Full wwPDB EM Validation Report (i)

Jun 28, 2023 – 12:28 pm BST

PDB ID	:	7ZN2
EMDB ID	:	EMD-14799
Title	:	Tail tip of siphophage T5 : full complex after interaction with its bacterial receptor FhuA
Authors	:	Linares, R.; Arnaud, C.A.; Effantin, G.; Darnault, C.; Epalle, N.; Boeri Erba, E.; Schoehn, G.; Breyton, C.
Deposited on	:	2022-04-20
Resolution	:	4.29 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

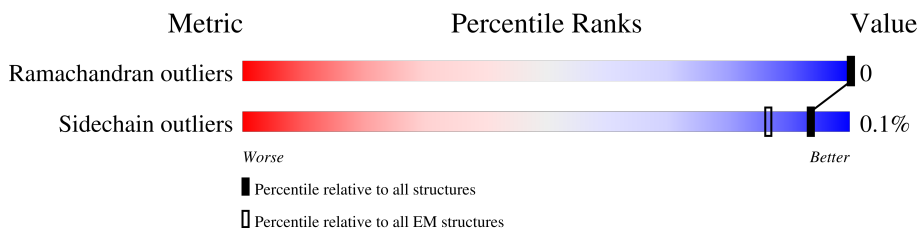The following versions of software and data (see references (i)) were used in the production of this report:

EMDB validation analysis	:	0.0.1.dev50
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)	:	2.33

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 4.29 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.
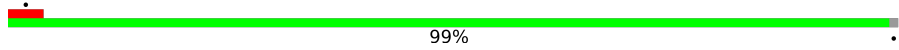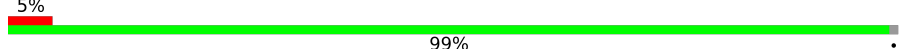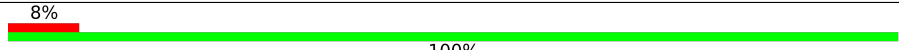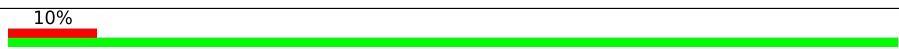
Metric	Percentile Ranks	Value
Ramachandran outliers		0
Sidechain outliers		0.1%

Worse   *Better*

▮ Percentile relative to all structures

▯ Percentile relative to all EM structures
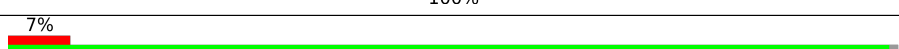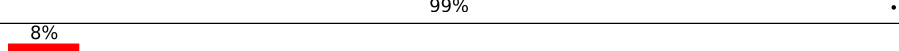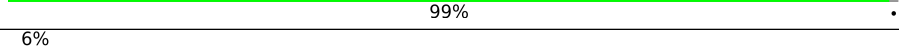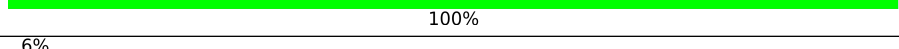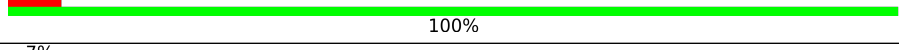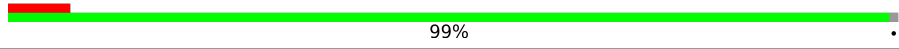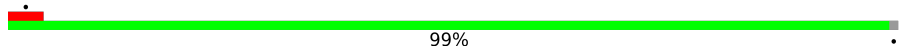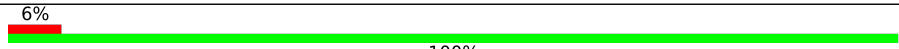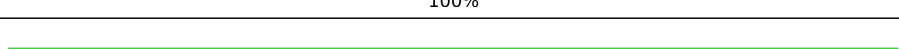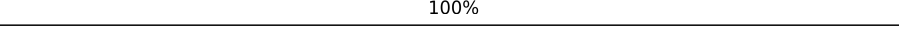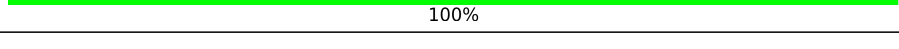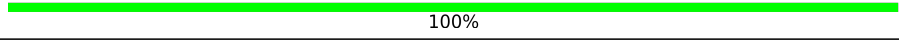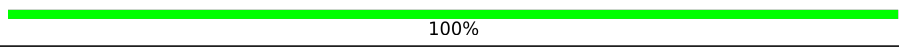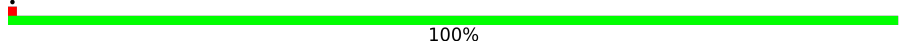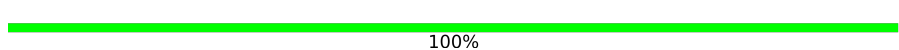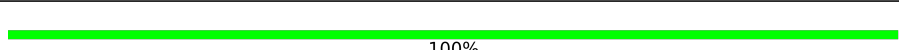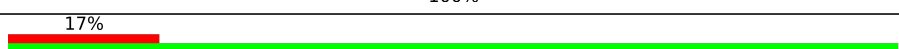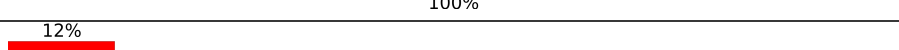
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	b	949	8% / 100%
1	c	949	9% / 100%
1	d	949	17% / 100%
2	h	1219	• / 96%
2	i	1219	• / 96%
2	j	1219	• / 96%
3	e	688	49% / 98% •
3	f	688	48% / 97% •
3	g	688	50% / 85% 14%
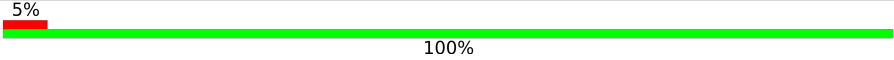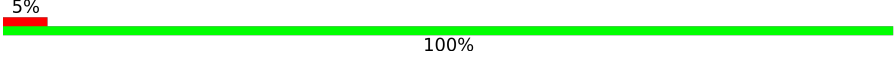
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Mol	Chain	Length	Quality of chain
4	J	140	99%
4	K	140	5% 99%
4	L	140	8% 100%
4	M	140	10% 100%
4	N	140	7% 99%
4	O	140	8% 99%
4	P	140	6% 100%
4	Q	140	6% 100%
4	R	140	7% 99%
4	S	140	99%
4	T	140	9% 100%
4	U	140	6% 100%
5	G	298	100%
5	H	298	100%
5	I	298	100%
6	V	204	100%
6	W	204	100%
6	X	204	100%
6	Y	204	100%
6	Z	204	100%
6	a	204	100%
7	A	464	17% 100%
7	B	464	12% 100%
7	C	464	14% 100%
7	D	464	5% 100%

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Mol	Chain	Length	Quality of chain
7	E	464	5% ▬ 100%
7	F	464	5% ▬ 100%

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 89393 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 Probable baseplate hub protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	d	949	Total	C	N	O	S	0	0
			7576	4811	1274	1481	10		
1	c	949	Total	C	N	O	S	0	0
			7576	4811	1274	1481	10		
1	b	949	Total	C	N	O	S	0	0
			7576	4811	1274	1481	10		

- Molecule 2 is a protein called Pore-forming tail tip protein pb2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	j	43	Total	C	N	O	S	0	0
			328	200	60	67	1		
2	h	43	Total	C	N	O	S	0	0
			328	200	60	67	1		
2	i	43	Total	C	N	O	S	0	0
			328	200	60	67	1		

- Molecule 3 is a protein called Straight fiber protein pb4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	f	669	Total	C	N	O	S	0	0
			5143	3274	854	1000	15		
3	e	671	Total	C	N	O	S	0	0
			5163	3285	859	1004	15		
3	g	589	Total	C	N	O	S	0	0
			4546	2897	758	877	14		

- Molecule 4 is a protein called L-shaped tail fiber protein p132.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	R	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	Q	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		
4	S	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
4	N	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
4	M	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		
4	O	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
4	J	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
4	L	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		
4	U	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		
4	K	139	Total	C	N	O	S	0	0
			1048	653	175	217	3		
4	P	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		
4	T	140	Total	C	N	O	S	0	0
			1056	658	176	218	4		

- Molecule 5 is a protein called Minor tail protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	298	Total	C	N	O	S	0	0
			2423	1551	398	464	10		
5	H	298	Total	C	N	O	S	0	0
			2423	1551	398	464	10		
5	G	298	Total	C	N	O	S	0	0
			2423	1551	398	464	10		

- Molecule 6 is a protein called Distal tail protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	a	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		
6	X	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		
6	Y	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	W	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		
6	V	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		
6	Z	204	Total	C	N	O	S	0	0
			1610	1030	264	313	3		

- Molecule 7 is a protein called Tail tube protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		
7	E	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		
7	C	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		
7	D	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		
7	A	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		
7	B	464	Total	C	N	O	S	0	0
			3546	2217	597	722	10		

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: Probable baseplate hub protein

Chain d:

• Molecule 1: Probable baseplate hub protein

Chain c:

• Molecule 1: Probable baseplate hub protein

Chain b:

D723 N724 S725 G726 N727 D728 I729 P730 D731 I732 S733 N734 G753 A754 N770 L790 E791 N792 N793 R822 R823 S843 R846 S852 G853 D854 K869 E874 I875 D914 A922 I949

