



# wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 10:37 PM UTC

PDB ID : 9LU6 / pdb\_00009lu6  
EMDB ID : EMD-63389  
Title : Structure of bacteriophage T4 protal-neck protein gp20-gp13-gp14-Hfq assembled in vitro in C6 symmetry  
Authors : Han, L.; Mao, Q.; Sun, L.  
Deposited on : 2025-02-07  
Resolution : 2.91 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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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

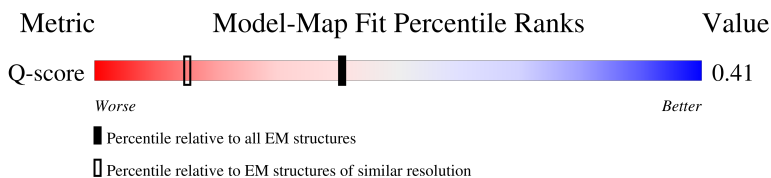
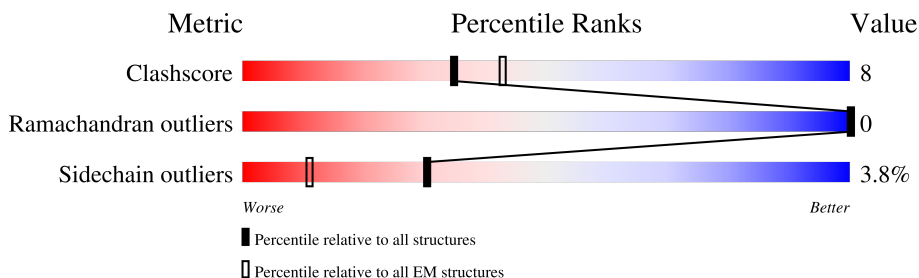
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.91 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.









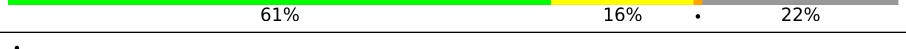
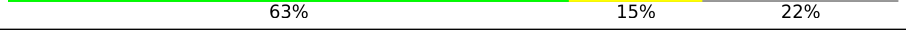
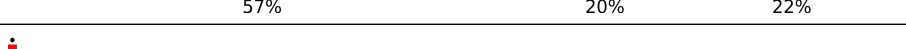
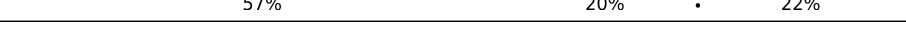
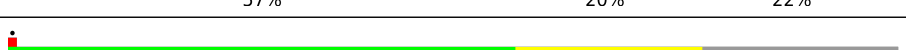

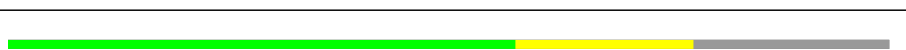

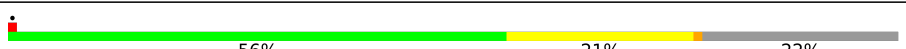




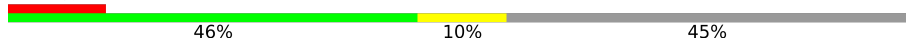
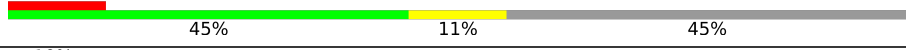
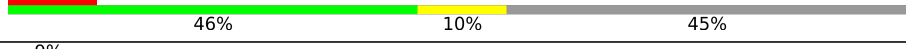
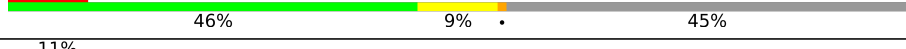
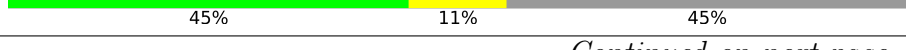

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12972 ( 2.41 - 3.41 )

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  $\geq 3$ , 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	315	61% 16% • 22%
1	B	315	59% 18% • 22%
1	C	315	60% 17% • 22%
1	D	315	61% 17% • 22%

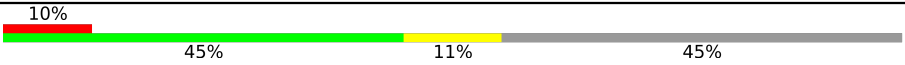

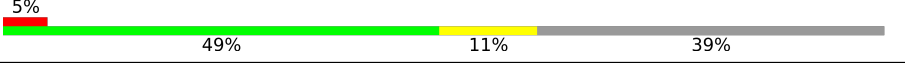
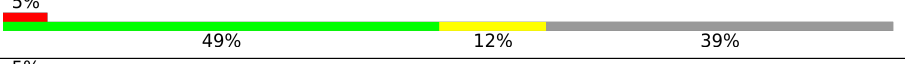
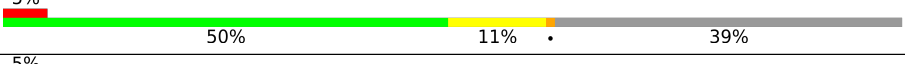
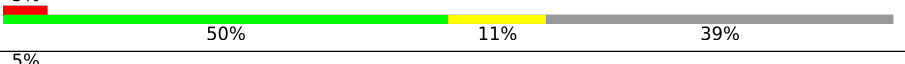
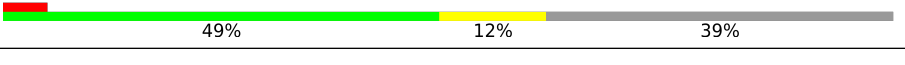
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Mol	Chain	Length	Quality of chain
1	E	315	
1	F	315	
1	G	315	
1	H	315	
1	I	315	
1	J	315	
1	K	315	
1	L	315	
2	a	533	
2	b	533	
2	c	533	
2	d	533	
2	e	533	
2	f	533	
2	g	533	
2	h	533	
2	i	533	
2	j	533	
2	k	533	
2	l	533	
3	S	114	
3	T	114	
3	U	114	
3	V	114	
3	W	114	

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Mol	Chain	Length	Quality of chain
3	X	114	
4	M	265	
4	N	265	
4	O	265	
4	P	265	
4	Q	265	
4	R	265	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 75102 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 Neck protein gp13.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	L	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	A	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	C	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	D	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	E	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	F	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	G	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	H	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	I	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	J	246	Total 1977	C 1273	N 330	O 363	S 11	0	0
1	K	246	Total 1977	C 1273	N 330	O 363	S 11	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	310	HIS	-	expression tag	UNP P11110
B	311	HIS	-	expression tag	UNP P11110
B	312	HIS	-	expression tag	UNP P11110
B	313	HIS	-	expression tag	UNP P11110
B	314	HIS	-	expression tag	UNP P11110
B	315	HIS	-	expression tag	UNP P11110

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Chain	Residue	Modelled	Actual	Comment	Reference
L	310	HIS	-	expression tag	UNP P11110
L	311	HIS	-	expression tag	UNP P11110
L	312	HIS	-	expression tag	UNP P11110
L	313	HIS	-	expression tag	UNP P11110
L	314	HIS	-	expression tag	UNP P11110
L	315	HIS	-	expression tag	UNP P11110
A	310	HIS	-	expression tag	UNP P11110
A	311	HIS	-	expression tag	UNP P11110
A	312	HIS	-	expression tag	UNP P11110
A	313	HIS	-	expression tag	UNP P11110
A	314	HIS	-	expression tag	UNP P11110
A	315	HIS	-	expression tag	UNP P11110
C	310	HIS	-	expression tag	UNP P11110
C	311	HIS	-	expression tag	UNP P11110
C	312	HIS	-	expression tag	UNP P11110
C	313	HIS	-	expression tag	UNP P11110
C	314	HIS	-	expression tag	UNP P11110
C	315	HIS	-	expression tag	UNP P11110
D	310	HIS	-	expression tag	UNP P11110
D	311	HIS	-	expression tag	UNP P11110
D	312	HIS	-	expression tag	UNP P11110
D	313	HIS	-	expression tag	UNP P11110
D	314	HIS	-	expression tag	UNP P11110
D	315	HIS	-	expression tag	UNP P11110
E	310	HIS	-	expression tag	UNP P11110
E	311	HIS	-	expression tag	UNP P11110
E	312	HIS	-	expression tag	UNP P11110
E	313	HIS	-	expression tag	UNP P11110
E	314	HIS	-	expression tag	UNP P11110
E	315	HIS	-	expression tag	UNP P11110
F	310	HIS	-	expression tag	UNP P11110
F	311	HIS	-	expression tag	UNP P11110
F	312	HIS	-	expression tag	UNP P11110
F	313	HIS	-	expression tag	UNP P11110
F	314	HIS	-	expression tag	UNP P11110
F	315	HIS	-	expression tag	UNP P11110
G	310	HIS	-	expression tag	UNP P11110
G	311	HIS	-	expression tag	UNP P11110
G	312	HIS	-	expression tag	UNP P11110
G	313	HIS	-	expression tag	UNP P11110
G	314	HIS	-	expression tag	UNP P11110
G	315	HIS	-	expression tag	UNP P11110

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Chain	Residue	Modelled	Actual	Comment	Reference
H	310	HIS	-	expression tag	UNP P11110
H	311	HIS	-	expression tag	UNP P11110
H	312	HIS	-	expression tag	UNP P11110
H	313	HIS	-	expression tag	UNP P11110
H	314	HIS	-	expression tag	UNP P11110
H	315	HIS	-	expression tag	UNP P11110
I	310	HIS	-	expression tag	UNP P11110
I	311	HIS	-	expression tag	UNP P11110
I	312	HIS	-	expression tag	UNP P11110
I	313	HIS	-	expression tag	UNP P11110
I	314	HIS	-	expression tag	UNP P11110
I	315	HIS	-	expression tag	UNP P11110
J	310	HIS	-	expression tag	UNP P11110
J	311	HIS	-	expression tag	UNP P11110
J	312	HIS	-	expression tag	UNP P11110
J	313	HIS	-	expression tag	UNP P11110
J	314	HIS	-	expression tag	UNP P11110
J	315	HIS	-	expression tag	UNP P11110
K	310	HIS	-	expression tag	UNP P11110
K	311	HIS	-	expression tag	UNP P11110
K	312	HIS	-	expression tag	UNP P11110
K	313	HIS	-	expression tag	UNP P11110
K	314	HIS	-	expression tag	UNP P11110
K	315	HIS	-	expression tag	UNP P11110

- Molecule 2 is a protein called Portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	l	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		
2	k	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		
2	j	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		
2	i	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		
2	h	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		
2	g	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		
2	f	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	e	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		
2	d	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		
2	c	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		
2	b	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		
2	a	415	Total	C	N	O	S	0	0
			3385	2138	593	635	19		

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
l	525	SER	-	expression tag	UNP A0A7S9SW10
l	526	SER	-	expression tag	UNP A0A7S9SW10
l	527	GLY	-	expression tag	UNP A0A7S9SW10
l	528	HIS	-	expression tag	UNP A0A7S9SW10
l	529	HIS	-	expression tag	UNP A0A7S9SW10
l	530	HIS	-	expression tag	UNP A0A7S9SW10
l	531	HIS	-	expression tag	UNP A0A7S9SW10
l	532	HIS	-	expression tag	UNP A0A7S9SW10
l	533	HIS	-	expression tag	UNP A0A7S9SW10
k	525	SER	-	expression tag	UNP A0A7S9SW10
k	526	SER	-	expression tag	UNP A0A7S9SW10
k	527	GLY	-	expression tag	UNP A0A7S9SW10
k	528	HIS	-	expression tag	UNP A0A7S9SW10
k	529	HIS	-	expression tag	UNP A0A7S9SW10
k	530	HIS	-	expression tag	UNP A0A7S9SW10
k	531	HIS	-	expression tag	UNP A0A7S9SW10
k	532	HIS	-	expression tag	UNP A0A7S9SW10
k	533	HIS	-	expression tag	UNP A0A7S9SW10
j	525	SER	-	expression tag	UNP A0A7S9SW10
j	526	SER	-	expression tag	UNP A0A7S9SW10
j	527	GLY	-	expression tag	UNP A0A7S9SW10
j	528	HIS	-	expression tag	UNP A0A7S9SW10
j	529	HIS	-	expression tag	UNP A0A7S9SW10
j	530	HIS	-	expression tag	UNP A0A7S9SW10
j	531	HIS	-	expression tag	UNP A0A7S9SW10
j	532	HIS	-	expression tag	UNP A0A7S9SW10
j	533	HIS	-	expression tag	UNP A0A7S9SW10
i	525	SER	-	expression tag	UNP A0A7S9SW10
i	526	SER	-	expression tag	UNP A0A7S9SW10

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Chain	Residue	Modelled	Actual	Comment	Reference
i	527	GLY	-	expression tag	UNP A0A7S9SW10
i	528	HIS	-	expression tag	UNP A0A7S9SW10
i	529	HIS	-	expression tag	UNP A0A7S9SW10
i	530	HIS	-	expression tag	UNP A0A7S9SW10
i	531	HIS	-	expression tag	UNP A0A7S9SW10
i	532	HIS	-	expression tag	UNP A0A7S9SW10
i	533	HIS	-	expression tag	UNP A0A7S9SW10
h	525	SER	-	expression tag	UNP A0A7S9SW10
h	526	SER	-	expression tag	UNP A0A7S9SW10
h	527	GLY	-	expression tag	UNP A0A7S9SW10
h	528	HIS	-	expression tag	UNP A0A7S9SW10
h	529	HIS	-	expression tag	UNP A0A7S9SW10
h	530	HIS	-	expression tag	UNP A0A7S9SW10
h	531	HIS	-	expression tag	UNP A0A7S9SW10
h	532	HIS	-	expression tag	UNP A0A7S9SW10
h	533	HIS	-	expression tag	UNP A0A7S9SW10
g	525	SER	-	expression tag	UNP A0A7S9SW10
g	526	SER	-	expression tag	UNP A0A7S9SW10
g	527	GLY	-	expression tag	UNP A0A7S9SW10
g	528	HIS	-	expression tag	UNP A0A7S9SW10
g	529	HIS	-	expression tag	UNP A0A7S9SW10
g	530	HIS	-	expression tag	UNP A0A7S9SW10
g	531	HIS	-	expression tag	UNP A0A7S9SW10
g	532	HIS	-	expression tag	UNP A0A7S9SW10
g	533	HIS	-	expression tag	UNP A0A7S9SW10
f	525	SER	-	expression tag	UNP A0A7S9SW10
f	526	SER	-	expression tag	UNP A0A7S9SW10
f	527	GLY	-	expression tag	UNP A0A7S9SW10
f	528	HIS	-	expression tag	UNP A0A7S9SW10
f	529	HIS	-	expression tag	UNP A0A7S9SW10
f	530	HIS	-	expression tag	UNP A0A7S9SW10
f	531	HIS	-	expression tag	UNP A0A7S9SW10
f	532	HIS	-	expression tag	UNP A0A7S9SW10
f	533	HIS	-	expression tag	UNP A0A7S9SW10
e	525	SER	-	expression tag	UNP A0A7S9SW10
e	526	SER	-	expression tag	UNP A0A7S9SW10
e	527	GLY	-	expression tag	UNP A0A7S9SW10
e	528	HIS	-	expression tag	UNP A0A7S9SW10
e	529	HIS	-	expression tag	UNP A0A7S9SW10
e	530	HIS	-	expression tag	UNP A0A7S9SW10
e	531	HIS	-	expression tag	UNP A0A7S9SW10
e	532	HIS	-	expression tag	UNP A0A7S9SW10

