



## Full wwPDB EM Validation Report ⓘ

Nov 12, 2022 – 07:11 AM EST

PDB ID : 6UPN  
EMDB ID : EMD-20842  
Title : Endophilin B1 helical scaffold  
Authors : Bhatt, V.S.; Sundborger-Lunna, A.C.  
Deposited on : 2019-10-17  
Resolution : 10.00 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](mailto: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>.

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

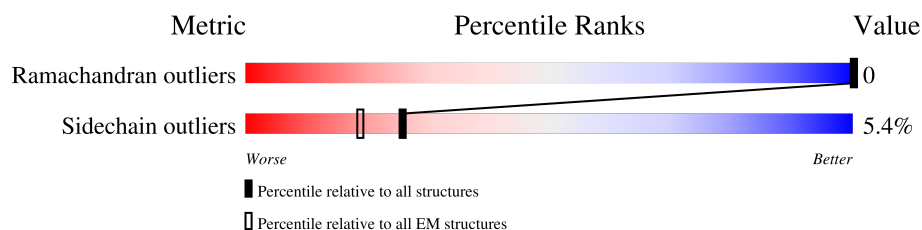
EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 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 10.00 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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

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	

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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	X	365	
1	Y	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	

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Mol	Chain	Length	Quality of chain
1	k	365	 64%33%
1	l	365	 64%33%
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%
1	x	365	 64%33%
1	y	365	 64%33%

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 94224 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	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	B	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	C	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	D	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	E	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	F	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	G	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	H	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	I	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	J	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	K	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	L	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	M	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	N	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	O	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	P	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	Q	245	Total 1963	C 1234	N 342	O 379	S 8	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	S	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	T	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	V	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	W	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	X	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	Y	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	a	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	b	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	c	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	d	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	e	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	f	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	g	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	h	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	i	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	j	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	k	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	l	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	m	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	n	245	Total 1963	C 1234	N 342	O 379	S 8	0	0

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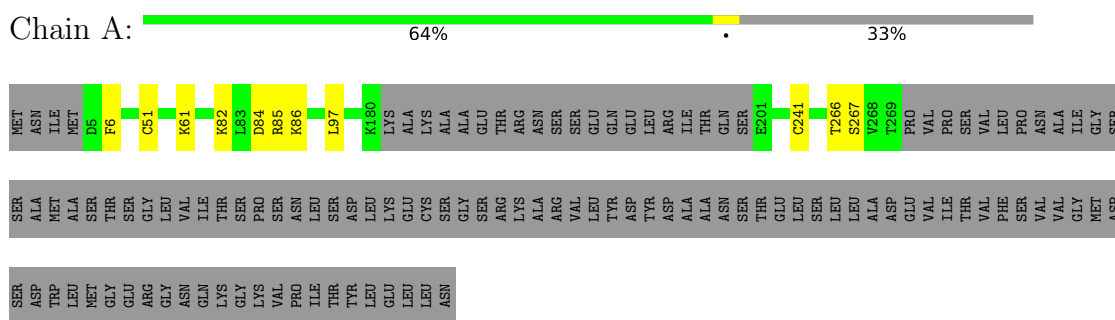
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	o	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	p	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	q	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	r	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	s	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	t	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	v	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	w	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	x	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	y	245	Total 1963	C 1234	N 342	O 379	S 8	0	0

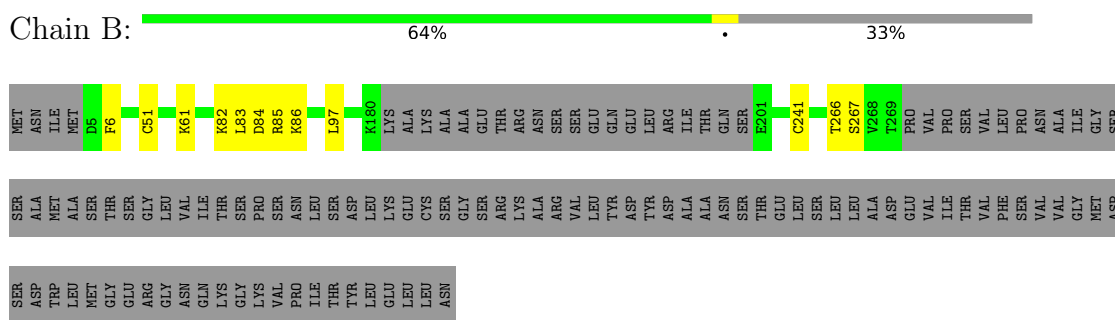
### 3 Residue-property plots [i](#)

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.

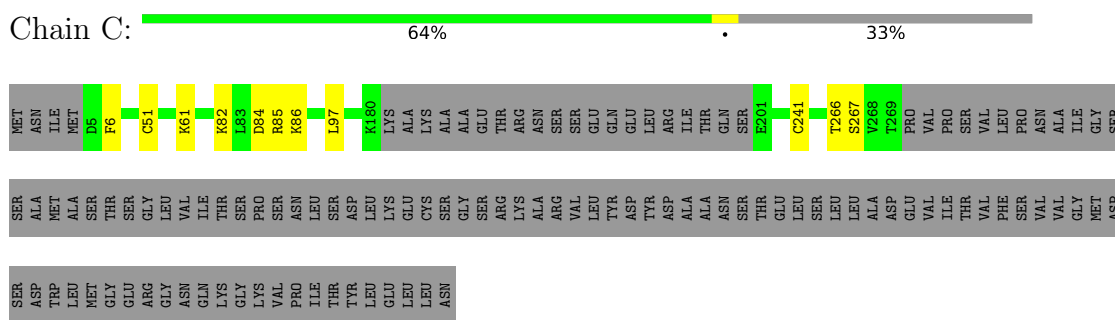
#### • Molecule 1: Endophilin-B1



#### • Molecule 1: Endophilin-B1



#### • Molecule 1: Endophilin-B1



#### • Molecule 1: Endophilin-B1



Chain D:  64% 33%

MET	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	LYS	ASN	SER	SER	GLU	GLN	GLU	LEU	ARG	ILE	THR	GLN	ASN	SER	E201	C241	T266	S267	V268	T289	PRO	VAL	PRO	SER	THR	VAL	PHE	LEU	VAL	ASN	ALA	ILE	GLY	MET
SER	ALA	MET	ALA	SER	THR	SER	GLY	LEU	VAL	ILE	THR	SER	ASP	LEU	LYS	GLU	CYS	GLY	SER	ARG	LYS	ALA	ASN	ARG	VAL	LEU	TYR	ASP	GLU	TYR	ASP	ALA	THR	GLN	THR	LEU	SER	LEU	VAL	ILE	THR	VAL	PHE	SER	VAL	ASN	ALA	ILE	GLY	MET					
SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLN	LYS	GLY	VAL	PRO	ILE	THR	TYR	LEU	GLU	LEU	LEU	LEU	ASN																																		

• Molecule 1: Endophilin-B1

Chain E:  64% 33%

SER	ALA	MET	ALA	SER	THR	SER	GLY	VAL	ILE	THR	PRO	SER	ASN	LEU	SER	ASP	LYS	GLU	CYS	SER	GLY	ARG	LYS	ALA	ARG	VAL	LEU	TYR	ASP	TYR	ASP	ALA	ALA	ASN	SER	THR	GLN	GLU	LEU	THR	GLN	SER	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	SER	THR	VAL	PHE	LEU	PRO	ASN	ALA	ILE	GLY	MET																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLN	LYS	GLY	LYS	VAL	PRO	ILE	THR	TYR	LEU	GLU	LEU	LEU	ASN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												

• Molecule 1: Endophilin-B1

Chain F:  64% 33%

MET	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	LYS	ASN	SER	SER	GLU	GLN	LEU	GLU	LEU	THR	GLN	ASN	SER	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	SER	THR	VAL	PHE	LEU	VAL	ASN	ALA	ILE	GLY	MET
SER	ALA	MET	ALA	SER	THR	SER	GLY	THR	SER	PRO	SER	ASN	LEU	SER	ASP	LEU	LYS	CYS	GLY	SER	ARG	LYS	ALA	ASN	ARG	VAL	LEU	TYR	ASP	GLU	TYR	ASP	ALA	ALA	ASN	SER	THR	GLU	LEU	SER	LEU	VAL	ILE	THR	VAL	PHE	SER	VAL	ASN	VAL	ALA	ILE	GLY	MET
SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLN	LYS	GLY	VAL	PRO	ILE	THR	TYR	LEU	GLU	LEU	LEU	LEU	ASN																																	

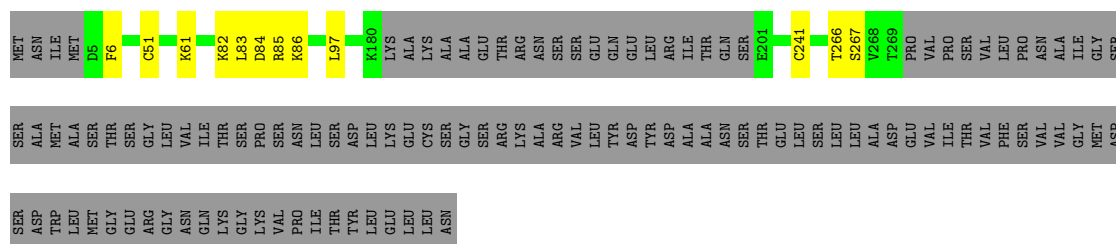
• Molecule 1: Endophilin-B1

Chain G:  64% 33%

SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLY	ASN	GLN	LYS	GLY	VAL	PRO	ILE	THR	TYR	LEU	GLU	LEU	LEU	ASN																																						
SER	ALA	MET	ALA	SER	THR	SER	GLY	LEU	VAL	ILE	THR	SER	PRO	SER	ASN	LEU	ASP	LEU	LYS	GLU	CYS	SER	GLY	ARG	LYS	ALA	ARG	VAL	LEU	TYR	ASP	THR	GLU	THR	LEU	THR	ASP	ALA	ASN	SER	THR	GLU	SER	LEU	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	LEU	VAL	ASN	ALA	ILE	GLY	MET
MET	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	LYS	ASN	SER	SER	GLU	GLN	LEU	GLU	LEU	THR	GLN	ASN	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	SER	THR	VAL	PHE	LEU	VAL	ASN	ALA	ILE	GLY								

