



wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 10:08 AM EST

PDB ID : 6BGL
EMDB ID : EMD-7097
Title : Doubly PafE-capped 20S core particle in Mycobacterium tuberculosis
Authors : Li, H.; Hu, K.
Deposited on : 2017-10-28
Resolution : 3.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

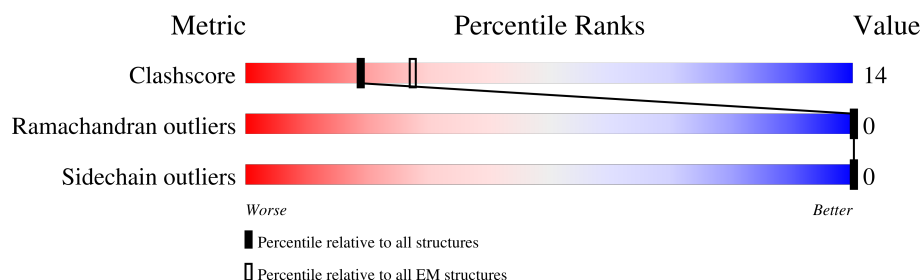
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.









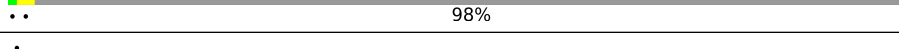
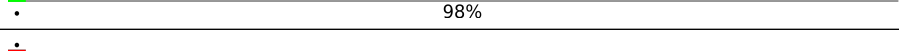
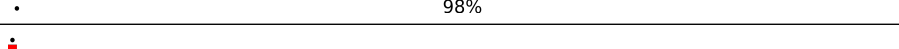
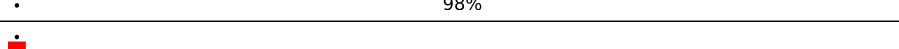
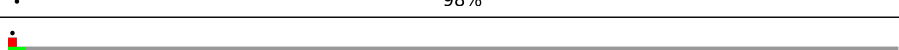
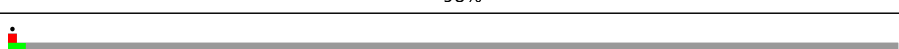

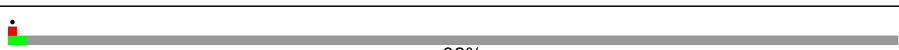
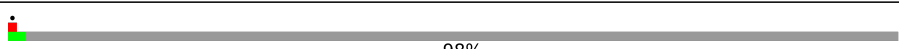


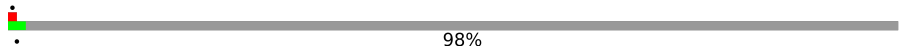
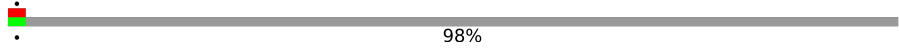

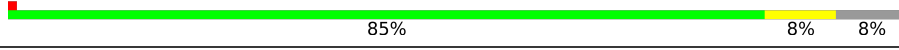
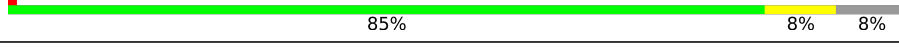



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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

Mol	Chain	Length	Quality of chain
1	A	248	
1	C	248	
1	D	248	
1	E	248	
1	F	248	
1	G	248	
1	H	248	
1	I	248	



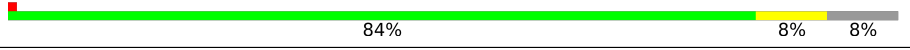



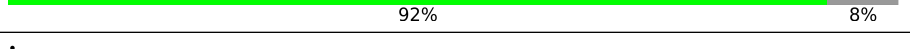
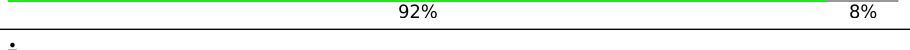
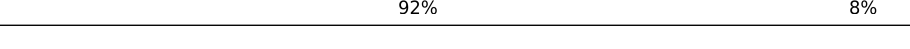
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Mol	Chain	Length	Quality of chain
1	J	248	
1	K	248	
1	L	248	
1	M	248	
1	N	248	
1	O	248	
2	B	174	
2	d	174	
2	e	174	
2	f	174	
2	g	174	
2	h	174	
2	i	174	
2	j	174	
2	k	174	
2	l	174	
2	m	174	
2	n	174	
2	o	174	
2	p	174	
3	P	240	
3	Q	240	
3	R	240	
3	S	240	
3	T	240	

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Mol	Chain	Length	Quality of chain
3	U	240	 85%8%8%
3	V	240	 84%9%8%
3	W	240	 84%8%8%
3	X	240	 85%8%8%
3	Y	240	 83%10%8%
3	Z	240	 85%8%8%
3	a	240	 92%8%
3	b	240	 92%8%
3	c	240	 92%8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 46618 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 Proteasome subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	C	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	D	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	E	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	F	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	G	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	H	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	I	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	J	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	K	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	L	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	M	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	N	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		
1	O	215	Total	C	N	O	S	0	0
			1658	1039	303	313	3		

- Molecule 2 is a protein called Bacterial proteasome activator.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	4	Total	C	N	O	0	0
			34	22	5	7		

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Mol	Chain	Residues	Atoms				AltConf	Trace
2	d	4	Total 34	C 22	N 5	O 7	0	0
2	e	4	Total 34	C 22	N 5	O 7	0	0
2	f	4	Total 34	C 22	N 5	O 7	0	0
2	g	4	Total 34	C 22	N 5	O 7	0	0
2	h	4	Total 34	C 22	N 5	O 7	0	0
2	i	4	Total 34	C 22	N 5	O 7	0	0
2	j	4	Total 34	C 22	N 5	O 7	0	0
2	k	4	Total 34	C 22	N 5	O 7	0	0
2	l	4	Total 34	C 22	N 5	O 7	0	0
2	m	4	Total 34	C 22	N 5	O 7	0	0
2	n	4	Total 34	C 22	N 5	O 7	0	0
2	o	4	Total 34	C 22	N 5	O 7	0	0
2	p	4	Total 34	C 22	N 5	O 7	0	0

- Molecule 3 is a protein called Proteasome subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	P	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	Q	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	R	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	S	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	T	222	Total 1636	C 1026	N 282	O 323	S 5	0	0
3	U	222	Total 1638	C 1027	N 282	O 324	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	V	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	W	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	X	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	Y	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	Z	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	a	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	b	222	Total 1638	C 1027	N 282	O 324	S 5	0	0
3	c	222	Total 1638	C 1027	N 282	O 324	S 5	0	0

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	535	HIS	-	expression tag	UNP A5U4D6
P	536	HIS	-	expression tag	UNP A5U4D6
P	537	HIS	-	expression tag	UNP A5U4D6
P	538	HIS	-	expression tag	UNP A5U4D6
P	539	HIS	-	expression tag	UNP A5U4D6
P	540	HIS	-	expression tag	UNP A5U4D6
Q	535	HIS	-	expression tag	UNP A5U4D6
Q	536	HIS	-	expression tag	UNP A5U4D6
Q	537	HIS	-	expression tag	UNP A5U4D6
Q	538	HIS	-	expression tag	UNP A5U4D6
Q	539	HIS	-	expression tag	UNP A5U4D6
Q	540	HIS	-	expression tag	UNP A5U4D6
R	535	HIS	-	expression tag	UNP A5U4D6
R	536	HIS	-	expression tag	UNP A5U4D6
R	537	HIS	-	expression tag	UNP A5U4D6
R	538	HIS	-	expression tag	UNP A5U4D6
R	539	HIS	-	expression tag	UNP A5U4D6
R	540	HIS	-	expression tag	UNP A5U4D6
S	535	HIS	-	expression tag	UNP A5U4D6
S	536	HIS	-	expression tag	UNP A5U4D6
S	537	HIS	-	expression tag	UNP A5U4D6
S	538	HIS	-	expression tag	UNP A5U4D6
S	539	HIS	-	expression tag	UNP A5U4D6

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Chain	Residue	Modelled	Actual	Comment	Reference
S	540	HIS	-	expression tag	UNP A5U4D6
T	535	HIS	-	expression tag	UNP A5U4D6
T	536	HIS	-	expression tag	UNP A5U4D6
T	537	HIS	-	expression tag	UNP A5U4D6
T	538	HIS	-	expression tag	UNP A5U4D6
T	539	HIS	-	expression tag	UNP A5U4D6
T	540	HIS	-	expression tag	UNP A5U4D6
U	535	HIS	-	expression tag	UNP A5U4D6
U	536	HIS	-	expression tag	UNP A5U4D6
U	537	HIS	-	expression tag	UNP A5U4D6
U	538	HIS	-	expression tag	UNP A5U4D6
U	539	HIS	-	expression tag	UNP A5U4D6
U	540	HIS	-	expression tag	UNP A5U4D6
V	535	HIS	-	expression tag	UNP A5U4D6
V	536	HIS	-	expression tag	UNP A5U4D6
V	537	HIS	-	expression tag	UNP A5U4D6
V	538	HIS	-	expression tag	UNP A5U4D6
V	539	HIS	-	expression tag	UNP A5U4D6
V	540	HIS	-	expression tag	UNP A5U4D6
W	535	HIS	-	expression tag	UNP A5U4D6
W	536	HIS	-	expression tag	UNP A5U4D6
W	537	HIS	-	expression tag	UNP A5U4D6
W	538	HIS	-	expression tag	UNP A5U4D6
W	539	HIS	-	expression tag	UNP A5U4D6
W	540	HIS	-	expression tag	UNP A5U4D6
X	535	HIS	-	expression tag	UNP A5U4D6
X	536	HIS	-	expression tag	UNP A5U4D6
X	537	HIS	-	expression tag	UNP A5U4D6
X	538	HIS	-	expression tag	UNP A5U4D6
X	539	HIS	-	expression tag	UNP A5U4D6
X	540	HIS	-	expression tag	UNP A5U4D6
Y	535	HIS	-	expression tag	UNP A5U4D6
Y	536	HIS	-	expression tag	UNP A5U4D6
Y	537	HIS	-	expression tag	UNP A5U4D6
Y	538	HIS	-	expression tag	UNP A5U4D6
Y	539	HIS	-	expression tag	UNP A5U4D6
Y	540	HIS	-	expression tag	UNP A5U4D6
Z	535	HIS	-	expression tag	UNP A5U4D6
Z	536	HIS	-	expression tag	UNP A5U4D6
Z	537	HIS	-	expression tag	UNP A5U4D6
Z	538	HIS	-	expression tag	UNP A5U4D6
Z	539	HIS	-	expression tag	UNP A5U4D6

