100%)	0	0	100	100
1	S	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	SA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	SB	156/258 (60%)	156 (100%)	0	0	100	100
1	SC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	T	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	TA	217/258 (84%)	217 (100%)	0	0	100	100
1	TB	131/258 (51%)	131 (100%)	0	0	100	100
1	TC	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	UA	217/258 (84%)	217 (100%)	0	0	100	100
1	UB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	UC	156/258 (60%)	156 (100%)	0	0	100	100
1	V	156/258 (60%)	156 (100%)	0	0	100	100
1	VA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	VB	217/258 (84%)	217 (100%)	0	0	100	100
1	VC	131/258 (51%)	131 (100%)	0	0	100	100
1	W	131/258 (51%)	131 (100%)	0	0	100	100
1	WA	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	WB	217/258 (84%)	217 (100%)	0	0	100	100
1	WC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	X	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	XA	156/258 (60%)	156 (100%)	0	0	100	100
1	XB	217/258 (84%)	216 (100%)	1 (0%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	XC	217/258 (84%)	217 (100%)	0	0	100	100
1	Y	217/258 (84%)	217 (100%)	0	0	100	100
1	YA	131/258 (51%)	131 (100%)	0	0	100	100
1	YB	216/258 (84%)	214 (99%)	2 (1%)	0	100	100
1	YC	217/258 (84%)	217 (100%)	0	0	100	100
1	Z	217/258 (84%)	217 (100%)	0	0	100	100
1	ZA	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
1	ZB	156/258 (60%)	156 (100%)	0	0	100	100
1	ZC	217/258 (84%)	216 (100%)	1 (0%)	0	100	100
All	All	21936/28896 (76%)	21872 (100%)	64 (0%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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.

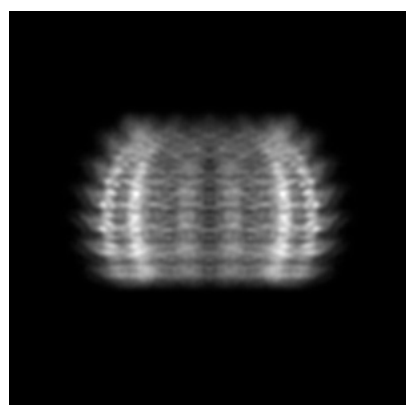
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11482. These allow visual inspection of the internal detail of the map and identification of artifacts.

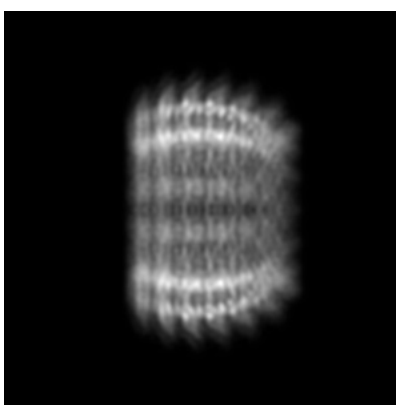
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

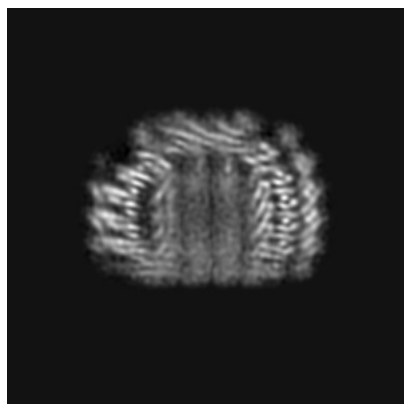


Z Index: 168

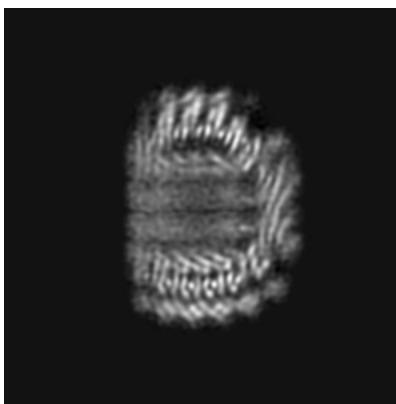
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 229



