



wwPDB EM Validation Summary Report ⓘ

Jan 26, 2023 – 07:01 PM EST

PDB ID : 8FM9
EMDB ID : EMD-29289
Title : Nodavirus RNA replication proto-crown, detergent-solublized C12 multimer
Authors : Zhan, H.; Unchwaniwala, N.; Rebolledo Viveros, A.; Pennington, J.; Horswill, M.; Broadberry, R.; Myers, J.; den Boon, J.; Grant, T.; Ahlquist, P.
Deposited on : 2022-12-22
Resolution : 3.20 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

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:

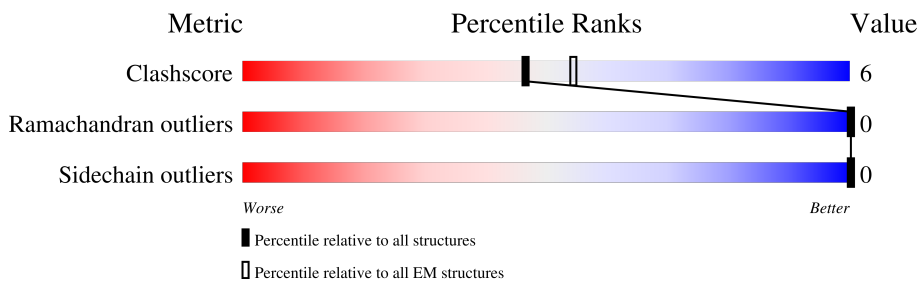
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 3.20 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	1011	
1	B	1011	
1	C	1011	
1	D	1011	
1	E	1011	
1	F	1011	
1	G	1011	
1	H	1011	

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Mol	Chain	Length	Quality of chain
1	I	1011	25% 6% 70%
1	J	1011	25% 6% 70%
1	K	1011	25% 6% 70%
1	L	1011	28% 6% 70%
1	M	1011	33% 28% 67%
1	N	1011	33% 28% 67%
1	O	1011	33% 28% 67%
1	P	1011	33% 28% 67%
1	Q	1011	33% 28% 67%
1	R	1011	33% 28% 67%
1	S	1011	33% 28% 67%
1	T	1011	33% 28% 67%
1	U	1011	33% 28% 67%
1	V	1011	33% 28% 67%
1	W	1011	33% 28% 67%
1	X	1011	33% 28% 67%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 76764 atoms, of which 29916 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 RNA-directed RNA polymerase.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	308	4986	1599	2493	435	450	9	0	0
1	B	308	4986	1599	2493	435	450	9	0	0
1	C	308	4986	1599	2493	435	450	9	0	0
1	D	308	4986	1599	2493	435	450	9	0	0
1	E	308	4986	1599	2493	435	450	9	0	0
1	F	308	4986	1599	2493	435	450	9	0	0
1	G	308	4986	1599	2493	435	450	9	0	0
1	H	308	4986	1599	2493	435	450	9	0	0
1	I	308	4986	1599	2493	435	450	9	0	0
1	J	308	4986	1599	2493	435	450	9	0	0
1	K	308	4986	1599	2493	435	450	9	0	0
1	L	308	4986	1599	2493	435	450	9	0	0
1	M	333	1411	724	338	349			0	0
1	N	333	1411	724	338	349			0	0
1	O	333	1411	724	338	349			0	0
1	P	333	1411	724	338	349			0	0
1	Q	333	1411	724	338	349			0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	R	333	Total	C	N	O	0	0
			1411	724	338	349		
1	S	333	Total	C	N	O	0	0
			1411	724	338	349		
1	T	333	Total	C	N	O	0	0
			1411	724	338	349		
1	U	333	Total	C	N	O	0	0
			1411	724	338	349		
1	V	333	Total	C	N	O	0	0
			1411	724	338	349		
1	W	333	Total	C	N	O	0	0
			1411	724	338	349		
1	X	333	Total	C	N	O	0	0
			1411	724	338	349		

There are 336 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	897	LEU	MET	conflict	UNP Q66929
A	999	SER	-	expression tag	UNP Q66929
A	1000	ARG	-	expression tag	UNP Q66929
A	1001	LEU	-	expression tag	UNP Q66929
A	1002	GLU	-	expression tag	UNP Q66929
A	1003	GLU	-	expression tag	UNP Q66929
A	1004	GLU	-	expression tag	UNP Q66929
A	1005	LEU	-	expression tag	UNP Q66929
A	1006	ARG	-	expression tag	UNP Q66929
A	1007	ARG	-	expression tag	UNP Q66929
A	1008	ARG	-	expression tag	UNP Q66929
A	1009	LEU	-	expression tag	UNP Q66929
A	1010	THR	-	expression tag	UNP Q66929
A	1011	GLU	-	expression tag	UNP Q66929
B	897	LEU	MET	conflict	UNP Q66929
B	999	SER	-	expression tag	UNP Q66929
B	1000	ARG	-	expression tag	UNP Q66929
B	1001	LEU	-	expression tag	UNP Q66929
B	1002	GLU	-	expression tag	UNP Q66929
B	1003	GLU	-	expression tag	UNP Q66929
B	1004	GLU	-	expression tag	UNP Q66929
B	1005	LEU	-	expression tag	UNP Q66929
B	1006	ARG	-	expression tag	UNP Q66929
B	1007	ARG	-	expression tag	UNP Q66929
B	1008	ARG	-	expression tag	UNP Q66929

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1009	LEU	-	expression tag	UNP Q66929
B	1010	THR	-	expression tag	UNP Q66929
B	1011	GLU	-	expression tag	UNP Q66929
C	897	LEU	MET	conflict	UNP Q66929
C	999	SER	-	expression tag	UNP Q66929
C	1000	ARG	-	expression tag	UNP Q66929
C	1001	LEU	-	expression tag	UNP Q66929
C	1002	GLU	-	expression tag	UNP Q66929
C	1003	GLU	-	expression tag	UNP Q66929
C	1004	GLU	-	expression tag	UNP Q66929
C	1005	LEU	-	expression tag	UNP Q66929
C	1006	ARG	-	expression tag	UNP Q66929
C	1007	ARG	-	expression tag	UNP Q66929
C	1008	ARG	-	expression tag	UNP Q66929
C	1009	LEU	-	expression tag	UNP Q66929
C	1010	THR	-	expression tag	UNP Q66929
C	1011	GLU	-	expression tag	UNP Q66929
D	897	LEU	MET	conflict	UNP Q66929
D	999	SER	-	expression tag	UNP Q66929
D	1000	ARG	-	expression tag	UNP Q66929
D	1001	LEU	-	expression tag	UNP Q66929
D	1002	GLU	-	expression tag	UNP Q66929
D	1003	GLU	-	expression tag	UNP Q66929
D	1004	GLU	-	expression tag	UNP Q66929
D	1005	LEU	-	expression tag	UNP Q66929
D	1006	ARG	-	expression tag	UNP Q66929
D	1007	ARG	-	expression tag	UNP Q66929
D	1008	ARG	-	expression tag	UNP Q66929
D	1009	LEU	-	expression tag	UNP Q66929
D	1010	THR	-	expression tag	UNP Q66929
D	1011	GLU	-	expression tag	UNP Q66929
E	897	LEU	MET	conflict	UNP Q66929
E	999	SER	-	expression tag	UNP Q66929
E	1000	ARG	-	expression tag	UNP Q66929
E	1001	LEU	-	expression tag	UNP Q66929
E	1002	GLU	-	expression tag	UNP Q66929
E	1003	GLU	-	expression tag	UNP Q66929
E	1004	GLU	-	expression tag	UNP Q66929
E	1005	LEU	-	expression tag	UNP Q66929
E	1006	ARG	-	expression tag	UNP Q66929
E	1007	ARG	-	expression tag	UNP Q66929
E	1008	ARG	-	expression tag	UNP Q66929

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1009	LEU	-	expression tag	UNP Q66929
E	1010	THR	-	expression tag	UNP Q66929
E	1011	GLU	-	expression tag	UNP Q66929
F	897	LEU	MET	conflict	UNP Q66929
F	999	SER	-	expression tag	UNP Q66929
F	1000	ARG	-	expression tag	UNP Q66929
F	1001	LEU	-	expression tag	UNP Q66929
F	1002	GLU	-	expression tag	UNP Q66929
F	1003	GLU	-	expression tag	UNP Q66929
F	1004	GLU	-	expression tag	UNP Q66929
F	1005	LEU	-	expression tag	UNP Q66929
F	1006	ARG	-	expression tag	UNP Q66929
F	1007	ARG	-	expression tag	UNP Q66929
F	1008	ARG	-	expression tag	UNP Q66929
F	1009	LEU	-	expression tag	UNP Q66929
F	1010	THR	-	expression tag	UNP Q66929
F	1011	GLU	-	expression tag	UNP Q66929
G	897	LEU	MET	conflict	UNP Q66929
G	999	SER	-	expression tag	UNP Q66929
G	1000	ARG	-	expression tag	UNP Q66929
G	1001	LEU	-	expression tag	UNP Q66929
G	1002	GLU	-	expression tag	UNP Q66929
G	1003	GLU	-	expression tag	UNP Q66929
G	1004	GLU	-	expression tag	UNP Q66929
G	1005	LEU	-	expression tag	UNP Q66929
G	1006	ARG	-	expression tag	UNP Q66929
G	1007	ARG	-	expression tag	UNP Q66929
G	1008	ARG	-	expression tag	UNP Q66929
G	1009	LEU	-	expression tag	UNP Q66929
G	1010	THR	-	expression tag	UNP Q66929
G	1011	GLU	-	expression tag	UNP Q66929
H	897	LEU	MET	conflict	UNP Q66929
H	999	SER	-	expression tag	UNP Q66929
H	1000	ARG	-	expression tag	UNP Q66929
H	1001	LEU	-	expression tag	UNP Q66929
H	1002	GLU	-	expression tag	UNP Q66929
H	1003	GLU	-	expression tag	UNP Q66929
H	1004	GLU	-	expression tag	UNP Q66929
H	1005	LEU	-	expression tag	UNP Q66929
H	1006	ARG	-	expression tag	UNP Q66929
H	1007	ARG	-	expression tag	UNP Q66929
H	1008	ARG	-	expression tag	UNP Q66929