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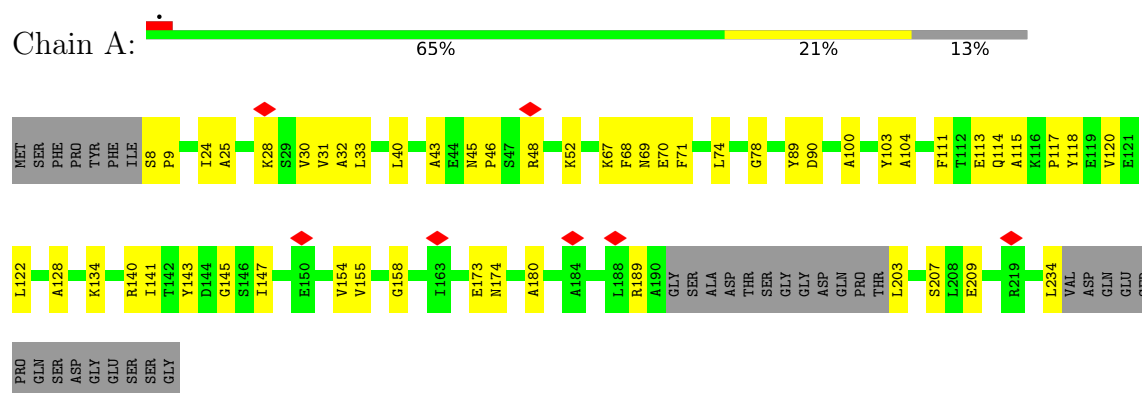
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Chain	Residue	Modelled	Actual	Comment	Reference
Z	540	HIS	-	expression tag	UNP A5U4D6
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a	536	HIS	-	expression tag	UNP A5U4D6
a	537	HIS	-	expression tag	UNP A5U4D6
a	538	HIS	-	expression tag	UNP A5U4D6
a	539	HIS	-	expression tag	UNP A5U4D6
a	540	HIS	-	expression tag	UNP A5U4D6
b	535	HIS	-	expression tag	UNP A5U4D6
b	536	HIS	-	expression tag	UNP A5U4D6
b	537	HIS	-	expression tag	UNP A5U4D6
b	538	HIS	-	expression tag	UNP A5U4D6
b	539	HIS	-	expression tag	UNP A5U4D6
b	540	HIS	-	expression tag	UNP A5U4D6
c	535	HIS	-	expression tag	UNP A5U4D6
c	536	HIS	-	expression tag	UNP A5U4D6
c	537	HIS	-	expression tag	UNP A5U4D6
c	538	HIS	-	expression tag	UNP A5U4D6
c	539	HIS	-	expression tag	UNP A5U4D6
c	540	HIS	-	expression tag	UNP A5U4D6

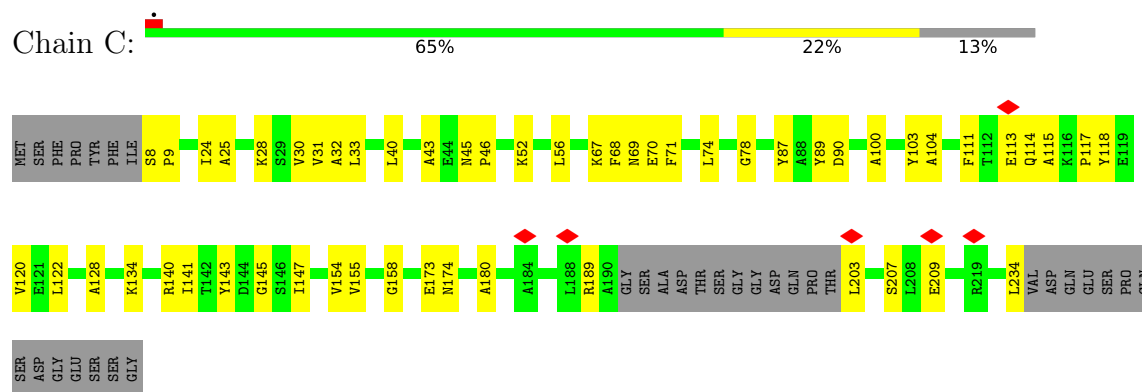
3 Residue-property plots

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.

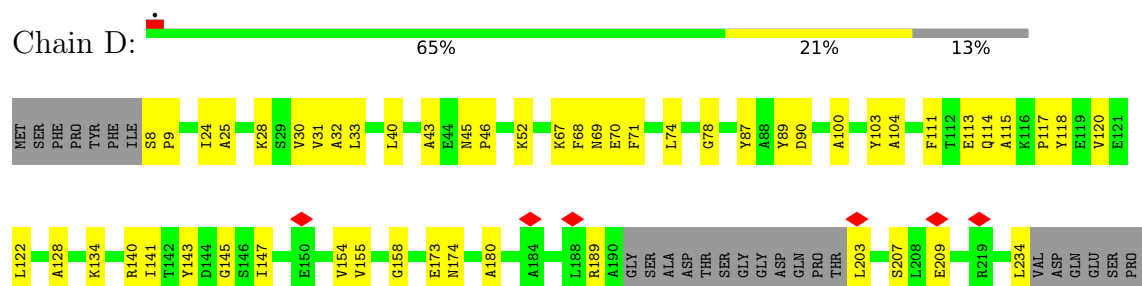
• Molecule 1: Proteasome subunit alpha



• Molecule 1: Proteasome subunit alpha



• Molecule 1: Proteasome subunit alpha



SER
ASP
SER
GLY
GLY
SER
SER
SER
GLY

• Molecule 1: Proteasome subunit alpha

Chain E:



MET SER PHE PRO TYR PHE ILE S8 P9 I24 A25 K28 S29 V30 V31 A32 L33 L40 A43 E44 N45 P46 K52 K67 F68 N69 E70 F71 L74 G78 Y87 A88 Y89 D90 A100 Y103 A104 F111 T112 E113 Q114 A115 K116 P117 Y118 F119 E120 E121

L122 A128 K134 R140 T141 Y143 G145 S146 T147 E150 V154 V155 G158 E173 N174 A180 A184 L188 R189 A190 GLY SER ALA ASP THR Y87 GLY ASP GLN PRO THR L203 S207 E209 L234 VAL ASP GLN SER PRO GLN SER ASP

GLY
GLY
SER
SER
GLY

• Molecule 1: Proteasome subunit alpha

Chain F:



MET SER PHE PRO TYR PHE ILE S8 P9 I24 A25 K28 S29 V30 V31 A32 L33 L40 A43 E44 N45 P46 K52 L56 K67 F68 N69 E70 F71 L74 G78 Y87 A88 Y89 D90 A100 Y103 A104 F111 T112 E113 Q114 A115 K116 P117 Y118 E119

Y120 E121 L122 A128 K134 R135 R140 I141 Y143 G145 S146 T147 E150 V154 V155 G158 T163 E173 N174 A180 A184 L188 R189 A190 GLY SER ALA ASP THR Y87 GLY ASP GLN PRO THR L203 S207 E209 L234 VAL ASP GLN SER PRO GLN

SER
PRO
GLN
SER
ASP
GLY
GLY
SER
SER
GLY

• Molecule 1: Proteasome subunit alpha

Chain G:



MET SER PHE PRO TYR PHE ILE S8 P9 I24 A25 K28 S29 V30 V31 A32 L33 L40 A43 E44 N45 P46 S47 R48 K52 L56 K67 F68 N69 E70 F71 L74 G78 Y87 A88 Y89 D90 A100 Y103 A104 F111 T112 E113 Q114 A115 K116 P117

Y118 E119 V120 E121 L122 A128 K134 R135 R140 I141 Y143 G145 S146 T147 E150 V154 V155 G158 T163 E173 N174 A180 A184 L188 R189 A190 GLY SER ALA ASP THR Y87 GLY ASP GLN PRO THR L203 S207 E209 L234 VAL ASP GLN SER PRO GLN

VAL
ASP
GLN
GLY
SER
PRO
GLN
SER
SER
GLY

• Molecule 1: Proteasome subunit alpha

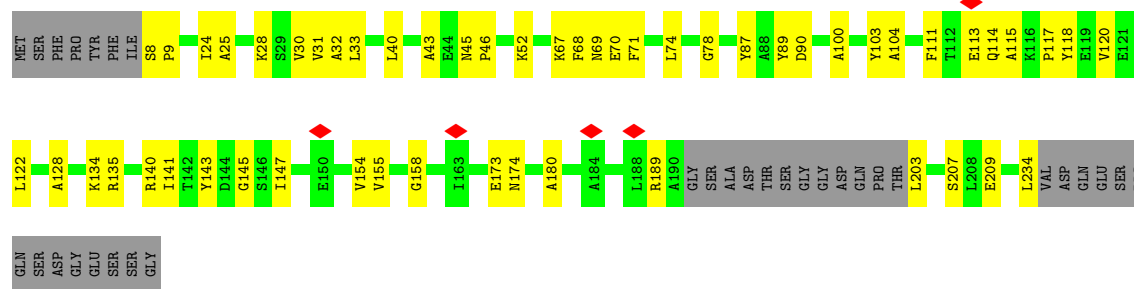
Chain H:



MET SER PHE PRO TYR PHE ILE S8 P9 I24 A25 K28 S29 V30 V31 A32 L33 L40 A43 E44 N45 P46 R48 K52 K67 F68 N69 E70 F71 L74 G78 Y87 A88 Y89 D90 A100 Y103 A104 F111 T112 E113 Q114 A115 K116 P117 Y118 E119

