



## Full wwPDB EM Validation Report ⓘ

May 25, 2024 – 09:26 PM EDT

PDB ID : 7RWL  
EMDB ID : EMD-24718  
Title : Envelope-associated Adeno-associated virus serotype 2  
Authors : Hull, J.A.; Mietzsch, M.; Chipman, P.; Strugatsky, D.; McKenna, R.  
Deposited on : 2021-08-20  
Resolution : 3.14 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.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*

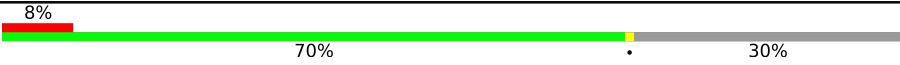


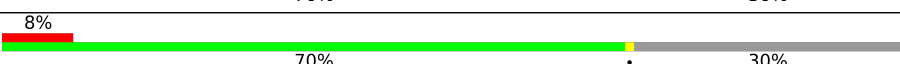


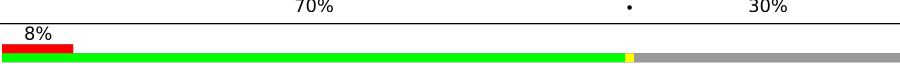


The reported resolution of this entry is 3.14 Å.

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)
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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	1	735	
1	2	735	
1	3	735	
1	4	735	
1	5	735	
1	6	735	
1	7	735	
1	8	735	
1	A	735	

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Mol	Chain	Length	Quality of chain
1	B	735	
1	C	735	
1	D	735	
1	E	735	
1	F	735	
1	G	735	
1	H	735	
1	I	735	
1	J	735	
1	K	735	
1	L	735	
1	M	735	
1	N	735	
1	O	735	
1	P	735	
1	Q	735	
1	R	735	
1	S	735	
1	T	735	
1	U	735	
1	V	735	
1	W	735	
1	X	735	
1	Y	735	
1	Z	735	

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Mol	Chain	Length	Quality of chain
1	a	735	
1	b	735	
1	c	735	
1	d	735	
1	e	735	
1	f	735	
1	g	735	
1	h	735	
1	i	735	
1	j	735	
1	k	735	
1	l	735	
1	m	735	
1	n	735	
1	o	735	
1	p	735	
1	q	735	
1	r	735	
1	s	735	
1	t	735	
1	u	735	
1	v	735	
1	w	735	
1	x	735	
1	y	735	

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Mol	Chain	Length	Quality of chain
1	z	735	<div><div></div><div>8%</div><div>70%</div><div></div><div>30%</div></div>

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 248580 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 Capsid protein VP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	B	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	C	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	D	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	E	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	F	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	G	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	H	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	I	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	J	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	K	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	L	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	M	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	N	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	O	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	P	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	Q	517	Total 4143	C 2607	N 723	O 800	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	S	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	T	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	U	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	V	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	W	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	X	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	Y	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	Z	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	a	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	b	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	c	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	d	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	e	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	f	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	g	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	h	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	i	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	j	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	k	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	l	517	Total 4143	C 2607	N 723	O 800	S 13	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	n	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	o	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	p	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	q	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	r	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	s	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	t	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	u	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	v	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	w	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	x	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	y	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	z	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	1	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	2	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	3	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	4	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	5	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
1	6	517	Total 4143	C 2607	N 723	O 800	S 13	0	0
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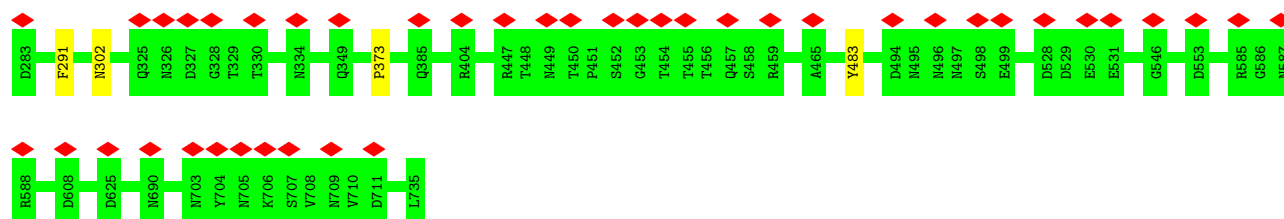
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	8	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		





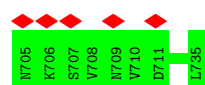
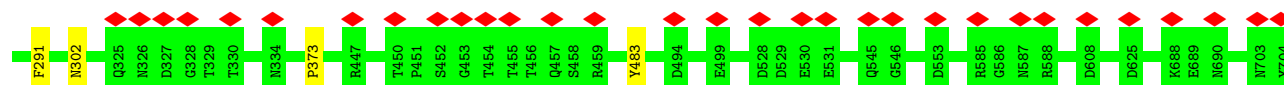
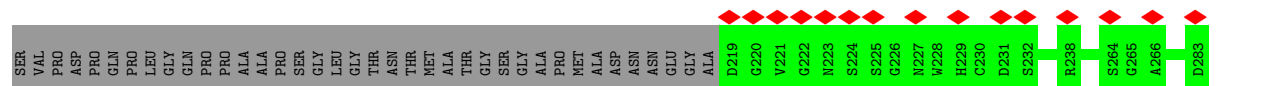
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LYS GLY PRO VAL ASN GLU ALA ASP TRP LEU HIS ASP LEU TYR ILE ARG GLN TRP LYS LEU LYS PRO GLY ASN HIS PRO TYR PRO LEU PRO LYS TYR ASN HIS ALA GLU ARG HIS LYS ASP PHE GLN ARG LEU LYS VAL PRO ARG LYS ARG LEU ASN PHE GLY ASP

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



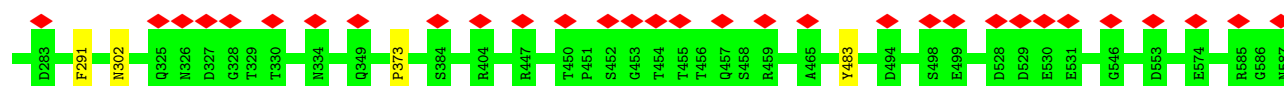
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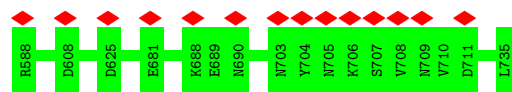


MET ALA ASP GLY TYR LEU PRO ASP TRP LEU ALA GLU THR ASP THR LEU HIS ASP LEU TYR ILE ARG GLN TRP LYS LEU LYS PRO GLY ASN HIS PRO TYR PRO LEU PRO LYS TYR ASN HIS ALA GLU ARG HIS LYS ASP PHE GLN ARG LEU LYS VAL PRO ARG LYS ARG LEU ASN PHE GLY ASP

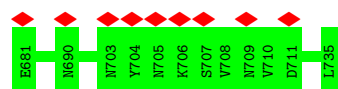
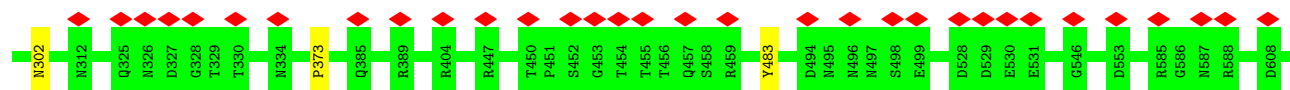
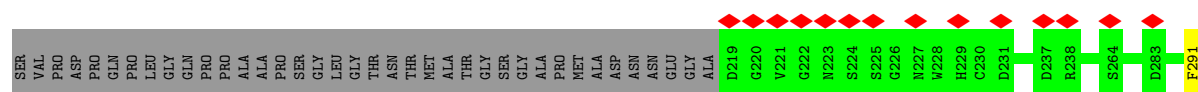
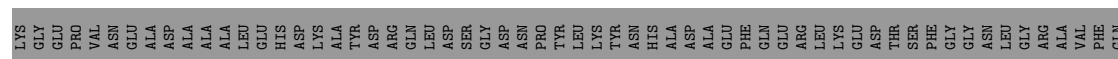
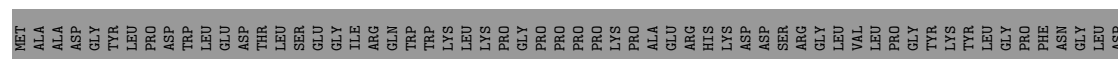
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ALA LYS LYS ARG VAL LEU PRO LEU ASP TRP LEU ALA GLU THR ASP THR LEU HIS ASP LEU TYR ILE ARG GLN TRP LYS LEU LYS PRO GLY ASN HIS PRO TYR PRO LEU PRO LYS TYR ASN HIS ALA GLU ARG HIS LYS ASP PHE GLN ARG LEU LYS VAL PRO ARG LYS ARG LEU ASN PHE GLY ASP

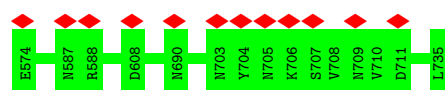
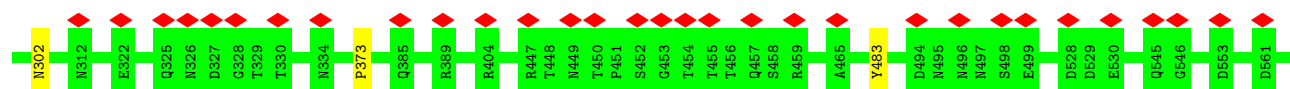
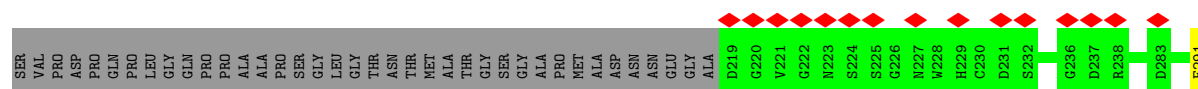
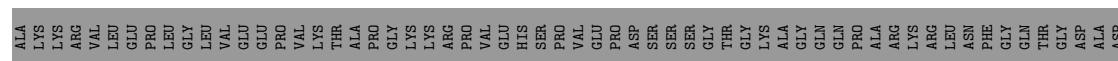
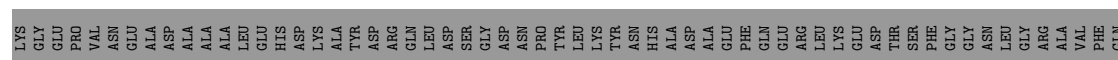
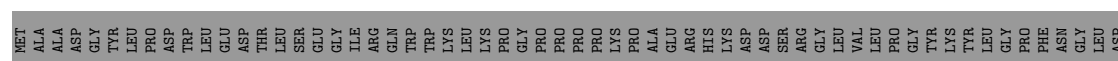




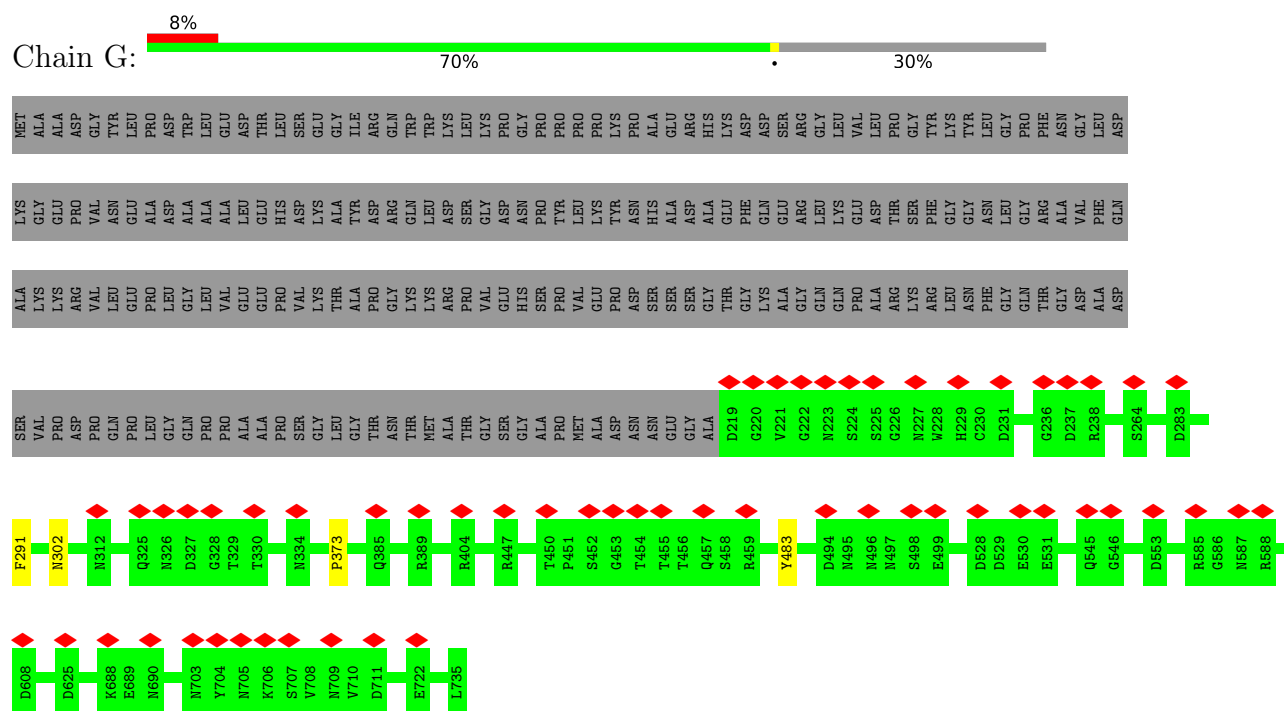
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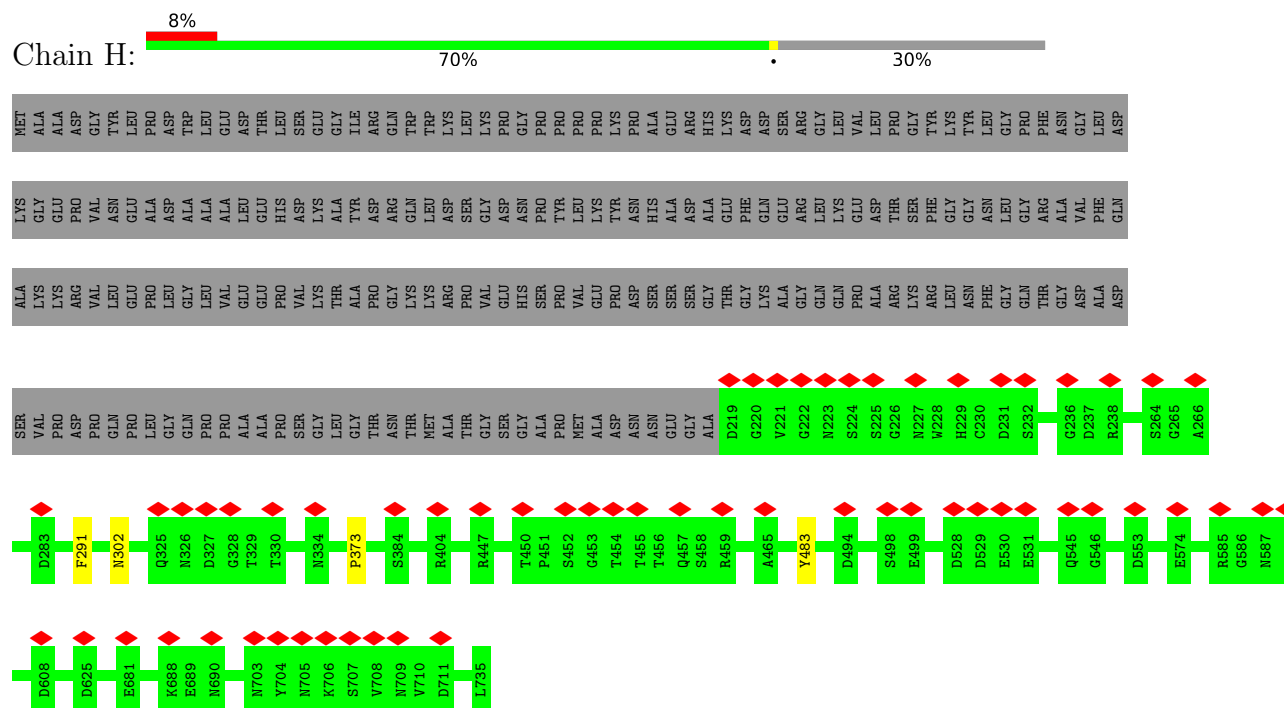
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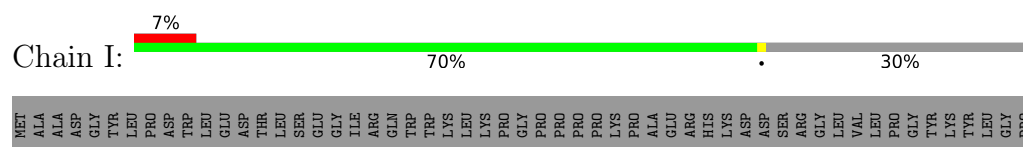
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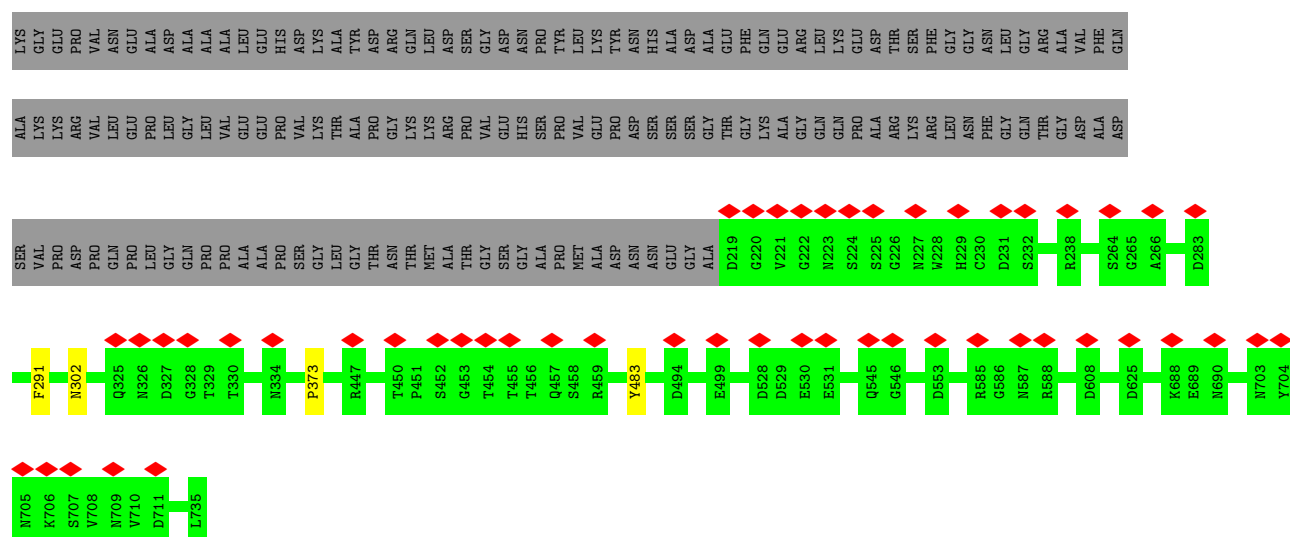


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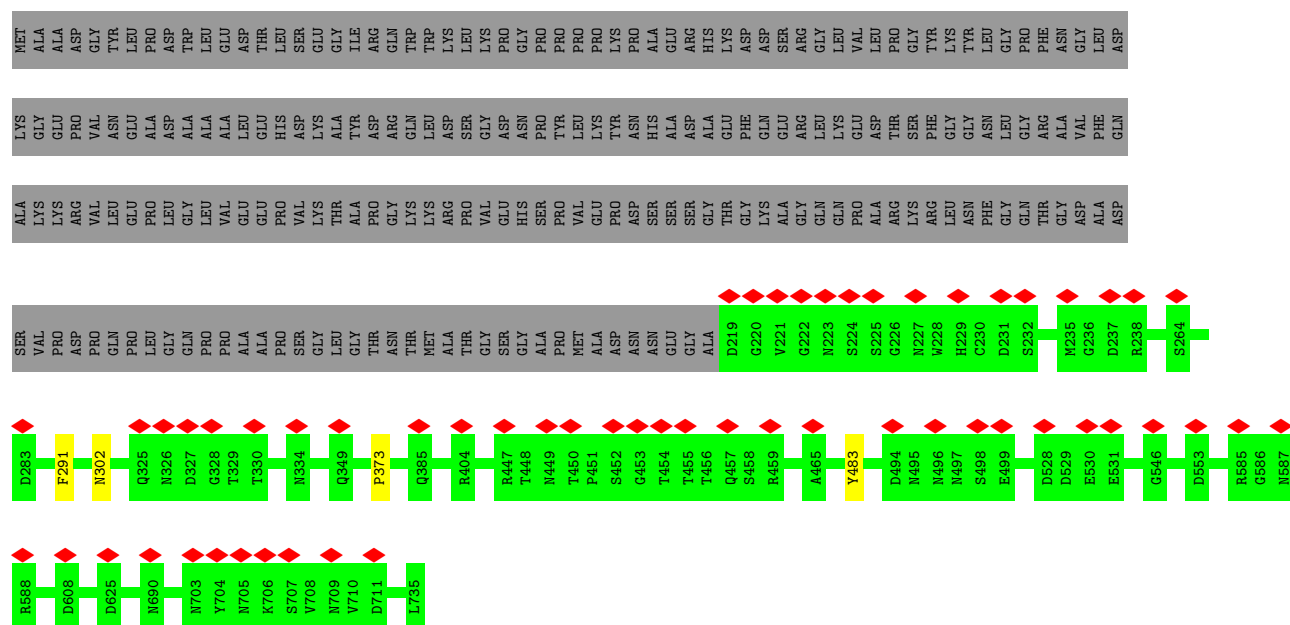