Y Index: 229

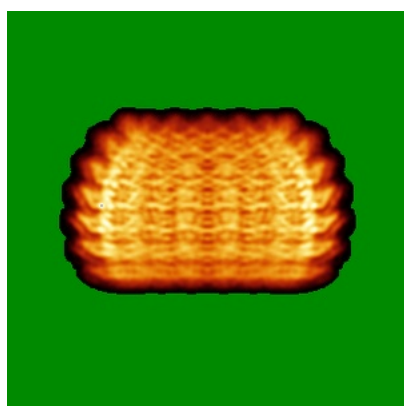


Z Index: 172

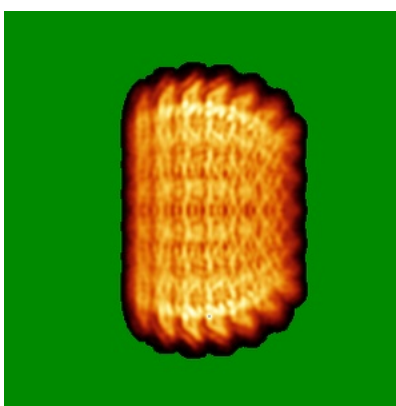
The images above show the largest variance slices of the map in three orthogonal directions.

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

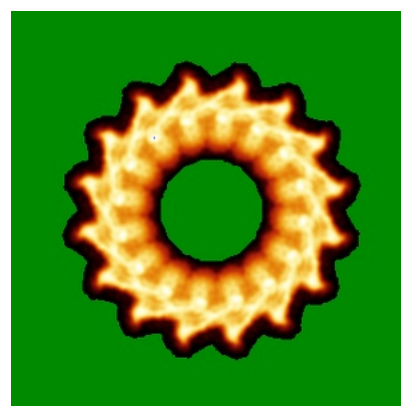
6.4.1 Primary map



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 0.014. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