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Chain	Residue	Modelled	Actual	Comment	Reference
e	533	HIS	-	expression tag	UNP A0A7S9SW10
d	525	SER	-	expression tag	UNP A0A7S9SW10
d	526	SER	-	expression tag	UNP A0A7S9SW10
d	527	GLY	-	expression tag	UNP A0A7S9SW10
d	528	HIS	-	expression tag	UNP A0A7S9SW10
d	529	HIS	-	expression tag	UNP A0A7S9SW10
d	530	HIS	-	expression tag	UNP A0A7S9SW10
d	531	HIS	-	expression tag	UNP A0A7S9SW10
d	532	HIS	-	expression tag	UNP A0A7S9SW10
d	533	HIS	-	expression tag	UNP A0A7S9SW10
c	525	SER	-	expression tag	UNP A0A7S9SW10
c	526	SER	-	expression tag	UNP A0A7S9SW10
c	527	GLY	-	expression tag	UNP A0A7S9SW10
c	528	HIS	-	expression tag	UNP A0A7S9SW10
c	529	HIS	-	expression tag	UNP A0A7S9SW10
c	530	HIS	-	expression tag	UNP A0A7S9SW10
c	531	HIS	-	expression tag	UNP A0A7S9SW10
c	532	HIS	-	expression tag	UNP A0A7S9SW10
c	533	HIS	-	expression tag	UNP A0A7S9SW10
b	525	SER	-	expression tag	UNP A0A7S9SW10
b	526	SER	-	expression tag	UNP A0A7S9SW10
b	527	GLY	-	expression tag	UNP A0A7S9SW10
b	528	HIS	-	expression tag	UNP A0A7S9SW10
b	529	HIS	-	expression tag	UNP A0A7S9SW10
b	530	HIS	-	expression tag	UNP A0A7S9SW10
b	531	HIS	-	expression tag	UNP A0A7S9SW10
b	532	HIS	-	expression tag	UNP A0A7S9SW10
b	533	HIS	-	expression tag	UNP A0A7S9SW10
a	525	SER	-	expression tag	UNP A0A7S9SW10
a	526	SER	-	expression tag	UNP A0A7S9SW10
a	527	GLY	-	expression tag	UNP A0A7S9SW10
a	528	HIS	-	expression tag	UNP A0A7S9SW10
a	529	HIS	-	expression tag	UNP A0A7S9SW10
a	530	HIS	-	expression tag	UNP A0A7S9SW10
a	531	HIS	-	expression tag	UNP A0A7S9SW10
a	532	HIS	-	expression tag	UNP A0A7S9SW10
a	533	HIS	-	expression tag	UNP A0A7S9SW10

- Molecule 3 is a protein called RNA-binding protein Hfq.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	X	63	Total	C	N	O	S	0	0
			504	326	88	89	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
3	W	63	Total	C	N	O	S	0	0
			504	326	88	89	1		
3	V	63	Total	C	N	O	S	0	0
			504	326	88	89	1		
3	U	63	Total	C	N	O	S	0	0
			504	326	88	89	1		
3	T	63	Total	C	N	O	S	0	0
			504	326	88	89	1		
3	S	63	Total	C	N	O	S	0	0
			504	326	88	89	1		

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	-11	MET	-	initiating methionine	UNP A7ZV41
X	-10	TRP	-	expression tag	UNP A7ZV41
X	-9	SER	-	expression tag	UNP A7ZV41
X	-8	HIS	-	expression tag	UNP A7ZV41
X	-7	PRO	-	expression tag	UNP A7ZV41
X	-6	GLN	-	expression tag	UNP A7ZV41
X	-5	PHE	-	expression tag	UNP A7ZV41
X	-4	GLU	-	expression tag	UNP A7ZV41
X	-3	LYS	-	expression tag	UNP A7ZV41
X	-2	GLY	-	expression tag	UNP A7ZV41
X	-1	SER	-	expression tag	UNP A7ZV41
X	0	SER	-	expression tag	UNP A7ZV41
W	-11	MET	-	initiating methionine	UNP A7ZV41
W	-10	TRP	-	expression tag	UNP A7ZV41
W	-9	SER	-	expression tag	UNP A7ZV41
W	-8	HIS	-	expression tag	UNP A7ZV41
W	-7	PRO	-	expression tag	UNP A7ZV41
W	-6	GLN	-	expression tag	UNP A7ZV41
W	-5	PHE	-	expression tag	UNP A7ZV41
W	-4	GLU	-	expression tag	UNP A7ZV41
W	-3	LYS	-	expression tag	UNP A7ZV41
W	-2	GLY	-	expression tag	UNP A7ZV41
W	-1	SER	-	expression tag	UNP A7ZV41
W	0	SER	-	expression tag	UNP A7ZV41
V	-11	MET	-	initiating methionine	UNP A7ZV41
V	-10	TRP	-	expression tag	UNP A7ZV41
V	-9	SER	-	expression tag	UNP A7ZV41
V	-8	HIS	-	expression tag	UNP A7ZV41
V	-7	PRO	-	expression tag	UNP A7ZV41

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Chain	Residue	Modelled	Actual	Comment	Reference
V	-6	GLN	-	expression tag	UNP A7ZV41
V	-5	PHE	-	expression tag	UNP A7ZV41
V	-4	GLU	-	expression tag	UNP A7ZV41
V	-3	LYS	-	expression tag	UNP A7ZV41
V	-2	GLY	-	expression tag	UNP A7ZV41
V	-1	SER	-	expression tag	UNP A7ZV41
V	0	SER	-	expression tag	UNP A7ZV41
U	-11	MET	-	initiating methionine	UNP A7ZV41
U	-10	TRP	-	expression tag	UNP A7ZV41
U	-9	SER	-	expression tag	UNP A7ZV41
U	-8	HIS	-	expression tag	UNP A7ZV41
U	-7	PRO	-	expression tag	UNP A7ZV41
U	-6	GLN	-	expression tag	UNP A7ZV41
U	-5	PHE	-	expression tag	UNP A7ZV41
U	-4	GLU	-	expression tag	UNP A7ZV41
U	-3	LYS	-	expression tag	UNP A7ZV41
U	-2	GLY	-	expression tag	UNP A7ZV41
U	-1	SER	-	expression tag	UNP A7ZV41
U	0	SER	-	expression tag	UNP A7ZV41
T	-11	MET	-	initiating methionine	UNP A7ZV41
T	-10	TRP	-	expression tag	UNP A7ZV41
T	-9	SER	-	expression tag	UNP A7ZV41
T	-8	HIS	-	expression tag	UNP A7ZV41
T	-7	PRO	-	expression tag	UNP A7ZV41
T	-6	GLN	-	expression tag	UNP A7ZV41
T	-5	PHE	-	expression tag	UNP A7ZV41
T	-4	GLU	-	expression tag	UNP A7ZV41
T	-3	LYS	-	expression tag	UNP A7ZV41
T	-2	GLY	-	expression tag	UNP A7ZV41
T	-1	SER	-	expression tag	UNP A7ZV41
T	0	SER	-	expression tag	UNP A7ZV41
S	-11	MET	-	initiating methionine	UNP A7ZV41
S	-10	TRP	-	expression tag	UNP A7ZV41
S	-9	SER	-	expression tag	UNP A7ZV41
S	-8	HIS	-	expression tag	UNP A7ZV41
S	-7	PRO	-	expression tag	UNP A7ZV41
S	-6	GLN	-	expression tag	UNP A7ZV41
S	-5	PHE	-	expression tag	UNP A7ZV41
S	-4	GLU	-	expression tag	UNP A7ZV41
S	-3	LYS	-	expression tag	UNP A7ZV41
S	-2	GLY	-	expression tag	UNP A7ZV41
S	-1	SER	-	expression tag	UNP A7ZV41

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Chain	Residue	Modelled	Actual	Comment	Reference
S	0	SER	-	expression tag	UNP A7ZV41

- Molecule 4 is a protein called Neck protein gp14.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	N	162	Total	C	N	O	S	0	0
			1289	832	212	242	3		
4	M	162	Total	C	N	O	S	0	0
			1289	832	212	242	3		
4	O	162	Total	C	N	O	S	0	0
			1289	832	212	242	3		
4	P	162	Total	C	N	O	S	0	0
			1289	832	212	242	3		
4	Q	162	Total	C	N	O	S	0	0
			1289	832	212	242	3		
4	R	162	Total	C	N	O	S	0	0
			1289	832	212	242	3		

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	-8	HIS	-	expression tag	UNP P11111
N	-7	HIS	-	expression tag	UNP P11111
N	-6	HIS	-	expression tag	UNP P11111
N	-5	HIS	-	expression tag	UNP P11111
N	-4	HIS	-	expression tag	UNP P11111
N	-3	HIS	-	expression tag	UNP P11111
N	-2	SER	-	expression tag	UNP P11111
N	-1	SER	-	expression tag	UNP P11111
N	0	GLY	-	expression tag	UNP P11111
M	-8	HIS	-	expression tag	UNP P11111
M	-7	HIS	-	expression tag	UNP P11111
M	-6	HIS	-	expression tag	UNP P11111
M	-5	HIS	-	expression tag	UNP P11111
M	-4	HIS	-	expression tag	UNP P11111
M	-3	HIS	-	expression tag	UNP P11111
M	-2	SER	-	expression tag	UNP P11111
M	-1	SER	-	expression tag	UNP P11111
M	0	GLY	-	expression tag	UNP P11111
O	-8	HIS	-	expression tag	UNP P11111
O	-7	HIS	-	expression tag	UNP P11111
O	-6	HIS	-	expression tag	UNP P11111

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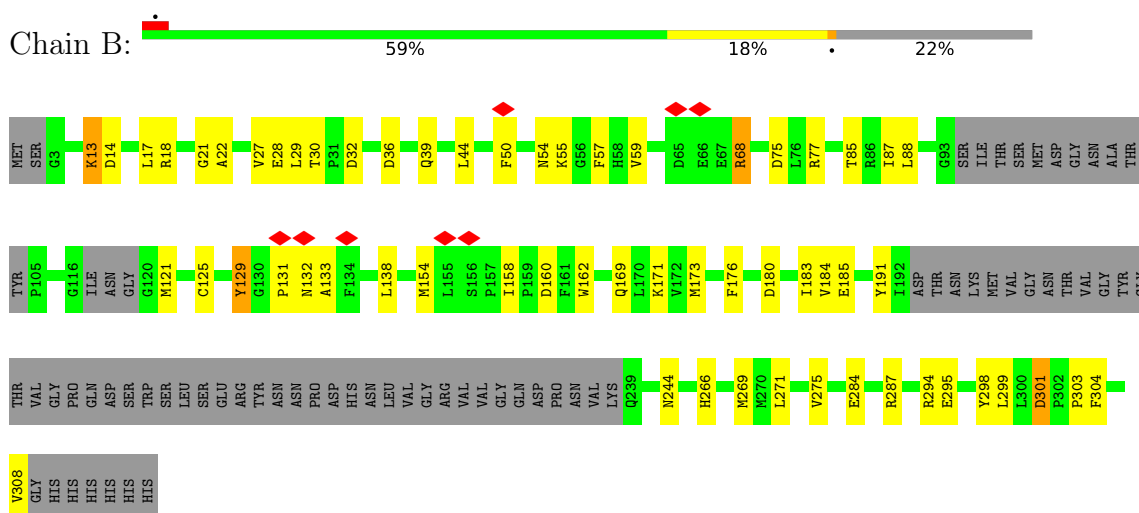
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Chain	Residue	Modelled	Actual	Comment	Reference
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O	-4	HIS	-	expression tag	UNP P11111
O	-3	HIS	-	expression tag	UNP P11111
O	-2	SER	-	expression tag	UNP P11111
O	-1	SER	-	expression tag	UNP P11111
O	0	GLY	-	expression tag	UNP P11111
P	-8	HIS	-	expression tag	UNP P11111
P	-7	HIS	-	expression tag	UNP P11111
P	-6	HIS	-	expression tag	UNP P11111
P	-5	HIS	-	expression tag	UNP P11111
P	-4	HIS	-	expression tag	UNP P11111
P	-3	HIS	-	expression tag	UNP P11111
P	-2	SER	-	expression tag	UNP P11111
P	-1	SER	-	expression tag	UNP P11111
P	0	GLY	-	expression tag	UNP P11111
Q	-8	HIS	-	expression tag	UNP P11111
Q	-7	HIS	-	expression tag	UNP P11111
Q	-6	HIS	-	expression tag	UNP P11111
Q	-5	HIS	-	expression tag	UNP P11111
Q	-4	HIS	-	expression tag	UNP P11111
Q	-3	HIS	-	expression tag	UNP P11111
Q	-2	SER	-	expression tag	UNP P11111
Q	-1	SER	-	expression tag	UNP P11111
Q	0	GLY	-	expression tag	UNP P11111
R	-8	HIS	-	expression tag	UNP P11111
R	-7	HIS	-	expression tag	UNP P11111
R	-6	HIS	-	expression tag	UNP P11111
R	-5	HIS	-	expression tag	UNP P11111
R	-4	HIS	-	expression tag	UNP P11111
R	-3	HIS	-	expression tag	UNP P11111
R	-2	SER	-	expression tag	UNP P11111
R	-1	SER	-	expression tag	UNP P11111
R	0	GLY	-	expression tag	UNP P11111

