



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 05:03 AM UTC

PDB ID : 6YT5 / pdb_00006yt5
EMDB ID : EMD-10912
Title : Cryo-EM structure of T7 bacteriophage DNA translocation gp15-gp16 core complex intermediate assembly
Authors : Perez-Ruiz, M.; Pulido-Cid, M.; Luque-Ortega, J.R.; Cuervo, A.; Carrascosa, J.L.
Deposited on : 2020-04-23
Resolution : 3.00 Å(reported)
Based on initial models : 1SLY, 4CFO

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

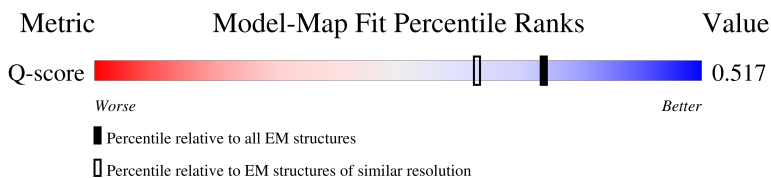
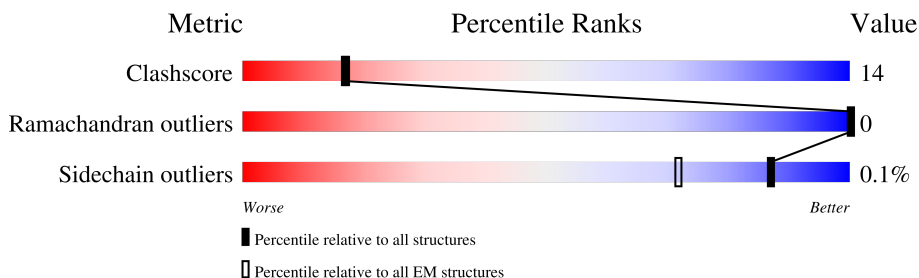
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	782	 54% 28% 18%
1	B	782	 55% 27% 18%
1	C	782	 54% 28% 18%
1	D	782	 55% 27% 18%

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Mol	Chain	Length	Quality of chain
1	E	782	 55%27%18%
1	F	782	 55%27%18%
2	G	1340	 12% • 85%
2	H	1340	 12% • 85%
2	I	1340	 12% • 85%
2	J	1340	 12% • 85%
2	K	1340	 12% • 85%
2	L	1340	 12% • 85%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 39078 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 Internal virion protein gp15.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	642	Total	C	N	O	S	0	0
			5116	3162	901	1024	29		
1	B	642	Total	C	N	O	S	0	0
			5116	3162	901	1024	29		
1	C	642	Total	C	N	O	S	0	0
			5116	3162	901	1024	29		
1	D	642	Total	C	N	O	S	0	0
			5116	3162	901	1024	29		
1	E	642	Total	C	N	O	S	0	0
			5116	3162	901	1024	29		
1	F	642	Total	C	N	O	S	0	0
			5116	3162	901	1024	29		

There are 210 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-34	MET	-	initiating methionine	UNP P03725
A	-33	ARG	-	expression tag	UNP P03725
A	-32	GLY	-	expression tag	UNP P03725
A	-31	SER	-	expression tag	UNP P03725
A	-30	HIS	-	expression tag	UNP P03725
A	-29	HIS	-	expression tag	UNP P03725
A	-28	HIS	-	expression tag	UNP P03725
A	-27	HIS	-	expression tag	UNP P03725
A	-26	HIS	-	expression tag	UNP P03725
A	-25	HIS	-	expression tag	UNP P03725
A	-24	GLY	-	expression tag	UNP P03725
A	-23	MET	-	expression tag	UNP P03725
A	-22	ALA	-	expression tag	UNP P03725
A	-21	SER	-	expression tag	UNP P03725
A	-20	MET	-	expression tag	UNP P03725
A	-19	THR	-	expression tag	UNP P03725
A	-18	GLY	-	expression tag	UNP P03725
A	-17	GLY	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	GLN	-	expression tag	UNP P03725
A	-15	GLN	-	expression tag	UNP P03725
A	-14	MET	-	expression tag	UNP P03725
A	-13	GLY	-	expression tag	UNP P03725
A	-12	ARG	-	expression tag	UNP P03725
A	-11	ASP	-	expression tag	UNP P03725
A	-10	LEU	-	expression tag	UNP P03725
A	-9	TYR	-	expression tag	UNP P03725
A	-8	ASP	-	expression tag	UNP P03725
A	-7	ASP	-	expression tag	UNP P03725
A	-6	ASP	-	expression tag	UNP P03725
A	-5	ASP	-	expression tag	UNP P03725
A	-4	LYS	-	expression tag	UNP P03725
A	-3	ASP	-	expression tag	UNP P03725
A	-2	PRO	-	expression tag	UNP P03725
A	-1	SER	-	expression tag	UNP P03725
A	0	SER	-	expression tag	UNP P03725
B	-34	MET	-	initiating methionine	UNP P03725
B	-33	ARG	-	expression tag	UNP P03725
B	-32	GLY	-	expression tag	UNP P03725
B	-31	SER	-	expression tag	UNP P03725
B	-30	HIS	-	expression tag	UNP P03725
B	-29	HIS	-	expression tag	UNP P03725
B	-28	HIS	-	expression tag	UNP P03725
B	-27	HIS	-	expression tag	UNP P03725
B	-26	HIS	-	expression tag	UNP P03725
B	-25	HIS	-	expression tag	UNP P03725
B	-24	GLY	-	expression tag	UNP P03725
B	-23	MET	-	expression tag	UNP P03725
B	-22	ALA	-	expression tag	UNP P03725
B	-21	SER	-	expression tag	UNP P03725
B	-20	MET	-	expression tag	UNP P03725
B	-19	THR	-	expression tag	UNP P03725
B	-18	GLY	-	expression tag	UNP P03725
B	-17	GLY	-	expression tag	UNP P03725
B	-16	GLN	-	expression tag	UNP P03725
B	-15	GLN	-	expression tag	UNP P03725
B	-14	MET	-	expression tag	UNP P03725
B	-13	GLY	-	expression tag	UNP P03725
B	-12	ARG	-	expression tag	UNP P03725
B	-11	ASP	-	expression tag	UNP P03725
B	-10	LEU	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	TYR	-	expression tag	UNP P03725
B	-8	ASP	-	expression tag	UNP P03725
B	-7	ASP	-	expression tag	UNP P03725
B	-6	ASP	-	expression tag	UNP P03725
B	-5	ASP	-	expression tag	UNP P03725
B	-4	LYS	-	expression tag	UNP P03725
B	-3	ASP	-	expression tag	UNP P03725
B	-2	PRO	-	expression tag	UNP P03725
B	-1	SER	-	expression tag	UNP P03725
B	0	SER	-	expression tag	UNP P03725
C	-34	MET	-	initiating methionine	UNP P03725
C	-33	ARG	-	expression tag	UNP P03725
C	-32	GLY	-	expression tag	UNP P03725
C	-31	SER	-	expression tag	UNP P03725
C	-30	HIS	-	expression tag	UNP P03725
C	-29	HIS	-	expression tag	UNP P03725
C	-28	HIS	-	expression tag	UNP P03725
C	-27	HIS	-	expression tag	UNP P03725
C	-26	HIS	-	expression tag	UNP P03725
C	-25	HIS	-	expression tag	UNP P03725
C	-24	GLY	-	expression tag	UNP P03725
C	-23	MET	-	expression tag	UNP P03725
C	-22	ALA	-	expression tag	UNP P03725
C	-21	SER	-	expression tag	UNP P03725
C	-20	MET	-	expression tag	UNP P03725
C	-19	THR	-	expression tag	UNP P03725
C	-18	GLY	-	expression tag	UNP P03725
C	-17	GLY	-	expression tag	UNP P03725
C	-16	GLN	-	expression tag	UNP P03725
C	-15	GLN	-	expression tag	UNP P03725
C	-14	MET	-	expression tag	UNP P03725
C	-13	GLY	-	expression tag	UNP P03725
C	-12	ARG	-	expression tag	UNP P03725
C	-11	ASP	-	expression tag	UNP P03725
C	-10	LEU	-	expression tag	UNP P03725
C	-9	TYR	-	expression tag	UNP P03725
C	-8	ASP	-	expression tag	UNP P03725
C	-7	ASP	-	expression tag	UNP P03725
C	-6	ASP	-	expression tag	UNP P03725
C	-5	ASP	-	expression tag	UNP P03725
C	-4	LYS	-	expression tag	UNP P03725
C	-3	ASP	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	PRO	-	expression tag	UNP P03725
C	-1	SER	-	expression tag	UNP P03725
C	0	SER	-	expression tag	UNP P03725
D	-34	MET	-	initiating methionine	UNP P03725
D	-33	ARG	-	expression tag	UNP P03725
D	-32	GLY	-	expression tag	UNP P03725
D	-31	SER	-	expression tag	UNP P03725
D	-30	HIS	-	expression tag	UNP P03725
D	-29	HIS	-	expression tag	UNP P03725
D	-28	HIS	-	expression tag	UNP P03725
D	-27	HIS	-	expression tag	UNP P03725
D	-26	HIS	-	expression tag	UNP P03725
D	-25	HIS	-	expression tag	UNP P03725
D	-24	GLY	-	expression tag	UNP P03725
D	-23	MET	-	expression tag	UNP P03725
D	-22	ALA	-	expression tag	UNP P03725
D	-21	SER	-	expression tag	UNP P03725
D	-20	MET	-	expression tag	UNP P03725
D	-19	THR	-	expression tag	UNP P03725
D	-18	GLY	-	expression tag	UNP P03725
D	-17	GLY	-	expression tag	UNP P03725
D	-16	GLN	-	expression tag	UNP P03725
D	-15	GLN	-	expression tag	UNP P03725
D	-14	MET	-	expression tag	UNP P03725
D	-13	GLY	-	expression tag	UNP P03725
D	-12	ARG	-	expression tag	UNP P03725
D	-11	ASP	-	expression tag	UNP P03725
D	-10	LEU	-	expression tag	UNP P03725
D	-9	TYR	-	expression tag	UNP P03725
D	-8	ASP	-	expression tag	UNP P03725
D	-7	ASP	-	expression tag	UNP P03725
D	-6	ASP	-	expression tag	UNP P03725
D	-5	ASP	-	expression tag	UNP P03725
D	-4	LYS	-	expression tag	UNP P03725
D	-3	ASP	-	expression tag	UNP P03725
D	-2	PRO	-	expression tag	UNP P03725
D	-1	SER	-	expression tag	UNP P03725
D	0	SER	-	expression tag	UNP P03725
E	-34	MET	-	initiating methionine	UNP P03725
E	-33	ARG	-	expression tag	UNP P03725
E	-32	GLY	-	expression tag	UNP P03725
E	-31	SER	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-30	HIS	-	expression tag	UNP P03725
E	-29	HIS	-	expression tag	UNP P03725
E	-28	HIS	-	expression tag	UNP P03725
E	-27	HIS	-	expression tag	UNP P03725
E	-26	HIS	-	expression tag	UNP P03725
E	-25	HIS	-	expression tag	UNP P03725
E	-24	GLY	-	expression tag	UNP P03725
E	-23	MET	-	expression tag	UNP P03725
E	-22	ALA	-	expression tag	UNP P03725
E	-21	SER	-	expression tag	UNP P03725
E	-20	MET	-	expression tag	UNP P03725
E	-19	THR	-	expression tag	UNP P03725
E	-18	GLY	-	expression tag	UNP P03725
E	-17	GLY	-	expression tag	UNP P03725
E	-16	GLN	-	expression tag	UNP P03725
E	-15	GLN	-	expression tag	UNP P03725
E	-14	MET	-	expression tag	UNP P03725
E	-13	GLY	-	expression tag	UNP P03725
E	-12	ARG	-	expression tag	UNP P03725
E	-11	ASP	-	expression tag	UNP P03725
E	-10	LEU	-	expression tag	UNP P03725
E	-9	TYR	-	expression tag	UNP P03725
E	-8	ASP	-	expression tag	UNP P03725
E	-7	ASP	-	expression tag	UNP P03725
E	-6	ASP	-	expression tag	UNP P03725
E	-5	ASP	-	expression tag	UNP P03725
E	-4	LYS	-	expression tag	UNP P03725
E	-3	ASP	-	expression tag	UNP P03725
E	-2	PRO	-	expression tag	UNP P03725
E	-1	SER	-	expression tag	UNP P03725
E	0	SER	-	expression tag	UNP P03725
F	-34	MET	-	initiating methionine	UNP P03725
F	-33	ARG	-	expression tag	UNP P03725
F	-32	GLY	-	expression tag	UNP P03725
F	-31	SER	-	expression tag	UNP P03725
F	-30	HIS	-	expression tag	UNP P03725
F	-29	HIS	-	expression tag	UNP P03725
F	-28	HIS	-	expression tag	UNP P03725
F	-27	HIS	-	expression tag	UNP P03725
F	-26	HIS	-	expression tag	UNP P03725
F	-25	HIS	-	expression tag	UNP P03725
F	-24	GLY	-	expression tag	UNP P03725