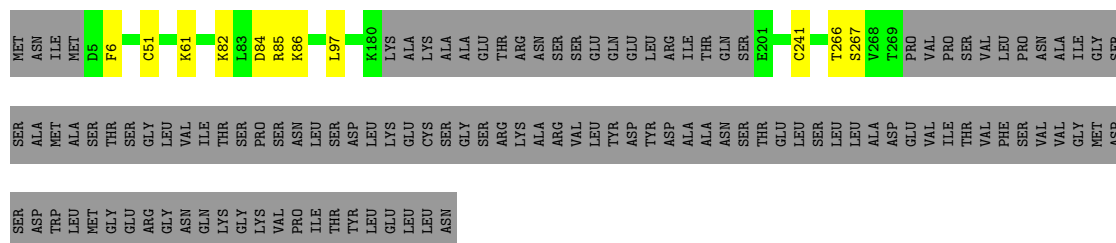
• Molecule 1: Endophilin-B1

Chain H:  64% 33%



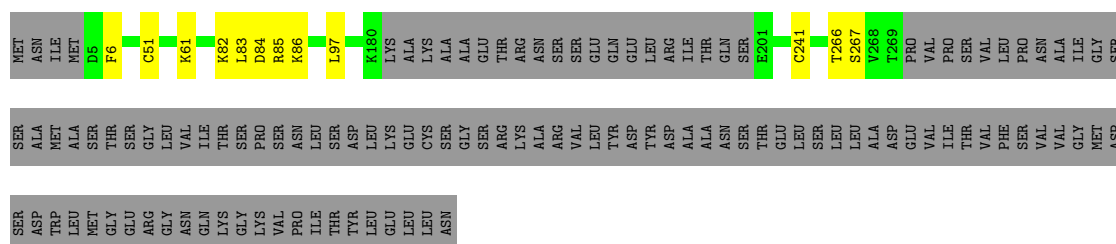
- Molecule 1: Endophilin-B1

Chain I: 



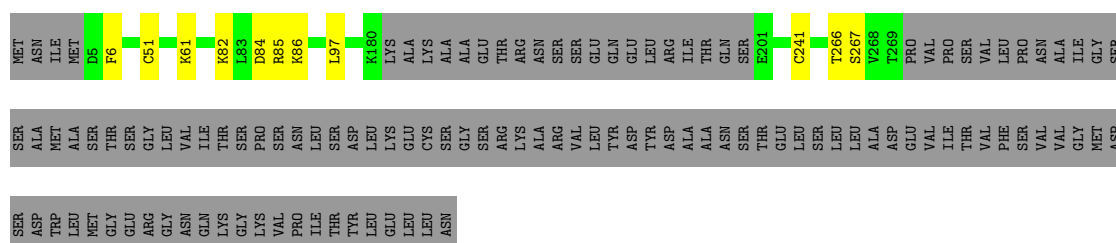
- Molecule 1: Endophilin-B1

Chain J: 



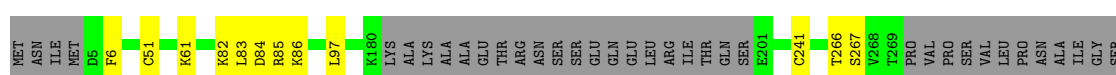
- Molecule 1: Endophilin-B1

Chain K: 



- Molecule 1: Endophilin-B1

Chain L: 



- Molecule 1: Endophilin-B1

Chain M:  64% . 33%

[illegible]

- Molecule 1: Endophilin-B1

Chain N:  64% . 33%

SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLY	ASN	GLN	LYS	GLY	LYS	VAL	ILE	THR	LEU	ASP	LEU	GLU	GLY	LEU	ASP	LYS	ALA	GLY	GLY	GLU	THR	ARG	LYS	ASN	ARG	SER	SER	GLU	GLN	GLU	LEU	LEU	ARG	ILE	THR	GLN	SER	SER	E201	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	SER	SER	VAL	LEU	PRO	ASN	ALA	ILE	GLY	MET	ASP
MET	ASN	ILE	ALA	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	ALA	GLU	GLU	THR	ARG	ASN	SER	SER	GLU	GLN	GLU	LEU	ARG	ILE	THR	GLN	SER	SER	E201	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	SER	SER	VAL	LEU	PRO	ASN	ALA	ILE	GLY	MET	ASP										

- Molecule 1: Endophilin-B1

Chain O:  64% 33%

[illegible]

- Molecule 1: Endophilin-B1

Chain P:  64% . 33%

[illegible]

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

• Molecule 1: Endophilin-B1

Chain Q: 64% 33%

MET ASN ILE MET D5 F6 C51 K61 K82 L83 D84 R85 R86 L97 K180 LYS ALA LYS ALA ALA GLU THR ARG ASN ARG SER GLU GLN TYR LEU LEU LEU LEU ASN

SER ALA MET ALA MET SER THR SER GLY LEU VAL ILE THR SER PRO SER R85 R86 L97 K180 LYS ALA LYS ALA GLU THR ARG ASN ARG SER GLU TYR ASP TYR ASP ALA ALA ASN THR SER THR LEU LEU ASP

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

• Molecule 1: Endophilin-B1

Chain R: 64% 33%

MET ASN ILE MET D5 F6 C51 K61 K82 L83 D84 R85 R86 L97 K180 LYS ALA LYS ALA ALA GLU THR ARG ASN ARG SER GLU GLN TYR LEU LEU LEU LEU ASN

SER ALA MET ALA MET SER THR SER GLY LEU VAL ILE THR SER PRO SER R85 R86 L97 K180 LYS ALA LYS ALA GLU THR ARG ASN ARG SER GLU TYR ASP TYR ASP ALA ALA ASN THR SER THR LEU LEU ASP

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

• Molecule 1: Endophilin-B1

Chain S: 64% 33%

MET ASN ILE MET D5 F6 C51 K61 K82 L83 D84 R85 R86 L97 K180 LYS ALA LYS ALA ALA GLU THR ARG ASN ARG SER GLU GLN TYR LEU LEU LEU LEU ASN

SER ALA MET ALA MET SER THR SER GLY LEU VAL ILE THR SER PRO SER R85 R86 L97 K180 LYS ALA LYS ALA GLU THR ARG ASN ARG SER GLU TYR ASP TYR ASP ALA ALA ASN THR SER THR LEU LEU ASP

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

• Molecule 1: Endophilin-B1

Chain T: 64% 33%

MET ASN ILE MET D5 F6 C51 K61 K82 L83 D84 R85 R86 L97 K180 LYS ALA LYS ALA ALA GLU THR ARG ASN ARG SER GLU GLN TYR LEU LEU LEU LEU ASN

SER ALA MET ALA MET SER THR SER GLY LEU VAL ILE THR SER PRO SER R85 R86 L97 K180 LYS ALA LYS ALA GLU THR ARG ASN ARG SER GLU TYR ASP TYR ASP ALA ALA ASN THR SER THR LEU LEU ASP

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

- Molecule 1: Endophilin-B1

Chain V:  64% 33%

SER	ASP	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	LYS	ASN	ARG	SER	VAL	LEU	GLN	TYR	ASP	GLU	LEU	THR	GLN	ASN	SER	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	THR	VAL	PHE	LEU	PRO	ASN	ALA	ILE	GLY	MET	SER							
SER	ALA	MET	ALA	MET	SER	THR	SER	GLY	THR	SER	PRO	SER	ASN	LEU	SER	LEU	ASP	LYS	CYS	GLY	SER	ARG	LYS	ALA	ASN	ARG	SER	VAL	LEU	GLN	TYR	ASP	GLU	LEU	THR	GLN	ASN	SER	THR	GLU	LEU	SER	LEU	LEU	VAL	ILE	THR	VAL	PHE	LEU	VAL	VAL	ASN	ALA	ILE	GLY	MET	SER						
SER	ASP	TRP	LEU	MET	MET	GLY	GLU	ARG	GLY	ASN	LYS	GLY	VAL	PRO	THR	LEU	TYR	LEU	LEU	ASN																																												

- Molecule 1: Endophilin-B1

Chain W:  64% 33%

MET	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	LYS	ASN	ARG	SER	VAL	LEU	GLN	TYR	ASP	GLU	LEU	THR	GLN	ASN	THR	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	THR	VAL	VAL	PHE	LEU	VAL	VAL	ASN	ALA	ILE	GLY	MET	SER						
SER	ALA	MET	ALA	MET	SER	THR	SER	GLY	THR	SER	PRO	SER	ASN	LEU	SER	LEU	ASP	LYS	CYS	GLY	SER	ARG	LYS	ALA	ASN	ARG	SER	VAL	LEU	GLN	TYR	ASP	GLU	LEU	THR	GLN	ASN	THR	THR	GLU	LEU	SER	LEU	LEU	VAL	ILE	THR	VAL	VAL	PHE	LEU	VAL	VAL	ASN	ALA	ILE	GLY	MET	SER					
SER	ASP	TRP	LEU	MET	MET	GLY	GLU	ARG	GLY	ASN	LYS	GLY	VAL	PRO	THR	LEU	TYR	LEU	LEU	ASN																																												

- Molecule 1: Endophilin-B1

Chain X:  64% 33%

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

- Molecule 1: Endophilin-B1

Chain Y:  64% 33%

SER	ASP	TRP	LEU	MET	MET	GLY	GLU	ARG	GLY	ASN	GLN	LYS	GLY	LYS	VAL	PRO	ILE	THR	TYR	LEU	LEU	LEU	ASN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
MET	ASN	ILE	MET	ALA	SER	THR	SER	GLY	LEU	VAL	ILE	THR	SER	LYS	ALA	LYS	CYS	GLY	SER	ARG	LYS	ALA	ARG	VAL	LEU	GLN	TYR	ASP	GLU	LEU	THR	GLN	ASN	SER	THR	GLU	LEU	SER	LEU	ALA	ASP	VAL	ILE	THR	VAL	PHE	LEU	VAL	PRO	ASN	ALA	ILE	GLY	MET	SER																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
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- Molecule 1: Endophilin-B1

Chain a:  64% 33%

SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLN	LYS	GLY	VAL	PRO	ILE	THR	TYR	LEU	GLU	LEU	LEU	ASN																																		
SER	ALA	MET	LEU	ALA	SER	GLY	GLY	ASN	THR	SER	PRO	ASN	LEU	SER	ASP	LEU	GLU	CYS	GLY	SER	ARG	LYS	ALA	ASN	ARG	VAL	LEU	TYR	ASP	THR	GLN	THR	SER	LEU	SER	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	LEU	SER	PRO	ASN	VAL	VAL	GLY	MET		
MET	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	LYS	ASN	SER	SER	GLU	GLU	LEU	TYR	ASP	THR	GLN	THR	SER	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	SER	THR	VAL	LEU	PHE	VAL	ASN	ALA	ILE	GLY	MET

• Molecule 1: Endophilin-B1

Chain b:  64% 33%

SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLN	LYS	GLY	VAL	PRO	ILE	THR	TYR	LEU	GLU	LEU	LEU	ASN																																				
SER	ALA	MET	ALA	SER	THR	SER	GLY	VAL	THR	SER	THR	PRO	SER	ASN	LEU	SER	ASP	LYS	GLU	CYS	SER	GLY	SER	ARG	LYS	ALA	ASN	ARG	VAL	LEU	TYR	ASP	THR	GLN	THR	SER	GLU	LEU	SER	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	LEU	SER	PRO	ASN	VAL	VAL	GLY	MET
MET	ASN	ILE	ALA	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	LYS	ASN	SER	SER	GLN	LEU	ARG	ILE	THR	ASN	SER	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	SER	THR	VAL	LEU	PHE	VAL	ASN	ALA	ILE	GLY					

