



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 09:42 AM UTC

PDB ID : 7RL1 / pdb_00007r11
EMDB ID : EMD-24513
Title : AAVrh.10-7x capsid
Authors : Mietzsch, M.; McKenna, R.
Deposited on : 2021-07-23
Resolution : 2.71 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:

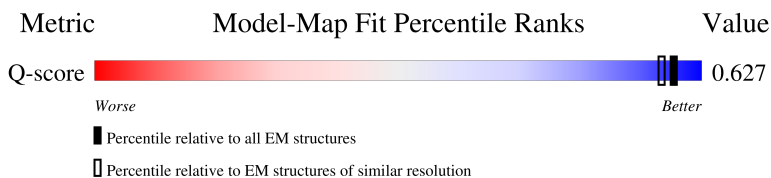
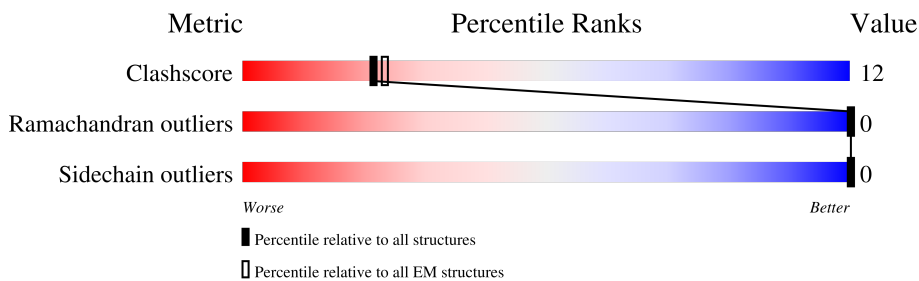
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.71 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.




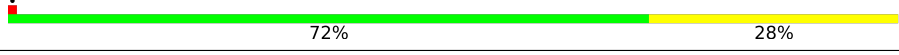

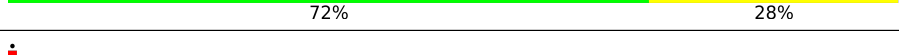
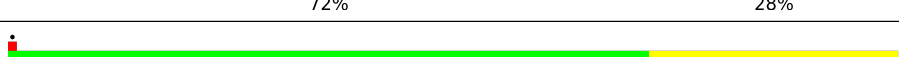
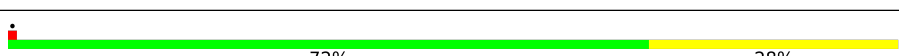












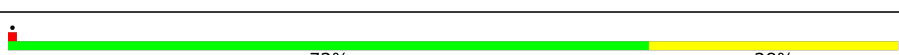
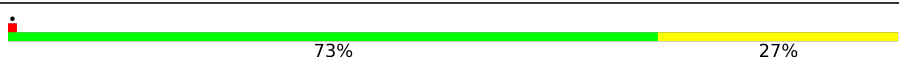

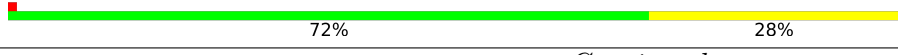



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10297 (2.21 - 3.21)

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	519	72% 28%
1	2	519	73% 27%
1	3	519	73% 27%
1	4	519	72% 28%





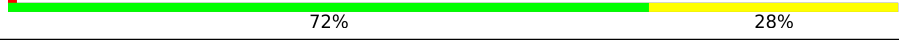


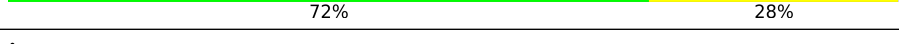
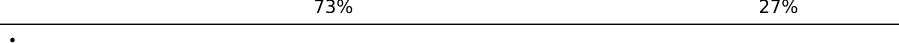
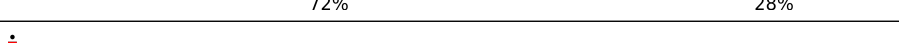
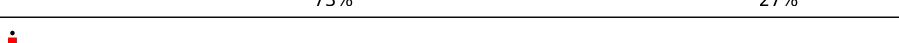











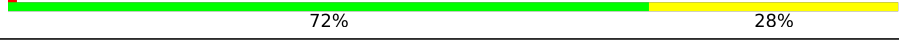


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Mol	Chain	Length	Quality of chain
1	5	519	 72% 28%
1	6	519	 72% 28%
1	7	519	 72% 28%
1	8	519	 72% 28%
1	A	519	 72% 28%
1	B	519	 72% 28%
1	C	519	 72% 28%
1	D	519	 72% 28%
1	E	519	 72% 28%
1	F	519	 73% 27%
1	G	519	 72% 28%
1	H	519	 72% 28%
1	I	519	 72% 28%
1	J	519	 73% 27%
1	K	519	 72% 28%
1	L	519	 72% 28%
1	M	519	 71% 29%
1	N	519	 72% 28%
1	O	519	 71% 29%
1	P	519	 74% 26%
1	Q	519	 72% 28%
1	R	519	 72% 28%
1	S	519	 73% 27%
1	T	519	 73% 27%
1	U	519	 72% 28%




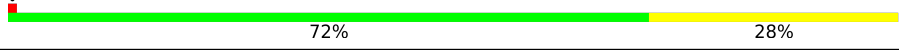
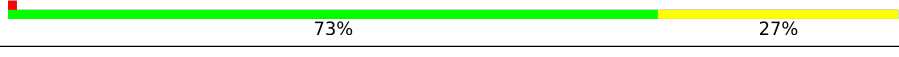

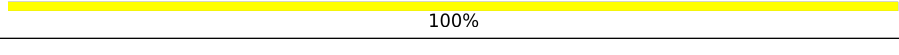
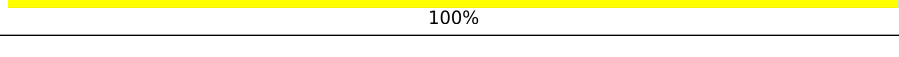
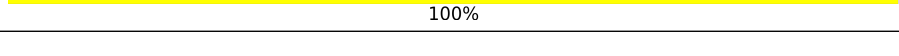
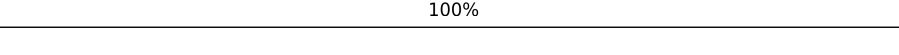
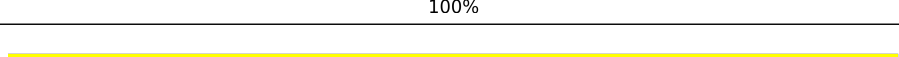
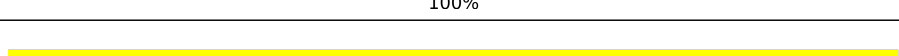
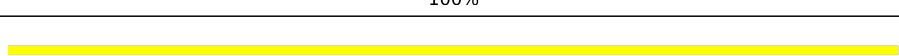
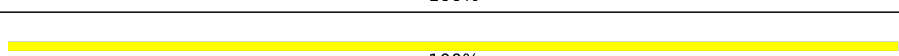
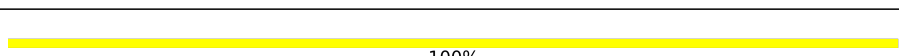
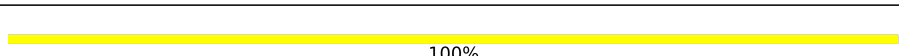
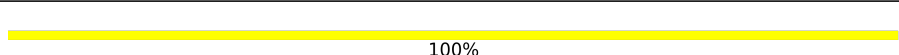
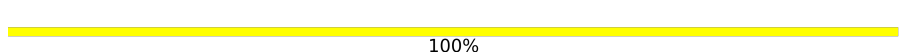
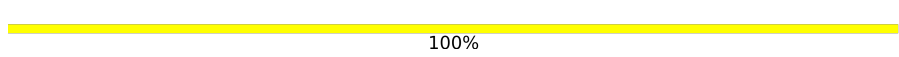
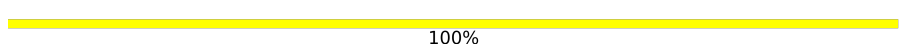
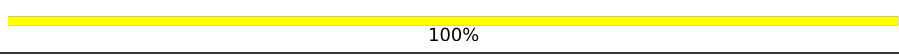
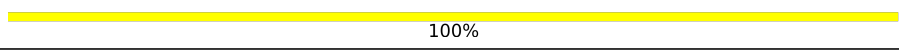
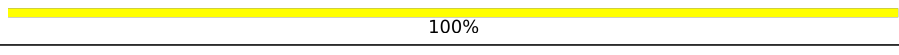
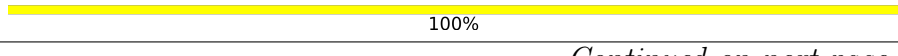

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Mol	Chain	Length	Quality of chain	
1	V	519		73% 27%
1	W	519		72% 28%
1	X	519		74% 26%
1	Y	519		72% 28%
1	Z	519		72% 28%
1	a	519		73% 27%
1	b	519		72% 28%
1	c	519		72% 28%
1	d	519		73% 27%
1	e	519		72% 28%
1	f	519		73% 27%
1	g	519		71% 29%
1	h	519		72% 28%
1	i	519		72% 28%
1	j	519		73% 27%
1	k	519		72% 28%
1	l	519		71% 29%
1	m	519		72% 28%
1	n	519		73% 27%
1	o	519		73% 27%
1	p	519		73% 27%
1	q	519		72% 28%
1	r	519		73% 27%
1	s	519		72% 28%
1	t	519		72% 28%

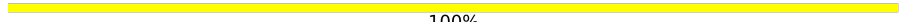
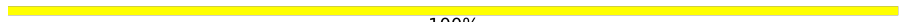
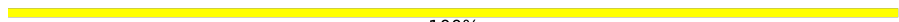
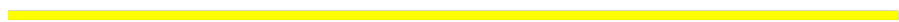











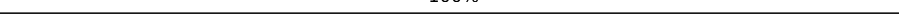
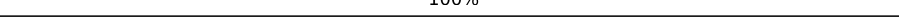
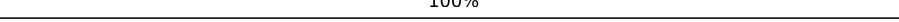
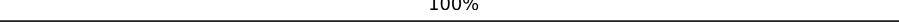
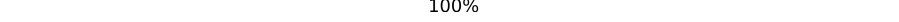
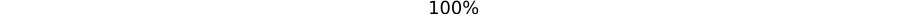
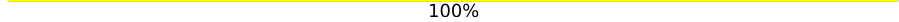
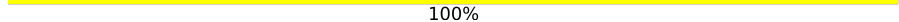
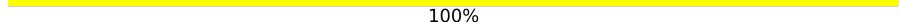
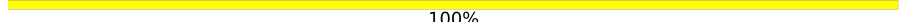
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Mol	Chain	Length	Quality of chain
1	u	519	 72% 28%
1	v	519	 72% 28%
1	w	519	 72% 28%
1	x	519	 72% 28%
1	y	519	 73% 27%
1	z	519	 72% 28%
2	0	2	 100%
2	0A	2	 100%
2	1A	2	 100%
2	2A	2	 100%
2	3A	2	 100%
2	4A	2	 100%
2	5A	2	 100%
2	9	2	 100%
2	AA	2	 100%
2	BA	2	 100%
2	CA	2	 100%
2	DA	2	 100%
2	EA	2	 100%
2	FA	2	 100%
2	GA	2	 100%
2	HA	2	 100%
2	IA	2	 100%
2	JA	2	 100%
2	KA	2	 100%

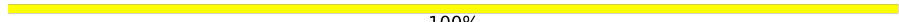
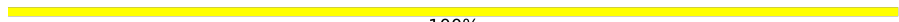

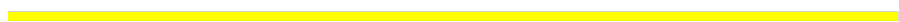






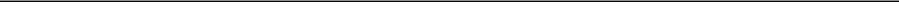

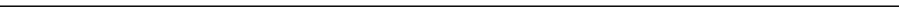


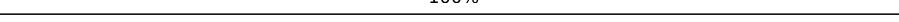
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Mol	Chain	Length	Quality of chain
2	LA	2	 100%
2	MA	2	 100%
2	NA	2	 100%
2	OA	2	 100%
2	PA	2	 100%
2	QA	2	 100%
2	RA	2	 100%
2	SA	2	 100%
2	TA	2	 100%
2	UA	2	 100%
2	VA	2	 100%
2	WA	2	 100%
2	XA	2	 100%
2	YA	2	 100%
2	ZA	2	 100%
2	aA	2	 100%
2	bA	2	 100%
2	cA	2	 100%
2	dA	2	 100%
2	eA	2	 100%
2	fA	2	 100%
2	gA	2	 100%
2	hA	2	 100%
2	iA	2	 100%
2	jA	2	 100%

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Mol	Chain	Length	Quality of chain
2	kA	2	 100%
2	lA	2	 100%
2	mA	2	 100%
2	nA	2	 100%
2	oA	2	 100%
2	pA	2	 100%
2	qA	2	 100%
2	rA	2	 100%
2	sA	2	 100%
2	tA	2	 100%
2	uA	2	 100%
2	vA	2	 100%
2	wA	2	 100%
2	xA	2	 100%
2	yA	2	 100%
2	zA	2	 100%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 249480 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
			Total	C	N	O	S		
1	A	519	4121	2606	711	790	14	0	0
1	B	519	4121	2606	711	790	14	0	0
1	C	519	4121	2606	711	790	14	0	0
1	D	519	4121	2606	711	790	14	0	0
1	E	519	4121	2606	711	790	14	0	0
1	F	519	4121	2606	711	790	14	0	0
1	G	519	4121	2606	711	790	14	0	0
1	H	519	4121	2606	711	790	14	0	0
1	I	519	4121	2606	711	790	14	0	0
1	J	519	4121	2606	711	790	14	0	0
1	K	519	4121	2606	711	790	14	0	0
1	L	519	4121	2606	711	790	14	0	0
1	M	519	4121	2606	711	790	14	0	0
1	N	519	4121	2606	711	790	14	0	0
1	O	519	4121	2606	711	790	14	0	0
1	P	519	4121	2606	711	790	14	0	0
1	Q	519	4121	2606	711	790	14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	S	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	T	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	U	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	V	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	W	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	X	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	Y	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	Z	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	a	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	b	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	c	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	d	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	e	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	f	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	g	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	h	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	i	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	j	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	k	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	l	519	Total 4121	C 2606	N 711	O 790	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	n	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	o	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	p	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	q	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	r	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	s	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	t	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	u	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	v	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	w	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	x	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	y	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	z	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	1	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	2	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	3	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	4	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	5	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	6	519	Total 4121	C 2606	N 711	O 790	S 14	0	0
1	7	519	Total 4121	C 2606	N 711	O 790	S 14	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	8	519	4121	2606	711	790	14	0	0