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Chain	Residue	Modelled	Actual	Comment	Reference
H	1009	LEU	-	expression tag	UNP Q66929
H	1010	THR	-	expression tag	UNP Q66929
H	1011	GLU	-	expression tag	UNP Q66929
I	897	LEU	MET	conflict	UNP Q66929
I	999	SER	-	expression tag	UNP Q66929
I	1000	ARG	-	expression tag	UNP Q66929
I	1001	LEU	-	expression tag	UNP Q66929
I	1002	GLU	-	expression tag	UNP Q66929
I	1003	GLU	-	expression tag	UNP Q66929
I	1004	GLU	-	expression tag	UNP Q66929
I	1005	LEU	-	expression tag	UNP Q66929
I	1006	ARG	-	expression tag	UNP Q66929
I	1007	ARG	-	expression tag	UNP Q66929
I	1008	ARG	-	expression tag	UNP Q66929
I	1009	LEU	-	expression tag	UNP Q66929
I	1010	THR	-	expression tag	UNP Q66929
I	1011	GLU	-	expression tag	UNP Q66929
J	897	LEU	MET	conflict	UNP Q66929
J	999	SER	-	expression tag	UNP Q66929
J	1000	ARG	-	expression tag	UNP Q66929
J	1001	LEU	-	expression tag	UNP Q66929
J	1002	GLU	-	expression tag	UNP Q66929
J	1003	GLU	-	expression tag	UNP Q66929
J	1004	GLU	-	expression tag	UNP Q66929
J	1005	LEU	-	expression tag	UNP Q66929
J	1006	ARG	-	expression tag	UNP Q66929
J	1007	ARG	-	expression tag	UNP Q66929
J	1008	ARG	-	expression tag	UNP Q66929
J	1009	LEU	-	expression tag	UNP Q66929
J	1010	THR	-	expression tag	UNP Q66929
J	1011	GLU	-	expression tag	UNP Q66929
K	897	LEU	MET	conflict	UNP Q66929
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K	1000	ARG	-	expression tag	UNP Q66929
K	1001	LEU	-	expression tag	UNP Q66929
K	1002	GLU	-	expression tag	UNP Q66929
K	1003	GLU	-	expression tag	UNP Q66929
K	1004	GLU	-	expression tag	UNP Q66929
K	1005	LEU	-	expression tag	UNP Q66929
K	1006	ARG	-	expression tag	UNP Q66929
K	1007	ARG	-	expression tag	UNP Q66929
K	1008	ARG	-	expression tag	UNP Q66929

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Chain	Residue	Modelled	Actual	Comment	Reference
K	1009	LEU	-	expression tag	UNP Q66929
K	1010	THR	-	expression tag	UNP Q66929
K	1011	GLU	-	expression tag	UNP Q66929
L	897	LEU	MET	conflict	UNP Q66929
L	999	SER	-	expression tag	UNP Q66929
L	1000	ARG	-	expression tag	UNP Q66929
L	1001	LEU	-	expression tag	UNP Q66929
L	1002	GLU	-	expression tag	UNP Q66929
L	1003	GLU	-	expression tag	UNP Q66929
L	1004	GLU	-	expression tag	UNP Q66929
L	1005	LEU	-	expression tag	UNP Q66929
L	1006	ARG	-	expression tag	UNP Q66929
L	1007	ARG	-	expression tag	UNP Q66929
L	1008	ARG	-	expression tag	UNP Q66929
L	1009	LEU	-	expression tag	UNP Q66929
L	1010	THR	-	expression tag	UNP Q66929
L	1011	GLU	-	expression tag	UNP Q66929
M	897	LEU	MET	conflict	UNP Q66929
M	999	SER	-	expression tag	UNP Q66929
M	1000	ARG	-	expression tag	UNP Q66929
M	1001	LEU	-	expression tag	UNP Q66929
M	1002	GLU	-	expression tag	UNP Q66929
M	1003	GLU	-	expression tag	UNP Q66929
M	1004	GLU	-	expression tag	UNP Q66929
M	1005	LEU	-	expression tag	UNP Q66929
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M	1007	ARG	-	expression tag	UNP Q66929
M	1008	ARG	-	expression tag	UNP Q66929
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M	1010	THR	-	expression tag	UNP Q66929
M	1011	GLU	-	expression tag	UNP Q66929
N	897	LEU	MET	conflict	UNP Q66929
N	999	SER	-	expression tag	UNP Q66929
N	1000	ARG	-	expression tag	UNP Q66929
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N	1006	ARG	-	expression tag	UNP Q66929
N	1007	ARG	-	expression tag	UNP Q66929
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Chain	Residue	Modelled	Actual	Comment	Reference
N	1009	LEU	-	expression tag	UNP Q66929
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N	1011	GLU	-	expression tag	UNP Q66929
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O	999	SER	-	expression tag	UNP Q66929
O	1000	ARG	-	expression tag	UNP Q66929
O	1001	LEU	-	expression tag	UNP Q66929
O	1002	GLU	-	expression tag	UNP Q66929
O	1003	GLU	-	expression tag	UNP Q66929
O	1004	GLU	-	expression tag	UNP Q66929
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O	1006	ARG	-	expression tag	UNP Q66929
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O	1011	GLU	-	expression tag	UNP Q66929
P	897	LEU	MET	conflict	UNP Q66929
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P	1002	GLU	-	expression tag	UNP Q66929
P	1003	GLU	-	expression tag	UNP Q66929
P	1004	GLU	-	expression tag	UNP Q66929
P	1005	LEU	-	expression tag	UNP Q66929
P	1006	ARG	-	expression tag	UNP Q66929
P	1007	ARG	-	expression tag	UNP Q66929
P	1008	ARG	-	expression tag	UNP Q66929
P	1009	LEU	-	expression tag	UNP Q66929
P	1010	THR	-	expression tag	UNP Q66929
P	1011	GLU	-	expression tag	UNP Q66929
Q	897	LEU	MET	conflict	UNP Q66929
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Q	1007	ARG	-	expression tag	UNP Q66929
Q	1008	ARG	-	expression tag	UNP Q66929

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Chain	Residue	Modelled	Actual	Comment	Reference
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Q	1010	THR	-	expression tag	UNP Q66929
Q	1011	GLU	-	expression tag	UNP Q66929
R	897	LEU	MET	conflict	UNP Q66929
R	999	SER	-	expression tag	UNP Q66929
R	1000	ARG	-	expression tag	UNP Q66929
R	1001	LEU	-	expression tag	UNP Q66929
R	1002	GLU	-	expression tag	UNP Q66929
R	1003	GLU	-	expression tag	UNP Q66929
R	1004	GLU	-	expression tag	UNP Q66929
R	1005	LEU	-	expression tag	UNP Q66929
R	1006	ARG	-	expression tag	UNP Q66929
R	1007	ARG	-	expression tag	UNP Q66929
R	1008	ARG	-	expression tag	UNP Q66929
R	1009	LEU	-	expression tag	UNP Q66929
R	1010	THR	-	expression tag	UNP Q66929
R	1011	GLU	-	expression tag	UNP Q66929
S	897	LEU	MET	conflict	UNP Q66929
S	999	SER	-	expression tag	UNP Q66929
S	1000	ARG	-	expression tag	UNP Q66929
S	1001	LEU	-	expression tag	UNP Q66929
S	1002	GLU	-	expression tag	UNP Q66929
S	1003	GLU	-	expression tag	UNP Q66929
S	1004	GLU	-	expression tag	UNP Q66929
S	1005	LEU	-	expression tag	UNP Q66929
S	1006	ARG	-	expression tag	UNP Q66929
S	1007	ARG	-	expression tag	UNP Q66929
S	1008	ARG	-	expression tag	UNP Q66929
S	1009	LEU	-	expression tag	UNP Q66929
S	1010	THR	-	expression tag	UNP Q66929
S	1011	GLU	-	expression tag	UNP Q66929
T	897	LEU	MET	conflict	UNP Q66929
T	999	SER	-	expression tag	UNP Q66929
T	1000	ARG	-	expression tag	UNP Q66929
T	1001	LEU	-	expression tag	UNP Q66929
T	1002	GLU	-	expression tag	UNP Q66929
T	1003	GLU	-	expression tag	UNP Q66929
T	1004	GLU	-	expression tag	UNP Q66929
T	1005	LEU	-	expression tag	UNP Q66929
T	1006	ARG	-	expression tag	UNP Q66929
T	1007	ARG	-	expression tag	UNP Q66929
T	1008	ARG	-	expression tag	UNP Q66929

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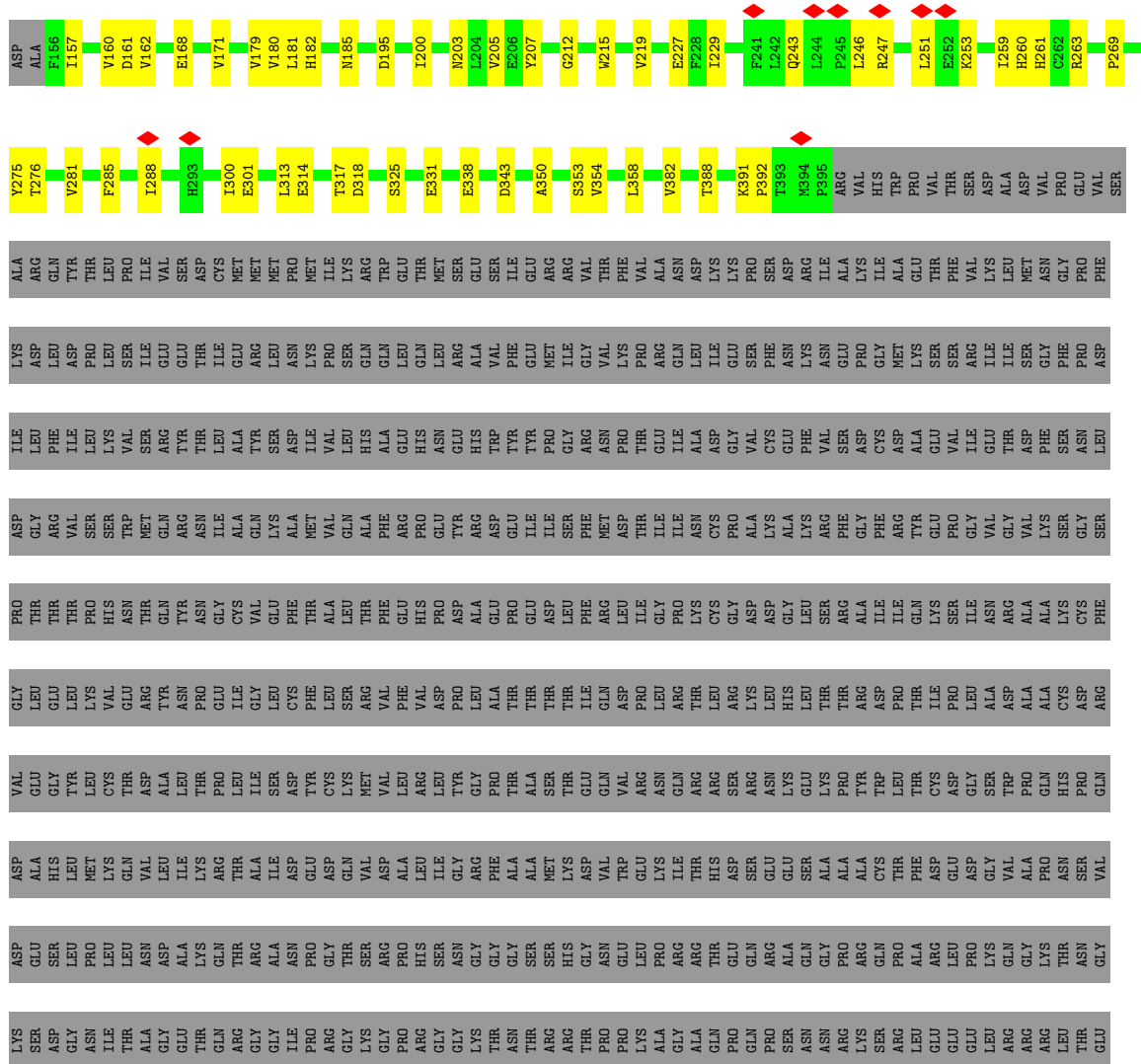
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Chain	Residue	Modelled	Actual	Comment	Reference
T	1009	LEU	-	expression tag	UNP Q66929
T	1010	THR	-	expression tag	UNP Q66929
T	1011	GLU	-	expression tag	UNP Q66929
U	897	LEU	MET	conflict	UNP Q66929
U	999	SER	-	expression tag	UNP Q66929
U	1000	ARG	-	expression tag	UNP Q66929
U	1001	LEU	-	expression tag	UNP Q66929
U	1002	GLU	-	expression tag	UNP Q66929
U	1003	GLU	-	expression tag	UNP Q66929
U	1004	GLU	-	expression tag	UNP Q66929
U	1005	LEU	-	expression tag	UNP Q66929
U	1006	ARG	-	expression tag	UNP Q66929
U	1007	ARG	-	expression tag	UNP Q66929
U	1008	ARG	-	expression tag	UNP Q66929
U	1009	LEU	-	expression tag	UNP Q66929
U	1010	THR	-	expression tag	UNP Q66929
U	1011	GLU	-	expression tag	UNP Q66929
V	897	LEU	MET	conflict	UNP Q66929
V	999	SER	-	expression tag	UNP Q66929
V	1000	ARG	-	expression tag	UNP Q66929
V	1001	LEU	-	expression tag	UNP Q66929
V	1002	GLU	-	expression tag	UNP Q66929
V	1003	GLU	-	expression tag	UNP Q66929
V	1004	GLU	-	expression tag	UNP Q66929
V	1005	LEU	-	expression tag	UNP Q66929
V	1006	ARG	-	expression tag	UNP Q66929
V	1007	ARG	-	expression tag	UNP Q66929
V	1008	ARG	-	expression tag	UNP Q66929
V	1009	LEU	-	expression tag	UNP Q66929
V	1010	THR	-	expression tag	UNP Q66929
V	1011	GLU	-	expression tag	UNP Q66929
W	897	LEU	MET	conflict	UNP Q66929
W	999	SER	-	expression tag	UNP Q66929
W	1000	ARG	-	expression tag	UNP Q66929
W	1001	LEU	-	expression tag	UNP Q66929
W	1002	GLU	-	expression tag	UNP Q66929
W	1003	GLU	-	expression tag	UNP Q66929
W	1004	GLU	-	expression tag	UNP Q66929
W	1005	LEU	-	expression tag	UNP Q66929
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W	1007	ARG	-	expression tag	UNP Q66929
W	1008	ARG	-	expression tag	UNP Q66929