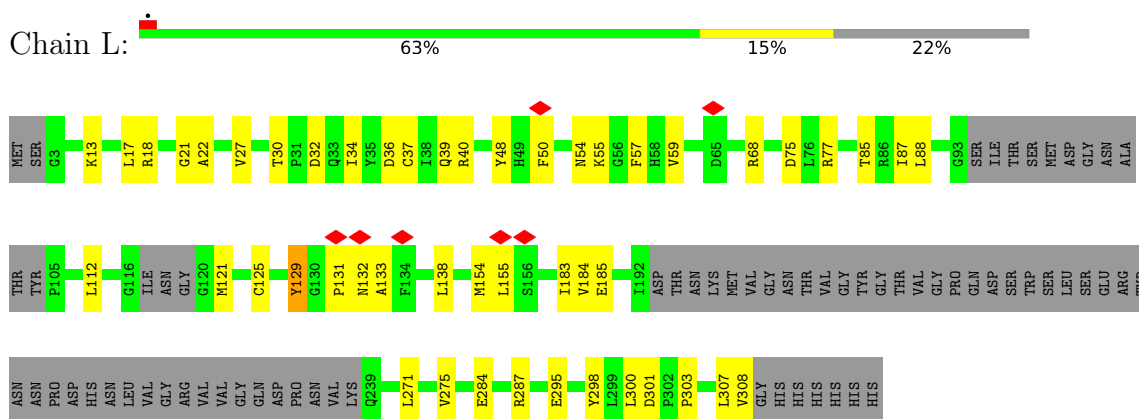
### 3 Residue-property plots

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: Neck protein gp13

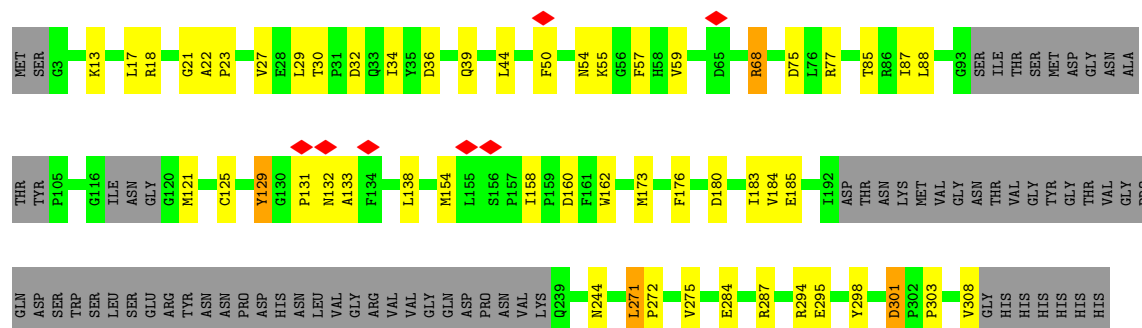


#### • Molecule 1: Neck protein gp13

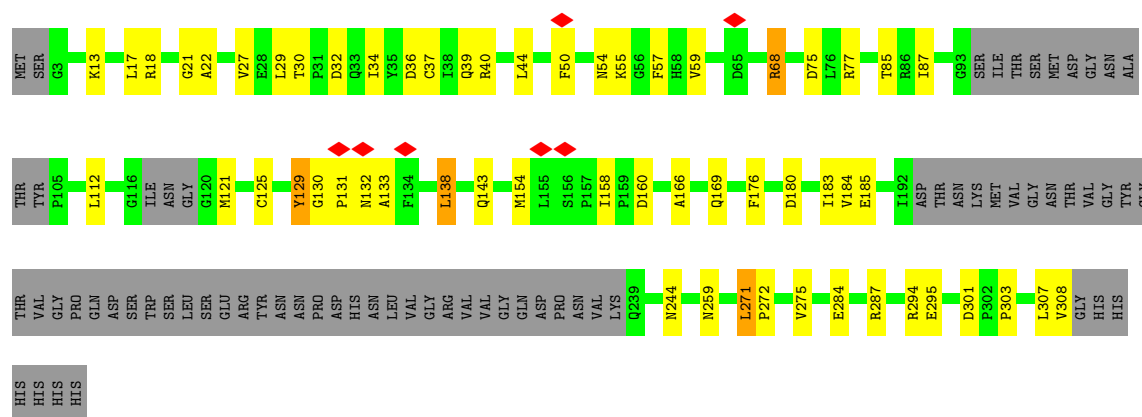


#### • Molecule 1: Neck protein gp13

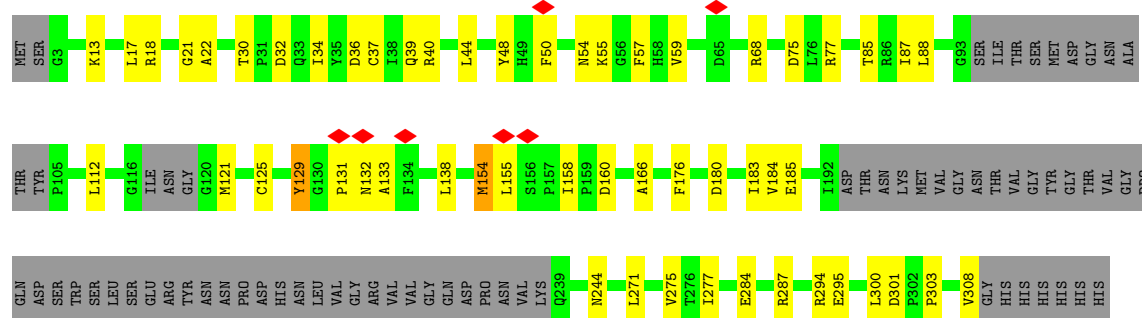




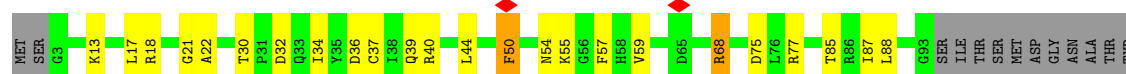
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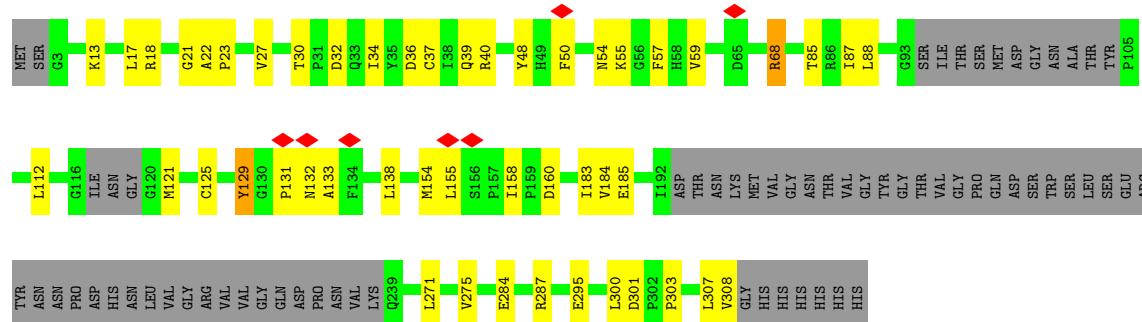
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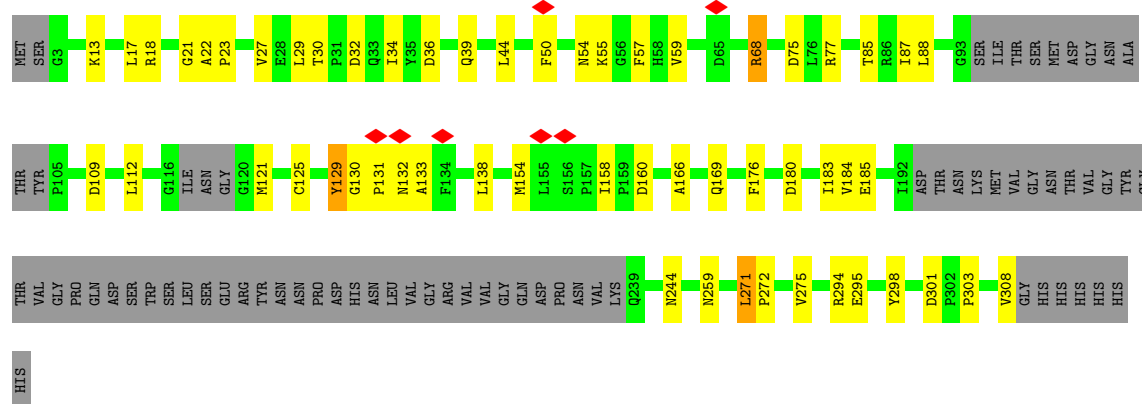
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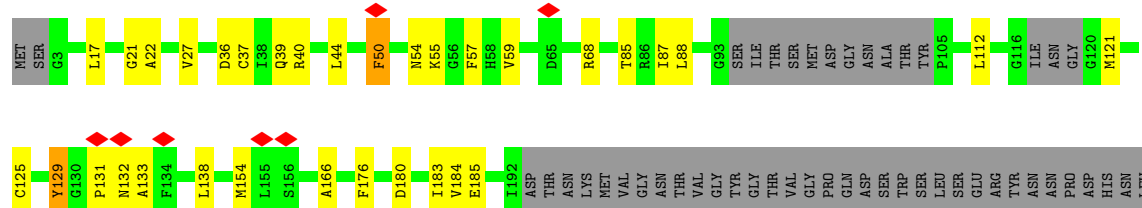
- Molecule 1: Neck protein gp13



- Molecule 1: Neck protein gp13

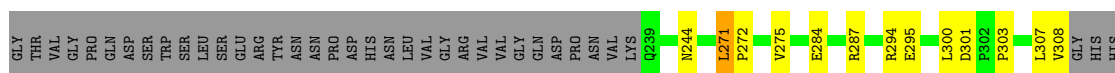
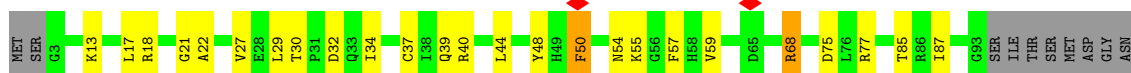


- Molecule 1: Neck protein gp13





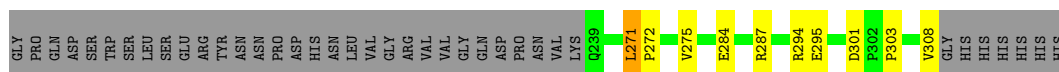
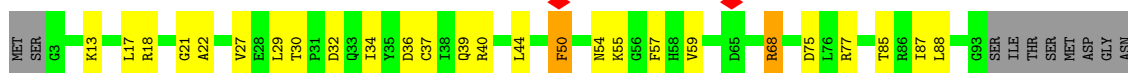
• Molecule 1: Neck protein gp13



