



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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

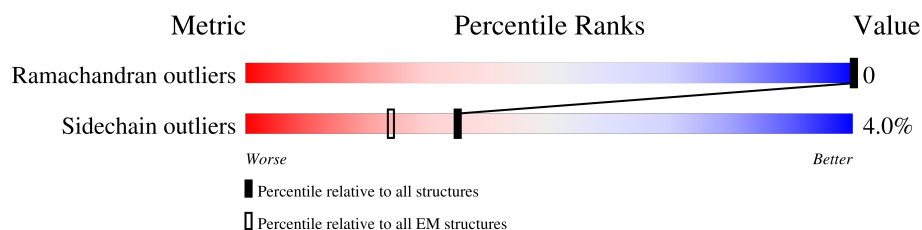
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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

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

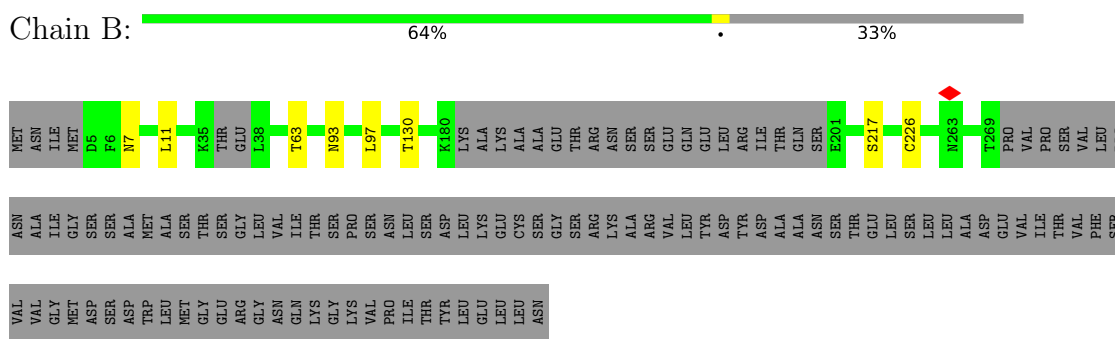
3 Residue-property plots [i](#)

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.

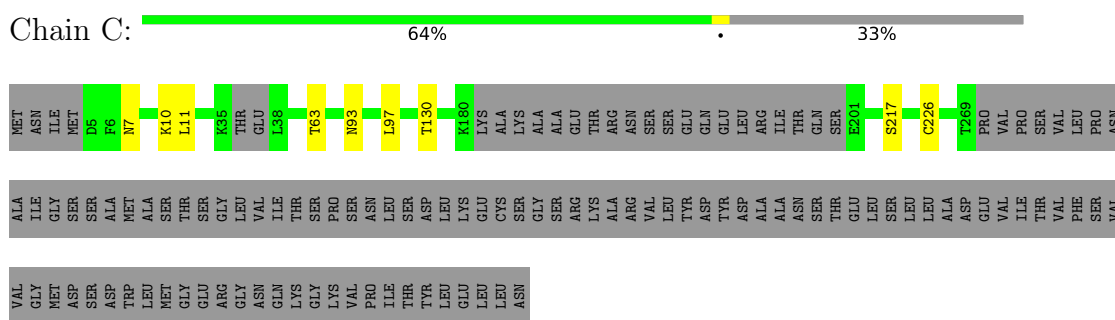
• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1

Chain D:  64% 33%

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

• Molecule 1: Endophilin-B1

Chain E:  64% 33%

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

• Molecule 1: Endophilin-B1

Chain F:  64% 33%

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

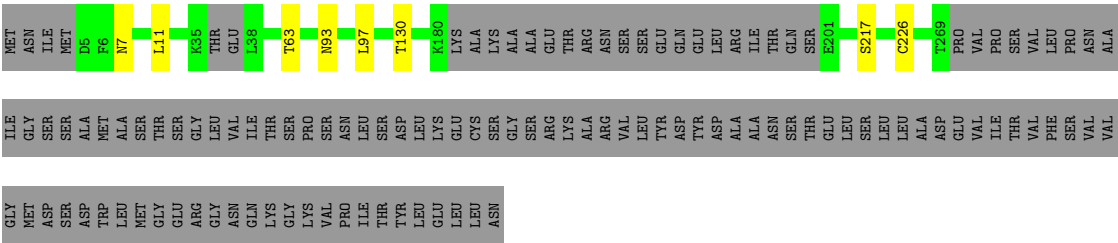
• Molecule 1: Endophilin-B1

Chain G:  64% 33%

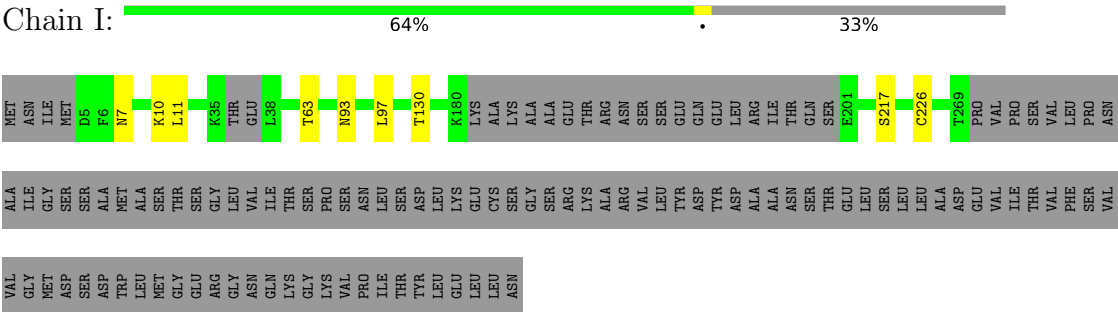
MET	ASN	ILE	MET	D5	F6	N7	K10	L11	K35	THR	GLU	L38	T63	N93	L97	T130	K180	LYS	ALA	LYS	ALA	ALA	GLU	THR	ARG	ASN	SER	SER	LEU	TYR	ASP	LEU	LYS	LYS	GLU	CYS	GLY	SER	ARG	LYS	ALA	ARG	VAL	SER	LEU	TYR	ASP	ALA	ALA	ASN	SER	THR	GLN	SER	E201	S217	C226	T269	PRO	VAL	PRO	SER	VAL	LEU	PRO	ASN																														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