• Molecule 1: Endophilin-B1

Chain c:  64% 33%

MET	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	ALA	GLU	THR	ARG	LYS	ASN	SER	SER	GLU	GLU	LEU	TYR	ASP	THR	GLN	THR	SER	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	SER	THR	VAL	LEU	PHE	VAL	ASN	ALA	ILE	GLY	MET
SER	ALA	MET	ALA	SER	THR	SER	GLY	THR	SER	PRO	SER	ASN	LEU	SER	LEU	LYS	CYS	GLY	SER	ARG	LYS	ALA	ASN	ARG	VAL	LEU	TYR	ASP	THR	GLN	THR	SER	LEU	SER	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	VAL	ASN	VAL	VAL	GLY	MET					
SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLN	LYS	GLY	VAL	PRO	ILE	THR	TYR	LEU	GLU	LEU	LEU	ASN	LYS	ALA	ASN	ARG	VAL	LEU	TYR	ASP	THR	GLN	THR	SER	LEU	SER	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	VAL	ASN	VAL	VAL	GLY	MET					

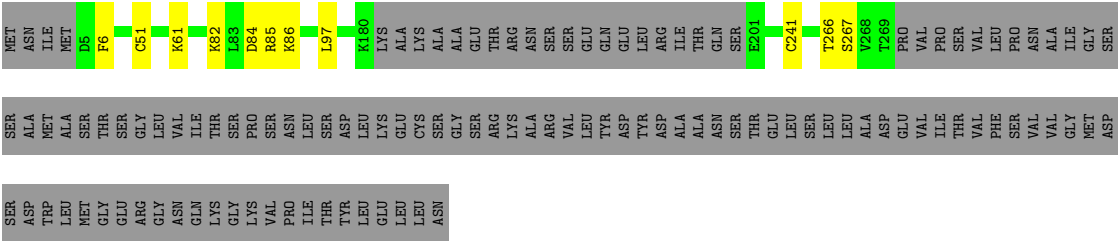
• Molecule 1: Endophilin-B1

Chain d:  64% 33%

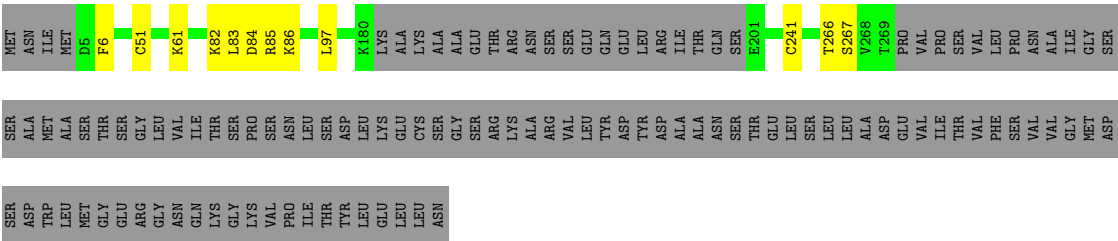
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SER	ALA	MET	ALA	SER	THR	SER	GLY	THR	SER	PRO	SER	ASN	LEU	SER	LEU	LYS	CYS	GLY	SER	ARG	LYS	ALA	ASN	ARG	VAL	LEU	TYR	ASP	THR	ASP	ALA	ALA	ASN	SER	THR	GLU	LEU	SER	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	SER	VAL	VAL	GLY	MET		
SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLN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

• Molecule 1: Endophilin-B1

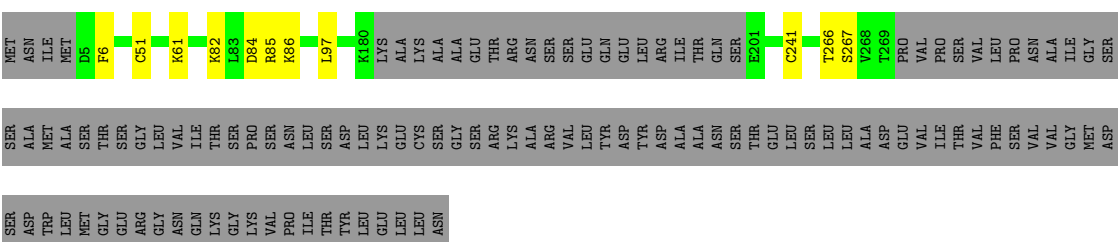
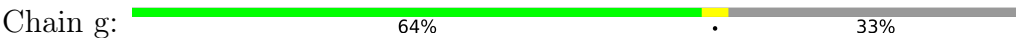
Chain e:  64% 33%



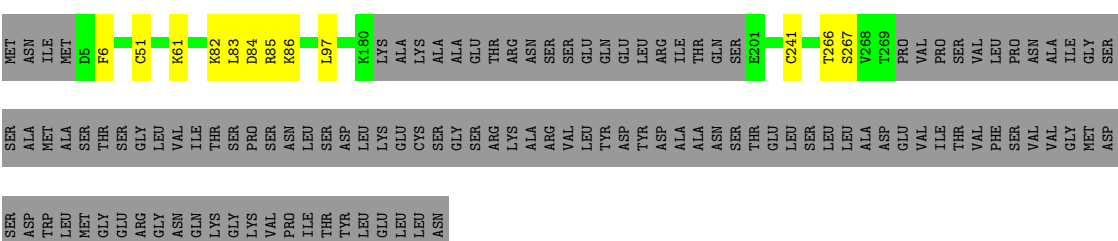
• Molecule 1: Endophilin-B1



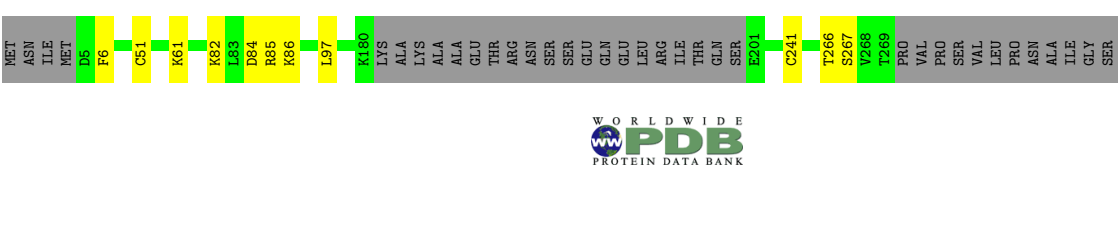
• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1



• Molecule 1: Endophilin-B1



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

- Molecule 1: Endophilin-B1

Chain j:  64% . 33%

[illegible]

- Molecule 1: Endophilin-B1

Chain k:  64% . 33%

[illegible]

- Molecule 1: Endophilin-B1

Chain 1:  64% . 33%

[illegible]

- Molecule 1: Endophilin-B1

Chain m:  64% . 33%

[illegible]



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

• Molecule 1: Endophilin-B1

Chain n:  64% 33%

MET ASN ILE MET D5 F6 C51 K61 K82 L83 D84 R85 K86 L97 K180 LYS ALA LYS ALA ALA GLU THR ARG ASN SER SER GLU GLN LEU LEU ARG ARG THR THR GLN SER E201 C241 T266 S267 V268 T269 PRO VAL PRO SER VAL LEU PHE SER PRO ASN ALA ILE GLY MET SER

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

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

• Molecule 1: Endophilin-B1

Chain o:  64% 33%

MET ASN ILE MET D5 F6 C51 K61 K82 L83 D84 R85 K86 L97 K180 LYS ALA LYS ALA ALA GLU THR ARG ASN SER SER GLU GLN LEU LEU ARG ARG THR THR GLN SER E201 C241 T266 S267 V268 T269 PRO VAL PRO SER VAL LEU PHE SER PRO ASN ALA ILE GLY MET SER

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

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

• Molecule 1: Endophilin-B1

Chain p:  64% 33%

MET ASN ILE MET D5 F6 C51 K61 K82 L83 D84 R85 K86 L97 K180 LYS ALA LYS ALA ALA GLU THR ARG ASN SER SER GLU GLN LEU LEU ARG ARG THR THR GLN SER E201 C241 T266 S267 V268 T269 PRO VAL PRO SER VAL LEU PHE SER PRO ASN ALA ILE GLY MET SER

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

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

• Molecule 1: Endophilin-B1

Chain q:  64% 33%

MET ASN ILE MET D5 F6 C51 K61 K82 L83 D84 R85 K86 L97 K180 LYS ALA LYS ALA ALA GLU THR ARG ASN SER SER GLU GLN LEU LEU ARG ARG THR THR GLN SER E201 C241 T266 S267 V268 T269 PRO VAL PRO SER VAL LEU PHE SER PRO ASN ALA ILE GLY MET SER

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

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

## ● Molecule 1: Endophilin-B1

Chain r:  64% 33%

MET	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	LYS	ALA	ALA	GLU	THR	ARG	LYS	ASN	ARG	SER	GLN	THR	GLU	GLN	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	PRO	SER	SER	VAL	VAL	PHE	LEU	PRO	ASN	ASN	ALA	ILE	GLY	MET	SER
SER	ALA	MET	ALA	SER	THR	SER	GLY	LEU	VAL	ILE	THR	SER	GLY	LYS	GLU	CYS	GLY	SER	SER	ARG	LYS	ALA	ASN	ARG	VAL	LEU	TYR	GLN	ASP	THR	GLU	LEU	SER	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	LEU	SER	VAL	VAL	VAL	GLY	ILE	ASP					
SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLY	ASN	LYS	GLY	LYS	VAL	PRO	ASN	ILE	THR	TYR	LEU	GLU	ASN																																		

## ● Molecule 1: Endophilin-B1

Chain s:  64% 33%

MET	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	LYS	ALA	ALA	GLU	THR	ARG	LYS	ASN	ARG	SER	SER	GLU	GLU	GLN	LEU	LEU	ARG	ILE	THR	GLN	SER	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	SER	SER	VAL	LEU	PRO	ASN	ALA	ILE	GLY	SER				
SER	ALA	MET	ALA	SER	THR	SER	GLY	LEU	VAL	ILE	THR	SER	PRO	SER	ASN	LEU	LEU	SER	ASP	LEU	LYS	GLY	CYS	SER	GLY	SER	ARG	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	THR	PHE	SER	VAL	VAL	GLY	ILE	ASP
SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLY	ASN	GLN	LYS	GLY	VAL	PRO	ASN	ILE	THR	TYR	LEU	GLU	LEU	ASN																																							