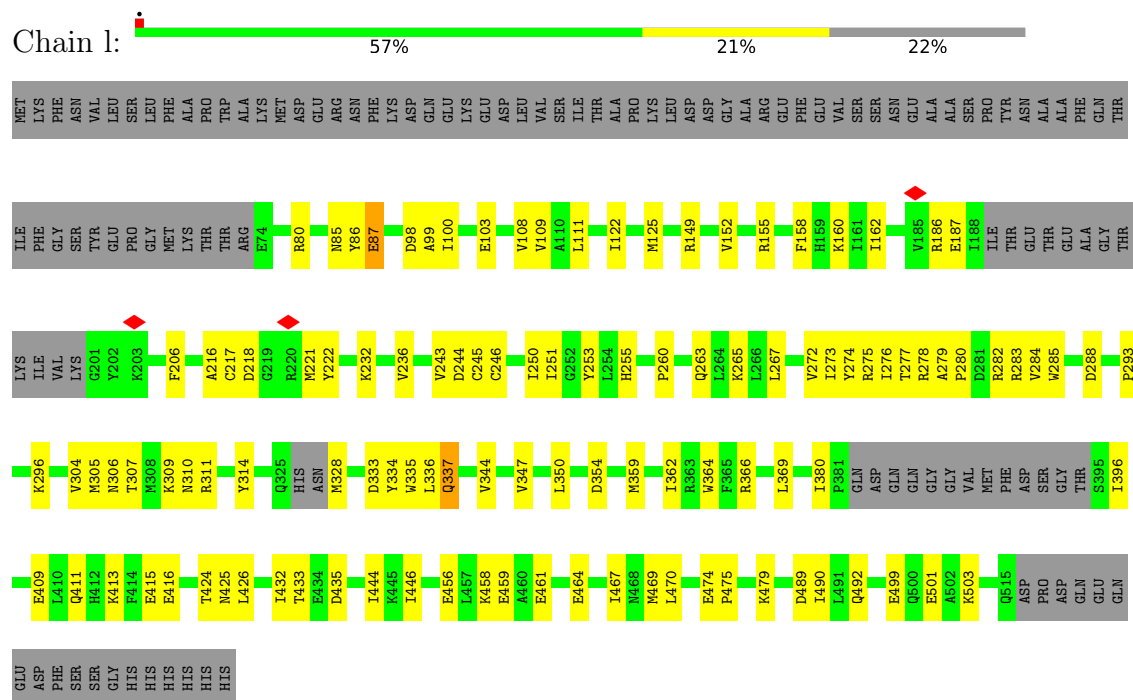
• Molecule 1: Neck protein gp13



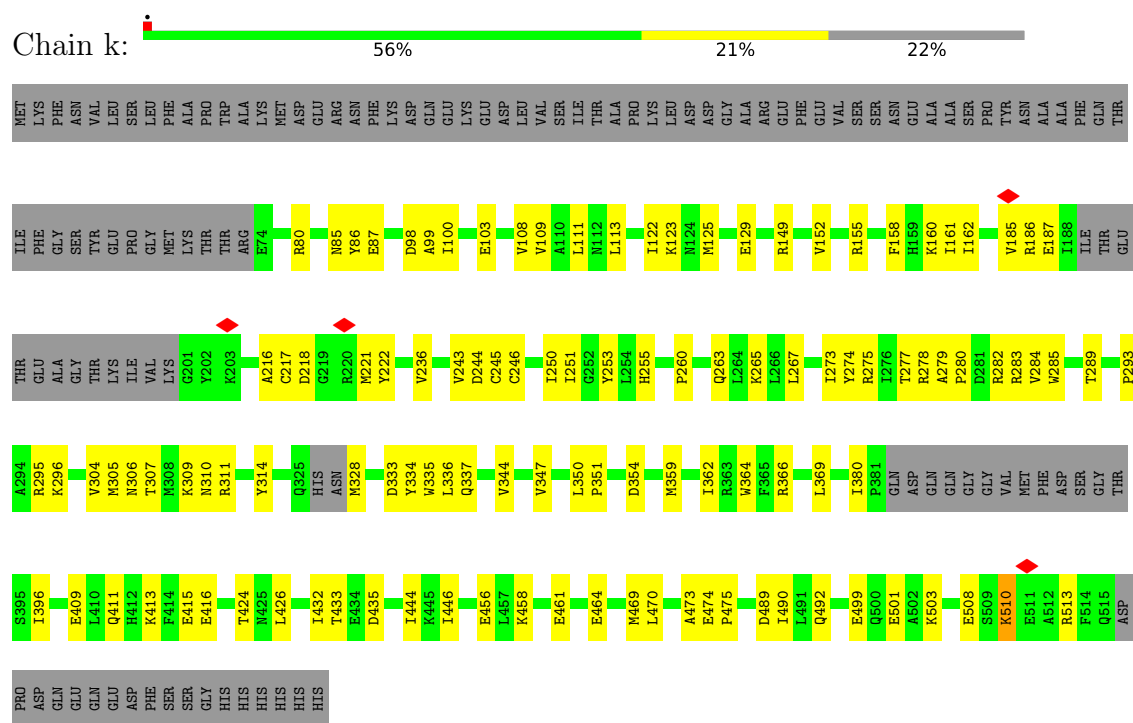
• Molecule 1: Neck protein gp13



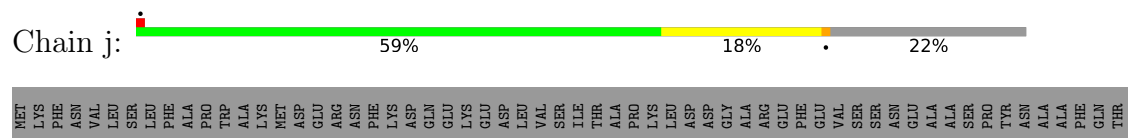
• Molecule 2: Portal protein

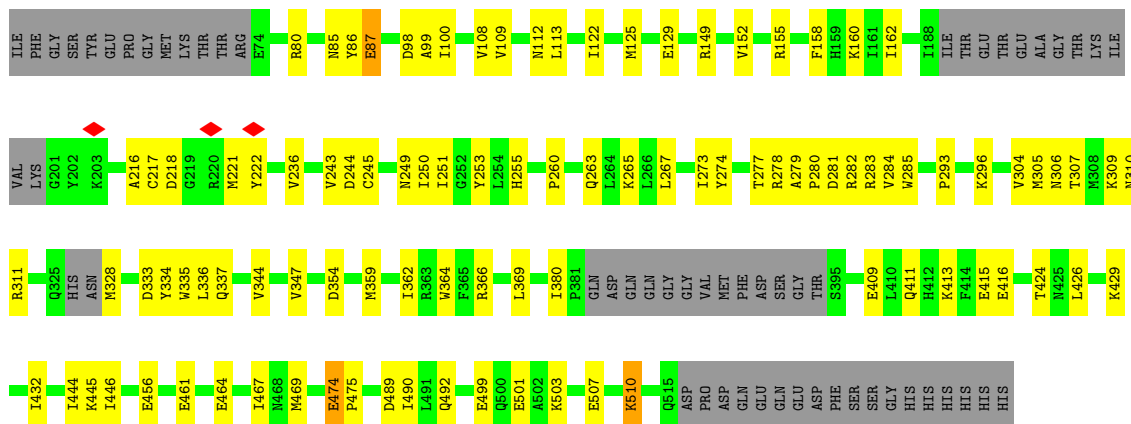


- Molecule 2: Portal protein

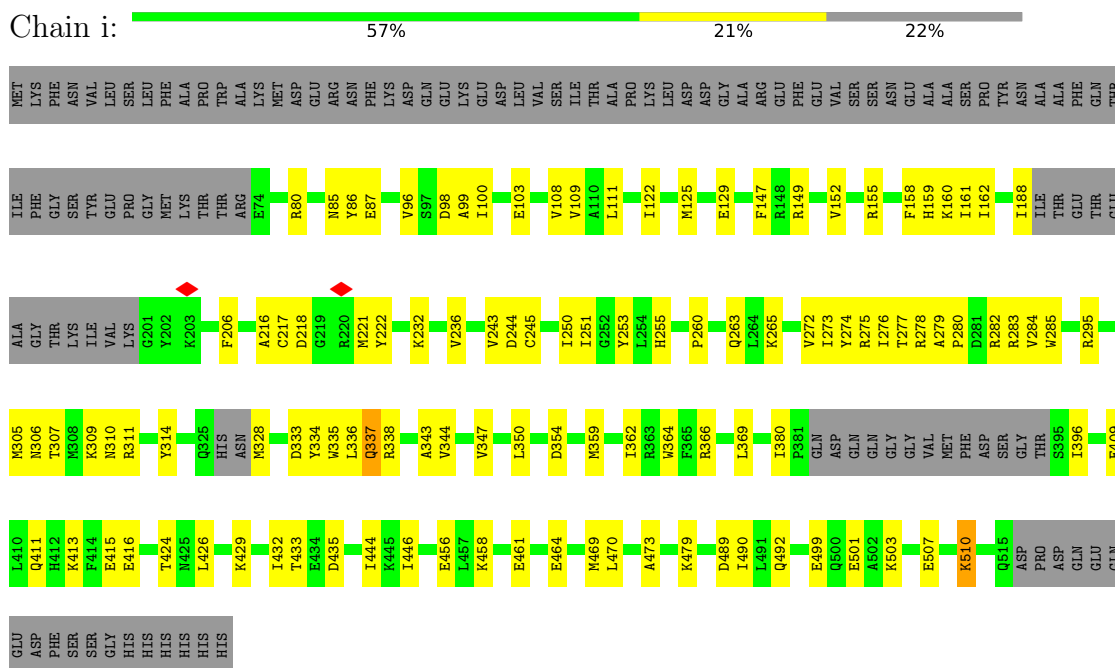


- Molecule 2: Portal protein

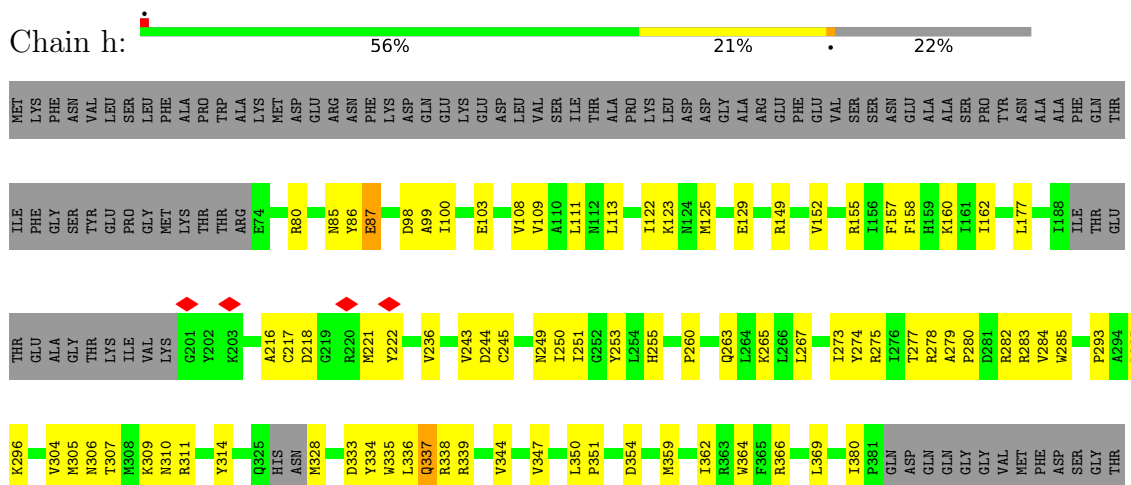


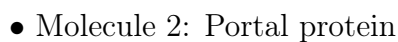


- Molecule 2: Portal protein

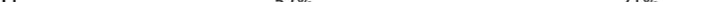


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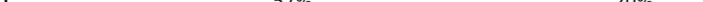




ASP	GLY	R295	THR	ILE	MET
GLN	S395	GLU	GLU	PHE	LYS
GLN	I396	GLN	GLY	ASN	PHE
ASP	E409	THR	THR	TYR	VAL
PHE	L410	LYS	LYS	GLU	LEU
SER	Q411	M305	ILE	PRO	SER
SER	H412	N306	VAL	GLY	LEU
GLY	K413	T307	GLY	MET	PHE
HIS	F414	K308	G201	LYS	ALA
HIS	E415	N309	Y202	THR	PRO
HIS	E416	N310	K203	THR	TRP
HIS	T424	R311	A216	ARG	ALA
HIS	N425	Y314	C217	E74	LYS
HIS	L426	Q325	D218	R80	MET
GLN	K429	HIS	G219	N81	GLU
GLN	L432	ASN	R220	L82	ARG
GLN	T433	M328	M221	N85	PHE
GLN	F434	D333	Y222	Y86	LYS
GLN	D435	Y334	V236	E87	ASP
GLN	L444	W335	V243	V88	GLN
GLN	K445	L336	D244	D98	LYS
GLN	L446	Q337	C245	A99	LYS
GLN	E456	V344	C246	I100	ASP
GLN	L457	T345	I250	E103	LEU
GLN	K458	E346	G252	I08	VAL
GLN	E461	V347	Y253	V108	SER
GLN	E464	L350	D254	A110	ILE
GLN	M469	P351	H255	L111	THR
GLN	L470	D354	P260	N112	ALA
GLN	A473	I362	Q263	L113	PRO
GLN	E474	K363	L264	I122	LYS
GLN	F475	W364	L266	M125	ASP
GLN	D489	F365	L267	E129	GLY
GLN	L490	R366	V272	E149	PHE
GLN	L491	L369	I273	R149	VAL
GLN	Q492	I380	Y274	V152	SER
GLN	E499	P391	R275	R155	SER
GLN	Q500	GLN	R277	F158	ASN
GLN	E501	ASP	R278	ALA	ALA
GLN	A502	GLN	A279	SER	ALA
GLN	K503	GLN	P280	H159	PRO
GLN	R513	GLY	D281	K160	TYR
GLN	F514	VAL	R282	I161	ASP
GLN	O515	THR	R283	I162	ASN
GLN	ASP	MET	V284	I188	ALA
GLN	R527	PHE	W285	ILE	ALA
GLN	P528	ASP	Y286	THR	PHE
GLN	P529	SER	V287	GLU	THR

Chain d:  57% 21% 22%

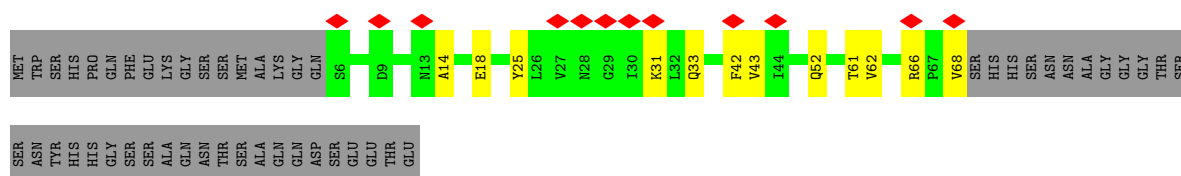
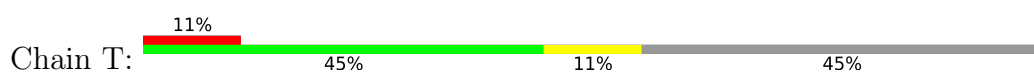
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GLU	L410	PHE	GLY	LYS	PHE	THR
GLN	Q411	ASN	VAL	ILE	GLY	ASP
GLU	R412	VAL	LYS	LYS	THR	GLN
ASP	K413	N306		G201	GLU	VAL
PHE	F414	T307		K203	PRO	LEU
SER	E415	M308		K202	GLY	SER
GLY	E416	K309			LEU	PHE
SER		N310		F206	MET	ALA
HIS	T424	R311			THR	ALA
HIS	M425			A216	THR	PRO
HIS	L426	Y314		C217	THR	TRP
HIS				D218	ARG	LYS
HIS	I432	Q325		G219	E74	MET
HIS	T433	HIS		R220	R80	GLY
ASP	F434	ASN		M221	N81	ASP
	D435	M328		Y222	L82	ARG
						ASN
	I444	D333		K232	N85	PHE
	K445	Y334			R86	LYS
	I446	W335		E37	E87	ASP
		L336		V236	V88	GLN
	E456	Q337		V243		GLU
SER	L457	R338		D244	D98	LYS
	K458	R339		C245	GLU	ASP
				C246	LEU	LEU
	E461	V944			V108	VAL
	E464	V347		I250	V109	SER
				I251	ILE	ILE
	I467	D354		G252	A110	THR
	M468	Y253		Y253	L111	ALA
	M469	L254		L254	ALA	PRO
	L470	M359		H255	M125	LYS
						LEU
	E474	I362		P260	E129	ASP
	P475	R363				ASP
		W364		Q263	R149	GLY
	K479	R365			V152	ARG
		R366		K265	L264	GLU
	D489	L369		L265	R155	PHE
	L490			L267		GLU
	L491	I380			F158	GLU
	Q492	P381		I273	H159	VAL
	E499	GLN		R275	Y274	SER
	Q500	ASP		K276	ILE	SER
	E501	GLN		T275	I161	ASN
	A502	GLN		T277	I162	GLU
	K503	GLY		R278		ALA
		GLY		A279	R186	ALA
		VAL		V280	E187	SER
	E507	MET		D281	PRO	PRO
		PHE		R282	ILE	TYR
	K510	ASP		R283	THR	ASN
	E511	SER		W284	GLU	ALA
		GLY		W285	THR	ALA
	Q515	THR			GLU	PHE
	ASP			T289	ALA	THR
	R500					

Chain c:  57% 20% 22%

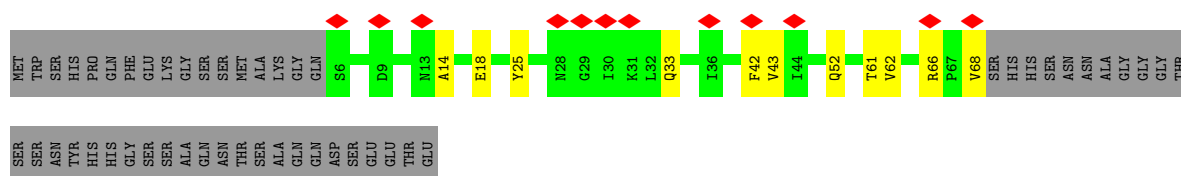
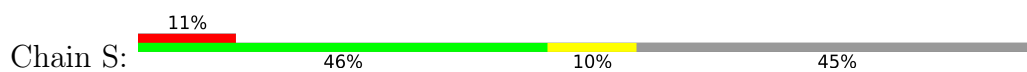
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-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



