



wwPDB EM Validation Summary Report ⓘ

Aug 8, 2026 – 10:38 AM EDT

PDB ID : 11LX / pdb_000011lx
EMDB ID : EMD-75829
Title : Bacteriophage Goslar Baseplate
Authors : Basu, D.; Gu, Y.; Corbett, K.D.
Deposited on : 2026-03-03
Resolution : 3.88 Å(reported)
Based on initial model : .

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:

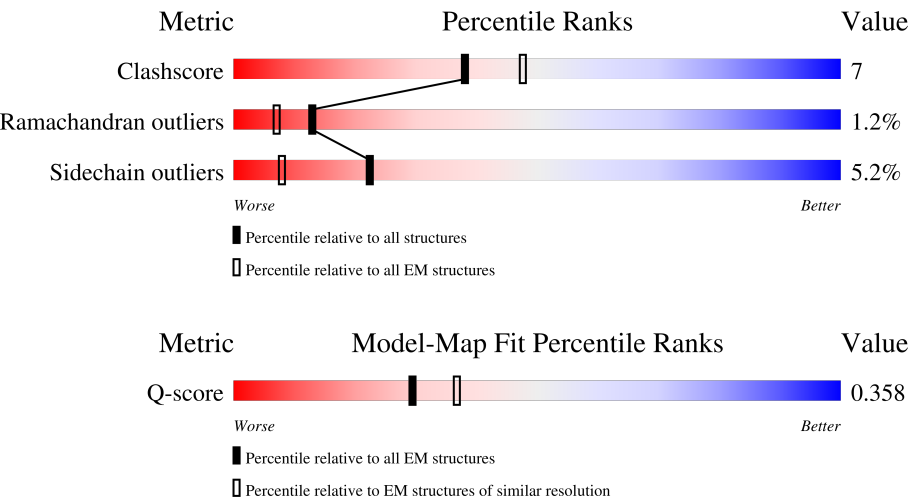
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.88 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



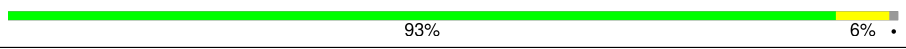
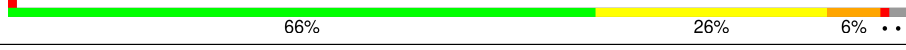
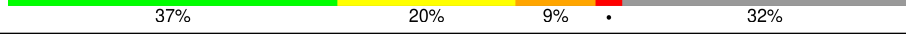
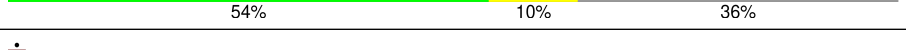
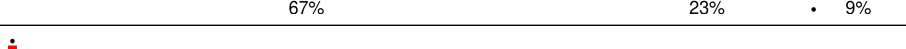
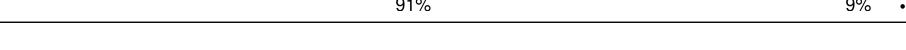
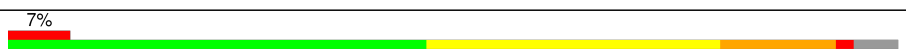
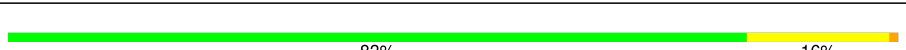
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8773 (3.38 - 4.38)

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	AJ	401	
2	AO	296	
3	Aa	294	
3	Ab	294	

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Mol	Chain	Length	Quality of chain
4	Ah	690	
4	An	690	
4	Az	690	
5	Aq	997	
5	M	997	
6	Bh	803	
7	CJ	355	
8	H	713	
9	I	117	
10	V	137	
10	W	137	
10	s	137	
10	t	137	
11	X	135	
12	n	208	
12	o	208	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 60205 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 Tail Tube Initiator Protein gp62.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AJ	361	Total	C	N	O	S	0	0
			2954	1884	508	548	14		

- Molecule 2 is a protein called Tail Tube of Bacteriophage Goslar.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AO	287	Total	C	N	O	S	0	0
			2259	1432	385	431	11		

- Molecule 3 is a protein called Virion structural protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	Aa	263	Total	C	N	O	S	0	0
			2093	1324	356	405	8		
3	Ab	269	Total	C	N	O	S	0	0
			2130	1348	361	413	8		

- Molecule 4 is a protein called Tail sheath protein gp29 gp29PR domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	Ah	680	Total	C	N	O	S	0	0
			5306	3345	895	1044	22		
4	An	661	Total	C	N	O	S	0	0
			5179	3263	876	1019	21		
4	Az	680	Total	C	N	O	S	0	0
			5306	3345	895	1044	22		

- Molecule 5 is a protein called Baseplate wedge protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	Aq	979	Total	C	N	O	S	0	0
			7770	4918	1285	1537	30		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	M	962	Total	C	N	O	S	0	0
			7629	4830	1263	1508	28		

- Molecule 6 is a protein called Virion structural protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	Bh	579	Total	C	N	O	S	0	0
			4793	3063	797	902	31		

- Molecule 7 is a protein called Inner baseplate protein gp202.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	CJ	243	Total	C	N	O	S	0	0
			1908	1202	319	381	6		

- Molecule 8 is a protein called Tail tube initiator complex protein gp203.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	457	Total	C	N	O	S	0	0
			3563	2253	598	694	18		

- Molecule 9 is a protein called Inner Baseplate Protein gp172.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	106	Total	C	N	O	S	0	0
			866	553	143	166	4		

- Molecule 10 is a protein called SH3 fold domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	V	137	Total	C	N	O	S	0	0
			1072	685	174	212	1		
10	W	137	Total	C	N	O	S	0	0
			1072	685	174	212	1		
10	s	137	Total	C	N	O	S	0	0
			1072	685	174	212	1		
10	t	137	Total	C	N	O	S	0	0
			1072	685	174	212	1		

- Molecule 11 is a protein called Inner Baseplate Protein gp180.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	X	128	Total	C	N	O	S	0	0
			1022	651	167	200	4		

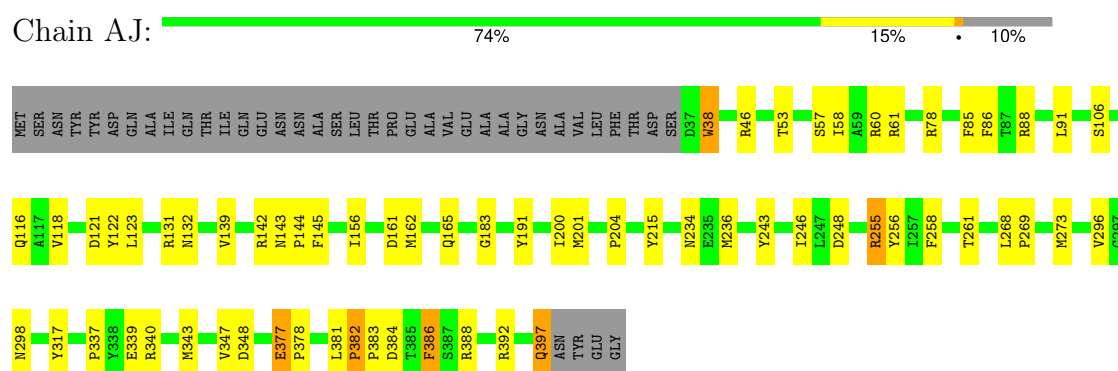
- Molecule 12 is a protein called Inner Baseplate Protein gp187.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	n	197	Total	C	N	O	S	0	0
			1538	981	253	301	3		
12	o	207	Total	C	N	O	S	0	0
			1601	1019	263	315	4		

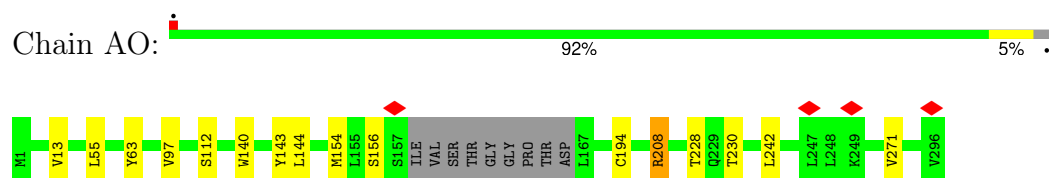
3 Residue-property plots

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.

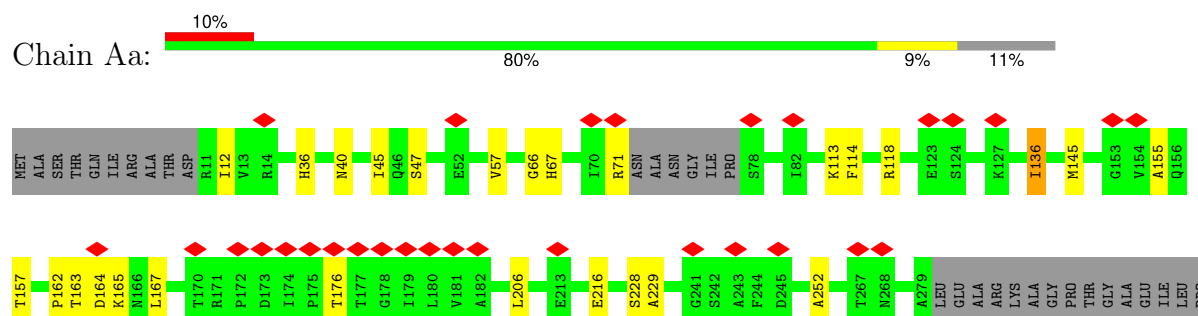
• Molecule 1: Tail Tube Initiator Protein gp62



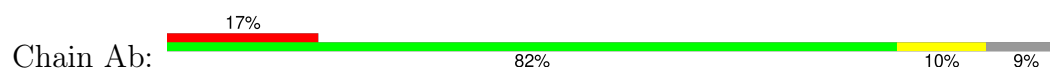
• Molecule 2: Tail Tube of Bacteriophage Goslar