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-23	MET	-	expression tag	UNP P03725
F	-22	ALA	-	expression tag	UNP P03725
F	-21	SER	-	expression tag	UNP P03725
F	-20	MET	-	expression tag	UNP P03725
F	-19	THR	-	expression tag	UNP P03725
F	-18	GLY	-	expression tag	UNP P03725
F	-17	GLY	-	expression tag	UNP P03725
F	-16	GLN	-	expression tag	UNP P03725
F	-15	GLN	-	expression tag	UNP P03725
F	-14	MET	-	expression tag	UNP P03725
F	-13	GLY	-	expression tag	UNP P03725
F	-12	ARG	-	expression tag	UNP P03725
F	-11	ASP	-	expression tag	UNP P03725
F	-10	LEU	-	expression tag	UNP P03725
F	-9	TYR	-	expression tag	UNP P03725
F	-8	ASP	-	expression tag	UNP P03725
F	-7	ASP	-	expression tag	UNP P03725
F	-6	ASP	-	expression tag	UNP P03725
F	-5	ASP	-	expression tag	UNP P03725
F	-4	LYS	-	expression tag	UNP P03725
F	-3	ASP	-	expression tag	UNP P03725
F	-2	PRO	-	expression tag	UNP P03725
F	-1	SER	-	expression tag	UNP P03725
F	0	SER	-	expression tag	UNP P03725

- Molecule 2 is a protein called Peptidoglycan transglycosylase gp16.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	198	Total	C	N	O	S	0	0
			1397	868	246	281	2		
2	H	198	Total	C	N	O	S	0	0
			1397	868	246	281	2		
2	I	198	Total	C	N	O	S	0	0
			1397	868	246	281	2		
2	J	198	Total	C	N	O	S	0	0
			1397	868	246	281	2		
2	K	198	Total	C	N	O	S	0	0
			1397	868	246	281	2		
2	L	198	Total	C	N	O	S	0	0
			1397	868	246	281	2		

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-21	MET	-	initiating methionine	UNP P03726
G	-20	GLY	-	expression tag	UNP P03726
G	-19	HIS	-	expression tag	UNP P03726
G	-18	HIS	-	expression tag	UNP P03726
G	-17	HIS	-	expression tag	UNP P03726
G	-16	HIS	-	expression tag	UNP P03726
G	-15	HIS	-	expression tag	UNP P03726
G	-14	HIS	-	expression tag	UNP P03726
G	-13	HIS	-	expression tag	UNP P03726
G	-12	HIS	-	expression tag	UNP P03726
G	-11	HIS	-	expression tag	UNP P03726
G	-10	HIS	-	expression tag	UNP P03726
G	-9	SER	-	expression tag	UNP P03726
G	-8	SER	-	expression tag	UNP P03726
G	-7	GLY	-	expression tag	UNP P03726
G	-6	HIS	-	expression tag	UNP P03726
G	-5	ILE	-	expression tag	UNP P03726
G	-4	GLU	-	expression tag	UNP P03726
G	-3	GLY	-	expression tag	UNP P03726
G	-2	ARG	-	expression tag	UNP P03726
G	-1	HIS	-	expression tag	UNP P03726
G	0	MET	-	expression tag	UNP P03726
H	-21	MET	-	initiating methionine	UNP P03726
H	-20	GLY	-	expression tag	UNP P03726
H	-19	HIS	-	expression tag	UNP P03726
H	-18	HIS	-	expression tag	UNP P03726
H	-17	HIS	-	expression tag	UNP P03726
H	-16	HIS	-	expression tag	UNP P03726
H	-15	HIS	-	expression tag	UNP P03726
H	-14	HIS	-	expression tag	UNP P03726
H	-13	HIS	-	expression tag	UNP P03726
H	-12	HIS	-	expression tag	UNP P03726
H	-11	HIS	-	expression tag	UNP P03726
H	-10	HIS	-	expression tag	UNP P03726
H	-9	SER	-	expression tag	UNP P03726
H	-8	SER	-	expression tag	UNP P03726
H	-7	GLY	-	expression tag	UNP P03726
H	-6	HIS	-	expression tag	UNP P03726
H	-5	ILE	-	expression tag	UNP P03726
H	-4	GLU	-	expression tag	UNP P03726
H	-3	GLY	-	expression tag	UNP P03726
H	-2	ARG	-	expression tag	UNP P03726
H	-1	HIS	-	expression tag	UNP P03726

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Chain	Residue	Modelled	Actual	Comment	Reference
H	0	MET	-	expression tag	UNP P03726
I	-21	MET	-	initiating methionine	UNP P03726
I	-20	GLY	-	expression tag	UNP P03726
I	-19	HIS	-	expression tag	UNP P03726
I	-18	HIS	-	expression tag	UNP P03726
I	-17	HIS	-	expression tag	UNP P03726
I	-16	HIS	-	expression tag	UNP P03726
I	-15	HIS	-	expression tag	UNP P03726
I	-14	HIS	-	expression tag	UNP P03726
I	-13	HIS	-	expression tag	UNP P03726
I	-12	HIS	-	expression tag	UNP P03726
I	-11	HIS	-	expression tag	UNP P03726
I	-10	HIS	-	expression tag	UNP P03726
I	-9	SER	-	expression tag	UNP P03726
I	-8	SER	-	expression tag	UNP P03726
I	-7	GLY	-	expression tag	UNP P03726
I	-6	HIS	-	expression tag	UNP P03726
I	-5	ILE	-	expression tag	UNP P03726
I	-4	GLU	-	expression tag	UNP P03726
I	-3	GLY	-	expression tag	UNP P03726
I	-2	ARG	-	expression tag	UNP P03726
I	-1	HIS	-	expression tag	UNP P03726
I	0	MET	-	expression tag	UNP P03726
J	-21	MET	-	initiating methionine	UNP P03726
J	-20	GLY	-	expression tag	UNP P03726
J	-19	HIS	-	expression tag	UNP P03726
J	-18	HIS	-	expression tag	UNP P03726
J	-17	HIS	-	expression tag	UNP P03726
J	-16	HIS	-	expression tag	UNP P03726
J	-15	HIS	-	expression tag	UNP P03726
J	-14	HIS	-	expression tag	UNP P03726
J	-13	HIS	-	expression tag	UNP P03726
J	-12	HIS	-	expression tag	UNP P03726
J	-11	HIS	-	expression tag	UNP P03726
J	-10	HIS	-	expression tag	UNP P03726
J	-9	SER	-	expression tag	UNP P03726
J	-8	SER	-	expression tag	UNP P03726
J	-7	GLY	-	expression tag	UNP P03726
J	-6	HIS	-	expression tag	UNP P03726
J	-5	ILE	-	expression tag	UNP P03726
J	-4	GLU	-	expression tag	UNP P03726
J	-3	GLY	-	expression tag	UNP P03726

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-2	ARG	-	expression tag	UNP P03726
J	-1	HIS	-	expression tag	UNP P03726
J	0	MET	-	expression tag	UNP P03726
K	-21	MET	-	initiating methionine	UNP P03726
K	-20	GLY	-	expression tag	UNP P03726
K	-19	HIS	-	expression tag	UNP P03726
K	-18	HIS	-	expression tag	UNP P03726
K	-17	HIS	-	expression tag	UNP P03726
K	-16	HIS	-	expression tag	UNP P03726
K	-15	HIS	-	expression tag	UNP P03726
K	-14	HIS	-	expression tag	UNP P03726
K	-13	HIS	-	expression tag	UNP P03726
K	-12	HIS	-	expression tag	UNP P03726
K	-11	HIS	-	expression tag	UNP P03726
K	-10	HIS	-	expression tag	UNP P03726
K	-9	SER	-	expression tag	UNP P03726
K	-8	SER	-	expression tag	UNP P03726
K	-7	GLY	-	expression tag	UNP P03726
K	-6	HIS	-	expression tag	UNP P03726
K	-5	ILE	-	expression tag	UNP P03726
K	-4	GLU	-	expression tag	UNP P03726
K	-3	GLY	-	expression tag	UNP P03726
K	-2	ARG	-	expression tag	UNP P03726
K	-1	HIS	-	expression tag	UNP P03726
K	0	MET	-	expression tag	UNP P03726
L	-21	MET	-	initiating methionine	UNP P03726
L	-20	GLY	-	expression tag	UNP P03726
L	-19	HIS	-	expression tag	UNP P03726
L	-18	HIS	-	expression tag	UNP P03726
L	-17	HIS	-	expression tag	UNP P03726
L	-16	HIS	-	expression tag	UNP P03726
L	-15	HIS	-	expression tag	UNP P03726
L	-14	HIS	-	expression tag	UNP P03726
L	-13	HIS	-	expression tag	UNP P03726
L	-12	HIS	-	expression tag	UNP P03726
L	-11	HIS	-	expression tag	UNP P03726
L	-10	HIS	-	expression tag	UNP P03726
L	-9	SER	-	expression tag	UNP P03726
L	-8	SER	-	expression tag	UNP P03726
L	-7	GLY	-	expression tag	UNP P03726
L	-6	HIS	-	expression tag	UNP P03726
L	-5	ILE	-	expression tag	UNP P03726