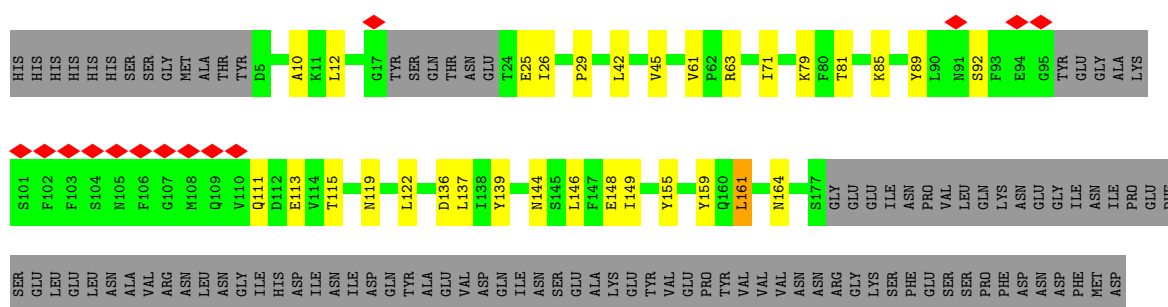




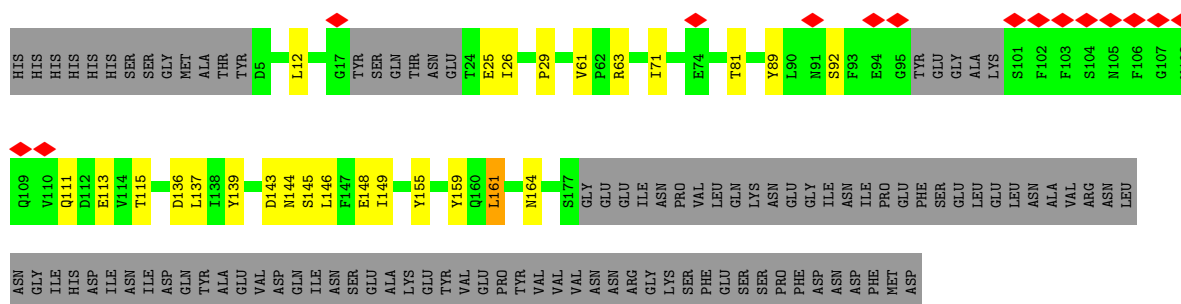
• Molecule 3: RNA-binding protein Hfq



• Molecule 4: Neck protein gp14

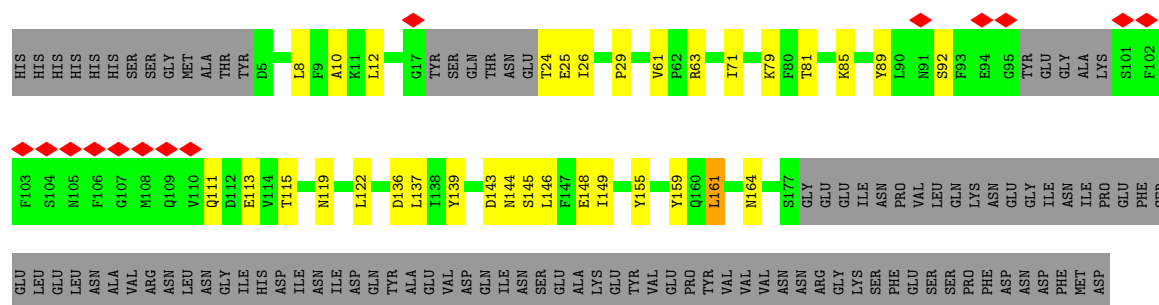


• Molecule 4: Neck protein gp14

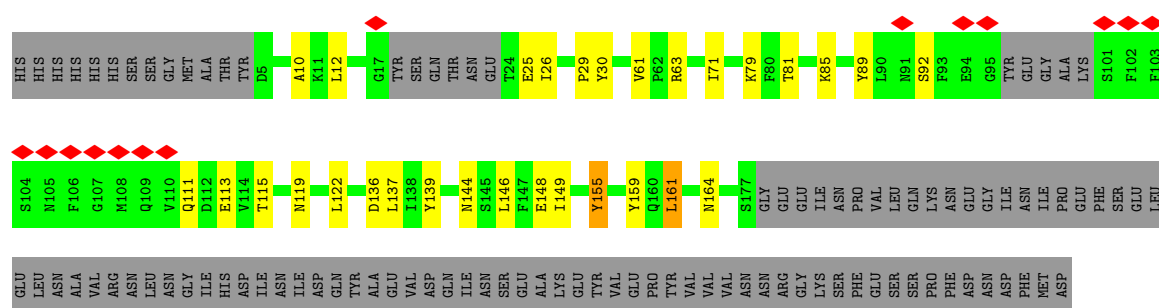


• Molecule 4: Neck protein gp14

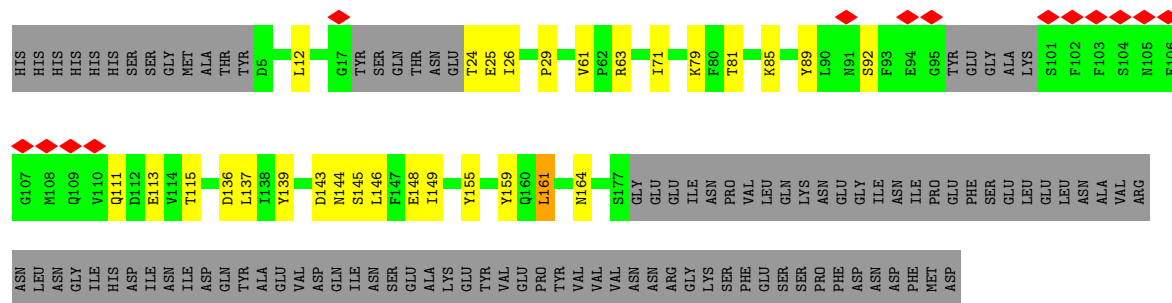




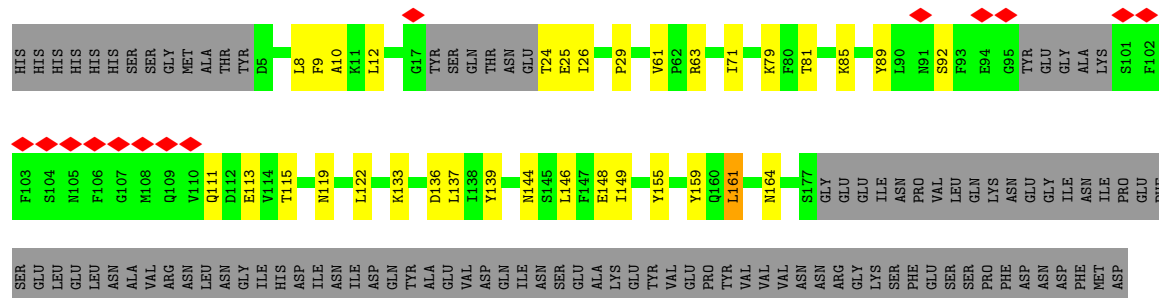
• Molecule 4: Neck protein gp14



• Molecule 4: Neck protein gp14



• Molecule 4: Neck protein gp14



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	80622	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 ( $e^-/\text{\AA}^2$ )	53.00, 53, 53, 53, 53, 53, 53	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k), FEI FALCON IV (4k x 4k), FEI FALCON IV (4k x 4k), FEI FALCON IV (4k x 4k), FEI FALCON IV (4k x 4k), FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.055	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00591	Depositor
Map size (Å)	334.72, 334.72, 334.72	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.046, 1.046, 1.046	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	0.11	0/2023	0.26	0/2732
1	B	0.23	0/2023	0.36	0/2732
1	C	0.11	0/2023	0.26	0/2732
1	D	0.10	0/2023	0.26	0/2732
1	E	0.10	0/2023	0.26	0/2732
1	F	0.11	0/2023	0.27	0/2732
1	G	0.10	0/2023	0.26	0/2732
1	H	0.11	0/2023	0.26	0/2732
1	I	0.10	0/2023	0.26	0/2732
1	J	0.10	0/2023	0.27	0/2732
1	K	0.10	0/2023	0.25	0/2732
1	L	0.10	0/2023	0.26	0/2732
2	a	0.10	0/3447	0.26	0/4644
2	b	0.11	0/3447	0.27	0/4644
2	c	0.10	0/3447	0.26	0/4644
2	d	0.11	0/3447	0.27	0/4644
2	e	0.10	0/3447	0.26	0/4644
2	f	0.11	0/3447	0.27	0/4644
2	g	0.10	0/3447	0.26	0/4644
2	h	0.11	0/3447	0.27	0/4644
2	i	0.10	0/3447	0.26	0/4644
2	j	0.11	0/3447	0.27	0/4644
2	k	0.10	0/3447	0.26	0/4644
2	l	0.11	0/3447	0.27	0/4644
3	S	0.10	0/513	0.26	0/696
3	T	0.09	0/513	0.25	0/696
3	U	0.09	0/513	0.24	0/696
3	V	0.11	0/513	0.26	0/696
3	W	0.09	0/513	0.25	0/696
3	X	0.09	0/513	0.24	0/696
4	M	0.11	0/1320	0.27	0/1788
4	N	0.11	0/1320	0.27	0/1788
4	O	0.10	0/1320	0.27	0/1788
4	P	0.11	0/1320	0.27	0/1788

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
4	Q	0.11	0/1320	0.27	0/1788
4	R	0.11	0/1320	0.27	0/1788
All	All	0.11	0/76638	0.27	0/103416

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1977	0	1926	31	0
1	B	1977	0	1926	46	0
1	C	1977	0	1926	34	0
1	D	1977	0	1926	31	0
1	E	1977	0	1926	33	0
1	F	1977	0	1926	29	0
1	G	1977	0	1926	33	0
1	H	1977	0	1926	26	0
1	I	1977	0	1926	34	0
1	J	1977	0	1926	31	0
1	K	1977	0	1926	33	0
1	L	1977	0	1926	29	0
2	a	3385	0	3331	70	0
2	b	3385	0	3331	74	0
2	c	3385	0	3331	74	0
2	d	3385	0	3331	71	0
2	e	3385	0	3331	75	0
2	f	3385	0	3331	69	0
2	g	3385	0	3331	72	0
2	h	3385	0	3331	72	0
2	i	3385	0	3331	69	0
2	j	3385	0	3331	62	0
2	k	3385	0	3331	73	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	I	3385	0	3331	73	0
3	S	504	0	530	7	0
3	T	504	0	530	9	0
3	U	504	0	530	7	0
3	V	504	0	530	8	0
3	W	504	0	530	9	0
3	X	504	0	530	9	0
4	M	1289	0	1212	20	0
4	N	1289	0	1212	23	0
4	O	1289	0	1212	26	0
4	P	1289	0	1212	23	0
4	Q	1289	0	1212	23	0
4	R	1289	0	1212	29	0
All	All	75102	0	73536	1194	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 8.

The worst 5 of 1194 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:303:PRO:HB3	2:c:300:HIS:NE2	1.94	0.82
1:D:59:VAL:O	1:D:125:CYS:HA	1.80	0.81
1:L:59:VAL:O	1:L:125:CYS:HA	1.82	0.79
1:B:28:GLU:OE2	4:N:42:LEU:HG	1.83	0.79
1:H:59:VAL:O	1:H:125:CYS:HA	1.84	0.78

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	238/315 (76%)	224 (94%)	14 (6%)	0	100	100
1	B	238/315 (76%)	222 (93%)	16 (7%)	0	100	100
1	C	238/315 (76%)	225 (94%)	13 (6%)	0	100	100
1	D	238/315 (76%)	225 (94%)	13 (6%)	0	100	100
1	E	238/315 (76%)	225 (94%)	13 (6%)	0	100	100
1	F	238/315 (76%)	222 (93%)	16 (7%)	0	100	100
1	G	238/315 (76%)	227 (95%)	11 (5%)	0	100	100
1	H	238/315 (76%)	222 (93%)	16 (7%)	0	100	100
1	I	238/315 (76%)	225 (94%)	13 (6%)	0	100	100
1	J	238/315 (76%)	224 (94%)	14 (6%)	0	100	100
1	K	238/315 (76%)	224 (94%)	14 (6%)	0	100	100
1	L	238/315 (76%)	222 (93%)	16 (7%)	0	100	100
2	a	407/533 (76%)	394 (97%)	13 (3%)	0	100	100
2	b	407/533 (76%)	393 (97%)	14 (3%)	0	100	100
2	c	407/533 (76%)	393 (97%)	14 (3%)	0	100	100
2	d	407/533 (76%)	392 (96%)	15 (4%)	0	100	100
2	e	407/533 (76%)	391 (96%)	16 (4%)	0	100	100
2	f	407/533 (76%)	394 (97%)	13 (3%)	0	100	100
2	g	407/533 (76%)	393 (97%)	14 (3%)	0	100	100
2	h	407/533 (76%)	394 (97%)	13 (3%)	0	100	100
2	i	407/533 (76%)	394 (97%)	13 (3%)	0	100	100
2	j	407/533 (76%)	394 (97%)	13 (3%)	0	100	100
2	k	407/533 (76%)	392 (96%)	15 (4%)	0	100	100
2	l	407/533 (76%)	393 (97%)	14 (3%)	0	100	100
3	S	61/114 (54%)	61 (100%)	0	0	100	100
3	T	61/114 (54%)	61 (100%)	0	0	100	100
3	U	61/114 (54%)	61 (100%)	0	0	100	100
3	V	61/114 (54%)	61 (100%)	0	0	100	100
3	W	61/114 (54%)	61 (100%)	0	0	100	100
3	X	61/114 (54%)	61 (100%)	0	0	100	100
4	M	156/265 (59%)	144 (92%)	12 (8%)	0	100	100
4	N	156/265 (59%)	146 (94%)	10 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	O	156/265 (59%)	143 (92%)	13 (8%)	0	100	100
4	P	156/265 (59%)	146 (94%)	10 (6%)	0	100	100
4	Q	156/265 (59%)	144 (92%)	12 (8%)	0	100	100
4	R	156/265 (59%)	144 (92%)	12 (8%)	0	100	100
All	All	9042/12450 (73%)	8637 (96%)	405 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	207/266 (78%)	197 (95%)	10 (5%)	23	54
1	B	207/266 (78%)	196 (95%)	11 (5%)	20	50
1	C	207/266 (78%)	196 (95%)	11 (5%)	20	50
1	D	207/266 (78%)	199 (96%)	8 (4%)	28	61
1	E	207/266 (78%)	199 (96%)	8 (4%)	28	61
1	F	207/266 (78%)	201 (97%)	6 (3%)	37	69
1	G	207/266 (78%)	197 (95%)	10 (5%)	23	54
1	H	207/266 (78%)	199 (96%)	8 (4%)	28	61
1	I	207/266 (78%)	197 (95%)	10 (5%)	23	54
1	J	207/266 (78%)	198 (96%)	9 (4%)	26	58
1	K	207/266 (78%)	199 (96%)	8 (4%)	28	61
1	L	207/266 (78%)	201 (97%)	6 (3%)	37	69
2	a	363/473 (77%)	350 (96%)	13 (4%)	31	63
2	b	363/473 (77%)	348 (96%)	15 (4%)	27	60
2	c	363/473 (77%)	349 (96%)	14 (4%)	28	61
2	d	363/473 (77%)	351 (97%)	12 (3%)	33	65
2	e	363/473 (77%)	350 (96%)	13 (4%)	31	63

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	f	363/473 (77%)	350 (96%)	13 (4%)	31	63
2	g	363/473 (77%)	350 (96%)	13 (4%)	31	63
2	h	363/473 (77%)	349 (96%)	14 (4%)	28	61
2	i	363/473 (77%)	348 (96%)	15 (4%)	27	60
2	j	363/473 (77%)	350 (96%)	13 (4%)	31	63
2	k	363/473 (77%)	350 (96%)	13 (4%)	31	63
2	l	363/473 (77%)	351 (97%)	12 (3%)	33	65
3	S	59/100 (59%)	57 (97%)	2 (3%)	32	65
3	T	59/100 (59%)	57 (97%)	2 (3%)	32	65
3	U	59/100 (59%)	57 (97%)	2 (3%)	32	65
3	V	59/100 (59%)	57 (97%)	2 (3%)	32	65
3	W	59/100 (59%)	57 (97%)	2 (3%)	32	65
3	X	59/100 (59%)	57 (97%)	2 (3%)	32	65
4	M	133/237 (56%)	129 (97%)	4 (3%)	36	68
4	N	133/237 (56%)	129 (97%)	4 (3%)	36	68
4	O	133/237 (56%)	129 (97%)	4 (3%)	36	68
4	P	133/237 (56%)	129 (97%)	4 (3%)	36	68
4	Q	133/237 (56%)	129 (97%)	4 (3%)	36	68
4	R	133/237 (56%)	129 (97%)	4 (3%)	36	68
All	All	7992/10890 (73%)	7691 (96%)	301 (4%)	30	62

5 of 301 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	271	LEU
1	J	121	MET
1	D	154	MET
1	G	138	LEU
1	K	295	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 171 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	39	GLN

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Mol	Chain	Res	Type
1	F	169	GLN
1	A	39	GLN
1	D	33	GLN
1	H	33	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](#)

There are no chain breaks in this entry.

