wwPDB EM Validation Summary Report

Jun 9, 2024 – 07:15 PM EDT

PDB ID	:	8FM9
EMDB ID	:	EMD-29289
Title	:	Nodavirus RNA replication proto-crown, detergent-solubliized 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:

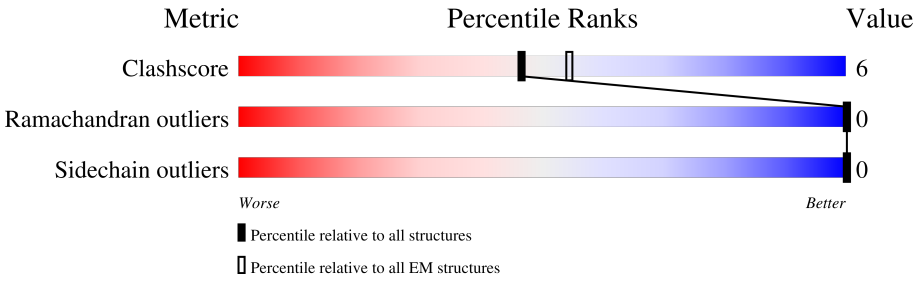
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.20 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 <=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	24% 6% 70%
1	B	1011	24% 6% 70%
1	C	1011	24% 6% 70%
1	D	1011	24% 6% 70%
1	E	1011	24% 6% 70%
1	F	1011	24% 6% 70%
1	G	1011	24% 6% 70%
1	H	1011	24% 6% 70%

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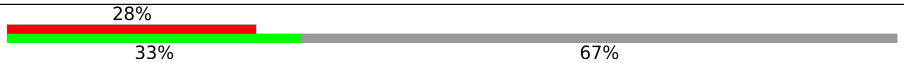
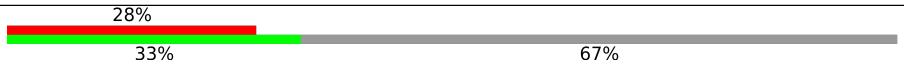
Mol	Chain	Length	Quality of chain
1	I	1011	
1	J	1011	
1	K	1011	
1	L	1011	
1	M	1011	
1	N	1011	
1	O	1011	
1	P	1011	
1	Q	1011	
1	R	1011	
1	S	1011	
1	T	1011	
1	U	1011	
1	V	1011	
1	W	1011	
1	X	1011	

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

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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
K	999	SER	-	expression tag	UNP Q66929
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
M	1006	ARG	-	expression tag	UNP Q66929
M	1007	ARG	-	expression tag	UNP Q66929
M	1008	ARG	-	expression tag	UNP Q66929
M	1009	LEU	-	expression tag	UNP Q66929
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
N	1001	LEU	-	expression tag	UNP Q66929
N	1002	GLU	-	expression tag	UNP Q66929
N	1003	GLU	-	expression tag	UNP Q66929
N	1004	GLU	-	expression tag	UNP Q66929
N	1005	LEU	-	expression tag	UNP Q66929
N	1006	ARG	-	expression tag	UNP Q66929
N	1007	ARG	-	expression tag	UNP Q66929
N	1008	ARG	-	expression tag	UNP Q66929

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

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	1009	LEU	-	expression tag	UNP Q66929
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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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
W	1006	ARG	-	expression tag	UNP Q66929
W	1007	ARG	-	expression tag	UNP Q66929
W	1008	ARG	-	expression tag	UNP Q66929

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Continued from previous page...

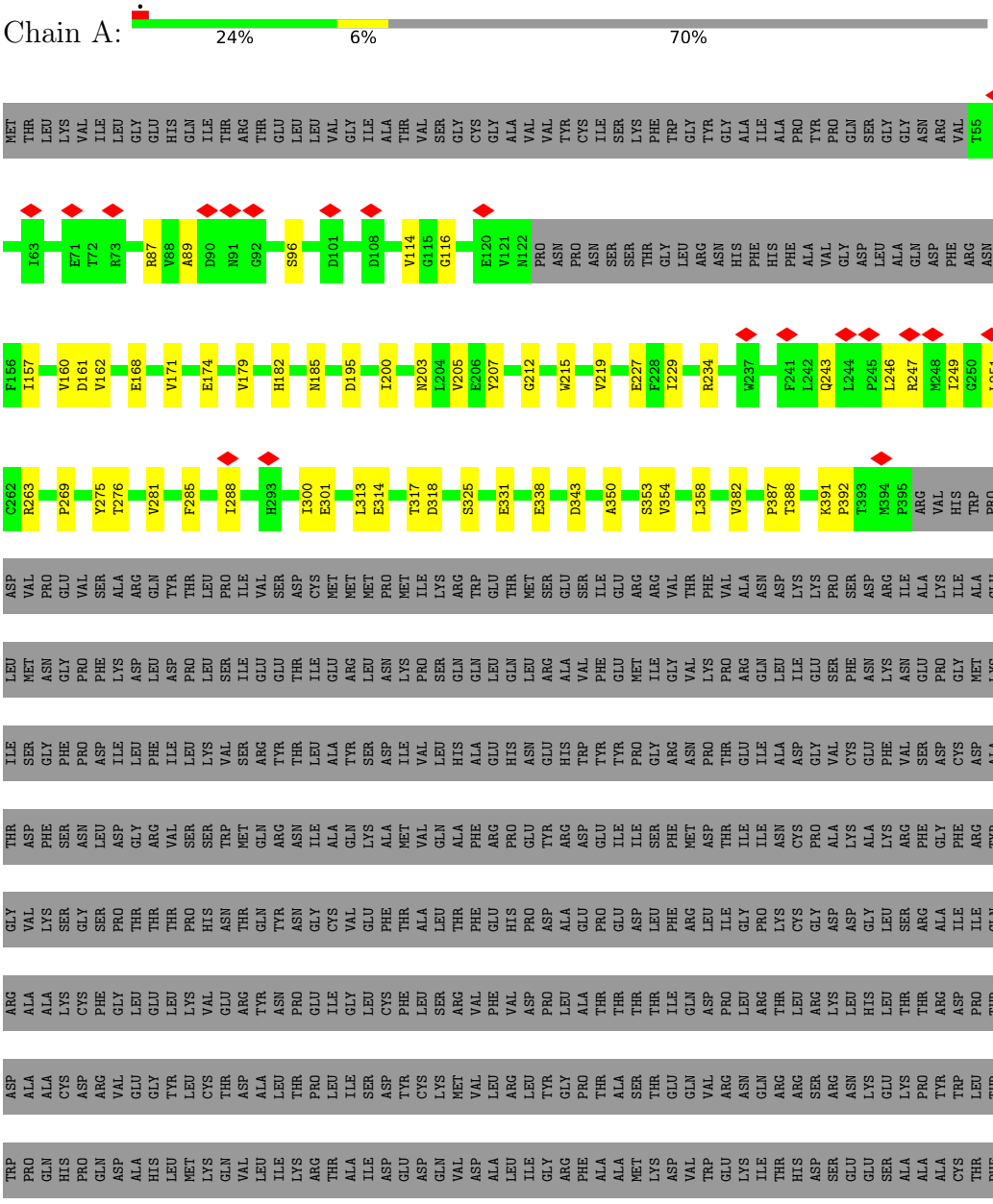
Chain	Residue	Modelled	Actual	Comment	Reference
W	1009	LEU	-	expression tag	UNP Q66929
W	1010	THR	-	expression tag	UNP Q66929
W	1011	GLU	-	expression tag	UNP Q66929
X	897	LEU	MET	conflict	UNP Q66929
X	999	SER	-	expression tag	UNP Q66929
X	1000	ARG	-	expression tag	UNP Q66929
X	1001	LEU	-	expression tag	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

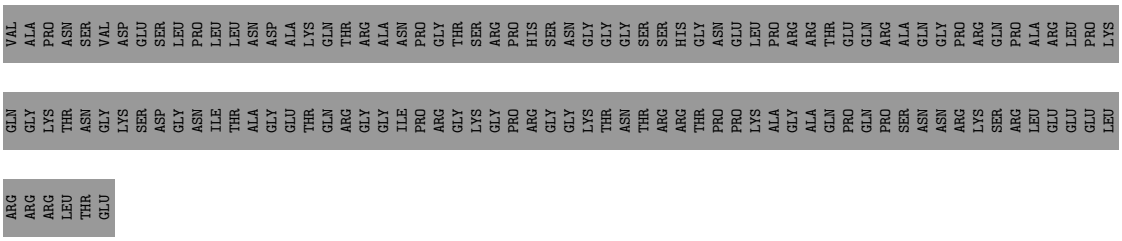
3 Residue-property plots (i)

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: RNA-directed RNA polymerase

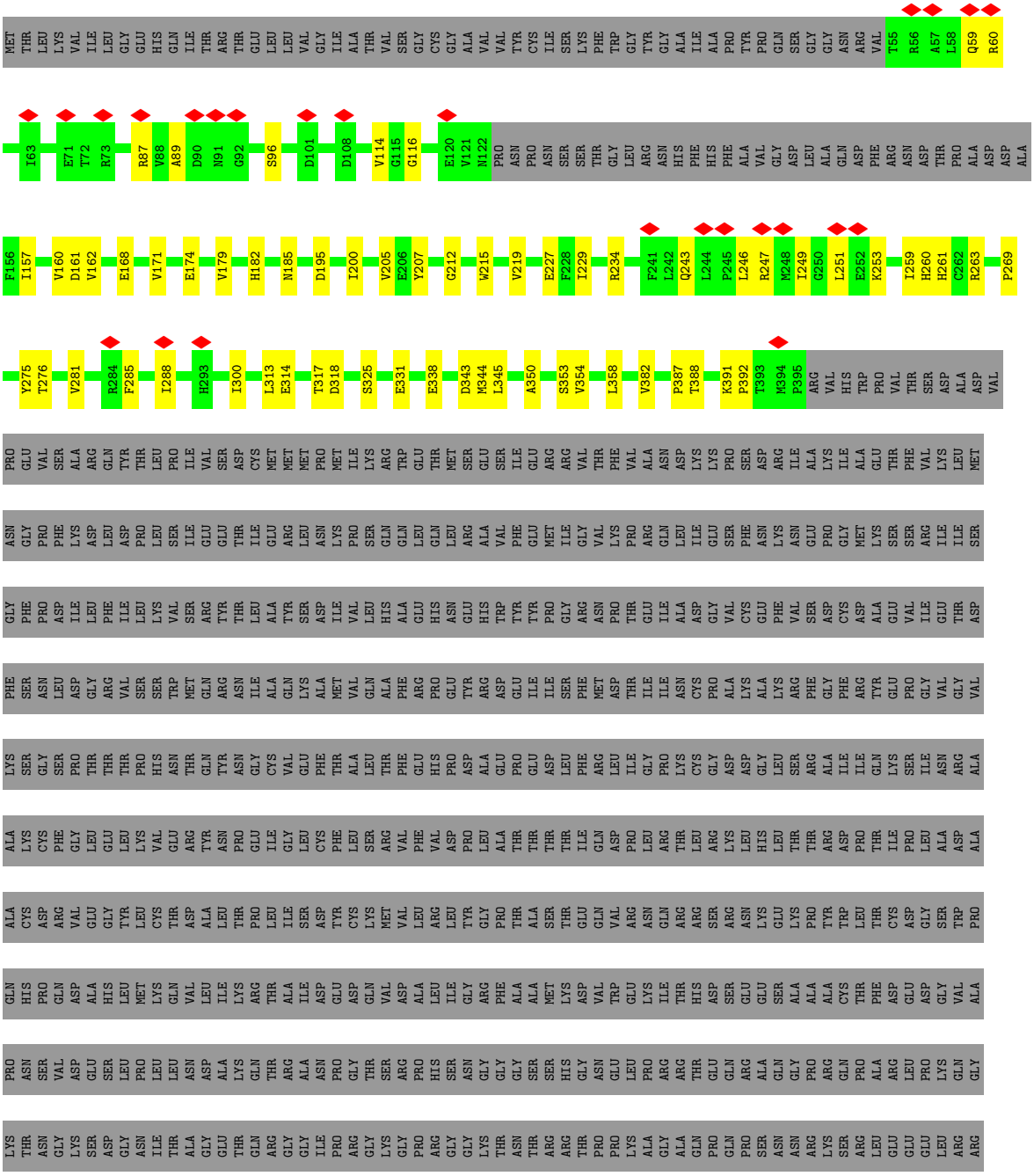
Chain A:





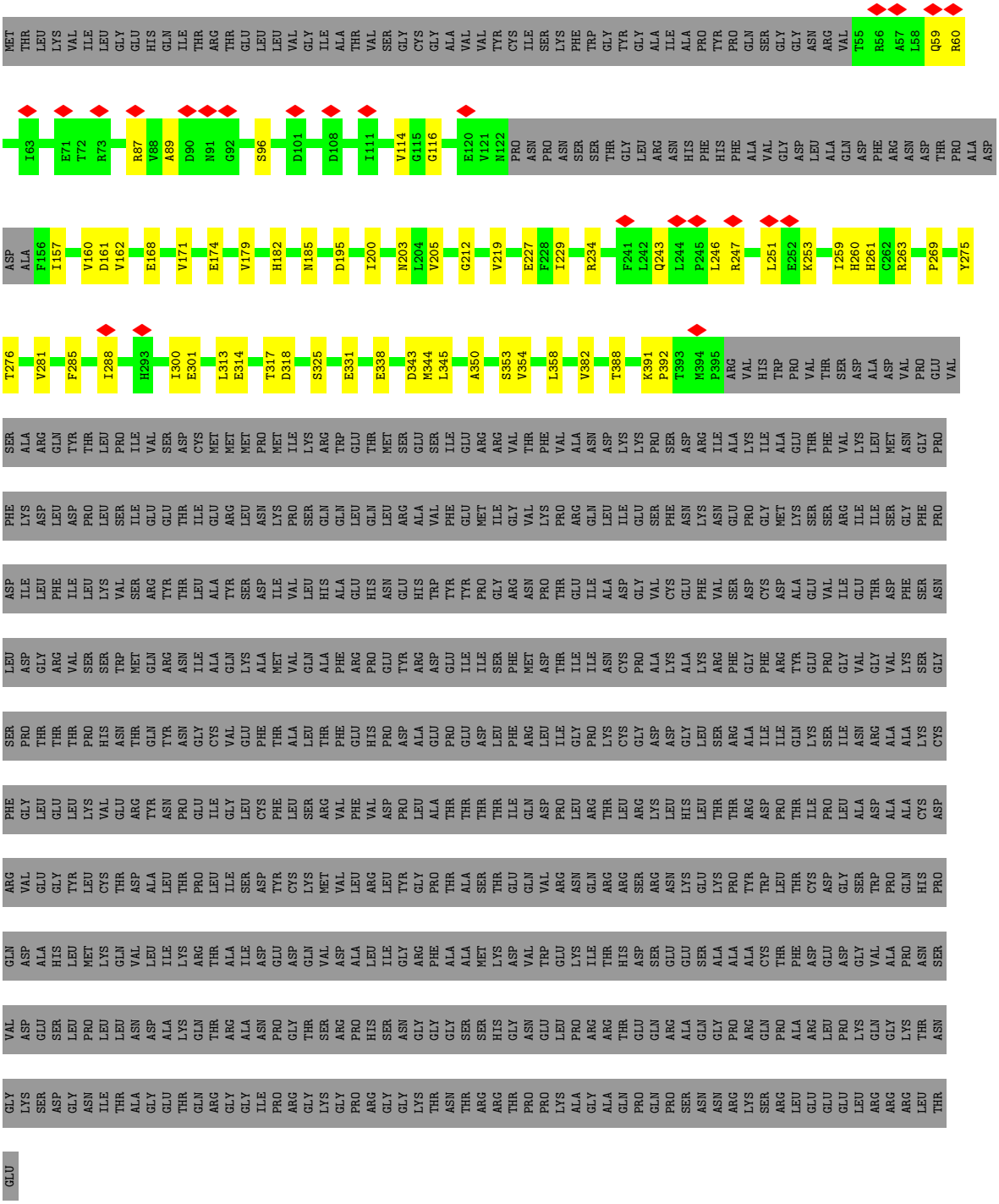
• Molecule 1: RNA-directed RNA polymerase

Chain B:



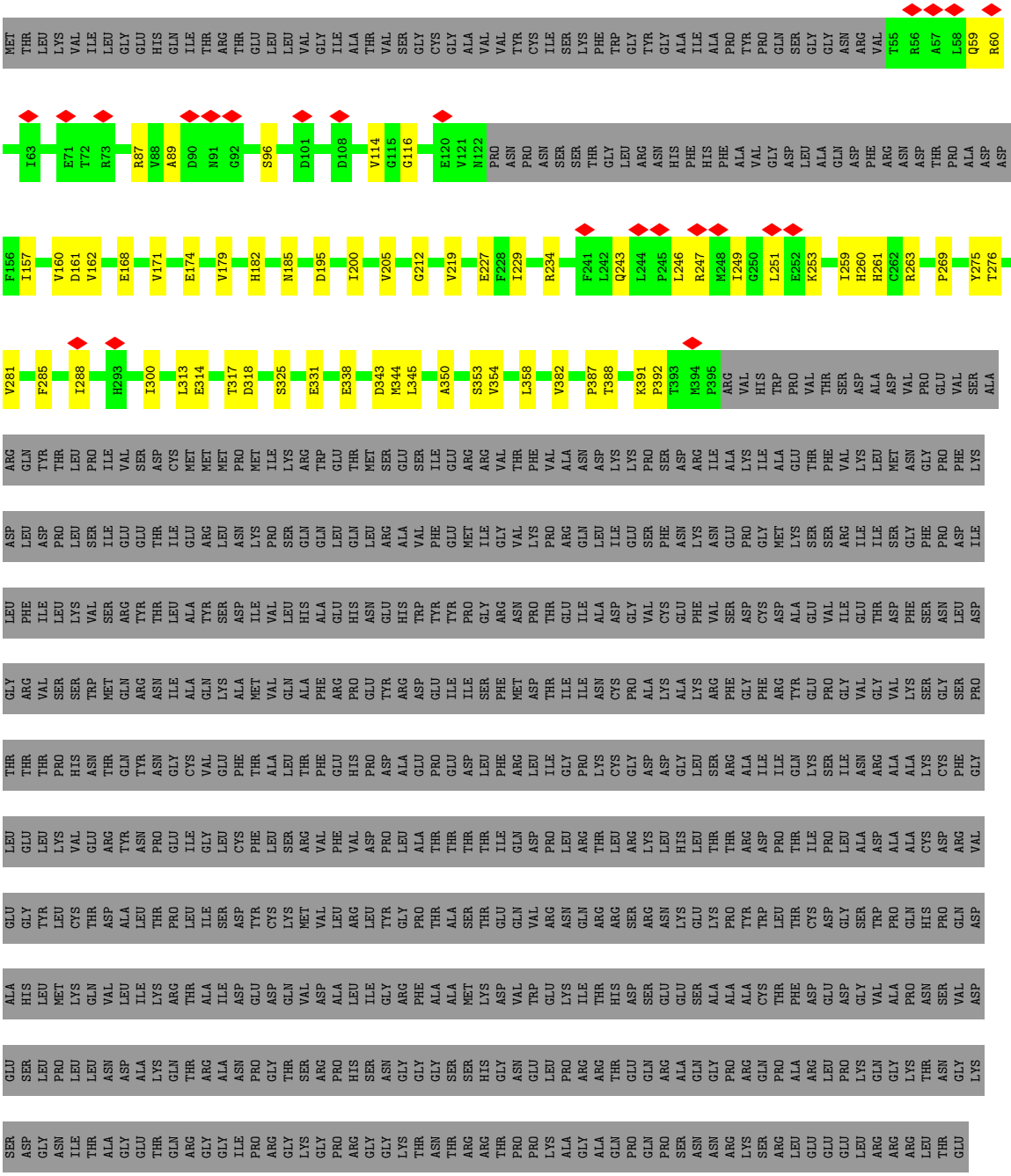
• Molecule 1: RNA-directed RNA polymerase

Chain C:



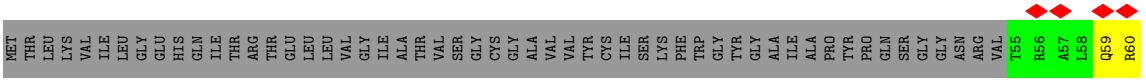
• Molecule 1: RNA-directed RNA polymerase

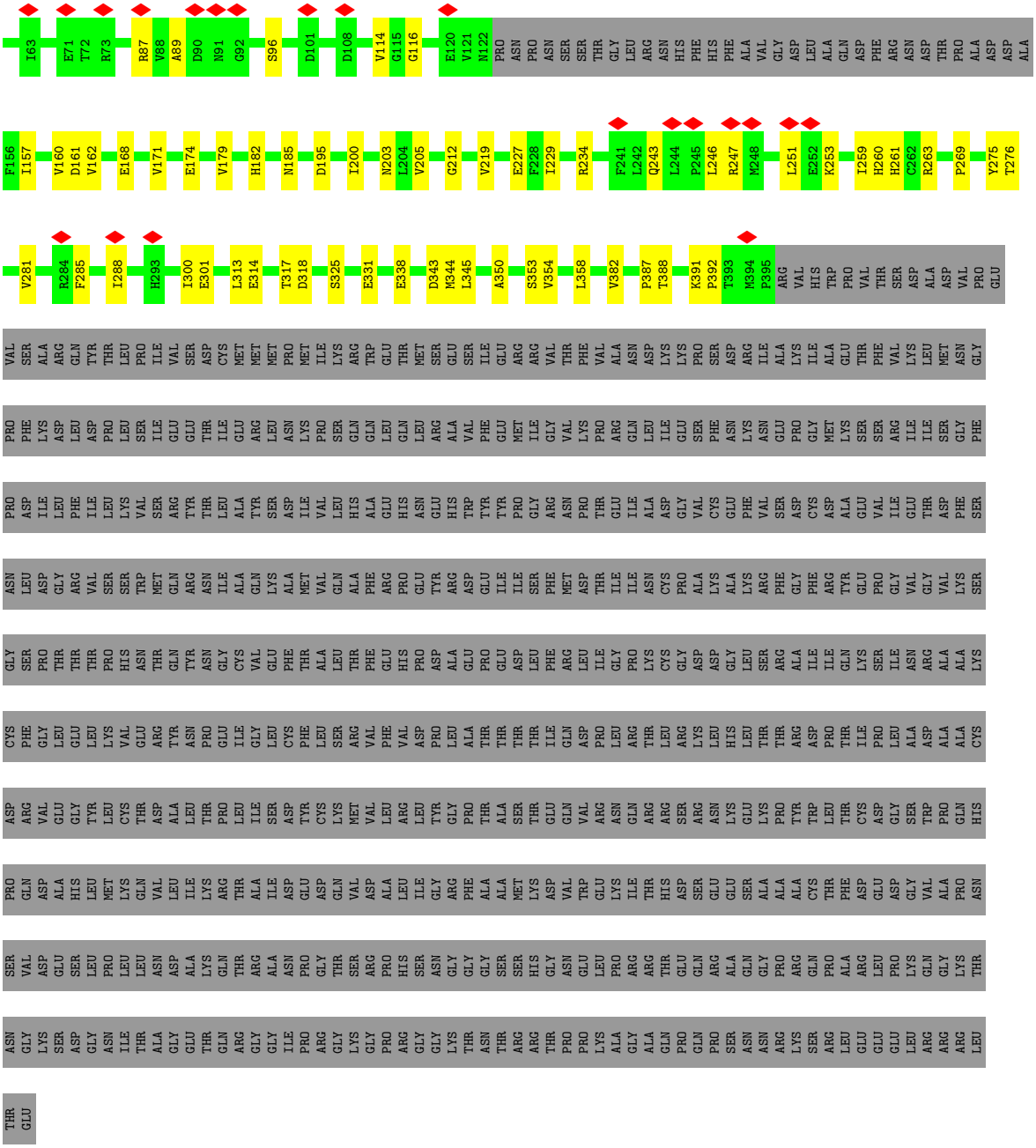
Chain D:



• Molecule 1: RNA-directed RNA polymerase

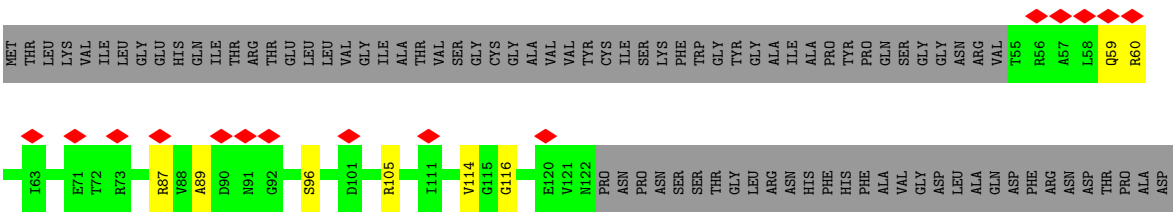
Chain E:

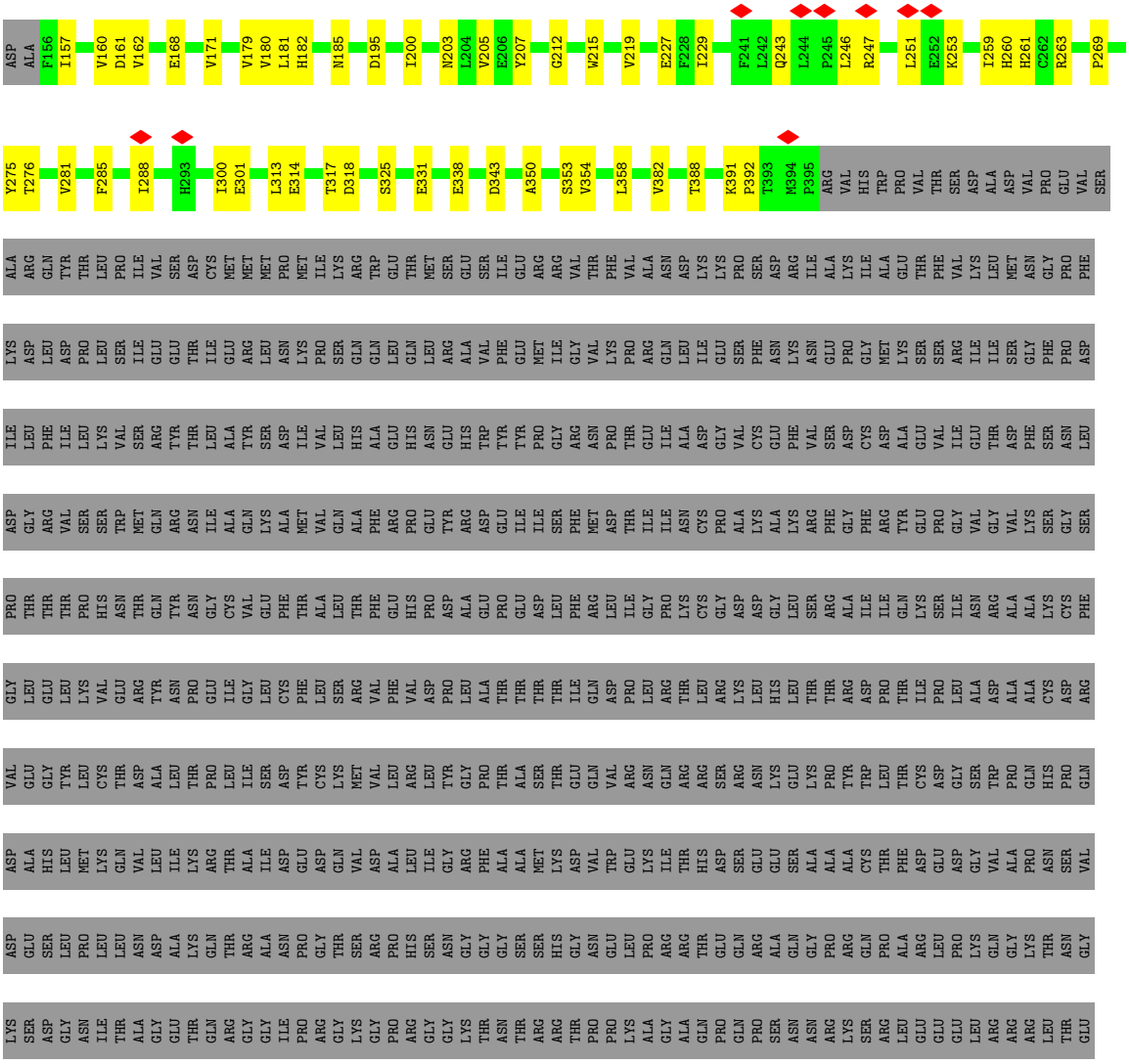




• Molecule 1: RNA-directed RNA polymerase

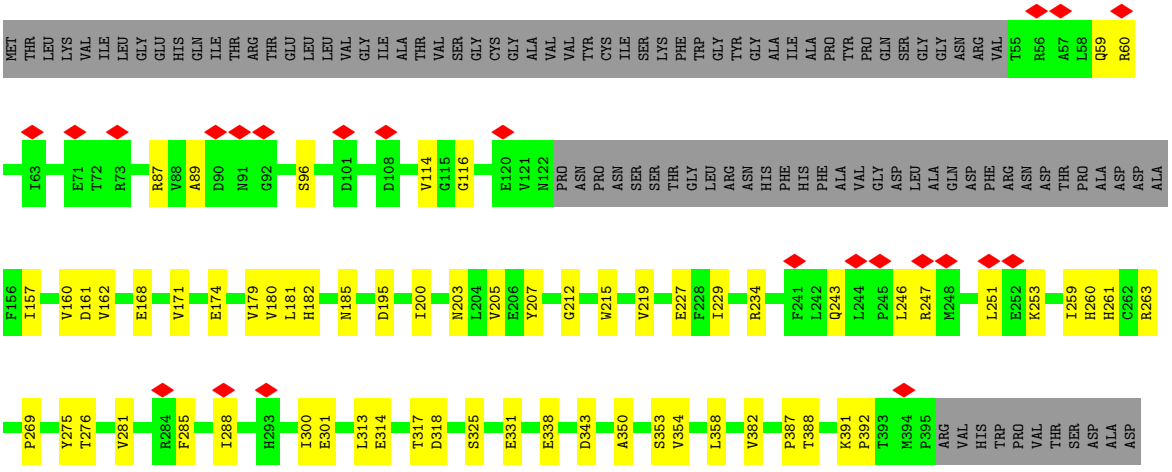
Chain F:

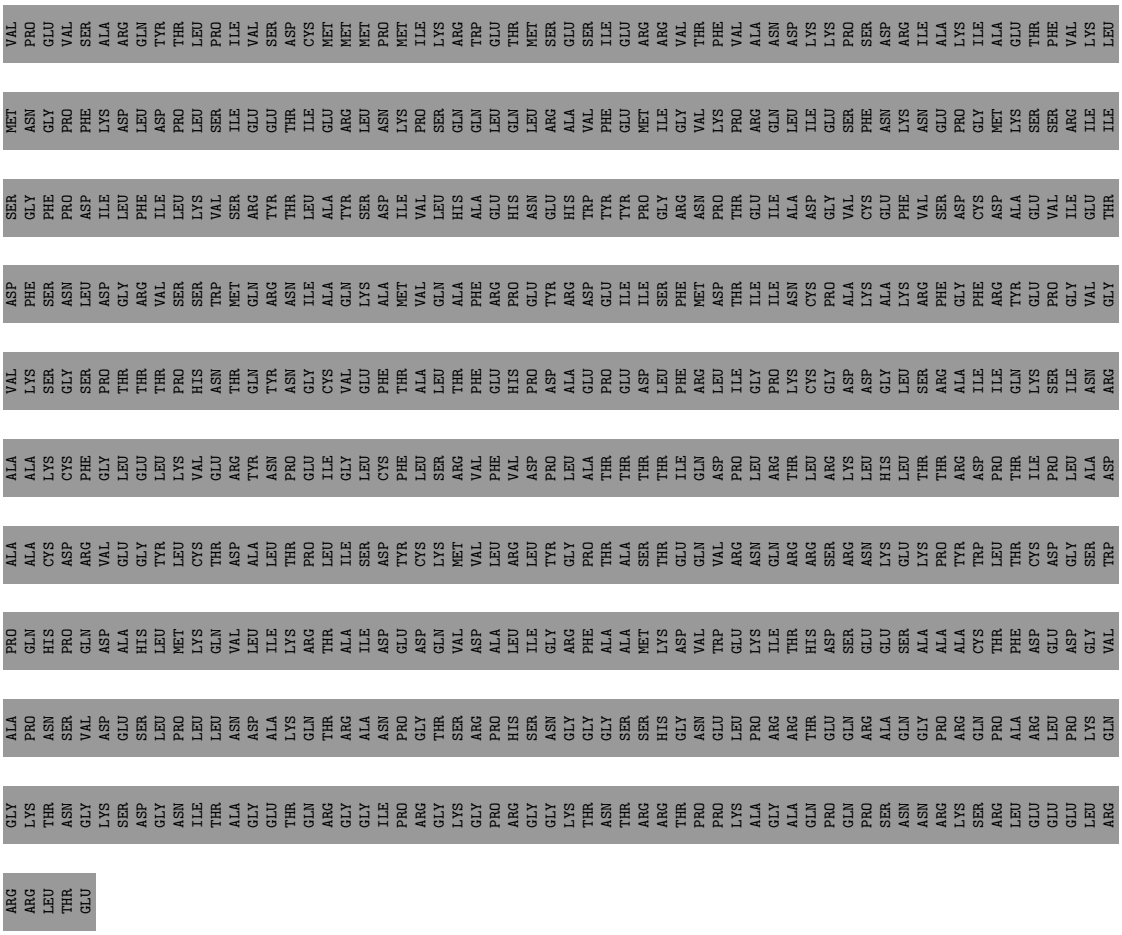




• Molecule 1: RNA-directed RNA polymerase

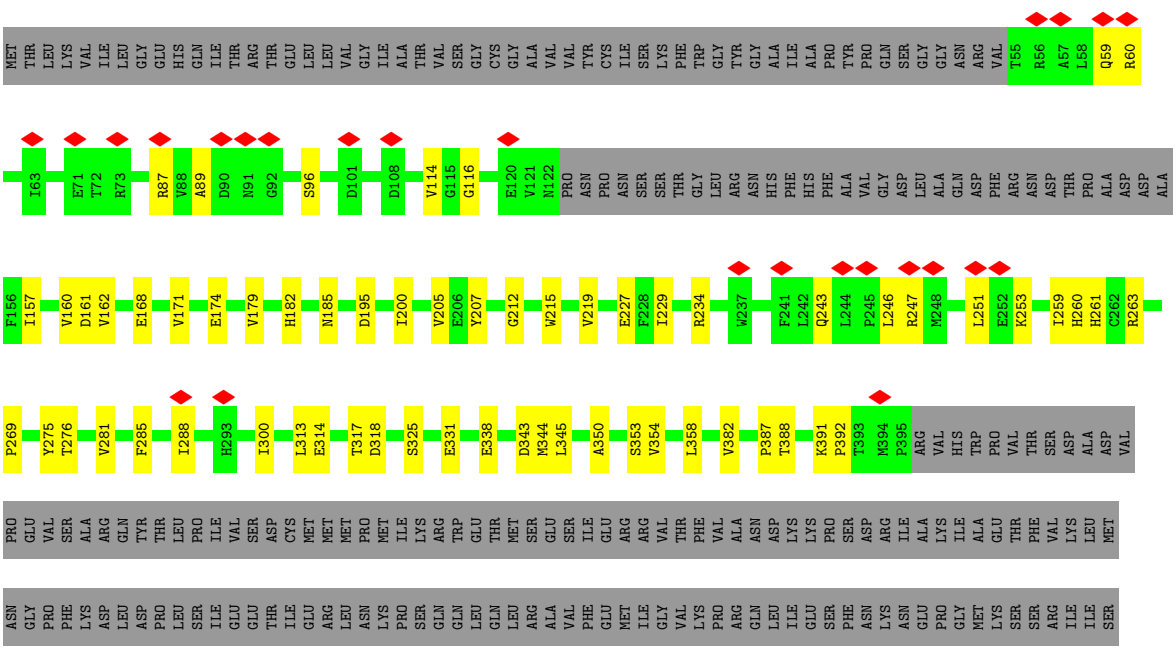
Chain G:

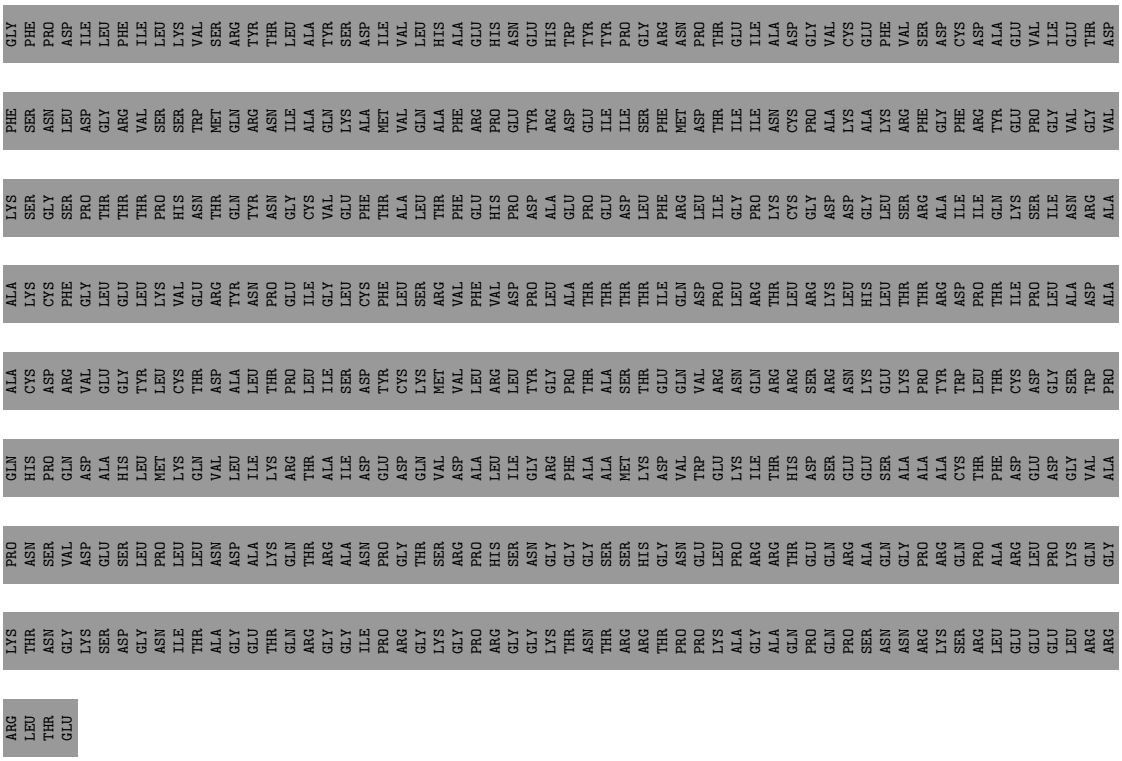




• Molecule 1: RNA-directed RNA polymerase

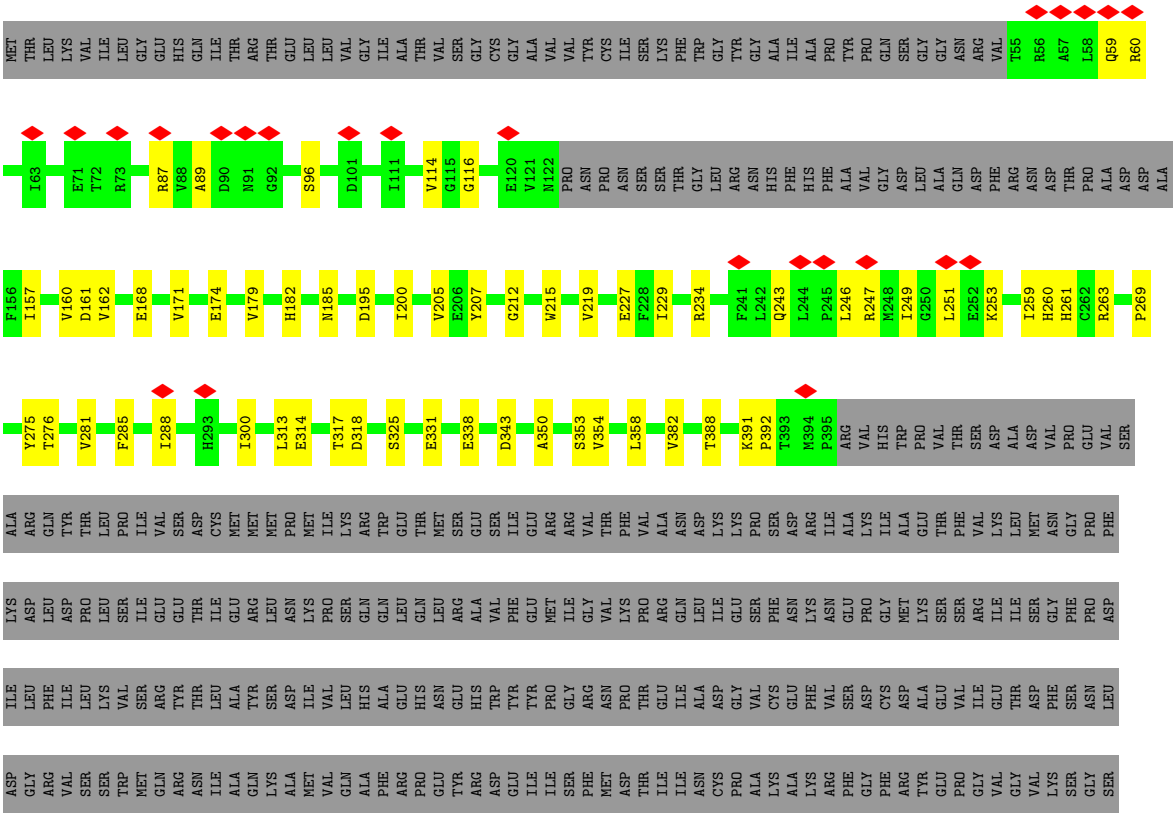
Chain H:

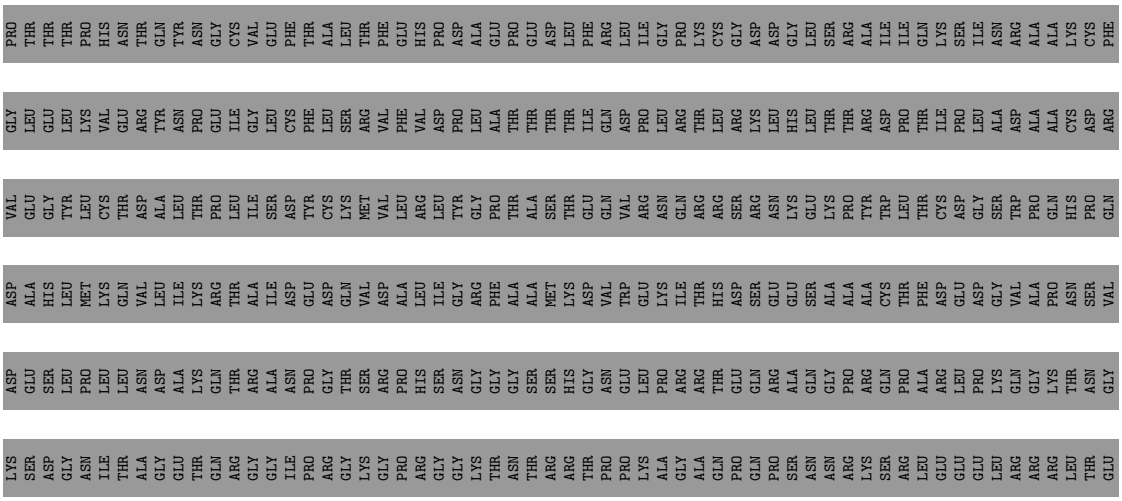




• Molecule 1: RNA-directed RNA polymerase

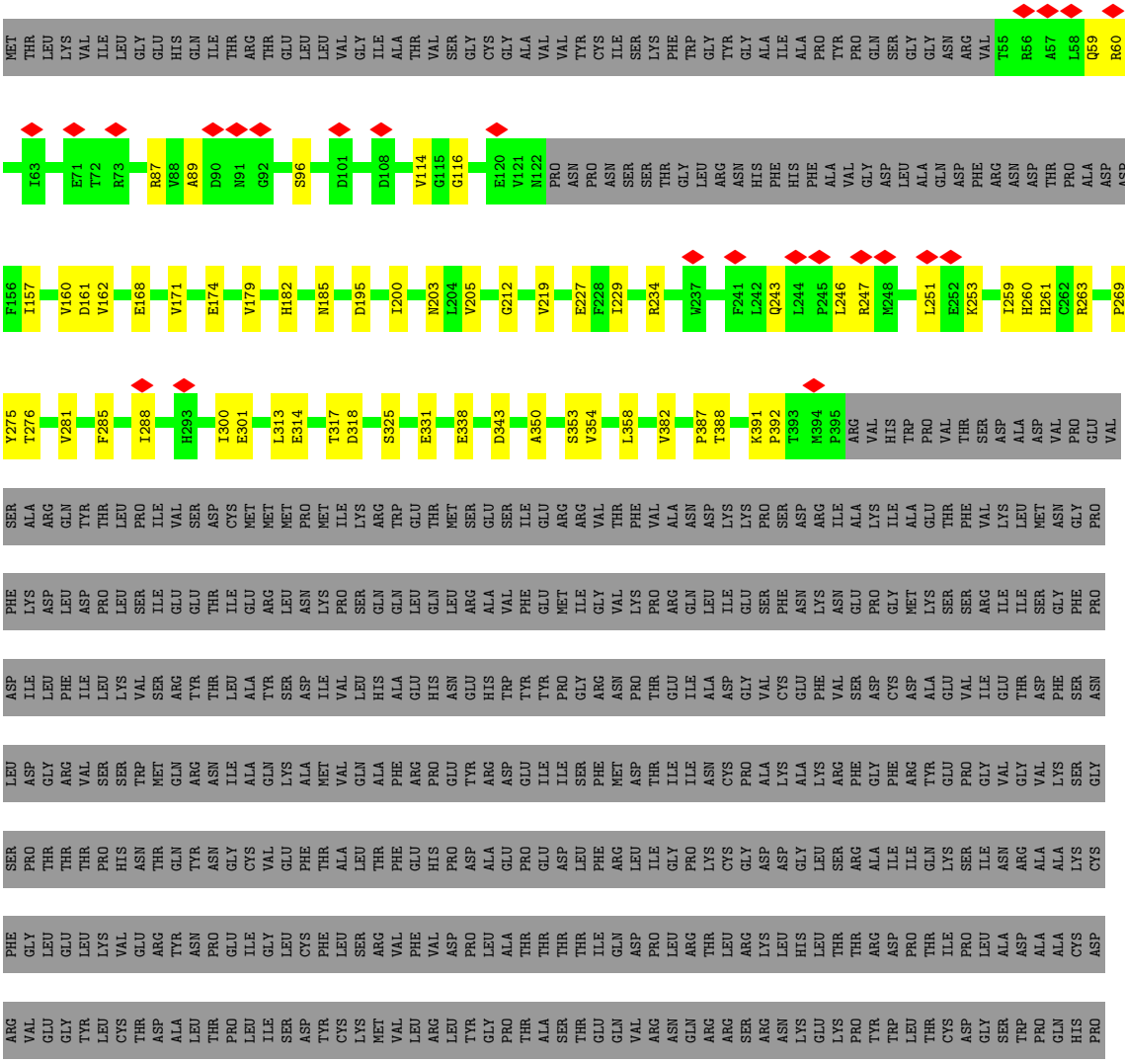
Chain I:

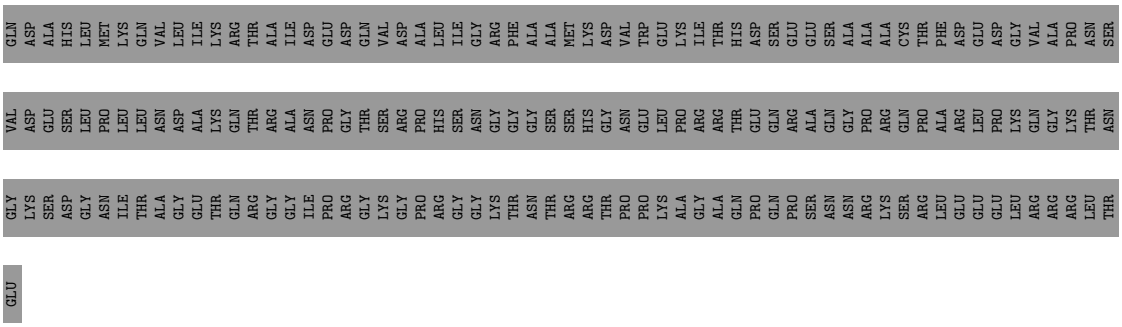




• Molecule 1: RNA-directed RNA polymerase

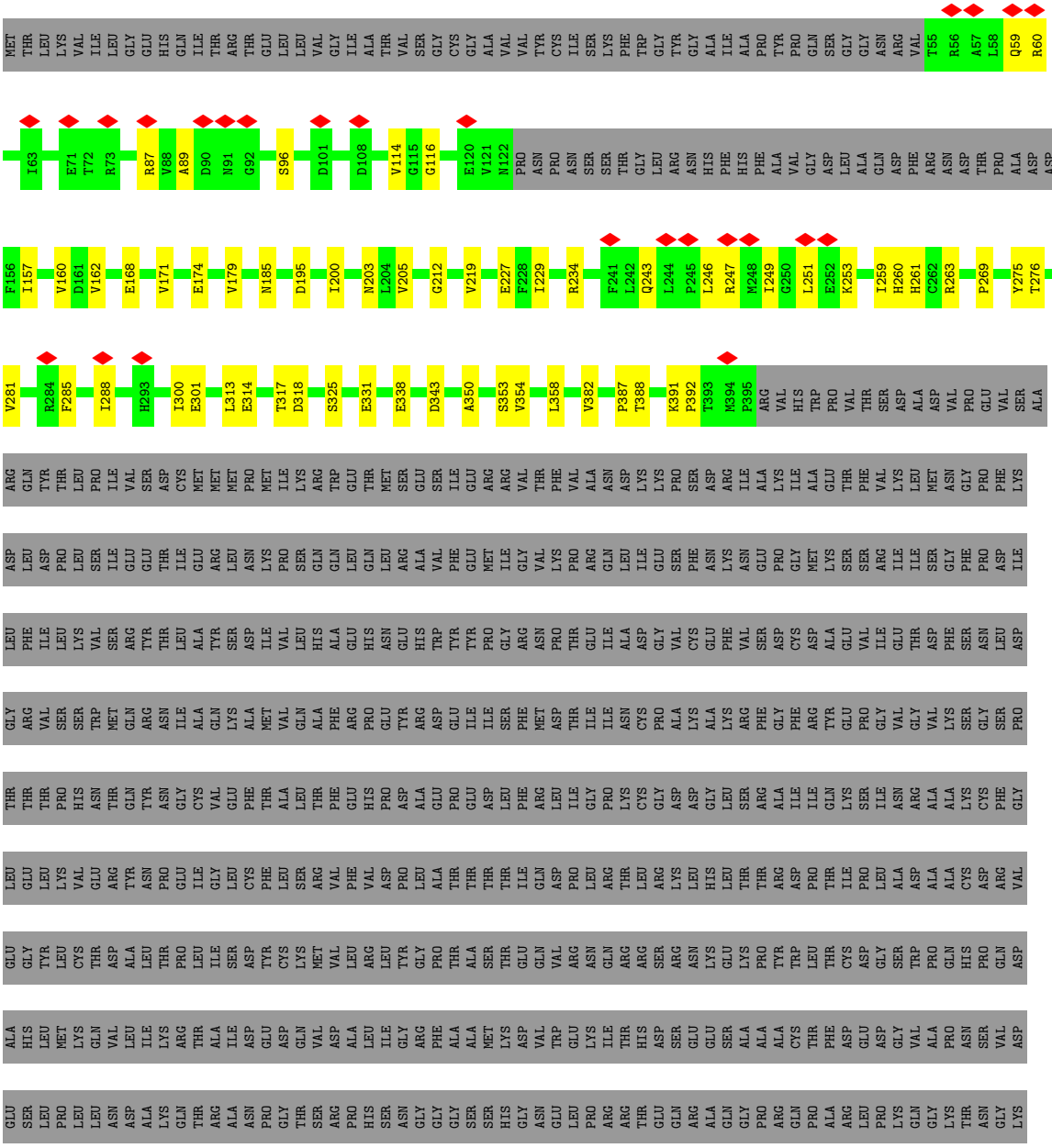
Chain J:





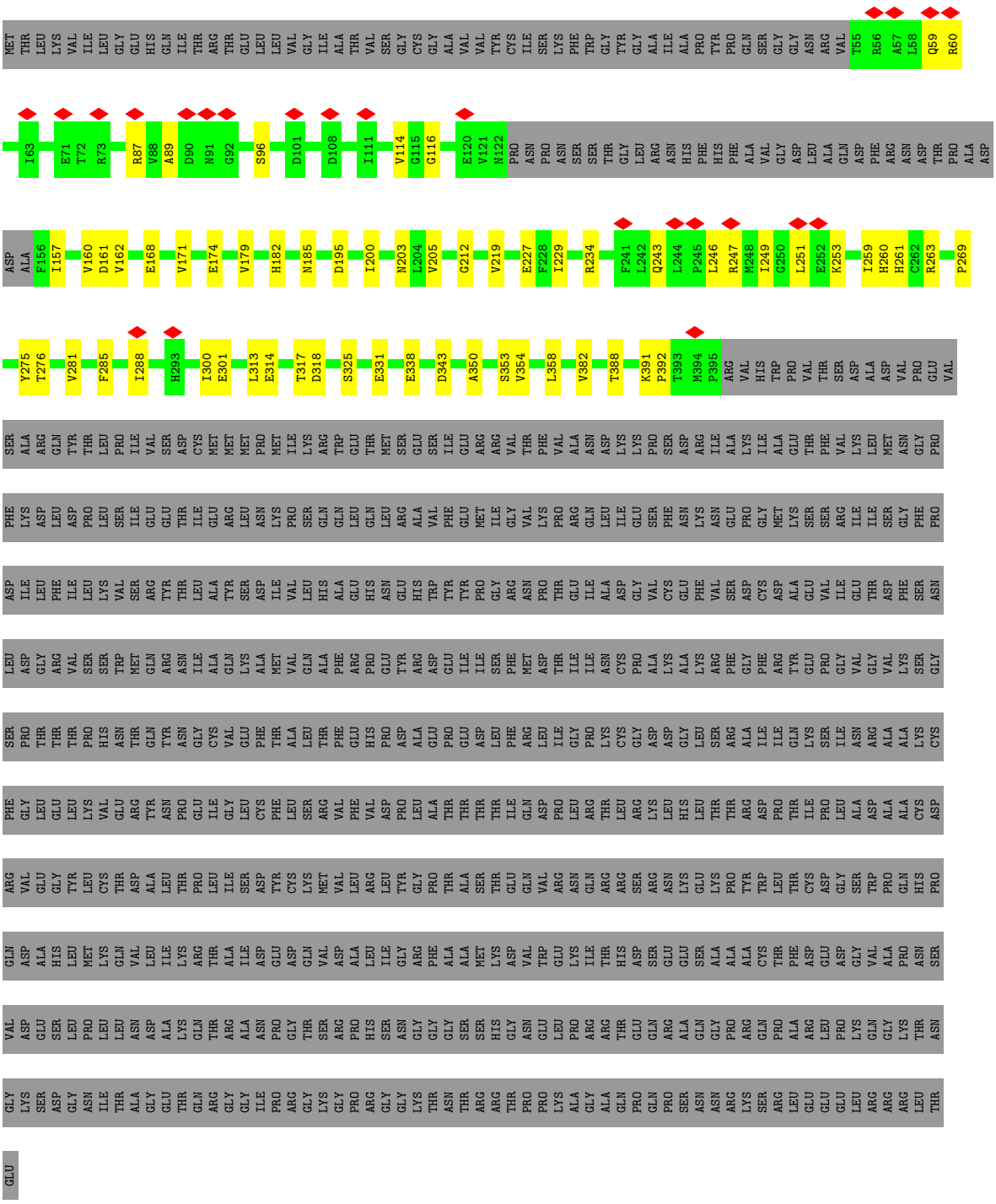
• Molecule 1: RNA-directed RNA polymerase

Chain K:



• Molecule 1: RNA-directed RNA polymerase

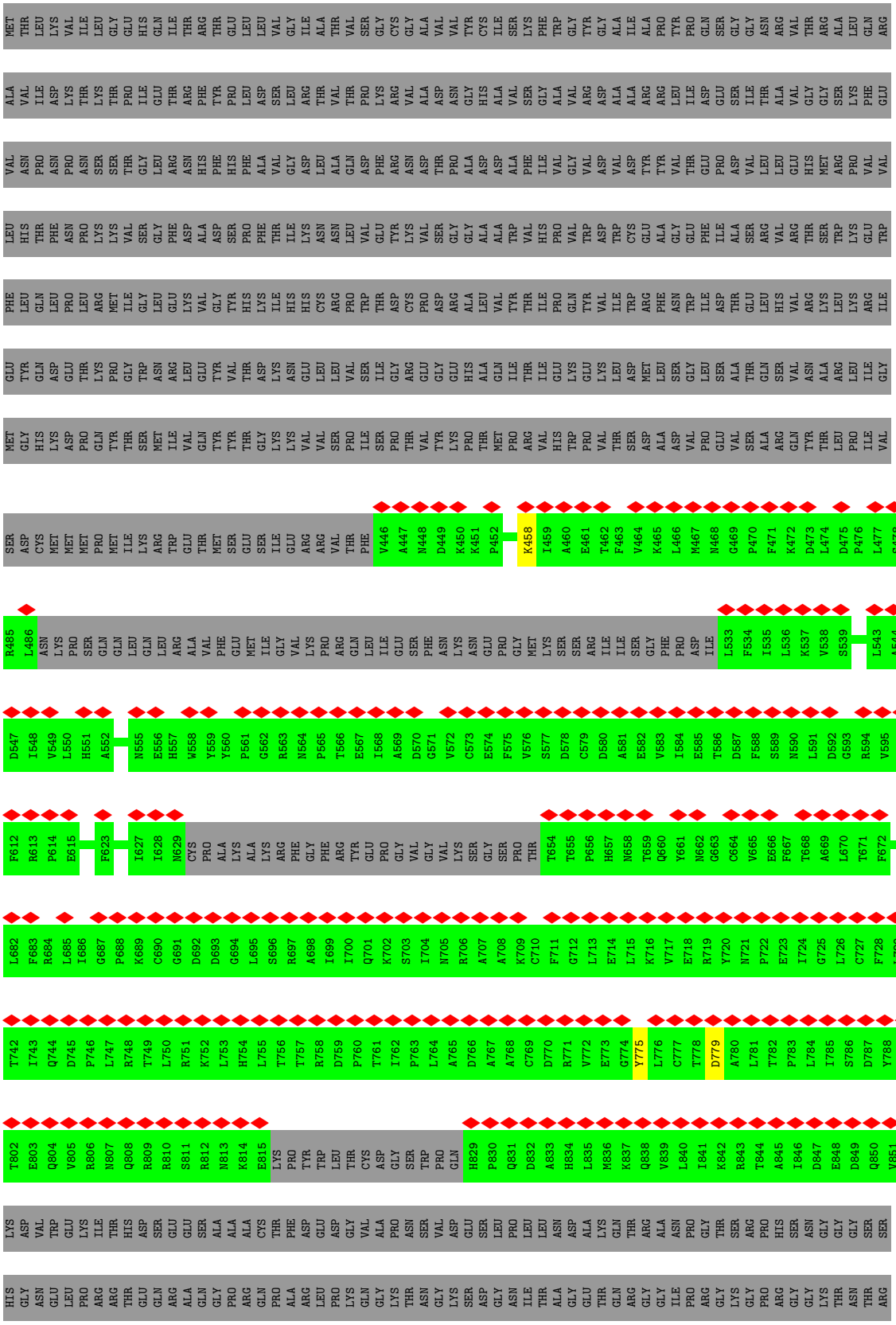
Chain L:



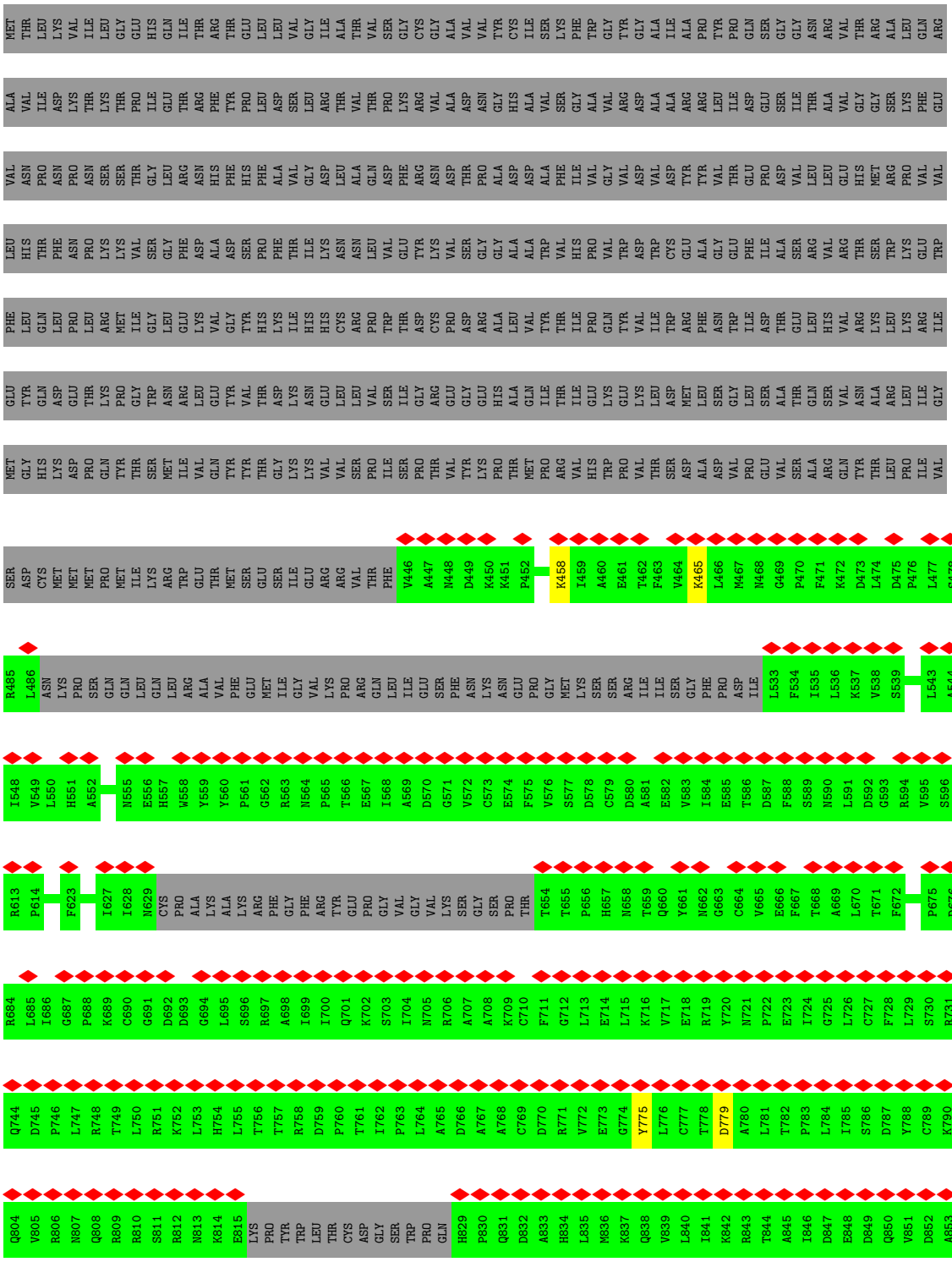
• Molecule 1: RNA-directed RNA polymerase

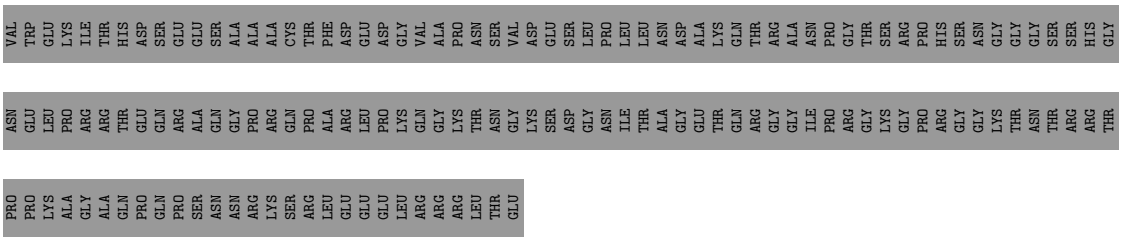
Chain M:

28%
33%
67%

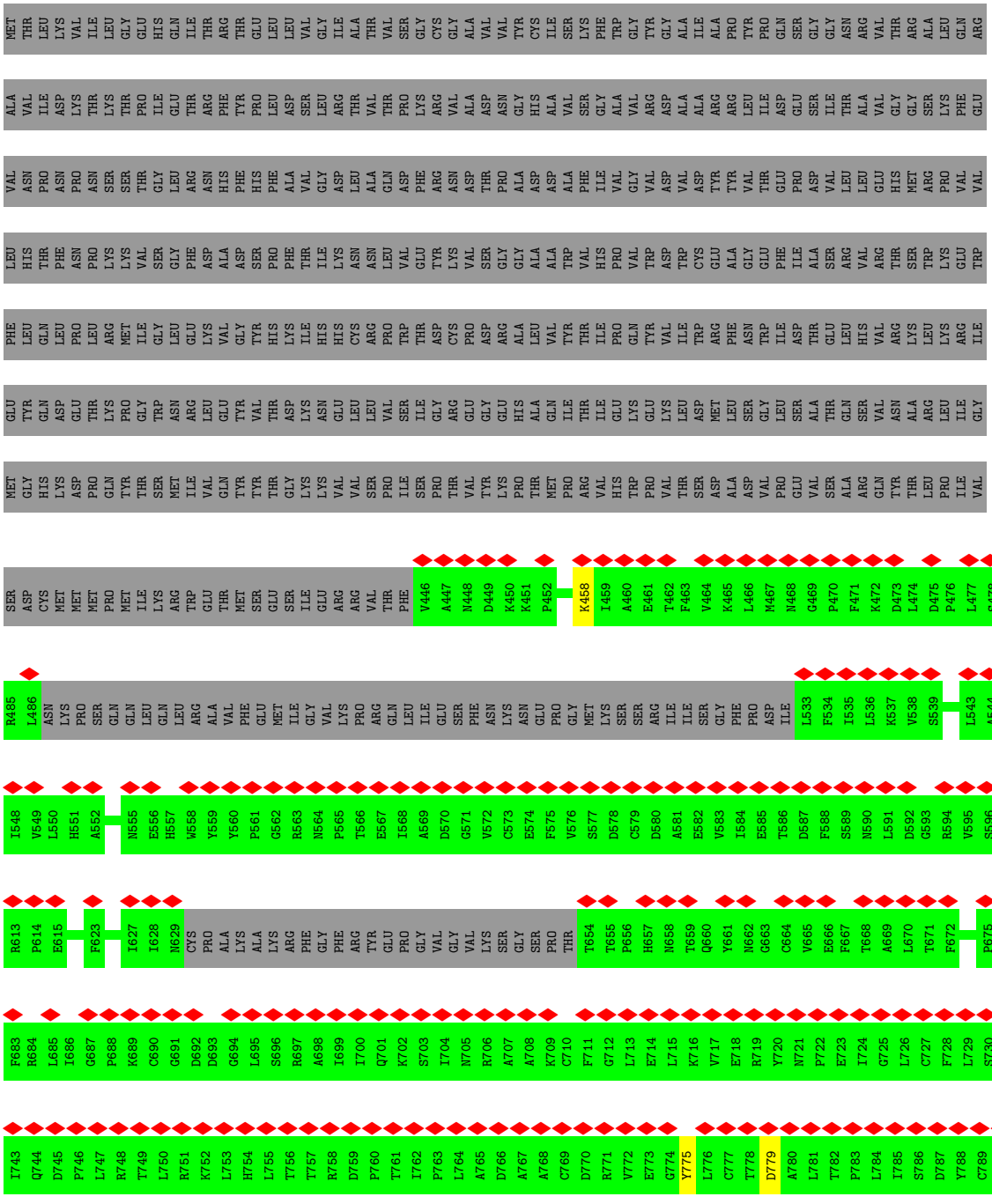

MET THR LEU LYS VAL ILE LEU GLY GLU HIS GLN ILE THR ARG THR GLU LEU LEU VAL GLY ILE ALA THR VAL SER GLY CYS GLY ALA VAL VAL TYR CYS ILE SER LYS PHE TRP GLY TYR GLY ALA ILE ALA PRO TYR PRO GLN SER GLY GLY ASN ARG VAL THR ARG ALA LEU GLN ARG
ALA VAL ILE ASP LYS THR LYS THR PRO ILE GLU THR ARG PHE TYR PRO LEU ASP SER LEU ARG THR VAL THR PRO LYS ARG VAL ALA ASP ASN GLY HIS ALA VAL SER GLY ALA VAL ARG ASP ALA ALA ARG ARG LEU ILE ASP GLU SER ILE THR ALA ALA VAL GLY GLY SER LYS PHE GLU
VAL ASN PRO ASN PRO ASN SER SER THR GLY LEU ARG ASN HIS PHE HIS PHE ALA VAL GLY ASP LEU ALA GLN ASP PHE ARG ASN ASP THR PRO ALA ASP ASP ALA PHE ILE VAL GLY VAL ASP VAL ASP TYR TYR VAL THR GLU PRO ASP VAL LEU LEU GLU HIS MET ARG PRO VAL VAL
LEU HIS THR PHE ASN PRO LYS LYS VAL SER GLY PHE ASP ALA ASP SER PRO PHE THR ILE LYS ASN ASN LEU VAL GLU TYR LYS VAL SER GLY GLY ALA ALA TRP VAL HIS PRO VAL TRP ASP TRP CYS GLU ALA GLY GLU PHE ILE ALA SER ARG VAL ARG THR SER TRP LYS GLU TRP
PHE LEU GLN LEU PRO LEU ARG MET ILE GLY LEU GLU LYS VAL GLY TYR HIS LYS ILE HIS HIS CYS ARG PRO TRP THR ASP CYS PRO PRO ASP ARG ALA LEU VAL TYR THR ILE PRO GLN TYR VAL ILE TRP ARG PHE ASN TRP ILE ASP THR GLU LEU HIS VAL ARG LYS LEU LYS ARG ILE
GLU TYR GLN ASP GLU THR LYS PRO GLY TRP ASN ARG LEU GLU GLU TYR VAL THR ASP LYS ASN GLU LEU GLU VAL SER ILE GLY ARG GLU GLY GLU GLU HIS ALA GLN ILE THR ILE GLU GLU LYS GLU LYS LEU ASP MET LEU SER GLY LEU SER ALA THR GLN SER VAL ASN ALA ARG LEU ILE GLY
MET GLY HIS LYS ASP PRO GLN TYR THR SER MET ILE VAL GLN GLU TYR VAL THR THR GLY LYS LYS VAL VAL SER PRO ILE SER PRO THR VAL TYR LYS PRO THR MET PRO ARG VAL HIS TRP PRO VAL THR SER ASP ALA ASP VAL PRO GLU VAL SER ALA ARG GLN TYR THR LEU PRO ILE VAL
SER ASP CYS MET MET MET PRO MET ILE LYS ARG TRP GLU THR MET SER GLU SER ILE GLU ARG ARG VAL THR PHE V446 A447 N448 D449 K450 K451 P452 K458 I459 A460 E461 T462 F463 V464 K465 L466 M467 N468 G469 P470 F471 K472 D473 L474 D475 P476 L477 S478 I479 E480 E481 T482 I483 E484
R485 L486 ASN LYS PRO SER GLN GLN LEU GLN LEU LEU ARG ALA VAL PHE GLU MET ILE GLY VAL LYS PRO ARG GLN LEU ILE GLU SER PHE ASN LYS ASN GLU PRO GLY MET LYS SER SER ARG ILE ILE SER GLY PHE PRO ASP ILE L533 F534 I535 L536 K537 V538 S539 L543 A544 Y545 S546
D547 I548 V549 L550 H551 A552 N555 E556 H557 W558 Y559 V560 P561 G562 R563 N564 P565 T566 E567 I568 A569 D570 G571 V572 C573 E574 F575 V576 S577 D578 C579 D580 A581 E582 V583 I584 E585 T586 D587 F588 S589 N590 L591 D592 G593 R594 V595 S596 S597 W598 N599 N602 I603 H608 V609 Q610 A611
F612 R613 P614 E615 F623 I627 I628 N629 CYS PRO ALA LYS ALA LYS ARG PHE GLY PHE ARG TYR GLU PRO GLY VAL GLY VAL LYS SER GLY SER PRO THR T654 T655 P656 H657 N658 T659 Q660 Y661 N662 G663 C664 V665 E666 F667 T668 A669 L670 T671 F672 P675 D676 P679 E680 D681
L682 F683 R684 L685 I686 G687 P688 K689 C690 G691 D692 D693 G694 L695 S696 R697 A698 I699 I700 Q701 K702 S703 I704 N705 R706 A707 A708 K709 C710 F711 G712 L713 E714 L715 K716 V717 E718 R719 Y720 N721 P722 E723 I724 G725 L726 C727 F728 L729 S730 R731 V732 F733 V734 D735 P736 L737 A738 T739 T740 T741
T742 I743 Q744 D745 P746 L747 R748 T749 L750 R751 K752 L753 H754 L755 T756 T757 R758 D759 P760 T761 I762 P763 L764 A765 D766 A767 A768 C769 D770 R771 V772 E773 G774 Y775 L776 C777 T778 D779 A780 L781 T782 P783 I784 I785 S786 D787 Y788 C789 K790 M791 V792 L793 R794 L795 Y796 G797 P798 T799 A800 S801
T802 E803 Q804 V805 R806 N807 Q808 R809 R810 S811 R812 N813 K814 E815 LYS PRO TYR TRP LEU THR CYS ASP GLY SER TRP PRO GLN H829 P830 Q831 D832 A833 H834 L835 M836 K837 Q838 V839 L840 I841 K842 R843 T844 A845 I846 D847 E848 D849 Q850 V851 D852 A853 L854 I855 G856 R857 F858 A859 A860 M861
LYS ASP VAL TRP GLU LYS ILE THR HIS ASP SER GLU GLU SER ALA ALA CYS THR PHE ASP GLU ASP GLY VAL ALA PRO ASN SER VAL ASP GLU SER LEU PRO LEU LEU ASN ASP ALA LYS GLN THR ARG ALA ASN PRO GLY THR SER ARG PRO HIS SER ASN GLY GLY GLY GLY SER SER
HIS GLY ASN GLU LEU PRO ARG THR GLU GLN ARG ALA GLN GLY PRO ARG GLN PRO ALA ARG LEU PRO LYS GLN GLY LYS THR ASN GLY LYS SER ASP GLY ASN ILE THR ALA GLY GLU THR GLN ARG GLY ALA ILE PRO ARG GLY LYS GLY PRO ARG GLY GLY LYS THR ASN THR ARG

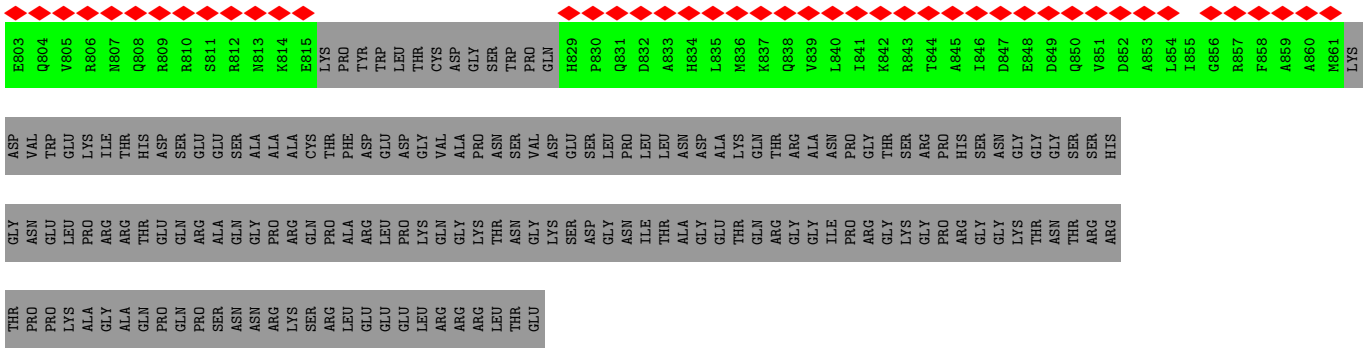
• Molecule 1: RNA-directed RNA polymerase





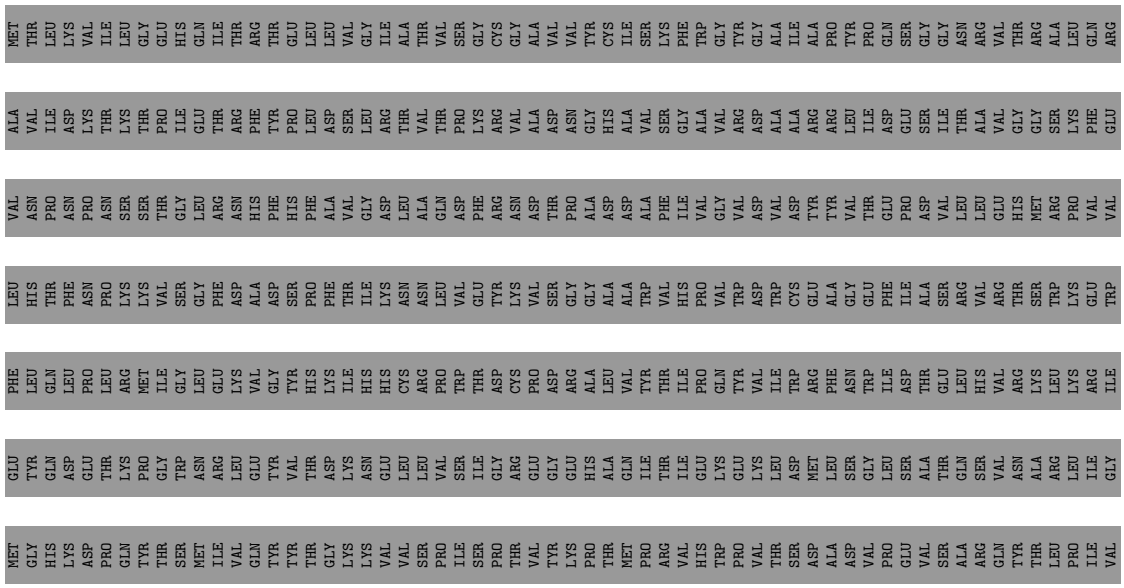
• Molecule 1: RNA-directed RNA polymerase

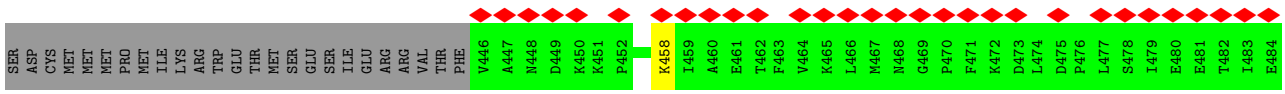


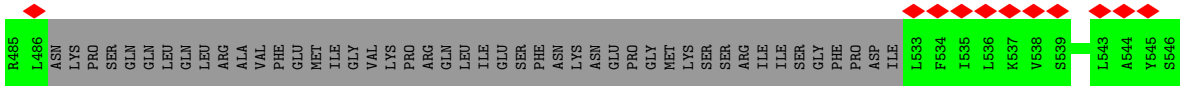


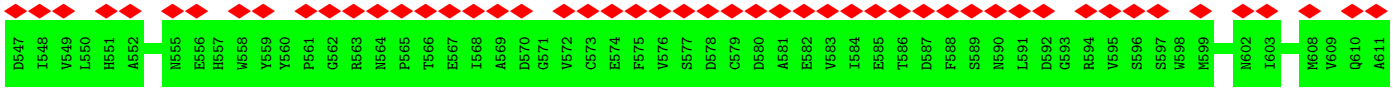
- Molecule 1: RNA-directed RNA polymerase

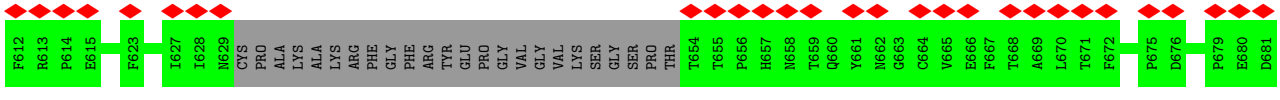
Chain P:

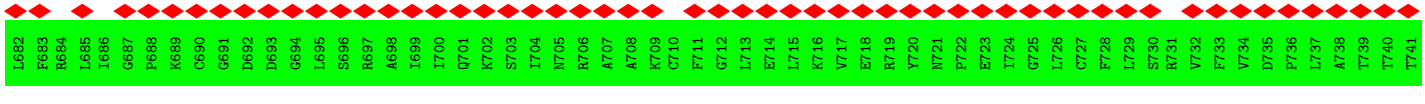


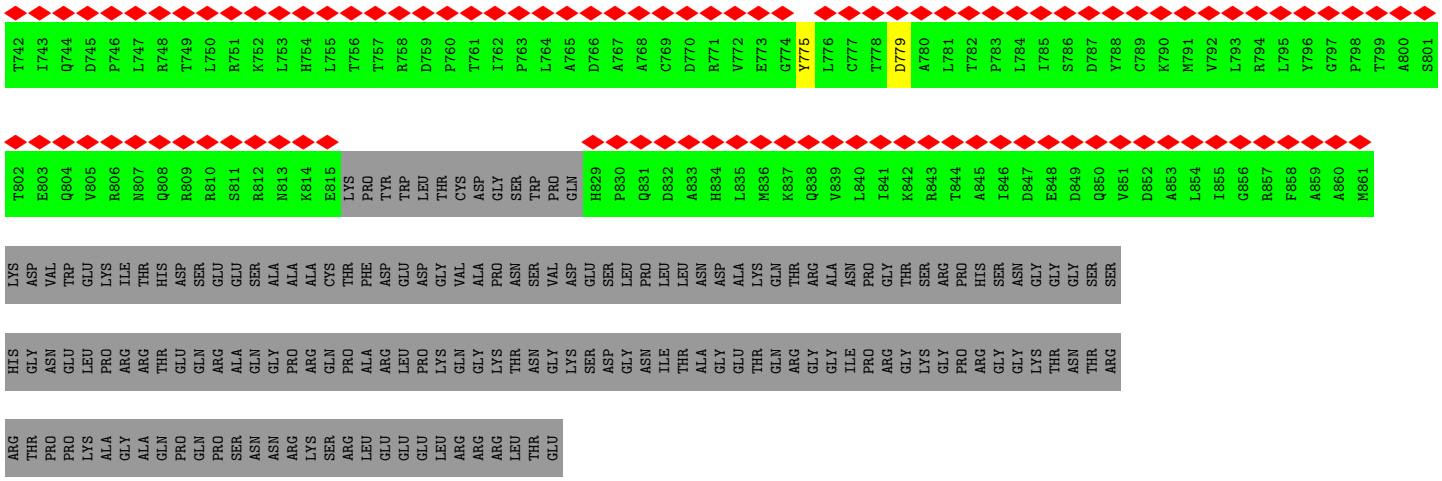






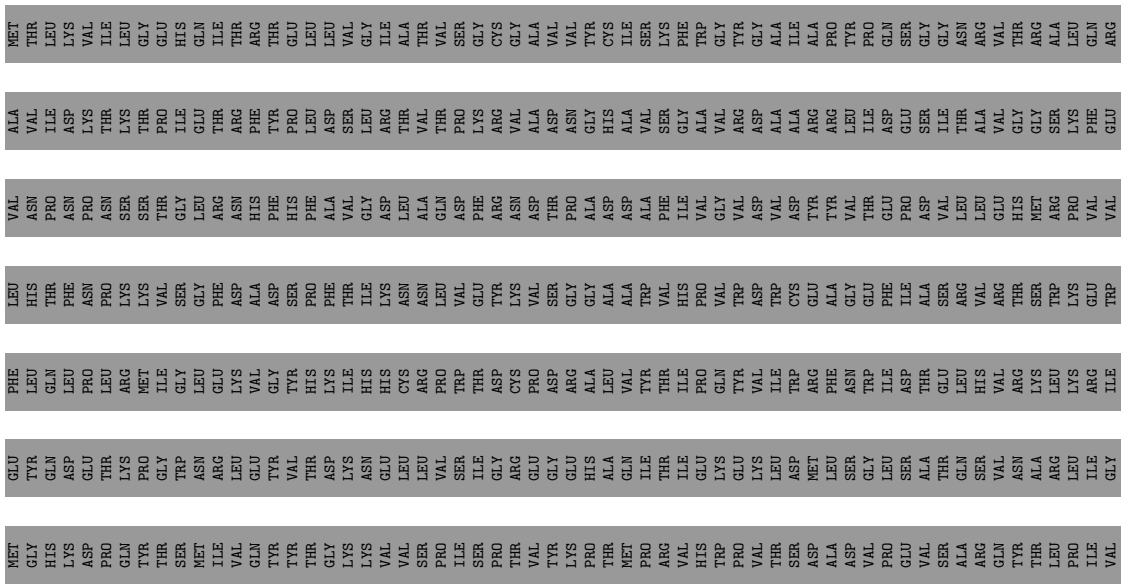


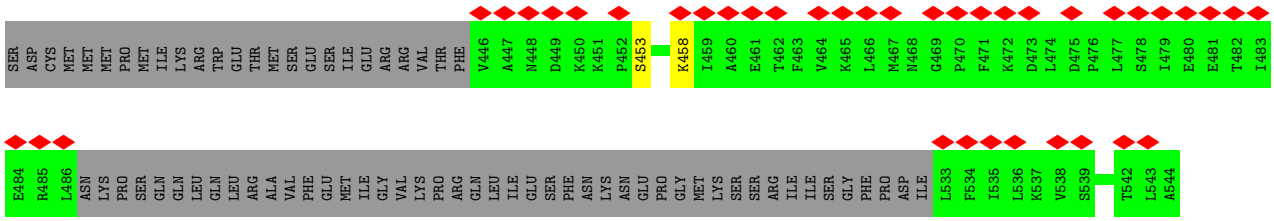


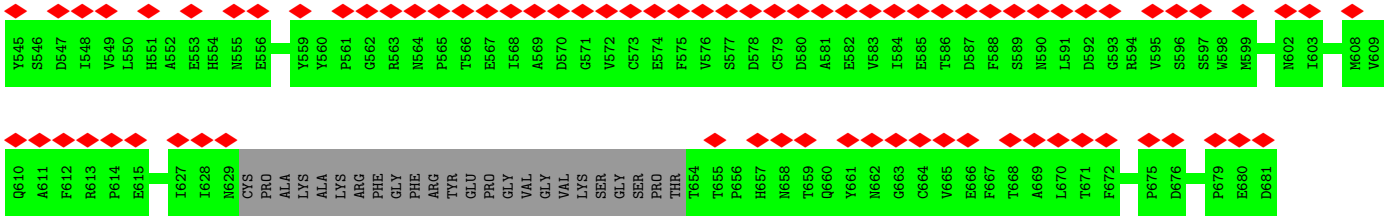


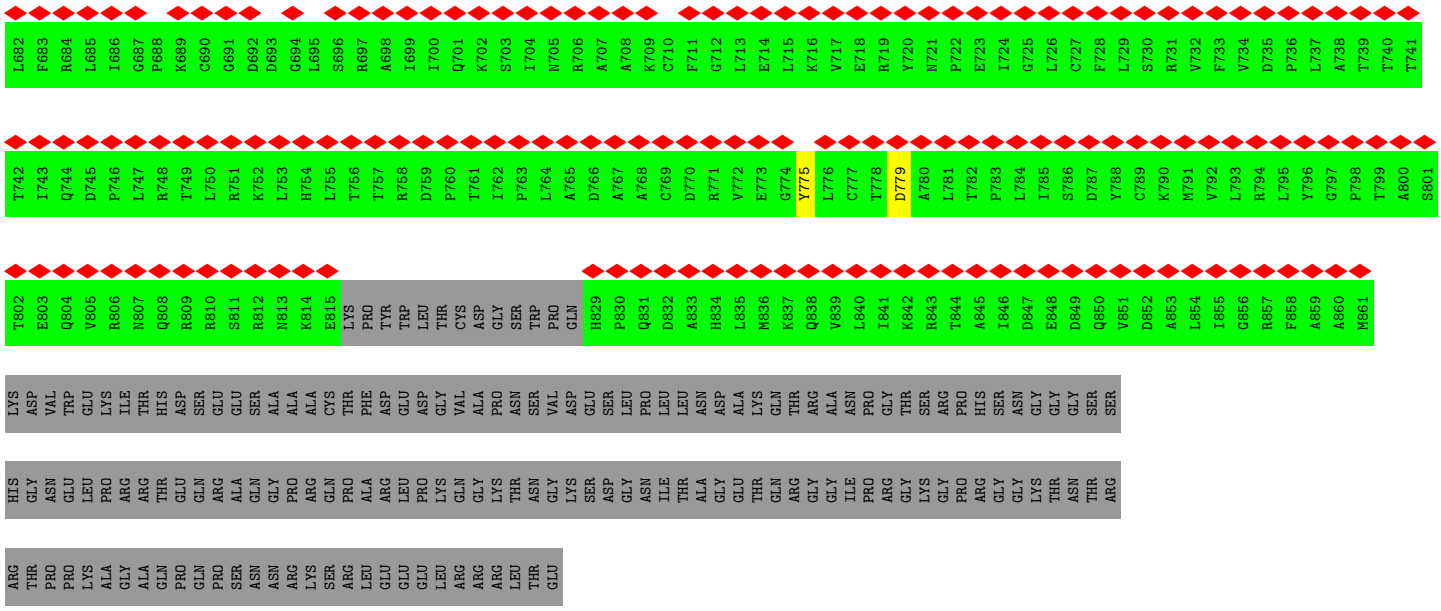
- Molecule 1: RNA-directed RNA polymerase

