



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 10:12 AM UTC

PDB ID : 6UPN / pdb_00006upn
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 wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

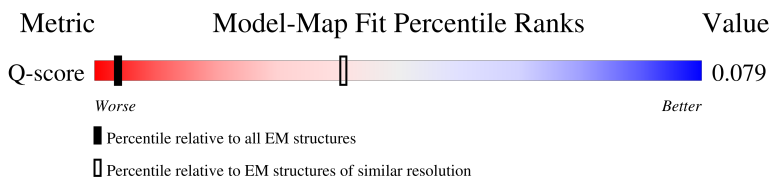
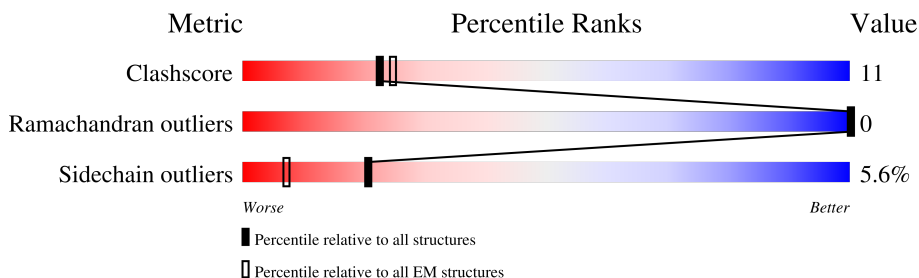
1 Overall quality at a glance i

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.



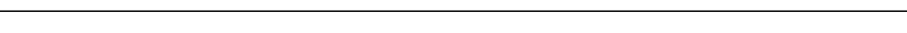
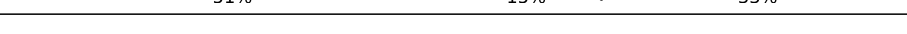
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	147 (9.50 - 10.50)

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

Mol	Chain	Length	Quality of chain
1	A	365	51% 15% • 33%
1	B	365	50% 15% • 33%
1	C	365	50% 16% • 33%
1	D	365	49% 16% • 33%

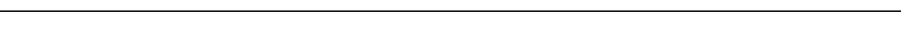
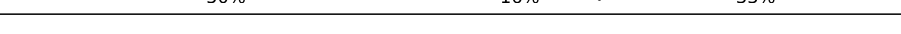
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Mol	Chain	Length	Quality of chain
1	E	365	
1	F	365	
1	G	365	
1	H	365	
1	I	365	
1	J	365	
1	K	365	
1	L	365	
1	M	365	
1	N	365	
1	O	365	
1	P	365	
1	Q	365	
1	R	365	
1	S	365	
1	T	365	
1	V	365	
1	W	365	
1	X	365	
1	Y	365	
1	a	365	
1	b	365	
1	c	365	
1	d	365	
1	e	365	

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Mol	Chain	Length	Quality of chain
1	f	365	
1	g	365	
1	h	365	
1	i	365	
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	

2 Entry composition

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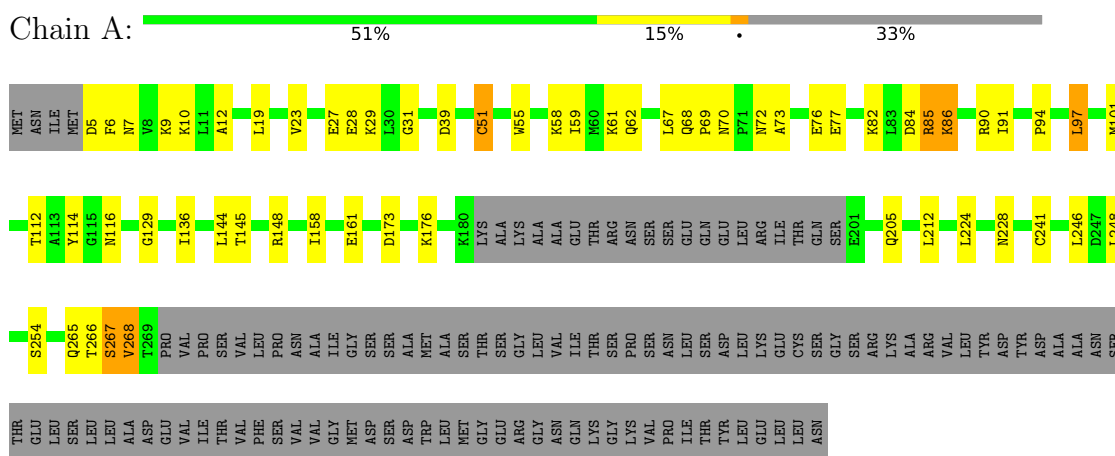
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	o	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	p	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	q	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	r	245	Total 1963	C 1234	N 342	O 379	S 8	0	0
1	s	245	Total 1963	C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