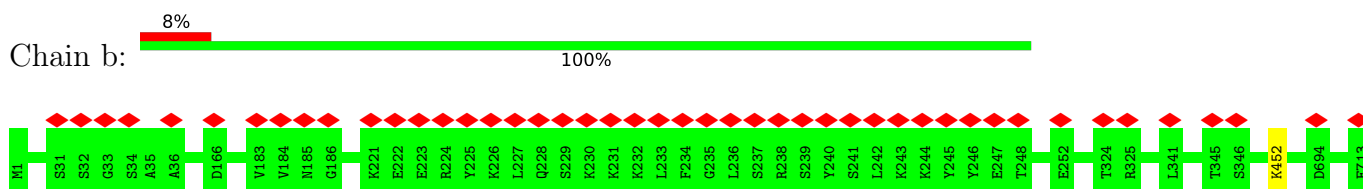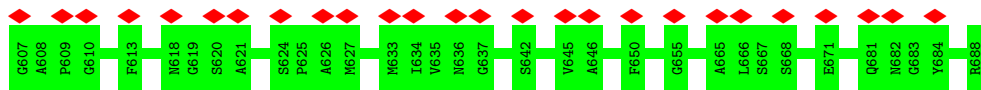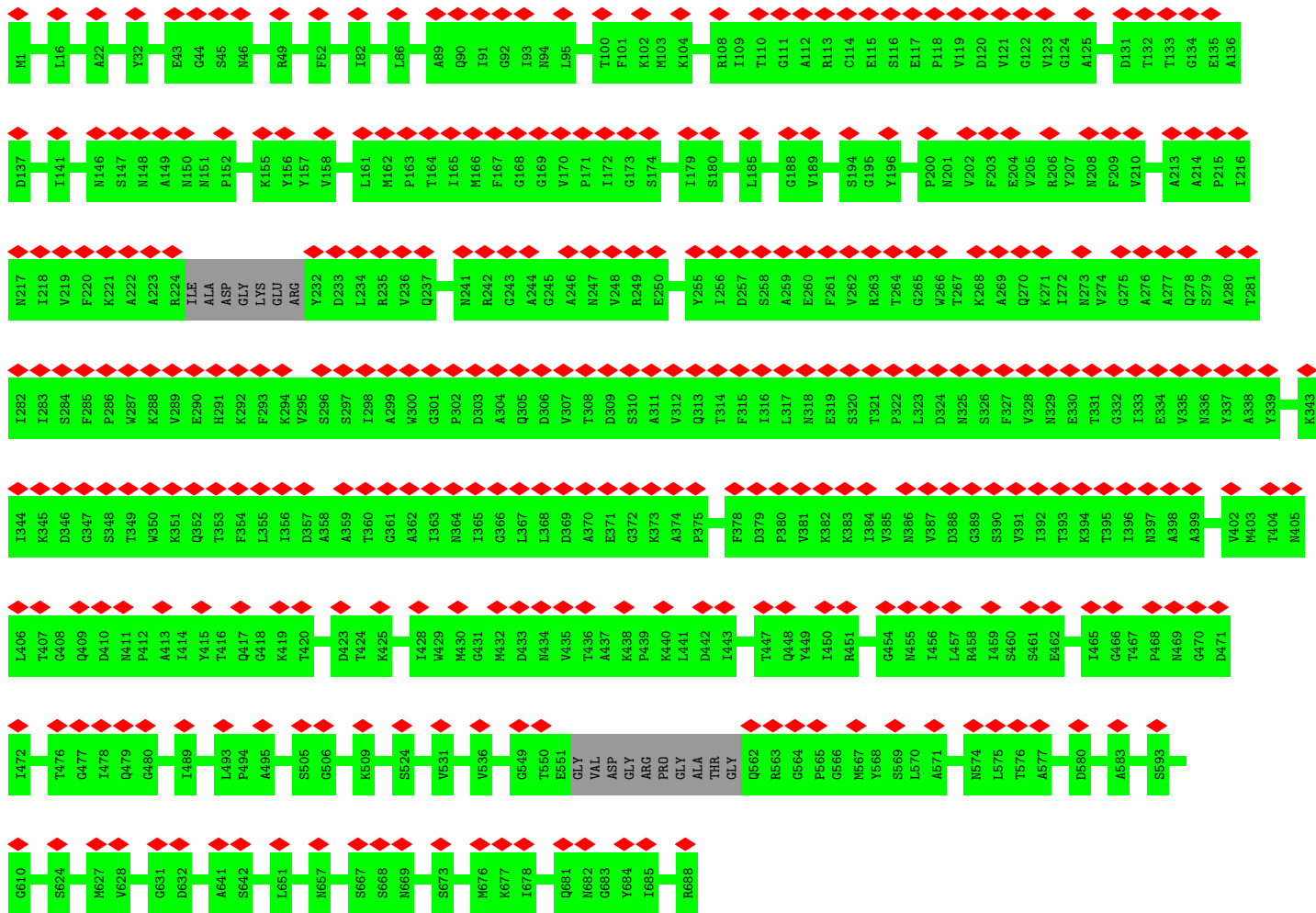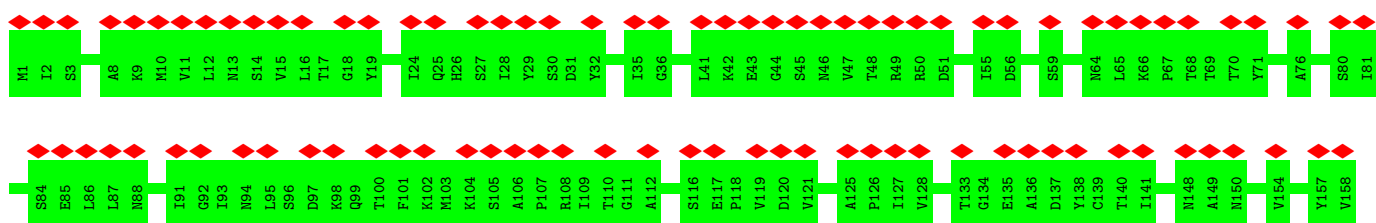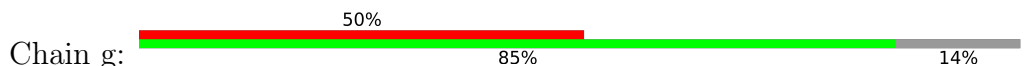• Molecule 2: Pore-forming tail tip protein pb2

Chain j: 96%

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

ASP ARG ALA ALA LYS SER LEU THR LYS MET GLN ALA SER ARG GLY MET ALA GLY ILE ILE THR LYS SER ILE ASP GLY ILE GLU ASP ARG LEU ASP ALA GLY ARG SER LEU ILE GLY ASN THR SER GLY SER ALA ARG GLY ALA THR ARG ASP PHE ALA ALA MET ALA LYS ASN GLY ASN

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

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

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

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

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

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

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

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

ALA LYS LYS ALA SER SER ASP ASN SER VAL VAL LYS VAL GLU ASP THR SER LYS VAL THR GLY GLN SER ALA ASP THR LEU LEU LYS ASN LEU ASN LEU GLY PHE SER PHE LEU LYS ASP MET LYS ALA ALA GLN LYS GLY LEU SER GLU GLU TYR VAL THR ALA MET ASP LYS SER

GLU GLN ASN ALA LEU GLU ASP VAL LYS ARG ASP GLU VAL TYR ASN GLN THR LYS ASP LYS ALA ALA GLU ALA ALA ARG GLU VAL LEU ARG GLN GLN GLN GLU LEU THR ALA ALA LYS ALA LEU GLU ALA ILE ASN PRO ASP PRO GLU ALA LEU LYS GLN GLN VAL

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

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

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

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

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

LYS ILE GLN GLN ASP ALA ALA LYS LYS GLN GLN ILE ILE ILE GLN THR ALA VAL ALA VAL MET GLN ALA ALA THR ALA VAL PRO TYR PRO PHE SER ILE PRO LEU MET VAL ALA ALA GLY LEU ALA GLY ALA LEU ALA LEU ALA GLN ALA SER ALA SER MET SER ILE ALA ASP

SER GLY ALA ASP **T1085** **T1086** **R1127** ALA GLU GLY GLY MET MET TYR PRO GLY VAL VAL SER TYR GLN MET GLY GLU HIS GLY THR GLU VAL VAL THR PRO MET VAL PRO MET LYS ALA THR PRO ASN ASP GLN LEU SER ASP GLY SER LYS THR SER GLY ARG PRO ILE ILE LEU ASN ILE

SER THR MET ASP ASP ALA ALA SER PHE ARG ASP PHE ALA SER ASN ASN SER THR ALA PHE ARG ASP ALA VAL GLU LEU ALA LEU ASN GLU ASN GLU THR THR LEU LYS SER LEU GLY ASN SER

• Molecule 2: Pore-forming tail tip protein pb2

Chain h: . ██████████████████████████████████████ 96%

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

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

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

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

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

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

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

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

ASN ALA LEU THR ALA GLY GLY ILE GLY GLY ASP GLU SER ASN LYS LEU VAL GLN LEU THR ASN GLU LEU ARG ASN LYS GLU LEU GLU ARG THR LYS VAL LEU ARG GLN ALA VAL GLN ASP THR GLY ALA LEU ARG ASN GLY LYS LEU LEU ALA GLU

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

ALA LYS LYS ALA SER SER ASP LEU ASN SER VAL VAL LYS ALA VAL GLU ASP THR SER LYS VAL THR GLY GLN SER ALA ASP THR VAL LYS ASN LEU ASN LEU GLY PHE SER LEU GLN MET LYS ALA ALA GLN LYS GLY LEU SER GLU GLU TYR VAL THR ALA MET ASP LYS SER

GLU GLN ASN ALA LEU GLU VAL ALA LYS ARG LYS ASP GLU VAL TYR ASN GLN THR LYS ASP LYS ALA GLU ALA ALA ARG GLU VAL LEU LEU ARG GLN ILE LEU ASN PRO ASN ASP GLU ALA LEU LYS GLN VAL

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

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

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

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

GLY SER LEU ASP THR THR SER SER MET ILE ALA SER GLY MET GLN THR VAL ALA SER MET ILE GLN SER THR SER GLN VAL SER ALA ILE ASP GLN ALA ALA ALA GLU GLN LYS ARG ASP LYS SER GLY LYS SER ALA SER LYS ALA LYS LYS LEU GLU GLU LYS LEU

LYS ILE GLN ASP ALA LYS LYS ILE ILE ILE GLN THR ALA VAL ALA VAL MET GLN ALA ALA THR ALA VAL PRO TYR PRO PHE SER ILE PRO MET VAL ALA GLY LEU ALA GLY LEU ALA GLN ALA SER ALA GLY MET SER ILE ALA ASP

SER GLY ALA ASP T1085 R1127 ALA GLU GLY GLY MET MET PRO GLY VAL VAL SER TYR GLN VAL MET GLY GLU GLU HIS GLY THR GLU GLU VAL VAL THR PRO MET VAL PRO MET LYS ALA THR PRO ASN ASP GLN LEU SER ASP GLY SER LYS THR THR SER GLY ARG PRO ILE ILE LEU ASN ILE SER