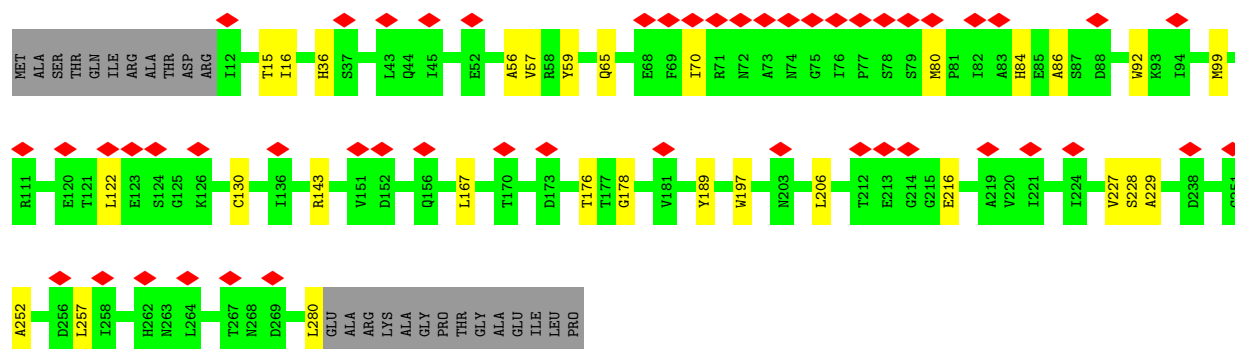


• Molecule 3: Virion structural protein



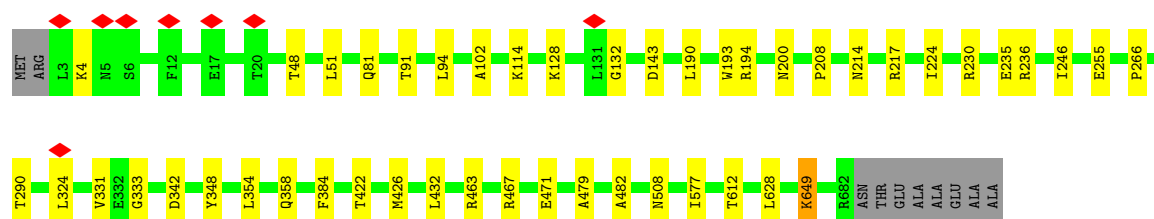
• Molecule 3: Virion structural protein





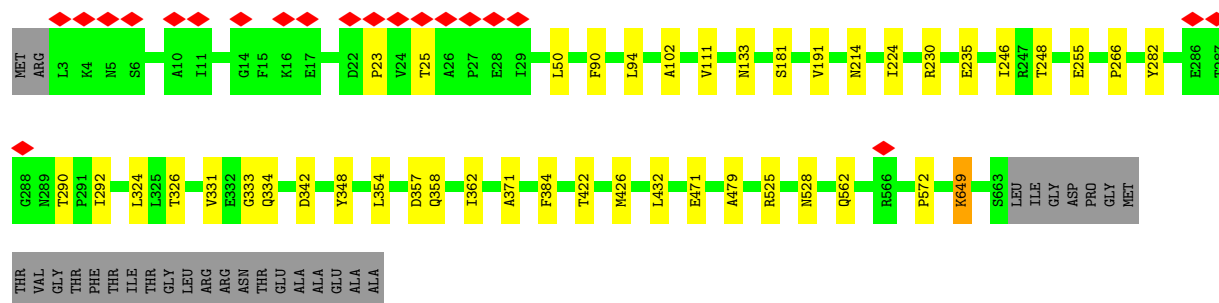
- Molecule 4: Tail sheath protein gp29 gp29PR domain-containing protein

Chain Ah: 92% 7%



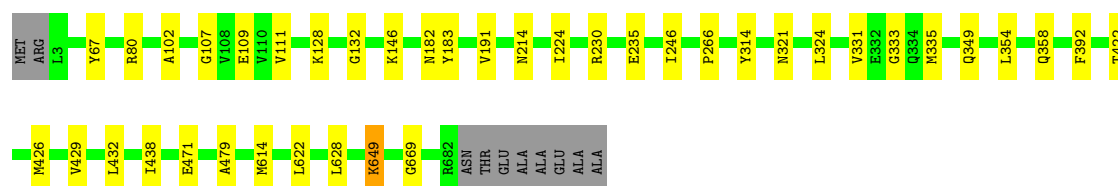
- Molecule 4: Tail sheath protein gp29 gp29PR domain-containing protein

Chain An: 89% 6%



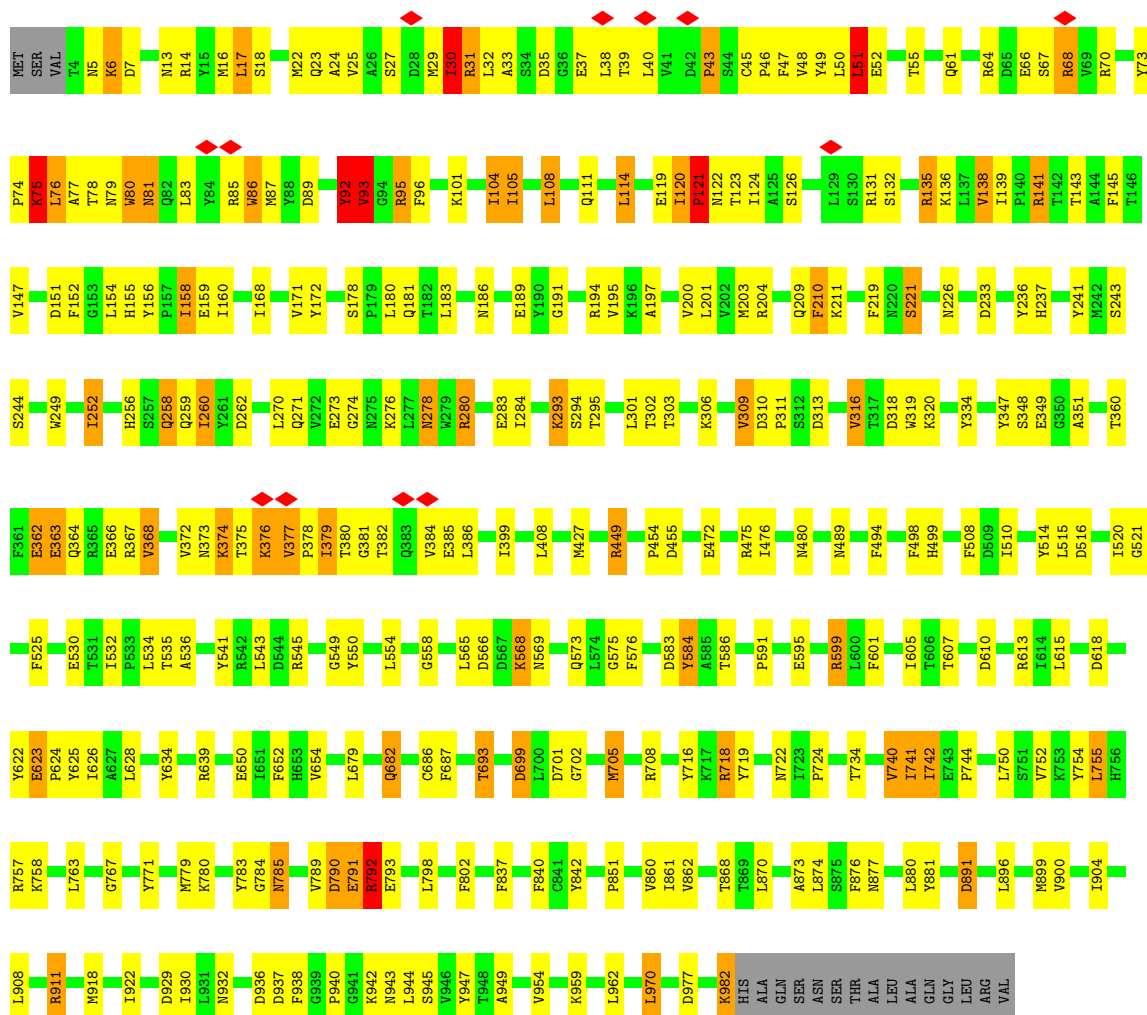
- Molecule 4: Tail sheath protein gp29 gp29PR domain-containing protein

