



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 04:45 PM UTC

PDB ID : 5TCP / pdb_00005tcp
EMDB ID : EMD-8398
Title : Near-atomic resolution cryo-EM structure of the periplasmic domains of PrgH and PrgK
Authors : Worrall, L.J.; Hong, C.; Vuckovic, M.; Bergeron, J.R.C.; Huang, R.K.; Yu, Z.; Strynadka, N.C.J.
Deposited on : 2016-09-15
Resolution : 4.30 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:

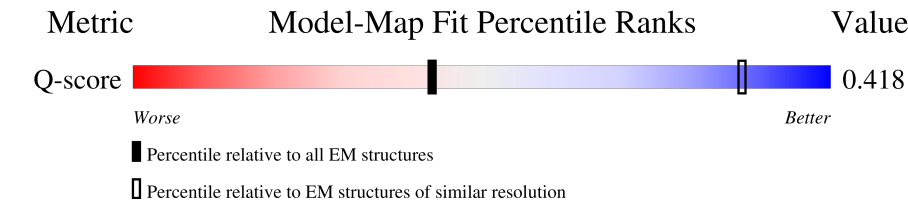
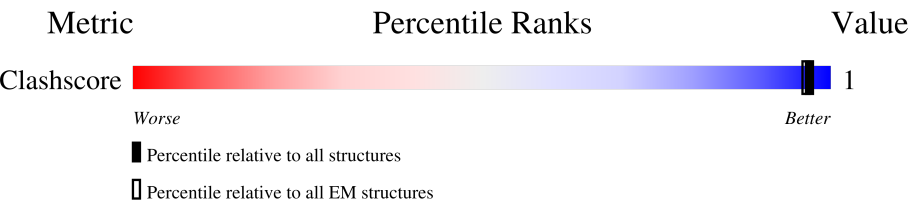
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 4.30 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.



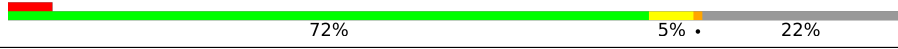
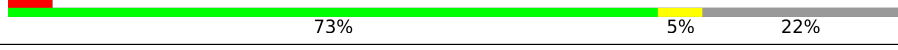
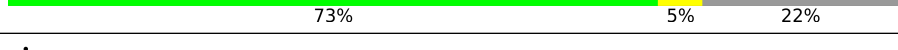
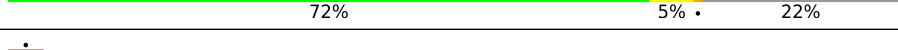
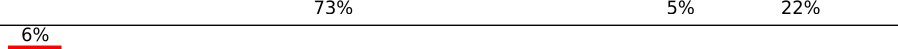
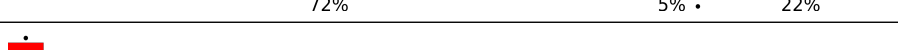
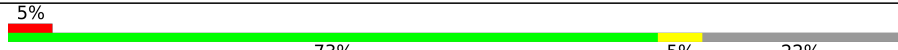
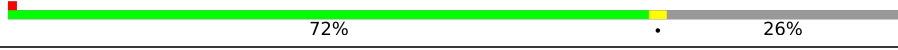
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	4585 (3.80 - 4.80)

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	0	235	72%5%•22%
1	2	235	5% 73%5%22%
1	4	235	6% 72%5%•22%
1	6	235	5% 72%5%•22%
1	8	235	6% 73%5%22%
1	B	235	72%5%•22%

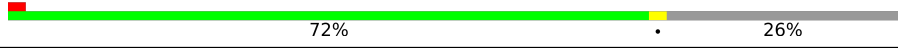
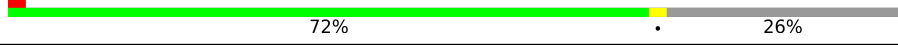
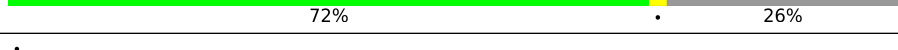
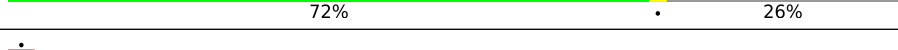
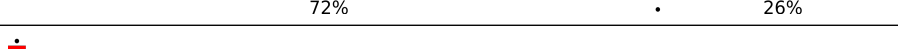
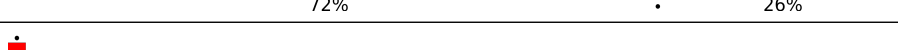
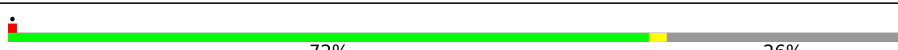
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Mol	Chain	Length	Quality of chain
1	D	235	
1	F	235	
1	H	235	
1	J	235	
1	L	235	
1	N	235	
1	P	235	
1	R	235	
1	T	235	
1	V	235	
1	X	235	
1	Z	235	
1	a	235	
1	c	235	
1	e	235	
1	g	235	
1	i	235	
1	k	235	
2	1	263	
2	3	263	
2	5	263	
2	7	263	
2	9	263	
2	A	263	
2	C	263	

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Mol	Chain	Length	Quality of chain
2	E	263	
2	G	263	
2	I	263	
2	K	263	
2	M	263	
2	O	263	
2	Q	263	
2	S	263	
2	U	263	
2	W	263	
2	Y	263	
2	b	263	
2	d	263	
2	f	263	
2	h	263	
2	j	263	
2	l	263	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 72888 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 Lipoprotein PrgK.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	2	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	4	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	6	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	8	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	B	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	D	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	F	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	H	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	J	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	L	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	N	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	P	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	R	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	T	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	V	184	Total 1437	C 905	N 250	O 279	S 3	0	0
1	X	184	Total 1437	C 905	N 250	O 279	S 3	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	Z	184	Total	C	N	O	S	0	0
			1437	905	250	279	3		
1	a	184	Total	C	N	O	S	0	0
			1437	905	250	279	3		
1	c	184	Total	C	N	O	S	0	0
			1437	905	250	279	3		
1	e	184	Total	C	N	O	S	0	0
			1437	905	250	279	3		
1	g	184	Total	C	N	O	S	0	0
			1437	905	250	279	3		
1	i	184	Total	C	N	O	S	0	0
			1437	905	250	279	3		
1	k	184	Total	C	N	O	S	0	0
			1437	905	250	279	3		

- Molecule 2 is a protein called Protein PrgH.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	3	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	5	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	7	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	9	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	A	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	C	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	E	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	G	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	I	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	K	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		
2	M	194	Total	C	N	O	S	0	0
			1600	1011	288	297	4		

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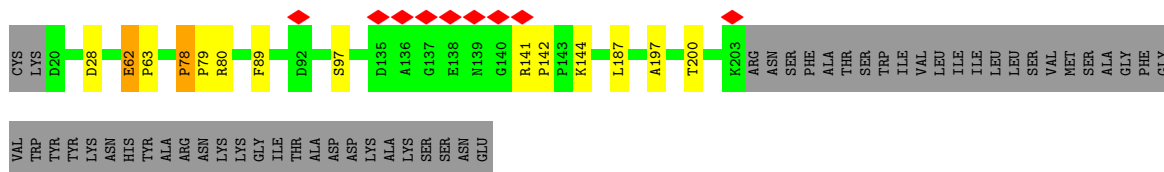
Mol	Chain	Residues	Atoms					AltConf	Trace
2	O	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	Q	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	S	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	U	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	W	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	Y	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	b	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	d	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	f	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	h	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	j	194	Total 1600	C 1011	N 288	O 297	S 4	0	0
2	l	194	Total 1600	C 1011	N 288	O 297	S 4	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.