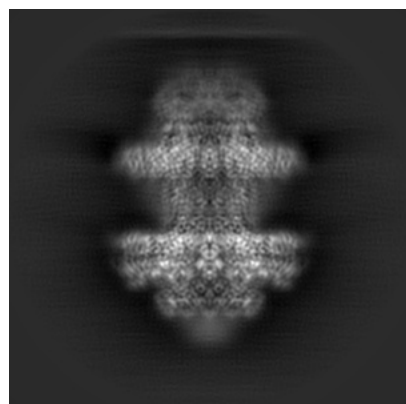
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63389. These allow visual inspection of the internal detail of the map and identification of artifacts.

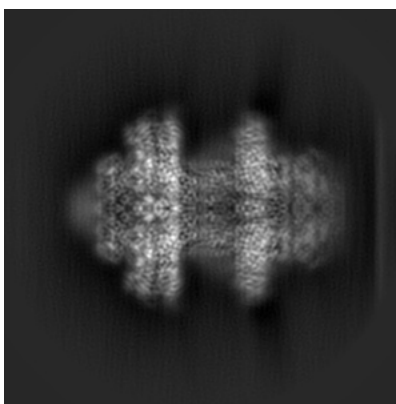
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

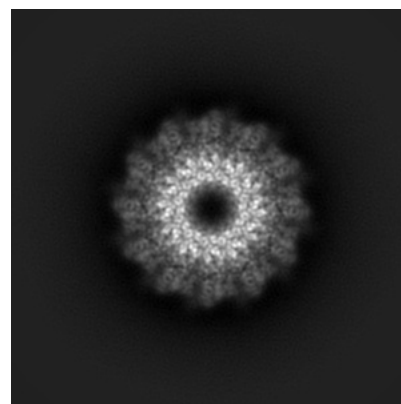
#### 6.1.1 Primary map



X

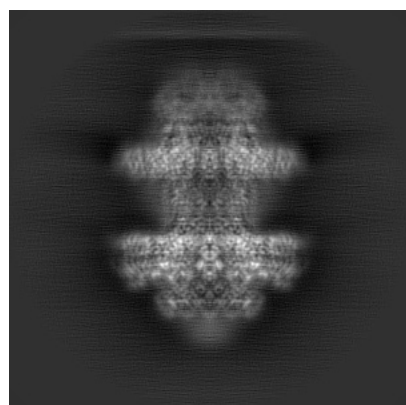


Y

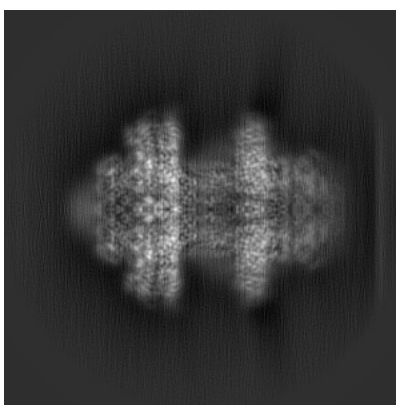


Z

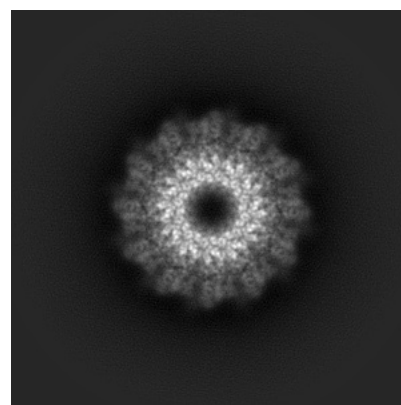
#### 6.1.2 Raw map



X



Y

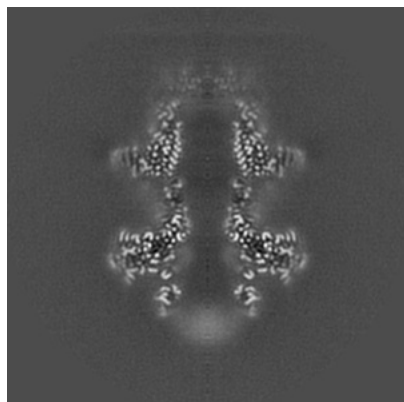


Z

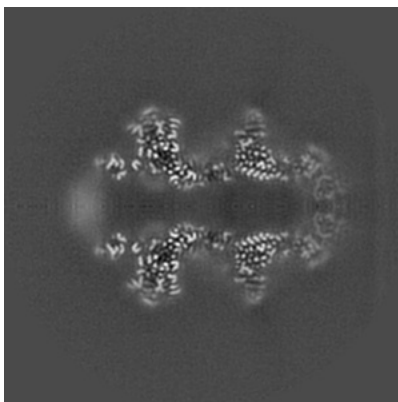
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

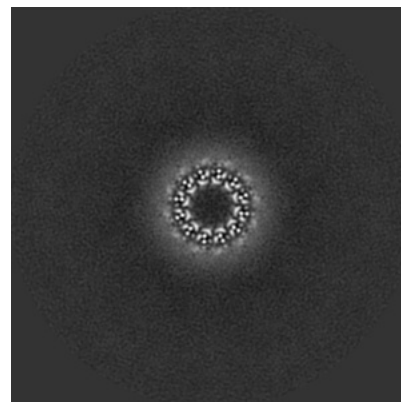
### 6.2.1 Primary map



X Index: 160

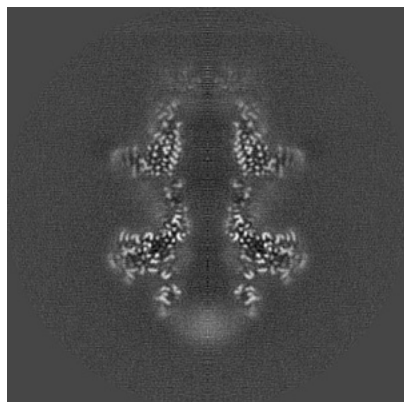


Y Index: 160

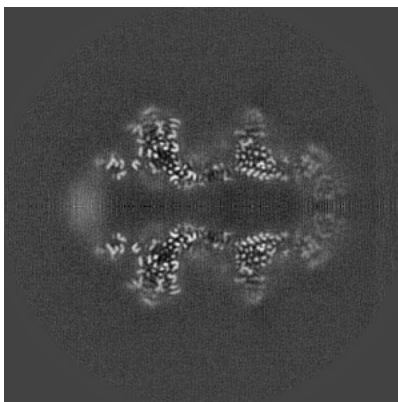


Z Index: 160

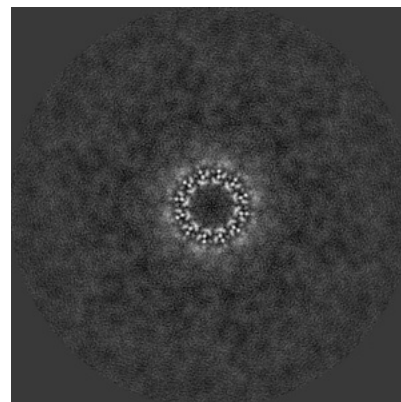
### 6.2.2 Raw map



X Index: 160



Y Index: 160

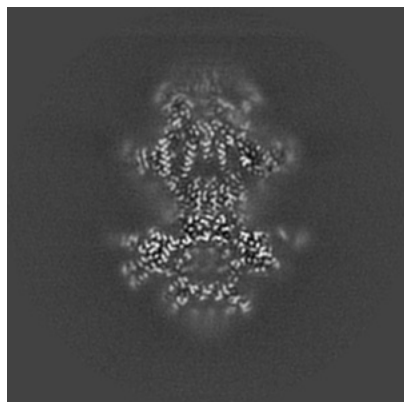


Z Index: 160

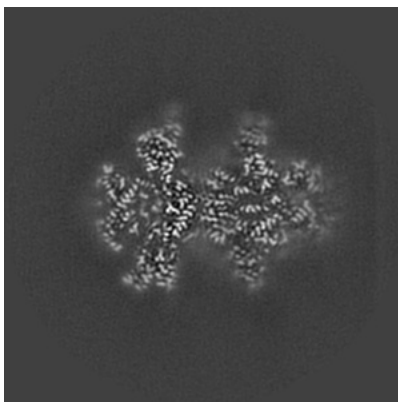
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

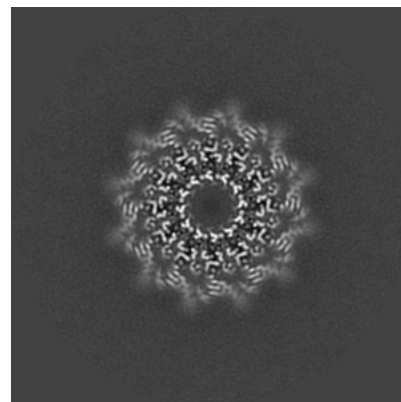
### 6.3.1 Primary map



X Index: 137

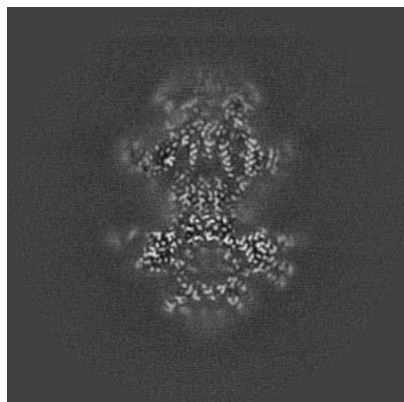


Y Index: 187

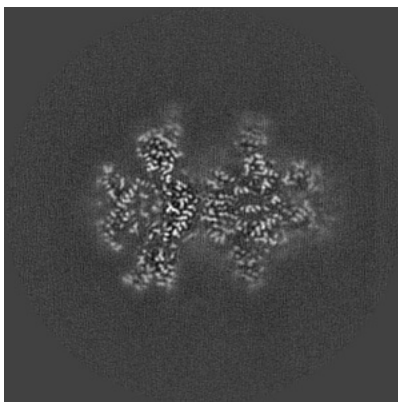


Z Index: 134

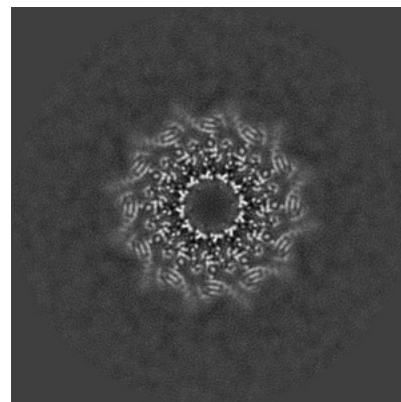
### 6.3.2 Raw map



X Index: 183



Y Index: 187

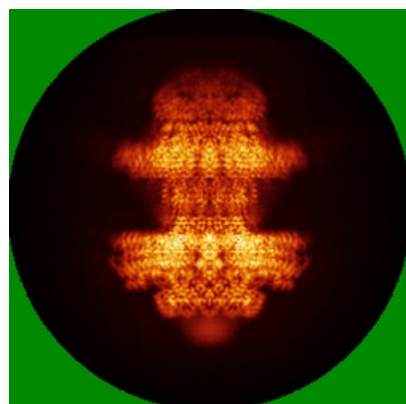


Z Index: 135

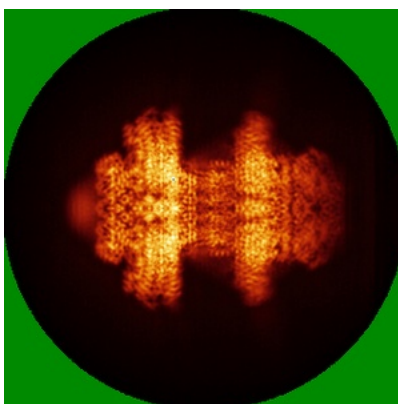
The images above show the largest variance slices of the map in three orthogonal directions.