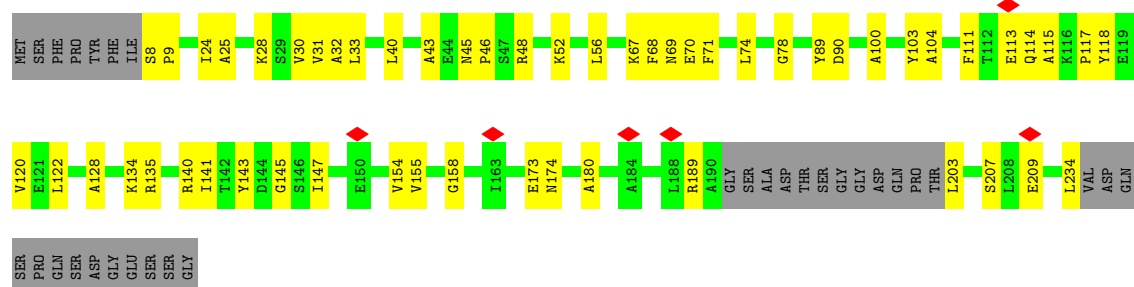


Chain L:  65% 22% 13%



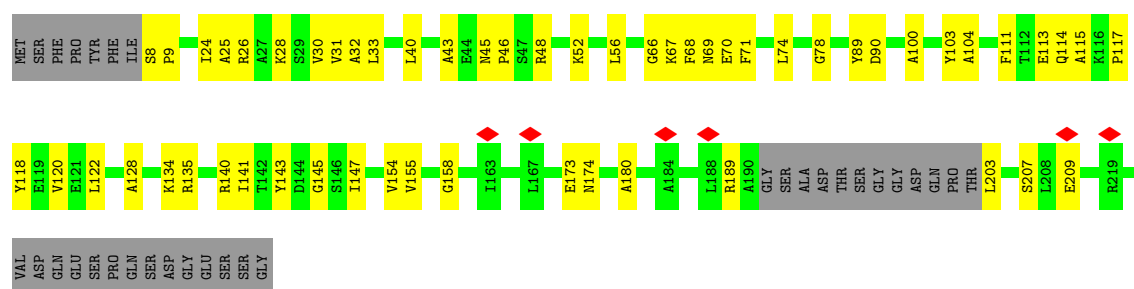
- Molecule 1: Proteasome subunit alpha

Chain M:  65% 22% 13%



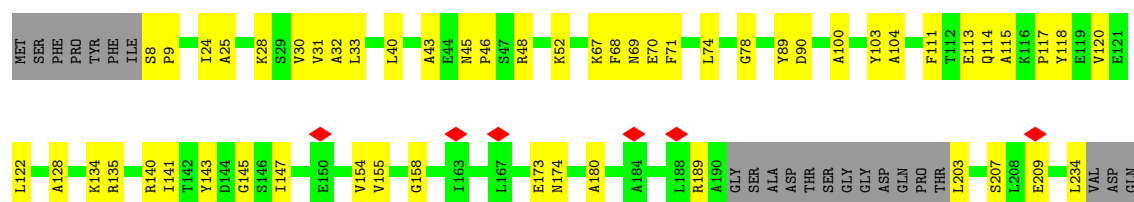
- Molecule 1: Proteasome subunit alpha

Chain N:  64% 23% 13%

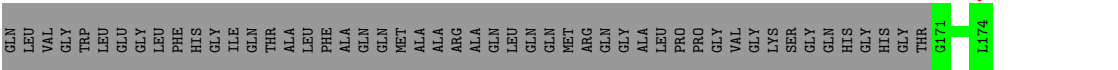


- Molecule 1: Proteasome subunit alpha

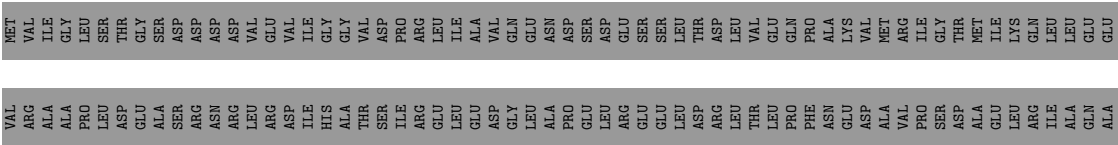
Chain O:  65% 22% 13%



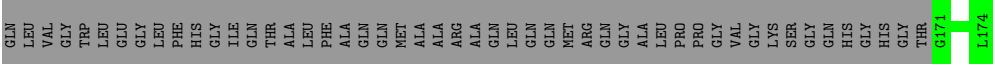
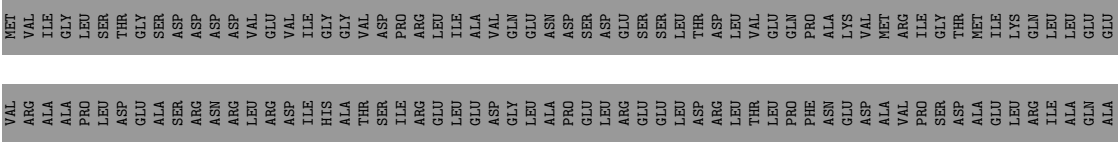
[illegible]



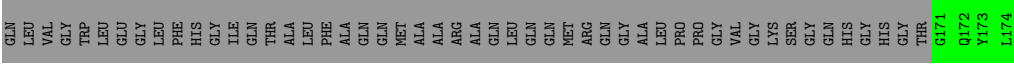
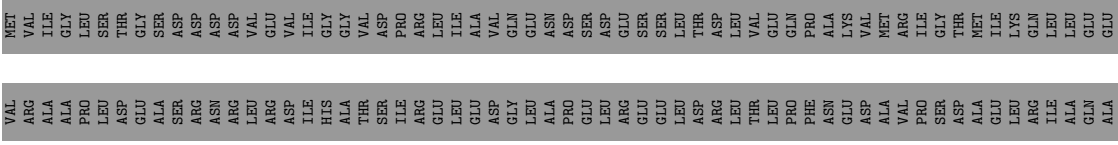
• Molecule 2: Bacterial proteasome activator



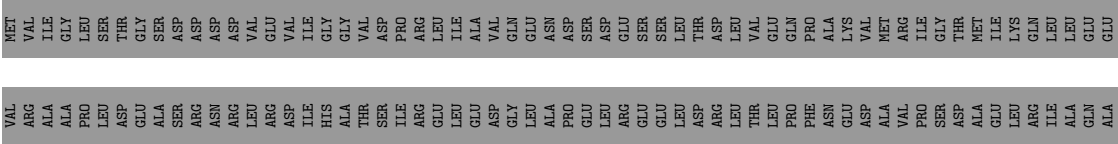
• Molecule 2: Bacterial proteasome activator

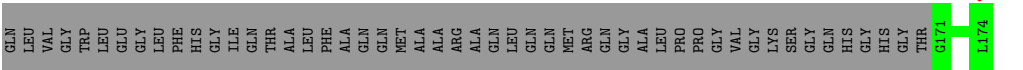


• Molecule 2: Bacterial proteasome activator

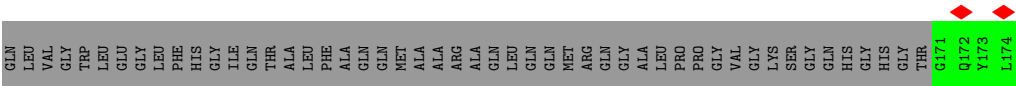
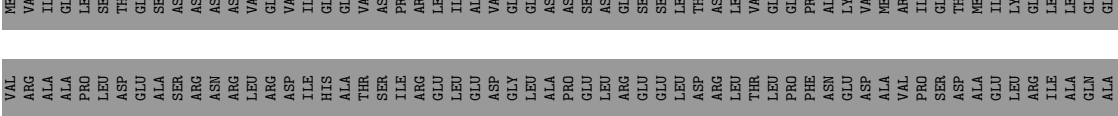


• Molecule 2: Bacterial proteasome activator

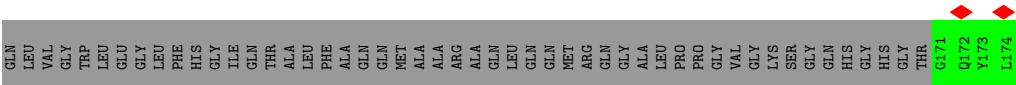
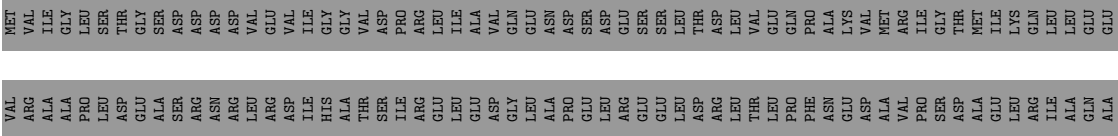




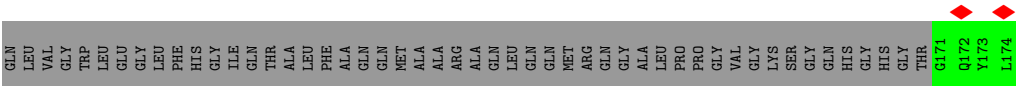
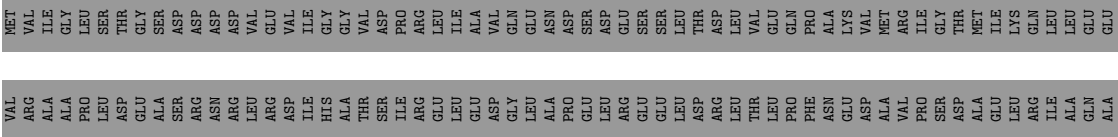
• Molecule 2: Bacterial proteasome activator



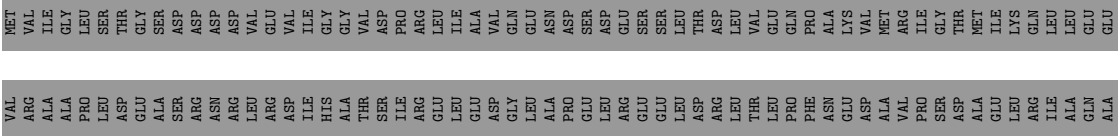
• Molecule 2: Bacterial proteasome activator

