



Full wwPDB EM Validation Report ⓘ

Nov 12, 2022 – 11:25 AM EST

PDB ID : 6UP6
EMDB ID : EMD-20835
Title : Endophilin B1 helical scaffold
Authors : Bhatt, V.S.; Sundborger-Lunna, A.C.
Deposited on : 2019-10-16
Resolution : 9.00 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:

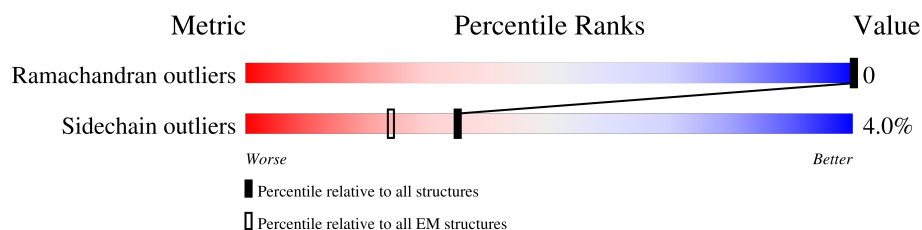
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 9.00 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	365	
1	B	365	
1	C	365	
1	D	365	
1	E	365	
1	F	365	
1	G	365	
1	H	365	
1	I	365	











Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	J	365	
1	K	365	
1	L	365	
1	M	365	
1	N	365	
1	O	365	
1	P	365	
1	Q	365	
1	R	365	
1	S	365	
1	T	365	
1	V	365	
1	W	365	
1	a	365	
1	b	365	
1	c	365	
1	d	365	
1	e	365	
1	f	365	
1	g	365	
1	h	365	
1	i	365	
1	j	365	
1	k	365	
1	l	365	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	m	365	 64%33%
1	n	365	 64%33%
1	o	365	 64%33%
1	p	365	 64%33%
1	q	365	 64%33%
1	r	365	 64%33%
1	s	365	 64%33%
1	t	365	 64%33%
1	v	365	 64%33%
1	w	365	 64%33%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 85668 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 Endophilin-B1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	B	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	C	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	D	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	E	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	F	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	G	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	H	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	I	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	J	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	K	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	L	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	M	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	N	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	O	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	P	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	Q	243	Total 1947	C 1225	N 340	O 374	S 8	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	S	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	T	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	V	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	W	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	a	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	b	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	c	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	d	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	e	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	f	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	g	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	h	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	i	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	j	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	k	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	l	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	m	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	n	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	o	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	p	243	Total 1947	C 1225	N 340	O 374	S 8	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					AltConf	Trace
1	q	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	r	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	s	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	t	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	v	243	Total 1947	C 1225	N 340	O 374	S 8	0	0
1	w	243	Total 1947	C 1225	N 340	O 374	S 8	0	0

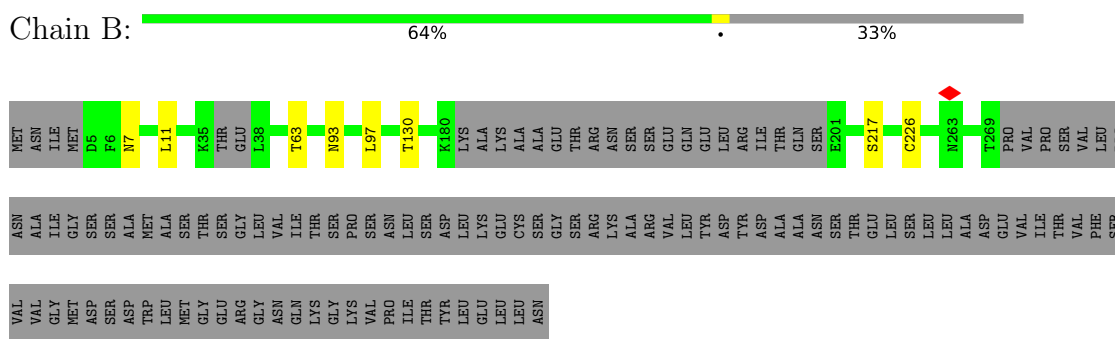
3 Residue-property plots [i](#)

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.

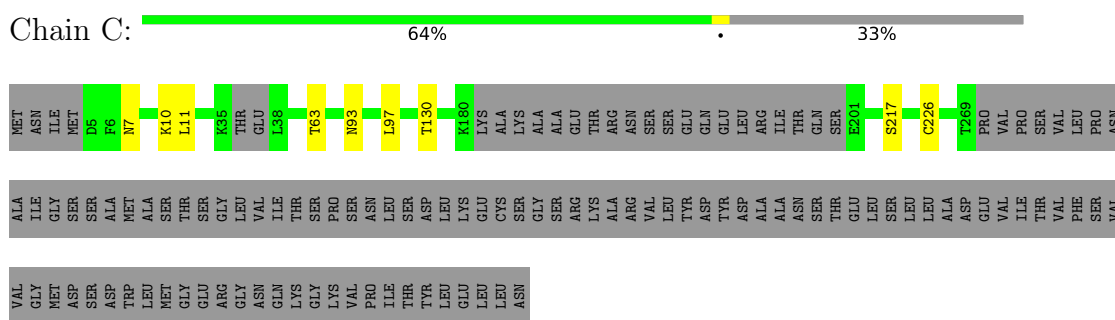
• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1