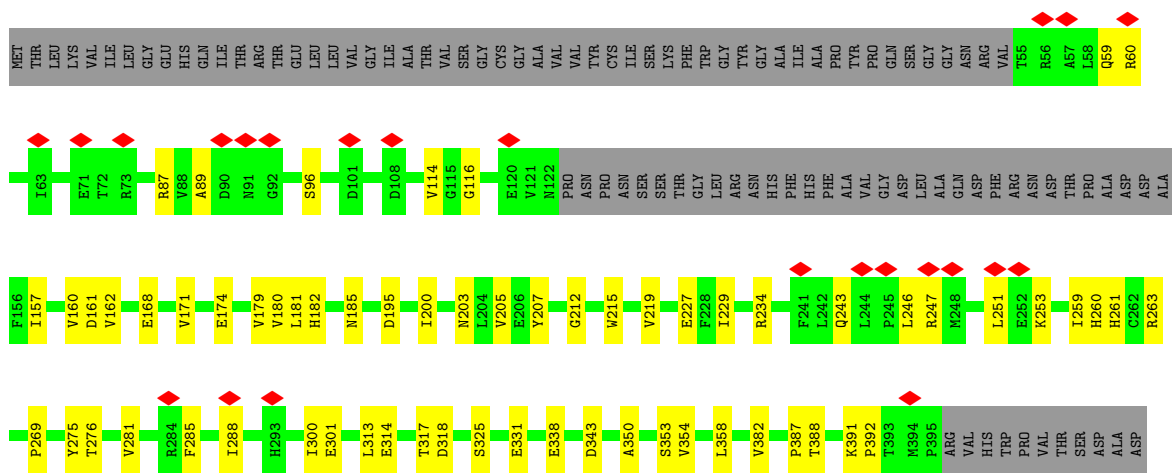
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Chain	Residue	Modelled	Actual	Comment	Reference
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W	1010	THR	-	expression tag	UNP Q66929
W	1011	GLU	-	expression tag	UNP Q66929
X	897	LEU	MET	conflict	UNP Q66929
X	999	SER	-	expression tag	UNP Q66929
X	1000	ARG	-	expression tag	UNP Q66929
X	1001	LEU	-	expression tag	UNP Q66929
X	1002	GLU	-	expression tag	UNP Q66929
X	1003	GLU	-	expression tag	UNP Q66929
X	1004	GLU	-	expression tag	UNP Q66929
X	1005	LEU	-	expression tag	UNP Q66929
X	1006	ARG	-	expression tag	UNP Q66929
X	1007	ARG	-	expression tag	UNP Q66929
X	1008	ARG	-	expression tag	UNP Q66929
X	1009	LEU	-	expression tag	UNP Q66929
X	1010	THR	-	expression tag	UNP Q66929
X	1011	GLU	-	expression tag	UNP Q66929



• Molecule 1: RNA-directed RNA polymerase



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

• Molecule 1: RNA-directed RNA polymerase



MET THR
LEU LEU
LYS VAL
VAL VAL
LEU LEU
GLY GLY
LEU LEU
GLU GLU
HIS HIS
Gln Gln
THR THR
ARG ARG
SER SER
ASN ASN
LEU LEU
ARG ARG
GLU GLU
THR THR
GLU GLU

ALA VAL
ILE ILE
ASP ASP
PRO PRO
THR THR
LYS LYS
THR THR
PRO PRO
THR THR
GLU GLU
HIS HIS
PHE PHE
TYR TYR
ARG ARG
LEU LEU
LEU LEU
SER SER
VAL VAL
GLY GLY
LEU LEU
ARG ARG
THR THR
ALA ALA
VAL VAL
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LEU LEU
THR THR
VAL VAL
SER SER
PRO PRO
LYS LYS

VAL ASN
PRO PRO
ASP ASP
LYS LYS
ASN ASN
PRO PRO
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SER SER
SER SER
THR THR
VAL VAL
Gln Gln
HIS HIS
PHE PHE
TYR TYR
ARG ARG
LEU LEU
LEU LEU
SER SER
VAL VAL
GLY GLY
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ARG ARG
THR THR
ALA ALA
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VAL VAL
SER SER
PRO PRO
LYS LYS

LEU HIS
THR THR
PHE PHE
ASN ASN
PRO PRO
LYS LYS
LYS LYS
VAL VAL
THR THR
TRP TRP
MET MET
MET MET
ILE ILE
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SER SER
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ARG ARG
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VAL VAL
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HIS HIS
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THR THR
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PRO PRO
LYS LYS

PHE LEU
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HIS HIS
PHE PHE
TYR TYR
ARG ARG
LEU LEU
LEU LEU
SER SER
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GLY GLY
LEU LEU
ARG ARG
THR THR
ALA ALA
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THR THR
LEU LEU
THR THR
VAL VAL
SER SER
PRO PRO
LYS LYS

GLU TYR
Gln Gln
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MET MET
MET MET
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VAL VAL
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LEU LEU
THR THR
VAL VAL
SER SER
PRO PRO
LYS LYS

MET GLY
HIS HIS
LYS LYS
ASP ASP
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THR THR
LYS LYS
Gln Gln
MET MET
MET MET
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VAL VAL
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PRO PRO
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CYS CYS
MET MET
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PRO PRO
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SER SER
VAL VAL
GLY GLY
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PRO PRO
LYS LYS

R485
L486
ASN LYS
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THR THR
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MET MET
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ARG ARG
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VAL VAL
VAL VAL
Gln Gln
HIS HIS
PHE PHE
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LEU LEU
SER SER
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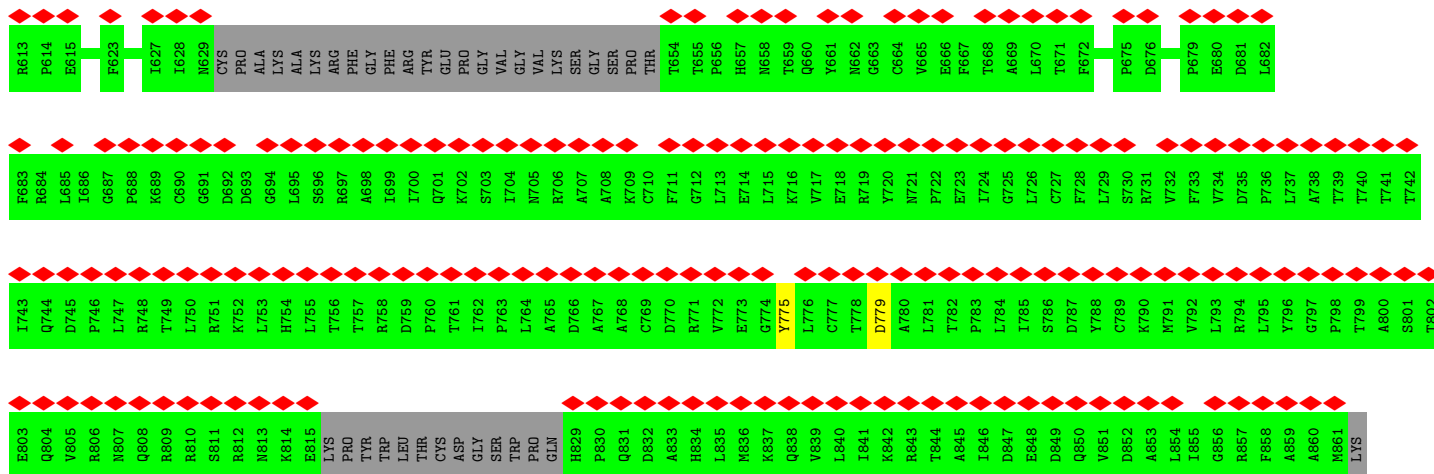
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E574
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D580
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V583
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D587
F588
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N590
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D592
G593
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V595
S596
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F612