Chain Az: 93% 6%

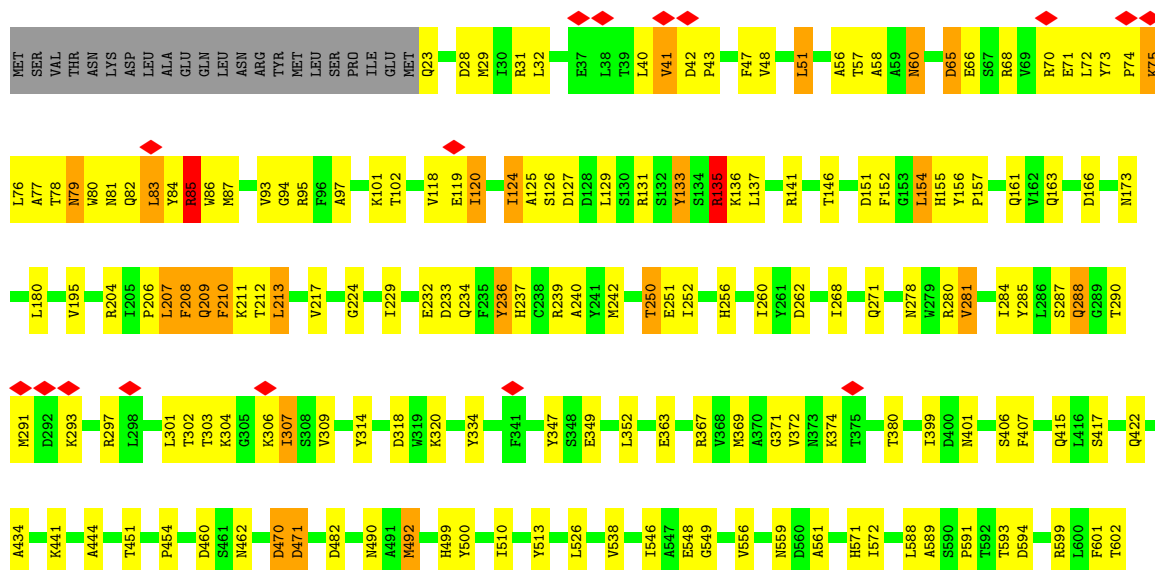


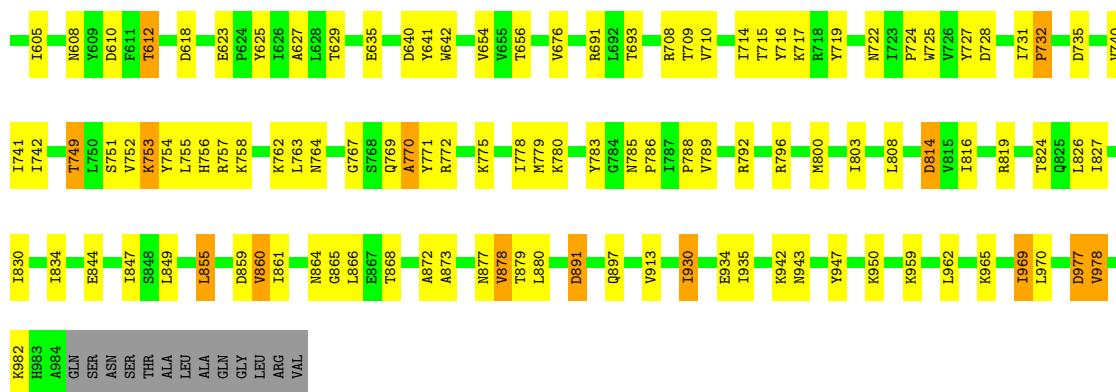
- Molecule 5: Baseplate wedge protein

Chain Aq: 66% 26% 6%

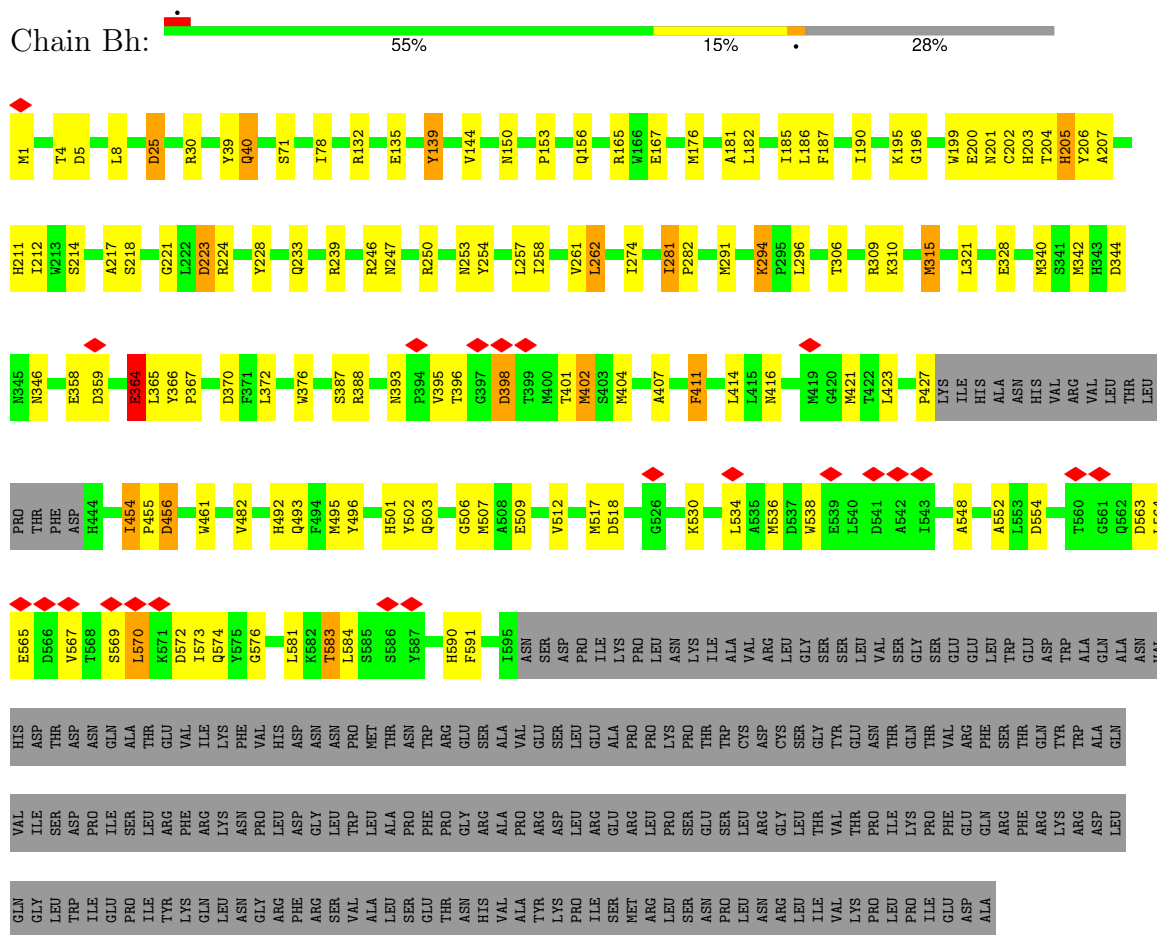


• Molecule 5: Baseplate wedge protein

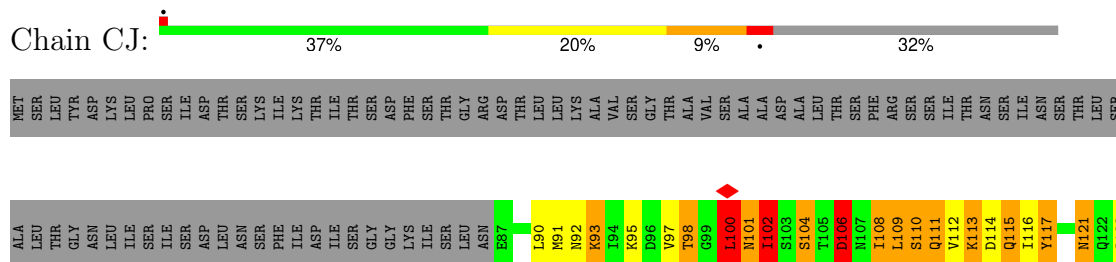


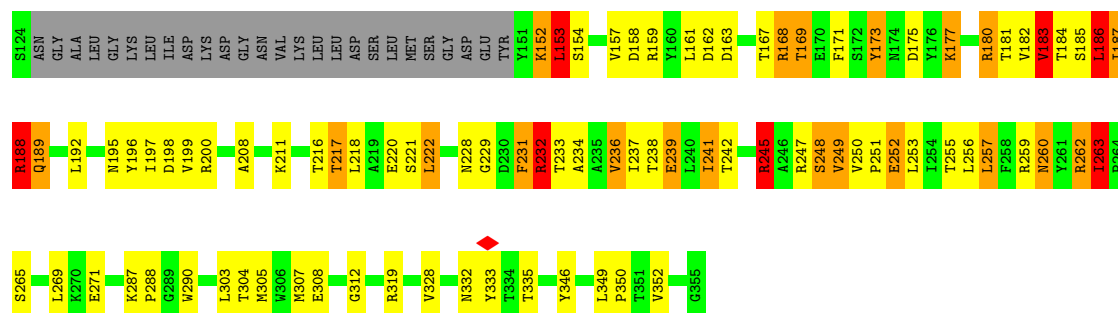


• Molecule 6: Virion structural protein



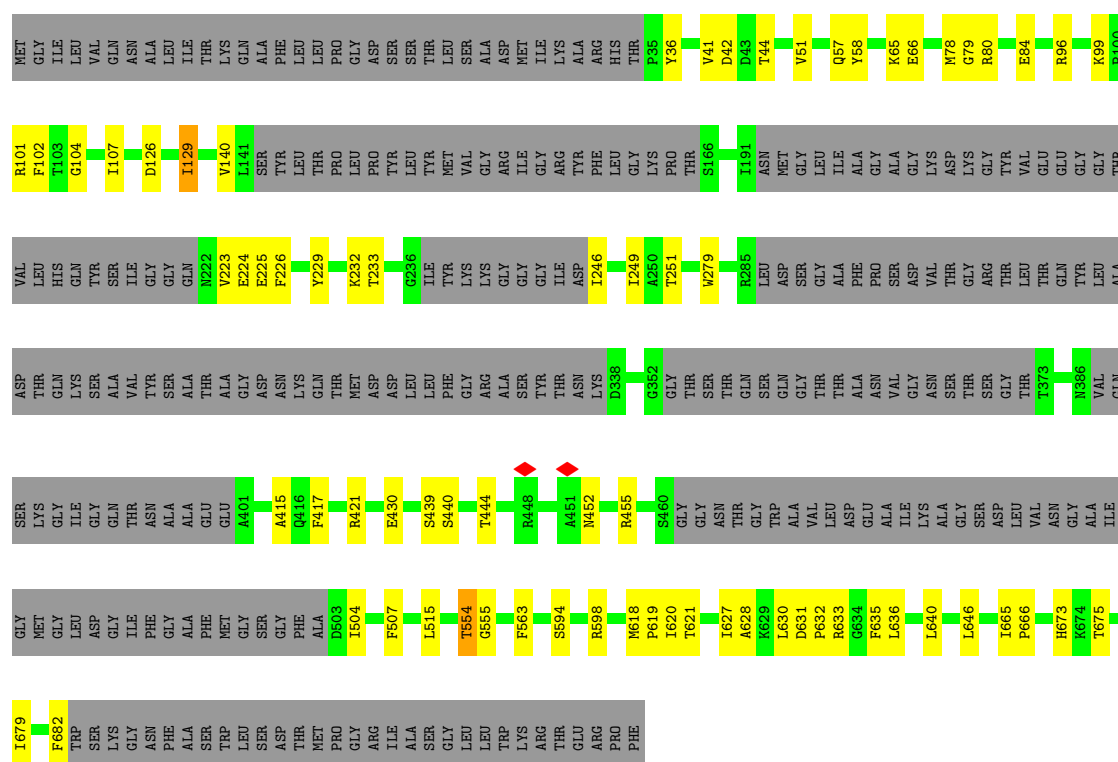
• Molecule 7: Inner baseplate protein gp202





• Molecule 8: Tail tube initiator complex protein gp203

Chain H: 54% 10% 36%



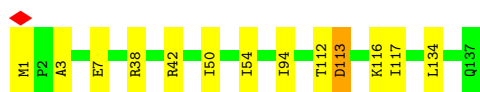
• Molecule 9: Inner Baseplate Protein gp172