There are 600 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	365	LEU	PRO	conflict	UNP Q6JC62
A	387	ALA	SER	conflict	UNP Q6JC62
A	406	LEU	ARG	conflict	UNP Q6JC62
A	?	-	SER	deletion	UNP Q6JC62
A	558	ALA	SER	conflict	UNP Q6JC62
A	588	ASN	GLN	conflict	UNP Q6JC62
A	589	SER	ASN	conflict	UNP Q6JC62
A	591	GLN	ALA	conflict	UNP Q6JC62
A	718	VAL	THR	conflict	UNP Q6JC62
A	719	ASP	GLU	conflict	UNP Q6JC62
B	365	LEU	PRO	conflict	UNP Q6JC62
B	387	ALA	SER	conflict	UNP Q6JC62
B	406	LEU	ARG	conflict	UNP Q6JC62
B	?	-	SER	deletion	UNP Q6JC62
B	558	ALA	SER	conflict	UNP Q6JC62
B	588	ASN	GLN	conflict	UNP Q6JC62
B	589	SER	ASN	conflict	UNP Q6JC62
B	591	GLN	ALA	conflict	UNP Q6JC62
B	718	VAL	THR	conflict	UNP Q6JC62
B	719	ASP	GLU	conflict	UNP Q6JC62
C	365	LEU	PRO	conflict	UNP Q6JC62
C	387	ALA	SER	conflict	UNP Q6JC62
C	406	LEU	ARG	conflict	UNP Q6JC62
C	?	-	SER	deletion	UNP Q6JC62
C	558	ALA	SER	conflict	UNP Q6JC62
C	588	ASN	GLN	conflict	UNP Q6JC62
C	589	SER	ASN	conflict	UNP Q6JC62
C	591	GLN	ALA	conflict	UNP Q6JC62
C	718	VAL	THR	conflict	UNP Q6JC62
C	719	ASP	GLU	conflict	UNP Q6JC62
D	365	LEU	PRO	conflict	UNP Q6JC62
D	387	ALA	SER	conflict	UNP Q6JC62
D	406	LEU	ARG	conflict	UNP Q6JC62
D	?	-	SER	deletion	UNP Q6JC62
D	558	ALA	SER	conflict	UNP Q6JC62
D	588	ASN	GLN	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
D	589	SER	ASN	conflict	UNP Q6JC62
D	591	GLN	ALA	conflict	UNP Q6JC62
D	718	VAL	THR	conflict	UNP Q6JC62
D	719	ASP	GLU	conflict	UNP Q6JC62
E	365	LEU	PRO	conflict	UNP Q6JC62
E	387	ALA	SER	conflict	UNP Q6JC62
E	406	LEU	ARG	conflict	UNP Q6JC62
E	?	-	SER	deletion	UNP Q6JC62
E	558	ALA	SER	conflict	UNP Q6JC62
E	588	ASN	GLN	conflict	UNP Q6JC62
E	589	SER	ASN	conflict	UNP Q6JC62
E	591	GLN	ALA	conflict	UNP Q6JC62
E	718	VAL	THR	conflict	UNP Q6JC62
E	719	ASP	GLU	conflict	UNP Q6JC62
F	365	LEU	PRO	conflict	UNP Q6JC62
F	387	ALA	SER	conflict	UNP Q6JC62
F	406	LEU	ARG	conflict	UNP Q6JC62
F	?	-	SER	deletion	UNP Q6JC62
F	558	ALA	SER	conflict	UNP Q6JC62
F	588	ASN	GLN	conflict	UNP Q6JC62
F	589	SER	ASN	conflict	UNP Q6JC62
F	591	GLN	ALA	conflict	UNP Q6JC62
F	718	VAL	THR	conflict	UNP Q6JC62
F	719	ASP	GLU	conflict	UNP Q6JC62
G	365	LEU	PRO	conflict	UNP Q6JC62
G	387	ALA	SER	conflict	UNP Q6JC62
G	406	LEU	ARG	conflict	UNP Q6JC62
G	?	-	SER	deletion	UNP Q6JC62
G	558	ALA	SER	conflict	UNP Q6JC62
G	588	ASN	GLN	conflict	UNP Q6JC62
G	589	SER	ASN	conflict	UNP Q6JC62
G	591	GLN	ALA	conflict	UNP Q6JC62
G	718	VAL	THR	conflict	UNP Q6JC62
G	719	ASP	GLU	conflict	UNP Q6JC62
H	365	LEU	PRO	conflict	UNP Q6JC62
H	387	ALA	SER	conflict	UNP Q6JC62
H	406	LEU	ARG	conflict	UNP Q6JC62
H	?	-	SER	deletion	UNP Q6JC62
H	558	ALA	SER	conflict	UNP Q6JC62
H	588	ASN	GLN	conflict	UNP Q6JC62
H	589	SER	ASN	conflict	UNP Q6JC62
H	591	GLN	ALA	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
H	718	VAL	THR	conflict	UNP Q6JC62
H	719	ASP	GLU	conflict	UNP Q6JC62
I	365	LEU	PRO	conflict	UNP Q6JC62
I	387	ALA	SER	conflict	UNP Q6JC62
I	406	LEU	ARG	conflict	UNP Q6JC62
I	?	-	SER	deletion	UNP Q6JC62
I	558	ALA	SER	conflict	UNP Q6JC62
I	588	ASN	GLN	conflict	UNP Q6JC62
I	589	SER	ASN	conflict	UNP Q6JC62
I	591	GLN	ALA	conflict	UNP Q6JC62
I	718	VAL	THR	conflict	UNP Q6JC62
I	719	ASP	GLU	conflict	UNP Q6JC62
J	365	LEU	PRO	conflict	UNP Q6JC62
J	387	ALA	SER	conflict	UNP Q6JC62
J	406	LEU	ARG	conflict	UNP Q6JC62
J	?	-	SER	deletion	UNP Q6JC62
J	558	ALA	SER	conflict	UNP Q6JC62
J	588	ASN	GLN	conflict	UNP Q6JC62
J	589	SER	ASN	conflict	UNP Q6JC62
J	591	GLN	ALA	conflict	UNP Q6JC62
J	718	VAL	THR	conflict	UNP Q6JC62
J	719	ASP	GLU	conflict	UNP Q6JC62
K	365	LEU	PRO	conflict	UNP Q6JC62
K	387	ALA	SER	conflict	UNP Q6JC62
K	406	LEU	ARG	conflict	UNP Q6JC62
K	?	-	SER	deletion	UNP Q6JC62
K	558	ALA	SER	conflict	UNP Q6JC62
K	588	ASN	GLN	conflict	UNP Q6JC62
K	589	SER	ASN	conflict	UNP Q6JC62
K	591	GLN	ALA	conflict	UNP Q6JC62
K	718	VAL	THR	conflict	UNP Q6JC62
K	719	ASP	GLU	conflict	UNP Q6JC62
L	365	LEU	PRO	conflict	UNP Q6JC62
L	387	ALA	SER	conflict	UNP Q6JC62
L	406	LEU	ARG	conflict	UNP Q6JC62
L	?	-	SER	deletion	UNP Q6JC62
L	558	ALA	SER	conflict	UNP Q6JC62
L	588	ASN	GLN	conflict	UNP Q6JC62
L	589	SER	ASN	conflict	UNP Q6JC62
L	591	GLN	ALA	conflict	UNP Q6JC62
L	718	VAL	THR	conflict	UNP Q6JC62
L	719	ASP	GLU	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
M	365	LEU	PRO	conflict	UNP Q6JC62
M	387	ALA	SER	conflict	UNP Q6JC62
M	406	LEU	ARG	conflict	UNP Q6JC62
M	?	-	SER	deletion	UNP Q6JC62
M	558	ALA	SER	conflict	UNP Q6JC62
M	588	ASN	GLN	conflict	UNP Q6JC62
M	589	SER	ASN	conflict	UNP Q6JC62
M	591	GLN	ALA	conflict	UNP Q6JC62
M	718	VAL	THR	conflict	UNP Q6JC62
M	719	ASP	GLU	conflict	UNP Q6JC62
N	365	LEU	PRO	conflict	UNP Q6JC62
N	387	ALA	SER	conflict	UNP Q6JC62
N	406	LEU	ARG	conflict	UNP Q6JC62
N	?	-	SER	deletion	UNP Q6JC62
N	558	ALA	SER	conflict	UNP Q6JC62
N	588	ASN	GLN	conflict	UNP Q6JC62
N	589	SER	ASN	conflict	UNP Q6JC62
N	591	GLN	ALA	conflict	UNP Q6JC62
N	718	VAL	THR	conflict	UNP Q6JC62
N	719	ASP	GLU	conflict	UNP Q6JC62
O	365	LEU	PRO	conflict	UNP Q6JC62
O	387	ALA	SER	conflict	UNP Q6JC62
O	406	LEU	ARG	conflict	UNP Q6JC62
O	?	-	SER	deletion	UNP Q6JC62
O	558	ALA	SER	conflict	UNP Q6JC62
O	588	ASN	GLN	conflict	UNP Q6JC62
O	589	SER	ASN	conflict	UNP Q6JC62
O	591	GLN	ALA	conflict	UNP Q6JC62
O	718	VAL	THR	conflict	UNP Q6JC62
O	719	ASP	GLU	conflict	UNP Q6JC62
P	365	LEU	PRO	conflict	UNP Q6JC62
P	387	ALA	SER	conflict	UNP Q6JC62
P	406	LEU	ARG	conflict	UNP Q6JC62
P	?	-	SER	deletion	UNP Q6JC62
P	558	ALA	SER	conflict	UNP Q6JC62
P	588	ASN	GLN	conflict	UNP Q6JC62
P	589	SER	ASN	conflict	UNP Q6JC62
P	591	GLN	ALA	conflict	UNP Q6JC62
P	718	VAL	THR	conflict	UNP Q6JC62
P	719	ASP	GLU	conflict	UNP Q6JC62
Q	365	LEU	PRO	conflict	UNP Q6JC62
Q	387	ALA	SER	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	406	LEU	ARG	conflict	UNP Q6JC62
Q	?	-	SER	deletion	UNP Q6JC62
Q	558	ALA	SER	conflict	UNP Q6JC62
Q	588	ASN	GLN	conflict	UNP Q6JC62
Q	589	SER	ASN	conflict	UNP Q6JC62
Q	591	GLN	ALA	conflict	UNP Q6JC62
Q	718	VAL	THR	conflict	UNP Q6JC62
Q	719	ASP	GLU	conflict	UNP Q6JC62
R	365	LEU	PRO	conflict	UNP Q6JC62
R	387	ALA	SER	conflict	UNP Q6JC62
R	406	LEU	ARG	conflict	UNP Q6JC62
R	?	-	SER	deletion	UNP Q6JC62
R	558	ALA	SER	conflict	UNP Q6JC62
R	588	ASN	GLN	conflict	UNP Q6JC62
R	589	SER	ASN	conflict	UNP Q6JC62
R	591	GLN	ALA	conflict	UNP Q6JC62
R	718	VAL	THR	conflict	UNP Q6JC62
R	719	ASP	GLU	conflict	UNP Q6JC62
S	365	LEU	PRO	conflict	UNP Q6JC62
S	387	ALA	SER	conflict	UNP Q6JC62
S	406	LEU	ARG	conflict	UNP Q6JC62
S	?	-	SER	deletion	UNP Q6JC62
S	558	ALA	SER	conflict	UNP Q6JC62
S	588	ASN	GLN	conflict	UNP Q6JC62
S	589	SER	ASN	conflict	UNP Q6JC62
S	591	GLN	ALA	conflict	UNP Q6JC62
S	718	VAL	THR	conflict	UNP Q6JC62
S	719	ASP	GLU	conflict	UNP Q6JC62
T	365	LEU	PRO	conflict	UNP Q6JC62
T	387	ALA	SER	conflict	UNP Q6JC62
T	406	LEU	ARG	conflict	UNP Q6JC62
T	?	-	SER	deletion	UNP Q6JC62
T	558	ALA	SER	conflict	UNP Q6JC62
T	588	ASN	GLN	conflict	UNP Q6JC62
T	589	SER	ASN	conflict	UNP Q6JC62
T	591	GLN	ALA	conflict	UNP Q6JC62
T	718	VAL	THR	conflict	UNP Q6JC62
T	719	ASP	GLU	conflict	UNP Q6JC62
U	365	LEU	PRO	conflict	UNP Q6JC62
U	387	ALA	SER	conflict	UNP Q6JC62
U	406	LEU	ARG	conflict	UNP Q6JC62
U	?	-	SER	deletion	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
U	558	ALA	SER	conflict	UNP Q6JC62
U	588	ASN	GLN	conflict	UNP Q6JC62
U	589	SER	ASN	conflict	UNP Q6JC62
U	591	GLN	ALA	conflict	UNP Q6JC62
U	718	VAL	THR	conflict	UNP Q6JC62
U	719	ASP	GLU	conflict	UNP Q6JC62
V	365	LEU	PRO	conflict	UNP Q6JC62
V	387	ALA	SER	conflict	UNP Q6JC62
V	406	LEU	ARG	conflict	UNP Q6JC62
V	?	-	SER	deletion	UNP Q6JC62
V	558	ALA	SER	conflict	UNP Q6JC62
V	588	ASN	GLN	conflict	UNP Q6JC62
V	589	SER	ASN	conflict	UNP Q6JC62
V	591	GLN	ALA	conflict	UNP Q6JC62
V	718	VAL	THR	conflict	UNP Q6JC62
V	719	ASP	GLU	conflict	UNP Q6JC62
W	365	LEU	PRO	conflict	UNP Q6JC62
W	387	ALA	SER	conflict	UNP Q6JC62
W	406	LEU	ARG	conflict	UNP Q6JC62
W	?	-	SER	deletion	UNP Q6JC62
W	558	ALA	SER	conflict	UNP Q6JC62
W	588	ASN	GLN	conflict	UNP Q6JC62
W	589	SER	ASN	conflict	UNP Q6JC62
W	591	GLN	ALA	conflict	UNP Q6JC62
W	718	VAL	THR	conflict	UNP Q6JC62
W	719	ASP	GLU	conflict	UNP Q6JC62
X	365	LEU	PRO	conflict	UNP Q6JC62
X	387	ALA	SER	conflict	UNP Q6JC62
X	406	LEU	ARG	conflict	UNP Q6JC62
X	?	-	SER	deletion	UNP Q6JC62
X	558	ALA	SER	conflict	UNP Q6JC62
X	588	ASN	GLN	conflict	UNP Q6JC62
X	589	SER	ASN	conflict	UNP Q6JC62
X	591	GLN	ALA	conflict	UNP Q6JC62
X	718	VAL	THR	conflict	UNP Q6JC62
X	719	ASP	GLU	conflict	UNP Q6JC62
Y	365	LEU	PRO	conflict	UNP Q6JC62
Y	387	ALA	SER	conflict	UNP Q6JC62
Y	406	LEU	ARG	conflict	UNP Q6JC62
Y	?	-	SER	deletion	UNP Q6JC62
Y	558	ALA	SER	conflict	UNP Q6JC62
Y	588	ASN	GLN	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
Y	589	SER	ASN	conflict	UNP Q6JC62
Y	591	GLN	ALA	conflict	UNP Q6JC62
Y	718	VAL	THR	conflict	UNP Q6JC62
Y	719	ASP	GLU	conflict	UNP Q6JC62
Z	365	LEU	PRO	conflict	UNP Q6JC62
Z	387	ALA	SER	conflict	UNP Q6JC62
Z	406	LEU	ARG	conflict	UNP Q6JC62
Z	?	-	SER	deletion	UNP Q6JC62
Z	558	ALA	SER	conflict	UNP Q6JC62
Z	588	ASN	GLN	conflict	UNP Q6JC62
Z	589	SER	ASN	conflict	UNP Q6JC62
Z	591	GLN	ALA	conflict	UNP Q6JC62
Z	718	VAL	THR	conflict	UNP Q6JC62
Z	719	ASP	GLU	conflict	UNP Q6JC62
a	365	LEU	PRO	conflict	UNP Q6JC62
a	387	ALA	SER	conflict	UNP Q6JC62
a	406	LEU	ARG	conflict	UNP Q6JC62
a	?	-	SER	deletion	UNP Q6JC62
a	558	ALA	SER	conflict	UNP Q6JC62
a	588	ASN	GLN	conflict	UNP Q6JC62
a	589	SER	ASN	conflict	UNP Q6JC62
a	591	GLN	ALA	conflict	UNP Q6JC62
a	718	VAL	THR	conflict	UNP Q6JC62
a	719	ASP	GLU	conflict	UNP Q6JC62
b	365	LEU	PRO	conflict	UNP Q6JC62
b	387	ALA	SER	conflict	UNP Q6JC62
b	406	LEU	ARG	conflict	UNP Q6JC62
b	?	-	SER	deletion	UNP Q6JC62
b	558	ALA	SER	conflict	UNP Q6JC62
b	588	ASN	GLN	conflict	UNP Q6JC62
b	589	SER	ASN	conflict	UNP Q6JC62
b	591	GLN	ALA	conflict	UNP Q6JC62
b	718	VAL	THR	conflict	UNP Q6JC62
b	719	ASP	GLU	conflict	UNP Q6JC62
c	365	LEU	PRO	conflict	UNP Q6JC62
c	387	ALA	SER	conflict	UNP Q6JC62
c	406	LEU	ARG	conflict	UNP Q6JC62
c	?	-	SER	deletion	UNP Q6JC62
c	558	ALA	SER	conflict	UNP Q6JC62
c	588	ASN	GLN	conflict	UNP Q6JC62
c	589	SER	ASN	conflict	UNP Q6JC62
c	591	GLN	ALA	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
c	718	VAL	THR	conflict	UNP Q6JC62
c	719	ASP	GLU	conflict	UNP Q6JC62
d	365	LEU	PRO	conflict	UNP Q6JC62
d	387	ALA	SER	conflict	UNP Q6JC62
d	406	LEU	ARG	conflict	UNP Q6JC62
d	?	-	SER	deletion	UNP Q6JC62
d	558	ALA	SER	conflict	UNP Q6JC62
d	588	ASN	GLN	conflict	UNP Q6JC62
d	589	SER	ASN	conflict	UNP Q6JC62
d	591	GLN	ALA	conflict	UNP Q6JC62
d	718	VAL	THR	conflict	UNP Q6JC62
d	719	ASP	GLU	conflict	UNP Q6JC62
e	365	LEU	PRO	conflict	UNP Q6JC62
e	387	ALA	SER	conflict	UNP Q6JC62
e	406	LEU	ARG	conflict	UNP Q6JC62
e	?	-	SER	deletion	UNP Q6JC62
e	558	ALA	SER	conflict	UNP Q6JC62
e	588	ASN	GLN	conflict	UNP Q6JC62
e	589	SER	ASN	conflict	UNP Q6JC62
e	591	GLN	ALA	conflict	UNP Q6JC62
e	718	VAL	THR	conflict	UNP Q6JC62
e	719	ASP	GLU	conflict	UNP Q6JC62
f	365	LEU	PRO	conflict	UNP Q6JC62
f	387	ALA	SER	conflict	UNP Q6JC62
f	406	LEU	ARG	conflict	UNP Q6JC62
f	?	-	SER	deletion	UNP Q6JC62
f	558	ALA	SER	conflict	UNP Q6JC62
f	588	ASN	GLN	conflict	UNP Q6JC62
f	589	SER	ASN	conflict	UNP Q6JC62
f	591	GLN	ALA	conflict	UNP Q6JC62
f	718	VAL	THR	conflict	UNP Q6JC62
f	719	ASP	GLU	conflict	UNP Q6JC62
g	365	LEU	PRO	conflict	UNP Q6JC62
g	387	ALA	SER	conflict	UNP Q6JC62
g	406	LEU	ARG	conflict	UNP Q6JC62
g	?	-	SER	deletion	UNP Q6JC62
g	558	ALA	SER	conflict	UNP Q6JC62
g	588	ASN	GLN	conflict	UNP Q6JC62
g	589	SER	ASN	conflict	UNP Q6JC62
g	591	GLN	ALA	conflict	UNP Q6JC62
g	718	VAL	THR	conflict	UNP Q6JC62
g	719	ASP	GLU	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
h	365	LEU	PRO	conflict	UNP Q6JC62
h	387	ALA	SER	conflict	UNP Q6JC62
h	406	LEU	ARG	conflict	UNP Q6JC62
h	?	-	SER	deletion	UNP Q6JC62
h	558	ALA	SER	conflict	UNP Q6JC62
h	588	ASN	GLN	conflict	UNP Q6JC62
h	589	SER	ASN	conflict	UNP Q6JC62
h	591	GLN	ALA	conflict	UNP Q6JC62
h	718	VAL	THR	conflict	UNP Q6JC62
h	719	ASP	GLU	conflict	UNP Q6JC62
i	365	LEU	PRO	conflict	UNP Q6JC62
i	387	ALA	SER	conflict	UNP Q6JC62
i	406	LEU	ARG	conflict	UNP Q6JC62
i	?	-	SER	deletion	UNP Q6JC62
i	558	ALA	SER	conflict	UNP Q6JC62
i	588	ASN	GLN	conflict	UNP Q6JC62
i	589	SER	ASN	conflict	UNP Q6JC62
i	591	GLN	ALA	conflict	UNP Q6JC62
i	718	VAL	THR	conflict	UNP Q6JC62
i	719	ASP	GLU	conflict	UNP Q6JC62
j	365	LEU	PRO	conflict	UNP Q6JC62
j	387	ALA	SER	conflict	UNP Q6JC62
j	406	LEU	ARG	conflict	UNP Q6JC62
j	?	-	SER	deletion	UNP Q6JC62
j	558	ALA	SER	conflict	UNP Q6JC62
j	588	ASN	GLN	conflict	UNP Q6JC62
j	589	SER	ASN	conflict	UNP Q6JC62
j	591	GLN	ALA	conflict	UNP Q6JC62
j	718	VAL	THR	conflict	UNP Q6JC62
j	719	ASP	GLU	conflict	UNP Q6JC62
k	365	LEU	PRO	conflict	UNP Q6JC62
k	387	ALA	SER	conflict	UNP Q6JC62
k	406	LEU	ARG	conflict	UNP Q6JC62
k	?	-	SER	deletion	UNP Q6JC62
k	558	ALA	SER	conflict	UNP Q6JC62
k	588	ASN	GLN	conflict	UNP Q6JC62
k	589	SER	ASN	conflict	UNP Q6JC62
k	591	GLN	ALA	conflict	UNP Q6JC62
k	718	VAL	THR	conflict	UNP Q6JC62
k	719	ASP	GLU	conflict	UNP Q6JC62
l	365	LEU	PRO	conflict	UNP Q6JC62
l	387	ALA	SER	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
l	406	LEU	ARG	conflict	UNP Q6JC62
l	?	-	SER	deletion	UNP Q6JC62
l	558	ALA	SER	conflict	UNP Q6JC62
l	588	ASN	GLN	conflict	UNP Q6JC62
l	589	SER	ASN	conflict	UNP Q6JC62
l	591	GLN	ALA	conflict	UNP Q6JC62
l	718	VAL	THR	conflict	UNP Q6JC62
l	719	ASP	GLU	conflict	UNP Q6JC62
m	365	LEU	PRO	conflict	UNP Q6JC62
m	387	ALA	SER	conflict	UNP Q6JC62
m	406	LEU	ARG	conflict	UNP Q6JC62
m	?	-	SER	deletion	UNP Q6JC62
m	558	ALA	SER	conflict	UNP Q6JC62
m	588	ASN	GLN	conflict	UNP Q6JC62
m	589	SER	ASN	conflict	UNP Q6JC62
m	591	GLN	ALA	conflict	UNP Q6JC62
m	718	VAL	THR	conflict	UNP Q6JC62
m	719	ASP	GLU	conflict	UNP Q6JC62
n	365	LEU	PRO	conflict	UNP Q6JC62
n	387	ALA	SER	conflict	UNP Q6JC62
n	406	LEU	ARG	conflict	UNP Q6JC62
n	?	-	SER	deletion	UNP Q6JC62
n	558	ALA	SER	conflict	UNP Q6JC62
n	588	ASN	GLN	conflict	UNP Q6JC62
n	589	SER	ASN	conflict	UNP Q6JC62
n	591	GLN	ALA	conflict	UNP Q6JC62
n	718	VAL	THR	conflict	UNP Q6JC62
n	719	ASP	GLU	conflict	UNP Q6JC62
o	365	LEU	PRO	conflict	UNP Q6JC62
o	387	ALA	SER	conflict	UNP Q6JC62
o	406	LEU	ARG	conflict	UNP Q6JC62
o	?	-	SER	deletion	UNP Q6JC62
o	558	ALA	SER	conflict	UNP Q6JC62
o	588	ASN	GLN	conflict	UNP Q6JC62
o	589	SER	ASN	conflict	UNP Q6JC62
o	591	GLN	ALA	conflict	UNP Q6JC62
o	718	VAL	THR	conflict	UNP Q6JC62
o	719	ASP	GLU	conflict	UNP Q6JC62
p	365	LEU	PRO	conflict	UNP Q6JC62
p	387	ALA	SER	conflict	UNP Q6JC62
p	406	LEU	ARG	conflict	UNP Q6JC62
p	?	-	SER	deletion	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
p	558	ALA	SER	conflict	UNP Q6JC62
p	588	ASN	GLN	conflict	UNP Q6JC62
p	589	SER	ASN	conflict	UNP Q6JC62
p	591	GLN	ALA	conflict	UNP Q6JC62
p	718	VAL	THR	conflict	UNP Q6JC62
p	719	ASP	GLU	conflict	UNP Q6JC62
q	365	LEU	PRO	conflict	UNP Q6JC62
q	387	ALA	SER	conflict	UNP Q6JC62
q	406	LEU	ARG	conflict	UNP Q6JC62
q	?	-	SER	deletion	UNP Q6JC62
q	558	ALA	SER	conflict	UNP Q6JC62
q	588	ASN	GLN	conflict	UNP Q6JC62
q	589	SER	ASN	conflict	UNP Q6JC62
q	591	GLN	ALA	conflict	UNP Q6JC62
q	718	VAL	THR	conflict	UNP Q6JC62
q	719	ASP	GLU	conflict	UNP Q6JC62
r	365	LEU	PRO	conflict	UNP Q6JC62
r	387	ALA	SER	conflict	UNP Q6JC62
r	406	LEU	ARG	conflict	UNP Q6JC62
r	?	-	SER	deletion	UNP Q6JC62
r	558	ALA	SER	conflict	UNP Q6JC62
r	588	ASN	GLN	conflict	UNP Q6JC62
r	589	SER	ASN	conflict	UNP Q6JC62
r	591	GLN	ALA	conflict	UNP Q6JC62
r	718	VAL	THR	conflict	UNP Q6JC62
r	719	ASP	GLU	conflict	UNP Q6JC62
s	365	LEU	PRO	conflict	UNP Q6JC62
s	387	ALA	SER	conflict	UNP Q6JC62
s	406	LEU	ARG	conflict	UNP Q6JC62
s	?	-	SER	deletion	UNP Q6JC62
s	558	ALA	SER	conflict	UNP Q6JC62
s	588	ASN	GLN	conflict	UNP Q6JC62
s	589	SER	ASN	conflict	UNP Q6JC62
s	591	GLN	ALA	conflict	UNP Q6JC62
s	718	VAL	THR	conflict	UNP Q6JC62
s	719	ASP	GLU	conflict	UNP Q6JC62
t	365	LEU	PRO	conflict	UNP Q6JC62
t	387	ALA	SER	conflict	UNP Q6JC62
t	406	LEU	ARG	conflict	UNP Q6JC62
t	?	-	SER	deletion	UNP Q6JC62
t	558	ALA	SER	conflict	UNP Q6JC62
t	588	ASN	GLN	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
t	589	SER	ASN	conflict	UNP Q6JC62
t	591	GLN	ALA	conflict	UNP Q6JC62
t	718	VAL	THR	conflict	UNP Q6JC62
t	719	ASP	GLU	conflict	UNP Q6JC62
u	365	LEU	PRO	conflict	UNP Q6JC62
u	387	ALA	SER	conflict	UNP Q6JC62
u	406	LEU	ARG	conflict	UNP Q6JC62
u	?	-	SER	deletion	UNP Q6JC62
u	558	ALA	SER	conflict	UNP Q6JC62
u	588	ASN	GLN	conflict	UNP Q6JC62
u	589	SER	ASN	conflict	UNP Q6JC62
u	591	GLN	ALA	conflict	UNP Q6JC62
u	718	VAL	THR	conflict	UNP Q6JC62
u	719	ASP	GLU	conflict	UNP Q6JC62
v	365	LEU	PRO	conflict	UNP Q6JC62
v	387	ALA	SER	conflict	UNP Q6JC62
v	406	LEU	ARG	conflict	UNP Q6JC62
v	?	-	SER	deletion	UNP Q6JC62
v	558	ALA	SER	conflict	UNP Q6JC62
v	588	ASN	GLN	conflict	UNP Q6JC62
v	589	SER	ASN	conflict	UNP Q6JC62
v	591	GLN	ALA	conflict	UNP Q6JC62
v	718	VAL	THR	conflict	UNP Q6JC62
v	719	ASP	GLU	conflict	UNP Q6JC62
w	365	LEU	PRO	conflict	UNP Q6JC62
w	387	ALA	SER	conflict	UNP Q6JC62
w	406	LEU	ARG	conflict	UNP Q6JC62
w	?	-	SER	deletion	UNP Q6JC62
w	558	ALA	SER	conflict	UNP Q6JC62
w	588	ASN	GLN	conflict	UNP Q6JC62
w	589	SER	ASN	conflict	UNP Q6JC62
w	591	GLN	ALA	conflict	UNP Q6JC62
w	718	VAL	THR	conflict	UNP Q6JC62
w	719	ASP	GLU	conflict	UNP Q6JC62
x	365	LEU	PRO	conflict	UNP Q6JC62
x	387	ALA	SER	conflict	UNP Q6JC62
x	406	LEU	ARG	conflict	UNP Q6JC62
x	?	-	SER	deletion	UNP Q6JC62
x	558	ALA	SER	conflict	UNP Q6JC62
x	588	ASN	GLN	conflict	UNP Q6JC62
x	589	SER	ASN	conflict	UNP Q6JC62
x	591	GLN	ALA	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
x	718	VAL	THR	conflict	UNP Q6JC62
x	719	ASP	GLU	conflict	UNP Q6JC62
y	365	LEU	PRO	conflict	UNP Q6JC62
y	387	ALA	SER	conflict	UNP Q6JC62
y	406	LEU	ARG	conflict	UNP Q6JC62
y	?	-	SER	deletion	UNP Q6JC62
y	558	ALA	SER	conflict	UNP Q6JC62
y	588	ASN	GLN	conflict	UNP Q6JC62
y	589	SER	ASN	conflict	UNP Q6JC62
y	591	GLN	ALA	conflict	UNP Q6JC62
y	718	VAL	THR	conflict	UNP Q6JC62
y	719	ASP	GLU	conflict	UNP Q6JC62
z	365	LEU	PRO	conflict	UNP Q6JC62
z	387	ALA	SER	conflict	UNP Q6JC62
z	406	LEU	ARG	conflict	UNP Q6JC62
z	?	-	SER	deletion	UNP Q6JC62
z	558	ALA	SER	conflict	UNP Q6JC62
z	588	ASN	GLN	conflict	UNP Q6JC62
z	589	SER	ASN	conflict	UNP Q6JC62
z	591	GLN	ALA	conflict	UNP Q6JC62
z	718	VAL	THR	conflict	UNP Q6JC62
z	719	ASP	GLU	conflict	UNP Q6JC62
1	365	LEU	PRO	conflict	UNP Q6JC62
1	387	ALA	SER	conflict	UNP Q6JC62
1	406	LEU	ARG	conflict	UNP Q6JC62
1	?	-	SER	deletion	UNP Q6JC62
1	558	ALA	SER	conflict	UNP Q6JC62
1	588	ASN	GLN	conflict	UNP Q6JC62
1	589	SER	ASN	conflict	UNP Q6JC62
1	591	GLN	ALA	conflict	UNP Q6JC62
1	718	VAL	THR	conflict	UNP Q6JC62
1	719	ASP	GLU	conflict	UNP Q6JC62
2	365	LEU	PRO	conflict	UNP Q6JC62
2	387	ALA	SER	conflict	UNP Q6JC62
2	406	LEU	ARG	conflict	UNP Q6JC62
2	?	-	SER	deletion	UNP Q6JC62
2	558	ALA	SER	conflict	UNP Q6JC62
2	588	ASN	GLN	conflict	UNP Q6JC62
2	589	SER	ASN	conflict	UNP Q6JC62
2	591	GLN	ALA	conflict	UNP Q6JC62
2	718	VAL	THR	conflict	UNP Q6JC62
2	719	ASP	GLU	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
3	365	LEU	PRO	conflict	UNP Q6JC62
3	387	ALA	SER	conflict	UNP Q6JC62
3	406	LEU	ARG	conflict	UNP Q6JC62
3	?	-	SER	deletion	UNP Q6JC62
3	558	ALA	SER	conflict	UNP Q6JC62
3	588	ASN	GLN	conflict	UNP Q6JC62
3	589	SER	ASN	conflict	UNP Q6JC62
3	591	GLN	ALA	conflict	UNP Q6JC62
3	718	VAL	THR	conflict	UNP Q6JC62
3	719	ASP	GLU	conflict	UNP Q6JC62
4	365	LEU	PRO	conflict	UNP Q6JC62
4	387	ALA	SER	conflict	UNP Q6JC62
4	406	LEU	ARG	conflict	UNP Q6JC62
4	?	-	SER	deletion	UNP Q6JC62
4	558	ALA	SER	conflict	UNP Q6JC62
4	588	ASN	GLN	conflict	UNP Q6JC62
4	589	SER	ASN	conflict	UNP Q6JC62
4	591	GLN	ALA	conflict	UNP Q6JC62
4	718	VAL	THR	conflict	UNP Q6JC62
4	719	ASP	GLU	conflict	UNP Q6JC62
5	365	LEU	PRO	conflict	UNP Q6JC62
5	387	ALA	SER	conflict	UNP Q6JC62
5	406	LEU	ARG	conflict	UNP Q6JC62
5	?	-	SER	deletion	UNP Q6JC62
5	558	ALA	SER	conflict	UNP Q6JC62
5	588	ASN	GLN	conflict	UNP Q6JC62
5	589	SER	ASN	conflict	UNP Q6JC62
5	591	GLN	ALA	conflict	UNP Q6JC62
5	718	VAL	THR	conflict	UNP Q6JC62
5	719	ASP	GLU	conflict	UNP Q6JC62
6	365	LEU	PRO	conflict	UNP Q6JC62
6	387	ALA	SER	conflict	UNP Q6JC62
6	406	LEU	ARG	conflict	UNP Q6JC62
6	?	-	SER	deletion	UNP Q6JC62
6	558	ALA	SER	conflict	UNP Q6JC62
6	588	ASN	GLN	conflict	UNP Q6JC62
6	589	SER	ASN	conflict	UNP Q6JC62
6	591	GLN	ALA	conflict	UNP Q6JC62
6	718	VAL	THR	conflict	UNP Q6JC62
6	719	ASP	GLU	conflict	UNP Q6JC62
7	365	LEU	PRO	conflict	UNP Q6JC62
7	387	ALA	SER	conflict	UNP Q6JC62