THR MET ASP ALA ALA SER PHE ARG ASP ASP PHE ALA SER ASN ASN SER THR ALA PHE ARG ASP ALA VAL GLU LEU LEU ASN GLU ASN GLY THR THR LEU LYS SER LEU GLY ASN SER

• Molecule 2: Pore-forming tail tip protein pb2

Chain i: _____ 96%

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

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

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

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

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

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

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

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

ASN ALA LEU THR ALA GLY GLY ILE GLY GLY ASP GLU ASN VAL THR ALA LEU ILE GLU LEU THR ASN ALA VAL GLN LEU GLY ALA ARG GLU ASP THR TYR LYS GLU LYS GLU GLU ARG THR LYS GLU LEU ASN LYS VAL LEU LEU ARG ASN GLY LEU ALA GLU

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

ALA LYS LYS ALA SER SER ASP LEU ASN SER VAL VAL LYS ALA VAL GLU ASP THR SER LYS VAL THR GLY GLN SER ALA ASP THR LEU VAL LYS ASN LEU ASN LEU GLY PHE SER LEU ASP MET LYS ALA ALA GLN GLY LEU SER GLU GLU TYR VAL THR ALA MET ASP LYS SER

GLU GLN ASN ALA LEU GLU VAL ALA LYS ARG LYS ASP GLU VAL TYR ASN GLN THR ASP LYS ALA LEU GLU LEU ALA ALA ALA ARG GLU ILE VAL LEU ARG GLN GLN GLU LEU THR ALA ALA LYS LEU LEU ILE ASN PRO ASP PRO GLU ALA LYS LYS GLN LEU VAL

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

• Molecule 3: Straight fiber protein pb4

Chain f:

48%

97%

• Molecule 3: Straight fiber protein pb4

Chain e:

• Molecule 3: Straight fiber protein pb4

Chain g:

G159 A160 I165 M166 F167 G168 G169 V170 P171 I172 G173 K176 I183 S184 L185 P186 D187 G188 V189 T190 I191 D192 Y197 E198 Y199 P200 N201 R206 Y207 N208 F209 A213 A214 P215 I216 N217 I218 V219 F220 K221 A222 A223 R224 ILE ALA ASP GLY LYS GLU ARG Y232 D233 L234 R235

V236 Q237 W238 D239 W240 M241 R242 G243 A244 N247 V248 R249 E250 F251 V252 L253 S254 A259 E260 F261 V262 R263 T264 G265 W266 T267 K268 A269 Q270 K271 I272 N273 V274 G275 A276 A277 Q278 S279 A280 T281 I282 I283 S284 F285 P286 W287 K288 V289 E290 H291 K292 F293 K294 V295 S296 S297 I298 A299

W300 G301 P302 D303 A304 T308 D309 S310 A311 V312 Q313 T314 F315 I316 L317 N318 E319 S320 T321 P322 L323 D324 N325 S326 N329 E330 T331 G332 I333 E334 V335 N336 Y337 A338 Y339 I340 K341 G342 K343 I344 K345 D346 G347 S348 T349 W350 K351 Q352 T353 F354 L355 I356 D357 A358 A359 T360 G361 A362

I363 N364 I365 G366 L367 L368 D369 A370 E371 G372 K373 S377 F378 D379 P380 V381 K382 K383 I384 V385 D388 G389 S390 V391 I392 T393 K394 T395 I396 N397 V402 M403 L406 Q409 D410 Q417 G418 K419 T420 W421 G422 K425 S426 G427 M430 G431 M432 D433 N434 P439

I443 G444 N445 A446 T447 Y452 D453 G454 N455 I456 L457 R458 I459 S460 S461 E462 V463 V464 I465 N469 GLY ASP ILE ASP ILE GLN THR GLY ILE GLN GLY LYS GLN THR VAL PHE ILE TYR ILE ILE GLY THR SER LEU PRO ALA LYS PRO THR SER PRO ALA TYR PRO PRO SER GLY TRP

SER LYS THR PRO PRO ASN ARG THR SER ASN THR GLN ASN ILE TYR CYS SER THR GLY THR LEU ASP PRO VAL THR ASN GLN LEU VAL SER GLY THR SER TRP SER ASP VAL VAL GLN TRP SER GLY THR GLU GLY VAL ASP GLY ARG PRO GLY ALA THR GLY Q562 R563 M567 Y568 S569

L570 A571 I572 A573 N574 L575 T576 A577 Q582 F586 N590 F591 G592 S593 G594 Y598 D599 K605 S606 G607 A608 P609 G610 Q616 Q620 M627 D632 M633 I634 V635 N636 G637 T638 V639 V645 N648 A649 R662 A663 A664 A665 L666 S667 K677 L680 Q681

R688

• Molecule 4: L-shaped tail fiber protein p132

Chain R:

7%

99%

• Molecule 4: L-shaped tail fiber protein p132

MET S2 D9 D29 S30 P33 S34 T35 E95 V118 G119 S120 Q140

• Molecule 4: L-shaped tail fiber protein p132

Chain Q:

6%

100%

M1 S30 V31 S34 A117 V118 G119 S120 A121 Q140

• Molecule 4: L-shaped tail fiber protein p132

Chain S:

99%

MET S2 T3 S30 A121 A122 Q140

• Molecule 4: L-shaped tail fiber protein p132

7%

Chain N:

99%

MET S2 D29 S30 V31 Y32 P33 S34 E95 V118 G119 S120 A121 A122 Q140

• Molecule 4: L-shaped tail fiber protein p132

10%

Chain M:

100%

M1 D29 S30 V31 S34 D56 A71 K91 A117 V118 G119 S120 A121 Q140

• Molecule 4: L-shaped tail fiber protein p132

8%

Chain O:

99%

MET S2 T3 E4 N5 S30 P33 V118 G119 S120 A121 A122 S123 Q140

• Molecule 4: L-shaped tail fiber protein p132

Chain J:

99%

MET S2 S30 V31 S34 V118 G119 A122 Q140

• Molecule 4: L-shaped tail fiber protein p132

8%

Chain L:

100%

M1 D29 S30 V31 Y32 A117 V118 G119 S120 A121 A122 Q140

• Molecule 4: L-shaped tail fiber protein p132

6%

Chain U:

100%

M1 D29 S30 V31 Y32 V118 G119 S120 A121 Q140

• Molecule 4: L-shaped tail fiber protein p132

Chain K:

5%

99%

MET S2 D29 P33 A117 V118 A121 A122 Q140

• Molecule 4: L-shaped tail fiber protein p132

Chain P:

6%

100%

M1 S30 V31 A117 V118 G119 S120 A121 A122 Q140

• Molecule 4: L-shaped tail fiber protein p132

Chain T:

9%

100%

M1 V31 Y32 P33 S34 T116 A117 V118 G119 S120 A121 A122 Q140
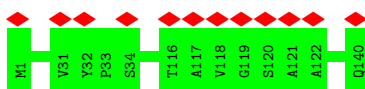
• Molecule 5: Minor tail protein

Chain I:

100%

There are no outlier residues recorded for this chain.

• Molecule 5: Minor tail protein

Chain H:

100%

There are no outlier residues recorded for this chain.

• Molecule 5: Minor tail protein

Chain G:

100%

M1 K133 G234 K298
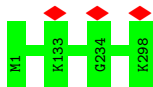
• Molecule 6: Distal tail protein

Chain a:

100%

There are no outlier residues recorded for this chain.

• Molecule 6: Distal tail protein

Chain X:

100%
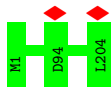
• Molecule 6: Distal tail protein

Chain Y:

100%

There are no outlier residues recorded for this chain.

• Molecule 6: Distal tail protein

Chain W:

100%

There are no outlier residues recorded for this chain.

• Molecule 6: Distal tail protein

Chain V:

100%

There are no outlier residues recorded for this chain.

• Molecule 6: Distal tail protein

Chain Z:

100%

There are no outlier residues recorded for this chain.

• Molecule 7: Tail tube protein

Chain F:

5%

100%
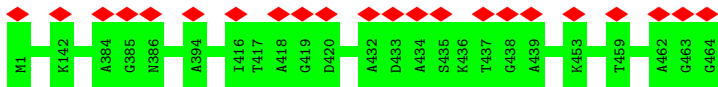
• Molecule 7: Tail tube protein

Chain E:

5%

100%
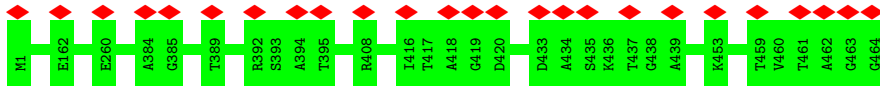
• Molecule 7: Tail tube protein

Chain C:

14%

100%

I416 T417 A418 G419 D420 T423 I424 N425 A426 T427 G428 L429 L430 R431 A432 D433 A434 S435 K436 T437 G438 A439 V440 K447 S450 K456 V457 I458 T459 A462 G463 G464

• Molecule 7: Tail tube protein

Chain D:

5%

100%

M1 D32 N386 T395 A418 G419 D420 A421 A426 L429 A432 D433 A434 S435 K436 T437 G438 A439 S450 G451 V452 K453 A462 G463 G464

• Molecule 7: Tail tube protein

Chain A:

17%

100%

M1 S2 N8 L29 I34 N83 K142 E162 D180 I191 D192 I199 Q200 G201 D217 I226 T227 G228 N270 S273 L274 L299 G300 G301 I324 E325 L330 D344 A375 I379 K382 S383 A384 G385 N386 V387 T388 T389 L390 N391

R392 S393 A394 T395 L396 Q397 S405 R408 N409 K410 E411 V412 A415 I416 T417 A418 G419 D420 A421 N425 A426 T427 G428 L429 L430 R431 A432 D433 A434 S435 K436 T437 G438 A439 V440 T441 K447 V452 K456 V457 I458 T459 V460 T461 A462 G463 G464

• Molecule 7: Tail tube protein

Chain B:

12%

100%

M1 S2 L3 Q4 L5 L6 R7 T18 L29 D32 I76 D141 K142 E181 Q188 I199 D217 D223 G301 E302 Y303 D304 D374 A384 G385 N386 V387 T388 T389 L390 N391 R392 S393 A394 T395 L396 Q397 T417 A418 G419 D420 A421 A426 T427 G428