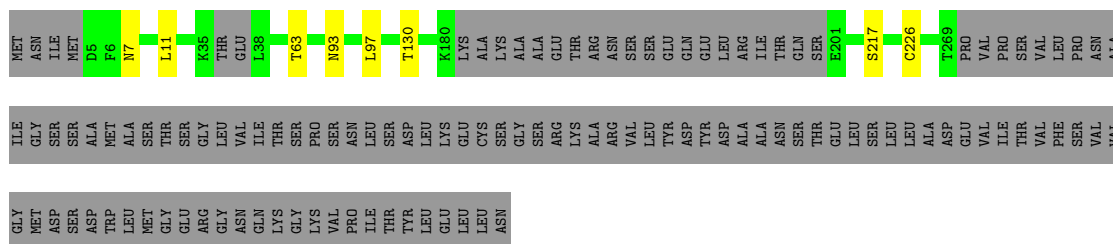


• Molecule 1: Endophilin-B1



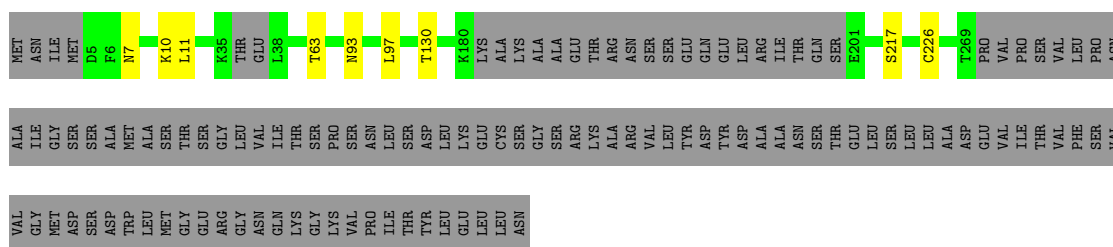
• Molecule 1: Endophilin-B1

Chain D:  64% 33%



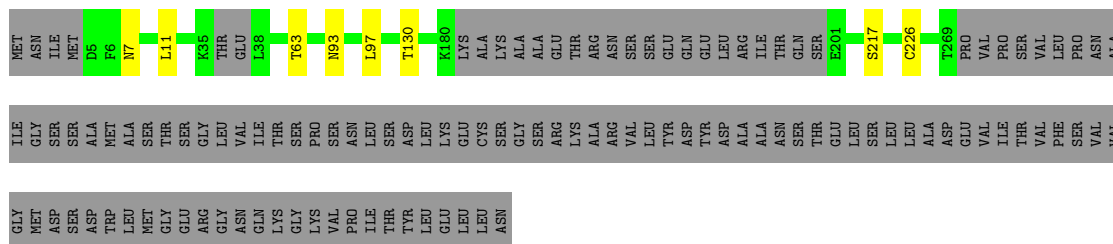
• Molecule 1: Endophilin-B1

Chain E:  64% 33%



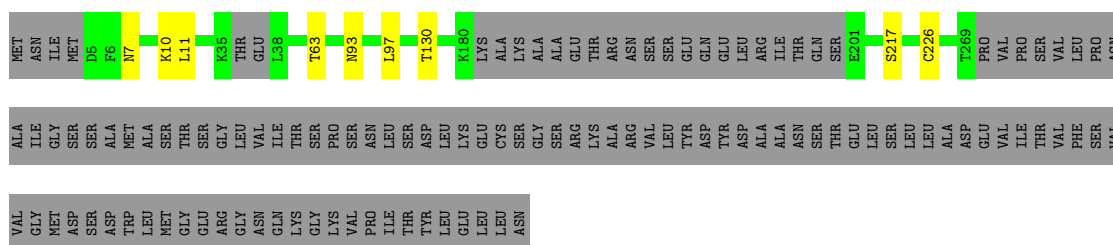
• Molecule 1: Endophilin-B1

Chain F:  64% 33%



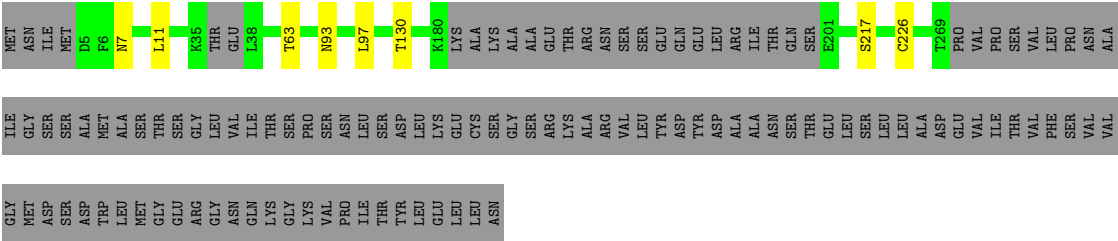
• Molecule 1: Endophilin-B1

Chain G:  64% 33%

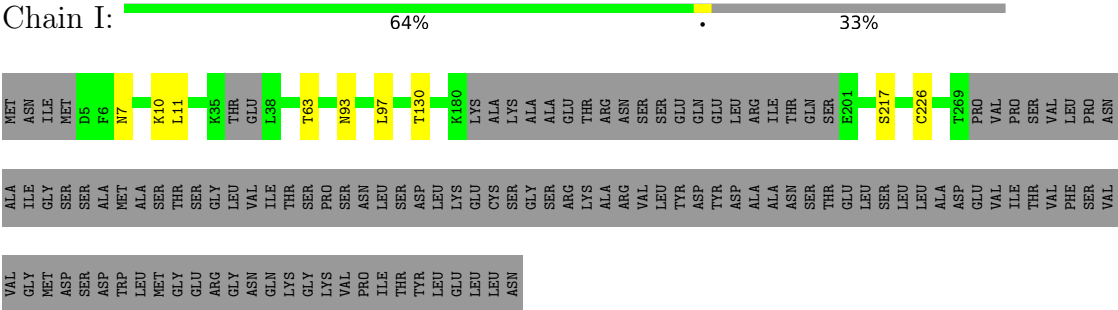


• Molecule 1: Endophilin-B1

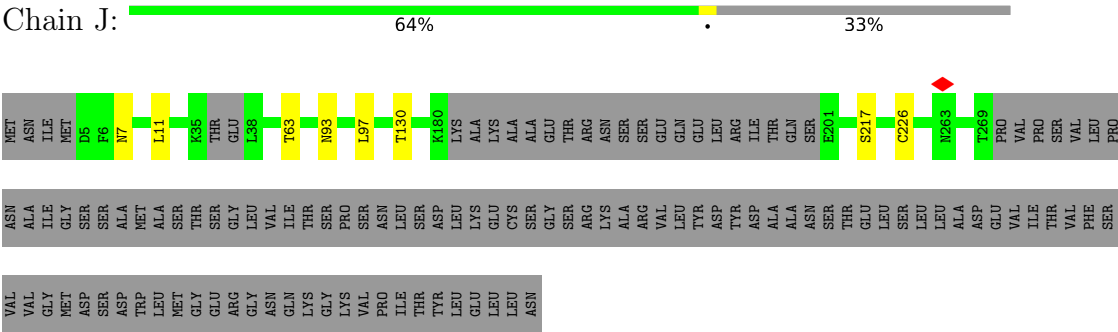
Chain H:  64% 33%



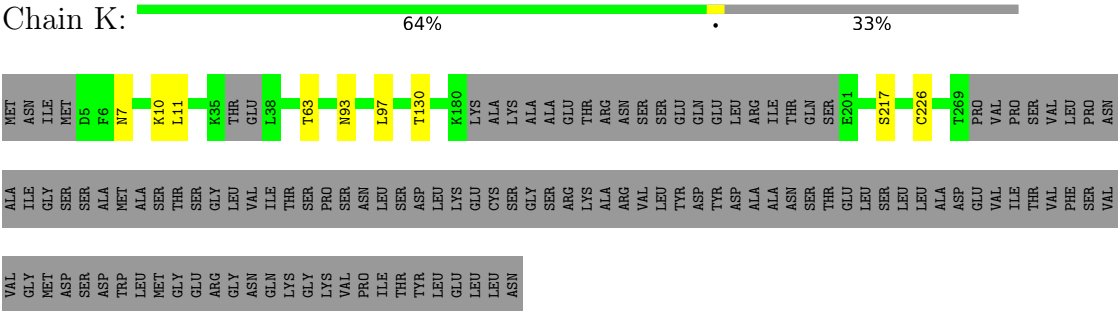
• Molecule 1: Endophilin-B1



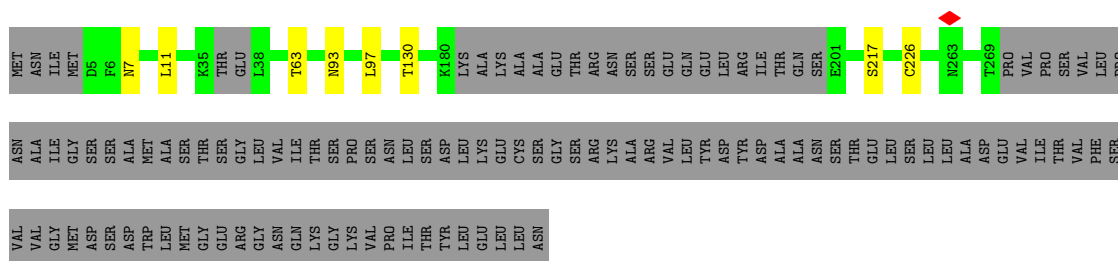
• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1

