



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 04:11 AM UTC

PDB ID : 3H3W / pdb_00003h3w
EMDB ID : EMD-1048
Title : Fitting of the gp6 crystal structure into 3D cryo-EM reconstruction of bacteriophage T4 dome-shaped baseplate
Authors : Aksyuk, A.A.; Leiman, P.G.; Shneider, M.M.; Mesyanzhinov, V.V.; Rossmann, M.G.
Deposited on : 2009-04-17
Resolution : 12.00 Å (reported)
Based on initial model : 3H2T

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

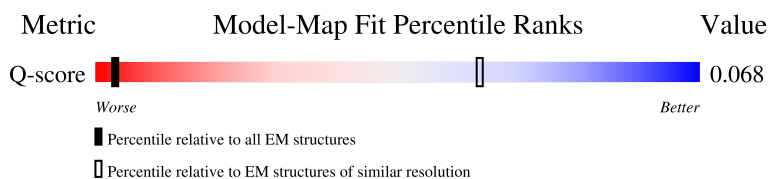
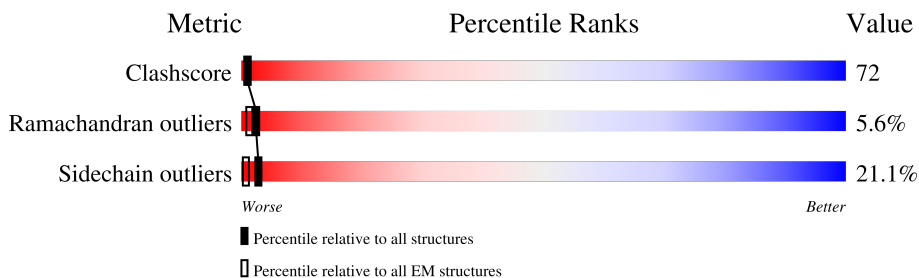
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 12.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	93 (11.50 - 12.50)

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

Mol	Chain	Length	Quality of chain
1	A	335	32% 32% 47% 16% . .
1	B	335	18% 33% 40% 20% . .
1	C	335	17% 32% 46% 16% . .
1	D	335	31% 33% 39% 20% . .

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Mol	Chain	Length	Quality of chain
1	E	335	32% 30% 48% 15%
1	F	335	17% 33% 40% 19%
1	G	335	32% 31% 47% 16%
1	H	335	18% 33% 40% 19%
1	I	335	32% 30% 49% 15%
1	J	335	17% 33% 40% 19%
1	K	335	32% 31% 47% 15%
1	L	335	17% 33% 40% 19%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 31380 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 Baseplate structural protein Gp6.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	326	Total	C	N	O	S	0	0
			2622	1667	424	528	3		
1	B	324	Total	C	N	O	S	0	0
			2608	1658	422	525	3		
1	C	326	Total	C	N	O	S	0	0
			2622	1667	424	528	3		
1	D	324	Total	C	N	O	S	0	0
			2608	1658	422	525	3		
1	E	326	Total	C	N	O	S	0	0
			2622	1667	424	528	3		
1	F	324	Total	C	N	O	S	0	0
			2608	1658	422	525	3		
1	G	326	Total	C	N	O	S	0	0
			2622	1667	424	528	3		
1	H	324	Total	C	N	O	S	0	0
			2608	1658	422	525	3		
1	I	326	Total	C	N	O	S	0	0
			2622	1667	424	528	3		
1	J	324	Total	C	N	O	S	0	0
			2608	1658	422	525	3		
1	K	326	Total	C	N	O	S	0	0
			2622	1667	424	528	3		
1	L	324	Total	C	N	O	S	0	0
			2608	1658	422	525	3		

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	661	LEU	-	expression tag	UNP P19060
A	662	GLU	-	expression tag	UNP P19060
A	663	HIS	-	expression tag	UNP P19060
A	664	HIS	-	expression tag	UNP P19060
A	665	HIS	-	expression tag	UNP P19060
A	666	HIS	-	expression tag	UNP P19060

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Chain	Residue	Modelled	Actual	Comment	Reference
A	667	HIS	-	expression tag	UNP P19060
A	668	HIS	-	expression tag	UNP P19060
B	661	LEU	-	expression tag	UNP P19060
B	662	GLU	-	expression tag	UNP P19060
B	663	HIS	-	expression tag	UNP P19060
B	664	HIS	-	expression tag	UNP P19060
B	665	HIS	-	expression tag	UNP P19060
B	666	HIS	-	expression tag	UNP P19060
B	667	HIS	-	expression tag	UNP P19060
B	668	HIS	-	expression tag	UNP P19060
C	661	LEU	-	expression tag	UNP P19060
C	662	GLU	-	expression tag	UNP P19060
C	663	HIS	-	expression tag	UNP P19060
C	664	HIS	-	expression tag	UNP P19060
C	665	HIS	-	expression tag	UNP P19060
C	666	HIS	-	expression tag	UNP P19060
C	667	HIS	-	expression tag	UNP P19060
C	668	HIS	-	expression tag	UNP P19060
D	661	LEU	-	expression tag	UNP P19060
D	662	GLU	-	expression tag	UNP P19060
D	663	HIS	-	expression tag	UNP P19060
D	664	HIS	-	expression tag	UNP P19060
D	665	HIS	-	expression tag	UNP P19060
D	666	HIS	-	expression tag	UNP P19060
D	667	HIS	-	expression tag	UNP P19060
D	668	HIS	-	expression tag	UNP P19060
E	661	LEU	-	expression tag	UNP P19060
E	662	GLU	-	expression tag	UNP P19060
E	663	HIS	-	expression tag	UNP P19060
E	664	HIS	-	expression tag	UNP P19060
E	665	HIS	-	expression tag	UNP P19060
E	666	HIS	-	expression tag	UNP P19060
E	667	HIS	-	expression tag	UNP P19060
E	668	HIS	-	expression tag	UNP P19060
F	661	LEU	-	expression tag	UNP P19060
F	662	GLU	-	expression tag	UNP P19060
F	663	HIS	-	expression tag	UNP P19060
F	664	HIS	-	expression tag	UNP P19060
F	665	HIS	-	expression tag	UNP P19060
F	666	HIS	-	expression tag	UNP P19060
F	667	HIS	-	expression tag	UNP P19060
F	668	HIS	-	expression tag	UNP P19060