Chain I: 67% 23% 9%



• Molecule 10: SH3 fold domain-containing protein

Chain V: 91% 9%



- Molecule 10: SH3 fold domain-containing protein

Chain W: 91% 9%



- Molecule 10: SH3 fold domain-containing protein

Chain s: 88% 12%



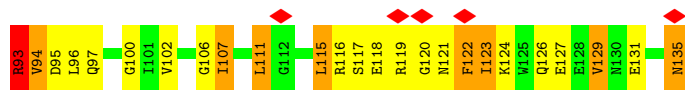
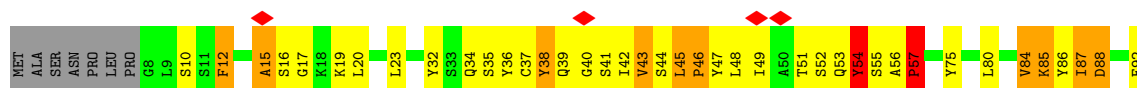
- Molecule 10: SH3 fold domain-containing protein

Chain t: 87% 12%



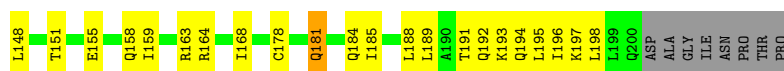
- Molecule 11: Inner Baseplate Protein gp180

Chain X: 7% 47% 33% 13% 5%



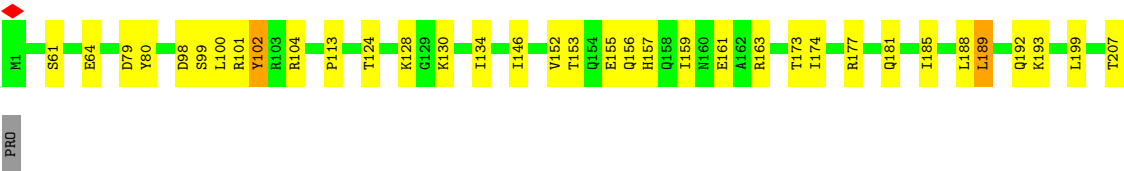
- Molecule 12: Inner Baseplate Protein gp187

Chain n: 68% 25% 5%



- Molecule 12: Inner Baseplate Protein gp187

Chain o: 83% 16%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31110	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	2.440	Depositor
Minimum map value	-1.154	Depositor
Average map value	-0.002	Depositor
Map value standard deviation	0.101	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	1120.2, 1120.2, 1120.2	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.8669999, 1.8669999, 1.8669999	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	AJ	0.19	0/3034	0.43	0/4133
2	AO	0.16	0/2310	0.33	0/3144
3	Aa	0.11	0/2138	0.35	0/2903
3	Ab	0.11	0/2178	0.33	0/2963
4	Ah	0.14	0/5414	0.31	0/7355
4	An	0.15	0/5285	0.34	0/7178
4	Az	0.14	0/5414	0.30	0/7355
5	Aq	0.19	0/7930	0.56	6/10787 (0.1%)
5	M	0.17	0/7787	0.42	0/10593
6	Bh	0.16	0/4905	0.40	0/6652
7	CJ	0.23	0/1937	0.81	5/2621 (0.2%)
8	H	0.17	0/3635	0.43	0/4932
9	I	0.20	0/886	0.49	0/1204
10	V	0.13	0/1092	0.29	0/1492
10	W	0.14	0/1092	0.32	0/1492
10	s	0.16	0/1092	0.35	0/1492
10	t	0.14	0/1092	0.32	0/1492
11	X	0.24	0/1042	0.72	2/1407 (0.1%)
12	n	0.16	0/1566	0.42	0/2133
12	o	0.15	0/1630	0.36	0/2223
All	All	0.17	0/61459	0.43	13/83551 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AJ	0	4
2	AO	0	1
5	Aq	0	8
5	M	0	1
7	CJ	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
11	X	0	2
12	n	0	1
All	All	0	23

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	Aq	792	ARG	CB-CG-CD	9.60	133.37	111.30
7	CJ	188	ARG	CA-CB-CG	9.56	133.22	114.10
5	Aq	791	GLU	CA-C-N	9.56	138.91	121.70
5	Aq	791	GLU	C-N-CA	9.56	138.91	121.70
7	CJ	100	LEU	CA-C-N	8.93	137.78	121.70

There are no chirality outliers.

5 of 23 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AJ	236	MET	Peptide
1	AJ	255	ARG	Sidechain
1	AJ	46	ARG	Sidechain
1	AJ	78	ARG	Sidechain
2	AO	208	ARG	Sidechain

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	AJ	2954	0	2864	45	0
2	AO	2259	0	2206	7	0
3	Aa	2093	0	2041	20	0
3	Ab	2130	0	2079	18	0
4	Ah	5306	0	5150	27	0
4	An	5179	0	5024	29	0
4	Az	5306	0	5150	21	0
5	Aq	7770	0	7582	224	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	M	7629	0	7436	185	0
6	Bh	4793	0	4686	108	0
7	CJ	1908	0	1900	76	0
8	H	3563	0	3472	38	0
9	I	866	0	839	19	0
10	V	1072	0	1077	7	0
10	W	1072	0	1077	9	0
10	s	1072	0	1077	12	0
10	t	1072	0	1077	11	0
11	X	1022	0	1007	47	0
12	n	1538	0	1564	41	0
12	o	1601	0	1622	30	0
All	All	60205	0	58930	877	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 7.

The worst 5 of 877 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)
5:Aq:50:LEU:HD21	6:Bh:185:ILE:HD13	1.51	0.92
5:Aq:5:ASN:H	5:M:40:LEU:HD22	1.35	0.91
5:Aq:791:GLU:HA	5:Aq:792:ARG:HD3	1.57	0.87
5:Aq:37:GLU:HB2	5:Aq:38:LEU:HA	1.59	0.83
5:Aq:6:LYS:HE2	5:Aq:7:ASP:H	1.42	0.83

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AJ	357/401 (89%)	316 (88%)	38 (11%)	3 (1%)	16	50
2	AO	283/296 (96%)	273 (96%)	10 (4%)	0	100	100
3	Aa	257/294 (87%)	244 (95%)	11 (4%)	2 (1%)	16	50
3	Ab	267/294 (91%)	256 (96%)	11 (4%)	0	100	100
4	Ah	678/690 (98%)	655 (97%)	23 (3%)	0	100	100
4	An	659/690 (96%)	637 (97%)	22 (3%)	0	100	100
4	Az	678/690 (98%)	653 (96%)	25 (4%)	0	100	100
5	Aq	977/997 (98%)	821 (84%)	125 (13%)	31 (3%)	3	25
5	M	958/997 (96%)	814 (85%)	129 (14%)	15 (2%)	7	36
6	Bh	575/803 (72%)	521 (91%)	51 (9%)	3 (0%)	24	59
7	CJ	237/355 (67%)	155 (65%)	59 (25%)	23 (10%)	0	8
8	H	441/713 (62%)	370 (84%)	68 (15%)	3 (1%)	18	52
9	I	104/117 (89%)	94 (90%)	9 (9%)	1 (1%)	12	45
10	V	135/137 (98%)	131 (97%)	4 (3%)	0	100	100
10	W	135/137 (98%)	135 (100%)	0	0	100	100
10	s	135/137 (98%)	119 (88%)	16 (12%)	0	100	100
10	t	135/137 (98%)	123 (91%)	12 (9%)	0	100	100
11	X	126/135 (93%)	83 (66%)	32 (25%)	11 (9%)	0	10
12	n	195/208 (94%)	170 (87%)	23 (12%)	2 (1%)	12	45
12	o	205/208 (99%)	186 (91%)	19 (9%)	0	100	100
All	All	7537/8436 (89%)	6756 (90%)	687 (9%)	94 (1%)	13	41

5 of 94 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	Aq	121	PRO
5	Aq	378	PRO
5	Aq	755	LEU
7	CJ	101	ASN
7	CJ	102	ILE

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	AJ	325/357 (91%)	316 (97%)	9 (3%)	38	59
2	AO	246/254 (97%)	241 (98%)	5 (2%)	48	65
3	Aa	228/250 (91%)	225 (99%)	3 (1%)	61	71
3	Ab	232/250 (93%)	230 (99%)	2 (1%)	70	75
4	Ah	569/579 (98%)	566 (100%)	3 (0%)	81	81
4	An	556/579 (96%)	553 (100%)	3 (0%)	81	81
4	Az	569/579 (98%)	566 (100%)	3 (0%)	81	81
5	Aq	854/868 (98%)	763 (89%)	91 (11%)	6	24
5	M	837/868 (96%)	752 (90%)	85 (10%)	7	26
6	Bh	521/724 (72%)	491 (94%)	30 (6%)	18	44
7	CJ	210/306 (69%)	159 (76%)	51 (24%)	1	4
8	H	389/582 (67%)	380 (98%)	9 (2%)	44	63
9	I	96/106 (91%)	93 (97%)	3 (3%)	35	57
10	V	121/121 (100%)	120 (99%)	1 (1%)	73	77
10	W	121/121 (100%)	118 (98%)	3 (2%)	42	62
10	s	121/121 (100%)	120 (99%)	1 (1%)	73	77
10	t	121/121 (100%)	118 (98%)	3 (2%)	42	62
11	X	111/117 (95%)	88 (79%)	23 (21%)	1	7
12	n	172/180 (96%)	164 (95%)	8 (5%)	23	48
12	o	178/180 (99%)	169 (95%)	9 (5%)	21	46
All	All	6577/7263 (91%)	6232 (95%)	345 (5%)	22	46

5 of 345 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	M	156	TYR
5	M	844	GLU
5	M	208	PHE
5	M	471	ASP
10	W	113	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 82 such sidechains are listed below:

Mol	Chain	Res	Type
5	M	62	ASN
11	X	126	GLN
5	M	81	ASN
5	M	653	HIS
12	o	158	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	CJ	1
3	Aa	1
1	AJ	1
5	M	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	CJ	332:ASN	C	333:TYR	N	7.28
1	Aa	195:LEU	C	196:VAL	N	3.10
1	AJ	93:LEU	C	94:THR	N	3.06
1	M	788:PRO	C	789:VAL	N	3.06

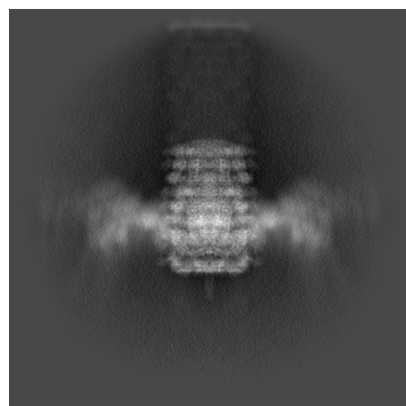
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-75829. These allow visual inspection of the internal detail of the map and identification of artifacts.

