



wwPDB EM Validation Summary Report ⓘ

Nov 24, 2022 – 11:37 AM EST

PDB ID : 7RWT
EMDB ID : EMD-24719
Title : Adeno-associated virus type 2
Authors : Hull, J.A.; Mietzsch, M.; Chipman, P.; Strugatsky, D.; McKenna, R.
Deposited on : 2021-08-20
Resolution : 2.43 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

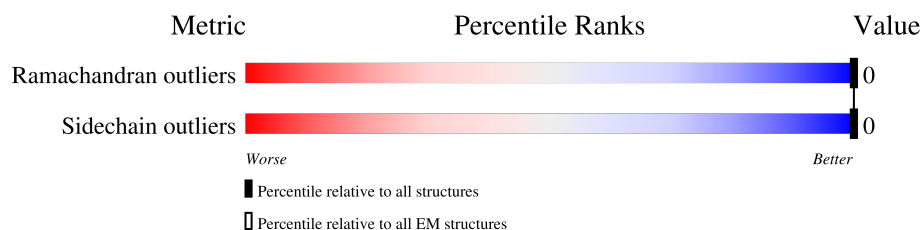
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.43 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.






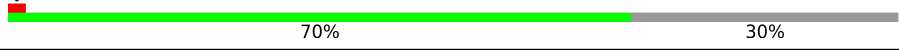
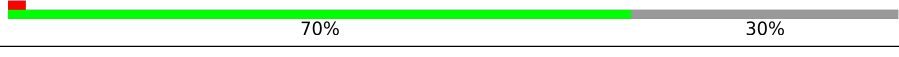



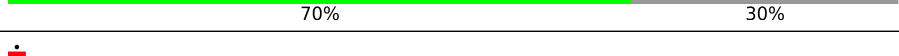
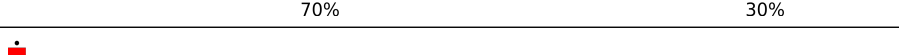
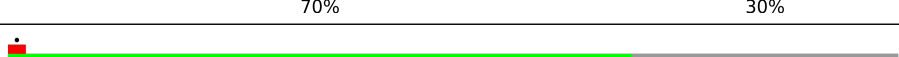
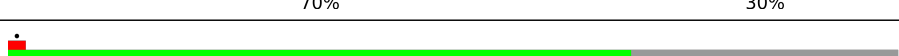

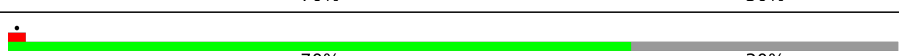
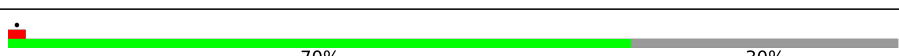
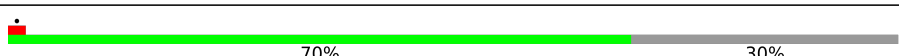





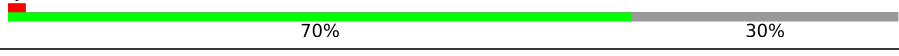

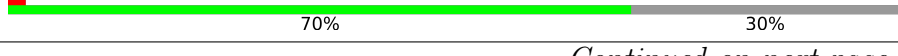

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 ≥ 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	70% 30%
1	2	735	70% 30%
1	3	735	70% 30%
1	4	735	70% 30%
1	5	735	70% 30%
1	6	735	70% 30%
1	7	735	70% 30%
1	8	735	70% 30%
1	A	735	70% 30%







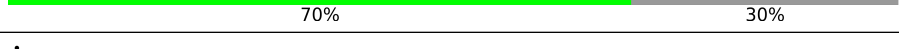
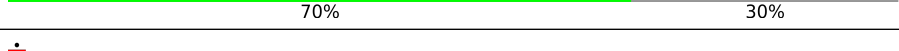
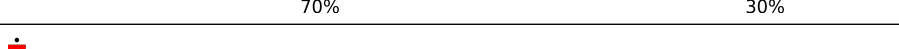
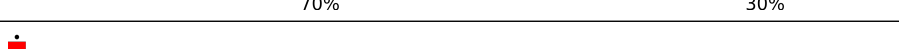
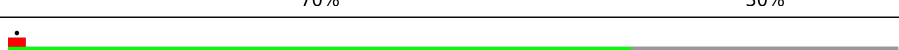

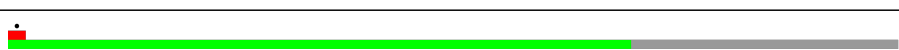

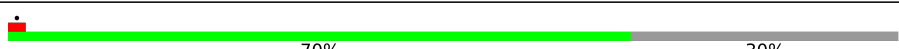





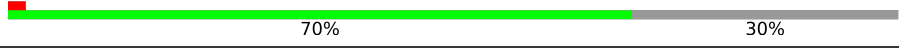
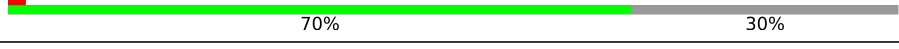



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Mol	Chain	Length	Quality of chain
1	B	735	
1	C	735	
1	D	735	
1	E	735	
1	F	735	
1	G	735	
1	H	735	
1	I	735	
1	J	735	
1	K	735	
1	L	735	
1	M	735	
1	N	735	
1	O	735	
1	P	735	
1	Q	735	
1	R	735	
1	S	735	
1	T	735	
1	U	735	
1	V	735	
1	W	735	
1	X	735	
1	Y	735	
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	 70% 30%

2 Entry composition

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
1	7	517	Total 4143	C 2607	N 723	O 800	S 13	0	0

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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		

Frequency	Percentage
Often	70%
Not often	30%

L735

-
- | Frequency | Percentage |
|-----------|------------|
| Often | 70% |
| Not often | 30% |

S707 **L735**

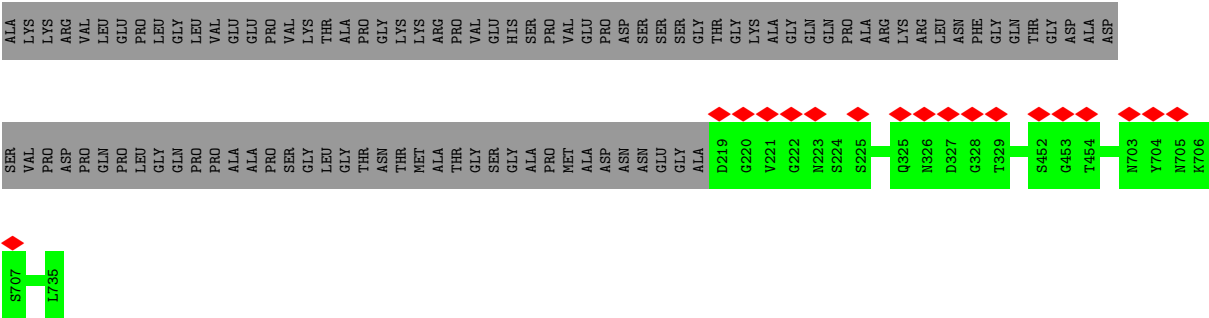
-
- | Frequency | Percentage |
|--------------|------------|
| Daily | 70% |
| Occasionally | 30% |