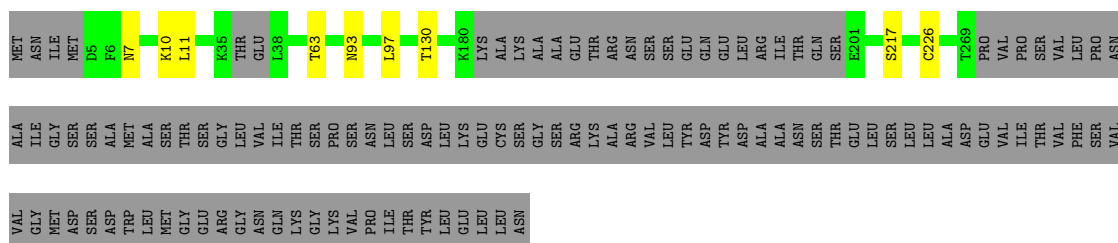


• Molecule 1: Endophilin-B1



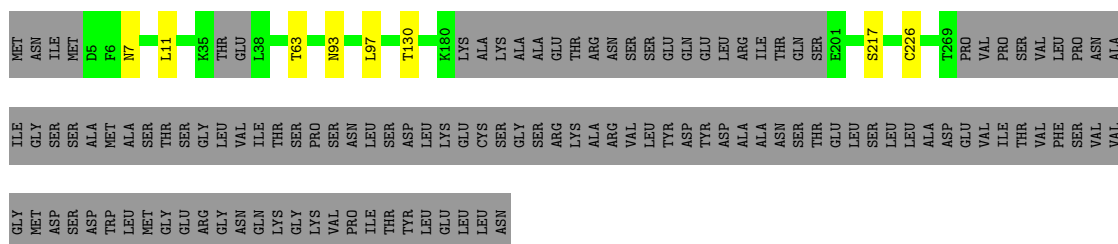
• Molecule 1: Endophilin-B1

Chain M: 64% 33%



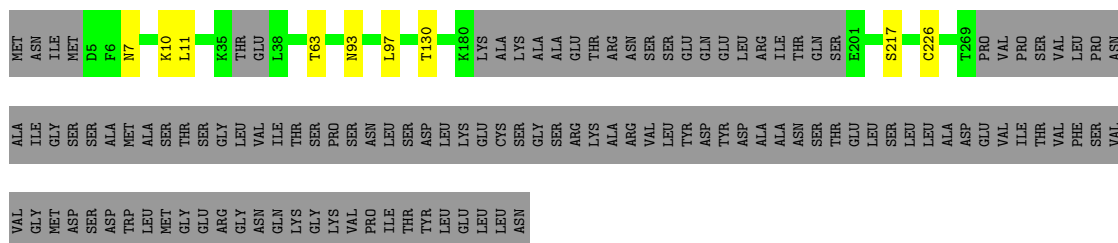
• Molecule 1: Endophilin-B1

Chain N: 64% 33%



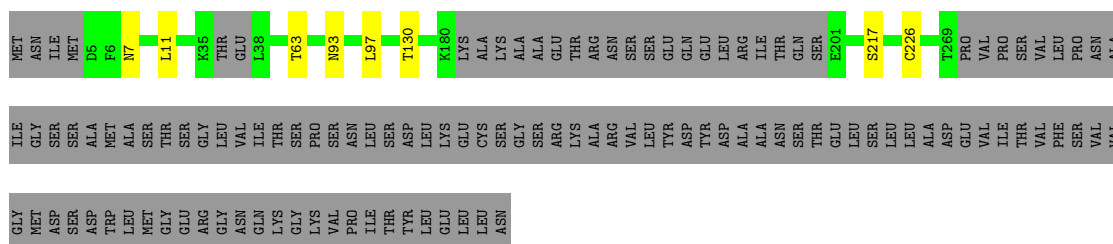
• Molecule 1: Endophilin-B1

Chain O: 64% 33%



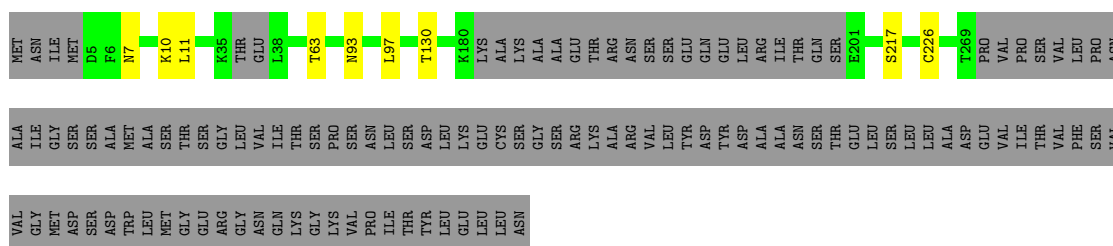
• Molecule 1: Endophilin-B1

Chain P: 64% 33%



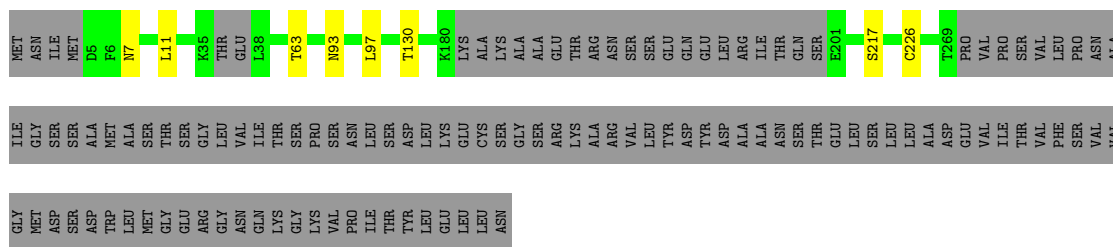
• Molecule 1: Endophilin-B1

Chain Q: 64% 33%



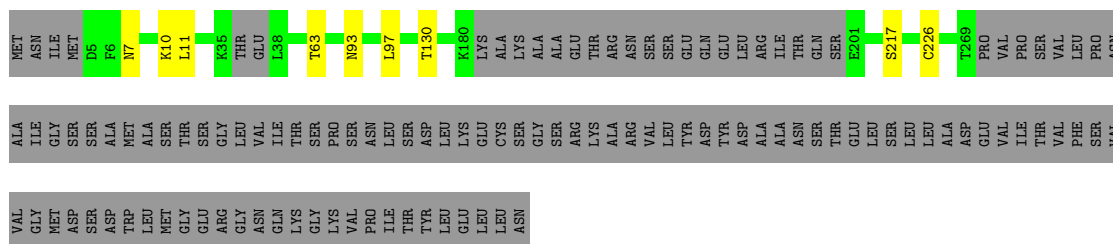
• Molecule 1: Endophilin-B1

Chain R: 64% 33%



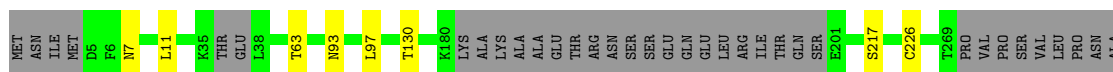
• Molecule 1: Endophilin-B1

Chain S: 64% 33%



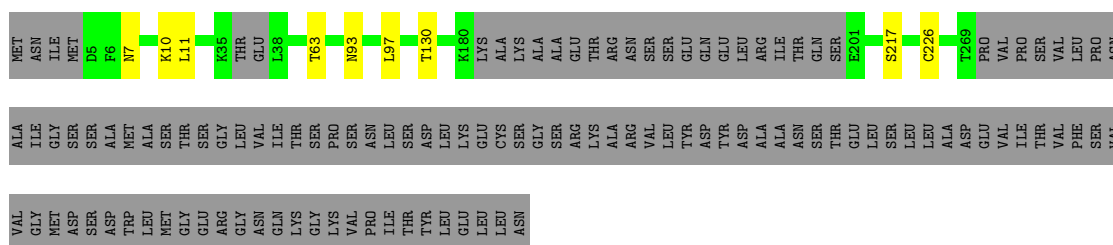
• Molecule 1: Endophilin-B1

Chain T: 64% 33%



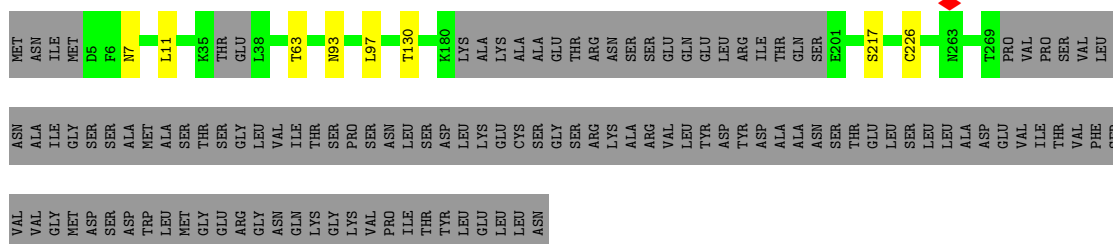
- Molecule 1: Endophilin-B1

Chain V:  64% 1% 33%



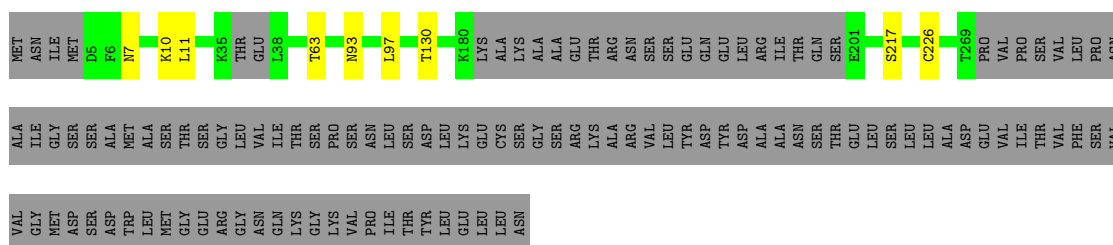
- Molecule 1: Endophilin-B1

Chain W: 64% 33%



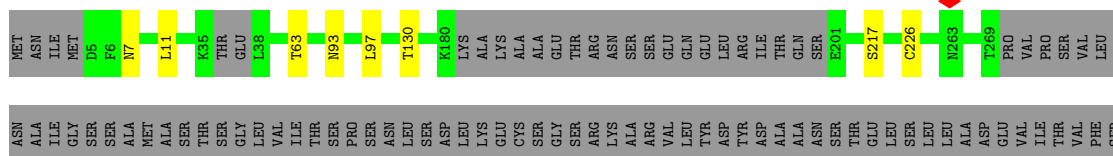
- Molecule 1: Endophilin-B1

Chain a: 64% . 33%



- Molecule 1: Endophilin-B1

Chain b: 64% 33%



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

• Molecule 1: Endophilin-B1

Chain c:  64% 33%

MET ASN ILE MET D5 F6 N7 K10 L11 K35 THR L38 T63 N93 L97 T130 K180 LYS ALA LYS LYS ALA ALA GLU THR ARG ASN ARG SER SER LEU GLN GLU LEU E201 S217 C226 T269 PRO VAL PRO SER VAL LEU ASN

ALA ILE GLY SER MET D5 F6 N7 K10 L11 K35 THR L38 T63 N93 L97 T130 K180 LYS GLU CYS LYS SER GLY ALA ALA GLU THR ARG LYS ALA ARG VAL SER LEU TYR ASP THR ASP TYR ALA ALA THR ASN SER THR LEU GLU SER E201 S217 C226 T269 ASP VAL ILE THR VAL PHE LEU VAL ASN VAL

VAL GLY MET ASP SER ASP TRP LEU MET GLY GLY ARG GLY ASN GLN LYS GLY LYS VAL PRO ILE THR TYR THR LEU LEU ASN

• Molecule 1: Endophilin-B1

Chain d:  64% 33%

MET ASN ILE MET D5 F6 N7 L11 K35 THR L38 T63 N93 L97 T130 K180 LYS ALA LYS LYS ALA ALA GLU THR ARG ASN ARG SER SER LEU GLN GLU LEU E201 S217 C226 T269 PRO VAL PRO SER VAL LEU ASN ALA

ILE GLY SER SER MET MET ALA SER THR THR GLY GLY VAL ILE THR SER PRO SER ASN LEU SER ASP LYS CYS SER LYS SER ARG LYS ALA ARG VAL SER LEU TYR ASP THR ASP TYR ALA ALA THR ASN SER THR LEU GLU SER E201 S217 C226 T269 ASP VAL ILE THR VAL PHE LEU VAL ASN VAL

GLY MET ASP SER ASP TRP LEU MET GLY GLY ARG GLY ASN GLN LYS GLY LYS VAL PRO ILE THR TYR THR LEU LEU ASN

• Molecule 1: Endophilin-B1

Chain e:  64% 33%

MET ASN ILE MET D5 F6 N7 K10 L11 K35 THR L38 T63 N93 L97 T130 K180 LYS LYS LYS ALA ALA GLU THR ARG ASN ARG SER SER LEU GLN GLU LEU E201 S217 C226 T269 PRO VAL PRO SER VAL LEU ASN

ALA ILE GLY SER MET D5 F6 N7 K10 L11 K35 THR L38 T63 N93 L97 T130 K180 LYS GLU CYS LYS SER GLY ALA ALA GLU THR ARG LYS ALA ARG VAL SER LEU TYR ASP THR ASP TYR ALA ALA THR ASN SER THR LEU GLU SER E201 S217 C226 T269 ASP VAL ILE THR VAL PHE LEU VAL ASN VAL

VAL GLY MET ASP SER ASP TRP LEU MET GLY GLY ARG GLY ASN GLN LYS GLY LYS VAL PRO ILE THR TYR THR LEU LEU ASN

• Molecule 1: Endophilin-B1

Chain f:  64% 33%

MET ASN ILE MET D5 F6 N7 L11 K35 THR L38 T63 N93 L97 T130 K180 LYS ALA LYS LYS ALA ALA GLU THR ARG ASN ARG SER SER LEU GLN GLU LEU E201 S217 C226 T269 PRO VAL PRO SER VAL LEU ASN ALA

ILE GLY SER SER MET MET ALA SER THR THR GLY GLY VAL ILE THR SER PRO SER ASN LEU SER ASP LYS CYS SER LYS SER ARG LYS ALA ARG VAL SER LEU TYR ASP THR ASP TYR ALA ALA THR ASN SER THR LEU GLU SER E201 S217 C226 T269 ASP VAL ILE THR VAL PHE LEU VAL ASN VAL

GLY MET ASP SER ASP TRP LEU MET GLY GLY ARG GLY ASN GLN LYS GLY LYS VAL PRO ILE THR TYR THR LEU LEU ASN

• Molecule 1: Endophilin-B1

Chain g:  64% 33%

MET	ASN	ILE	MET	D5	F6	N7	K10	L11	K35	THR	L38	T63	N93	L97	T130	K180	LYS	ALA	LYS	ALA	ALA	GLU	THR	LYS	ARG	ASN	SER	SER	GLU	GLN	GLU	LEU	ARG	ALA	ILE	THR	GLN	SER	E201	S217	C226	T269	PRO	VAL	PRO	VAL	THR	VAL	LEU	PRO	ASN	
ALA	ILE	GLY	SER	SER	ASP	ALA	MET	ALA	SER	THR	GLY	SER	PRO	ASN	SER	LYS	GLU	CYS	GLY	SER	ARG	LYS	LYS	ALA	ARG	VAL	LEU	TYR	ASP	TYR	ASP	ALA	ALA	ASN	SER	THR	THR	GLU	LEU	SER	LEU	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	SER	VAL
VAL	GLY	MET	ASP	SER	ASP	TRP	LEU	MET	GLY	ARG	GLY	ASN	GLN	LYS	LYS	VAL	PRO	ILE	THR	TYR	THR	ASP	LEU	GLU	LEU	LEU	ASN																									

• Molecule 1: Endophilin-B1

Chain h:  64% 33%

MET	ASN	ILE	MET	D5	F6	N7	L11	K35	THR	GLU	L38	T63	N93	L97	T130	K180	LYS	ALA	LYS	ALA	GLU	THR	LYS	ARG	ASN	VAL	SER	GLY	TYR	ASP	LEU	GLY	CYS	SER	GLY	ALA	SER	GLY	ARG	LYS	ALA	THR	LYS	ALA	ASN	VAL	SER	GLY	TYR	ASP	LEU	GLY	LEU	LEU	ASN	
ILE	GLY	SER	SER	ALA	MET	ALA	SER	THR	GLY	VAL	ILE	THR	SER	PRO	LYS	ASN	LEU	THR	ASP	LEU	LYS	GLU	CYS	SER	GLY	ALA	VAL	THR	TYR	GLY	LEU	GLY	ASP	TYR	ALA	ALA	ASN	SER	THR	GLU	LEU	SER	LEU	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	SER	VAL	VAL	VAL
GLY	MET	ASP	SER	ASP	TRP	LEU	MET	GLY	ARG	ASN	GLN	LYS	GLY	VAL	PRO	ILE	THR	TYR	THR	ASP	LEU	LYS	GLY	LEU	LEU	ASN																														

• Molecule 1: Endophilin-B1

Chain i:  64% 33%

ALA	ILE	GLY	SER	SER	ALA	MET	ALA	SER	THR	GLY	LEU	VAL	ILE	THR	SER	PRO	SER	ASN	LEU	SER	LEU	ASP	LEU	LYS	GLU	CYS	SER	GLY	SER	ARG	LYS	ALA	ARG	VAL	LEU	TYR	ASP	ASP	ALA	ALA	ASN	SER	THR	GLU	LEU	SER	LEU	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	SER	VAL	VAL
MET	ASN	ILE	MET	D5	F6	N7	K10	L11	K35	THR	THR	GLU	L38	T63	N93	L97	T130	K180	LYS	ALA	LYS	ALA	ALA	GLU	THR	ALA	ARG	ASN	SER	SER	GLU	GLN	TYR	LEU	ASP	LEU	GLY	ALA	ASN	SER	THR	GLU	LEU	LEU	ALA	E201	S217	C226	T269	PRO	VAL	PRO	THR	VAL	LEU	VAL	PRO	ASN	
VAL	GLY	MET	ASP	SER	ASP	TRP	LEU	MET	GLY	ARG	GLY	ASN	GLN	LYS	LYS	VAL	PRO	ILE	THR	TYR	THR	ASP	LEU	GLU	LEU	LEU	ASN																																

• Molecule 1: Endophilin-B1

Chain j:  64% 33%

ILE	GLY	ASN	THR	GLY	LEU	VAL	ILE	THR	SER	PRO	SER	ASN	LEU	SER	ASP	LEU	LYS	GLU	CYS	SER	GLY	ALA	SER	GLY	ARG	LYS	ALA	ARG	ASN	SER	VAL	TYR	ASP	TYR	GLU	ASN	ALA	ALA	ASN	SER	THR	GLU	SER	LEU	ASP	GLU	VAL	ILE	THR	VAL	VAL	VAL	ASN	ALA	
MET	ASN	ILE	MET	D5	F6	N7	L11	K35	THR	GLU	L38	T63	N93	L97	T130	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	ASN	SER	GLU	GLN	GLU	ARG	ASN	SER	THR	TYR	GLU	LEU	GLY	ASN	THR	GLN	THR	ILE	THR	GLU	SER	LEU	GLU	VAL	PRO	VAL	THR	PRO	VAL	THR	ASN	ALA

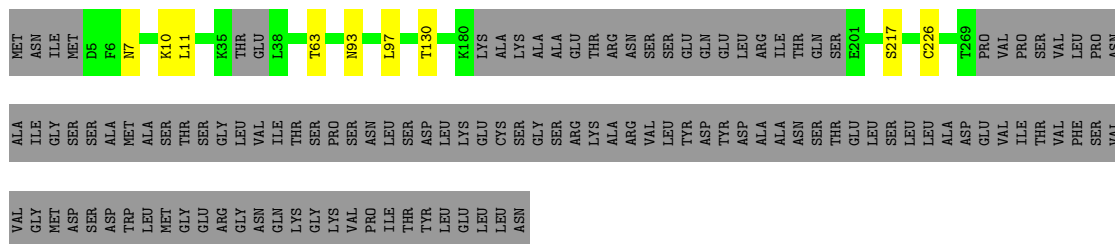
• Molecule 1: Endophilin-B1

[illegible][illegible]