• Molecule 1: Endophilin-B1

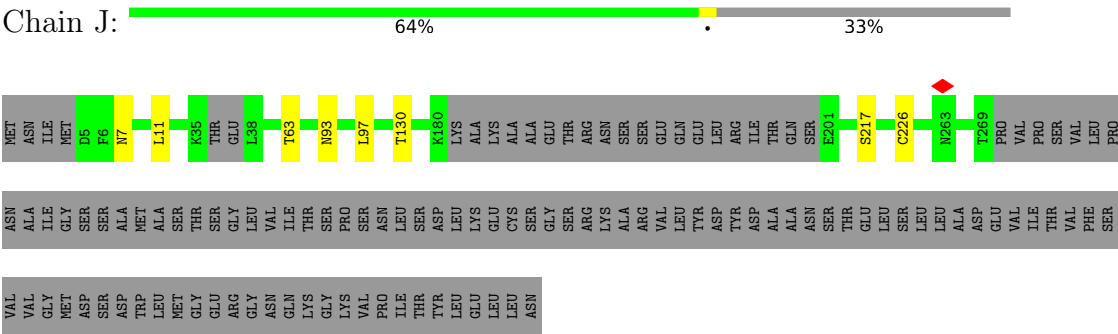
Chain H:  64% 33%



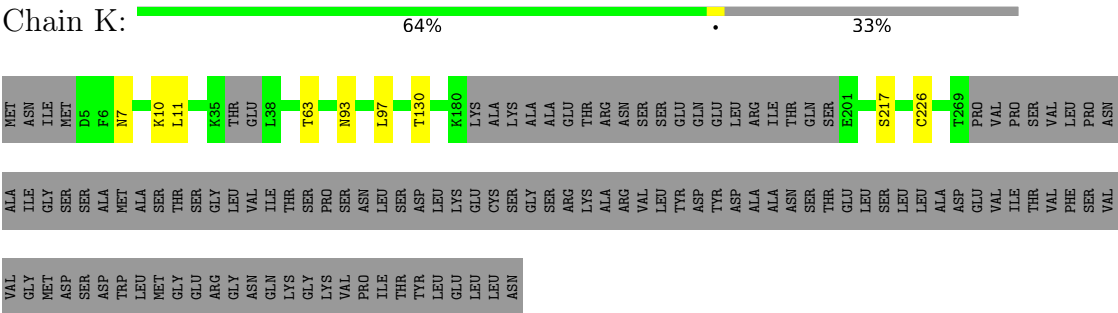
• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1

