



wwPDB EM Validation Summary Report ⓘ

Apr 29, 2024 – 10:44 pm BST

PDB ID : 4BBL
EMDB ID : EMD-2205
Title : Cryo-electron microscopy reconstruction of the helical part of influenza A virus ribonucleoprotein isolated from virions.
Authors : Arranz, R.; Coloma, R.; Chichon, F.J.; Conesa, J.J.; Carrascosa, J.L.; Valpuesta, J.M.; Ortin, J.; Martin-Benito, J.
Deposited on : 2012-09-26
Resolution : 18.00 Å(reported)
Based on initial model : 2IQH

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

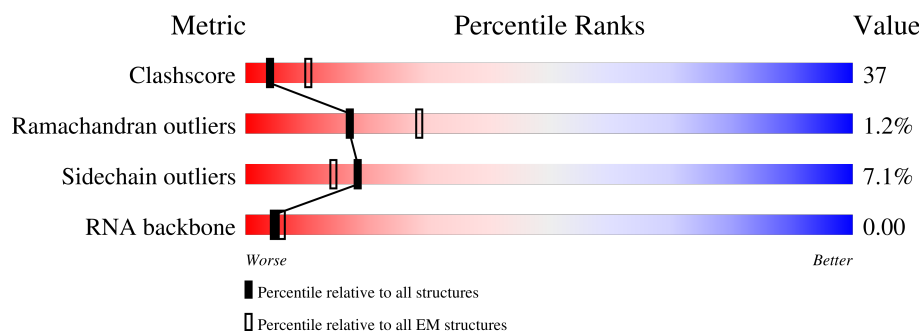
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 18.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	499	<div> <div>9%</div> <div>40%</div> <div>38%</div> <div>5%</div> <div>17%</div> </div>
1	B	499	<div> <div>9%</div> <div>39%</div> <div>36%</div> <div>5%</div> <div>20%</div> </div>
1	C	499	<div> <div>9%</div> <div>38%</div> <div>39%</div> <div>5%</div> <div>17%</div> </div>
1	D	499	<div> <div>11%</div> <div>38%</div> <div>39%</div> <div>5%</div> <div>17%</div> </div>
1	E	499	<div> <div>9%</div> <div>38%</div> <div>39%</div> <div>5%</div> <div>17%</div> </div>
1	F	499	<div> <div>11%</div> <div>39%</div> <div>39%</div> <div>5%</div> <div>17%</div> </div>
1	G	499	<div> <div>10%</div> <div>39%</div> <div>39%</div> <div>5%</div> <div>17%</div> </div>

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Mol	Chain	Length	Quality of chain
1	H	499	
1	I	499	
1	J	499	
1	K	499	
1	L	499	
1	M	499	
1	N	499	
1	O	499	
1	P	499	
1	Q	499	
1	R	499	
1	S	499	
1	T	499	
1	U	499	
1	V	499	
1	W	499	
1	X	499	
2	Y	308	
2	Z	308	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 78901 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called NUCLEOPROTEIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	B	399	Total	C	N	O	S	0	0
			3151	1954	586	586	25		
1	C	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	D	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	E	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	F	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	G	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	H	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	I	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	J	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	K	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	L	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	M	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	N	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	O	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	P	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	Q	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	S	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	T	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	U	414	Total	C	N	O	S	0	0
			3271	2031	607	608	25		
1	V	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		
1	W	399	Total	C	N	O	S	0	0
			3151	1954	586	586	25		
1	X	414	Total	C	N	O	S	0	0
			3272	2031	608	608	25		

There are 312 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	499	LEU	-	expression tag	UNP P15682
A	500	GLU	-	expression tag	UNP P15682
A	501	HIS	-	expression tag	UNP P15682
A	502	HIS	-	expression tag	UNP P15682
A	503	HIS	-	expression tag	UNP P15682
A	504	HIS	-	expression tag	UNP P15682
A	505	HIS	-	expression tag	UNP P15682
A	506	HIS	-	expression tag	UNP P15682
A	34	ASP	GLY	conflict	UNP P15682
A	105	ARG	MET	conflict	UNP P15682
A	237	THR	ALA	conflict	UNP P15682
A	283	SER	PRO	conflict	UNP P15682
A	472	THR	ALA	conflict	UNP P15682
B	499	LEU	-	expression tag	UNP P15682
B	500	GLU	-	expression tag	UNP P15682
B	501	HIS	-	expression tag	UNP P15682
B	502	HIS	-	expression tag	UNP P15682
B	503	HIS	-	expression tag	UNP P15682
B	504	HIS	-	expression tag	UNP P15682
B	505	HIS	-	expression tag	UNP P15682
B	506	HIS	-	expression tag	UNP P15682
B	34	ASP	GLY	conflict	UNP P15682
B	105	ARG	MET	conflict	UNP P15682
B	237	THR	ALA	conflict	UNP P15682
B	283	SER	PRO	conflict	UNP P15682

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Chain	Residue	Modelled	Actual	Comment	Reference
B	472	THR	ALA	conflict	UNP P15682
C	499	LEU	-	expression tag	UNP P15682
C	500	GLU	-	expression tag	UNP P15682
C	501	HIS	-	expression tag	UNP P15682
C	502	HIS	-	expression tag	UNP P15682
C	503	HIS	-	expression tag	UNP P15682
C	504	HIS	-	expression tag	UNP P15682
C	505	HIS	-	expression tag	UNP P15682
C	506	HIS	-	expression tag	UNP P15682
C	34	ASP	GLY	conflict	UNP P15682
C	105	ARG	MET	conflict	UNP P15682
C	237	THR	ALA	conflict	UNP P15682
C	283	SER	PRO	conflict	UNP P15682
C	472	THR	ALA	conflict	UNP P15682
D	499	LEU	-	expression tag	UNP P15682
D	500	GLU	-	expression tag	UNP P15682
D	501	HIS	-	expression tag	UNP P15682
D	502	HIS	-	expression tag	UNP P15682
D	503	HIS	-	expression tag	UNP P15682
D	504	HIS	-	expression tag	UNP P15682
D	505	HIS	-	expression tag	UNP P15682
D	506	HIS	-	expression tag	UNP P15682
D	34	ASP	GLY	conflict	UNP P15682
D	105	ARG	MET	conflict	UNP P15682
D	237	THR	ALA	conflict	UNP P15682
D	283	SER	PRO	conflict	UNP P15682
D	472	THR	ALA	conflict	UNP P15682
E	499	LEU	-	expression tag	UNP P15682
E	500	GLU	-	expression tag	UNP P15682
E	501	HIS	-	expression tag	UNP P15682
E	502	HIS	-	expression tag	UNP P15682
E	503	HIS	-	expression tag	UNP P15682
E	504	HIS	-	expression tag	UNP P15682
E	505	HIS	-	expression tag	UNP P15682
E	506	HIS	-	expression tag	UNP P15682
E	34	ASP	GLY	conflict	UNP P15682
E	105	ARG	MET	conflict	UNP P15682
E	237	THR	ALA	conflict	UNP P15682
E	283	SER	PRO	conflict	UNP P15682
E	472	THR	ALA	conflict	UNP P15682
F	499	LEU	-	expression tag	UNP P15682
F	500	GLU	-	expression tag	UNP P15682

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Chain	Residue	Modelled	Actual	Comment	Reference
F	501	HIS	-	expression tag	UNP P15682
F	502	HIS	-	expression tag	UNP P15682
F	503	HIS	-	expression tag	UNP P15682
F	504	HIS	-	expression tag	UNP P15682
F	505	HIS	-	expression tag	UNP P15682
F	506	HIS	-	expression tag	UNP P15682
F	34	ASP	GLY	conflict	UNP P15682
F	105	ARG	MET	conflict	UNP P15682
F	237	THR	ALA	conflict	UNP P15682
F	283	SER	PRO	conflict	UNP P15682
F	472	THR	ALA	conflict	UNP P15682
G	499	LEU	-	expression tag	UNP P15682
G	500	GLU	-	expression tag	UNP P15682
G	501	HIS	-	expression tag	UNP P15682
G	502	HIS	-	expression tag	UNP P15682
G	503	HIS	-	expression tag	UNP P15682
G	504	HIS	-	expression tag	UNP P15682
G	505	HIS	-	expression tag	UNP P15682
G	506	HIS	-	expression tag	UNP P15682
G	34	ASP	GLY	conflict	UNP P15682
G	105	ARG	MET	conflict	UNP P15682
G	237	THR	ALA	conflict	UNP P15682
G	283	SER	PRO	conflict	UNP P15682
G	472	THR	ALA	conflict	UNP P15682
H	499	LEU	-	expression tag	UNP P15682
H	500	GLU	-	expression tag	UNP P15682
H	501	HIS	-	expression tag	UNP P15682
H	502	HIS	-	expression tag	UNP P15682
H	503	HIS	-	expression tag	UNP P15682
H	504	HIS	-	expression tag	UNP P15682
H	505	HIS	-	expression tag	UNP P15682
H	506	HIS	-	expression tag	UNP P15682
H	34	ASP	GLY	conflict	UNP P15682
H	105	ARG	MET	conflict	UNP P15682
H	237	THR	ALA	conflict	UNP P15682
H	283	SER	PRO	conflict	UNP P15682
H	472	THR	ALA	conflict	UNP P15682
I	499	LEU	-	expression tag	UNP P15682
I	500	GLU	-	expression tag	UNP P15682
I	501	HIS	-	expression tag	UNP P15682
I	502	HIS	-	expression tag	UNP P15682
I	503	HIS	-	expression tag	UNP P15682

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Chain	Residue	Modelled	Actual	Comment	Reference
I	504	HIS	-	expression tag	UNP P15682
I	505	HIS	-	expression tag	UNP P15682
I	506	HIS	-	expression tag	UNP P15682
I	34	ASP	GLY	conflict	UNP P15682
I	105	ARG	MET	conflict	UNP P15682
I	237	THR	ALA	conflict	UNP P15682
I	283	SER	PRO	conflict	UNP P15682
I	472	THR	ALA	conflict	UNP P15682
J	499	LEU	-	expression tag	UNP P15682
J	500	GLU	-	expression tag	UNP P15682
J	501	HIS	-	expression tag	UNP P15682
J	502	HIS	-	expression tag	UNP P15682
J	503	HIS	-	expression tag	UNP P15682
J	504	HIS	-	expression tag	UNP P15682
J	505	HIS	-	expression tag	UNP P15682
J	506	HIS	-	expression tag	UNP P15682
J	34	ASP	GLY	conflict	UNP P15682
J	105	ARG	MET	conflict	UNP P15682
J	237	THR	ALA	conflict	UNP P15682
J	283	SER	PRO	conflict	UNP P15682
J	472	THR	ALA	conflict	UNP P15682
K	499	LEU	-	expression tag	UNP P15682
K	500	GLU	-	expression tag	UNP P15682
K	501	HIS	-	expression tag	UNP P15682
K	502	HIS	-	expression tag	UNP P15682
K	503	HIS	-	expression tag	UNP P15682
K	504	HIS	-	expression tag	UNP P15682
K	505	HIS	-	expression tag	UNP P15682
K	506	HIS	-	expression tag	UNP P15682
K	34	ASP	GLY	conflict	UNP P15682
K	105	ARG	MET	conflict	UNP P15682
K	237	THR	ALA	conflict	UNP P15682
K	283	SER	PRO	conflict	UNP P15682
K	472	THR	ALA	conflict	UNP P15682
L	499	LEU	-	expression tag	UNP P15682
L	500	GLU	-	expression tag	UNP P15682
L	501	HIS	-	expression tag	UNP P15682
L	502	HIS	-	expression tag	UNP P15682
L	503	HIS	-	expression tag	UNP P15682
L	504	HIS	-	expression tag	UNP P15682
L	505	HIS	-	expression tag	UNP P15682
L	506	HIS	-	expression tag	UNP P15682

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Chain	Residue	Modelled	Actual	Comment	Reference
L	34	ASP	GLY	conflict	UNP P15682
L	105	ARG	MET	conflict	UNP P15682
L	237	THR	ALA	conflict	UNP P15682
L	283	SER	PRO	conflict	UNP P15682
L	472	THR	ALA	conflict	UNP P15682
M	499	LEU	-	expression tag	UNP P15682
M	500	GLU	-	expression tag	UNP P15682
M	501	HIS	-	expression tag	UNP P15682
M	502	HIS	-	expression tag	UNP P15682
M	503	HIS	-	expression tag	UNP P15682
M	504	HIS	-	expression tag	UNP P15682
M	505	HIS	-	expression tag	UNP P15682
M	506	HIS	-	expression tag	UNP P15682
M	34	ASP	GLY	conflict	UNP P15682
M	105	ARG	MET	conflict	UNP P15682
M	237	THR	ALA	conflict	UNP P15682
M	283	SER	PRO	conflict	UNP P15682
M	472	THR	ALA	conflict	UNP P15682
N	499	LEU	-	expression tag	UNP P15682
N	500	GLU	-	expression tag	UNP P15682
N	501	HIS	-	expression tag	UNP P15682
N	502	HIS	-	expression tag	UNP P15682
N	503	HIS	-	expression tag	UNP P15682
N	504	HIS	-	expression tag	UNP P15682
N	505	HIS	-	expression tag	UNP P15682
N	506	HIS	-	expression tag	UNP P15682
N	34	ASP	GLY	conflict	UNP P15682
N	105	ARG	MET	conflict	UNP P15682
N	237	THR	ALA	conflict	UNP P15682
N	283	SER	PRO	conflict	UNP P15682
N	472	THR	ALA	conflict	UNP P15682
O	499	LEU	-	expression tag	UNP P15682
O	500	GLU	-	expression tag	UNP P15682
O	501	HIS	-	expression tag	UNP P15682
O	502	HIS	-	expression tag	UNP P15682
O	503	HIS	-	expression tag	UNP P15682
O	504	HIS	-	expression tag	UNP P15682
O	505	HIS	-	expression tag	UNP P15682
O	506	HIS	-	expression tag	UNP P15682
O	34	ASP	GLY	conflict	UNP P15682
O	105	ARG	MET	conflict	UNP P15682
O	237	THR	ALA	conflict	UNP P15682

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Chain	Residue	Modelled	Actual	Comment	Reference
O	283	SER	PRO	conflict	UNP P15682
O	472	THR	ALA	conflict	UNP P15682
P	499	LEU	-	expression tag	UNP P15682
P	500	GLU	-	expression tag	UNP P15682
P	501	HIS	-	expression tag	UNP P15682
P	502	HIS	-	expression tag	UNP P15682
P	503	HIS	-	expression tag	UNP P15682
P	504	HIS	-	expression tag	UNP P15682
P	505	HIS	-	expression tag	UNP P15682
P	506	HIS	-	expression tag	UNP P15682
P	34	ASP	GLY	conflict	UNP P15682
P	105	ARG	MET	conflict	UNP P15682
P	237	THR	ALA	conflict	UNP P15682
P	283	SER	PRO	conflict	UNP P15682
P	472	THR	ALA	conflict	UNP P15682
Q	499	LEU	-	expression tag	UNP P15682
Q	500	GLU	-	expression tag	UNP P15682
Q	501	HIS	-	expression tag	UNP P15682
Q	502	HIS	-	expression tag	UNP P15682
Q	503	HIS	-	expression tag	UNP P15682
Q	504	HIS	-	expression tag	UNP P15682
Q	505	HIS	-	expression tag	UNP P15682
Q	506	HIS	-	expression tag	UNP P15682
Q	34	ASP	GLY	conflict	UNP P15682
Q	105	ARG	MET	conflict	UNP P15682
Q	237	THR	ALA	conflict	UNP P15682
Q	283	SER	PRO	conflict	UNP P15682
Q	472	THR	ALA	conflict	UNP P15682
R	499	LEU	-	expression tag	UNP P15682
R	500	GLU	-	expression tag	UNP P15682
R	501	HIS	-	expression tag	UNP P15682
R	502	HIS	-	expression tag	UNP P15682
R	503	HIS	-	expression tag	UNP P15682
R	504	HIS	-	expression tag	UNP P15682
R	505	HIS	-	expression tag	UNP P15682
R	506	HIS	-	expression tag	UNP P15682
R	34	ASP	GLY	conflict	UNP P15682
R	105	ARG	MET	conflict	UNP P15682
R	237	THR	ALA	conflict	UNP P15682
R	283	SER	PRO	conflict	UNP P15682
R	472	THR	ALA	conflict	UNP P15682
S	499	LEU	-	expression tag	UNP P15682