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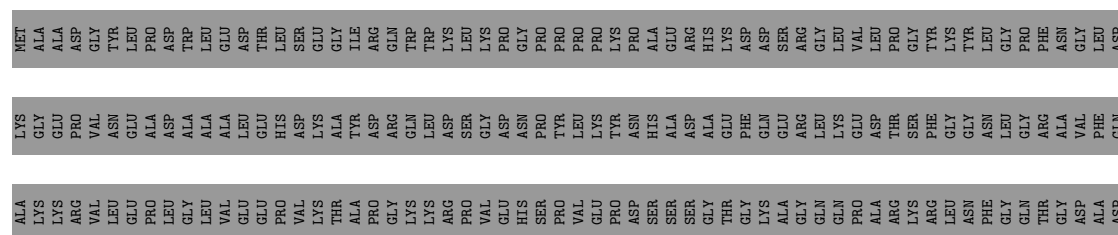


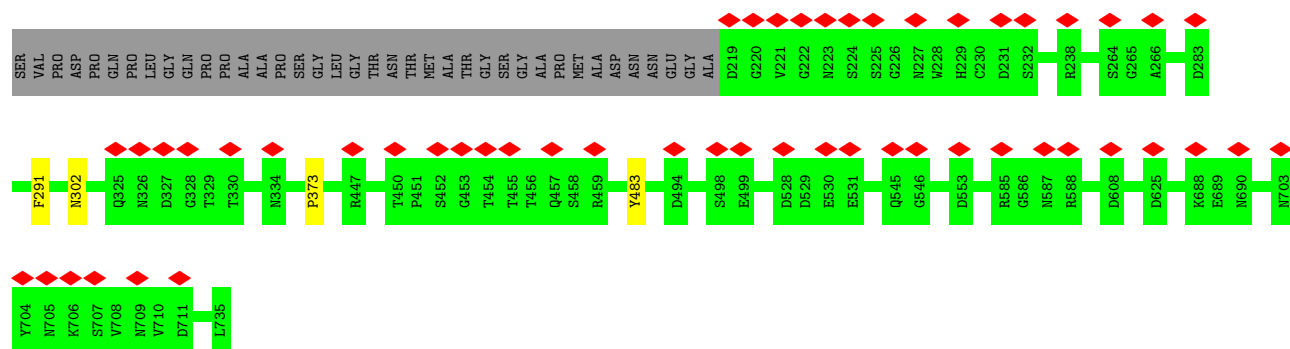


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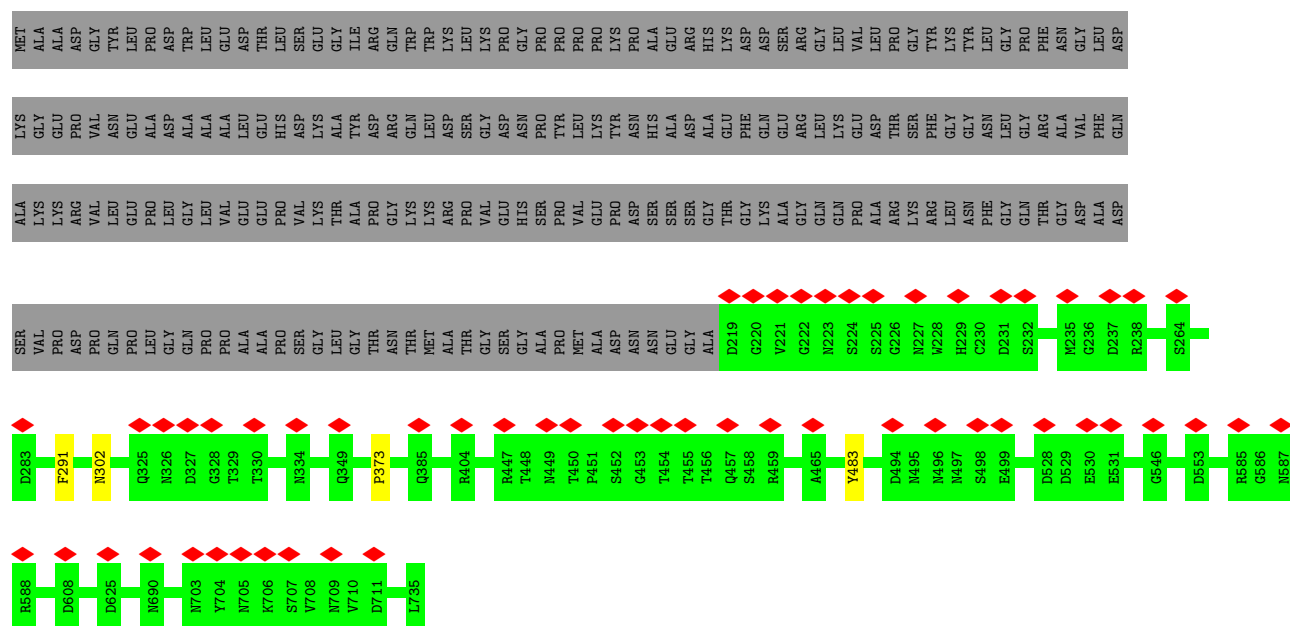


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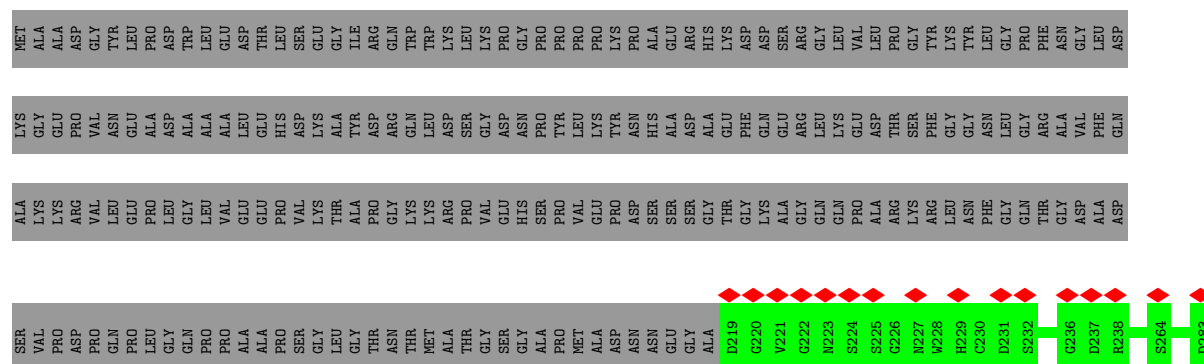


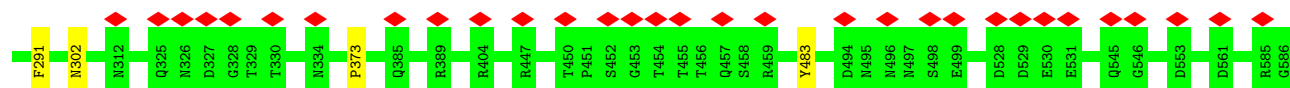


- Molecule 1: Capsid protein VP1



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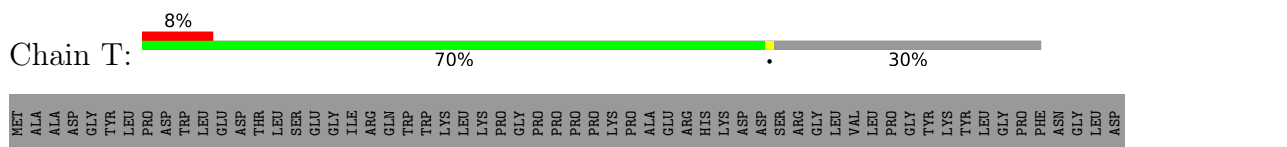




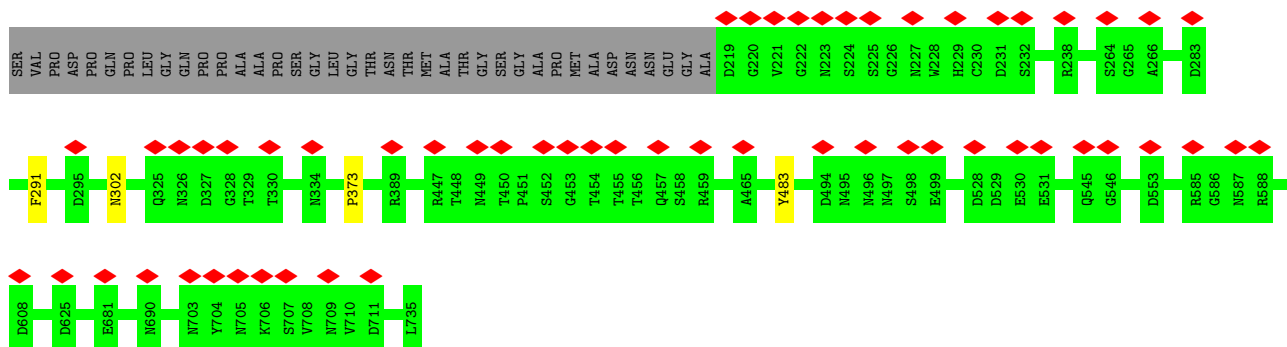


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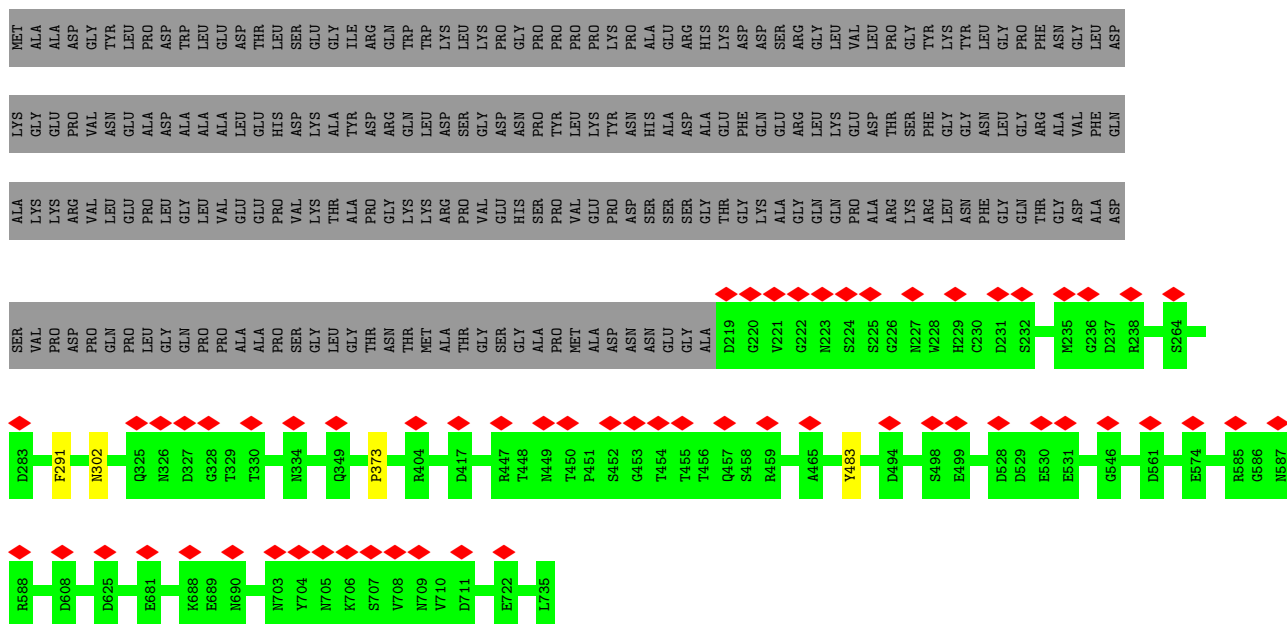
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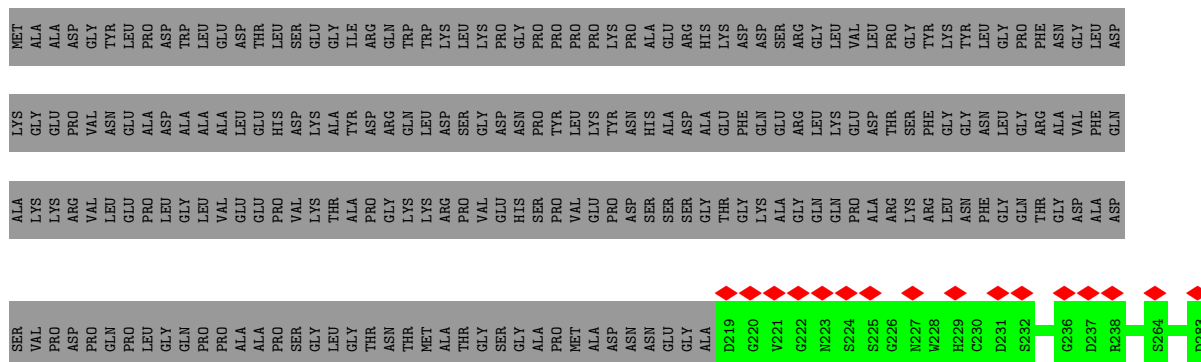


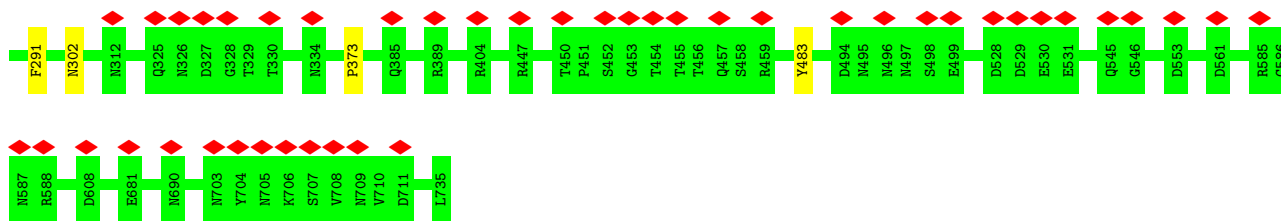


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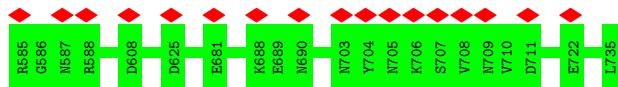
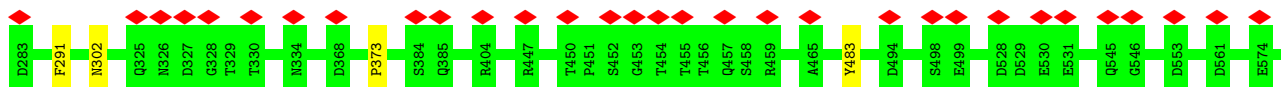
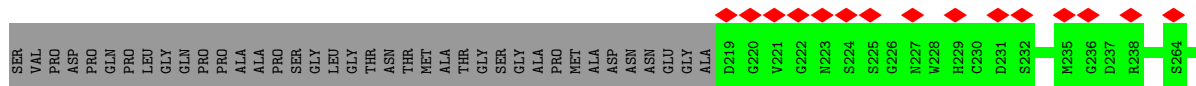
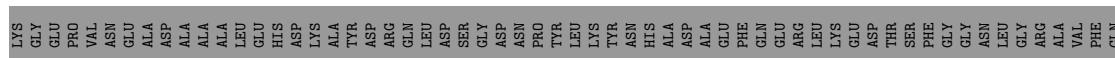


- Molecule 1: Capsid protein VP1

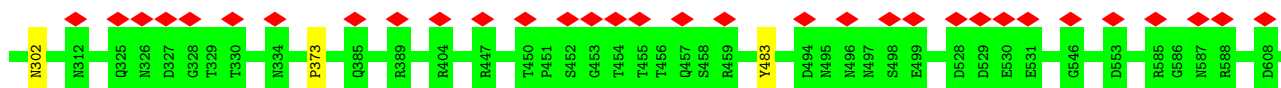
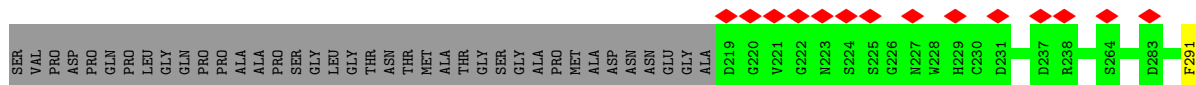
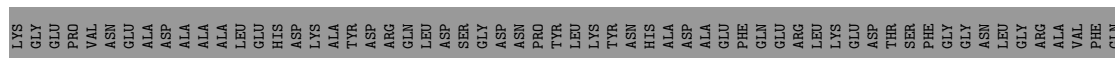
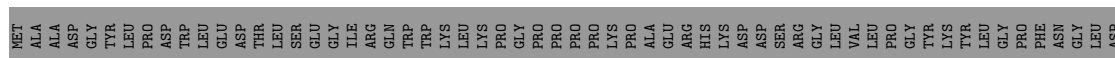