## ● Molecule 1: Endophilin-B1

Chain t:  64% 33%

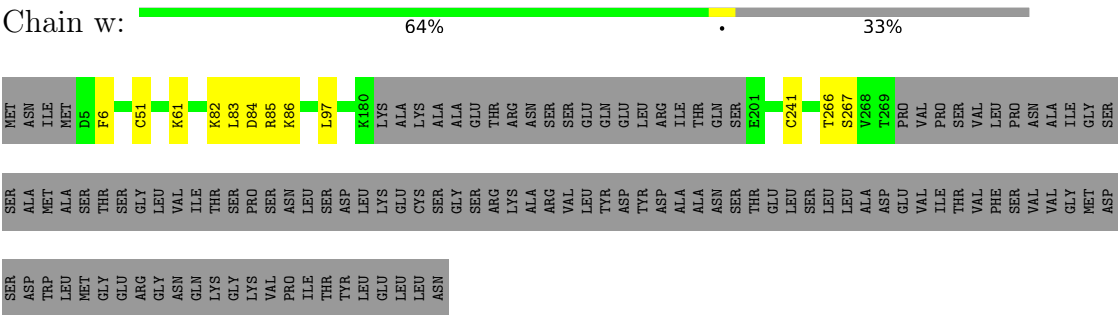
MET	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	LYS	ALA	ALA	GLU	THR	ARG	LYS	ASN	ARG	SER	GLU	GLN	GLU	LEU	ARG	ILE	THR	GLN	SER	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	THR	SER	VAL	PHE	LEU	PRO	ASN	VAL	VAL	GLY	ILE	GLY	MET	SER										
SER	ALA	MET	ALA	SER	THR	GLY	GLY	THR	SER	PRO	SER	ASN	LEU	SER	ASP	LEU	LYS	GLY	CYS	GLY	SER	SER	ARG	LYS	ALA	ASN	ARG	VAL	LEU	TYR	ASP	THR	TYR	ASP	ALA	ALA	ALA	ASN	SER	SER	THR	THR	GLU	LEU	SER	SER	LEU	LEU	ALA	ALA	ASP	GLY	VAL	ILE	THR	VAL	VAL	PHE	LEU	PRO	SER	VAL	VAL	VAL	GLY	ILE	GLY	MET	SER
SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLY	ASN	LYS	GLY	LYS	VAL	PRO	ASN	ILE	THR	TYR	LEU	GLU	ASN	ASN	ASN	ASN	ALA	ALA	ARG	VAL	LEU	TYR	ASP	THR	TYR	ASP	ALA	ALA	ALA	ASN	SER	SER	THR	THR	GLU	LEU	SER	SER	LEU	LEU	ALA	ALA	ASP	GLY	VAL	ILE	THR	VAL	VAL	PHE	LEU	PRO	SER	VAL	VAL	VAL	GLY	ILE	GLY	MET	SER

## ● Molecule 1: Endophilin-B1

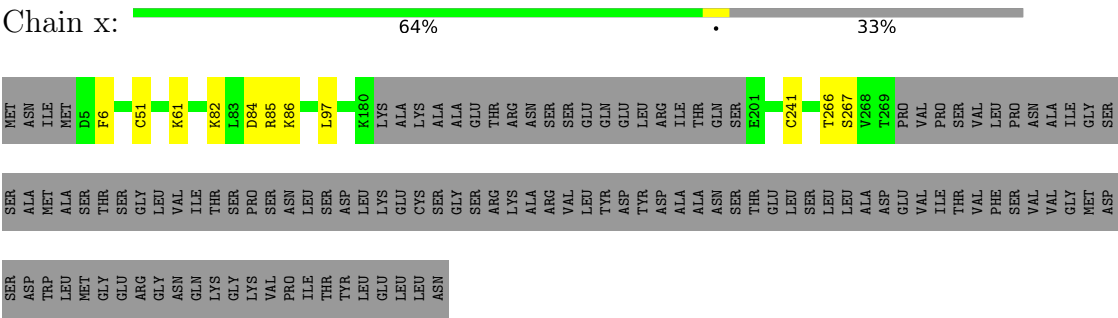
Chain v:  64% 33%

MET	ASN	ILE	MET	D5	F6	C51	K61	K82	L83	D84	R85	K86	L97	K180	LYS	ALA	LYS	LYS	ALA	ALA	GLU	THR	ARG	LYS	ASN	ARG	SER	GLU	GLN	THR	GLN	SER	E201	C241	T266	S267	V268	T269	PRO	VAL	PRO	THR	SER	VAL	VAL	LEU	PRO	ASN	ALA	ILE	GLY	MET	SER																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
SER	ALA	MET	ALA	SER	THR	GLY	LEU	ILE	THR	SER	PRO	ASN	LEU	SER	ASP	LEU	GLU	CYS	SER	GLY	SER	ARG	LYS	ALA	ASN	ARG	VAL	LEU	TYR	ASP	THR	THR	GLU	LEU	LEU	ALA	ASP	GLU	VAL	ILE	THR	VAL	PHE	SER	VAL	VAL	GLY	ILE	ASP																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
SER	ASP	TRP	LEU	MET	GLY	GLU	ARG	GLN	LYS	GLY	LYS	VAL	PRO	ASN	ILE	THR	TYR	LEU	GLU	ASN																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												

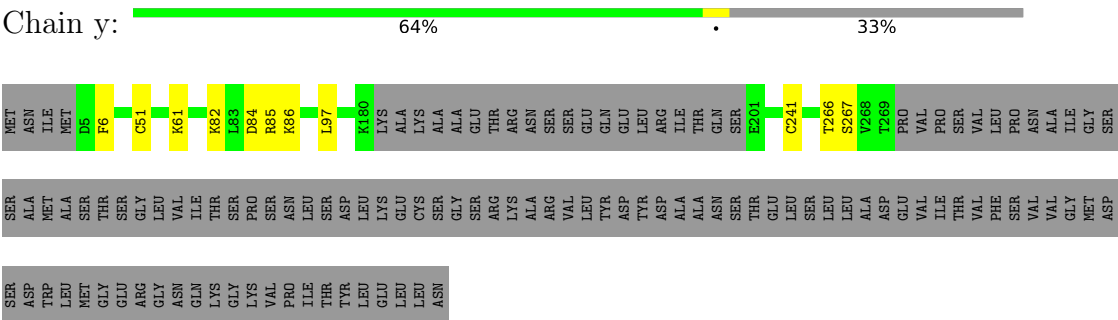
## ● Molecule 1: Endophilin-B1



● Molecule 1: Endophilin-B1



● Molecule 1: Endophilin-B1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=59.1°, rise=17.8 Å, axial sym=C1	Depositor
Number of segments used	21197	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	0.062	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	490.9588, 490.9588, 490.9588	wwPDB
Map dimensions	214, 214, 214	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.2942, 2.2942, 2.2942	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	0.35	0/1993	0.58	0/2685
1	B	0.36	0/1993	0.58	0/2685
1	C	0.35	0/1993	0.58	0/2685
1	D	0.36	0/1993	0.58	0/2685
1	E	0.35	0/1993	0.58	0/2685
1	F	0.36	0/1993	0.59	0/2685
1	G	0.35	0/1993	0.58	0/2685
1	H	0.36	0/1993	0.58	0/2685
1	I	0.35	0/1993	0.58	0/2685
1	J	0.36	0/1993	0.58	0/2685
1	K	0.35	0/1993	0.58	0/2685
1	L	0.36	0/1993	0.59	0/2685
1	M	0.35	0/1993	0.58	0/2685
1	N	0.36	0/1993	0.58	0/2685
1	O	0.35	0/1993	0.58	0/2685
1	P	0.36	0/1993	0.59	0/2685
1	Q	0.35	0/1993	0.58	0/2685
1	R	0.36	0/1993	0.59	0/2685
1	S	0.35	0/1993	0.58	0/2685
1	T	0.36	0/1993	0.58	0/2685
1	V	0.35	0/1993	0.58	0/2685
1	W	0.36	0/1993	0.59	0/2685
1	X	0.35	0/1993	0.58	0/2685
1	Y	0.36	0/1993	0.59	0/2685
1	a	0.35	0/1993	0.58	0/2685
1	b	0.36	0/1993	0.58	0/2685
1	c	0.35	0/1993	0.58	0/2685
1	d	0.36	0/1993	0.59	0/2685
1	e	0.35	0/1993	0.58	0/2685
1	f	0.36	0/1993	0.59	0/2685
1	g	0.35	0/1993	0.58	0/2685
1	h	0.36	0/1993	0.58	0/2685
1	i	0.35	0/1993	0.58	0/2685
1	j	0.36	0/1993	0.59	0/2685

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	k	0.35	0/1993	0.59	0/2685
1	l	0.36	0/1993	0.59	0/2685
1	m	0.35	0/1993	0.58	0/2685
1	n	0.36	0/1993	0.58	0/2685
1	o	0.35	0/1993	0.58	0/2685
1	p	0.36	0/1993	0.59	0/2685
1	q	0.35	0/1993	0.58	0/2685
1	r	0.36	0/1993	0.58	0/2685
1	s	0.35	0/1993	0.58	0/2685
1	t	0.36	0/1993	0.58	0/2685
1	v	0.35	0/1993	0.58	0/2685
1	w	0.36	0/1993	0.59	0/2685
1	x	0.35	0/1993	0.58	0/2685
1	y	0.36	0/1993	0.59	0/2685
All	All	0.35	0/95664	0.58	0/128880

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	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	B	241/365 (66%)	213 (88%)	28 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	D	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	E	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	F	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	G	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	H	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	I	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	J	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	K	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	L	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	M	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	N	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	O	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	P	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	Q	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	R	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	S	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	T	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	V	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	W	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	X	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	Y	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	a	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	b	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	c	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	d	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	e	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	f	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	g	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	h	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	i	241/365 (66%)	215 (89%)	26 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	j	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	k	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	l	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	m	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	n	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	o	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	p	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	q	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	r	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	s	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	t	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	v	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	w	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
1	x	241/365 (66%)	215 (89%)	26 (11%)	0	100	100
1	y	241/365 (66%)	213 (88%)	28 (12%)	0	100	100
All	All	11568/17520 (66%)	10272 (89%)	1296 (11%)	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	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	B	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	C	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	D	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	E	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	F	212/315 (67%)	200 (94%)	12 (6%)	20	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	H	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	I	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	J	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	K	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	L	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	M	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	N	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	O	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	P	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	Q	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	R	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	S	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	T	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	V	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	W	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	X	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	Y	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	a	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	b	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	c	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	d	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	e	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	f	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	g	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	h	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	i	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	j	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	k	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	l	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	m	212/315 (67%)	201 (95%)	11 (5%)	23	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	n	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	o	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	p	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	q	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	r	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	s	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	t	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	v	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	w	212/315 (67%)	200 (94%)	12 (6%)	20	45
1	x	212/315 (67%)	201 (95%)	11 (5%)	23	48
1	y	212/315 (67%)	201 (95%)	11 (5%)	23	48
All	All	10176/15120 (67%)	9627 (95%)	549 (5%)	26	47

All (549) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	PHE
1	A	51	CYS
1	A	61	LYS
1	A	82	LYS
1	A	84	ASP
1	A	85	ARG
1	A	86	LYS
1	A	97	LEU
1	A	241	CYS
1	A	266	THR
1	A	267	SER
1	B	6	PHE
1	B	51	CYS
1	B	61	LYS
1	B	82	LYS
1	B	83	LEU
1	B	84	ASP
1	B	85	ARG
1	B	86	LYS
1	B	97	LEU
1	B	241	CYS
1	B	266	THR