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Chain	Residue	Modelled	Actual	Comment	Reference
S	500	GLU	-	expression tag	UNP P15682
S	501	HIS	-	expression tag	UNP P15682
S	502	HIS	-	expression tag	UNP P15682
S	503	HIS	-	expression tag	UNP P15682
S	504	HIS	-	expression tag	UNP P15682
S	505	HIS	-	expression tag	UNP P15682
S	506	HIS	-	expression tag	UNP P15682
S	34	ASP	GLY	conflict	UNP P15682
S	105	ARG	MET	conflict	UNP P15682
S	237	THR	ALA	conflict	UNP P15682
S	283	SER	PRO	conflict	UNP P15682
S	472	THR	ALA	conflict	UNP P15682
T	499	LEU	-	expression tag	UNP P15682
T	500	GLU	-	expression tag	UNP P15682
T	501	HIS	-	expression tag	UNP P15682
T	502	HIS	-	expression tag	UNP P15682
T	503	HIS	-	expression tag	UNP P15682
T	504	HIS	-	expression tag	UNP P15682
T	505	HIS	-	expression tag	UNP P15682
T	506	HIS	-	expression tag	UNP P15682
T	34	ASP	GLY	conflict	UNP P15682
T	105	ARG	MET	conflict	UNP P15682
T	237	THR	ALA	conflict	UNP P15682
T	283	SER	PRO	conflict	UNP P15682
T	472	THR	ALA	conflict	UNP P15682
U	499	LEU	-	expression tag	UNP P15682
U	500	GLU	-	expression tag	UNP P15682
U	501	HIS	-	expression tag	UNP P15682
U	502	HIS	-	expression tag	UNP P15682
U	503	HIS	-	expression tag	UNP P15682
U	504	HIS	-	expression tag	UNP P15682
U	505	HIS	-	expression tag	UNP P15682
U	506	HIS	-	expression tag	UNP P15682
U	34	ASP	GLY	conflict	UNP P15682
U	105	ARG	MET	conflict	UNP P15682
U	237	THR	ALA	conflict	UNP P15682
U	283	SER	PRO	conflict	UNP P15682
U	472	THR	ALA	conflict	UNP P15682
V	499	LEU	-	expression tag	UNP P15682
V	500	GLU	-	expression tag	UNP P15682
V	501	HIS	-	expression tag	UNP P15682
V	502	HIS	-	expression tag	UNP P15682

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Chain	Residue	Modelled	Actual	Comment	Reference
V	503	HIS	-	expression tag	UNP P15682
V	504	HIS	-	expression tag	UNP P15682
V	505	HIS	-	expression tag	UNP P15682
V	506	HIS	-	expression tag	UNP P15682
V	34	ASP	GLY	conflict	UNP P15682
V	105	ARG	MET	conflict	UNP P15682
V	237	THR	ALA	conflict	UNP P15682
V	283	SER	PRO	conflict	UNP P15682
V	472	THR	ALA	conflict	UNP P15682
W	499	LEU	-	expression tag	UNP P15682
W	500	GLU	-	expression tag	UNP P15682
W	501	HIS	-	expression tag	UNP P15682
W	502	HIS	-	expression tag	UNP P15682
W	503	HIS	-	expression tag	UNP P15682
W	504	HIS	-	expression tag	UNP P15682
W	505	HIS	-	expression tag	UNP P15682
W	506	HIS	-	expression tag	UNP P15682
W	34	ASP	GLY	conflict	UNP P15682
W	105	ARG	MET	conflict	UNP P15682
W	237	THR	ALA	conflict	UNP P15682
W	283	SER	PRO	conflict	UNP P15682
W	472	THR	ALA	conflict	UNP P15682
X	499	LEU	-	expression tag	UNP P15682
X	500	GLU	-	expression tag	UNP P15682
X	501	HIS	-	expression tag	UNP P15682
X	502	HIS	-	expression tag	UNP P15682
X	503	HIS	-	expression tag	UNP P15682
X	504	HIS	-	expression tag	UNP P15682
X	505	HIS	-	expression tag	UNP P15682
X	506	HIS	-	expression tag	UNP P15682
X	34	ASP	GLY	conflict	UNP P15682
X	105	ARG	MET	conflict	UNP P15682
X	237	THR	ALA	conflict	UNP P15682
X	283	SER	PRO	conflict	UNP P15682
X	472	THR	ALA	conflict	UNP P15682

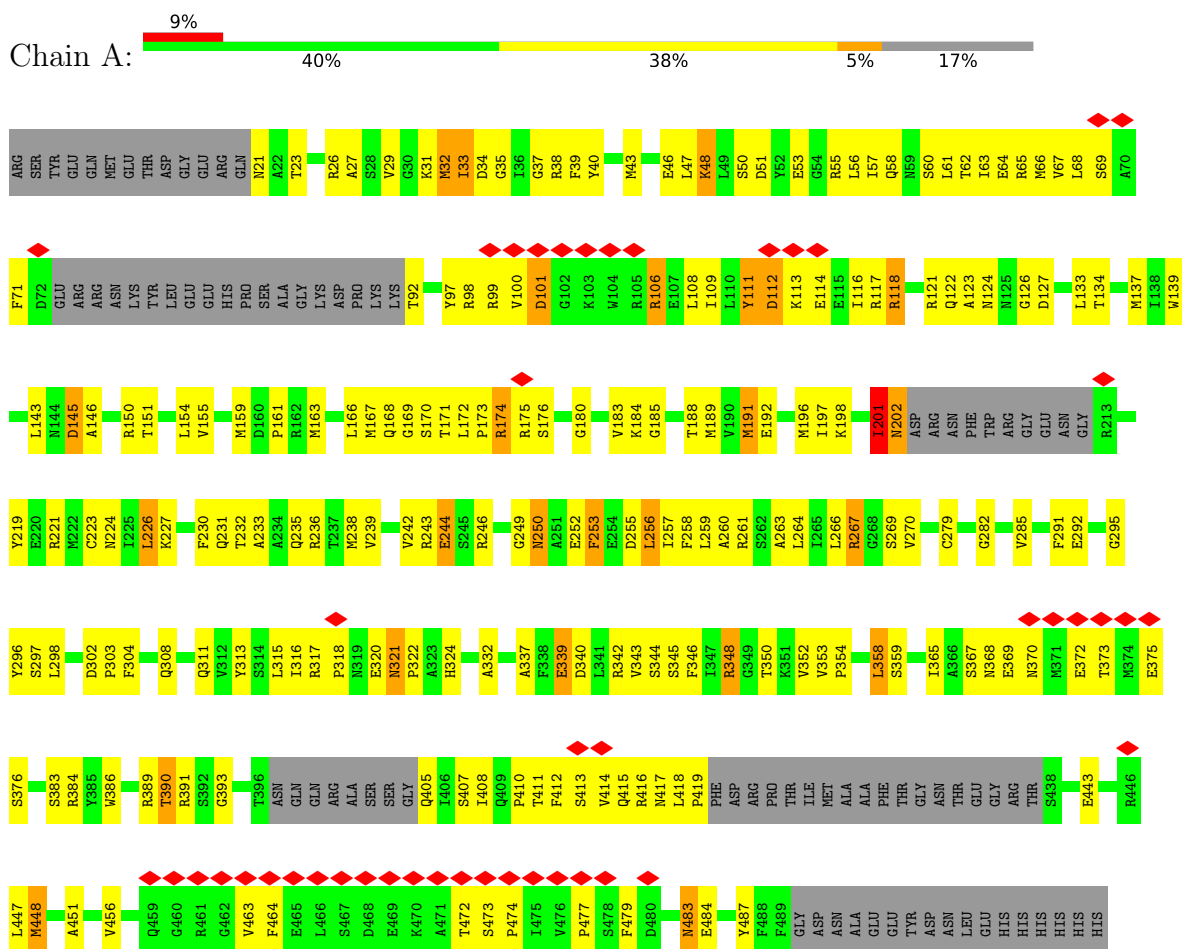
- Molecule 2 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	Y	308	Total P 308 308	0	308
2	Z	308	Total P 308 308	0	308

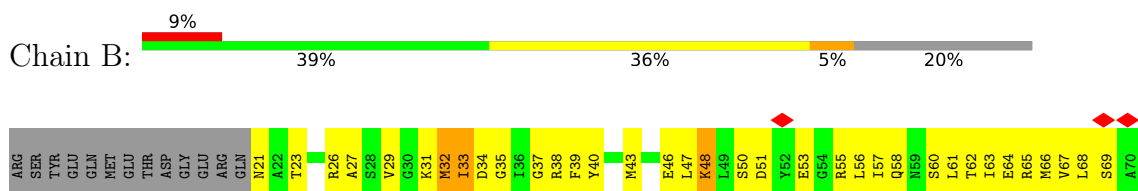
3 Residue-property plots

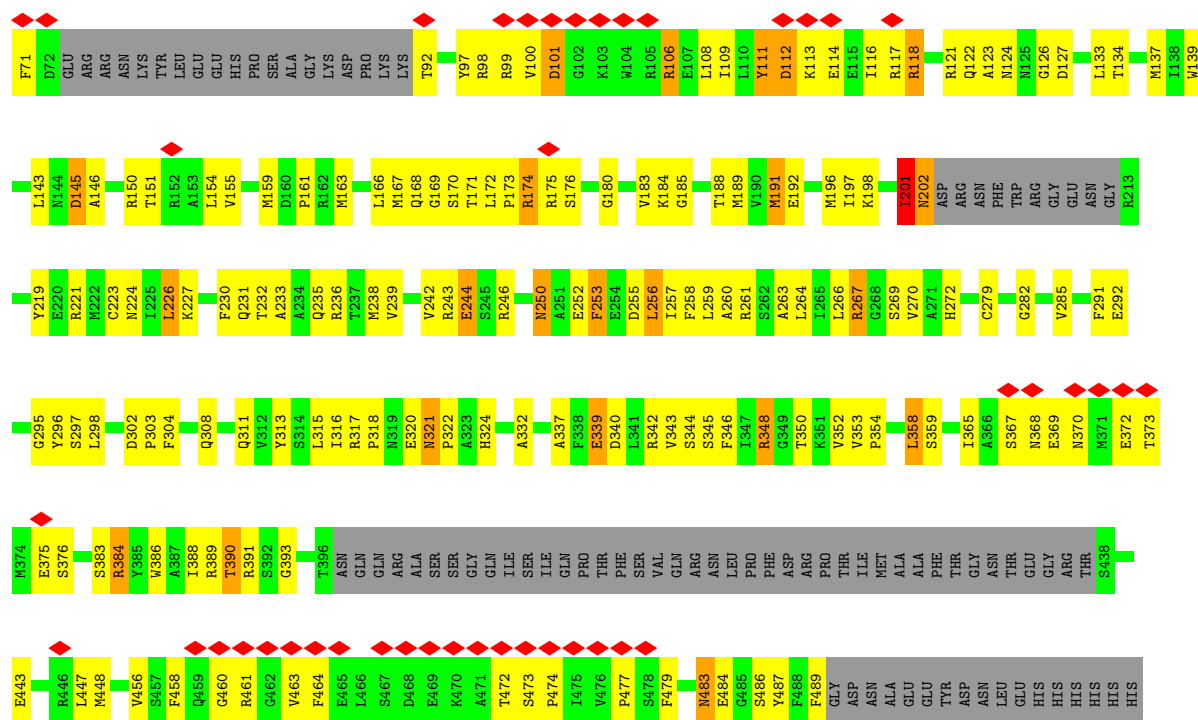
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: NUCLEOPROTEIN