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Chain	Residue	Modelled	Actual	Comment	Reference
7	406	LEU	ARG	conflict	UNP Q6JC62
7	?	-	SER	deletion	UNP Q6JC62
7	558	ALA	SER	conflict	UNP Q6JC62
7	588	ASN	GLN	conflict	UNP Q6JC62
7	589	SER	ASN	conflict	UNP Q6JC62
7	591	GLN	ALA	conflict	UNP Q6JC62
7	718	VAL	THR	conflict	UNP Q6JC62
7	719	ASP	GLU	conflict	UNP Q6JC62
8	365	LEU	PRO	conflict	UNP Q6JC62
8	387	ALA	SER	conflict	UNP Q6JC62
8	406	LEU	ARG	conflict	UNP Q6JC62
8	?	-	SER	deletion	UNP Q6JC62
8	558	ALA	SER	conflict	UNP Q6JC62
8	588	ASN	GLN	conflict	UNP Q6JC62
8	589	SER	ASN	conflict	UNP Q6JC62
8	591	GLN	ALA	conflict	UNP Q6JC62
8	718	VAL	THR	conflict	UNP Q6JC62
8	719	ASP	GLU	conflict	UNP Q6JC62

- Molecule 2 is a DNA chain called DNA (5'-D(*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
2	0	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	9	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	AA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	BA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	CA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	DA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	EA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	FA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	GA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	HA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	IA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	JA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	KA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	LA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	MA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	NA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	OA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	PA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	QA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	RA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	SA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	TA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	UA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	VA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	WA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	XA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	YA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	ZA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	aA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	bA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	cA	2	Total 37	C 19	N 8	O 9	P 1	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	dA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	eA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	fA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	gA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	hA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	iA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	jA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	kA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	lA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	mA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	nA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	oA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	pA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	qA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	rA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	sA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	tA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	uA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	vA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	wA	2	Total 37	C 19	N 8	O 9	P 1	0	0
2	xA	2	Total 37	C 19	N 8	O 9	P 1	0	0

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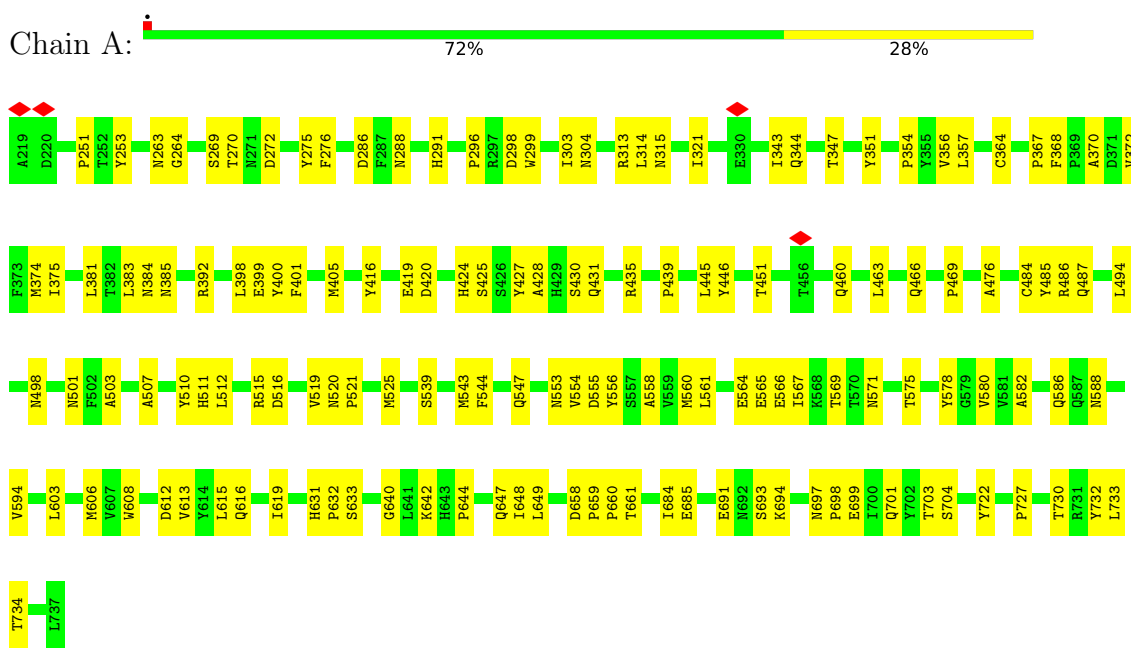
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	yA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	zA	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	0A	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	1A	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	2A	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	3A	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	4A	2	Total	C	N	O	P	0	0
			37	19	8	9	1		
2	5A	2	Total	C	N	O	P	0	0
			37	19	8	9	1		

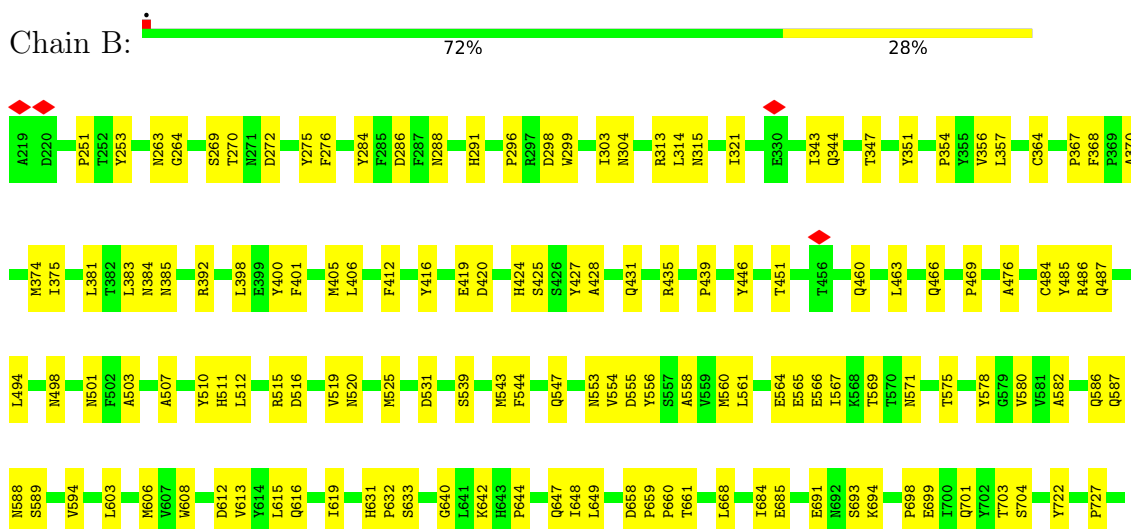
3 Residue-property plots

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

- Molecule 1: Capsid protein VP1

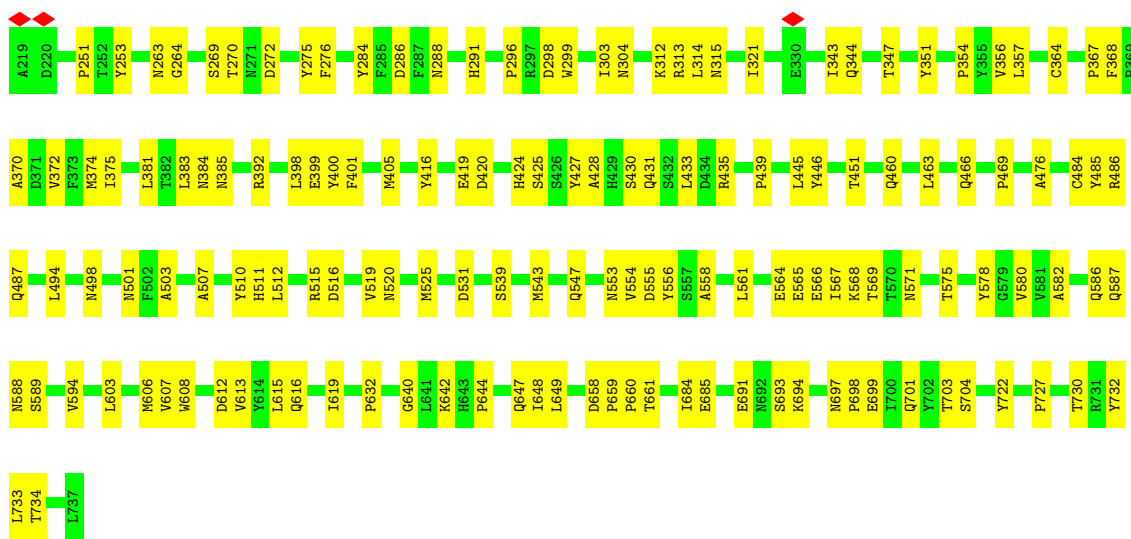


- Molecule 1: Capsid protein VP1

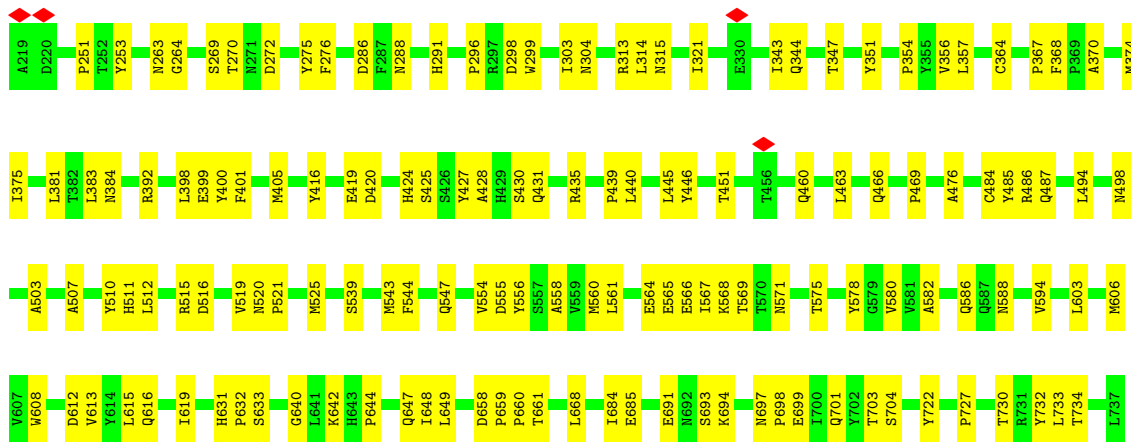


T730
R731
Y732
L733
T734
L737

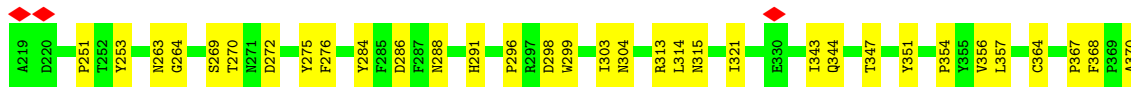
• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1