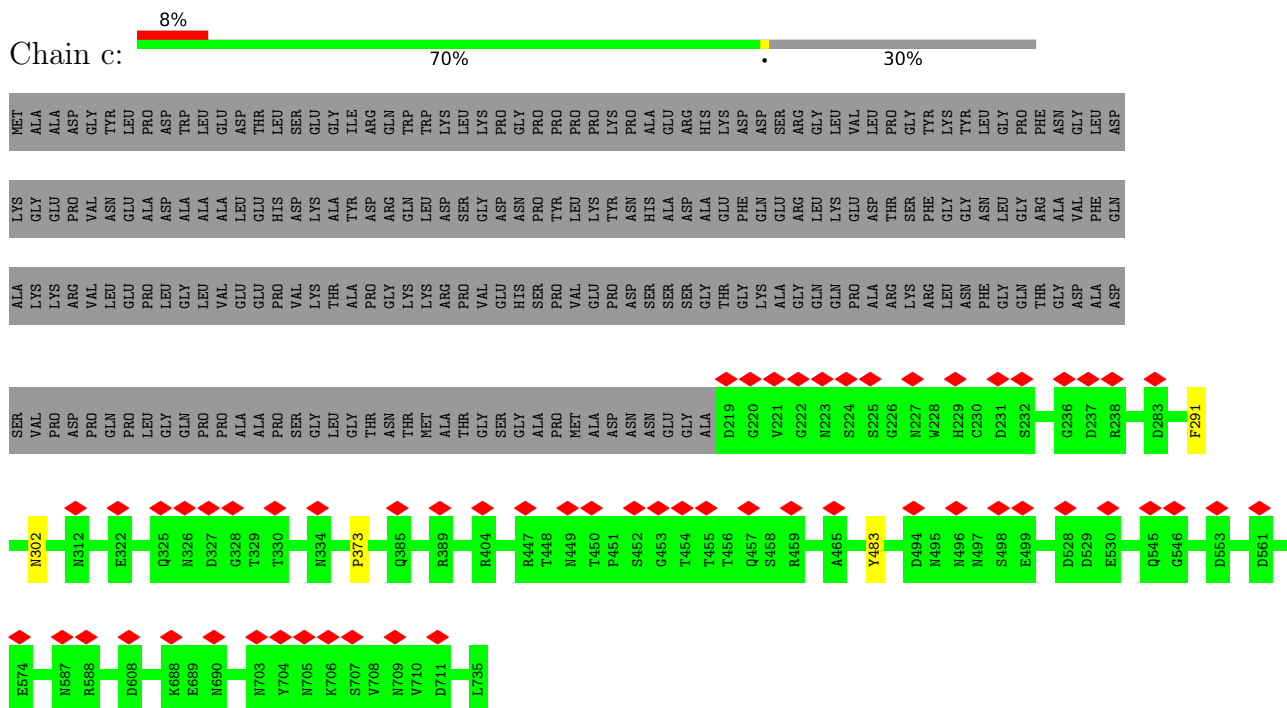
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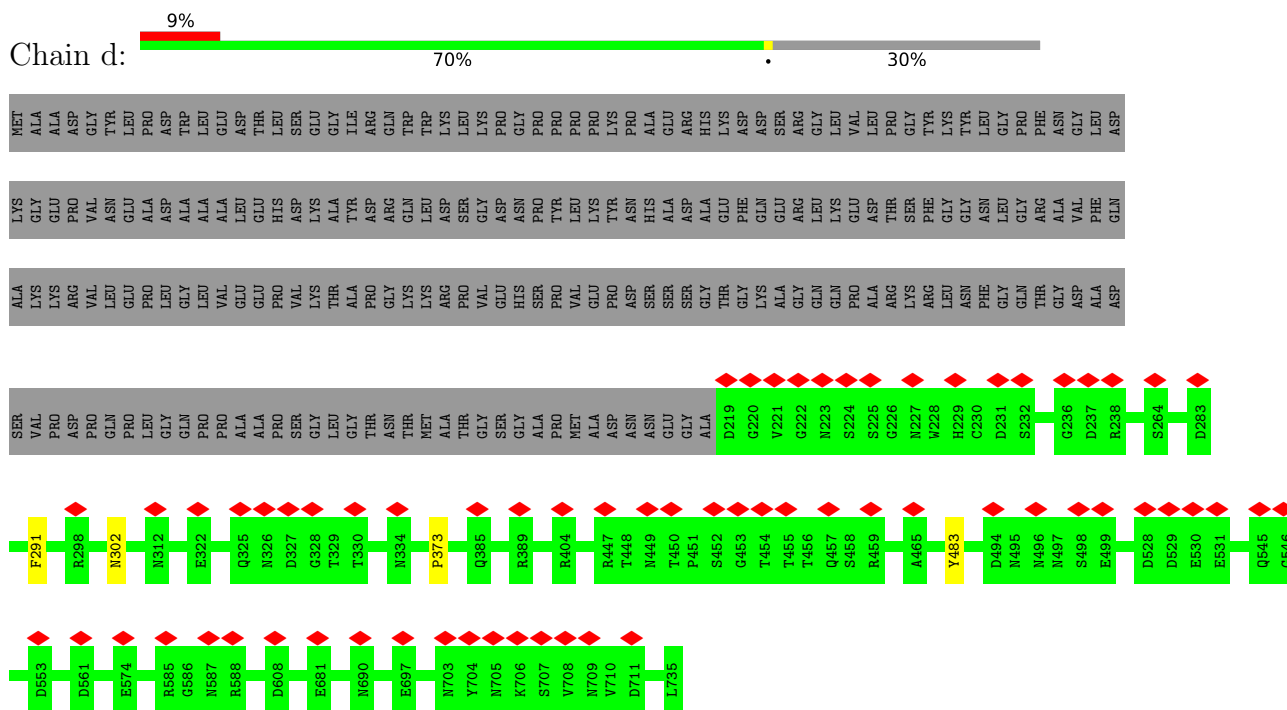
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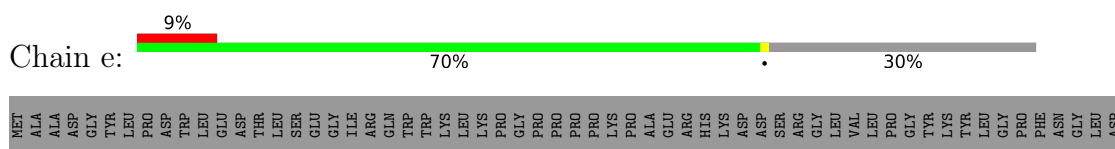




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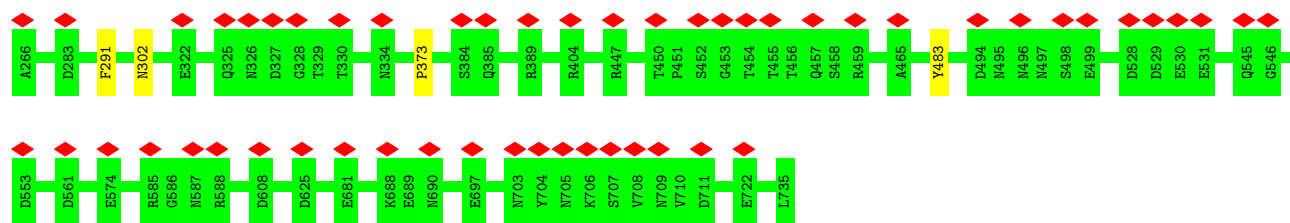
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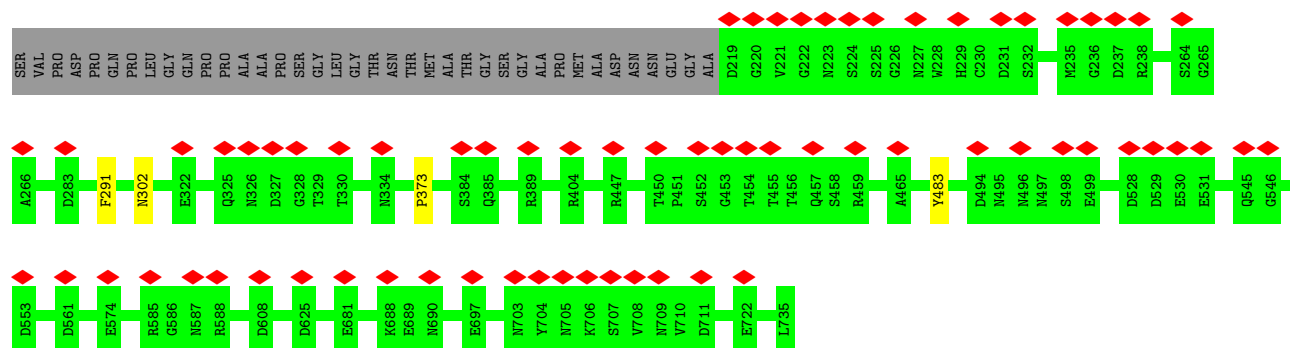
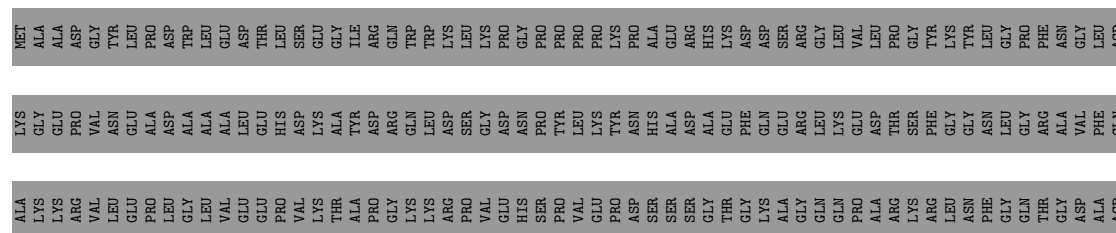




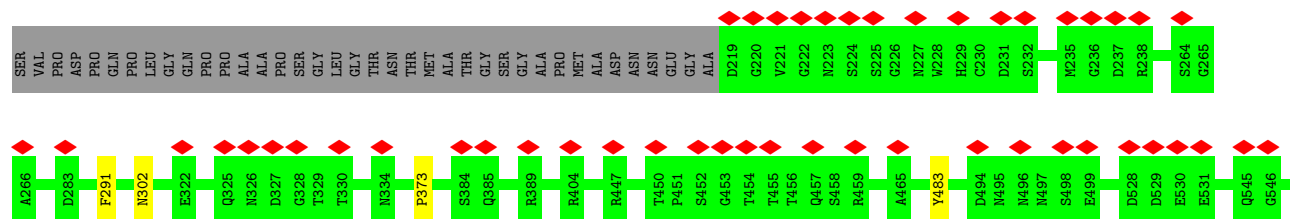
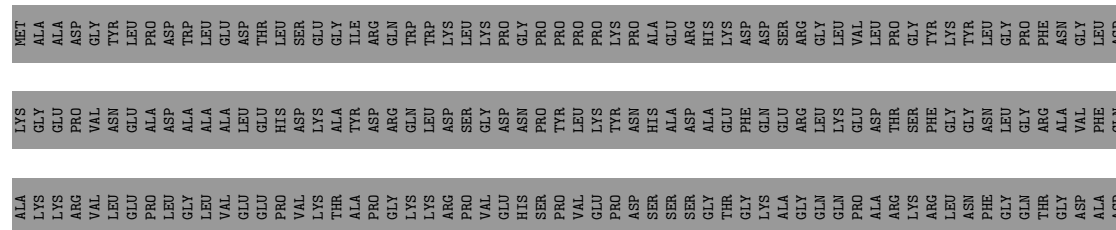




• Molecule 1: Capsid protein VP1



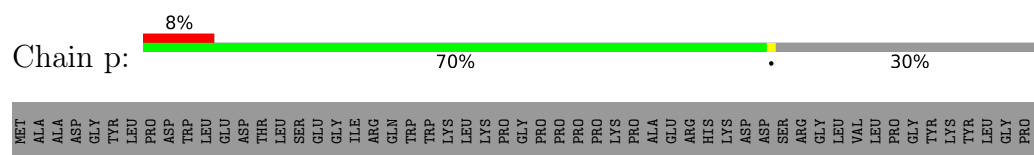
• Molecule 1: Capsid protein VP1

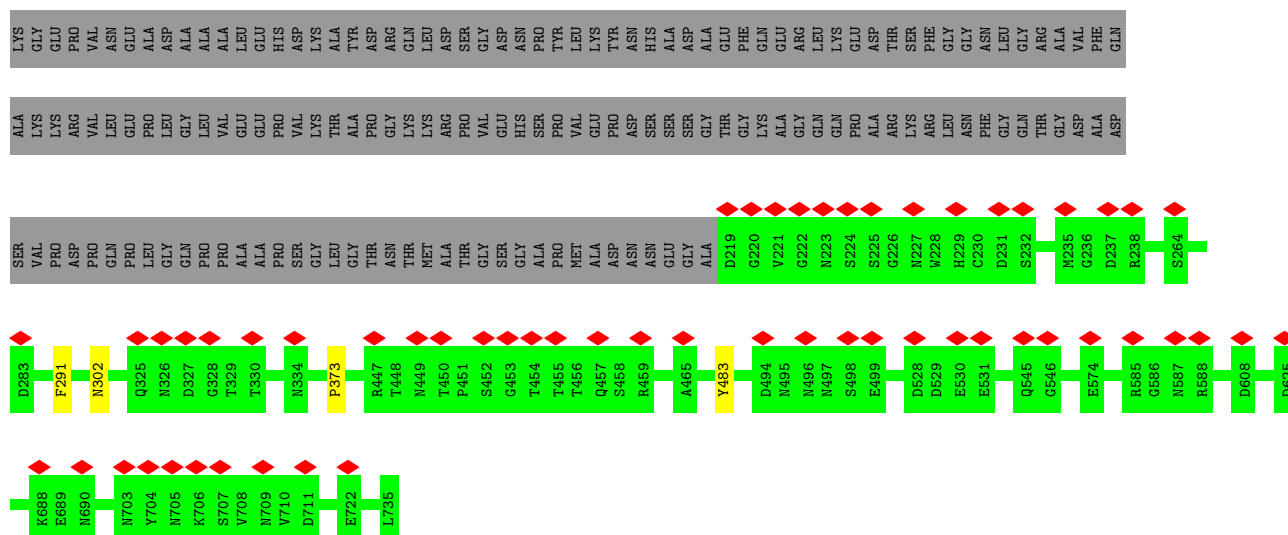




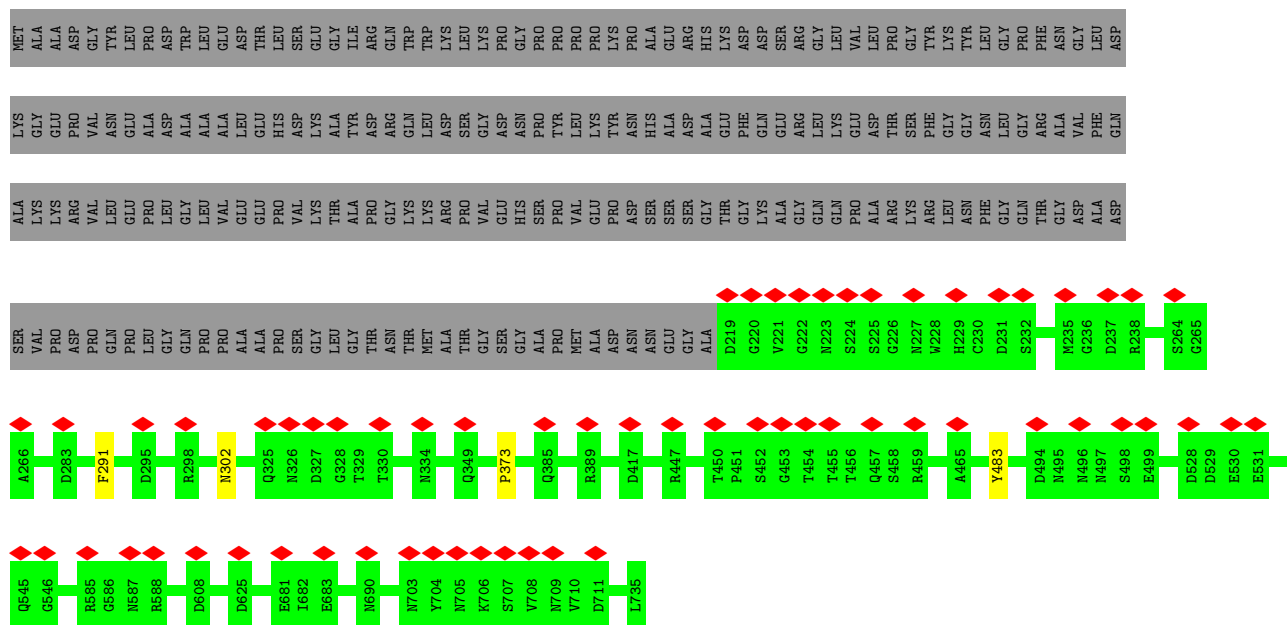
- Molecule 1: Capsid protein VP1

- Molecule 1: Capsid protein VP1

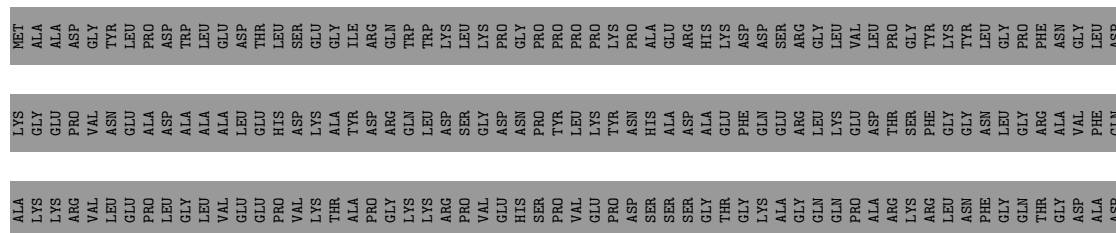


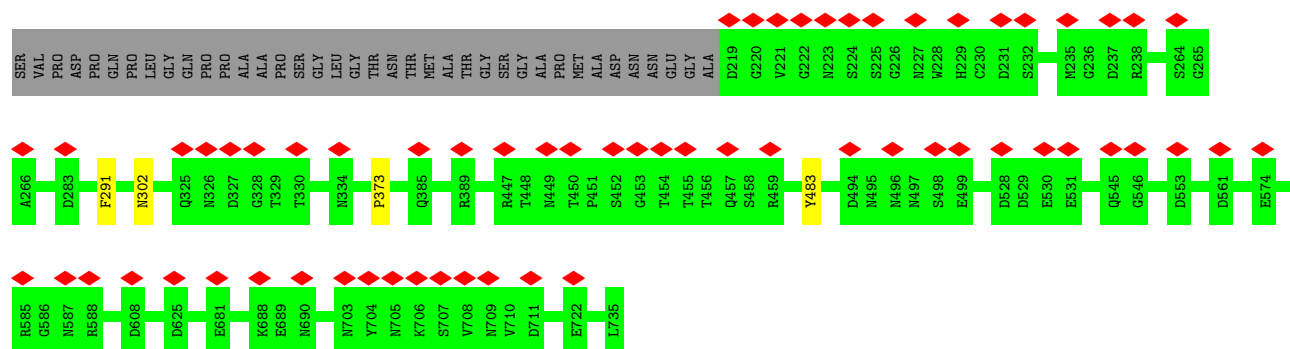


• Molecule 1: Capsid protein VP1

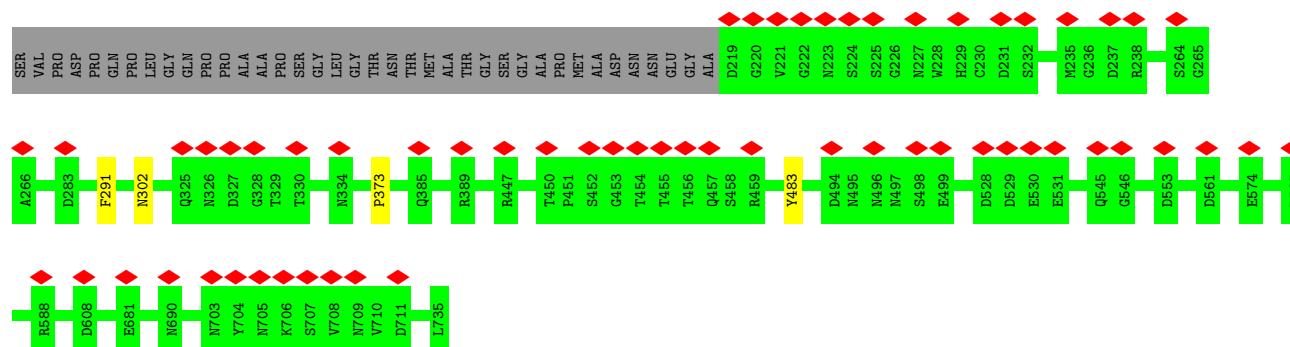
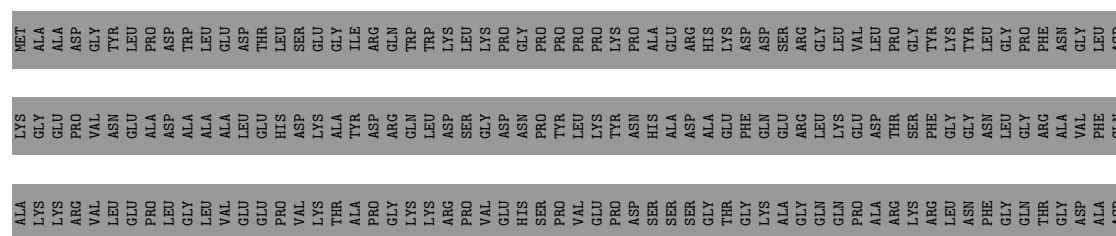


• Molecule 1: Capsid protein VP1

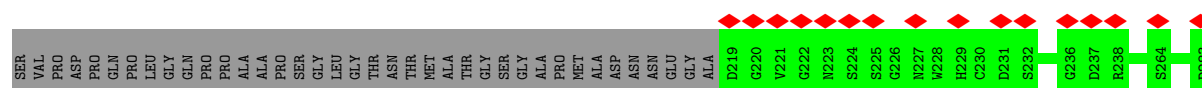
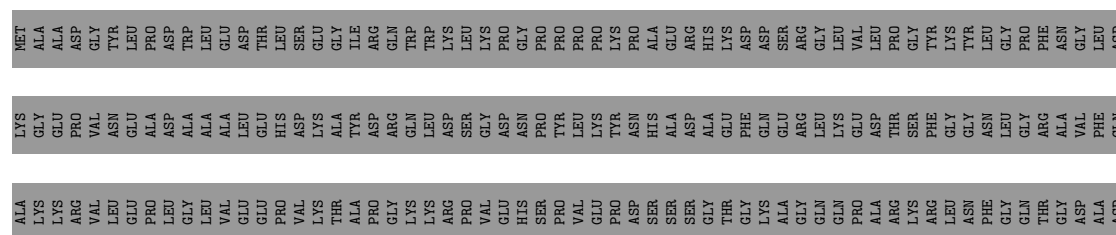