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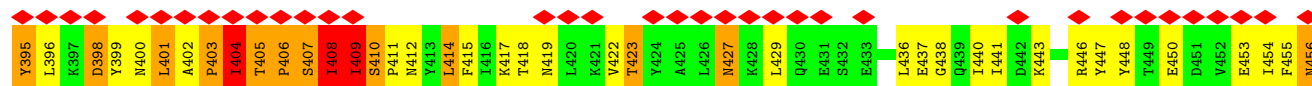
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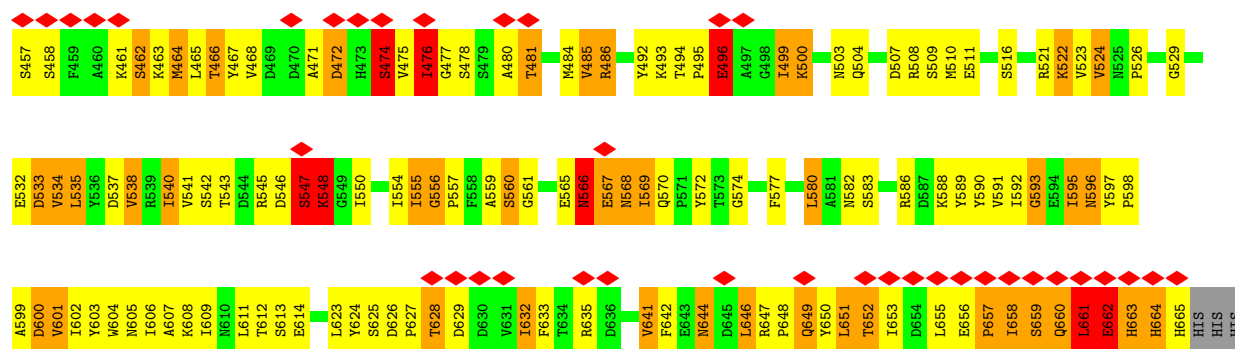
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G	661	LEU	-	expression tag	UNP P19060
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G	664	HIS	-	expression tag	UNP P19060
G	665	HIS	-	expression tag	UNP P19060
G	666	HIS	-	expression tag	UNP P19060
G	667	HIS	-	expression tag	UNP P19060
G	668	HIS	-	expression tag	UNP P19060
H	661	LEU	-	expression tag	UNP P19060
H	662	GLU	-	expression tag	UNP P19060
H	663	HIS	-	expression tag	UNP P19060
H	664	HIS	-	expression tag	UNP P19060
H	665	HIS	-	expression tag	UNP P19060
H	666	HIS	-	expression tag	UNP P19060
H	667	HIS	-	expression tag	UNP P19060
H	668	HIS	-	expression tag	UNP P19060
I	661	LEU	-	expression tag	UNP P19060
I	662	GLU	-	expression tag	UNP P19060
I	663	HIS	-	expression tag	UNP P19060
I	664	HIS	-	expression tag	UNP P19060
I	665	HIS	-	expression tag	UNP P19060
I	666	HIS	-	expression tag	UNP P19060
I	667	HIS	-	expression tag	UNP P19060
I	668	HIS	-	expression tag	UNP P19060
J	661	LEU	-	expression tag	UNP P19060
J	662	GLU	-	expression tag	UNP P19060
J	663	HIS	-	expression tag	UNP P19060
J	664	HIS	-	expression tag	UNP P19060
J	665	HIS	-	expression tag	UNP P19060
J	666	HIS	-	expression tag	UNP P19060
J	667	HIS	-	expression tag	UNP P19060
J	668	HIS	-	expression tag	UNP P19060
K	661	LEU	-	expression tag	UNP P19060
K	662	GLU	-	expression tag	UNP P19060
K	663	HIS	-	expression tag	UNP P19060
K	664	HIS	-	expression tag	UNP P19060
K	665	HIS	-	expression tag	UNP P19060
K	666	HIS	-	expression tag	UNP P19060
K	667	HIS	-	expression tag	UNP P19060
K	668	HIS	-	expression tag	UNP P19060
L	661	LEU	-	expression tag	UNP P19060
L	662	GLU	-	expression tag	UNP P19060

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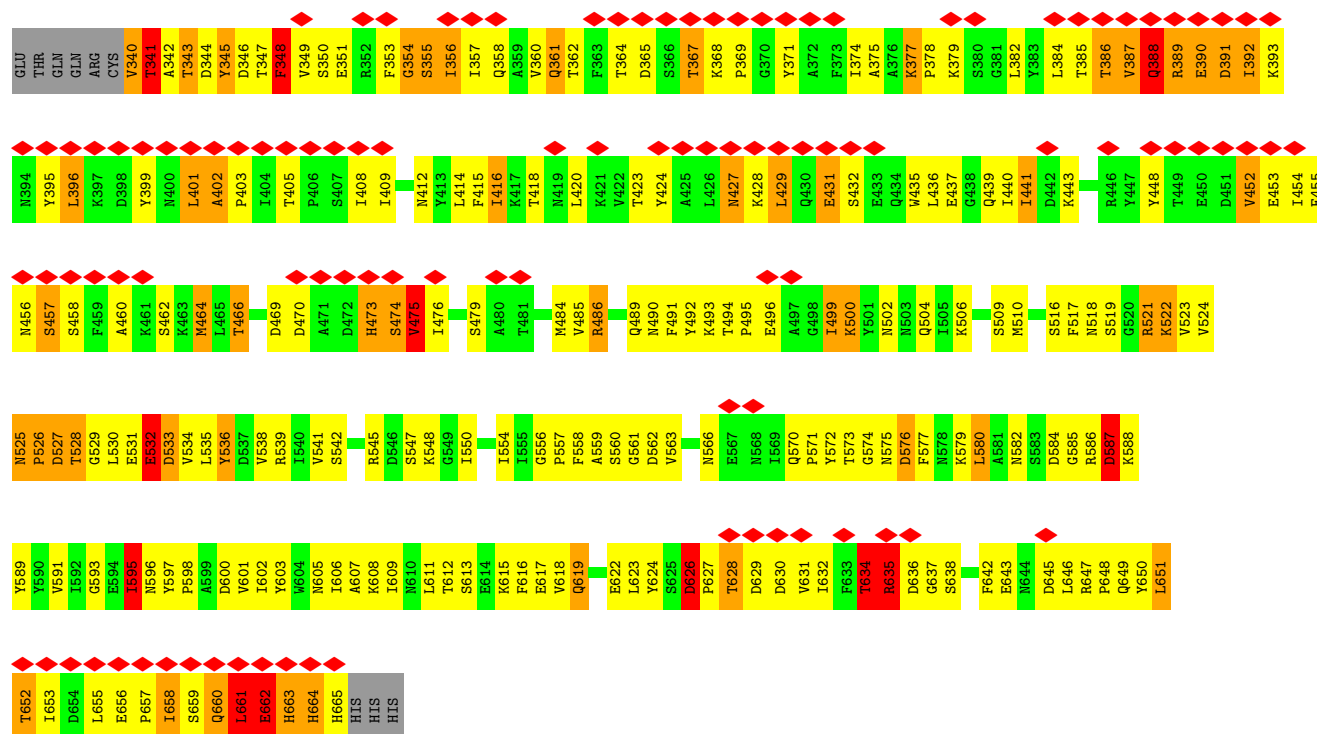
Chain	Residue	Modelled	Actual	Comment	Reference
L	663	HIS	-	expression tag	UNP P19060
L	664	HIS	-	expression tag	UNP P19060
L	665	HIS	-	expression tag	UNP P19060
L	666	HIS	-	expression tag	UNP P19060
L	667	HIS	-	expression tag	UNP P19060
L	668	HIS	-	expression tag	UNP P19060





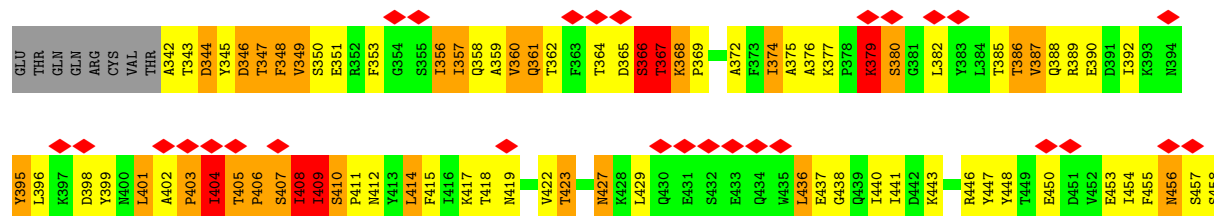
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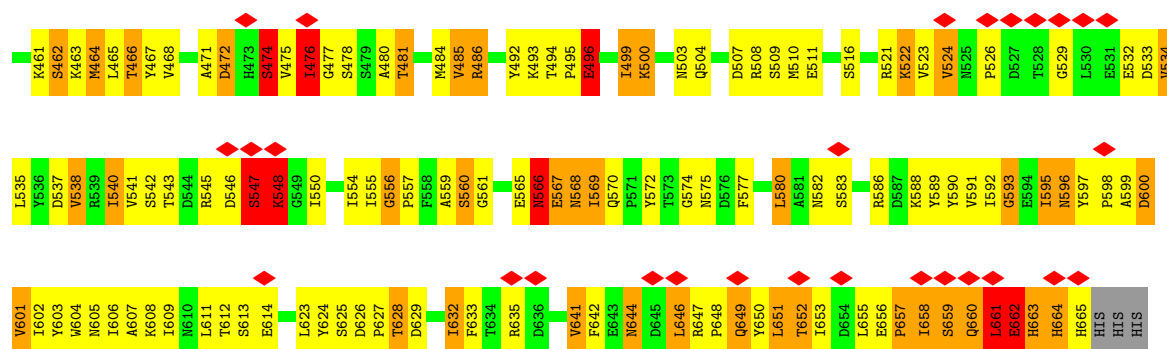
Chain E: 32% 30% 48% 15%