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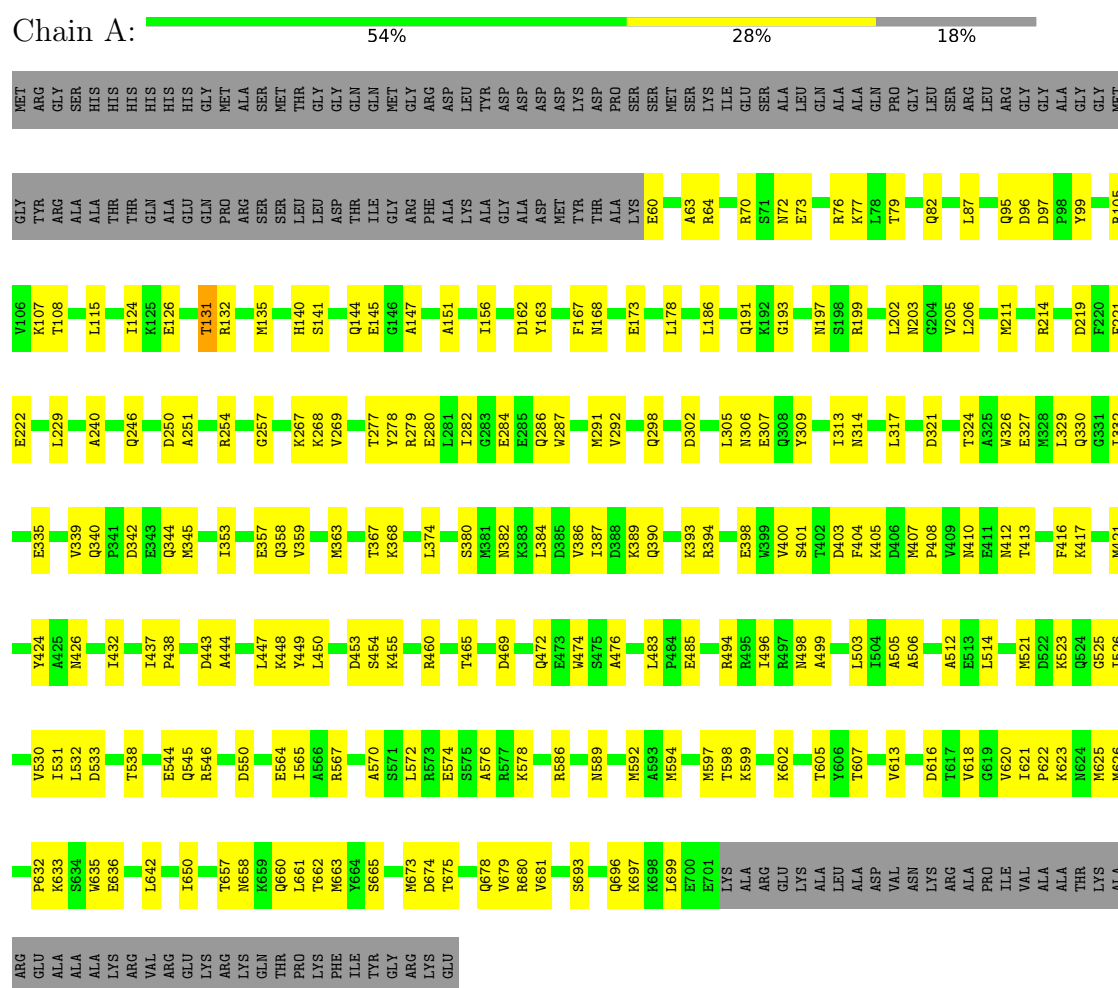
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
L	-4	GLU	-	expression tag	UNP P03726
L	-3	GLY	-	expression tag	UNP P03726
L	-2	ARG	-	expression tag	UNP P03726
L	-1	HIS	-	expression tag	UNP P03726
L	0	MET	-	expression tag	UNP P03726

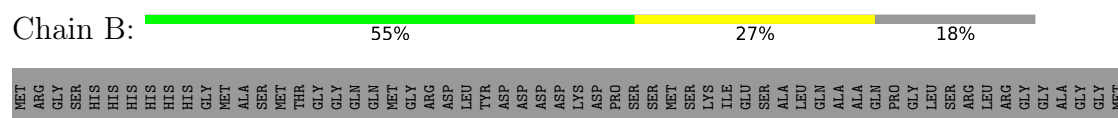
3 Residue-property plots

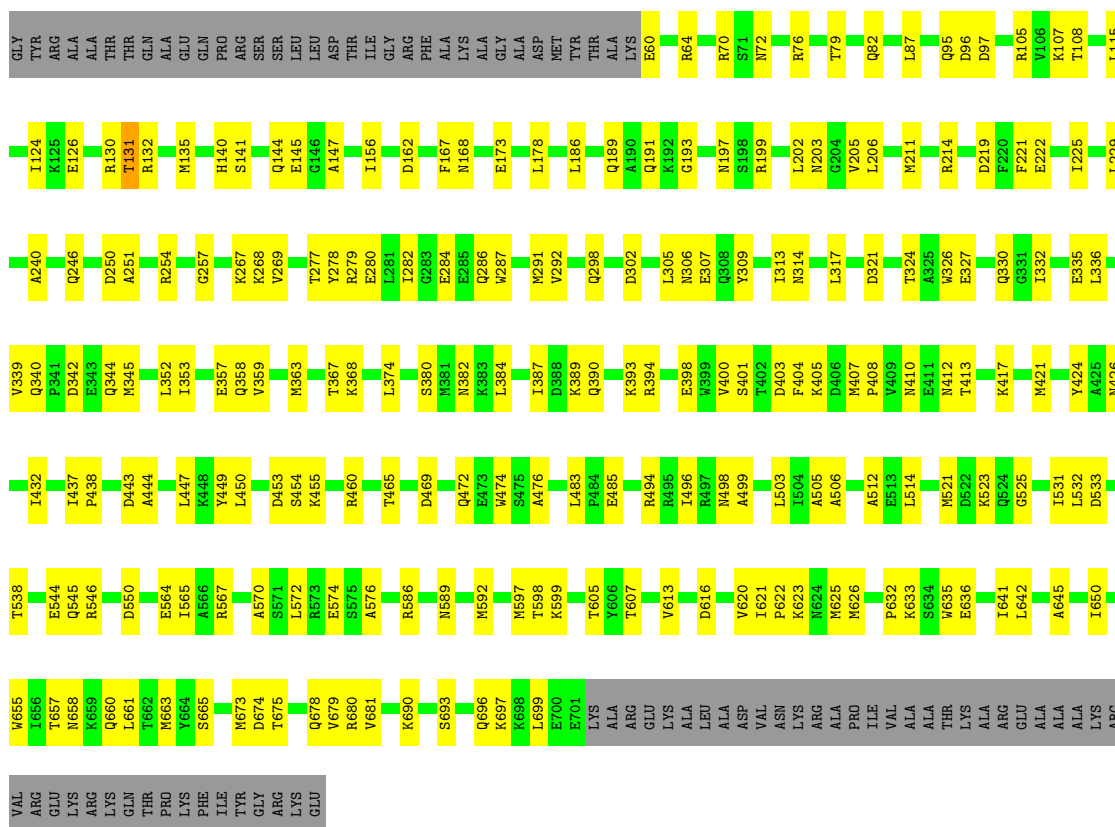
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Internal virion protein gp15



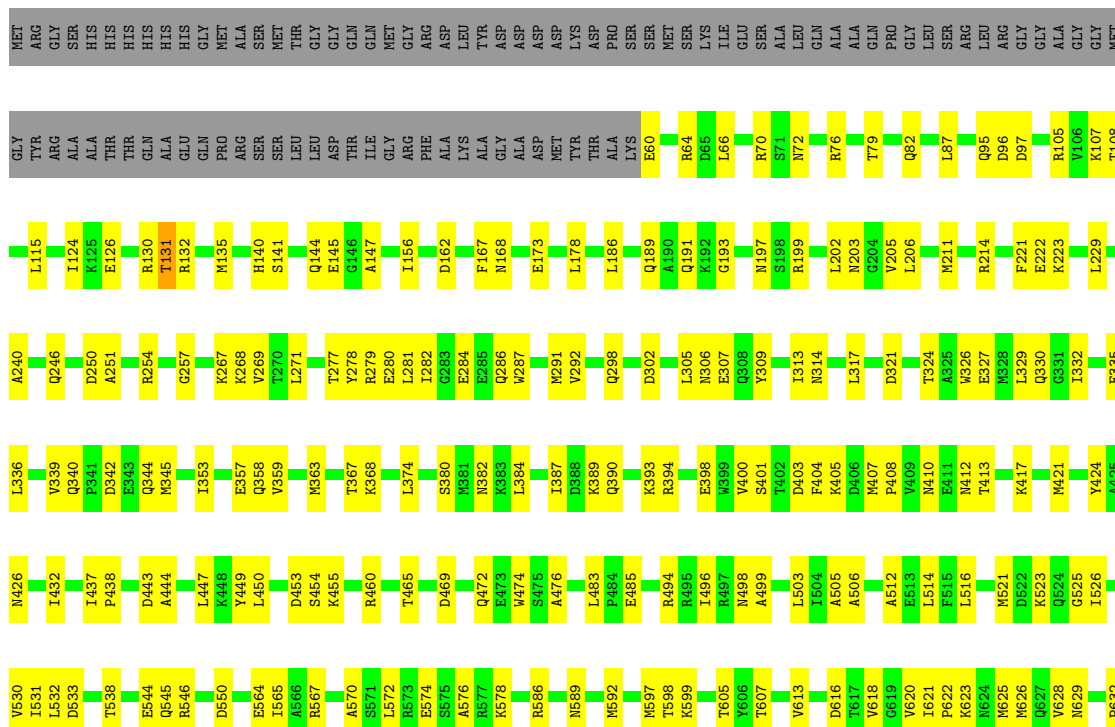
• Molecule 1: Internal virion protein gp15