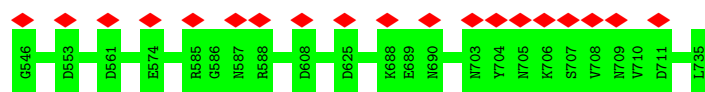
• Molecule 1: Capsid protein VP1



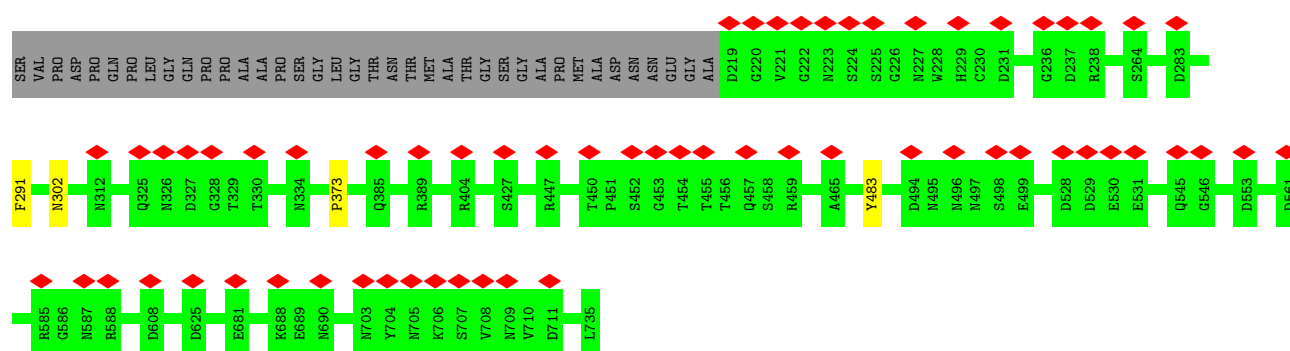
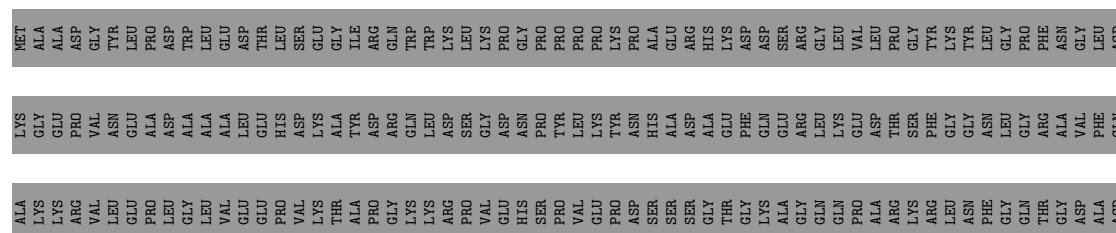
• Molecule 1: Capsid protein VP1



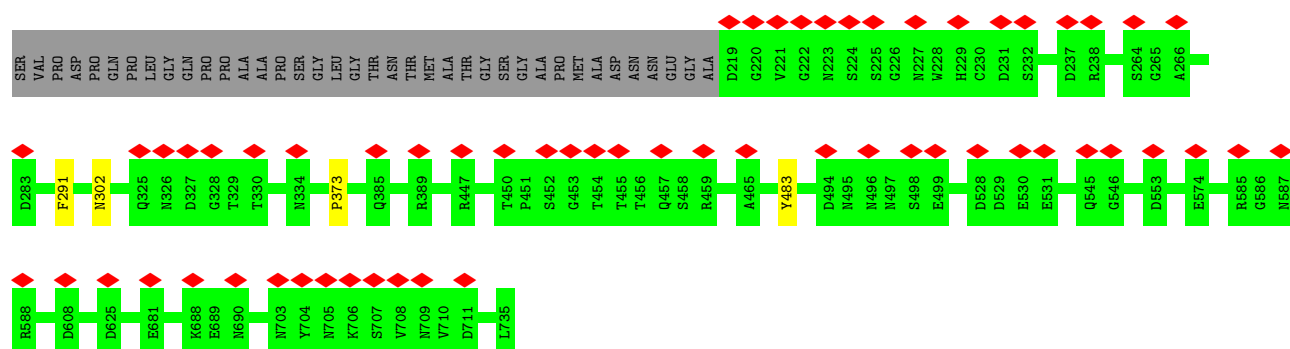
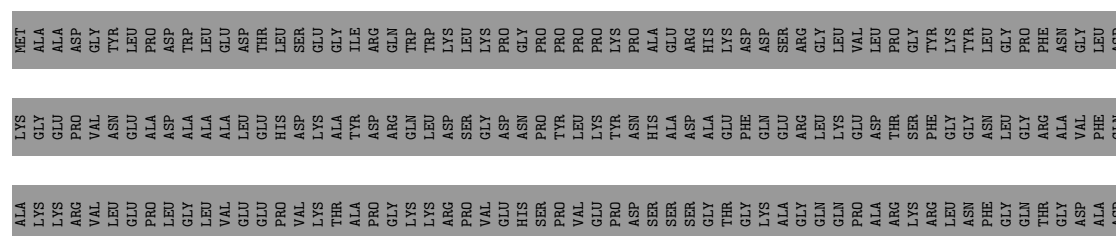




• Molecule 1: Capsid protein VP1

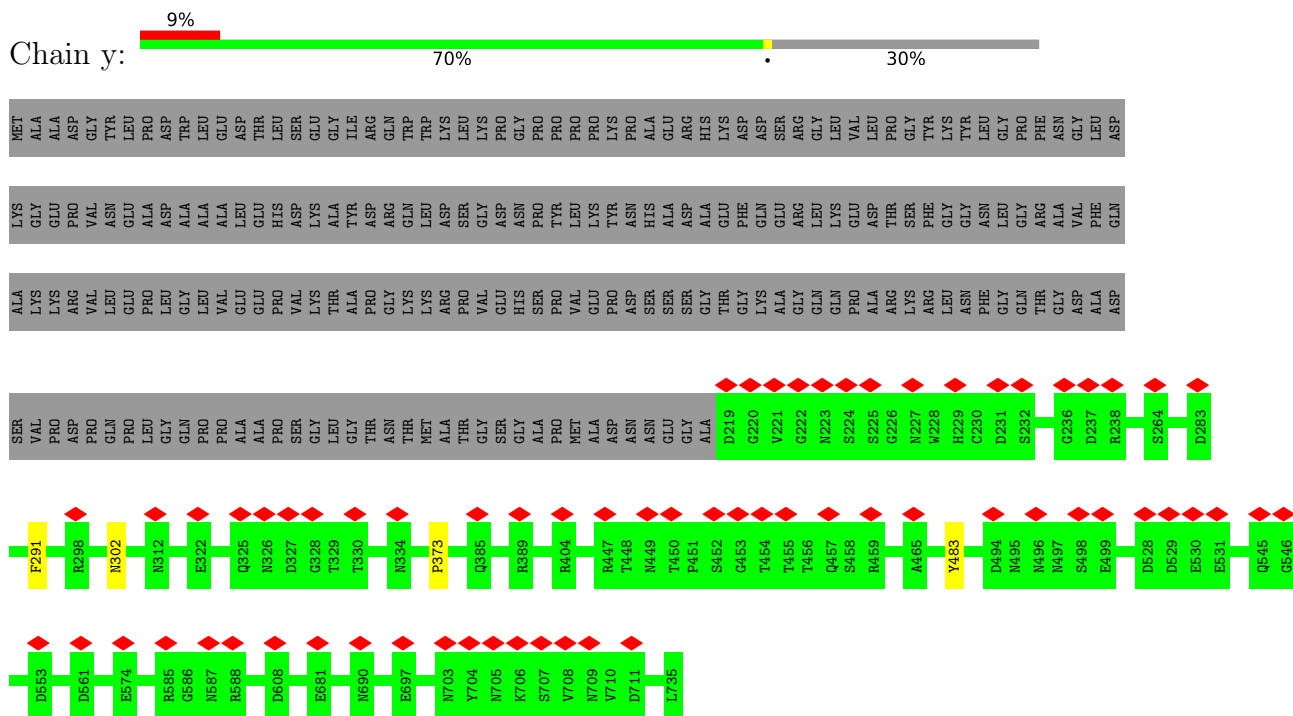


• Molecule 1: Capsid protein VP1

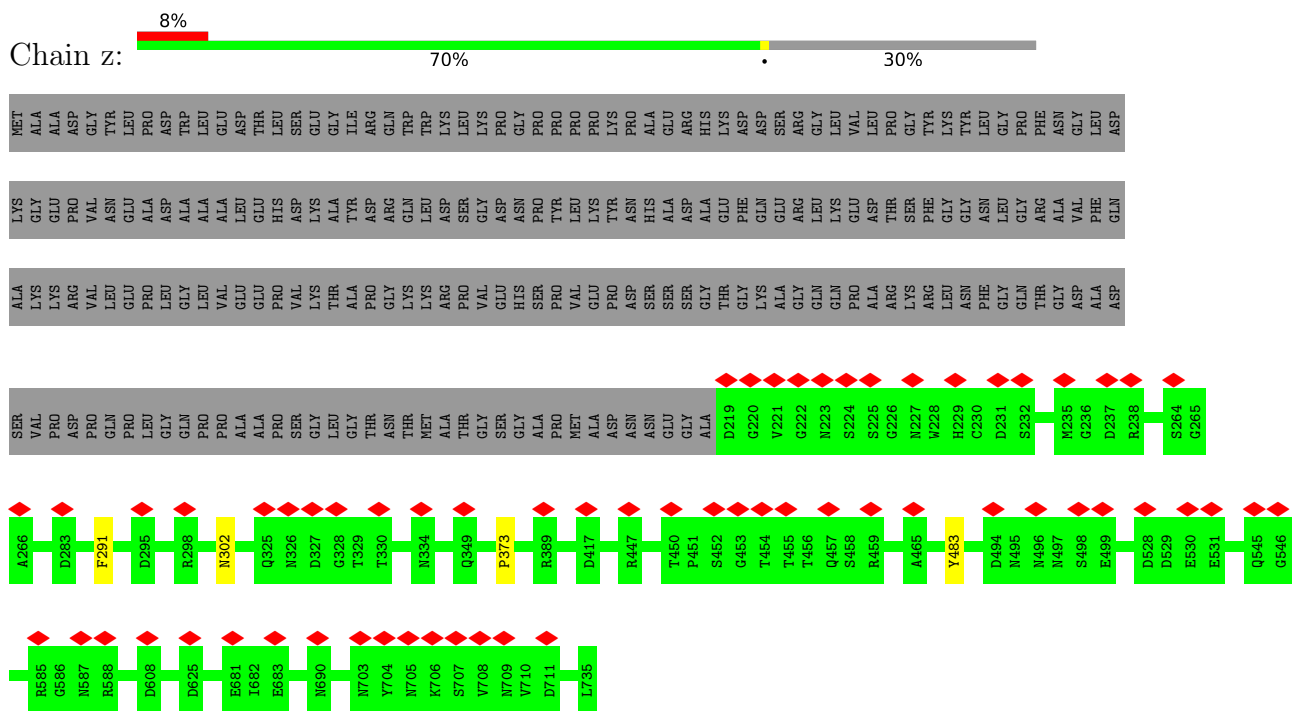


• Molecule 1: Capsid protein VP1

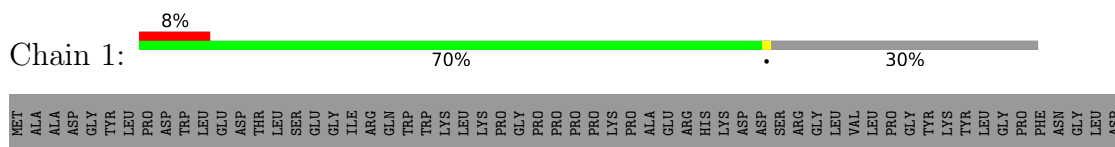




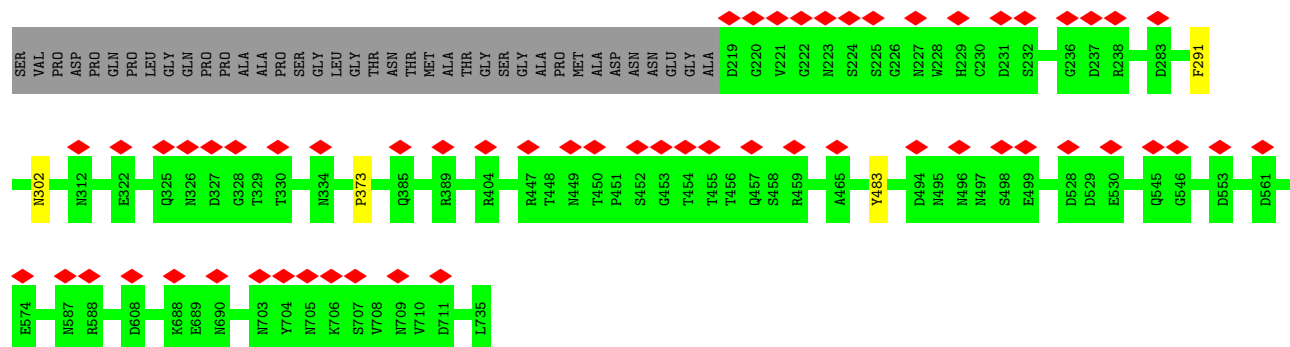
- Molecule 1: Capsid protein VP1



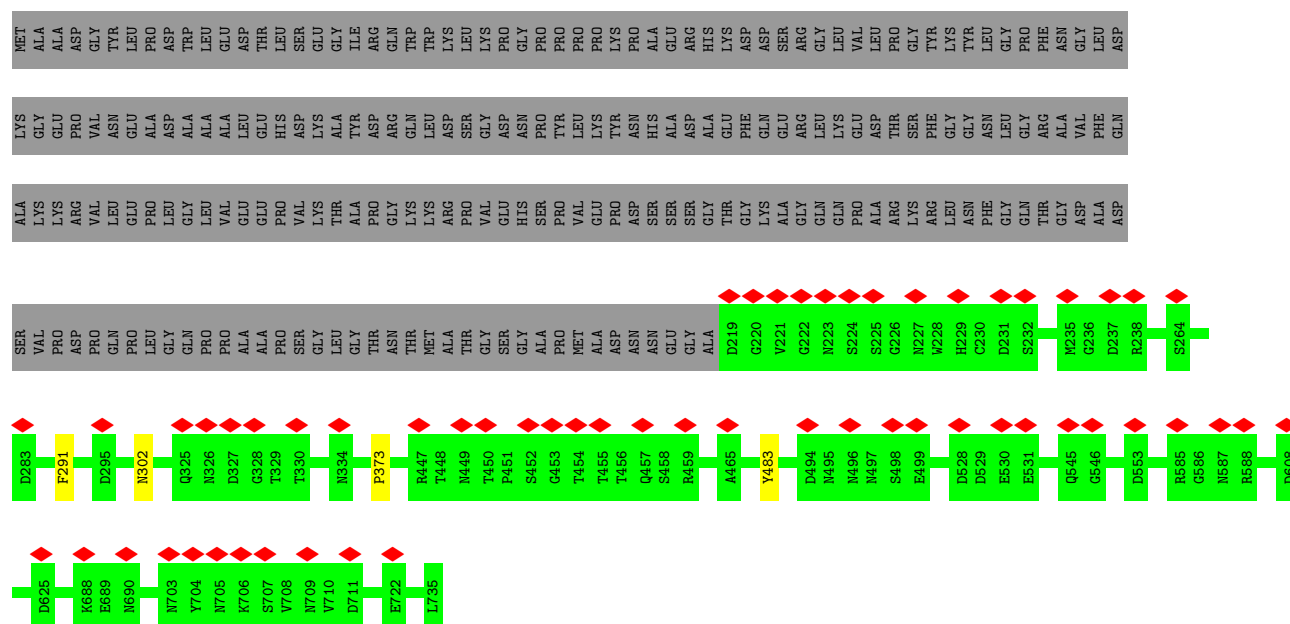
- Molecule 1: Capsid protein VP1



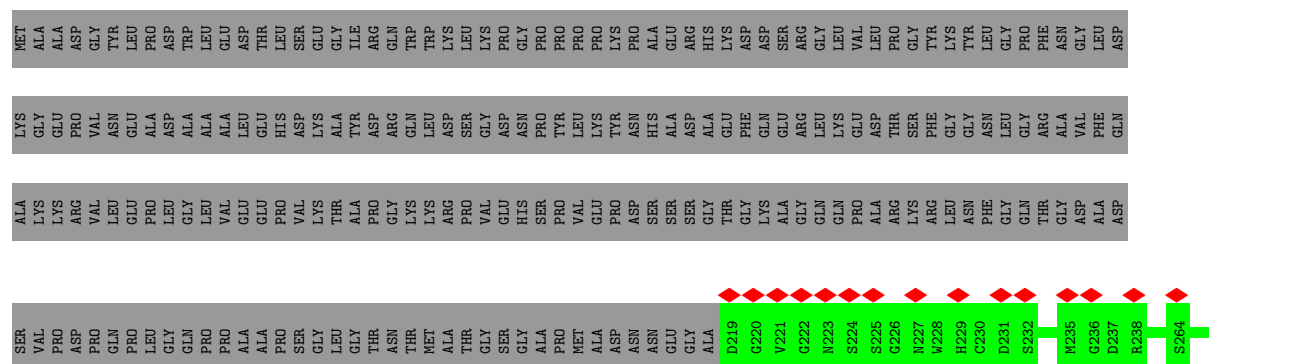


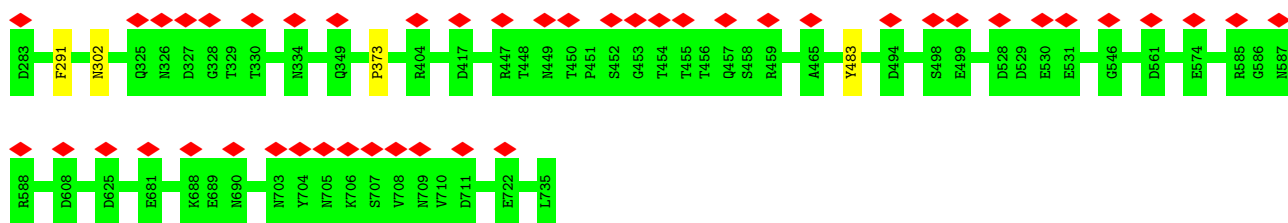


• Molecule 1: Capsid protein VP1

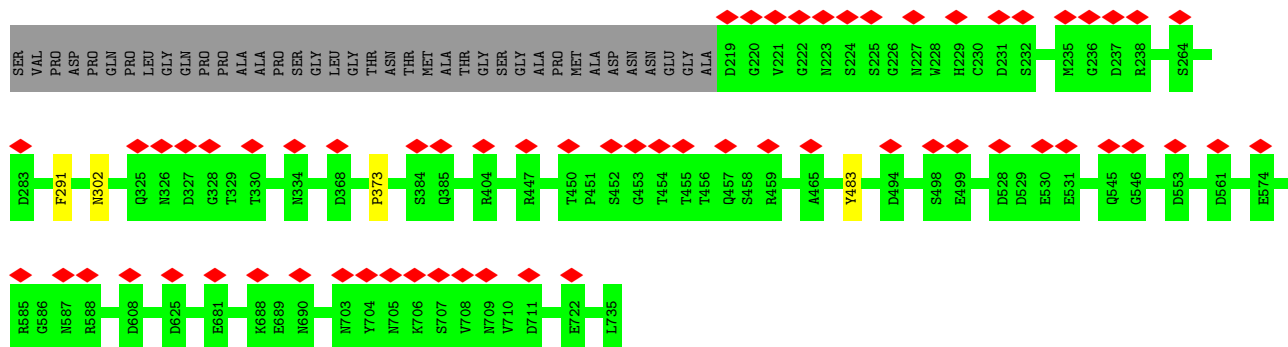
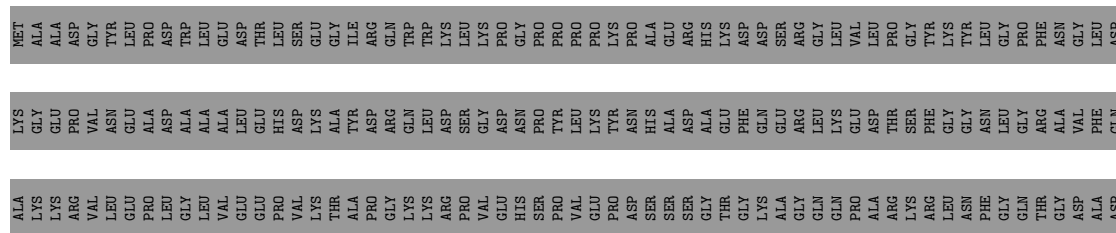