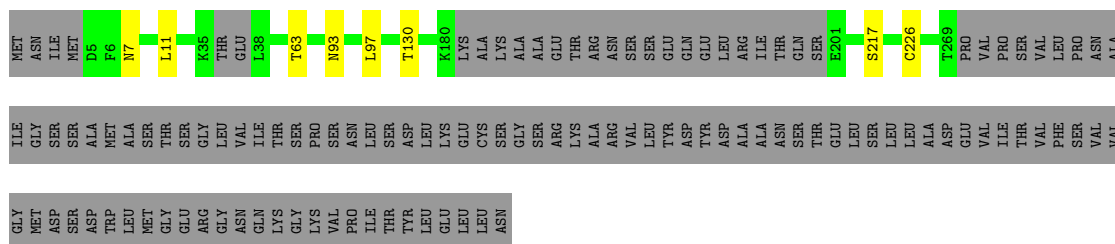
VAL	GLY	MET	ASP	SER	ASP	TRP	LEU	MET	MET	GLY	GLU	ARG	GLY	GLY	ASN	GLN	LYS	GLY	LYS	VAL	PRO	ASN	ILE	THR	TYR	LEU	LEU	LEU	ASN																	
ALA	ILE	SER	SER	ALA	MET	ALA	ALA	SER	THR	SER	GLY	LEU	VAL	THR	PRO	ASN	LEU	SER	ASP	LEU	LYS	GLU	GLY	GLY	SER	ARG	ASP	TYR	ASN																	
MET	ASN	ILE	MET	P6	M7	K10	L11	K35	THR	L38	T63	M93	L97	T130	K190	LYS	ALA	LYS	ALA	ALA	GLU	THR	ARG	ASN	SER	SER	GLU	GLN	GLU	ARG	ILE	THR	GLN	SER	E201	S217	C226	T269	PRO	VAL	PRO	SER	VAL	LEU	PRO	ASN

GLY	MET	ASP	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLY	ASN	GLN	LYS	GLY	LYS	VAL	PRO	ASN	LEU	SER	ASP	LEU	LYS	GLU	LEU	LEU	ASN																
ILE	GLY	SER	SER	ALA	MET	ALA	THR	SER	GLY	LEU	VAL	ILE	THR	SER	PRO	SER	ASN	LEU	SER	ASP	LEU	LYS	GLU	GLY	CYS	ARG	ALA	LYS															
MET	ASN	ILE	MET	P6	N7	L11	K35	THR	GLU	L38	T63	N93	L97	T130	K180	LYS	ALA	LYS	ALA	GLU	THR	ASN	SER	GLU	GLN	LEU	ARG	ILE	THR	GLN	SER	E201	S217	C226	T269	PRO	VAL	PRO	VAL	LEU	PRO	ASN	ALA

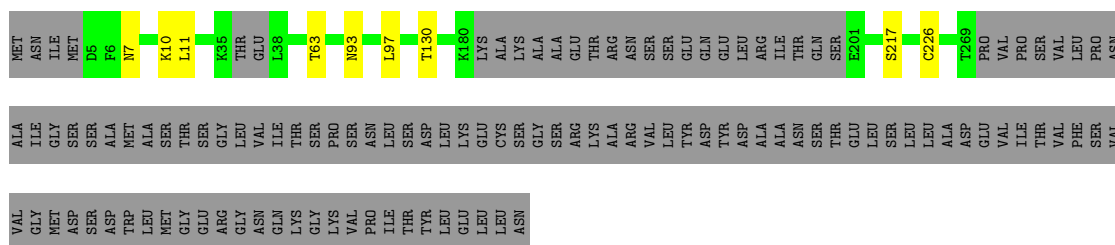
Chain o:  64% 1% 33%



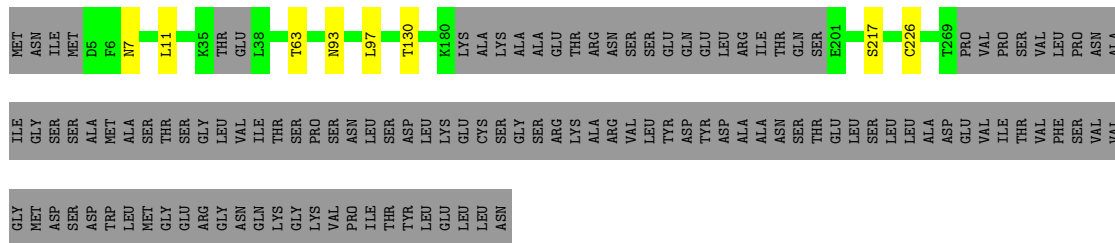
- Molecule 1: Endophilin-B1



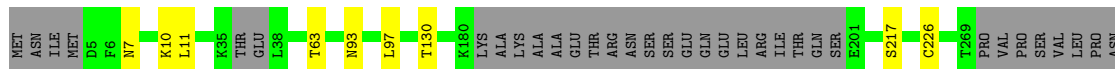
- Molecule 1: Endophilin-B1



- Molecule 1: Endophilin-B1



- Molecule 1: Endophilin-B1



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

● Molecule 1: Endophilin-B1



ILE	GLY	ASP	SER	SER	ALA	MET	ALA	SER	THR	SER	GLY	LEU	VAL	ILE	THR	SER	PRO	SER	ASN	LEU	SER	ASP	LYS	GLY	CYS	SER	GLY	SER	ALA	GLU	THR	LYS	ALA	ARG	ASN	SER	SER	GLU	GLN	GLU	LEU	LEU	ARG	ILE	THR	GLN	SER	E201	S217	C226	T269	PRO	VAL	VAL	ILE	THR	THR	PHE	SER	VAL	VAL	ALA	
GLY	MET	ASP	SER	ASP	TRP	LEU	MET	MET	GLY	GLU	ARG	GLY	ASN	GLN	LYS	GLY	LYS	VAL	PRO	PRO	ILE	THR	TYR	LEU	LEU	ASN	GLY	LEU	LEU	LEU	ASN	ARG	VAL	VAL	TYR	ASP	ASP	ASP	TYR	ASP	ALA	ALA	ASN	ASN	THR	SER	GLU	LEU	SER	LEU	LEU	ALA	ASP	GLU	VAL	ILE	THR	THR	PHE	SER	VAL	VAL	ALA
MET	ASN	MET	ILE	D5	F6	N7	L11	K35	THR	L38	T63	N93	L97	T130	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	ASN	ALA	ARG	ASN	SER	SER	GLU	GLN	GLU	LEU	LEU	ARG	ILE	THR	GLN	SER	E201	S217	C226	T269	PRO	VAL	VAL	THR	GLN	SER	LEU	VAL	ASN	ALA											

● Molecule 1: Endophilin-B1



VAL	GLY	MET	ASP	SER	ASP	TRP	LEU	LEU	MET	GLY	ARG	GLY	ASN	GLN	LYS	GLY	VAL	LYS	VAL	PRO	ASN	LEU	THR	TYR	GLU	LEU	LEU	LEU	ASN																																	
ALA	ILE	GLY	SER	SER	ALA	MET	ALA	SER	THR	THR	GLY	LEU	VAL	ILE	THR	THR	SER	PRO	SER	ASN	ASP	LYS	GLU	CYS	SER	GLY	SER	ALA	ARG	LYS	ALA	ARG	VAL	SER	LEU	TYR	ASP	TYR	ASP	ALA	ALA	ASN	SER	THR	GLU	LEU	SER	LEU	ALA	ASP	GLU	VAL	ILE	THR	THR	PHE	VAL	LEU	PRO	SER	ASN	VAL
MET	ASN	MET	D5	F6	N7	K10	L11	K35	THR	L38	T63	N93	L97	T130	K180	LYS	ALA	LYS	ALA	ALA	GLU	THR	ARG	ASN	ALA	ARG	ASN	SER	SER	SER	GLU	GLN	GLU	LEU	ARG	ILE	THR	GLN	SER	E201	S217	C226	T269	PRO	VAL	VAL	PRO	SER	SER	VAL	VAL	LEU	PRO	SER	ASN	VAL						

● Molecule 1: Endophilin-B1



ILE	GLY	SER	ILE	SER	ALA	MET	ALA	SER	THR	THR	SER	GLY	LEU	VAL	ILE	THR	SER	PRO	ASN	ASN	LEU	SER	ASP	LEU	LYS	GLU	CYS	SER	GLY	SER	ALA	GLU	THR	ARG	ALA	ARG	ASN	SER	SER	GLU	GLN	GLU	LEU	ASP	ALA	ALA	ASN	THR	GLN	SER	E201	S217	C226	T269	PRO	VAL	VAL	ILE	THR	THR	VAL	PHE	SER	PRO	ASN	VAL	ALA
GLY	MET	ASP	SER	ASP	TRP	LEU	MET	LEU	THR	GLY	ARG	GLY	ASN	GLN	LYS	THR	VAL	LYS	VAL	PRO	ASN	LEU	THR	TYR	GLU	LEU	LEU	ASN	ASN	GLY	THR	LYS	GLY	VAL	PRO	ASN	GLN	GLY	GLU	ARG	THR	GLU	LEU	GLY	LEU	GLY	LEU	ASP	GLU	VAL	ILE	THR	THR	VAL	PHE	SER	PRO	ASN	VAL	VAL							
MET	ASN	MET	ILE	SER	D5	F6	N7	L11	K35	THR	L38	T63	N93	L97	T130	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	ASN	SER	ALA	GLY	SER	GLY	SER	ALA	GLU	THR	ARG	ALA	ARG	ASN	SER	SER	GLU	GLN	GLU	LEU	ASP	ALA	ALA	ASN	THR	GLN	SER	E201	S217	C226	T269	PRO	VAL	VAL	ILE	THR	THR	VAL	PHE	SER	PRO	ASN	VAL	ALA

4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=66.6°, rise=18.7 Å, axial sym=C1	Depositor
Number of segments used	12300	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.037	Depositor
Minimum map value	-0.017	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.009	Depositor
Map size (Å)	490.06, 490.06, 490.06	wwPDB
Map dimensions	214, 214, 214	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.29, 2.29, 2.29	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.33	0/1976	0.55	0/2660
1	B	0.34	0/1976	0.55	0/2660
1	C	0.33	0/1976	0.55	0/2660
1	D	0.34	0/1976	0.55	0/2660
1	E	0.33	0/1976	0.55	0/2660
1	F	0.34	0/1976	0.55	0/2660
1	G	0.33	0/1976	0.55	0/2660
1	H	0.34	0/1976	0.55	0/2660
1	I	0.33	0/1976	0.55	0/2660
1	J	0.34	0/1976	0.55	0/2660
1	K	0.33	0/1976	0.55	0/2660
1	L	0.34	0/1976	0.55	0/2660
1	M	0.33	0/1976	0.55	0/2660
1	N	0.34	0/1976	0.55	0/2660
1	O	0.34	0/1976	0.55	0/2660
1	P	0.34	0/1976	0.55	0/2660
1	Q	0.34	0/1976	0.55	0/2660
1	R	0.34	0/1976	0.55	0/2660
1	S	0.33	0/1976	0.55	0/2660
1	T	0.34	0/1976	0.55	0/2660
1	V	0.33	0/1976	0.55	0/2660
1	W	0.34	0/1976	0.55	0/2660
1	a	0.34	0/1976	0.55	0/2660
1	b	0.34	0/1976	0.55	0/2660
1	c	0.33	0/1976	0.55	0/2660
1	d	0.34	0/1976	0.55	0/2660
1	e	0.34	0/1976	0.55	0/2660
1	f	0.34	0/1976	0.55	0/2660
1	g	0.33	0/1976	0.55	0/2660
1	h	0.34	0/1976	0.55	0/2660
1	i	0.33	0/1976	0.55	0/2660
1	j	0.34	0/1976	0.55	0/2660
1	k	0.34	0/1976	0.55	0/2660
1	l	0.34	0/1976	0.55	0/2660