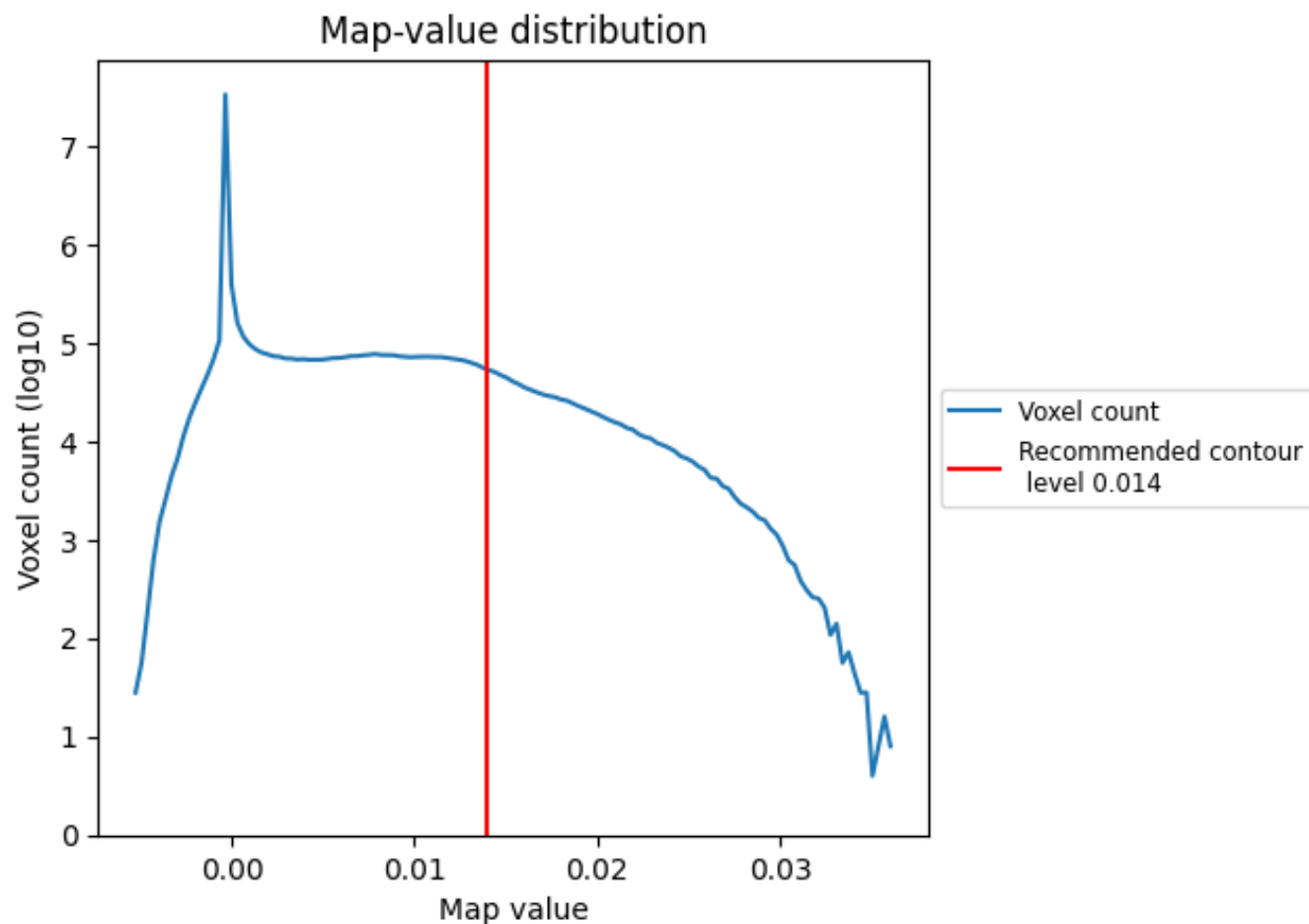
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

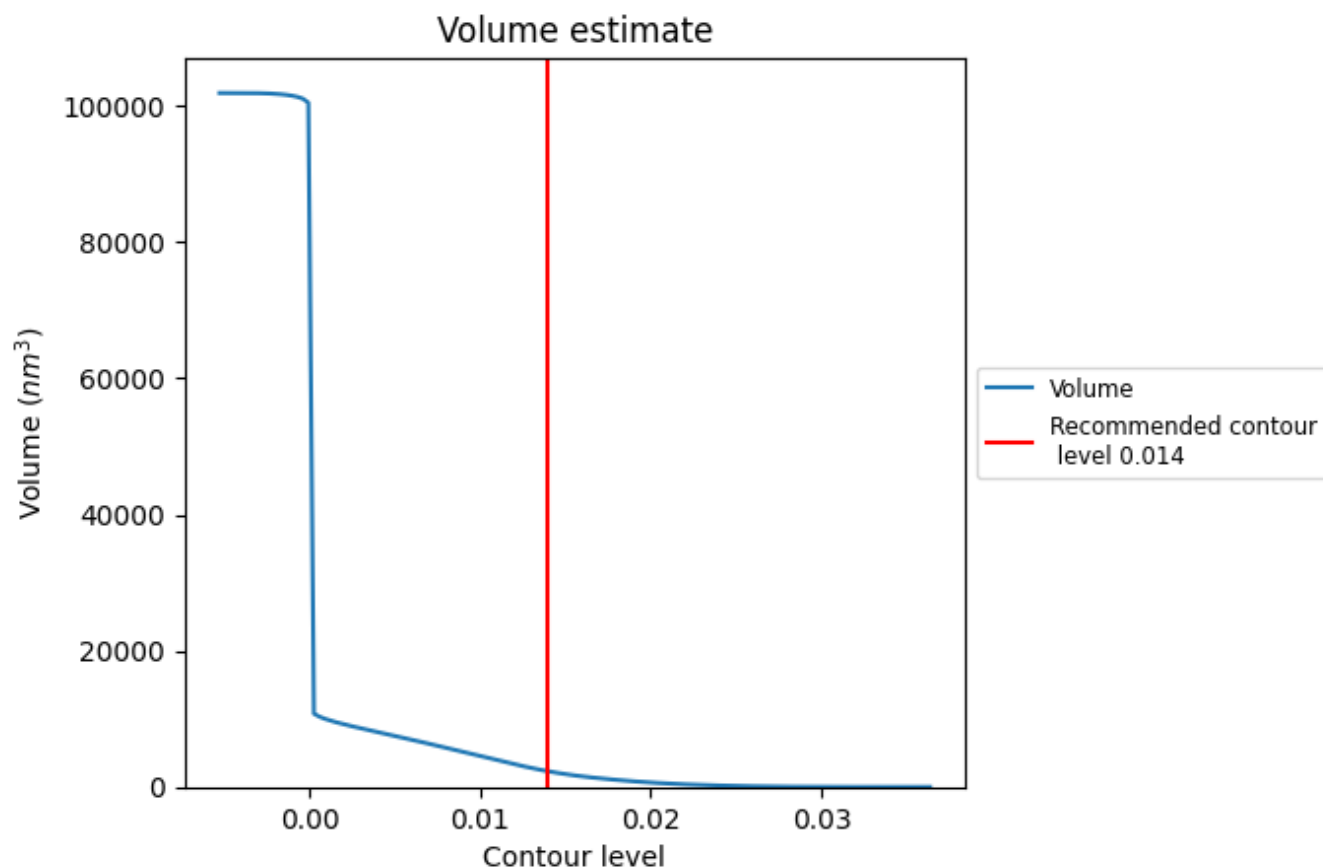
This section contains the results of statistical analysis of the map.