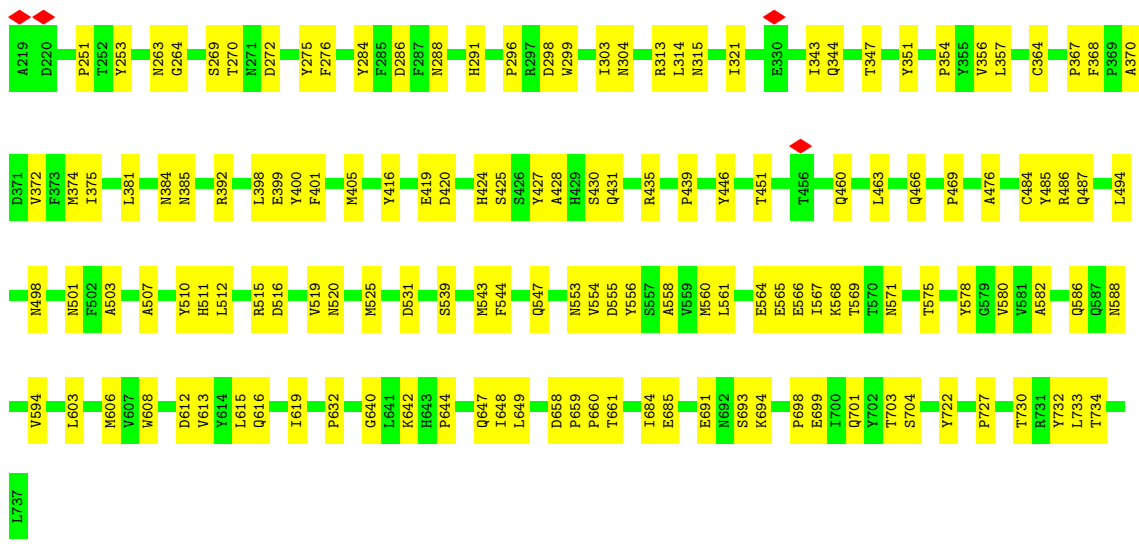


• Molecule 1: Capsid protein VP1

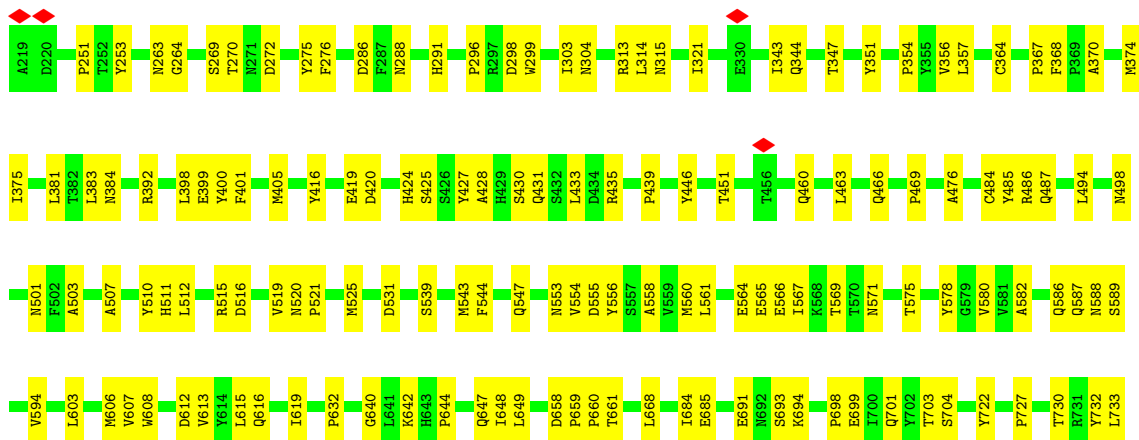




• Molecule 1: Capsid protein VP1

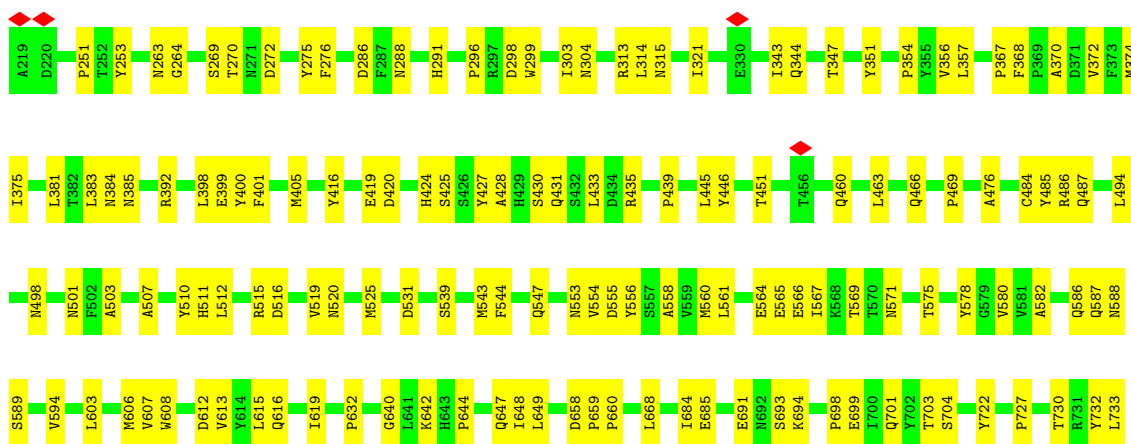


• Molecule 1: Capsid protein VP1



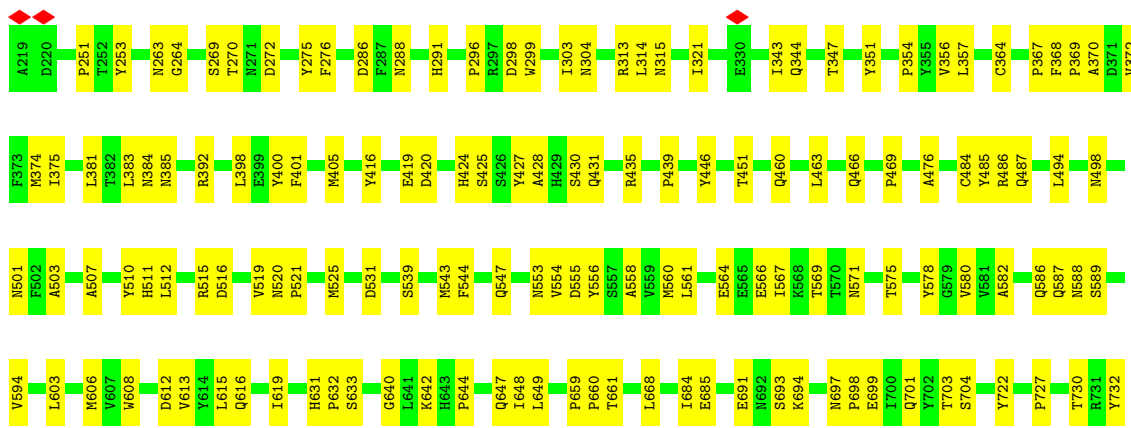
T734
L737

• Molecule 1: Capsid protein VP1



T734
L737

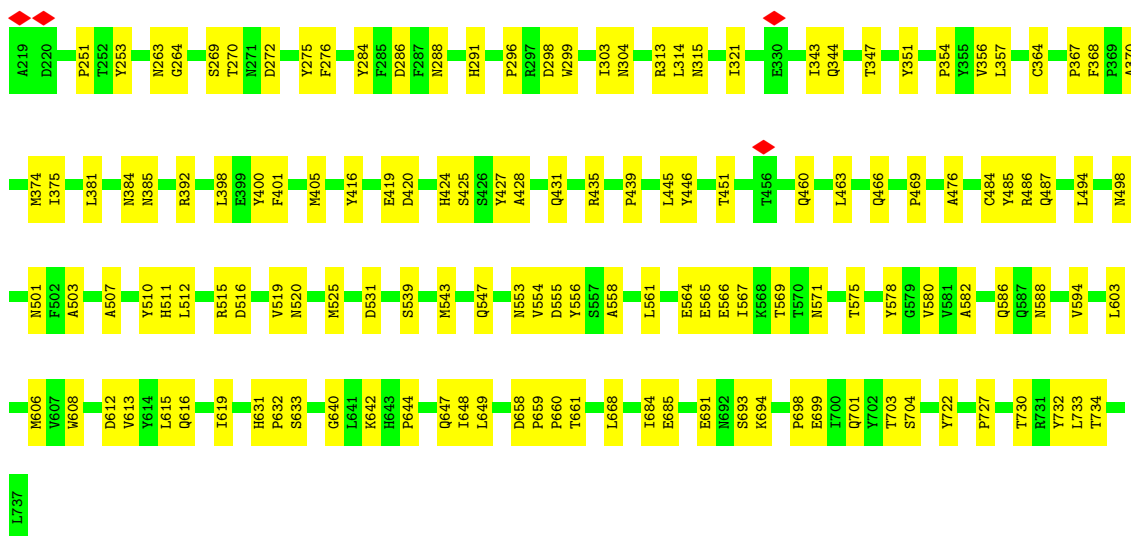
• Molecule 1: Capsid protein VP1



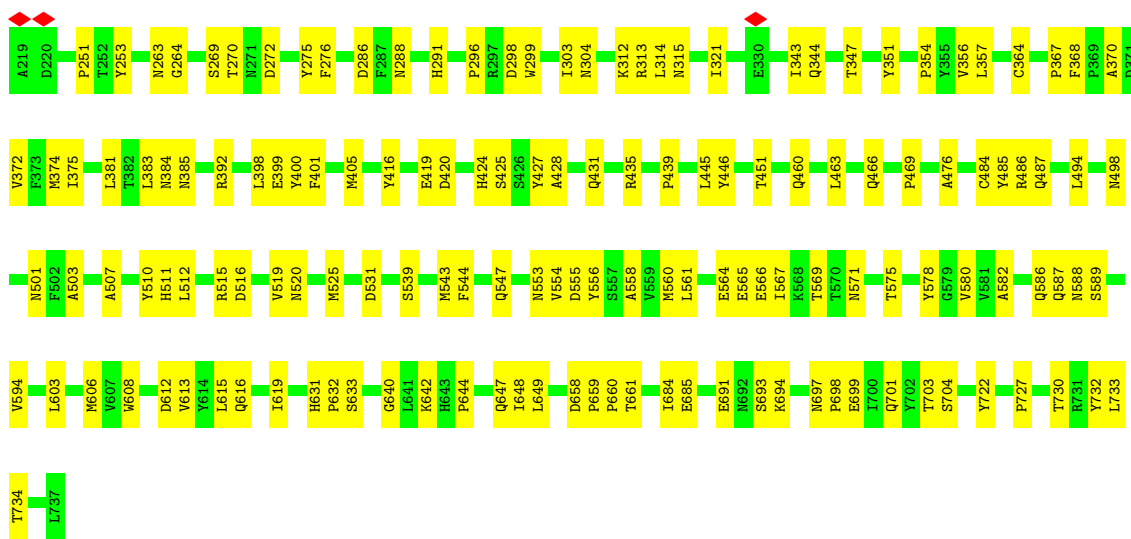
L733
T734
L737

• Molecule 1: Capsid protein VP1

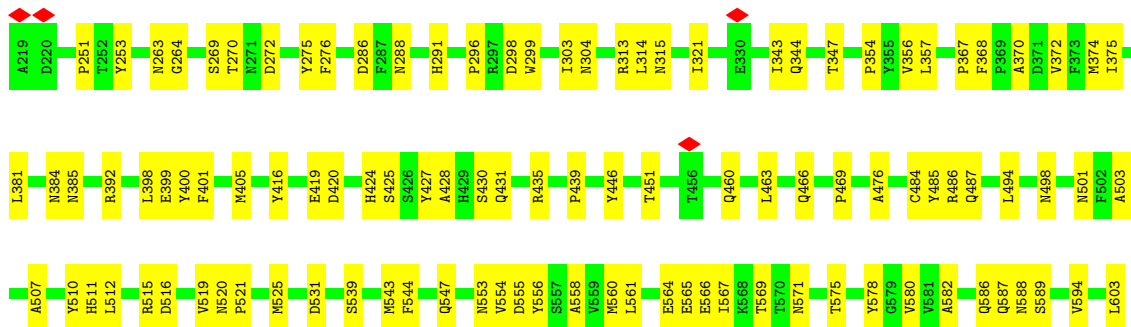




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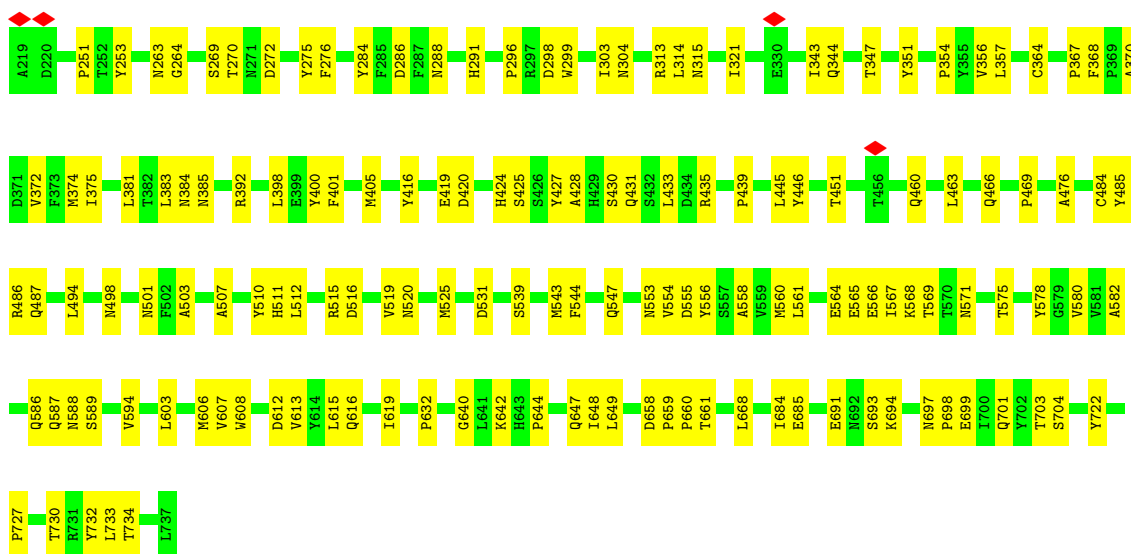


• Molecule 1: Capsid protein VP1

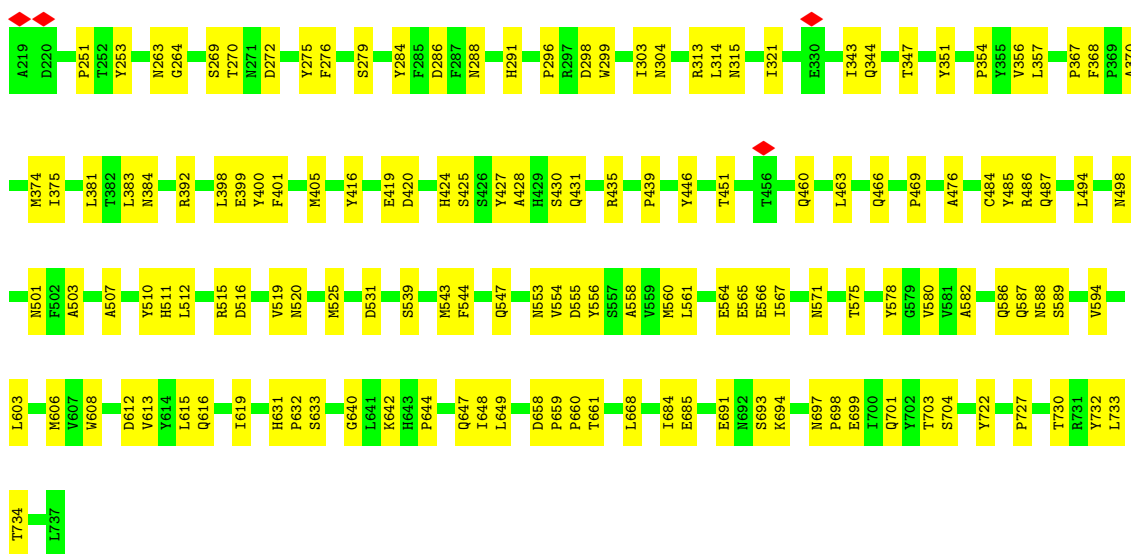




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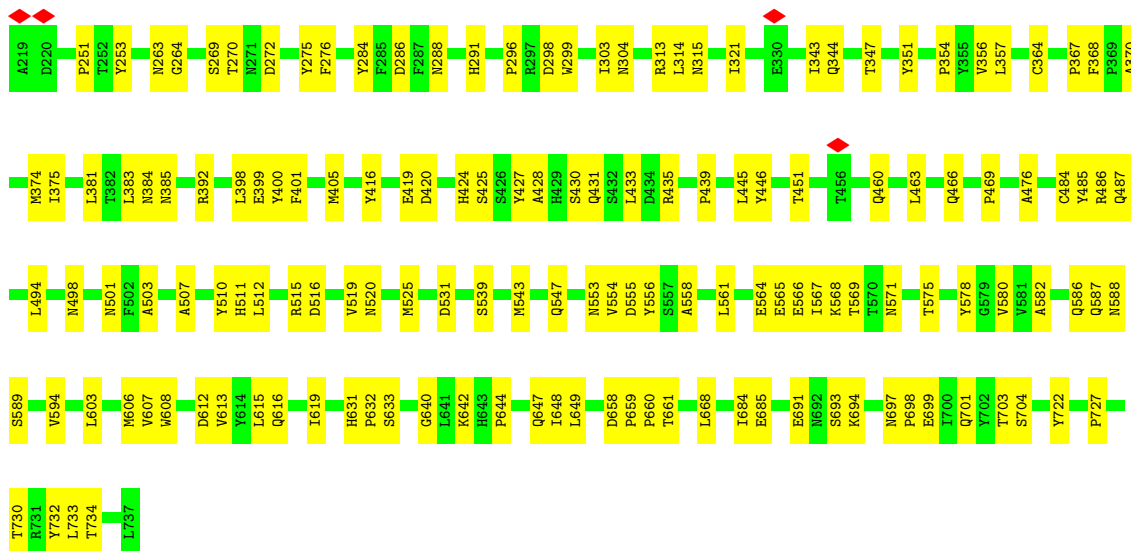


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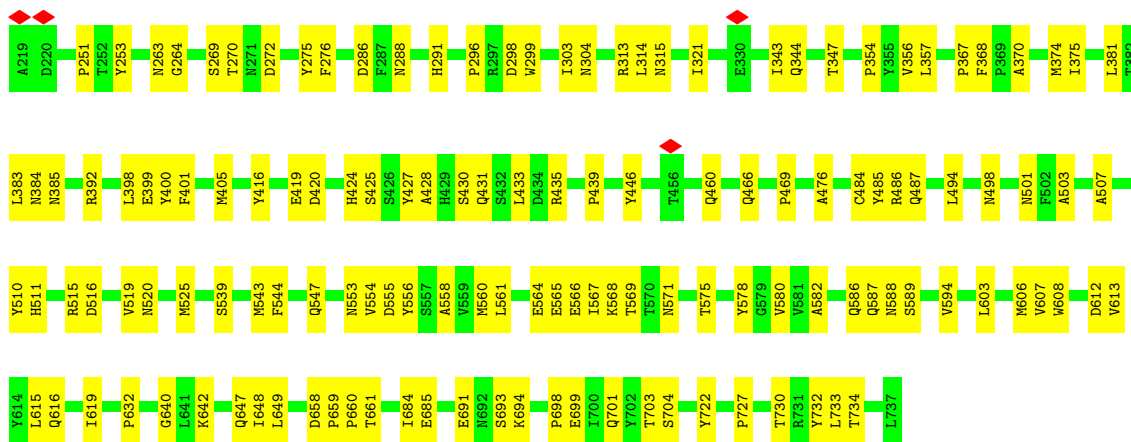