R613
P614
F623
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N629
CYS PRO
ALA ALA
LYS LYS
LYS LYS
PHE PHE
PHE PHE
PHE PHE
ARG ARG
TYR TYR
PRO PRO
PRO PRO
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Gln Gln
Gln Gln
VAL VAL
Gln Gln
PHE PHE
TYR TYR
ARG ARG
LEU LEU
LEU LEU
SER SER
VAL VAL
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LEU LEU
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LYS LYS

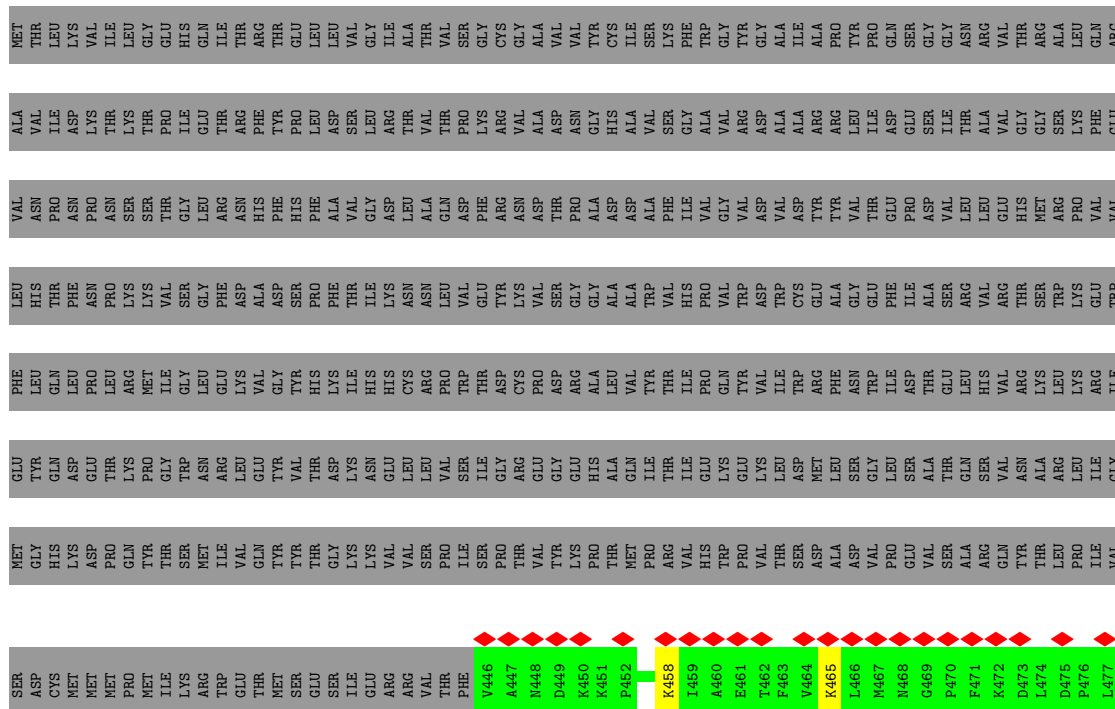
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Q701
K702
S703
I704
N705
R706
A707
A708
K709
C710
F711
G712
L713
E714
L715
K716
V717
E718
R719
Y720
N721
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E723
I724
G725
L726
C727
F728
L729
S730
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T742
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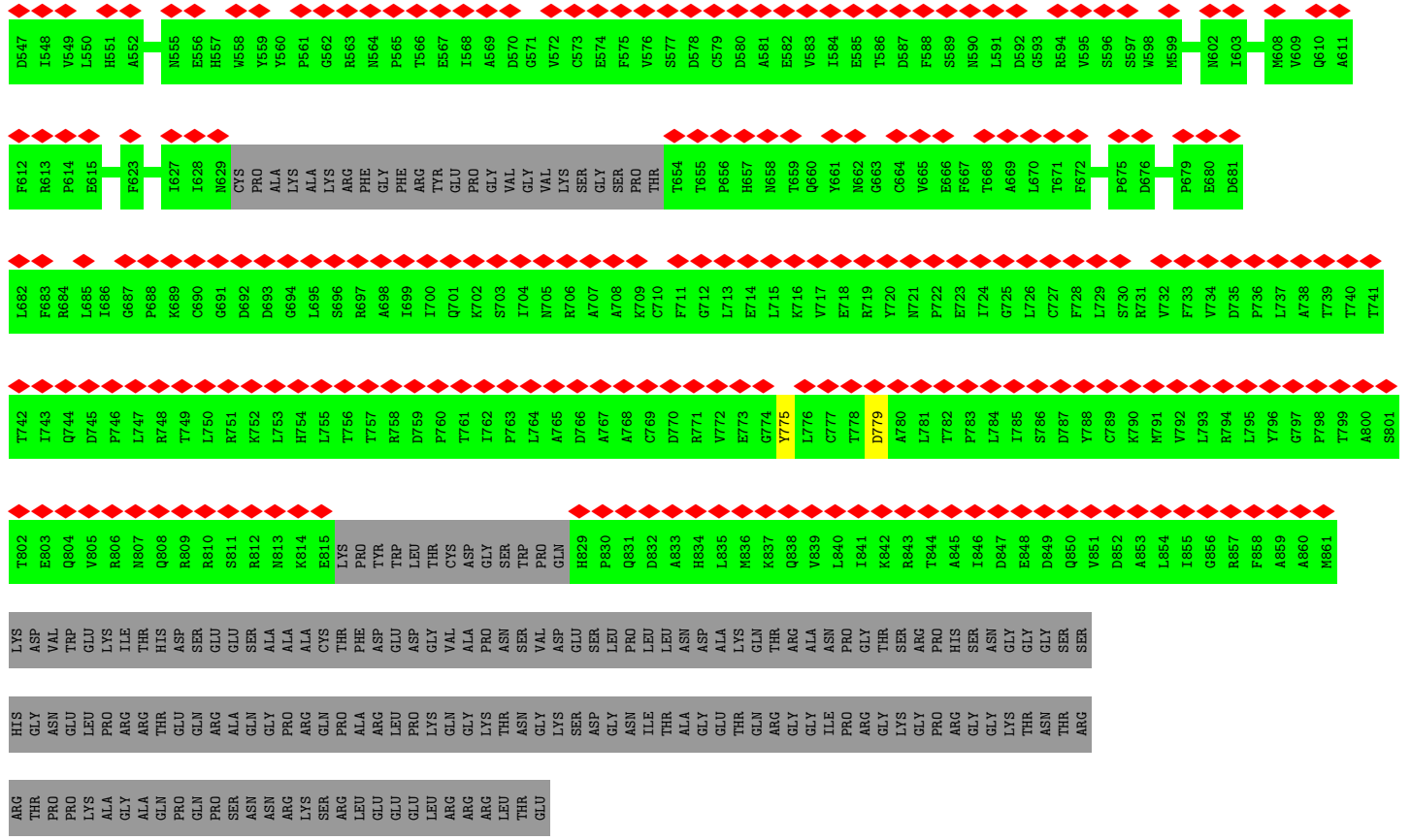
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T761
I762
P763
L764
A765
D766
A767
A768
C769
D770
R771
W772
E773
G774
Y775
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C777
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D779
A780
L781
T782
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L784
D847
E848
D849
Q850
W851
D852
A853
L854
G855
R857
F858
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A860
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R804
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R806
N807
R808
R809
R810
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R812
N813
R814
E815
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THR THR
CYS CYS
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PRO PRO
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L835
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K837
Q838
W839
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I841
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R843
T844
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L846
D847
E848
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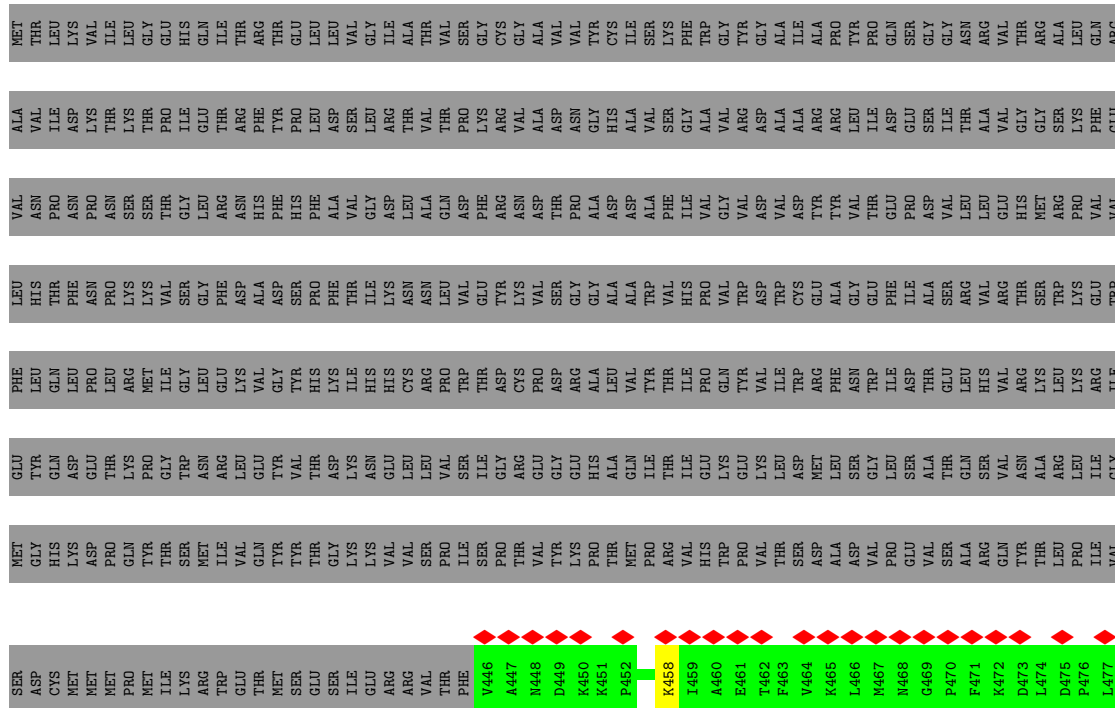