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.

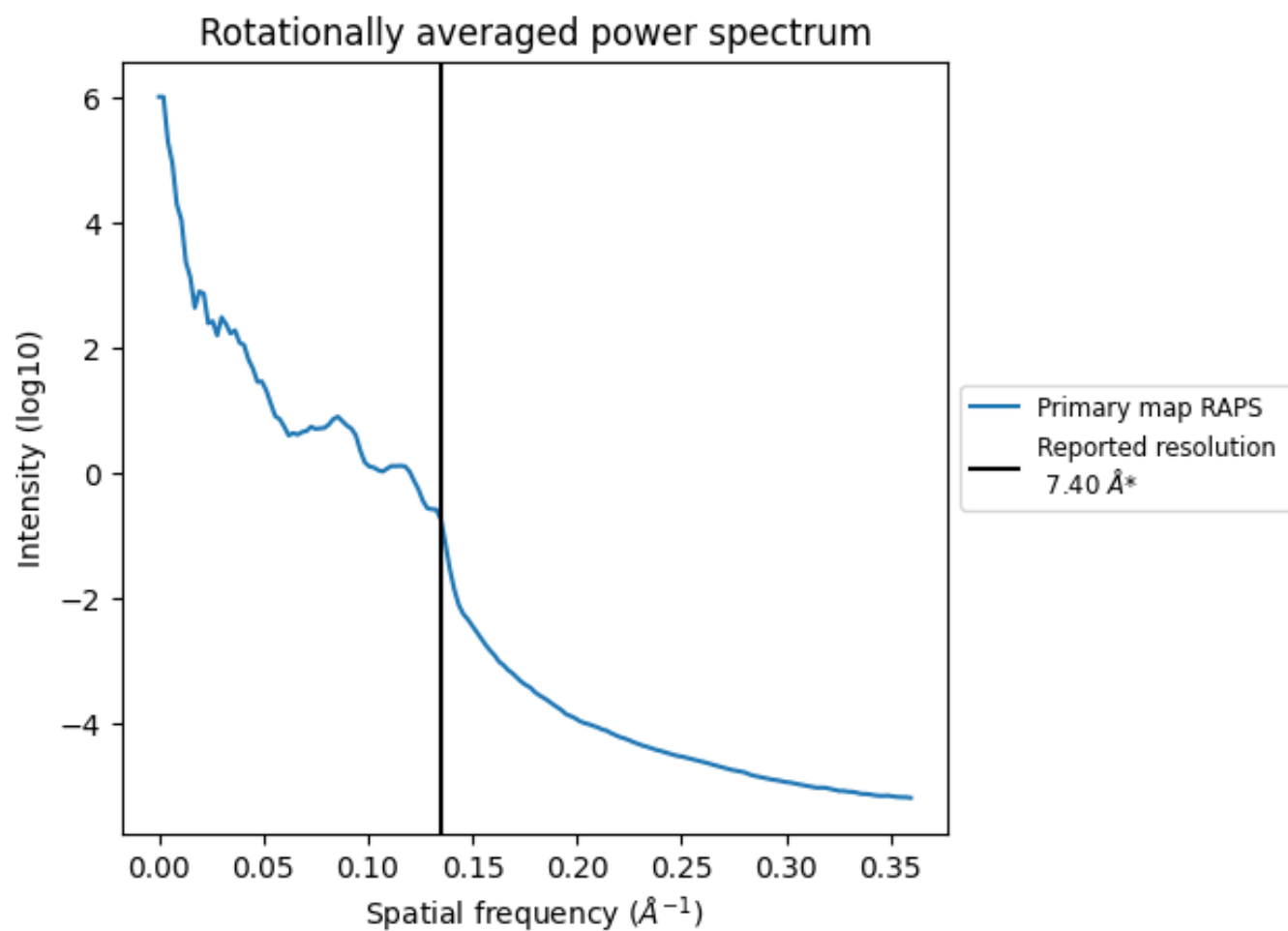
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2305 nm³; this corresponds to an approximate mass of 2082 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 0.135 Å⁻¹