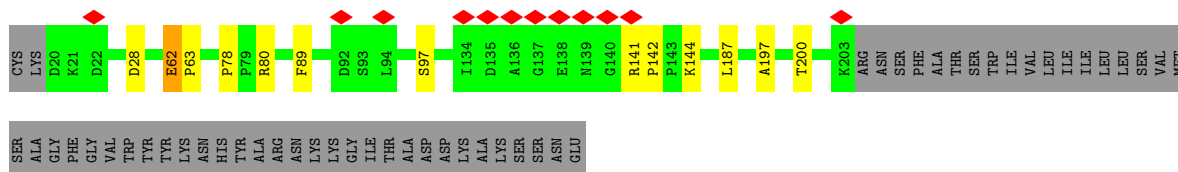
• Molecule 1: Lipoprotein PrgK

Chain 0: 



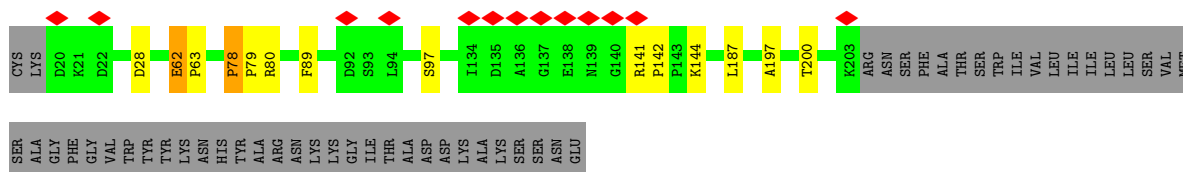
• Molecule 1: Lipoprotein PrgK

Chain 2: 



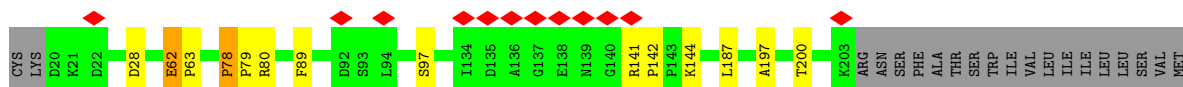
• Molecule 1: Lipoprotein PrgK

Chain 4: 



• Molecule 1: Lipoprotein PrgK

Chain 6: 



SER
ALA
GLY
PHE
GLY
VAL
TRP
TYR
TYR
LYS
ASN
HIS
TYR
ALA
ALA
ASN
LYS
LYS
GLY
ILE
THR
ALA
ASP
ASP
LYS
ALA
LYS
SER
SER
ASN
ASN
GLU

• Molecule 1: Lipoprotein PrgK

Chain 8:  6% 73% 5% 22%

CYS
LYS
D20
K21
D22
D28
E62
P63
P78
P79
R80
F89
D92
S93
L94
S97
D133
I134
D135
A136
G137
E138
N139
G140
R141
P142
P143
K144
L187
A197
T200
K203
ARG
ASN
SER
PHE
ALA
THR
SER
ILE
VAL
LEU
ILE
LEU
SER
MET
SER
ALA
GLY
PHE
VAL

MET
SER
ALA
GLY
PHE
GLY
VAL
TRP
TYR
TYR
LYS
ASN
HIS
TYR
ALA
ALA
ASN
LYS
LYS
GLY
ILE
THR
ALA
ASP
ASP
LYS
LYS
ALA
LYS
SER
SER
ASN
ASN
GLU

• Molecule 1: Lipoprotein PrgK

Chain B:  0% 72% 5% 22%

CYS
LYS
D20
D28
E62
P63
P78
P79
R80
F89
D92
S97
D135
A136
G137
E138
N139
G140
R141
P142
P143
K144
L187
A197
T200
K203
ARG
ASN
SER
PHE
ALA
THR
SER
ILE
VAL
LEU
ILE
LEU
SER
MET
SER
ALA
GLY
PHE
VAL

VAL
TRP
TYR
LYS
ASN
HIS
TYR
ALA
ALA
ASN
LYS
LYS
GLY
ILE
THR
ASP
ASP
LYS
LYS
ALA
LYS
SER
SER
ASN
ASN
GLU

• Molecule 1: Lipoprotein PrgK

Chain D:  0% 72% 5% 22%

CYS
LYS
D20
D28
E62
P63
P78
P79
R80
F89
D92
S97
D135
A136
G137
E138
N139
G140
R141
P142
P143
K144
L187
A197
T200
K203
ARG
ASN
SER
PHE
ALA
THR
SER
ILE
VAL
LEU
ILE
LEU
SER
MET
SER
ALA
GLY
PHE
VAL

VAL
TRP
TYR
LYS
ASN
HIS
TYR
ALA
ALA
ASN
LYS
LYS
GLY
ILE
THR
ASP
ASP
LYS
LYS
ALA
LYS
SER
SER
ASN
ASN
GLU

• Molecule 1: Lipoprotein PrgK

Chain F:  0% 72% 5% 22%

CYS
LYS
D20
D28
E62
P63
P78
P79
R80
F89
D92
S97
I134
D135
A136
G137
E138
N139
G140
R141
P142
P143
K144
L187
A197
T200
K203
ARG
ASN
SER
PHE
ALA
THR
SER
ILE
VAL
LEU
ILE
LEU
SER
MET
SER
ALA
GLY
PHE
VAL

GLY
VAL
TRP
TYR
LYS
ASN
HIS
TYR
ALA
ALA
ASN
LYS
LYS
GLY
ILE
THR
ASP
ASP
LYS
LYS
ALA
LYS
SER
SER
ASN
ASN
GLU

• Molecule 1: Lipoprotein PrgK

Chain H:  5% 72% 5% 22%

CYS
LYS
D20
D28
E62
P63
P78
P79
R80
F89
D92
S97
D135
A136
G137
E138
N139
G140
R141
P142
P143
K144
G157
D177
L187
A197
T200
K203
ARG
ASN
SER
PHE
ALA
THR
SER
ILE
VAL
LEU
ILE
LEU
SER
MET
SER
ALA
GLY
PHE
VAL
MET
SER

GLY
VAL
TRP
TYR
LYS
ASN
HIS
TYR
ALA
ALA
ASN
LYS
LYS
GLY
ILE
THR
ASP
ASP
LYS
LYS
ALA
LYS
SER
SER
ASN
ASN
GLU

ALA
GLY
PHE
GLY
VAL
TRP
TYR
LYS
ASN
HIS
TYR
ALA
ARG
ASN
LYS
GLY
ILE
THR
ASP
ASP
LYS
ALA
LYS
SER
SER
ASN
GLU

• Molecule 1: Lipoprotein PrgK

Chain J: 5% 73% 5% 22%

CYS
LYS
D20
D28
E62
P63
P78
P79
R80
F89
D92
S97
D135
A136
G137
E138
N139
G140
P142
P143
K144
D177
D181
L187
A197
T200
K203
ARG
ASN
PHE
THR
SER
TRP
VAL
ILE
LEU
LEU
SER
VAL

• Molecule 1: Lipoprotein PrgK

Chain L: 5% 73% 5% 22%

CYS
LYS
D20
D28
E62
P63
P78
P79
R80
F89
D92
S97
D135
A136
G137
E138
N139
G140
P142
P143
K144
L187
A197
T200
K203
ARG
ASN
PHE
THR
SER
TRP
VAL
ILE
LEU
LEU
SER
VAL
MET
SER
ALA
GLY
PHE
GLY
VAL

• Molecule 1: Lipoprotein PrgK

Chain N: 5% 73% 5% 22%

CYS
LYS
D20
D28
E62
P63
P78
P79
R80
F89
D92
S97
D135
A136
G137
E138
N139
G140
P142
P143
K144
G157
L187
A197
T200
K203
ARG
ASN
PHE
THR
SER
TRP
VAL
ILE
LEU
LEU
SER
VAL
MET
SER
ALA
GLY
PHE
GLY
VAL

• Molecule 1: Lipoprotein PrgK

Chain P: 5% 73% 5% 22%

CYS
LYS
D20
D28
E62
P63
P78
P79
R80
F89
D92
S97
D135
A136
G137
E138
N139
G140
P142
P143
K144
L187
A197
T200
K203
ARG
ASN
PHE
THR
SER
TRP
VAL
ILE
LEU
LEU
SER
VAL
MET
SER
ALA
GLY
PHE
GLY
VAL

• Molecule 1: Lipoprotein PrgK

Chain R: 5% 72% 5% 22%

CYS
LYS
D20
D28
E62
P63
P78
P79
R80
F89
D92
S97
I134
D135
A136
G137
E138
N139
G140
R141
P142
P143
K144
L187
A197
T200
K203
ARG
ASN
PHE
THR
SER
TRP
VAL
ILE
LEU
LEU
SER
VAL
MET
SER
ALA
GLY
PHE
GLY
VAL

GLY VAL TRP TYR LYS ASN HIS TYR ARG ALA ASN LYS GLY ILE THR ALA ASP ASP LYS LYS LYS SER SER ASN GLU

• Molecule 1: Lipoprotein PrgK

Chain T:



CYS LYS D20 D28 E62 P63 P78 P79 R80 F89 D92 S97 I134 D135 A136 G137 E138 N139 G140 R141 P142 P143 K144 L187 A197 T200 K203 ARG ASN SER PHE ALA THR TRP TRP ILE VAL LEU ILE ILE LEU LEU SER VAL MET SER ALA GLY PHE

GLY VAL TRP TYR LYS ASN HIS TYR ARG ALA ASN LYS GLY ILE THR ALA ASP ASP LYS LYS LYS SER SER ASN GLU

• Molecule 1: Lipoprotein PrgK

Chain V:



CYS LYS D20 K21 D22 D28 E62 P63 P78 P79 R80 F89 D92 S97 I134 D135 A136 G137 E138 N139 G140 R141 P142 P143 K144 L187 A197 T200 K203 ARG ASN SER PHE ALA THR TRP TRP ILE VAL LEU ILE ILE LEU LEU SER VAL MET SER ALA GLY PHE

VAL MET SER ALA GLY PHE GLY VAL TRP TYR LYS ASN HIS TYR ARG ALA ASN LYS GLY ILE THR ALA ASP ASP LYS LYS LYS SER SER ASN GLU

• Molecule 1: Lipoprotein PrgK

Chain X:



CYS LYS D20 K21 D22 D28 E62 P63 P78 P79 R80 F89 D92 S97 I134 D135 A136 G137 E138 N139 G140 R141 P142 P143 K144 L187 A197 T200 K203 ARG ASN SER PHE ALA THR TRP TRP ILE VAL LEU ILE ILE LEU LEU SER VAL MET SER ALA GLY PHE

PHE GLY VAL TRP TYR LYS ASN HIS TYR ARG ALA ASN LYS GLY ILE THR ALA ASP ASP LYS LYS LYS SER SER ASN GLU

• Molecule 1: Lipoprotein PrgK

Chain Z:



CYS LYS D20 D28 E62 P63 P78 P79 R80 F89 D92 S97 I134 D135 A136 G137 E138 N139 G140 R141 P142 P143 K144 L187 A197 T200 K203 ARG ASN SER PHE ALA THR TRP TRP ILE VAL LEU ILE ILE LEU LEU SER VAL MET SER ALA GLY PHE

GLY PHE GLY VAL TRP TYR LYS ASN HIS TYR ARG ALA ASN LYS GLY ILE THR ALA ASP ASP LYS LYS LYS SER SER ASN GLU

• Molecule 1: Lipoprotein PrgK

Chain a:



CYS LYS D20 D28 E62 P63 P78 P79 R80 F89 D92 S93 L94 S97 I134 D135 A136 G137 E138 N139 G140 R141 P142 P143 K144 L187 A197 T200 K203 ARG ASN SER PHE ALA THR TRP TRP ILE VAL LEU ILE ILE LEU LEU SER VAL MET SER ALA GLY PHE

GLY PHE GLY VAL TRP TYR TYR LYS HIS TYR TYR ALA ARG ASN LYS LYS GLY ILE THR ALA ASP ASP LYS LYS ALA LYS SER SER ASN ASN GLU

• Molecule 1: Lipoprotein PrgK

Chain c: 5% 73% 5% 22%

CYS LYS D20 D28 E62 P63 P78 P79 R80 F89 D92 S97 D133 I134 D135 A136 G137 E138 N139 G140 R141 P142 P143 K144 L187 A197 T200 K203 ARG ASN SER PHE ALA THR SER TRP ILE VAL LEU ILE ILE LEU SER VAL MET SER ALA GLY

• Molecule 1: Lipoprotein PrgK

Chain e: 5% 73% 5% 22%

CYS LYS D20 D28 E62 P63 P78 P79 R80 F89 D92 S93 L94 S97 I134 D135 A136 G137 E138 N139 G140 R141 P142 P143 K144 L187 A197 T200 K203 ARG ASN SER PHE ALA THR SER TRP ILE VAL LEU ILE ILE LEU SER VAL MET SER ALA

• Molecule 1: Lipoprotein PrgK

Chain g: 5% 73% 5% 22%

CYS LYS D20 D28 E62 P63 P78 P79 R80 F89 D92 S93 L94 S97 I134 D135 A136 G137 E138 N139 G140 R141 P142 P143 K144 L187 A197 T200 K203 ARG ASN SER PHE ALA THR SER TRP ILE VAL LEU ILE ILE LEU SER VAL MET SER ALA

• Molecule 1: Lipoprotein PrgK

Chain i: 5% 72% 5% 22%

CYS LYS D20 D28 E62 P63 P78 P79 R80 F89 D92 S93 L94 S97 I134 D135 A136 G137 E138 N139 G140 R141 P142 P143 K144 L187 A197 T200 K203 ARG ASN SER PHE ALA THR SER TRP ILE VAL LEU ILE ILE LEU SER VAL MET SER ALA

• Molecule 1: Lipoprotein PrgK

Chain k: 5% 72% 5% 22%

CYS LYS D20 D28 E62 P63 P78 P79 R80 F89 D92 S93 L94 S97 D135 A136 G137 E138 N139 G140 R141 P142 P143 K144 D181 L187 A197 T200 K203 ARG ASN SER PHE ALA THR SER TRP ILE VAL LEU ILE ILE LEU SER VAL MET SER

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• Molecule 2: Protein PrgH



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• Molecule 2: Protein PrgH



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• Molecule 2: Protein PrgH



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• Molecule 2: Protein PrgH



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• Molecule 2: Protein PrgH



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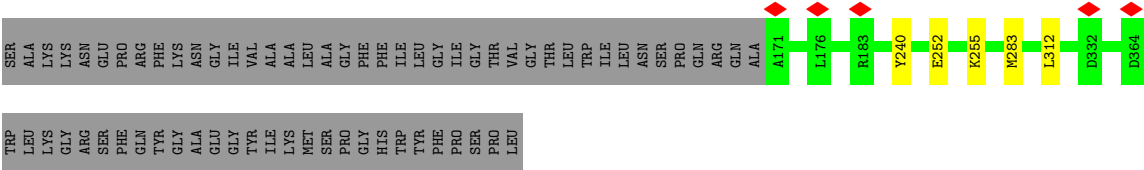
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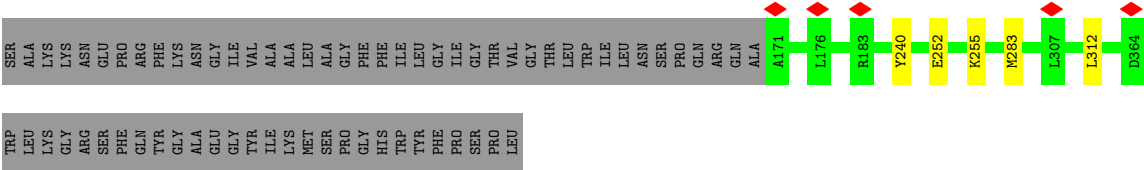
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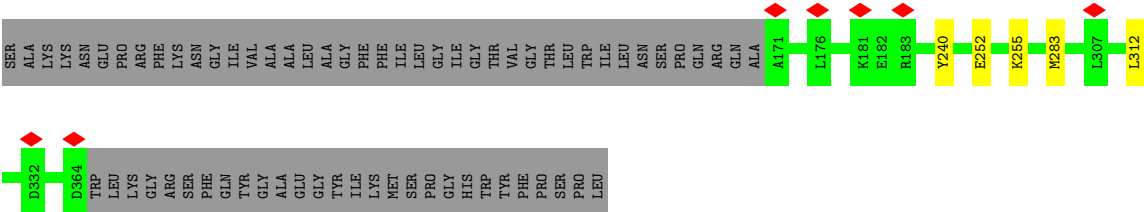
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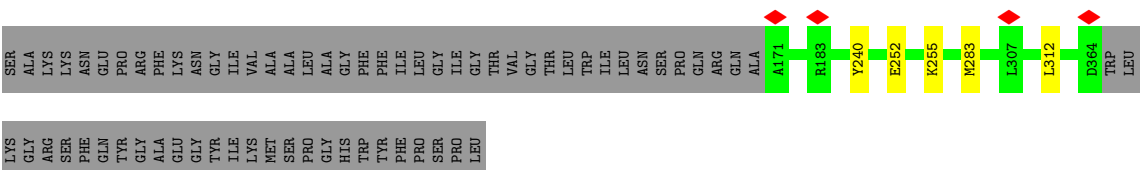
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• Molecule 2: Protein PrgH