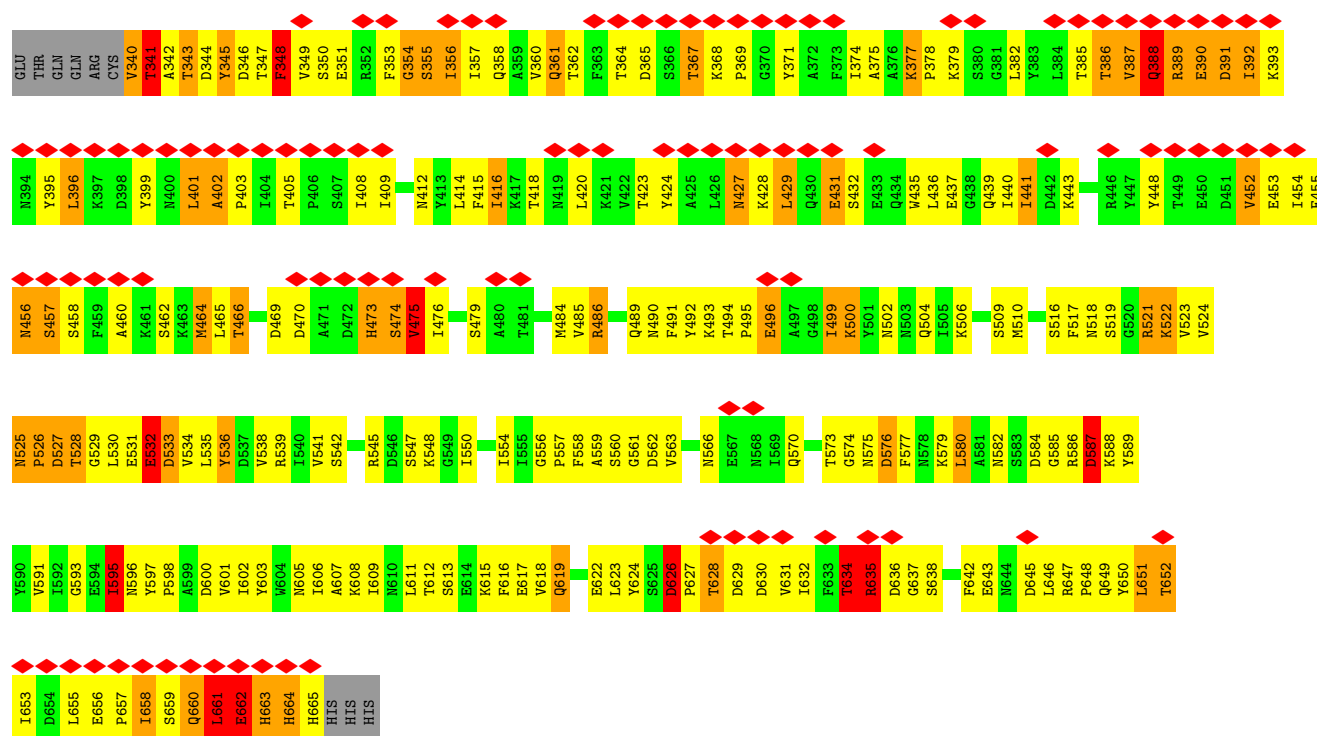
• Molecule 1: Baseplate structural protein Gp6