• Molecule 1: Capsid protein VP1



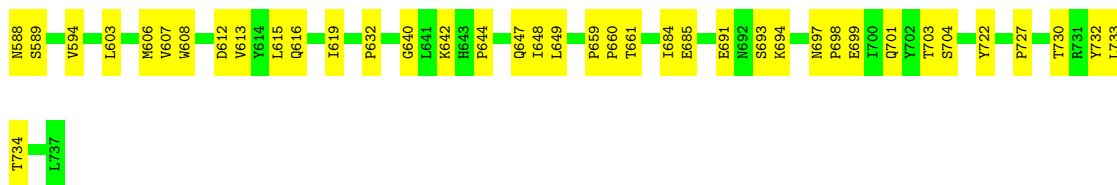


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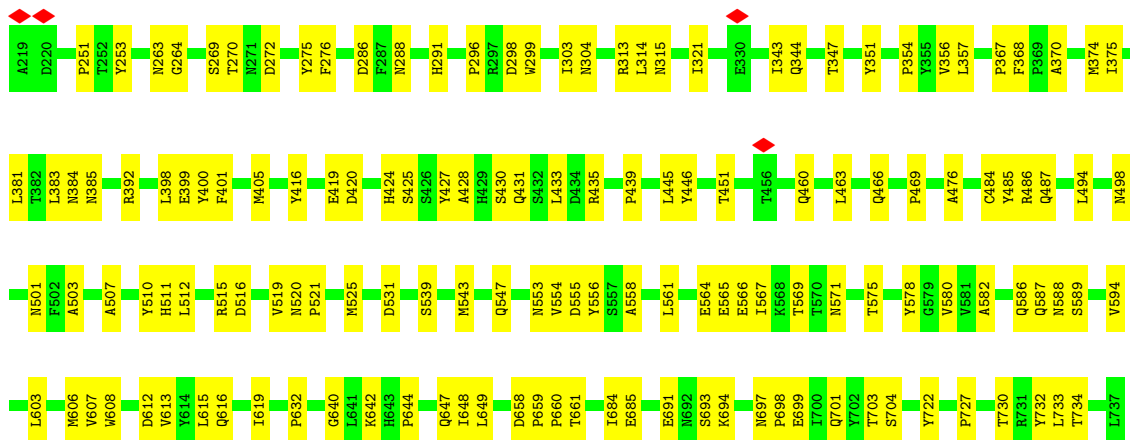


• Molecule 1: Capsid protein VP1

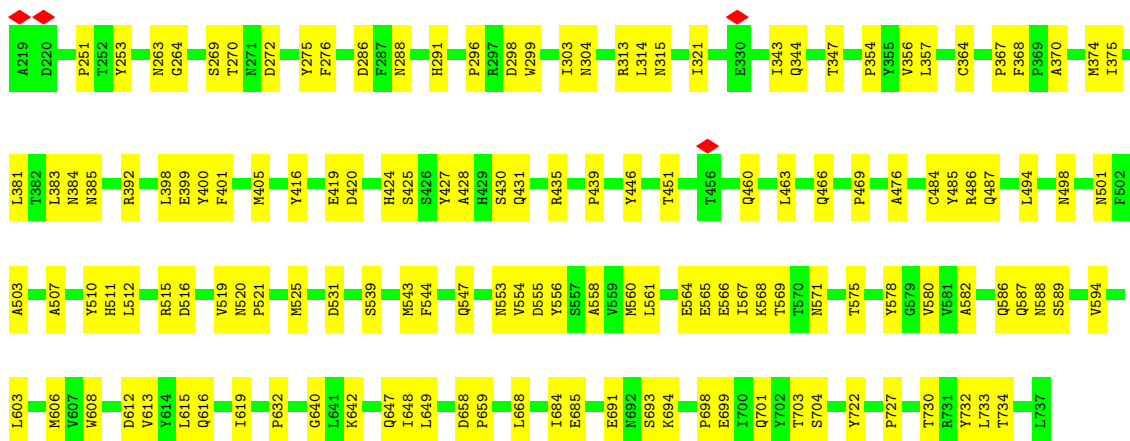




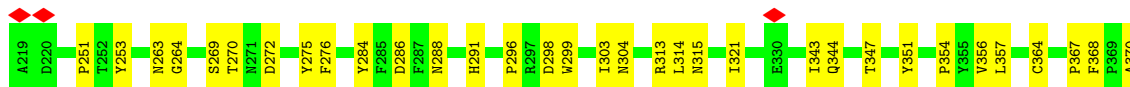
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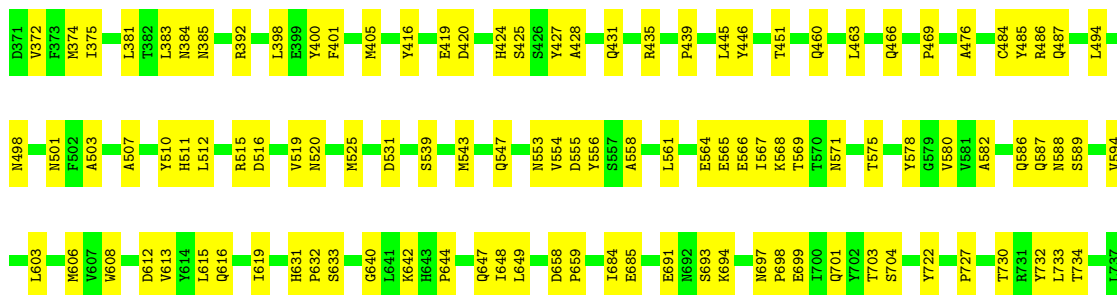


• Molecule 1: Capsid protein VP1

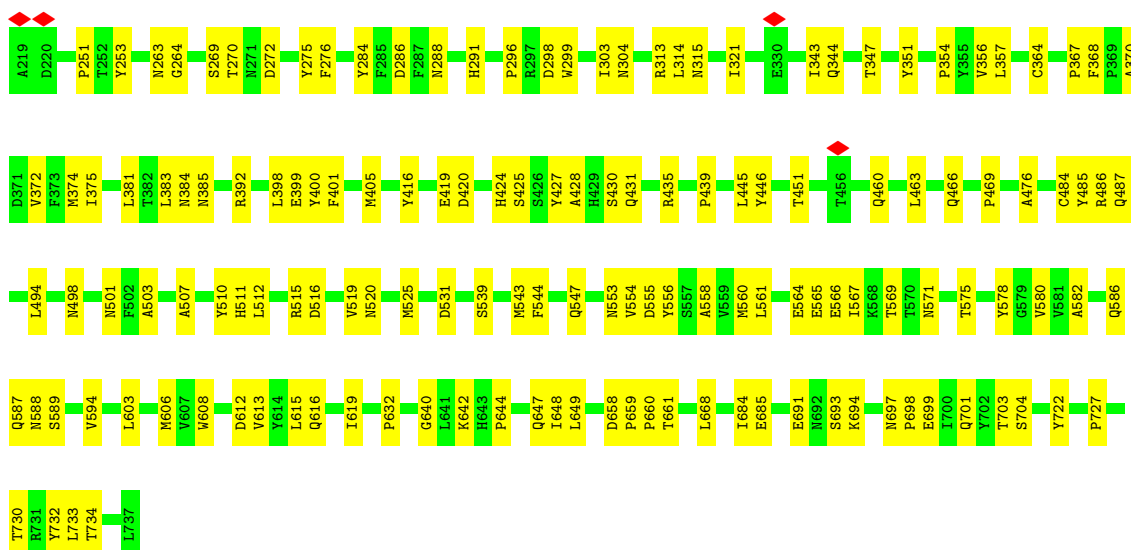


• Molecule 1: Capsid protein VP1

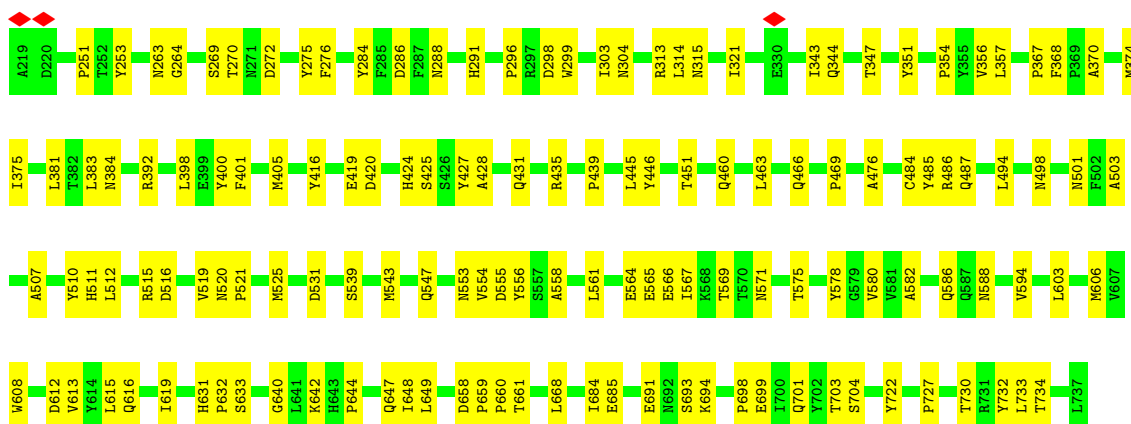




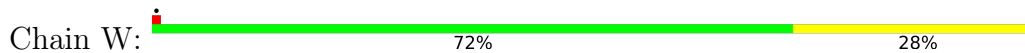
• Molecule 1: Capsid protein VP1

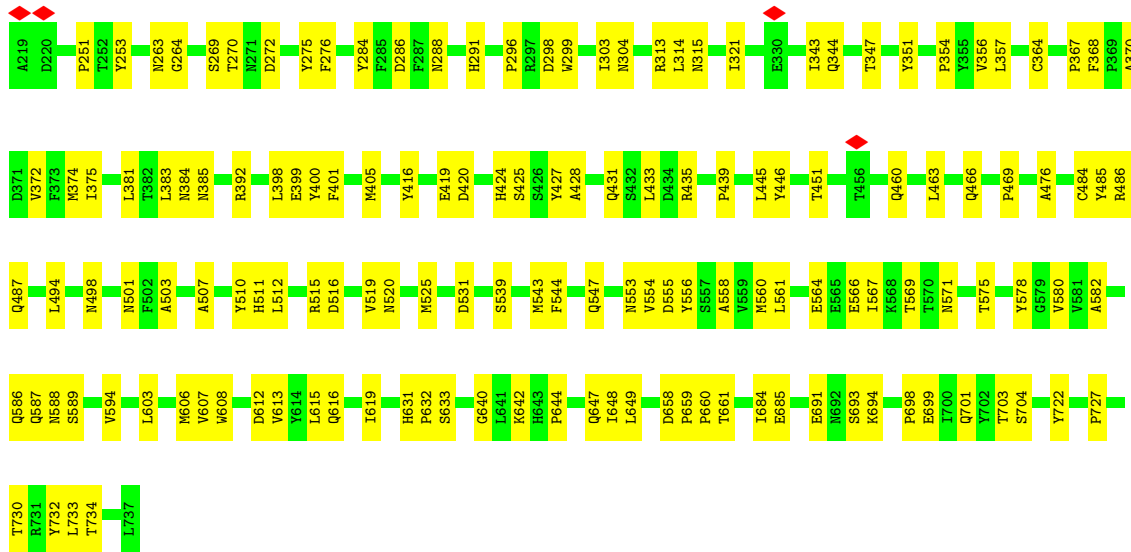


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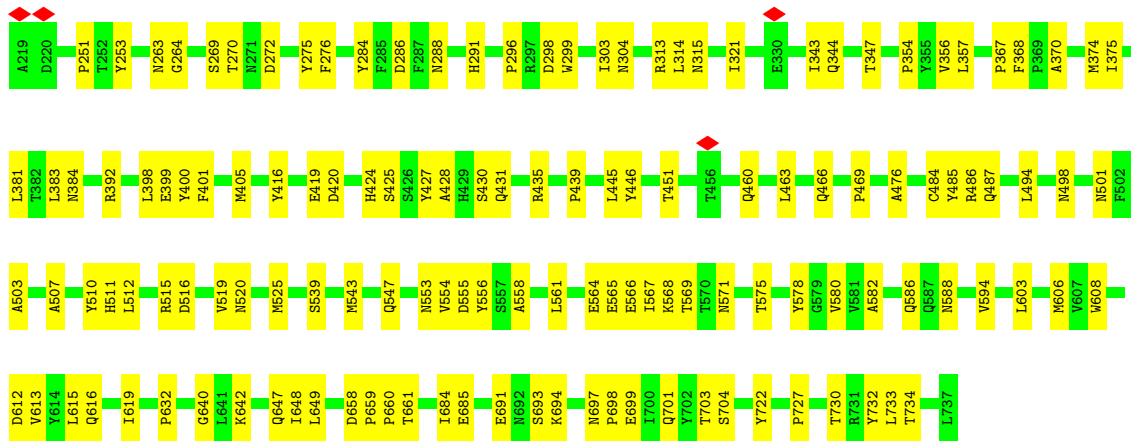


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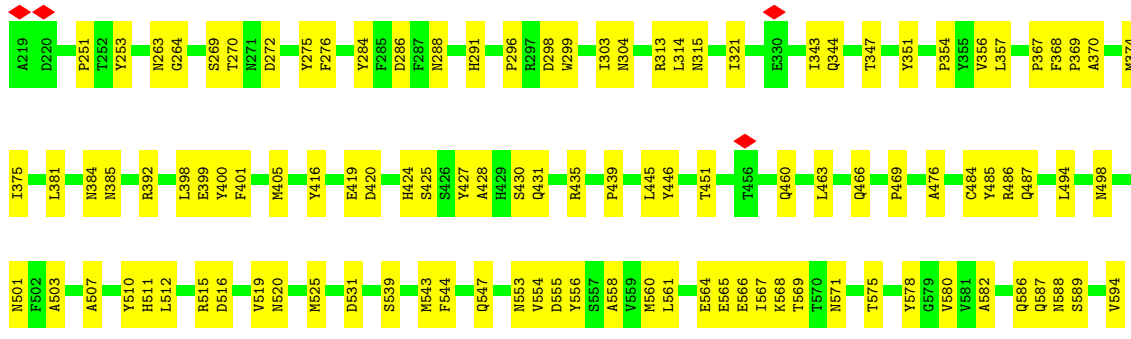


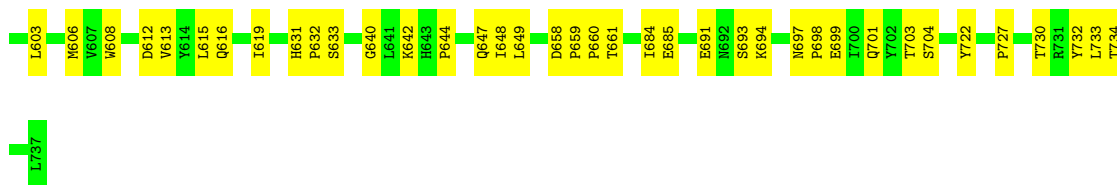


• Molecule 1: Capsid protein VP1

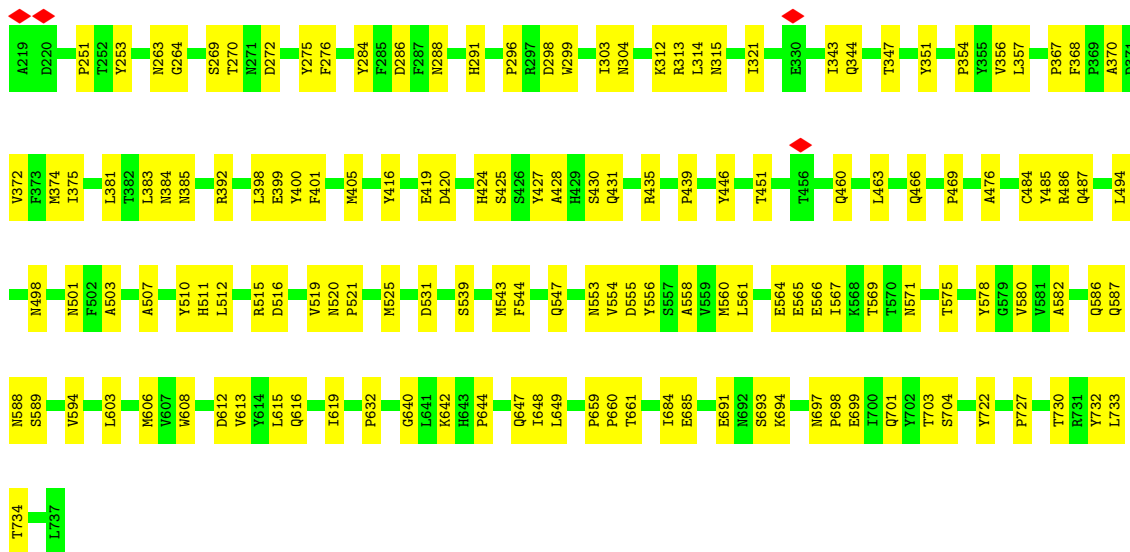


• Molecule 1: Capsid protein VP1

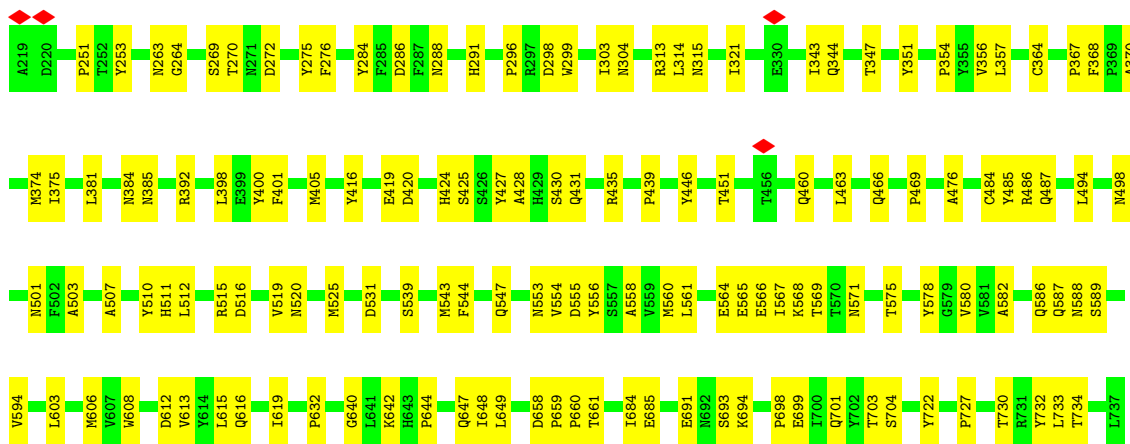




• Molecule 1: Capsid protein VP1

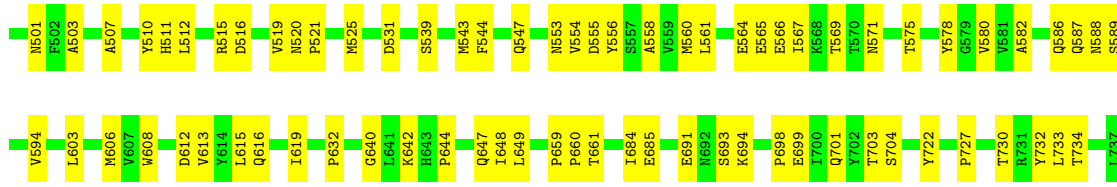


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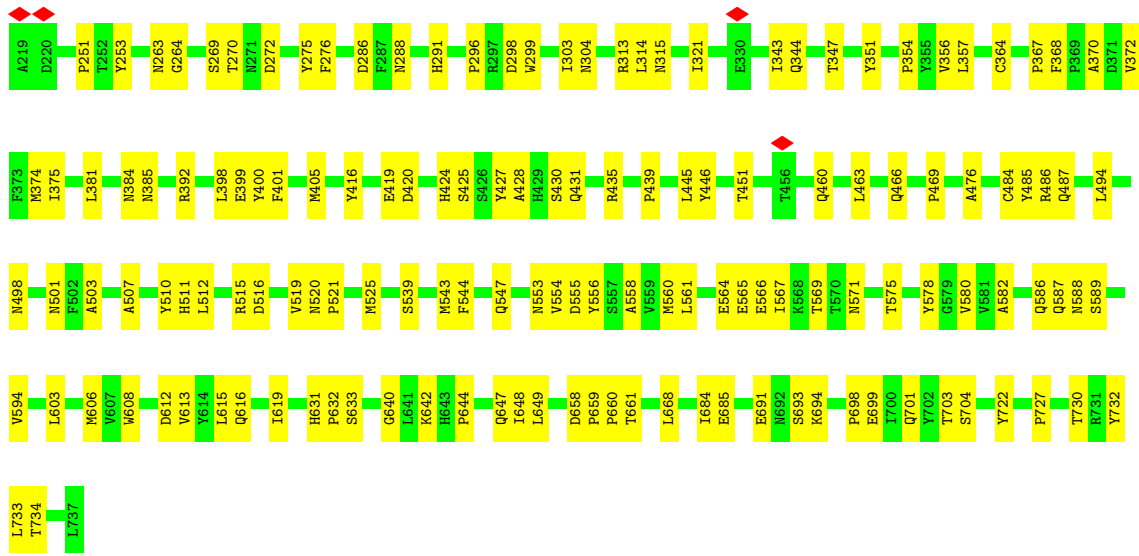