• Molecule 1: RNA-directed RNA polymerase





● Molecule 1: RNA-directed RNA polymerase



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C12	Depositor
Number of particles used	11093	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 ($e^-/\text{\AA}^2$)	100	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	26.494	Depositor
Minimum map value	-16.121	Depositor
Average map value	-0.008	Depositor
Map value standard deviation	0.814	Depositor
Recommended contour level	3.05	Depositor
Map size (Å)	479.9808, 479.9808, 479.9808	wwPDB
Map dimensions	576, 576, 576	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8333, 0.8333, 0.8333	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	0.26	0/2559	0.49	0/3479
1	B	0.26	0/2559	0.49	0/3479
1	C	0.26	0/2559	0.49	0/3479
1	D	0.26	0/2559	0.49	0/3479
1	E	0.26	0/2559	0.49	0/3479
1	F	0.26	0/2559	0.49	0/3479
1	G	0.26	0/2559	0.49	0/3479
1	H	0.26	0/2559	0.49	0/3479
1	I	0.26	0/2559	0.49	0/3479
1	J	0.26	0/2559	0.49	0/3479
1	K	0.26	0/2559	0.49	0/3479
1	L	0.26	0/2559	0.49	0/3479
1	M	0.23	0/1409	0.43	0/1766
1	N	0.23	0/1409	0.43	0/1766
1	O	0.23	0/1409	0.43	0/1766
1	P	0.23	0/1409	0.43	0/1766
1	Q	0.23	0/1409	0.43	0/1766
1	R	0.23	0/1409	0.43	0/1766
1	S	0.23	0/1409	0.43	0/1766
1	T	0.23	0/1409	0.43	0/1766
1	U	0.23	0/1409	0.43	0/1766
1	V	0.23	0/1409	0.43	0/1766
1	W	0.23	0/1409	0.43	0/1766
1	X	0.23	0/1409	0.43	0/1766
All	All	0.25	0/47616	0.47	0/62940

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	2493	2493	2491	48	0
1	B	2493	2493	2491	50	0
1	C	2493	2493	2491	47	0
1	D	2493	2493	2491	47	0
1	E	2493	2493	2491	48	0
1	F	2493	2493	2491	49	0
1	G	2493	2493	2491	48	0
1	H	2493	2493	2491	48	0
1	I	2493	2493	2491	47	0
1	J	2493	2493	2491	46	0
1	K	2493	2493	2491	47	0
1	L	2493	2493	2491	47	0
1	M	1411	0	464	3	0
1	N	1411	0	464	4	0
1	O	1411	0	464	3	0
1	P	1411	0	464	3	0
1	Q	1411	0	464	5	0
1	R	1411	0	464	3	0
1	S	1411	0	464	4	0
1	T	1411	0	464	3	0
1	U	1411	0	464	3	0
1	V	1411	0	464	4	0
1	W	1411	0	464	3	0
1	X	1411	0	464	3	0
All	All	46848	29916	35460	531	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 6.

The worst 5 of 531 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:388:THR:OG1	1:C:314:GLU:OE2	1.81	0.99
1:A:388:THR:OG1	1:B:314:GLU:OE2	1.82	0.98
1:G:388:THR:OG1	1:H:314:GLU:OE2	1.82	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:388:THR:OG1	1:D:314:GLU:OE2	1.84	0.96
1:D:388:THR:OG1	1:E:314:GLU:OE2	1.83	0.96

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	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	B	304/1011 (30%)	294 (97%)	10 (3%)	0	100	100
1	C	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	D	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	E	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	F	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	G	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	H	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	I	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	J	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	K	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	L	304/1011 (30%)	293 (96%)	11 (4%)	0	100	100
1	M	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
1	N	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
1	O	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
1	P	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
1	Q	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
1	R	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	S	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
1	T	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
1	U	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
1	V	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
1	W	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
1	X	325/1011 (32%)	319 (98%)	6 (2%)	0	100	100
All	All	7548/24264 (31%)	7345 (97%)	203 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	273/877 (31%)	273 (100%)	0	100	100
1	B	273/877 (31%)	273 (100%)	0	100	100
1	C	273/877 (31%)	273 (100%)	0	100	100
1	D	273/877 (31%)	273 (100%)	0	100	100
1	E	273/877 (31%)	273 (100%)	0	100	100
1	F	273/877 (31%)	273 (100%)	0	100	100
1	G	273/877 (31%)	273 (100%)	0	100	100
1	H	273/877 (31%)	273 (100%)	0	100	100
1	I	273/877 (31%)	273 (100%)	0	100	100
1	J	273/877 (31%)	273 (100%)	0	100	100
1	K	273/877 (31%)	273 (100%)	0	100	100
1	L	273/877 (31%)	273 (100%)	0	100	100
1	M	17/877 (2%)	17 (100%)	0	100	100
1	N	17/877 (2%)	17 (100%)	0	100	100
1	O	17/877 (2%)	17 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	P	17/877 (2%)	17 (100%)	0	100	100
1	Q	17/877 (2%)	17 (100%)	0	100	100
1	R	17/877 (2%)	17 (100%)	0	100	100
1	S	17/877 (2%)	17 (100%)	0	100	100
1	T	17/877 (2%)	17 (100%)	0	100	100
1	U	17/877 (2%)	17 (100%)	0	100	100
1	V	17/877 (2%)	17 (100%)	0	100	100
1	W	17/877 (2%)	17 (100%)	0	100	100
1	X	17/877 (2%)	17 (100%)	0	100	100
All	All	3480/21048 (16%)	3480 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides 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

There are no chain breaks in this entry.

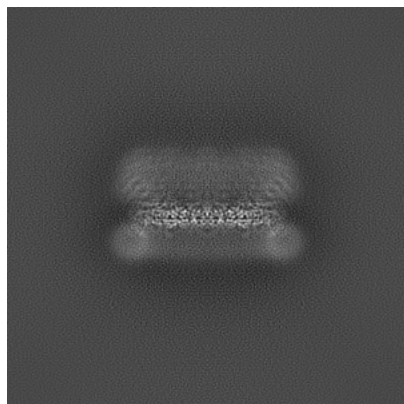
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-29289. These allow visual inspection of the internal detail of the map and identification of artifacts.

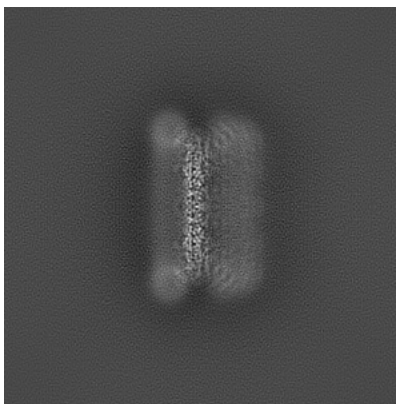
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

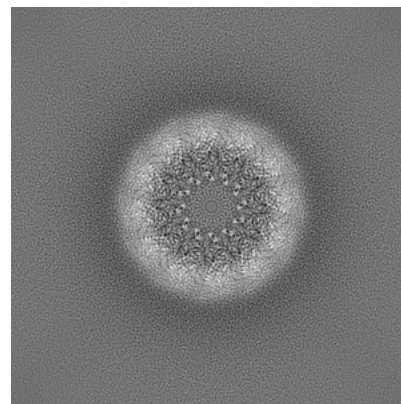
6.1.1 Primary map



X

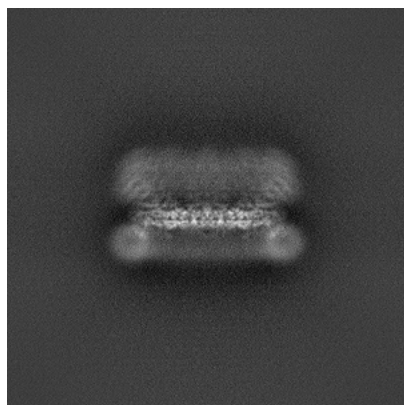


Y

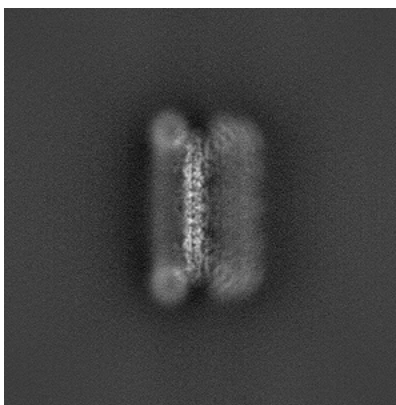


Z

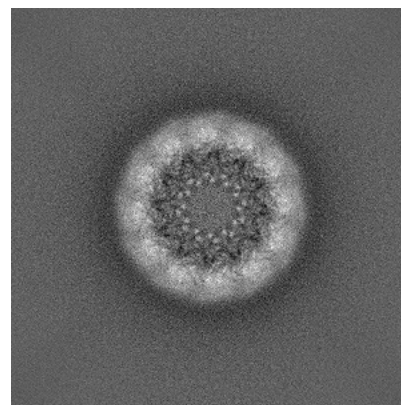
6.1.2 Raw map



X



Y

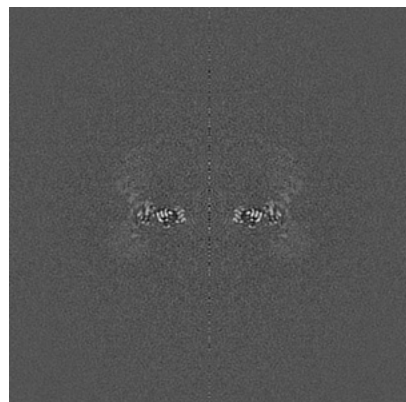


Z

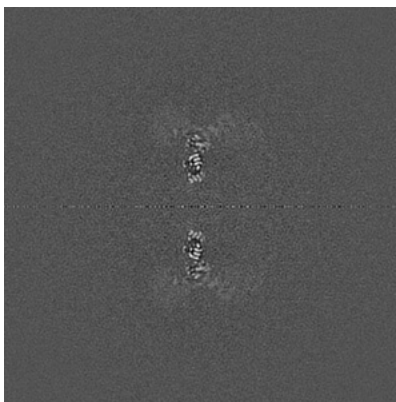
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