L429 L430 R431 A432 D433 A434 G438 A439 G451 T455 K456 V457 I458 T459 A462 G463 G464

4 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25558	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 $(e^-/\text{Å}^2)$	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.038	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0214	Depositor
Map size (Å)	459.34, 459.34, 459.34	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.351, 1.351, 1.351	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	b	0.27	0/7740	0.49	0/10500
1	c	0.27	0/7740	0.49	0/10500
1	d	0.27	0/7740	0.49	0/10500
2	h	0.26	0/331	0.54	0/444
2	i	0.25	0/331	0.54	0/444
2	j	0.26	0/331	0.53	0/444
3	e	0.26	0/5285	0.47	0/7208
3	f	0.26	0/5265	0.47	0/7182
3	g	0.26	0/4650	0.48	0/6332
4	J	0.26	0/1062	0.54	0/1443
4	K	0.26	0/1062	0.54	0/1443
4	L	0.30	0/1070	0.55	0/1453
4	M	0.26	0/1070	0.54	0/1453
4	N	0.26	0/1062	0.54	0/1443
4	O	0.27	0/1062	0.54	0/1443
4	P	0.30	0/1070	0.55	0/1453
4	Q	0.26	0/1070	0.54	0/1453
4	R	0.26	0/1062	0.54	0/1443
4	S	0.26	0/1062	0.54	0/1443
4	T	0.30	0/1070	0.55	0/1453
4	U	0.26	0/1070	0.53	0/1453
5	G	0.28	0/2483	0.50	0/3370
5	H	0.28	0/2483	0.50	0/3370
5	I	0.28	0/2483	0.50	0/3370
6	V	0.28	0/1649	0.48	0/2239
6	W	0.27	0/1649	0.47	0/2239
6	X	0.28	0/1649	0.48	0/2239
6	Y	0.27	0/1649	0.47	0/2239
6	Z	0.28	0/1649	0.48	0/2239
6	a	0.27	0/1649	0.47	0/2239
7	A	0.27	0/3604	0.50	0/4904
7	B	0.26	0/3604	0.50	0/4904
7	C	0.26	0/3604	0.50	0/4904
7	D	0.26	0/3604	0.50	0/4904

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
7	E	0.26	0/3604	0.50	0/4904
7	F	0.26	0/3604	0.50	0/4904
All	All	0.27	0/91172	0.50	0/123898

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 ⓘ

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	b	947/949 (100%)	903 (95%)	44 (5%)	0	100	100
1	c	947/949 (100%)	918 (97%)	29 (3%)	0	100	100
1	d	947/949 (100%)	898 (95%)	49 (5%)	0	100	100
2	h	41/1219 (3%)	41 (100%)	0	0	100	100
2	i	41/1219 (3%)	40 (98%)	1 (2%)	0	100	100
2	j	41/1219 (3%)	41 (100%)	0	0	100	100
3	e	665/688 (97%)	636 (96%)	29 (4%)	0	100	100
3	f	663/688 (96%)	648 (98%)	15 (2%)	0	100	100
3	g	583/688 (85%)	568 (97%)	15 (3%)	0	100	100
4	J	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
4	K	137/140 (98%)	133 (97%)	4 (3%)	0	100	100

Continued on next page...

W O R L D W I D E
wwPDB
PROTEIN DATA BANK

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	L	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
4	M	138/140 (99%)	131 (95%)	7 (5%)	0	100	100
4	N	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
4	O	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
4	P	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
4	Q	138/140 (99%)	131 (95%)	7 (5%)	0	100	100
4	R	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
4	S	137/140 (98%)	133 (97%)	4 (3%)	0	100	100
4	T	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
4	U	138/140 (99%)	131 (95%)	7 (5%)	0	100	100
5	G	296/298 (99%)	286 (97%)	10 (3%)	0	100	100
5	H	296/298 (99%)	286 (97%)	10 (3%)	0	100	100
5	I	296/298 (99%)	287 (97%)	9 (3%)	0	100	100
6	V	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
6	W	202/204 (99%)	196 (97%)	6 (3%)	0	100	100
6	X	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
6	Y	202/204 (99%)	197 (98%)	5 (2%)	0	100	100
6	Z	202/204 (99%)	198 (98%)	4 (2%)	0	100	100
6	a	202/204 (99%)	197 (98%)	5 (2%)	0	100	100
7	A	462/464 (100%)	445 (96%)	17 (4%)	0	100	100
7	B	462/464 (100%)	445 (96%)	17 (4%)	0	100	100
7	C	462/464 (100%)	445 (96%)	17 (4%)	0	100	100
7	D	462/464 (100%)	446 (96%)	16 (4%)	0	100	100
7	E	462/464 (100%)	444 (96%)	18 (4%)	0	100	100
7	F	462/464 (100%)	446 (96%)	16 (4%)	0	100	100
All	All	11397/15150 (75%)	10997 (96%)	400 (4%)	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	b	834/834 (100%)	832 (100%)	2 (0%)	93	96
1	c	834/834 (100%)	832 (100%)	2 (0%)	93	96
1	d	834/834 (100%)	832 (100%)	2 (0%)	93	96
2	h	36/980 (4%)	36 (100%)	0	100	100
2	i	36/980 (4%)	36 (100%)	0	100	100
2	j	36/980 (4%)	36 (100%)	0	100	100
3	e	562/572 (98%)	562 (100%)	0	100	100
3	f	560/572 (98%)	559 (100%)	1 (0%)	93	96
3	g	490/572 (86%)	489 (100%)	1 (0%)	93	96
4	J	118/119 (99%)	118 (100%)	0	100	100
4	K	118/119 (99%)	118 (100%)	0	100	100
4	L	119/119 (100%)	119 (100%)	0	100	100
4	M	119/119 (100%)	119 (100%)	0	100	100
4	N	118/119 (99%)	118 (100%)	0	100	100
4	O	118/119 (99%)	118 (100%)	0	100	100
4	P	119/119 (100%)	119 (100%)	0	100	100
4	Q	119/119 (100%)	119 (100%)	0	100	100
4	R	118/119 (99%)	118 (100%)	0	100	100
4	S	118/119 (99%)	118 (100%)	0	100	100
4	T	119/119 (100%)	119 (100%)	0	100	100
4	U	119/119 (100%)	119 (100%)	0	100	100
5	G	273/273 (100%)	273 (100%)	0	100	100
5	H	273/273 (100%)	273 (100%)	0	100	100
5	I	273/273 (100%)	273 (100%)	0	100	100
6	V	181/181 (100%)	181 (100%)	0	100	100
6	W	181/181 (100%)	181 (100%)	0	100	100
6	X	181/181 (100%)	181 (100%)	0	100	100
6	Y	181/181 (100%)	181 (100%)	0	100	100
6	Z	181/181 (100%)	181 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	a	181/181 (100%)	181 (100%)	0	100	100
7	A	394/394 (100%)	394 (100%)	0	100	100
7	B	394/394 (100%)	394 (100%)	0	100	100
7	C	394/394 (100%)	394 (100%)	0	100	100
7	D	394/394 (100%)	394 (100%)	0	100	100
7	E	394/394 (100%)	394 (100%)	0	100	100
7	F	394/394 (100%)	394 (100%)	0	100	100
All	All	9913/12855 (77%)	9905 (100%)	8 (0%)	93	97

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	d	452	LYS
1	d	846	ARG
1	c	224	ARG
1	c	452	LYS
3	f	206	ARG
3	g	206	ARG
1	b	452	LYS
1	b	846	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	c	911	ASN
3	f	386	ASN
3	g	13	ASN
3	g	25	GLN
7	F	31	GLN
5	H	216	ASN
7	C	151	GLN
7	A	151	GLN
7	B	151	GLN

5.3.3　RNA　ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-14799. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections ⓘ
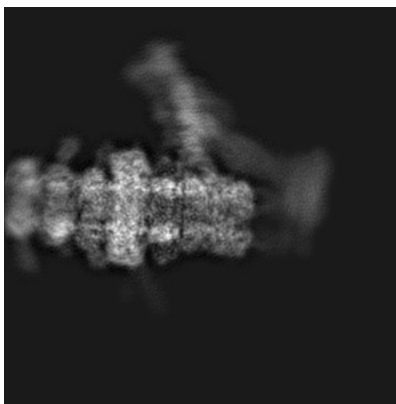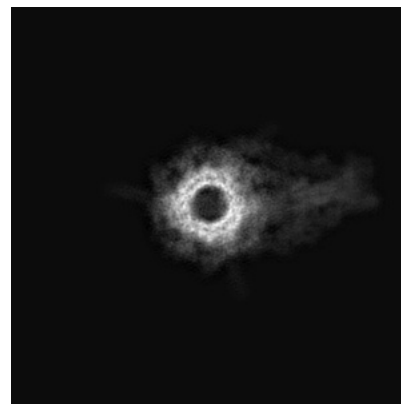
6.1.1 Primary map

X   Y   Z

6.1.2 Raw map

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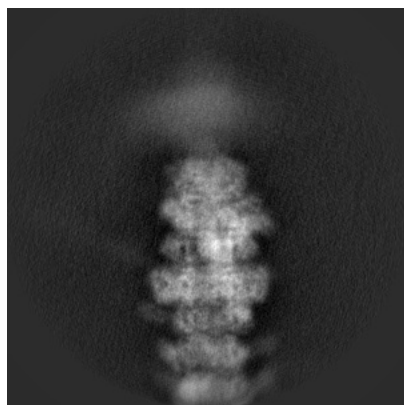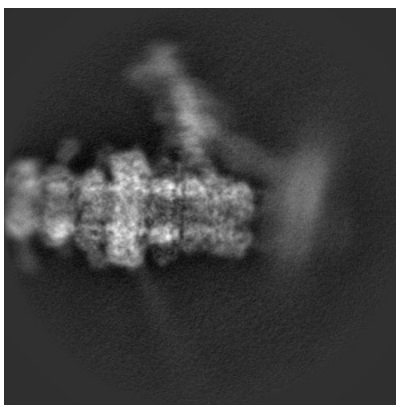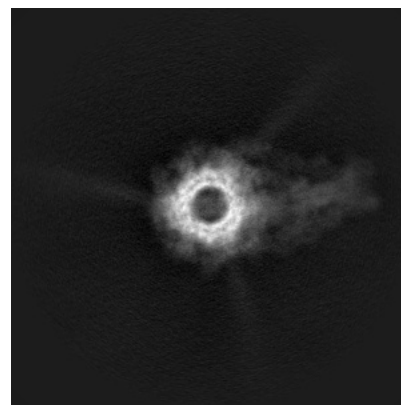
The images above show the map projected in three orthogonal directions.