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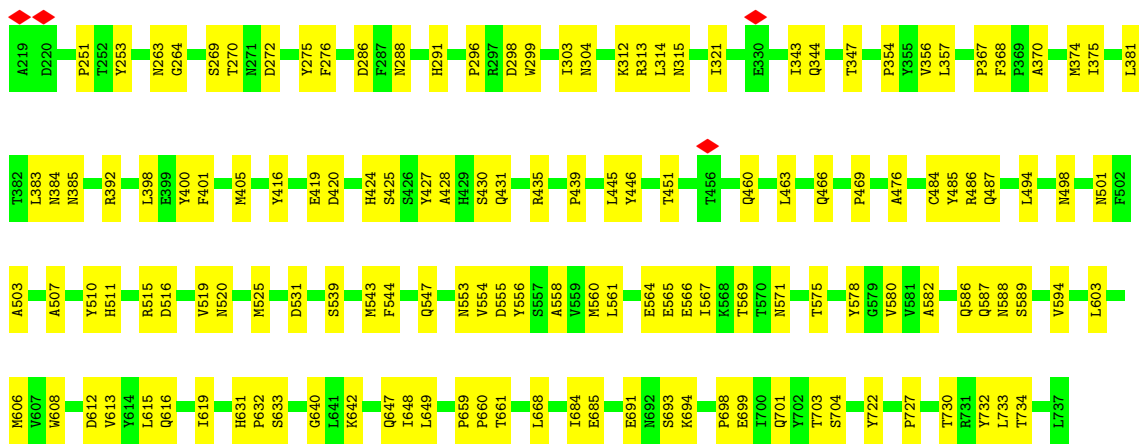




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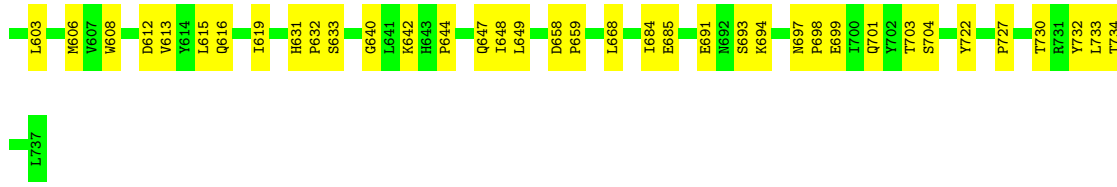


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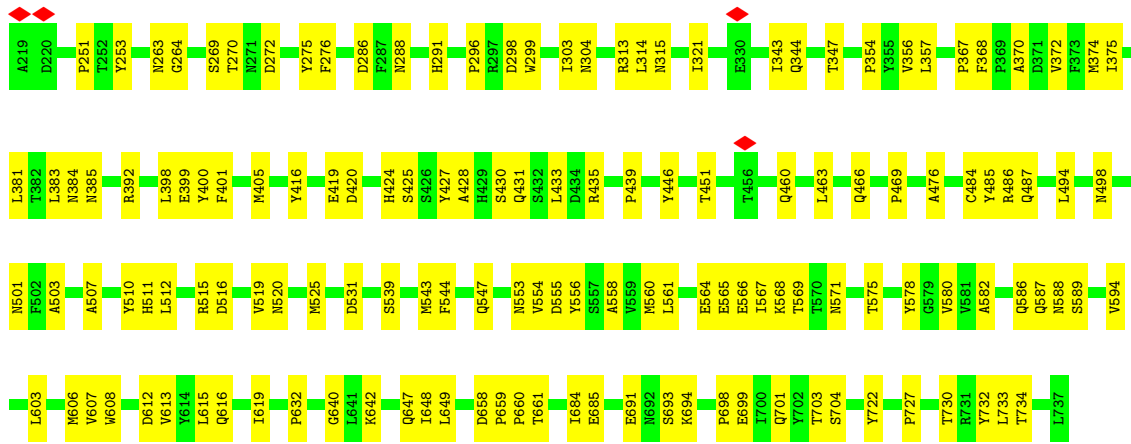


• Molecule 1: Capsid protein VP1

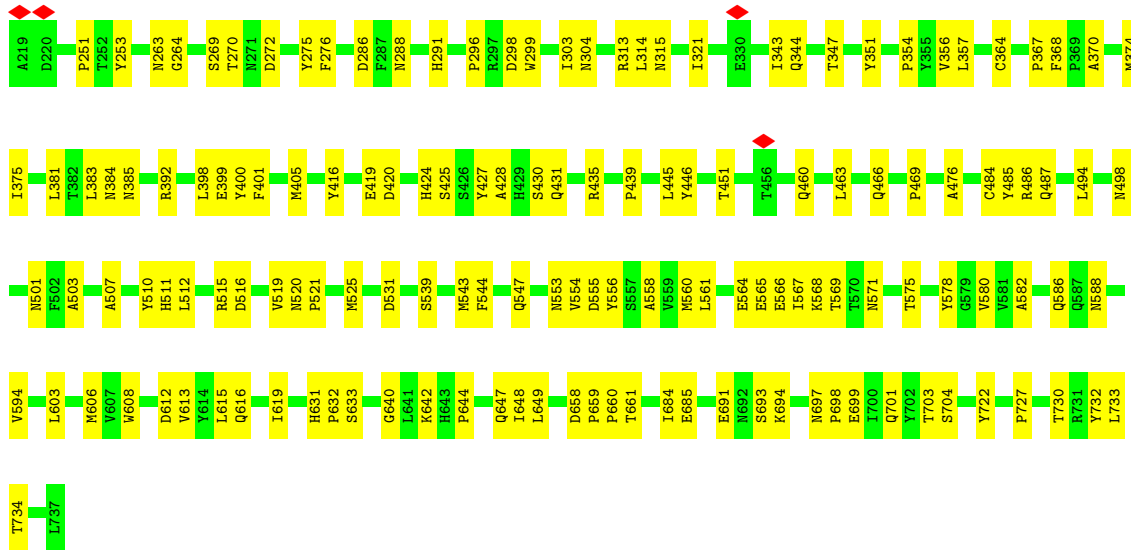




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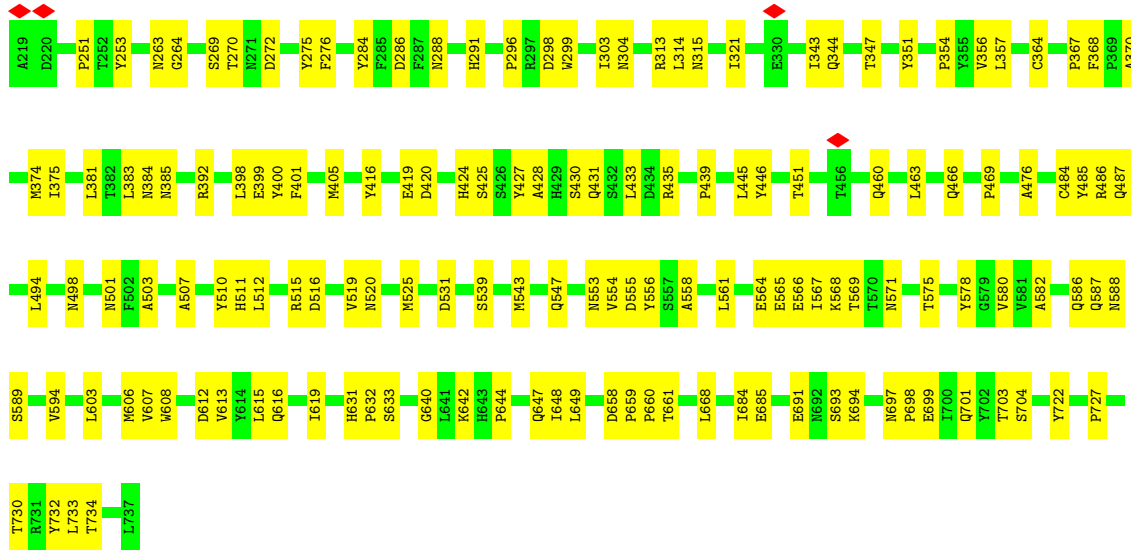


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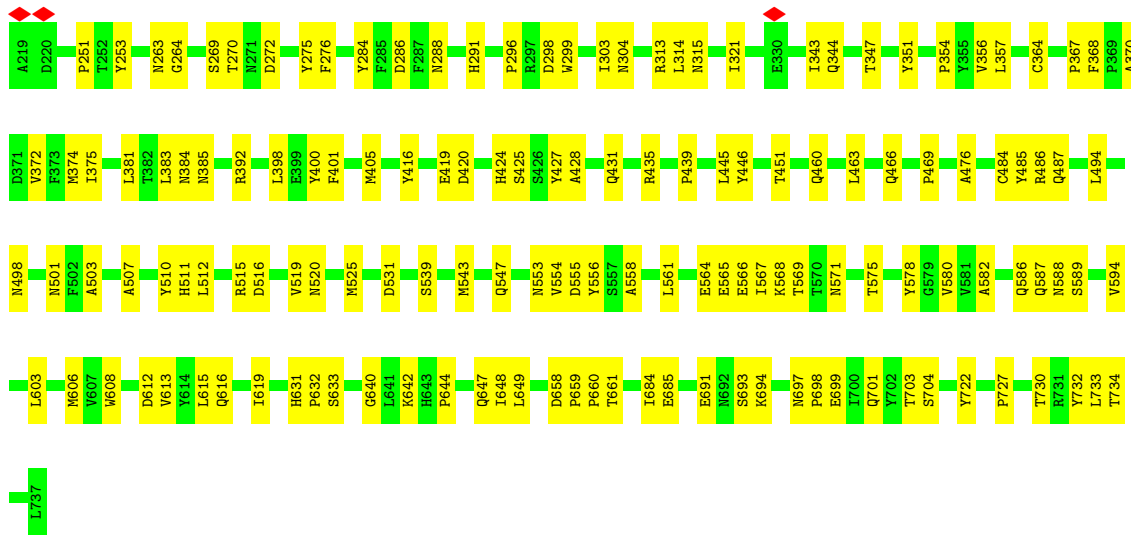


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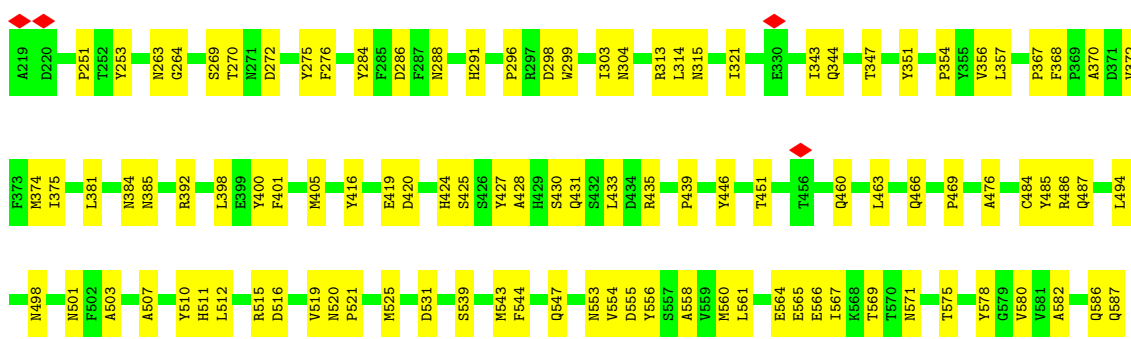


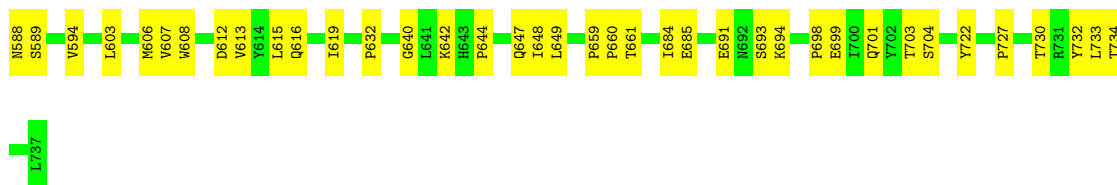


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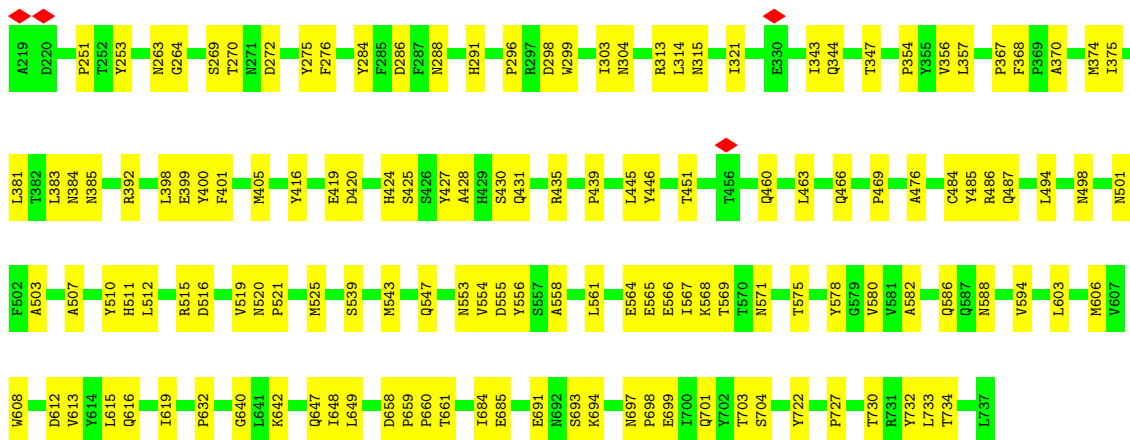


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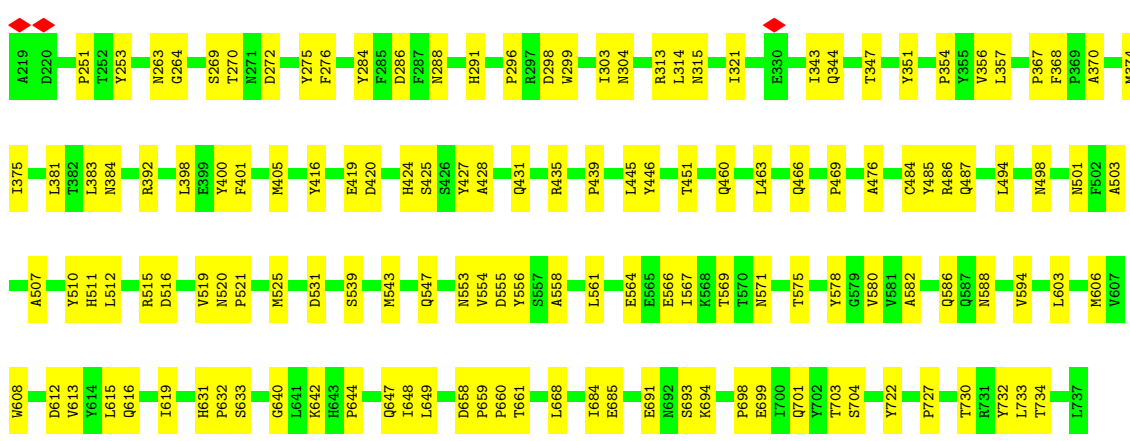




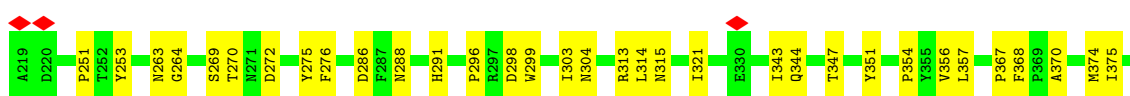
• Molecule 1: Capsid protein VP1

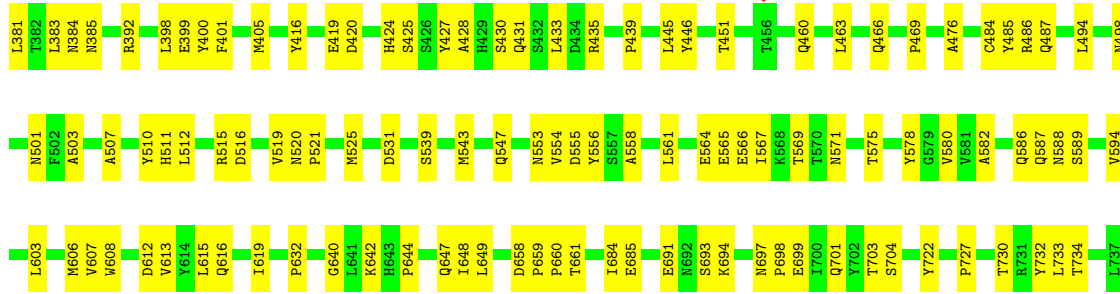


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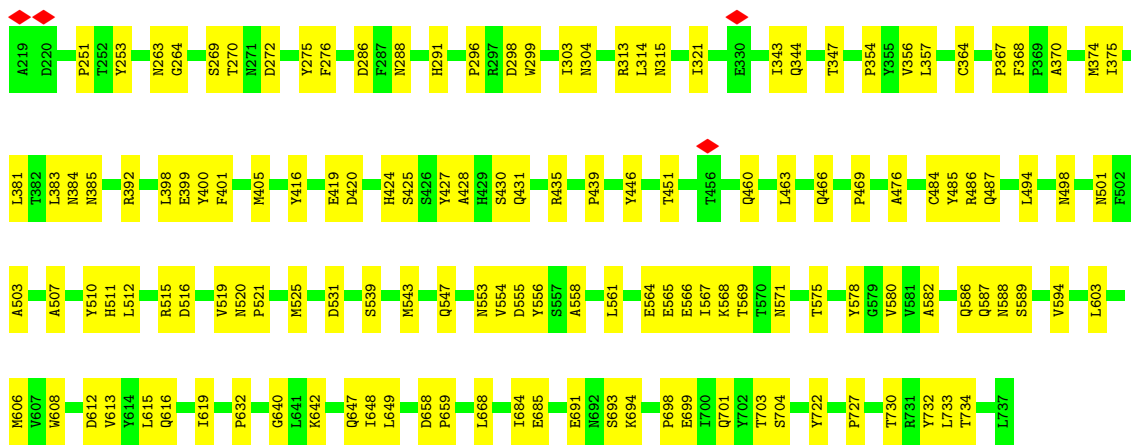