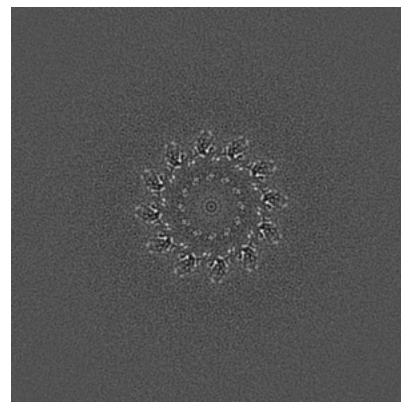
6.2.1 Primary map



X Index: 288

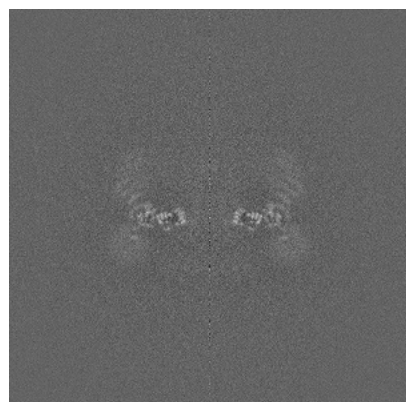


Y Index: 288

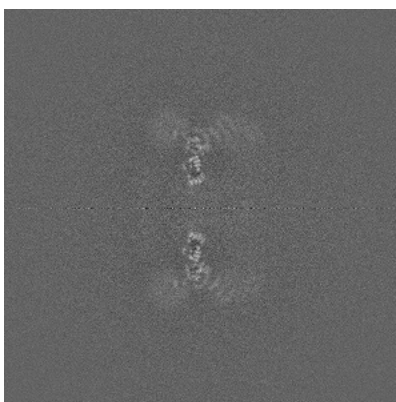


Z Index: 288

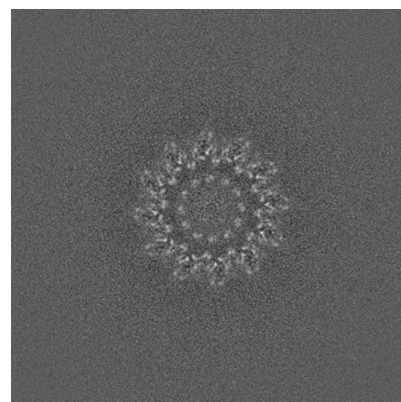
6.2.2 Raw map



X Index: 288



Y Index: 288

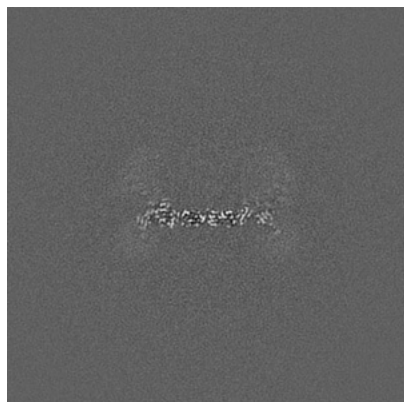


Z Index: 288

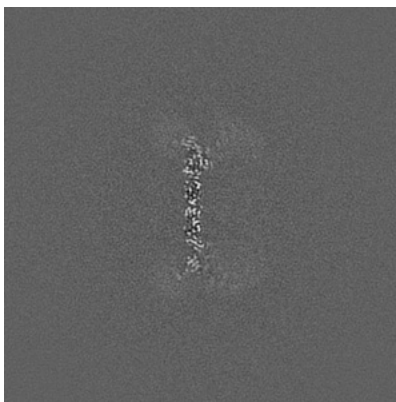
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

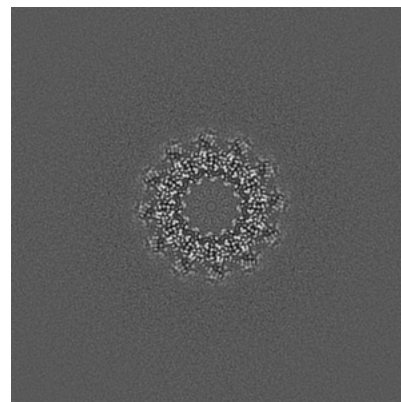
6.3.1 Primary map



X Index: 337

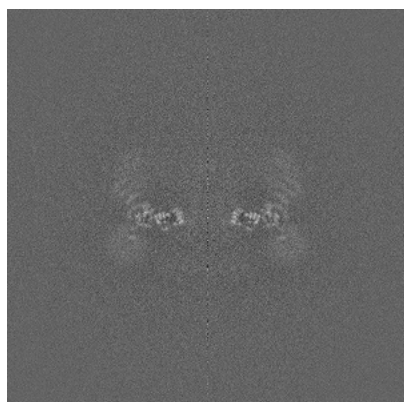


Y Index: 337

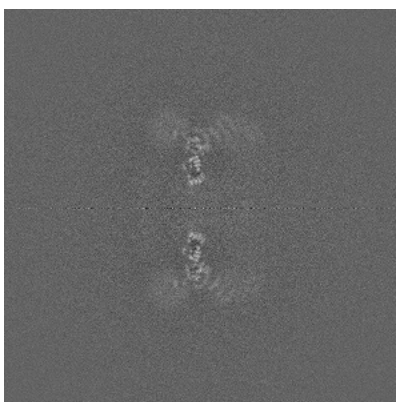


Z Index: 277

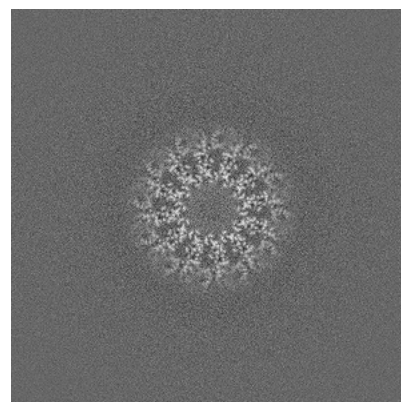
6.3.2 Raw map



X Index: 288



Y Index: 288

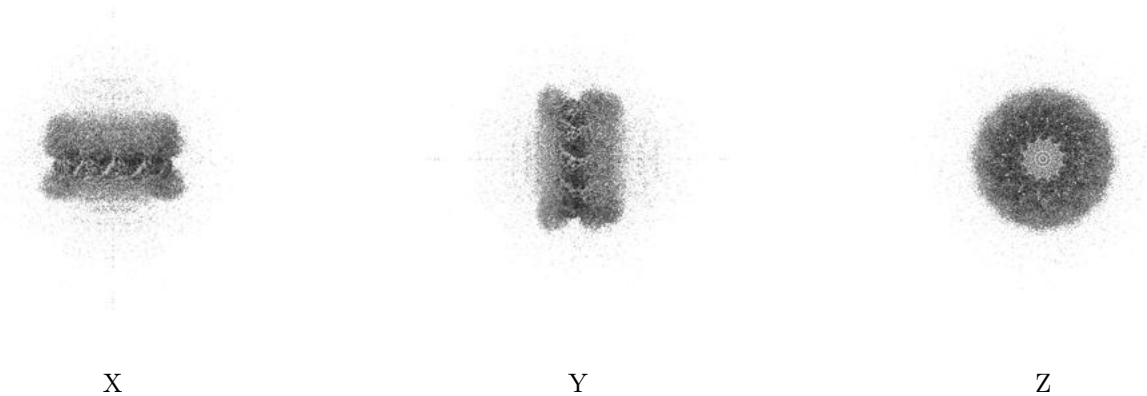


Z Index: 267

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

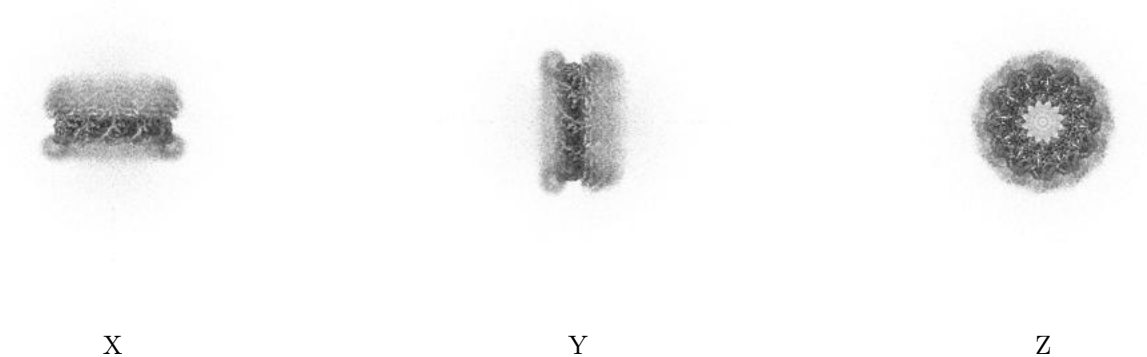
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

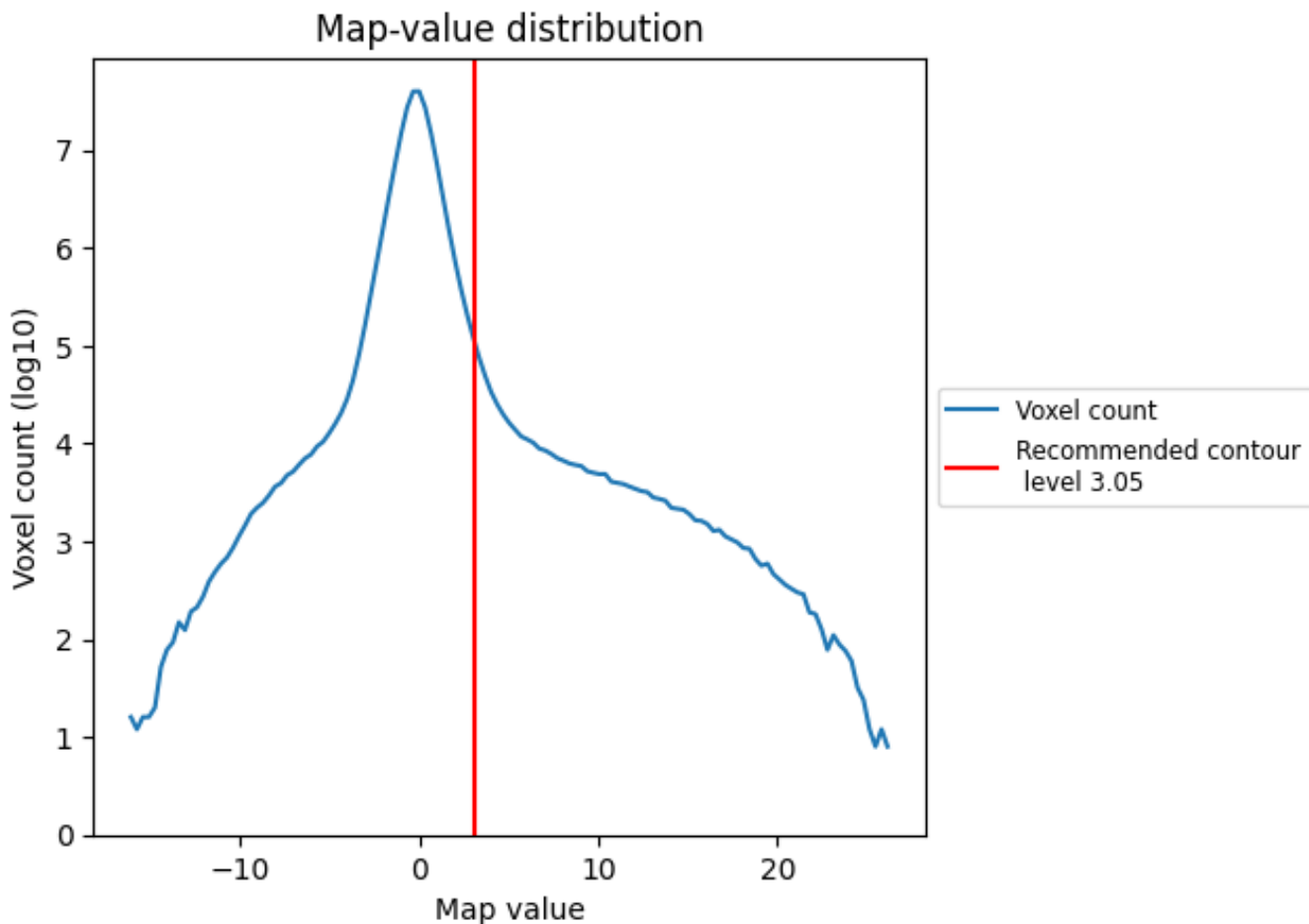
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