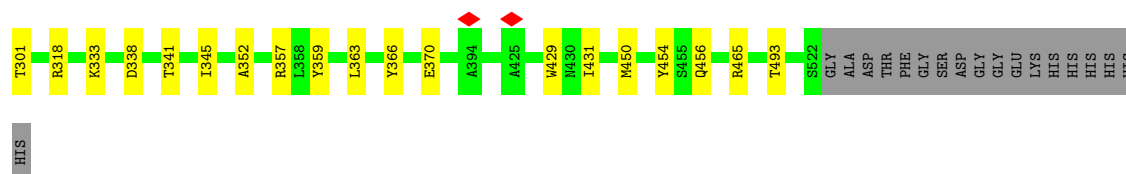
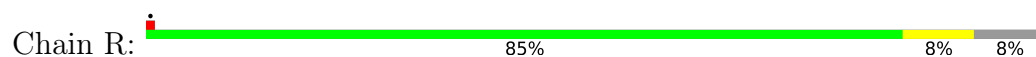


• Molecule 2: Bacterial proteasome activator

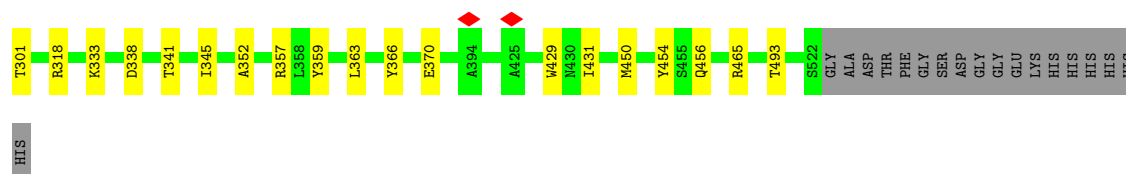
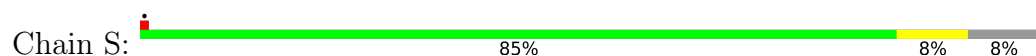


• Molecule 2: Bacterial proteasome activator

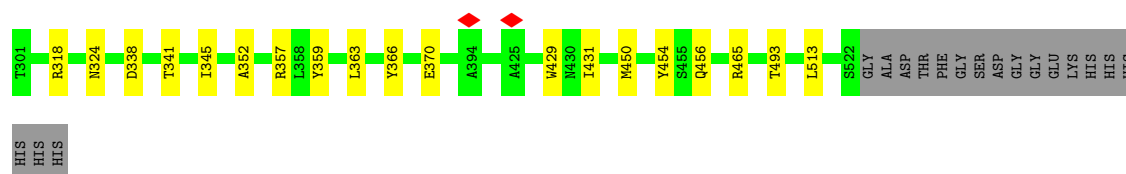
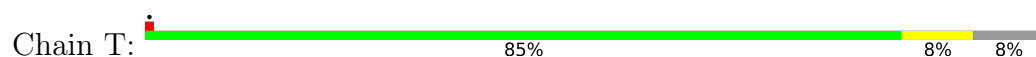




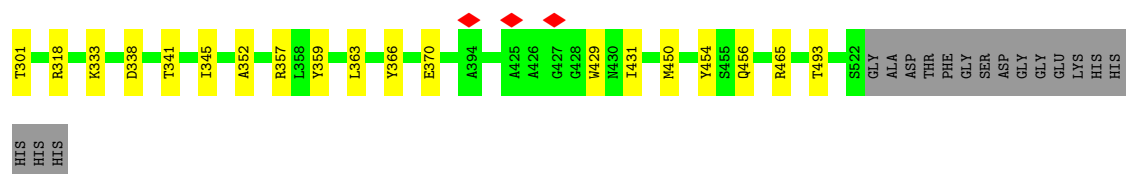
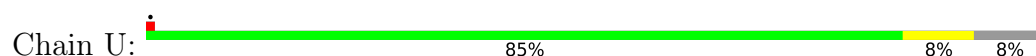
- Molecule 3: Proteasome subunit beta



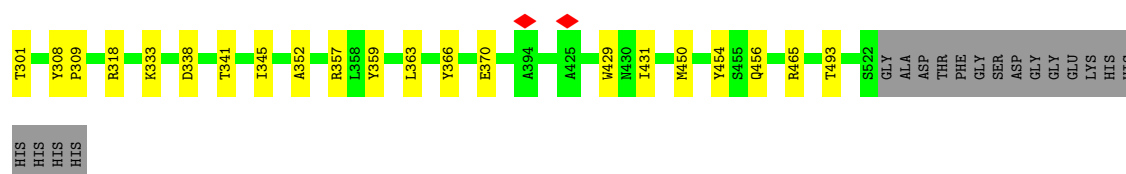
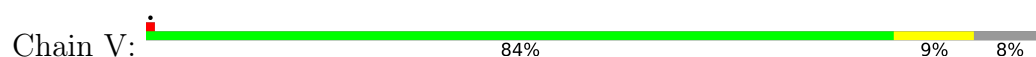
- Molecule 3: Proteasome subunit beta



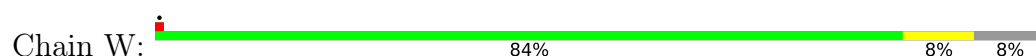
- Molecule 3: Proteasome subunit beta

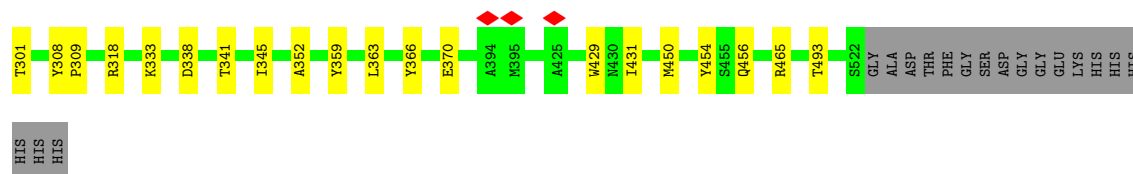


- Molecule 3: Proteasome subunit beta

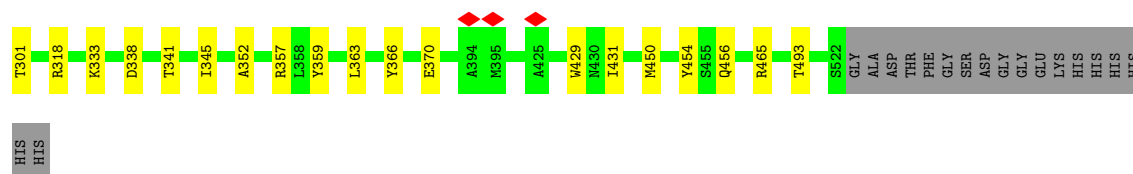
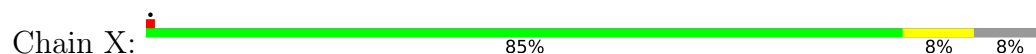


- Molecule 3: Proteasome subunit beta

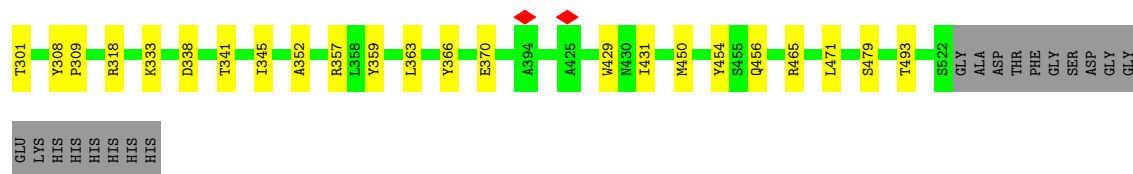
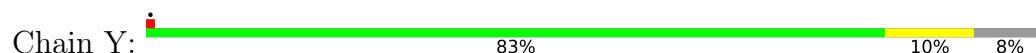




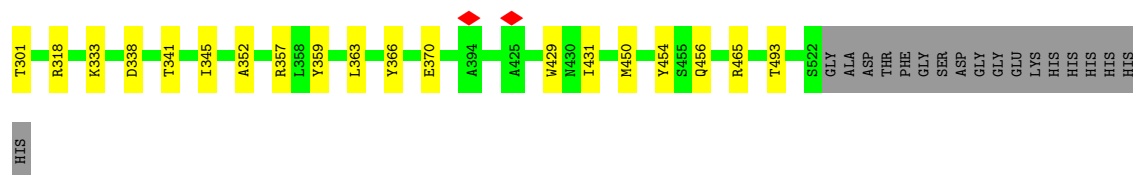
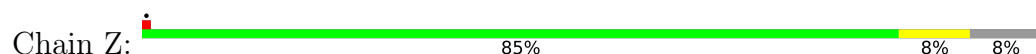
- Molecule 3: Proteasome subunit beta



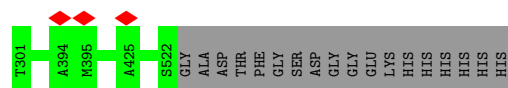
- Molecule 3: Proteasome subunit beta



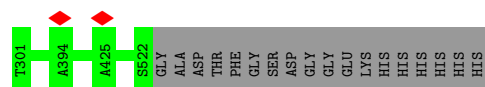
- Molecule 3: Proteasome subunit beta



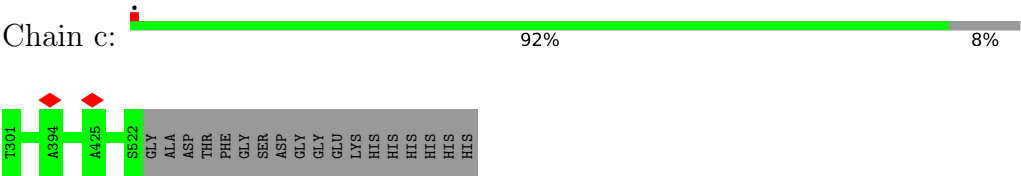
- Molecule 3: Proteasome subunit beta



- Molecule 3: Proteasome subunit beta



● Molecule 3: Proteasome subunit beta



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D7	Depositor
Number of particles used	51091	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 ($e^-/\text{\AA}^2$)	1.9	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.031	Depositor
Minimum map value	-0.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00742	Depositor
Map size (Å)	436.0, 436.0, 436.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	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	0.37	0/1683	0.56	0/2274
1	C	0.38	0/1683	0.56	0/2274
1	D	0.38	0/1683	0.56	0/2274
1	E	0.38	0/1683	0.56	0/2274
1	F	0.38	0/1683	0.56	0/2274
1	G	0.38	0/1683	0.56	0/2274
1	H	0.38	0/1683	0.56	0/2274
1	I	0.38	0/1683	0.56	0/2274
1	J	0.38	0/1683	0.56	0/2274
1	K	0.38	0/1683	0.56	0/2274
1	L	0.38	0/1683	0.56	0/2274
1	M	0.38	0/1683	0.56	0/2274
1	N	0.38	0/1683	0.56	0/2274
1	O	0.38	0/1683	0.56	0/2274
2	B	0.25	0/34	0.39	0/43
2	d	0.25	0/34	0.39	0/43
2	e	0.26	0/34	0.39	0/43
2	f	0.26	0/34	0.39	0/43
2	g	0.24	0/34	0.39	0/43
2	h	0.24	0/34	0.39	0/43
2	i	0.25	0/34	0.39	0/43
2	j	0.25	0/34	0.39	0/43
2	k	0.25	0/34	0.39	0/43
2	l	0.25	0/34	0.39	0/43
2	m	0.25	0/34	0.39	0/43
2	n	0.25	0/34	0.39	0/43
2	o	0.26	0/34	0.39	0/43
2	p	0.25	0/34	0.39	0/43
3	P	0.38	0/1662	0.59	0/2254
3	Q	0.38	0/1662	0.58	0/2254
3	R	0.38	0/1662	0.58	0/2254
3	S	0.38	0/1662	0.59	0/2254
3	T	0.38	0/1660	0.58	0/2251
3	U	0.38	0/1662	0.59	0/2254