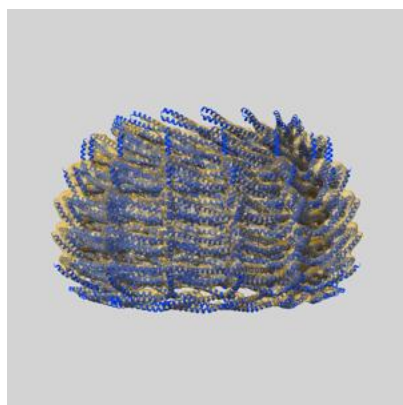
8 Fourier-Shell correlation

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

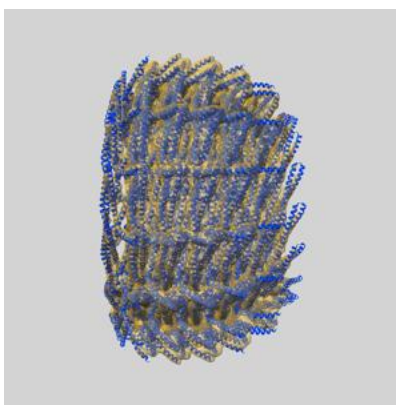
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11482 and PDB model 6ZW6. Per-residue inclusion information can be found in section 3 on page 14.

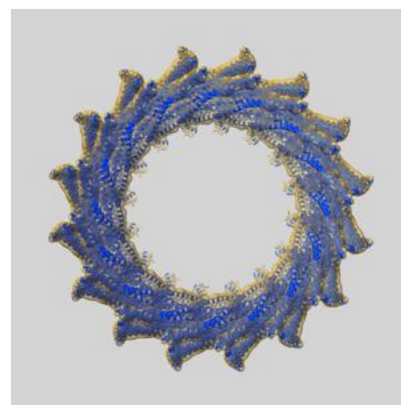
9.1 Map-model overlay [i](#)