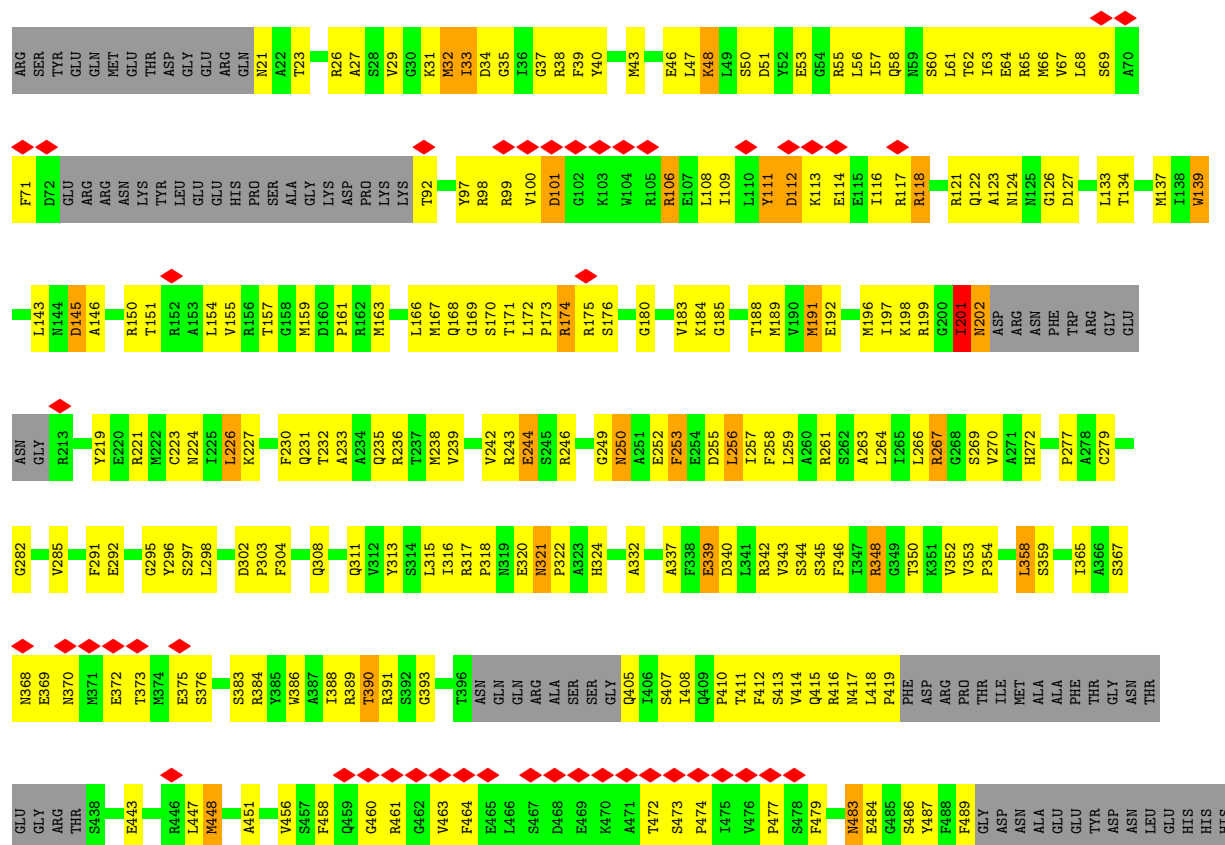


• Molecule 1: NUCLEOPROTEIN





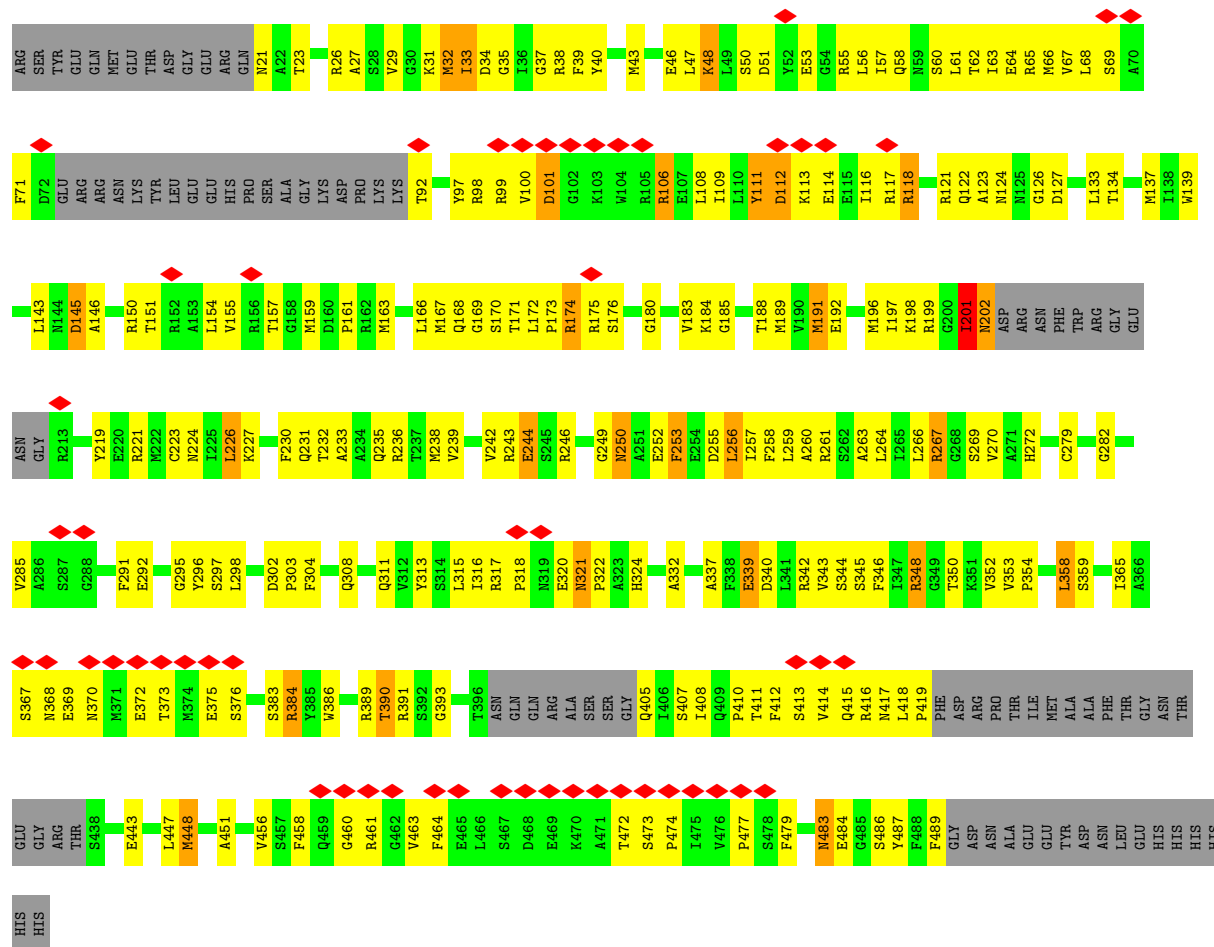
• Molecule 1: NUCLEOPROTEIN



HIS
HIS
HIS

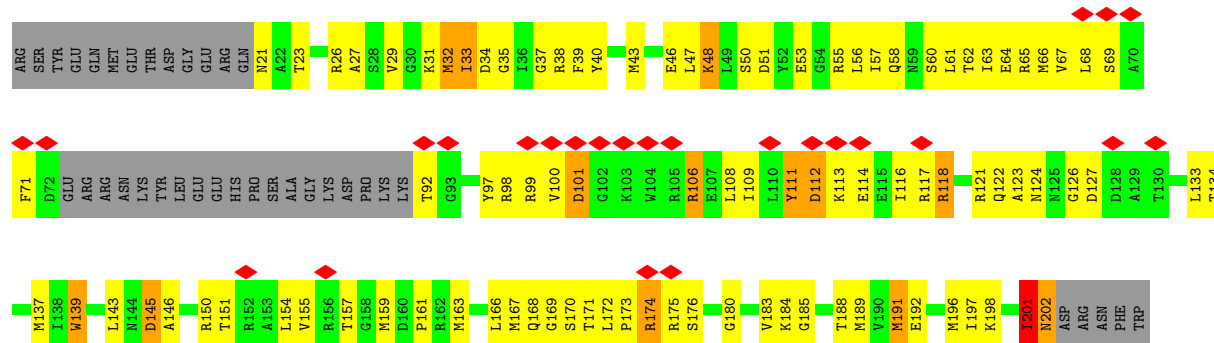
● Molecule 1: NUCLEOPROTEIN

Chain D: 11% 38% 39% 5% 17%

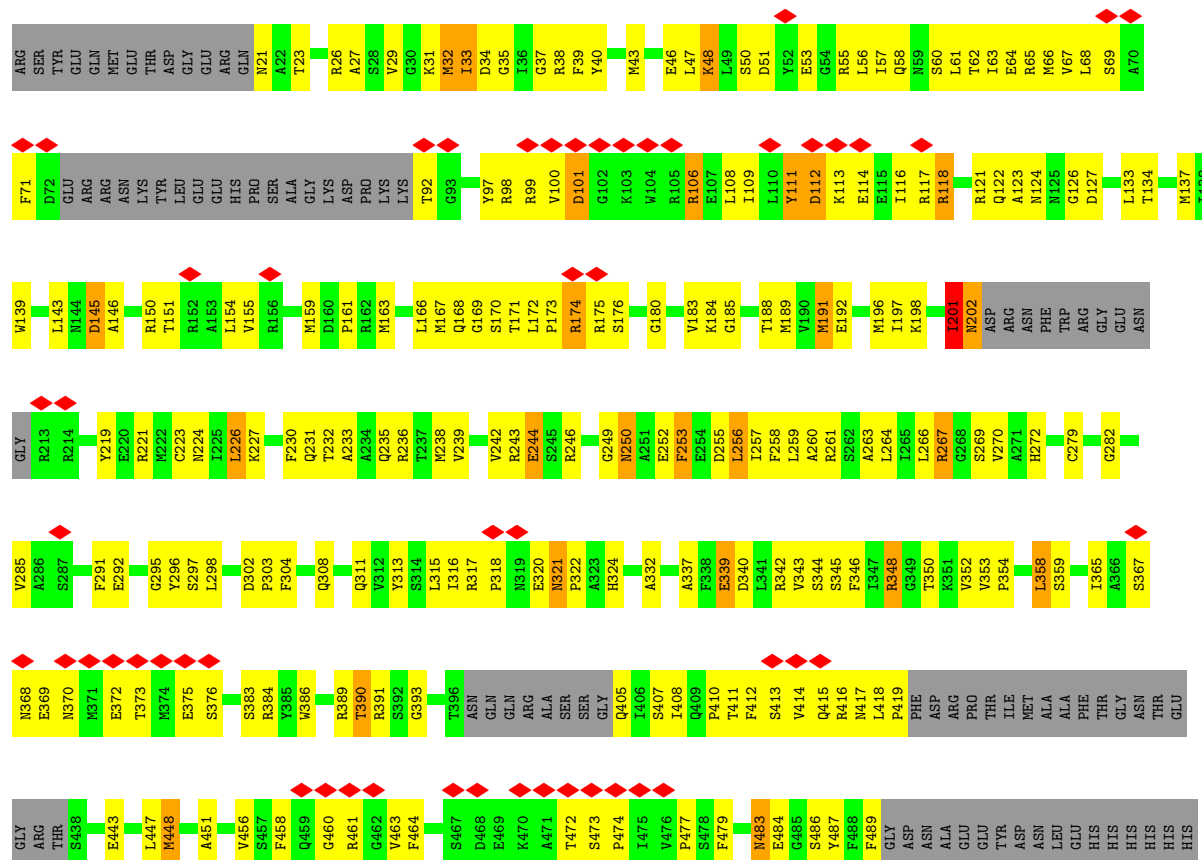
HIS
HIS

● Molecule 1: NUCLEOPROTEIN

Chain E: 9% 38% 39% 5% 17%

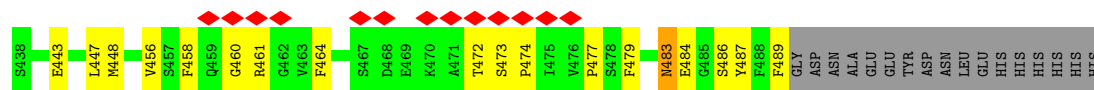


- Molecule 1: NUCLEOPROTEIN

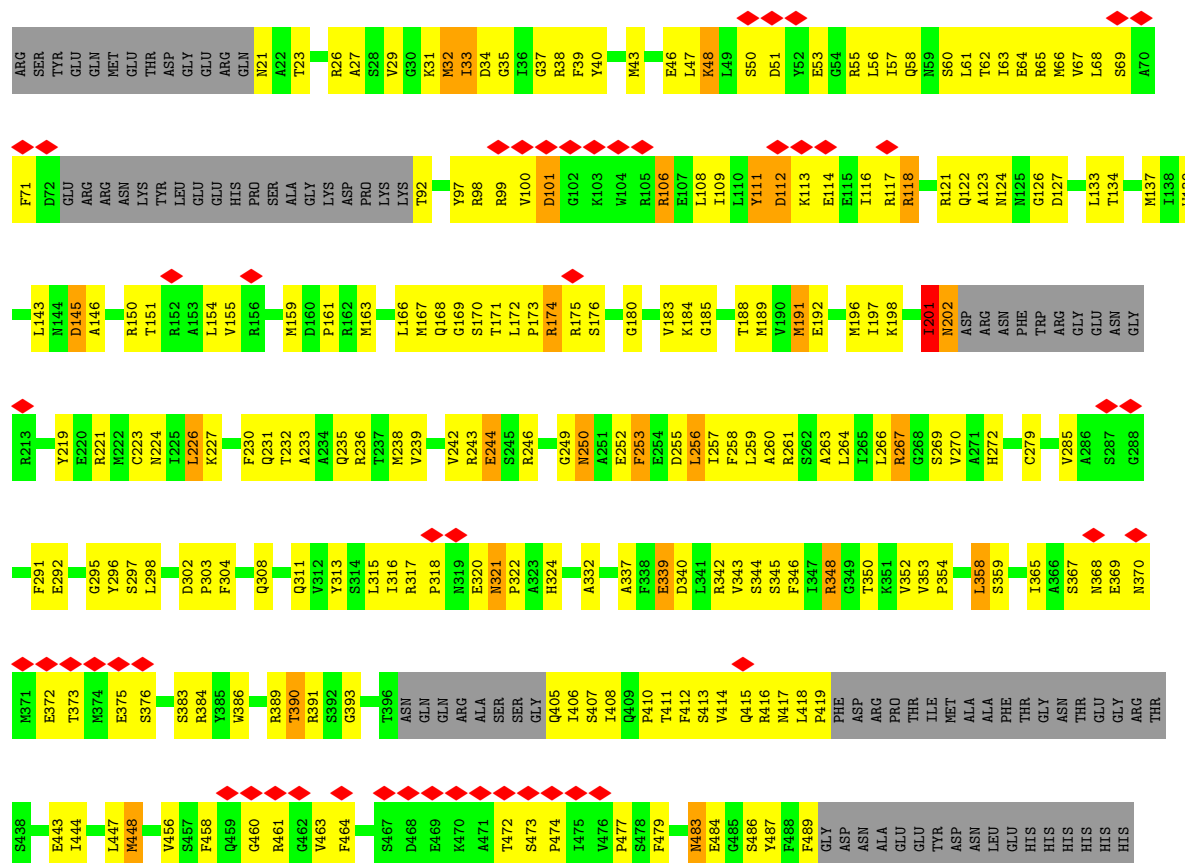


- Molecule 1: NUCLEOPROTEIN

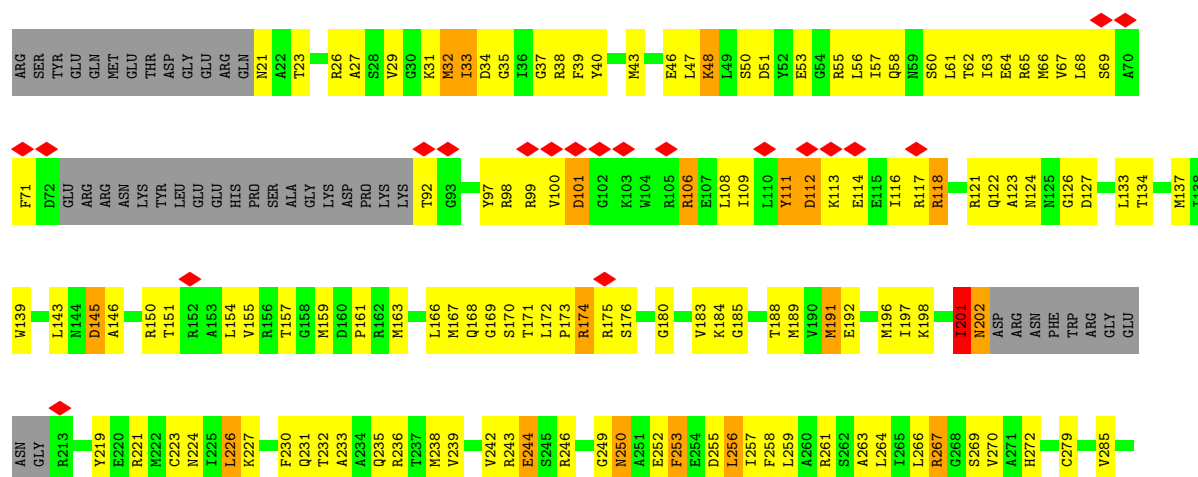
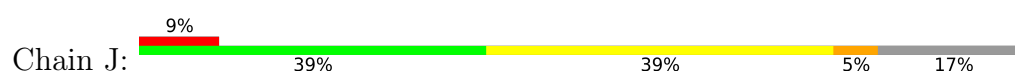