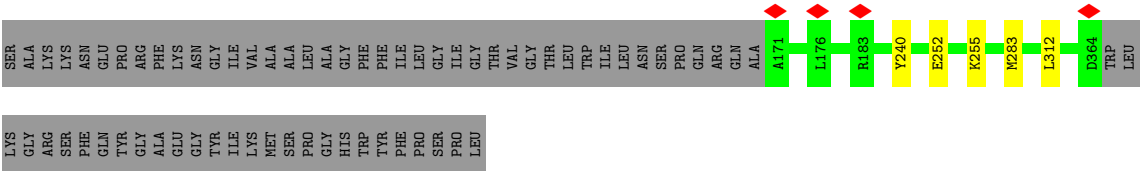


• Molecule 2: Protein PrgH

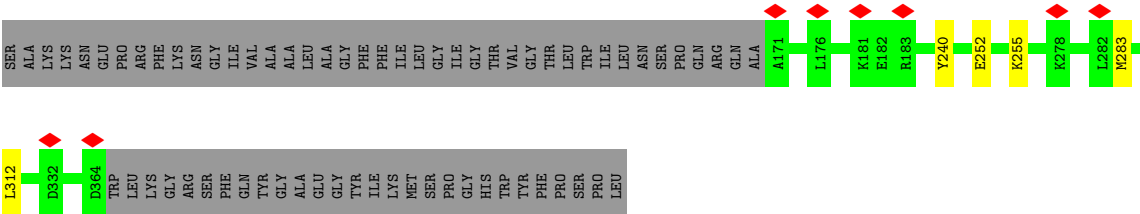


• Molecule 2: Protein PrgH

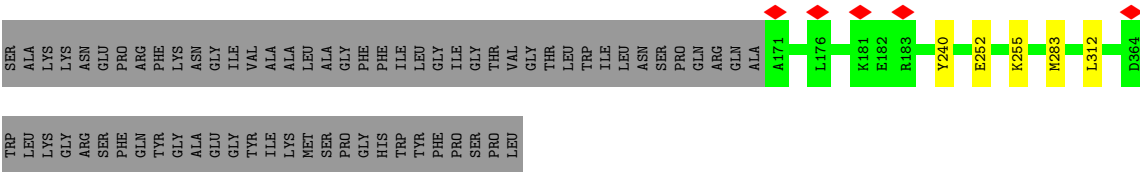




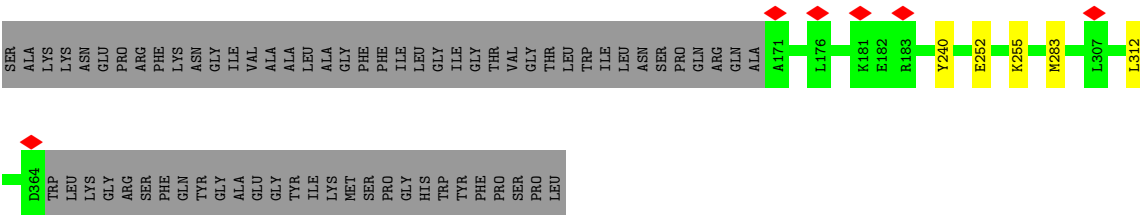
• Molecule 2: Protein PrgH



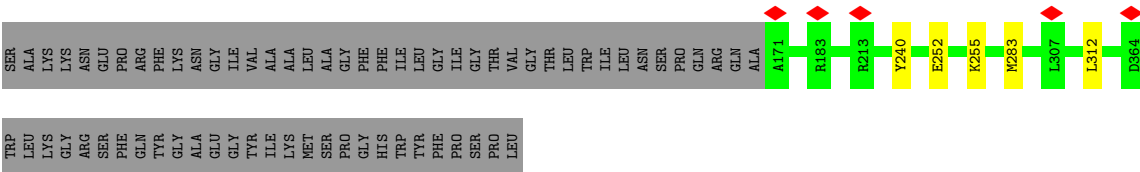
• Molecule 2: Protein PrgH



• Molecule 2: Protein PrgH

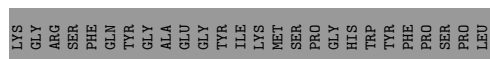
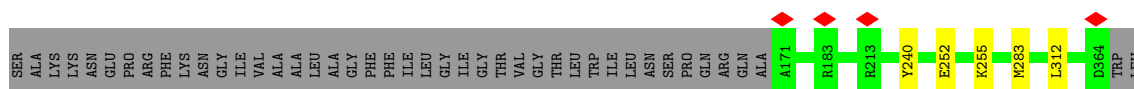


• Molecule 2: Protein PrgH



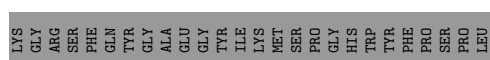
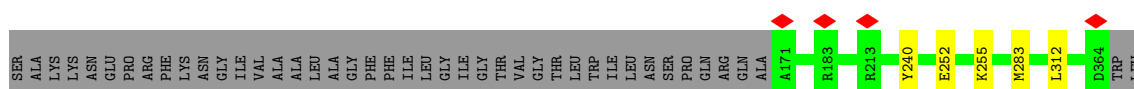
• Molecule 2: Protein PrgH

Chain d:  72% 26%



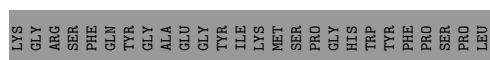
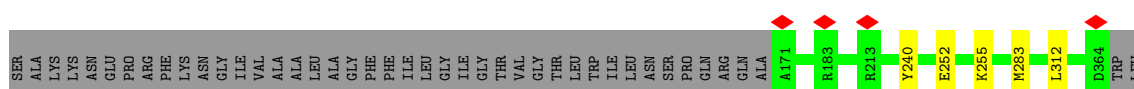
• Molecule 2: Protein PrgH

Chain f:  72% 26%



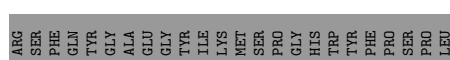
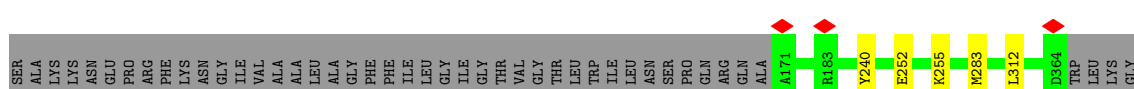
• Molecule 2: Protein PrgH

Chain h:  72% 26%



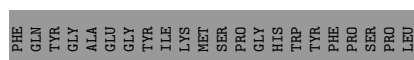
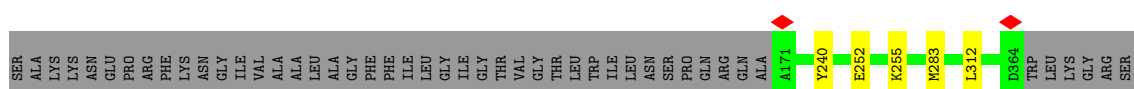
• Molecule 2: Protein PrgH