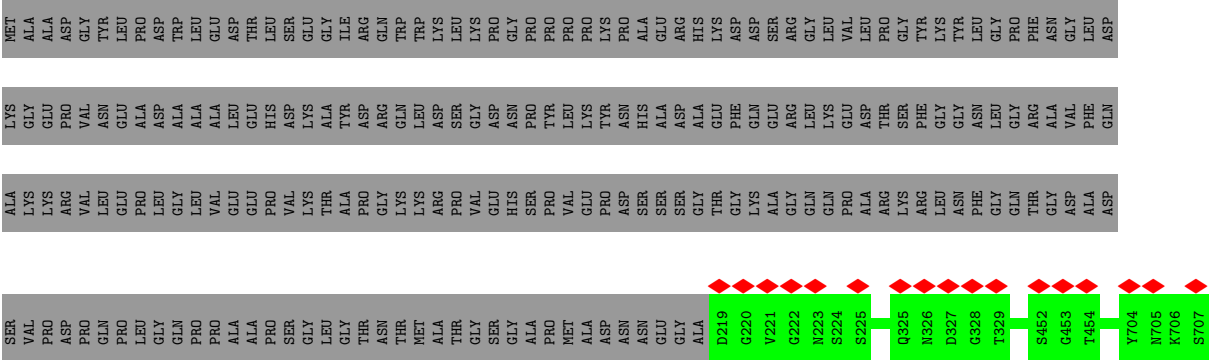
- Molecule 1: Capsid protein VP1

- Molecule 1: Capsid protein VP1

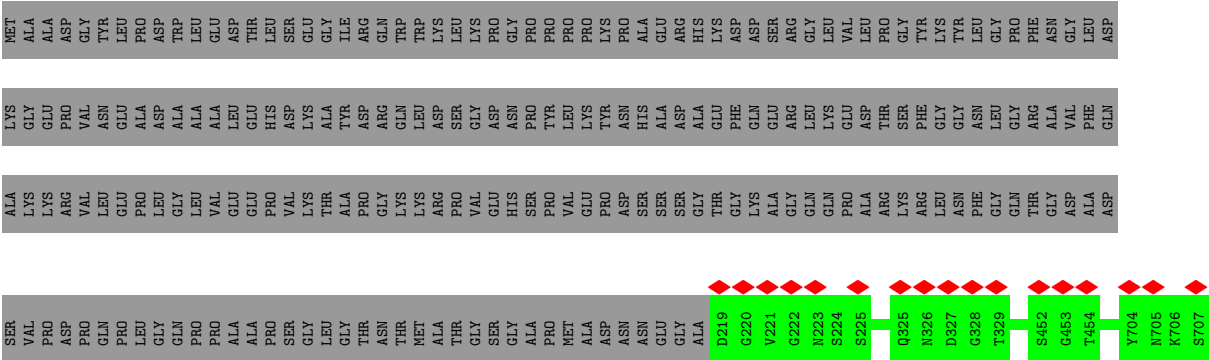
- Molecule 1: Capsid protein VP1



● Molecule 1: Capsid protein VP1

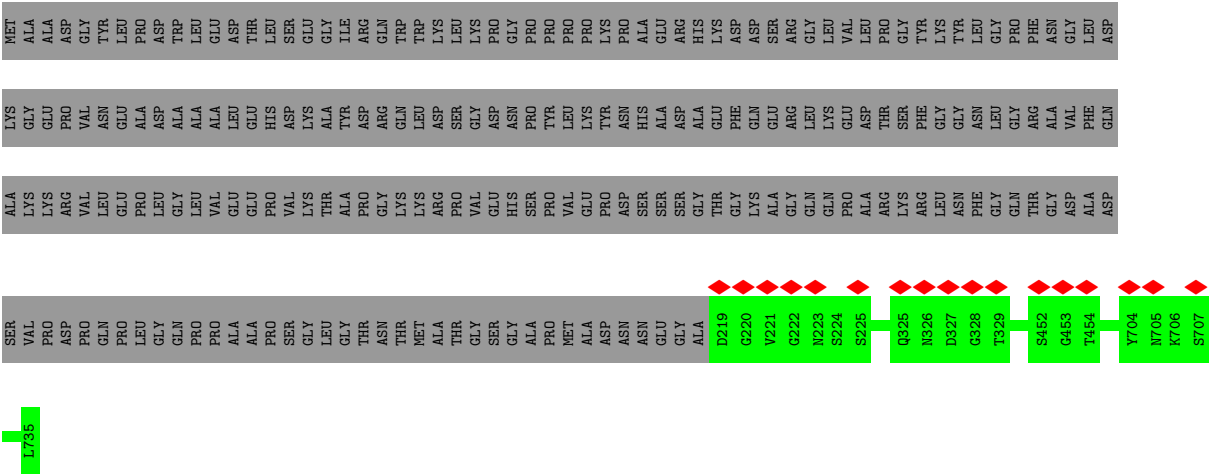


● Molecule 1: Capsid protein VP1

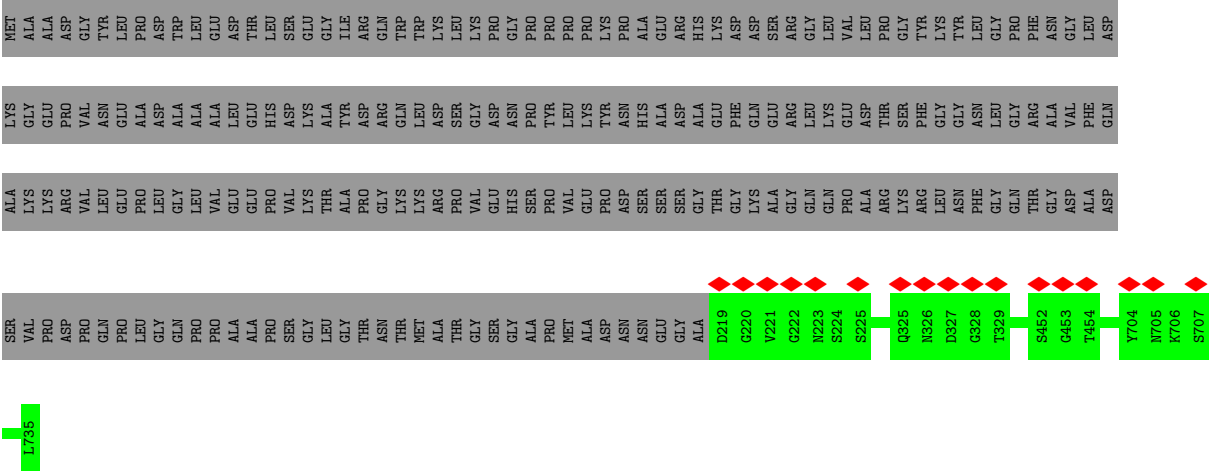


● Molecule 1: Capsid protein VP1

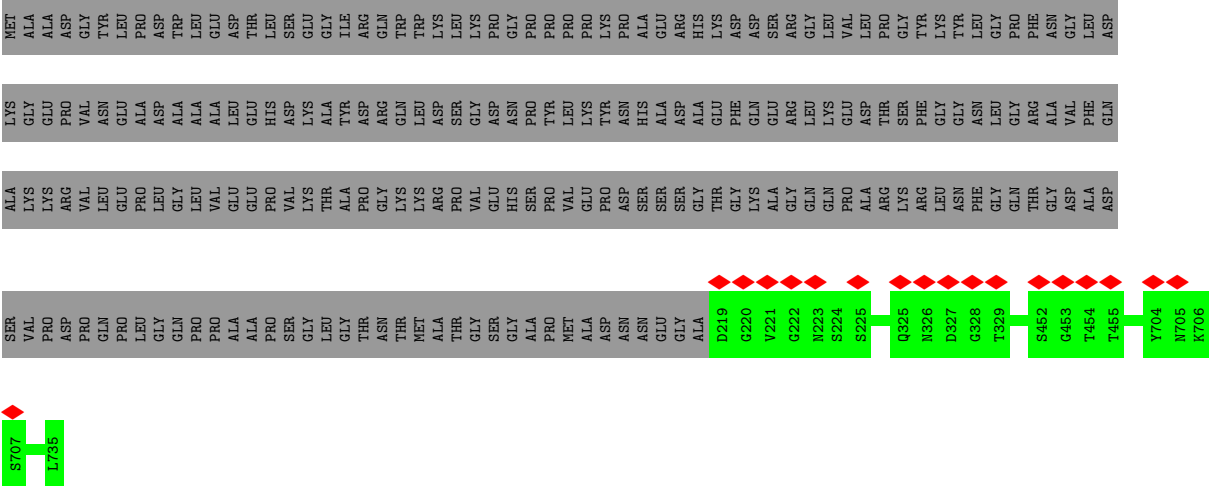




• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1



SER	VAL	PRO	ASP	PRO	GLN	PRO	LEU	GLY	GLN	PRO	PRO	ALA	ALA	PRO	SER	SER	GLY	LEU	GLY	THR	ASN	THR	MET	ALA	THR	GLY	SER	GLY	ALA	PRO	PRO	MET	ALA	ASP	ASN	ASN	GLU	GLY	ALA	D219	G220	V221	G222	N223	S224	S225	Q325	N326	D327	G328	T329	S452	G453	T454	N703	Y704	N705	K706
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• Molecule 1: Capsid protein VP1



MET	ALA	ALA	ASP	GLY	TYR	LEU	PRO	ASP	TRP	ALA	LEU	GLU	ASP	THR	LEU	GLY	TYR	ILE	ARG	GLN	TRP	TRP	LEU	ASP	LYS	LEU	GLY	PRO	ASP	GLY	ALA	PRO	PRO	PRO	PRO	GLU	ALA	HIS	LYS	ASP	ASP	SER	ARG	GLY	LEU	VAL	LEU	ASP	LEU	PRO	GLY	TYR	LYS	LEU	ASN	GLY	ARG	PHE	ASN	GLY	LEU	ASP
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LYS	GLY	GLU	PRO	ASN	GLU	ALA	PRO	ALA	ASP	ALA	LEU	GLU	HIS	ASP	GLU	LYS	ALA	TYR	ASP	ARG	GLN	TRP	LEU	ASP	SER	GLY	THR	GLY	ASP	ASN	GLU	ALA	THR	LYS	TYR	ASN	HIS	ALA	ALA	ASP	ALA	GLY	ARG	LEU	LEU	LYS	GLU	GLU	VAL	LEU	THR	PHE	SER	GLY	TYR	LYS	ASN	PHE	GLY	ARG	ALA	VAL	PHE	GLN
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ALA	LYS	LYS	ARG	VAL	LEU	GLU	PRO	GLY	GLY	ALA	LEU	VAL	GLU	GLU	PRO	VAL	THR	ALA	PRO	GLY	LYS	TRP	LEU	ASP	PRO	VAL	GLU	GLY	THR	GLY	GLY	ALA	GLY	HIS	SER	ALA	SER	ALA	SER	ASP	GLY	GLY	THR	GLY	VAL	GLU	VAL	PRO	GLU	GLY	THR	ARG	LYS	LEU	ASN	PHE	GLY	GLY	THR	GLY	ASP	ALA	ALA	ASP
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SER	VAL	PRO	ASP	PRO	GLN	PRO	PRO	LEU	GLY	GLN	PRO	PRO	ALA	ALA	PRO	SER	GLY	LEU	GLY	THR	ASN	THR	MET	ALA	THR	GLY	SER	ASP	GLY	ALA	PRO	PRO	MET	ALA	ASP	ASN	ASN	GLU	GLY	ALA	HIS	LYS	D219	G220	V221	G222	N223	S224	S225	Q325	N326	D327	G328	T329	S452	G453	T454	Y704	N705	K706	S707
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• Molecule 1: Capsid protein VP1