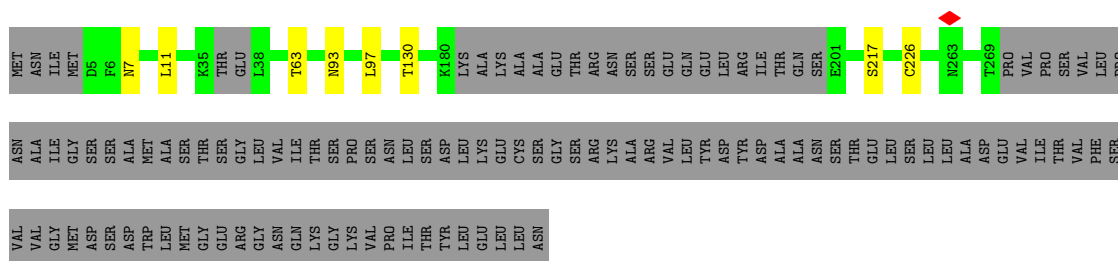


• Molecule 1: Endophilin-B1



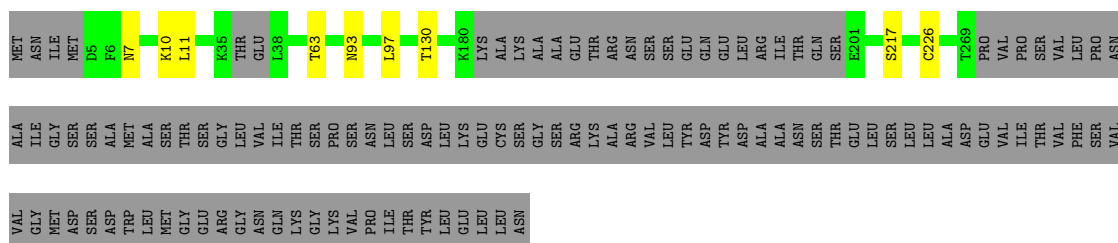
• Molecule 1: Endophilin-B1





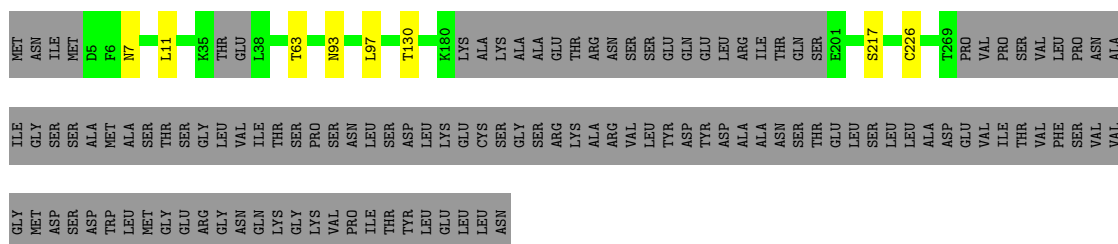
• Molecule 1: Endophilin-B1

Chain M: 64% 33%



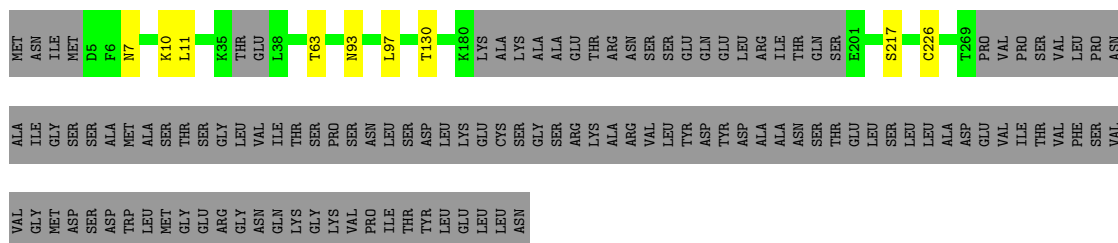
• Molecule 1: Endophilin-B1

Chain N: 64% 33%



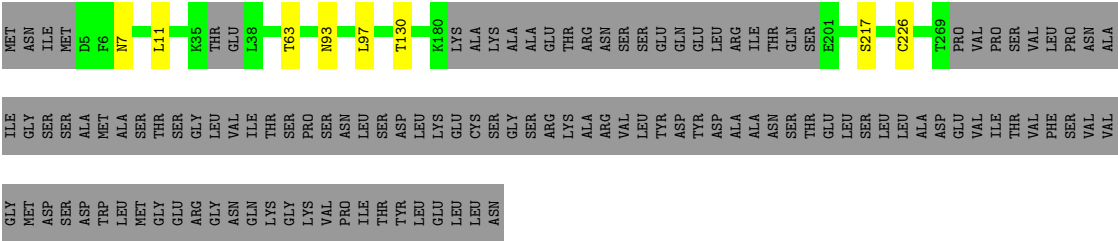
• Molecule 1: Endophilin-B1

Chain O: 64% 33%

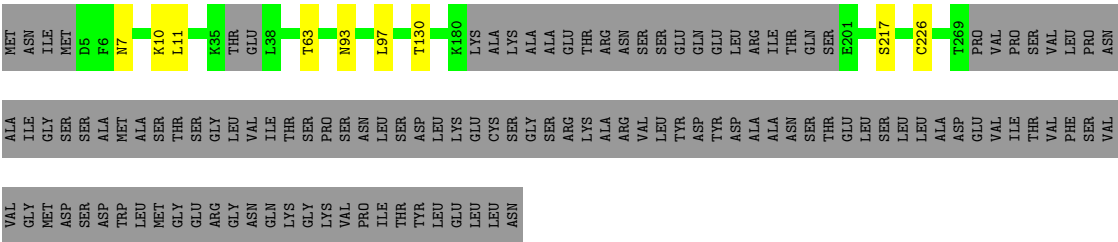


• Molecule 1: Endophilin-B1

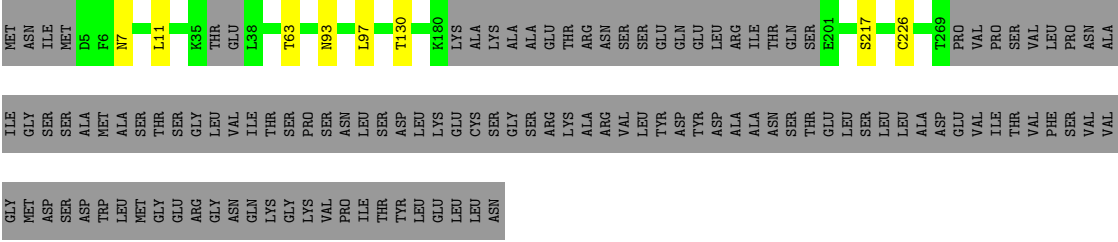
Chain P: 64% 33%



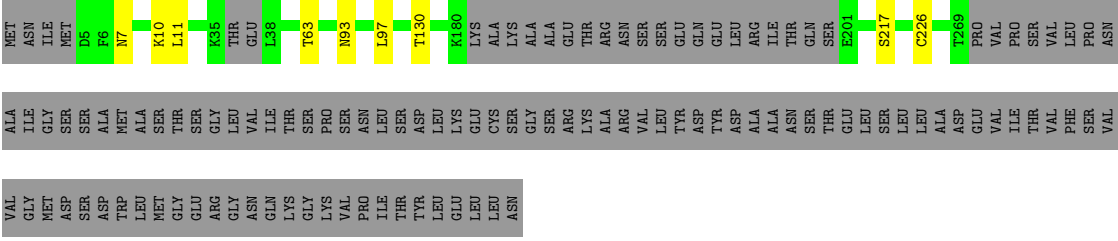
• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1



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

- Molecule 1: Endophilin-B1

Chain V: 64% . 33%

[illegible]

- Molecule 1: Endophilin-B1

Chain W: 64% 33%

[illegible]

- Molecule 1: Endophilin-B1

Chain a: 64% 33%

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

- Molecule 1: Endophilin-B1

Chain b:  64% 33%

[illegible]

- Molecule 1: Endophilin-B1

Chain c: 64% . 33%

ME1	ASW	ME1	D5	F6	N7		K10	L11		K35	THR	GLU	L38		T63		N93	L97		T130	K160	LYS	ALA	ALA	ALA	ALA	ALA	GLU	GLU	THR	ARG	ASN	SER	SER	GLU	GLN	GLU	LEU	ARG	ILE	THR	GLN	S201	E201		S217	C236	T269	PRO	VAL	PRO	SER	PRO	VAL	LEU	PRO	ASN
-----	-----	-----	----	----	----	--	-----	-----	--	-----	-----	-----	-----	--	-----	--	-----	-----	--	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	--	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

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

- Molecule 1: Endophilin-B1

Chain d: 64% . 33%

NET	ASN	ILE	MET	D5	F6	N7	L11	K35	THR	GLU	L38	T63	N83	L97	T130	K130	LYS	ALA	LYS	ALA	ALA	ALA	GLU	THR	ARG	ASN	SER	SER	SER	GLU	GLN	GLU	GLU	LEU	LEU	ARG	ARG	ILE	THR	GLN	THR	SER	SER	E201	S217	C226	T269	PRO	VAL	PRO	PRO	SER	VAL	LEU	PRO	PRO	ASN	ALA
-----	-----	-----	-----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

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

- Molecule 1: Endophilin-B1

Chain e: 64% . 33%

ME1	ME2	ME3	ME4	ME5	ME6	ME7	ME8	ME9	ME10	ME11	ME12	ME13	ME14	ME15	ME16	ME17	ME18	ME19	ME20	ME21	ME22	ME23	ME24	ME25	ME26	ME27	ME28	ME29	ME30	ME31	ME32	ME33	ME34	ME35	ME36	ME37	ME38	ME39	ME40	ME41	ME42	ME43	ME44	ME45	ME46	ME47	ME48	ME49	ME50	ME51	ME52	ME53	ME54	ME55	ME56	ME57	ME58	ME59	ME60	ME61	ME62	ME63	ME64	ME65	ME66	ME67	ME68	ME69	ME70	ME71	ME72	ME73	ME74	ME75	ME76	ME77	ME78	ME79	ME80	ME81	ME82	ME83	ME84	ME85	ME86	ME87	ME88	ME89	ME90	ME91	ME92	ME93	ME94	ME95	ME96	ME97	ME98	ME99	ME100	ME101	ME102	ME103	ME104	ME105	ME106	ME107	ME108	ME109	ME110	ME111	ME112	ME113	ME114	ME115	ME116	ME117	ME118	ME119	ME120	ME121	ME122	ME123	ME124	ME125	ME126	ME127	ME128	ME129	ME130	ME131	ME132	ME133	ME134	ME135	ME136	ME137	ME138	ME139	ME140	ME141	ME142	ME143	ME144	ME145	ME146	ME147	ME148	ME149	ME150	ME151	ME152	ME153	ME154	ME155	ME156	ME157	ME158	ME159	ME160	ME161	ME162	ME163	ME164	ME165	ME166	ME167	ME168	ME169	ME170	ME171	ME172	ME173	ME174	ME175	ME176	ME177	ME178	ME179	ME180	ME181	ME182	ME183	ME184	ME185	ME186	ME187	ME188	ME189	ME190	ME191	ME192	ME193	ME194	ME195	ME196	ME197	ME198	ME199	ME200	ME201	ME202	ME203	ME204	ME205	ME206	ME207	ME208	ME209	ME210	ME211	ME212	ME213	ME214	ME215	ME216	ME217	ME218	ME219	ME220	ME221	ME222	ME223	ME224	ME225	ME226	ME227	ME228	ME229	ME230	ME231	ME232	ME233	ME234	ME235	ME236	ME237	ME238	ME239	ME240	ME241	ME242	ME243	ME244	ME245	ME246	ME247	ME248	ME249	ME250	ME251	ME252	ME253	ME254	ME255	ME256	ME257	ME258	ME259	ME260	ME261	ME262	ME263	ME264	ME265	ME266	ME267	ME268	ME269	ME270	ME271	ME272	ME273	ME274	ME275	ME276	ME277	ME278	ME279	ME280	ME281	ME282	ME283	ME284	ME285	ME286	ME287	ME288	ME289	ME290	ME291	ME292	ME293	ME294	ME295	ME296	ME297	ME298	ME299	ME300	ME301	ME302	ME303	ME304	ME305	ME306	ME307	ME308	ME309	ME310	ME311	ME312	ME313	ME314	ME315	ME316	ME317	ME318	ME319	ME320	ME321	ME322	ME323	ME324	ME325	ME326	ME327	ME328	ME329	ME330	ME331	ME332	ME333	ME334	ME335	ME336	ME337	ME338	ME339	ME340	ME341	ME342	ME343	ME344	ME345	ME346	ME347	ME348	ME349	ME350	ME351	ME352	ME353	ME354	ME355	ME356	ME357	ME358	ME359	ME360	ME361	ME362	ME363	ME364	ME365	ME366	ME367	ME368	ME369	ME370	ME371	ME372	ME373	ME374	ME375	ME376	ME377	ME378	ME379	ME380	ME381	ME382	ME383	ME384	ME385	ME386	ME387	ME388	ME389	ME390	ME391	ME392	ME393	ME394	ME395	ME396	ME397	ME398	ME399	ME400	ME401	ME402	ME403	ME404	ME405	ME406	ME407	ME408	ME409	ME410	ME411	ME412	ME413	ME414	ME415	ME416	ME417	ME418	ME419	ME420	ME421	ME422	ME423	ME424	ME425	ME426	ME427	ME428	ME429	ME430	ME431	ME432	ME433	ME434	ME435	ME436	ME437	ME438	ME439	ME440	ME441	ME442	ME443	ME444	ME445	ME446	ME447	ME448	ME449	ME450	ME451	ME452	ME453	ME454	ME455	ME456	ME457	ME458	ME459	ME460	ME461	ME462	ME463	ME464	ME465	ME466
-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