• Molecule 1: Capsid protein VP1





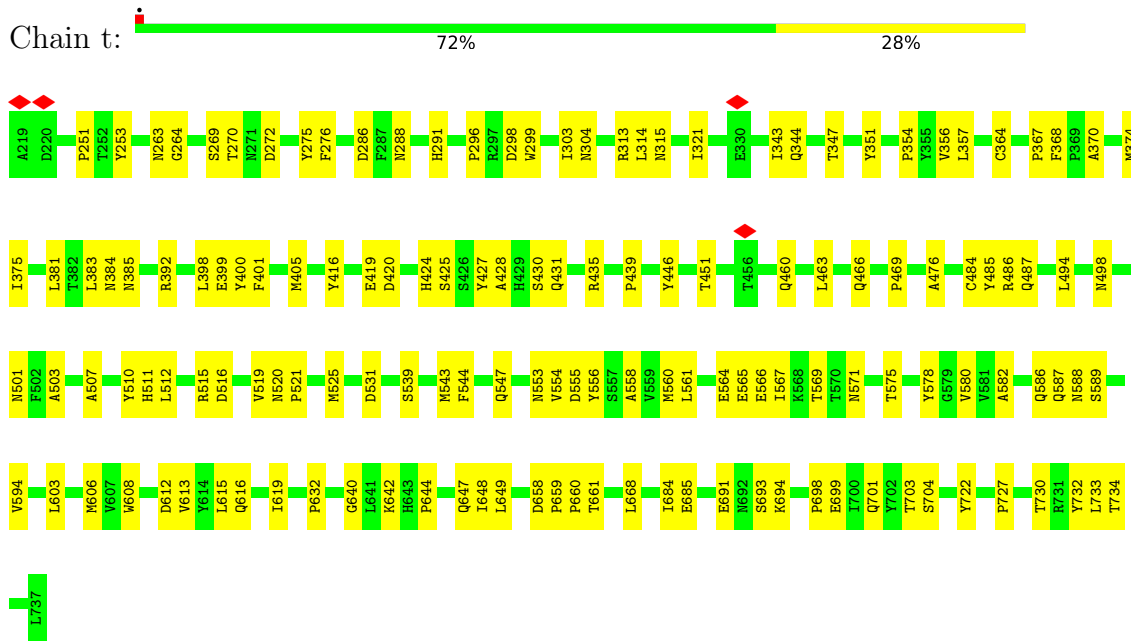
• Molecule 1: Capsid protein VP1



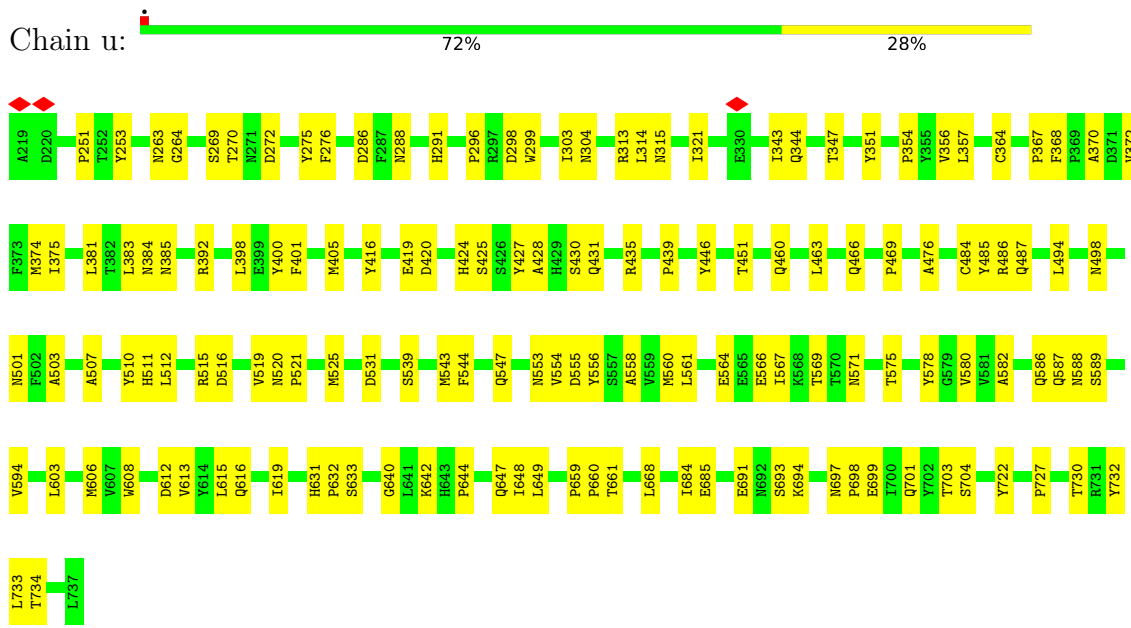
• Molecule 1: Capsid protein VP1



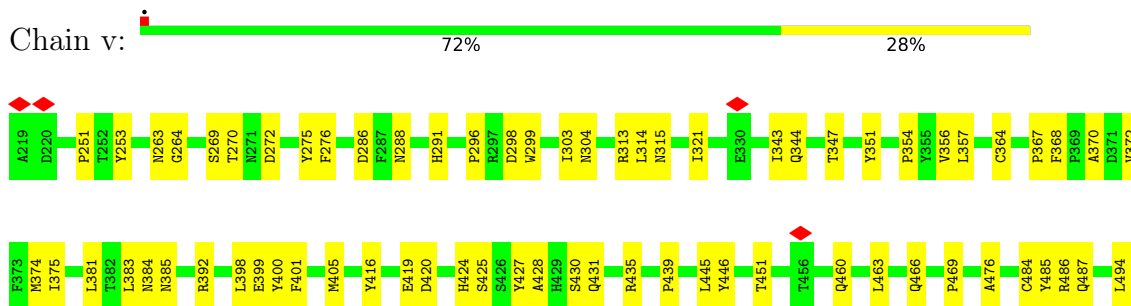
• Molecule 1: Capsid protein VP1

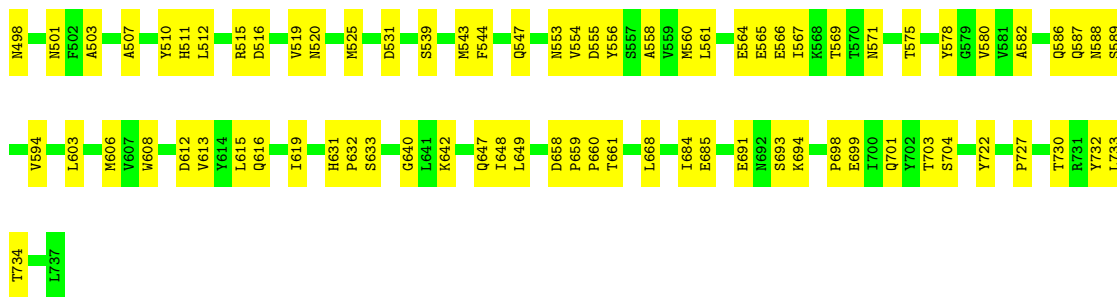


• Molecule 1: Capsid protein VP1

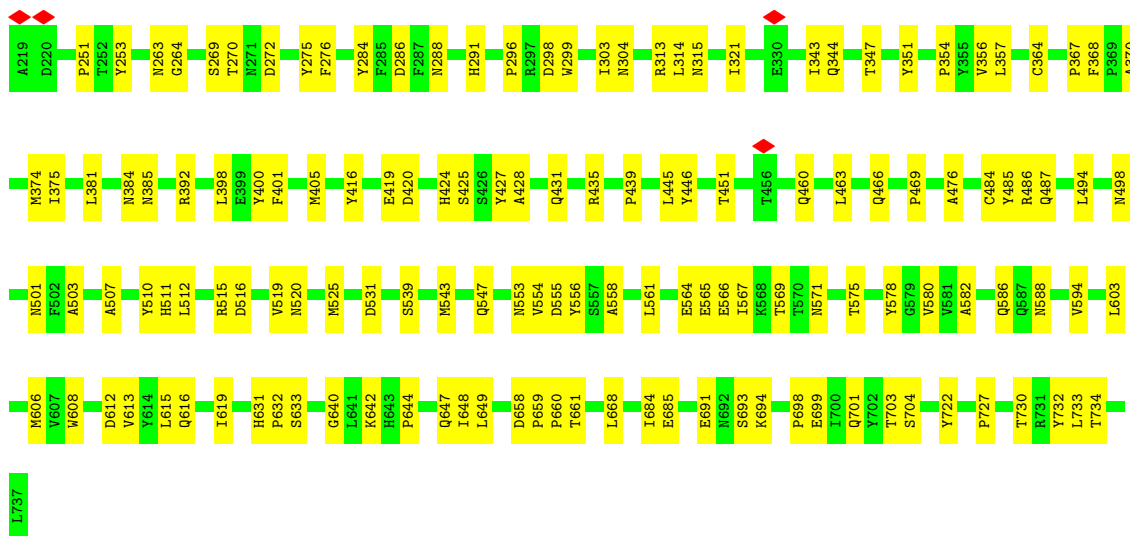


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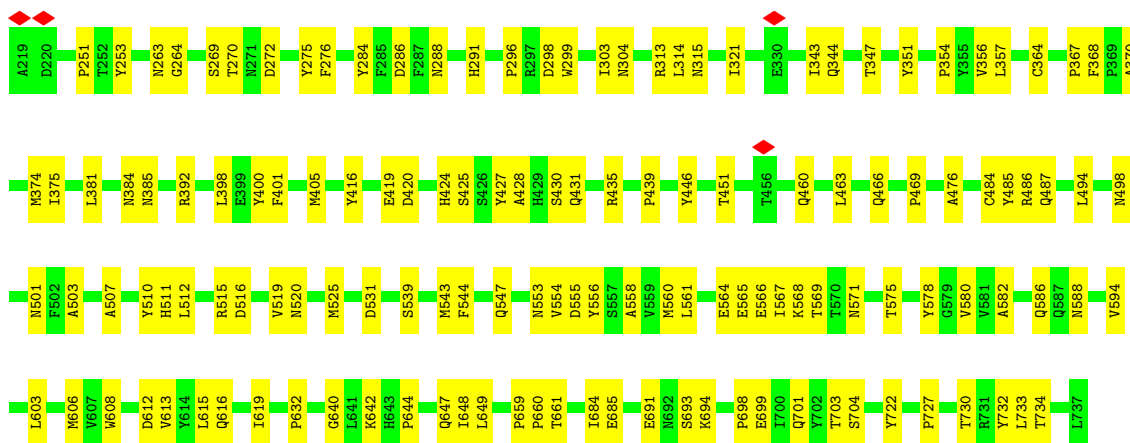




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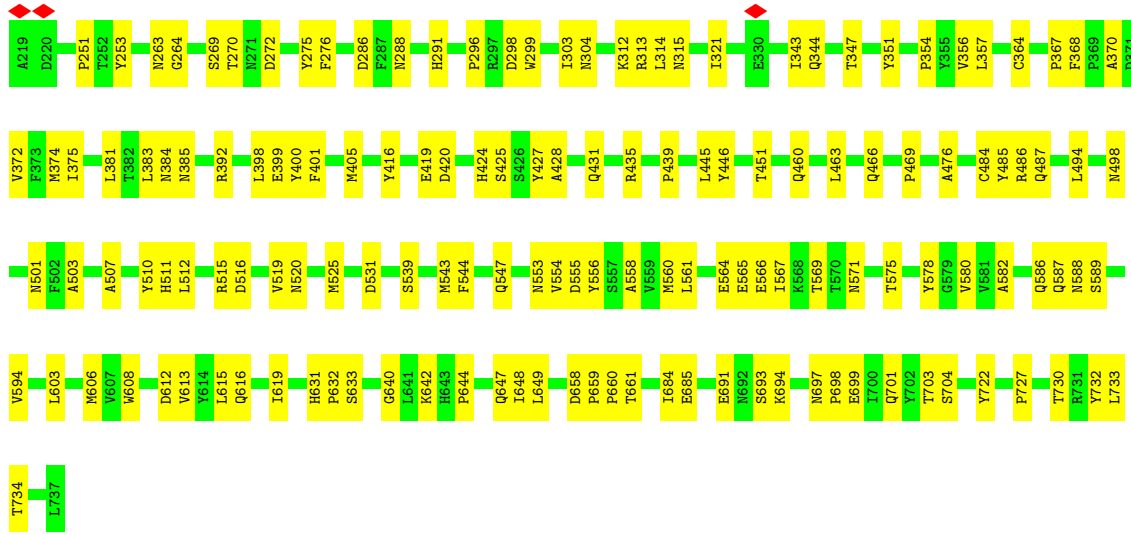


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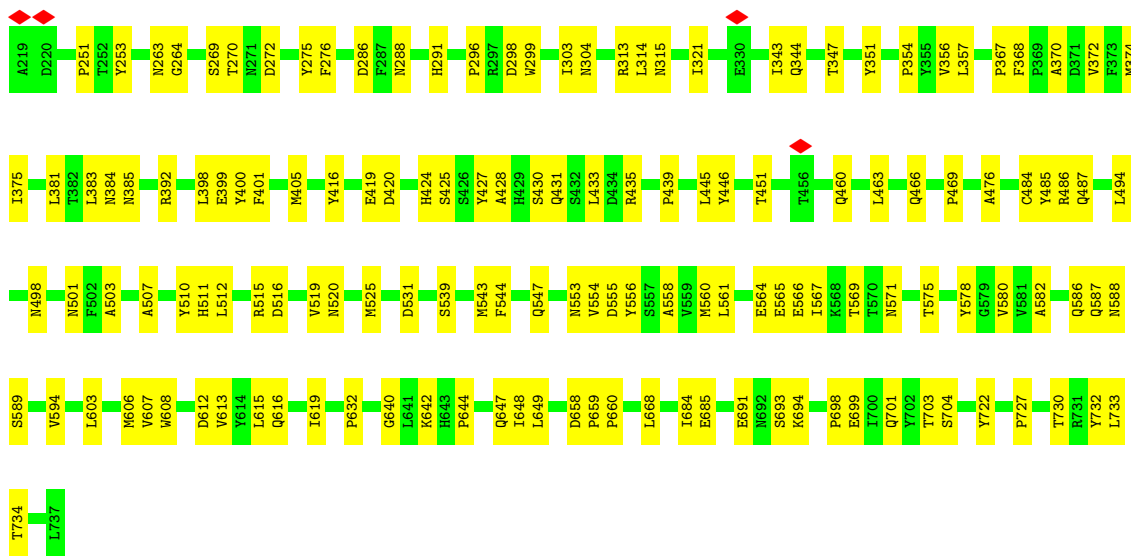


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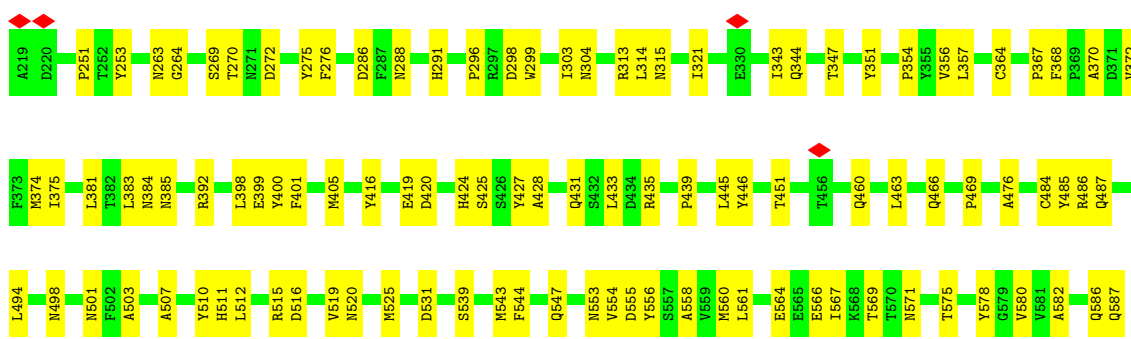


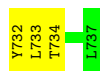
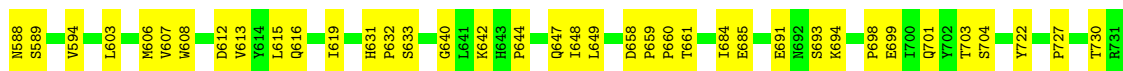


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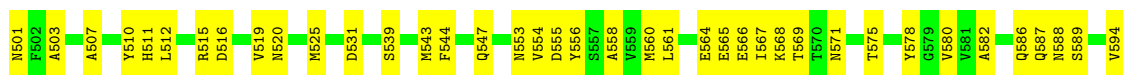
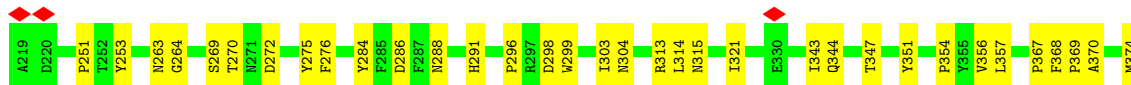


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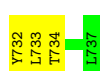
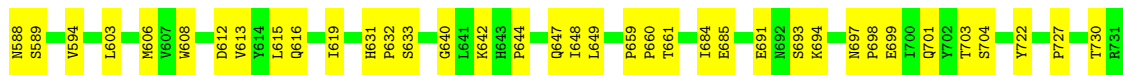





• Molecule 1: Capsid protein VP1



• Molecule 1: Capsid protein VP1



• Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 0:  100%

C901
A902

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 9:  100%


C903
A904

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain AA:  100%


C905
A906

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain BA:  100%

C907
A908

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain CA:  100%


C909
A910

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain DA:  100%

C911
A912

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain EA:  100%


C913
A914

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain FA:  100%

C915
A916

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain GA:  100%C917
A918

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain HA:  100%C919
A920

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain IA:  100%C921
A922

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain JA:  100%C923
A924

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain KA:  100%C925
A926


- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain LA:  100%C927
A928

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain MA:  100%C929
A930

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain NA:  100%

C931
A932

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain OA:  100%


C933
A934

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain PA:  100%

C935
A936

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain QA:  100%

C937
A938

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain RA:  100%


C939
A940

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain SA:  100%


C941
A942

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain TA:  100%


C943
A944

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain UA:  100%

C945
A946

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain VA:  100%C947
A948

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain WA:  100%C949
A950


- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain XA:  100%C951
A952

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain YA:  100%C953
A954

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain ZA:  100%C955
A956

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain aA:  100%C957
A958

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain bA:  100%C959
A960

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain cA:  100%

C961
A962

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain dA:  100%

C963
A964

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain eA:  100%

C965
A966

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain fA:  100%

C967
A968

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain gA:  100%

C969
A970

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain hA:  100%


C971
A972

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain iA:  100%


C973
A974

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain jA:  100%

C975
A976

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain kA:  100%C977
A978

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain lA:  100%C979
A980


- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain mA:  100%C981
A982

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain nA:  100%C983
A984

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain oA:  100%C985
A986

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain pA:  100%C987
A988

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain qA:  100%C989
A990

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain rA:  100%

C991
A992

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain sA:  100%

C993
A994

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain tA:  100%

C995
A996

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain uA:  100%

C997
A998

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain vA:  100%

C999
A1000

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain wA:  100%


C1001
A1002

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain xA:  100%

C1003
A1004

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain yA:  100%

C1005
A1006

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain zA:  100%C1007
A1008

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 0A:  100%C1009
A1010

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 1A:  100%C1011
A1012


- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 2A:  100%C1013
A1014

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 3A:  100%C1015
A1016

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 4A:  100%C1017
A1018

- Molecule 2: DNA (5'-D(*CP*A)-3')

Chain 5A:  100%C1019
A1020

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	17861	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 ($e^-/\text{\AA}^2$)	75	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	14.012	Depositor
Minimum map value	-7.303	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	419.6, 419.6, 419.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.049, 1.049, 1.049	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	0.40	0/4244	0.53	0/5788
1	2	0.40	0/4244	0.53	0/5788
1	3	0.40	0/4244	0.53	0/5788
1	4	0.40	0/4244	0.53	0/5788
1	5	0.40	0/4244	0.53	0/5788
1	6	0.40	0/4244	0.53	0/5788
1	7	0.40	0/4244	0.53	0/5788
1	8	0.40	0/4244	0.53	0/5788
1	A	0.40	0/4244	0.53	0/5788
1	B	0.40	0/4244	0.53	0/5788
1	C	0.40	0/4244	0.53	0/5788
1	D	0.40	0/4244	0.53	0/5788
1	E	0.40	0/4244	0.53	0/5788
1	F	0.40	0/4244	0.53	0/5788
1	G	0.40	0/4244	0.53	0/5788
1	H	0.40	0/4244	0.53	0/5788
1	I	0.40	0/4244	0.53	0/5788
1	J	0.40	0/4244	0.53	0/5788
1	K	0.40	0/4244	0.53	0/5788
1	L	0.40	0/4244	0.53	0/5788
1	M	0.40	0/4244	0.53	0/5788
1	N	0.40	0/4244	0.53	0/5788
1	O	0.40	0/4244	0.53	0/5788
1	P	0.40	0/4244	0.53	0/5788
1	Q	0.40	0/4244	0.53	0/5788
1	R	0.40	0/4244	0.53	0/5788
1	S	0.40	0/4244	0.53	0/5788
1	T	0.40	0/4244	0.53	0/5788
1	U	0.40	0/4244	0.53	0/5788
1	V	0.40	0/4244	0.53	0/5788
1	W	0.40	0/4244	0.53	0/5788
1	X	0.40	0/4244	0.53	0/5788
1	Y	0.40	0/4244	0.53	0/5788
1	Z	0.40	0/4244	0.53	0/5788