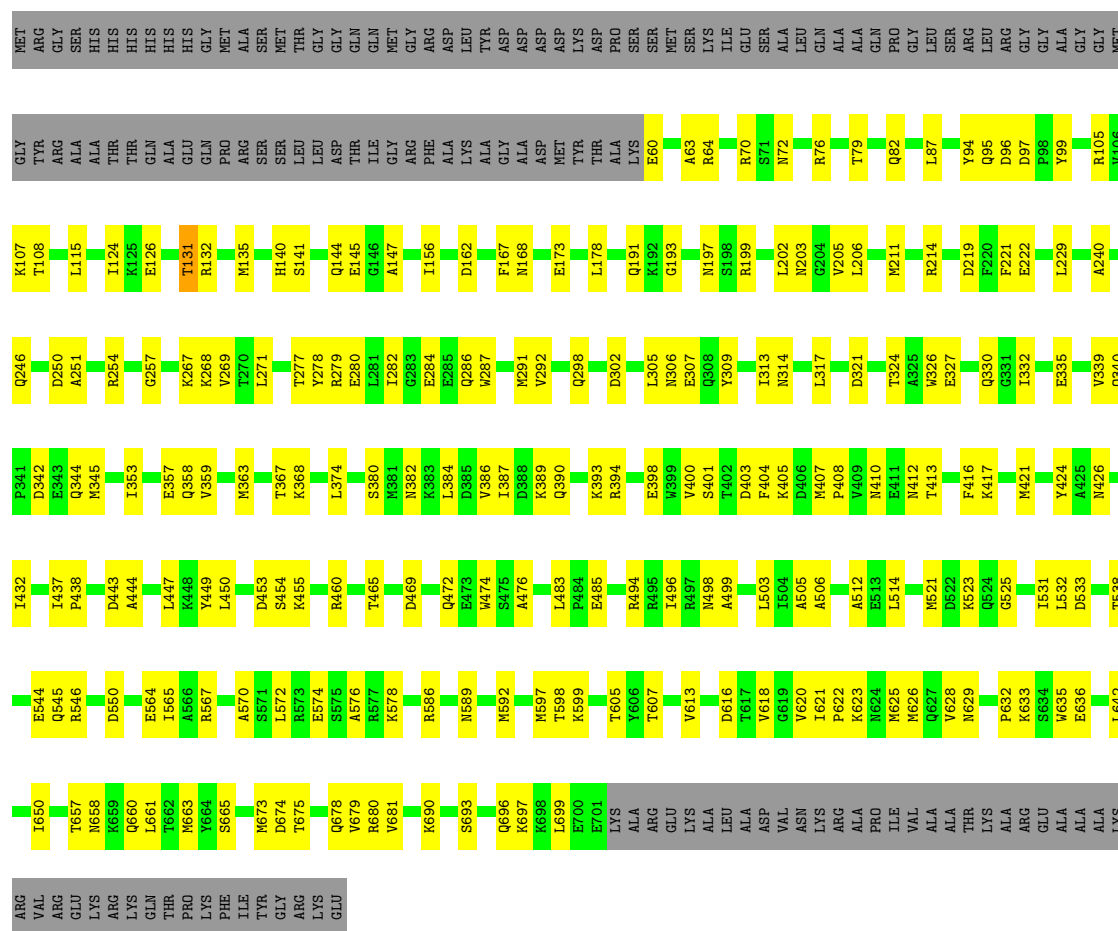
• Molecule 1: Internal virion protein gp15

Chain C:



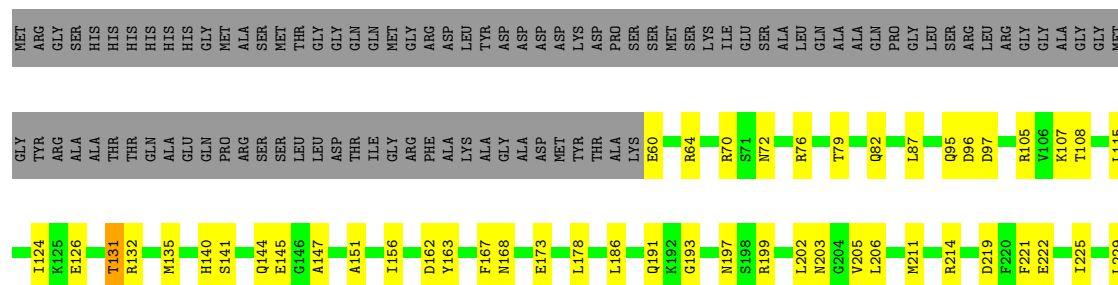
- Molecule 1: Internal virion protein gp15