6.2　Central slices　ⓘ
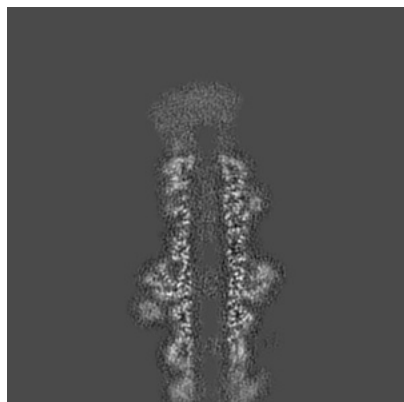
6.2.1　Primary map
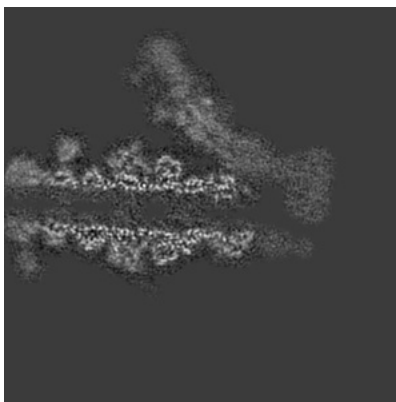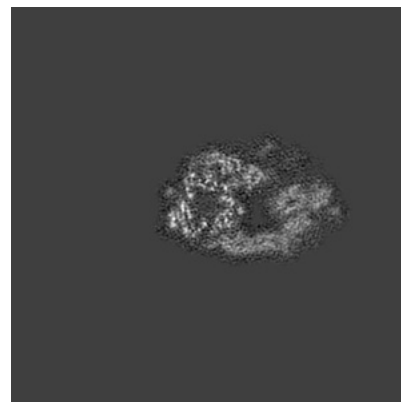
| X Index: 170 | Y Index: 170 | Z Index: 170 |

6.2.2　Raw map
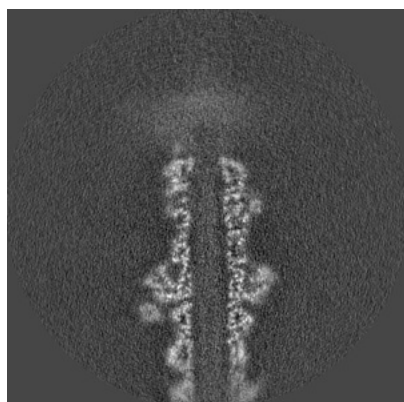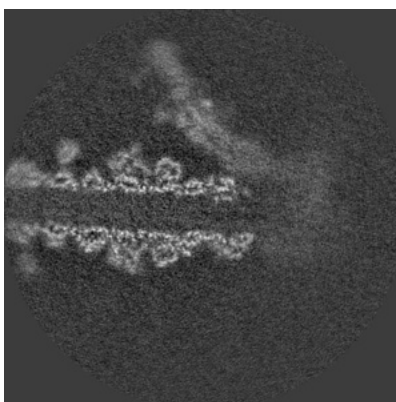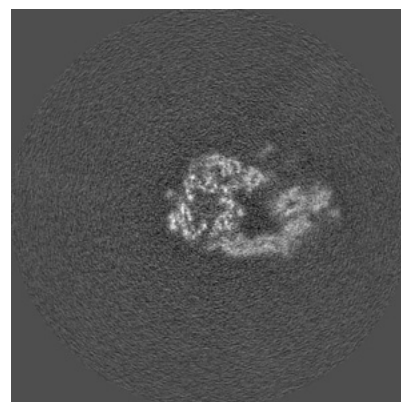
| X Index: 170 | Y Index: 170 | Z Index: 170 |

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

6.3 Largest variance slices ⓘ
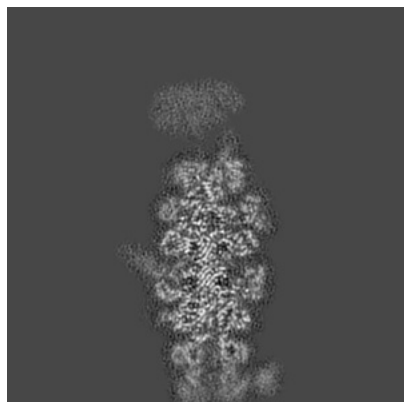
6.3.1 Primary map
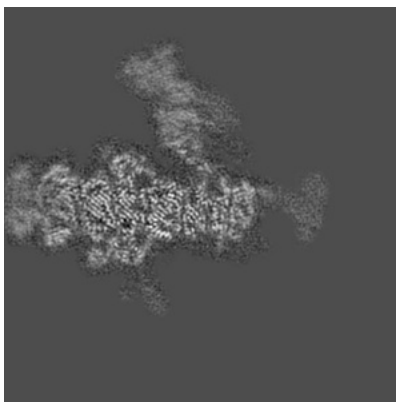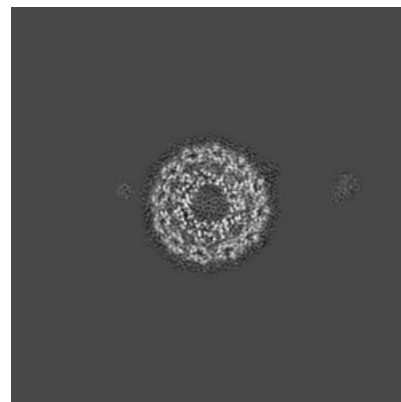
X Index: 186	Y Index: 189	Z Index: 99

6.3.2 Raw map
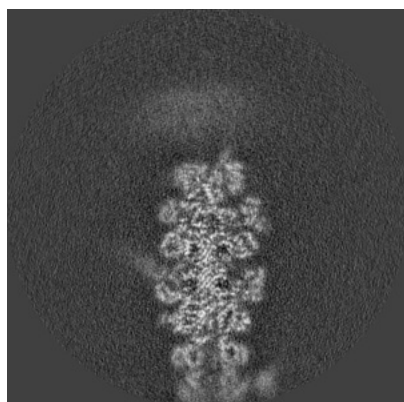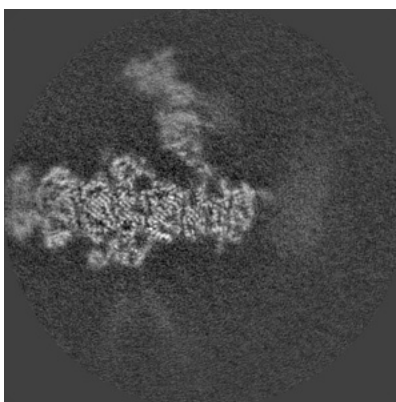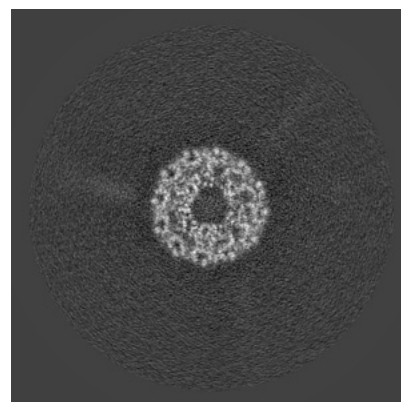
X Index: 186	Y Index: 189	Z Index: 97

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

6.4 Orthogonal standard-deviation projections (False-color) ⓘ

6.4.1 Primary map

X   Y   Z

6.4.2 Raw map

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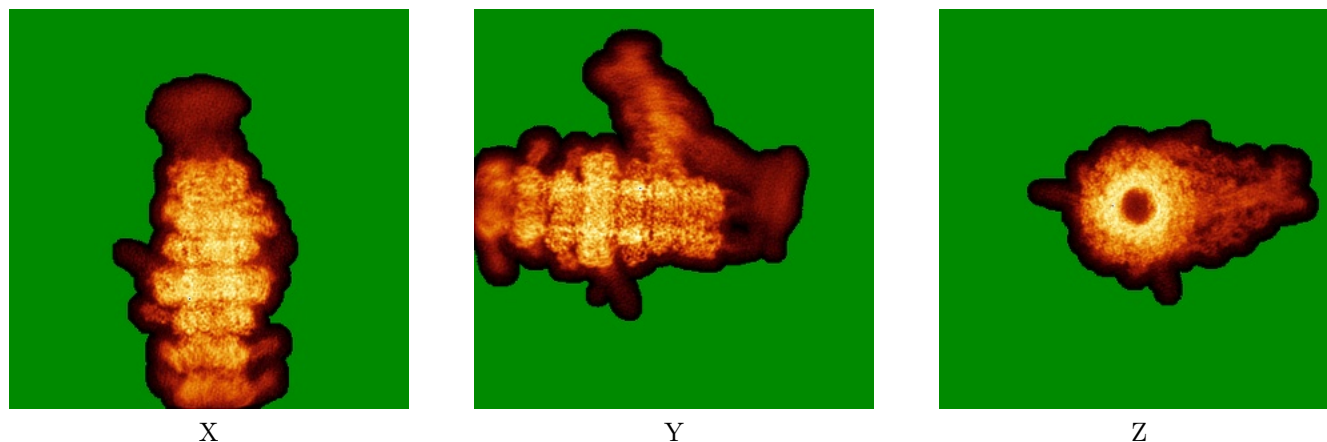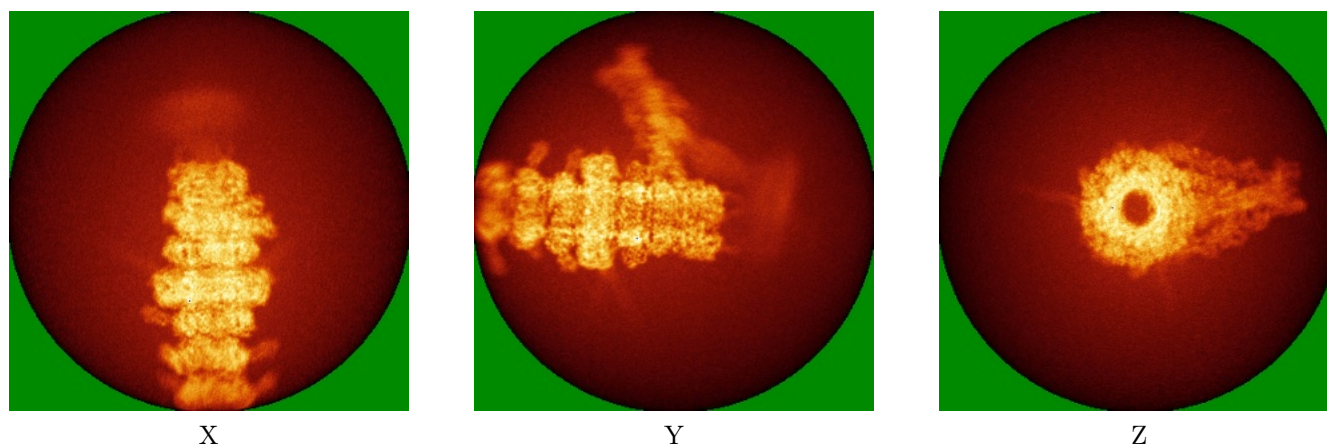
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views ⓘ