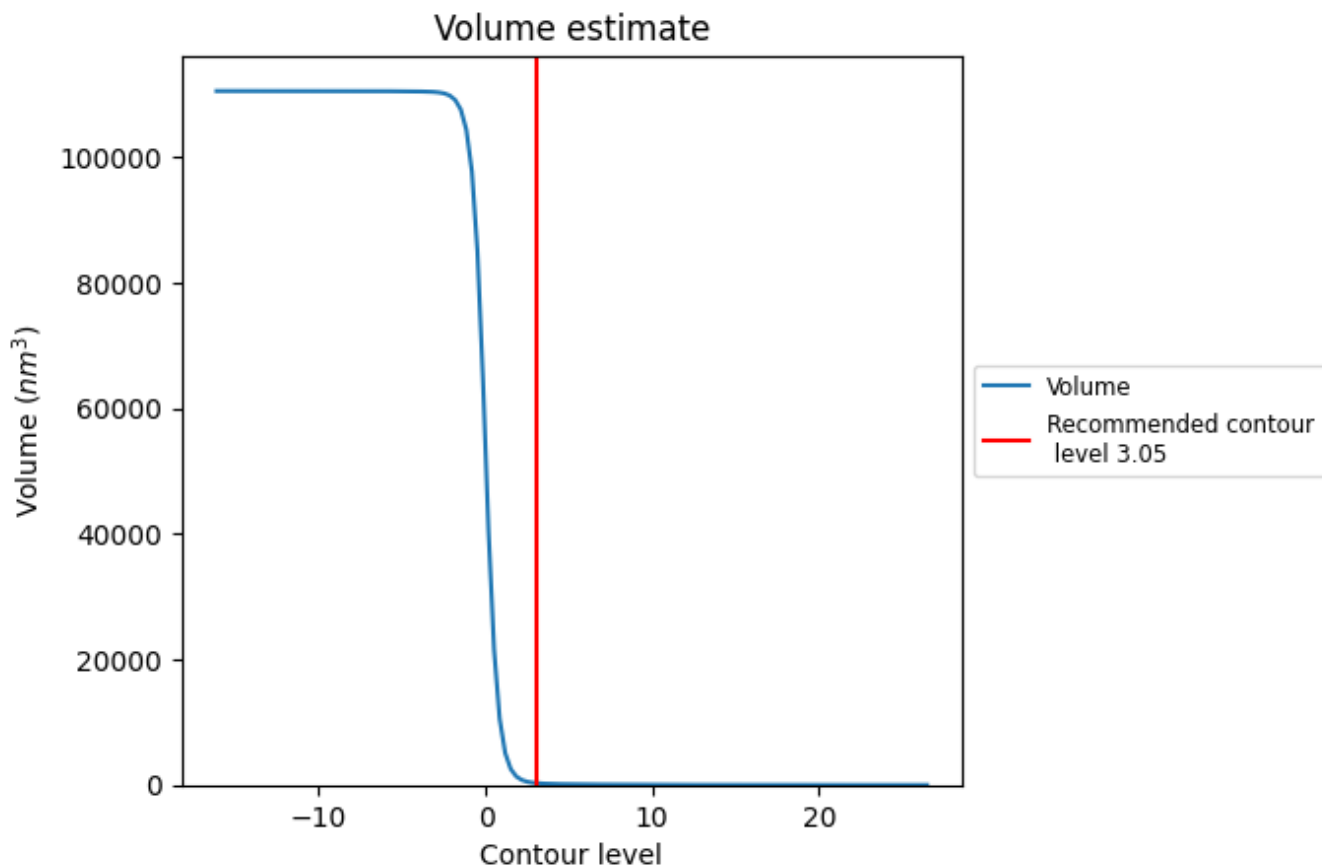
This section contains the results of statistical analysis of the map.

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.

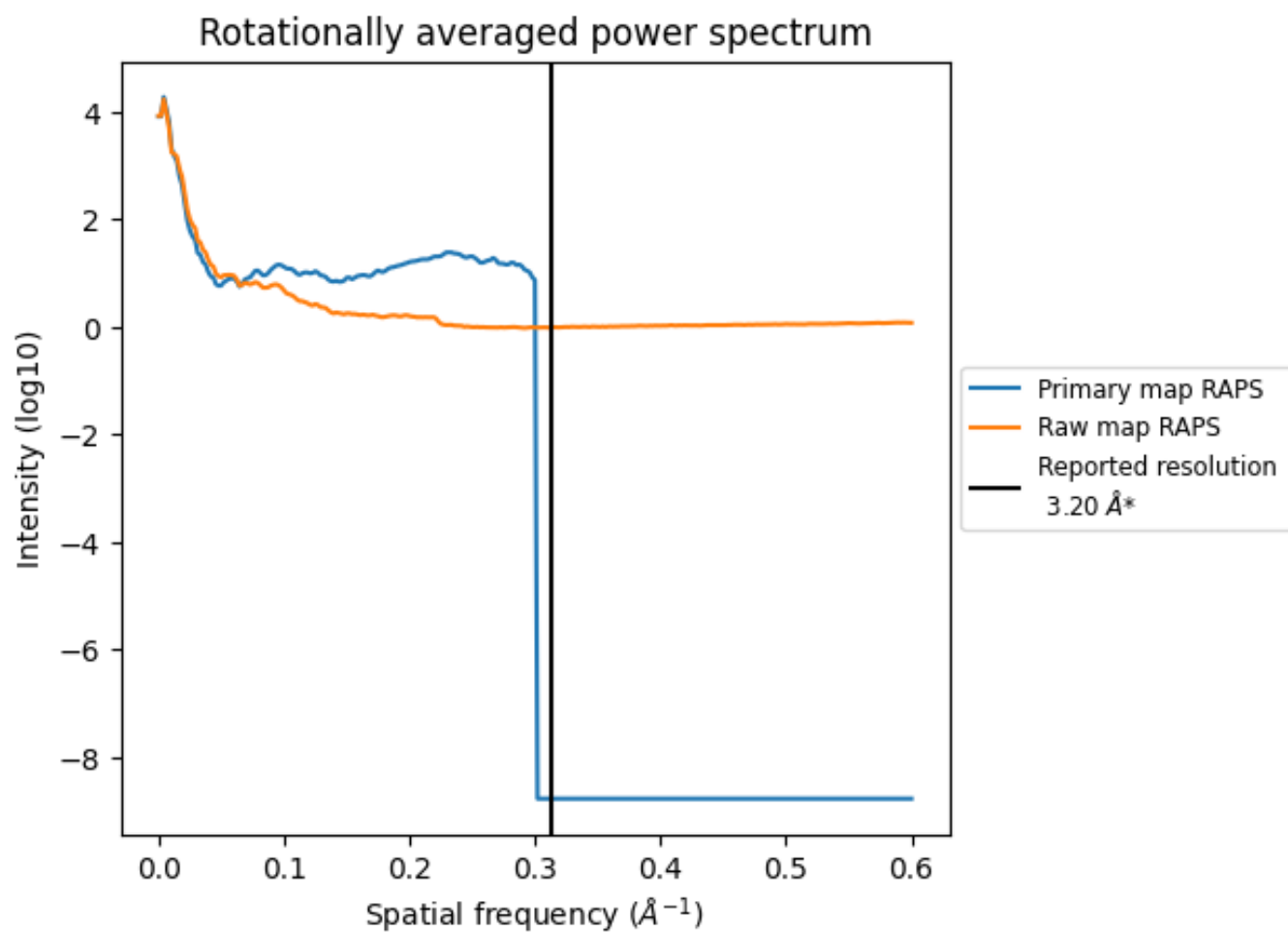
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 297 nm^3 ; this corresponds to an approximate mass of 268 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 [\(i\)](#)