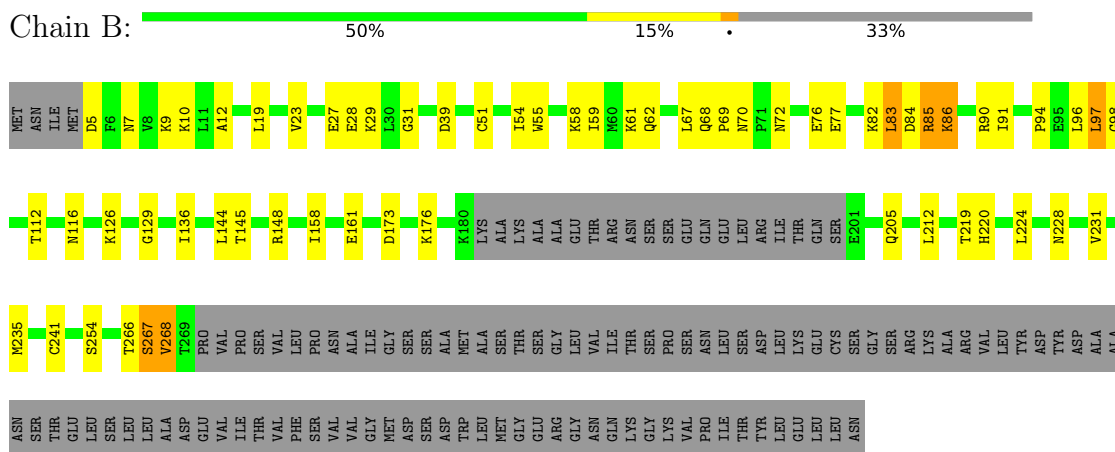
3 Residue-property plots

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

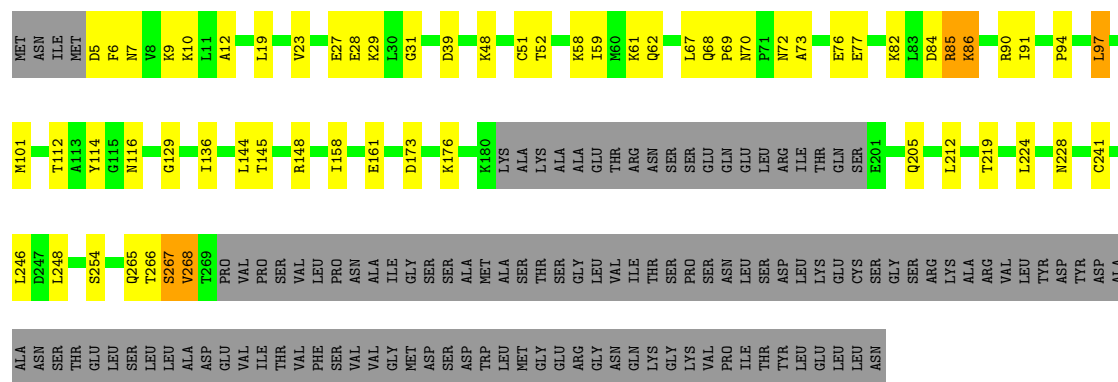


• Molecule 1: Endophilin-B1



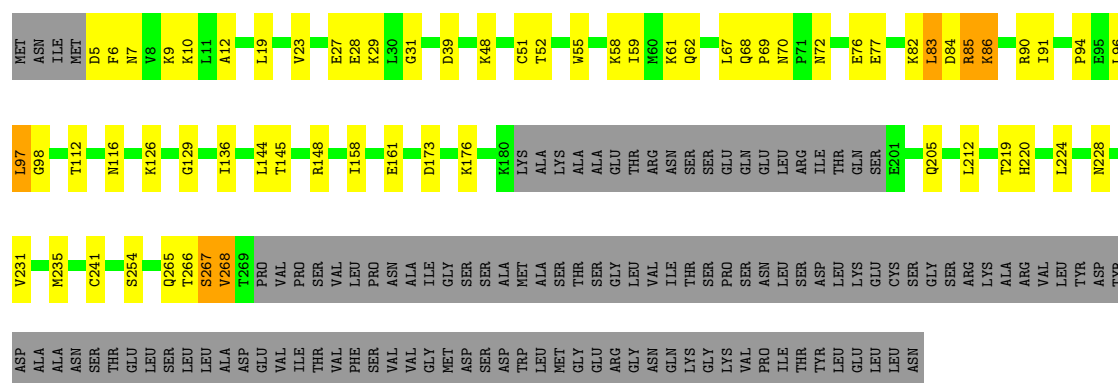
• Molecule 1: Endophilin-B1





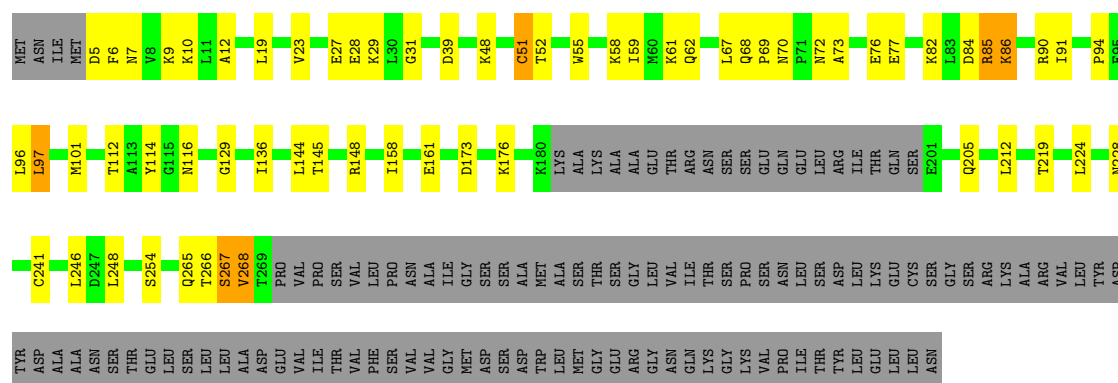
• Molecule 1: Endophilin-B1

Chain D: 49% 16% 33%



• Molecule 1: Endophilin-B1

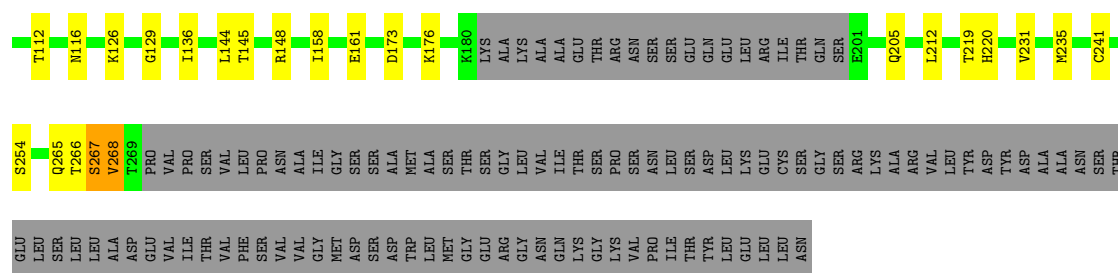
Chain E: 50% 16% 33%



• Molecule 1: Endophilin-B1

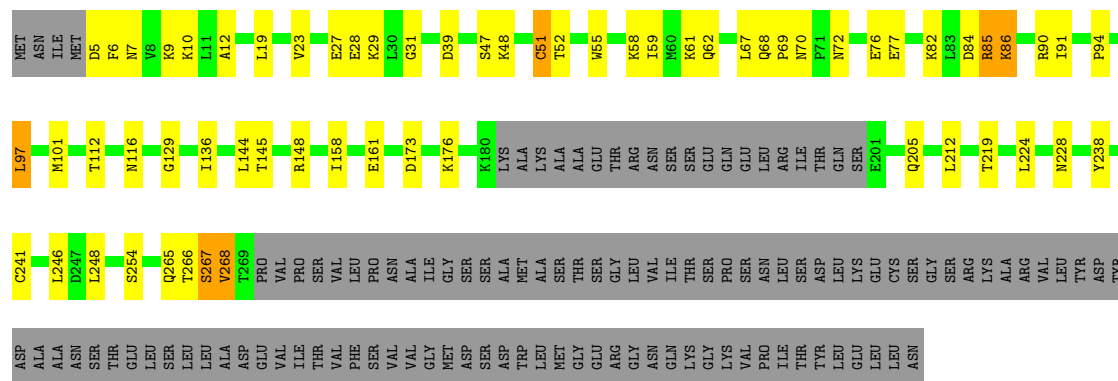
Chain F: 50% 15% 33%





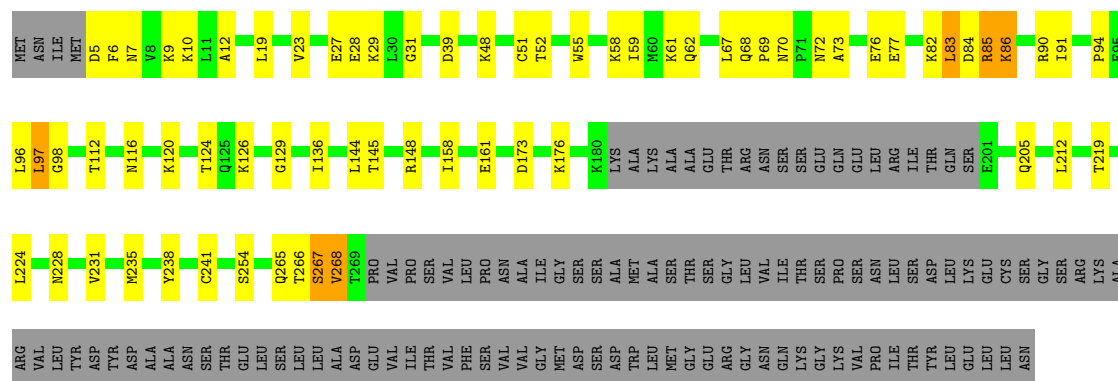
• Molecule 1: Endophilin-B1

Chain G: 50% 16% 33%



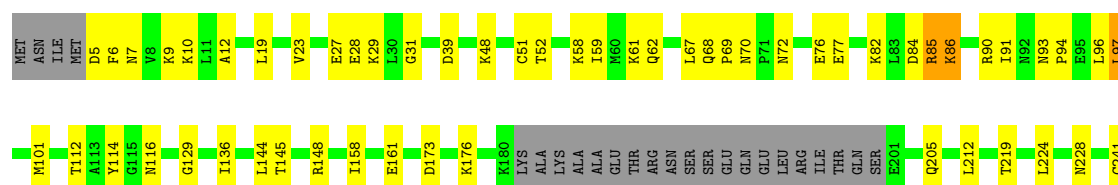
• Molecule 1: Endophilin-B1

Chain H: 48% 17% 33%

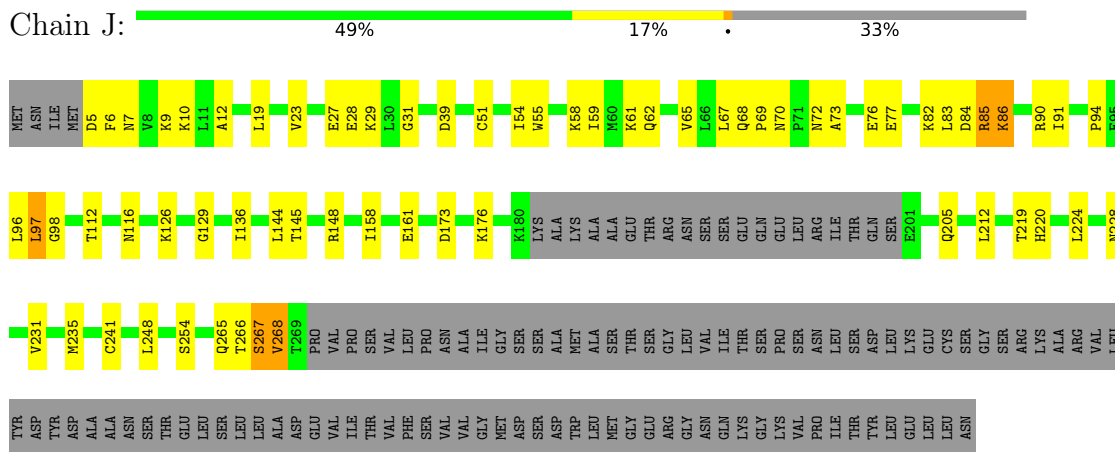


• Molecule 1: Endophilin-B1

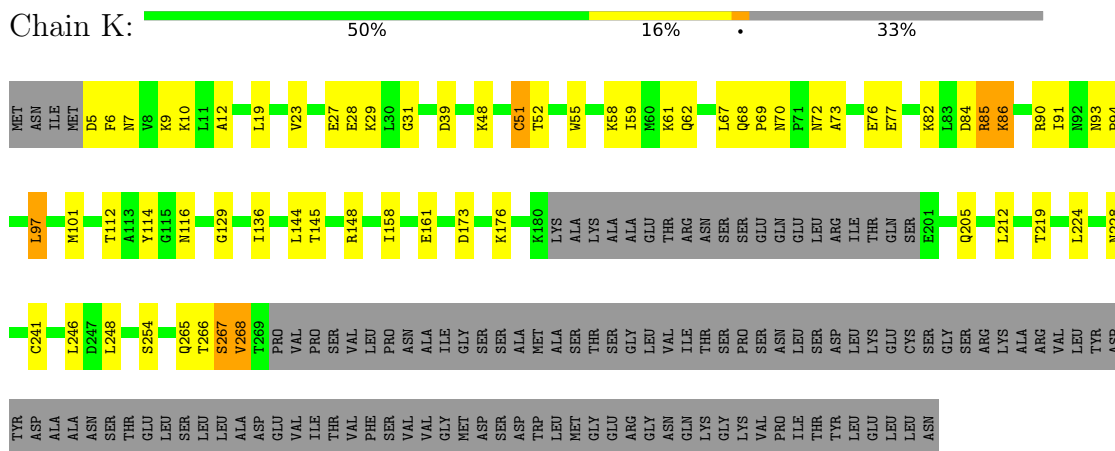
Chain I: 50% 16% 33%



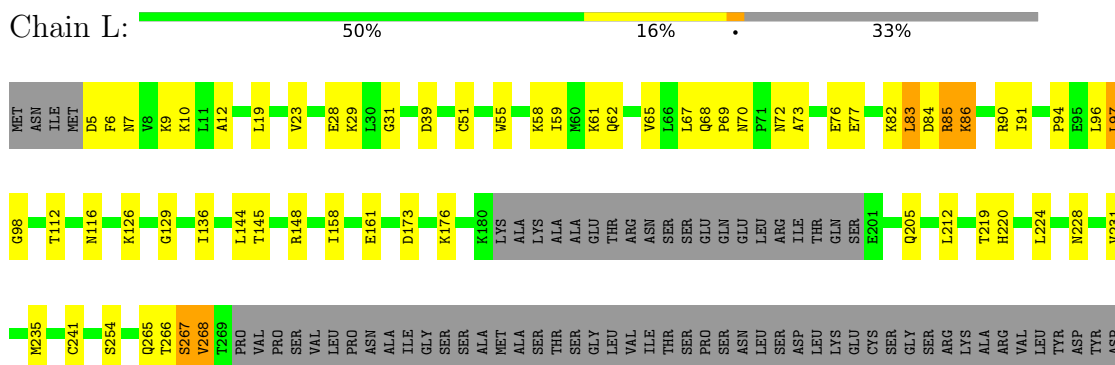
- Molecule 1: Endophilin-B1



- Molecule 1: Endophilin-B1



- Molecule 1: Endophilin-B1



ALA
ALA
ASN
SER
THR
GLU
LEU
SER
LEU
LEU
LEU
ALA
ASP
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SER
SER
VAL
VAL
GLY
MET
MET
ASP
SER
ASP
TRP

• Molecule 1: Endophilin-B1

Chain M:  50% 15% 33%

MET
ASN
ILE
MET
D5
F6
N7
V8
K9
K10
L11
A12
L19
V23
E28
K29
L30
G31
D39
C51
W55
K58
I59
M60
K61
Q62
L67
Q68
P69
N70
P71
N72
A73
E76
E77
K82
L83
D84
R85
K86
R90
I91
P94
F95
L96
L97
M101

T112
A113
Y114
N116
G129
I136
L144
T145
R148
I158
E161
D173
K176
K180
LYS
ALA
LYS
ALA
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GLY
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LEU
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SER
E201
Q205
L212
T219
L224
N228
C241
L246

D247
L248
S254
Q265
T266
V267
T268
PRO
VAL
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ASN

• Molecule 1: Endophilin-B1

Chain N:  49% 16% 33%

MET
ASN
ILE
MET
D5
F6
N7
V8
K9
K10
L11
A12
L19
V23
E27
E28
K29
L30
G31
D39
K48
C51
T52
W55
K58
I59
M60
K61
Q62
L67
Q68
P69
N70
P71
N72
E76
E77
K82
L83
D84
R85
K86
R90
I91
P94
E95
L96

L97
G98
T112
M116
K126
G129
I136
L144
T145
R148
I158
E161
D173
K176
K180
ALA
ALA
ALA
GLU
THR
ARG
ASN
SER
SER
SER
PRO
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LEU
LEU
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SER
E201
Q205
L212
T219
H220
L224
N228

V231
M235
C241
S254
Q265
T266
S267
V268
T269
PRO
VAL
VAL
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SER
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• Molecule 1: Endophilin-B1

Chain O:  49% 16% 33%

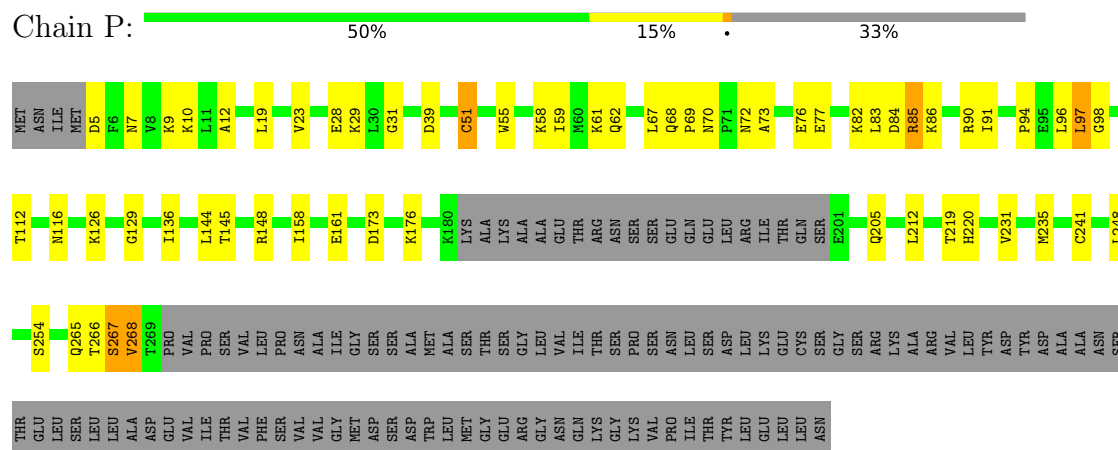
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D5
F6
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V8
K9
K10
L11
A12
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V23
E27
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K29
G31
D39
K48
C51
T52
K53
I54
W55
K58
I59
M60
K61
Q62
L67
Q68
P69
N70
P71
N72
A73
E76
E77
K82
L83
D84
R85
K86
R90
I91
P94