Chain j:  72% 26%



• Molecule 2: Protein PrgH

Chain l:  72% 26%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C24	Depositor
Number of particles used	67800	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.3	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	3200	Depositor
Magnification	29240	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.247	Depositor
Minimum map value	-0.223	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	513.0, 513.0, 513.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.71, 1.71, 1.71	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	0	0.77	0/1465	1.19	20/1989 (1.0%)
1	2	0.77	0/1465	1.20	20/1989 (1.0%)
1	4	0.77	0/1465	1.19	20/1989 (1.0%)
1	6	0.77	0/1465	1.19	20/1989 (1.0%)
1	8	0.77	0/1465	1.19	20/1989 (1.0%)
1	B	0.77	0/1465	1.20	20/1989 (1.0%)
1	D	0.77	0/1465	1.19	20/1989 (1.0%)
1	F	0.77	0/1465	1.19	20/1989 (1.0%)
1	H	0.77	0/1465	1.19	20/1989 (1.0%)
1	J	0.77	0/1465	1.19	20/1989 (1.0%)
1	L	0.77	0/1465	1.19	20/1989 (1.0%)
1	N	0.77	0/1465	1.19	20/1989 (1.0%)
1	P	0.77	0/1465	1.19	20/1989 (1.0%)
1	R	0.77	0/1465	1.19	20/1989 (1.0%)
1	T	0.77	0/1465	1.19	20/1989 (1.0%)
1	V	0.77	0/1465	1.19	20/1989 (1.0%)
1	X	0.77	0/1465	1.19	20/1989 (1.0%)
1	Z	0.77	0/1465	1.19	20/1989 (1.0%)
1	a	0.77	0/1465	1.20	20/1989 (1.0%)
1	c	0.77	0/1465	1.19	20/1989 (1.0%)
1	e	0.77	0/1465	1.19	20/1989 (1.0%)
1	g	0.77	0/1465	1.20	20/1989 (1.0%)
1	i	0.77	0/1465	1.19	20/1989 (1.0%)
1	k	0.77	0/1465	1.19	20/1989 (1.0%)
2	1	0.76	0/1632	0.99	10/2204 (0.5%)
2	3	0.76	0/1632	0.99	10/2204 (0.5%)
2	5	0.76	0/1632	0.99	10/2204 (0.5%)
2	7	0.76	0/1632	0.99	10/2204 (0.5%)
2	9	0.76	0/1632	0.99	10/2204 (0.5%)
2	A	0.76	0/1632	0.99	10/2204 (0.5%)
2	C	0.76	0/1632	0.99	10/2204 (0.5%)
2	E	0.76	0/1632	0.99	10/2204 (0.5%)
2	G	0.76	0/1632	0.99	10/2204 (0.5%)
2	I	0.76	0/1632	0.99	10/2204 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	K	0.76	0/1632	0.99	10/2204 (0.5%)
2	M	0.76	0/1632	0.99	10/2204 (0.5%)
2	O	0.76	0/1632	0.99	10/2204 (0.5%)
2	Q	0.76	0/1632	0.99	10/2204 (0.5%)
2	S	0.76	0/1632	0.99	10/2204 (0.5%)
2	U	0.76	0/1632	0.99	10/2204 (0.5%)
2	W	0.76	0/1632	0.99	10/2204 (0.5%)
2	Y	0.76	0/1632	0.99	10/2204 (0.5%)
2	b	0.76	0/1632	0.99	10/2204 (0.5%)
2	d	0.76	0/1632	0.99	10/2204 (0.5%)
2	f	0.76	0/1632	0.99	10/2204 (0.5%)
2	h	0.76	0/1632	0.99	10/2204 (0.5%)
2	j	0.76	0/1632	0.99	10/2204 (0.5%)
2	l	0.76	0/1632	0.99	10/2204 (0.5%)
All	All	0.76	0/74328	1.09	720/100632 (0.7%)

There are no bond length outliers.

The worst 5 of 720 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	0	141	ARG	CA-C-N	10.30	127.08	119.66
1	0	141	ARG	C-N-CA	10.30	127.08	119.66
1	F	141	ARG	CA-C-N	10.30	127.08	119.66
1	F	141	ARG	C-N-CA	10.30	127.08	119.66
1	2	141	ARG	CA-C-N	10.29	127.07	119.66

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	1437	0	1434	5	0
1	2	1437	0	1434	4	0
1	4	1437	0	1434	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	6	1437	0	1434	5	0
1	8	1437	0	1434	4	0
1	B	1437	0	1434	5	0
1	D	1437	0	1434	5	0
1	F	1437	0	1434	5	0
1	H	1437	0	1434	5	0
1	J	1437	0	1434	4	0
1	L	1437	0	1434	4	0
1	N	1437	0	1434	4	0
1	P	1437	0	1434	4	0
1	R	1437	0	1434	5	0
1	T	1437	0	1434	4	0
1	V	1437	0	1434	5	0
1	X	1437	0	1434	4	0
1	Z	1437	0	1434	4	0
1	a	1437	0	1434	5	0
1	c	1437	0	1434	4	0
1	e	1437	0	1434	4	0
1	g	1437	0	1434	4	0
1	i	1437	0	1434	5	0
1	k	1437	0	1434	5	0
2	1	1600	0	1580	0	0
2	3	1600	0	1580	0	0
2	5	1600	0	1580	0	0
2	7	1600	0	1580	0	0
2	9	1600	0	1580	0	0
2	A	1600	0	1580	0	0
2	C	1600	0	1580	0	0
2	E	1600	0	1580	0	0
2	G	1600	0	1580	0	0
2	I	1600	0	1580	0	0
2	K	1600	0	1580	0	0
2	M	1600	0	1580	0	0
2	O	1600	0	1580	0	0
2	Q	1600	0	1580	0	0
2	S	1600	0	1580	0	0
2	U	1600	0	1580	0	0
2	W	1600	0	1580	0	0
2	Y	1600	0	1580	0	0
2	b	1600	0	1580	0	0
2	d	1600	0	1580	0	0
2	f	1600	0	1580	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	h	1600	0	1580	0	0
2	j	1600	0	1580	0	0
2	l	1600	0	1580	0	0
All	All	72888	0	72336	108	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 1.

The worst 5 of 108 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:a:28:ASP:OD1	1:a:28:ASP:C	2.48	0.57
1:8:28:ASP:OD1	1:8:28:ASP:C	2.48	0.57
1:e:28:ASP:OD1	1:e:28:ASP:C	2.48	0.56
1:2:187:LEU:C	1:2:187:LEU:HD12	2.31	0.56
1:k:187:LEU:C	1:k:187:LEU:HD12	2.31	0.56

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

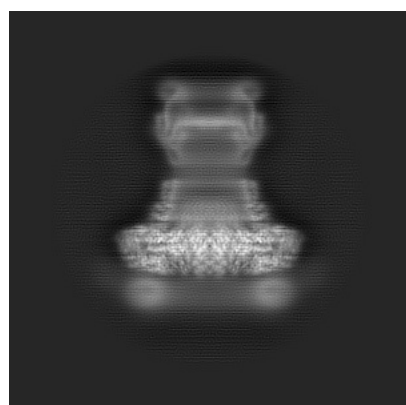
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8398. These allow visual inspection of the internal detail of the map and identification of artifacts.

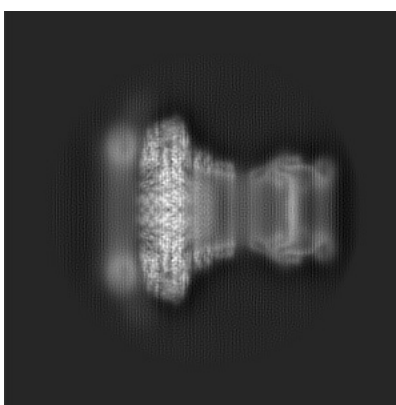
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

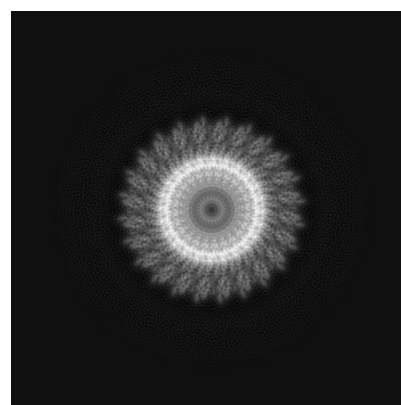
6.1.1 Primary map



X



Y

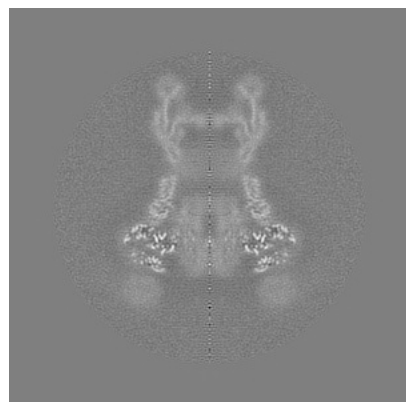


Z

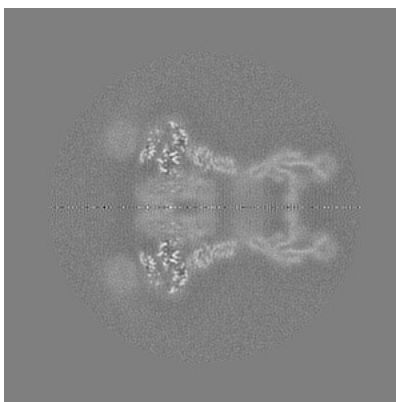
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