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

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

- Molecule 1: Endophilin-B1

Chain f:  64% 33%

MET	ASW	D5	F6	M7	L11	K35	THR	GLU	L38	TE3	N93	L97	T130	L130	L15	ALA	ALA	ALA	ALA	GLU	THR	ARG	ASN	SER	SER	GLU	GLN	GLU	LEU	LEU	ALA	ARG	ILE	THR	GLN	SER	SER	E201	S217	C226	T269	VAL	PRO	PRO	SER	VAL	LEU	PRO	PRO	ASN	ALA
-----	-----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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

GLY MET ASP SER ASP TRP LEU MET GLY GLU ARG GLY ASN GLN LYS GLY LYS VAL PRO ILE THR TYR LEU GLU 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	ALA	MET	ALA	SER	GLY	LEU	VAL	ILE	THR	SER	PRO	LYS	GLU	CYS	GLY	SER	ARG	LYS	ALA	ALA	VAL	VAL	LEU	TYR	ASP	TYR	ASP	ALA	ALA	ASN	SER	THR	GLU	LEU	SER	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	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 h:  64% 33%

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

• Molecule 1: Endophilin-B1

Chain i:  64% 33%

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

• Molecule 1: Endophilin-B1

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

• Molecule 1: Endophilin-B1

Chain k:  64% 33%

ALA	ILE	GLY	SER	SER	ASP	ALA	MET	ALA	K10	SER	GLY	LEU	VAL	ILE	THR	SER	PRO	SER	ASN	LEU	SER	ASP	LEU	LYS	GLY	CYS	GLY	SER	ARG	LYS	ALA	ALA	ARG	VAL	LEU	TYR	ASP	ASP	ASP	ALA	ALA	ASN	THR	GLN	SER	THR	GLU	LEU	SER	E201	S217	C226	T269	PRO	VAL	PRO	PRO	VAL	VAL	PHE	LEU	PRO	ASN	VAL																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
VAL	GLY	MET	ASP	SER	ASP	TRP	LEU	MET	GLY	ARG	GLY	ASN	GLN	LYS	GLY	LYS	VAL	PRO	ILE	THR	TYR	LEU	GLU	LEU	LEU	LEU	ASN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										