E95
L96
L97
M101
T112
A113
Y114
G115
N116
K120
T124
G129
I136
L144
T145
R148
I158
E161
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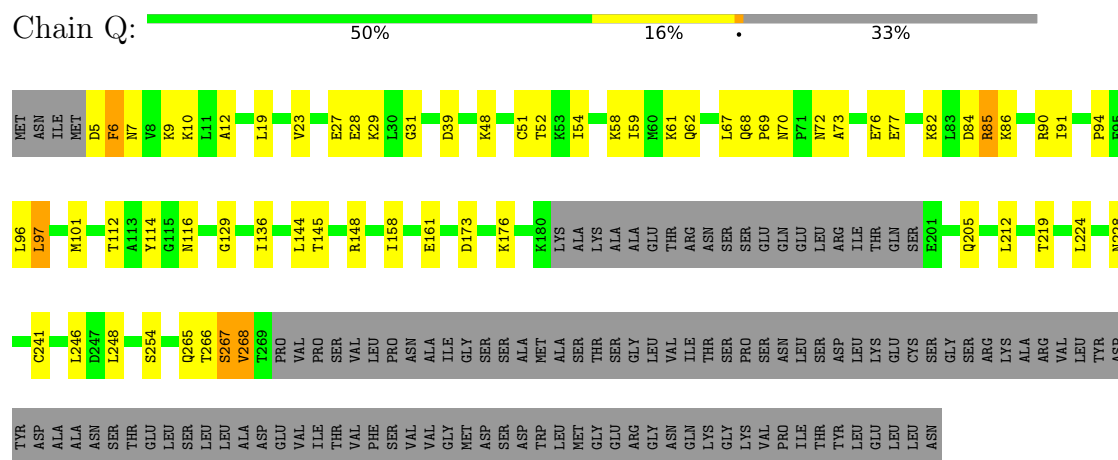
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L248
S254
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T266
S267
V268
T269
PRO
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PRO
SER
VAL
LEU
PRO
ASN
VAL
ILE
MET
GLY
SER
SER
SER
ASP
ASP
TRP
MET
ALA
SER
SER
GLY
THR
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LYS
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TYR
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ALA
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SER
THR
GLU
LEU
SER
SER
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PHE
SER
VAL
VAL
GLY
MET
GLY
ASP
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SER
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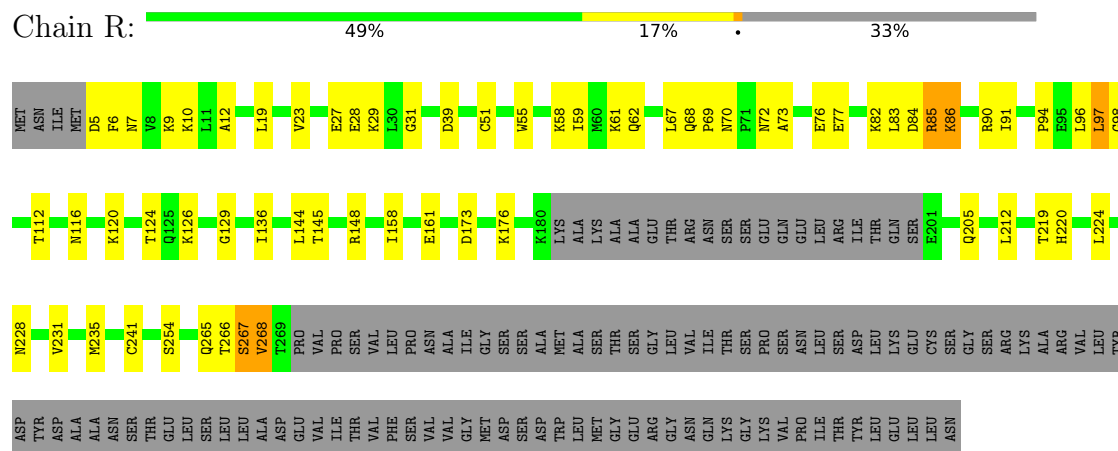
- Molecule 1: Endophilin-B1