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	m	0.34	0/1976	0.55	0/2660
1	n	0.34	0/1976	0.55	0/2660
1	o	0.34	0/1976	0.55	0/2660
1	p	0.34	0/1976	0.55	0/2660
1	q	0.34	0/1976	0.55	0/2660
1	r	0.34	0/1976	0.55	0/2660
1	s	0.34	0/1976	0.55	0/2660
1	t	0.34	0/1976	0.55	0/2660
1	v	0.33	0/1976	0.55	0/2660
1	w	0.34	0/1976	0.55	0/2660
All	All	0.34	0/86944	0.55	0/117040

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	B	237/365 (65%)	221 (93%)	16 (7%)	0	100	100
1	C	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	D	237/365 (65%)	223 (94%)	14 (6%)	0	100	100
1	E	237/365 (65%)	222 (94%)	15 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	237/365 (65%)	223 (94%)	14 (6%)	0	100	100
1	G	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	H	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	I	237/365 (65%)	223 (94%)	14 (6%)	0	100	100
1	J	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	K	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	L	237/365 (65%)	224 (94%)	13 (6%)	0	100	100
1	M	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	N	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	O	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	P	237/365 (65%)	224 (94%)	13 (6%)	0	100	100
1	Q	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	R	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	S	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	T	237/365 (65%)	221 (93%)	16 (7%)	0	100	100
1	V	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	W	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	a	237/365 (65%)	223 (94%)	14 (6%)	0	100	100
1	b	237/365 (65%)	221 (93%)	16 (7%)	0	100	100
1	c	237/365 (65%)	221 (93%)	16 (7%)	0	100	100
1	d	237/365 (65%)	223 (94%)	14 (6%)	0	100	100
1	e	237/365 (65%)	223 (94%)	14 (6%)	0	100	100
1	f	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	g	237/365 (65%)	221 (93%)	16 (7%)	0	100	100
1	h	237/365 (65%)	221 (93%)	16 (7%)	0	100	100
1	i	237/365 (65%)	223 (94%)	14 (6%)	0	100	100
1	j	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	k	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	l	237/365 (65%)	224 (94%)	13 (6%)	0	100	100
1	m	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	n	237/365 (65%)	224 (94%)	13 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	o	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	p	237/365 (65%)	224 (94%)	13 (6%)	0	100	100
1	q	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	r	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	s	237/365 (65%)	224 (94%)	13 (6%)	0	100	100
1	t	237/365 (65%)	221 (93%)	16 (7%)	0	100	100
1	v	237/365 (65%)	222 (94%)	15 (6%)	0	100	100
1	w	237/365 (65%)	223 (94%)	14 (6%)	0	100	100
All	All	10428/16060 (65%)	9781 (94%)	647 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	B	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	C	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	D	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	E	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	F	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	G	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	H	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	I	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	J	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	K	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	L	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	M	210/315 (67%)	201 (96%)	9 (4%)	29	53

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	N	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	O	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	P	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	Q	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	R	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	S	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	T	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	V	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	W	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	a	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	b	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	c	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	d	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	e	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	f	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	g	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	h	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	i	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	j	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	k	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	l	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	m	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	n	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	o	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	p	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	q	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	r	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	s	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	t	210/315 (67%)	202 (96%)	8 (4%)	33	57
1	v	210/315 (67%)	201 (96%)	9 (4%)	29	53
1	w	210/315 (67%)	202 (96%)	8 (4%)	33	57

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	9240/13860 (67%)	8866 (96%)	374 (4%)	35 55

All (374) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	10	LYS
1	A	11	LEU
1	A	63	THR
1	A	93	ASN
1	A	97	LEU
1	A	130	THR
1	A	217	SER
1	A	226	CYS
1	B	7	ASN
1	B	11	LEU
1	B	63	THR
1	B	93	ASN
1	B	97	LEU
1	B	130	THR
1	B	217	SER
1	B	226	CYS
1	C	7	ASN
1	C	10	LYS
1	C	11	LEU
1	C	63	THR
1	C	93	ASN
1	C	97	LEU
1	C	130	THR
1	C	217	SER
1	C	226	CYS
1	D	7	ASN
1	D	11	LEU
1	D	63	THR
1	D	93	ASN
1	D	97	LEU
1	D	130	THR
1	D	217	SER
1	D	226	CYS
1	E	7	ASN
1	E	10	LYS
1	E	11	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	63	THR
1	E	93	ASN
1	E	97	LEU
1	E	130	THR
1	E	217	SER
1	E	226	CYS
1	F	7	ASN
1	F	11	LEU
1	F	63	THR
1	F	93	ASN
1	F	97	LEU
1	F	130	THR
1	F	217	SER
1	F	226	CYS
1	G	7	ASN
1	G	10	LYS
1	G	11	LEU
1	G	63	THR
1	G	93	ASN
1	G	97	LEU
1	G	130	THR
1	G	217	SER
1	G	226	CYS
1	H	7	ASN
1	H	11	LEU
1	H	63	THR
1	H	93	ASN
1	H	97	LEU
1	H	130	THR
1	H	217	SER
1	H	226	CYS
1	I	7	ASN
1	I	10	LYS
1	I	11	LEU
1	I	63	THR
1	I	93	ASN
1	I	97	LEU
1	I	130	THR
1	I	217	SER
1	I	226	CYS
1	J	7	ASN
1	J	11	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	J	63	THR
1	J	93	ASN
1	J	97	LEU
1	J	130	THR
1	J	217	SER
1	J	226	CYS
1	K	7	ASN
1	K	10	LYS
1	K	11	LEU
1	K	63	THR
1	K	93	ASN
1	K	97	LEU
1	K	130	THR
1	K	217	SER
1	K	226	CYS
1	L	7	ASN
1	L	11	LEU
1	L	63	THR
1	L	93	ASN
1	L	97	LEU
1	L	130	THR
1	L	217	SER
1	L	226	CYS
1	M	7	ASN
1	M	10	LYS
1	M	11	LEU
1	M	63	THR
1	M	93	ASN
1	M	97	LEU
1	M	130	THR
1	M	217	SER
1	M	226	CYS
1	N	7	ASN
1	N	11	LEU
1	N	63	THR
1	N	93	ASN
1	N	97	LEU
1	N	130	THR
1	N	217	SER
1	N	226	CYS
1	O	7	ASN
1	O	10	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	O	11	LEU
1	O	63	THR
1	O	93	ASN
1	O	97	LEU
1	O	130	THR
1	O	217	SER
1	O	226	CYS
1	P	7	ASN
1	P	11	LEU
1	P	63	THR
1	P	93	ASN
1	P	97	LEU
1	P	130	THR
1	P	217	SER
1	P	226	CYS
1	Q	7	ASN
1	Q	10	LYS
1	Q	11	LEU
1	Q	63	THR
1	Q	93	ASN
1	Q	97	LEU
1	Q	130	THR
1	Q	217	SER
1	Q	226	CYS
1	R	7	ASN
1	R	11	LEU
1	R	63	THR
1	R	93	ASN
1	R	97	LEU
1	R	130	THR
1	R	217	SER
1	R	226	CYS
1	S	7	ASN
1	S	10	LYS
1	S	11	LEU
1	S	63	THR
1	S	93	ASN
1	S	97	LEU
1	S	130	THR
1	S	217	SER
1	S	226	CYS
1	T	7	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	T	11	LEU
1	T	63	THR
1	T	93	ASN
1	T	97	LEU
1	T	130	THR
1	T	217	SER
1	T	226	CYS
1	V	7	ASN
1	V	10	LYS
1	V	11	LEU
1	V	63	THR
1	V	93	ASN
1	V	97	LEU
1	V	130	THR
1	V	217	SER
1	V	226	CYS
1	W	7	ASN
1	W	11	LEU
1	W	63	THR
1	W	93	ASN
1	W	97	LEU
1	W	130	THR
1	W	217	SER
1	W	226	CYS
1	a	7	ASN
1	a	10	LYS
1	a	11	LEU
1	a	63	THR
1	a	93	ASN
1	a	97	LEU
1	a	130	THR
1	a	217	SER
1	a	226	CYS
1	b	7	ASN
1	b	11	LEU
1	b	63	THR
1	b	93	ASN
1	b	97	LEU
1	b	130	THR
1	b	217	SER
1	b	226	CYS
1	c	7	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	c	10	LYS
1	c	11	LEU
1	c	63	THR
1	c	93	ASN
1	c	97	LEU
1	c	130	THR
1	c	217	SER
1	c	226	CYS
1	d	7	ASN
1	d	11	LEU
1	d	63	THR
1	d	93	ASN
1	d	97	LEU
1	d	130	THR
1	d	217	SER
1	d	226	CYS
1	e	7	ASN
1	e	10	LYS
1	e	11	LEU
1	e	63	THR
1	e	93	ASN
1	e	97	LEU
1	e	130	THR
1	e	217	SER
1	e	226	CYS
1	f	7	ASN
1	f	11	LEU
1	f	63	THR
1	f	93	ASN
1	f	97	LEU
1	f	130	THR
1	f	217	SER
1	f	226	CYS
1	g	7	ASN
1	g	10	LYS
1	g	11	LEU
1	g	63	THR
1	g	93	ASN
1	g	97	LEU
1	g	130	THR
1	g	217	SER
1	g	226	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	h	7	ASN
1	h	11	LEU
1	h	63	THR
1	h	93	ASN
1	h	97	LEU
1	h	130	THR
1	h	217	SER
1	h	226	CYS
1	i	7	ASN
1	i	10	LYS
1	i	11	LEU
1	i	63	THR
1	i	93	ASN
1	i	97	LEU
1	i	130	THR
1	i	217	SER
1	i	226	CYS
1	j	7	ASN
1	j	11	LEU
1	j	63	THR
1	j	93	ASN
1	j	97	LEU
1	j	130	THR
1	j	217	SER
1	j	226	CYS
1	k	7	ASN
1	k	10	LYS
1	k	11	LEU
1	k	63	THR
1	k	93	ASN
1	k	97	LEU
1	k	130	THR
1	k	217	SER
1	k	226	CYS
1	l	7	ASN
1	l	11	LEU
1	l	63	THR
1	l	93	ASN
1	l	97	LEU
1	l	130	THR
1	l	217	SER
1	l	226	CYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	m	7	ASN
1	m	10	LYS
1	m	11	LEU
1	m	63	THR
1	m	93	ASN
1	m	97	LEU
1	m	130	THR
1	m	217	SER
1	m	226	CYS
1	n	7	ASN
1	n	11	LEU
1	n	63	THR
1	n	93	ASN
1	n	97	LEU
1	n	130	THR
1	n	217	SER
1	n	226	CYS
1	o	7	ASN
1	o	10	LYS
1	o	11	LEU
1	o	63	THR
1	o	93	ASN
1	o	97	LEU
1	o	130	THR
1	o	217	SER
1	o	226	CYS
1	p	7	ASN
1	p	11	LEU
1	p	63	THR
1	p	93	ASN
1	p	97	LEU
1	p	130	THR
1	p	217	SER
1	p	226	CYS
1	q	7	ASN
1	q	10	LYS
1	q	11	LEU
1	q	63	THR
1	q	93	ASN
1	q	97	LEU
1	q	130	THR
1	q	217	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	q	226	CYS
1	r	7	ASN
1	r	11	LEU
1	r	63	THR
1	r	93	ASN
1	r	97	LEU
1	r	130	THR
1	r	217	SER
1	r	226	CYS
1	s	7	ASN
1	s	10	LYS
1	s	11	LEU
1	s	63	THR
1	s	93	ASN
1	s	97	LEU
1	s	130	THR
1	s	217	SER
1	s	226	CYS
1	t	7	ASN
1	t	11	LEU
1	t	63	THR
1	t	93	ASN
1	t	97	LEU
1	t	130	THR
1	t	217	SER
1	t	226	CYS
1	v	7	ASN
1	v	10	LYS
1	v	11	LEU
1	v	63	THR
1	v	93	ASN
1	v	97	LEU
1	v	130	THR
1	v	217	SER
1	v	226	CYS
1	w	7	ASN
1	w	11	LEU
1	w	63	THR
1	w	93	ASN
1	w	97	LEU
1	w	130	THR
1	w	217	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	w	226	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (283) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	142	ASN
1	A	205	GLN
1	A	220	HIS
1	A	222	HIS
1	A	234	GLN
1	A	251	GLN
1	B	68	GLN
1	B	142	ASN
1	B	205	GLN
1	B	222	HIS
1	B	234	GLN
1	B	251	GLN
1	B	265	GLN
1	C	142	ASN
1	C	205	GLN
1	C	220	HIS
1	C	222	HIS
1	C	234	GLN
1	C	251	GLN
1	D	68	GLN
1	D	142	ASN
1	D	205	GLN
1	D	222	HIS
1	D	234	GLN
1	D	251	GLN
1	D	265	GLN
1	E	142	ASN
1	E	205	GLN
1	E	220	HIS
1	E	222	HIS
1	E	234	GLN
1	E	251	GLN
1	F	68	GLN
1	F	142	ASN
1	F	205	GLN
1	F	222	HIS
1	F	234	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	251	GLN
1	F	265	GLN
1	G	142	ASN
1	G	205	GLN
1	G	222	HIS
1	G	234	GLN
1	G	251	GLN
1	H	68	GLN
1	H	142	ASN
1	H	205	GLN
1	H	222	HIS
1	H	234	GLN
1	H	251	GLN
1	H	265	GLN
1	I	142	ASN
1	I	205	GLN
1	I	220	HIS
1	I	222	HIS
1	I	234	GLN
1	I	251	GLN
1	J	68	GLN
1	J	142	ASN
1	J	205	GLN
1	J	222	HIS
1	J	234	GLN
1	J	251	GLN
1	J	265	GLN
1	K	142	ASN
1	K	205	GLN
1	K	220	HIS
1	K	222	HIS
1	K	234	GLN
1	K	251	GLN
1	L	68	GLN
1	L	205	GLN
1	L	222	HIS
1	L	234	GLN
1	L	251	GLN
1	L	265	GLN
1	M	142	ASN
1	M	205	GLN
1	M	220	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	M	222	HIS
1	M	234	GLN
1	M	251	GLN
1	N	68	GLN
1	N	142	ASN
1	N	205	GLN
1	N	222	HIS
1	N	234	GLN
1	N	251	GLN
1	N	265	GLN
1	O	142	ASN
1	O	205	GLN
1	O	220	HIS
1	O	222	HIS
1	O	234	GLN
1	O	251	GLN
1	P	68	GLN
1	P	142	ASN
1	P	205	GLN
1	P	222	HIS
1	P	234	GLN
1	P	251	GLN
1	P	265	GLN
1	Q	142	ASN
1	Q	205	GLN
1	Q	220	HIS
1	Q	222	HIS
1	Q	234	GLN
1	Q	251	GLN
1	R	68	GLN
1	R	142	ASN
1	R	205	GLN
1	R	222	HIS
1	R	234	GLN
1	R	251	GLN
1	R	265	GLN
1	S	142	ASN
1	S	205	GLN
1	S	220	HIS
1	S	222	HIS
1	S	234	GLN
1	S	251	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	T	68	GLN
1	T	142	ASN
1	T	205	GLN
1	T	222	HIS
1	T	234	GLN
1	T	251	GLN
1	T	265	GLN
1	V	142	ASN
1	V	205	GLN
1	V	220	HIS
1	V	222	HIS
1	V	234	GLN
1	V	251	GLN
1	W	68	GLN
1	W	142	ASN
1	W	205	GLN
1	W	222	HIS
1	W	234	GLN
1	W	251	GLN
1	W	265	GLN
1	a	142	ASN
1	a	205	GLN
1	a	220	HIS
1	a	222	HIS
1	a	234	GLN
1	a	251	GLN
1	b	68	GLN
1	b	142	ASN
1	b	205	GLN
1	b	222	HIS
1	b	234	GLN
1	b	251	GLN
1	b	265	GLN
1	c	142	ASN
1	c	205	GLN
1	c	220	HIS
1	c	222	HIS
1	c	234	GLN
1	c	251	GLN
1	d	68	GLN
1	d	142	ASN
1	d	205	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	d	222	HIS
1	d	234	GLN
1	d	251	GLN
1	d	265	GLN
1	e	142	ASN
1	e	205	GLN
1	e	220	HIS
1	e	222	HIS
1	e	234	GLN
1	e	251	GLN
1	f	68	GLN
1	f	142	ASN
1	f	205	GLN
1	f	222	HIS
1	f	234	GLN
1	f	251	GLN
1	f	265	GLN
1	g	142	ASN
1	g	205	GLN
1	g	220	HIS
1	g	222	HIS
1	g	234	GLN
1	g	251	GLN
1	h	68	GLN
1	h	142	ASN
1	h	205	GLN
1	h	222	HIS
1	h	234	GLN
1	h	251	GLN
1	h	265	GLN
1	i	142	ASN
1	i	205	GLN
1	i	220	HIS
1	i	222	HIS
1	i	234	GLN
1	i	251	GLN
1	j	68	GLN
1	j	142	ASN
1	j	205	GLN
1	j	222	HIS
1	j	234	GLN
1	j	251	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	j	265	GLN
1	k	142	ASN
1	k	205	GLN
1	k	222	HIS
1	k	234	GLN
1	k	251	GLN
1	l	68	GLN
1	l	142	ASN
1	l	205	GLN
1	l	222	HIS
1	l	234	GLN
1	l	251	GLN
1	l	265	GLN
1	m	142	ASN
1	m	205	GLN
1	m	220	HIS
1	m	222	HIS
1	m	234	GLN
1	m	251	GLN
1	n	68	GLN
1	n	142	ASN
1	n	205	GLN
1	n	222	HIS
1	n	234	GLN
1	n	251	GLN
1	n	265	GLN
1	o	142	ASN
1	o	205	GLN
1	o	220	HIS
1	o	222	HIS
1	o	234	GLN
1	o	251	GLN
1	p	68	GLN
1	p	142	ASN
1	p	205	GLN
1	p	222	HIS
1	p	234	GLN
1	p	251	GLN
1	p	265	GLN
1	q	142	ASN
1	q	205	GLN
1	q	220	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	q	222	HIS
1	q	234	GLN
1	q	251	GLN
1	r	68	GLN
1	r	142	ASN
1	r	205	GLN
1	r	222	HIS
1	r	234	GLN
1	r	251	GLN
1	r	265	GLN
1	s	142	ASN
1	s	205	GLN
1	s	220	HIS
1	s	222	HIS
1	s	234	GLN
1	s	251	GLN
1	t	68	GLN
1	t	142	ASN
1	t	205	GLN
1	t	222	HIS
1	t	234	GLN
1	t	251	GLN
1	t	265	GLN
1	v	142	ASN
1	v	205	GLN
1	v	220	HIS
1	v	222	HIS
1	v	234	GLN
1	v	251	GLN
1	w	68	GLN
1	w	142	ASN
1	w	205	GLN
1	w	222	HIS
1	w	234	GLN
1	w	251	GLN
1	w	265	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