X

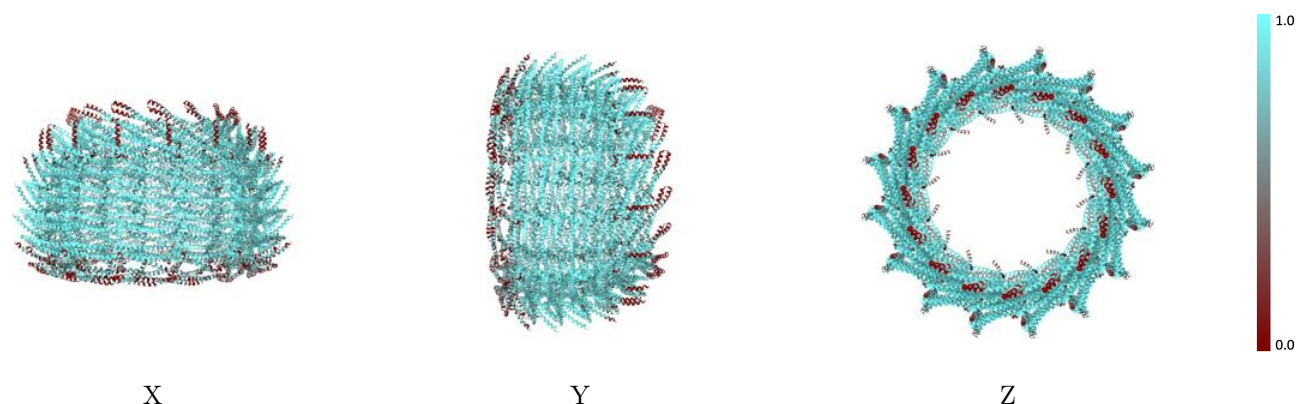
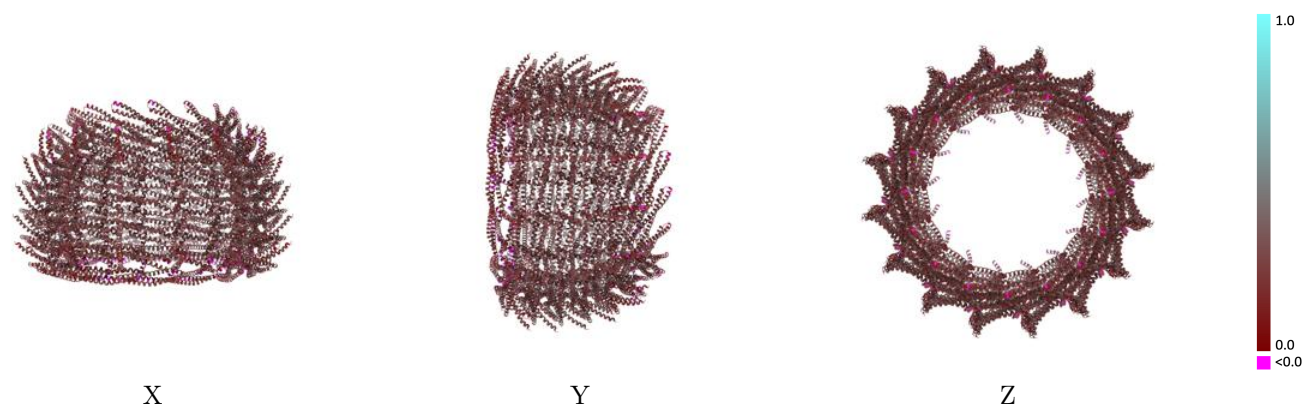