- Molecule 1: Endophilin-B1

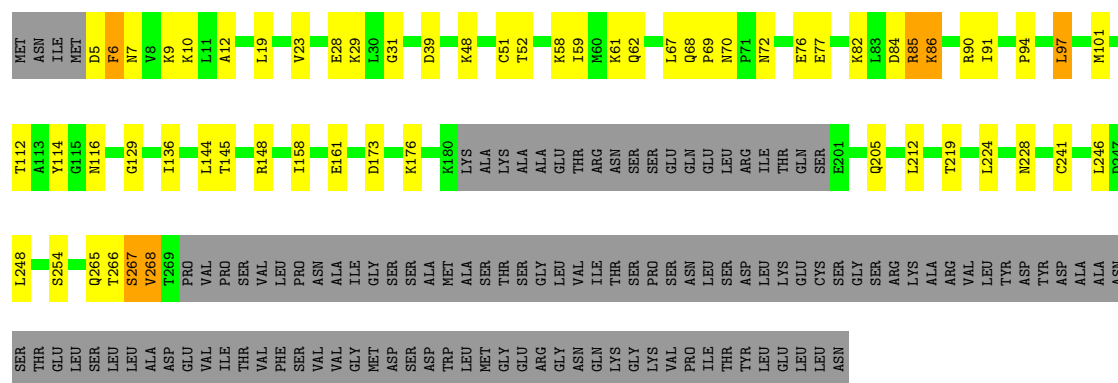


- Molecule 1: Endophilin-B1



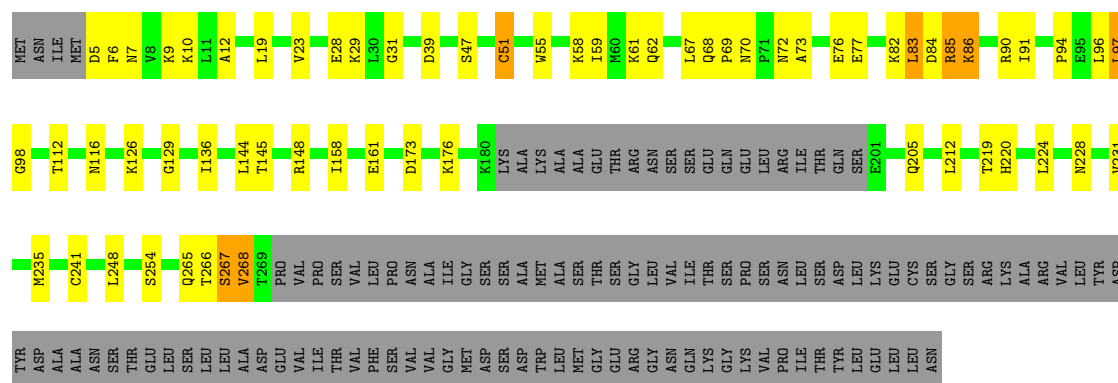
- Molecule 1: Endophilin-B1

Chain S:  51% 15% 33%



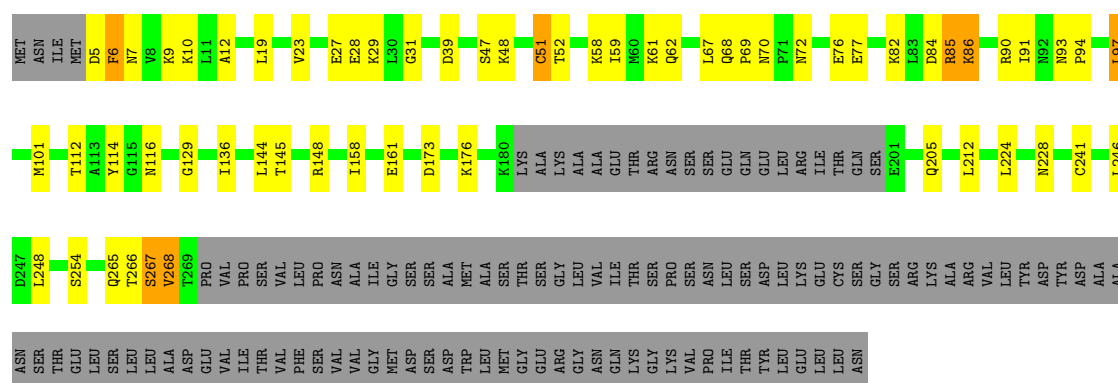
• Molecule 1: Endophilin-B1

Chain T:  49% 16% 33%



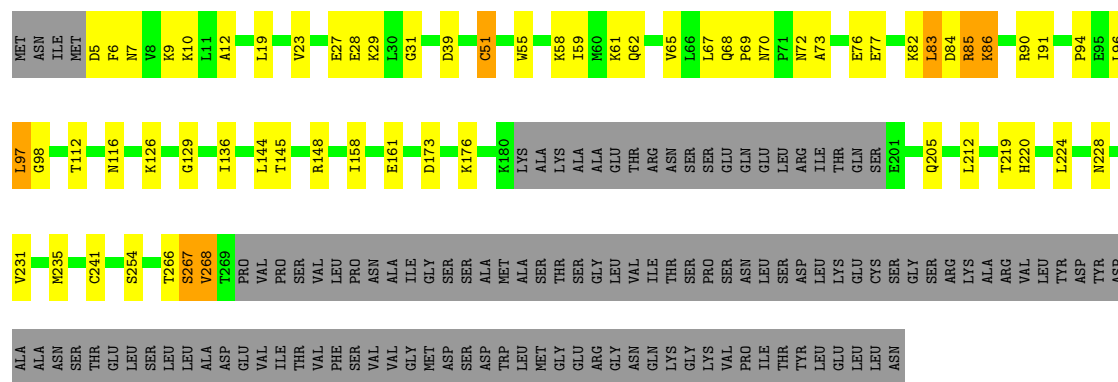
• Molecule 1: Endophilin-B1

Chain V:  50% 15% 33%



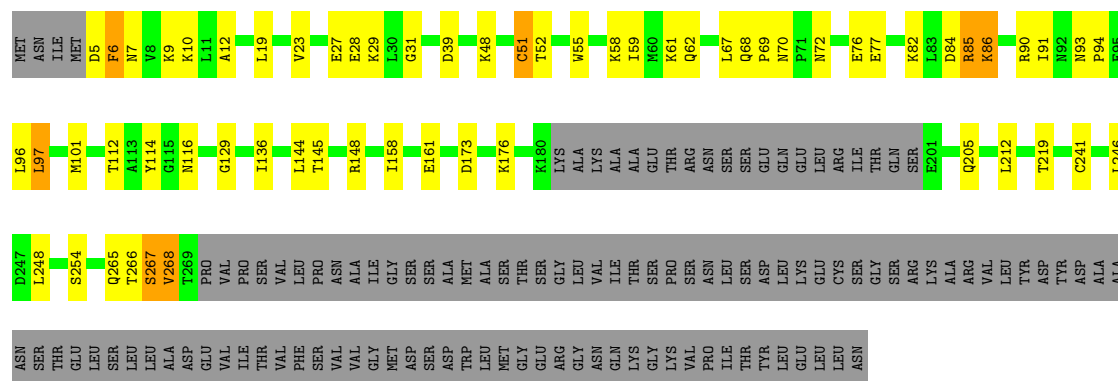
• Molecule 1: Endophilin-B1

Chain W:  50% 16% 33%



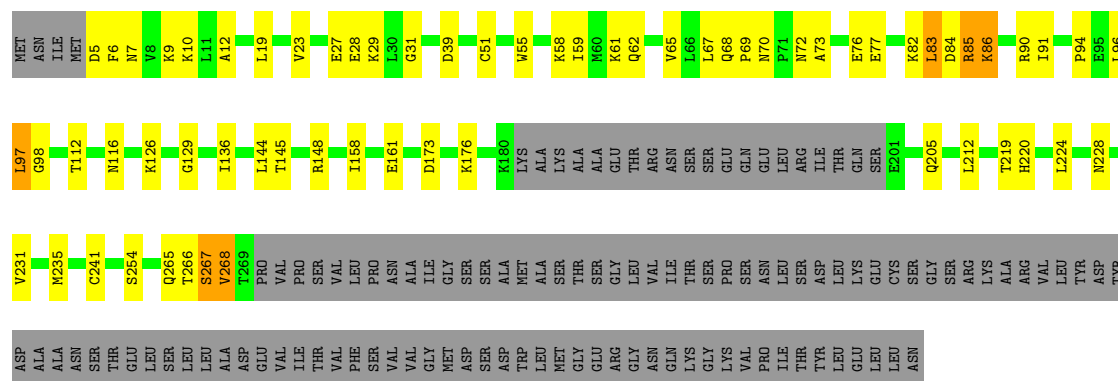
• Molecule 1: Endophilin-B1

Chain X: 50% 15% 33%



• Molecule 1: Endophilin-B1

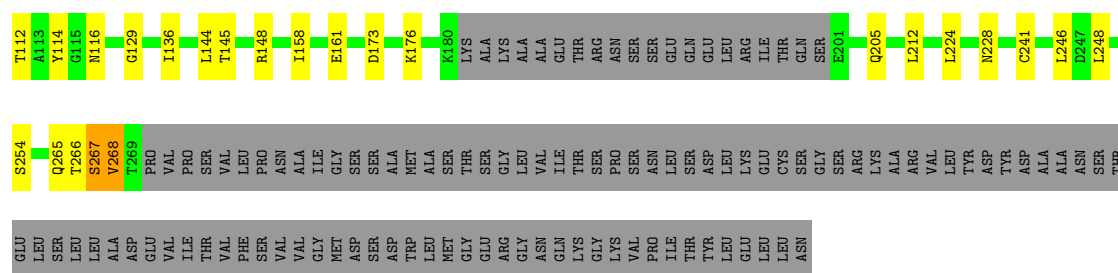
Chain Y: 49% 16% 33%



• Molecule 1: Endophilin-B1

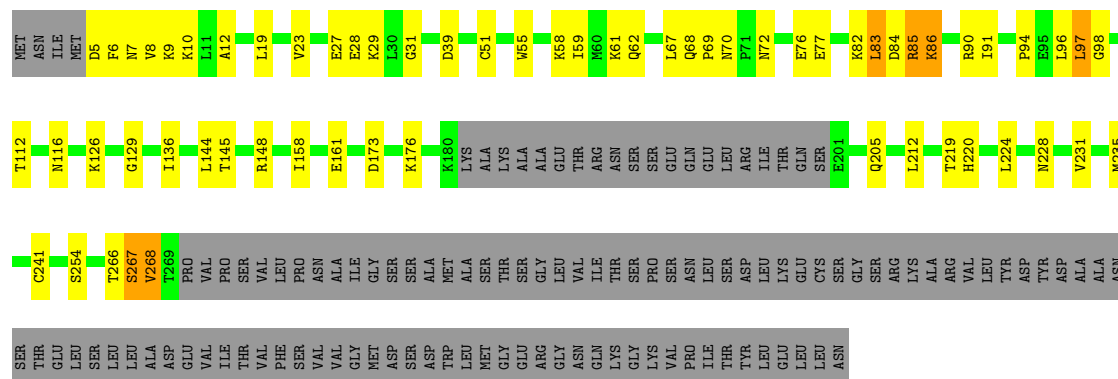
Chain a: 50% 15% 33%





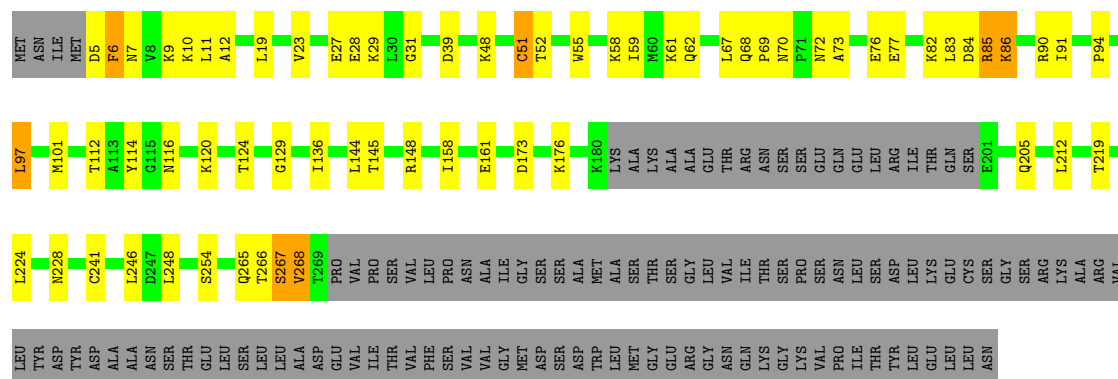
• Molecule 1: Endophilin-B1

Chain b: 50% 16% 33%



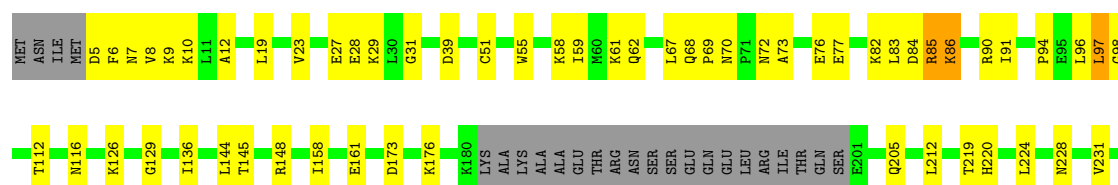
• Molecule 1: Endophilin-B1

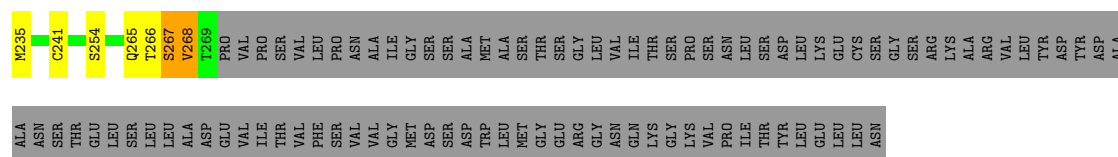
Chain c: 49% 16% 33%



• Molecule 1: Endophilin-B1

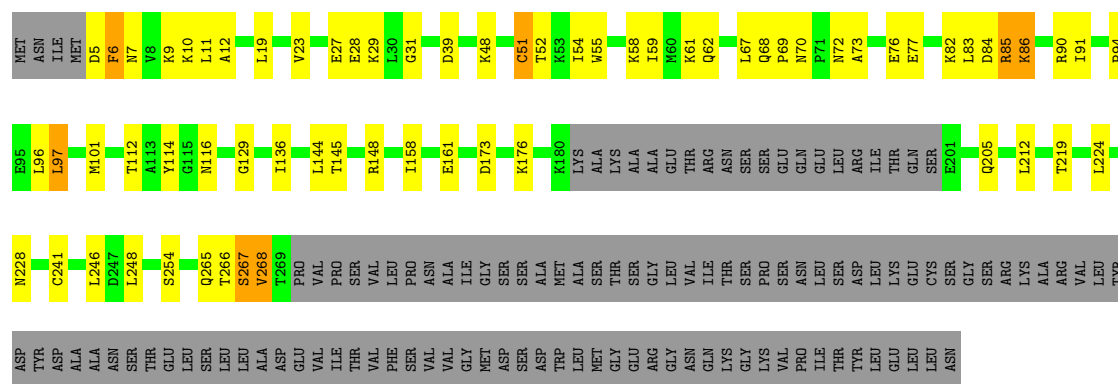
Chain d: 49% 16% 33%





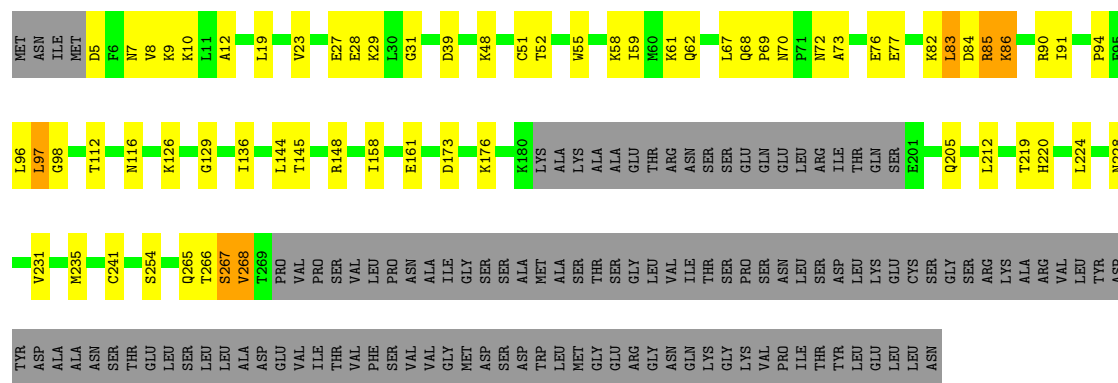
• Molecule 1: Endophilin-B1

Chain e: 49% 16% 33%



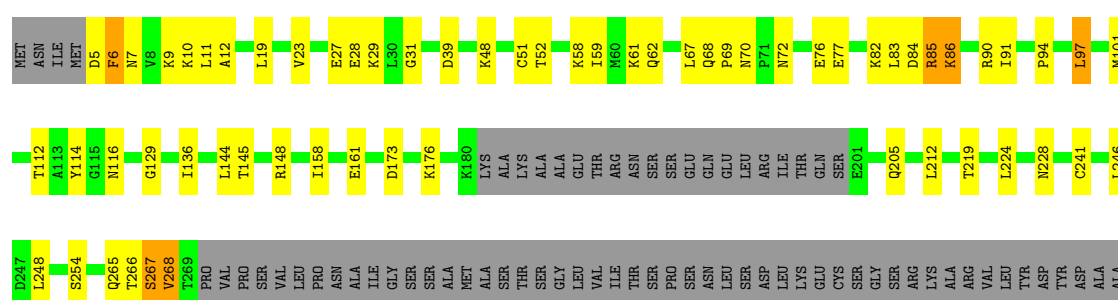
• Molecule 1: Endophilin-B1

Chain f: 49% 16% 33%

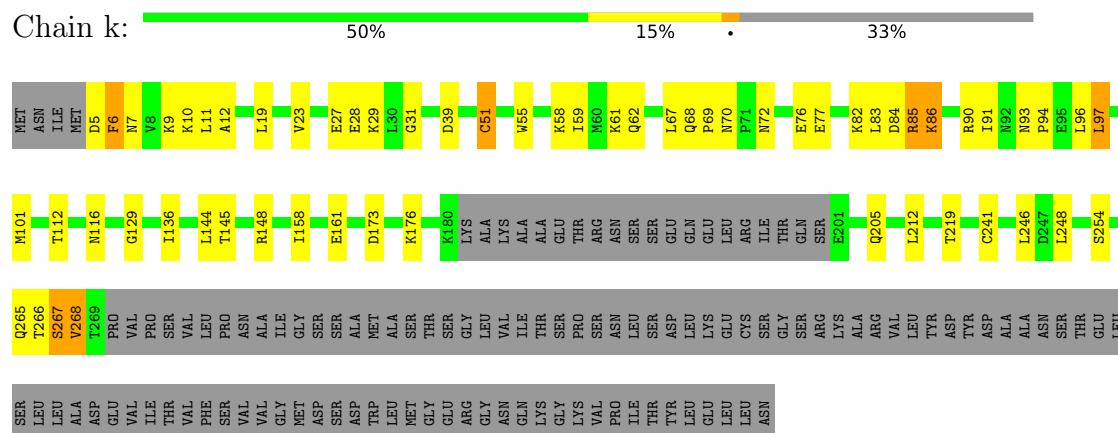


• Molecule 1: Endophilin-B1

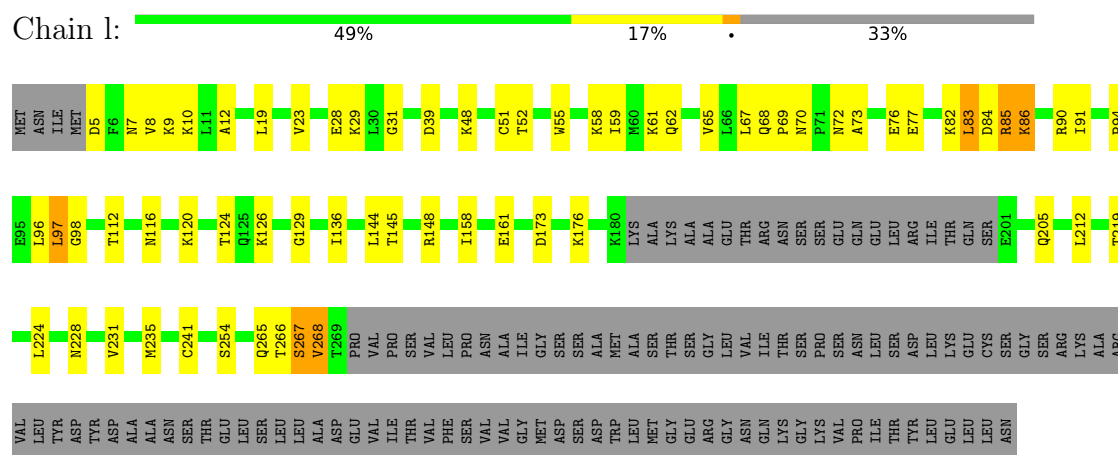
Chain g: 50% 16% 33%



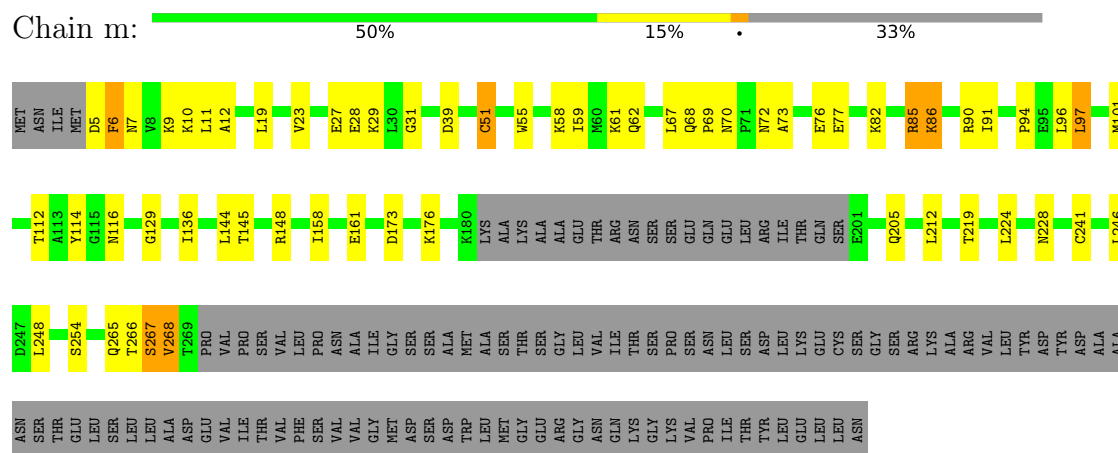
● Molecule 1: Endophilin-B1



● Molecule 1: Endophilin-B1

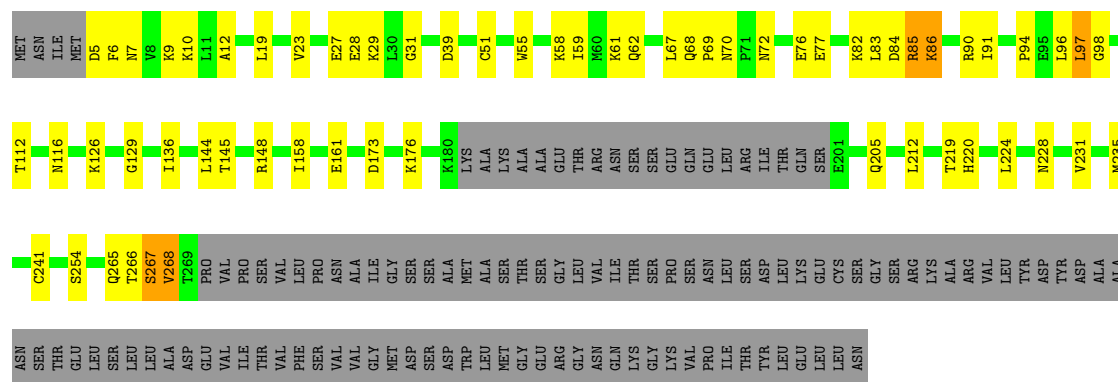


● Molecule 1: Endophilin-B1



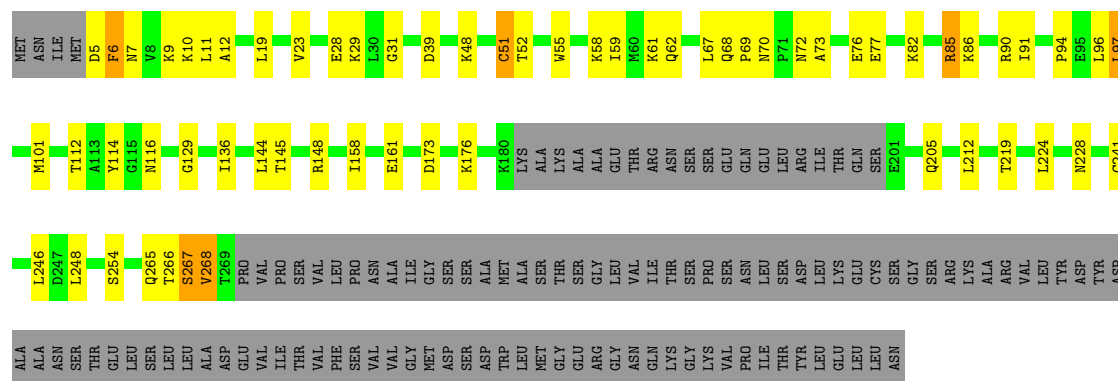
● Molecule 1: Endophilin-B1





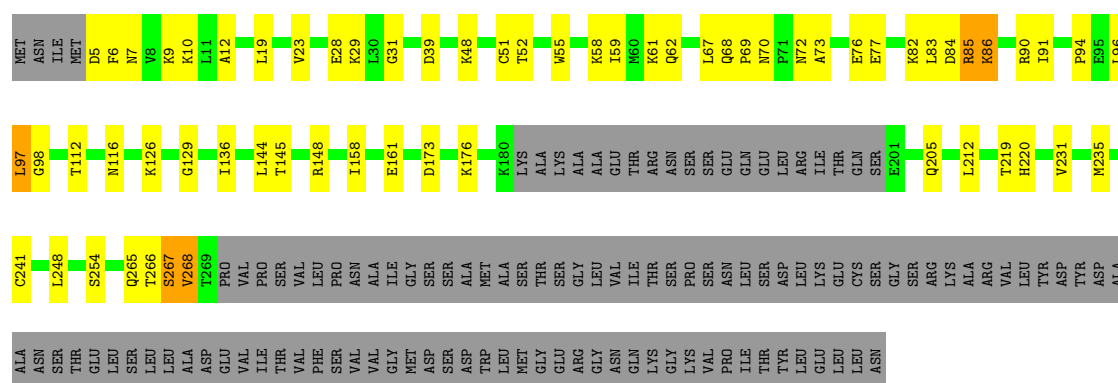
• Molecule 1: Endophilin-B1

Chain o: 50% 16% 33%



• Molecule 1: Endophilin-B1

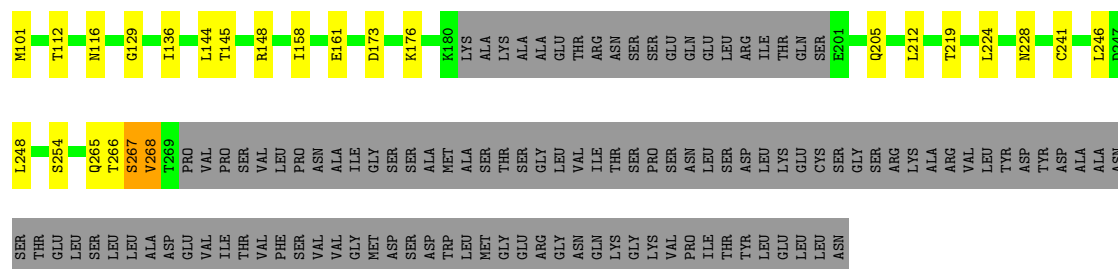
Chain p: 50% 16% 33%



• Molecule 1: Endophilin-B1

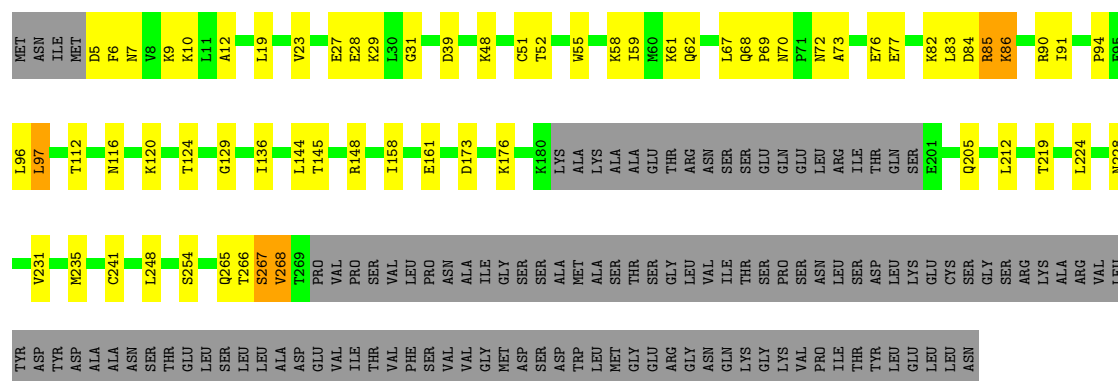
Chain q: 50% 15% 33%





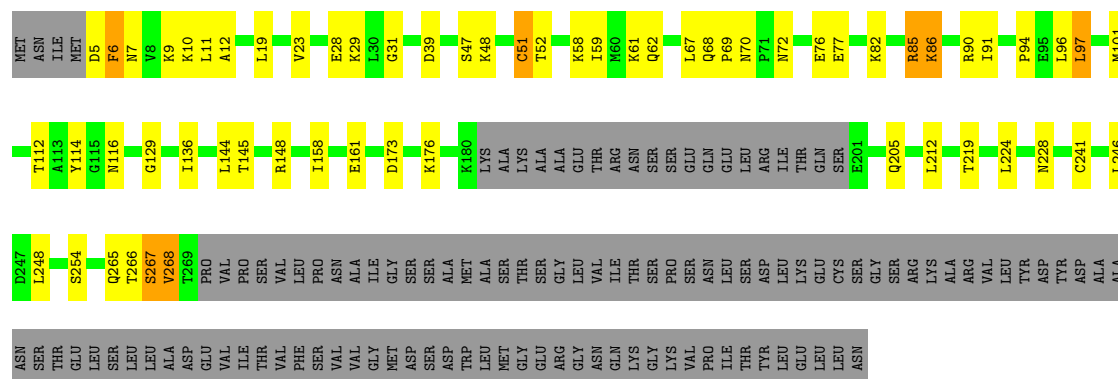
• Molecule 1: Endophilin-B1

Chain r: 49% 17% 33%



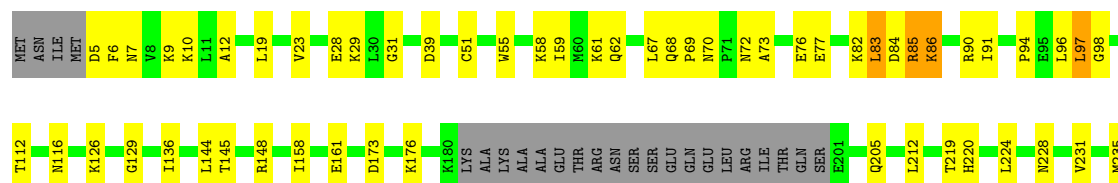
• Molecule 1: Endophilin-B1

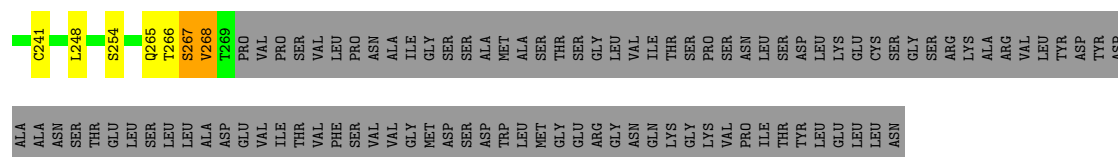
Chain s: 50% 15% 33%



• Molecule 1: Endophilin-B1

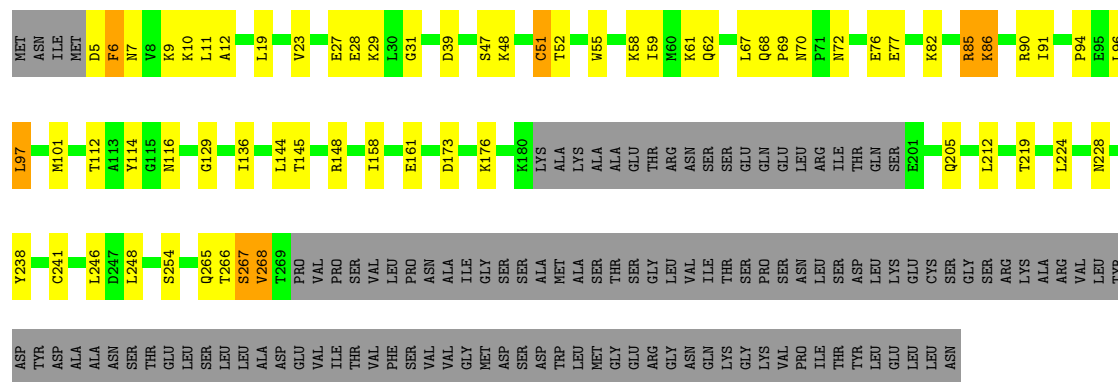
Chain t: 50% 16% 33%





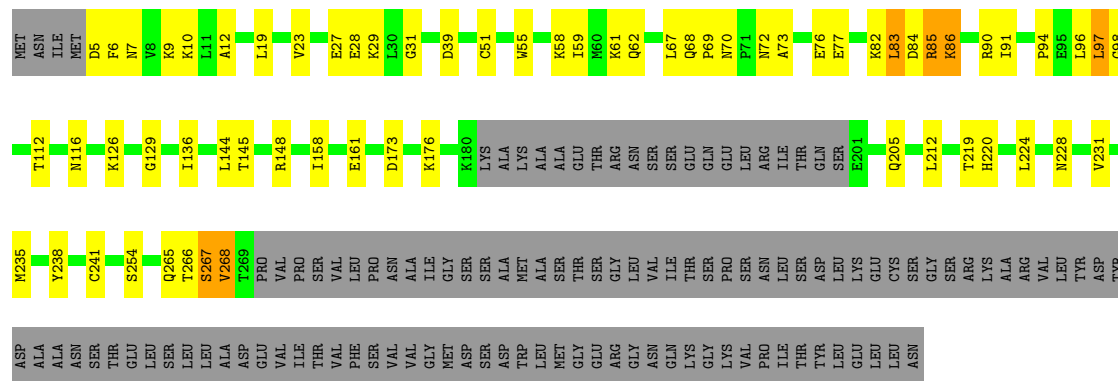
• Molecule 1: Endophilin-B1

Chain v: 49% 16% 33%



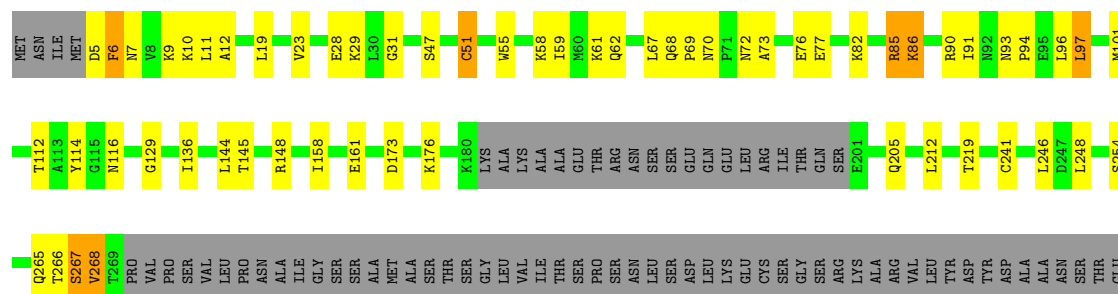
• Molecule 1: Endophilin-B1

Chain w: 49% 16% 33%



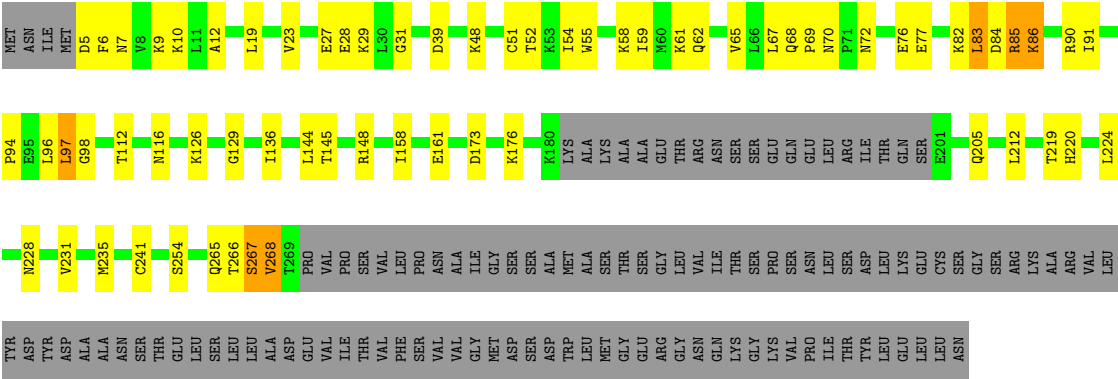
• Molecule 1: Endophilin-B1

Chain x: 51% 15% 33%



LEU
SER
LEU
LEU
LEU
ALA
ASP
GLU
VAL
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
ASN

● 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 ($e^-/\text{Å}^2$)	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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.34	0/1993	0.76	2/2685 (0.1%)
1	B	0.35	0/1993	0.76	2/2685 (0.1%)
1	C	0.34	0/1993	0.76	2/2685 (0.1%)
1	D	0.35	0/1993	0.77	2/2685 (0.1%)
1	E	0.34	0/1993	0.76	2/2685 (0.1%)
1	F	0.35	0/1993	0.77	2/2685 (0.1%)
1	G	0.34	0/1993	0.76	2/2685 (0.1%)
1	H	0.35	0/1993	0.76	2/2685 (0.1%)
1	I	0.34	0/1993	0.76	2/2685 (0.1%)
1	J	0.35	0/1993	0.77	2/2685 (0.1%)