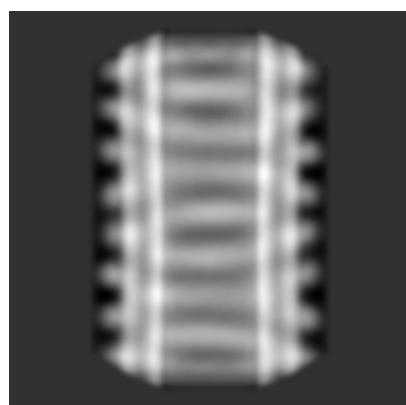
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20835. These allow visual inspection of the internal detail of the map and identification of artifacts.

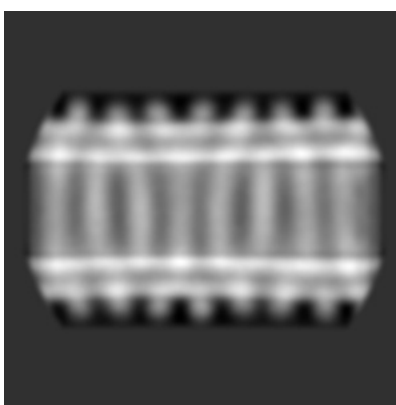
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

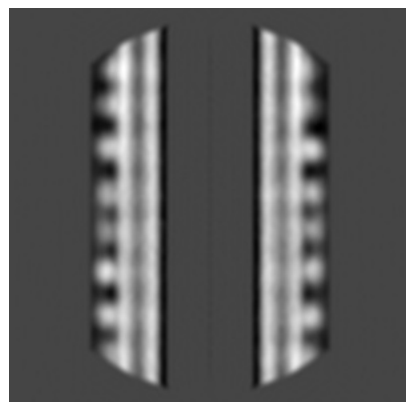


Z

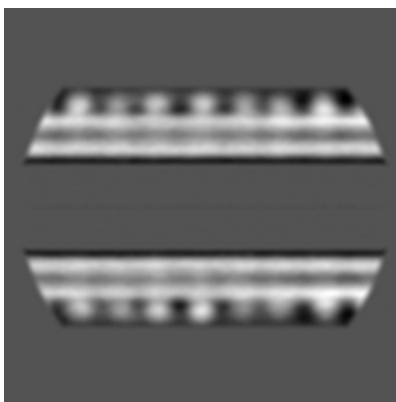
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

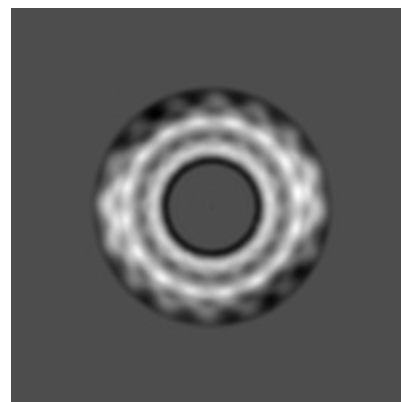
6.2.1 Primary map



X Index: 107



Y Index: 107

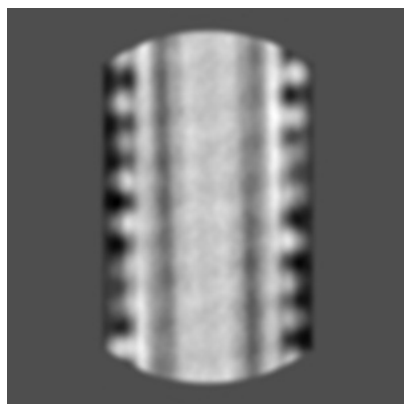


Z Index: 107

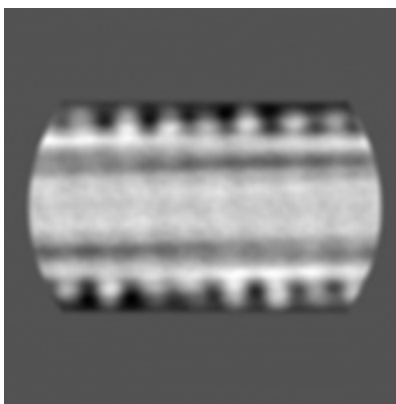
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