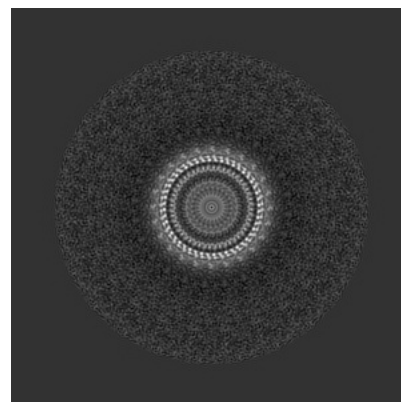
6.2.1 Primary map



X Index: 150



Y Index: 150

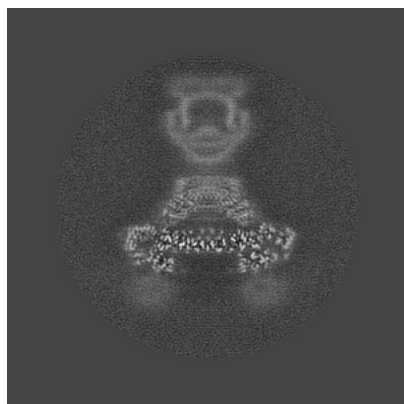


Z Index: 150

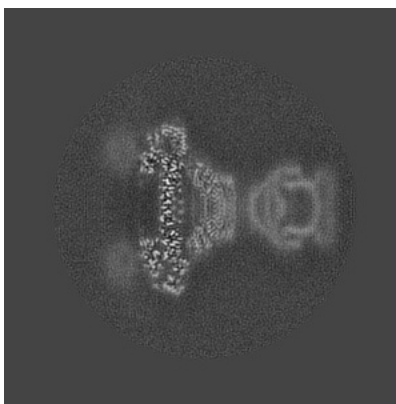
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

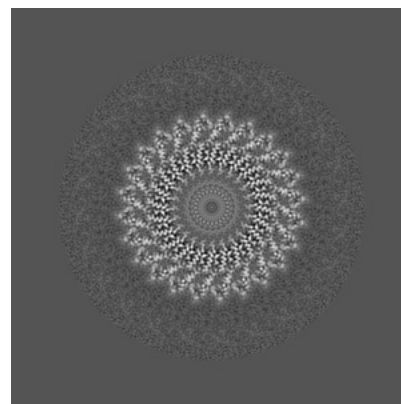
6.3.1 Primary map



X Index: 178



Y Index: 178

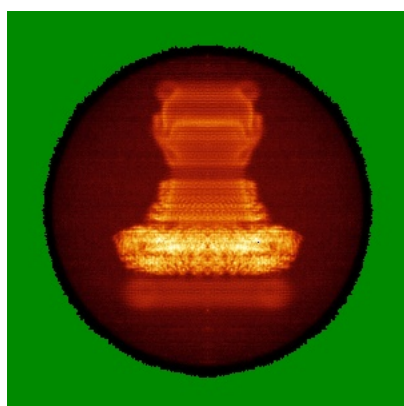


Z Index: 127

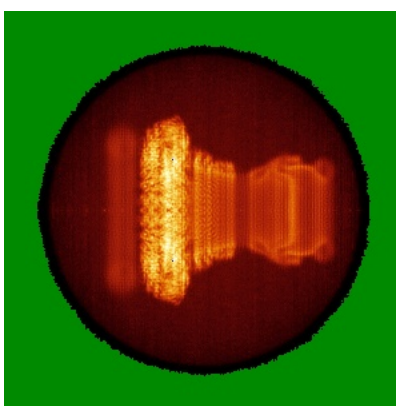
The images above show the largest variance slices of the map in three orthogonal directions.

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

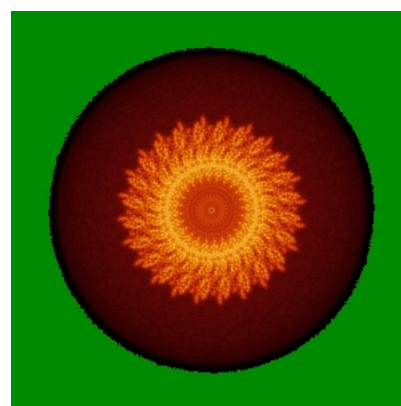
6.4.1 Primary map



X



Y

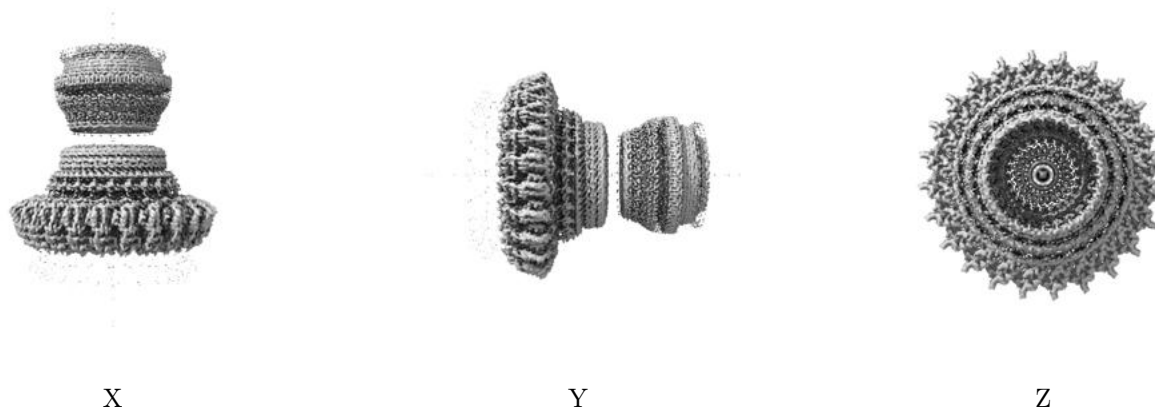


Z

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

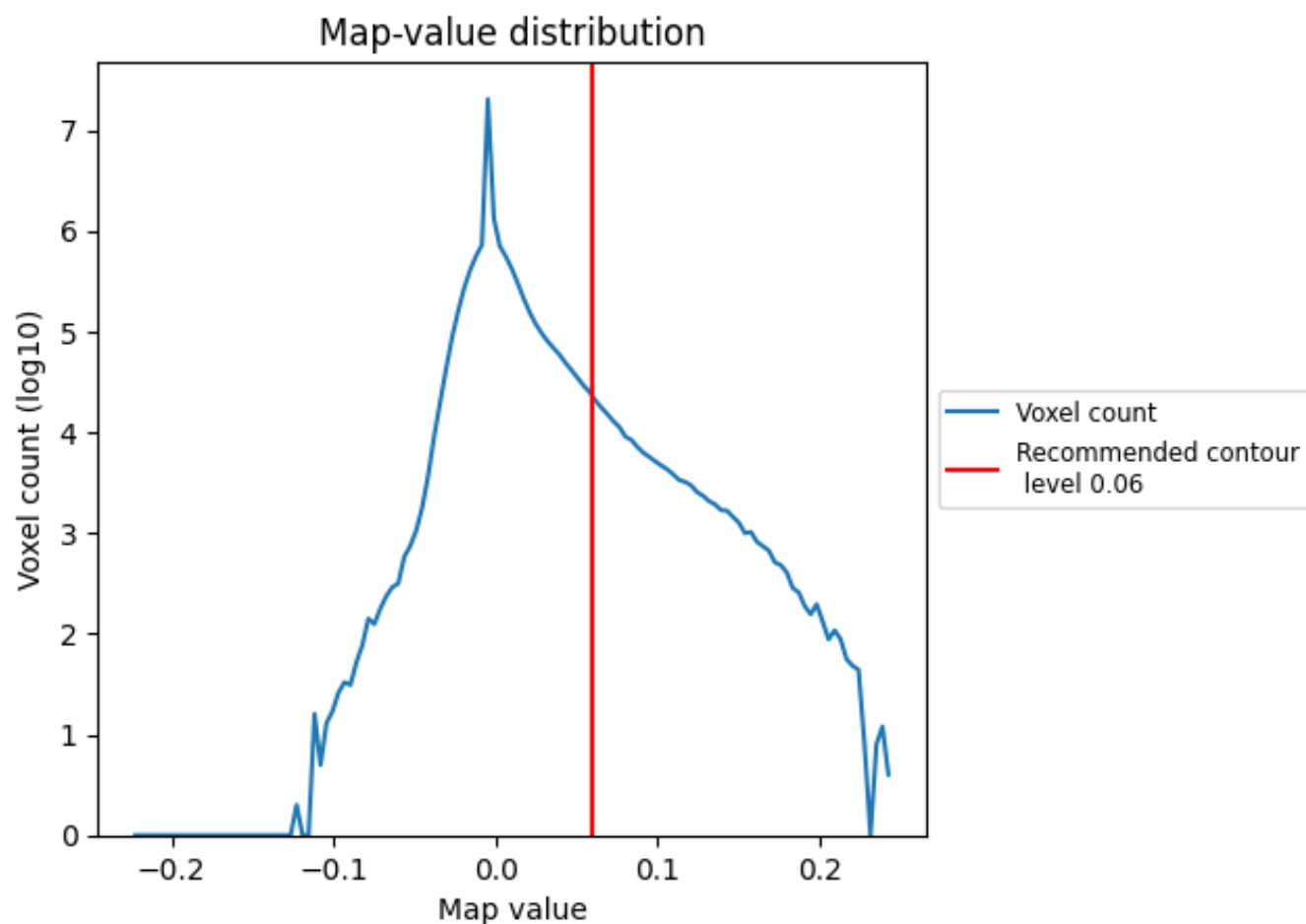
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