1	K	0.34	0/1993	0.76	2/2685 (0.1%)
1	L	0.35	0/1993	0.77	1/2685 (0.0%)
1	M	0.34	0/1993	0.76	1/2685 (0.0%)
1	N	0.35	0/1993	0.77	2/2685 (0.1%)
1	O	0.34	0/1993	0.76	2/2685 (0.1%)
1	P	0.35	0/1993	0.77	1/2685 (0.0%)
1	Q	0.34	0/1993	0.76	2/2685 (0.1%)
1	R	0.35	0/1993	0.77	2/2685 (0.1%)
1	S	0.34	0/1993	0.76	1/2685 (0.0%)
1	T	0.35	0/1993	0.77	1/2685 (0.0%)
1	V	0.34	0/1993	0.76	2/2685 (0.1%)
1	W	0.35	0/1993	0.77	2/2685 (0.1%)
1	X	0.34	0/1993	0.76	2/2685 (0.1%)
1	Y	0.35	0/1993	0.77	2/2685 (0.1%)
1	a	0.34	0/1993	0.76	2/2685 (0.1%)
1	b	0.35	0/1993	0.77	2/2685 (0.1%)
1	c	0.34	0/1993	0.76	2/2685 (0.1%)
1	d	0.35	0/1993	0.77	2/2685 (0.1%)
1	e	0.34	0/1993	0.76	2/2685 (0.1%)
1	f	0.35	0/1993	0.77	2/2685 (0.1%)
1	g	0.34	0/1993	0.76	2/2685 (0.1%)
1	h	0.35	0/1993	0.76	2/2685 (0.1%)
1	i	0.34	0/1993	0.76	1/2685 (0.0%)
1	j	0.35	0/1993	0.77	2/2685 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	k	0.34	0/1993	0.76	2/2685 (0.1%)
1	l	0.35	0/1993	0.77	1/2685 (0.0%)
1	m	0.34	0/1993	0.76	2/2685 (0.1%)
1	n	0.36	0/1993	0.77	2/2685 (0.1%)
1	o	0.34	0/1993	0.76	1/2685 (0.0%)
1	p	0.36	0/1993	0.77	1/2685 (0.0%)
1	q	0.34	0/1993	0.76	2/2685 (0.1%)
1	r	0.35	0/1993	0.77	2/2685 (0.1%)
1	s	0.34	0/1993	0.76	1/2685 (0.0%)
1	t	0.35	0/1993	0.77	1/2685 (0.0%)
1	v	0.34	0/1993	0.76	2/2685 (0.1%)
1	w	0.35	0/1993	0.77	2/2685 (0.1%)
1	x	0.34	0/1993	0.76	1/2685 (0.0%)
1	y	0.35	0/1993	0.77	2/2685 (0.1%)
All	All	0.35	0/95664	0.76	84/128880 (0.1%)

There are no bond length outliers.

The worst 5 of 84 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	v	254	SER	N-CA-C	-8.31	105.15	114.62
1	N	254	SER	N-CA-C	-8.30	105.16	114.62
1	c	254	SER	N-CA-C	-8.30	105.16	114.62
1	C	254	SER	N-CA-C	-8.29	105.17	114.62
1	E	254	SER	N-CA-C	-8.29	105.17	114.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1963	0	1963	56	0
1	B	1963	0	1963	51	0
1	C	1963	0	1963	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1963	0	1963	52	0
1	E	1963	0	1963	62	0
1	F	1963	0	1963	51	0
1	G	1963	0	1963	61	0
1	H	1963	0	1963	53	0
1	I	1963	0	1963	61	0
1	J	1963	0	1963	53	0
1	K	1963	0	1963	61	0
1	L	1963	0	1963	54	0
1	M	1963	0	1963	71	0
1	N	1963	0	1963	54	0
1	O	1963	0	1963	74	0
1	P	1963	0	1963	53	0
1	Q	1963	0	1963	73	0
1	R	1963	0	1963	53	0
1	S	1963	0	1963	69	0
1	T	1963	0	1963	54	0
1	V	1963	0	1963	70	0
1	W	1963	0	1963	54	0
1	X	1963	0	1963	73	0
1	Y	1963	0	1963	55	0
1	a	1963	0	1963	68	0
1	b	1963	0	1963	53	0
1	c	1963	0	1963	73	0
1	d	1963	0	1963	51	0
1	e	1963	0	1963	74	0
1	f	1963	0	1963	53	0
1	g	1963	0	1963	70	0
1	h	1963	0	1963	54	0
1	i	1963	0	1963	74	0
1	j	1963	0	1963	55	0
1	k	1963	0	1963	71	0
1	l	1963	0	1963	54	0
1	m	1963	0	1963	62	0
1	n	1963	0	1963	50	0
1	o	1963	0	1963	60	0
1	p	1963	0	1963	52	0
1	q	1963	0	1963	62	0
1	r	1963	0	1963	51	0
1	s	1963	0	1963	61	0
1	t	1963	0	1963	55	0
1	v	1963	0	1963	60	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	w	1963	0	1963	53	0
1	x	1963	0	1963	60	0
1	y	1963	0	1963	53	0
All	All	94224	0	94224	2131	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 2131 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:62:GLN:CG	1:F:97:LEU:HD22	1.43	1.49
1:s:62:GLN:CG	1:t:97:LEU:HD22	1.43	1.49
1:c:62:GLN:CG	1:d:97:LEU:HD22	1.43	1.49
1:O:62:GLN:CG	1:P:97:LEU:HD22	1.43	1.48
1:C:62:GLN:CG	1:D:97:LEU:HD22	1.43	1.48