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
3	V	0.38	0/1662	0.59	0/2254
3	W	0.38	0/1662	0.59	0/2254
3	X	0.38	0/1662	0.59	0/2254
3	Y	0.38	0/1662	0.59	0/2254
3	Z	0.38	0/1662	0.59	0/2254
3	a	0.38	0/1662	0.59	0/2254
3	b	0.38	0/1662	0.59	0/2254
3	c	0.38	0/1662	0.59	0/2254
All	All	0.38	0/47304	0.57	0/63991

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

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	1658	0	1657	67	0
1	C	1658	0	1654	61	0
1	D	1658	0	1654	61	0
1	E	1658	0	1655	62	0
1	F	1658	0	1657	68	0
1	G	1658	0	1659	73	0
1	H	1658	0	1658	69	0
1	I	1658	0	1654	67	0
1	J	1658	0	1658	68	0
1	K	1658	0	1657	68	0
1	L	1658	0	1658	68	0
1	M	1658	0	1659	73	0
1	N	1658	0	1658	77	0
1	O	1658	0	1657	69	0
2	B	34	0	30	9	0
2	d	34	0	30	0	0
2	e	34	0	30	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	f	34	0	30	0	0
2	g	34	0	30	0	0
2	h	34	0	30	0	0
2	i	34	0	30	0	0
2	j	34	0	30	0	0
2	k	34	0	30	0	0
2	l	34	0	30	0	0
2	m	34	0	30	0	0
2	n	34	0	30	0	0
2	o	34	0	30	0	0
2	p	34	0	30	0	0
3	P	1638	0	1630	16	0
3	Q	1638	0	1630	15	0
3	R	1638	0	1630	14	0
3	S	1638	0	1630	15	0
3	T	1636	0	1625	11	0
3	U	1638	0	1630	14	0
3	V	1638	0	1630	15	0
3	W	1638	0	1630	14	0
3	X	1638	0	1630	15	0
3	Y	1638	0	1630	18	0
3	Z	1638	0	1630	15	0
3	a	1638	0	1630	0	0
3	b	1638	0	1630	0	0
3	c	1638	0	1630	0	0
All	All	46618	0	46430	1060	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 14.

The worst 5 of 1060 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:H:135:ARG:NH2	1:I:48:ARG:NH1	1.62	1.42
1:J:135:ARG:NH2	1:K:48:ARG:NH1	1.66	1.42
1:J:135:ARG:NH2	1:K:48:ARG:HH12	1.05	1.40
1:G:135:ARG:NH2	1:H:48:ARG:HH12	1.17	1.40
1:L:135:ARG:NH2	1:M:48:ARG:HH12	1.16	1.39

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	C	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	D	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	E	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	F	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	G	211/248 (85%)	204 (97%)	7 (3%)	0	100	100
1	H	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	I	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	J	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	K	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	L	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	M	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	N	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
1	O	211/248 (85%)	205 (97%)	6 (3%)	0	100	100
2	B	2/174 (1%)	2 (100%)	0	0	100	100
2	d	2/174 (1%)	2 (100%)	0	0	100	100
2	e	2/174 (1%)	2 (100%)	0	0	100	100
2	f	2/174 (1%)	2 (100%)	0	0	100	100
2	g	2/174 (1%)	2 (100%)	0	0	100	100
2	h	2/174 (1%)	2 (100%)	0	0	100	100
2	i	2/174 (1%)	2 (100%)	0	0	100	100
2	j	2/174 (1%)	2 (100%)	0	0	100	100
2	k	2/174 (1%)	2 (100%)	0	0	100	100
2	l	2/174 (1%)	2 (100%)	0	0	100	100
2	m	2/174 (1%)	2 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	n	2/174 (1%)	2 (100%)	0	0	100	100
2	o	2/174 (1%)	2 (100%)	0	0	100	100
2	p	2/174 (1%)	2 (100%)	0	0	100	100
3	P	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	Q	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	R	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	S	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	T	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	U	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	V	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	W	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	X	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	Y	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	Z	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	a	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	b	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
3	c	220/240 (92%)	214 (97%)	6 (3%)	0	100	100
All	All	6062/9268 (65%)	5893 (97%)	169 (3%)	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	165/192 (86%)	165 (100%)	0	100	100
1	C	165/192 (86%)	165 (100%)	0	100	100
1	D	165/192 (86%)	165 (100%)	0	100	100
1	E	165/192 (86%)	165 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	165/192 (86%)	165 (100%)	0	100	100
1	G	165/192 (86%)	165 (100%)	0	100	100
1	H	165/192 (86%)	165 (100%)	0	100	100
1	I	165/192 (86%)	165 (100%)	0	100	100
1	J	165/192 (86%)	165 (100%)	0	100	100
1	K	165/192 (86%)	165 (100%)	0	100	100
1	L	165/192 (86%)	165 (100%)	0	100	100
1	M	165/192 (86%)	165 (100%)	0	100	100
1	N	165/192 (86%)	165 (100%)	0	100	100
1	O	165/192 (86%)	165 (100%)	0	100	100
2	B	3/141 (2%)	3 (100%)	0	100	100
2	d	3/141 (2%)	3 (100%)	0	100	100
2	e	3/141 (2%)	3 (100%)	0	100	100
2	f	3/141 (2%)	3 (100%)	0	100	100
2	g	3/141 (2%)	3 (100%)	0	100	100
2	h	3/141 (2%)	3 (100%)	0	100	100
2	i	3/141 (2%)	3 (100%)	0	100	100
2	j	3/141 (2%)	3 (100%)	0	100	100
2	k	3/141 (2%)	3 (100%)	0	100	100
2	l	3/141 (2%)	3 (100%)	0	100	100
2	m	3/141 (2%)	3 (100%)	0	100	100
2	n	3/141 (2%)	3 (100%)	0	100	100
2	o	3/141 (2%)	3 (100%)	0	100	100
2	p	3/141 (2%)	3 (100%)	0	100	100
3	P	165/178 (93%)	165 (100%)	0	100	100
3	Q	165/178 (93%)	165 (100%)	0	100	100
3	R	165/178 (93%)	165 (100%)	0	100	100
3	S	165/178 (93%)	165 (100%)	0	100	100
3	T	164/178 (92%)	164 (100%)	0	100	100
3	U	165/178 (93%)	165 (100%)	0	100	100
3	V	165/178 (93%)	165 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	W	165/178 (93%)	165 (100%)	0	100	100
3	X	165/178 (93%)	165 (100%)	0	100	100
3	Y	165/178 (93%)	165 (100%)	0	100	100
3	Z	165/178 (93%)	165 (100%)	0	100	100
3	a	165/178 (93%)	165 (100%)	0	100	100
3	b	165/178 (93%)	165 (100%)	0	100	100
3	c	165/178 (93%)	165 (100%)	0	100	100
All	All	4661/7154 (65%)	4661 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 47 such sidechains are listed below:

Mol	Chain	Res	Type
1	N	11	GLN
3	S	456	GLN
1	N	80	GLN
3	P	456	GLN
3	U	456	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

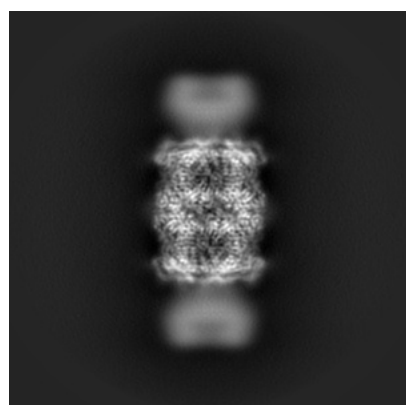
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7097. These allow visual inspection of the internal detail of the map and identification of artifacts.