Chain F: 17% 33% 40% 19%

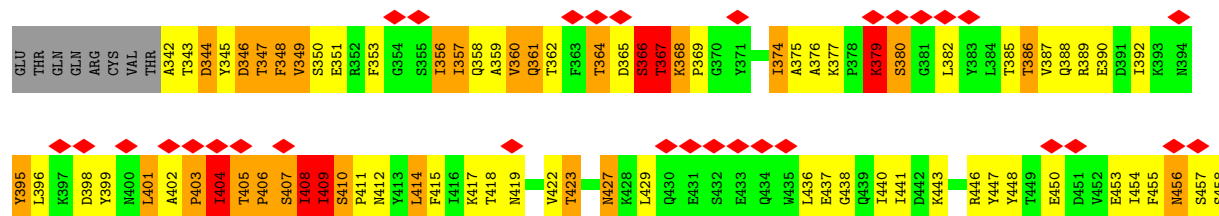


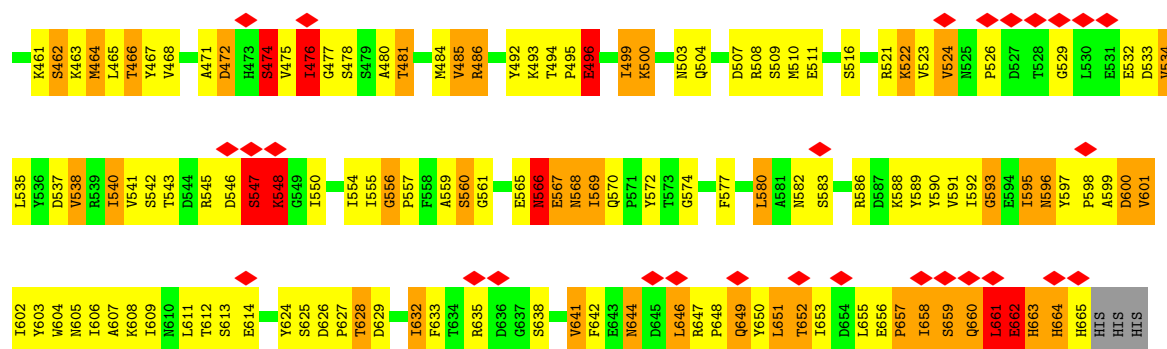


• Molecule 1: Baseplate structural protein Gp6

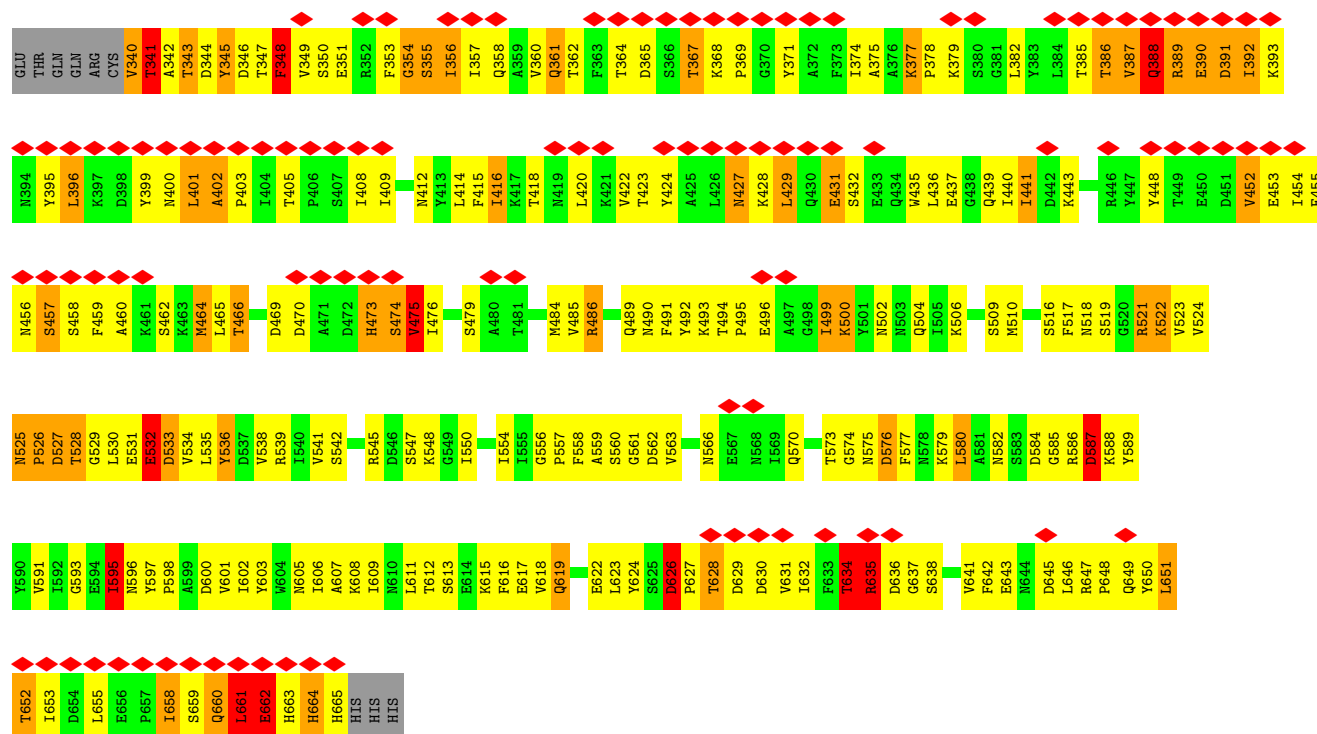


• Molecule 1: Baseplate structural protein Gp6

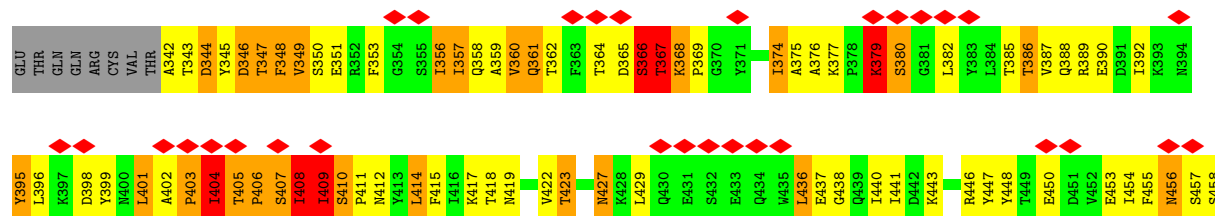


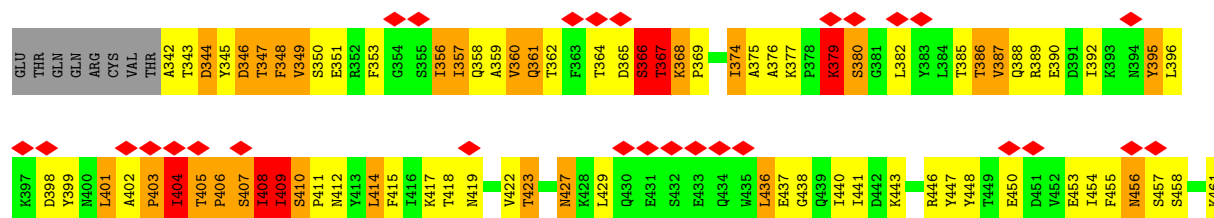


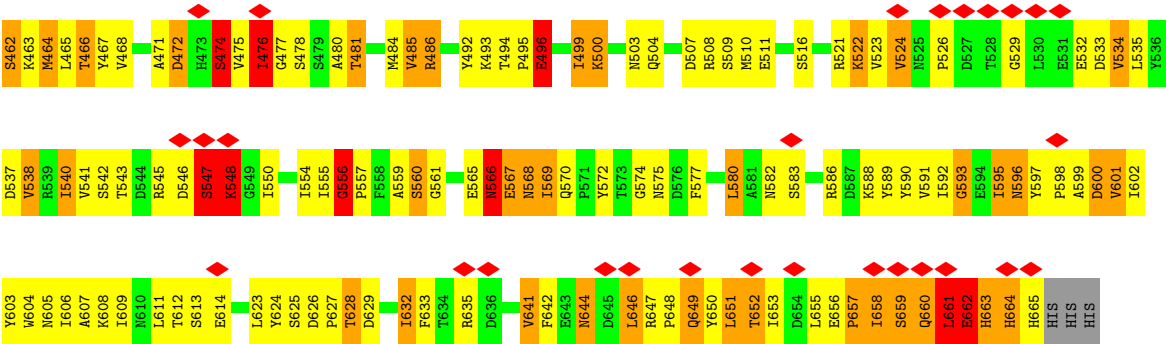
• Molecule 1: Baseplate structural protein Gp6



• Molecule 1: Baseplate structural protein Gp6







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	945	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	47000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	10.345	Depositor
Minimum map value	-7.648	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.45	Depositor
Map size ($\text{\AA}$)	583.8291, 583.8291, 583.8291	wwPDB
Map dimensions	196, 196, 196	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	2.97872, 2.97872, 2.97872	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.67	0/2677	1.20	39/3637 (1.1%)
1	B	0.73	3/2663 (0.1%)	1.29	42/3617 (1.2%)
1	C	0.67	0/2677	1.19	39/3637 (1.1%)
1	D	0.73	3/2663 (0.1%)	1.29	43/3617 (1.2%)
1	E	0.67	0/2677	1.20	38/3637 (1.0%)
1	F	0.73	3/2663 (0.1%)	1.29	42/3617 (1.2%)
1	G	0.67	0/2677	1.20	39/3637 (1.1%)
1	H	0.73	3/2663 (0.1%)	1.29	42/3617 (1.2%)
1	I	0.67	0/2677	1.19	38/3637 (1.0%)
1	J	0.73	3/2663 (0.1%)	1.29	43/3617 (1.2%)
1	K	0.67	0/2677	1.20	39/3637 (1.1%)
1	L	0.73	3/2663 (0.1%)	1.29	42/3617 (1.2%)
All	All	0.70	18/32040 (0.1%)	1.25	486/43524 (1.1%)

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	409	ILE	CA-CB	-9.72	1.48	1.55
1	D	409	ILE	CA-CB	-9.70	1.48	1.55
1	L	409	ILE	CA-CB	-9.68	1.48	1.55
1	B	409	ILE	CA-CB	-9.67	1.48	1.55
1	H	409	ILE	CA-CB	-9.64	1.48	1.55

The worst 5 of 486 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	548	LYS	N-CA-C	17.52	137.91	113.56
1	D	548	LYS	N-CA-C	17.50	137.88	113.56
1	L	548	LYS	N-CA-C	17.48	137.85	113.56
1	F	548	LYS	N-CA-C	17.46	137.84	113.56
1	H	548	LYS	N-CA-C	17.46	137.83	113.56

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	2622	0	2545	409	0
1	B	2608	0	2530	387	0
1	C	2622	0	2545	411	0
1	D	2608	0	2530	389	0
1	E	2622	0	2543	455	0
1	F	2608	0	2530	348	0
1	G	2622	0	2543	387	0
1	H	2608	0	2530	379	0
1	I	2622	0	2544	392	0
1	J	2608	0	2530	350	0
1	K	2622	0	2543	427	0
1	L	2608	0	2530	350	0
All	All	31380	0	30443	4423	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 72.