MET	ALA	ALA	ASP	GLY	TYR	LEU	PRO	ASP	TRP	ALA	LEU	GLU	ASP	THR	LEU	GLY	TYR	ILE	ARG	GLN	TRP	TRP	LEU	ASP	LYS	LEU	GLY	PRO	ASP	GLY	ALA	PRO	PRO	PRO	PRO	GLU	ALA	HIS	LYS	ASP	ASP	SER	ARG	GLY	LEU	VAL	LEU	ASP	LEU	PRO	GLY	TYR	LYS	LEU	ASN	PHE	ASN	GLY	LEU	ASP
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LYS	GLY	GLU	PRO	ASN	GLU	ALA	PRO	ALA	ASP	ALA	LEU	GLU	HIS	ASP	GLU	LYS	ALA	TYR	ASP	ARG	GLN	TRP	LEU	ASP	SER	GLY	THR	GLY	ASP	ASN	GLU	ALA	THR	LYS	TYR	ASN	HIS	ALA	SER	ALA	SER	ASP	ALA	GLY	THR	GLY	VAL	GLU	VAL	LEU	THR	PHE	SER	GLY	TYR	LYS	ASN	PHE	GLY	ARG	ALA	VAL	PHE	GLN
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ALA	LYS	LYS	ARG	VAL	LEU	GLU	PRO	GLY	GLY	ALA	LEU	VAL	GLU	GLU	PRO	VAL	THR	ALA	PRO	GLY	LYS	TRP	LEU	ASP	PRO	VAL	GLU	GLY	THR	GLY	GLY	ALA	GLY	HIS	SER	ALA	SER	ALA	SER	ASP	GLY	THR	GLY	VAL	GLU	VAL	PRO	GLU	GLY	THR	ARG	LYS	LEU	ASN	PHE	GLY	GLY	THR	GLY	ASP	ALA	ALA	ASP
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SER	VAL	PRO	ASP	PRO	GLN	PRO	PRO	LEU	GLY	GLN	PRO	PRO	ALA	ALA	PRO	SER	GLY	LEU	GLY	THR	ASN	THR	MET	ALA	THR	GLY	SER	ASP	GLY	ALA	PRO	PRO	MET	ALA	ASP	ASN	ASN	GLU	GLY	ALA	HIS	LYS	D219	G220	V221	G222	N223	S224	S225	Q325	N326	D327	G328	T329	S452	G453	T454	Y704	N705	K706	S707
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• Molecule 1: Capsid protein VP1



MET	ALA	ALA	ASP	GLY	TYR	LEU	PRO	ASP	TRP	ALA	LEU	GLU	ASP	THR	LEU	GLY	TYR	ILE	ARG	GLN	TRP	TRP	LEU	ASP	LYS	LEU	GLY	PRO	ASP	GLY	ALA	PRO	PRO	PRO	PRO	GLU	ALA	SER	ALA	SER	ASP	GLY	THR	GLY	VAL	LEU	LEU	VAL	PRO	GLY	TYR	LYS	LEU	GLY	GLY	PHE	ASN	GLY	LEU	LEU	ASP
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Frequency	Percentage
Often	70%
Not often	30%

L735

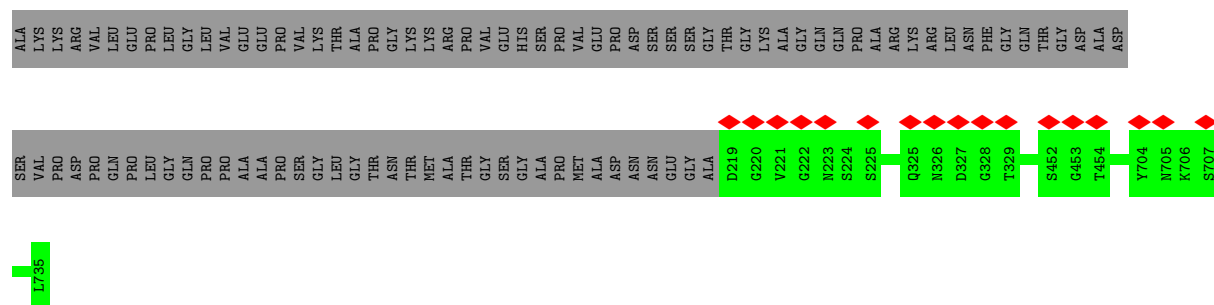
- Chain W:



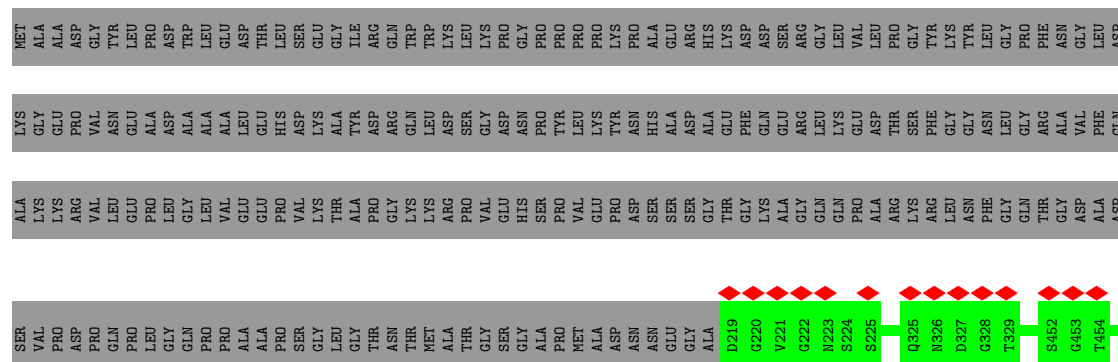
S707

- Chain X:

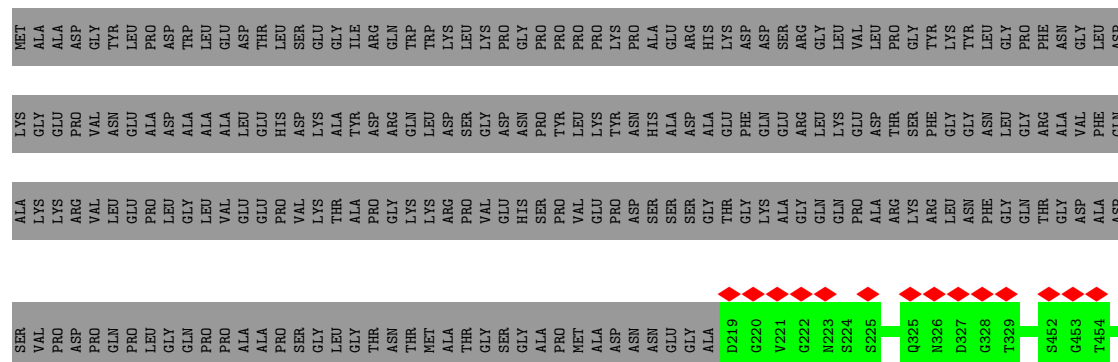
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- Molecule 1: Capsid protein VP1



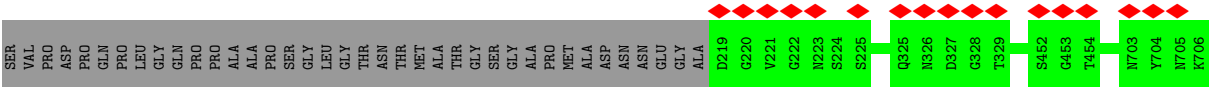
- Molecule 1: Capsid protein VP1



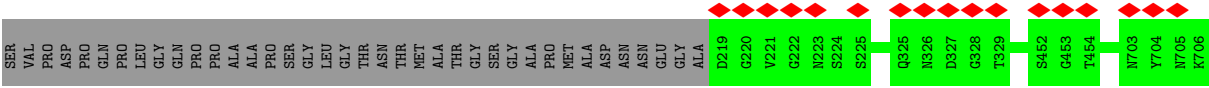
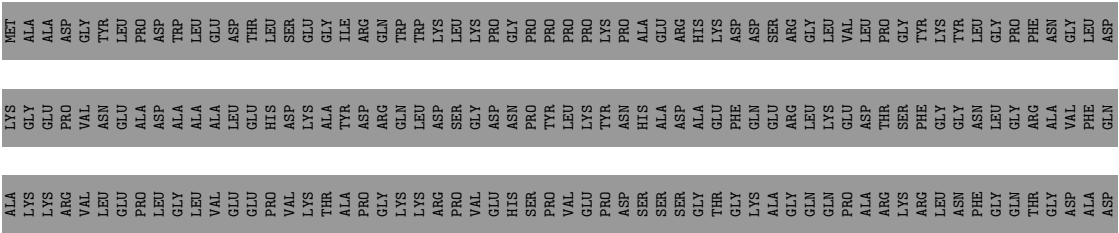
- Molecule 1: Capsid protein VP1



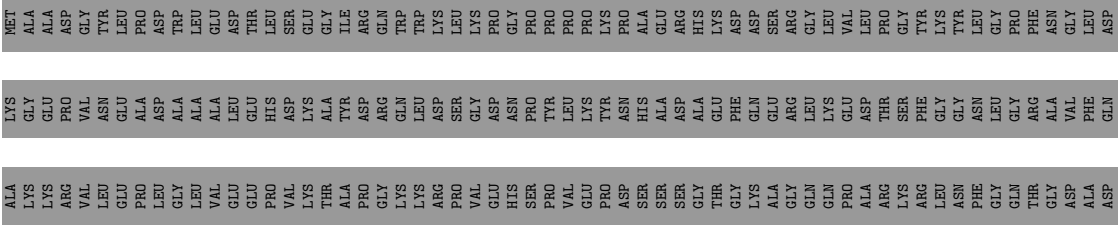




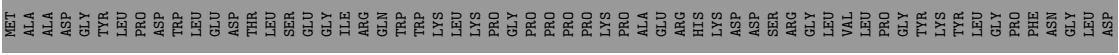
• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1