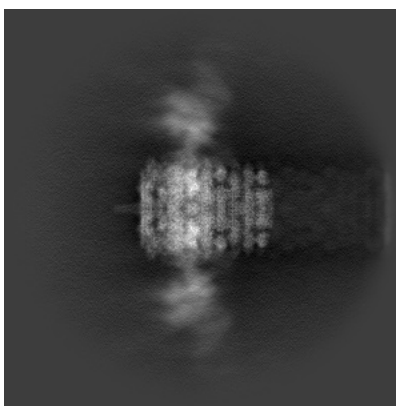
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

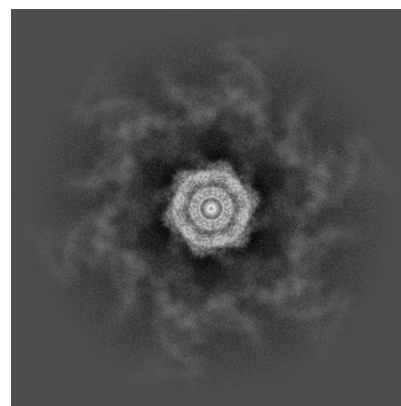
6.1.1 Primary map



X

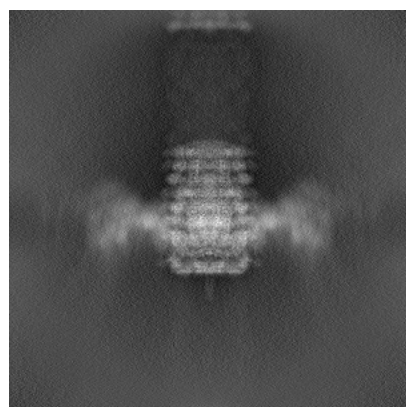


Y

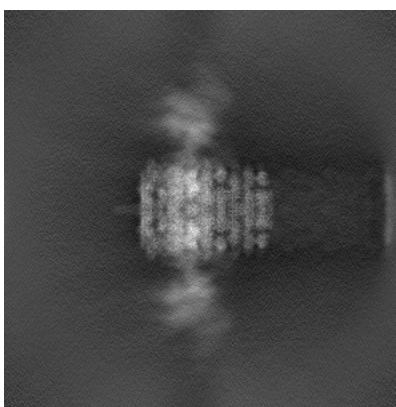


Z

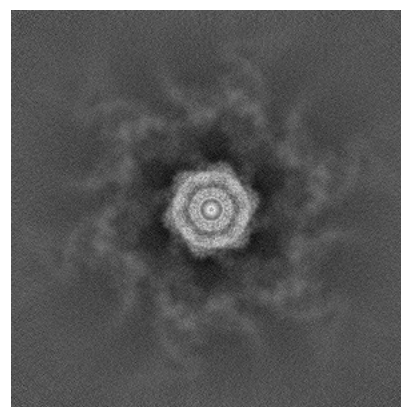
6.1.2 Raw map



X



Y

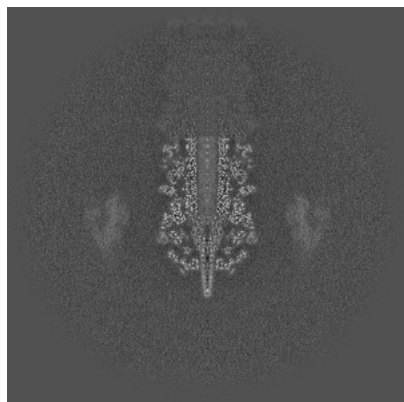


Z

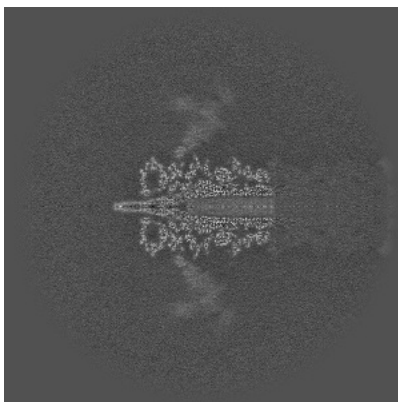
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

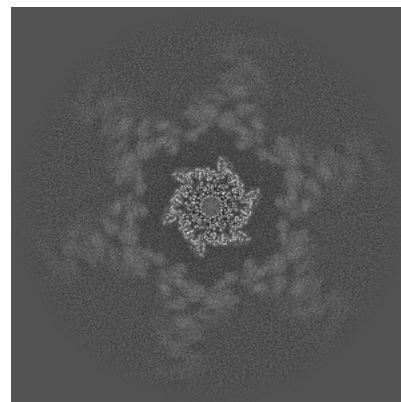
6.2.1 Primary map



X Index: 300

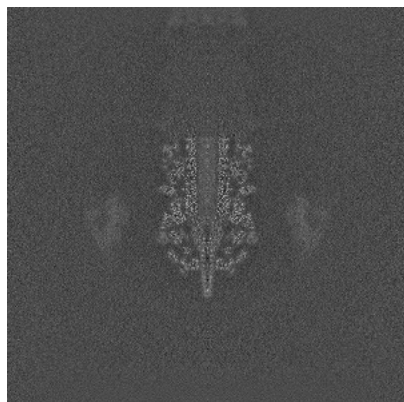


Y Index: 300

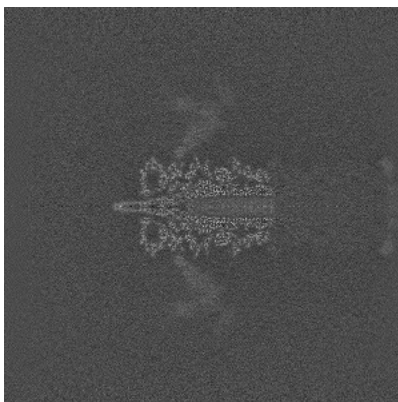


Z Index: 300

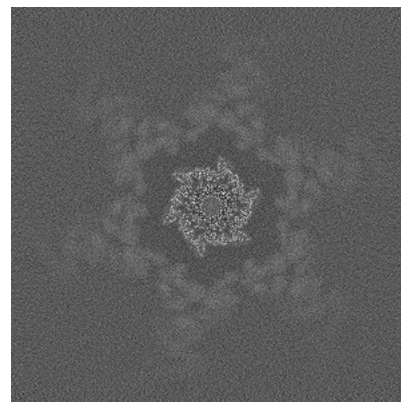
6.2.2 Raw map



X Index: 300



Y Index: 300

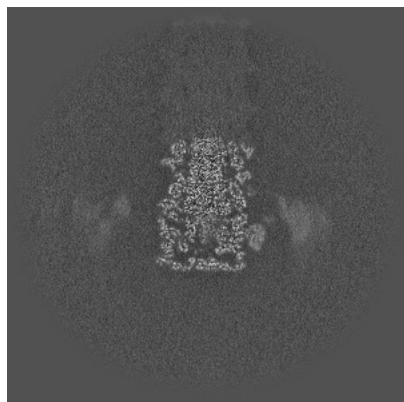


Z Index: 300

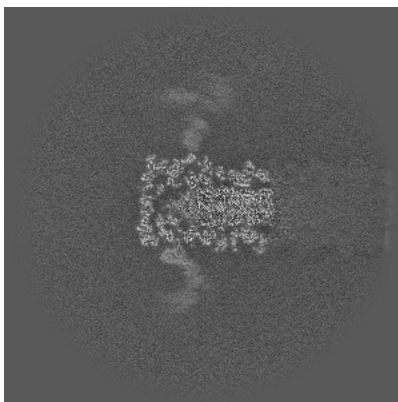
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

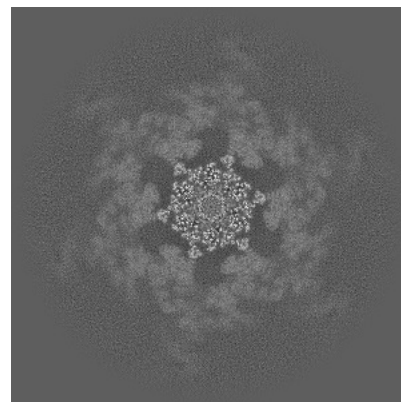
6.3.1 Primary map



X Index: 281

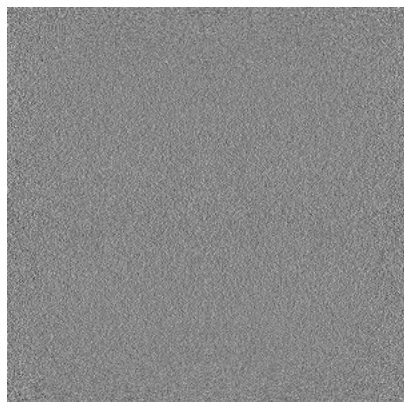


Y Index: 317

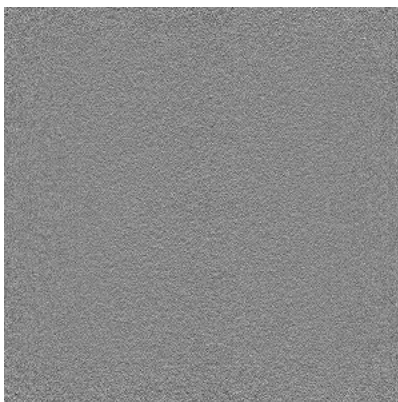


Z Index: 281

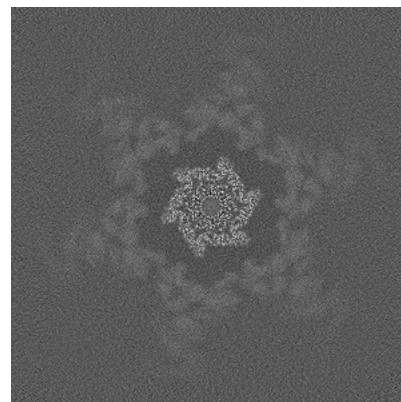
6.3.2 Raw map



X Index: 0



Y Index: 0

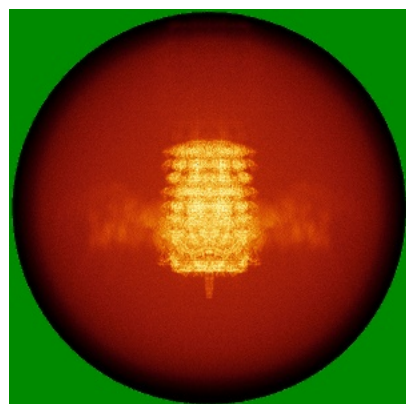


Z Index: 301

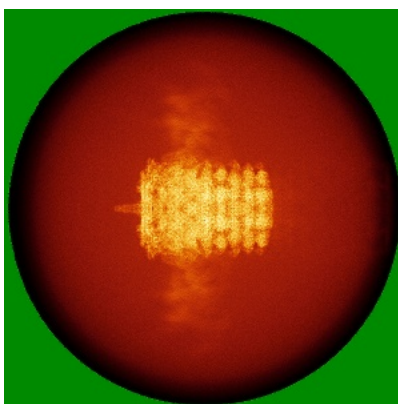
The images above show the largest variance slices of the map in three orthogonal directions.