• Molecule 1: Capsid protein VP1

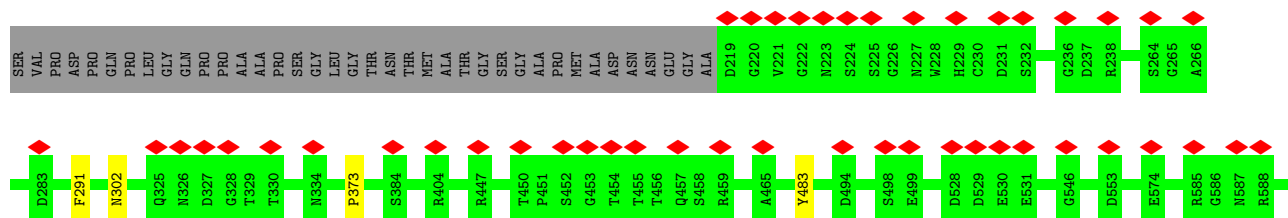
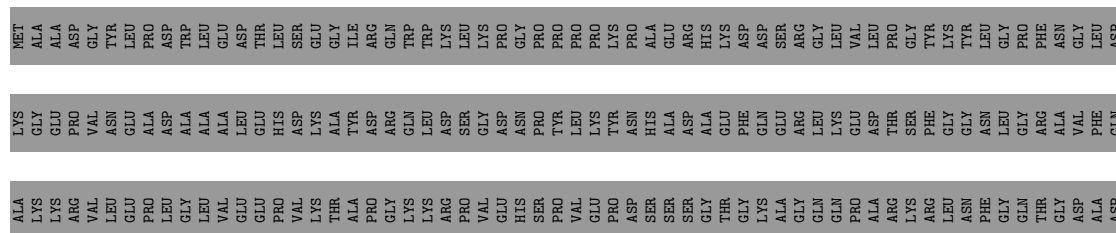


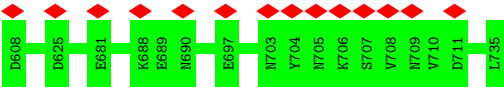


• Molecule 1: Capsid protein VP1

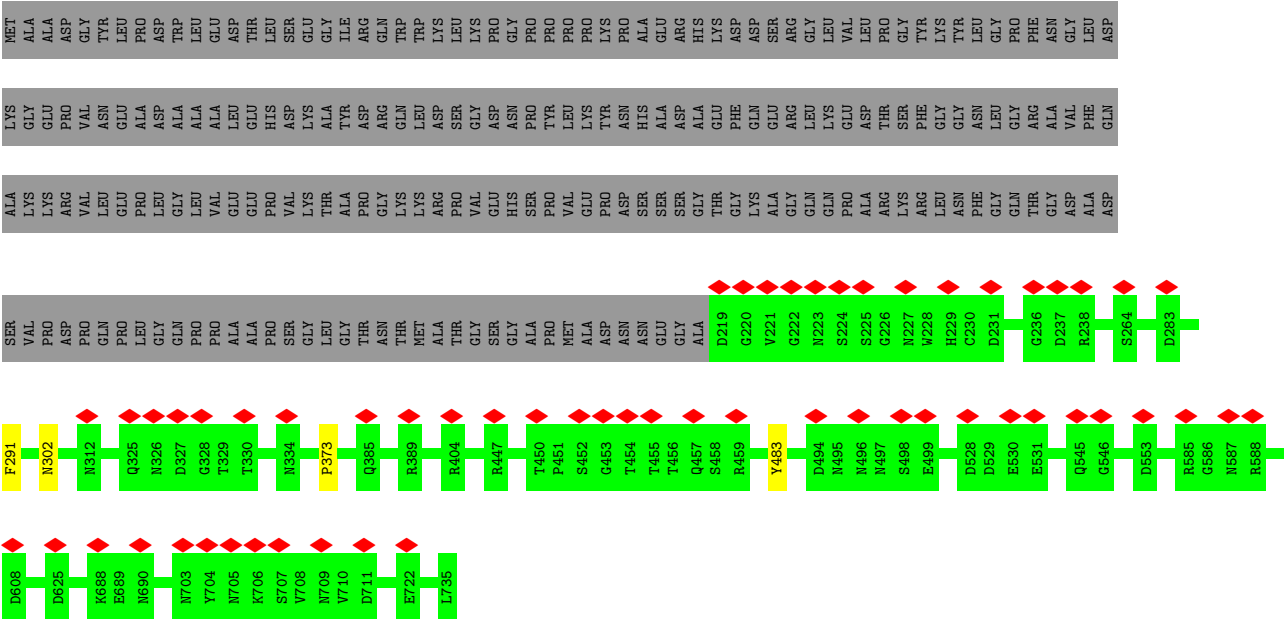


• Molecule 1: Capsid protein VP1





• Molecule 1: Capsid protein VP1



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	291	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	34	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	30.997	Depositor
Minimum map value	-13.154	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	5.0	Depositor
Map size (Å)	821.76, 821.76, 821.76	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.07, 1.07, 1.07	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	1	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	2	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	3	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	4	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	5	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	6	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	7	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	8	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	A	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	B	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	C	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	D	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	E	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	F	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	G	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	H	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	I	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	J	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	K	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	L	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	M	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	N	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	O	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	P	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	Q	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	R	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	S	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	T	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	U	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	V	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	W	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	X	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	Y	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	Z	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	a	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	b	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	c	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	d	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	e	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	f	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	g	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	h	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	i	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	j	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	k	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	l	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	m	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	n	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	o	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	p	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	q	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	r	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	s	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	t	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	u	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	v	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	w	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	x	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	y	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	z	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
All	All	0.55	120/255960 (0.0%)	0.67	120/348900 (0.0%)

All (120) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	291	PHE	C-N	-5.45	1.21	1.34
1	H	291	PHE	C-N	-5.45	1.21	1.34
1	N	291	PHE	C-N	-5.45	1.21	1.34
1	P	291	PHE	C-N	-5.45	1.21	1.34
1	W	291	PHE	C-N	-5.45	1.21	1.34
1	Y	291	PHE	C-N	-5.45	1.21	1.34
1	i	291	PHE	C-N	-5.45	1.21	1.34
1	j	291	PHE	C-N	-5.45	1.21	1.34
1	k	291	PHE	C-N	-5.45	1.21	1.34
1	5	291	PHE	C-N	-5.45	1.21	1.34
1	6	291	PHE	C-N	-5.45	1.21	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	7	291	PHE	C-N	-5.45	1.21	1.34
1	B	291	PHE	C-N	-5.45	1.21	1.34
1	E	291	PHE	C-N	-5.45	1.21	1.34
1	G	291	PHE	C-N	-5.45	1.21	1.34
1	J	291	PHE	C-N	-5.45	1.21	1.34
1	L	291	PHE	C-N	-5.45	1.21	1.34
1	M	291	PHE	C-N	-5.45	1.21	1.34
1	O	291	PHE	C-N	-5.45	1.21	1.34
1	R	291	PHE	C-N	-5.45	1.21	1.34
1	S	291	PHE	C-N	-5.45	1.21	1.34
1	U	291	PHE	C-N	-5.45	1.21	1.34
1	X	291	PHE	C-N	-5.45	1.21	1.34
1	Z	291	PHE	C-N	-5.45	1.21	1.34
1	h	291	PHE	C-N	-5.45	1.21	1.34
1	l	291	PHE	C-N	-5.45	1.21	1.34
1	o	291	PHE	C-N	-5.45	1.21	1.34
1	q	291	PHE	C-N	-5.45	1.21	1.34
1	r	291	PHE	C-N	-5.45	1.21	1.34
1	s	291	PHE	C-N	-5.45	1.21	1.34
1	t	291	PHE	C-N	-5.45	1.21	1.34
1	w	291	PHE	C-N	-5.45	1.21	1.34
1	z	291	PHE	C-N	-5.45	1.21	1.34
1	1	291	PHE	C-N	-5.45	1.21	1.34
1	2	291	PHE	C-N	-5.45	1.21	1.34
1	8	291	PHE	C-N	-5.45	1.21	1.34
1	A	291	PHE	C-N	-5.44	1.21	1.34
1	F	291	PHE	C-N	-5.44	1.21	1.34
1	a	291	PHE	C-N	-5.44	1.21	1.34
1	b	291	PHE	C-N	-5.44	1.21	1.34
1	c	291	PHE	C-N	-5.44	1.21	1.34
1	d	291	PHE	C-N	-5.44	1.21	1.34
1	e	291	PHE	C-N	-5.44	1.21	1.34
1	f	291	PHE	C-N	-5.44	1.21	1.34
1	n	291	PHE	C-N	-5.44	1.21	1.34
1	v	291	PHE	C-N	-5.44	1.21	1.34
1	y	291	PHE	C-N	-5.44	1.21	1.34
1	3	291	PHE	C-N	-5.44	1.21	1.34
1	C	291	PHE	C-N	-5.43	1.21	1.34
1	I	291	PHE	C-N	-5.43	1.21	1.34
1	K	291	PHE	C-N	-5.43	1.21	1.34
1	Q	291	PHE	C-N	-5.43	1.21	1.34
1	T	291	PHE	C-N	-5.43	1.21	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	V	291	PHE	C-N	-5.43	1.21	1.34
1	g	291	PHE	C-N	-5.43	1.21	1.34
1	m	291	PHE	C-N	-5.43	1.21	1.34
1	p	291	PHE	C-N	-5.43	1.21	1.34
1	u	291	PHE	C-N	-5.43	1.21	1.34
1	x	291	PHE	C-N	-5.43	1.21	1.34
1	4	291	PHE	C-N	-5.43	1.21	1.34
1	A	373	PRO	N-CD	5.37	1.55	1.47
1	F	373	PRO	N-CD	5.37	1.55	1.47
1	a	373	PRO	N-CD	5.37	1.55	1.47
1	b	373	PRO	N-CD	5.37	1.55	1.47
1	c	373	PRO	N-CD	5.37	1.55	1.47
1	d	373	PRO	N-CD	5.37	1.55	1.47
1	e	373	PRO	N-CD	5.37	1.55	1.47
1	f	373	PRO	N-CD	5.37	1.55	1.47
1	n	373	PRO	N-CD	5.37	1.55	1.47
1	v	373	PRO	N-CD	5.37	1.55	1.47
1	y	373	PRO	N-CD	5.37	1.55	1.47
1	3	373	PRO	N-CD	5.37	1.55	1.47
1	C	373	PRO	N-CD	5.36	1.55	1.47
1	I	373	PRO	N-CD	5.36	1.55	1.47
1	K	373	PRO	N-CD	5.36	1.55	1.47
1	Q	373	PRO	N-CD	5.36	1.55	1.47
1	T	373	PRO	N-CD	5.36	1.55	1.47
1	V	373	PRO	N-CD	5.36	1.55	1.47
1	g	373	PRO	N-CD	5.36	1.55	1.47
1	m	373	PRO	N-CD	5.36	1.55	1.47
1	p	373	PRO	N-CD	5.36	1.55	1.47
1	u	373	PRO	N-CD	5.36	1.55	1.47
1	x	373	PRO	N-CD	5.36	1.55	1.47
1	4	373	PRO	N-CD	5.36	1.55	1.47
1	E	373	PRO	N-CD	5.33	1.55	1.47
1	G	373	PRO	N-CD	5.33	1.55	1.47
1	M	373	PRO	N-CD	5.33	1.55	1.47
1	O	373	PRO	N-CD	5.33	1.55	1.47
1	X	373	PRO	N-CD	5.33	1.55	1.47
1	Z	373	PRO	N-CD	5.33	1.55	1.47
1	h	373	PRO	N-CD	5.33	1.55	1.47
1	l	373	PRO	N-CD	5.33	1.55	1.47
1	o	373	PRO	N-CD	5.33	1.55	1.47
1	t	373	PRO	N-CD	5.33	1.55	1.47
1	w	373	PRO	N-CD	5.33	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	8	373	PRO	N-CD	5.33	1.55	1.47
1	D	373	PRO	N-CD	5.33	1.55	1.47
1	H	373	PRO	N-CD	5.33	1.55	1.47
1	N	373	PRO	N-CD	5.33	1.55	1.47
1	P	373	PRO	N-CD	5.33	1.55	1.47
1	W	373	PRO	N-CD	5.33	1.55	1.47
1	Y	373	PRO	N-CD	5.33	1.55	1.47
1	i	373	PRO	N-CD	5.33	1.55	1.47
1	j	373	PRO	N-CD	5.33	1.55	1.47
1	k	373	PRO	N-CD	5.33	1.55	1.47
1	5	373	PRO	N-CD	5.33	1.55	1.47
1	6	373	PRO	N-CD	5.33	1.55	1.47
1	7	373	PRO	N-CD	5.33	1.55	1.47
1	B	373	PRO	N-CD	5.33	1.55	1.47
1	J	373	PRO	N-CD	5.33	1.55	1.47
1	L	373	PRO	N-CD	5.33	1.55	1.47
1	R	373	PRO	N-CD	5.33	1.55	1.47
1	S	373	PRO	N-CD	5.33	1.55	1.47
1	U	373	PRO	N-CD	5.33	1.55	1.47
1	q	373	PRO	N-CD	5.33	1.55	1.47
1	r	373	PRO	N-CD	5.33	1.55	1.47
1	s	373	PRO	N-CD	5.33	1.55	1.47
1	z	373	PRO	N-CD	5.33	1.55	1.47
1	1	373	PRO	N-CD	5.33	1.55	1.47
1	2	373	PRO	N-CD	5.33	1.55	1.47

All (120) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	302	ASN	N-CA-C	5.94	127.04	111.00
1	J	302	ASN	N-CA-C	5.94	127.04	111.00
1	L	302	ASN	N-CA-C	5.94	127.04	111.00
1	R	302	ASN	N-CA-C	5.94	127.04	111.00
1	S	302	ASN	N-CA-C	5.94	127.04	111.00
1	U	302	ASN	N-CA-C	5.94	127.04	111.00
1	q	302	ASN	N-CA-C	5.94	127.04	111.00
1	r	302	ASN	N-CA-C	5.94	127.04	111.00
1	s	302	ASN	N-CA-C	5.94	127.04	111.00
1	z	302	ASN	N-CA-C	5.94	127.04	111.00
1	1	302	ASN	N-CA-C	5.94	127.04	111.00
1	2	302	ASN	N-CA-C	5.94	127.04	111.00
1	C	302	ASN	N-CA-C	5.93	127.01	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	302	ASN	N-CA-C	5.93	127.01	111.00
1	K	302	ASN	N-CA-C	5.93	127.01	111.00
1	Q	302	ASN	N-CA-C	5.93	127.01	111.00
1	T	302	ASN	N-CA-C	5.93	127.01	111.00
1	V	302	ASN	N-CA-C	5.93	127.01	111.00
1	g	302	ASN	N-CA-C	5.93	127.01	111.00
1	m	302	ASN	N-CA-C	5.93	127.01	111.00
1	p	302	ASN	N-CA-C	5.93	127.01	111.00
1	u	302	ASN	N-CA-C	5.93	127.01	111.00
1	x	302	ASN	N-CA-C	5.93	127.01	111.00
1	4	302	ASN	N-CA-C	5.93	127.01	111.00
1	E	302	ASN	N-CA-C	5.93	127.00	111.00
1	G	302	ASN	N-CA-C	5.93	127.00	111.00
1	M	302	ASN	N-CA-C	5.93	127.00	111.00
1	O	302	ASN	N-CA-C	5.93	127.00	111.00
1	X	302	ASN	N-CA-C	5.93	127.00	111.00
1	Z	302	ASN	N-CA-C	5.93	127.00	111.00
1	h	302	ASN	N-CA-C	5.93	127.00	111.00
1	l	302	ASN	N-CA-C	5.93	127.00	111.00
1	o	302	ASN	N-CA-C	5.93	127.00	111.00
1	t	302	ASN	N-CA-C	5.93	127.00	111.00
1	w	302	ASN	N-CA-C	5.93	127.00	111.00
1	8	302	ASN	N-CA-C	5.93	127.00	111.00
1	D	302	ASN	N-CA-C	5.93	127.00	111.00
1	H	302	ASN	N-CA-C	5.93	127.00	111.00
1	N	302	ASN	N-CA-C	5.93	127.00	111.00
1	P	302	ASN	N-CA-C	5.93	127.00	111.00
1	W	302	ASN	N-CA-C	5.93	127.00	111.00
1	Y	302	ASN	N-CA-C	5.93	127.00	111.00
1	i	302	ASN	N-CA-C	5.93	127.00	111.00
1	j	302	ASN	N-CA-C	5.93	127.00	111.00
1	k	302	ASN	N-CA-C	5.93	127.00	111.00
1	5	302	ASN	N-CA-C	5.93	127.00	111.00
1	6	302	ASN	N-CA-C	5.93	127.00	111.00
1	7	302	ASN	N-CA-C	5.93	127.00	111.00
1	A	302	ASN	N-CA-C	5.92	127.00	111.00
1	F	302	ASN	N-CA-C	5.92	127.00	111.00
1	a	302	ASN	N-CA-C	5.92	127.00	111.00
1	b	302	ASN	N-CA-C	5.92	127.00	111.00
1	c	302	ASN	N-CA-C	5.92	127.00	111.00
1	d	302	ASN	N-CA-C	5.92	127.00	111.00
1	e	302	ASN	N-CA-C	5.92	127.00	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	f	302	ASN	N-CA-C	5.92	127.00	111.00
1	n	302	ASN	N-CA-C	5.92	127.00	111.00
1	v	302	ASN	N-CA-C	5.92	127.00	111.00
1	y	302	ASN	N-CA-C	5.92	127.00	111.00
1	3	302	ASN	N-CA-C	5.92	127.00	111.00
1	B	483	TYR	N-CA-C	-5.10	97.24	111.00
1	J	483	TYR	N-CA-C	-5.10	97.24	111.00
1	L	483	TYR	N-CA-C	-5.10	97.24	111.00
1	R	483	TYR	N-CA-C	-5.10	97.24	111.00
1	S	483	TYR	N-CA-C	-5.10	97.24	111.00
1	U	483	TYR	N-CA-C	-5.10	97.24	111.00
1	q	483	TYR	N-CA-C	-5.10	97.24	111.00
1	r	483	TYR	N-CA-C	-5.10	97.24	111.00
1	s	483	TYR	N-CA-C	-5.10	97.24	111.00
1	z	483	TYR	N-CA-C	-5.10	97.24	111.00
1	1	483	TYR	N-CA-C	-5.10	97.24	111.00
1	2	483	TYR	N-CA-C	-5.10	97.24	111.00
1	A	483	TYR	N-CA-C	-5.08	97.28	111.00
1	D	483	TYR	N-CA-C	-5.08	97.28	111.00
1	F	483	TYR	N-CA-C	-5.08	97.28	111.00
1	H	483	TYR	N-CA-C	-5.08	97.28	111.00
1	N	483	TYR	N-CA-C	-5.08	97.28	111.00
1	P	483	TYR	N-CA-C	-5.08	97.28	111.00
1	W	483	TYR	N-CA-C	-5.08	97.28	111.00
1	Y	483	TYR	N-CA-C	-5.08	97.28	111.00
1	a	483	TYR	N-CA-C	-5.08	97.28	111.00
1	b	483	TYR	N-CA-C	-5.08	97.28	111.00
1	c	483	TYR	N-CA-C	-5.08	97.28	111.00
1	d	483	TYR	N-CA-C	-5.08	97.28	111.00
1	e	483	TYR	N-CA-C	-5.08	97.28	111.00
1	f	483	TYR	N-CA-C	-5.08	97.28	111.00
1	i	483	TYR	N-CA-C	-5.08	97.28	111.00
1	j	483	TYR	N-CA-C	-5.08	97.28	111.00
1	k	483	TYR	N-CA-C	-5.08	97.28	111.00
1	n	483	TYR	N-CA-C	-5.08	97.28	111.00
1	v	483	TYR	N-CA-C	-5.08	97.28	111.00
1	y	483	TYR	N-CA-C	-5.08	97.28	111.00
1	3	483	TYR	N-CA-C	-5.08	97.28	111.00
1	5	483	TYR	N-CA-C	-5.08	97.28	111.00
1	6	483	TYR	N-CA-C	-5.08	97.28	111.00
1	7	483	TYR	N-CA-C	-5.08	97.28	111.00
1	C	483	TYR	N-CA-C	-5.08	97.29	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	483	TYR	N-CA-C	-5.08	97.29	111.00
1	K	483	TYR	N-CA-C	-5.08	97.29	111.00
1	Q	483	TYR	N-CA-C	-5.08	97.29	111.00
1	T	483	TYR	N-CA-C	-5.08	97.29	111.00
1	V	483	TYR	N-CA-C	-5.08	97.29	111.00
1	g	483	TYR	N-CA-C	-5.08	97.29	111.00
1	m	483	TYR	N-CA-C	-5.08	97.29	111.00
1	p	483	TYR	N-CA-C	-5.08	97.29	111.00
1	u	483	TYR	N-CA-C	-5.08	97.29	111.00
1	x	483	TYR	N-CA-C	-5.08	97.29	111.00
1	4	483	TYR	N-CA-C	-5.08	97.29	111.00
1	E	483	TYR	N-CA-C	-5.07	97.31	111.00
1	G	483	TYR	N-CA-C	-5.07	97.31	111.00
1	M	483	TYR	N-CA-C	-5.07	97.31	111.00
1	O	483	TYR	N-CA-C	-5.07	97.31	111.00
1	X	483	TYR	N-CA-C	-5.07	97.31	111.00
1	Z	483	TYR	N-CA-C	-5.07	97.31	111.00
1	h	483	TYR	N-CA-C	-5.07	97.31	111.00
1	l	483	TYR	N-CA-C	-5.07	97.31	111.00
1	o	483	TYR	N-CA-C	-5.07	97.31	111.00
1	t	483	TYR	N-CA-C	-5.07	97.31	111.00
1	w	483	TYR	N-CA-C	-5.07	97.31	111.00
1	8	483	TYR	N-CA-C	-5.07	97.31	111.00

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	1	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	2	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	3	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	4	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	5	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	6	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	7	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	8	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	A	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	B	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	C	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	D	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	E	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	F	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	G	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	H	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	I	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	J	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	K	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	L	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	M	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	N	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	O	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	P	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	Q	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	R	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	S	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	T	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	U	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	V	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	W	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	X	515/735 (70%)	506 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Y	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	Z	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	a	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	b	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	c	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	d	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	e	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	f	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	g	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	h	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	i	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	j	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	k	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	l	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	m	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	n	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	o	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	p	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	q	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	r	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	s	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	t	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	u	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	v	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	w	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	x	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	y	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	z	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
All	All	30900/44100 (70%)	30360 (98%)	540 (2%)	0	100	100

There are no Ramachandran outliers to report.



### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	459/630 (73%)	459 (100%)	0	100	100
1	2	459/630 (73%)	459 (100%)	0	100	100
1	3	459/630 (73%)	459 (100%)	0	100	100
1	4	459/630 (73%)	459 (100%)	0	100	100
1	5	459/630 (73%)	459 (100%)	0	100	100
1	6	459/630 (73%)	459 (100%)	0	100	100
1	7	459/630 (73%)	459 (100%)	0	100	100
1	8	459/630 (73%)	459 (100%)	0	100	100
1	A	459/630 (73%)	459 (100%)	0	100	100
1	B	459/630 (73%)	459 (100%)	0	100	100
1	C	459/630 (73%)	459 (100%)	0	100	100
1	D	459/630 (73%)	459 (100%)	0	100	100
1	E	459/630 (73%)	459 (100%)	0	100	100
1	F	459/630 (73%)	459 (100%)	0	100	100
1	G	459/630 (73%)	459 (100%)	0	100	100
1	H	459/630 (73%)	459 (100%)	0	100	100
1	I	459/630 (73%)	459 (100%)	0	100	100
1	J	459/630 (73%)	459 (100%)	0	100	100
1	K	459/630 (73%)	459 (100%)	0	100	100
1	L	459/630 (73%)	459 (100%)	0	100	100
1	M	459/630 (73%)	459 (100%)	0	100	100
1	N	459/630 (73%)	459 (100%)	0	100	100
1	O	459/630 (73%)	459 (100%)	0	100	100
1	P	459/630 (73%)	459 (100%)	0	100	100
1	Q	459/630 (73%)	459 (100%)	0	100	100
1	R	459/630 (73%)	459 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S	459/630 (73%)	459 (100%)	0	100	100
1	T	459/630 (73%)	459 (100%)	0	100	100
1	U	459/630 (73%)	459 (100%)	0	100	100
1	V	459/630 (73%)	459 (100%)	0	100	100
1	W	459/630 (73%)	459 (100%)	0	100	100
1	X	459/630 (73%)	459 (100%)	0	100	100
1	Y	459/630 (73%)	459 (100%)	0	100	100
1	Z	459/630 (73%)	459 (100%)	0	100	100
1	a	459/630 (73%)	459 (100%)	0	100	100
1	b	459/630 (73%)	459 (100%)	0	100	100
1	c	459/630 (73%)	459 (100%)	0	100	100
1	d	459/630 (73%)	459 (100%)	0	100	100
1	e	459/630 (73%)	459 (100%)	0	100	100
1	f	459/630 (73%)	459 (100%)	0	100	100
1	g	459/630 (73%)	459 (100%)	0	100	100
1	h	459/630 (73%)	459 (100%)	0	100	100
1	i	459/630 (73%)	459 (100%)	0	100	100
1	j	459/630 (73%)	459 (100%)	0	100	100
1	k	459/630 (73%)	459 (100%)	0	100	100
1	l	459/630 (73%)	459 (100%)	0	100	100
1	m	459/630 (73%)	459 (100%)	0	100	100
1	n	459/630 (73%)	459 (100%)	0	100	100
1	o	459/630 (73%)	459 (100%)	0	100	100
1	p	459/630 (73%)	459 (100%)	0	100	100
1	q	459/630 (73%)	459 (100%)	0	100	100
1	r	459/630 (73%)	459 (100%)	0	100	100
1	s	459/630 (73%)	459 (100%)	0	100	100
1	t	459/630 (73%)	459 (100%)	0	100	100
1	u	459/630 (73%)	459 (100%)	0	100	100
1	v	459/630 (73%)	459 (100%)	0	100	100
1	w	459/630 (73%)	459 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	x	459/630 (73%)	459 (100%)	0	100	100
1	y	459/630 (73%)	459 (100%)	0	100	100
1	z	459/630 (73%)	459 (100%)	0	100	100
All	All	27540/37800 (73%)	27540 (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. All (1020) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	270	ASN
1	A	288	HIS
1	A	297	GLN
1	A	317	ASN
1	A	334	ASN
1	A	349	GLN
1	A	374	GLN
1	A	428	GLN
1	A	496	ASN
1	A	526	HIS
1	A	536	GLN
1	A	598	GLN
1	A	623	HIS
1	A	645	GLN
1	A	672	GLN
1	A	677	GLN
1	A	734	ASN
1	B	270	ASN
1	B	288	HIS
1	B	297	GLN
1	B	317	ASN
1	B	334	ASN
1	B	349	GLN
1	B	374	GLN
1	B	428	GLN
1	B	496	ASN
1	B	526	HIS
1	B	536	GLN
1	B	598	GLN
1	B	623	HIS
1	B	645	GLN

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Mol	Chain	Res	Type
1	B	672	GLN
1	B	677	GLN
1	B	734	ASN
1	C	270	ASN
1	C	288	HIS
1	C	297	GLN
1	C	317	ASN
1	C	334	ASN
1	C	349	GLN
1	C	374	GLN
1	C	428	GLN
1	C	496	ASN
1	C	526	HIS
1	C	536	GLN
1	C	598	GLN
1	C	623	HIS
1	C	645	GLN
1	C	672	GLN
1	C	677	GLN
1	C	734	ASN
1	D	270	ASN
1	D	288	HIS
1	D	297	GLN
1	D	317	ASN
1	D	334	ASN
1	D	335	ASN
1	D	349	GLN
1	D	374	GLN
1	D	428	GLN
1	D	496	ASN
1	D	526	HIS
1	D	536	GLN
1	D	598	GLN
1	D	623	HIS
1	D	645	GLN
1	D	677	GLN
1	D	734	ASN
1	E	270	ASN
1	E	288	HIS
1	E	297	GLN
1	E	317	ASN
1	E	334	ASN

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Mol	Chain	Res	Type
1	E	349	GLN
1	E	374	GLN
1	E	428	GLN
1	E	496	ASN
1	E	526	HIS
1	E	536	GLN
1	E	598	GLN
1	E	623	HIS
1	E	645	GLN
1	E	672	GLN
1	E	677	GLN
1	E	734	ASN
1	F	270	ASN
1	F	288	HIS
1	F	297	GLN
1	F	317	ASN
1	F	334	ASN
1	F	349	GLN
1	F	374	GLN
1	F	428	GLN
1	F	496	ASN
1	F	526	HIS
1	F	536	GLN
1	F	598	GLN
1	F	623	HIS
1	F	645	GLN
1	F	672	GLN
1	F	677	GLN
1	F	734	ASN
1	G	270	ASN
1	G	288	HIS
1	G	297	GLN
1	G	317	ASN
1	G	334	ASN
1	G	349	GLN
1	G	374	GLN
1	G	428	GLN
1	G	496	ASN
1	G	526	HIS
1	G	536	GLN
1	G	598	GLN
1	G	623	HIS

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Mol	Chain	Res	Type
1	G	645	GLN
1	G	672	GLN
1	G	677	GLN
1	G	734	ASN
1	H	270	ASN
1	H	288	HIS
1	H	297	GLN
1	H	317	ASN
1	H	334	ASN
1	H	349	GLN
1	H	374	GLN
1	H	428	GLN
1	H	496	ASN
1	H	526	HIS
1	H	536	GLN
1	H	598	GLN
1	H	623	HIS
1	H	645	GLN
1	H	672	GLN
1	H	677	GLN
1	H	734	ASN
1	I	270	ASN
1	I	288	HIS
1	I	297	GLN
1	I	317	ASN
1	I	334	ASN
1	I	335	ASN
1	I	349	GLN
1	I	374	GLN
1	I	428	GLN
1	I	496	ASN
1	I	526	HIS
1	I	536	GLN
1	I	598	GLN
1	I	623	HIS
1	I	645	GLN
1	I	677	GLN
1	I	734	ASN
1	J	270	ASN
1	J	288	HIS
1	J	297	GLN
1	J	317	ASN

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Mol	Chain	Res	Type
1	J	334	ASN
1	J	349	GLN
1	J	374	GLN
1	J	428	GLN
1	J	496	ASN
1	J	526	HIS
1	J	536	GLN
1	J	598	GLN
1	J	623	HIS
1	J	645	GLN
1	J	672	GLN
1	J	677	GLN
1	J	734	ASN
1	K	270	ASN
1	K	288	HIS
1	K	297	GLN
1	K	317	ASN
1	K	334	ASN
1	K	349	GLN
1	K	374	GLN
1	K	428	GLN
1	K	496	ASN
1	K	526	HIS
1	K	536	GLN
1	K	598	GLN
1	K	623	HIS
1	K	645	GLN
1	K	672	GLN
1	K	677	GLN
1	K	734	ASN
1	L	270	ASN
1	L	288	HIS
1	L	297	GLN
1	L	317	ASN
1	L	334	ASN
1	L	349	GLN
1	L	374	GLN
1	L	428	GLN
1	L	496	ASN
1	L	526	HIS
1	L	536	GLN
1	L	598	GLN

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Mol	Chain	Res	Type
1	L	623	HIS
1	L	645	GLN
1	L	672	GLN
1	L	677	GLN
1	L	734	ASN
1	M	270	ASN
1	M	288	HIS
1	M	297	GLN
1	M	317	ASN
1	M	334	ASN
1	M	349	GLN
1	M	374	GLN
1	M	428	GLN
1	M	496	ASN
1	M	526	HIS
1	M	536	GLN
1	M	598	GLN
1	M	623	HIS
1	M	645	GLN
1	M	672	GLN
1	M	677	GLN
1	M	734	ASN
1	N	270	ASN
1	N	288	HIS
1	N	297	GLN
1	N	317	ASN
1	N	334	ASN
1	N	335	ASN
1	N	349	GLN
1	N	374	GLN
1	N	428	GLN
1	N	496	ASN
1	N	526	HIS
1	N	536	GLN
1	N	598	GLN
1	N	623	HIS
1	N	645	GLN
1	N	677	GLN
1	N	734	ASN
1	O	270	ASN
1	O	288	HIS
1	O	297	GLN

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Mol	Chain	Res	Type
1	O	317	ASN
1	O	334	ASN
1	O	349	GLN
1	O	374	GLN
1	O	428	GLN
1	O	496	ASN
1	O	526	HIS
1	O	536	GLN
1	O	598	GLN
1	O	623	HIS
1	O	645	GLN
1	O	672	GLN
1	O	677	GLN
1	O	734	ASN
1	P	270	ASN
1	P	288	HIS
1	P	297	GLN
1	P	317	ASN
1	P	334	ASN
1	P	349	GLN
1	P	374	GLN
1	P	428	GLN
1	P	496	ASN
1	P	526	HIS
1	P	536	GLN
1	P	598	GLN
1	P	623	HIS
1	P	645	GLN
1	P	672	GLN
1	P	677	GLN
1	P	734	ASN
1	Q	270	ASN
1	Q	288	HIS
1	Q	297	GLN
1	Q	317	ASN
1	Q	334	ASN
1	Q	335	ASN
1	Q	349	GLN
1	Q	374	GLN
1	Q	428	GLN
1	Q	496	ASN
1	Q	526	HIS

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Mol	Chain	Res	Type
1	Q	536	GLN
1	Q	598	GLN
1	Q	623	HIS
1	Q	645	GLN
1	Q	677	GLN
1	Q	734	ASN
1	R	270	ASN
1	R	288	HIS
1	R	297	GLN
1	R	317	ASN
1	R	334	ASN
1	R	335	ASN
1	R	349	GLN
1	R	374	GLN
1	R	428	GLN
1	R	496	ASN
1	R	526	HIS
1	R	536	GLN
1	R	598	GLN
1	R	623	HIS
1	R	645	GLN
1	R	677	GLN
1	R	734	ASN
1	S	270	ASN
1	S	288	HIS
1	S	297	GLN
1	S	317	ASN
1	S	334	ASN
1	S	349	GLN
1	S	374	GLN
1	S	428	GLN
1	S	496	ASN
1	S	526	HIS
1	S	536	GLN
1	S	598	GLN
1	S	623	HIS
1	S	645	GLN
1	S	672	GLN
1	S	677	GLN
1	S	734	ASN
1	T	270	ASN
1	T	288	HIS

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Mol	Chain	Res	Type
1	T	297	GLN
1	T	317	ASN
1	T	334	ASN
1	T	349	GLN
1	T	374	GLN
1	T	428	GLN
1	T	496	ASN
1	T	526	HIS
1	T	536	GLN
1	T	598	GLN
1	T	623	HIS
1	T	645	GLN
1	T	672	GLN
1	T	677	GLN
1	T	734	ASN
1	U	270	ASN
1	U	288	HIS
1	U	297	GLN
1	U	317	ASN
1	U	334	ASN
1	U	349	GLN
1	U	374	GLN
1	U	428	GLN
1	U	496	ASN
1	U	526	HIS
1	U	536	GLN
1	U	598	GLN
1	U	623	HIS
1	U	645	GLN
1	U	672	GLN
1	U	677	GLN
1	U	734	ASN
1	V	270	ASN
1	V	288	HIS
1	V	297	GLN
1	V	317	ASN
1	V	334	ASN
1	V	349	GLN
1	V	374	GLN
1	V	428	GLN
1	V	496	ASN
1	V	526	HIS

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Mol	Chain	Res	Type
1	V	536	GLN
1	V	598	GLN
1	V	623	HIS
1	V	645	GLN
1	V	672	GLN
1	V	677	GLN
1	V	734	ASN
1	W	270	ASN
1	W	288	HIS
1	W	297	GLN
1	W	317	ASN
1	W	334	ASN
1	W	349	GLN
1	W	374	GLN
1	W	428	GLN
1	W	496	ASN
1	W	526	HIS
1	W	536	GLN
1	W	598	GLN
1	W	623	HIS
1	W	645	GLN
1	W	672	GLN
1	W	677	GLN
1	W	734	ASN
1	X	270	ASN
1	X	288	HIS
1	X	297	GLN
1	X	317	ASN
1	X	334	ASN
1	X	349	GLN
1	X	374	GLN
1	X	428	GLN
1	X	496	ASN
1	X	526	HIS
1	X	536	GLN
1	X	598	GLN
1	X	623	HIS
1	X	645	GLN
1	X	672	GLN
1	X	677	GLN
1	X	734	ASN
1	Y	270	ASN

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Mol	Chain	Res	Type
1	Y	288	HIS
1	Y	297	GLN
1	Y	317	ASN
1	Y	334	ASN
1	Y	349	GLN
1	Y	374	GLN
1	Y	428	GLN
1	Y	496	ASN
1	Y	526	HIS
1	Y	536	GLN
1	Y	598	GLN
1	Y	623	HIS
1	Y	645	GLN
1	Y	672	GLN
1	Y	677	GLN
1	Y	734	ASN
1	Z	270	ASN
1	Z	288	HIS
1	Z	297	GLN
1	Z	317	ASN
1	Z	334	ASN
1	Z	349	GLN
1	Z	374	GLN
1	Z	428	GLN
1	Z	496	ASN
1	Z	526	HIS
1	Z	536	GLN
1	Z	598	GLN
1	Z	623	HIS
1	Z	645	GLN
1	Z	672	GLN
1	Z	677	GLN
1	Z	734	ASN
1	a	270	ASN
1	a	288	HIS
1	a	297	GLN
1	a	317	ASN
1	a	334	ASN
1	a	349	GLN
1	a	374	GLN
1	a	428	GLN
1	a	496	ASN

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Mol	Chain	Res	Type
1	a	526	HIS
1	a	536	GLN
1	a	598	GLN
1	a	623	HIS
1	a	645	GLN
1	a	672	GLN
1	a	677	GLN
1	a	734	ASN
1	b	270	ASN
1	b	288	HIS
1	b	297	GLN
1	b	317	ASN
1	b	334	ASN
1	b	349	GLN
1	b	374	GLN
1	b	428	GLN
1	b	496	ASN
1	b	526	HIS
1	b	536	GLN
1	b	598	GLN
1	b	623	HIS
1	b	645	GLN
1	b	672	GLN
1	b	677	GLN
1	b	734	ASN
1	c	270	ASN
1	c	288	HIS
1	c	297	GLN
1	c	317	ASN
1	c	334	ASN
1	c	349	GLN
1	c	374	GLN
1	c	428	GLN
1	c	496	ASN
1	c	526	HIS
1	c	536	GLN
1	c	598	GLN
1	c	623	HIS
1	c	645	GLN
1	c	672	GLN
1	c	677	GLN
1	c	734	ASN

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Mol	Chain	Res	Type
1	d	270	ASN
1	d	288	HIS
1	d	297	GLN
1	d	317	ASN
1	d	334	ASN
1	d	335	ASN
1	d	349	GLN
1	d	374	GLN
1	d	428	GLN
1	d	496	ASN
1	d	526	HIS
1	d	536	GLN
1	d	598	GLN
1	d	623	HIS
1	d	645	GLN
1	d	677	GLN
1	d	734	ASN
1	e	270	ASN
1	e	288	HIS
1	e	297	GLN
1	e	317	ASN
1	e	334	ASN
1	e	349	GLN
1	e	374	GLN
1	e	428	GLN
1	e	496	ASN
1	e	526	HIS
1	e	536	GLN
1	e	598	GLN
1	e	623	HIS
1	e	645	GLN
1	e	672	GLN
1	e	677	GLN
1	e	734	ASN
1	f	270	ASN
1	f	288	HIS
1	f	297	GLN
1	f	317	ASN
1	f	334	ASN
1	f	349	GLN
1	f	374	GLN
1	f	428	GLN

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Mol	Chain	Res	Type
1	f	496	ASN
1	f	526	HIS
1	f	536	GLN
1	f	598	GLN
1	f	623	HIS
1	f	645	GLN
1	f	672	GLN
1	f	677	GLN
1	f	734	ASN
1	g	270	ASN
1	g	288	HIS
1	g	297	GLN
1	g	317	ASN
1	g	334	ASN
1	g	349	GLN
1	g	374	GLN
1	g	428	GLN
1	g	496	ASN
1	g	526	HIS
1	g	536	GLN
1	g	598	GLN
1	g	623	HIS
1	g	645	GLN
1	g	672	GLN
1	g	677	GLN
1	g	734	ASN
1	h	270	ASN
1	h	288	HIS
1	h	297	GLN
1	h	317	ASN
1	h	334	ASN
1	h	349	GLN
1	h	374	GLN
1	h	428	GLN
1	h	496	ASN
1	h	526	HIS
1	h	536	GLN
1	h	598	GLN
1	h	623	HIS
1	h	645	GLN
1	h	672	GLN
1	h	677	GLN

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Mol	Chain	Res	Type
1	h	734	ASN
1	i	270	ASN
1	i	288	HIS
1	i	297	GLN
1	i	317	ASN
1	i	334	ASN
1	i	335	ASN
1	i	349	GLN
1	i	374	GLN
1	i	428	GLN
1	i	496	ASN
1	i	526	HIS
1	i	536	GLN
1	i	598	GLN
1	i	623	HIS
1	i	645	GLN
1	i	677	GLN
1	i	734	ASN
1	j	270	ASN
1	j	288	HIS
1	j	297	GLN
1	j	317	ASN
1	j	334	ASN
1	j	349	GLN
1	j	374	GLN
1	j	428	GLN
1	j	496	ASN
1	j	526	HIS
1	j	536	GLN
1	j	598	GLN
1	j	623	HIS
1	j	645	GLN
1	j	672	GLN
1	j	677	GLN
1	j	734	ASN
1	k	270	ASN
1	k	288	HIS
1	k	297	GLN
1	k	317	ASN
1	k	334	ASN
1	k	349	GLN
1	k	374	GLN