- Molecule 1: Endophilin-B1

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

- Molecule 1: Endophilin-B1

Chain m:  64% 33%

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

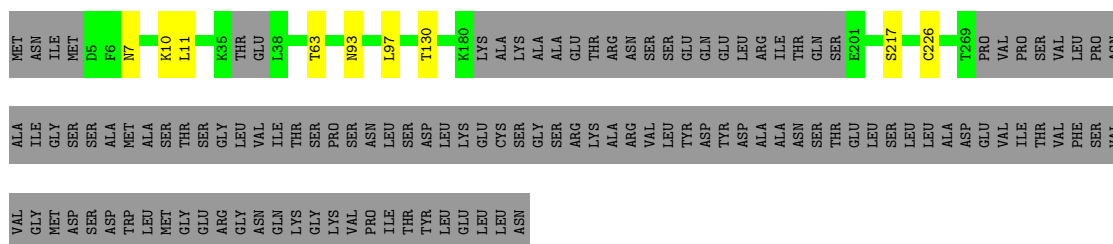
- Molecule 1: Endophilin-B1

Chain n:  64% 33%

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

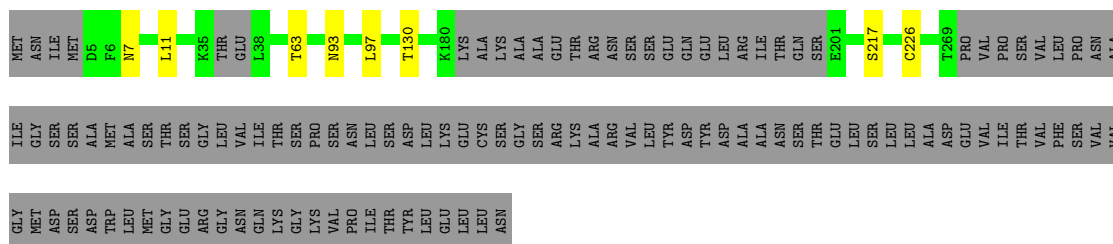
- Molecule 1: Endophilin-B1

Chain o:  64% 33%



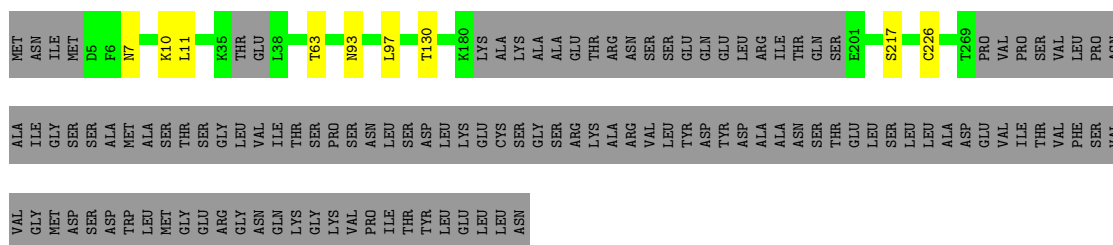
• Molecule 1: Endophilin-B1

Chain p: 64% 33%



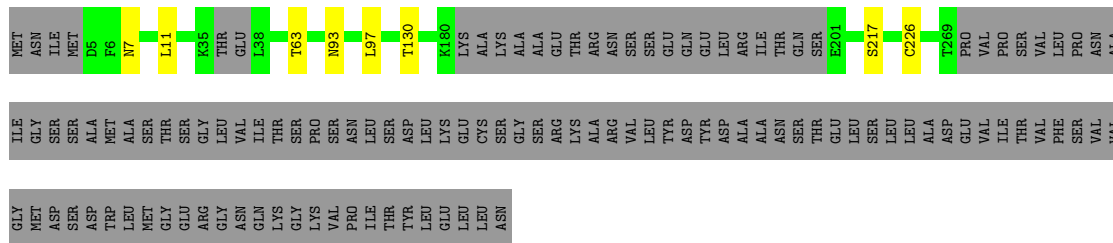
• Molecule 1: Endophilin-B1

Chain q: 64% 33%



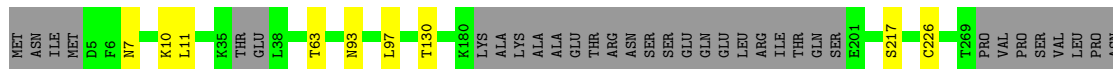
• Molecule 1: Endophilin-B1

Chain r: 64% 33%

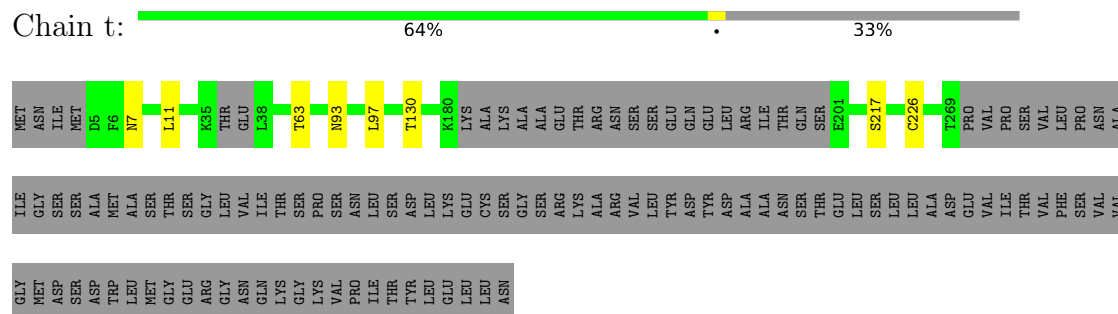


• Molecule 1: Endophilin-B1

Chain s: 64% 33%



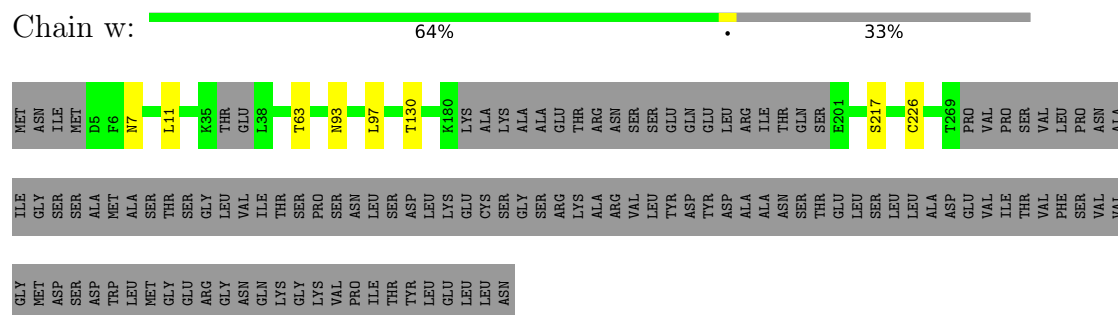
- Molecule 1: Endophilin-B1



- Molecule 1: Endophilin-B1



- Molecule 1: Endophilin-B1



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 ⓘ

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

5 of 374 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	f	11	LEU
1	l	130	THR
1	g	7	ASN
1	i	97	LEU
1	n	63	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 283 such sidechains are listed below:

Mol	Chain	Res	Type
1	o	142	ASN
1	p	142	ASN
1	s	222	HIS
1	P	205	GLN
1	O	251	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

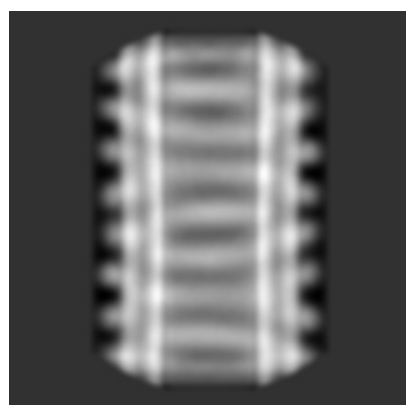
6 Map visualisation [i](#)

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.

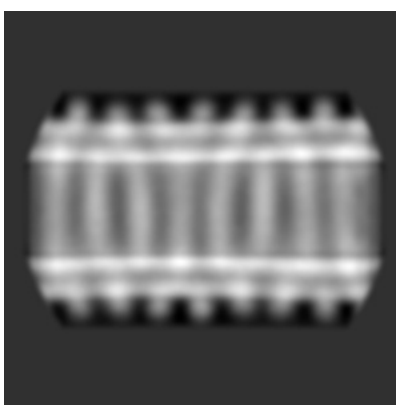
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

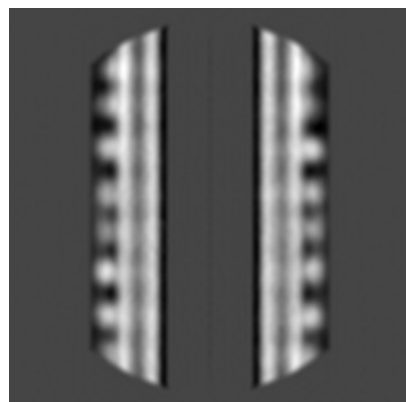


Z

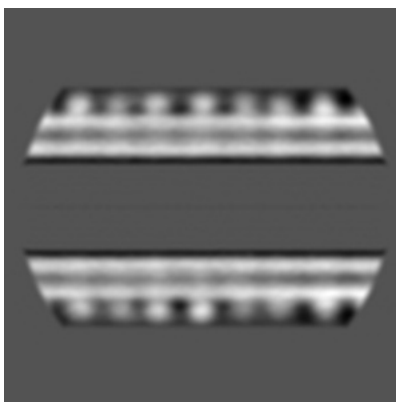
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

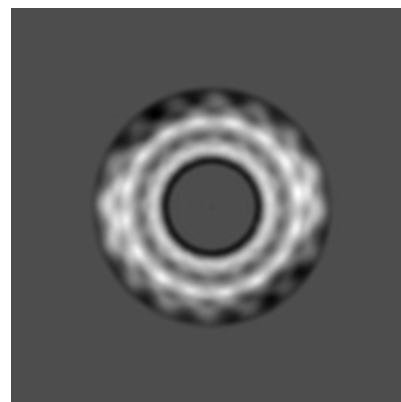
6.2.1 Primary map



X Index: 107



Y Index: 107

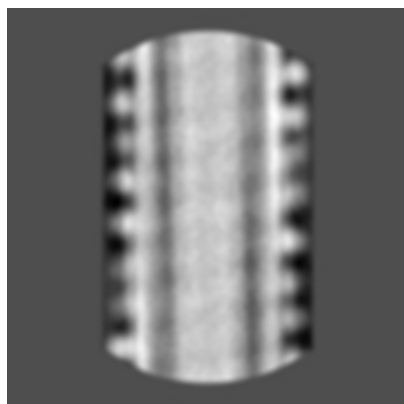


Z Index: 107

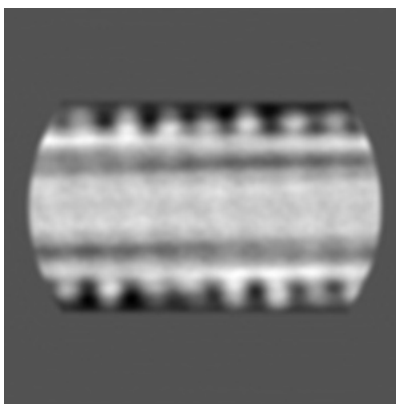
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

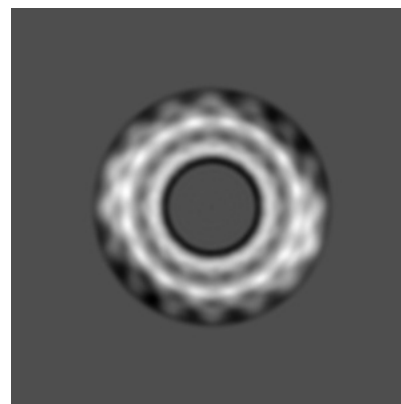
6.3.1 Primary map



X Index: 137



Y Index: 137

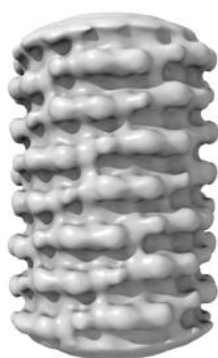


Z Index: 80

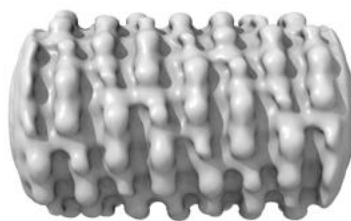
The images above show the largest variance slices of the map in three orthogonal directions.