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	21	42
1	B	212/315 (67%)	200 (94%)	12 (6%)	18	40
1	C	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	D	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	E	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	F	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	G	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	H	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	I	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	J	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	K	212/315 (67%)	201 (95%)	11 (5%)	21	42

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	M	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	N	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	O	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	P	212/315 (67%)	200 (94%)	12 (6%)	18	40
1	Q	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	R	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	S	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	T	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	V	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	W	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	X	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	Y	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	a	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	b	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	c	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	d	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	e	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	f	212/315 (67%)	200 (94%)	12 (6%)	18	40
1	g	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	h	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	i	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	j	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	k	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	l	212/315 (67%)	200 (94%)	12 (6%)	18	40
1	m	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	n	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	o	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	p	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	q	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	r	212/315 (67%)	199 (94%)	13 (6%)	17	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	s	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	t	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	v	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	w	212/315 (67%)	199 (94%)	13 (6%)	17	38
1	x	212/315 (67%)	201 (95%)	11 (5%)	21	42
1	y	212/315 (67%)	199 (94%)	13 (6%)	17	38
All	All	10176/15120 (67%)	9604 (94%)	572 (6%)	21	40

5 of 572 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	p	6	PHE
1	q	6	PHE
1	o	268	VAL
1	t	241	CYS
1	Q	85	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 156 such sidechains are listed below:

Mol	Chain	Res	Type
1	m	32	GLN
1	v	72	ASN
1	n	72	ASN
1	q	72	ASN
1	x	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 oligosaccharides 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.

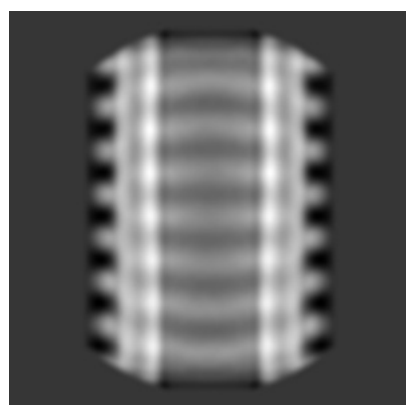
6 Map visualisation [i](#)

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.