The worst 5 of 4423 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:B:366:SER:CB	1:K:403:PRO:HB3	1.21	1.65
1:A:664:HIS:NE2	1:K:348:PHE:CZ	1.70	1.60
1:I:400:ASN:ND2	1:K:664:HIS:CE1	1.69	1.58
1:B:364:THR:CG2	1:K:401:LEU:CD1	1.79	1.58
1:E:348:PHE:CZ	1:G:664:HIS:NE2	1.68	1.57

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	324/335 (97%)	260 (80%)	47 (14%)	17 (5%)	1	15
1	B	322/335 (96%)	261 (81%)	42 (13%)	19 (6%)	1	13
1	C	324/335 (97%)	260 (80%)	47 (14%)	17 (5%)	1	15
1	D	322/335 (96%)	262 (81%)	41 (13%)	19 (6%)	1	13
1	E	324/335 (97%)	260 (80%)	47 (14%)	17 (5%)	1	15
1	F	322/335 (96%)	262 (81%)	41 (13%)	19 (6%)	1	13
1	G	324/335 (97%)	260 (80%)	47 (14%)	17 (5%)	1	15
1	H	322/335 (96%)	262 (81%)	41 (13%)	19 (6%)	1	13
1	I	324/335 (97%)	260 (80%)	47 (14%)	17 (5%)	1	15
1	J	322/335 (96%)	261 (81%)	42 (13%)	19 (6%)	1	13
1	K	324/335 (97%)	260 (80%)	47 (14%)	17 (5%)	1	15
1	L	322/335 (96%)	261 (81%)	42 (13%)	19 (6%)	1	13
All	All	3876/4020 (96%)	3129 (81%)	531 (14%)	216 (6%)	2	14

5 of 216 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	348	PHE
1	A	354	GLY
1	A	389	ARG
1	A	390	GLU
1	A	526	PRO

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	295/304 (97%)	236 (80%)	59 (20%)	1	7
1	B	293/304 (96%)	228 (78%)	65 (22%)	1	6
1	C	295/304 (97%)	236 (80%)	59 (20%)	1	7
1	D	293/304 (96%)	228 (78%)	65 (22%)	1	6
1	E	295/304 (97%)	236 (80%)	59 (20%)	1	7
1	F	293/304 (96%)	227 (78%)	66 (22%)	1	6
1	G	295/304 (97%)	236 (80%)	59 (20%)	1	7
1	H	293/304 (96%)	228 (78%)	65 (22%)	1	6
1	I	295/304 (97%)	236 (80%)	59 (20%)	1	7
1	J	293/304 (96%)	228 (78%)	65 (22%)	1	6
1	K	295/304 (97%)	236 (80%)	59 (20%)	1	7
1	L	293/304 (96%)	227 (78%)	66 (22%)	1	6
All	All	3528/3648 (97%)	2782 (79%)	746 (21%)	3	6

5 of 746 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	476	ILE
1	J	409	ILE
1	H	547	SER
1	H	474	SER
1	I	441	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 154 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	361	GLN
1	L	412	ASN
1	J	489	GLN
1	K	427	ASN
1	L	582	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

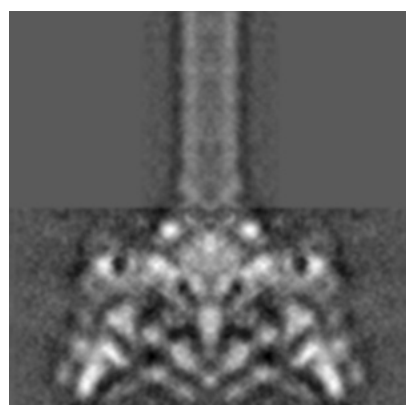
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1048. These allow visual inspection of the internal detail of the map and identification of artifacts.

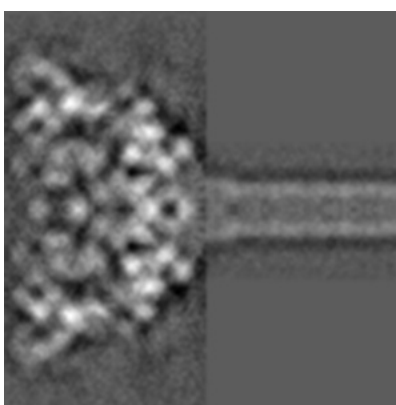
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

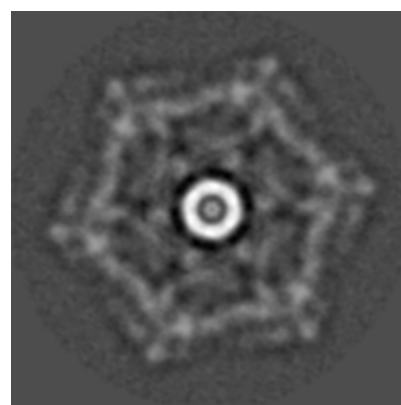
6.1.1 Primary map



X



Y

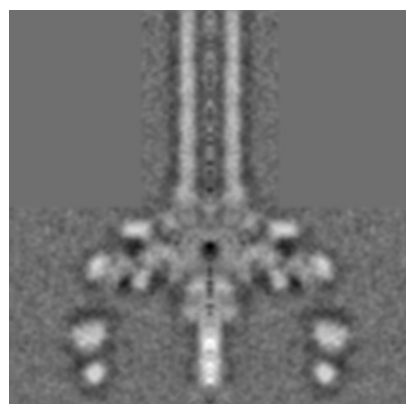


Z

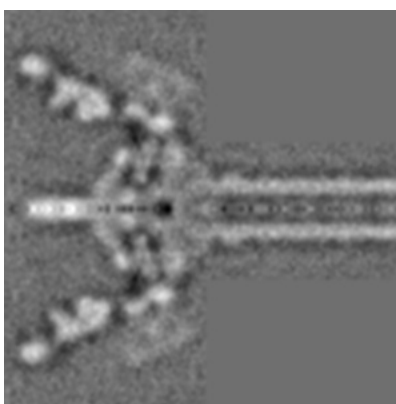
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

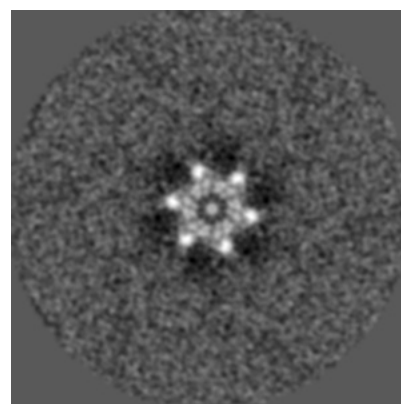
6.2.1 Primary map



X Index: 98



Y Index: 98

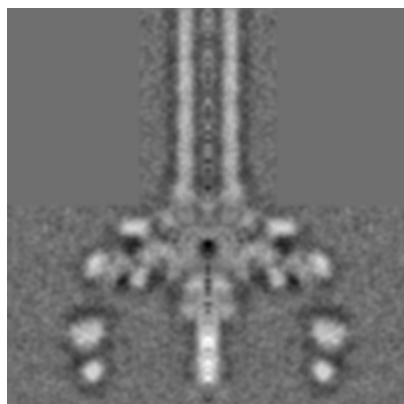


Z Index: 98

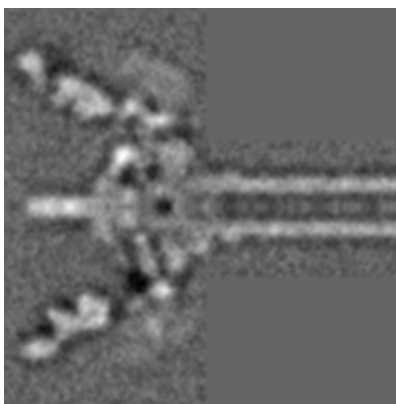
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