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.

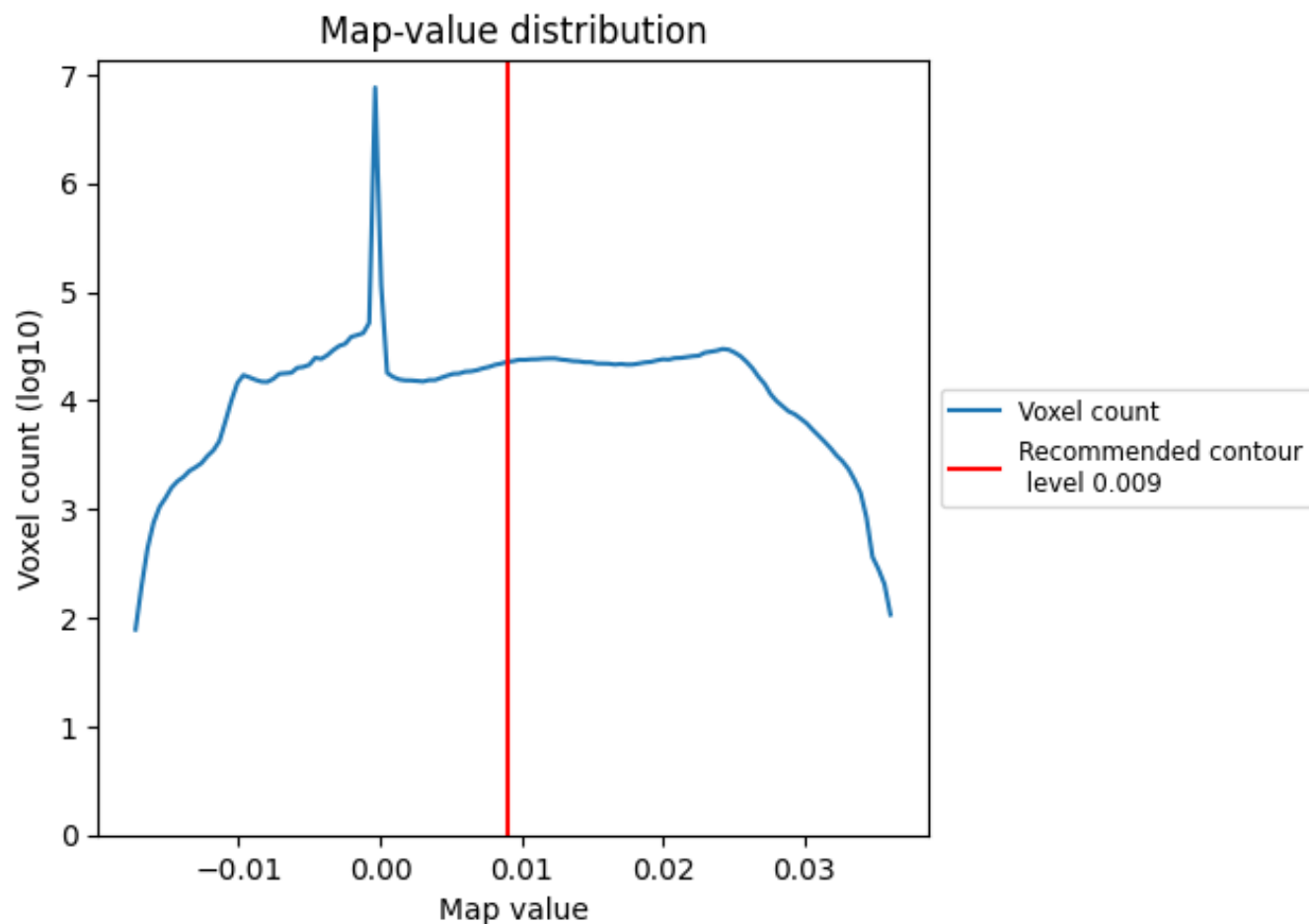
6.5 Mask visualisation

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

7 Map analysis [i](#)

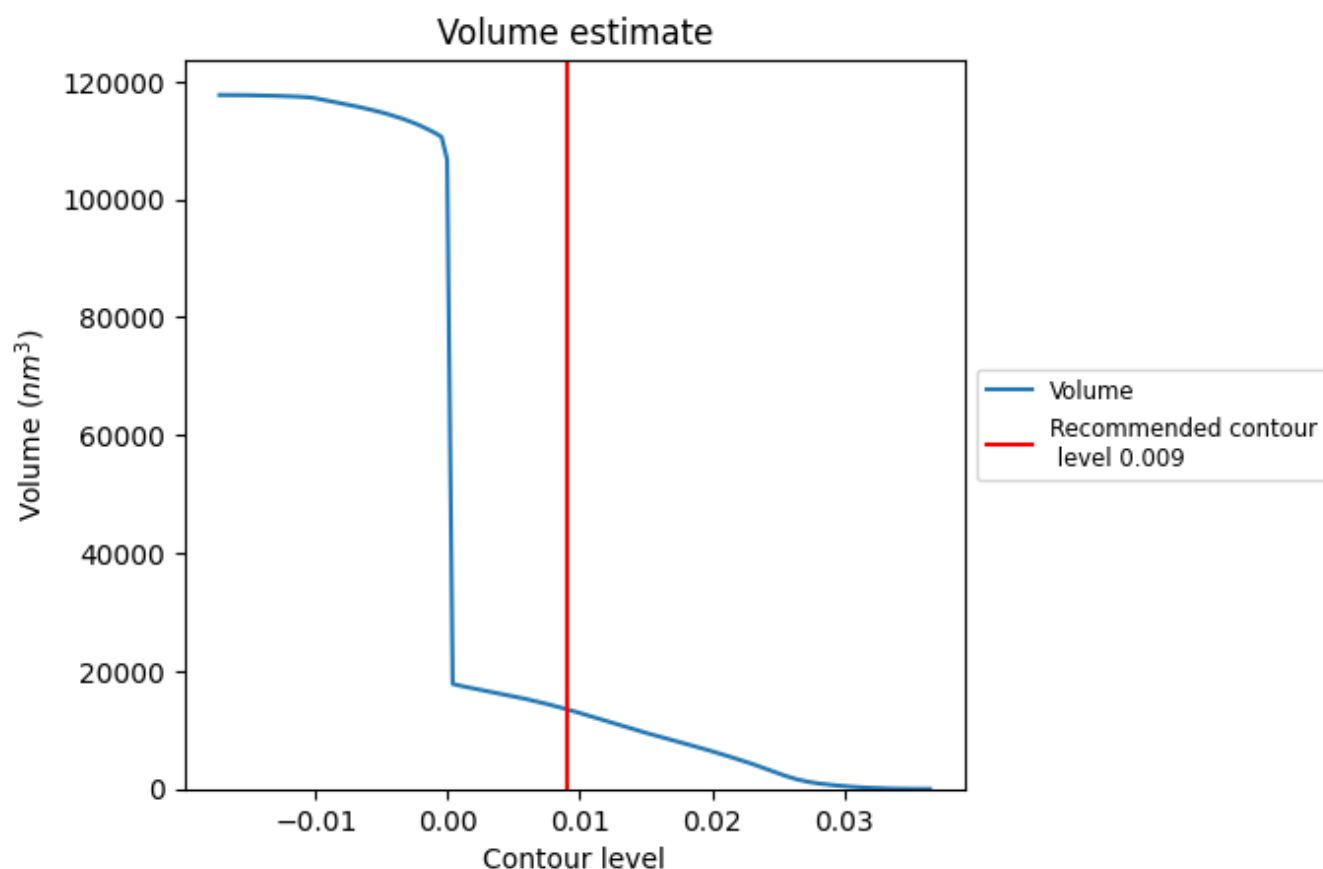
This section contains the results of statistical analysis of the map.