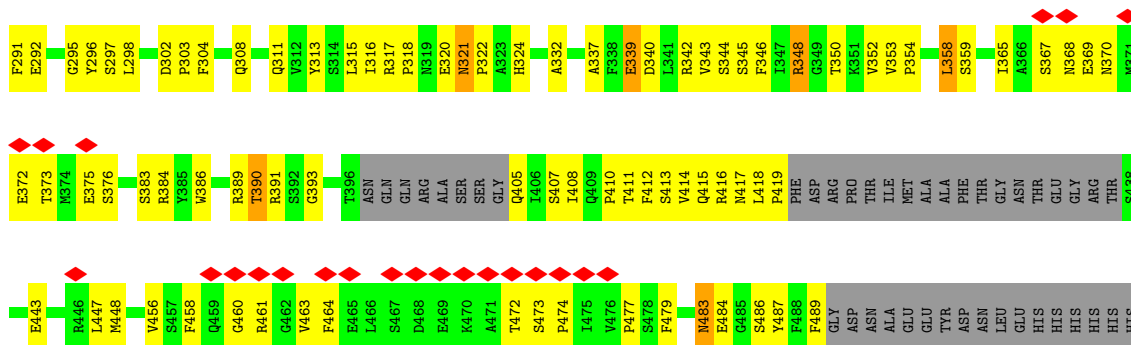


• Molecule 1: NUCLEOPROTEIN

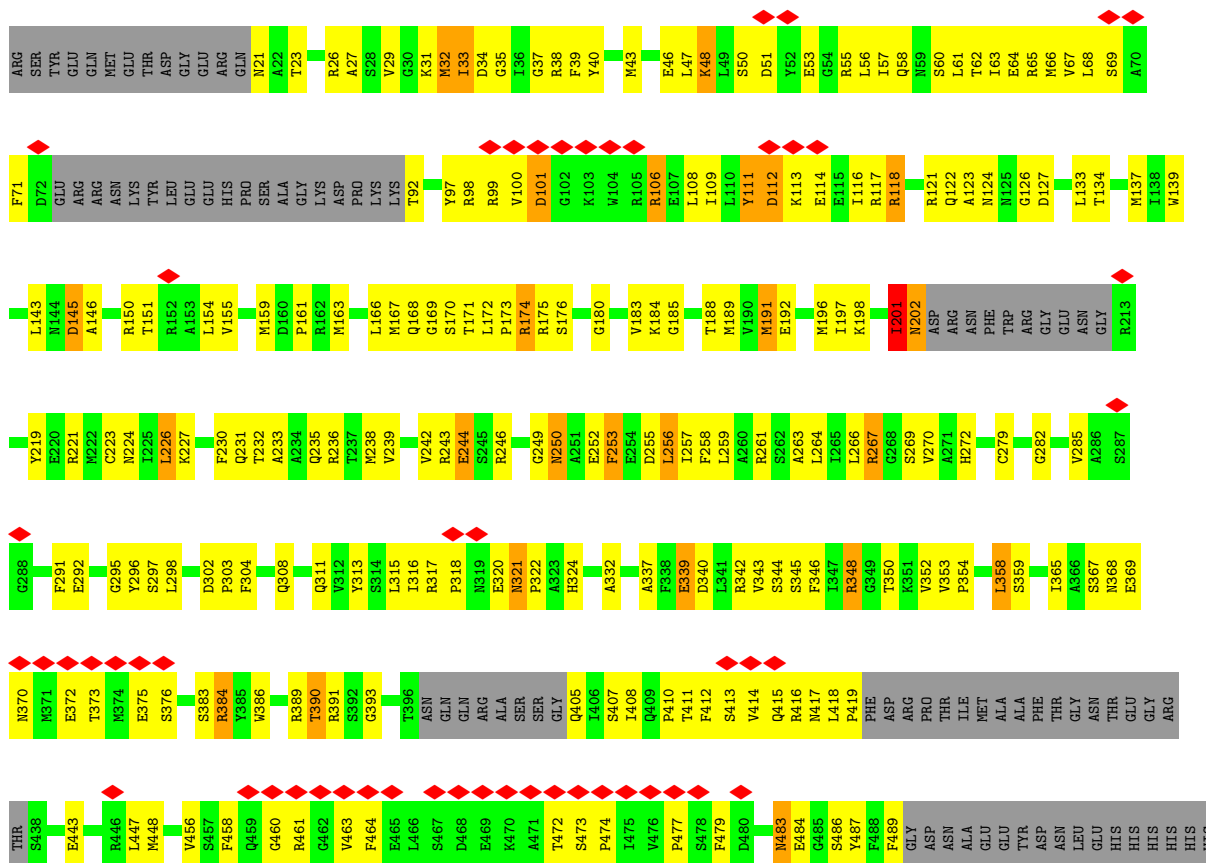


• Molecule 1: NUCLEOPROTEIN

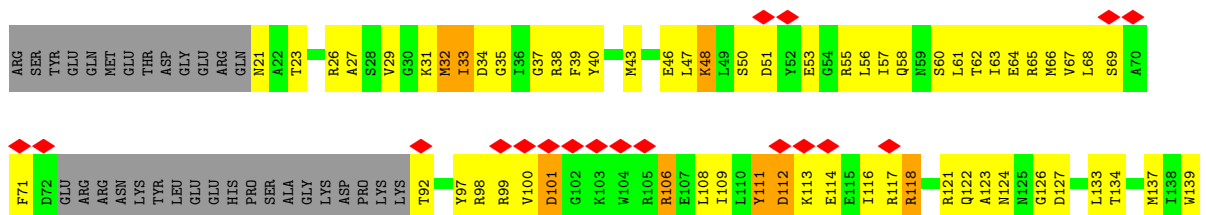


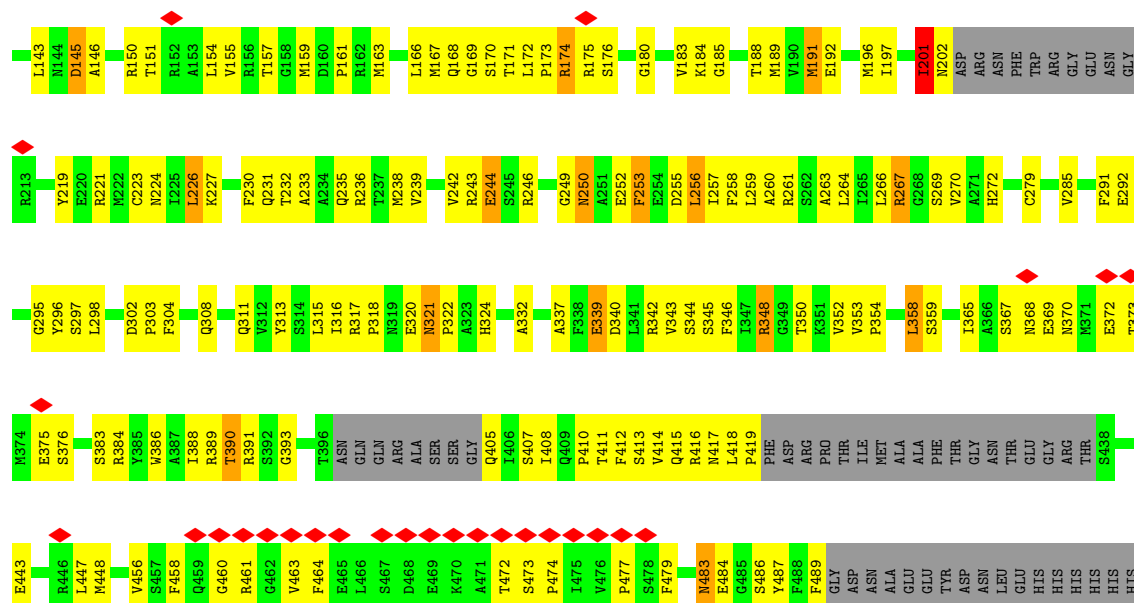


• Molecule 1: NUCLEOPROTEIN

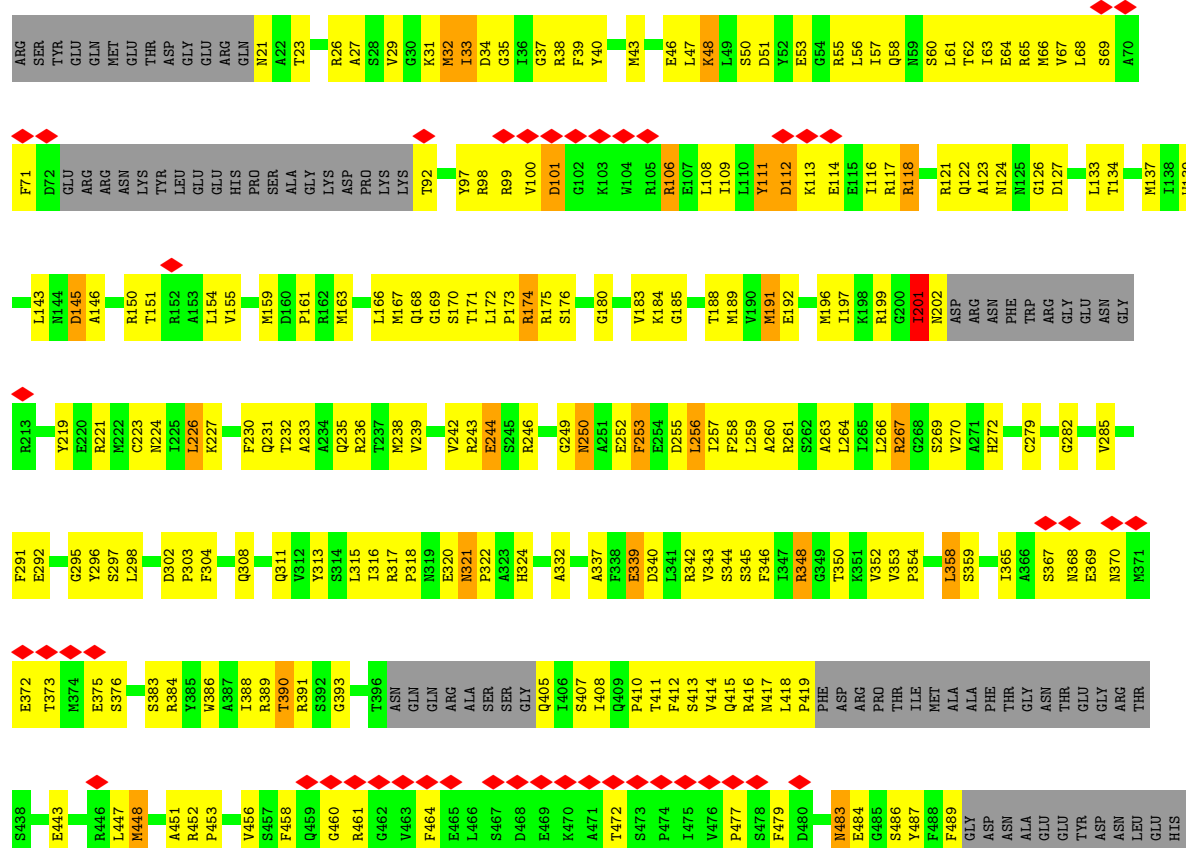


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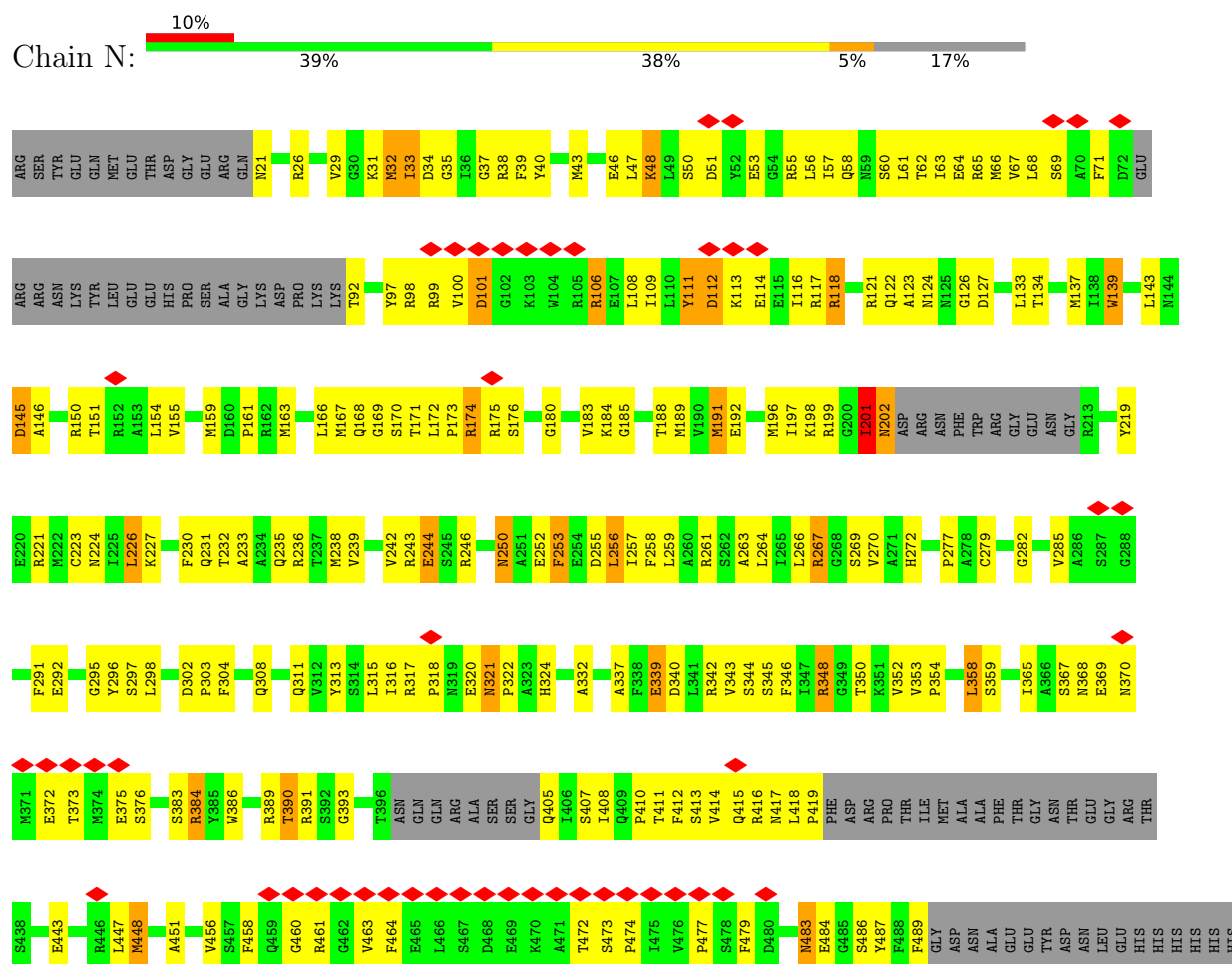