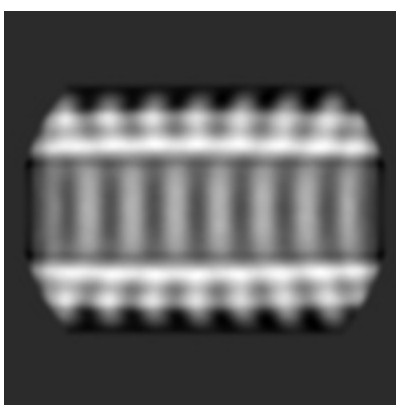
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y



Z

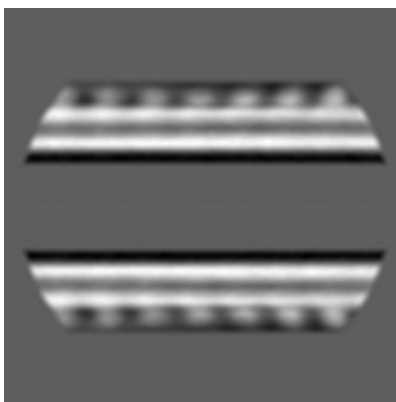
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

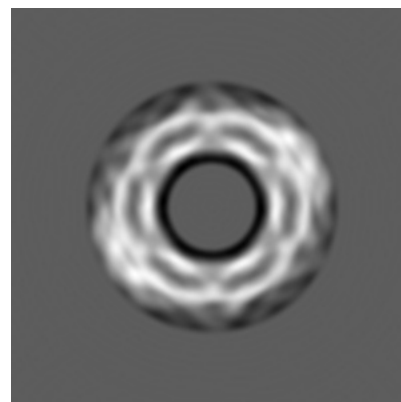
6.2.1 Primary map



X Index: 107



Y Index: 107



Z Index: 107

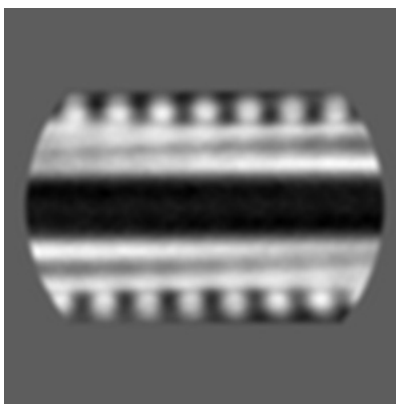
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

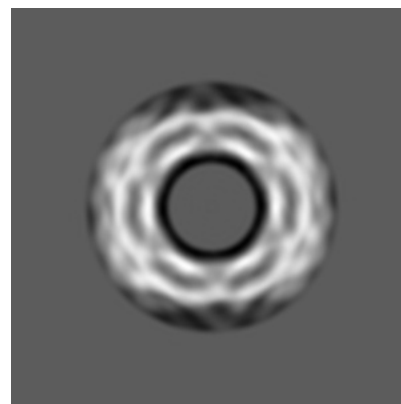
6.3.1 Primary map



X Index: 73



Y Index: 132

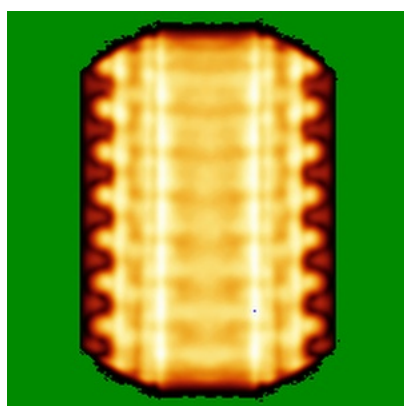


Z Index: 80

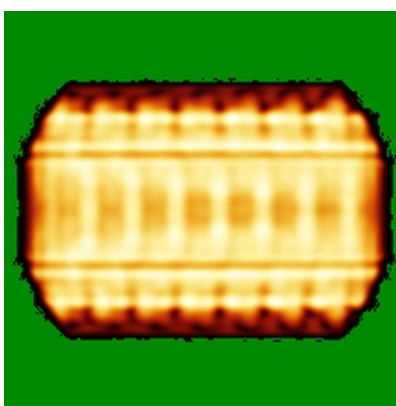
The images above show the largest variance slices of the map in three orthogonal directions.

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

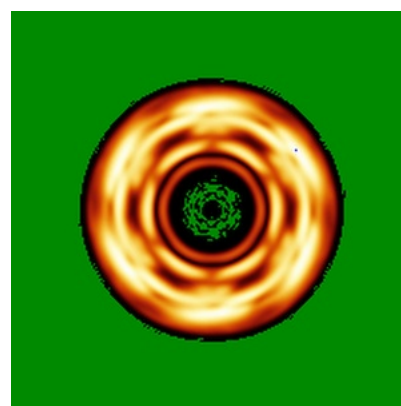
6.4.1 Primary map



X



Y

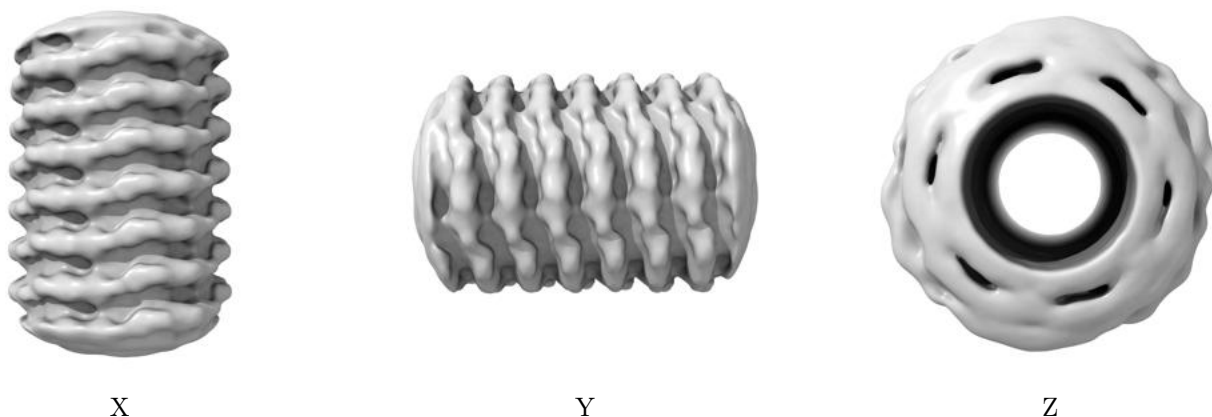


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

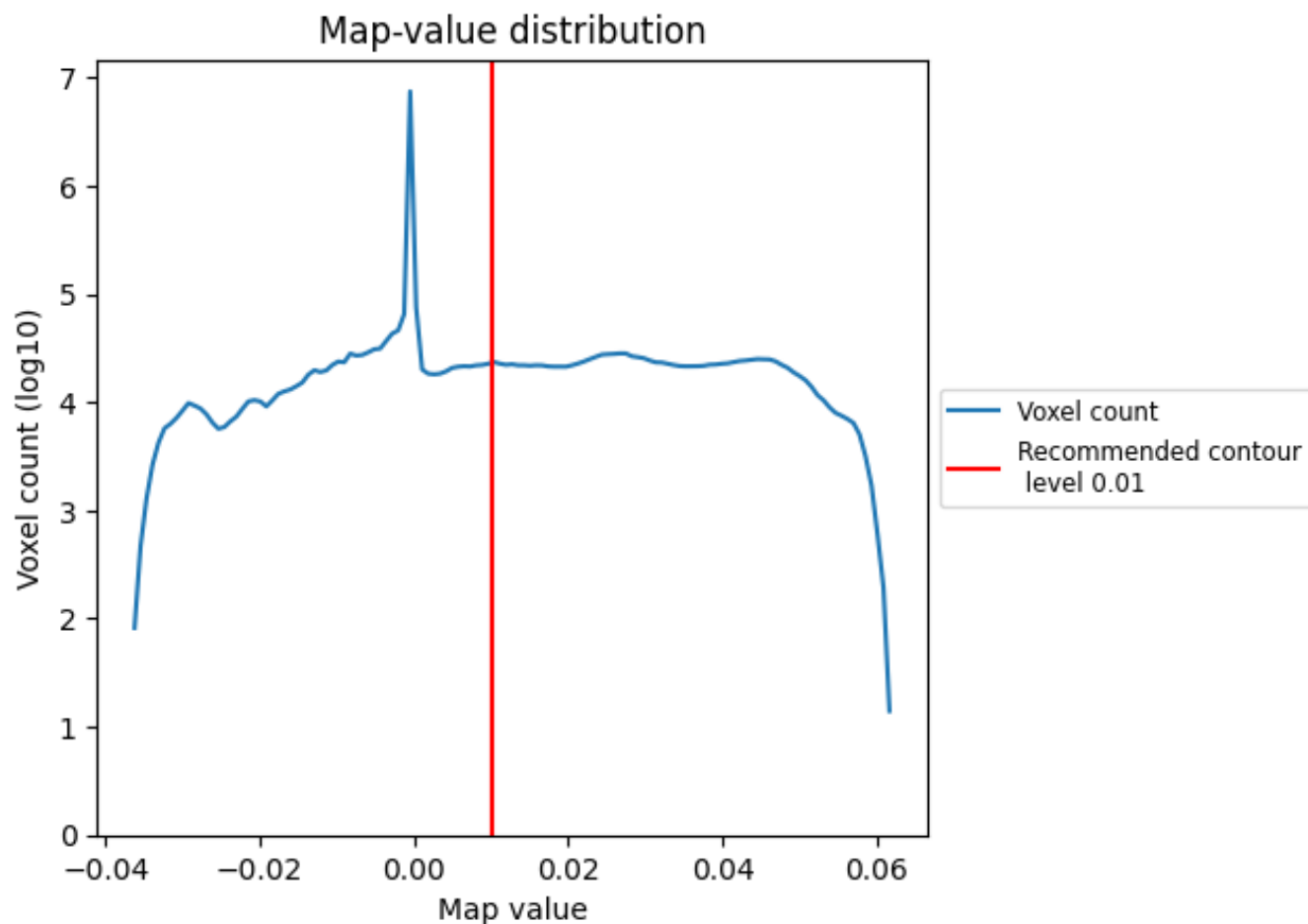
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

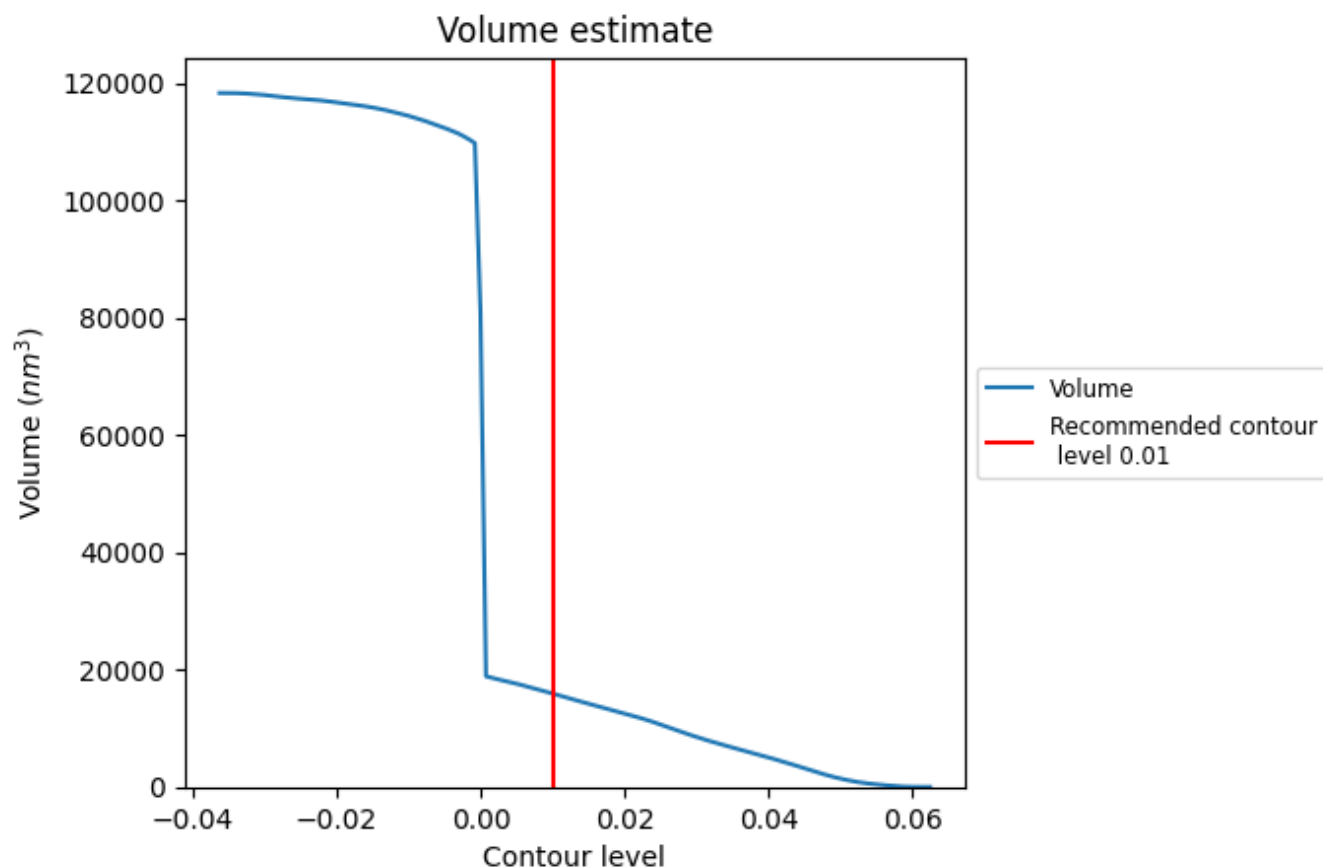
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