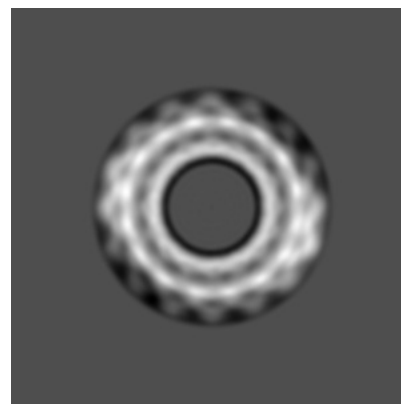
6.3.1 Primary map



X Index: 137



Y Index: 137

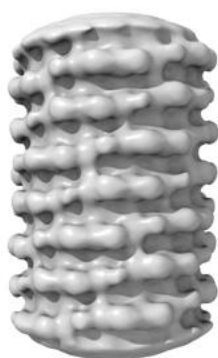


Z Index: 80

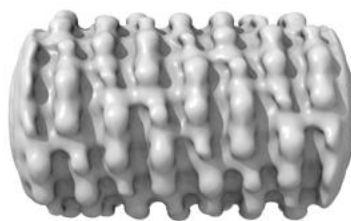
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.009. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

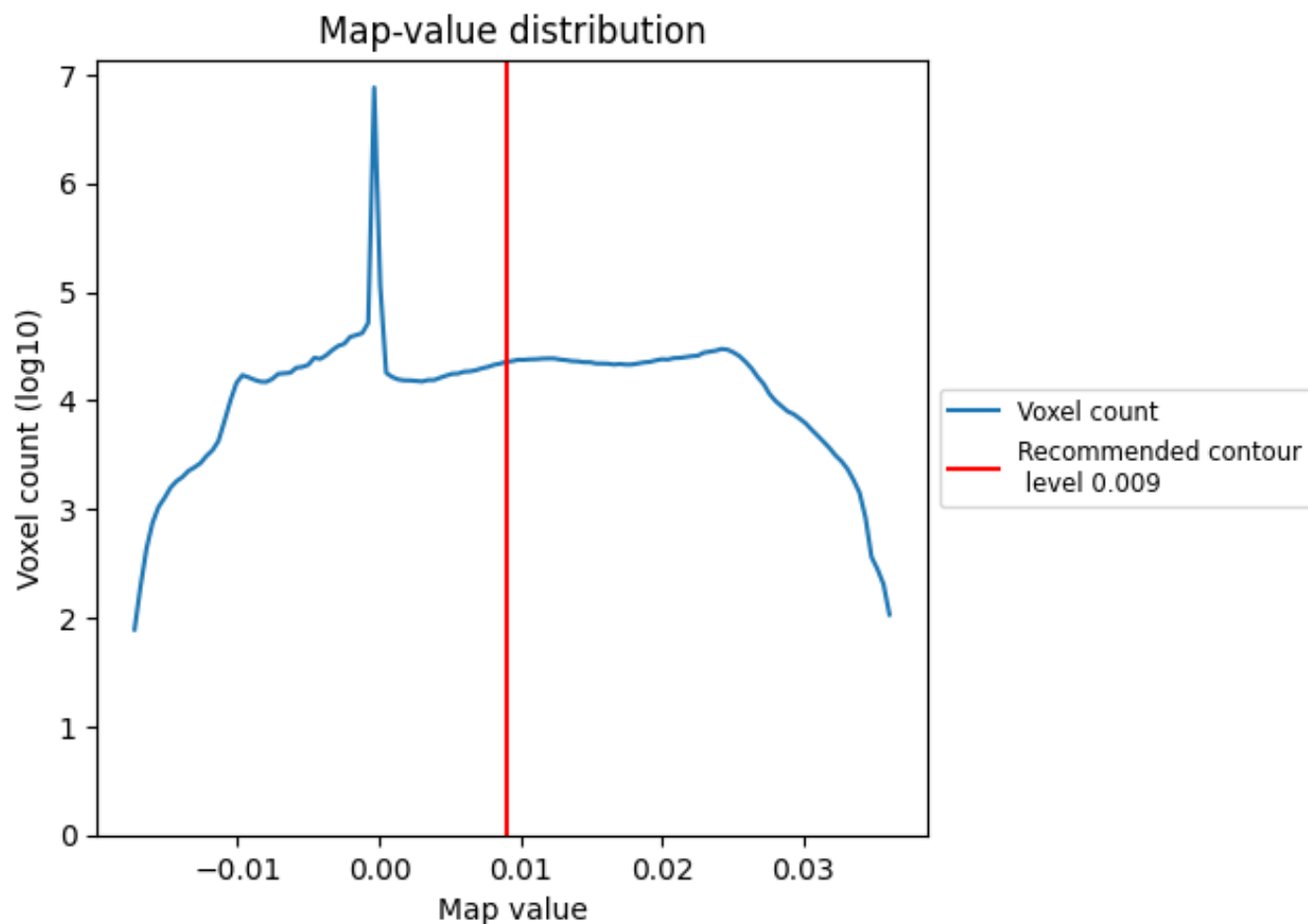
6.5 Mask visualisation

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

7 Map analysis [i](#)

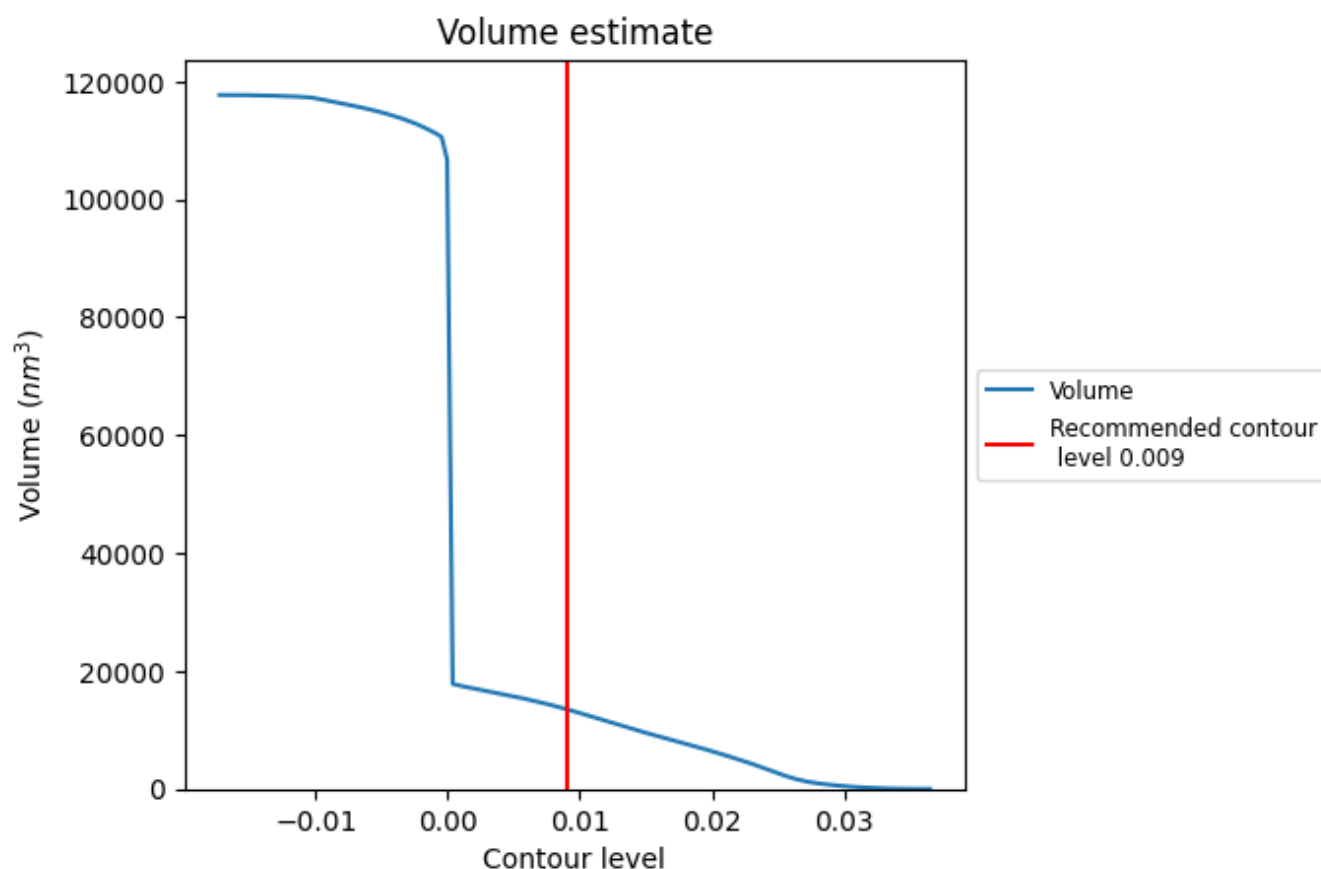
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

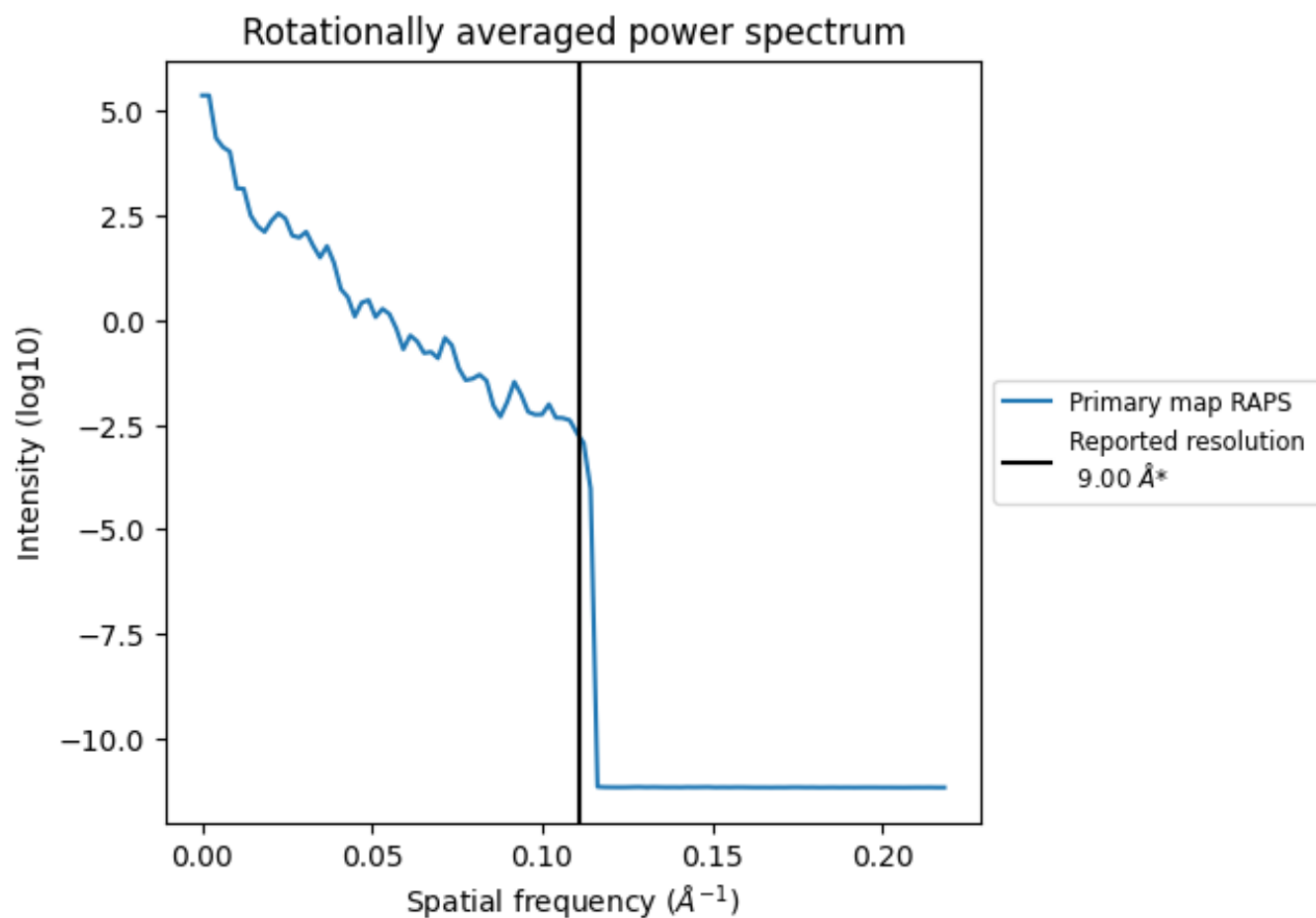
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 13522 nm^3 ; this corresponds to an approximate mass of 12215 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 0.111 Å⁻¹