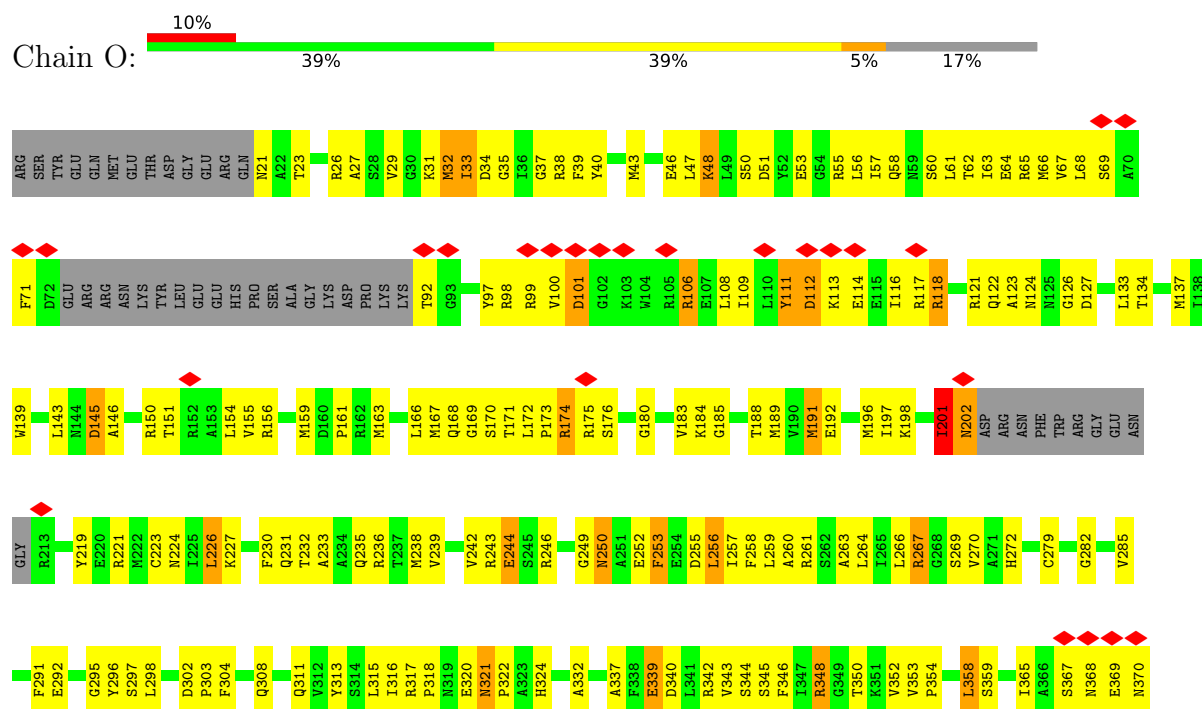
Molecule 1: NUCLEOPROTEIN

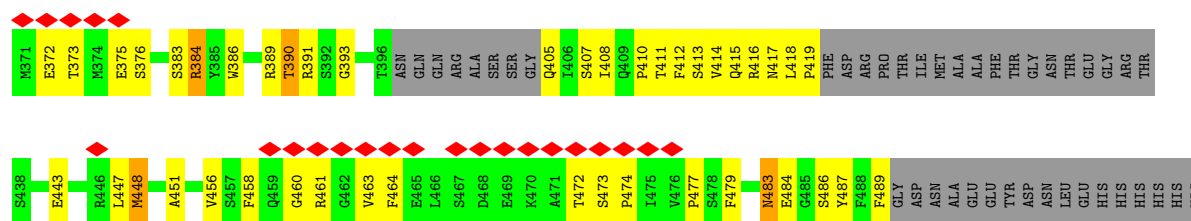


• Molecule 1: NUCLEOPROTEIN

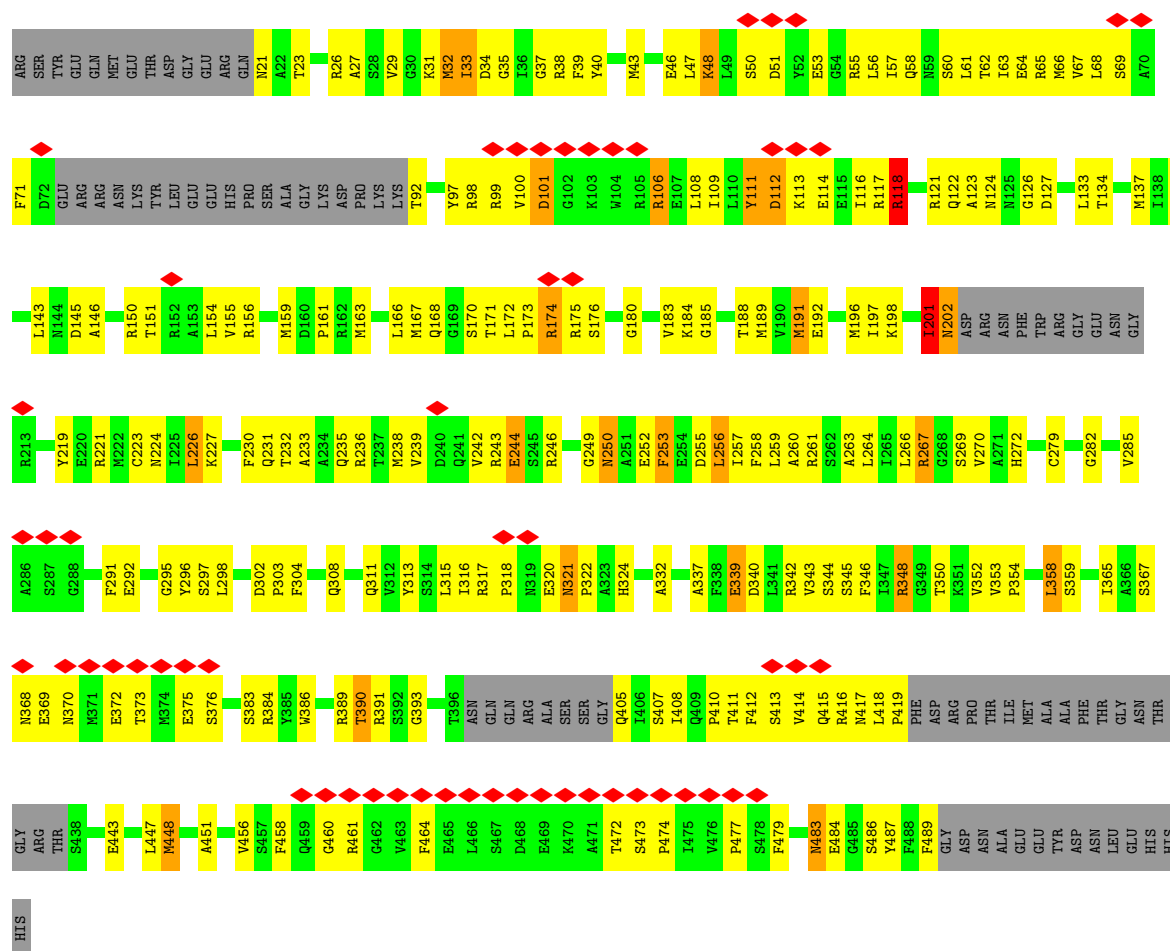


• Molecule 1: NUCLEOPROTEIN

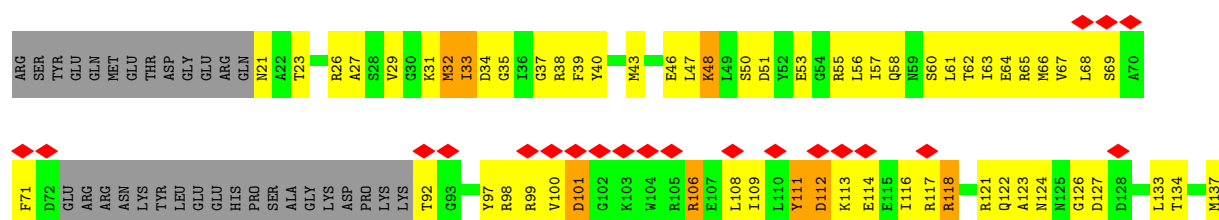
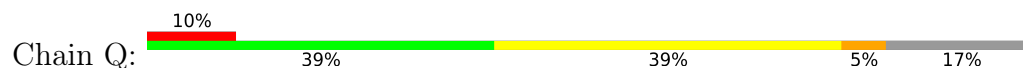