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Mol	Chain	Res	Type
1	k	428	GLN
1	k	496	ASN
1	k	526	HIS
1	k	536	GLN
1	k	598	GLN
1	k	623	HIS
1	k	645	GLN
1	k	672	GLN
1	k	677	GLN
1	k	734	ASN
1	l	270	ASN
1	l	288	HIS
1	l	297	GLN
1	l	317	ASN
1	l	334	ASN
1	l	349	GLN
1	l	374	GLN
1	l	428	GLN
1	l	496	ASN
1	l	526	HIS
1	l	536	GLN
1	l	598	GLN
1	l	623	HIS
1	l	645	GLN
1	l	672	GLN
1	l	677	GLN
1	l	734	ASN
1	m	270	ASN
1	m	288	HIS
1	m	297	GLN
1	m	317	ASN
1	m	334	ASN
1	m	349	GLN
1	m	374	GLN
1	m	428	GLN
1	m	496	ASN
1	m	526	HIS
1	m	536	GLN
1	m	598	GLN
1	m	623	HIS
1	m	645	GLN
1	m	672	GLN

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Mol	Chain	Res	Type
1	m	677	GLN
1	m	734	ASN
1	n	270	ASN
1	n	288	HIS
1	n	297	GLN
1	n	317	ASN
1	n	334	ASN
1	n	335	ASN
1	n	349	GLN
1	n	374	GLN
1	n	428	GLN
1	n	496	ASN
1	n	526	HIS
1	n	536	GLN
1	n	598	GLN
1	n	623	HIS
1	n	645	GLN
1	n	677	GLN
1	n	734	ASN
1	o	270	ASN
1	o	288	HIS
1	o	297	GLN
1	o	317	ASN
1	o	334	ASN
1	o	349	GLN
1	o	374	GLN
1	o	428	GLN
1	o	496	ASN
1	o	526	HIS
1	o	536	GLN
1	o	598	GLN
1	o	623	HIS
1	o	645	GLN
1	o	672	GLN
1	o	677	GLN
1	o	734	ASN
1	p	270	ASN
1	p	288	HIS
1	p	297	GLN
1	p	317	ASN
1	p	334	ASN
1	p	349	GLN

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Mol	Chain	Res	Type
1	p	374	GLN
1	p	428	GLN
1	p	496	ASN
1	p	526	HIS
1	p	536	GLN
1	p	598	GLN
1	p	623	HIS
1	p	645	GLN
1	p	672	GLN
1	p	677	GLN
1	p	734	ASN
1	q	270	ASN
1	q	288	HIS
1	q	297	GLN
1	q	317	ASN
1	q	334	ASN
1	q	335	ASN
1	q	349	GLN
1	q	374	GLN
1	q	428	GLN
1	q	496	ASN
1	q	526	HIS
1	q	536	GLN
1	q	598	GLN
1	q	623	HIS
1	q	645	GLN
1	q	677	GLN
1	q	734	ASN
1	r	270	ASN
1	r	288	HIS
1	r	297	GLN
1	r	317	ASN
1	r	334	ASN
1	r	349	GLN
1	r	374	GLN
1	r	428	GLN
1	r	496	ASN
1	r	526	HIS
1	r	536	GLN
1	r	598	GLN
1	r	623	HIS
1	r	645	GLN

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Mol	Chain	Res	Type
1	r	672	GLN
1	r	677	GLN
1	r	734	ASN
1	s	270	ASN
1	s	288	HIS
1	s	297	GLN
1	s	317	ASN
1	s	334	ASN
1	s	349	GLN
1	s	374	GLN
1	s	428	GLN
1	s	496	ASN
1	s	526	HIS
1	s	536	GLN
1	s	598	GLN
1	s	623	HIS
1	s	645	GLN
1	s	672	GLN
1	s	677	GLN
1	s	734	ASN
1	t	270	ASN
1	t	288	HIS
1	t	297	GLN
1	t	317	ASN
1	t	334	ASN
1	t	335	ASN
1	t	349	GLN
1	t	374	GLN
1	t	428	GLN
1	t	496	ASN
1	t	526	HIS
1	t	536	GLN
1	t	598	GLN
1	t	623	HIS
1	t	645	GLN
1	t	677	GLN
1	t	734	ASN
1	u	270	ASN
1	u	288	HIS
1	u	297	GLN
1	u	317	ASN
1	u	334	ASN

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Mol	Chain	Res	Type
1	u	335	ASN
1	u	349	GLN
1	u	374	GLN
1	u	428	GLN
1	u	496	ASN
1	u	526	HIS
1	u	536	GLN
1	u	598	GLN
1	u	623	HIS
1	u	645	GLN
1	u	677	GLN
1	u	734	ASN
1	v	270	ASN
1	v	288	HIS
1	v	297	GLN
1	v	317	ASN
1	v	334	ASN
1	v	349	GLN
1	v	374	GLN
1	v	428	GLN
1	v	496	ASN
1	v	526	HIS
1	v	536	GLN
1	v	598	GLN
1	v	623	HIS
1	v	645	GLN
1	v	672	GLN
1	v	677	GLN
1	v	734	ASN
1	w	270	ASN
1	w	288	HIS
1	w	297	GLN
1	w	317	ASN
1	w	334	ASN
1	w	349	GLN
1	w	374	GLN
1	w	428	GLN
1	w	496	ASN
1	w	526	HIS
1	w	536	GLN
1	w	598	GLN
1	w	623	HIS

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Mol	Chain	Res	Type
1	w	645	GLN
1	w	672	GLN
1	w	677	GLN
1	w	734	ASN
1	x	270	ASN
1	x	288	HIS
1	x	297	GLN
1	x	317	ASN
1	x	334	ASN
1	x	335	ASN
1	x	349	GLN
1	x	374	GLN
1	x	428	GLN
1	x	496	ASN
1	x	526	HIS
1	x	536	GLN
1	x	598	GLN
1	x	623	HIS
1	x	645	GLN
1	x	677	GLN
1	x	734	ASN
1	y	270	ASN
1	y	288	HIS
1	y	297	GLN
1	y	317	ASN
1	y	334	ASN
1	y	349	GLN
1	y	374	GLN
1	y	428	GLN
1	y	496	ASN
1	y	526	HIS
1	y	536	GLN
1	y	598	GLN
1	y	623	HIS
1	y	645	GLN
1	y	672	GLN
1	y	677	GLN
1	y	734	ASN
1	z	270	ASN
1	z	288	HIS
1	z	297	GLN
1	z	317	ASN

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Mol	Chain	Res	Type
1	z	334	ASN
1	z	349	GLN
1	z	374	GLN
1	z	428	GLN
1	z	496	ASN
1	z	526	HIS
1	z	536	GLN
1	z	598	GLN
1	z	623	HIS
1	z	645	GLN
1	z	672	GLN
1	z	677	GLN
1	z	734	ASN
1	1	270	ASN
1	1	288	HIS
1	1	297	GLN
1	1	317	ASN
1	1	334	ASN
1	1	349	GLN
1	1	374	GLN
1	1	428	GLN
1	1	496	ASN
1	1	526	HIS
1	1	536	GLN
1	1	598	GLN
1	1	623	HIS
1	1	645	GLN
1	1	672	GLN
1	1	677	GLN
1	1	734	ASN
1	2	270	ASN
1	2	288	HIS
1	2	297	GLN
1	2	317	ASN
1	2	334	ASN
1	2	349	GLN
1	2	374	GLN
1	2	428	GLN
1	2	496	ASN
1	2	526	HIS
1	2	536	GLN
1	2	598	GLN

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Mol	Chain	Res	Type
1	2	623	HIS
1	2	645	GLN
1	2	672	GLN
1	2	677	GLN
1	2	734	ASN
1	3	270	ASN
1	3	288	HIS
1	3	297	GLN
1	3	317	ASN
1	3	334	ASN
1	3	349	GLN
1	3	374	GLN
1	3	428	GLN
1	3	496	ASN
1	3	526	HIS
1	3	536	GLN
1	3	598	GLN
1	3	623	HIS
1	3	645	GLN
1	3	672	GLN
1	3	677	GLN
1	3	734	ASN
1	4	270	ASN
1	4	288	HIS
1	4	297	GLN
1	4	317	ASN
1	4	334	ASN
1	4	349	GLN
1	4	374	GLN
1	4	428	GLN
1	4	496	ASN
1	4	526	HIS
1	4	536	GLN
1	4	598	GLN
1	4	623	HIS
1	4	645	GLN
1	4	672	GLN
1	4	677	GLN
1	4	734	ASN
1	5	270	ASN
1	5	288	HIS
1	5	297	GLN

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Mol	Chain	Res	Type
1	5	317	ASN
1	5	334	ASN
1	5	349	GLN
1	5	374	GLN
1	5	428	GLN
1	5	496	ASN
1	5	526	HIS
1	5	536	GLN
1	5	598	GLN
1	5	623	HIS
1	5	645	GLN
1	5	672	GLN
1	5	677	GLN
1	5	734	ASN
1	6	270	ASN
1	6	288	HIS
1	6	297	GLN
1	6	317	ASN
1	6	334	ASN
1	6	335	ASN
1	6	349	GLN
1	6	374	GLN
1	6	428	GLN
1	6	496	ASN
1	6	526	HIS
1	6	536	GLN
1	6	598	GLN
1	6	623	HIS
1	6	645	GLN
1	6	677	GLN
1	6	734	ASN
1	7	270	ASN
1	7	288	HIS
1	7	297	GLN
1	7	317	ASN
1	7	334	ASN
1	7	349	GLN
1	7	374	GLN
1	7	428	GLN
1	7	496	ASN
1	7	526	HIS
1	7	536	GLN

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Mol	Chain	Res	Type
1	7	598	GLN
1	7	623	HIS
1	7	645	GLN
1	7	672	GLN
1	7	677	GLN
1	7	734	ASN
1	8	270	ASN
1	8	288	HIS
1	8	297	GLN
1	8	317	ASN
1	8	334	ASN
1	8	349	GLN
1	8	374	GLN
1	8	428	GLN
1	8	496	ASN
1	8	526	HIS
1	8	536	GLN
1	8	598	GLN
1	8	623	HIS
1	8	645	GLN
1	8	672	GLN
1	8	677	GLN
1	8	734	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

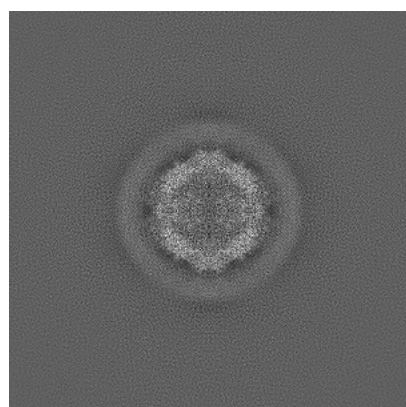
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24718. These allow visual inspection of the internal detail of the map and identification of artifacts.

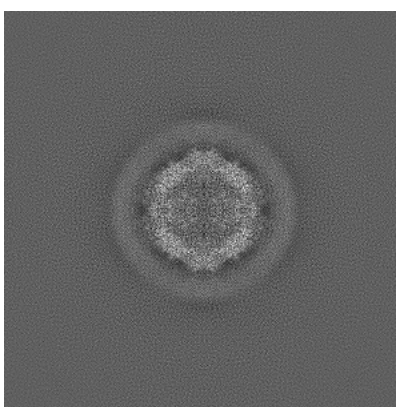
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

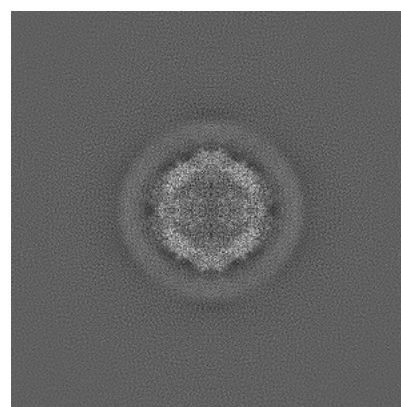
#### 6.1.1 Primary map



X



Y

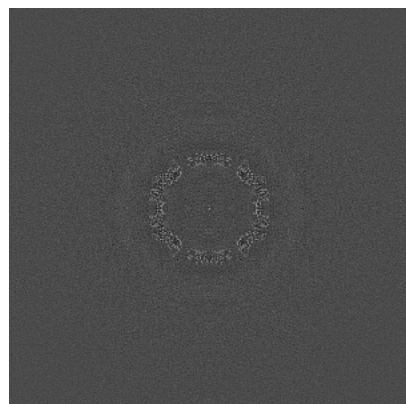


Z

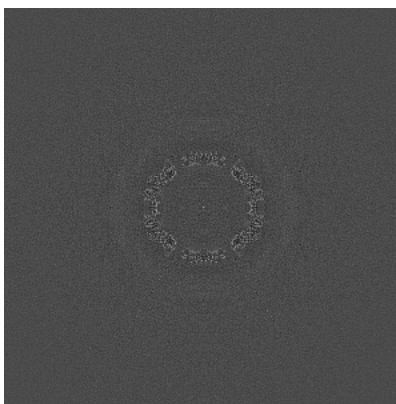
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

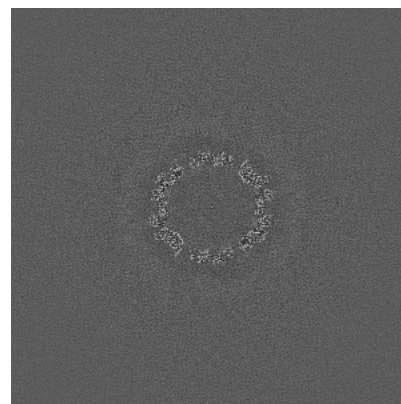
#### 6.2.1 Primary map



X Index: 384



Y Index: 384

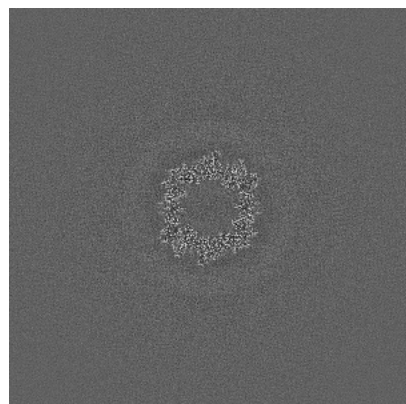


Z Index: 384

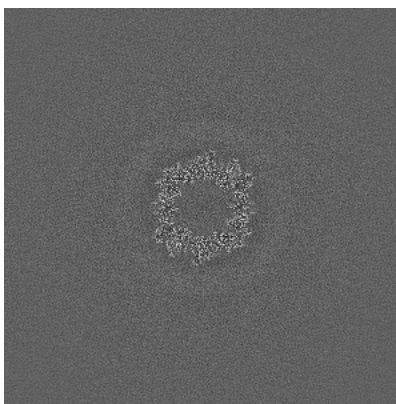
The images above show central slices of the map in three orthogonal directions.

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

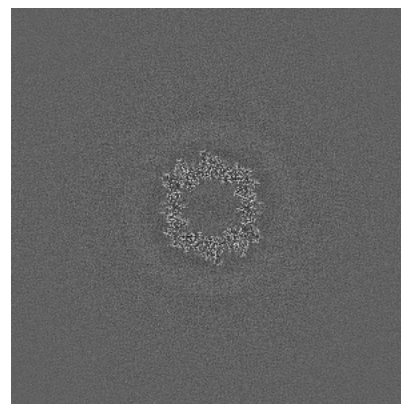
### 6.3.1 Primary map



X Index: 446



Y Index: 446

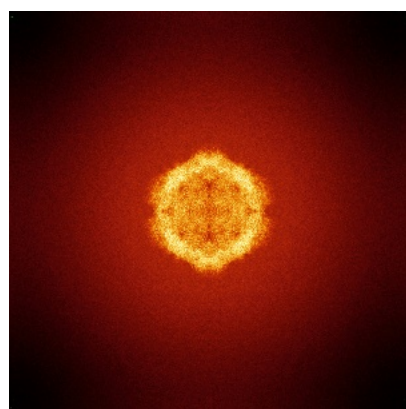


Z Index: 321

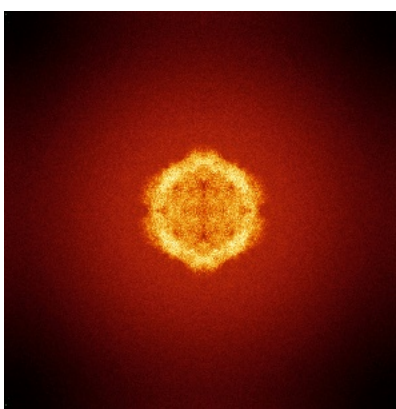
The images above show the largest variance slices of the map in three orthogonal directions.

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

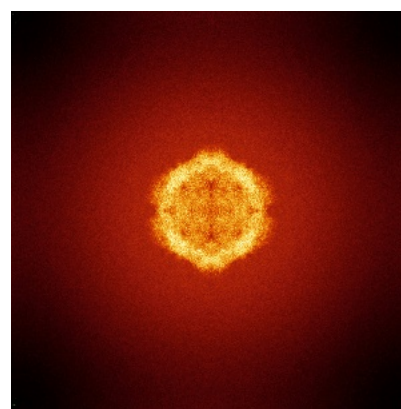
### 6.4.1 Primary map



X



Y

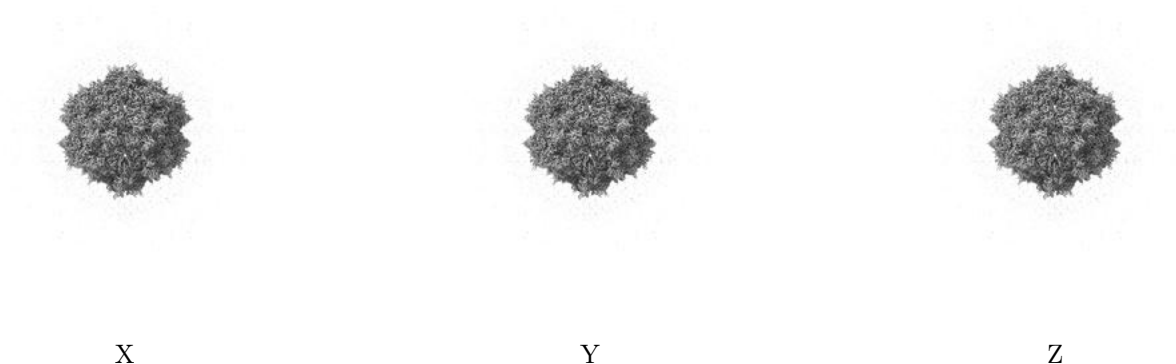


Z

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 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

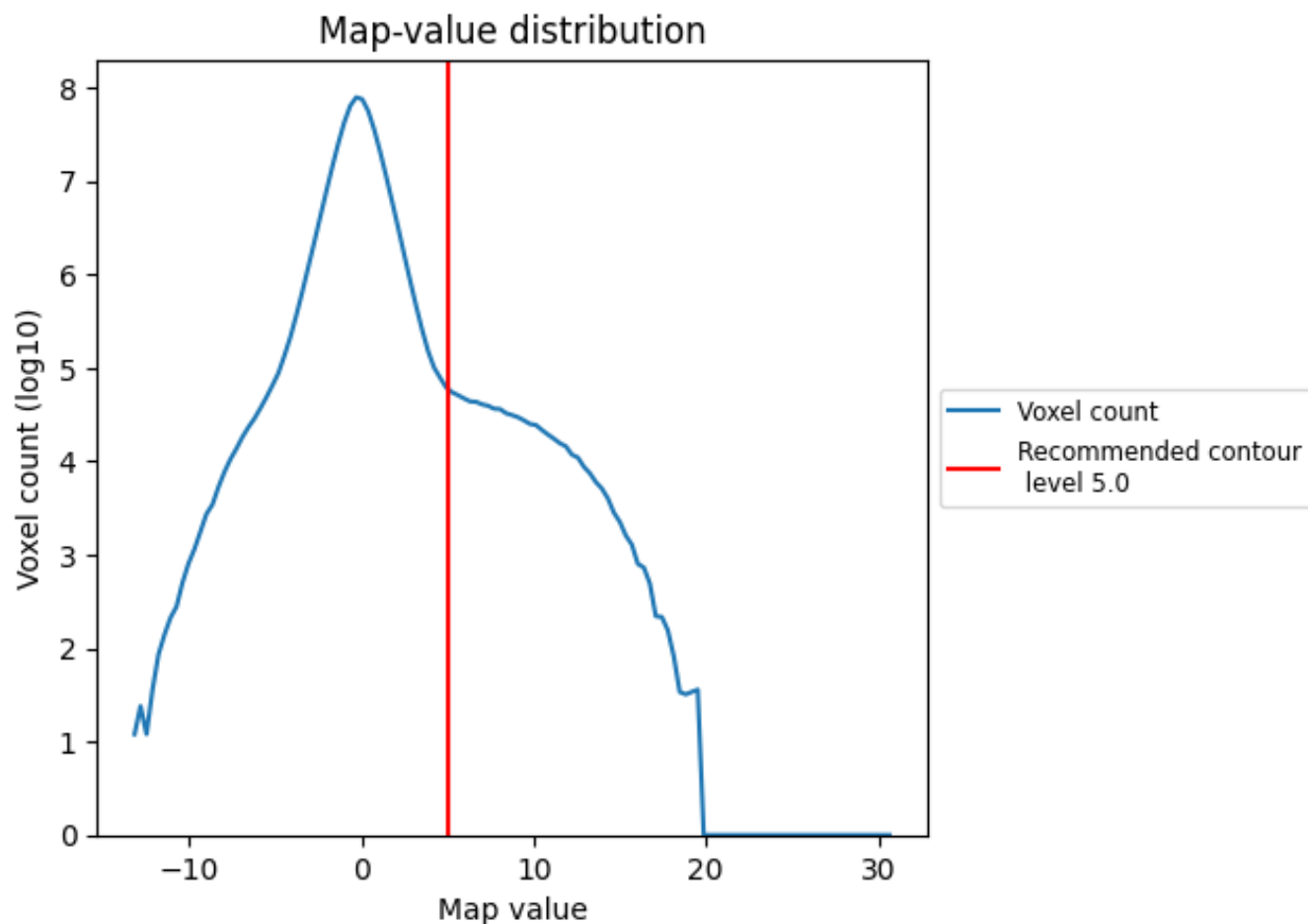
## 6.6 Mask visualisation [i](#)

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.