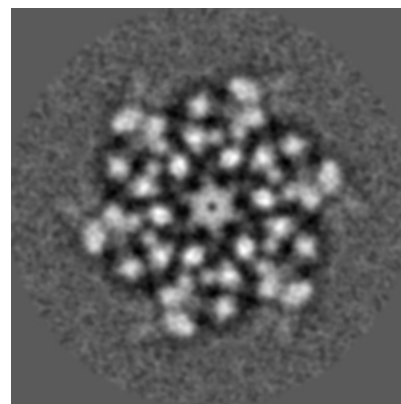
6.3.1 Primary map



X Index: 98



Y Index: 100

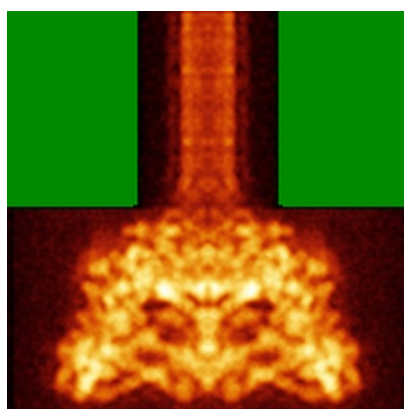


Z Index: 60

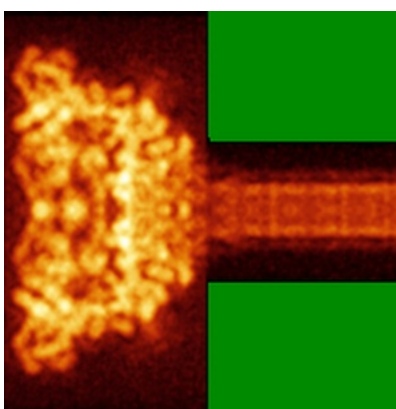
The images above show the largest variance slices of the map in three orthogonal directions.

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

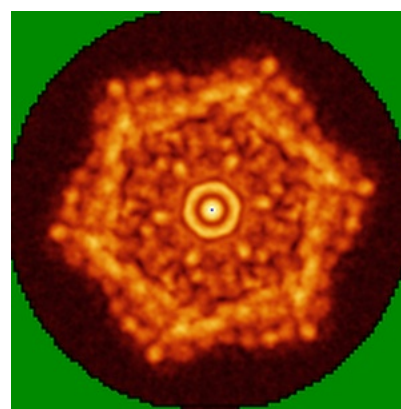
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

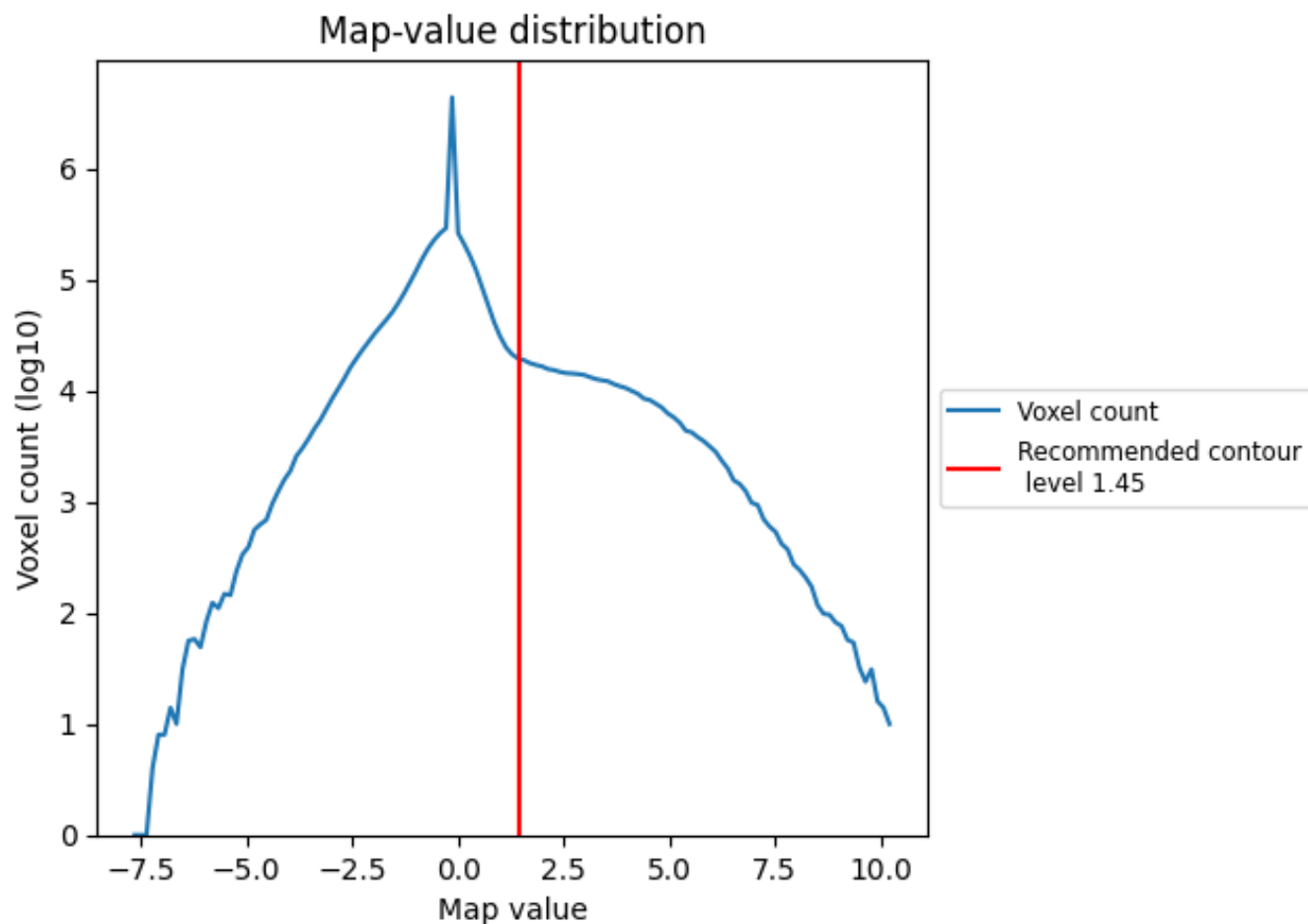
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