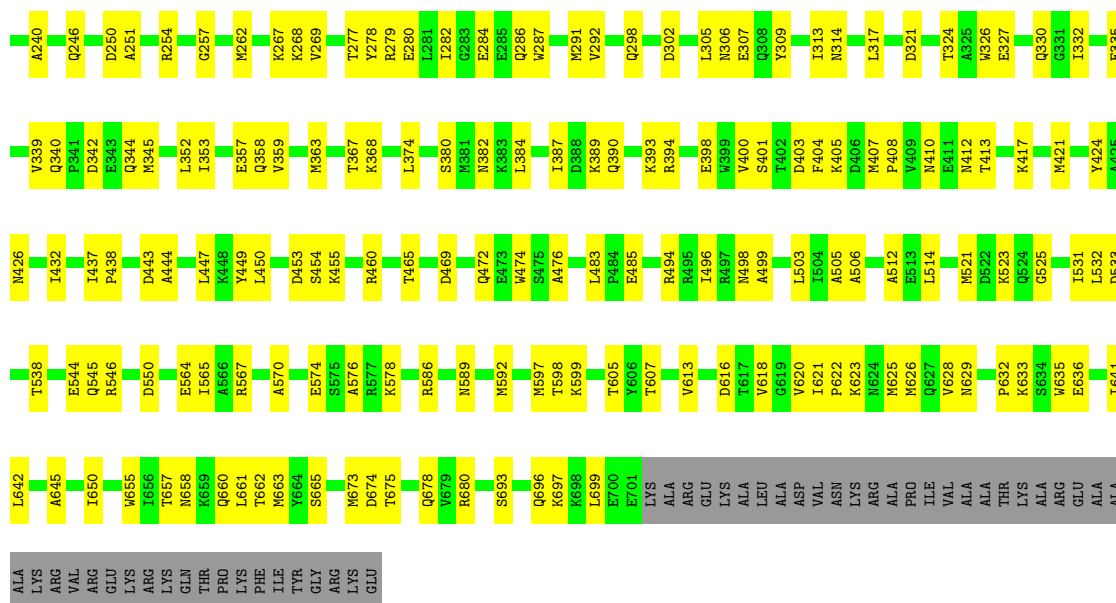
Chain D: 55% 27% 18%



- Molecule 1: Internal virion protein gp15

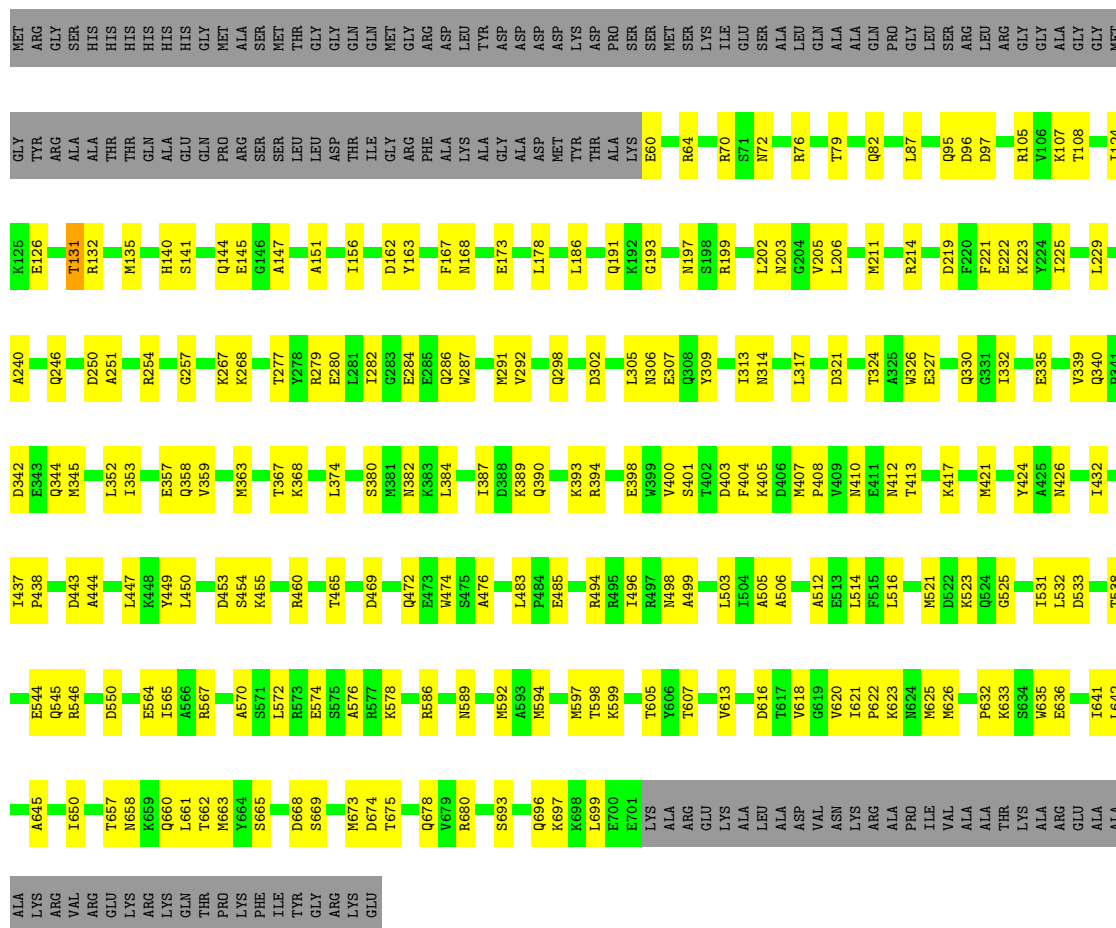
Chain E: 55% 27% 18%





• Molecule 1: Internal virion protein gp15

Chain F: 55% 27% 18%

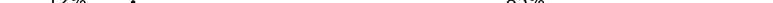


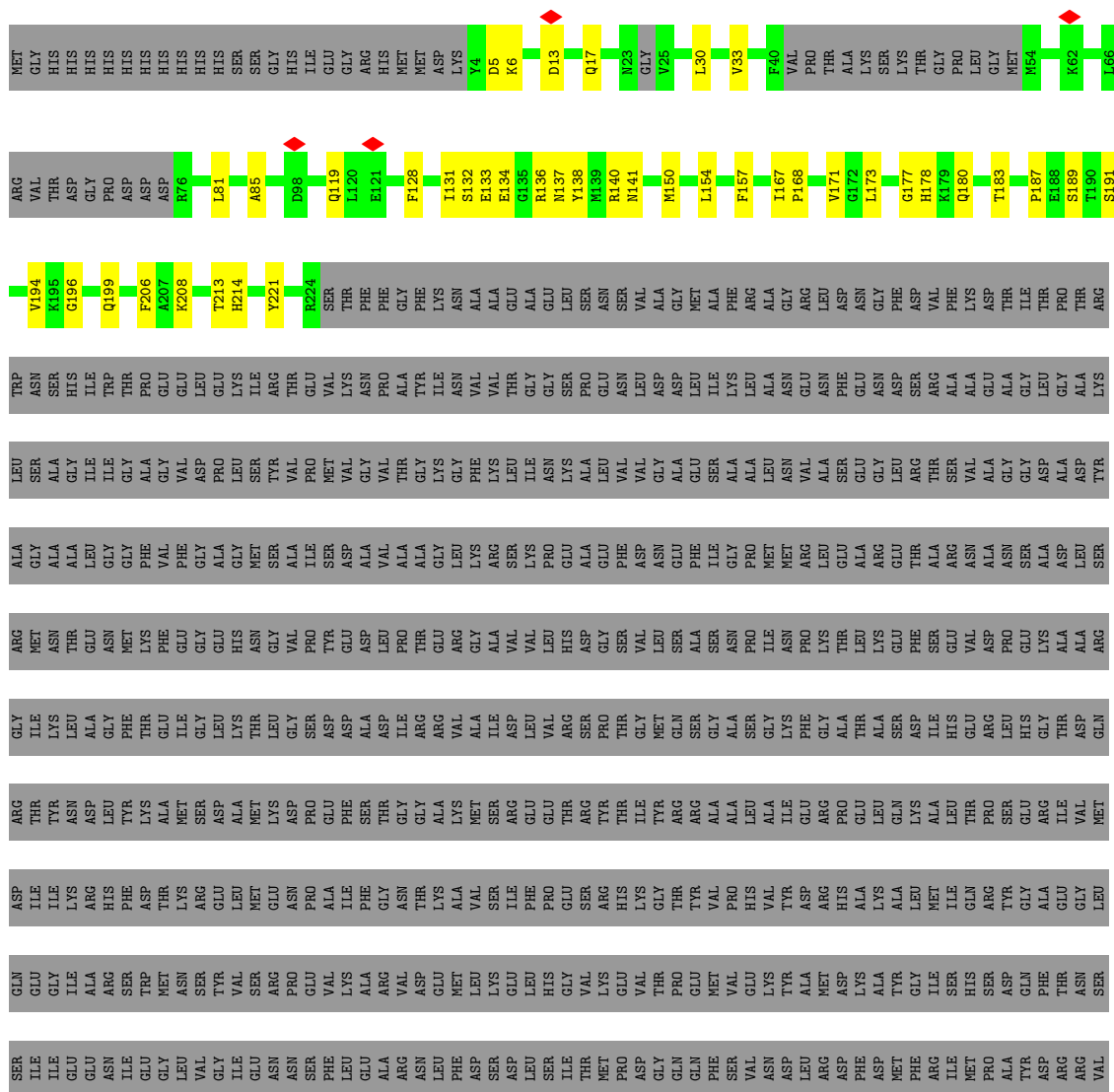
• Molecule 2: Peptidoglycan transglycosylase gp16

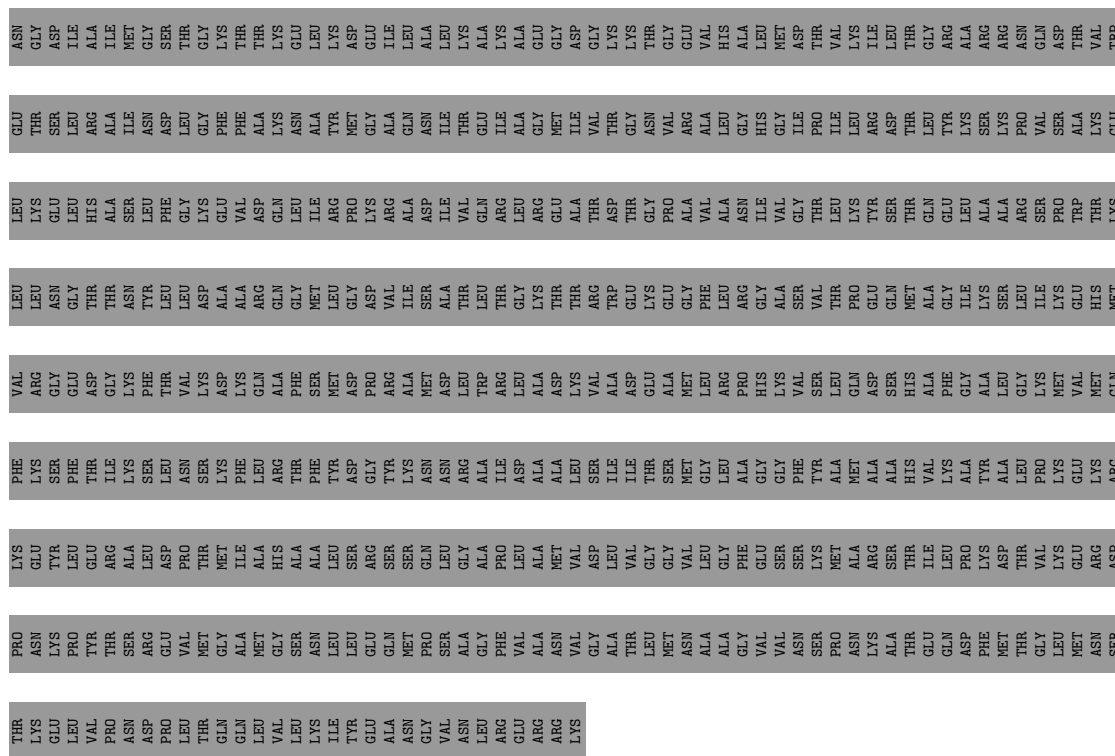
[illegible]

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

- Molecule 2: Peptidoglycan transglycosylase gp16

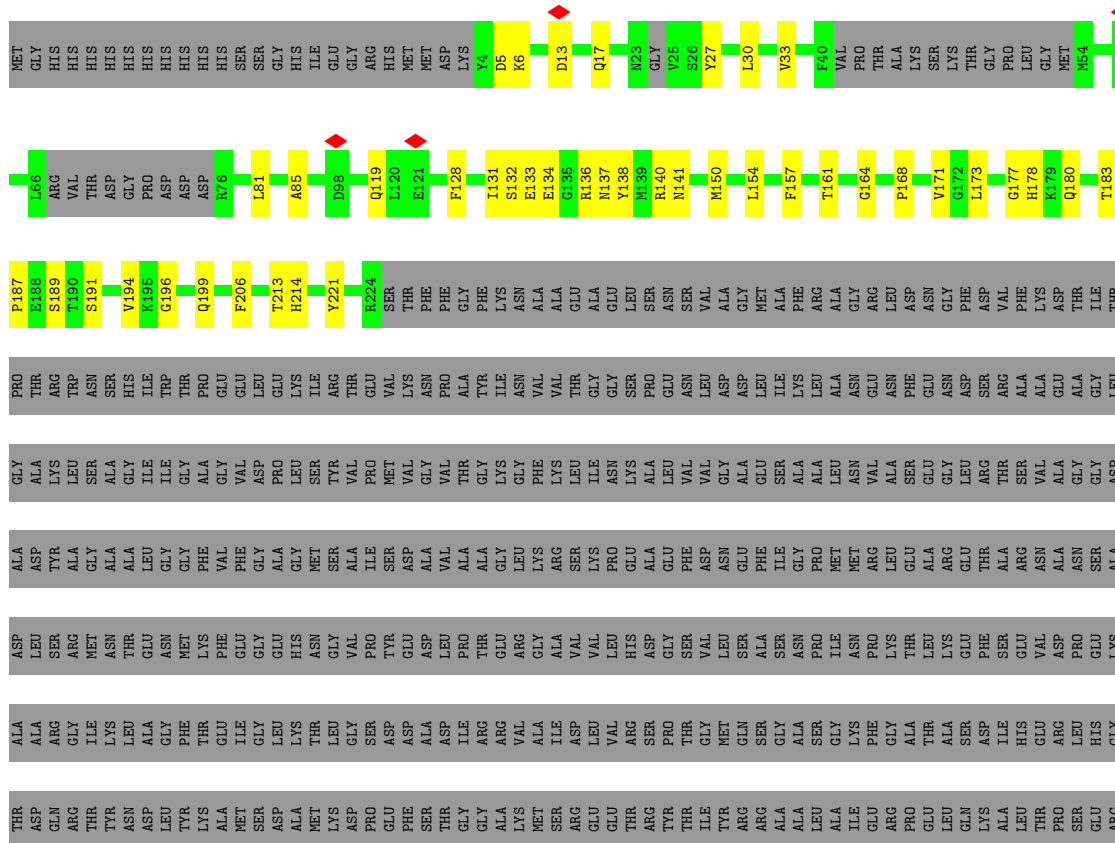
Chain I:  12% . 85%





- Molecule 2: Peptidoglycan transglycosylase gp16

Chain J: 12% 1% 85%







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C6	Depositor
Number of particles used	72882	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	47619	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.151	Depositor
Minimum map value	-0.012	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.006	Depositor
Map size (Å)	335.04, 335.04, 335.04	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.047, 1.047, 1.047	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	0.43	0/5194	0.44	0/6996
1	B	0.43	0/5194	0.44	0/6996
1	C	0.43	0/5194	0.44	0/6996
1	D	0.43	0/5194	0.44	0/6996
1	E	0.43	0/5194	0.44	0/6996
1	F	0.43	0/5194	0.44	0/6996
2	G	0.27	0/1419	0.37	0/1920
2	H	0.27	0/1419	0.37	0/1920
2	I	0.27	0/1419	0.37	0/1920
2	J	0.27	0/1419	0.37	0/1920
2	K	0.27	0/1419	0.37	0/1920
2	L	0.27	0/1419	0.37	0/1920
All	All	0.40	0/39678	0.43	0/53496

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 [i](#)

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	5116	0	4998	179	0
1	B	5116	0	4998	172	0
1	C	5116	0	4998	180	0
1	D	5116	0	4998	174	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	5116	0	4998	177	0
1	F	5116	0	4998	175	0
2	G	1397	0	1242	42	0
2	H	1397	0	1242	44	0
2	I	1397	0	1242	46	0
2	J	1397	0	1242	47	0
2	K	1397	0	1242	47	0
2	L	1397	0	1242	46	0
All	All	39078	0	37440	1066	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

The worst 5 of 1066 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:E:314:ASN:HD22	1:F:357:GLU:HB2	1.09	1.13
1:B:314:ASN:HD22	1:C:357:GLU:HB2	1.09	1.12
1:C:314:ASN:HD22	1:D:357:GLU:HB2	1.09	1.12
1:A:357:GLU:HB2	1:F:314:ASN:HD22	1.09	1.09
1:A:314:ASN:HD22	1:B:357:GLU:HB2	1.08	1.09

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	A	640/782 (82%)	599 (94%)	41 (6%)	0	100	100
1	B	640/782 (82%)	598 (93%)	42 (7%)	0	100	100
1	C	640/782 (82%)	599 (94%)	41 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	640/782 (82%)	599 (94%)	41 (6%)	0	100	100
1	E	640/782 (82%)	599 (94%)	41 (6%)	0	100	100
1	F	640/782 (82%)	599 (94%)	41 (6%)	0	100	100
2	G	190/1340 (14%)	165 (87%)	25 (13%)	0	100	100
2	H	190/1340 (14%)	165 (87%)	25 (13%)	0	100	100
2	I	190/1340 (14%)	165 (87%)	25 (13%)	0	100	100
2	J	190/1340 (14%)	165 (87%)	25 (13%)	0	100	100
2	K	190/1340 (14%)	165 (87%)	25 (13%)	0	100	100
2	L	190/1340 (14%)	165 (87%)	25 (13%)	0	100	100
All	All	4980/12732 (39%)	4583 (92%)	397 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	548/653 (84%)	547 (100%)	1 (0%)	87	92
1	B	548/653 (84%)	547 (100%)	1 (0%)	87	92
1	C	548/653 (84%)	547 (100%)	1 (0%)	87	92
1	D	548/653 (84%)	547 (100%)	1 (0%)	87	92
1	E	548/653 (84%)	547 (100%)	1 (0%)	87	92
1	F	548/653 (84%)	547 (100%)	1 (0%)	87	92
2	G	120/1078 (11%)	120 (100%)	0	100	100
2	H	120/1078 (11%)	120 (100%)	0	100	100
2	I	120/1078 (11%)	120 (100%)	0	100	100
2	J	120/1078 (11%)	120 (100%)	0	100	100
2	K	120/1078 (11%)	120 (100%)	0	100	100
2	L	120/1078 (11%)	120 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	4008/10386 (39%)	4002 (100%)	6 (0%)	87 93

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	131	THR
1	E	131	THR
1	F	131	THR
1	B	131	THR
1	A	131	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 170 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	653	ASN
2	G	180	GLN
1	F	164	GLN
1	F	356	GLN
2	H	222	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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.