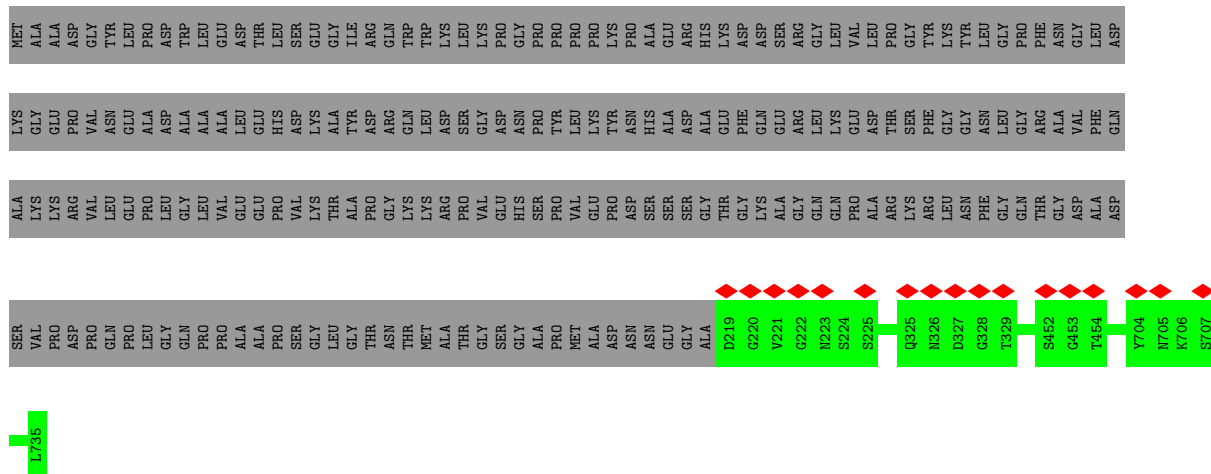


• Molecule 1: Capsid protein VP1

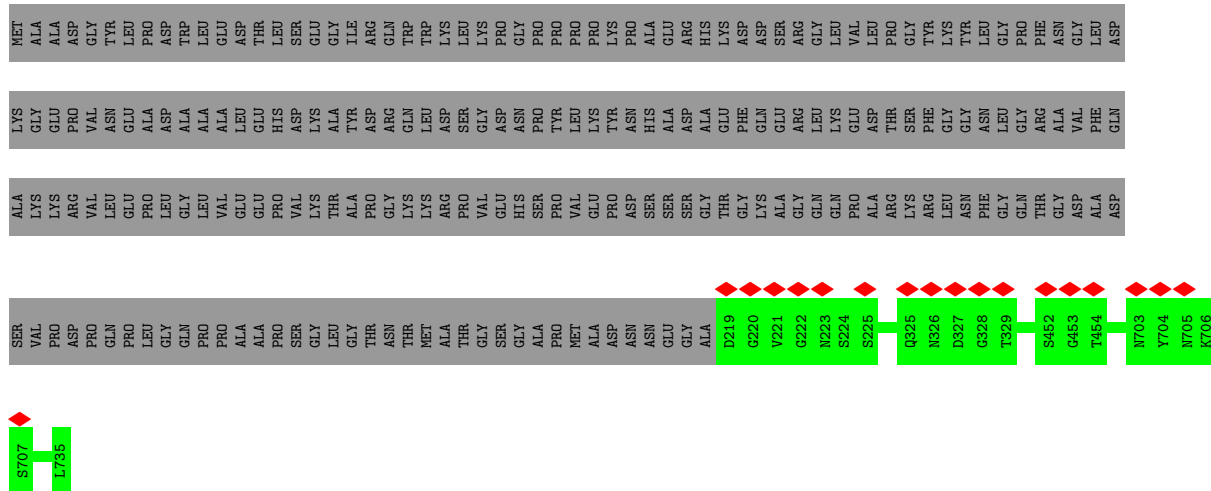




- Chain m: 



- Chain n:  70% 30%



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MET	ALA	LYS	GLY	GLU	PRO	VAL	ASN	GLU	PRO	ASP	ALA	GLY	LEU	THR	LEU	HIS	ASP	ARG	GLN	TRP	LYS	LEU	PRO	GLY	ASP	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO	PRO
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• Molecule 1: Capsid protein VP1



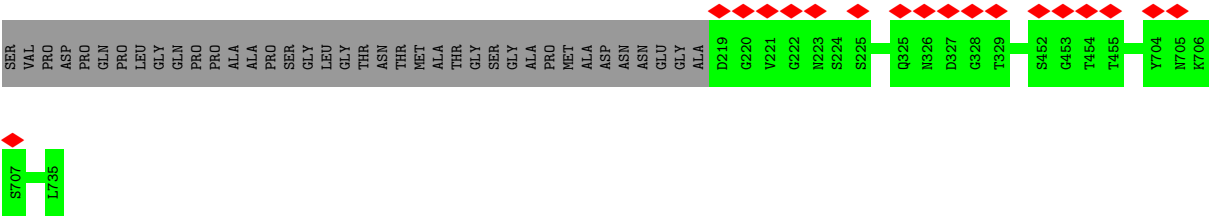
MET	LYS	GLY	ALA	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY</
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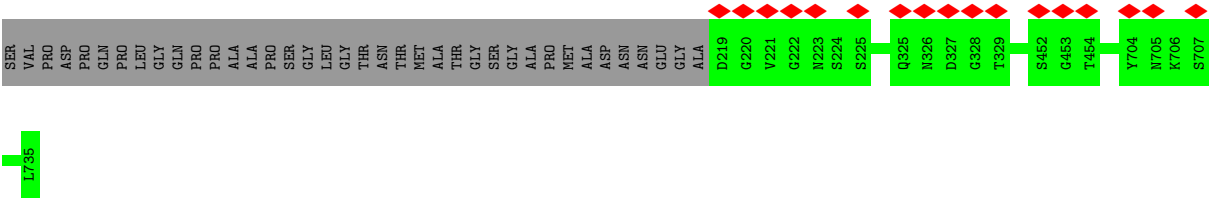
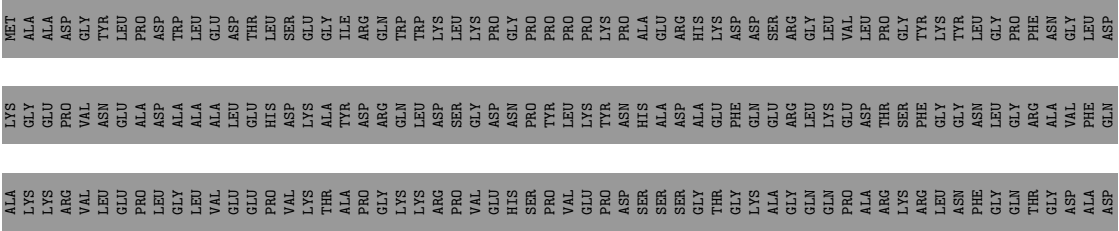
• Molecule 1: Capsid protein VP1



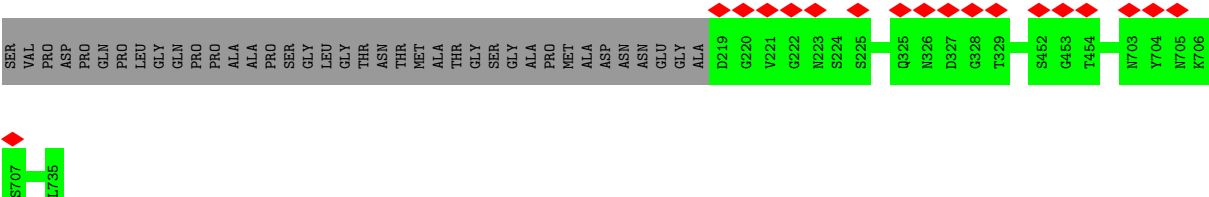
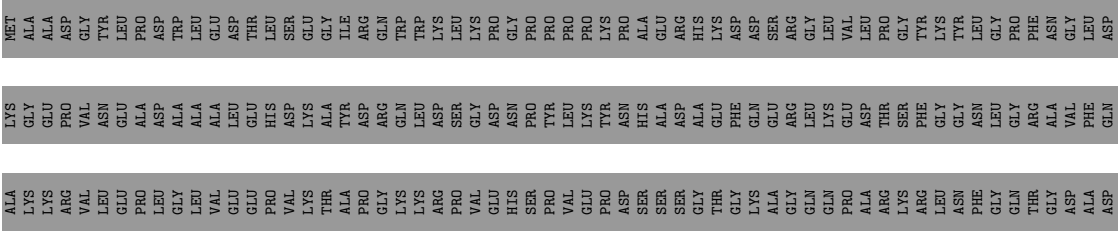
MET	LYS	ALA	GLY	GLU	PRO	VAL	ASN	GLU	ASP	ALA	ASP	TRP	LEU	GLU	GLY	ILE	ARG	GLN	TRP	LYS	LEU	LYS	PRO	GLY	ASP	PRO	PRO	PRO	PRO	PRO	PRO	GLU	ALA	GLY	ASP	ARG	HIS	LYS	ASP	PHE	GLY	LYS	TYR	LEU	VAL	PRO	PRO	GLY	THR	PRO	GLY	THR	LEU	ASP																																																																																	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



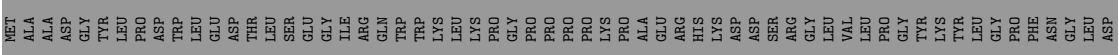
• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1