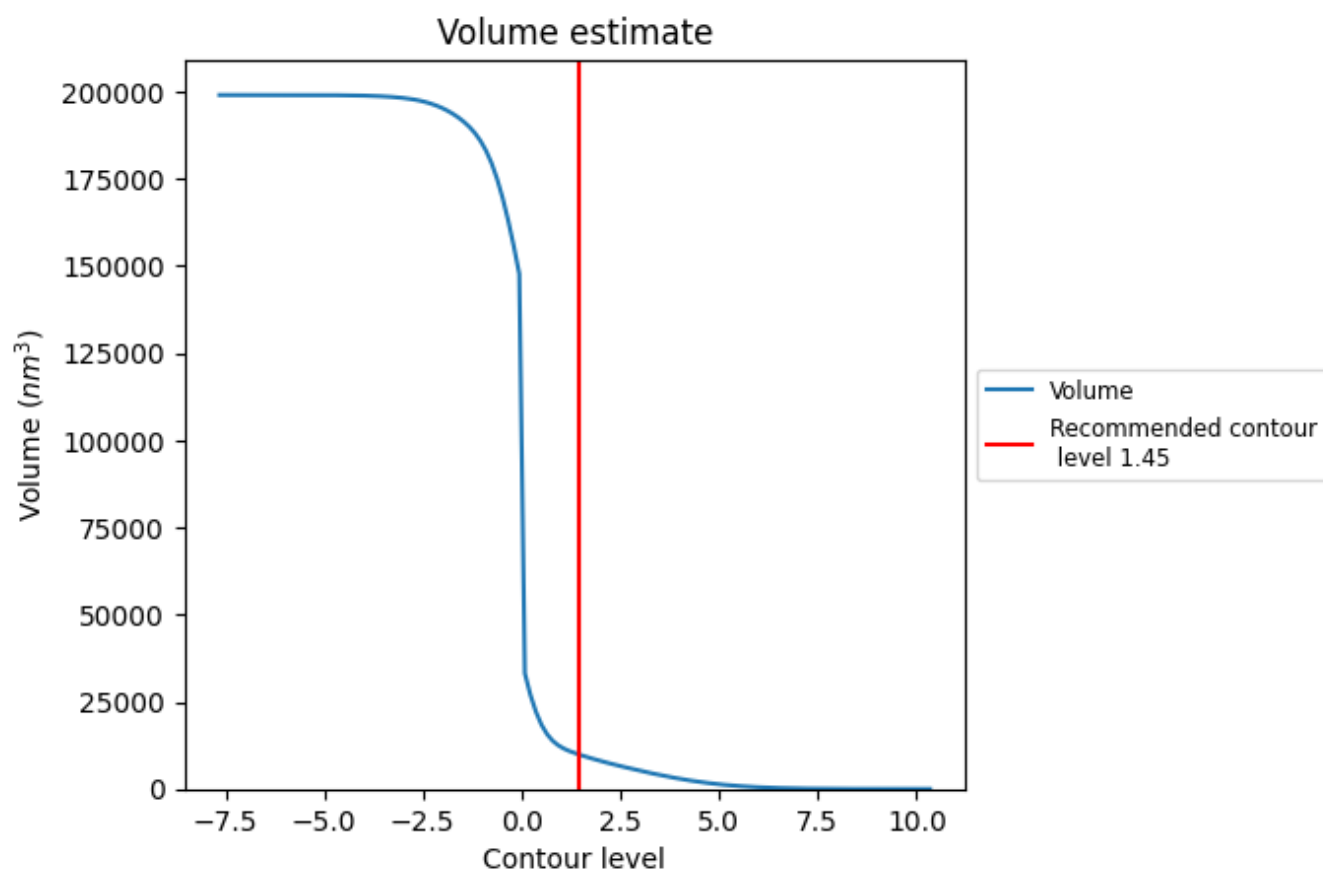
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

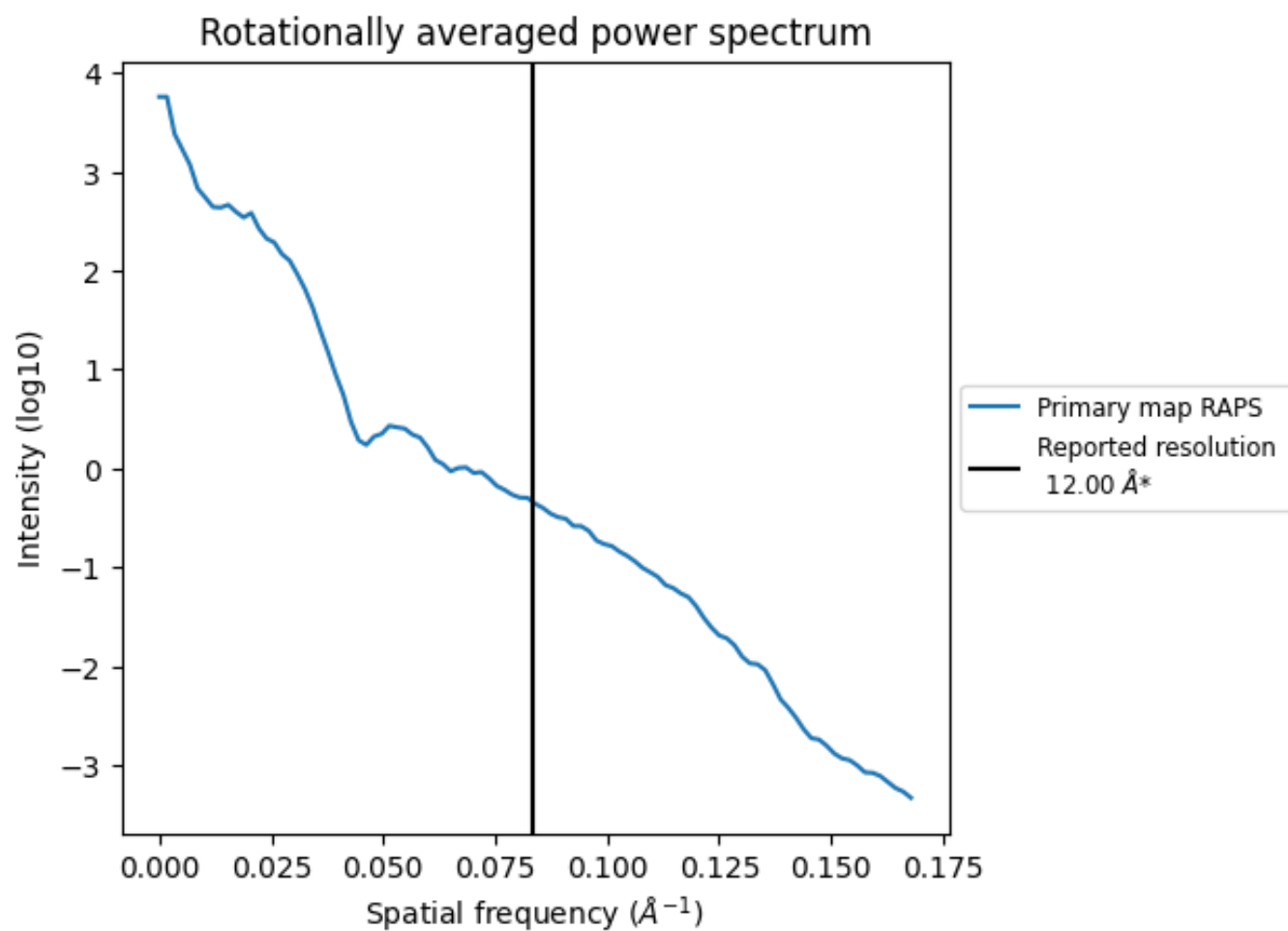
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 9896 nm^3 ; this corresponds to an approximate mass of 8939 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 0.083 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