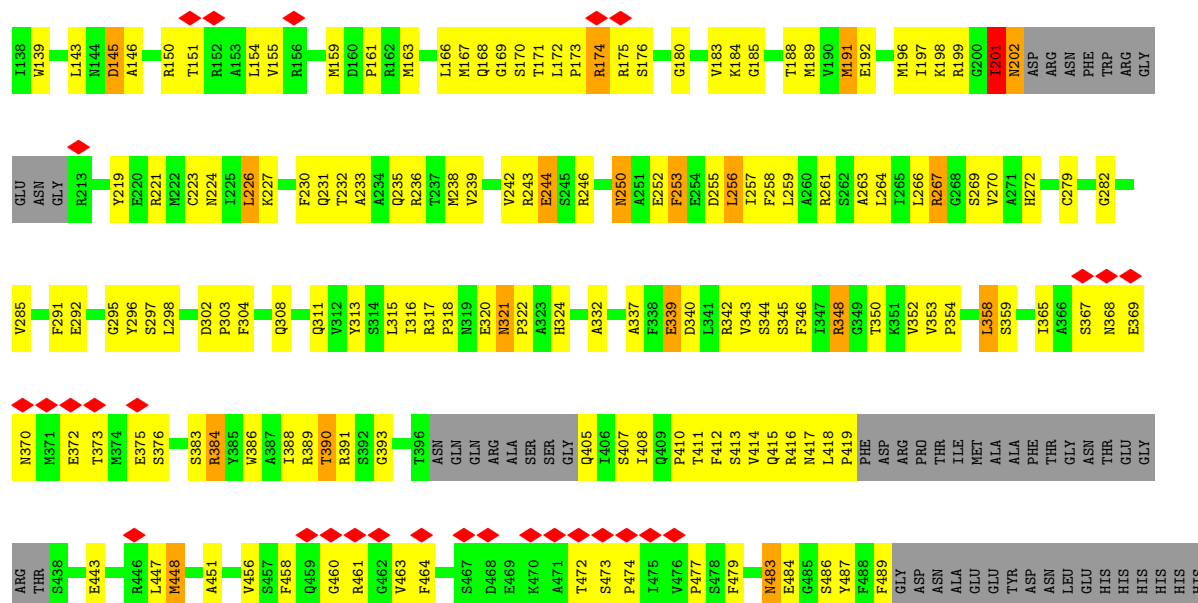


• Molecule 1: NUCLEOPROTEIN

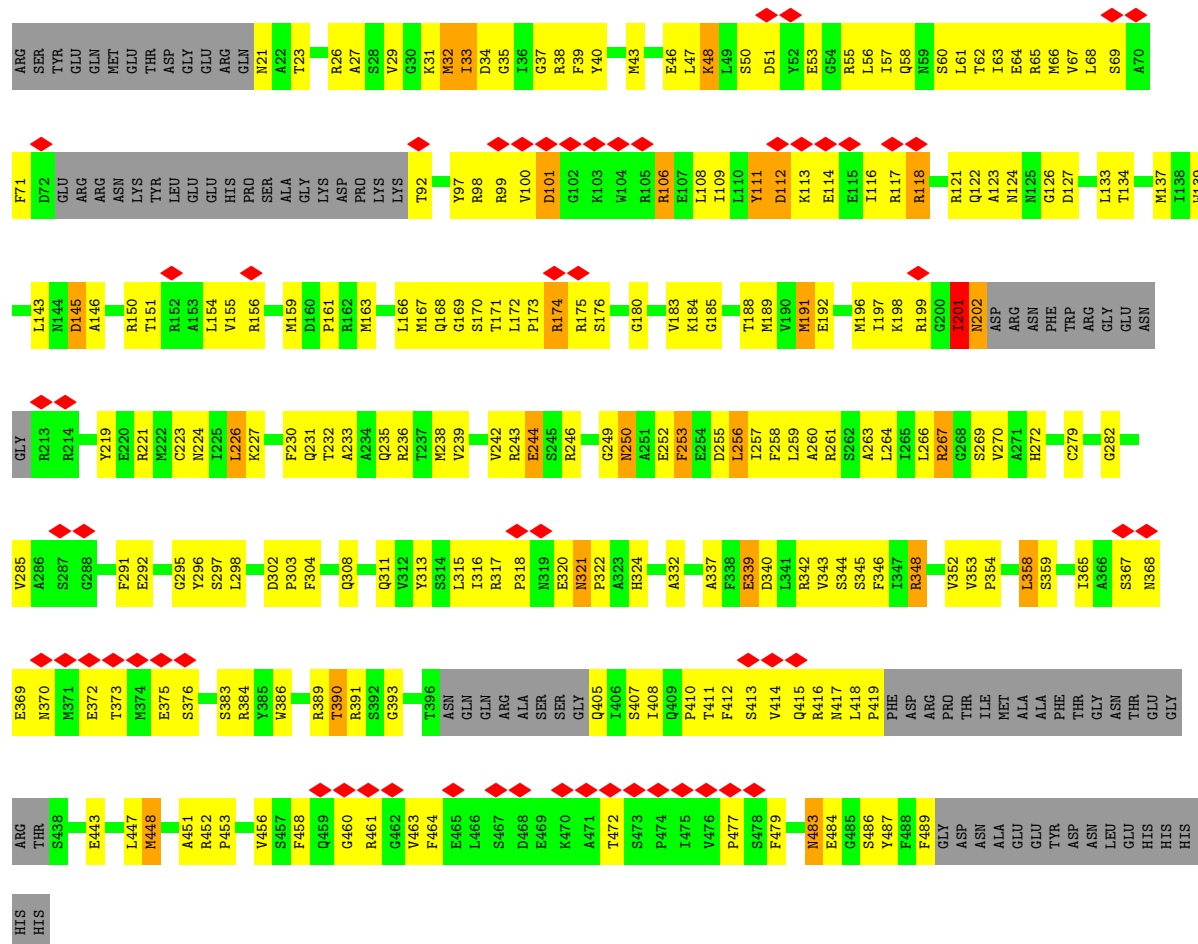


• Molecule 1: NUCLEOPROTEIN

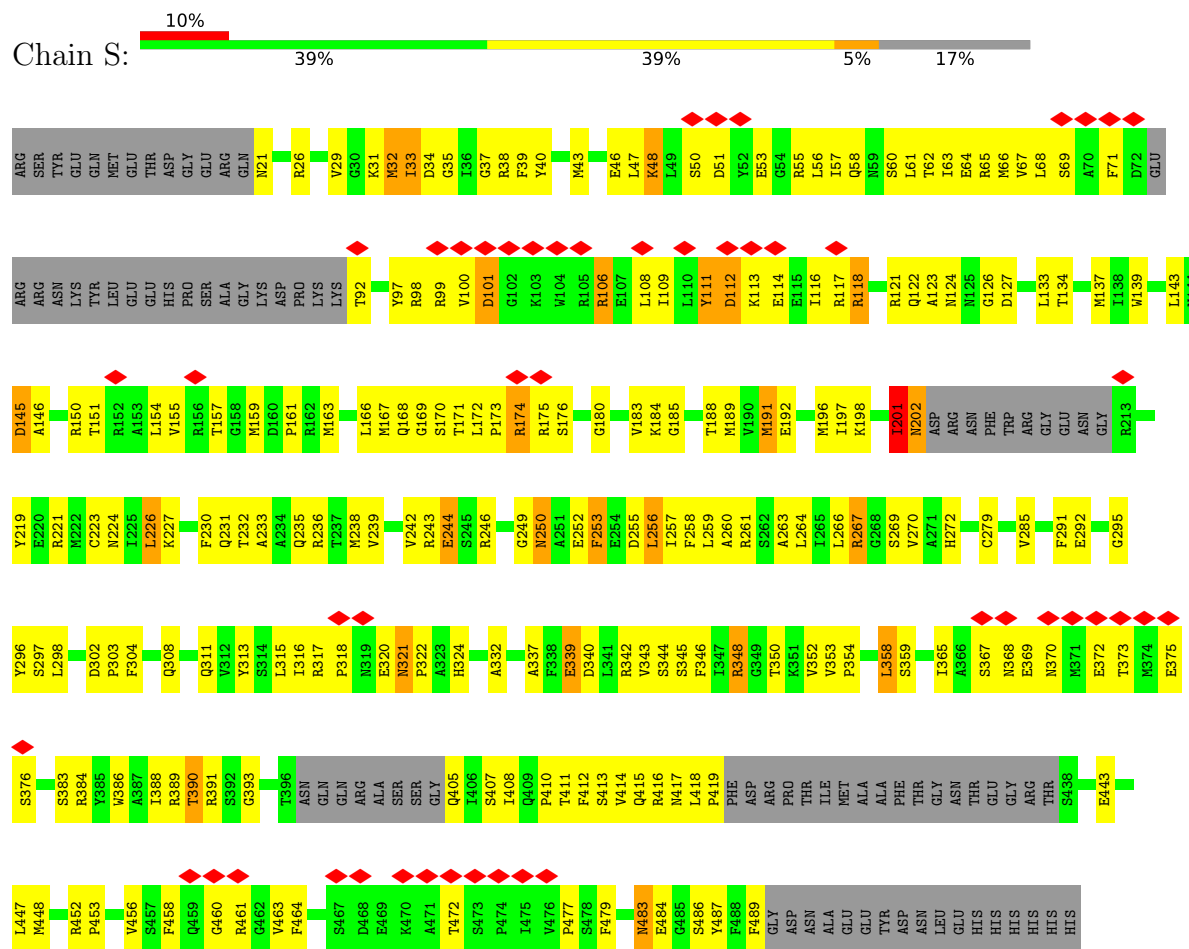




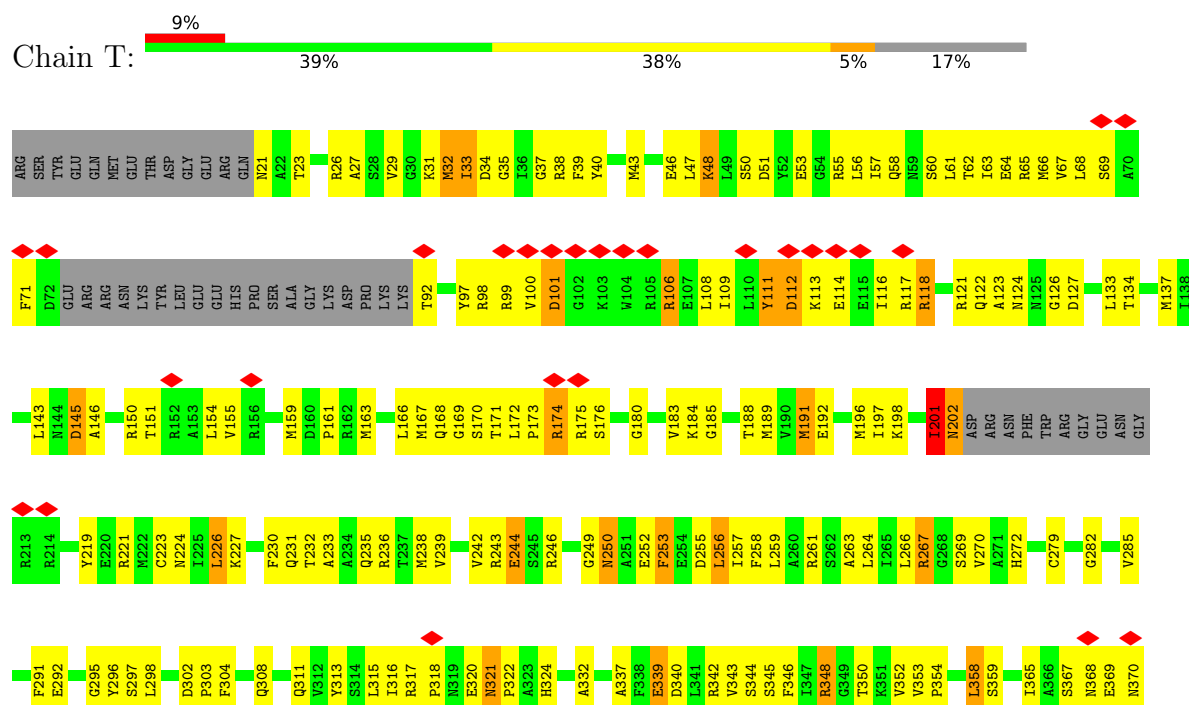
• Molecule 1: NUCLEOPROTEIN

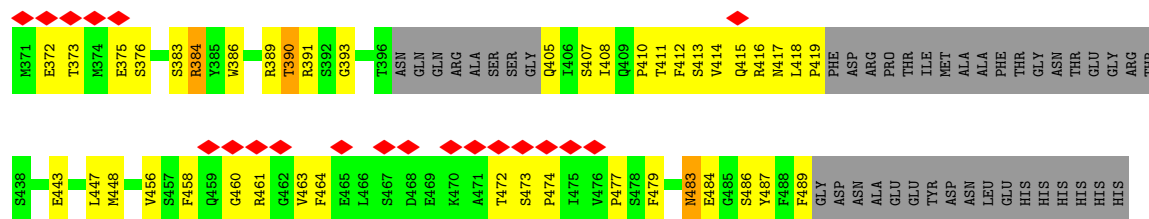


• Molecule 1: NUCLEOPROTEIN

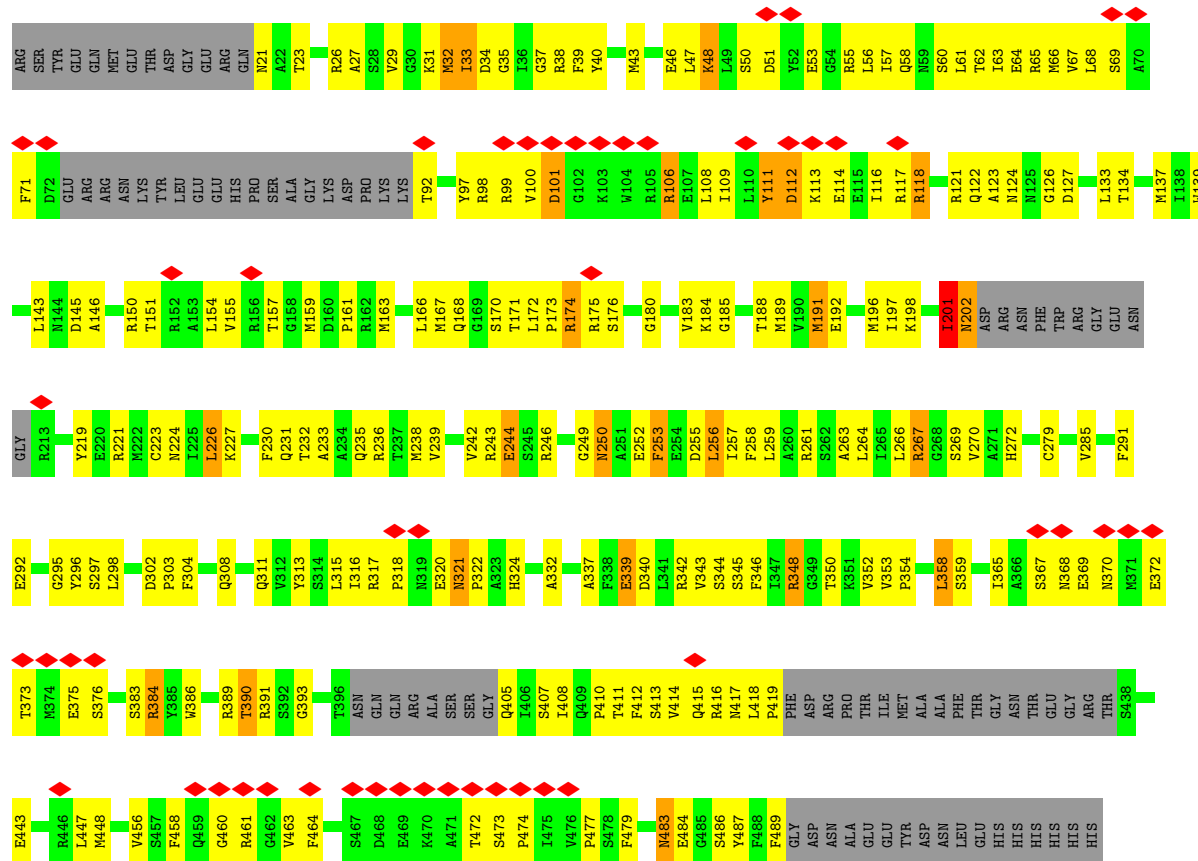


• Molecule 1: NUCLEOPROTEIN

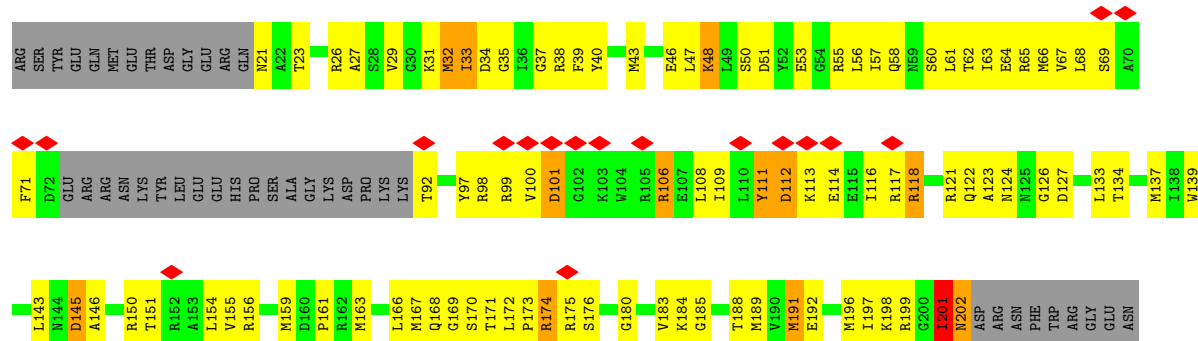
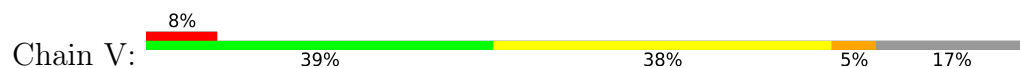


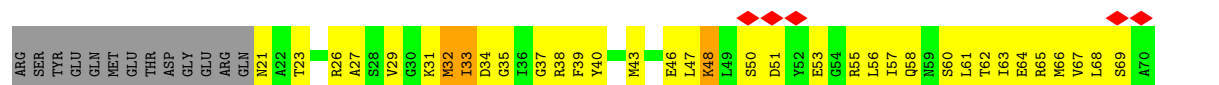


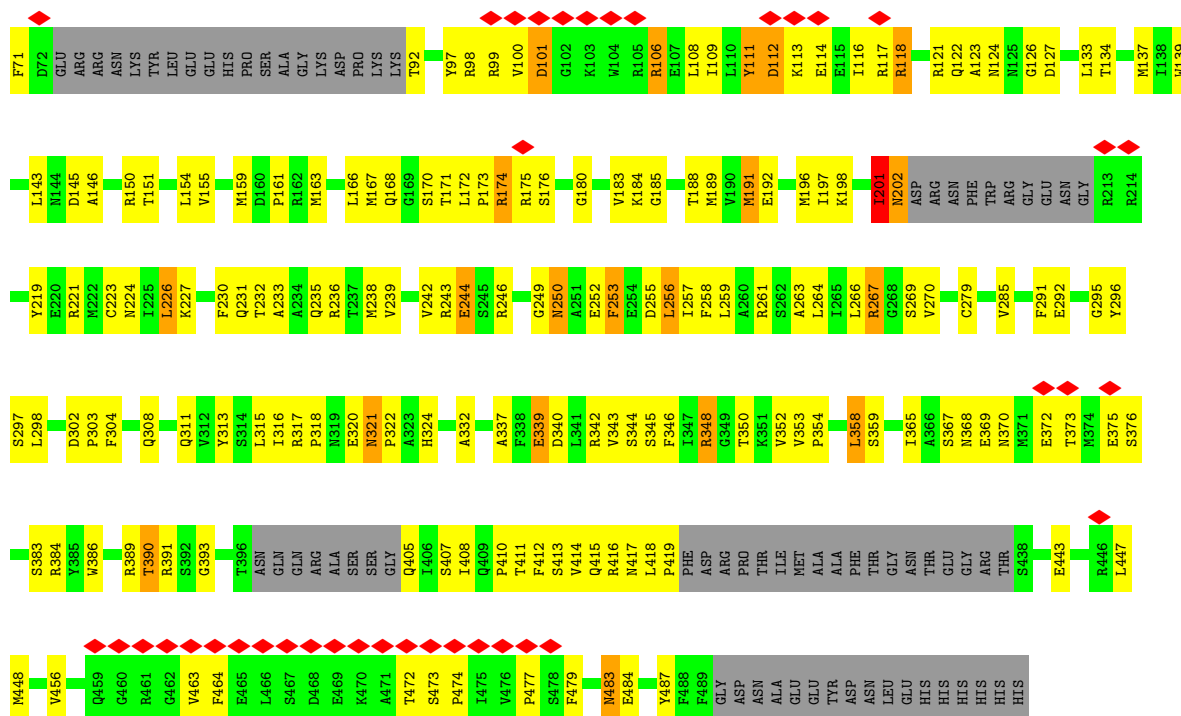
• Molecule 1: NUCLEOPROTEIN



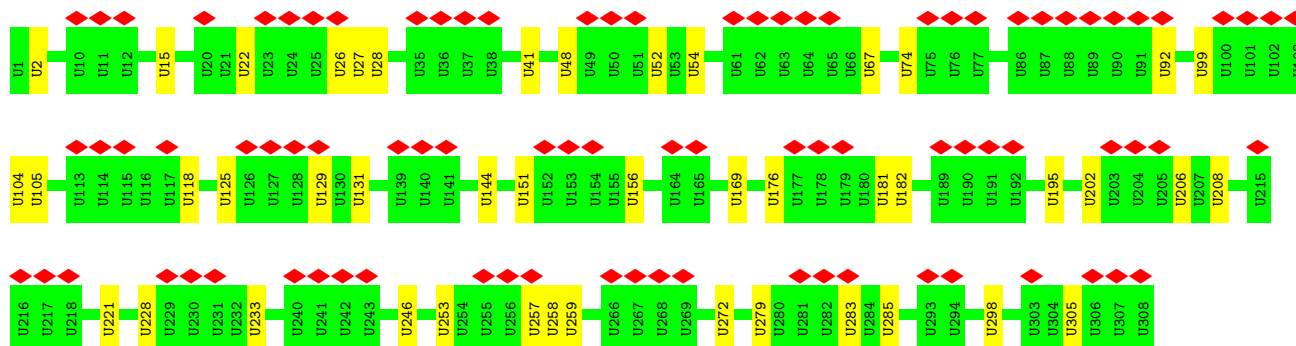
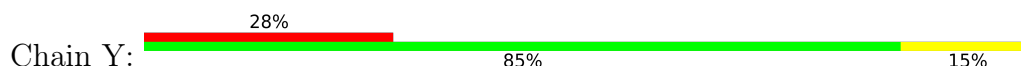
• Molecule 1: NUCLEOPROTEIN



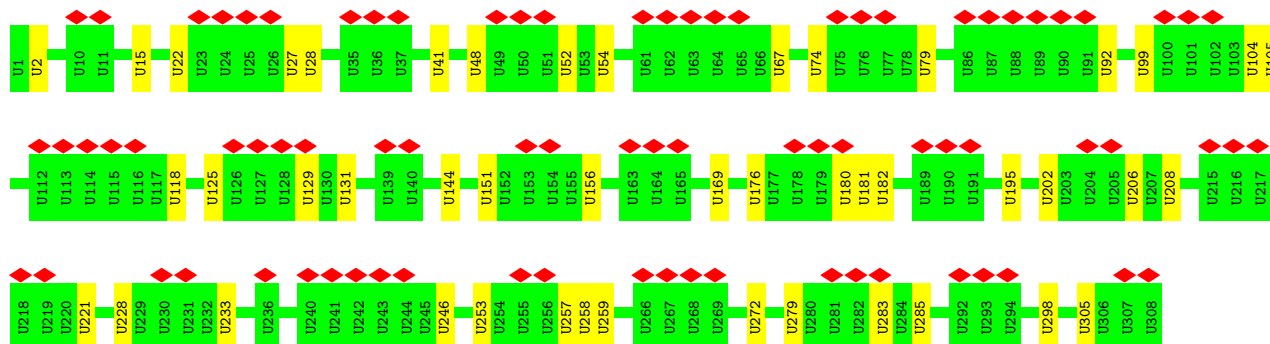
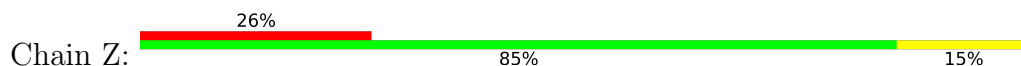




• Molecule 2: RNA



• Molecule 2: RNA



4 Experimental information

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=Not provided°, rise=Not provided Å, axial sym=Not provided	Depositor
Number of segments used	876	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH PLATE	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	65000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	0.039	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	442.0, 442.0, 442.0	wwPDB
Map dimensions	100, 100, 100	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	4.42, 4.42, 4.42	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	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	B	0.92	1/3200 (0.0%)	0.92	6/4299 (0.1%)
1	C	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	D	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	E	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	F	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	G	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	H	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	I	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	J	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	K	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	L	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	M	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	N	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	O	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	P	0.92	1/3323 (0.0%)	0.92	7/4466 (0.2%)
1	Q	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	R	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	S	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	T	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	U	0.92	1/3322 (0.0%)	0.92	6/4464 (0.1%)
1	V	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
1	W	0.92	1/3200 (0.0%)	0.92	6/4299 (0.1%)
1	X	0.92	1/3323 (0.0%)	0.92	6/4466 (0.1%)
All	All	0.92	24/79505 (0.0%)	0.92	145/106848 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
1	O	0	1
1	P	0	1
1	Q	0	1
1	R	0	1
1	S	0	1
1	T	0	1
1	U	0	1
1	V	0	1
1	W	0	1
1	X	0	1
All	All	0	24

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	201	ILE	C-N	-5.31	1.21	1.34
1	T	201	ILE	C-N	-5.27	1.22	1.34
1	W	201	ILE	C-N	-5.27	1.22	1.34
1	Q	201	ILE	C-N	-5.27	1.22	1.34
1	F	201	ILE	C-N	-5.26	1.22	1.34

The worst 5 of 145 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	201	ILE	O-C-N	-6.22	112.74	122.70
1	M	201	ILE	O-C-N	-6.22	112.75	122.70
1	W	201	ILE	O-C-N	-6.22	112.75	122.70
1	A	201	ILE	O-C-N	-6.22	112.75	122.70
1	B	201	ILE	O-C-N	-6.21	112.76	122.70

There are no chirality outliers.