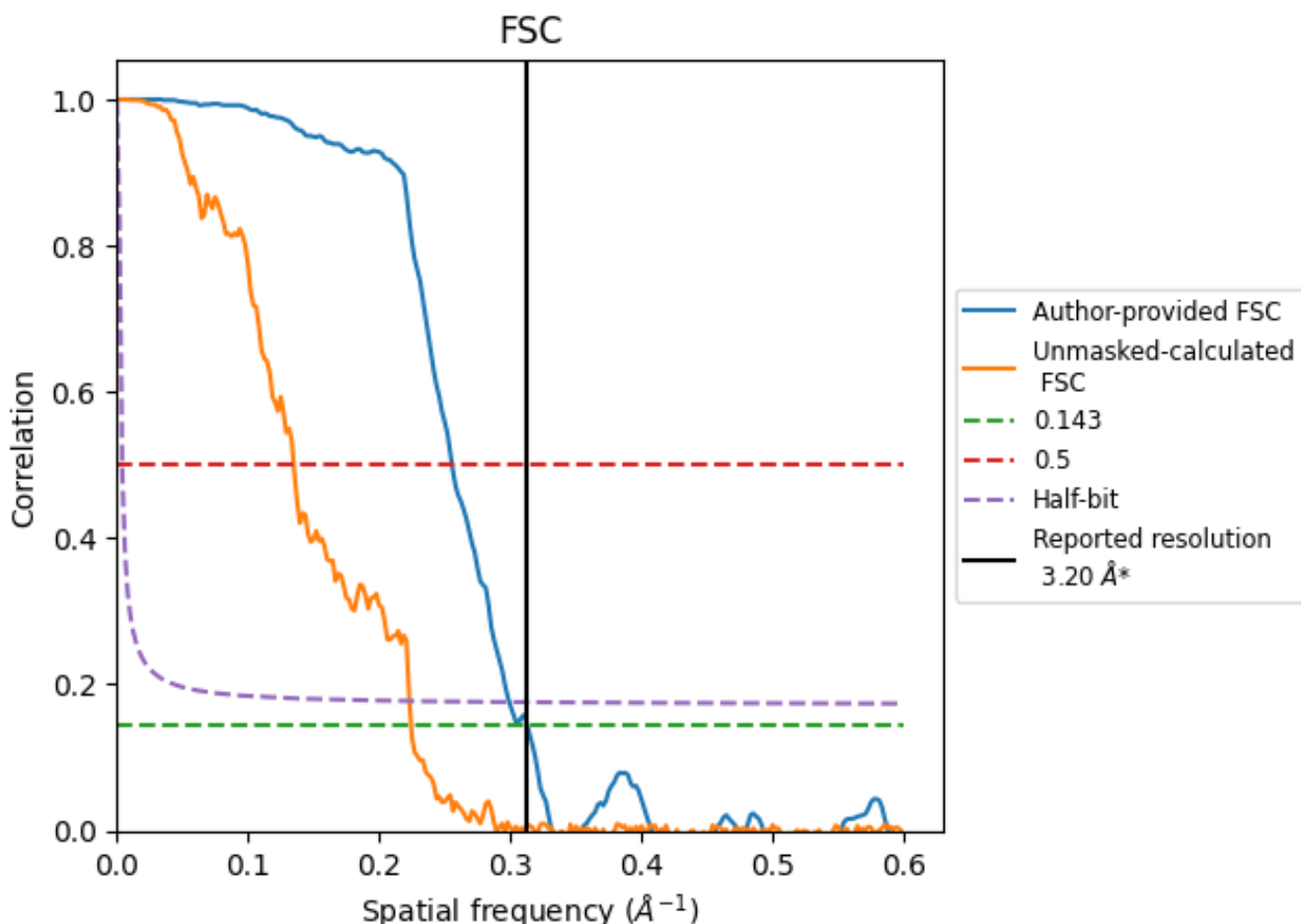


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

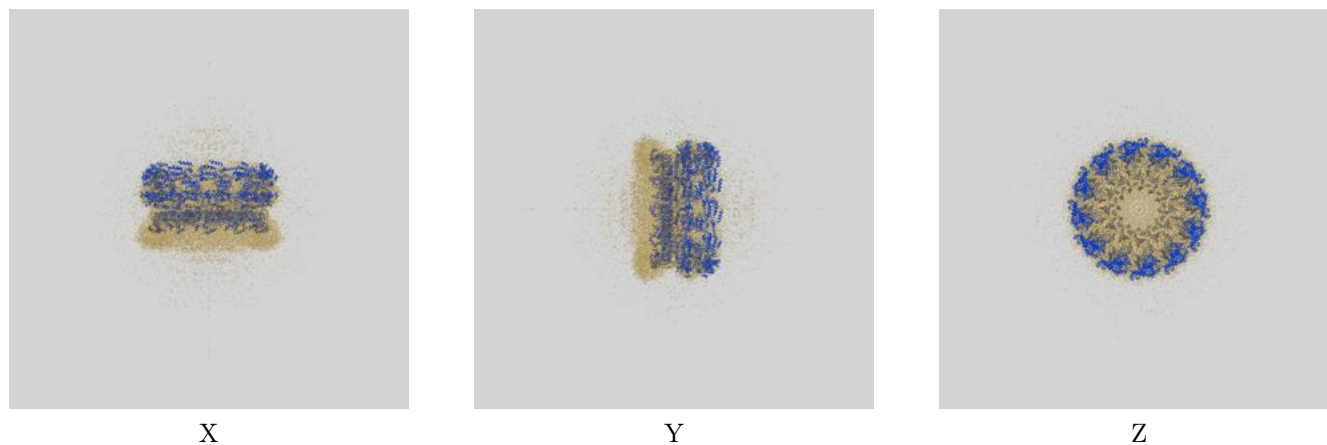
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.19	3.91	3.34
Unmasked-calculated*	4.46	7.41	4.48

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.46 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

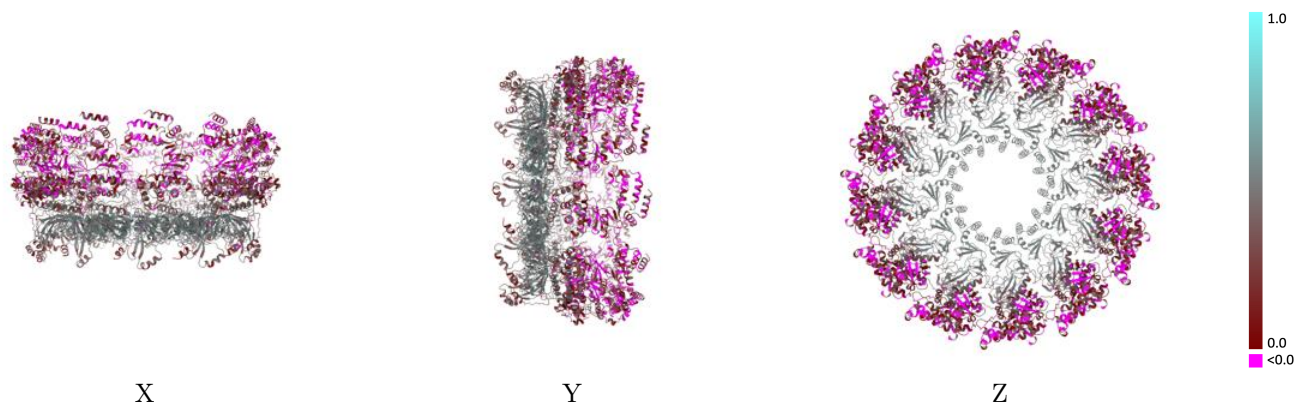
This section contains information regarding the fit between EMDB map EMD-29289 and PDB model 8FM9. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)



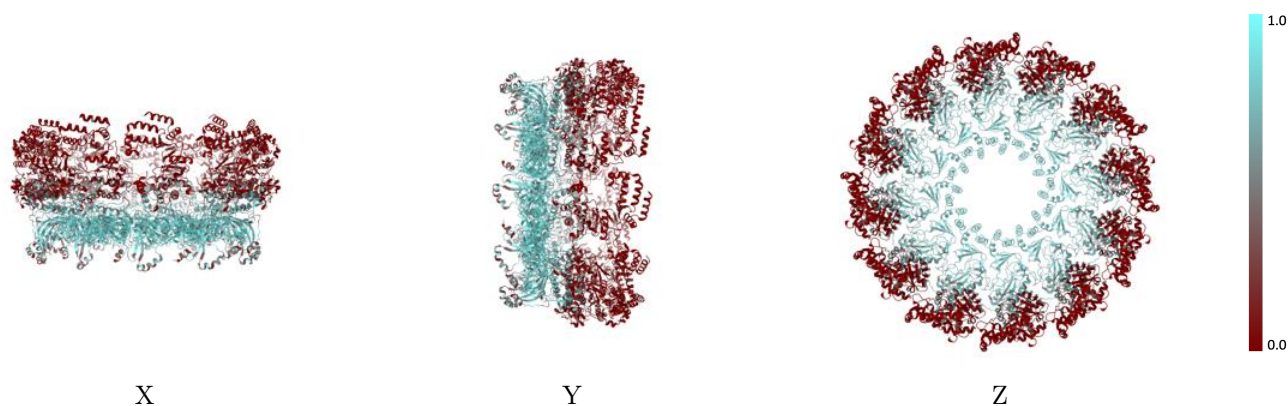
The images above show the 3D surface view of the map at the recommended contour level 3.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



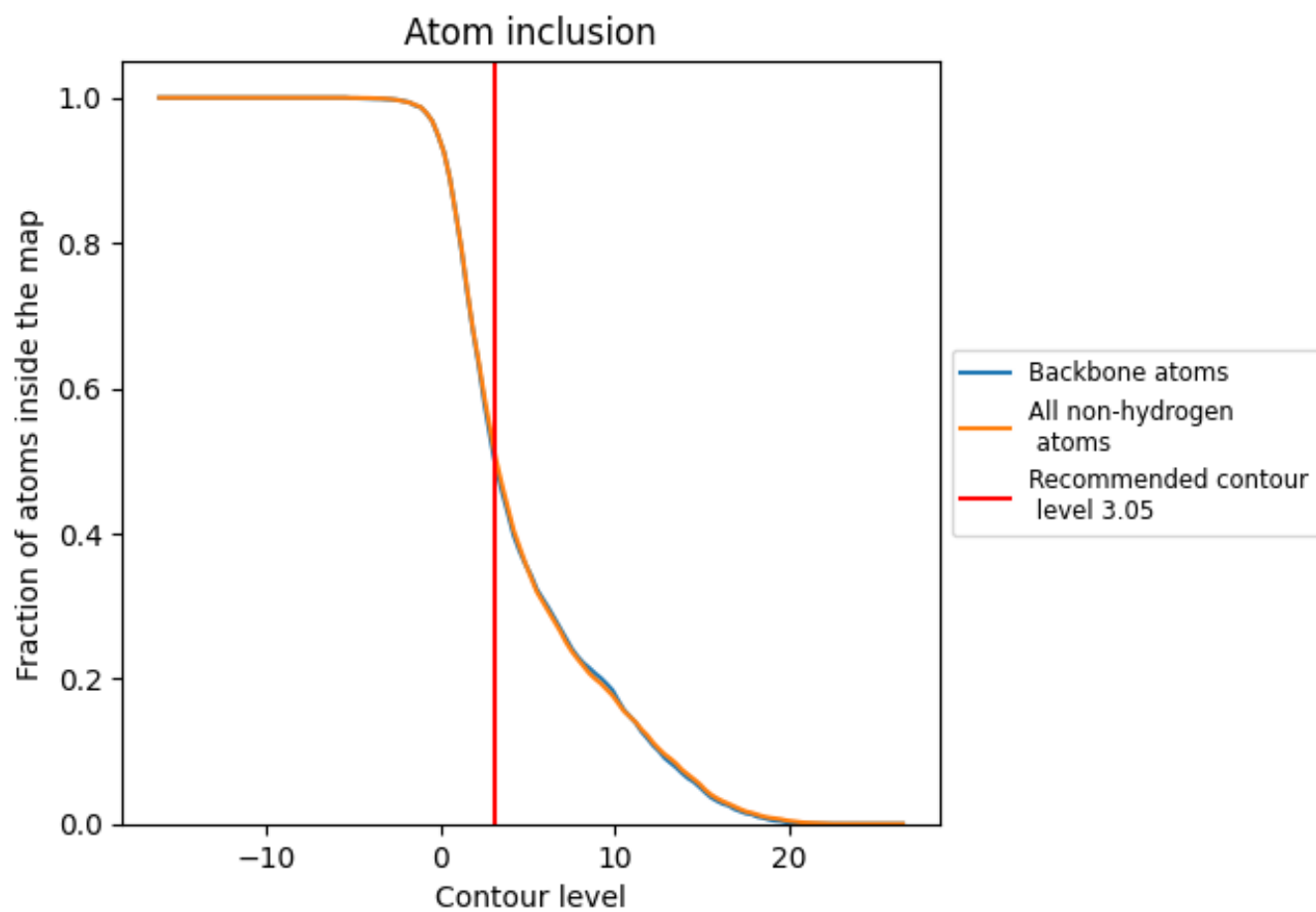
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3.05).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 50% of all backbone atoms, 52% 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 (3.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5162	 0.3340
A	 0.7343	 0.4420
B	 0.7343	 0.4420
C	 0.7355	 0.4410
D	 0.7334	 0.4430
E	 0.7347	 0.4420
F	 0.7343	 0.4410
G	 0.7347	 0.4430
H	 0.7318	 0.4410
I	 0.7343	 0.4420
J	 0.7339	 0.4420
K	 0.7343	 0.4410
L	 0.7359	 0.4420
M	 0.1474	 0.1460
N	 0.1446	 0.1470
O	 0.1467	 0.1470
P	 0.1474	 0.1460
Q	 0.1453	 0.1330
R	 0.1460	 0.1460
S	 0.1474	 0.1470
T	 0.1446	 0.1440
U	 0.1467	 0.1440
V	 0.1467	 0.1440
W	 0.1460	 0.1420
X	 0.1467	 0.1450