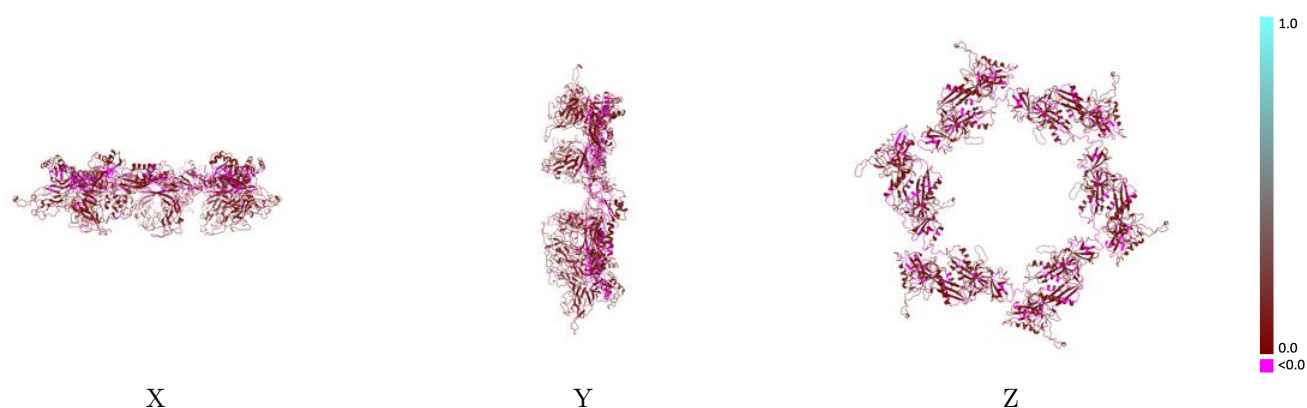
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-1048 and PDB model 3H3W. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

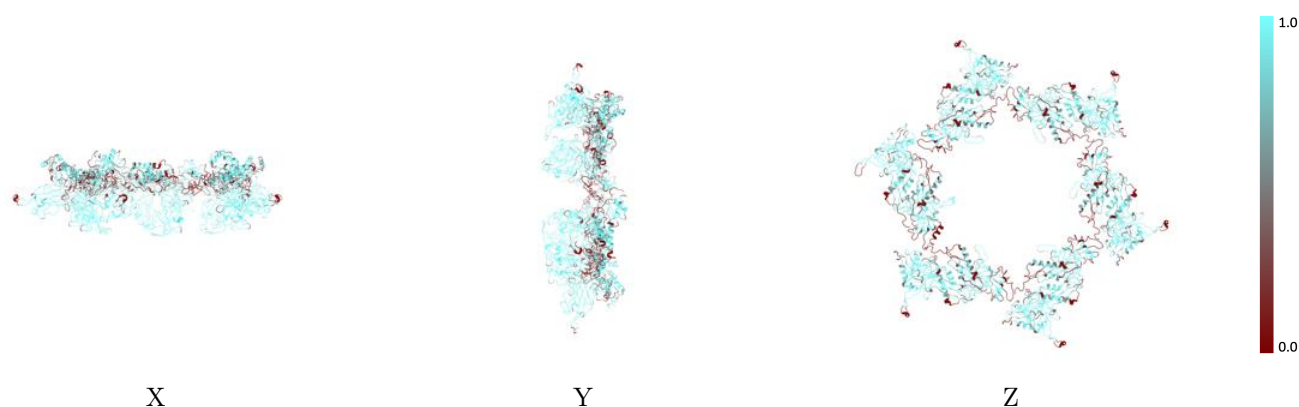
This section was not generated.

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



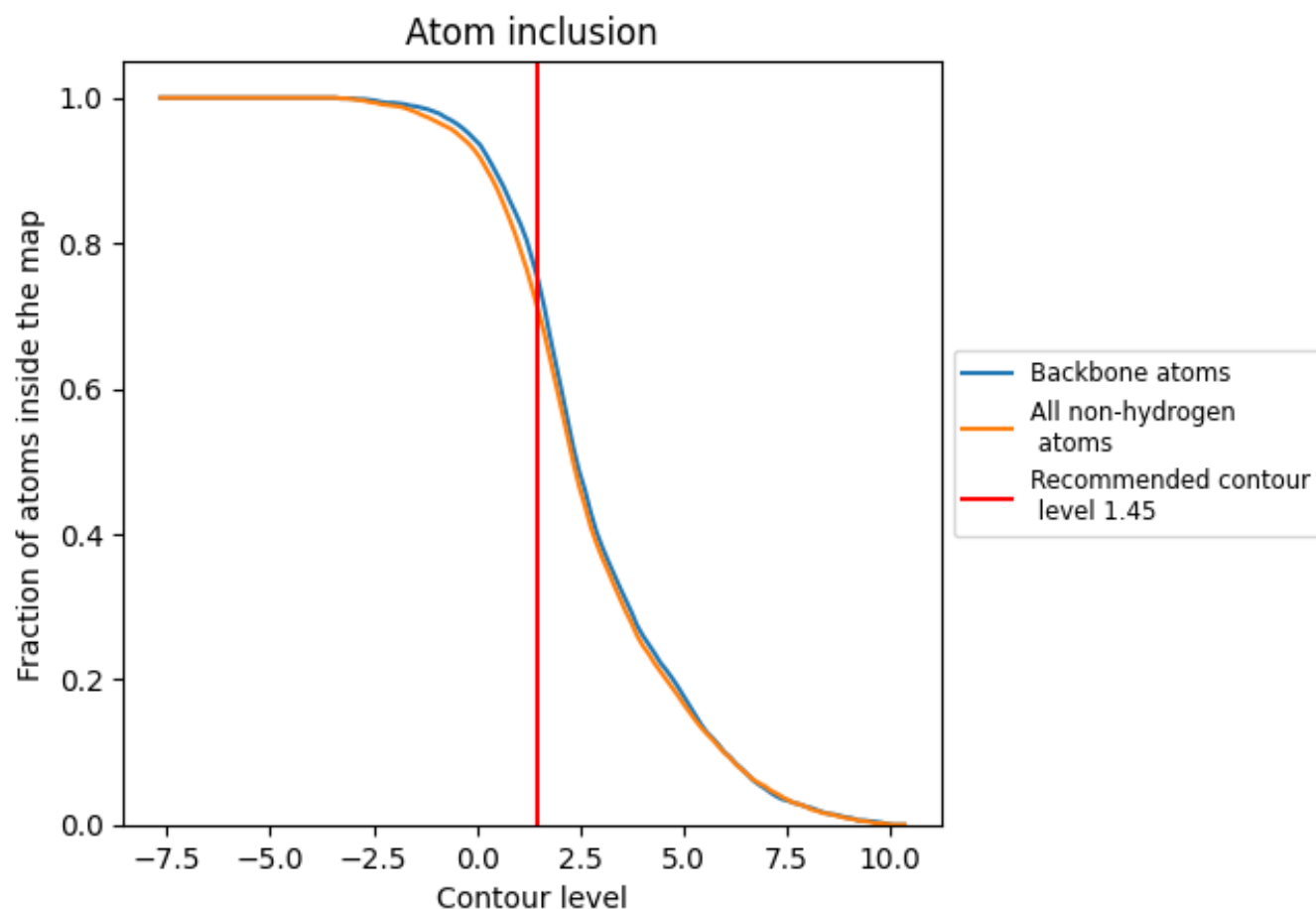
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 72% 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 (1.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7150	0.0680
A	0.6560	0.0630
B	0.7730	0.0750
C	0.7700	0.0760
D	0.6550	0.0630
E	0.6540	0.0630
F	0.7800	0.0730
G	0.6550	0.0600
H	0.7730	0.0740
I	0.6540	0.0630
J	0.7740	0.0720
K	0.6540	0.0640
L	0.7800	0.0750

1.0

0.0

<0.0