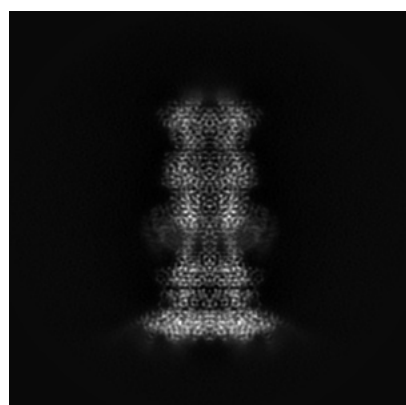
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10912. These allow visual inspection of the internal detail of the map and identification of artifacts.

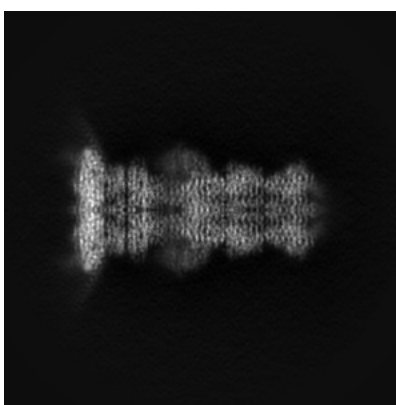
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

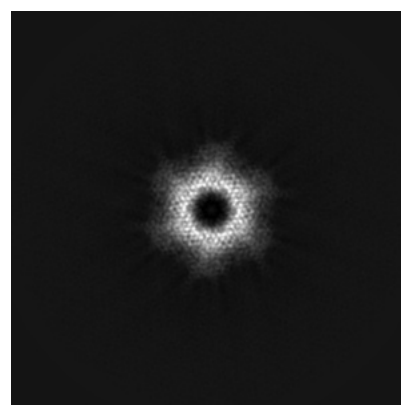
6.1.1 Primary map



X



Y

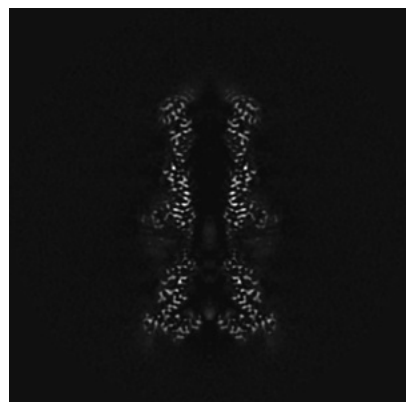


Z

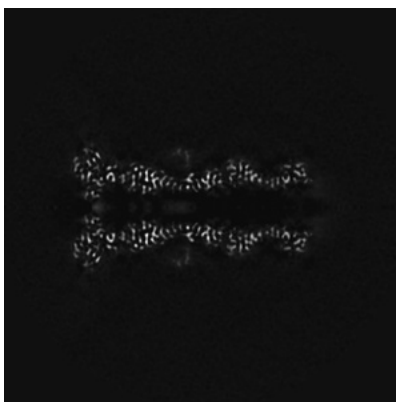
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

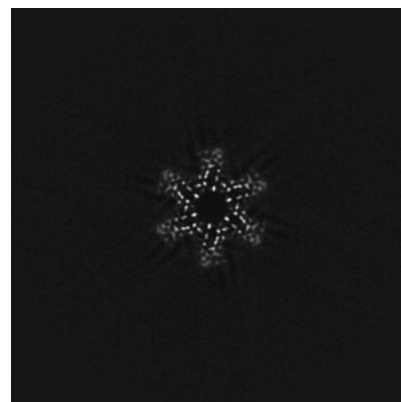
6.2.1 Primary map



X Index: 160



Y Index: 160

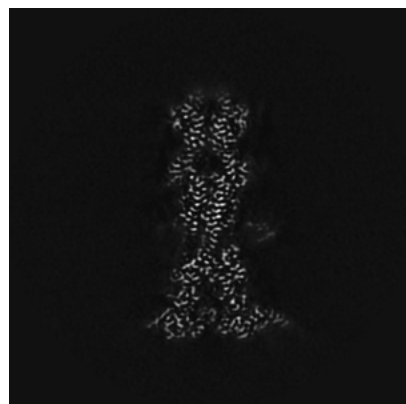


Z Index: 160

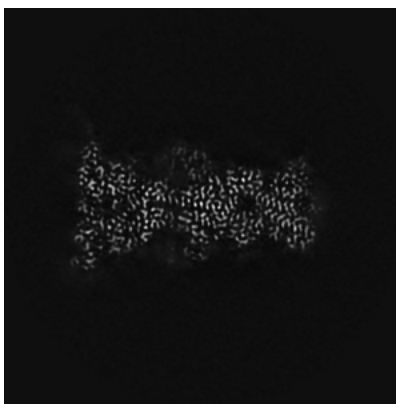
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

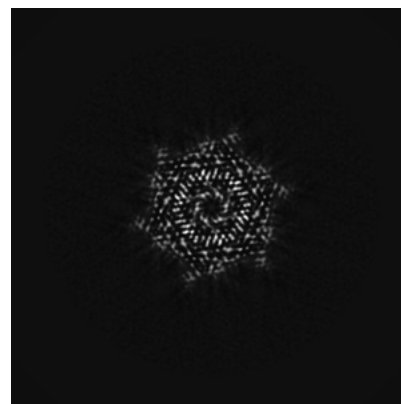
6.3.1 Primary map



X Index: 177



Y Index: 179

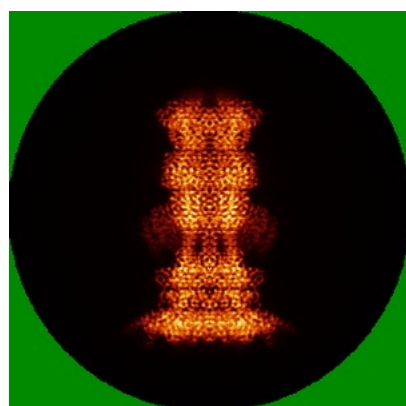


Z Index: 70

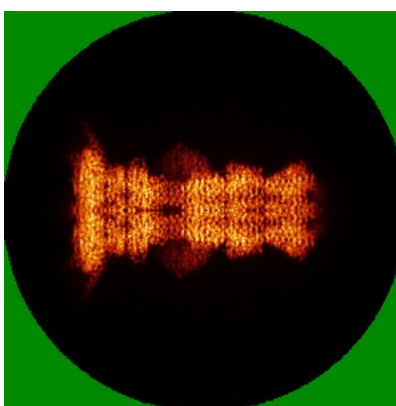
The images above show the largest variance slices of the map in three orthogonal directions.

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

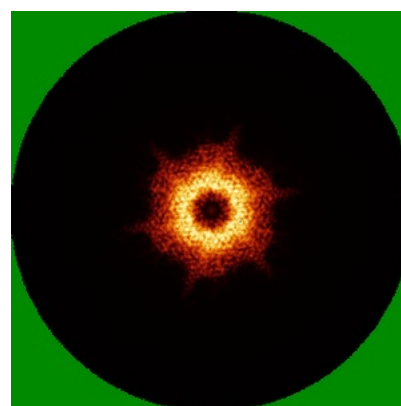
6.4.1 Primary map



X



Y

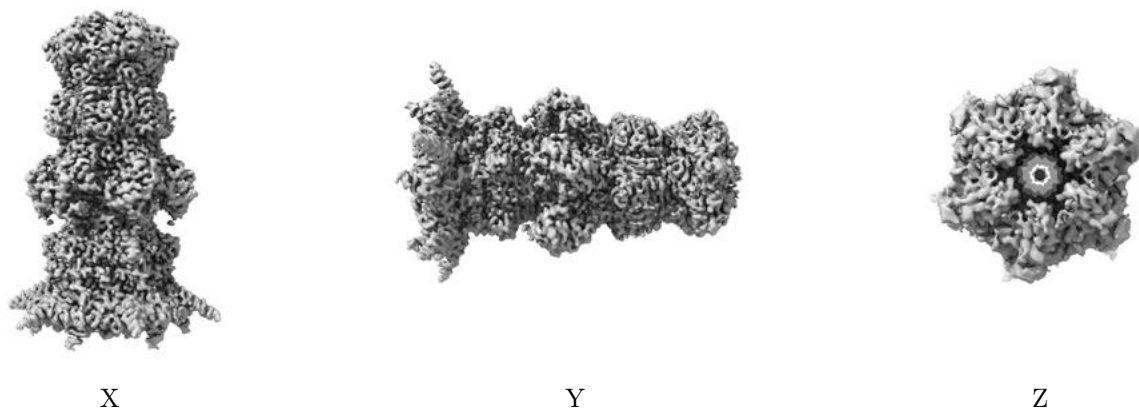


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.006. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