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Mol	Chain	Res	Type
1	B	267	SER
1	C	6	PHE
1	C	51	CYS
1	C	61	LYS
1	C	82	LYS
1	C	84	ASP
1	C	85	ARG
1	C	86	LYS
1	C	97	LEU
1	C	241	CYS
1	C	266	THR
1	C	267	SER
1	D	6	PHE
1	D	51	CYS
1	D	61	LYS
1	D	82	LYS
1	D	83	LEU
1	D	84	ASP
1	D	85	ARG
1	D	86	LYS
1	D	97	LEU
1	D	241	CYS
1	D	266	THR
1	D	267	SER
1	E	6	PHE
1	E	51	CYS
1	E	61	LYS
1	E	82	LYS
1	E	84	ASP
1	E	85	ARG
1	E	86	LYS
1	E	97	LEU
1	E	241	CYS
1	E	266	THR
1	E	267	SER
1	F	6	PHE
1	F	51	CYS
1	F	61	LYS
1	F	82	LYS
1	F	83	LEU
1	F	84	ASP
1	F	85	ARG

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Mol	Chain	Res	Type
1	F	86	LYS
1	F	97	LEU
1	F	241	CYS
1	F	266	THR
1	F	267	SER
1	G	6	PHE
1	G	51	CYS
1	G	61	LYS
1	G	82	LYS
1	G	84	ASP
1	G	85	ARG
1	G	86	LYS
1	G	97	LEU
1	G	241	CYS
1	G	266	THR
1	G	267	SER
1	H	6	PHE
1	H	51	CYS
1	H	61	LYS
1	H	82	LYS
1	H	83	LEU
1	H	84	ASP
1	H	85	ARG
1	H	86	LYS
1	H	97	LEU
1	H	241	CYS
1	H	266	THR
1	H	267	SER
1	I	6	PHE
1	I	51	CYS
1	I	61	LYS
1	I	82	LYS
1	I	84	ASP
1	I	85	ARG
1	I	86	LYS
1	I	97	LEU
1	I	241	CYS
1	I	266	THR
1	I	267	SER
1	J	6	PHE
1	J	51	CYS
1	J	61	LYS

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Mol	Chain	Res	Type
1	J	82	LYS
1	J	83	LEU
1	J	84	ASP
1	J	85	ARG
1	J	86	LYS
1	J	97	LEU
1	J	241	CYS
1	J	266	THR
1	J	267	SER
1	K	6	PHE
1	K	51	CYS
1	K	61	LYS
1	K	82	LYS
1	K	84	ASP
1	K	85	ARG
1	K	86	LYS
1	K	97	LEU
1	K	241	CYS
1	K	266	THR
1	K	267	SER
1	L	6	PHE
1	L	51	CYS
1	L	61	LYS
1	L	82	LYS
1	L	83	LEU
1	L	84	ASP
1	L	85	ARG
1	L	86	LYS
1	L	97	LEU
1	L	241	CYS
1	L	266	THR
1	L	267	SER
1	M	6	PHE
1	M	51	CYS
1	M	61	LYS
1	M	82	LYS
1	M	84	ASP
1	M	85	ARG
1	M	86	LYS
1	M	97	LEU
1	M	241	CYS
1	M	266	THR

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Mol	Chain	Res	Type
1	M	267	SER
1	N	6	PHE
1	N	51	CYS
1	N	61	LYS
1	N	82	LYS
1	N	83	LEU
1	N	84	ASP
1	N	85	ARG
1	N	86	LYS
1	N	97	LEU
1	N	241	CYS
1	N	266	THR
1	N	267	SER
1	O	6	PHE
1	O	51	CYS
1	O	61	LYS
1	O	82	LYS
1	O	84	ASP
1	O	85	ARG
1	O	86	LYS
1	O	97	LEU
1	O	241	CYS
1	O	266	THR
1	O	267	SER
1	P	6	PHE
1	P	51	CYS
1	P	61	LYS
1	P	82	LYS
1	P	83	LEU
1	P	84	ASP
1	P	85	ARG
1	P	86	LYS
1	P	97	LEU
1	P	241	CYS
1	P	266	THR
1	P	267	SER
1	Q	6	PHE
1	Q	51	CYS
1	Q	61	LYS
1	Q	82	LYS
1	Q	84	ASP
1	Q	85	ARG

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Mol	Chain	Res	Type
1	Q	86	LYS
1	Q	97	LEU
1	Q	241	CYS
1	Q	266	THR
1	Q	267	SER
1	R	6	PHE
1	R	51	CYS
1	R	61	LYS
1	R	82	LYS
1	R	83	LEU
1	R	84	ASP
1	R	85	ARG
1	R	86	LYS
1	R	97	LEU
1	R	241	CYS
1	R	266	THR
1	R	267	SER
1	S	6	PHE
1	S	51	CYS
1	S	61	LYS
1	S	82	LYS
1	S	84	ASP
1	S	85	ARG
1	S	86	LYS
1	S	97	LEU
1	S	241	CYS
1	S	266	THR
1	S	267	SER
1	T	6	PHE
1	T	51	CYS
1	T	61	LYS
1	T	82	LYS
1	T	83	LEU
1	T	84	ASP
1	T	85	ARG
1	T	86	LYS
1	T	97	LEU
1	T	241	CYS
1	T	266	THR
1	T	267	SER
1	V	6	PHE
1	V	51	CYS

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Mol	Chain	Res	Type
1	V	61	LYS
1	V	82	LYS
1	V	84	ASP
1	V	85	ARG
1	V	86	LYS
1	V	97	LEU
1	V	241	CYS
1	V	266	THR
1	V	267	SER
1	W	6	PHE
1	W	51	CYS
1	W	61	LYS
1	W	82	LYS
1	W	83	LEU
1	W	84	ASP
1	W	85	ARG
1	W	86	LYS
1	W	97	LEU
1	W	241	CYS
1	W	266	THR
1	W	267	SER
1	X	6	PHE
1	X	51	CYS
1	X	61	LYS
1	X	82	LYS
1	X	84	ASP
1	X	85	ARG
1	X	86	LYS
1	X	97	LEU
1	X	241	CYS
1	X	266	THR
1	X	267	SER
1	Y	6	PHE
1	Y	51	CYS
1	Y	61	LYS
1	Y	82	LYS
1	Y	84	ASP
1	Y	85	ARG
1	Y	86	LYS
1	Y	97	LEU
1	Y	241	CYS
1	Y	266	THR

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Mol	Chain	Res	Type
1	Y	267	SER
1	a	6	PHE
1	a	51	CYS
1	a	61	LYS
1	a	82	LYS
1	a	84	ASP
1	a	85	ARG
1	a	86	LYS
1	a	97	LEU
1	a	241	CYS
1	a	266	THR
1	a	267	SER
1	b	6	PHE
1	b	51	CYS
1	b	61	LYS
1	b	82	LYS
1	b	83	LEU
1	b	84	ASP
1	b	85	ARG
1	b	86	LYS
1	b	97	LEU
1	b	241	CYS
1	b	266	THR
1	b	267	SER
1	c	6	PHE
1	c	51	CYS
1	c	61	LYS
1	c	82	LYS
1	c	84	ASP
1	c	85	ARG
1	c	86	LYS
1	c	97	LEU
1	c	241	CYS
1	c	266	THR
1	c	267	SER
1	d	6	PHE
1	d	51	CYS
1	d	61	LYS
1	d	82	LYS
1	d	83	LEU
1	d	84	ASP
1	d	85	ARG

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Mol	Chain	Res	Type
1	d	86	LYS
1	d	97	LEU
1	d	241	CYS
1	d	266	THR
1	d	267	SER
1	e	6	PHE
1	e	51	CYS
1	e	61	LYS
1	e	82	LYS
1	e	84	ASP
1	e	85	ARG
1	e	86	LYS
1	e	97	LEU
1	e	241	CYS
1	e	266	THR
1	e	267	SER
1	f	6	PHE
1	f	51	CYS
1	f	61	LYS
1	f	82	LYS
1	f	83	LEU
1	f	84	ASP
1	f	85	ARG
1	f	86	LYS
1	f	97	LEU
1	f	241	CYS
1	f	266	THR
1	f	267	SER
1	g	6	PHE
1	g	51	CYS
1	g	61	LYS
1	g	82	LYS
1	g	84	ASP
1	g	85	ARG
1	g	86	LYS
1	g	97	LEU
1	g	241	CYS
1	g	266	THR
1	g	267	SER
1	h	6	PHE
1	h	51	CYS
1	h	61	LYS

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Mol	Chain	Res	Type
1	h	82	LYS
1	h	83	LEU
1	h	84	ASP
1	h	85	ARG
1	h	86	LYS
1	h	97	LEU
1	h	241	CYS
1	h	266	THR
1	h	267	SER
1	i	6	PHE
1	i	51	CYS
1	i	61	LYS
1	i	82	LYS
1	i	84	ASP
1	i	85	ARG
1	i	86	LYS
1	i	97	LEU
1	i	241	CYS
1	i	266	THR
1	i	267	SER
1	j	6	PHE
1	j	51	CYS
1	j	61	LYS
1	j	82	LYS
1	j	83	LEU
1	j	84	ASP
1	j	85	ARG
1	j	86	LYS
1	j	97	LEU
1	j	241	CYS
1	j	266	THR
1	j	267	SER
1	k	6	PHE
1	k	51	CYS
1	k	61	LYS
1	k	82	LYS
1	k	84	ASP
1	k	85	ARG
1	k	86	LYS
1	k	97	LEU
1	k	241	CYS
1	k	266	THR

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Mol	Chain	Res	Type
1	k	267	SER
1	l	6	PHE
1	l	51	CYS
1	l	61	LYS
1	l	82	LYS
1	l	83	LEU
1	l	84	ASP
1	l	85	ARG
1	l	86	LYS
1	l	97	LEU
1	l	241	CYS
1	l	266	THR
1	l	267	SER
1	m	6	PHE
1	m	51	CYS
1	m	61	LYS
1	m	82	LYS
1	m	84	ASP
1	m	85	ARG
1	m	86	LYS
1	m	97	LEU
1	m	241	CYS
1	m	266	THR
1	m	267	SER
1	n	6	PHE
1	n	51	CYS
1	n	61	LYS
1	n	82	LYS
1	n	84	ASP
1	n	85	ARG
1	n	86	LYS
1	n	97	LEU
1	n	241	CYS
1	n	266	THR
1	n	267	SER
1	o	6	PHE
1	o	51	CYS
1	o	61	LYS
1	o	82	LYS
1	o	84	ASP
1	o	85	ARG
1	o	86	LYS

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Mol	Chain	Res	Type
1	o	97	LEU
1	o	241	CYS
1	o	266	THR
1	o	267	SER
1	p	6	PHE
1	p	51	CYS
1	p	61	LYS
1	p	82	LYS
1	p	83	LEU
1	p	84	ASP
1	p	85	ARG
1	p	86	LYS
1	p	97	LEU
1	p	241	CYS
1	p	266	THR
1	p	267	SER
1	q	6	PHE
1	q	51	CYS
1	q	61	LYS
1	q	82	LYS
1	q	84	ASP
1	q	85	ARG
1	q	86	LYS
1	q	97	LEU
1	q	241	CYS
1	q	266	THR
1	q	267	SER
1	r	6	PHE
1	r	51	CYS
1	r	61	LYS
1	r	82	LYS
1	r	83	LEU
1	r	84	ASP
1	r	85	ARG
1	r	86	LYS
1	r	97	LEU
1	r	241	CYS
1	r	266	THR
1	r	267	SER
1	s	6	PHE
1	s	51	CYS
1	s	61	LYS