6.5.1 Primary map

| X | Y | Z |
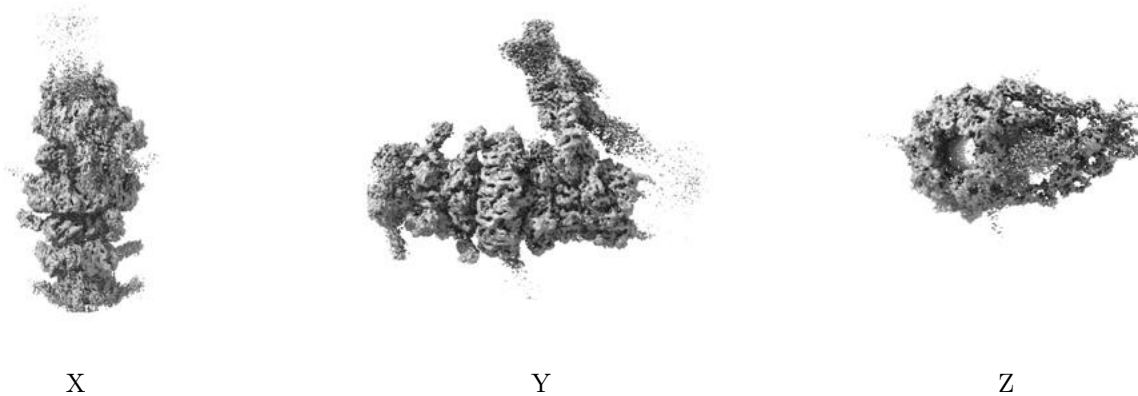
The images above show the 3D surface view of the map at the recommended contour level 0.0214. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

| X | Y | Z |
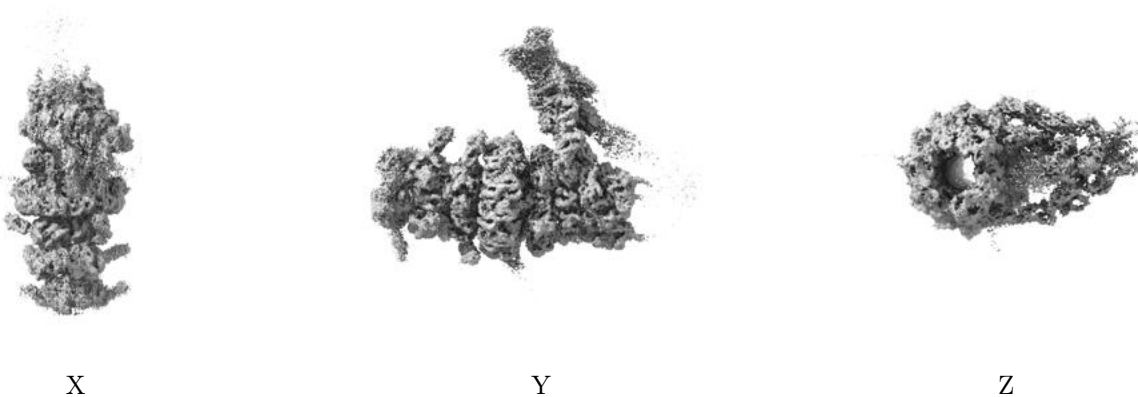
These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

6.6 Mask visualisation ⓘ

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

7 Map analysis ⓘ

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

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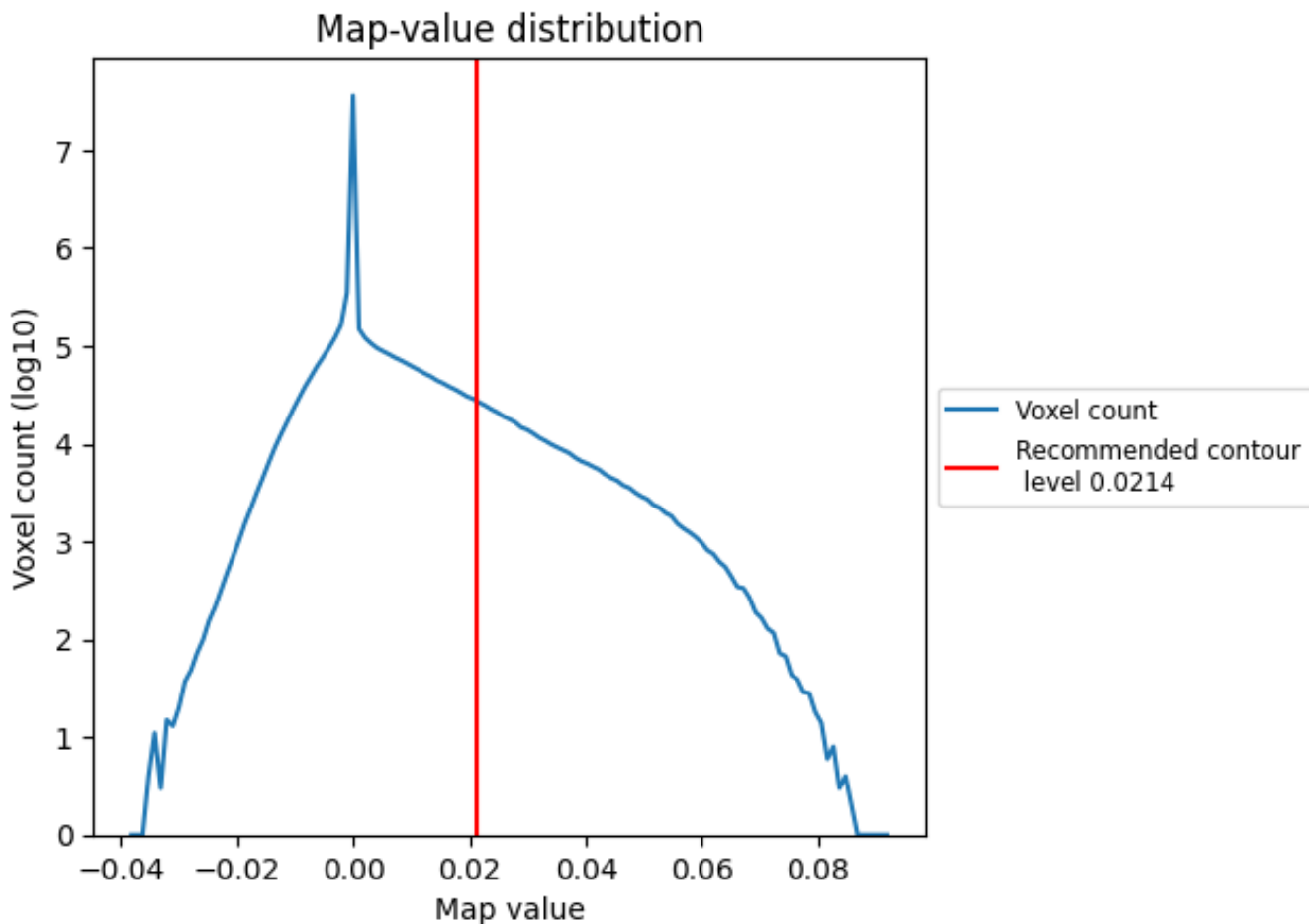
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate (i)
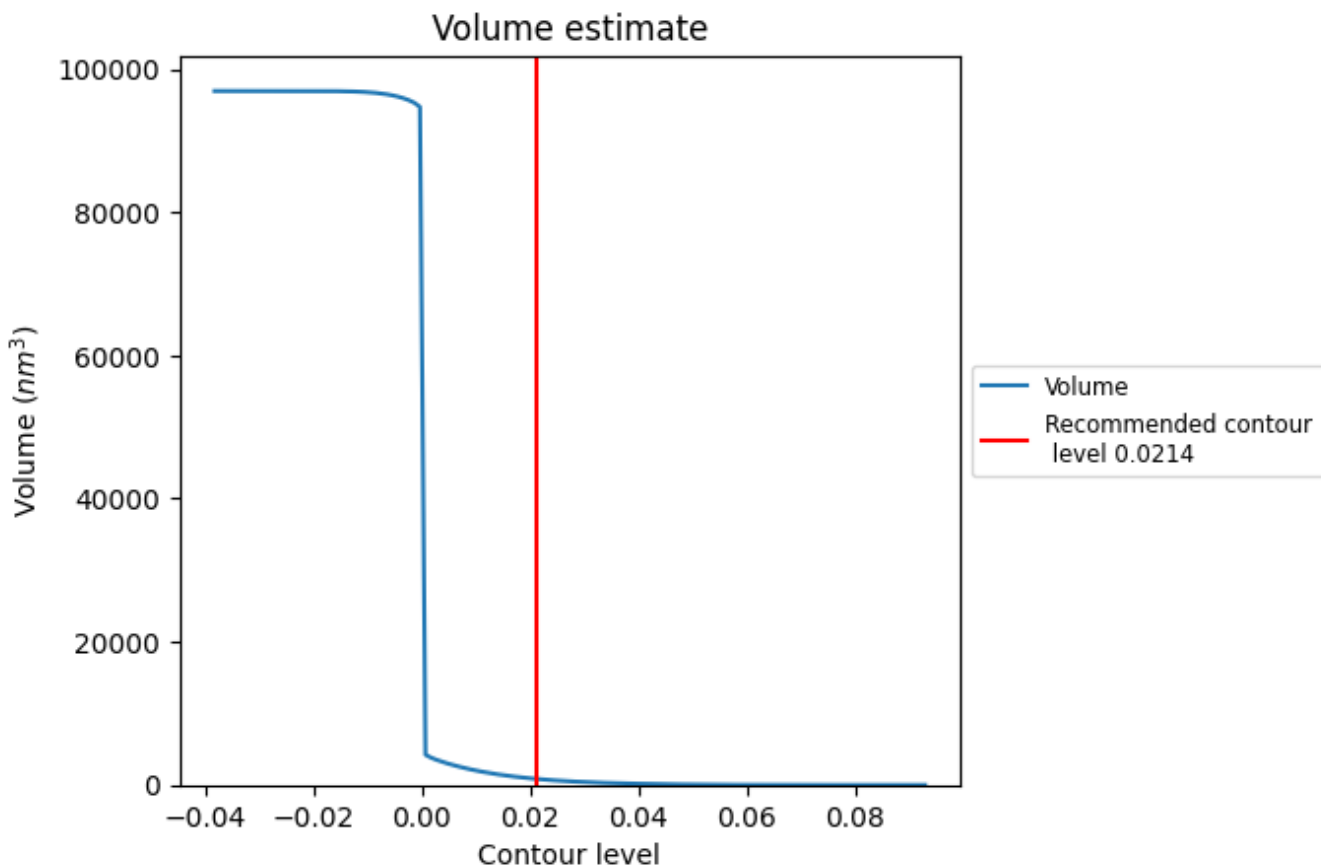
The volume at the recommended contour level is 830 nm^3; this corresponds to an approximate mass of 750 kDa.