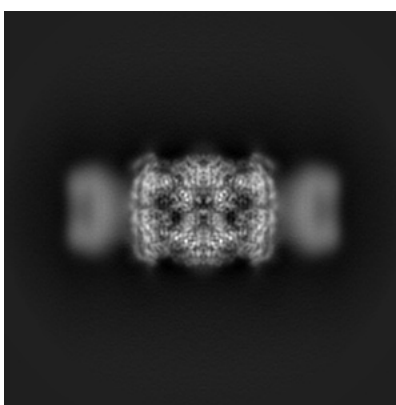
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

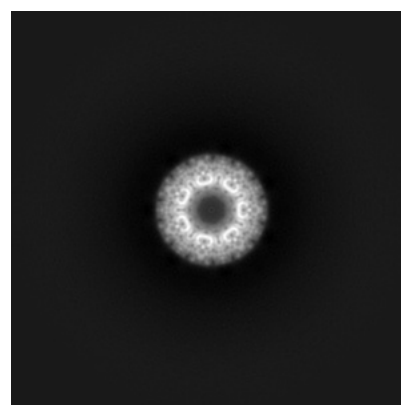
6.1.1 Primary map



X



Y

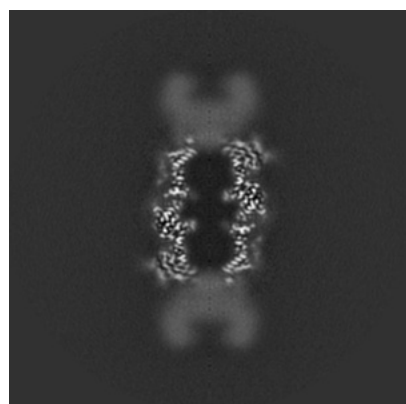


Z

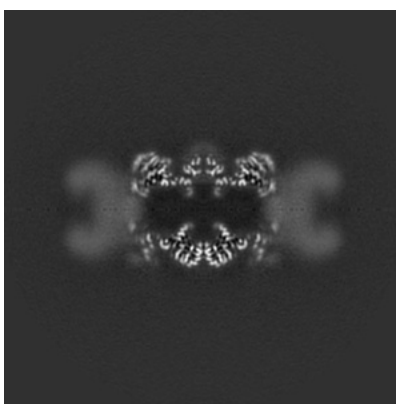
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

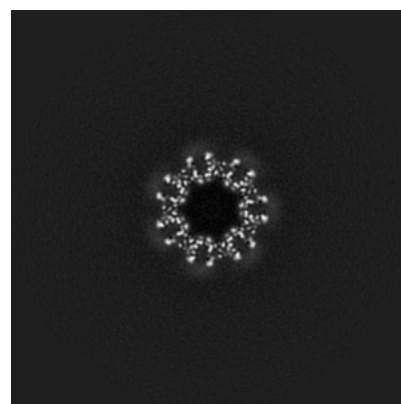
6.2.1 Primary map



X Index: 200



Y Index: 200

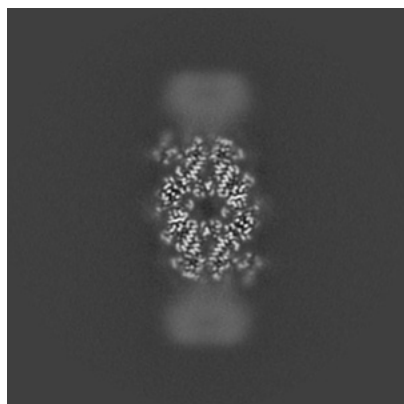


Z Index: 200

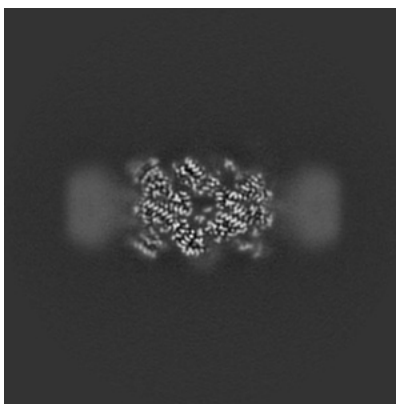
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

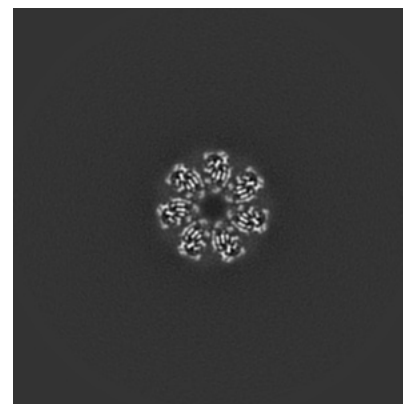
6.3.1 Primary map



X Index: 176



Y Index: 172



Z Index: 216

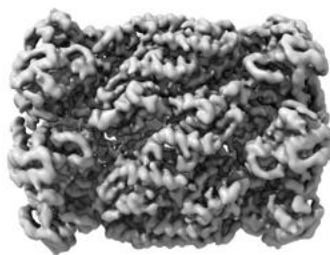
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

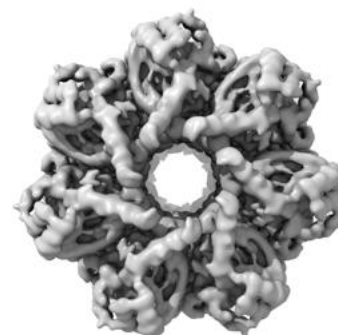
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.00742. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

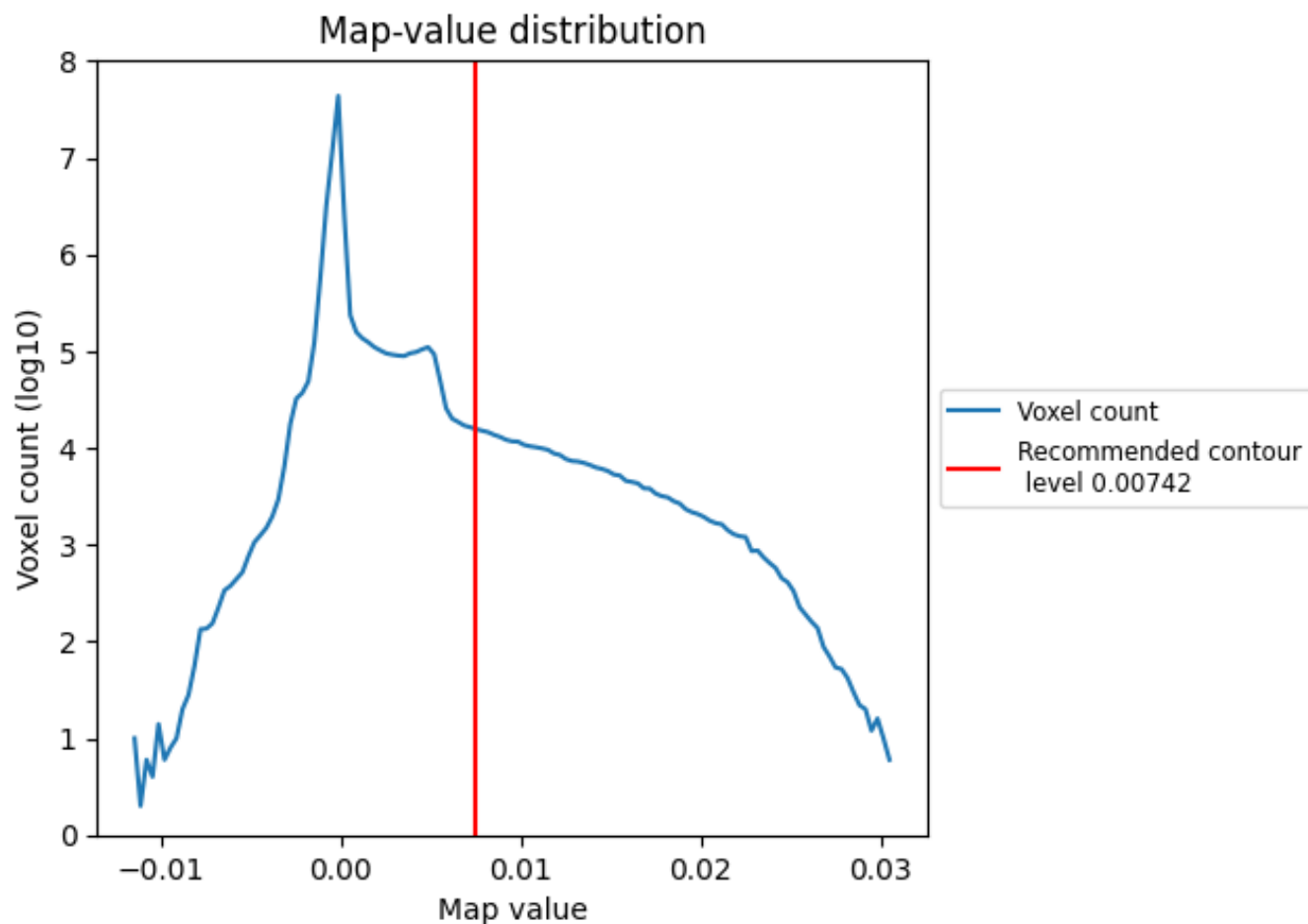
6.5 Mask visualisation

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

7 Map analysis [i](#)

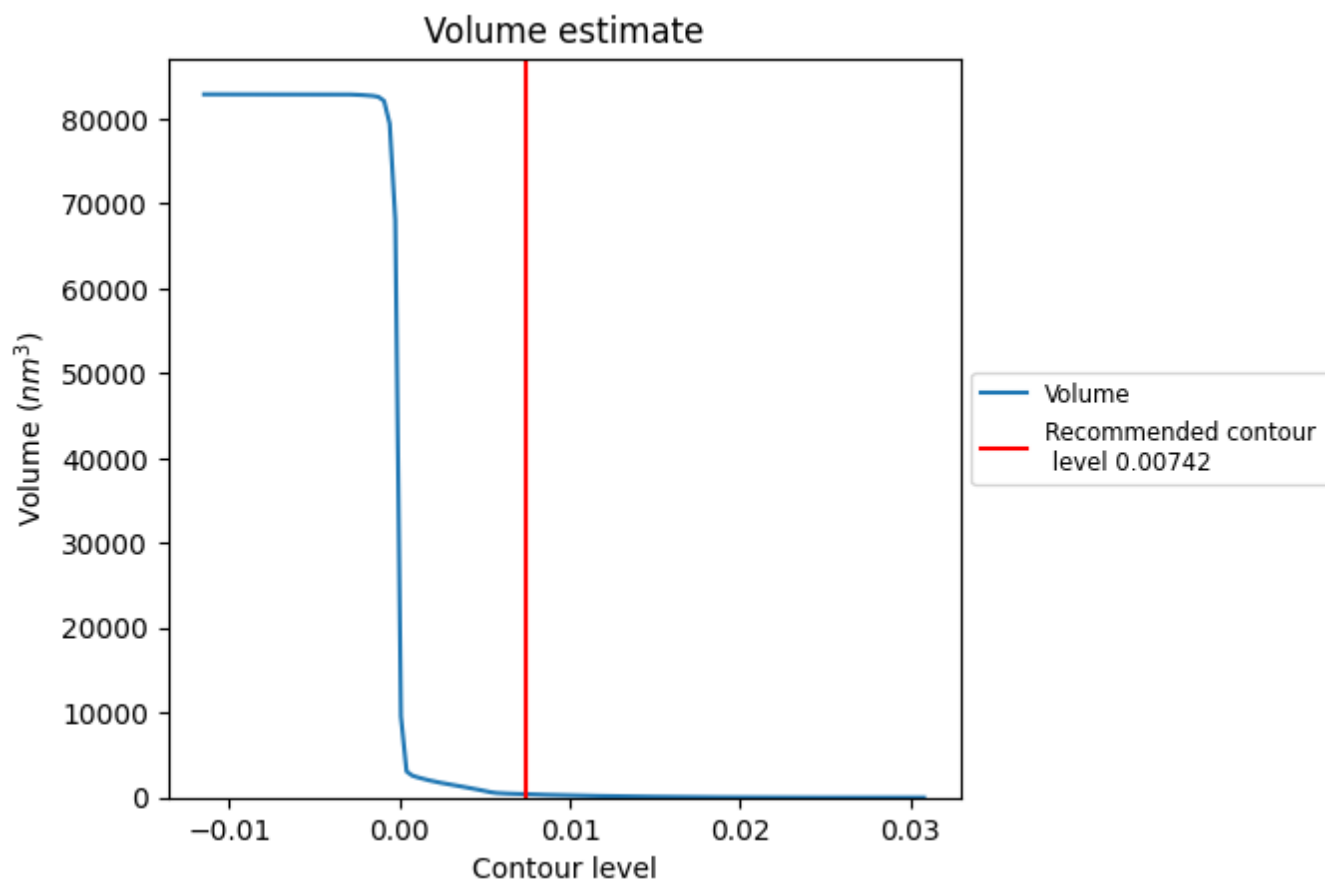
This section contains the results of statistical analysis of the map.