5 of 24 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	201	ILE	Mainchain
1	B	201	ILE	Mainchain
1	C	201	ILE	Mainchain
1	D	201	ILE	Mainchain
1	E	201	ILE	Mainchain

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	3272	0	3272	249	0
1	B	3151	0	3148	236	0
1	C	3272	0	3272	267	0
1	D	3272	0	3272	264	0
1	E	3272	0	3272	271	0
1	F	3272	0	3272	261	0
1	G	3272	0	3272	262	0
1	H	3272	0	3272	264	0
1	I	3272	0	3272	262	0
1	J	3272	0	3272	259	0
1	K	3272	0	3272	260	0
1	L	3272	0	3272	269	0
1	M	3272	0	3272	265	0
1	N	3272	0	3272	268	0
1	O	3272	0	3272	268	0
1	P	3272	0	3272	262	0
1	Q	3272	0	3272	263	0
1	R	3272	0	3272	263	0
1	S	3272	0	3272	266	0
1	T	3272	0	3272	265	0
1	U	3271	0	3271	260	0
1	V	3272	0	3272	259	0
1	W	3151	0	3148	239	0
1	X	3272	0	3272	241	0
2	Y	308	0	0	95	0
2	Z	308	0	0	98	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	78901	0	78279	5798	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 37.

The worst 5 of 5798 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:D:221:ARG:HH22	2:Y:272:U:P	1.81	1.04
1:K:221:ARG:HH22	2:Z:144:U:P	1.81	1.04
1:T:221:ARG:HH22	2:Y:67:U:P	1.81	1.04
1:A:221:ARG:HH22	2:Z:15:U:P	1.81	1.04
1:B:221:ARG:HH22	2:Y:298:U:P	1.81	1.04

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	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	B	391/499 (78%)	339 (87%)	47 (12%)	5 (1%)	12	48
1	C	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	D	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	E	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	F	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	G	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	H	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	I	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	J	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	K	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	L	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	M	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	N	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	O	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	P	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	Q	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	R	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	S	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	T	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	U	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	V	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
1	W	391/499 (78%)	339 (87%)	47 (12%)	5 (1%)	12	48
1	X	404/499 (81%)	350 (87%)	49 (12%)	5 (1%)	13	50
All	All	9670/11976 (81%)	8378 (87%)	1172 (12%)	120 (1%)	17	50

5 of 120 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	233	ALA
1	A	472	THR
1	B	233	ALA
1	B	472	THR
1	C	233	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	353/425 (83%)	328 (93%)	25 (7%)	14	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	338/425 (80%)	313 (93%)	25 (7%)	13	38
1	C	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	D	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	E	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	F	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	G	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	H	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	I	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	J	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	K	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	L	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	M	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	N	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	O	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	P	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	Q	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	R	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	S	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	T	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	U	352/425 (83%)	327 (93%)	25 (7%)	14	39
1	V	353/425 (83%)	328 (93%)	25 (7%)	14	39
1	W	338/425 (80%)	313 (93%)	25 (7%)	13	38
1	X	353/425 (83%)	328 (93%)	25 (7%)	14	39
All	All	8441/10200 (83%)	7841 (93%)	600 (7%)	18	39

5 of 600 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	S	244	GLU
1	W	483	ASN
1	T	32	MET
1	S	202	ASN
1	U	384	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 296 such sidechains are listed below:

Mol	Chain	Res	Type
1	S	370	ASN
1	X	231	GLN
1	T	308	GLN
1	V	202	ASN
1	H	415	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	Y	0/308	-	-
2	Z	0/308	-	-
All	All	0/616	-	-

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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 [i](#)

There are no chain breaks in this entry.

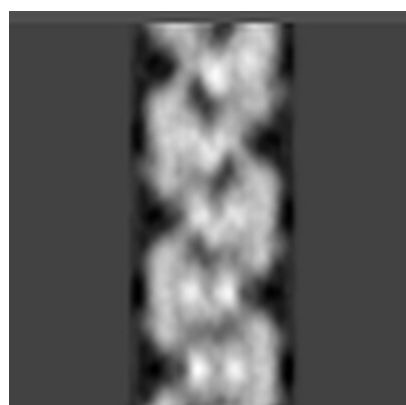
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2205. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

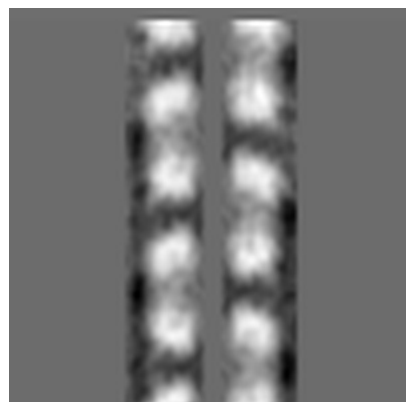


Z

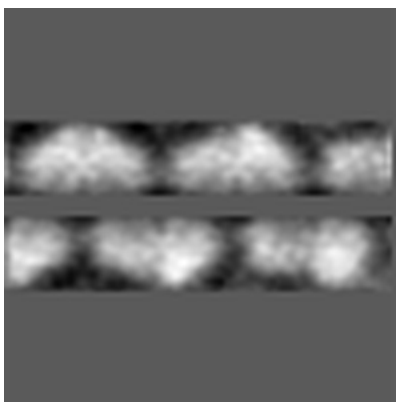
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

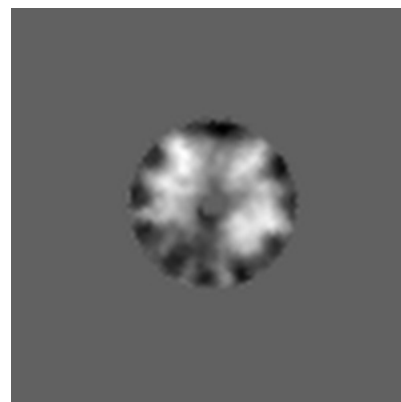
6.2.1 Primary map



X Index: 50



Y Index: 50

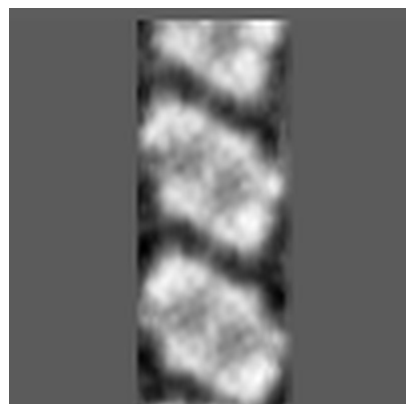


Z Index: 50

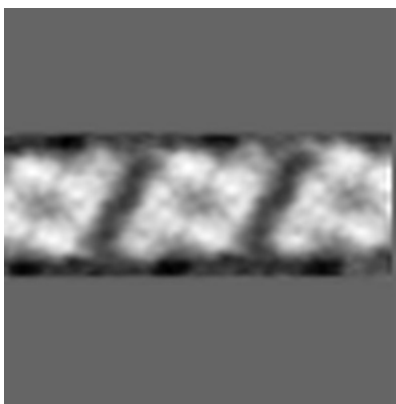
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

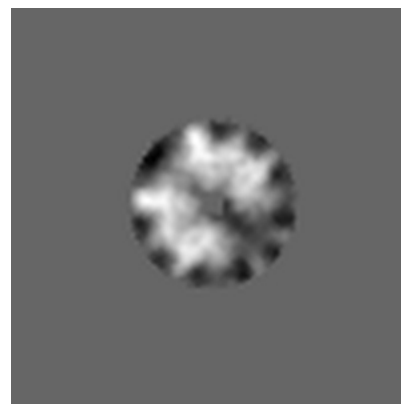
6.3.1 Primary map



X Index: 59



Y Index: 61

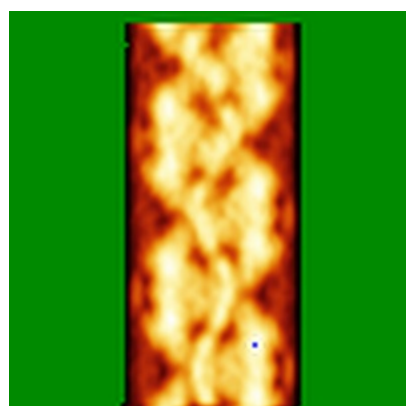


Z Index: 80

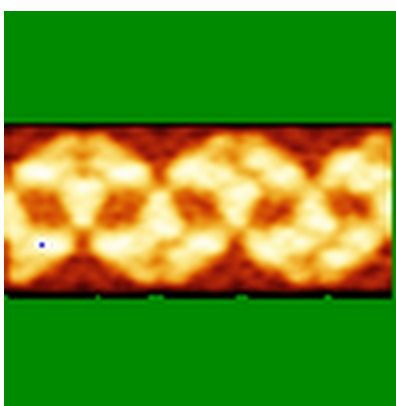
The images above show the largest variance slices of the map in three orthogonal directions.

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

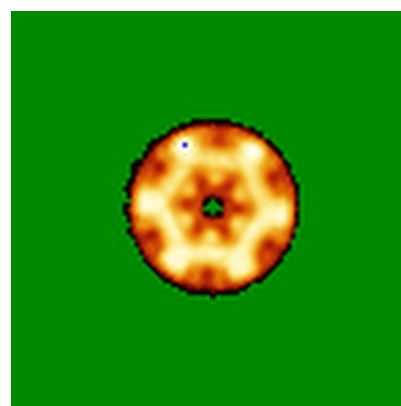
6.4.1 Primary map



X



Y

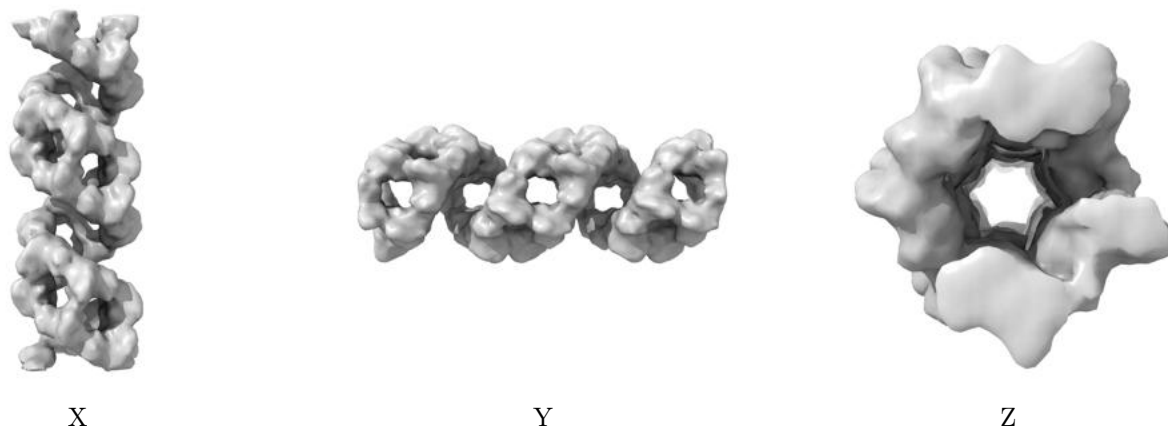


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

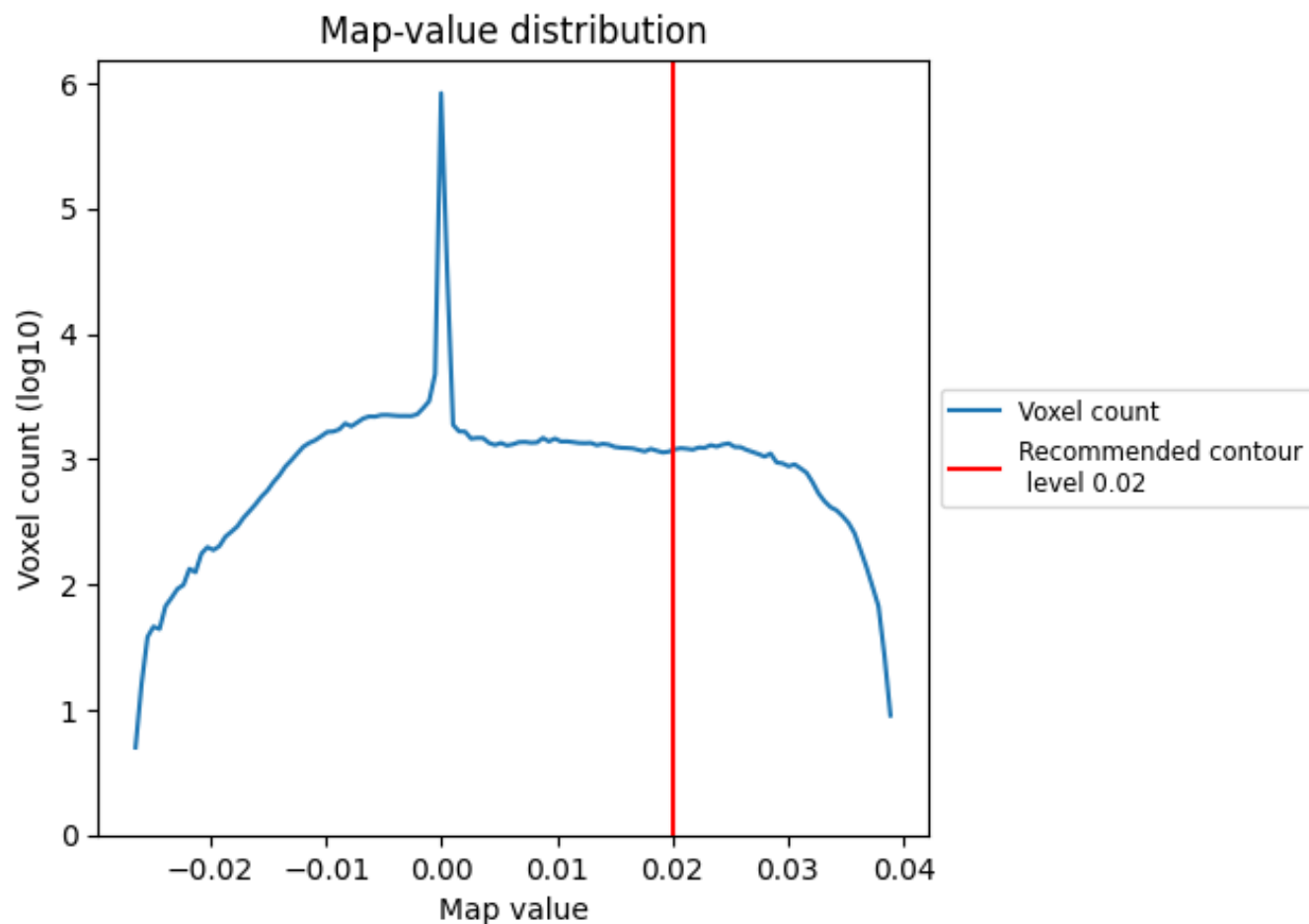
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