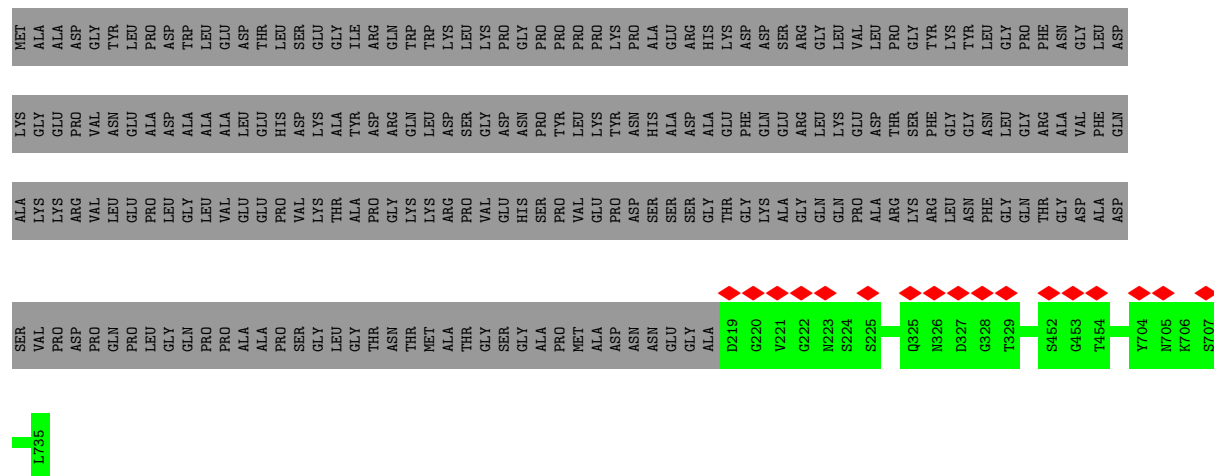


• Molecule 1: Capsid protein VP1

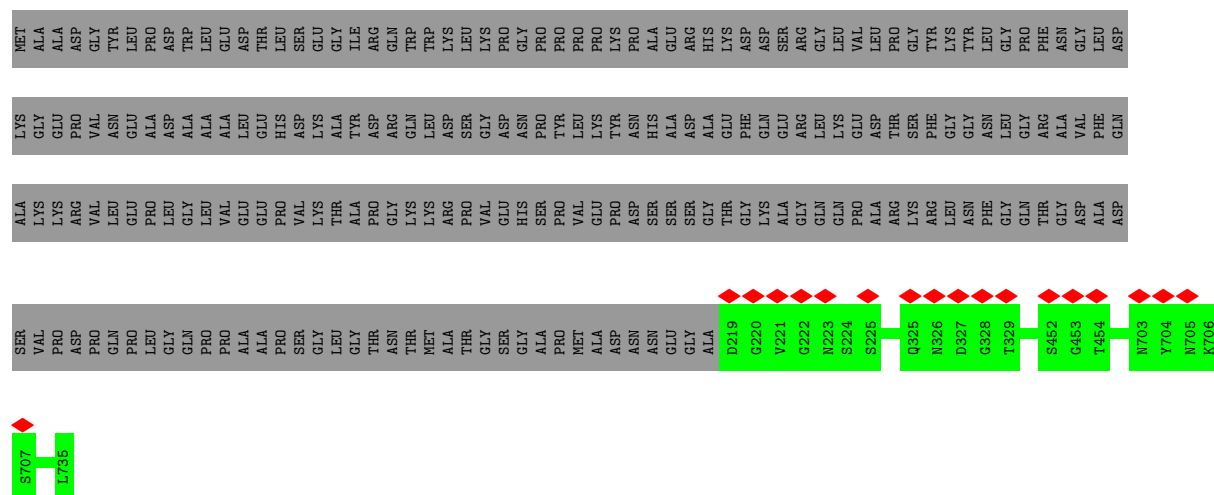




- Chain x:  70% 30%



- Chain γ : 



- Molecule 1: Capsid protein VP1

Frequency	Percentage
Often	70%
Not often	30%

L735

-
- | Frequency | Percentage |
|-----------|------------|
| Often | 70% |
| Not often | 30% |

L735

-
- | Frequency | Percentage |
|-----------|------------|
| Often | 70% |
| Not often | 30% |





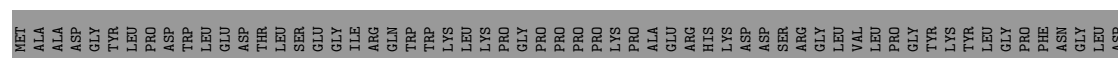
- Chain 6:  70% 30%

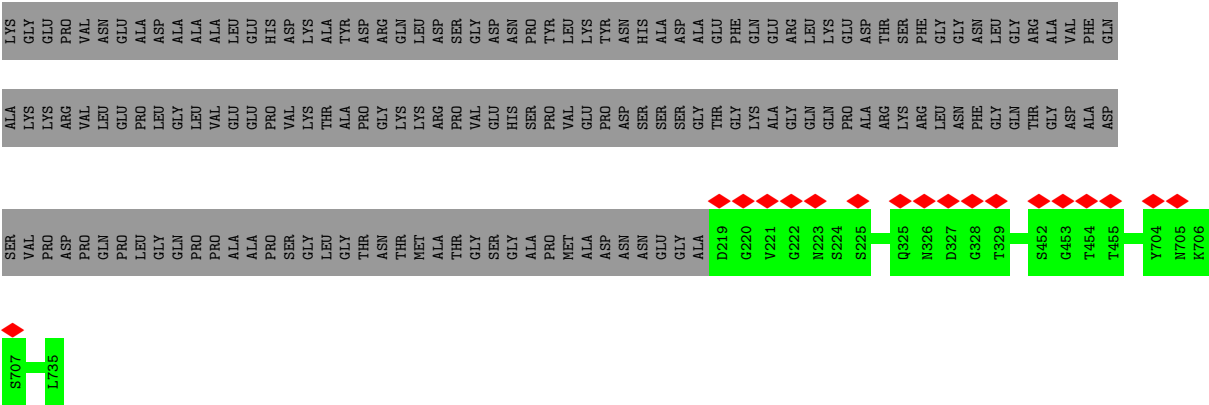


- Chain 7: 



- Chain 8:  70% 30%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46289	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	21.906	Depositor
Minimum map value	-12.086	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	3.0	Depositor
Map size (\AA)	535.0, 535.0, 535.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.42	0/4266	0.51	0/5815
1	2	0.42	0/4266	0.51	0/5815
1	3	0.42	0/4266	0.51	0/5815
1	4	0.42	0/4266	0.51	0/5815
1	5	0.42	0/4266	0.51	0/5815
1	6	0.42	0/4266	0.51	0/5815
1	7	0.42	0/4266	0.51	0/5815
1	8	0.42	0/4266	0.51	0/5815
1	A	0.42	0/4266	0.51	0/5815
1	B	0.42	0/4266	0.51	0/5815
1	C	0.42	0/4266	0.51	0/5815
1	D	0.42	0/4266	0.51	0/5815
1	E	0.42	0/4266	0.51	0/5815
1	F	0.42	0/4266	0.51	0/5815
1	G	0.42	0/4266	0.51	0/5815
1	H	0.42	0/4266	0.51	0/5815
1	I	0.42	0/4266	0.51	0/5815
1	J	0.42	0/4266	0.51	0/5815
1	K	0.42	0/4266	0.51	0/5815
1	L	0.42	0/4266	0.51	0/5815
1	M	0.42	0/4266	0.51	0/5815
1	N	0.42	0/4266	0.51	0/5815
1	O	0.42	0/4266	0.51	0/5815
1	P	0.42	0/4266	0.51	0/5815
1	Q	0.42	0/4266	0.51	0/5815
1	R	0.42	0/4266	0.51	0/5815
1	S	0.42	0/4266	0.51	0/5815
1	T	0.42	0/4266	0.51	0/5815
1	U	0.42	0/4266	0.51	0/5815
1	V	0.42	0/4266	0.51	0/5815
1	W	0.42	0/4266	0.51	0/5815
1	X	0.42	0/4266	0.51	0/5815
1	Y	0.42	0/4266	0.51	0/5815
1	Z	0.42	0/4266	0.51	0/5815

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.42	0/4266	0.51	0/5815
1	b	0.42	0/4266	0.51	0/5815
1	c	0.42	0/4266	0.51	0/5815
1	d	0.42	0/4266	0.51	0/5815
1	e	0.42	0/4266	0.51	0/5815
1	f	0.42	0/4266	0.51	0/5815
1	g	0.42	0/4266	0.51	0/5815
1	h	0.42	0/4266	0.51	0/5815
1	i	0.42	0/4266	0.51	0/5815
1	j	0.42	0/4266	0.51	0/5815
1	k	0.42	0/4266	0.51	0/5815
1	l	0.42	0/4266	0.51	0/5815
1	m	0.42	0/4266	0.51	0/5815
1	n	0.42	0/4266	0.51	0/5815
1	o	0.42	0/4266	0.51	0/5815
1	p	0.42	0/4266	0.51	0/5815
1	q	0.42	0/4266	0.51	0/5815
1	r	0.42	0/4266	0.51	0/5815
1	s	0.42	0/4266	0.51	0/5815
1	t	0.42	0/4266	0.51	0/5815
1	u	0.42	0/4266	0.51	0/5815
1	v	0.42	0/4266	0.51	0/5815
1	w	0.42	0/4266	0.51	0/5815
1	x	0.42	0/4266	0.51	0/5815
1	y	0.42	0/4266	0.51	0/5815
1	z	0.42	0/4266	0.51	0/5815
All	All	0.42	0/255960	0.51	0/348900

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	502 (98%)	13 (2%)	0	100	100
1	2	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	3	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	4	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	5	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	6	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	7	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	8	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	A	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	B	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	C	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	D	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	E	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	F	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	G	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	H	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	I	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	J	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	K	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	L	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	M	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	N	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	O	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	P	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	Q	515/735 (70%)	501 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	S	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	T	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	U	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	V	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	W	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	X	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	Y	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	Z	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	a	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	b	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	c	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	d	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	e	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	f	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	g	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	h	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	i	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	j	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	k	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	l	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	m	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	n	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	o	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	p	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	q	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	r	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	s	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	t	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	u	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	v	515/735 (70%)	501 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	w	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	x	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
1	y	515/735 (70%)	501 (97%)	14 (3%)	0	100	100
1	z	515/735 (70%)	502 (98%)	13 (2%)	0	100	100
All	All	30900/44100 (70%)	30094 (97%)	806 (3%)	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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
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. 5 of 600 such sidechains are listed below:

Mol	Chain	Res	Type
1	u	319	GLN
1	6	319	GLN
1	v	623	HIS
1	u	270	ASN
1	1	229	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry [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.