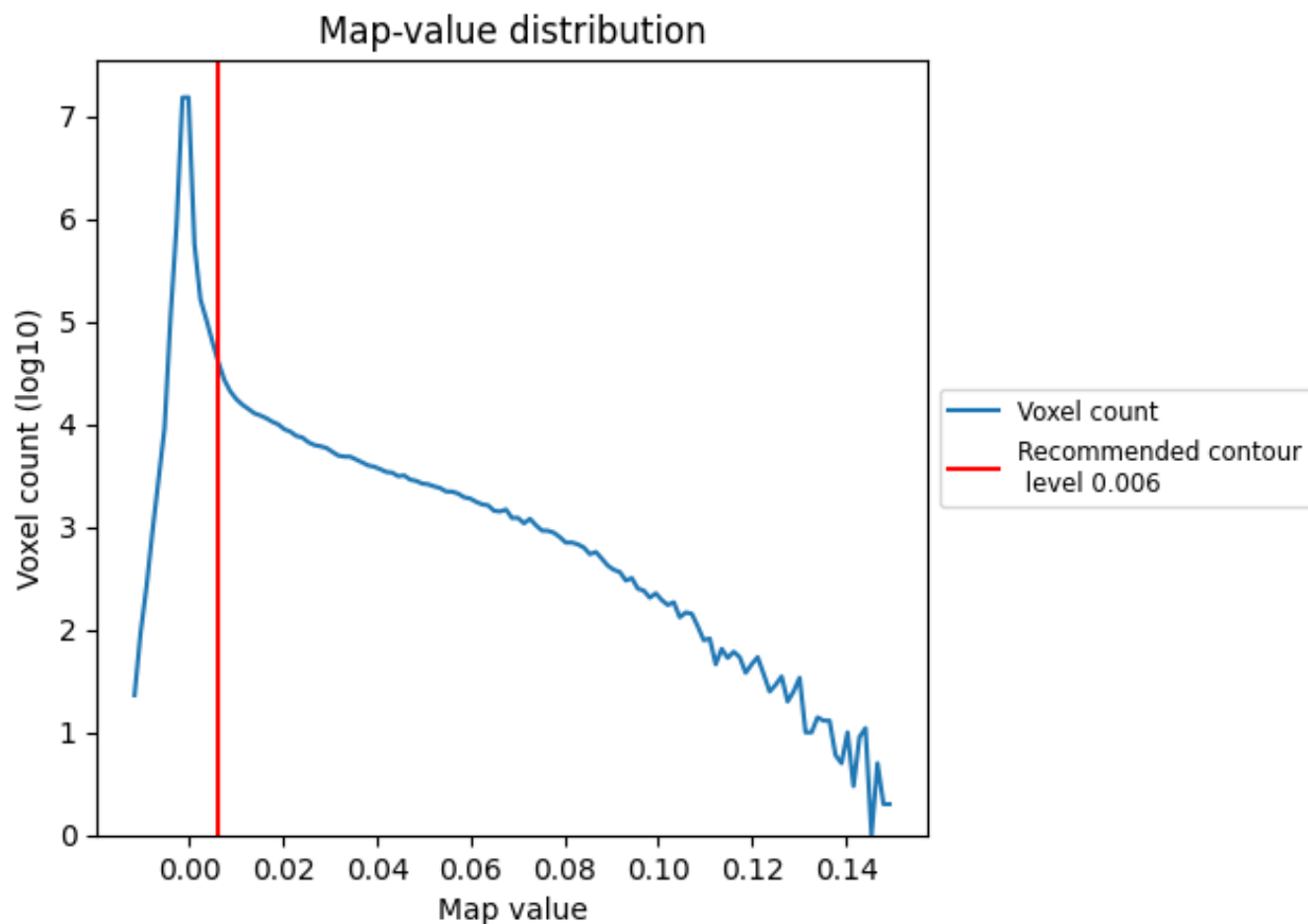
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

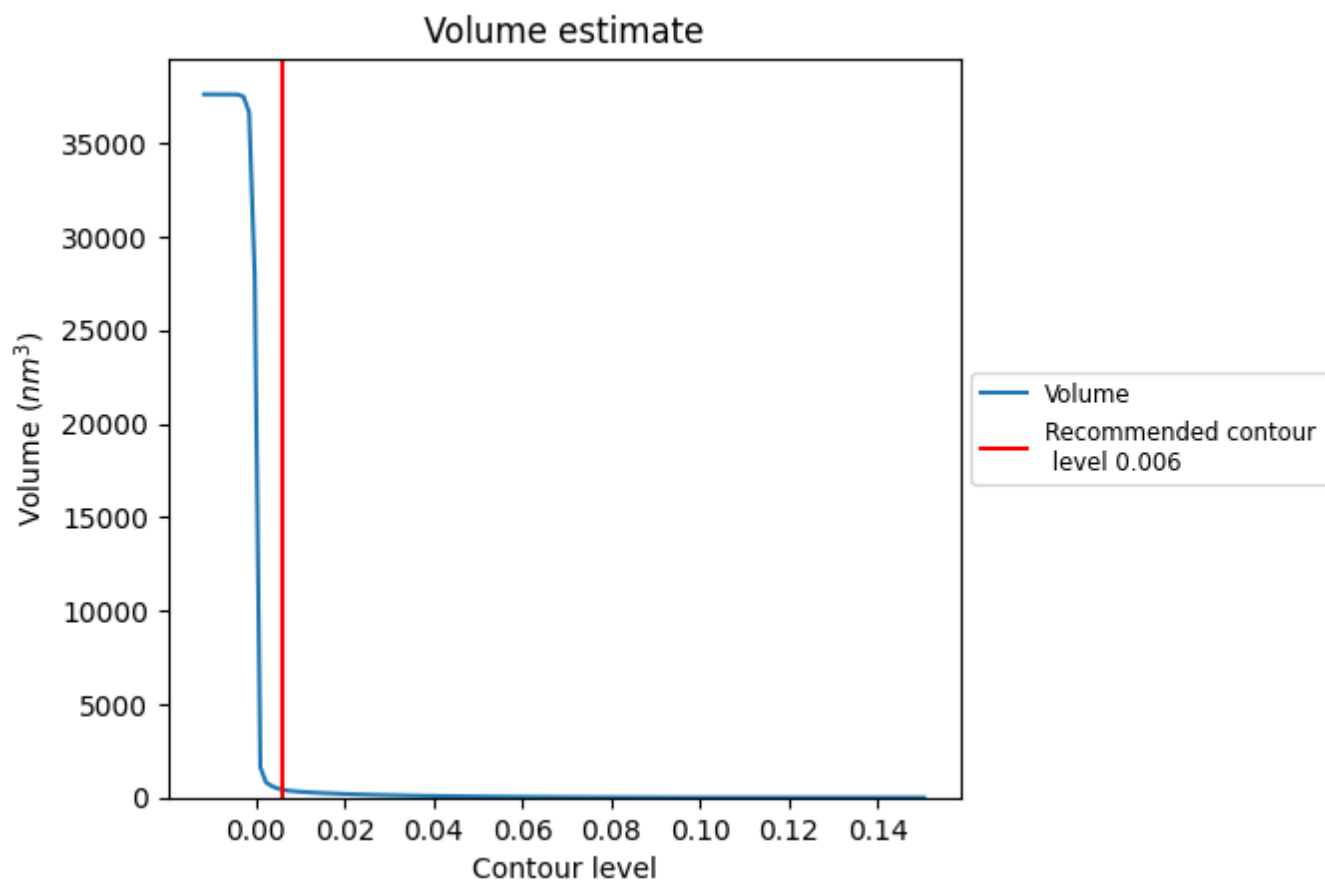
This section contains the results of statistical analysis of the map.

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.

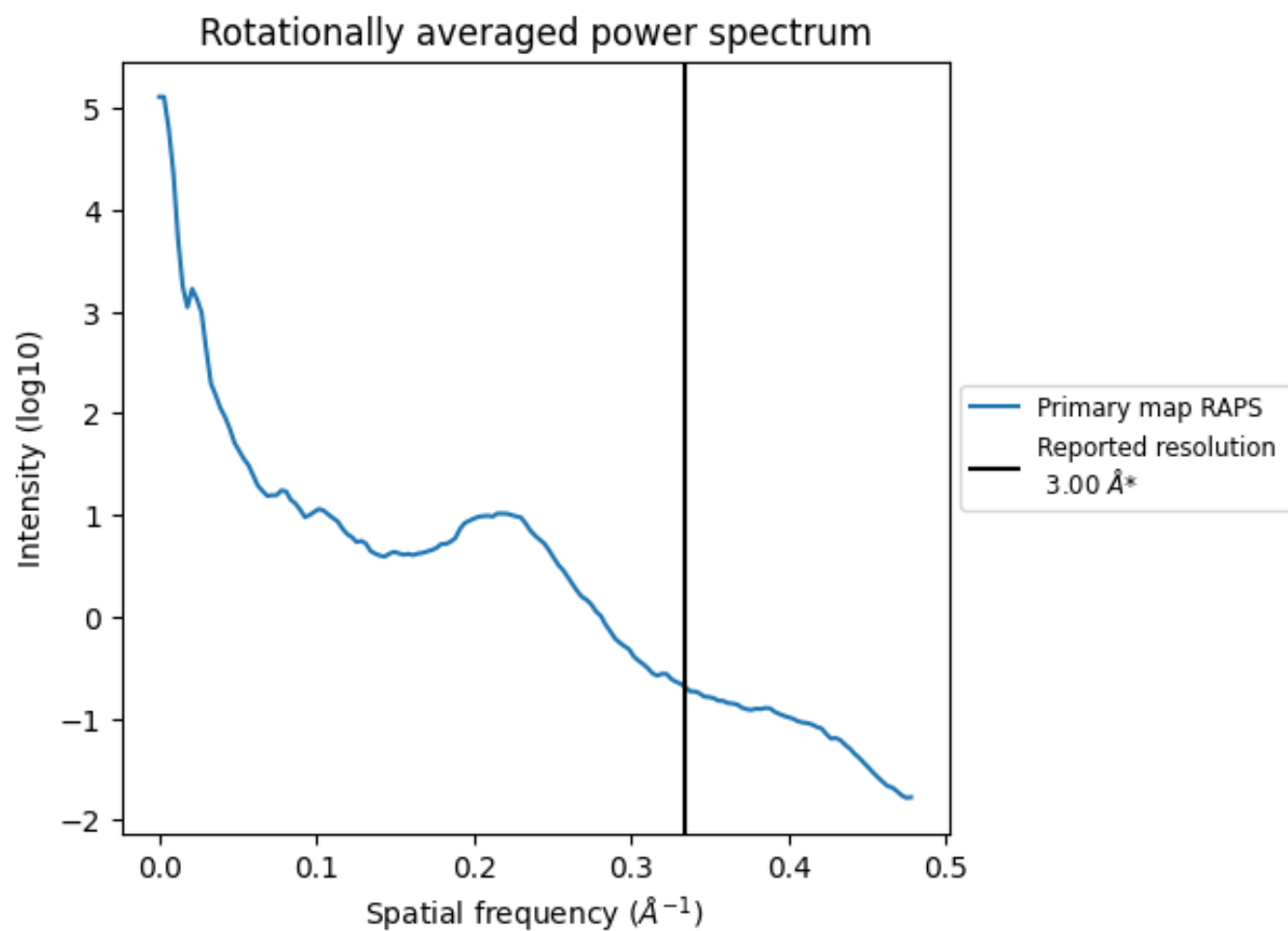
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 420 nm^3 ; this corresponds to an approximate mass of 379 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 ⓘ