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

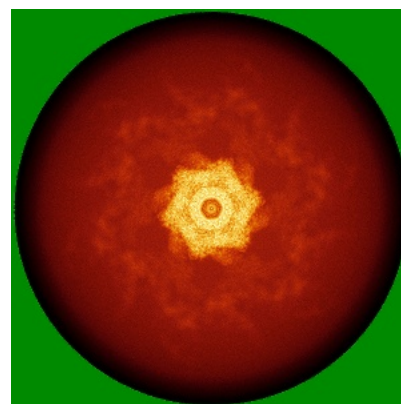
6.4.1 Primary map



X

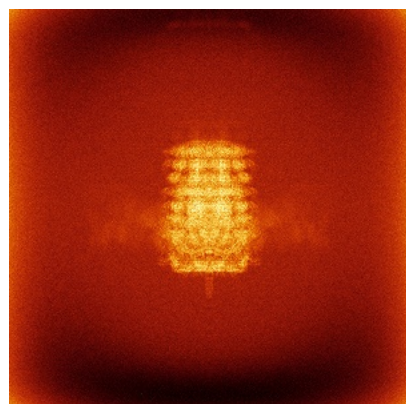


Y

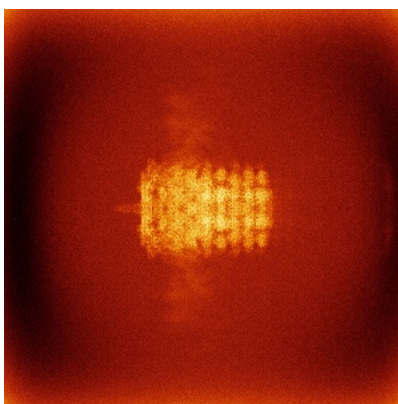


Z

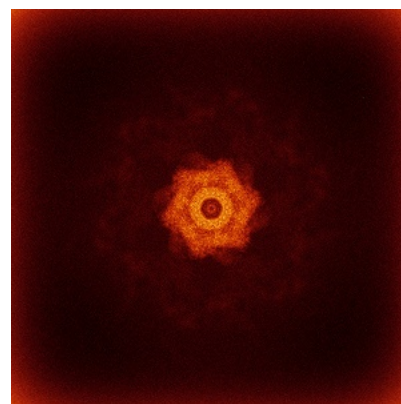
6.4.2 Raw map



X



Y

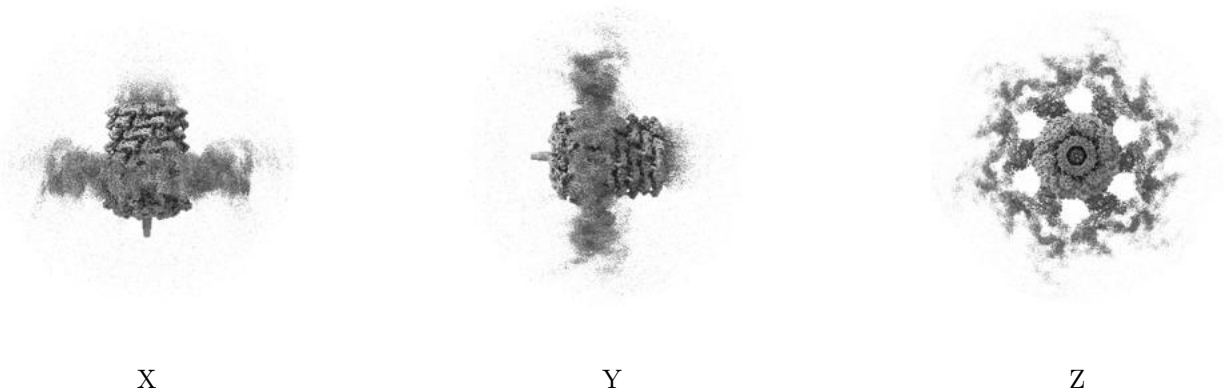


Z

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.

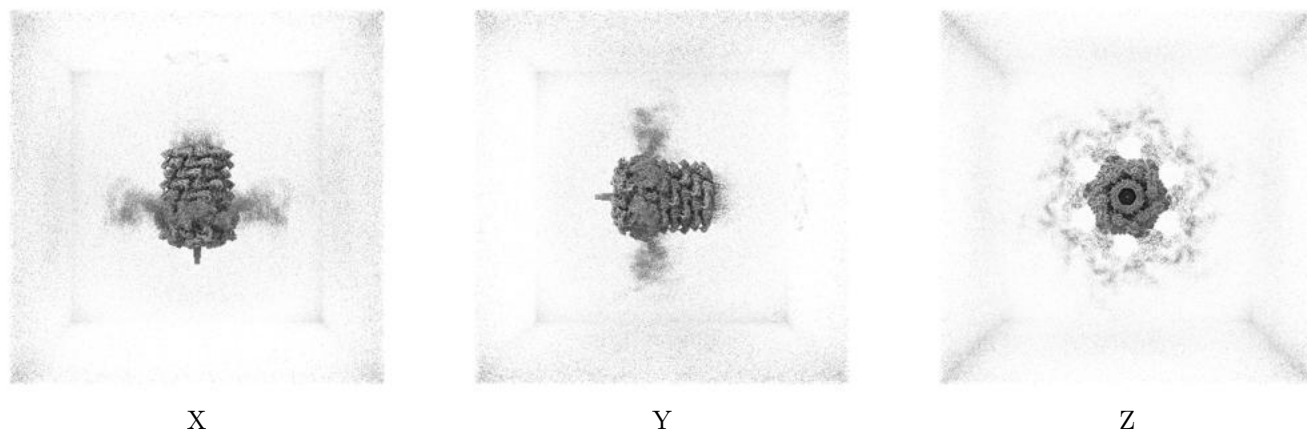
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. 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



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.

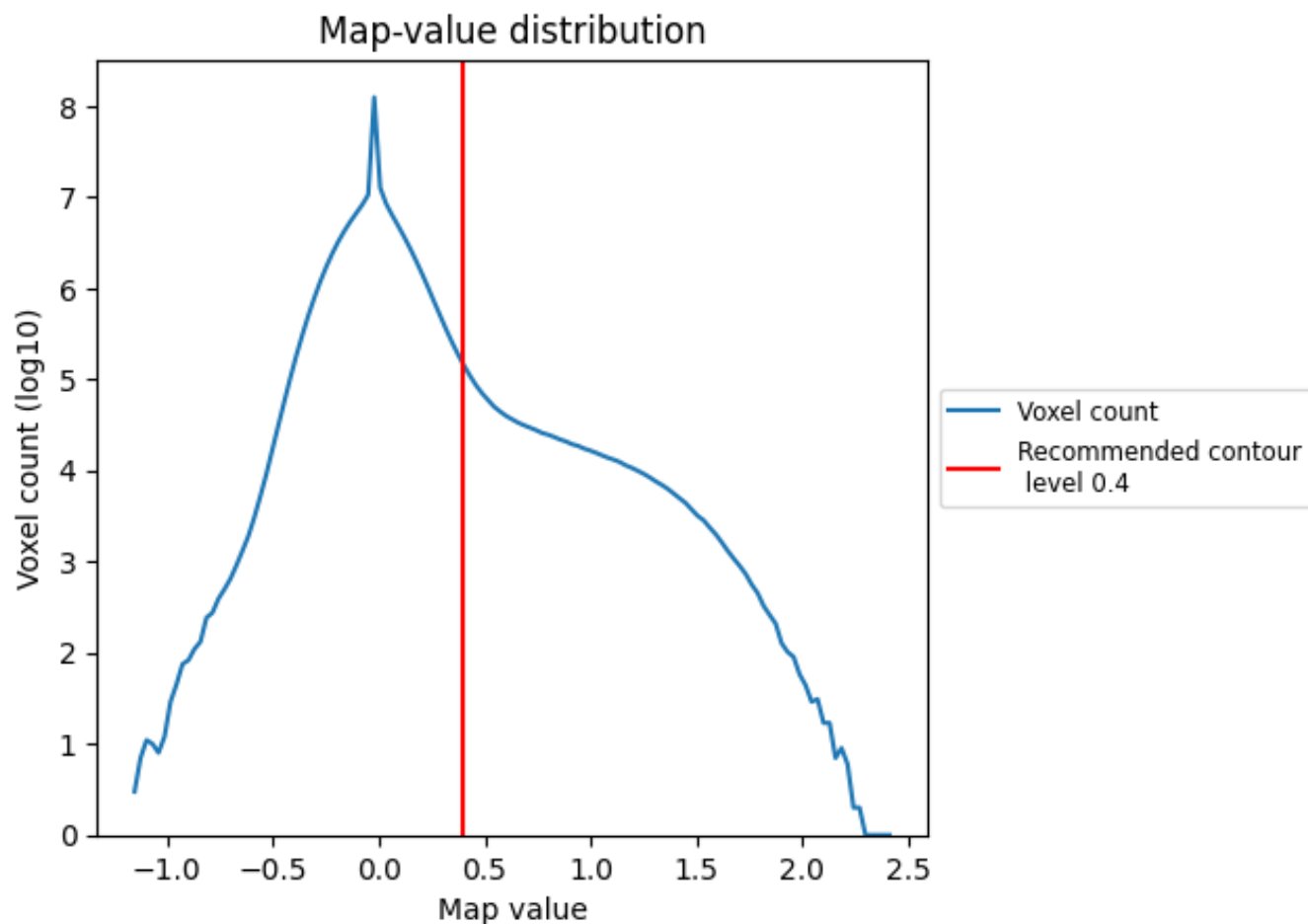
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