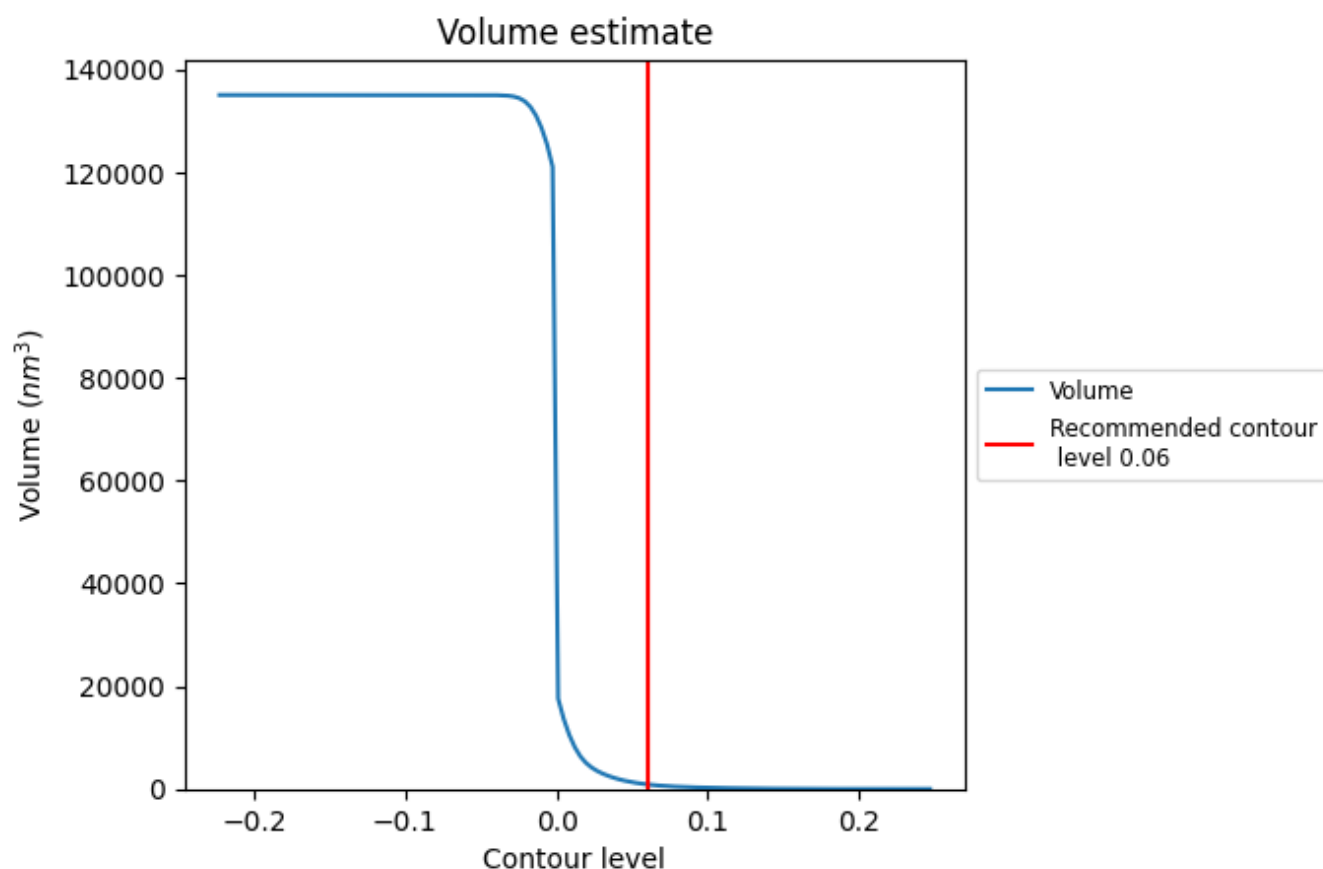
This section contains the results of statistical analysis of the map.

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.

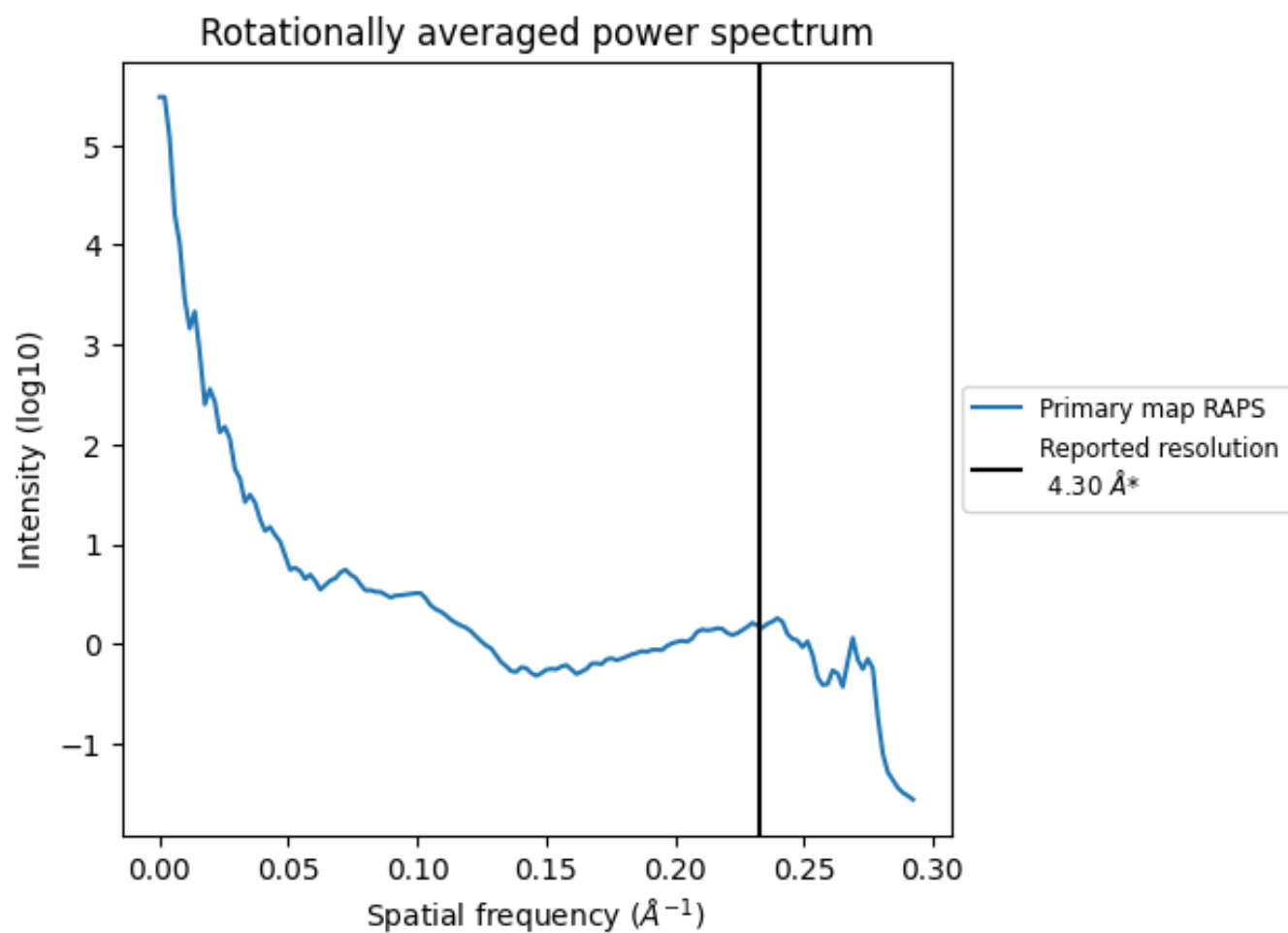
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 883 nm³; this corresponds to an approximate mass of 797 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 0.233 Å⁻¹