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.

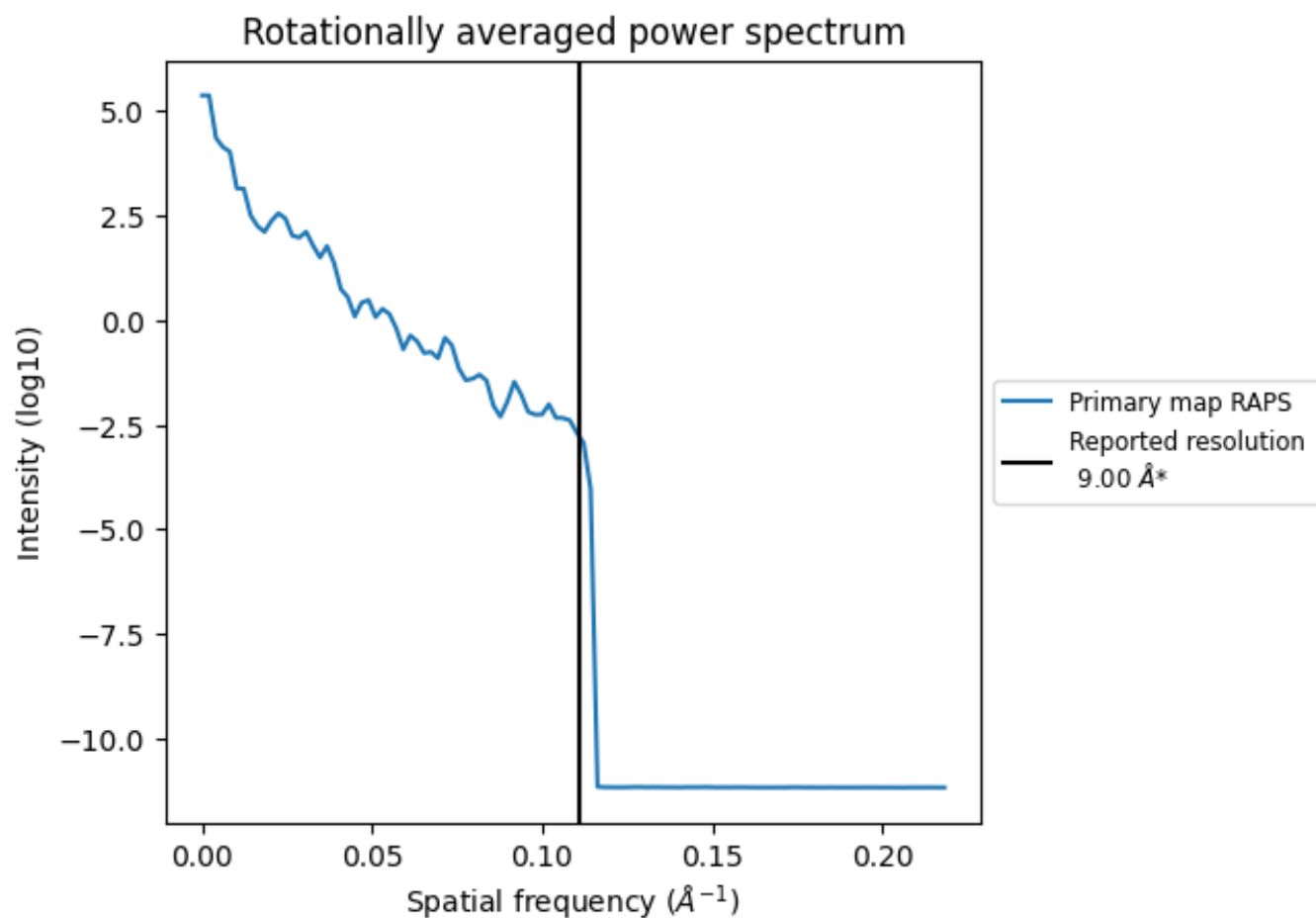
7.2 Volume estimate [i](#)



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

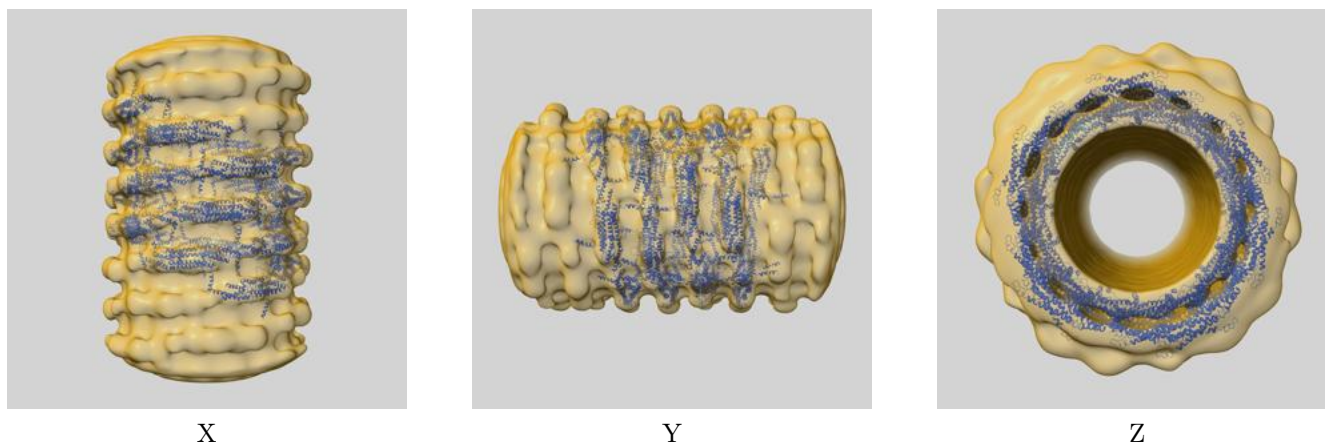
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