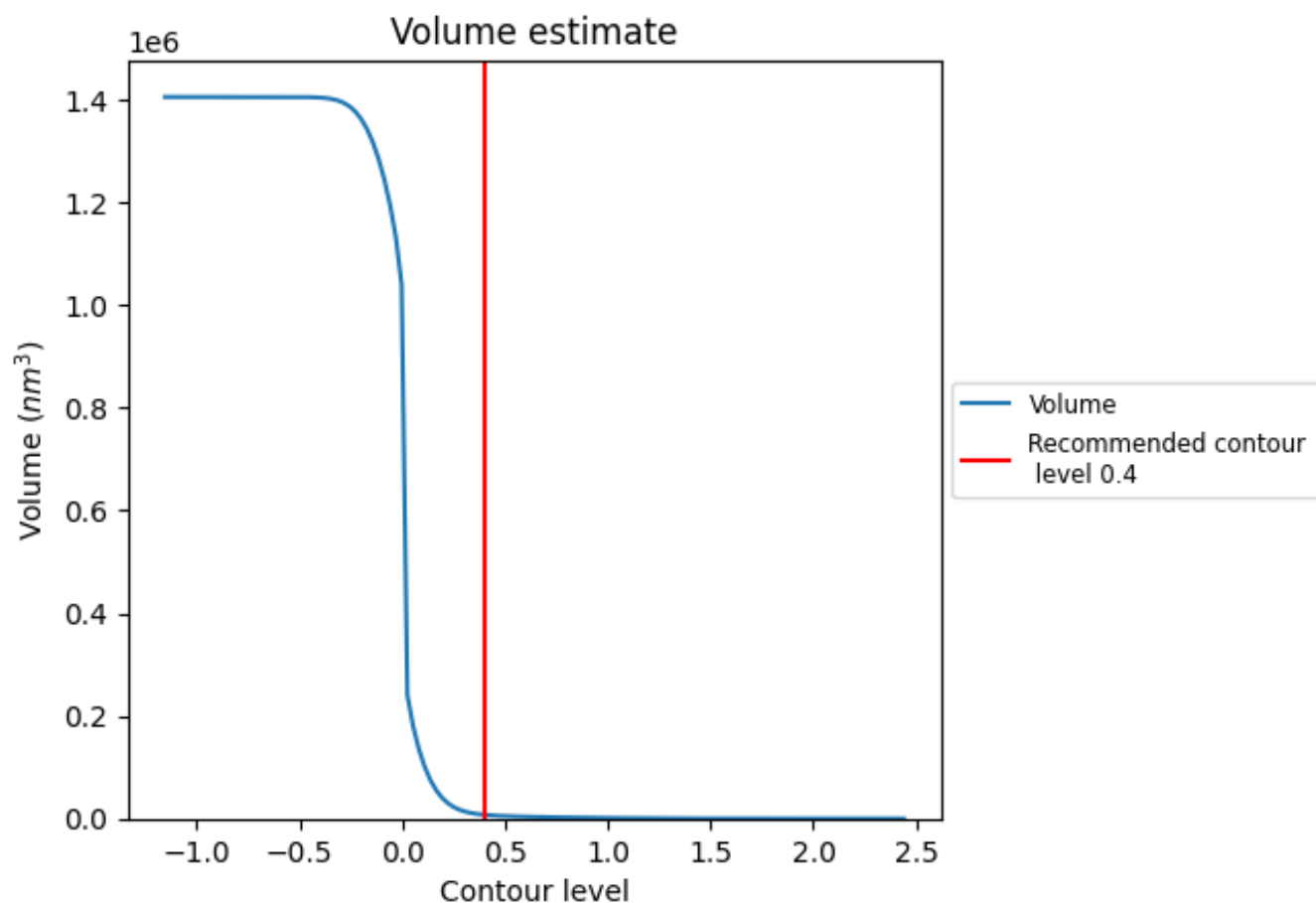
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

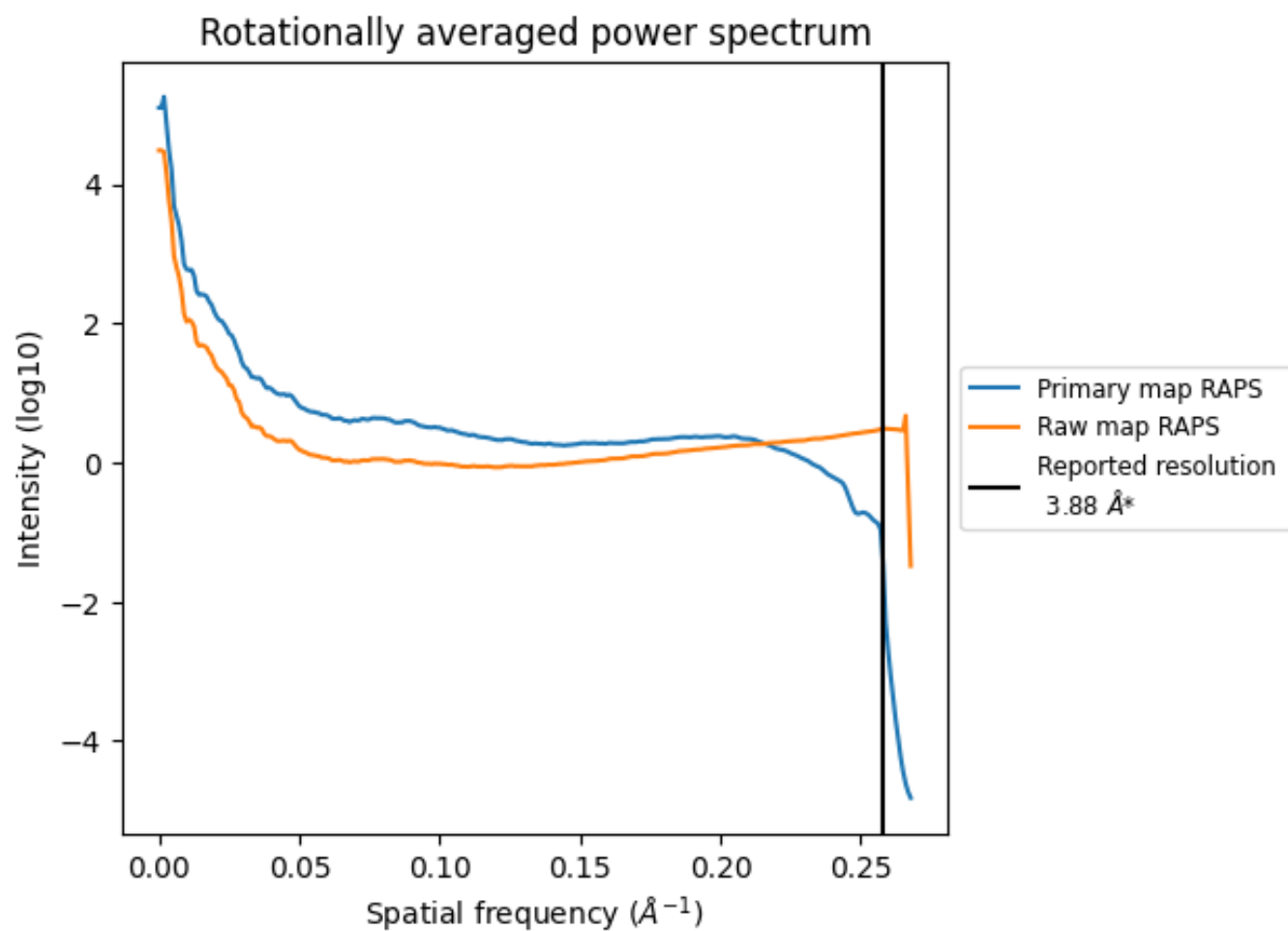
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 7436 nm^3 ; this corresponds to an approximate mass of 6717 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 ⓘ