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

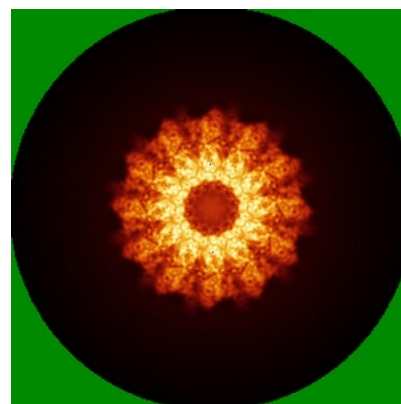
### 6.4.1 Primary map



X

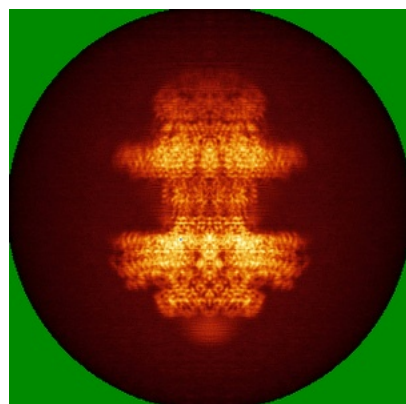


Y

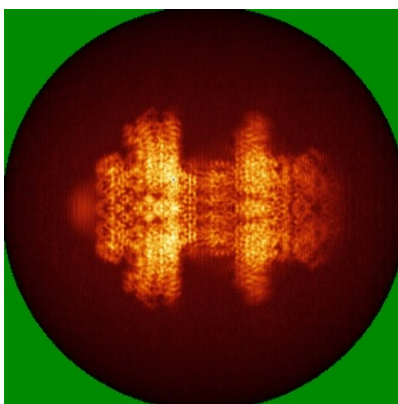


Z

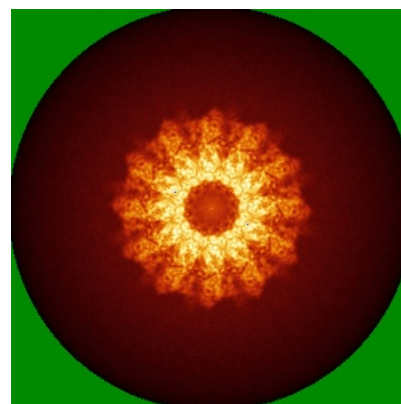
### 6.4.2 Raw map



X



Y

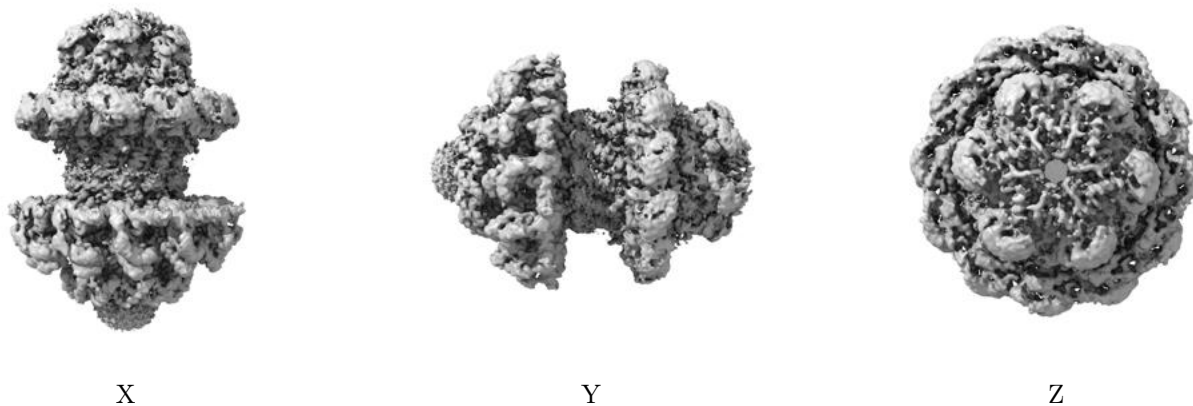


Z

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.

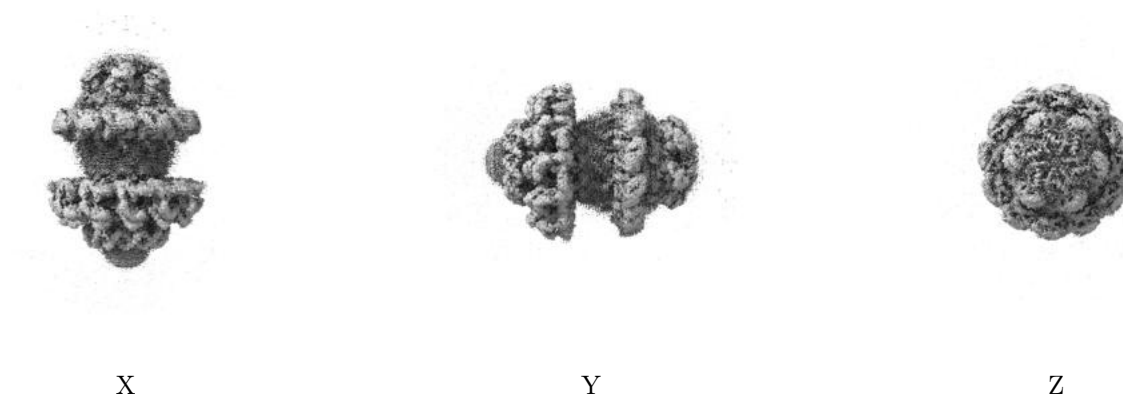
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00591. 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.

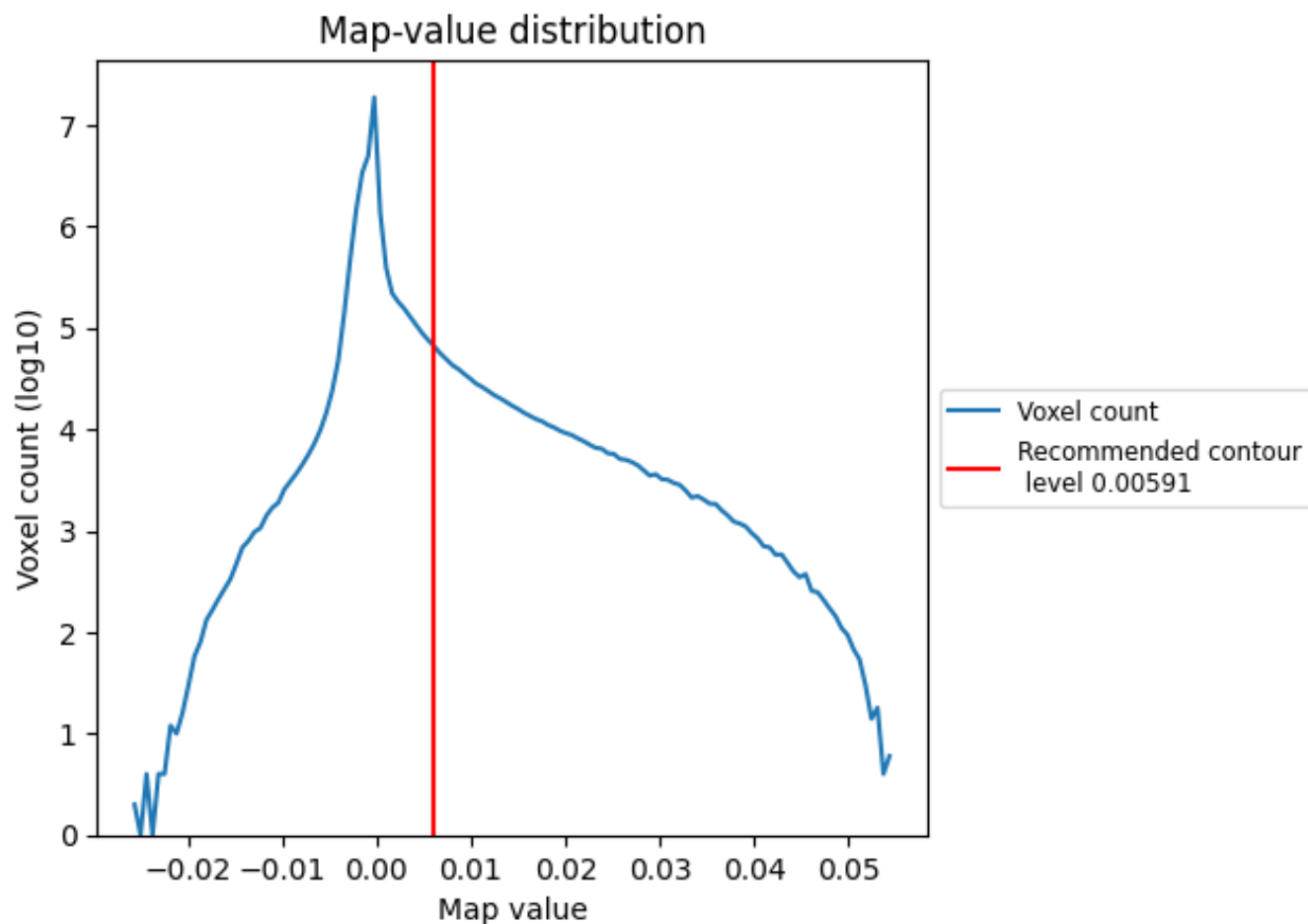
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

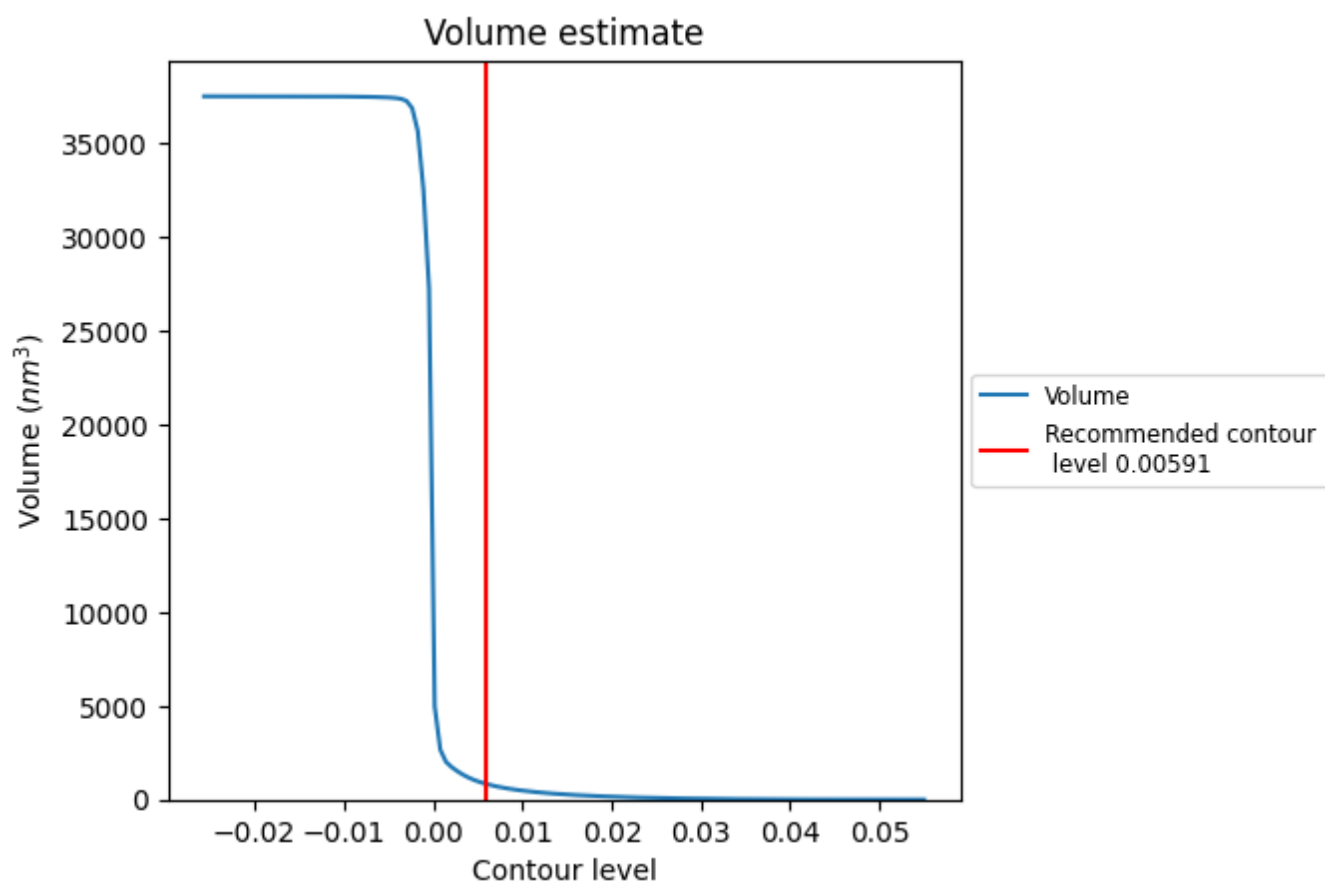
This section contains the results of statistical analysis of the map.

### 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.

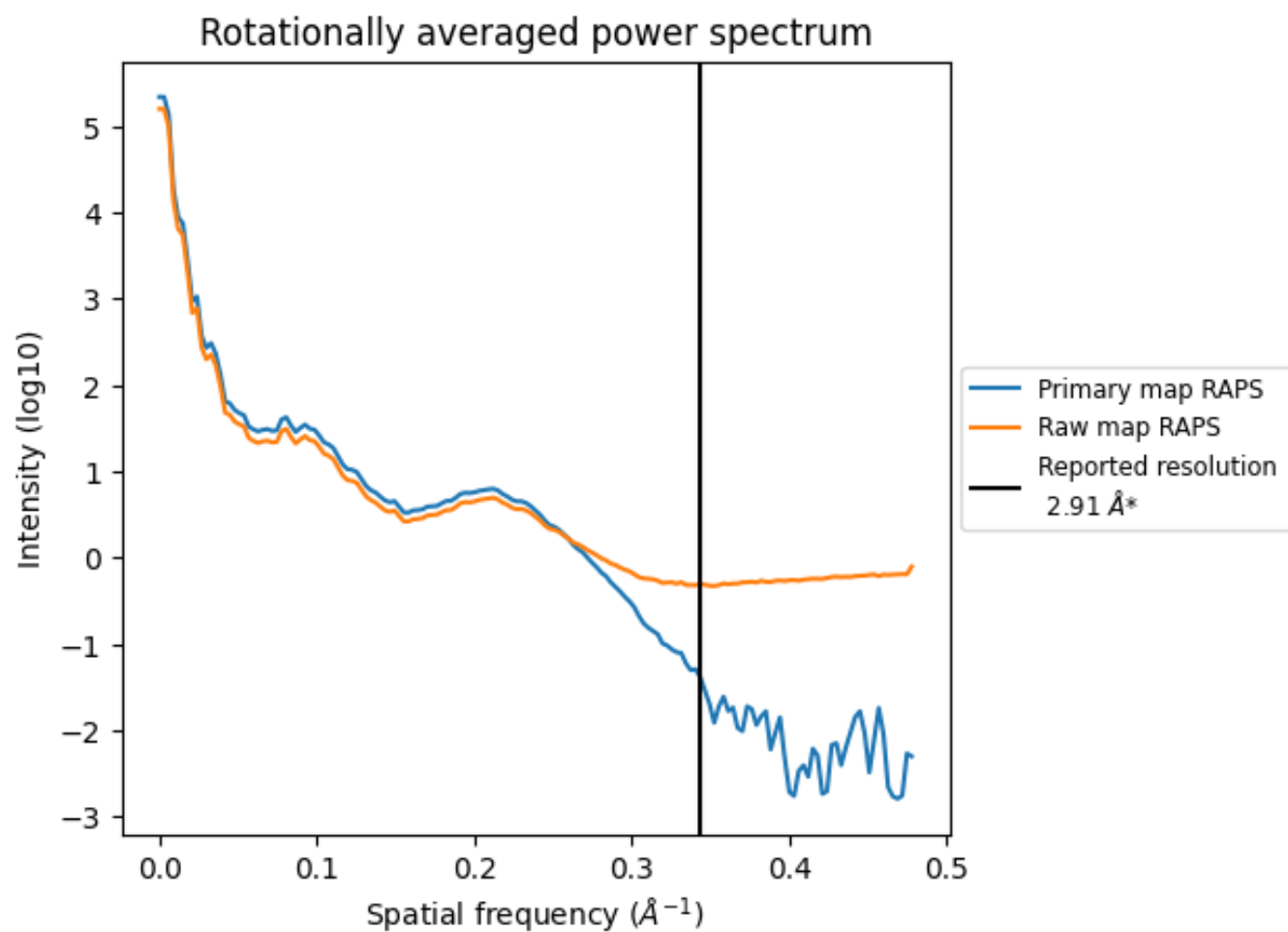
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 838 nm<sup>3</sup>; this corresponds to an approximate mass of 757 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 ⓘ