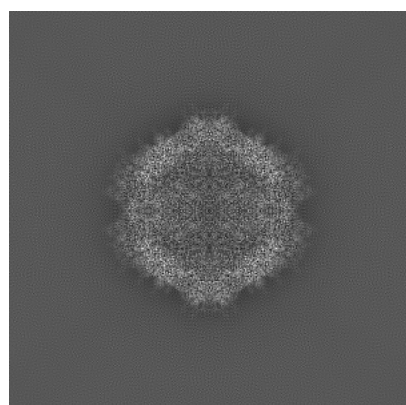
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24719. These allow visual inspection of the internal detail of the map and identification of artifacts.

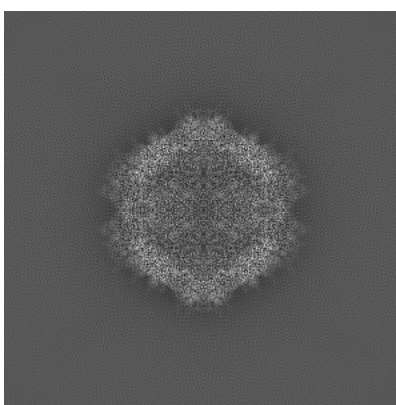
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

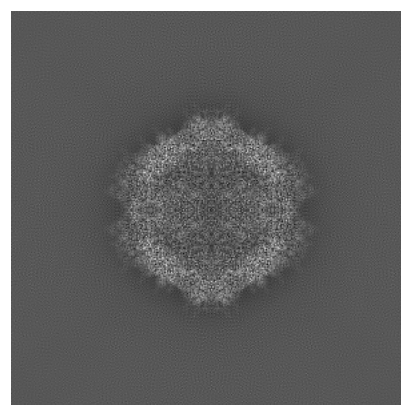
6.1.1 Primary map



X



Y

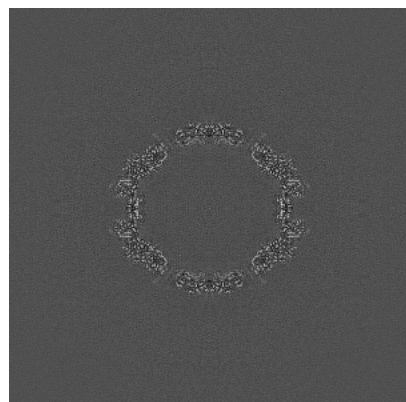


Z

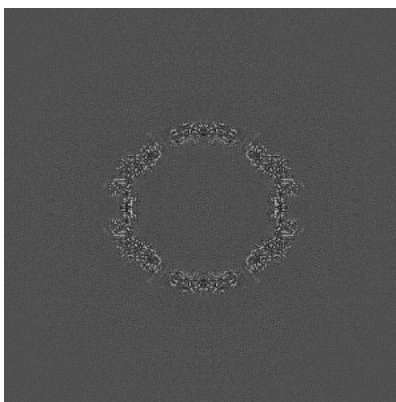
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

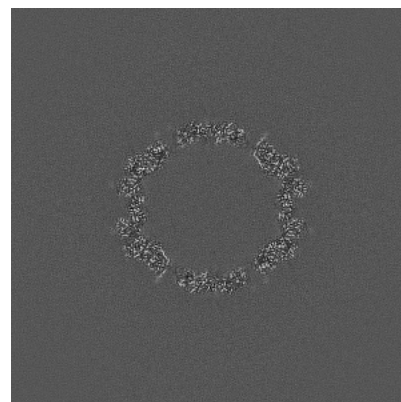
6.2.1 Primary map



X Index: 250



Y Index: 250

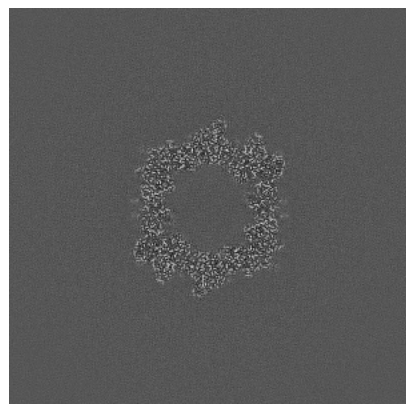


Z Index: 250

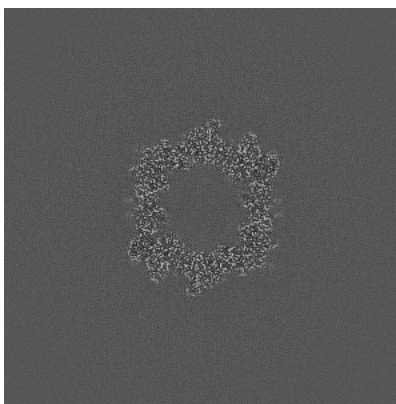
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