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 ⓘ
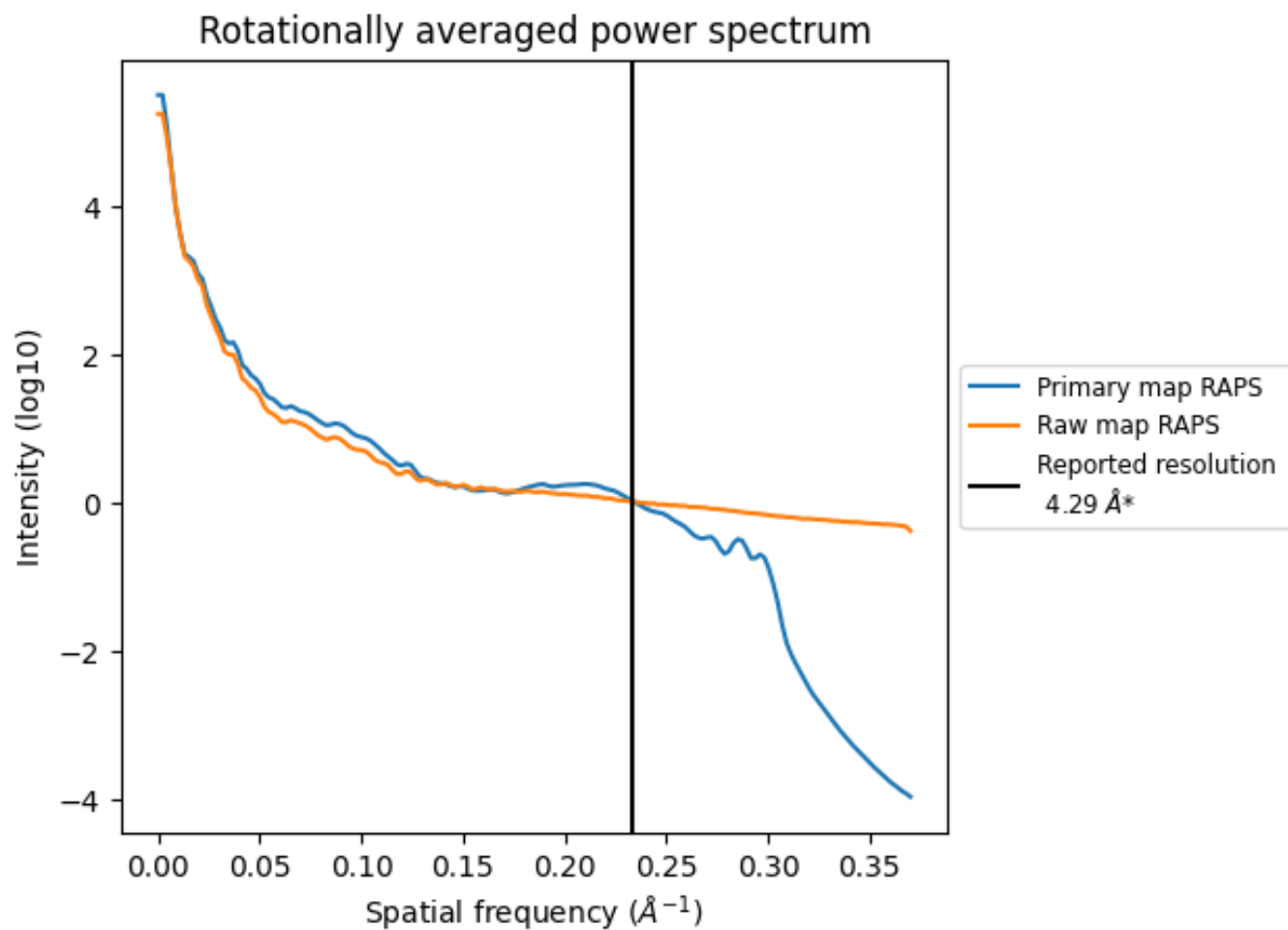
*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

8 Fourier-Shell correlation ⓘ

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 ⓘ
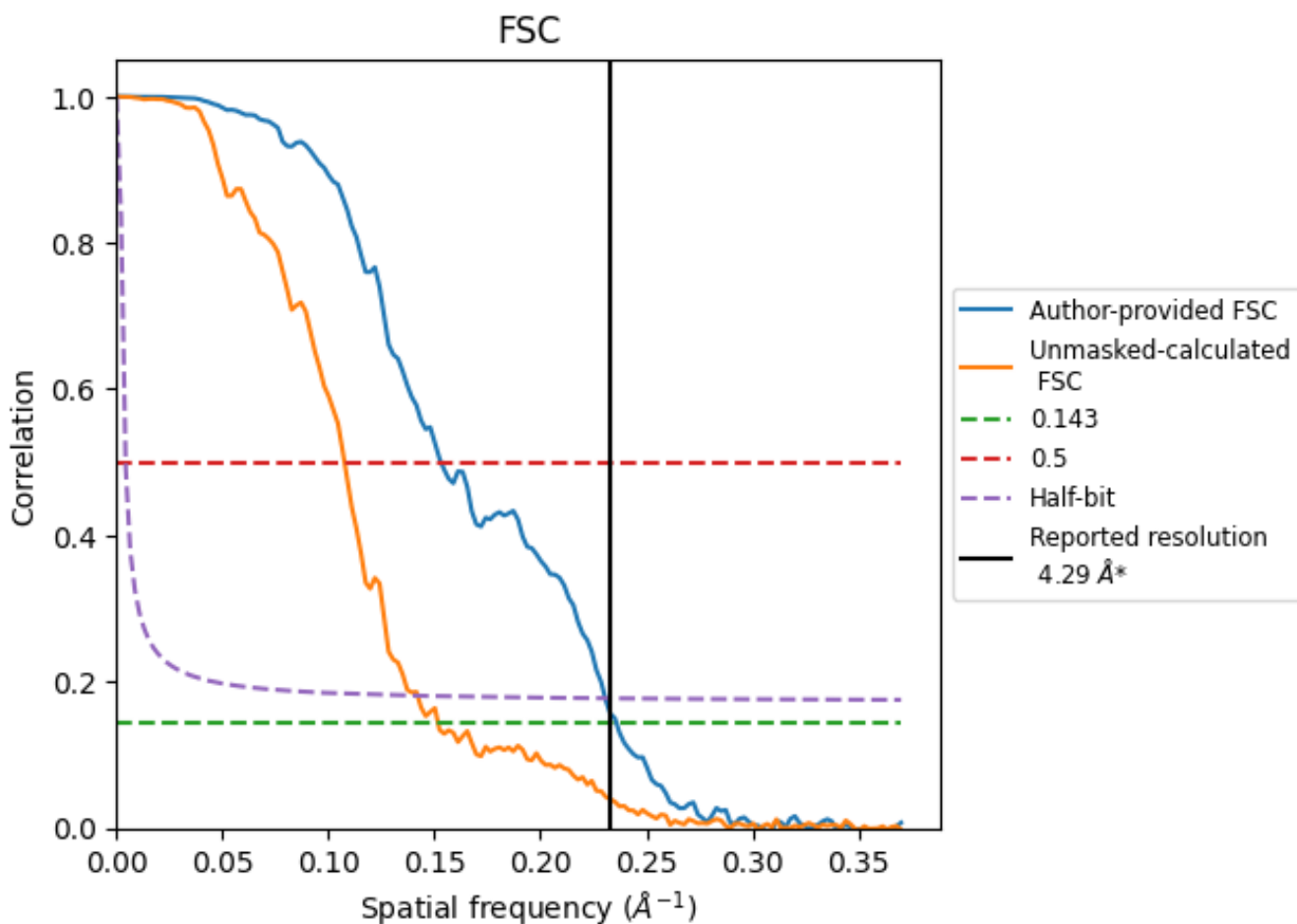
*Reported resolution corresponds to spatial frequency of 0.233 Å^{-1}

8.2　Resolution estimates ⓘ

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.29	-	-
Author-provided FSC curve	4.24	6.53	4.34
Unmasked-calculated*	6.59	9.30	7.04

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.59 differs from the reported value 4.29 by more than 10 %