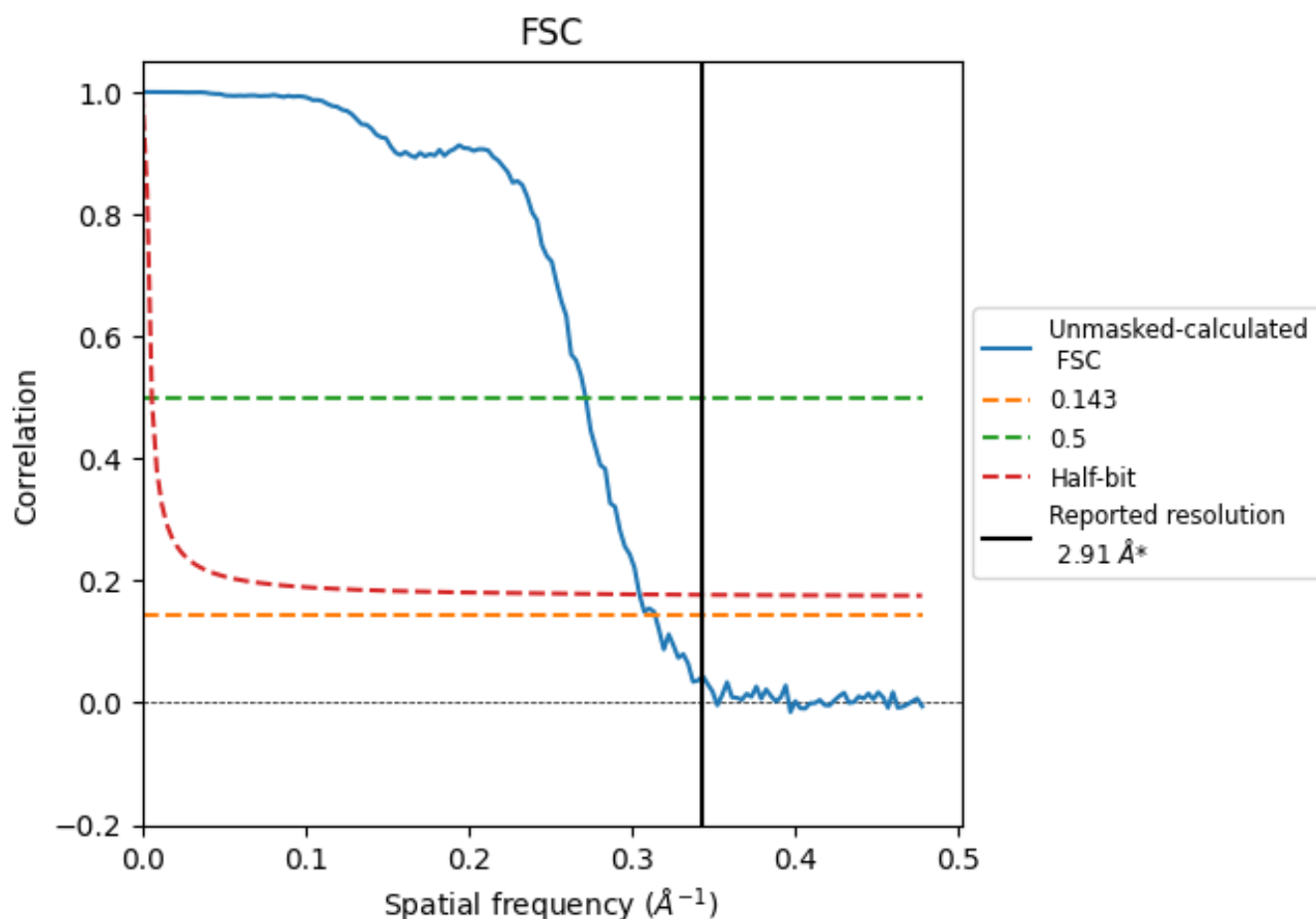


\*Reported resolution corresponds to spatial frequency of  $0.344 \text{ \AA}^{-1}$

## 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 0.344 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

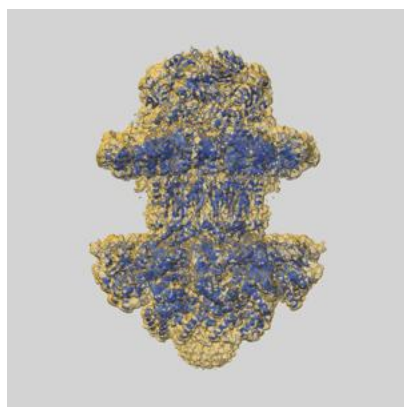
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.91	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.18	3.68	3.28

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

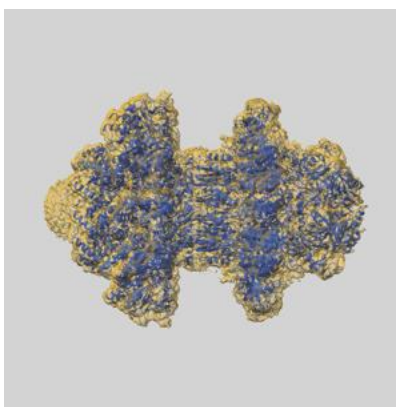
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-63389 and PDB model 9LU6. Per-residue inclusion information can be found in section [3](#) on page [15](#).

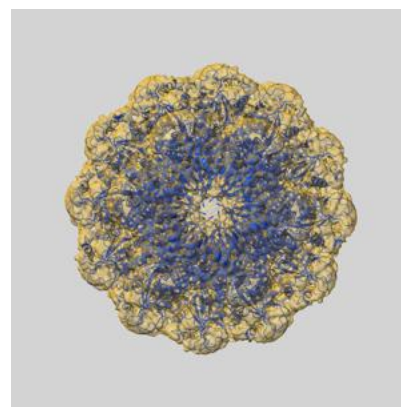
### 9.1 Map-model overlay [i](#)



X



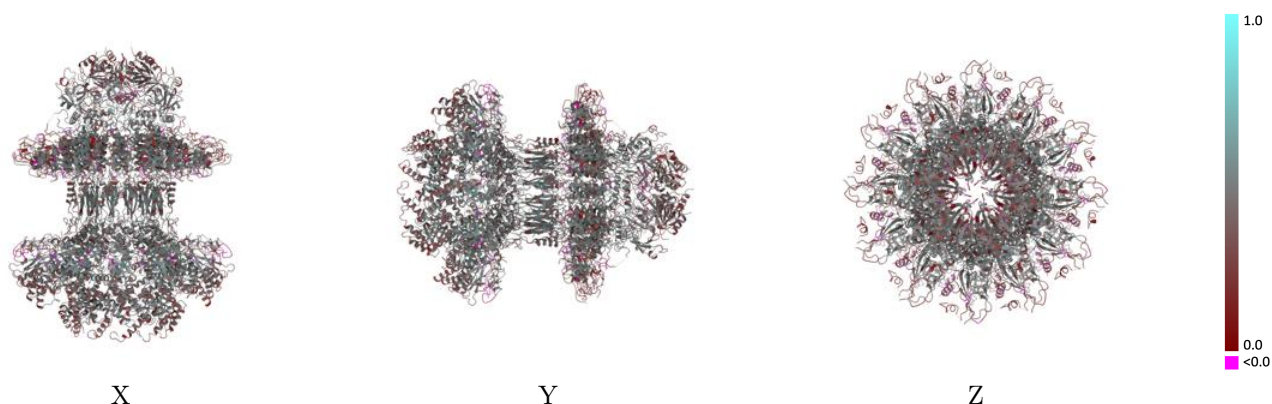
Y



Z

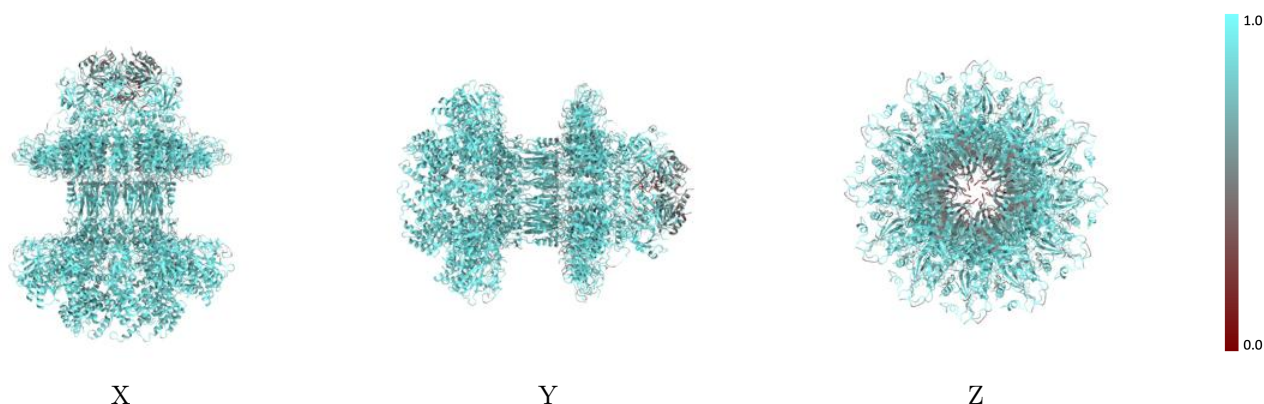
The images above show the 3D surface view of the map at the recommended contour level 0.00591 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



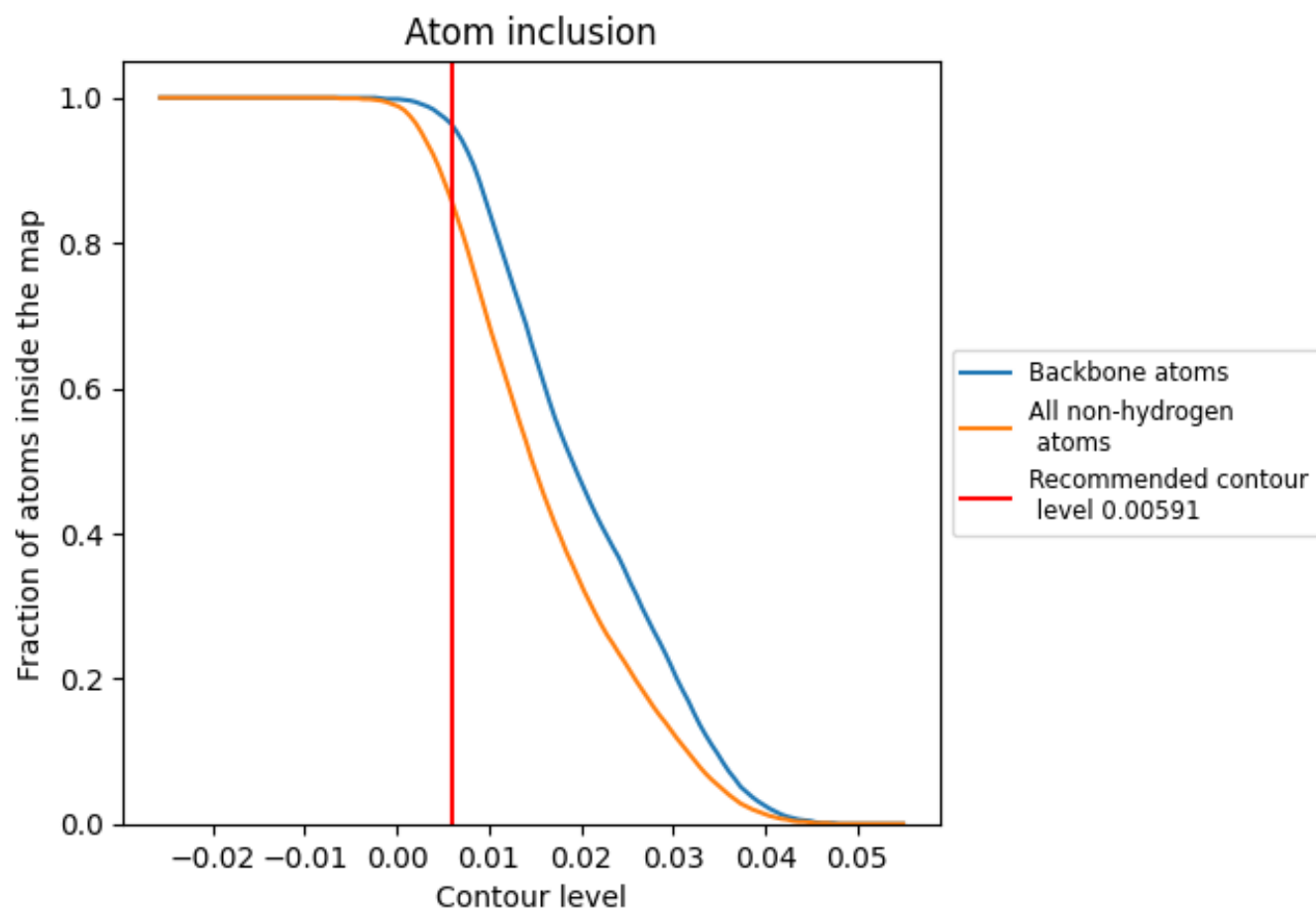
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00591).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% 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 (0.00591) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8600	 0.4100
A	 0.8550	 0.3850
B	 0.8440	 0.3810
C	 0.8510	 0.3880
D	 0.8480	 0.3930
E	 0.8550	 0.3870
F	 0.8530	 0.3930
G	 0.8520	 0.3870
H	 0.8480	 0.3940
I	 0.8520	 0.3900
J	 0.8510	 0.3910
K	 0.8560	 0.3880
L	 0.8510	 0.3920
M	 0.8320	 0.3840
N	 0.8350	 0.3870
O	 0.8360	 0.3850
P	 0.8380	 0.3880
Q	 0.8330	 0.3880
R	 0.8350	 0.3820
S	 0.5690	 0.3740
T	 0.5650	 0.3690
U	 0.5610	 0.3700
V	 0.5730	 0.3730
W	 0.5710	 0.3660
X	 0.5610	 0.3650
a	 0.8930	 0.4320
b	 0.8900	 0.4300
c	 0.8940	 0.4320
d	 0.8900	 0.4280
e	 0.8910	 0.4340
f	 0.8920	 0.4300
g	 0.8930	 0.4320
h	 0.8920	 0.4320
i	 0.8930	 0.4320
j	 0.8930	 0.4290



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Chain	Atom inclusion	Q-score
k	 0.8890	 0.4290
l	 0.8860	 0.4280