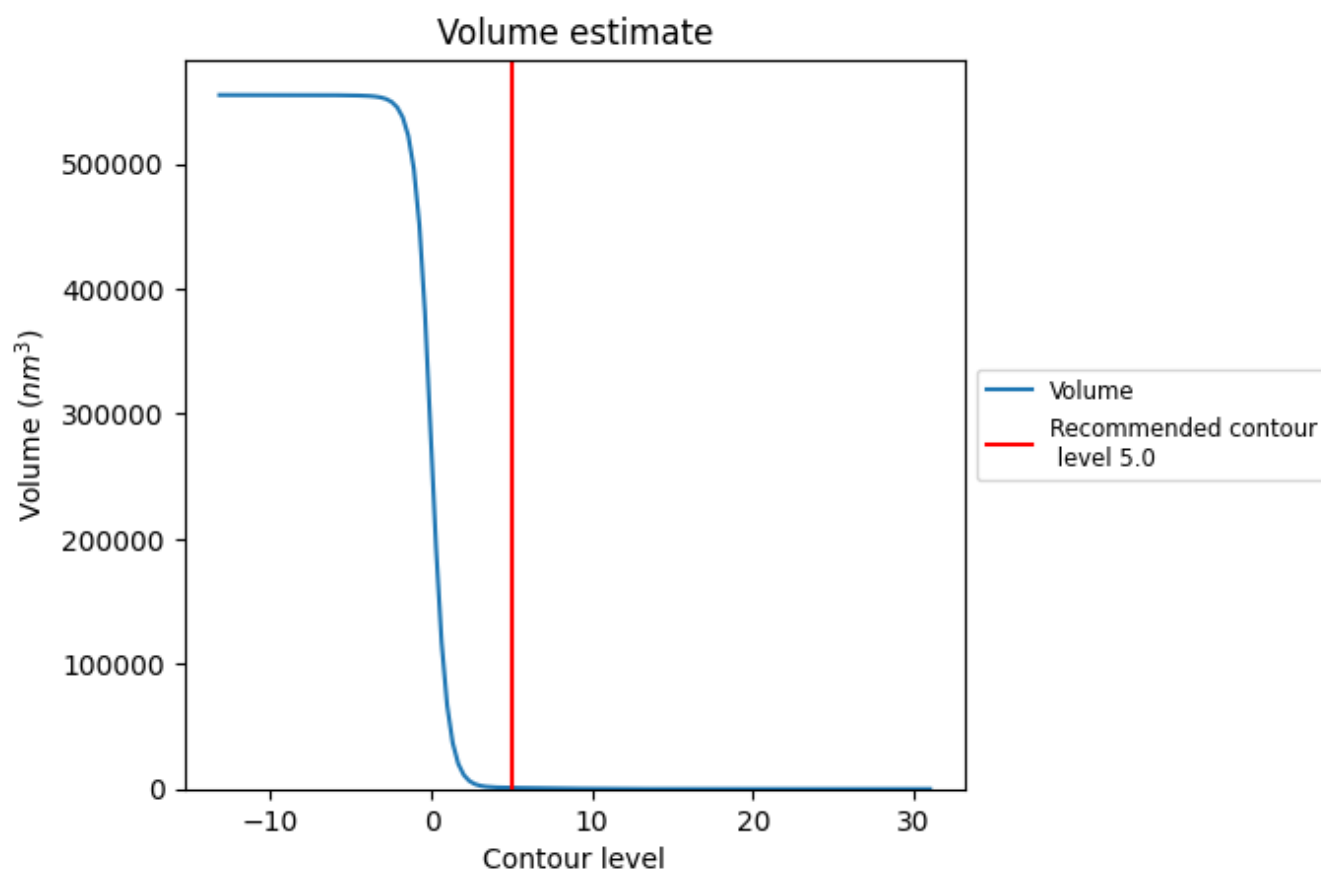
### 7.1 Map-value distribution [i](#)



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.



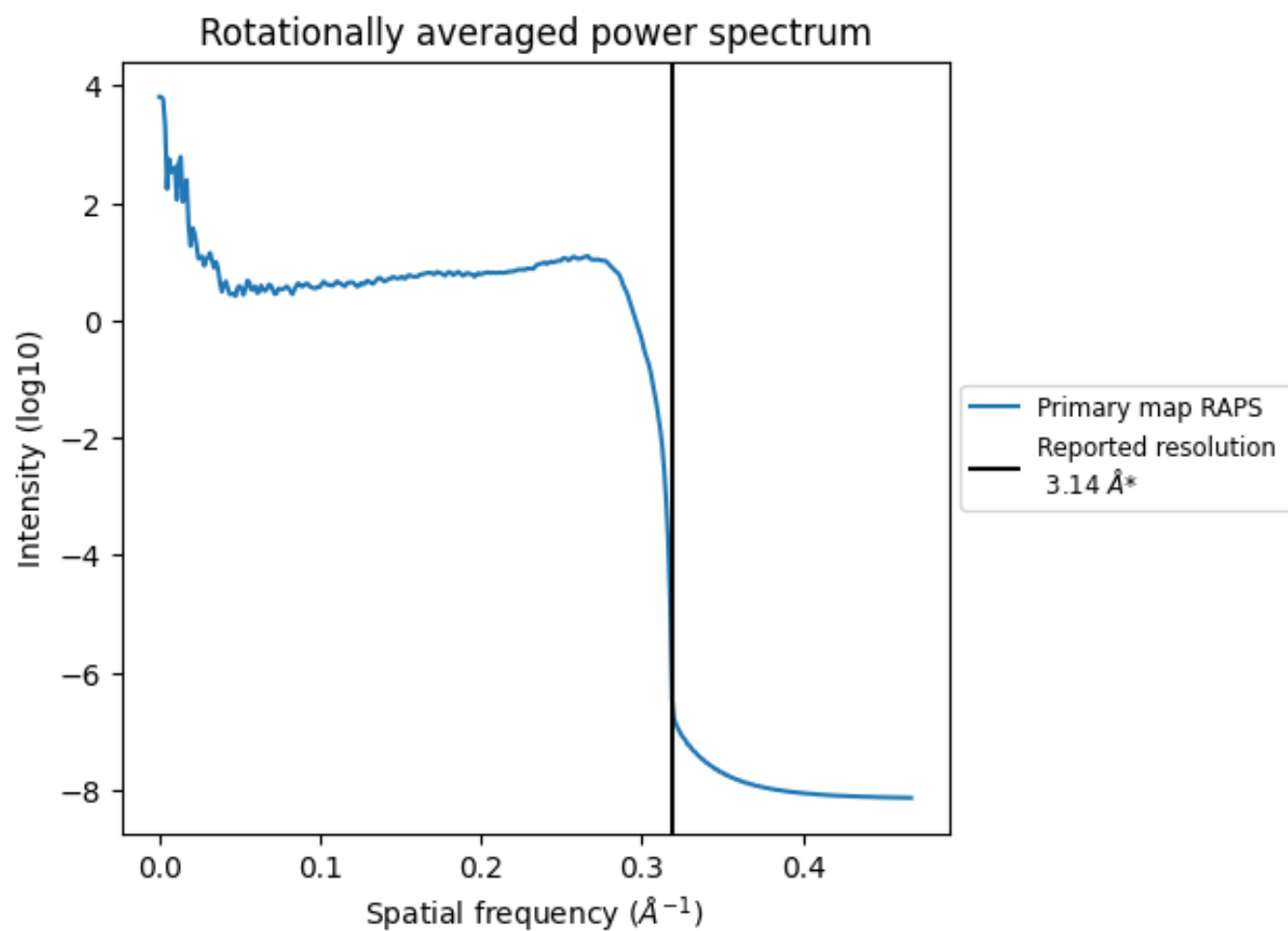
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 938 nm<sup>3</sup>; this corresponds to an approximate mass of 847 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 0.318 Å<sup>-1</sup>

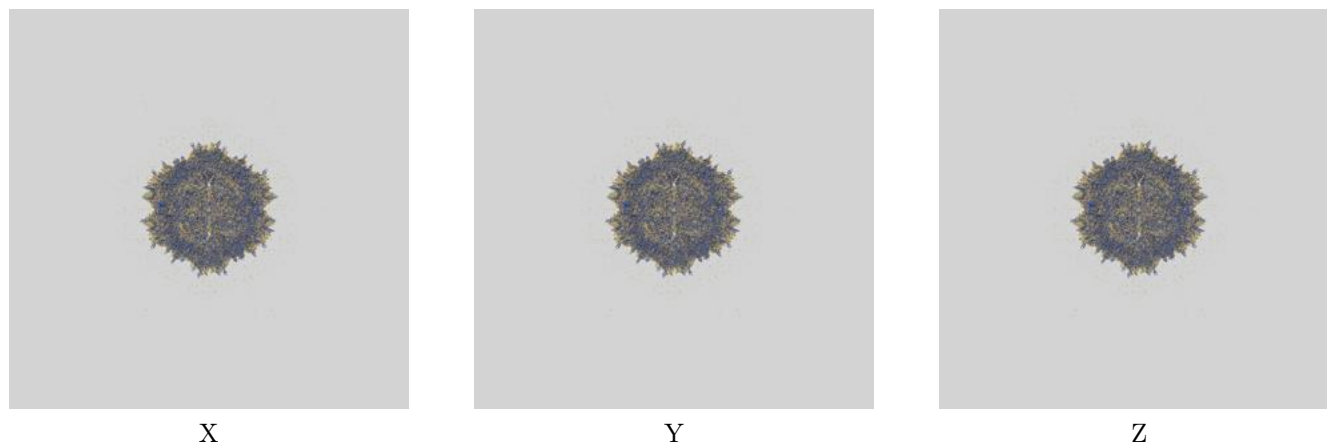
## 8 Fourier-Shell correlation

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

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

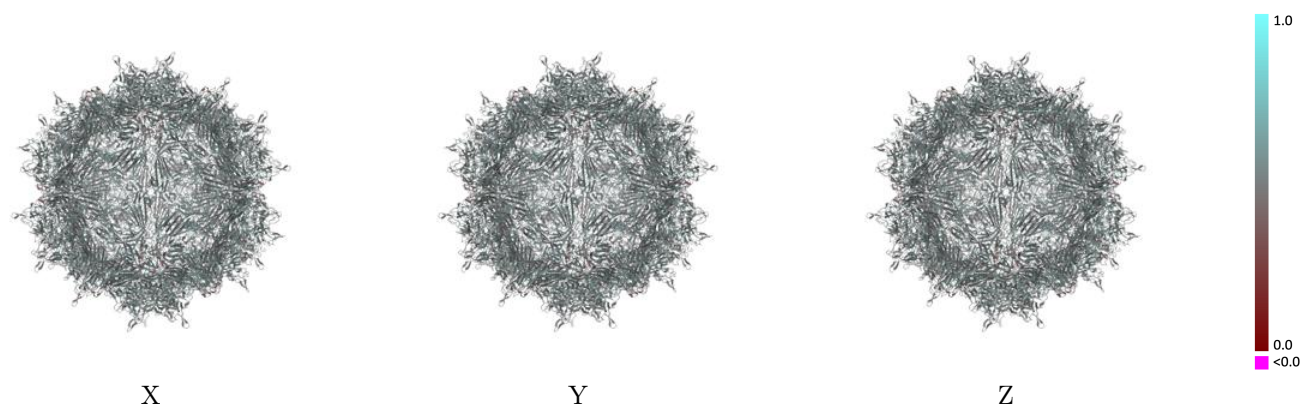
This section contains information regarding the fit between EMDB map EMD-24718 and PDB model 7RWL. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

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



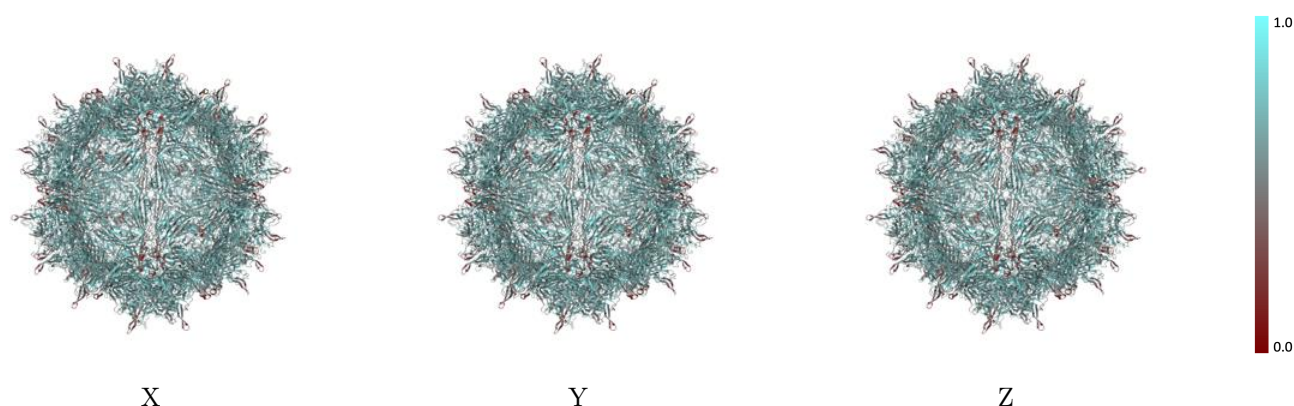
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



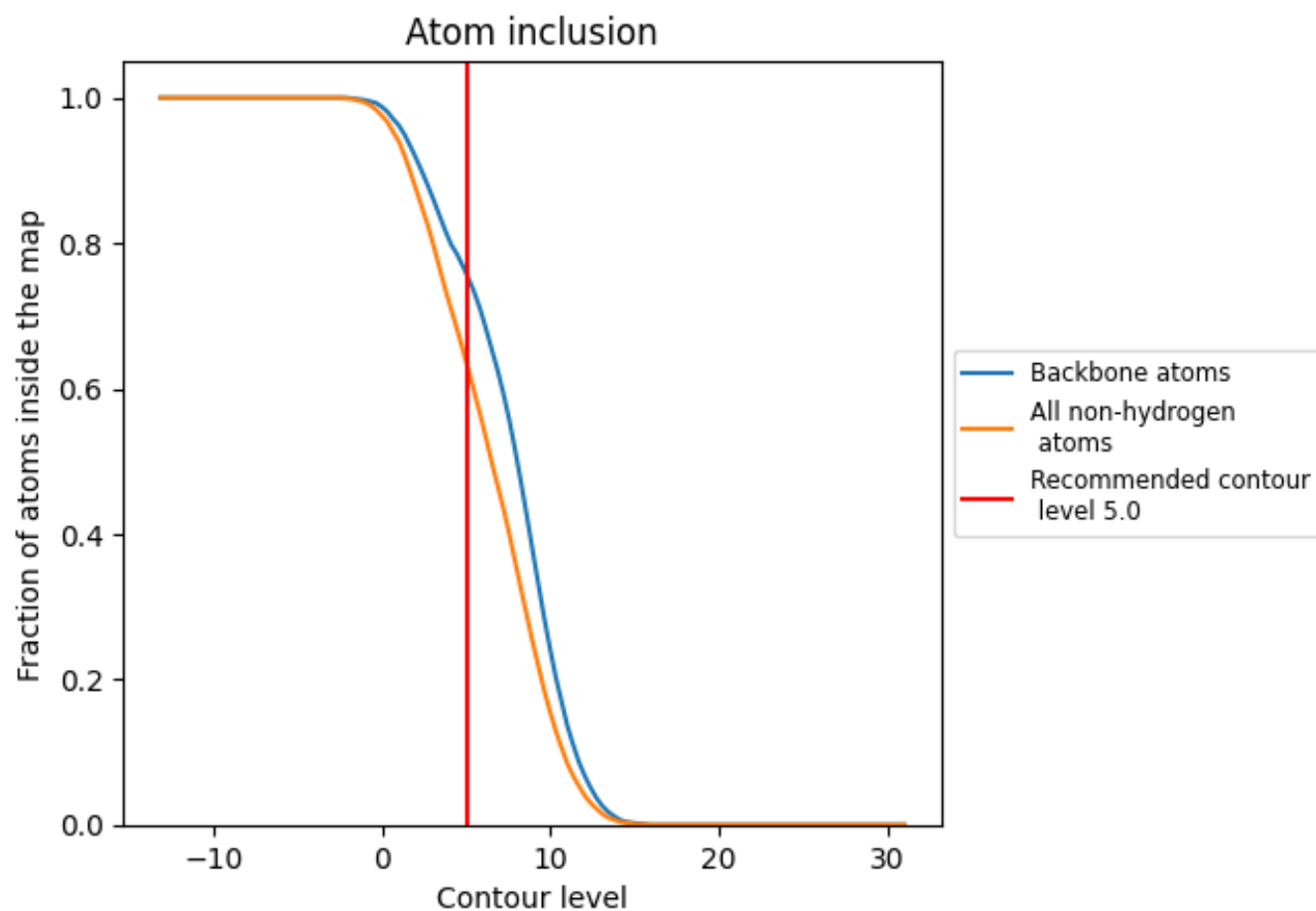
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (5.0).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 76% of all backbone atoms, 64% 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 (5.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6360	 0.5150
1	 0.6370	 0.5140
2	 0.6350	 0.5170
3	 0.6370	 0.5200
4	 0.6360	 0.5180
5	 0.6370	 0.5190
6	 0.6350	 0.5180
7	 0.6380	 0.5210
8	 0.6410	 0.5210
A	 0.6400	 0.5180
B	 0.6410	 0.5200
C	 0.6410	 0.5190
D	 0.6390	 0.5170
E	 0.6410	 0.5170
F	 0.6380	 0.5150
G	 0.6400	 0.5170
H	 0.6380	 0.5190
I	 0.6420	 0.5190
J	 0.6410	 0.5210
K	 0.6410	 0.5210
L	 0.6410	 0.5210
M	 0.6400	 0.5180
N	 0.6350	 0.5150
O	 0.6350	 0.5130
P	 0.6340	 0.5140
Q	 0.6360	 0.5130
R	 0.6350	 0.5130
S	 0.6320	 0.5120
T	 0.6330	 0.5100
U	 0.6360	 0.5110
V	 0.6340	 0.5130
W	 0.6350	 0.5160
X	 0.6340	 0.5140
Y	 0.6350	 0.5180
Z	 0.6410	 0.5200



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Chain	Atom inclusion	Q-score
a	 0.6390	 0.5220
b	 0.6390	 0.5220
c	 0.6370	 0.5190
d	 0.6320	 0.5120
e	 0.6310	 0.5120
f	 0.6310	 0.5130
g	 0.6330	 0.5100
h	 0.6310	 0.5110
i	 0.6310	 0.5080
j	 0.6310	 0.5080
k	 0.6310	 0.5090
l	 0.6310	 0.5090
m	 0.6340	 0.5130
n	 0.6310	 0.5100
o	 0.6400	 0.5200
p	 0.6370	 0.5170
q	 0.6320	 0.5120
r	 0.6360	 0.5110
s	 0.6350	 0.5140
t	 0.6350	 0.5160
u	 0.6340	 0.5160
v	 0.6320	 0.5130
w	 0.6300	 0.5090
x	 0.6330	 0.5080
y	 0.6320	 0.5110
z	 0.6330	 0.5140