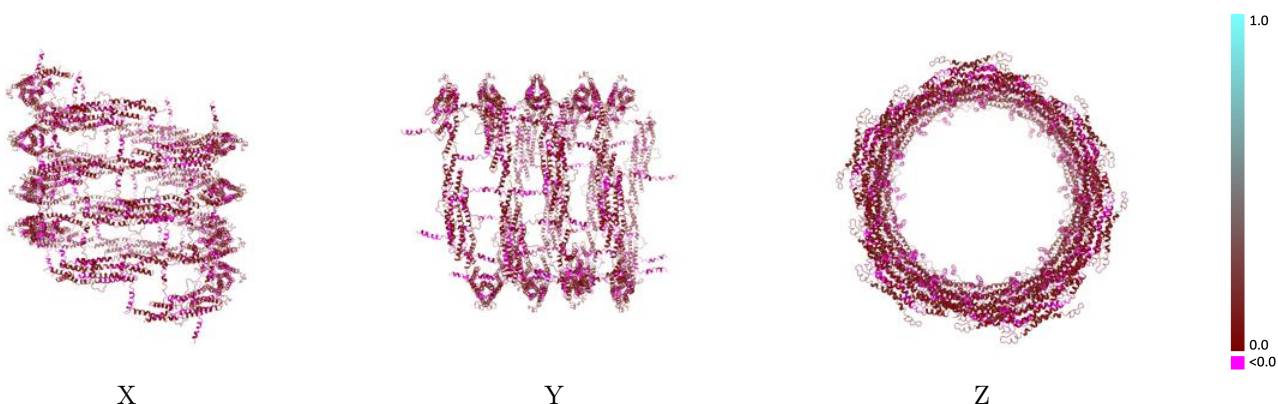
This section contains information regarding the fit between EMDB map EMD-20835 and PDB model 6UP6. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



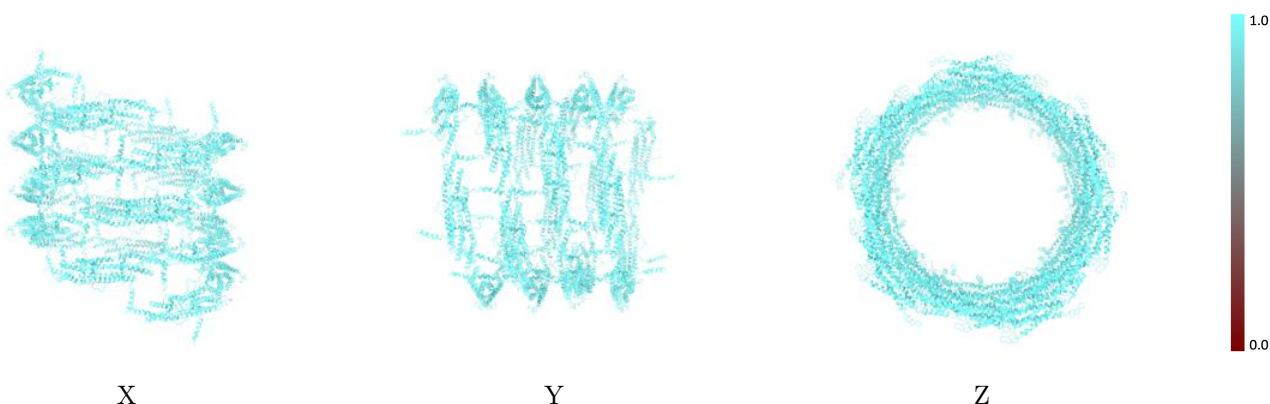
The images above show the 3D surface view of the map at the recommended contour level 0.009 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



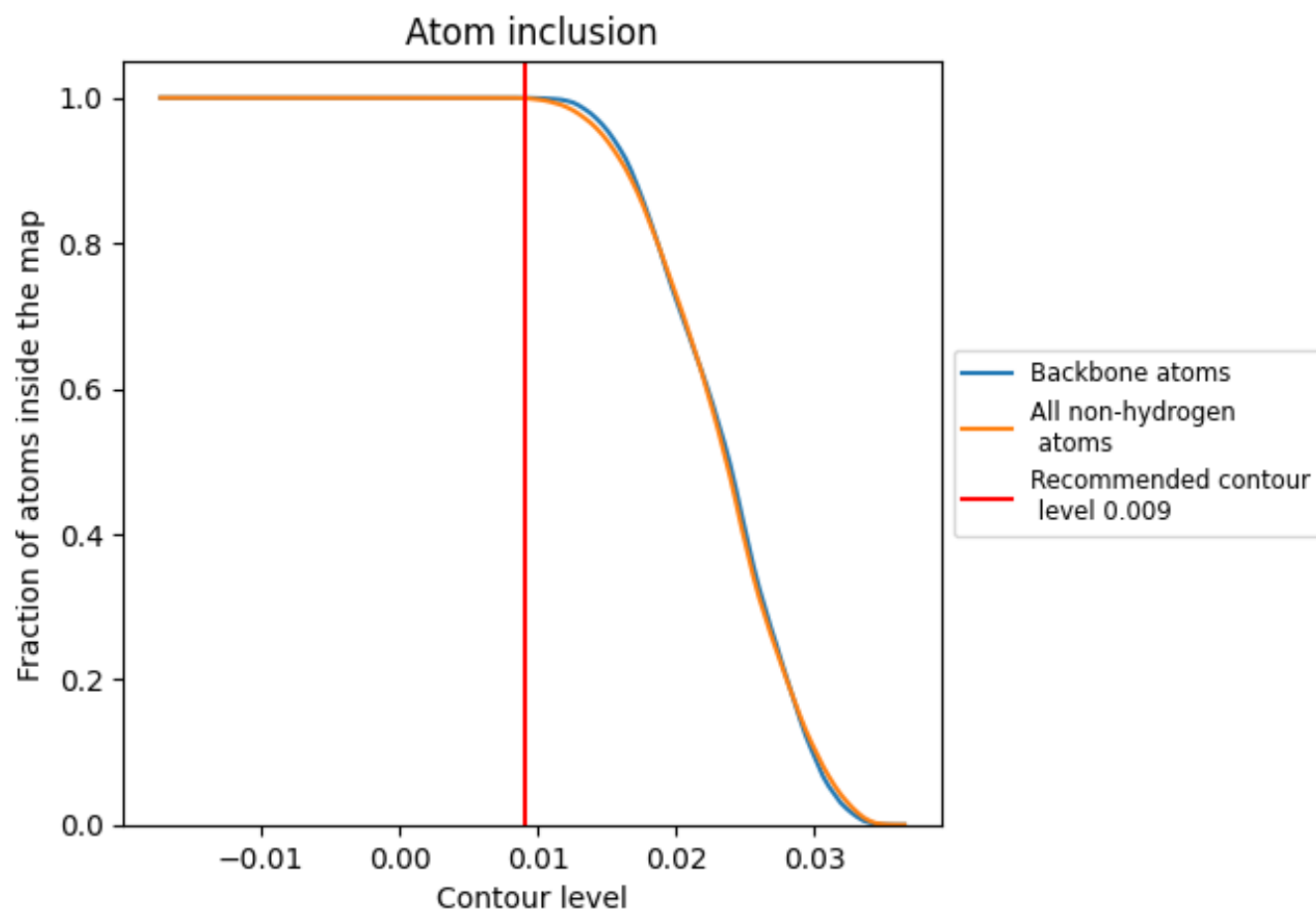
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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







































































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