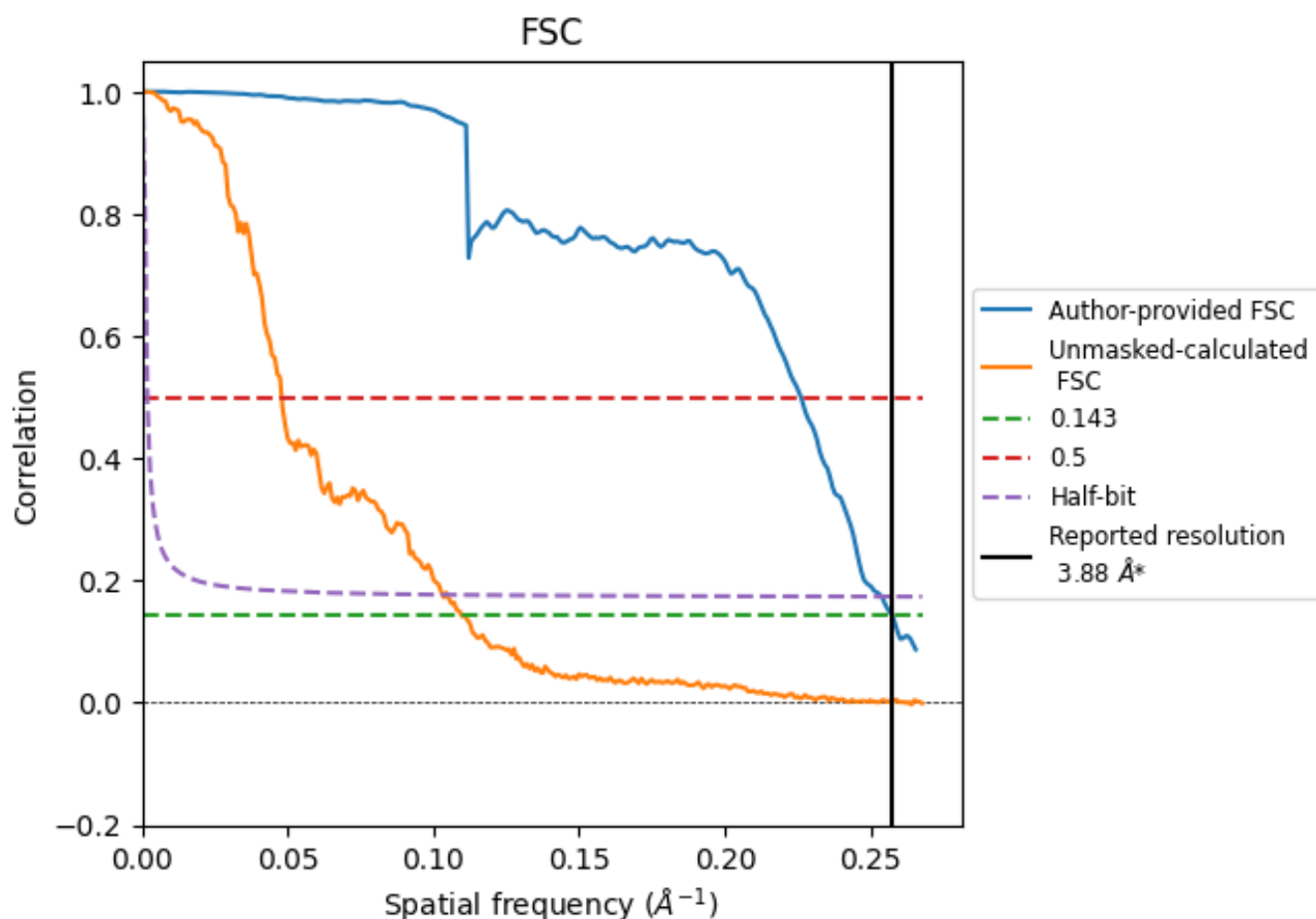


*Reported resolution corresponds to spatial frequency of 0.258 Å⁻¹

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 0.258 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

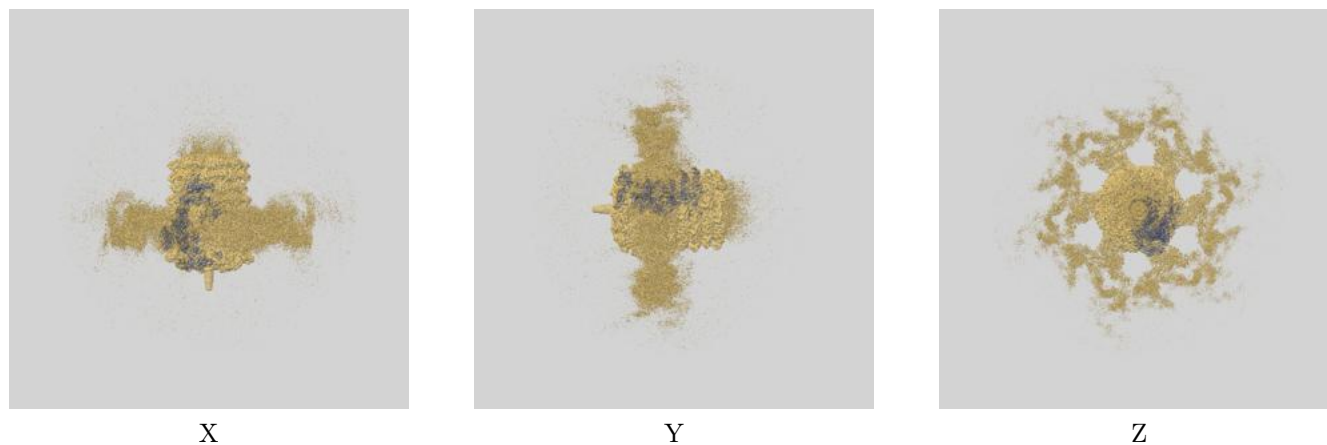
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.88	-	-
Author-provided FSC curve	3.88	4.42	3.94
Unmasked-calculated*	9.12	20.88	9.70

*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 9.12 differs from the reported value 3.88 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-75829 and PDB model 11LX. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



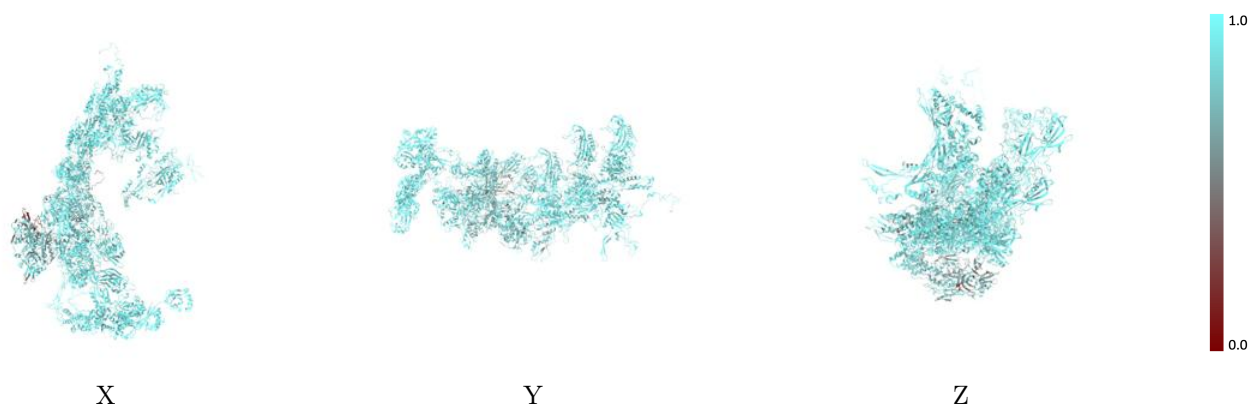
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



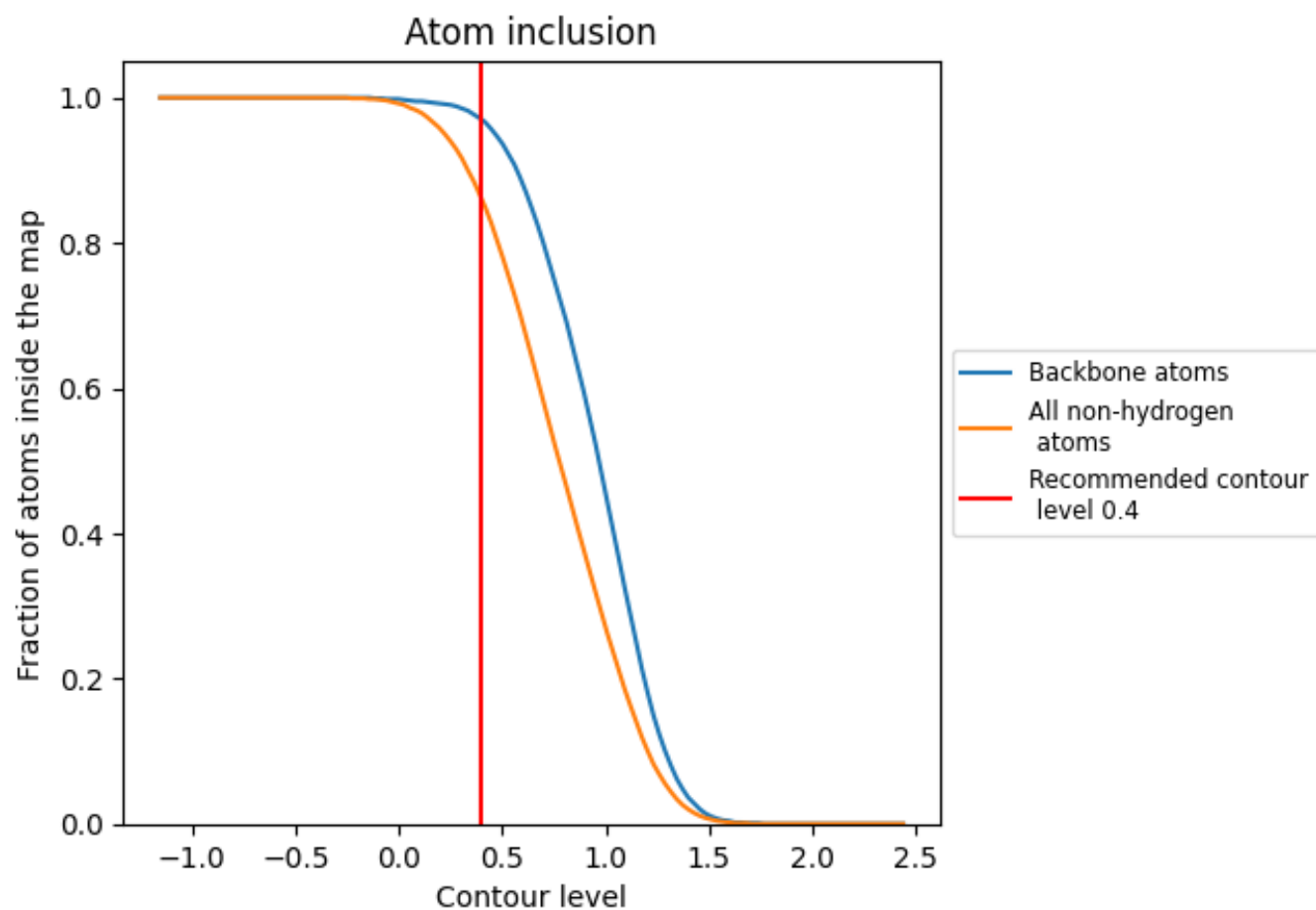
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 86% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8610	 0.3580
AJ	 0.8880	 0.4270
AO	 0.8740	 0.4270
Aa	 0.7630	 0.1880
Ab	 0.6460	 0.1510
Ah	 0.8800	 0.3770
An	 0.8690	 0.3790
Aq	 0.8670	 0.3580
Az	 0.8840	 0.3790
Bh	 0.8240	 0.3200
CJ	 0.8930	 0.3380
H	 0.8760	 0.3920
I	 0.8510	 0.3930
M	 0.8680	 0.3710
V	 0.9070	 0.3740
W	 0.9090	 0.3630
X	 0.7740	 0.3100
n	 0.9190	 0.3640
o	 0.9130	 0.3710
s	 0.8950	 0.3990
t	 0.8880	 0.3780