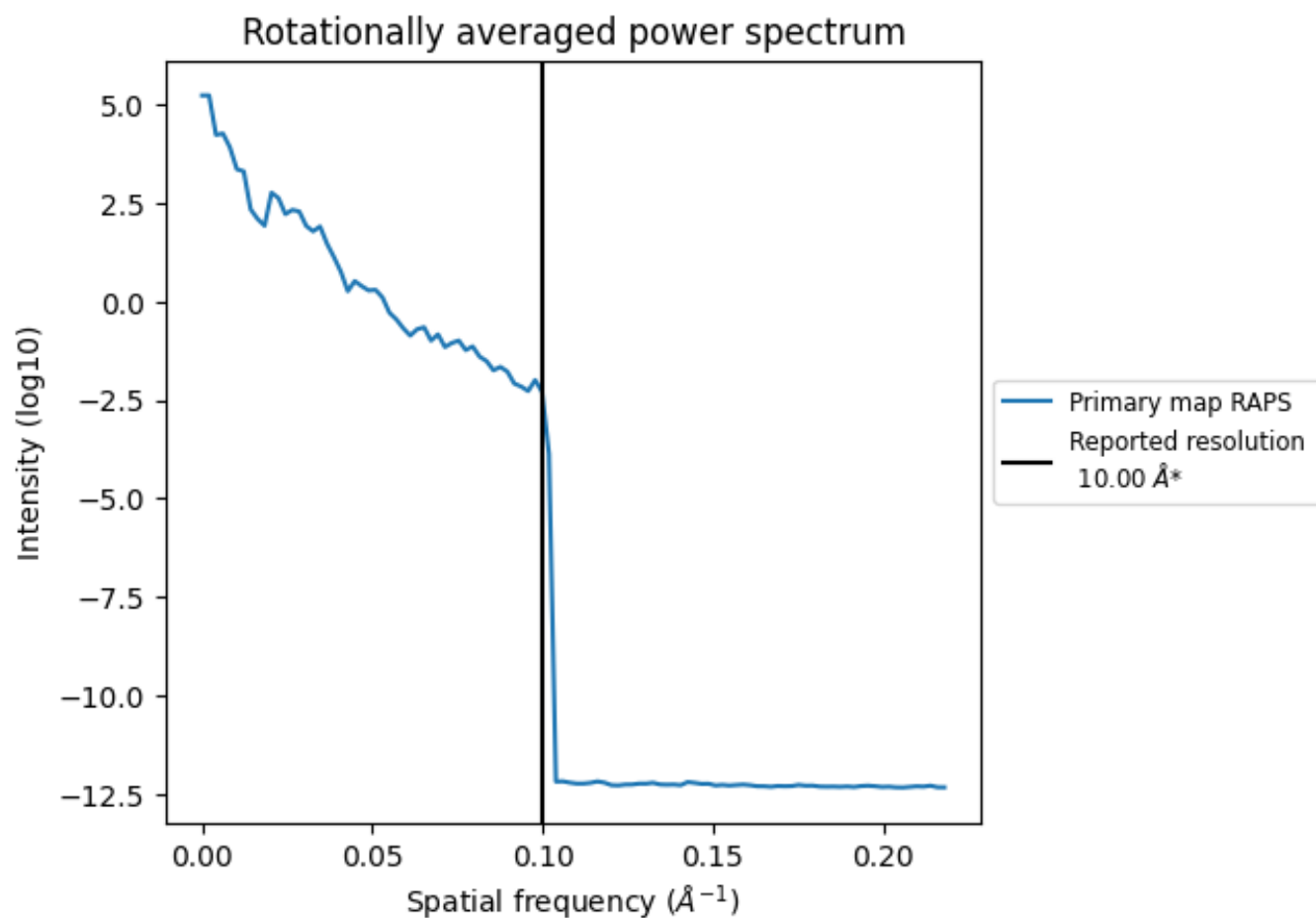
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 15935 nm^3 ; 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 Å⁻¹

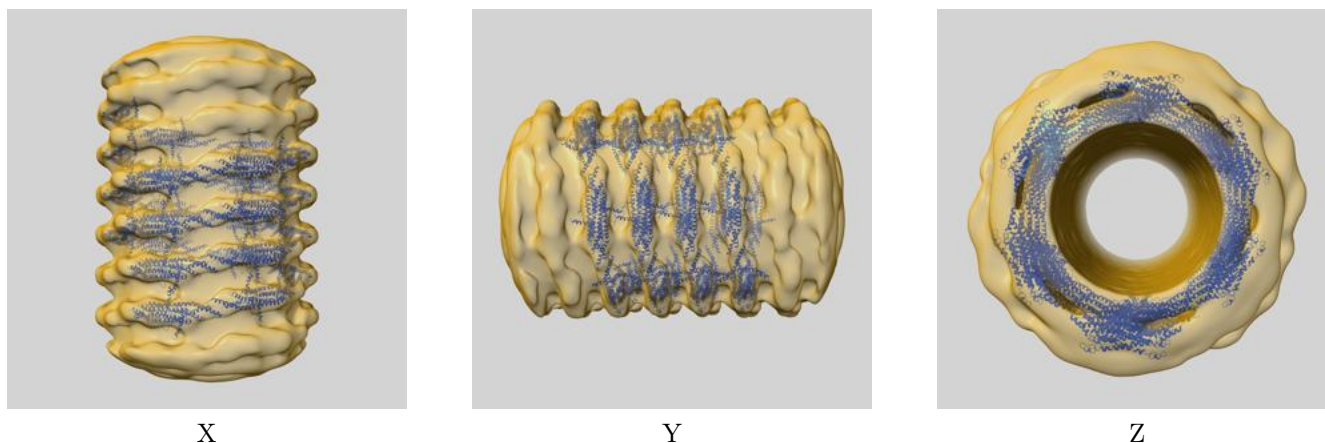
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

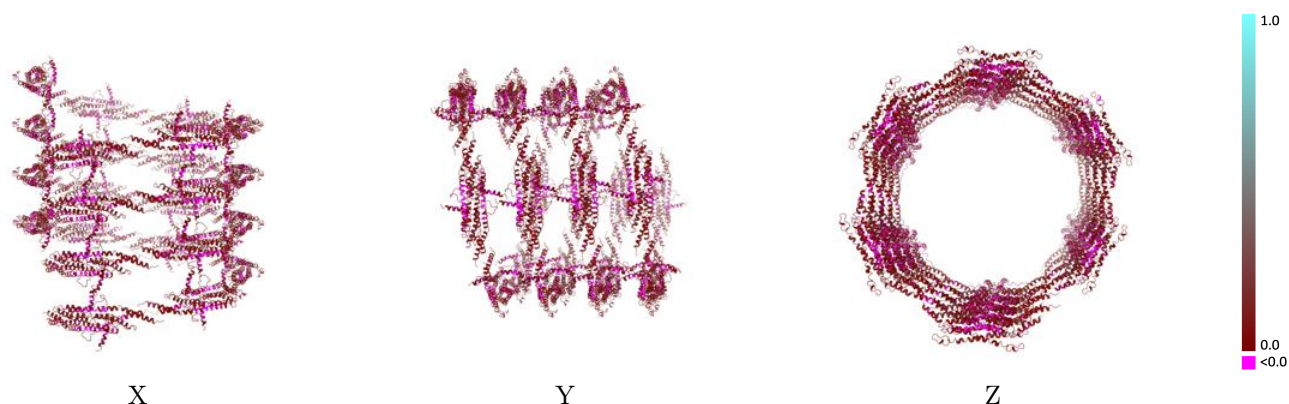
This section contains information regarding the fit between EMDB map EMD-20842 and PDB model 6UPN. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



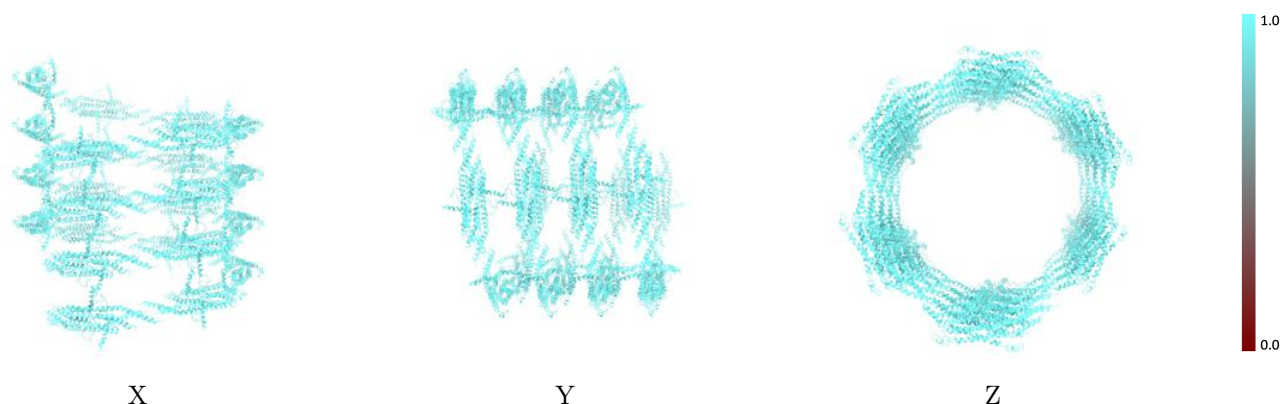
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



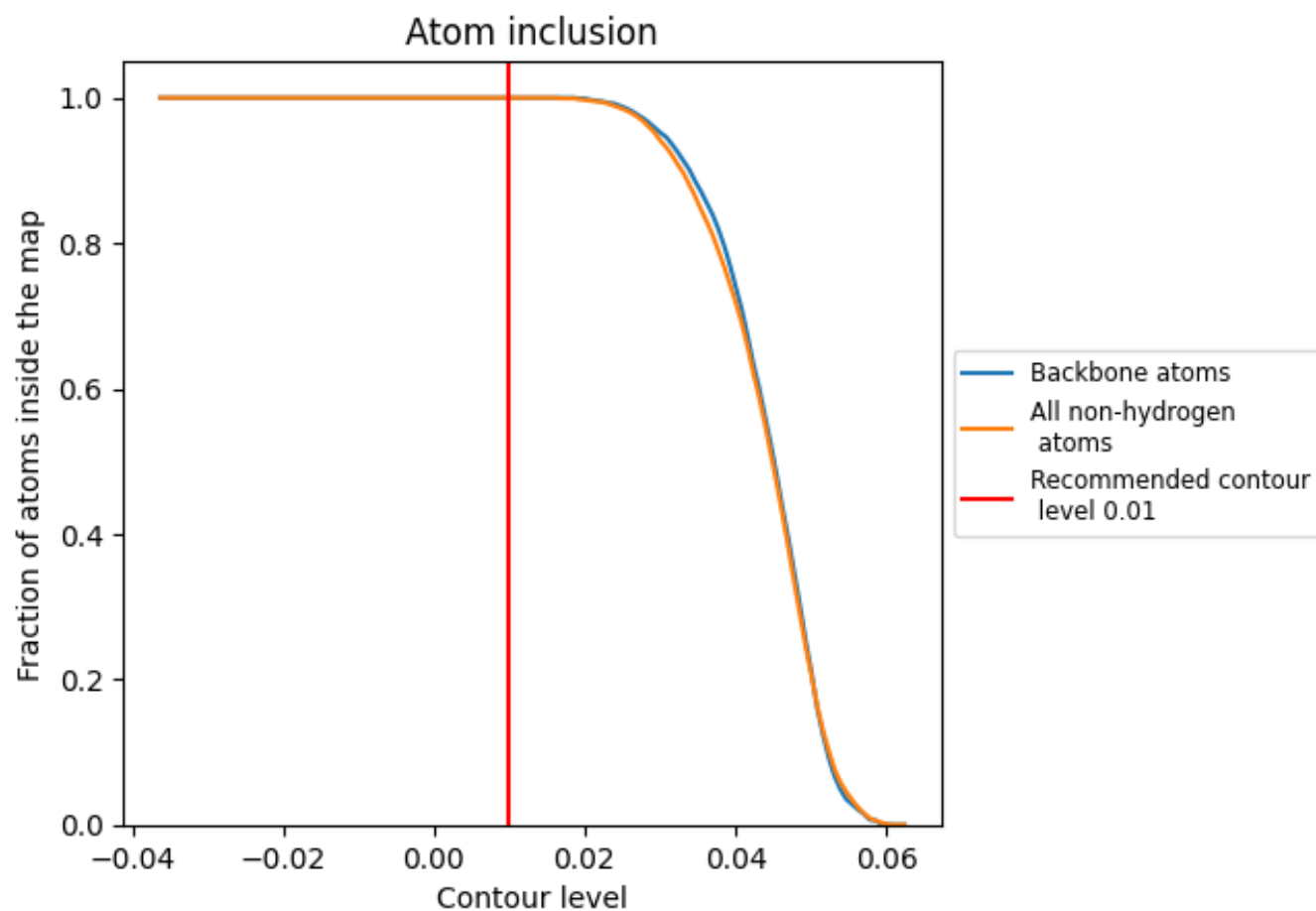
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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