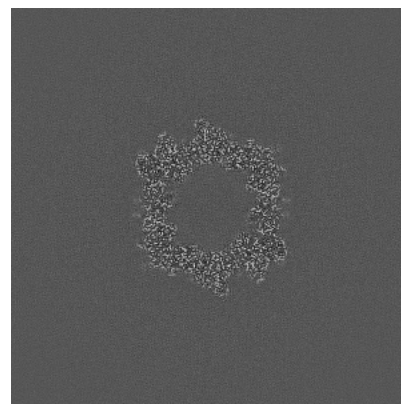
6.3.1 Primary map



X Index: 312



Y Index: 312

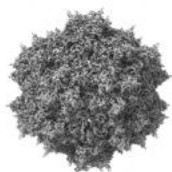


Z Index: 187

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

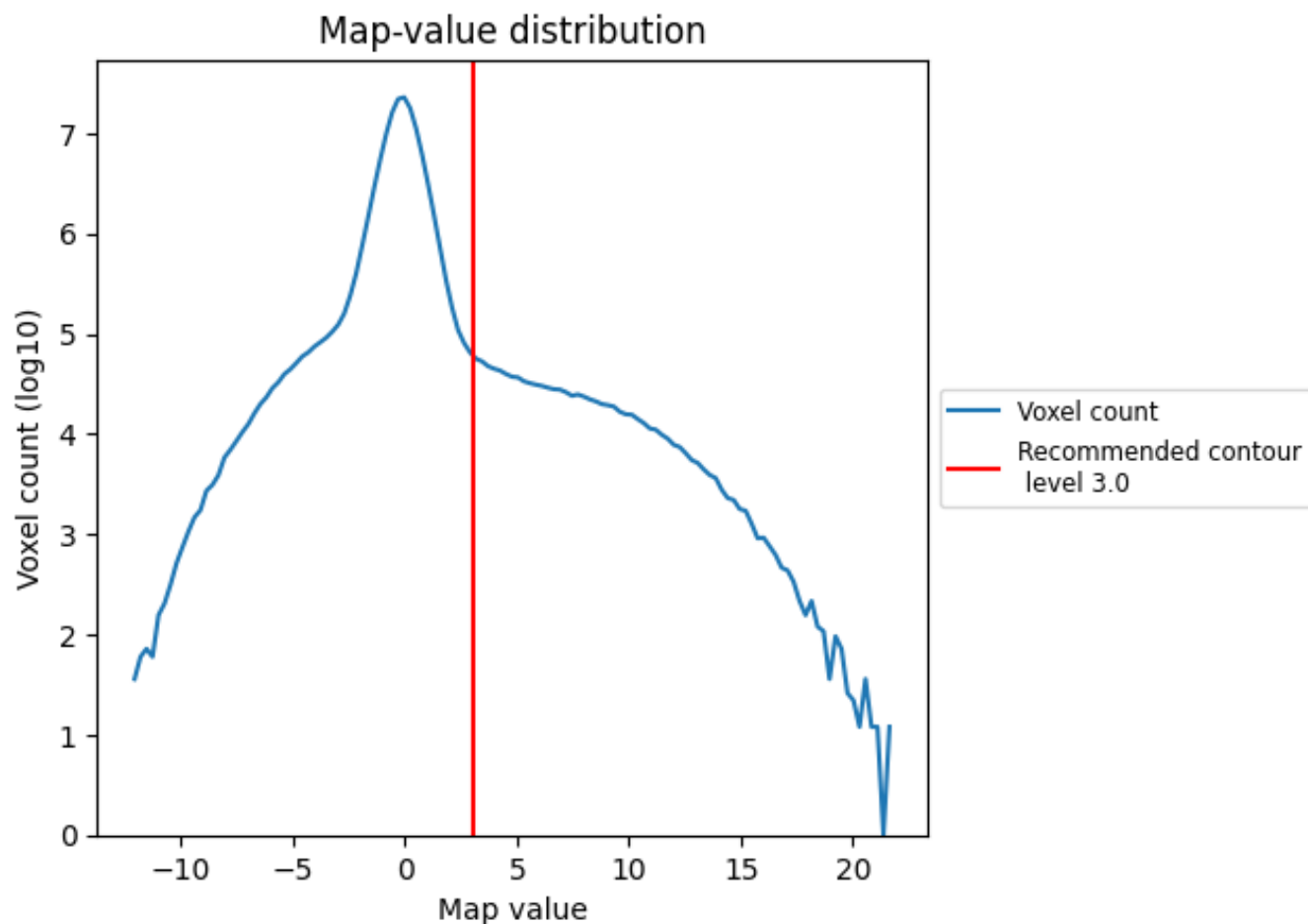
6.5 Mask visualisation

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

7 Map analysis [i](#)

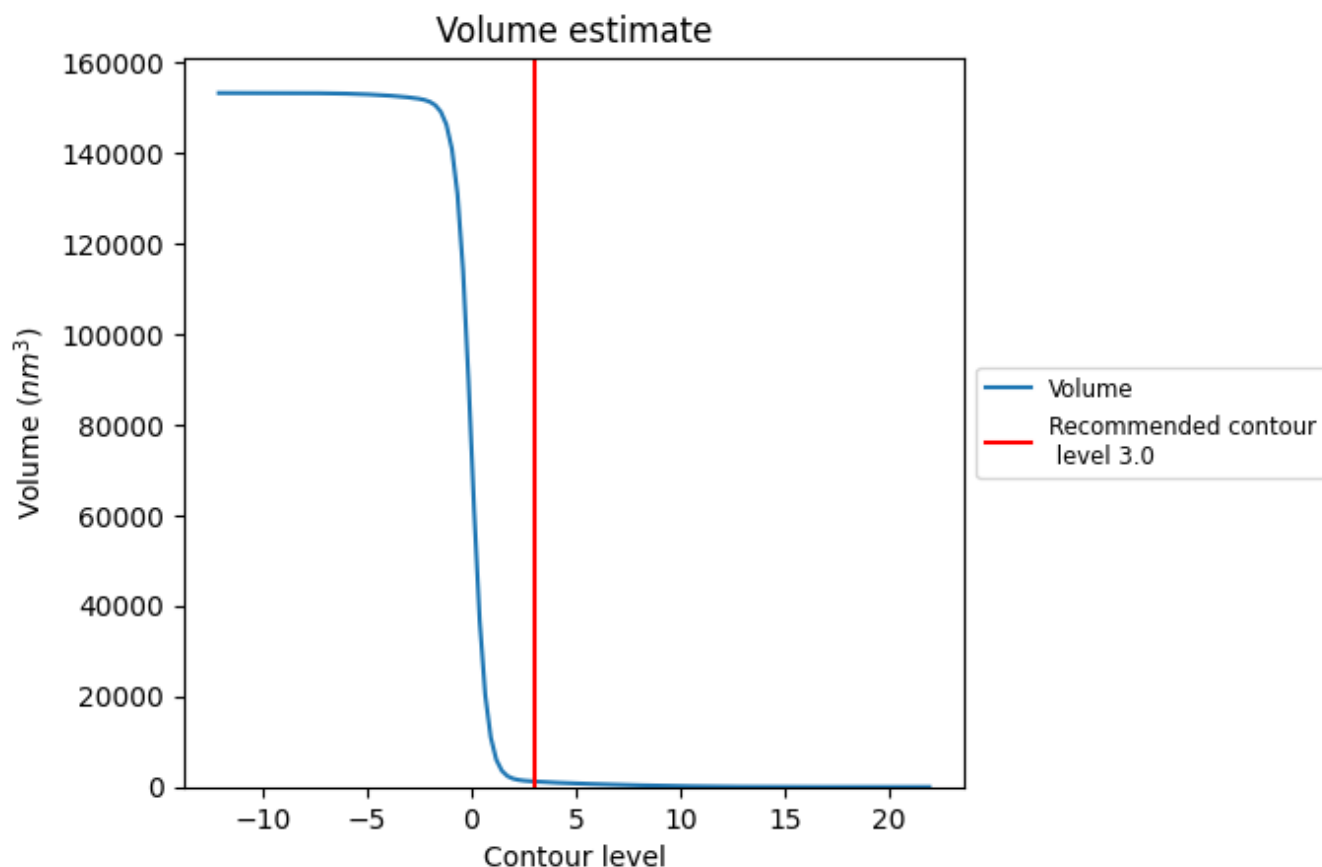
This section contains the results of statistical analysis of the map.

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.

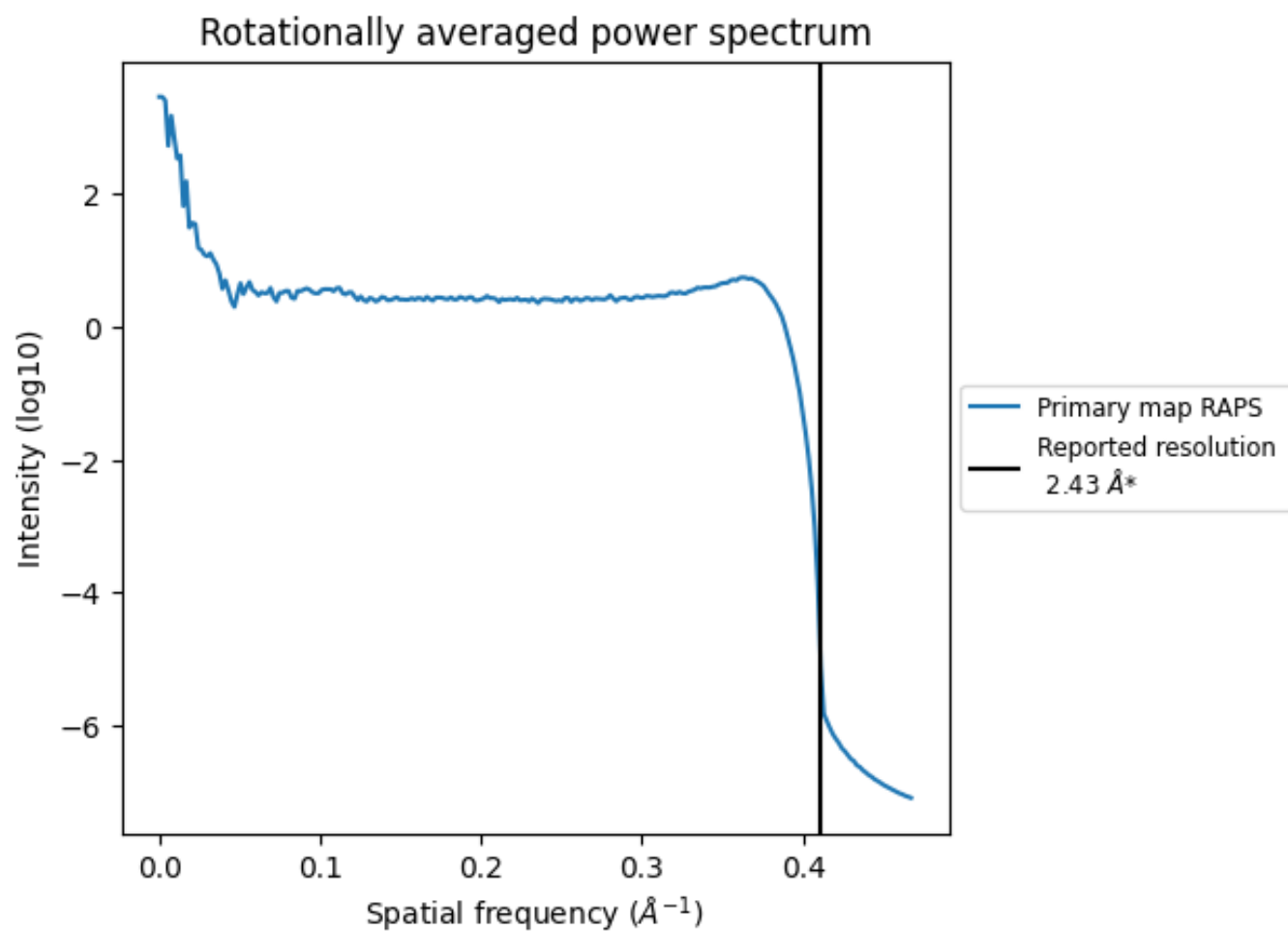
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1211 nm³; this corresponds to an approximate mass of 1094 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 0.412 Å⁻¹

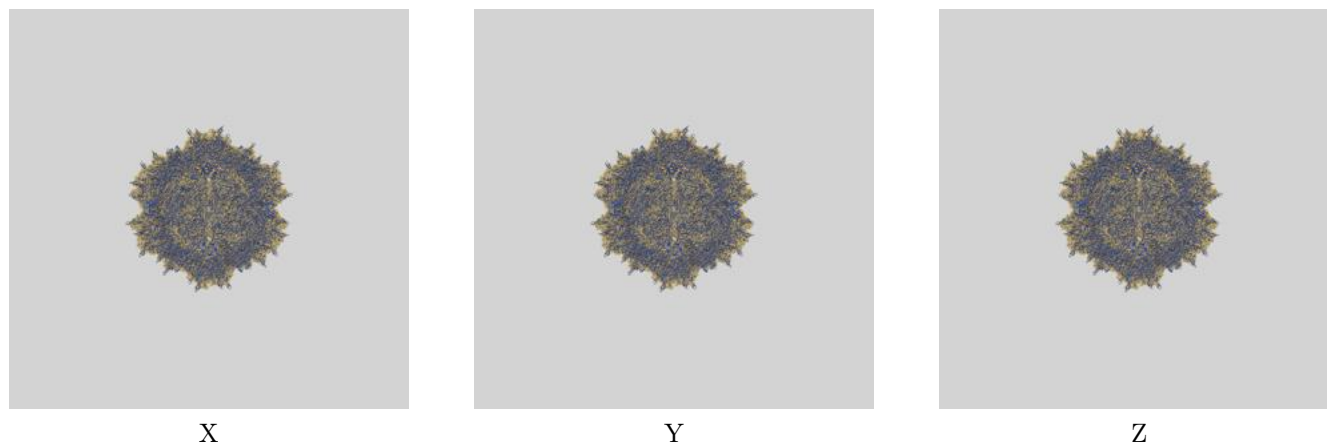
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