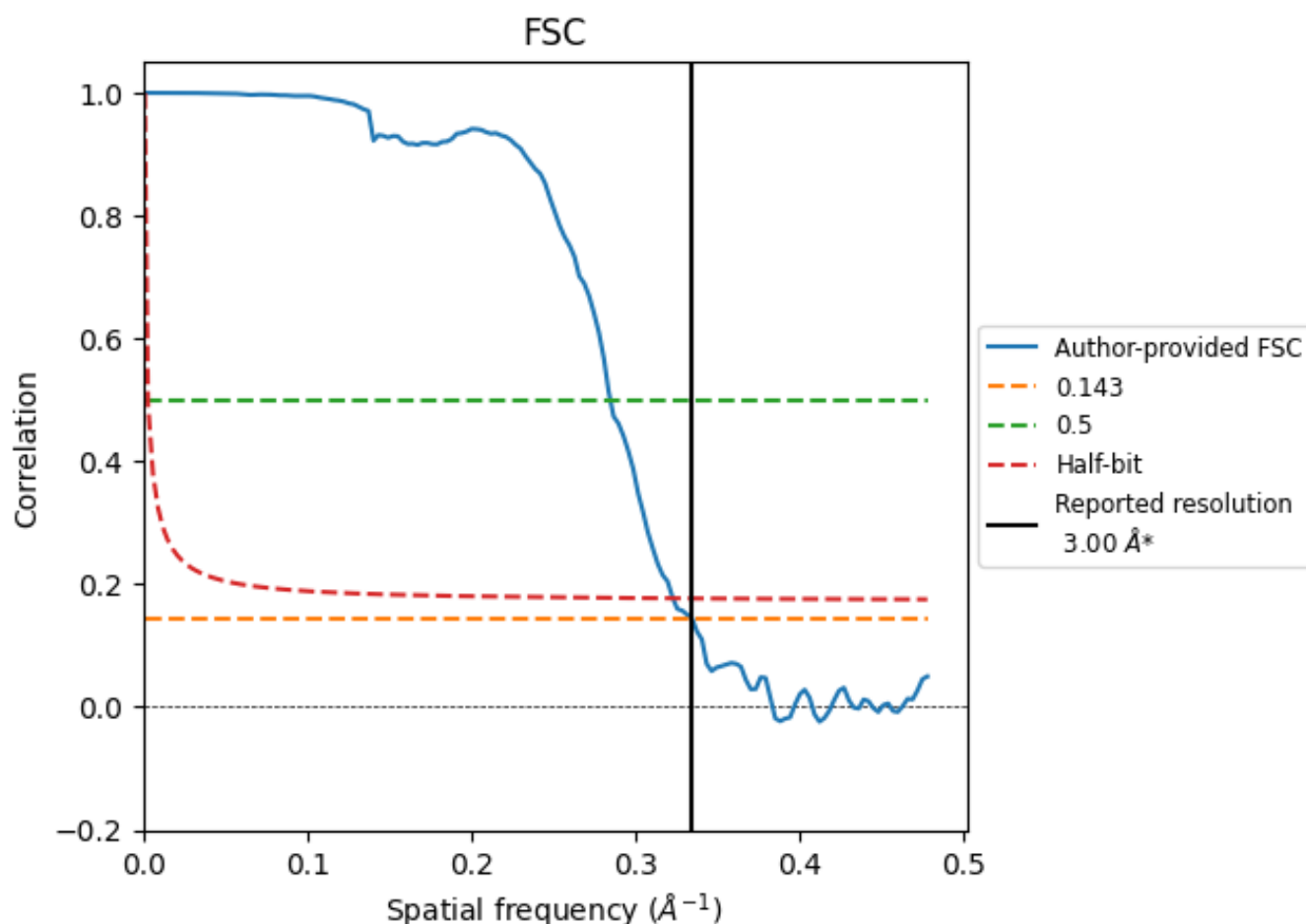


*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

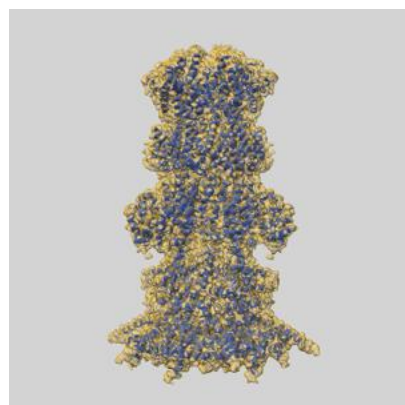
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	2.99	3.51	3.10
Unmasked-calculated*	-	-	-

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

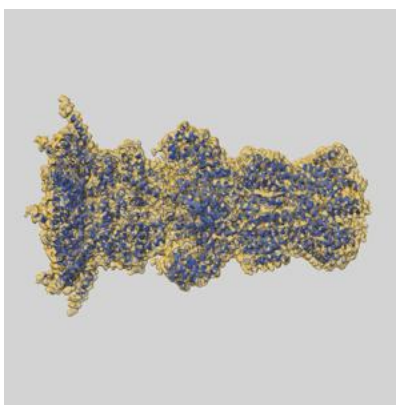
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10912 and PDB model 6YT5. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

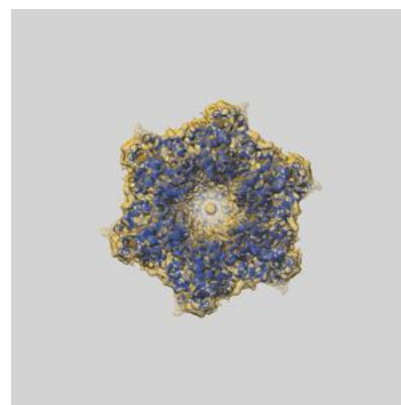
9.1 Map-model overlay [i](#)



X



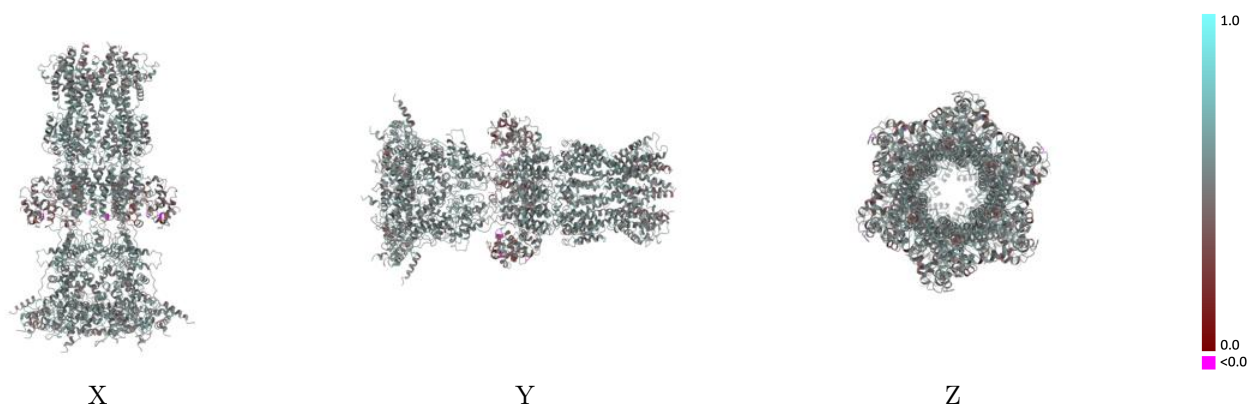
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.006 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

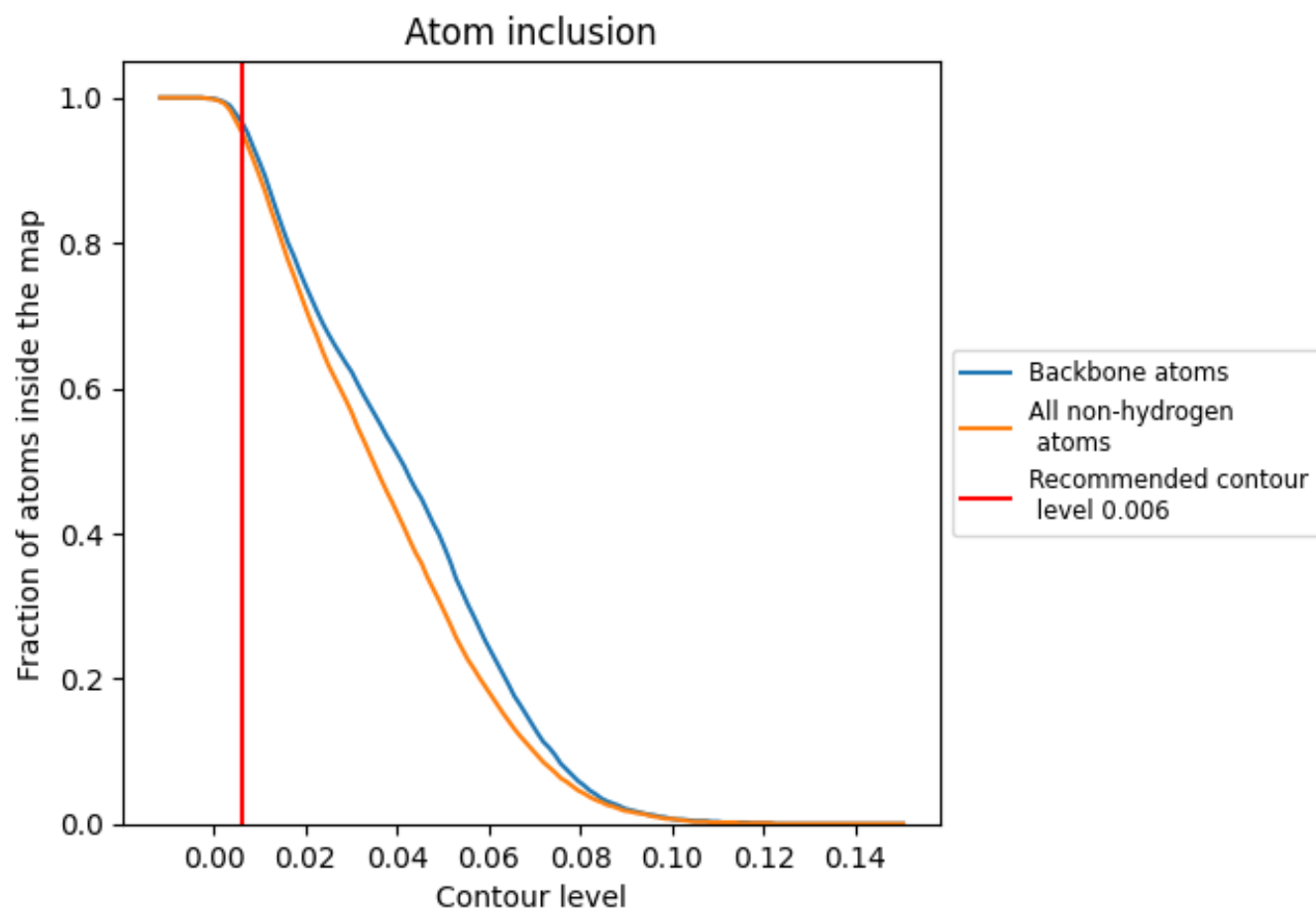


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 95% 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 (0.006) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9540	0.5170
A	0.9660	0.5280
B	0.9640	0.5250
C	0.9640	0.5250
D	0.9660	0.5290
E	0.9640	0.5260
F	0.9640	0.5260
G	0.9160	0.4850
H	0.9190	0.4790
I	0.9140	0.4800
J	0.9190	0.4800
K	0.9170	0.4840
L	0.9140	0.4760