Y

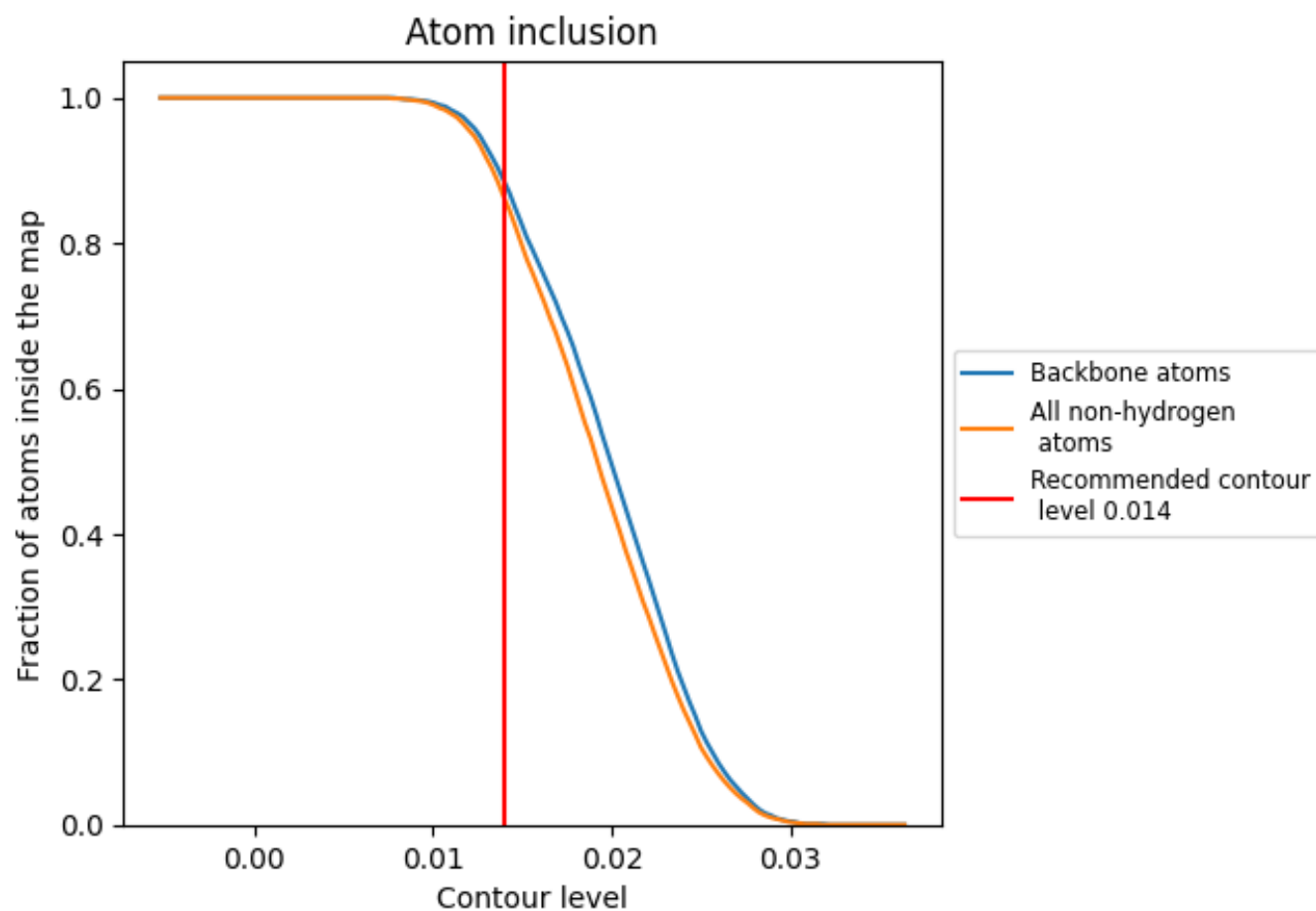


Z

The images above show the 3D surface view of the map at the recommended contour level 0.014 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.