Chain Q:



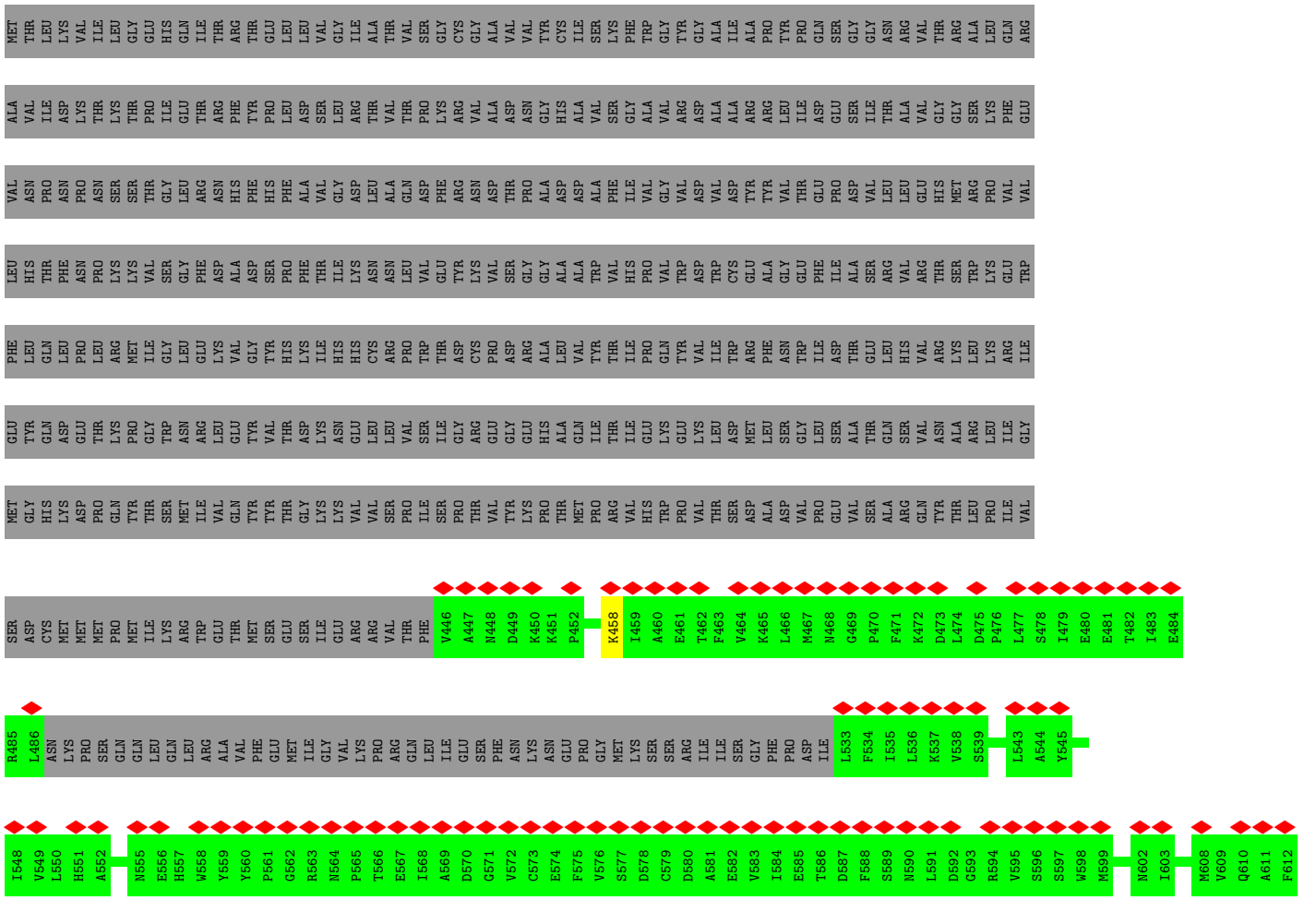


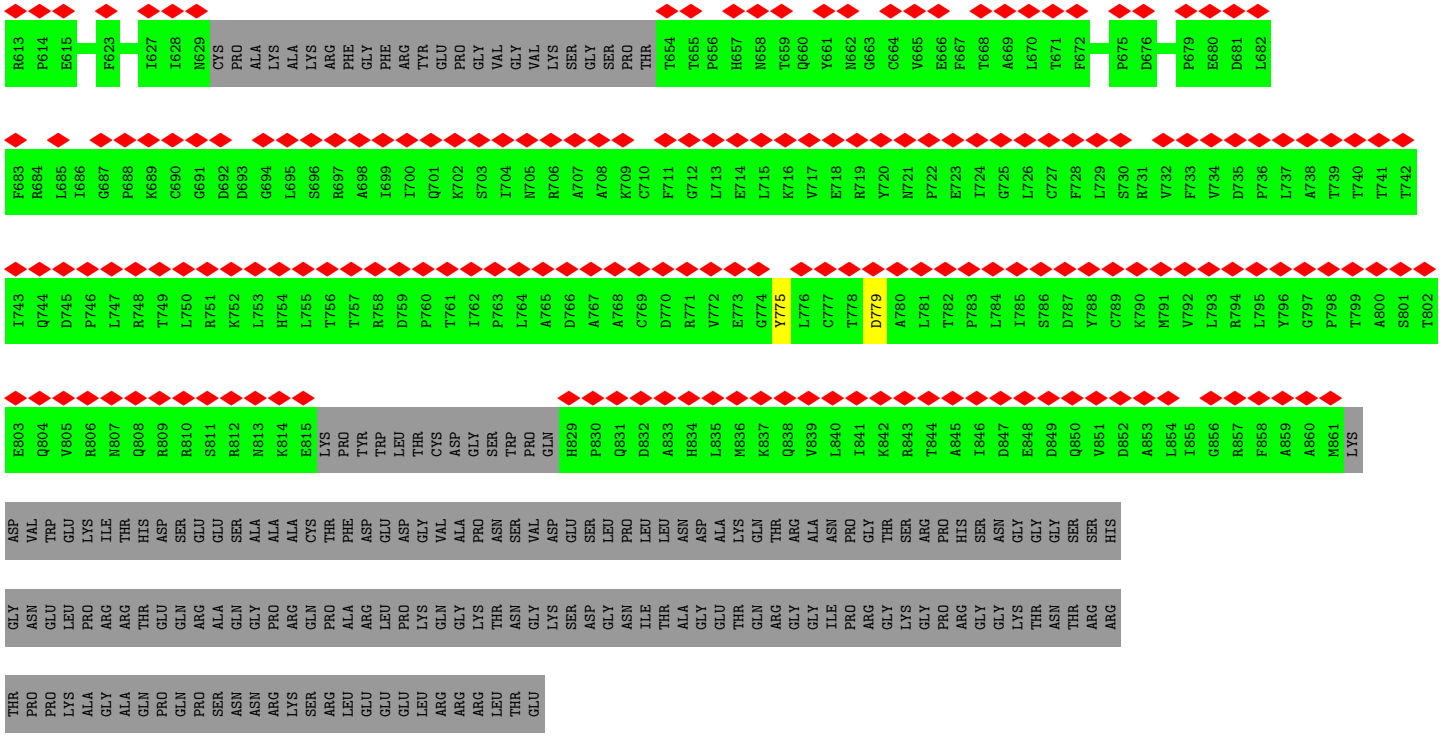




- Molecule 1: RNA-directed RNA polymerase

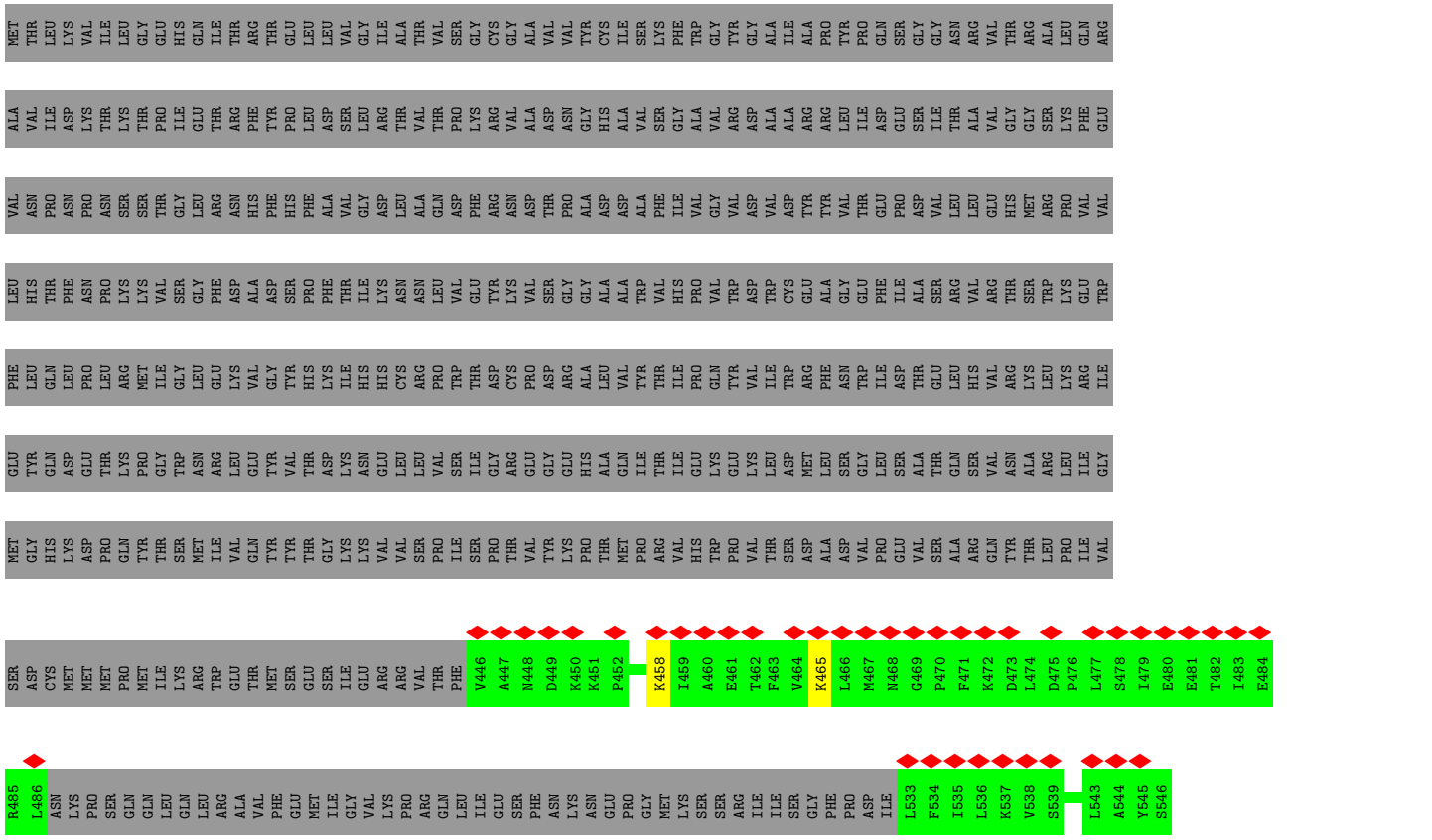
Chain R:

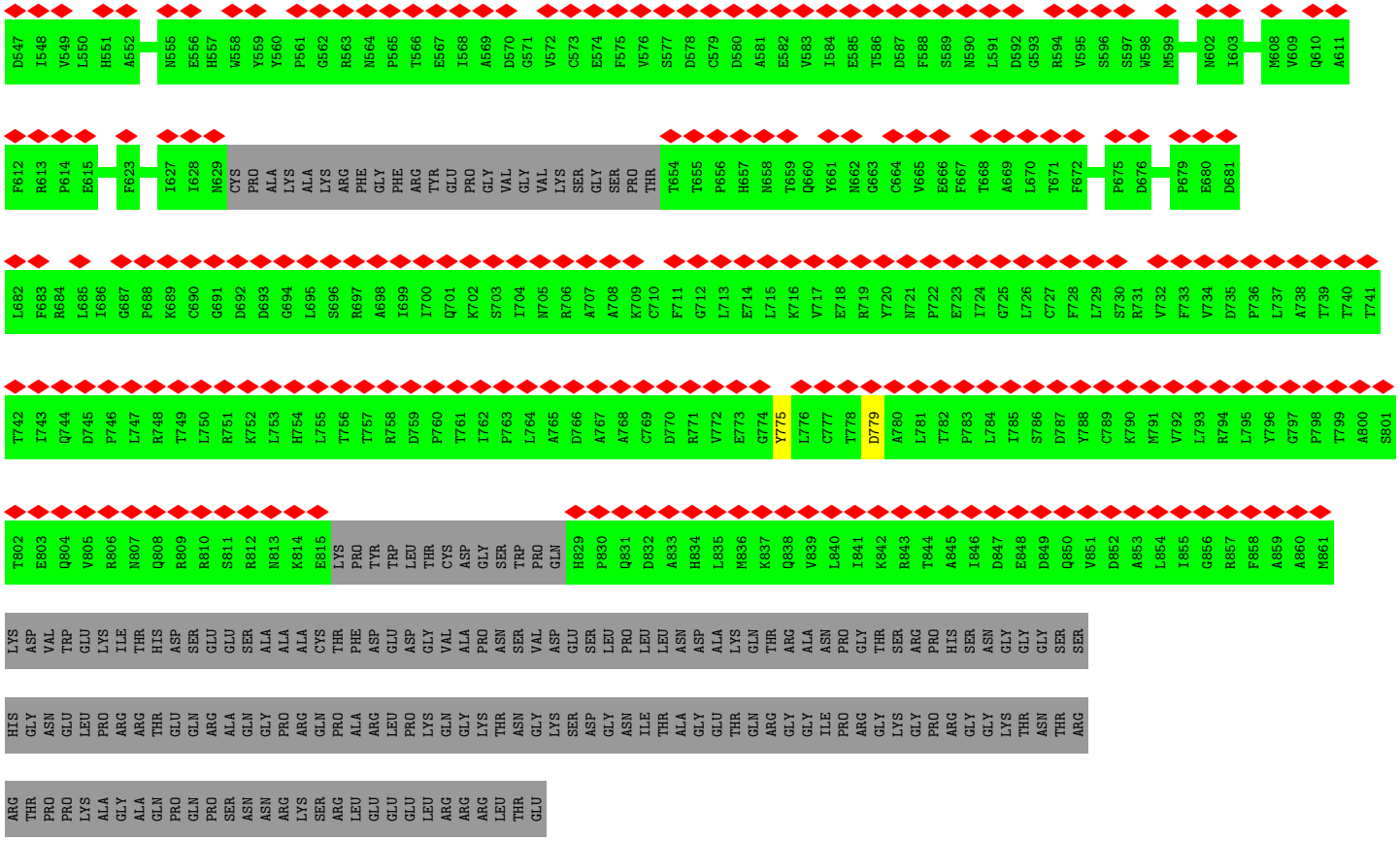




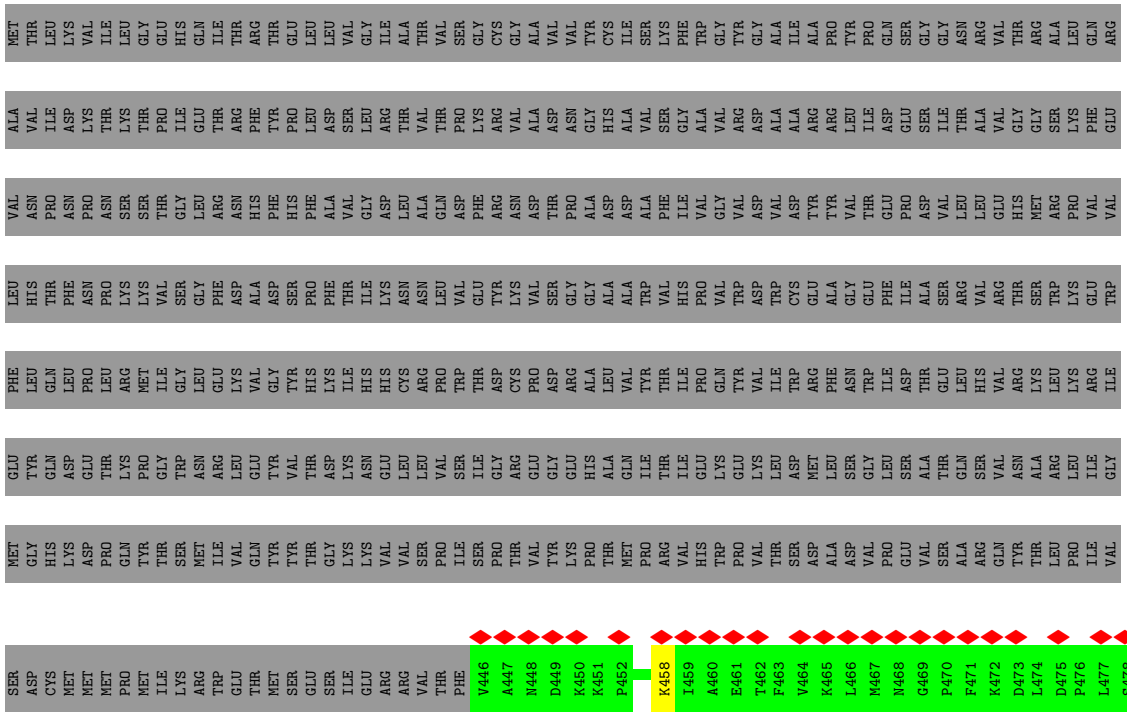
• Molecule 1: RNA-directed RNA polymerase

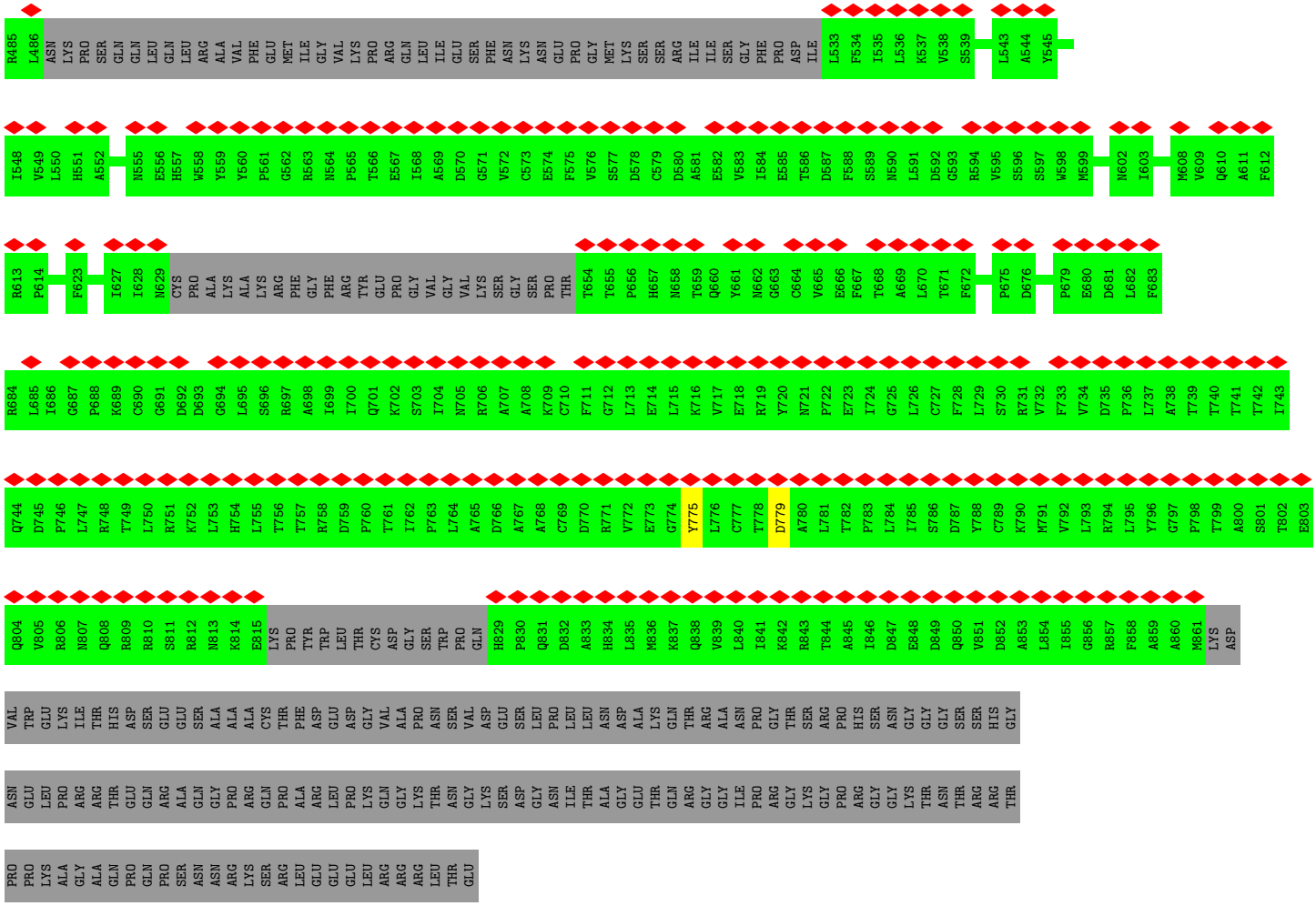
Chain S:





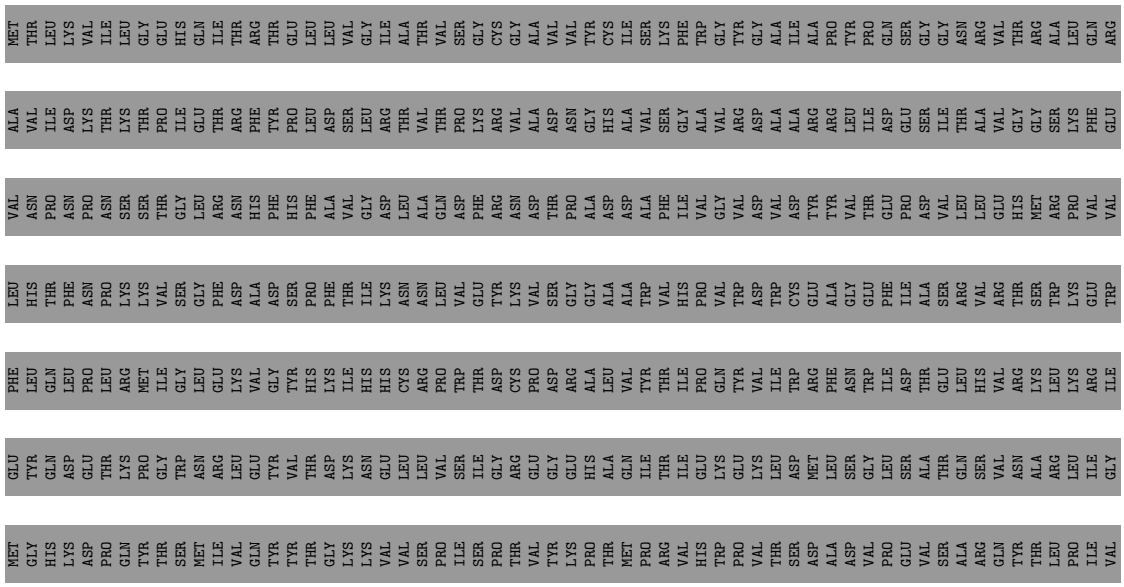
- Molecule 1: RNA-directed RNA polymerase

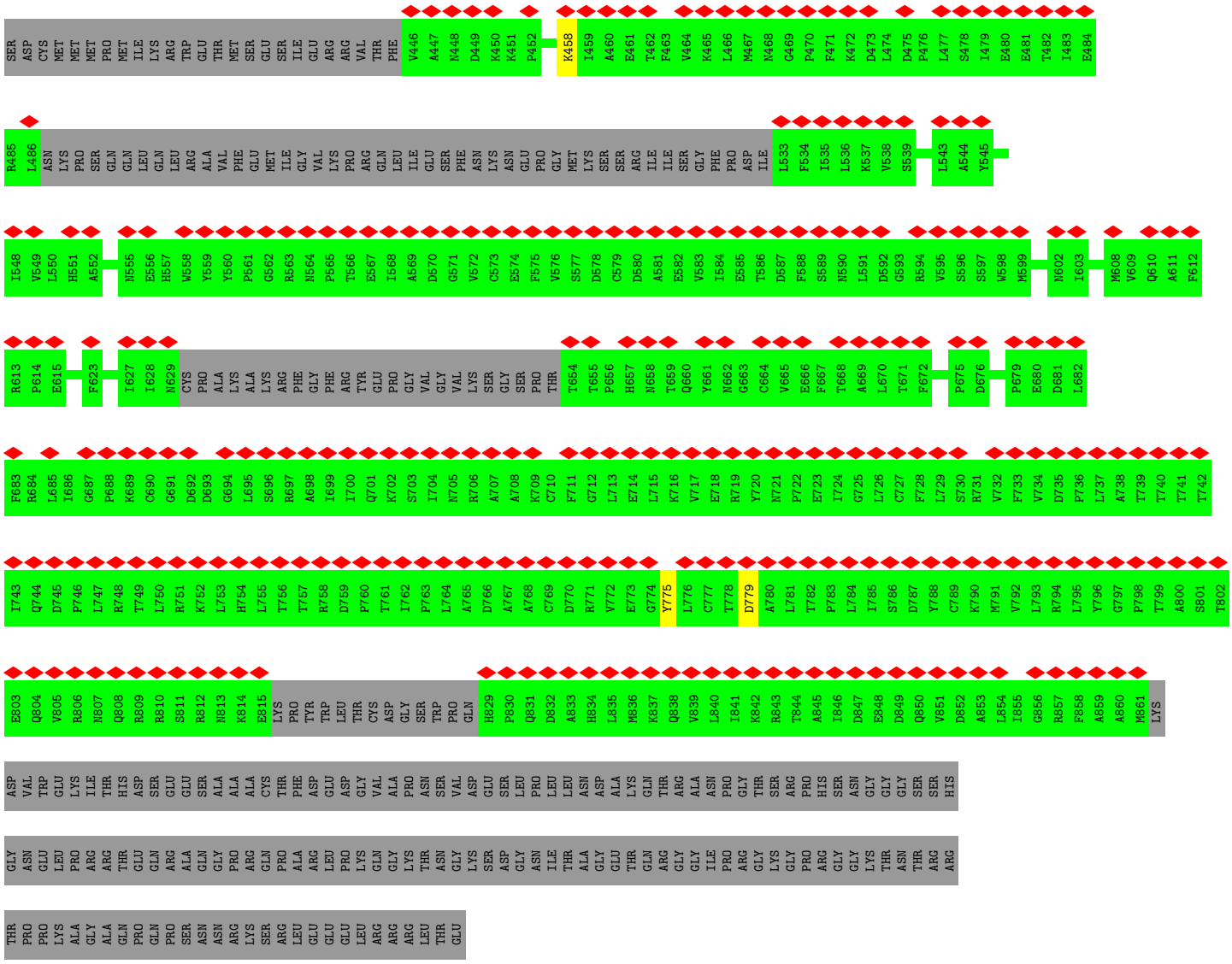




• Molecule 1: RNA-directed RNA polymerase

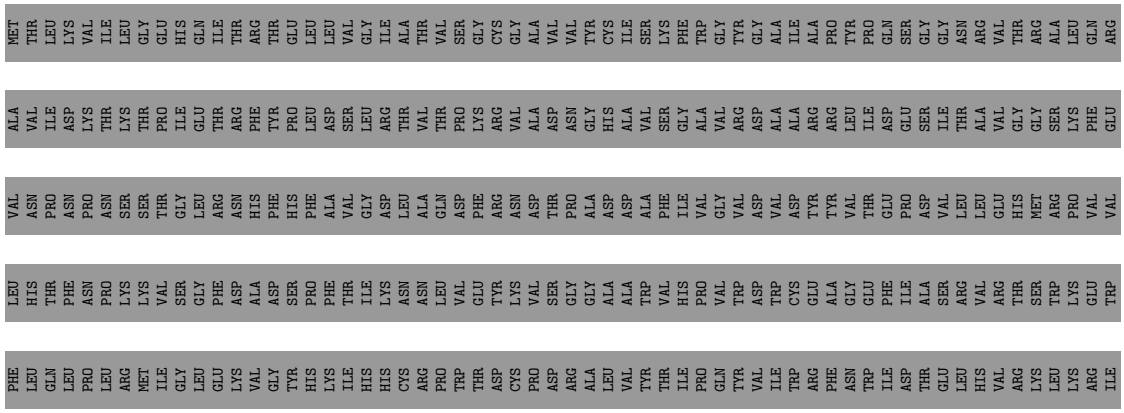
Chain U:

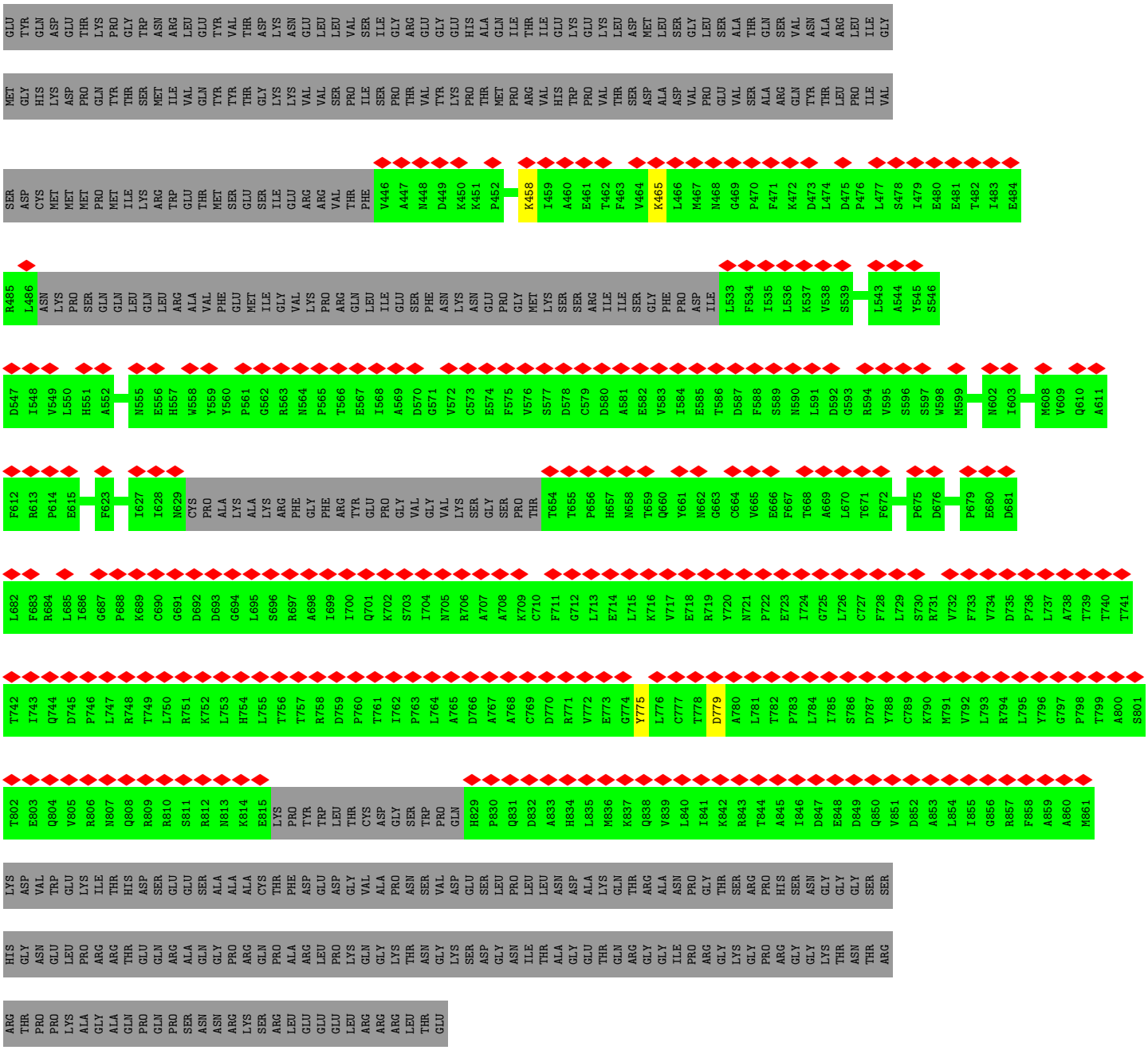




• Molecule 1: RNA-directed RNA polymerase

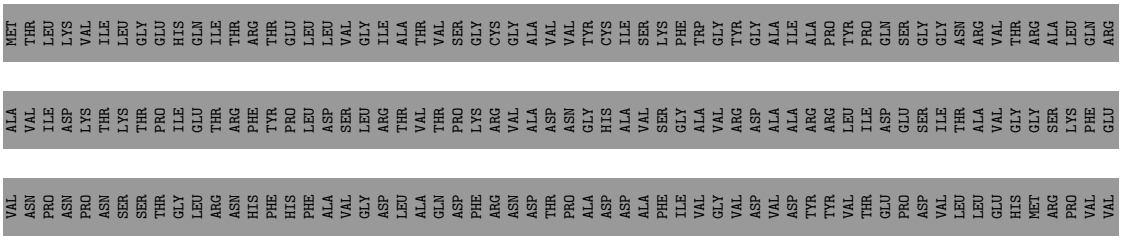
Chain V:

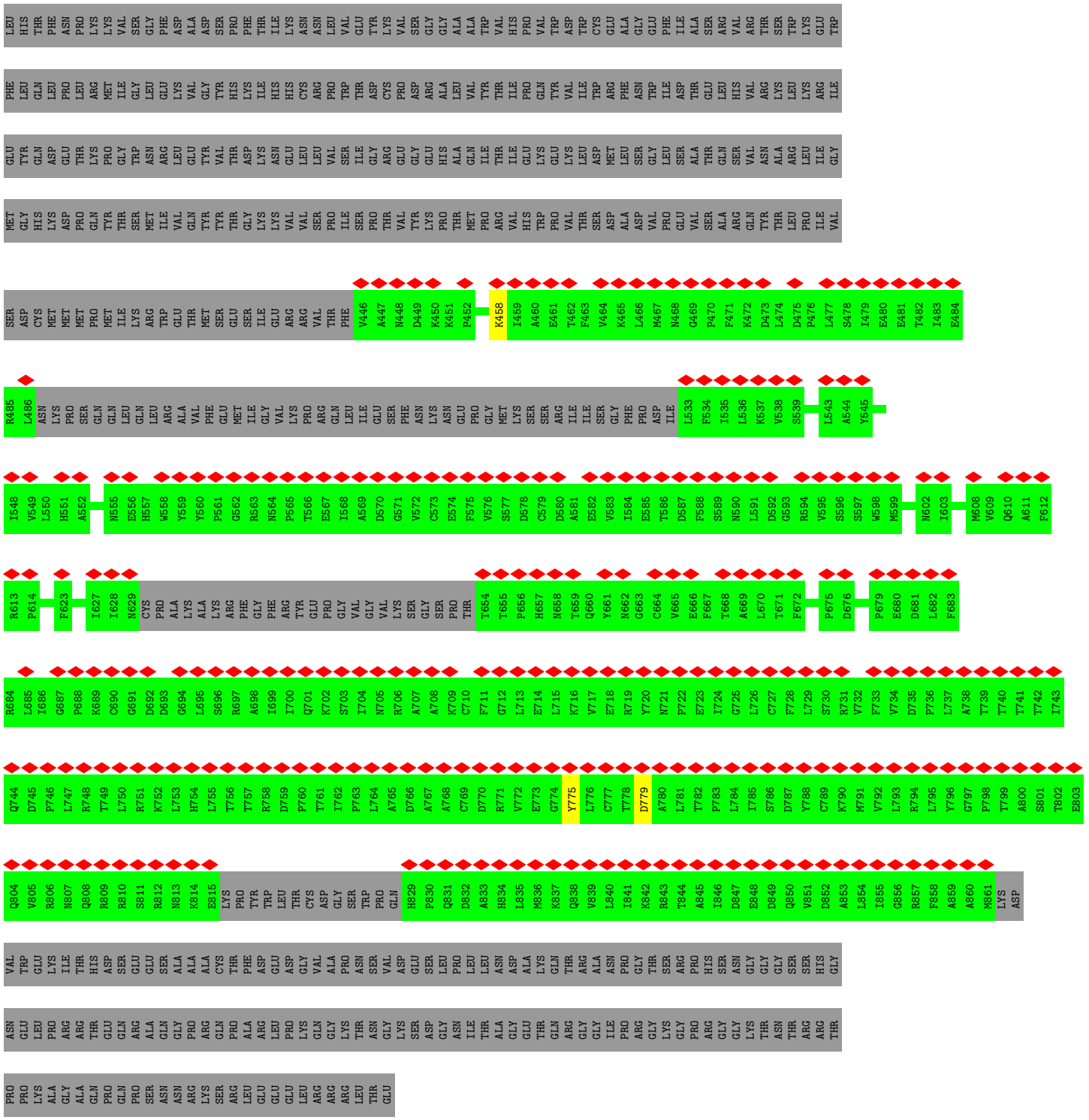




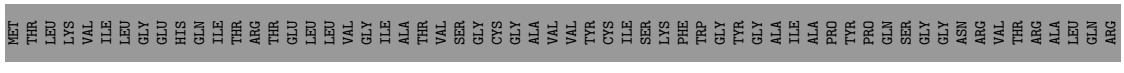
• Molecule 1: RNA-directed RNA polymerase

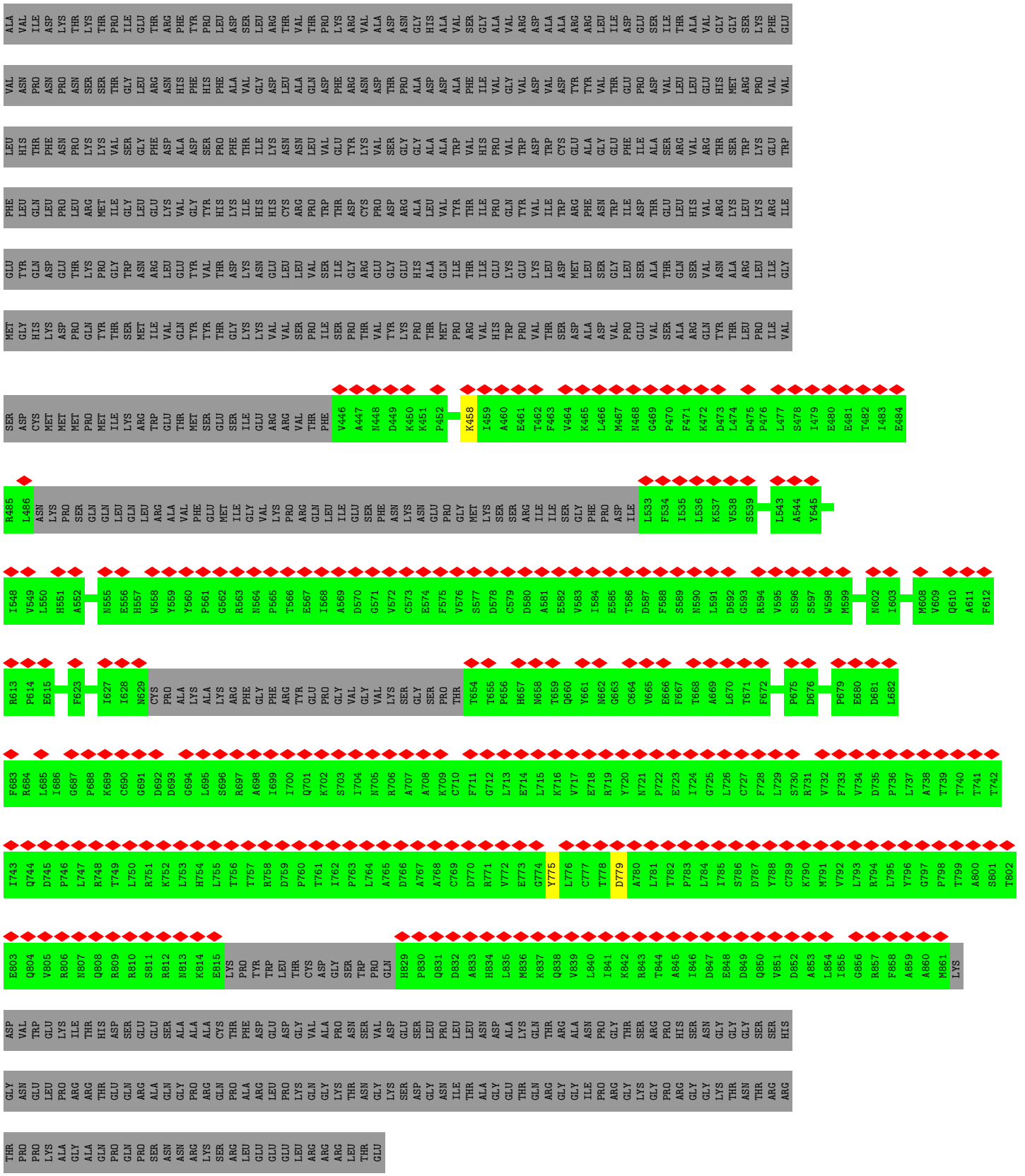
Chain W:





• Molecule 1: RNA-directed RNA polymerase




ALA VAL ILE ASP LYS THR LYS THR PRO ILE GLU THR ARG PHE TYR PRO LEU ASP SER LEU ARG THR VAL THR PRO LYS ARG VAL ALA ASP ASN GLY HIS ALA VAL SER GLY ALA VAL ARG ASP ALA ALA ARG ARG LEU ILE ASP GLU SER ILE THR ALA VAL GLY GLY SER LYS PHE GLU
VAL ASN PRO ASN PRO ASN SER SER THR GLY LEU ARG ASN HIS PHE HIS PHE ALA VAL GLY ASP LEU ALA GLN ASP PHE ARG ASN ASP THR PRO ALA ASP ASP ALA PHE ILE VAL GLY VAL ASP VAL ASP TYR TYR VAL THR GLU PRO ASP SER ILE THR LEU LEU GLU HIS MET ARG PRO VAL VAL
LEU HIS THR PHE ASN PRO LYS LYS VAL SER GLY PHE ASP ALA ASP SER PRO PHE THR ILE ILE GLU LYS ASN ASN LEU VAL GLY ASP LEU ALA GLN ASP PHE ARG MET ILE GLY LEU GLU LYS VAL GLY TYR HIS LYS ILE HIS HIS CYS ARG PRO TRP THR ASP LYS ASN GLU LEU LEU VAL SER LYS PRO GLY TRP ASN ARG LEU GLU GLU TYR VAL THR ASP LYS ASN GLU LEU LYS PRO GLY GLU GLY GLU HIS ALA GLN ILE THR ILE GLU GLY LYS GLU LYS LEU ASP MET LEU SER GLY LEU SER ALA THR GLN SER VAL ASN ALA ARG LEU ILE GLY
PHE LEU GLN LEU PRO LEU ARG MET ILE GLY LEU GLU GLU LYS VAL GLY TYR HIS LYS ILE HIS HIS CYS ARG PRO TRP THR ASP CYS PRO ASP ARG ALA LEU VAL THR TYR THR ILE PRO GLN TYR VAL ILE TRP ARG PHE ASN TRP ILE ASP THR GLU LEU HIS VAL ARG LYS LEU LYS ARG ILE
GLU TYR GLN ASP GLU THR LYS PRO GLY TRP ASN ARG LEU GLU VAL SER ILE GLY ARG GLU GLY GLU HIS ALA GLN ILE THR ILE GLU GLU LYS GLU LYS LEU ASP MET LEU SER GLY LEU SER ALA THR GLN SER VAL ASN ALA ARG LEU ILE GLY
MET GLY HIS LYS ASP PRO GLN TYR THR SER MET ILE VAL GLN TYR TYR THR GLY LYS LYS VAL VAL SER PRO ILE SER PRO THR VAL TYR LYS PRO THR MET PRO ARG VAL HIS TRP PRO VAL THR SER ASP ALA ASP VAL PRO GLU VAL SER ALA ARG GLN TYR THR LEU PRO ILE VAL
SER ASP CYS MET MET MET PRO MET ILE LYS ARG TRP GLU THR MET SER GLU SER ILE GLU GLY ARG ARG VAL THR PHE V446 A447 N448 D449 K450 K451 P452 K458 I459 A460 E461 T462 F463 V464 K465 L466 M467 N468 G469 P470 F471 K472 D473 L474 D475 P476 L477 S478 I479 E480 E481 T482 I483 E484
R485 L486 ASN LYS PRO SER GLN GLN LEU GLN LEU ARG ALA VAL PHE GLU MET ILE GLY VAL LYS PRO ARG GLN LEU ILE GLU SER PHE ASN LYS ASN GLU PRO GLY MET LYS SER SER ARG ILE ILE SER GLY PHE PRO ASP ILE L533 F534 I535 L536 K537 V538 S539 L543 A544 Y545
I548 V549 L550 H551 A552 N555 E556 H557 W558 Y559 Y560 P561 G562 R563 N564 P565 T566 E567 I568 A569 D570 G571 V572 C573 E574 F575 V576 S577 D578 C579 D580 A581 E582 V583 I584 E585 T586 D587 F588 S589 N590 L591 D592 G593 R594 V595 S596 S597 W598 M599 N602 I603 M608 V609 Q610 A611 F612
R613 P614 E615 F623 I627 I628 N629 CYS PRO ALA LYS ALA LYS ARG PHE GLY PHE ARG TYR GLU PRO GLY VAL GLY VAL LYS SER GLY SER PRO THR T654 T655 P656 H657 N658 T659 Q660 Y661 N662 G663 C664 V665 E666 F667 T668 A669 L670 T671 F672 P675 D676 P679 E680 D681 L682
F683 R684 L685 I686 G687 P688 K689 C690 G691 D692 D693 G694 L695 S696 R697 A698 I699 I700 Q701 K702 S703 I704 N705 R706 A707 A708 K709 C710 F711 G712 L713 E714 L715 K716 V717 E718 R719 Y720 N721 P722 E723 I724 G725 L726 C727 F728 L729 S730 R731 V732 F733 V734 D735 P736 L737 A738 T739 T740 T741 T742
I743 Q744 D745 P746 L747 R748 T749 L750 R751 K752 L753 H754 L755 T756 T757 R758 D759 P760 T761 I762 P763 L764 A765 D766 A767 A768 C769 D770 R771 V772 E773 G774 Y775 L776 C777 T778 D779 A780 L781 T782 P783 L784 T785 S786 D787 Y788 C789 K790 M791 V792 L793 R794 L795 Y796 G797 P798 T799 A800 S801 T802
E803 Q804 V805 R806 N807 Q808 R809 R810 S811 R812 N813 K814 E815 LYS PRO TYR TRP LEU THR CYS ASP GLY SER TRP PRO GLN H829 P830 Q831 D832 A833 H834 L835 M836 K837 Q838 V839 L840 I841 K842 R843 T844 A845 I846 D847 E848 D849 Q850 V851 D852 A853 L854 I855 G856 R857 F858 A859 A860 M861 LYS
ASP VAL TRP GLU LYS ILE THR HIS ASP SER GLU GLU SER ALA ALA ALA CYS THR PHE ASP GLU ASP GLY VAL ALA PRO ASN SER VAL ASP GLU SER LEU PRO LEU LEU LEU ASN ASP ALA LYS GLN THR ARG ALA ASN PRO GLY THR SER ARG PRO HIS SER ASN GLY GLY GLY SER SER HIS
GLY ASN GLU LEU PRO ARG ARG THR GLU GLN ARG ALA GLN GLY PRO ALA ARG LEU PRO LYS GLN LEU GLY LYS THR ASN GLY LYS SER ASP GLY ASN ILE THR ALA GLY GLU THR GLN ARG GLY GLY ILE PRO ARG GLY LYS GLY PRO ARG GLY GLY LYS THR ASN THR ARG ARG
THR PRO PRO LYS ALA GLY ALA GLN PRO PRO SER ASN ASN ARG LYS SER ARG LEU GLU GLU GLU LEU ARG ARG ARG LEU THR GLU

4 Experimental information (i)

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 ($e^-/Å^2$)	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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	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 (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	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

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

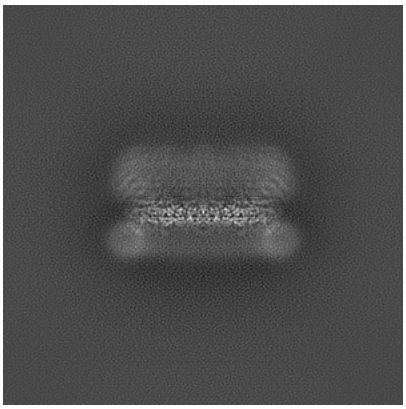
6 Map visualisation

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.

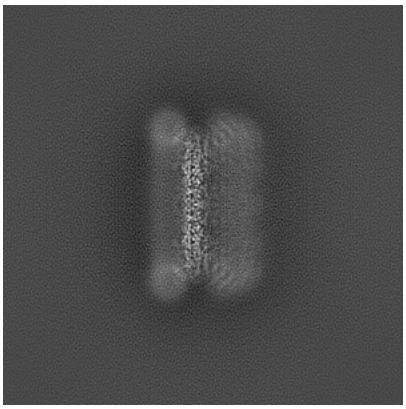
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

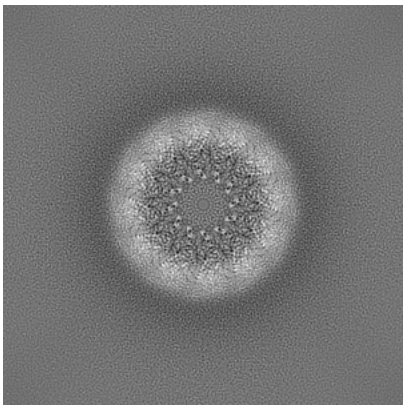
6.1.1 Primary map



X

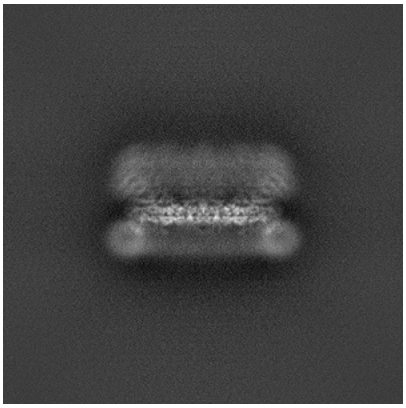


Y

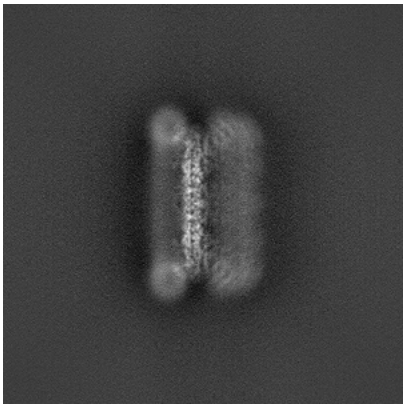


Z

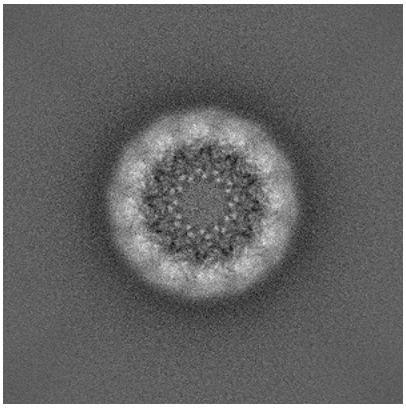
6.1.2 Raw map



X



Y

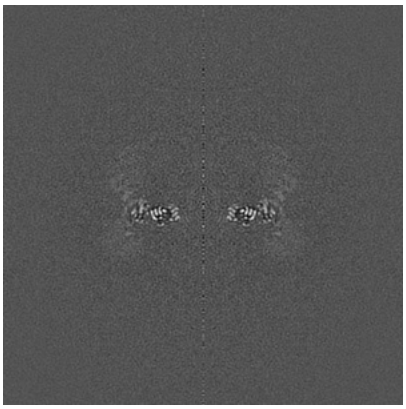


Z

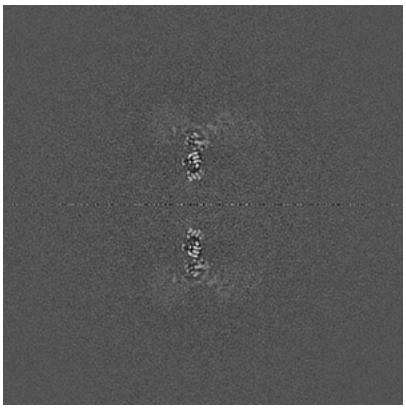
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

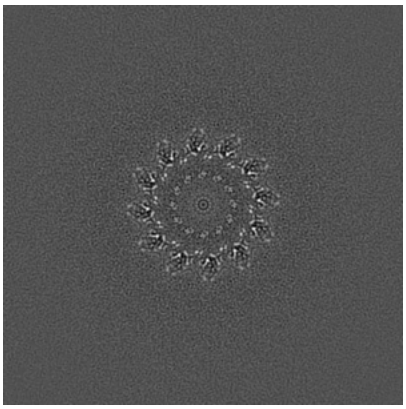
6.2.1 Primary map



X Index: 288

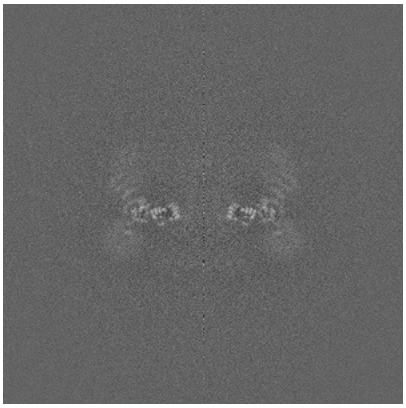


Y Index: 288

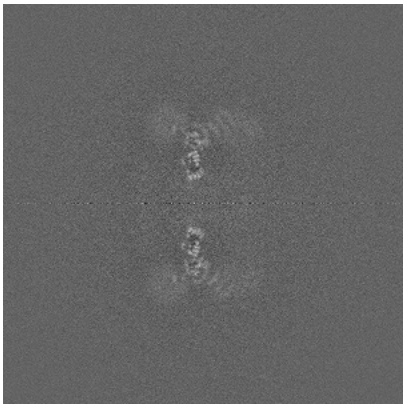


Z Index: 288

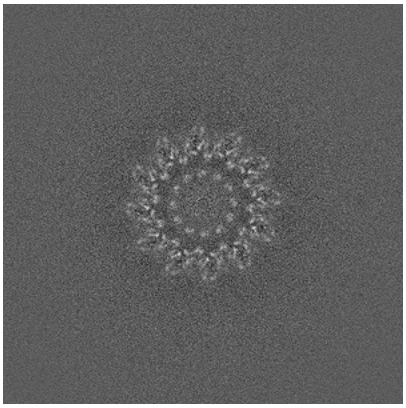
6.2.2 Raw map



X Index: 288



Y Index: 288

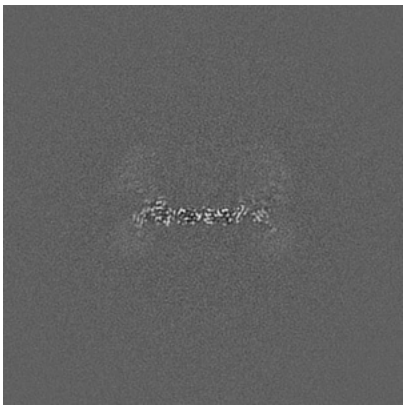


Z Index: 288

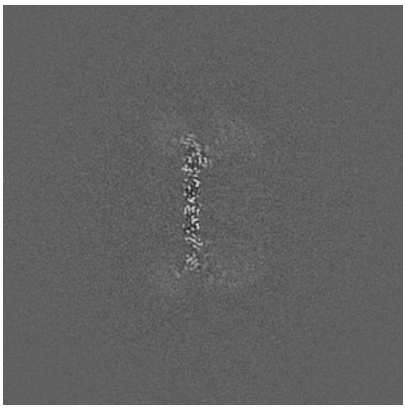
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

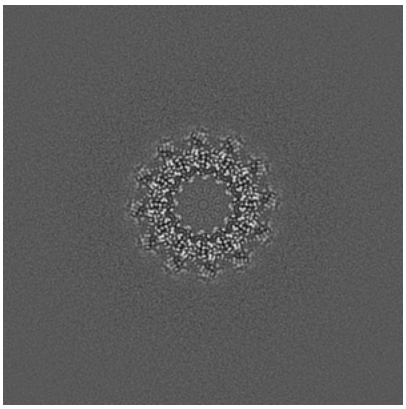
6.3.1 Primary map



X Index: 337

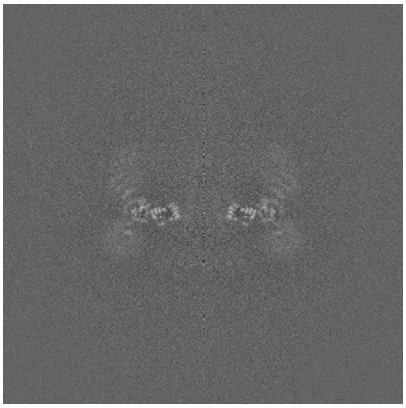


Y Index: 337

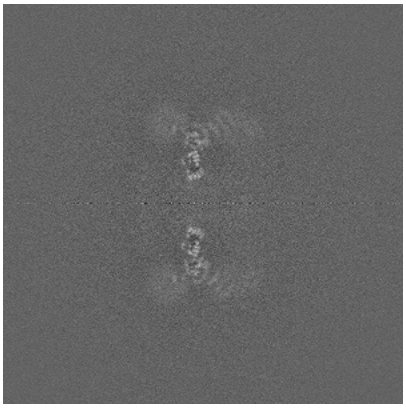


Z Index: 277

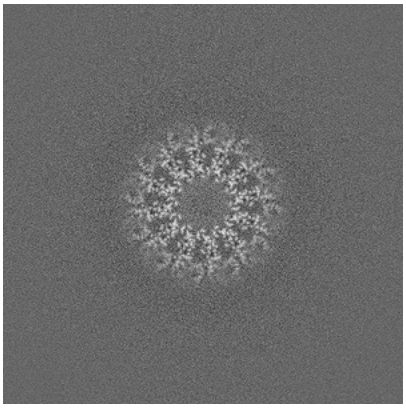
6.3.2 Raw map



X Index: 288



Y Index: 288

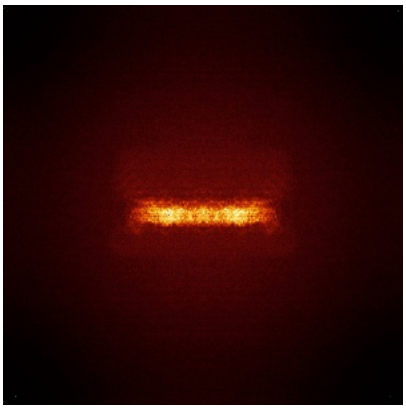


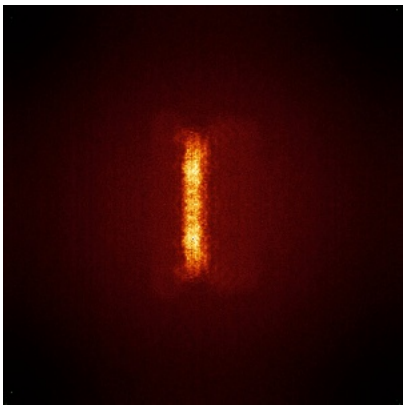
Z Index: 267

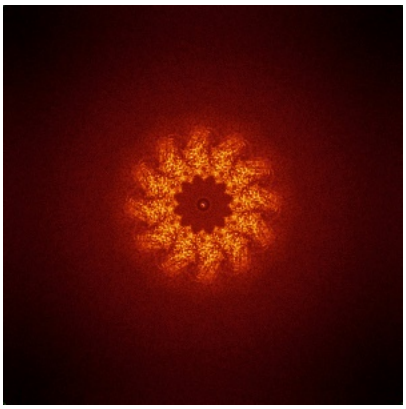
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

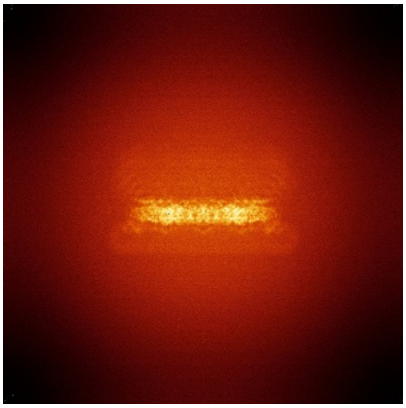
6.4.1 Primary map

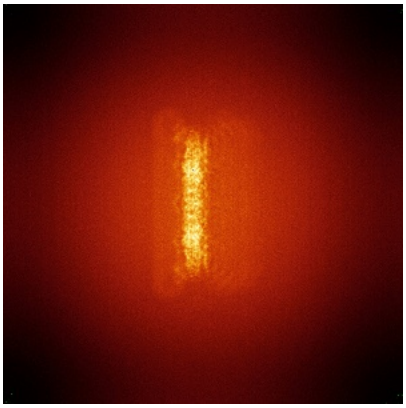

X

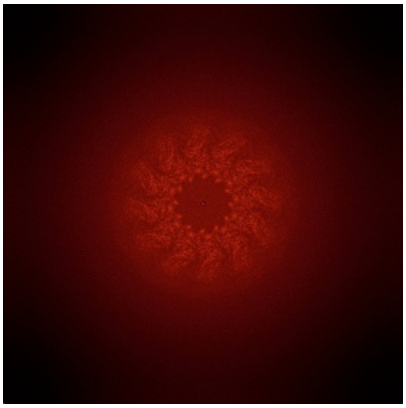

Y


Z

6.4.2 Raw map


X

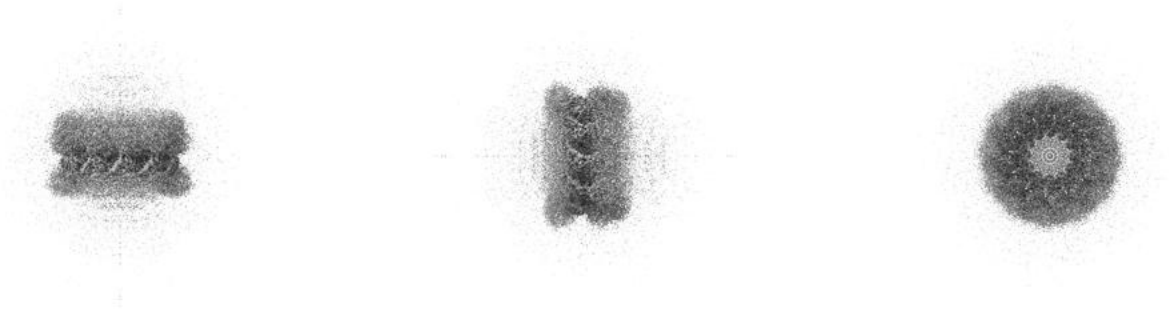

Y


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



X Y Z

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.

6.5.2 Raw map

X Y Z

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.