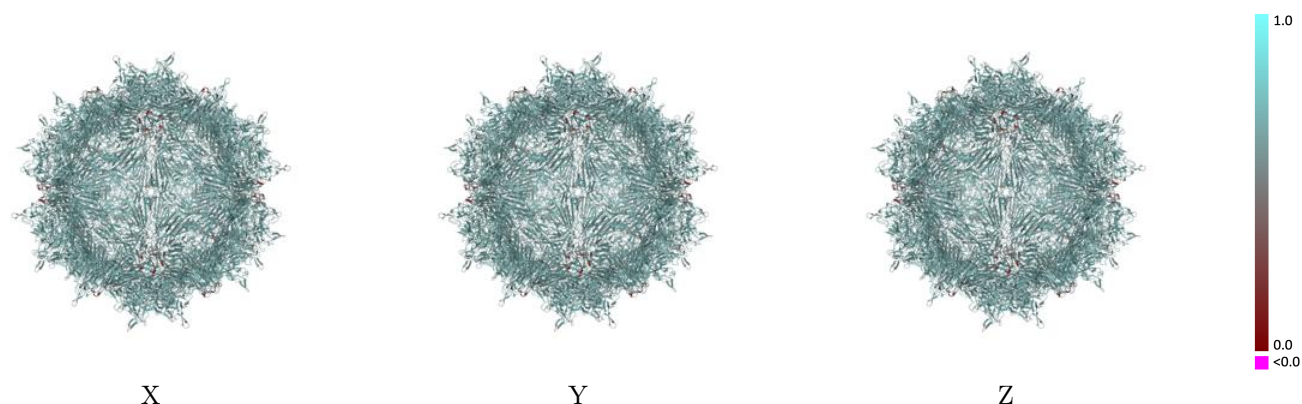
This section contains information regarding the fit between EMDB map EMD-24719 and PDB model 7RWT. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

9.1 Map-model overlay [i](#)



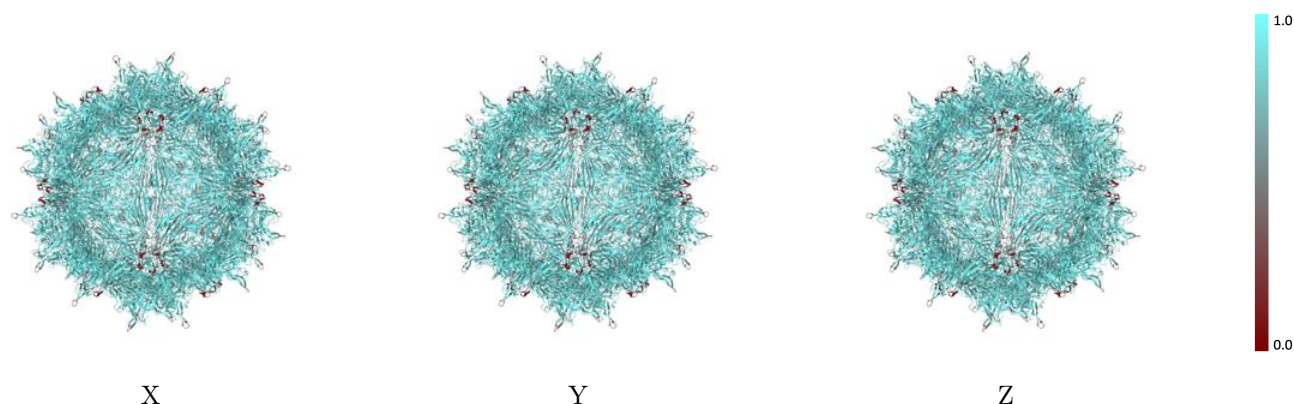
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



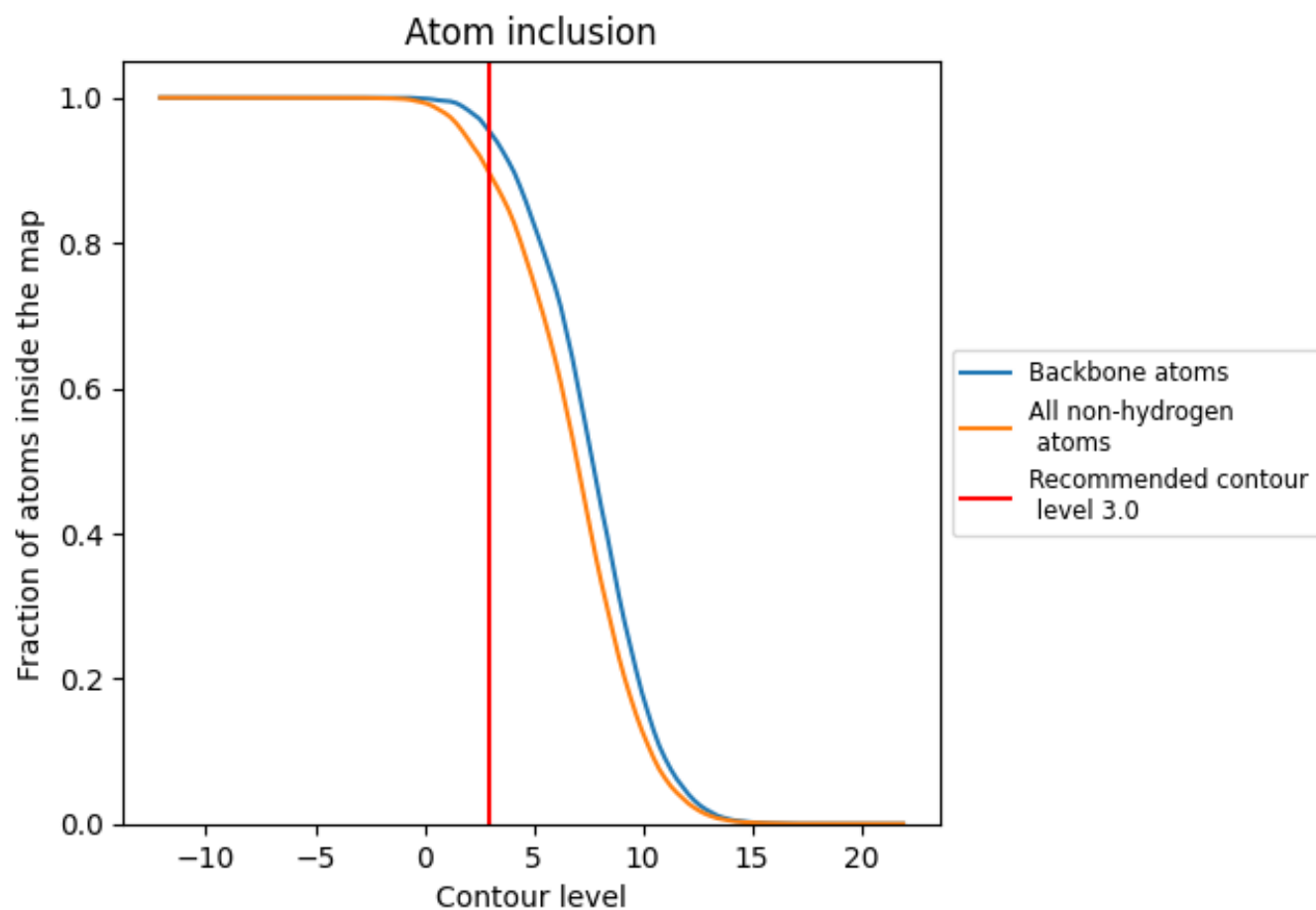
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (3.0).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ




















































The table lists the average atom inclusion at the recommended contour level (3.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8947	 0.6480
1	 0.8962	 0.6510
2	 0.8969	 0.6520
3	 0.8974	 0.6540
4	 0.8940	 0.6530
5	 0.8945	 0.6510
6	 0.8940	 0.6490
7	 0.8940	 0.6510
8	 0.8945	 0.6530
A	 0.8974	 0.6460
B	 0.8962	 0.6470
C	 0.8912	 0.6480
D	 0.8940	 0.6450
E	 0.8947	 0.6450
F	 0.8964	 0.6460
G	 0.8945	 0.6460
H	 0.8937	 0.6490
I	 0.8937	 0.6490
J	 0.8969	 0.6490
K	 0.8930	 0.6510
L	 0.8962	 0.6490
M	 0.8937	 0.6480
N	 0.8940	 0.6460
O	 0.8942	 0.6460
P	 0.8937	 0.6450
Q	 0.8925	 0.6460
R	 0.8972	 0.6460
S	 0.8952	 0.6460
T	 0.8920	 0.6490
U	 0.8964	 0.6480
V	 0.8945	 0.6490
W	 0.8935	 0.6490
X	 0.8945	 0.6500
Y	 0.8940	 0.6510
Z	 0.8952	 0.6520



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Chain	Atom inclusion	Q-score
a	 0.8974	 0.6530
b	 0.8962	 0.6500
c	 0.8952	 0.6480
d	 0.8962	 0.6480
e	 0.8984	 0.6510
f	 0.8972	 0.6520
g	 0.8935	 0.6500
h	 0.8949	 0.6490
i	 0.8937	 0.6480
j	 0.8942	 0.6460
k	 0.8940	 0.6470
l	 0.8937	 0.6470
m	 0.8905	 0.6470
n	 0.8954	 0.6470
o	 0.8940	 0.6490
p	 0.8905	 0.6490
q	 0.8949	 0.6440
r	 0.8959	 0.6440
s	 0.8945	 0.6460
t	 0.8945	 0.6490
u	 0.8932	 0.6520
v	 0.8962	 0.6490
w	 0.8942	 0.6460
x	 0.8910	 0.6450
y	 0.8959	 0.6460
z	 0.8969	 0.6510