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Mol	Chain	Res	Type
1	s	82	LYS
1	s	84	ASP
1	s	85	ARG
1	s	86	LYS
1	s	97	LEU
1	s	241	CYS
1	s	266	THR
1	s	267	SER
1	t	6	PHE
1	t	51	CYS
1	t	61	LYS
1	t	82	LYS
1	t	83	LEU
1	t	84	ASP
1	t	85	ARG
1	t	86	LYS
1	t	97	LEU
1	t	241	CYS
1	t	266	THR
1	t	267	SER
1	v	6	PHE
1	v	51	CYS
1	v	61	LYS
1	v	82	LYS
1	v	84	ASP
1	v	85	ARG
1	v	86	LYS
1	v	97	LEU
1	v	241	CYS
1	v	266	THR
1	v	267	SER
1	w	6	PHE
1	w	51	CYS
1	w	61	LYS
1	w	82	LYS
1	w	83	LEU
1	w	84	ASP
1	w	85	ARG
1	w	86	LYS
1	w	97	LEU
1	w	241	CYS
1	w	266	THR

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Mol	Chain	Res	Type
1	w	267	SER
1	x	6	PHE
1	x	51	CYS
1	x	61	LYS
1	x	82	LYS
1	x	84	ASP
1	x	85	ARG
1	x	86	LYS
1	x	97	LEU
1	x	241	CYS
1	x	266	THR
1	x	267	SER
1	y	6	PHE
1	y	51	CYS
1	y	61	LYS
1	y	82	LYS
1	y	84	ASP
1	y	85	ARG
1	y	86	LYS
1	y	97	LEU
1	y	241	CYS
1	y	266	THR
1	y	267	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (169) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	116	ASN
1	A	251	GLN
1	B	72	ASN
1	B	116	ASN
1	B	251	GLN
1	C	72	ASN
1	C	116	ASN
1	C	251	GLN
1	D	72	ASN
1	D	116	ASN
1	D	251	GLN
1	D	258	ASN
1	E	72	ASN
1	E	116	ASN

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Mol	Chain	Res	Type
1	E	251	GLN
1	E	258	ASN
1	F	72	ASN
1	F	116	ASN
1	F	251	GLN
1	F	258	ASN
1	G	72	ASN
1	G	116	ASN
1	G	251	GLN
1	G	258	ASN
1	H	72	ASN
1	H	116	ASN
1	H	251	GLN
1	I	72	ASN
1	I	116	ASN
1	I	251	GLN
1	I	258	ASN
1	J	72	ASN
1	J	116	ASN
1	J	251	GLN
1	J	258	ASN
1	K	72	ASN
1	K	116	ASN
1	K	251	GLN
1	K	258	ASN
1	L	72	ASN
1	L	116	ASN
1	L	251	GLN
1	L	258	ASN
1	M	72	ASN
1	M	116	ASN
1	M	251	GLN
1	N	72	ASN
1	N	116	ASN
1	N	251	GLN
1	O	72	ASN
1	O	116	ASN
1	O	251	GLN
1	P	72	ASN
1	P	116	ASN
1	P	251	GLN
1	P	258	ASN

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Mol	Chain	Res	Type
1	Q	72	ASN
1	Q	116	ASN
1	Q	251	GLN
1	R	72	ASN
1	R	116	ASN
1	R	251	GLN
1	R	258	ASN
1	S	72	ASN
1	S	116	ASN
1	S	251	GLN
1	T	72	ASN
1	T	116	ASN
1	T	251	GLN
1	T	258	ASN
1	V	72	ASN
1	V	116	ASN
1	V	251	GLN
1	V	258	ASN
1	W	72	ASN
1	W	116	ASN
1	W	251	GLN
1	W	258	ASN
1	X	72	ASN
1	X	116	ASN
1	X	251	GLN
1	Y	72	ASN
1	Y	116	ASN
1	Y	251	GLN
1	Y	258	ASN
1	a	72	ASN
1	a	116	ASN
1	a	251	GLN
1	b	72	ASN
1	b	116	ASN
1	b	251	GLN
1	b	258	ASN
1	c	72	ASN
1	c	116	ASN
1	c	251	GLN
1	d	72	ASN
1	d	116	ASN
1	d	251	GLN

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Mol	Chain	Res	Type
1	d	258	ASN
1	e	72	ASN
1	e	116	ASN
1	e	251	GLN
1	f	72	ASN
1	f	116	ASN
1	f	251	GLN
1	f	258	ASN
1	g	72	ASN
1	g	116	ASN
1	g	251	GLN
1	h	72	ASN
1	h	116	ASN
1	h	251	GLN
1	h	258	ASN
1	i	72	ASN
1	i	116	ASN
1	i	251	GLN
1	i	258	ASN
1	j	72	ASN
1	j	116	ASN
1	j	251	GLN
1	k	72	ASN
1	k	116	ASN
1	k	251	GLN
1	l	72	ASN
1	l	116	ASN
1	l	251	GLN
1	l	258	ASN
1	m	72	ASN
1	m	116	ASN
1	m	251	GLN
1	n	72	ASN
1	n	116	ASN
1	n	251	GLN
1	n	258	ASN
1	o	72	ASN
1	o	116	ASN
1	o	251	GLN
1	o	258	ASN
1	p	72	ASN
1	p	116	ASN

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Mol	Chain	Res	Type
1	p	251	GLN
1	p	258	ASN
1	q	72	ASN
1	q	116	ASN
1	q	251	GLN
1	q	258	ASN
1	r	72	ASN
1	r	116	ASN
1	r	251	GLN
1	s	72	ASN
1	s	116	ASN
1	s	251	GLN
1	t	72	ASN
1	t	116	ASN
1	t	251	GLN
1	v	72	ASN
1	v	116	ASN
1	v	251	GLN
1	w	72	ASN
1	w	116	ASN
1	w	251	GLN
1	w	258	ASN
1	x	72	ASN
1	x	116	ASN
1	x	251	GLN
1	y	72	ASN
1	y	116	ASN
1	y	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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

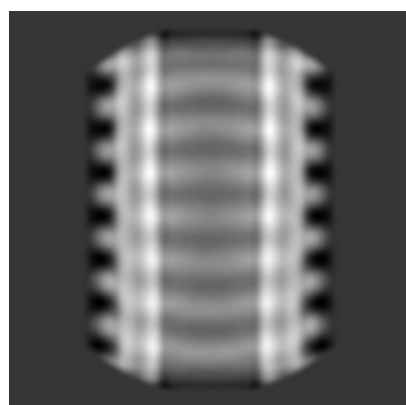
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20842. These allow visual inspection of the internal detail of the map and identification of artifacts.

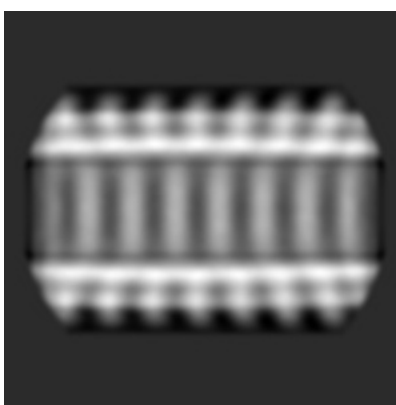
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

#### 6.1.1 Primary map



X



Y



Z

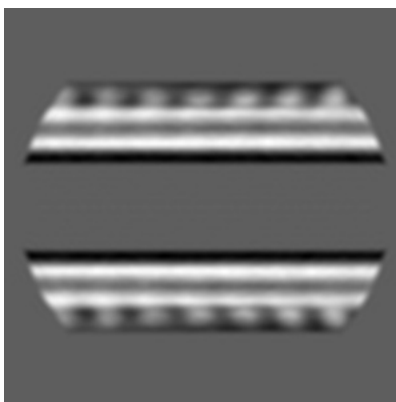
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

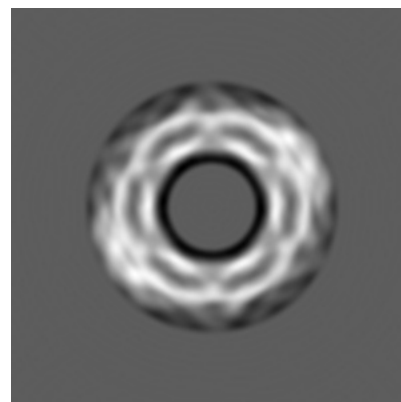
#### 6.2.1 Primary map



X Index: 107



Y Index: 107



Z Index: 107

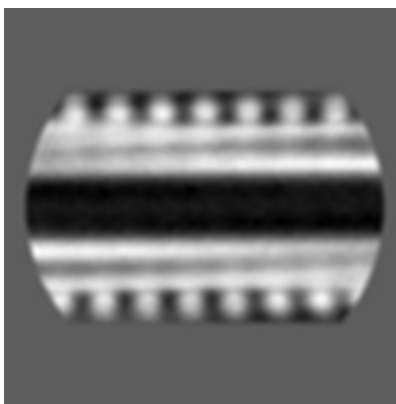
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

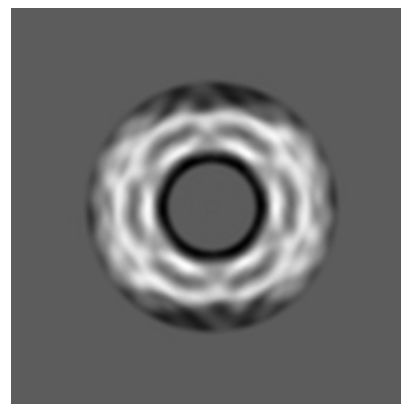
### 6.3.1 Primary map



X Index: 73



Y Index: 132

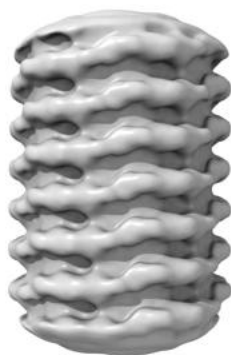


Z Index: 80

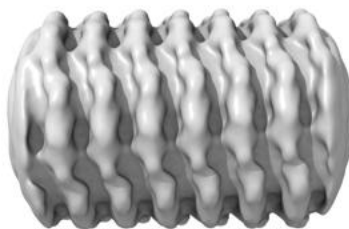
The images above show the largest variance slices of the map in three orthogonal directions.