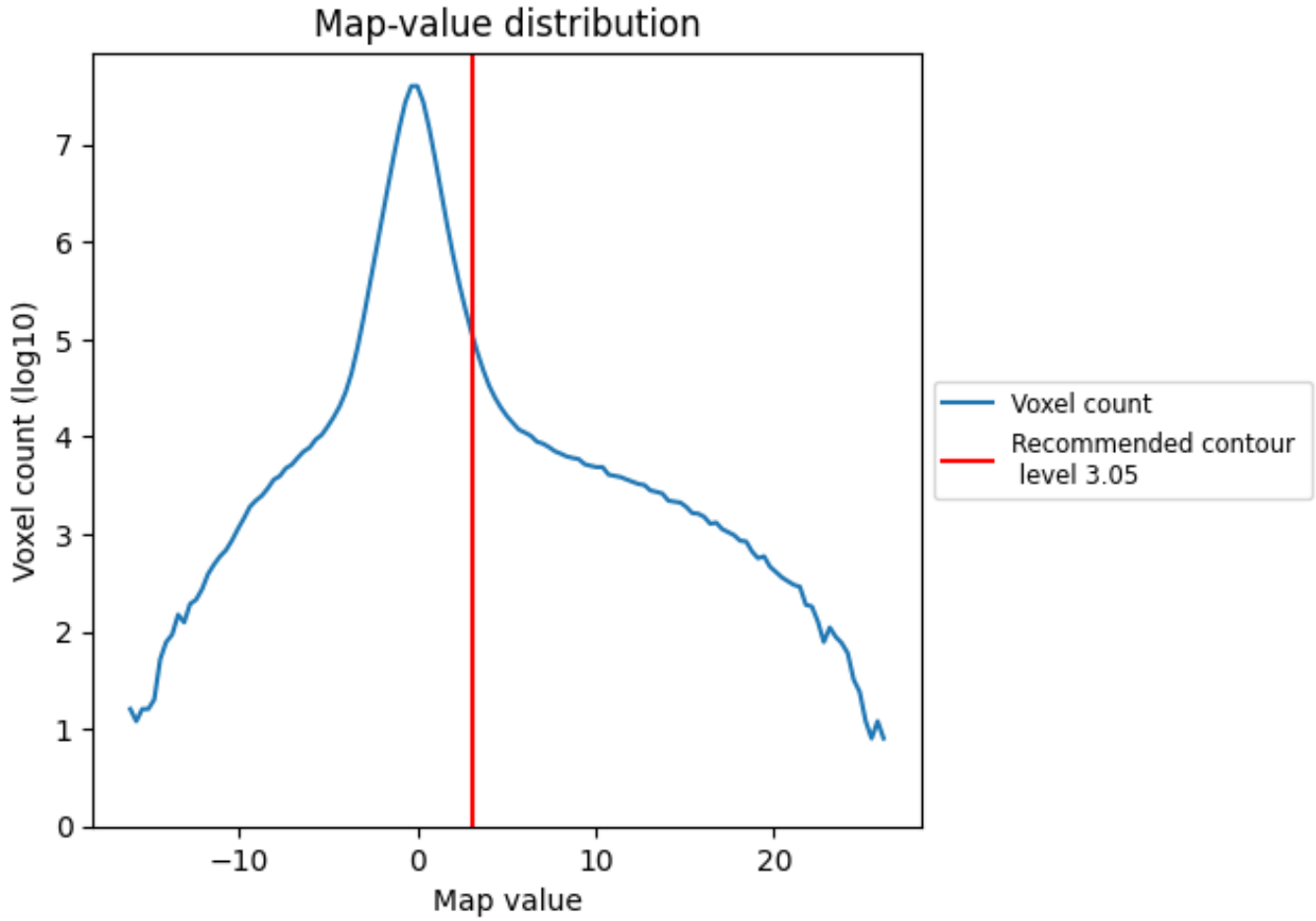
6.6 Mask visualisation (i)

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

7 Map analysis

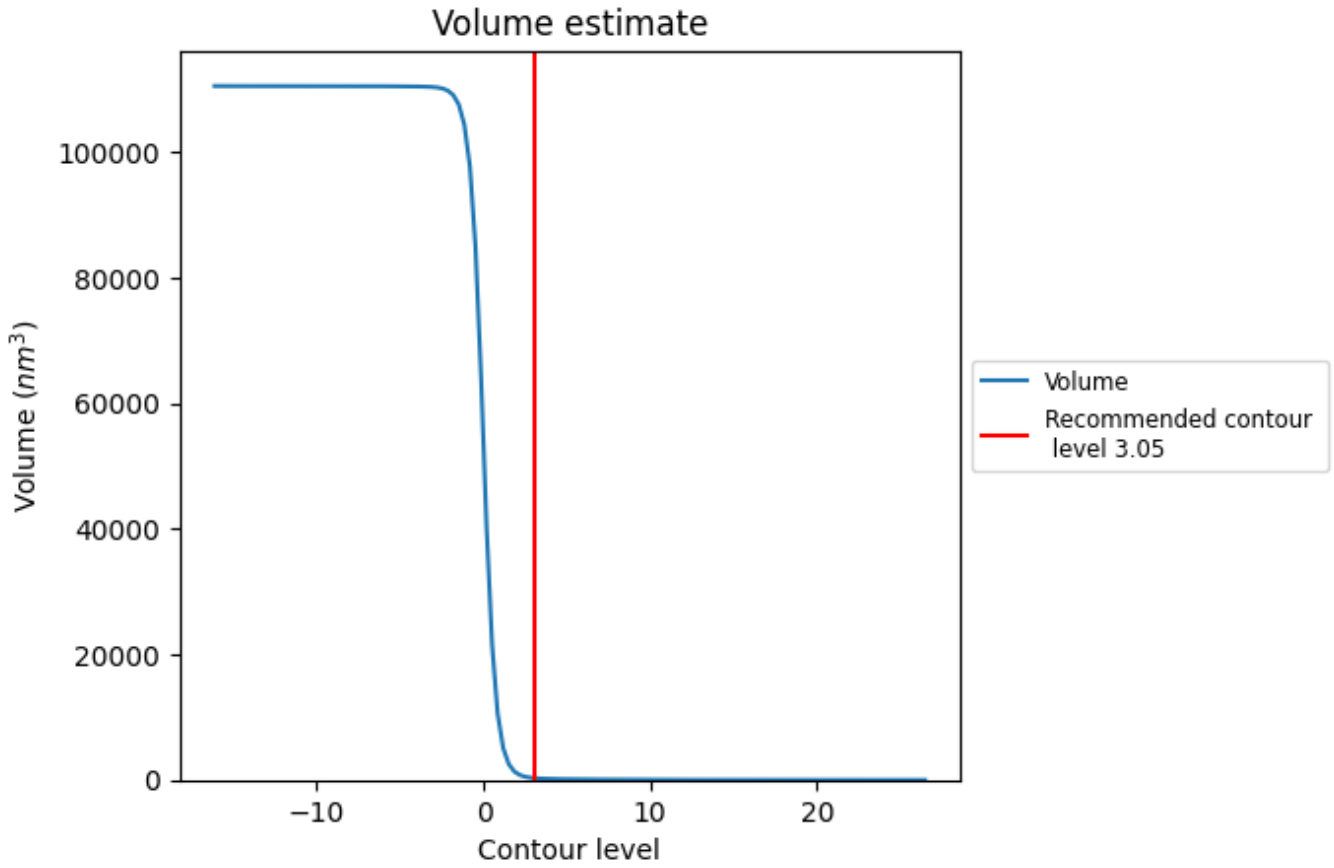
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

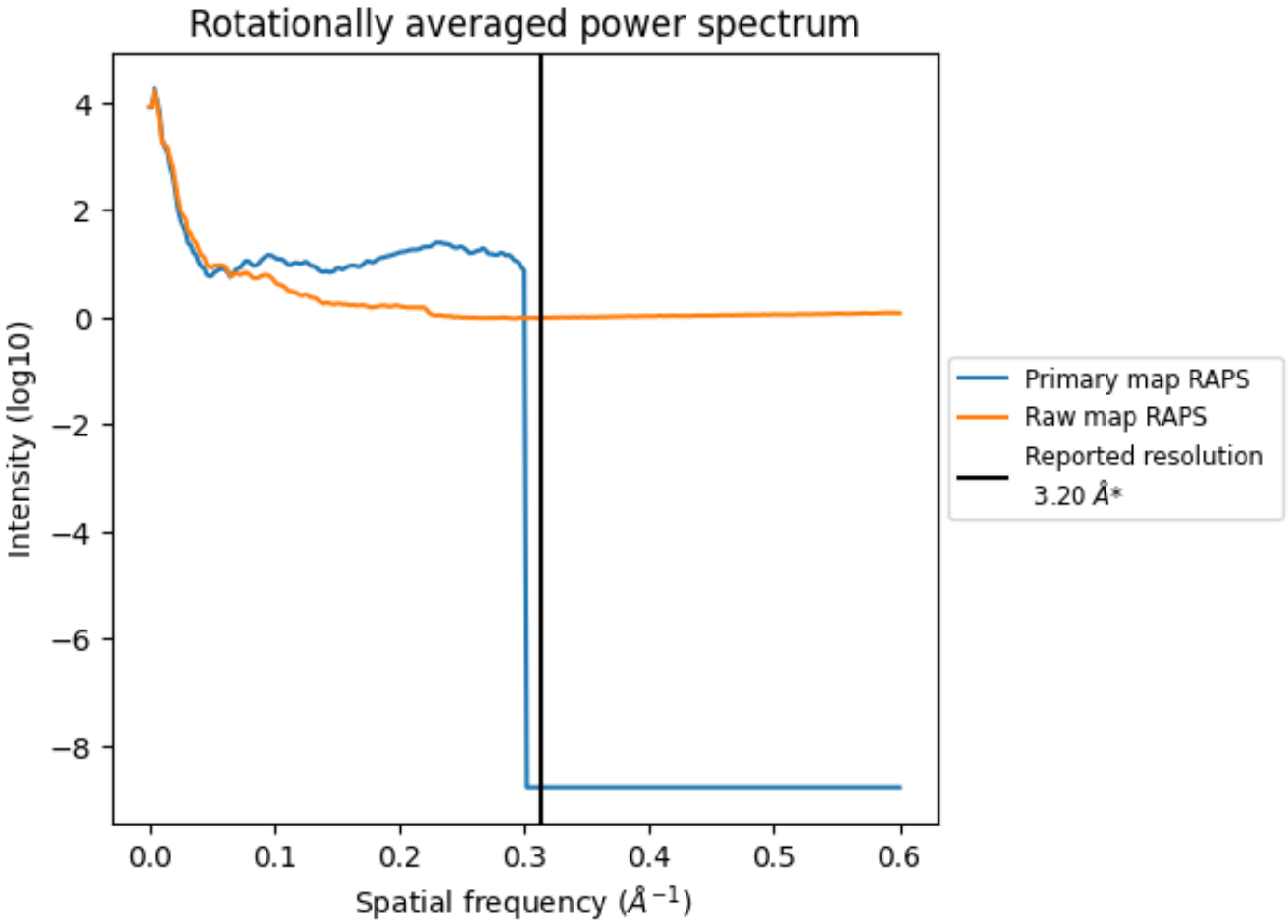
7.2 Volume estimate (i)



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)

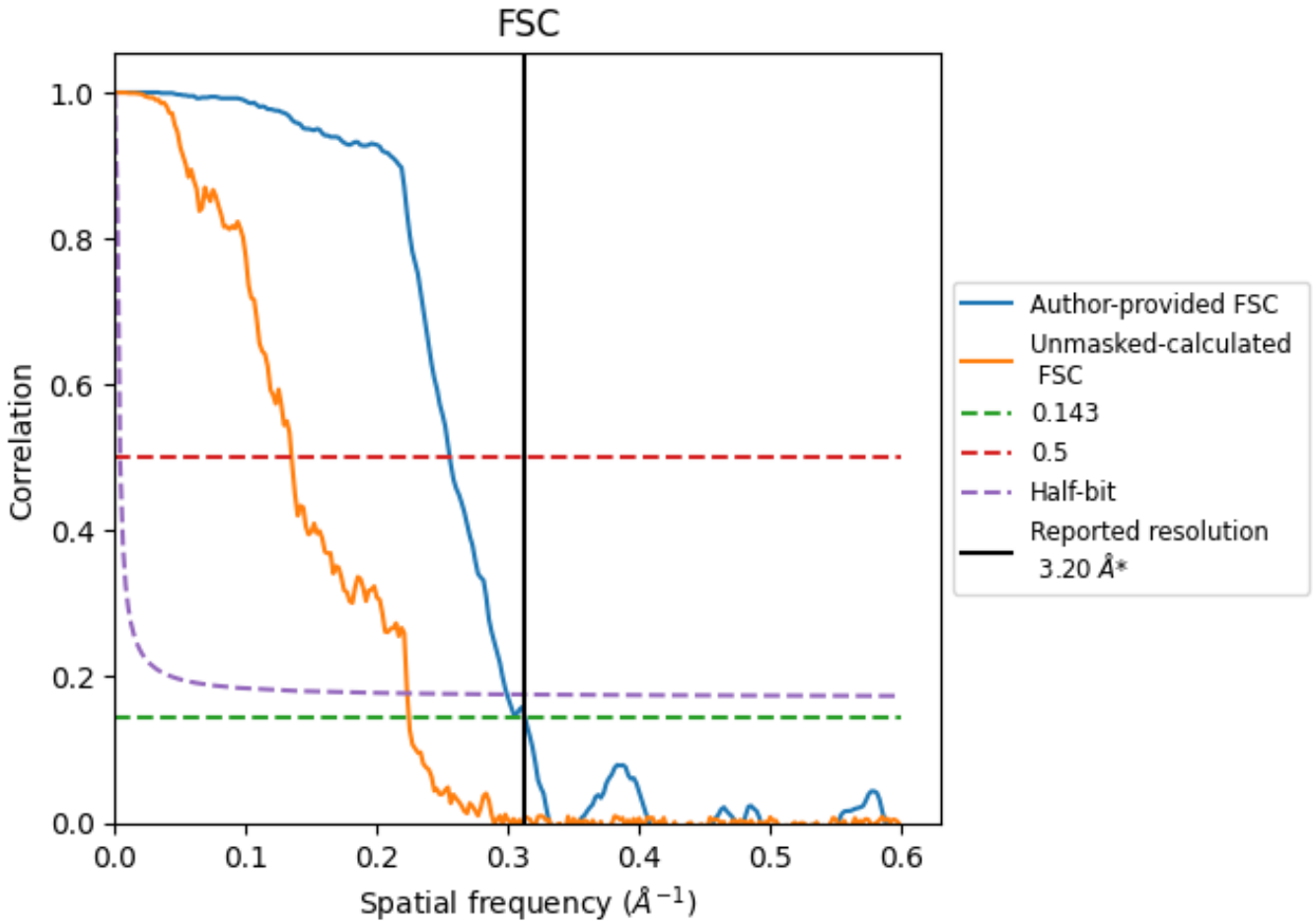


*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.312 $Å^{-1}$

8.2 Resolution estimates (i)

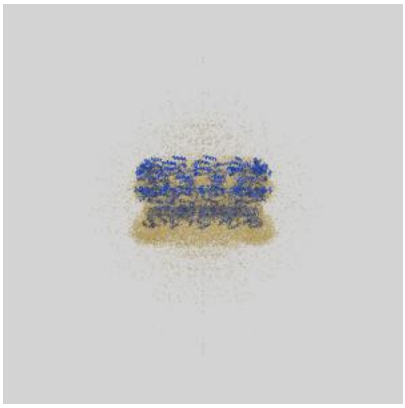
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.19	3.91	3.34
Unmasked-calculated*	4.46	7.41	4.48

*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 %

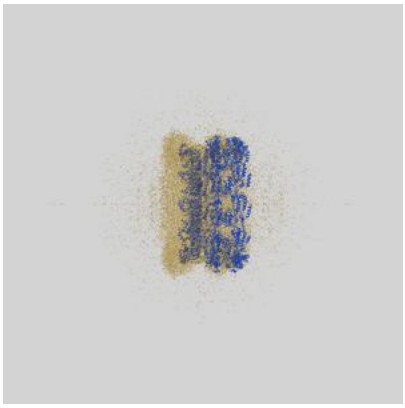
9 Map-model fit

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.

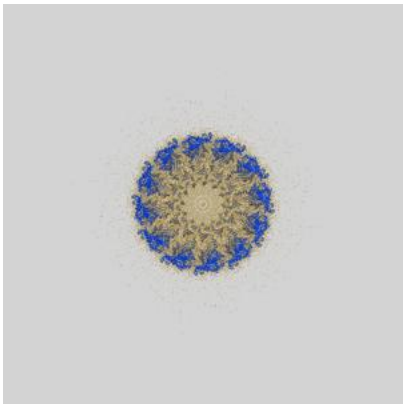
9.1 Map-model overlay



X



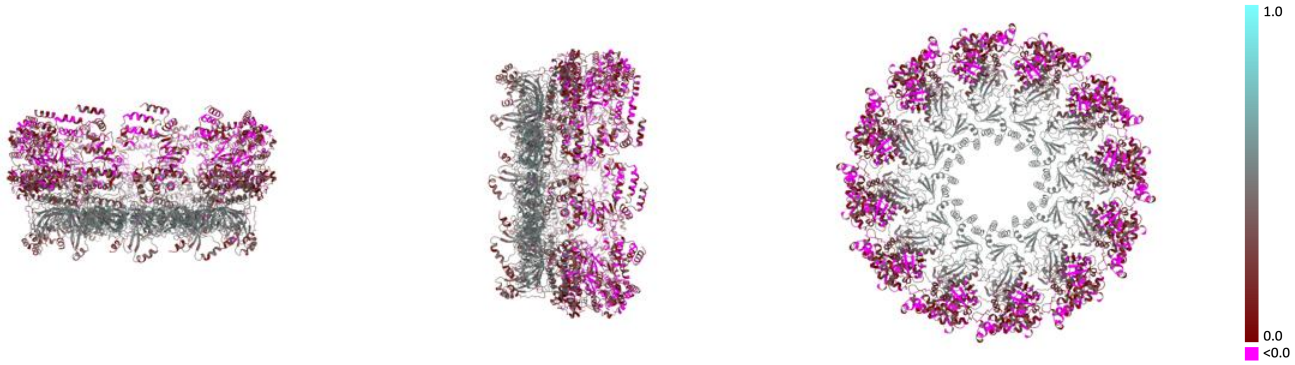
Y



Z

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.

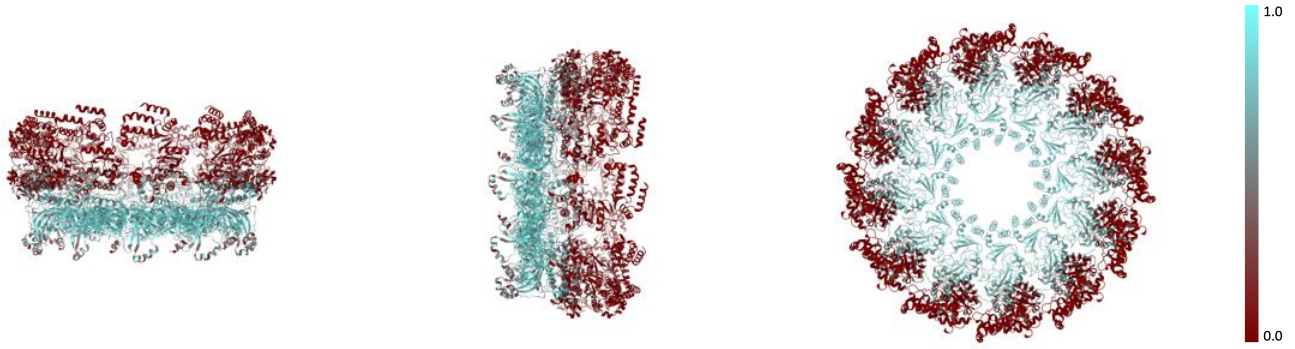
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

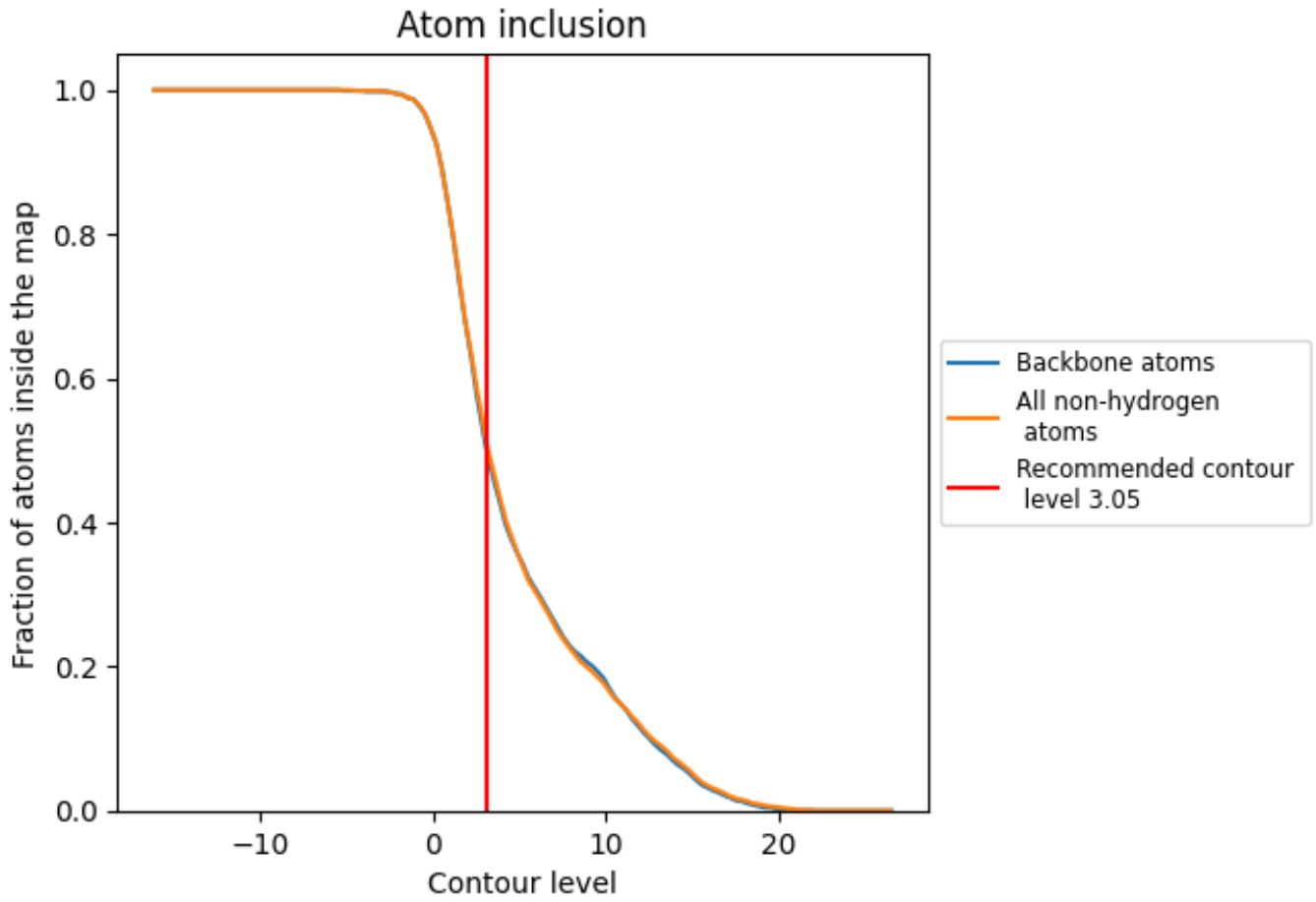
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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	0.5160	0.3340
A	0.7340	0.4420
B	0.7340	0.4420
C	0.7360	0.4410
D	0.7330	0.4430
E	0.7350	0.4420
F	0.7340	0.4410
G	0.7350	0.4430
H	0.7320	0.4410
I	0.7340	0.4420
J	0.7340	0.4420
K	0.7340	0.4410
L	0.7360	0.4410
M	0.1470	0.1460
N	0.1450	0.1460
O	0.1470	0.1470
P	0.1470	0.1460
Q	0.1450	0.1330
R	0.1460	0.1460
S	0.1470	0.1470
T	0.1450	0.1440
U	0.1470	0.1440
V	0.1470	0.1440
W	0.1460	0.1420
X	0.1470	0.1450