9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% 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 (0.014) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8610	 0.2500
A	 0.5580	 0.2160
AA	 0.9440	 0.2630
AB	 0.9690	 0.2630
AC	 0.5610	 0.2170
AD	 0.8760	 0.2500
B	 0.8170	 0.2240
BA	 0.8790	 0.2530
BB	 0.9770	 0.2680
BC	 0.8080	 0.2220
BD	 0.7360	 0.2470
C	 0.9700	 0.2620
CA	 0.7350	 0.2550
CB	 0.9440	 0.2620
CC	 0.9700	 0.2630
CD	 0.5630	 0.2150
D	 0.9790	 0.2680
DA	 0.5580	 0.2150
DB	 0.8790	 0.2520
DC	 0.9770	 0.2680
DD	 0.8090	 0.2240
E	 0.9480	 0.2600
EA	 0.8170	 0.2220
EB	 0.7350	 0.2550
EC	 0.9440	 0.2600
ED	 0.9700	 0.2650
F	 0.8820	 0.2510
FA	 0.9700	 0.2630
FB	 0.5580	 0.2140
FC	 0.8790	 0.2480
FD	 0.9780	 0.2690
G	 0.7330	 0.2500
GA	 0.9790	 0.2690
GB	 0.8170	 0.2200
GC	 0.7340	 0.2500



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Chain	Atom inclusion	Q-score
GD	 0.9440	 0.2610
H	 0.5400	 0.2160
HA	 0.9480	 0.2620
HB	 0.9700	 0.2610
HC	 0.5580	 0.2160
HD	 0.8790	 0.2490
I	 0.8200	 0.2230
IA	 0.8820	 0.2500
IB	 0.9790	 0.2670
IC	 0.8170	 0.2220
ID	 0.7340	 0.2510
J	 0.9700	 0.2620
JA	 0.7330	 0.2530
JB	 0.9480	 0.2590
JC	 0.9700	 0.2650
K	 0.9790	 0.2700
KA	 0.5420	 0.2140
KB	 0.8820	 0.2500
KC	 0.9790	 0.2710
L	 0.9440	 0.2610
LA	 0.8190	 0.2230
LB	 0.7330	 0.2530
LC	 0.9480	 0.2640
M	 0.8830	 0.2500
MA	 0.9700	 0.2640
MB	 0.5400	 0.2160
MC	 0.8820	 0.2530
N	 0.7340	 0.2510
NA	 0.9790	 0.2710
NB	 0.8190	 0.2220
NC	 0.7330	 0.2510
O	 0.5540	 0.2170
OA	 0.9440	 0.2640
OB	 0.9700	 0.2620
OC	 0.5420	 0.2150
P	 0.8140	 0.2250
PA	 0.8830	 0.2550
PB	 0.9790	 0.2690
PC	 0.8200	 0.2220
Q	 0.9670	 0.2640
QA	 0.7350	 0.2550
QB	 0.9440	 0.2610

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Chain	Atom inclusion	Q-score
QC	 0.9700	 0.2610
R	 0.9780	 0.2710
RA	 0.5540	 0.2170
RB	 0.8830	 0.2510
RC	 0.9790	 0.2680
S	 0.9430	 0.2620
SA	 0.8140	 0.2230
SB	 0.7350	 0.2530
SC	 0.9440	 0.2590
T	 0.8760	 0.2520
TA	 0.9670	 0.2630
TB	 0.5550	 0.2170
TC	 0.8830	 0.2500
UA	 0.9780	 0.2700
UB	 0.8140	 0.2220
UC	 0.7350	 0.2500
V	 0.7360	 0.2500
VA	 0.9430	 0.2630
VB	 0.9670	 0.2630
VC	 0.5550	 0.2160
W	 0.5610	 0.2170
WA	 0.8760	 0.2530
WB	 0.9780	 0.2690
WC	 0.8140	 0.2220
X	 0.8090	 0.2250
XA	 0.7360	 0.2540
XB	 0.9430	 0.2610
XC	 0.9670	 0.2630
Y	 0.9700	 0.2640
YA	 0.5610	 0.2160
YB	 0.8760	 0.2510
YC	 0.9780	 0.2680
Z	 0.9770	 0.2690
ZA	 0.8080	 0.2220
ZB	 0.7360	 0.2520
ZC	 0.9430	 0.2610