9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-14799 and PDB model 7ZN2. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay (i)
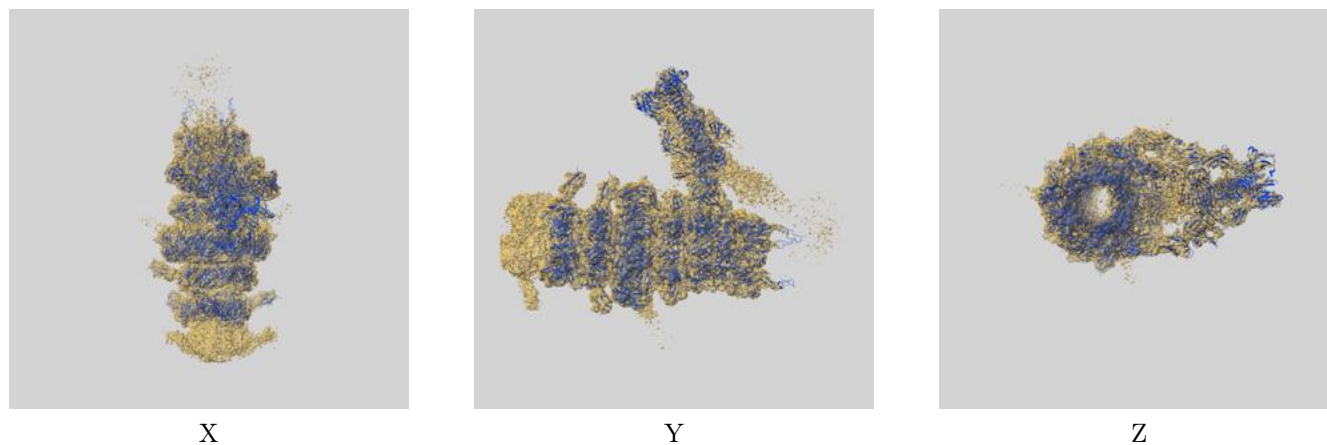
X	Y	Z

The images above show the 3D surface view of the map at the recommended contour level 0.0214 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 ⓘ

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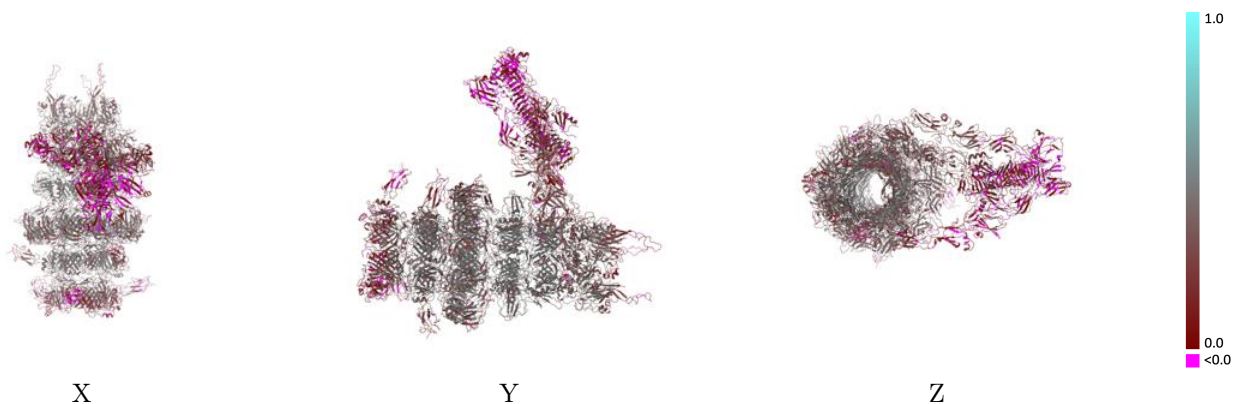
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

X　　　　　　　　　　　Y　　　　　　　　　　　Z
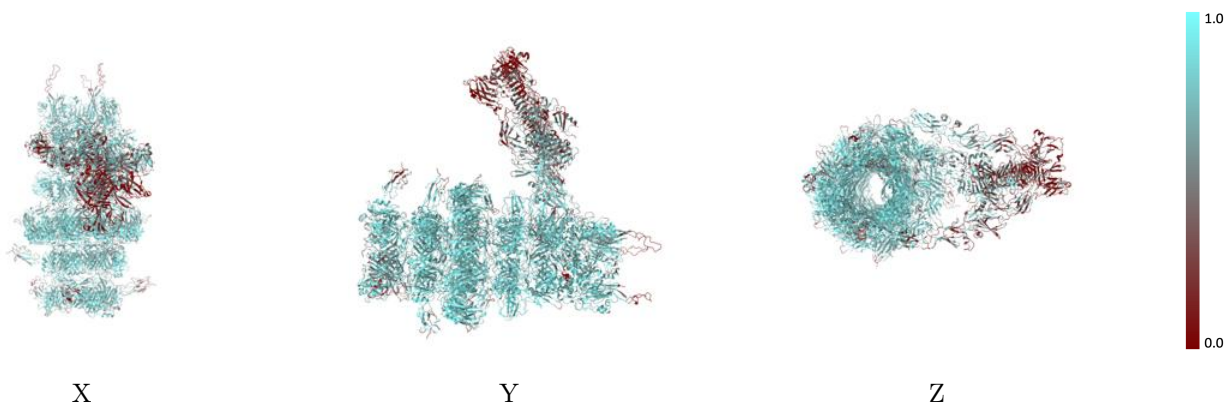
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0214).

9.4　Atom inclusion ⓘ
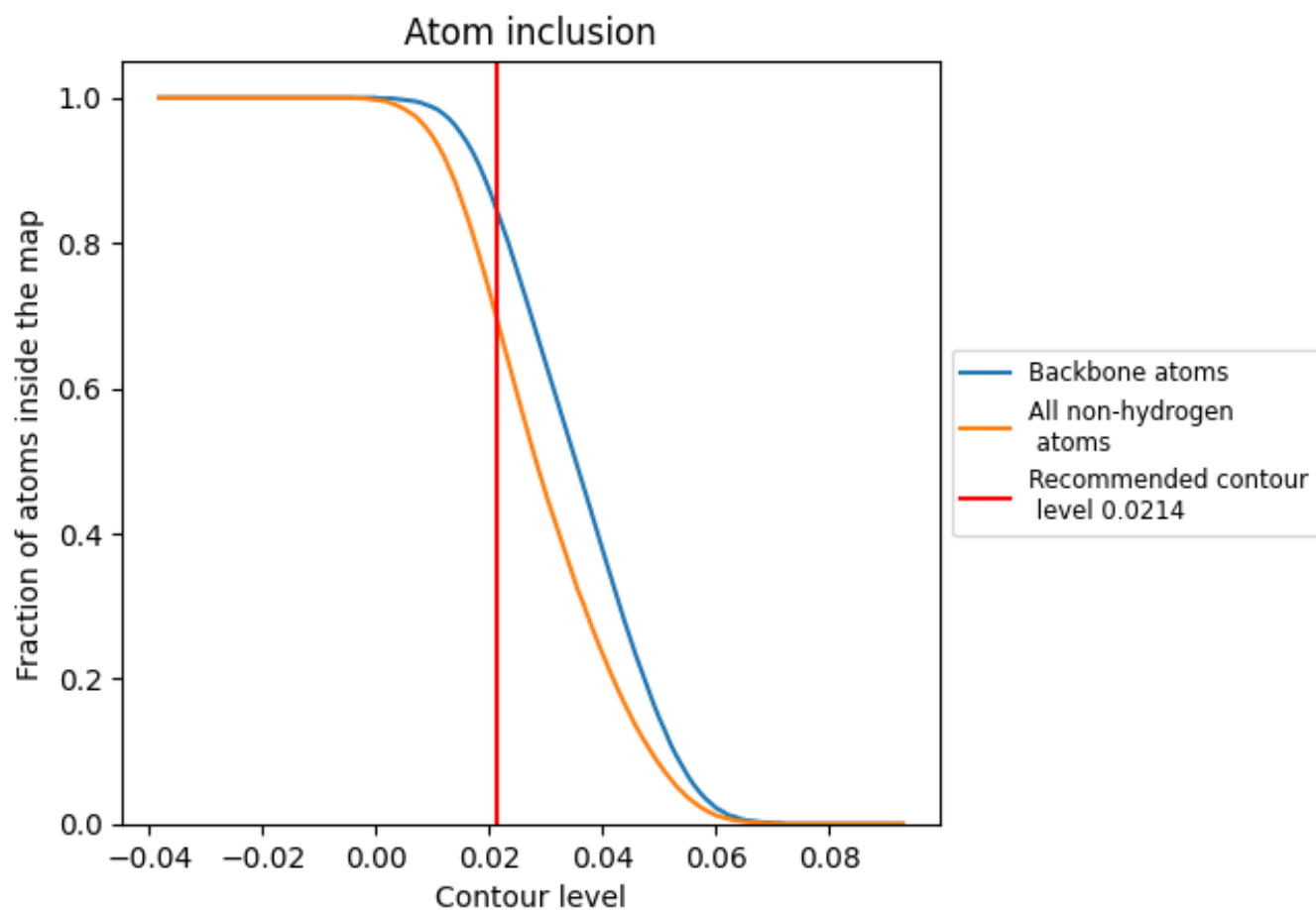
At the recommended contour level, 84% of all backbone atoms, 69% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0214) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6930	0.3200
A	0.6820	0.2530
B	0.6860	0.2560
C	0.6750	0.2500
D	0.7840	0.3770
E	0.7730	0.3780
F	0.7840	0.3810
G	0.8300	0.4530
H	0.8350	0.4410
I	0.8350	0.4490
J	0.7690	0.3530
K	0.7490	0.3230
L	0.7280	0.3410
M	0.7480	0.3490
N	0.7560	0.3210
O	0.7480	0.3280
P	0.7500	0.3500
Q	0.7700	0.3660
R	0.7640	0.3370
S	0.7720	0.3530
T	0.7520	0.3560
U	0.7780	0.3700
V	0.8250	0.4360
W	0.8300	0.4350
X	0.8290	0.4220
Y	0.8430	0.4390
Z	0.8580	0.4340
a	0.8640	0.4430
b	0.7250	0.3550
c	0.7280	0.3500
d	0.6870	0.3150
e	0.4020	0.1680
f	0.4090	0.1340
g	0.3460	0.1050
h	0.7280	0.3450

1.0

0.0
<0.0

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Chain	Atom inclusion	Q-score
i	0.6690	0.3230
j	0.7590	0.3630