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.

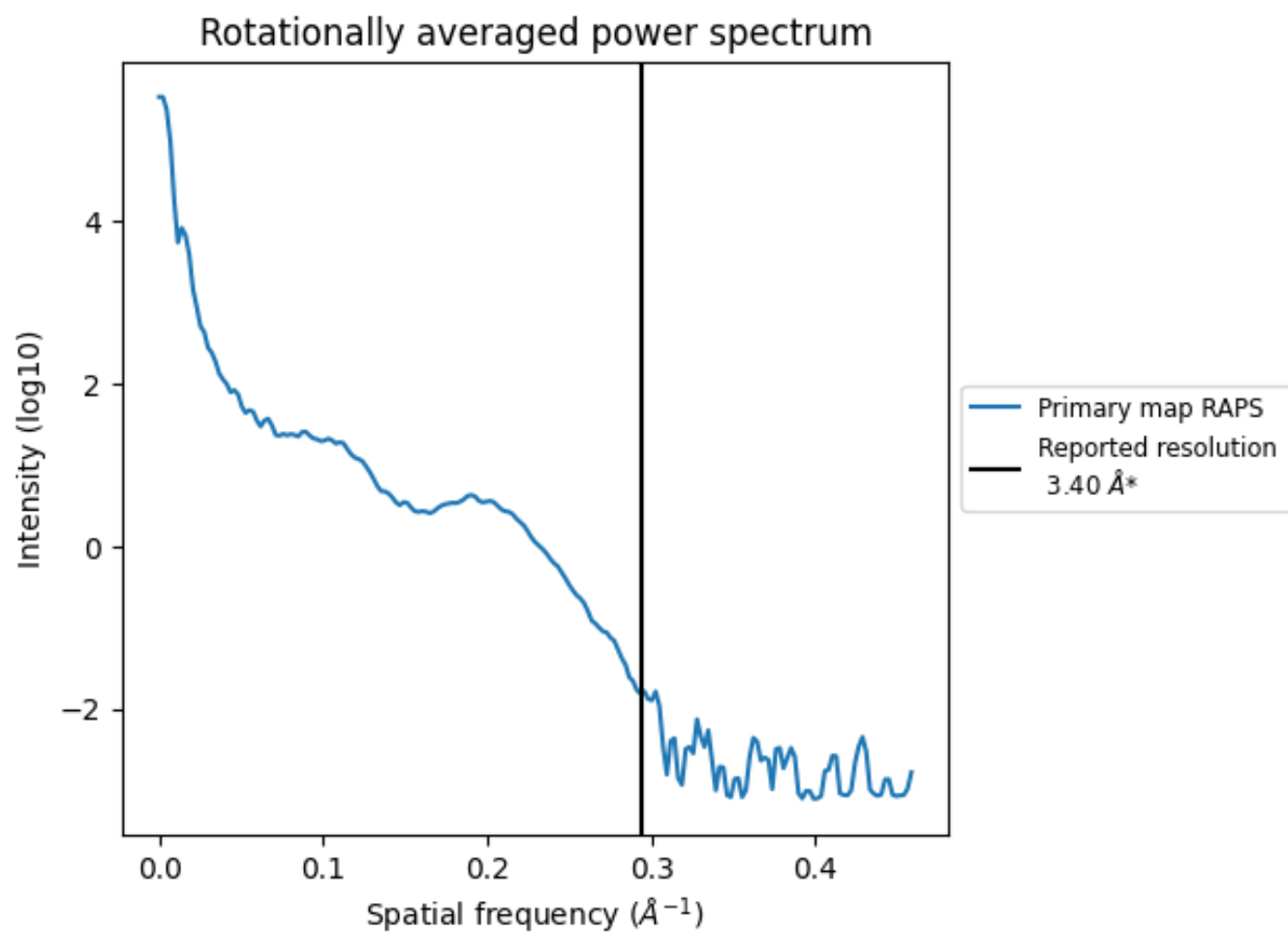
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 395 nm^3 ; this corresponds to an approximate mass of 357 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 ⓘ

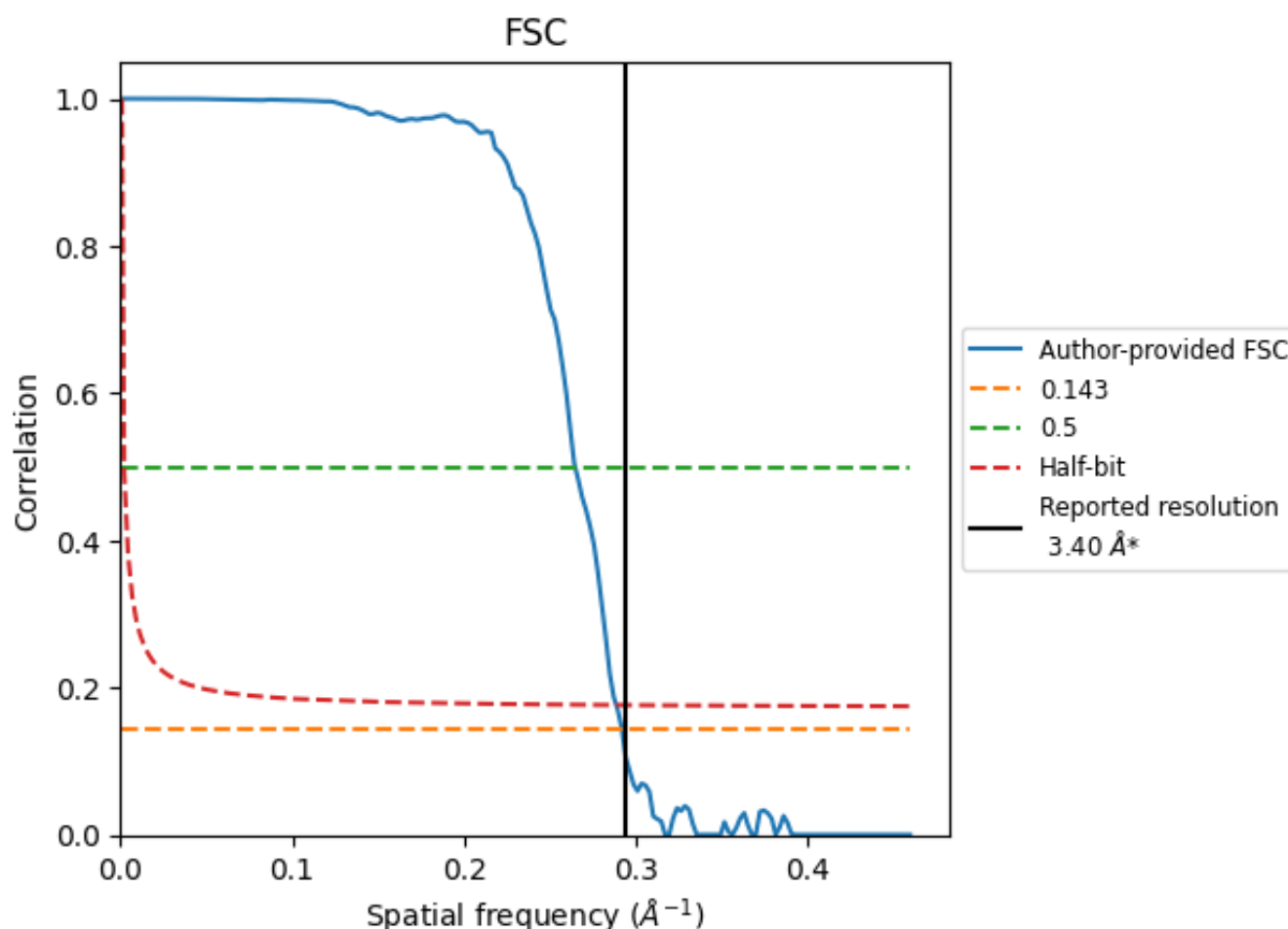


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

8.2 Resolution estimates [i](#)

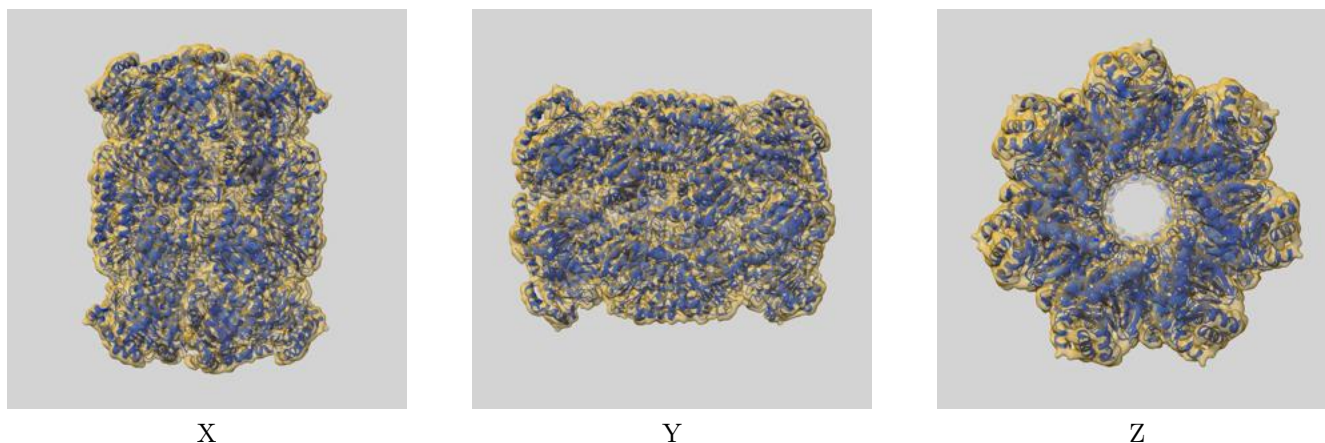
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.43	3.78	3.47
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