8 Fourier-Shell correlation

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

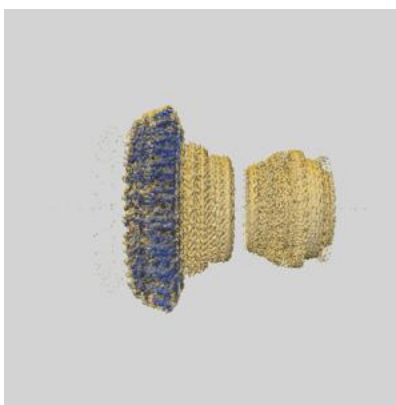
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-8398 and PDB model 5TCP. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



X



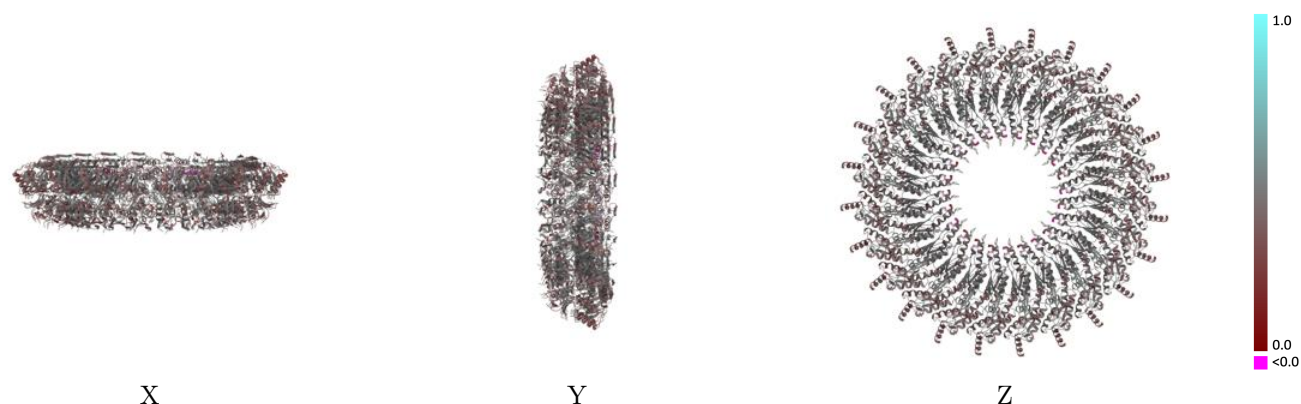
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.06 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](#)

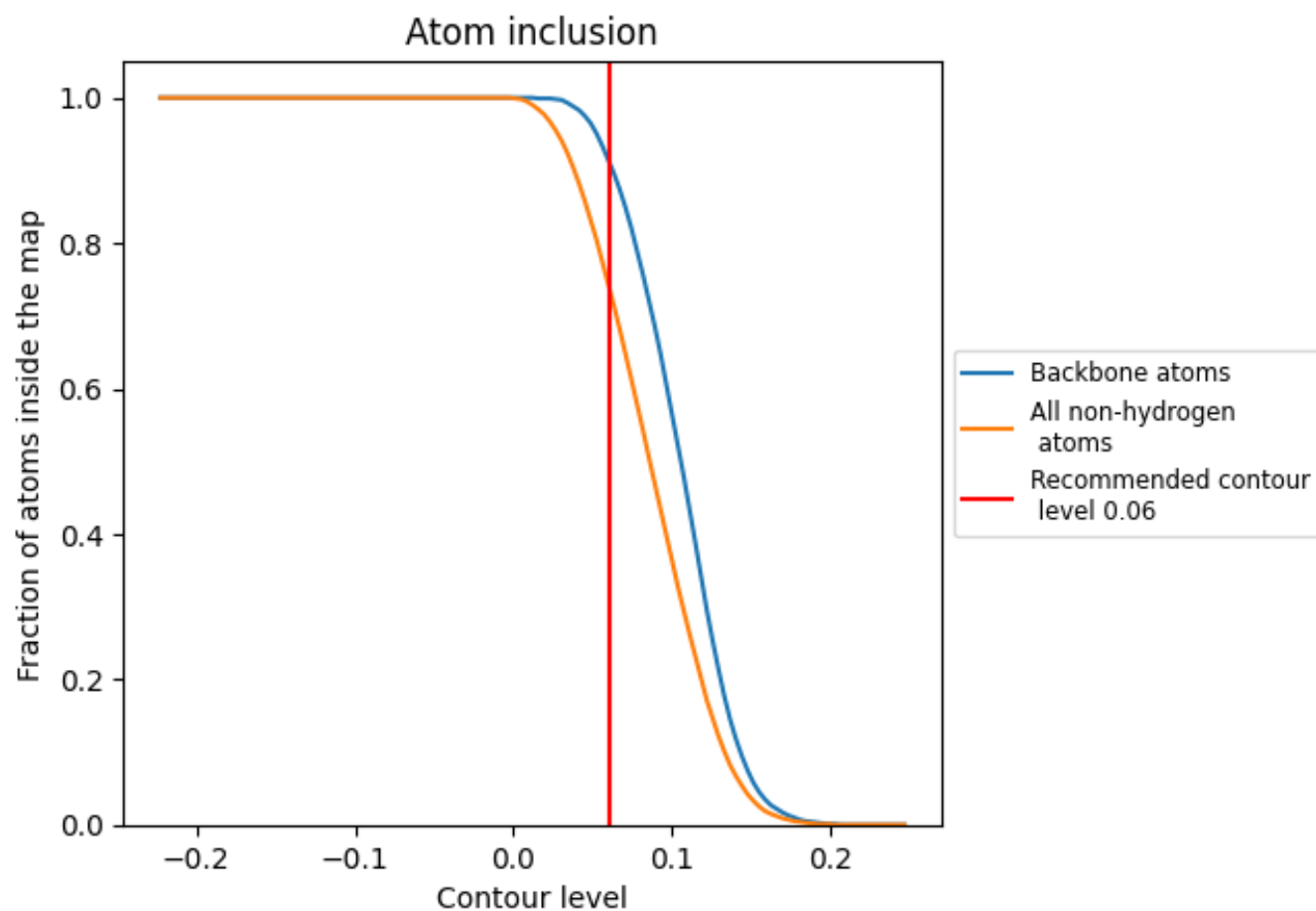


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 74% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7440	 0.4180
0	 0.7590	 0.4460
1	 0.7490	 0.4050
2	 0.7350	 0.4280
3	 0.7550	 0.4020
4	 0.7360	 0.4240
5	 0.7520	 0.3990
6	 0.7340	 0.4270
7	 0.7480	 0.3980
8	 0.7370	 0.4270
9	 0.7360	 0.3910
A	 0.7500	 0.4170
B	 0.7490	 0.4400
C	 0.7530	 0.4150
D	 0.7460	 0.4380
E	 0.7440	 0.4080
F	 0.7370	 0.4320
G	 0.7490	 0.4070
H	 0.7400	 0.4330
I	 0.7450	 0.4020
J	 0.7390	 0.4330
K	 0.7350	 0.3960
L	 0.7380	 0.4320
M	 0.7410	 0.4030
N	 0.7370	 0.4290
O	 0.7380	 0.4010
P	 0.7400	 0.4300
Q	 0.7390	 0.4000
R	 0.7360	 0.4260
S	 0.7520	 0.4040
T	 0.7420	 0.4310
U	 0.7440	 0.4070
V	 0.7340	 0.4340
W	 0.7460	 0.4050
X	 0.7420	 0.4360



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Chain	Atom inclusion	Q-score
Y	 0.7510	 0.4130
Z	 0.7370	 0.4290
a	 0.7370	 0.4310
b	 0.7410	 0.3970
c	 0.7370	 0.4310
d	 0.7420	 0.3950
e	 0.7450	 0.4340
f	 0.7450	 0.4000
g	 0.7450	 0.4360
h	 0.7550	 0.4040
i	 0.7500	 0.4430
j	 0.7520	 0.4090
k	 0.7550	 0.4440
l	 0.7450	 0.4090