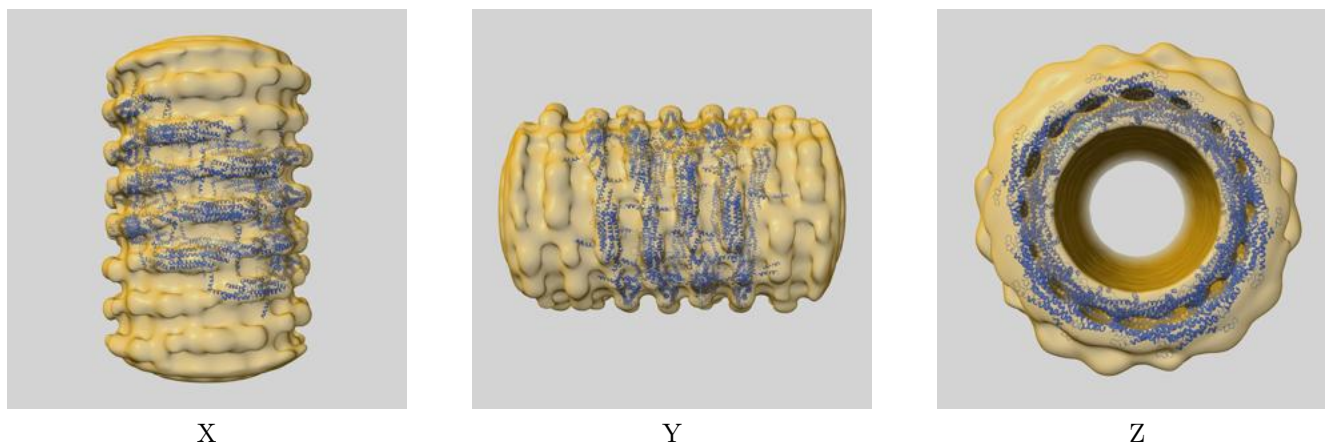
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

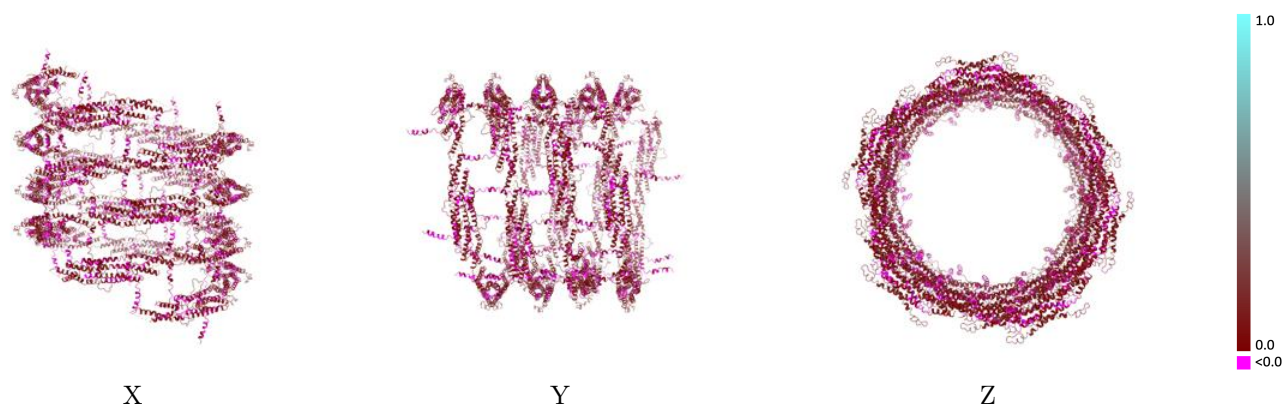
This section contains information regarding the fit between EMDB map EMD-20835 and PDB model 6UP6. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



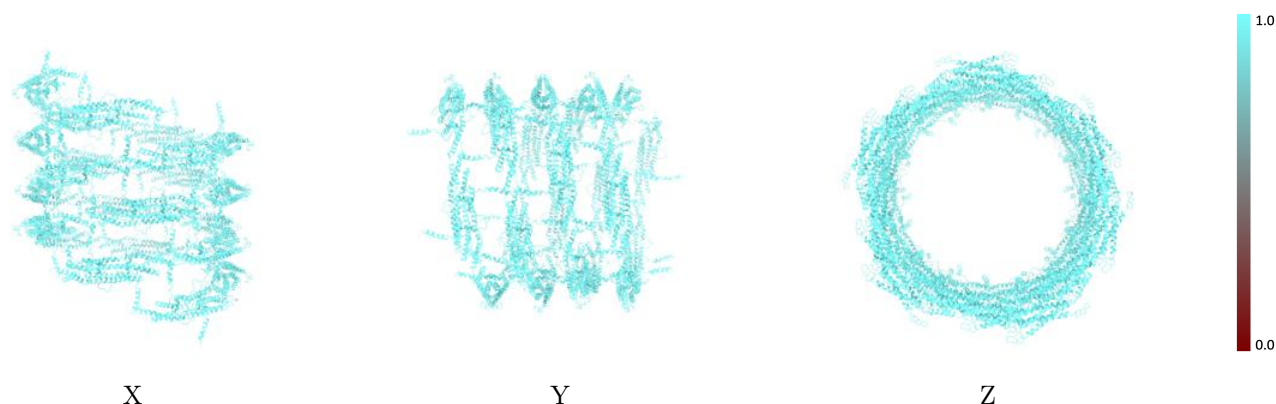
The images above show the 3D surface view of the map at the recommended contour level 0.009 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



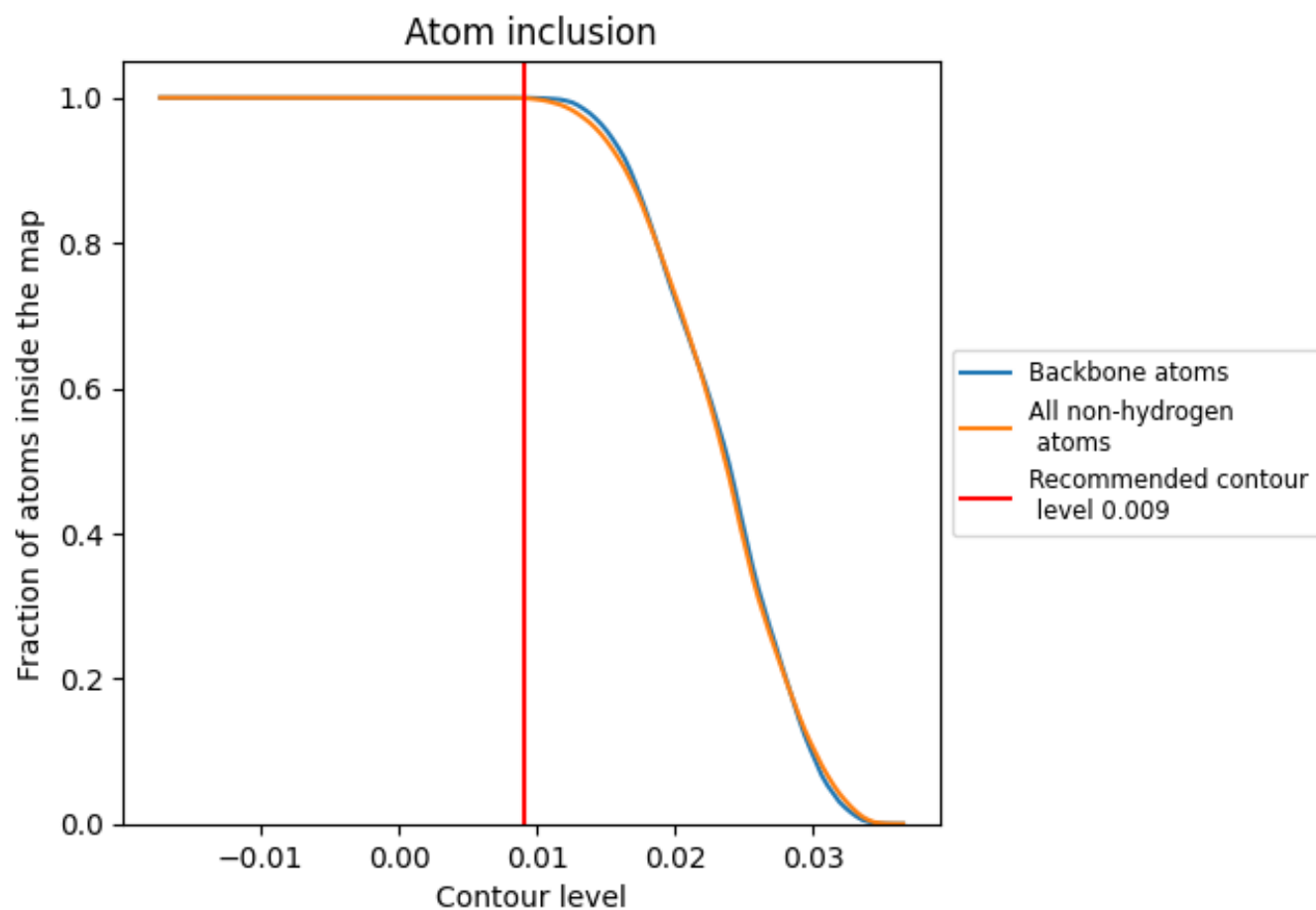
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.009).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 100% 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 (0.009) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9994	 0.0610
A	 1.0000	 0.0600
B	 0.9969	 0.0550
C	 0.9995	 0.0620
D	 0.9995	 0.0560
E	 1.0000	 0.0620
F	 0.9995	 0.0560
G	 1.0000	 0.0650
H	 0.9995	 0.0580
I	 1.0000	 0.0640
J	 0.9969	 0.0550
K	 1.0000	 0.0620
L	 0.9969	 0.0530
M	 0.9995	 0.0630
N	 0.9984	 0.0550
O	 0.9995	 0.0620
P	 1.0000	 0.0550
Q	 1.0000	 0.0630
R	 1.0000	 0.0520
S	 1.0000	 0.0660
T	 0.9995	 0.0530
V	 1.0000	 0.0660
W	 0.9974	 0.0500
a	 1.0000	 0.0590
b	 0.9974	 0.0680
c	 1.0000	 0.0590
d	 0.9995	 0.0700
e	 1.0000	 0.0590
f	 0.9995	 0.0690
g	 1.0000	 0.0580
h	 0.9990	 0.0650
i	 1.0000	 0.0600
j	 0.9990	 0.0630
k	 1.0000	 0.0620
l	 0.9990	 0.0640



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
m	 1.0000	 0.0620
n	 0.9995	 0.0670
o	 1.0000	 0.0610
p	 1.0000	 0.0650
q	 1.0000	 0.0590
r	 0.9995	 0.0650
s	 1.0000	 0.0630
t	 0.9990	 0.0610
v	 1.0000	 0.0640
w	 0.9990	 0.0610