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

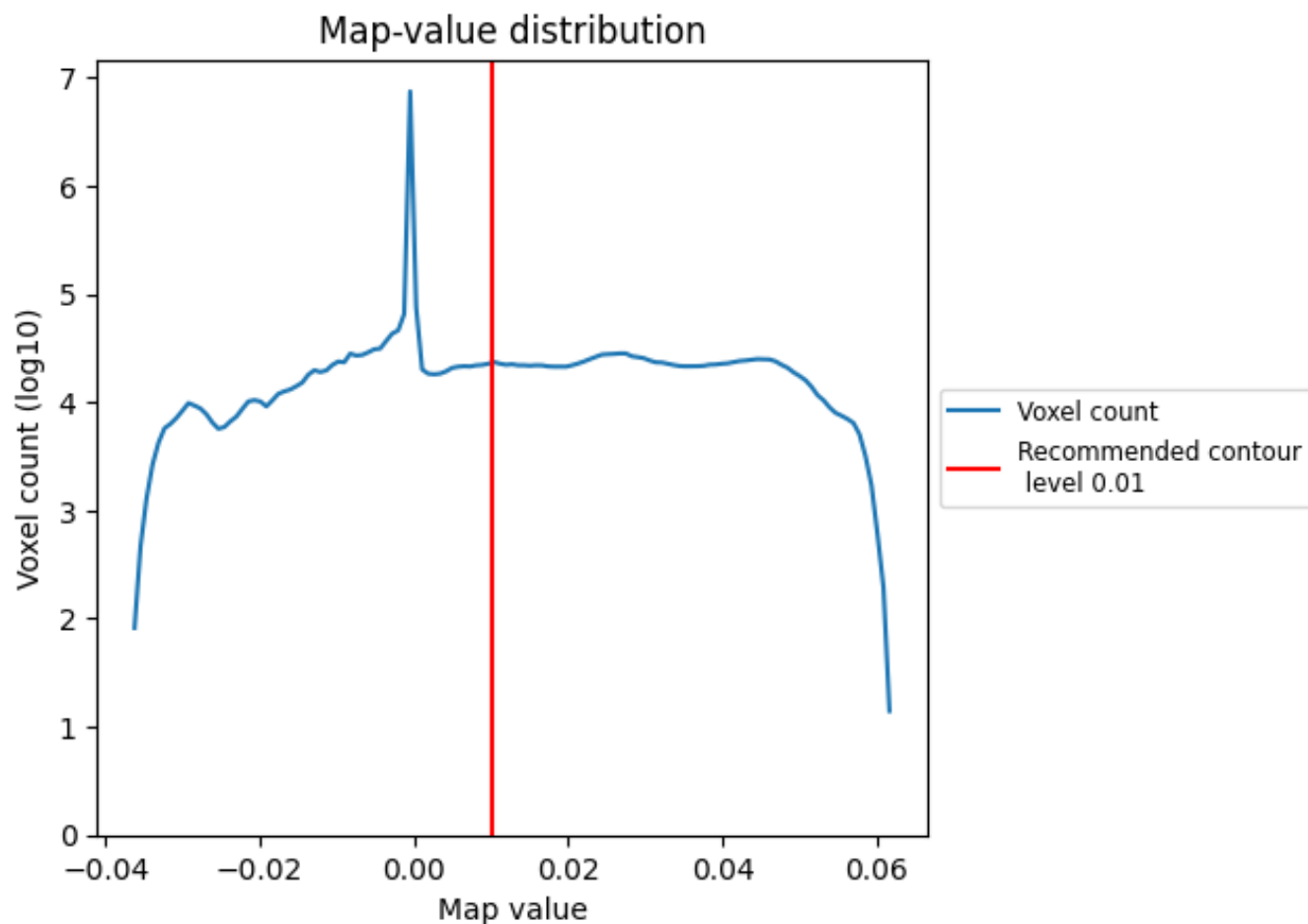
## 6.5 Mask visualisation

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.

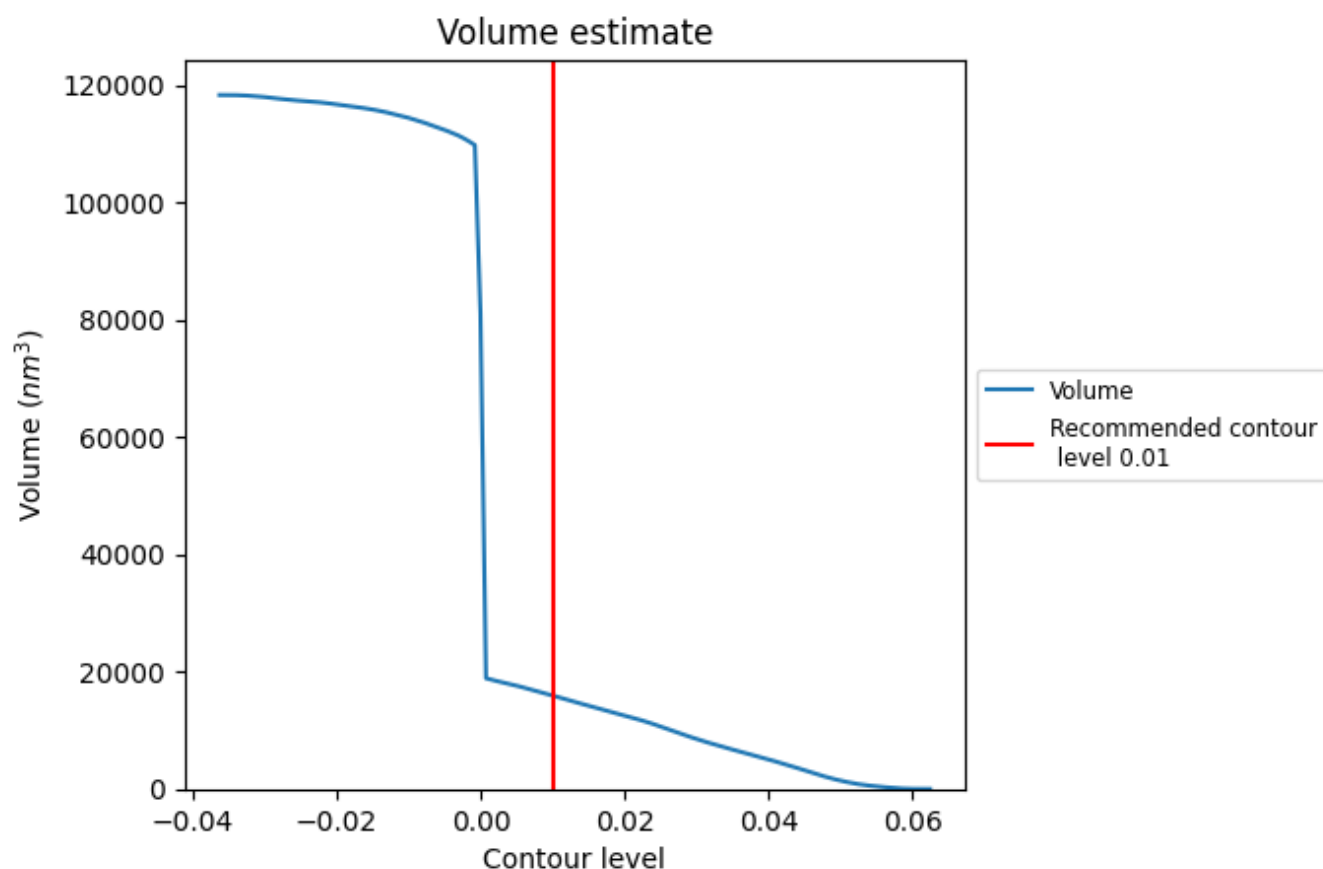
### 7.1 Map-value distribution [i](#)



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.



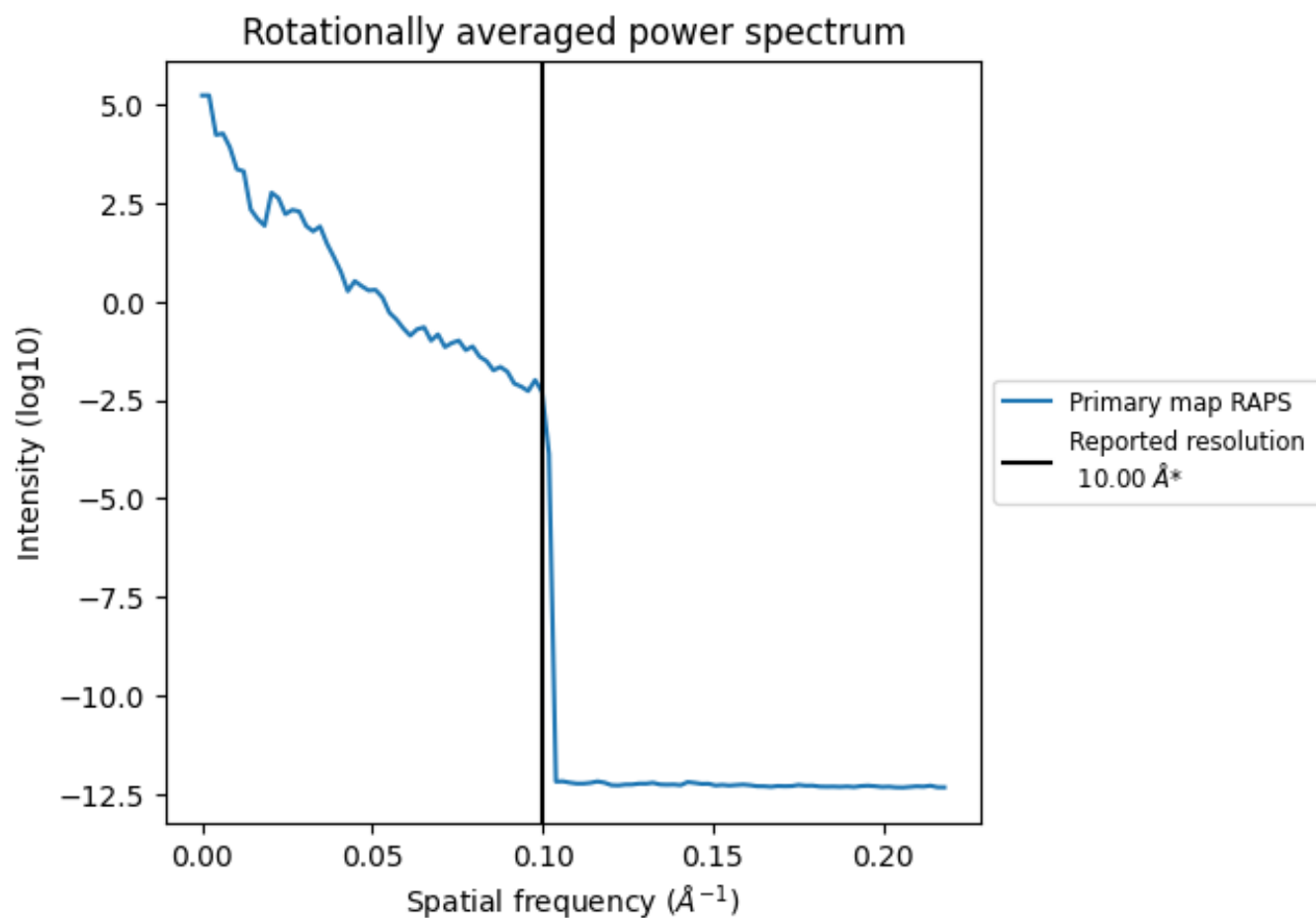
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 15935 nm<sup>3</sup>; this corresponds to an approximate mass of 14395 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 0.100  $\text{\AA}^{-1}$