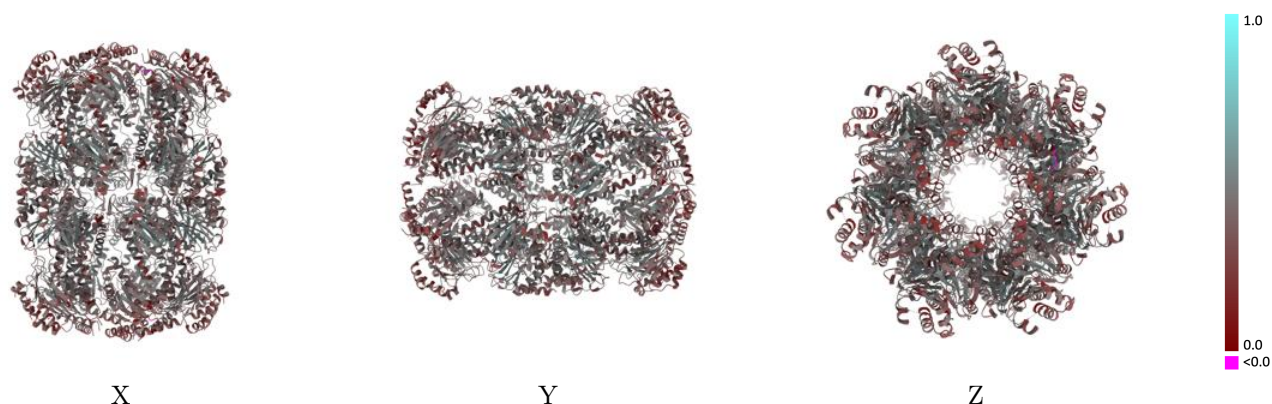
This section contains information regarding the fit between EMDB map EMD-7097 and PDB model 6BGL. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



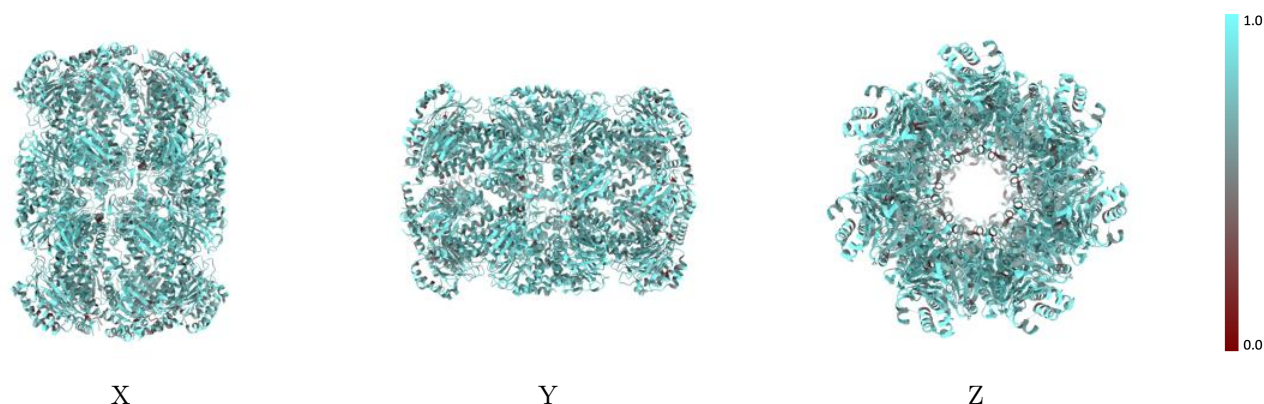
The images above show the 3D surface view of the map at the recommended contour level 0.00742 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



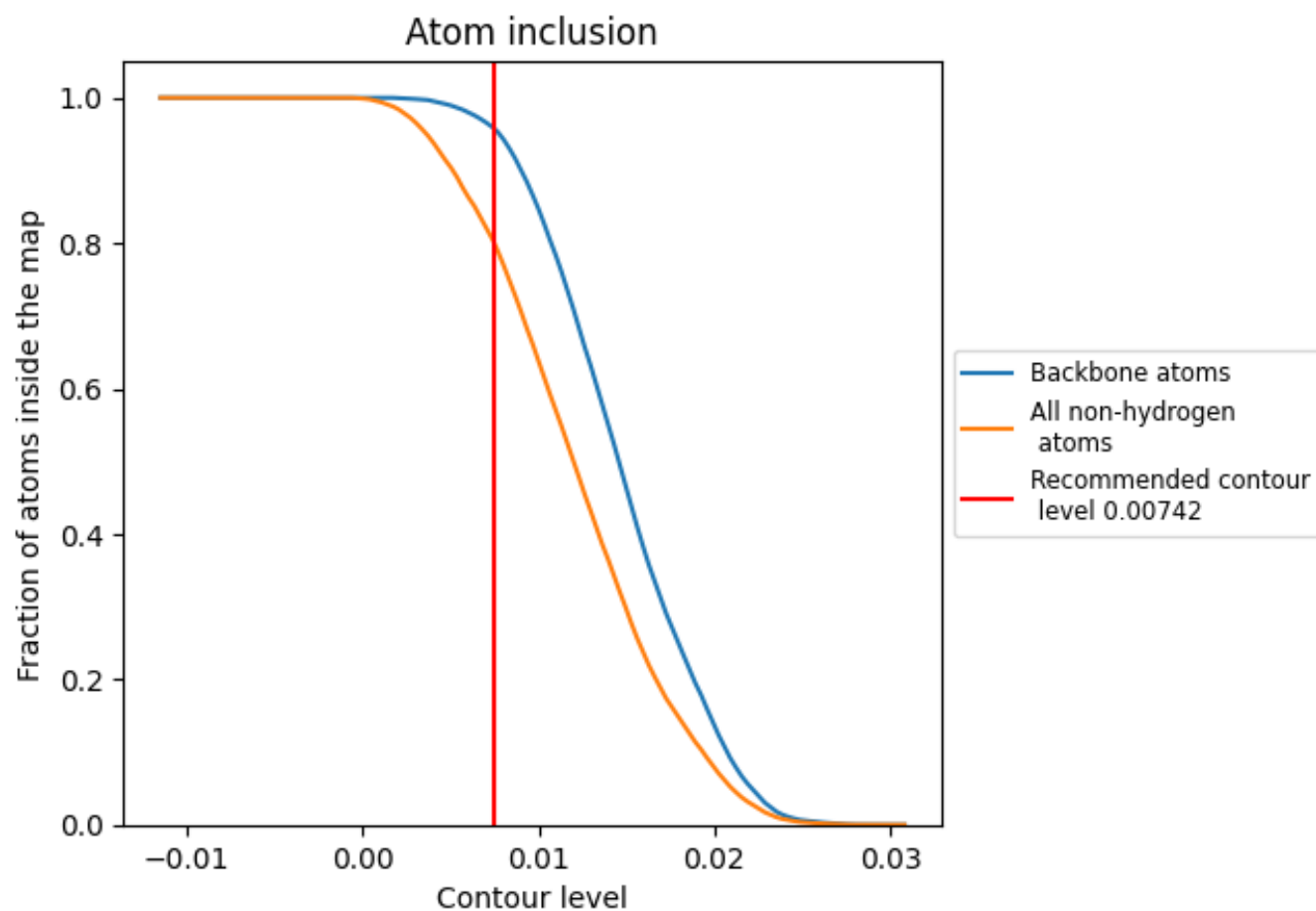
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00742).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 80% 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 (0.00742) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8038	 0.3970
A	 0.7833	 0.3760
B	 0.4242	 0.3300
C	 0.7771	 0.3730
D	 0.7802	 0.3740
E	 0.7677	 0.3660
F	 0.7790	 0.3810
G	 0.7852	 0.3800
H	 0.7777	 0.3790
I	 0.7771	 0.3760
J	 0.7790	 0.3720
K	 0.7846	 0.3710
L	 0.7796	 0.3780
M	 0.7808	 0.3730
N	 0.7858	 0.3750
O	 0.7827	 0.3730
P	 0.8346	 0.4210
Q	 0.8321	 0.4170
R	 0.8321	 0.4180
S	 0.8408	 0.4200
T	 0.8387	 0.4190
U	 0.8365	 0.4190
V	 0.8340	 0.4220
W	 0.8390	 0.4240
X	 0.8383	 0.4240
Y	 0.8346	 0.4230
Z	 0.8358	 0.4240
a	 0.8308	 0.4220
b	 0.8390	 0.4240
c	 0.8390	 0.4220
d	 0.1818	 0.0370
e	 0.3030	 0.2080
f	 0.5455	 0.3790
g	 0.2727	 0.1240
h	 0.5152	 0.3730



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Chain	Atom inclusion	Q-score
i	 0.4545	 0.3750
j	 0.5455	 0.3850
k	 0.4242	 0.4040
l	 0.3939	 0.3460
m	 0.4545	 0.3580
n	 0.4242	 0.2990
o	 0.5152	 0.3950
p	 0.0909	 -0.1440