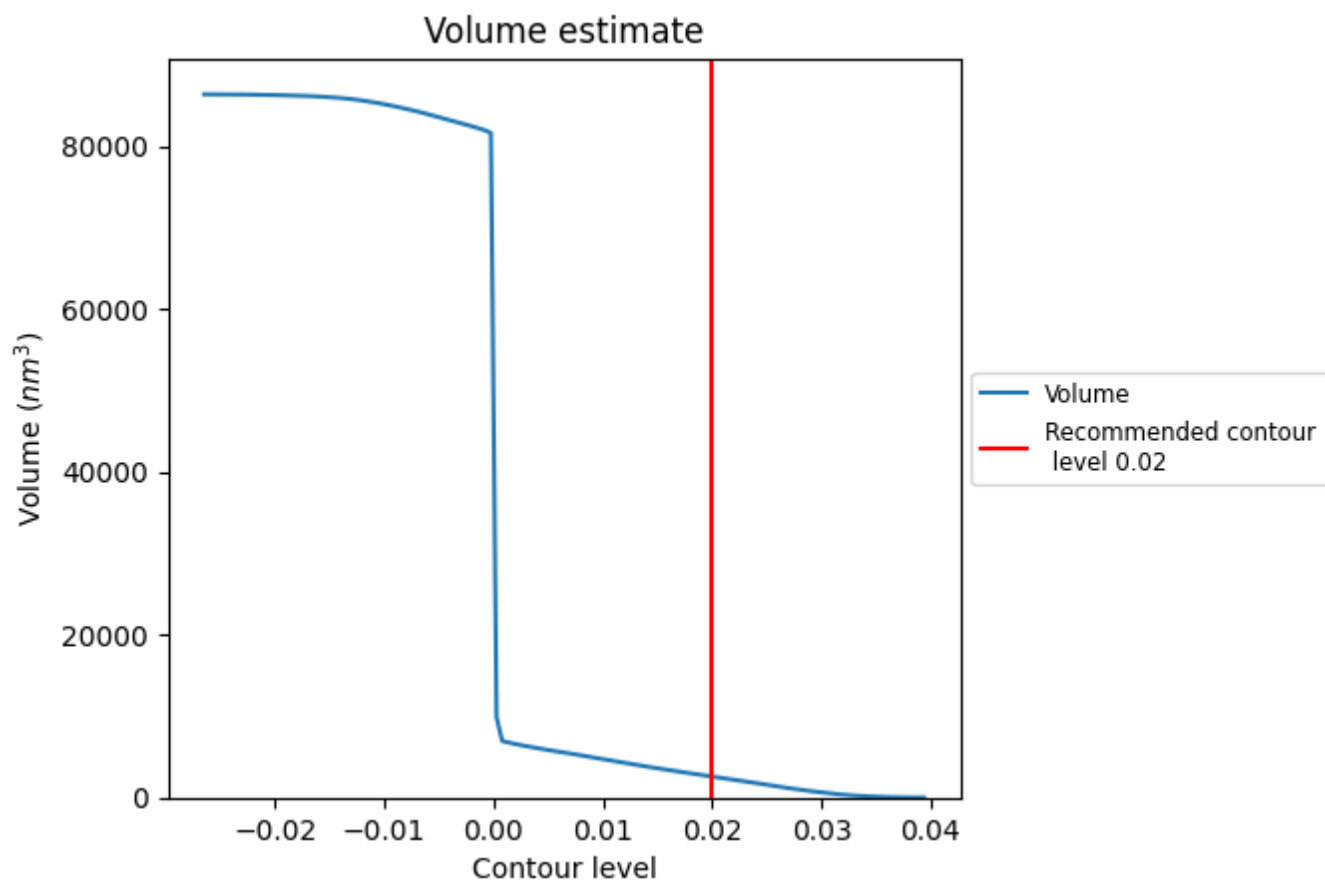
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

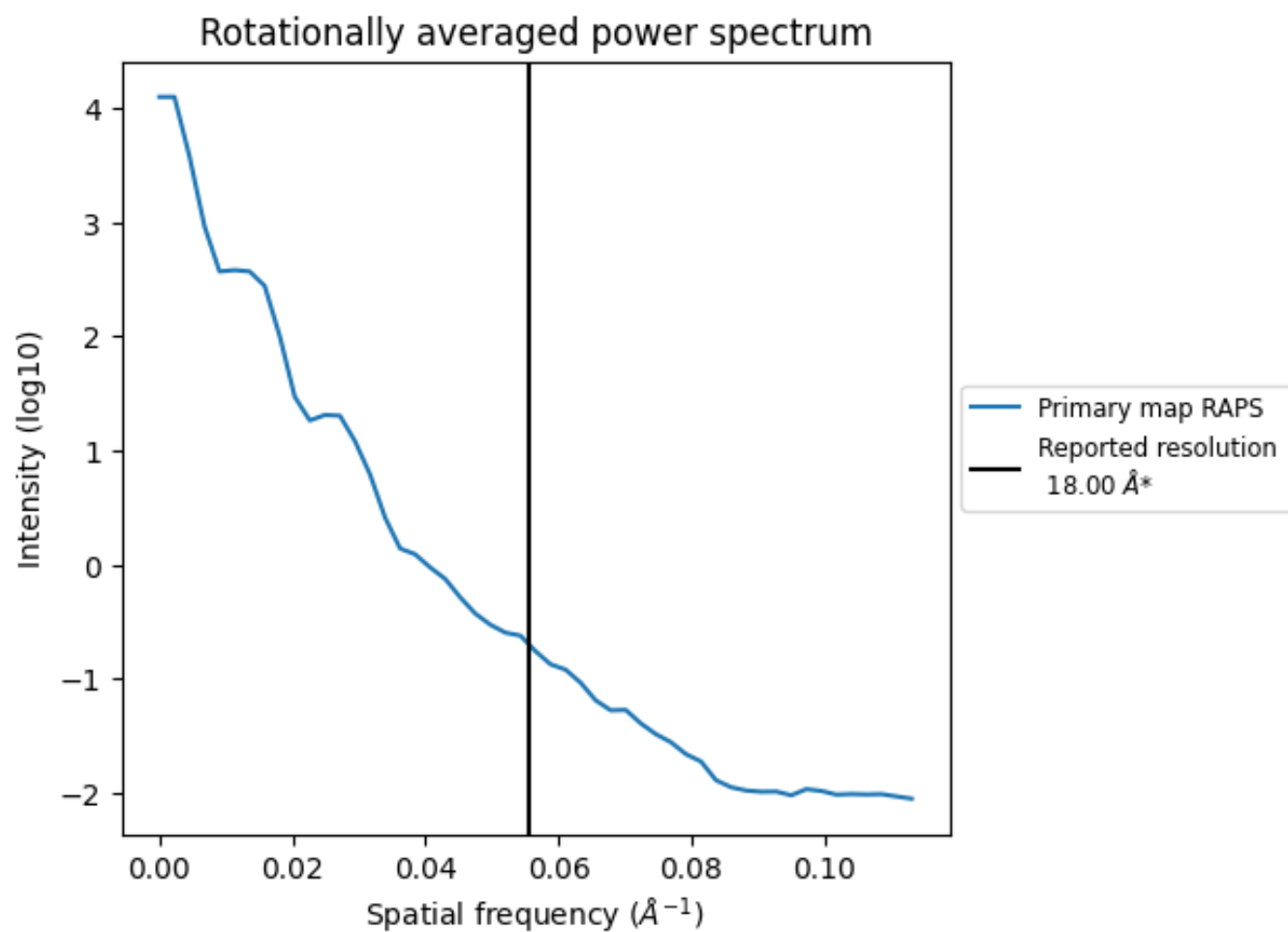
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2597 nm³; this corresponds to an approximate mass of 2346 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.056 Å⁻¹

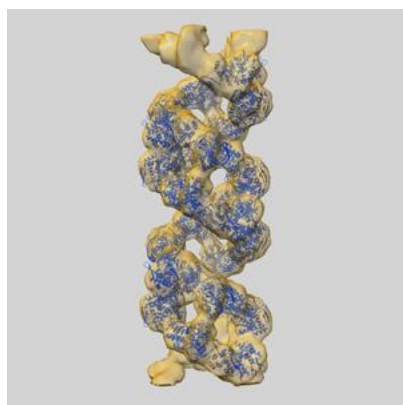
8 Fourier-Shell correlation

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

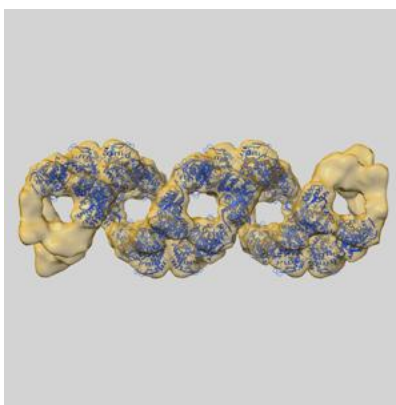
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2205 and PDB model 4BBL. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

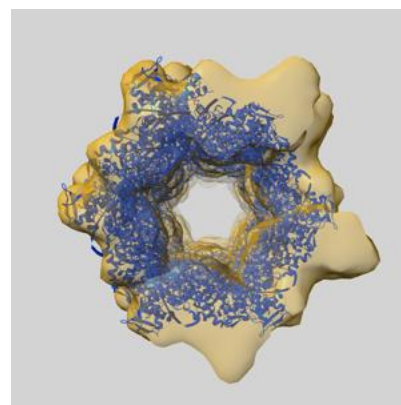
9.1 Map-model overlay [i](#)



X



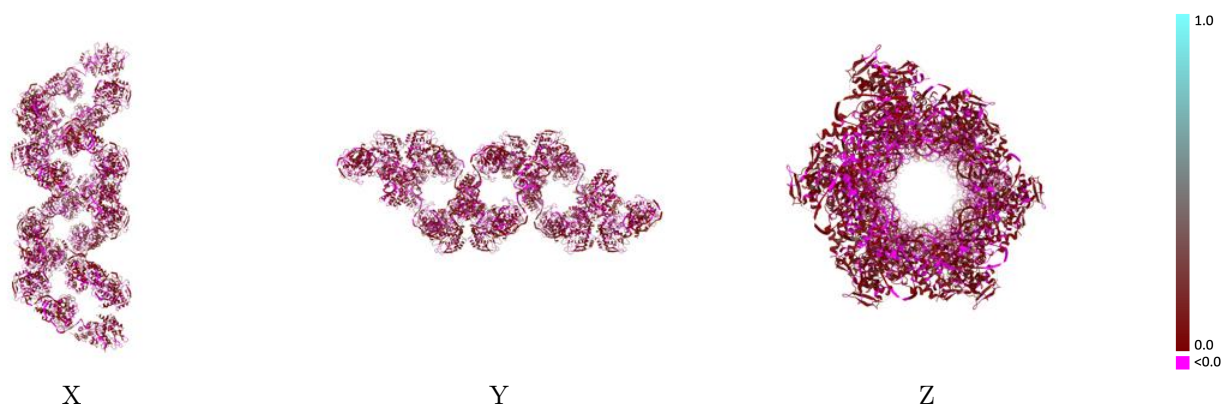
Y



Z

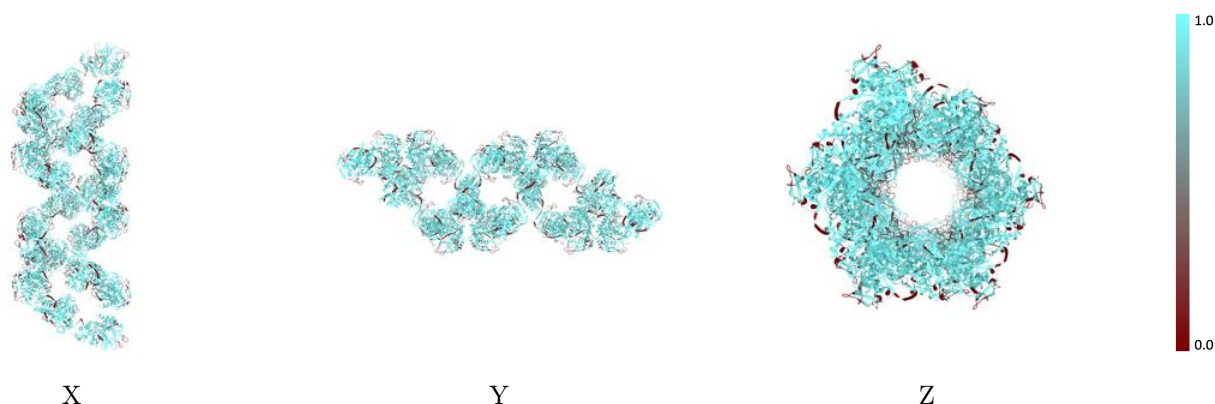
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



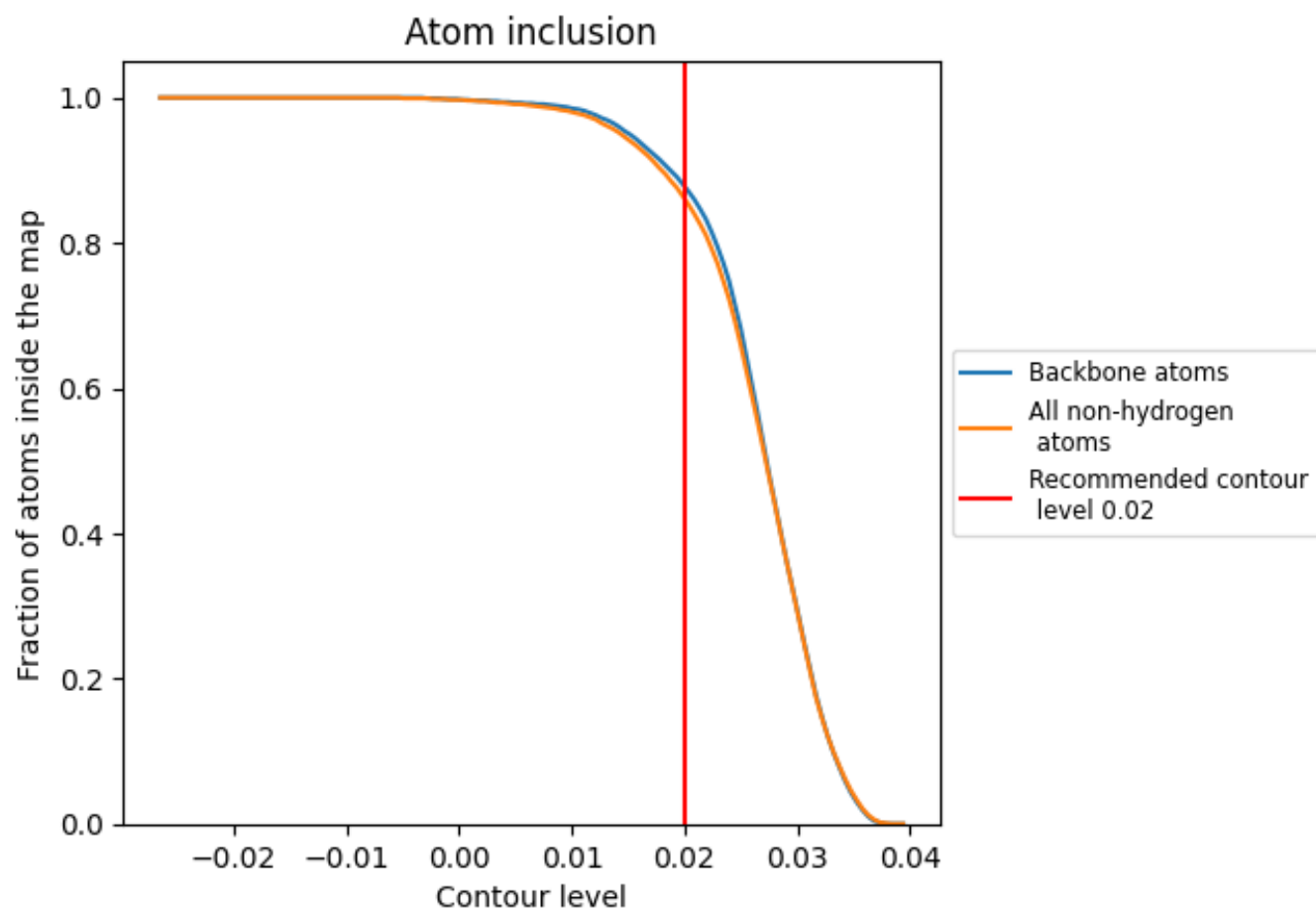
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).























































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8610	 0.0530
A	 0.8690	 0.0560
B	 0.8640	 0.0520
C	 0.8760	 0.0540
D	 0.8580	 0.0550
E	 0.8580	 0.0550
F	 0.8560	 0.0550
G	 0.8490	 0.0520
H	 0.8660	 0.0590
I	 0.8590	 0.0520
J	 0.8720	 0.0550
K	 0.8670	 0.0560
L	 0.8700	 0.0460
M	 0.8740	 0.0580
N	 0.8660	 0.0480
O	 0.8660	 0.0570
P	 0.8550	 0.0530
Q	 0.8520	 0.0550
R	 0.8500	 0.0520
S	 0.8500	 0.0550
T	 0.8620	 0.0510
U	 0.8590	 0.0530
V	 0.8740	 0.0500
W	 0.8570	 0.0580
X	 0.8640	 0.0470
Y	 0.7180	 0.0250
Z	 0.7400	 0.0250