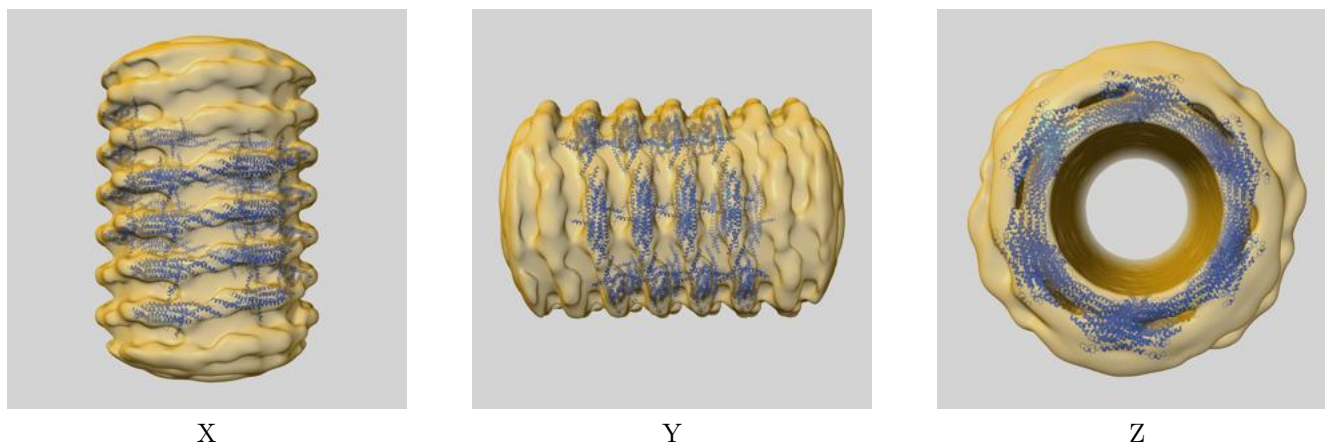
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

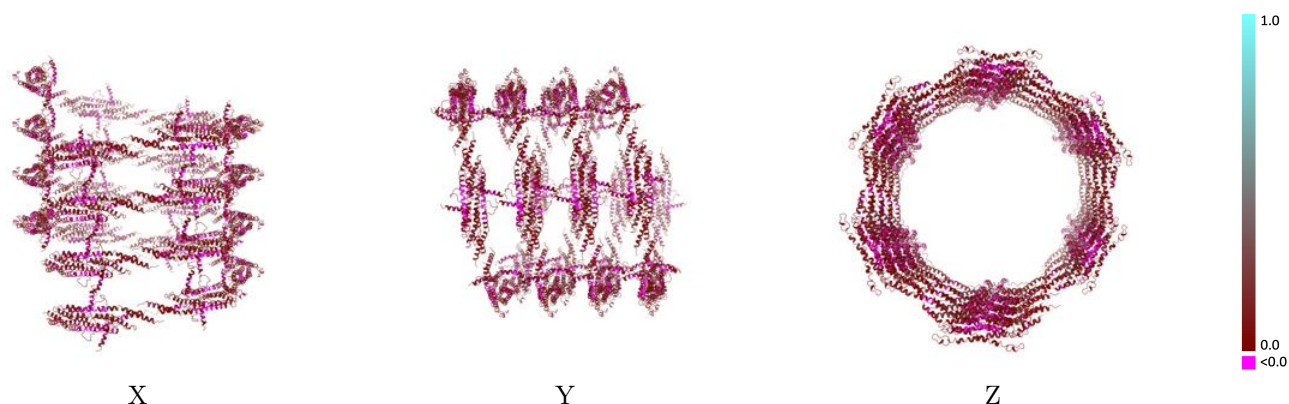
This section contains information regarding the fit between EMDB map EMD-20842 and PDB model 6UPN. Per-residue inclusion information can be found in section [3](#) on page [8](#).

### 9.1 Map-model overlay [i](#)



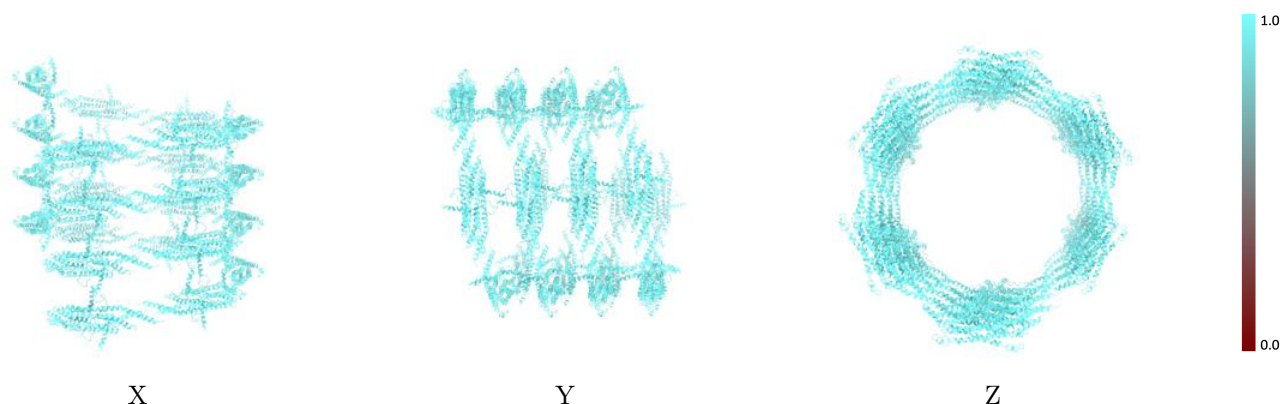
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



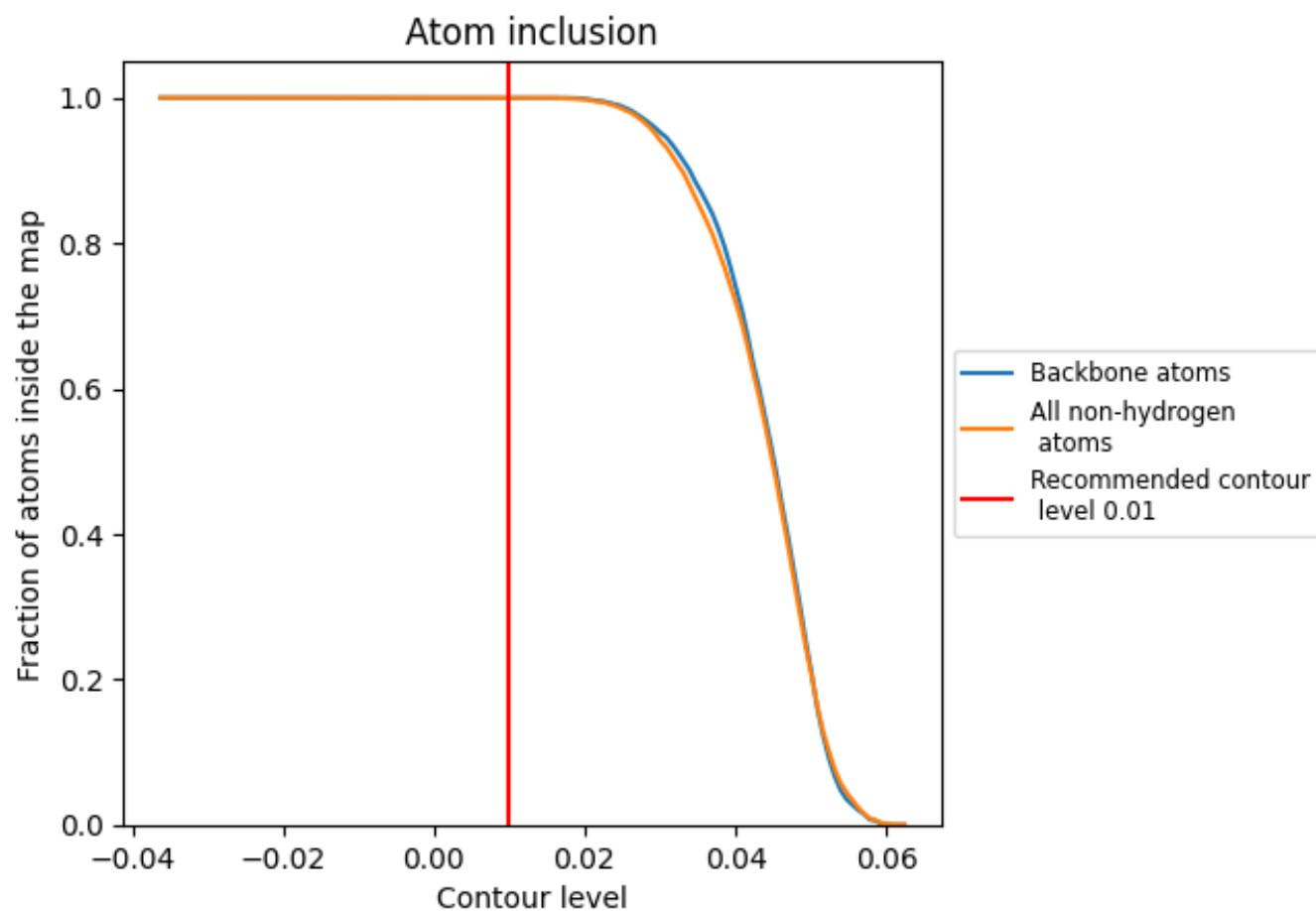
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).







































































## 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 1.0000	 0.0790
A	 1.0000	 0.0880
B	 1.0000	 0.0710
C	 1.0000	 0.0890
D	 1.0000	 0.0710
E	 1.0000	 0.0870
F	 1.0000	 0.0700
G	 1.0000	 0.0850
H	 1.0000	 0.0730
I	 1.0000	 0.0850
J	 1.0000	 0.0730
K	 1.0000	 0.0850
L	 1.0000	 0.0710
M	 1.0000	 0.0870
N	 1.0000	 0.0710
O	 1.0000	 0.0890
P	 1.0000	 0.0690
Q	 1.0000	 0.0880
R	 1.0000	 0.0700
S	 1.0000	 0.0870
T	 1.0000	 0.0720
V	 1.0000	 0.0850
W	 1.0000	 0.0730
X	 1.0000	 0.0860
Y	 1.0000	 0.0730
a	 1.0000	 0.0890
b	 1.0000	 0.0710
c	 1.0000	 0.0890
d	 1.0000	 0.0720
e	 1.0000	 0.0870
f	 1.0000	 0.0680
g	 1.0000	 0.0860
h	 1.0000	 0.0730
i	 1.0000	 0.0870
j	 1.0000	 0.0710



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Chain	Atom inclusion	Q-score
k	 1.0000	 0.0860
l	 1.0000	 0.0720
m	 1.0000	 0.0880
n	 1.0000	 0.0690
o	 1.0000	 0.0890
p	 1.0000	 0.0710
q	 1.0000	 0.0890
r	 1.0000	 0.0720
s	 1.0000	 0.0880
t	 1.0000	 0.0730
v	 1.0000	 0.0860
w	 1.0000	 0.0690
x	 1.0000	 0.0860
y	 1.0000	 0.0720