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	a	0.40	0/4244	0.53	0/5788
1	b	0.40	0/4244	0.53	0/5788
1	c	0.40	0/4244	0.53	0/5788
1	d	0.40	0/4244	0.53	0/5788
1	e	0.40	0/4244	0.53	0/5788
1	f	0.40	0/4244	0.53	0/5788
1	g	0.40	0/4244	0.53	0/5788
1	h	0.40	0/4244	0.53	0/5788
1	i	0.40	0/4244	0.53	0/5788
1	j	0.40	0/4244	0.53	0/5788
1	k	0.40	0/4244	0.53	0/5788
1	l	0.40	0/4244	0.53	0/5788
1	m	0.40	0/4244	0.53	0/5788
1	n	0.40	0/4244	0.53	0/5788
1	o	0.40	0/4244	0.53	0/5788
1	p	0.40	0/4244	0.53	0/5788
1	q	0.40	0/4244	0.53	0/5788
1	r	0.40	0/4244	0.53	0/5788
1	s	0.40	0/4244	0.53	0/5788
1	t	0.40	0/4244	0.53	0/5788
1	u	0.40	0/4244	0.53	0/5788
1	v	0.40	0/4244	0.53	0/5788
1	w	0.40	0/4244	0.53	0/5788
1	x	0.40	0/4244	0.53	0/5788
1	y	0.40	0/4244	0.53	0/5788
1	z	0.40	0/4244	0.53	0/5788
2	0	0.27	0/41	0.31	0/61
2	0A	0.27	0/41	0.31	0/61
2	1A	0.27	0/41	0.31	0/61
2	2A	0.28	0/41	0.30	0/61
2	3A	0.28	0/41	0.31	0/61
2	4A	0.28	0/41	0.31	0/61
2	5A	0.27	0/41	0.31	0/61
2	9	0.28	0/41	0.31	0/61
2	AA	0.27	0/41	0.31	0/61
2	BA	0.28	0/41	0.31	0/61
2	CA	0.28	0/41	0.30	0/61
2	DA	0.27	0/41	0.31	0/61
2	EA	0.27	0/41	0.31	0/61
2	FA	0.28	0/41	0.31	0/61
2	GA	0.28	0/41	0.30	0/61
2	HA	0.28	0/41	0.30	0/61
2	IA	0.27	0/41	0.31	0/61

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	JA	0.27	0/41	0.31	0/61
2	KA	0.28	0/41	0.31	0/61
2	LA	0.28	0/41	0.30	0/61
2	MA	0.27	0/41	0.31	0/61
2	NA	0.27	0/41	0.31	0/61
2	OA	0.27	0/41	0.31	0/61
2	PA	0.28	0/41	0.31	0/61
2	QA	0.28	0/41	0.30	0/61
2	RA	0.27	0/41	0.31	0/61
2	SA	0.27	0/41	0.31	0/61
2	TA	0.27	0/41	0.31	0/61
2	UA	0.28	0/41	0.30	0/61
2	VA	0.27	0/41	0.31	0/61
2	WA	0.27	0/41	0.31	0/61
2	XA	0.27	0/41	0.31	0/61
2	YA	0.27	0/41	0.31	0/61
2	ZA	0.27	0/41	0.31	0/61
2	aA	0.27	0/41	0.31	0/61
2	bA	0.27	0/41	0.31	0/61
2	cA	0.28	0/41	0.31	0/61
2	dA	0.27	0/41	0.31	0/61
2	eA	0.27	0/41	0.31	0/61
2	fA	0.27	0/41	0.31	0/61
2	gA	0.27	0/41	0.31	0/61
2	hA	0.28	0/41	0.31	0/61
2	iA	0.28	0/41	0.30	0/61
2	jA	0.27	0/41	0.31	0/61
2	kA	0.27	0/41	0.31	0/61
2	lA	0.27	0/41	0.31	0/61
2	mA	0.27	0/41	0.31	0/61
2	nA	0.27	0/41	0.31	0/61
2	oA	0.28	0/41	0.31	0/61
2	pA	0.28	0/41	0.30	0/61
2	qA	0.27	0/41	0.31	0/61
2	rA	0.27	0/41	0.31	0/61
2	sA	0.28	0/41	0.30	0/61
2	tA	0.27	0/41	0.31	0/61
2	uA	0.27	0/41	0.31	0/61
2	vA	0.28	0/41	0.30	0/61
2	wA	0.27	0/41	0.31	0/61
2	xA	0.27	0/41	0.31	0/61
2	yA	0.28	0/41	0.31	0/61
2	zA	0.28	0/41	0.30	0/61

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.40	0/257100	0.53	0/350940

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	4121	0	3890	117	0
1	2	4121	0	3890	112	0
1	3	4121	0	3890	113	0
1	4	4121	0	3890	116	0
1	5	4121	0	3890	116	0
1	6	4121	0	3890	115	0
1	7	4121	0	3890	119	0
1	8	4121	0	3890	120	0
1	A	4121	0	3890	116	0
1	B	4121	0	3890	118	0
1	C	4121	0	3890	122	0
1	D	4121	0	3890	121	0
1	E	4121	0	3890	122	0
1	F	4121	0	3890	116	0
1	G	4121	0	3890	115	0
1	H	4121	0	3890	115	0
1	I	4121	0	3890	118	0
1	J	4121	0	3890	112	0
1	K	4121	0	3890	117	0
1	L	4121	0	3890	117	0
1	M	4121	0	3890	121	0
1	N	4121	0	3890	117	0
1	O	4121	0	3890	119	0
1	P	4121	0	3890	112	0
1	Q	4121	0	3890	118	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	4121	0	3890	113	0
1	S	4121	0	3890	114	0
1	T	4121	0	3890	114	0
1	U	4121	0	3890	120	0
1	V	4121	0	3890	113	0
1	W	4121	0	3890	116	0
1	X	4121	0	3890	112	0
1	Y	4121	0	3890	119	0
1	Z	4121	0	3890	118	0
1	a	4121	0	3890	114	0
1	b	4121	0	3890	116	0
1	c	4121	0	3890	117	0
1	d	4121	0	3890	112	0
1	e	4121	0	3890	116	0
1	f	4121	0	3890	114	0
1	g	4121	0	3890	121	0
1	h	4121	0	3890	118	0
1	i	4121	0	3890	117	0
1	j	4121	0	3890	117	0
1	k	4121	0	3890	119	0
1	l	4121	0	3890	118	0
1	m	4121	0	3890	115	0
1	n	4121	0	3890	114	0
1	o	4121	0	3890	114	0
1	p	4121	0	3890	112	0
1	q	4121	0	3890	114	0
1	r	4121	0	3890	112	0
1	s	4121	0	3890	120	0
1	t	4121	0	3890	117	0
1	u	4121	0	3890	116	0
1	v	4121	0	3890	118	0
1	w	4121	0	3890	120	0
1	x	4121	0	3890	119	0
1	y	4121	0	3890	117	0
1	z	4121	0	3890	116	0
2	0	37	0	24	3	0
2	0A	37	0	24	3	0
2	1A	37	0	24	3	0
2	2A	37	0	24	3	0
2	3A	37	0	24	3	0
2	4A	37	0	24	3	0
2	5A	37	0	24	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	9	37	0	24	3	0
2	AA	37	0	24	3	0
2	BA	37	0	24	3	0
2	CA	37	0	24	3	0
2	DA	37	0	24	3	0
2	EA	37	0	24	3	0
2	FA	37	0	24	3	0
2	GA	37	0	24	3	0
2	HA	37	0	24	3	0
2	IA	37	0	24	3	0
2	JA	37	0	24	3	0
2	KA	37	0	24	3	0
2	LA	37	0	24	3	0
2	MA	37	0	24	3	0
2	NA	37	0	24	3	0
2	OA	37	0	24	3	0
2	PA	37	0	24	3	0
2	QA	37	0	24	3	0
2	RA	37	0	24	3	0
2	SA	37	0	24	3	0
2	TA	37	0	24	3	0
2	UA	37	0	24	3	0
2	VA	37	0	24	3	0
2	WA	37	0	24	3	0
2	XA	37	0	24	3	0
2	YA	37	0	24	3	0
2	ZA	37	0	24	3	0
2	aA	37	0	24	3	0
2	bA	37	0	24	3	0
2	cA	37	0	24	3	0
2	dA	37	0	24	3	0
2	eA	37	0	24	3	0
2	fA	37	0	24	3	0
2	gA	37	0	24	3	0
2	hA	37	0	24	3	0
2	iA	37	0	24	3	0
2	jA	37	0	24	3	0
2	kA	37	0	24	3	0
2	lA	37	0	24	3	0
2	mA	37	0	24	3	0
2	nA	37	0	24	3	0
2	oA	37	0	24	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	pA	37	0	24	3	0
2	qA	37	0	24	3	0
2	rA	37	0	24	3	0
2	sA	37	0	24	3	0
2	tA	37	0	24	3	0
2	uA	37	0	24	3	0
2	vA	37	0	24	3	0
2	wA	37	0	24	3	0
2	xA	37	0	24	3	0
2	yA	37	0	24	3	0
2	zA	37	0	24	3	0
All	All	249480	0	234840	5646	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

The worst 5 of 5646 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:632:PRO:HD2	2:RA:940:DA:H2'	1.62	0.82
1:m:632:PRO:HD2	2:kA:978:DA:H2'	1.62	0.82
1:o:632:PRO:HD2	2:mA:982:DA:H2'	1.62	0.82
1:X:632:PRO:HD2	2:VA:948:DA:H2'	1.62	0.82
1:C:632:PRO:HD2	2:AA:906:DA:H2'	1.62	0.82

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	1	517/519 (100%)	510 (99%)	7 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	3	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	4	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	5	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	6	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	7	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	8	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	A	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	B	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	C	517/519 (100%)	509 (98%)	8 (2%)	0	100	100
1	D	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	E	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	F	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	G	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	H	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	I	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	J	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	K	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	L	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	M	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	N	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	O	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	P	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	Q	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	R	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	S	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	T	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	U	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	V	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	W	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	X	517/519 (100%)	510 (99%)	7 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Y	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	Z	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	a	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	b	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	c	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	d	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	e	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	f	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	g	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	h	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	i	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	j	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	k	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	l	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	m	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	n	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	o	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	p	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	q	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	r	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	s	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	t	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	u	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	v	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	w	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	x	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	y	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
1	z	517/519 (100%)	510 (99%)	7 (1%)	0	100	100
All	All	31020/31140 (100%)	30599 (99%)	421 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	450/450 (100%)	450 (100%)	0	100	100
1	2	450/450 (100%)	450 (100%)	0	100	100
1	3	450/450 (100%)	450 (100%)	0	100	100
1	4	450/450 (100%)	450 (100%)	0	100	100
1	5	450/450 (100%)	450 (100%)	0	100	100
1	6	450/450 (100%)	450 (100%)	0	100	100
1	7	450/450 (100%)	450 (100%)	0	100	100
1	8	450/450 (100%)	450 (100%)	0	100	100
1	A	450/450 (100%)	450 (100%)	0	100	100
1	B	450/450 (100%)	450 (100%)	0	100	100
1	C	450/450 (100%)	450 (100%)	0	100	100
1	D	450/450 (100%)	450 (100%)	0	100	100
1	E	450/450 (100%)	450 (100%)	0	100	100
1	F	450/450 (100%)	450 (100%)	0	100	100
1	G	450/450 (100%)	450 (100%)	0	100	100
1	H	450/450 (100%)	450 (100%)	0	100	100
1	I	450/450 (100%)	450 (100%)	0	100	100
1	J	450/450 (100%)	450 (100%)	0	100	100
1	K	450/450 (100%)	450 (100%)	0	100	100
1	L	450/450 (100%)	450 (100%)	0	100	100
1	M	450/450 (100%)	450 (100%)	0	100	100
1	N	450/450 (100%)	450 (100%)	0	100	100
1	O	450/450 (100%)	450 (100%)	0	100	100
1	P	450/450 (100%)	450 (100%)	0	100	100
1	Q	450/450 (100%)	450 (100%)	0	100	100
1	R	450/450 (100%)	450 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S	450/450 (100%)	450 (100%)	0	100	100
1	T	450/450 (100%)	450 (100%)	0	100	100
1	U	450/450 (100%)	450 (100%)	0	100	100
1	V	450/450 (100%)	450 (100%)	0	100	100
1	W	450/450 (100%)	450 (100%)	0	100	100
1	X	450/450 (100%)	450 (100%)	0	100	100
1	Y	450/450 (100%)	450 (100%)	0	100	100
1	Z	450/450 (100%)	450 (100%)	0	100	100
1	a	450/450 (100%)	450 (100%)	0	100	100
1	b	450/450 (100%)	450 (100%)	0	100	100
1	c	450/450 (100%)	450 (100%)	0	100	100
1	d	450/450 (100%)	450 (100%)	0	100	100
1	e	450/450 (100%)	450 (100%)	0	100	100
1	f	450/450 (100%)	450 (100%)	0	100	100
1	g	450/450 (100%)	450 (100%)	0	100	100
1	h	450/450 (100%)	450 (100%)	0	100	100
1	i	450/450 (100%)	450 (100%)	0	100	100
1	j	450/450 (100%)	450 (100%)	0	100	100
1	k	450/450 (100%)	450 (100%)	0	100	100
1	l	450/450 (100%)	450 (100%)	0	100	100
1	m	450/450 (100%)	450 (100%)	0	100	100
1	n	450/450 (100%)	450 (100%)	0	100	100
1	o	450/450 (100%)	450 (100%)	0	100	100
1	p	450/450 (100%)	450 (100%)	0	100	100
1	q	450/450 (100%)	450 (100%)	0	100	100
1	r	450/450 (100%)	450 (100%)	0	100	100
1	s	450/450 (100%)	450 (100%)	0	100	100
1	t	450/450 (100%)	450 (100%)	0	100	100
1	u	450/450 (100%)	450 (100%)	0	100	100
1	v	450/450 (100%)	450 (100%)	0	100	100
1	w	450/450 (100%)	450 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	x	450/450 (100%)	450 (100%)	0	100	100
1	y	450/450 (100%)	450 (100%)	0	100	100
1	z	450/450 (100%)	450 (100%)	0	100	100
All	All	27000/27000 (100%)	27000 (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 874 such sidechains are listed below:

Mol	Chain	Res	Type
1	f	674	GLN
1	n	487	GLN
1	3	736	ASN
1	g	647	GLN
1	f	652	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

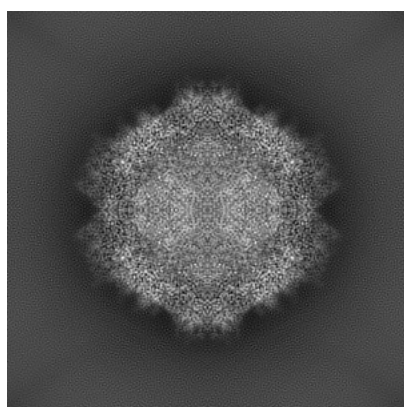
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24513. These allow visual inspection of the internal detail of the map and identification of artifacts.

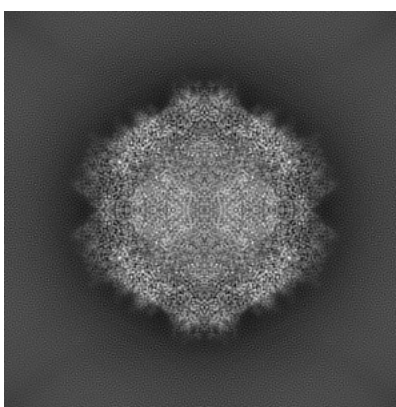
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

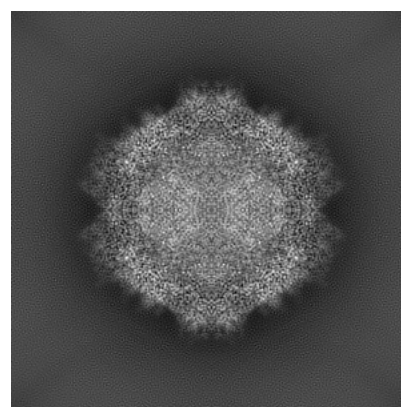
6.1.1 Primary map



X



Y

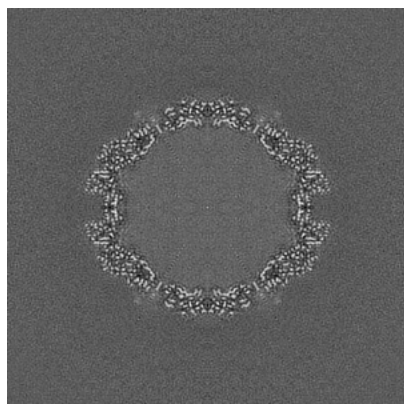


Z

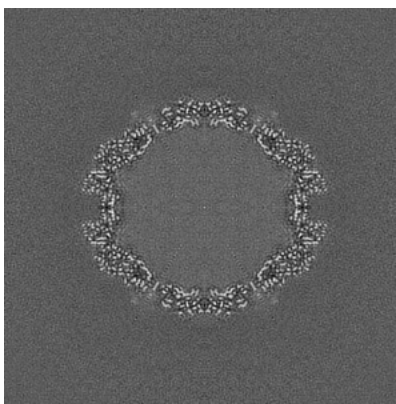
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

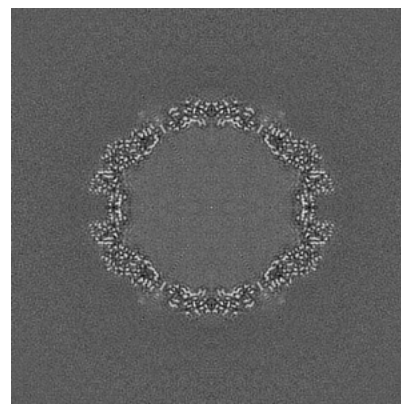
6.2.1 Primary map



X Index: 200



Y Index: 200

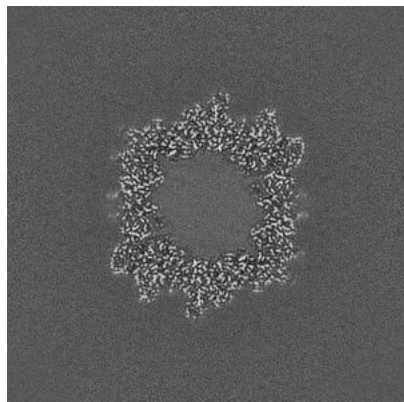


Z Index: 200

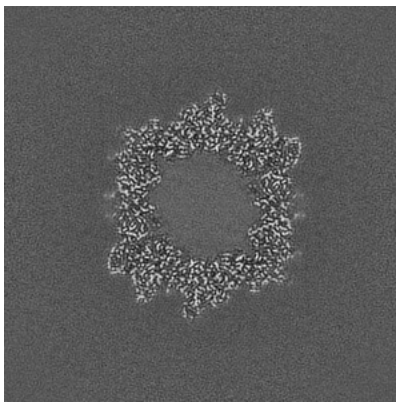
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

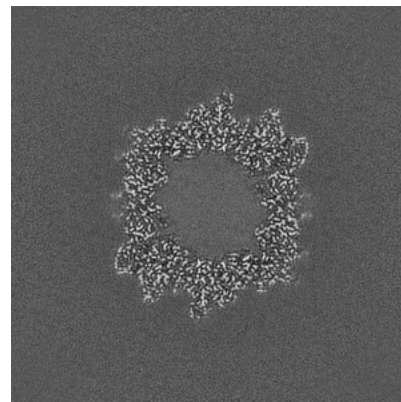
6.3.1 Primary map



X Index: 263



Y Index: 263

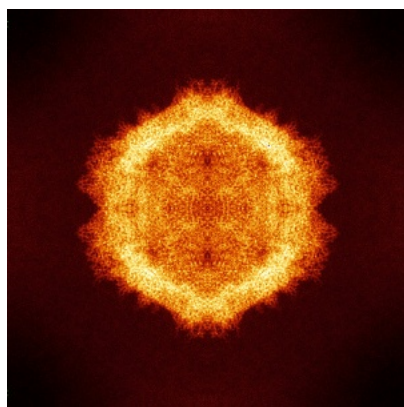


Z Index: 263

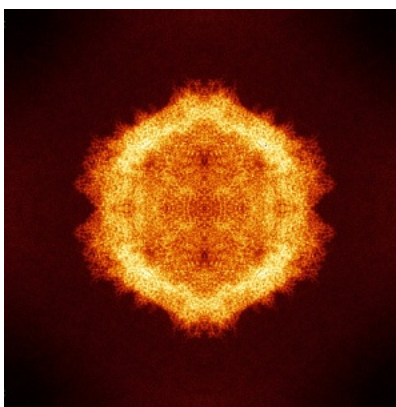
The images above show the largest variance slices of the map in three orthogonal directions.

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

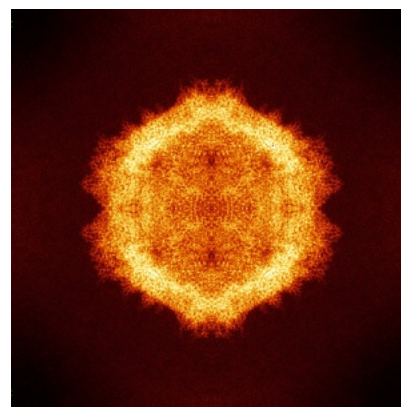
6.4.1 Primary map



X



Y

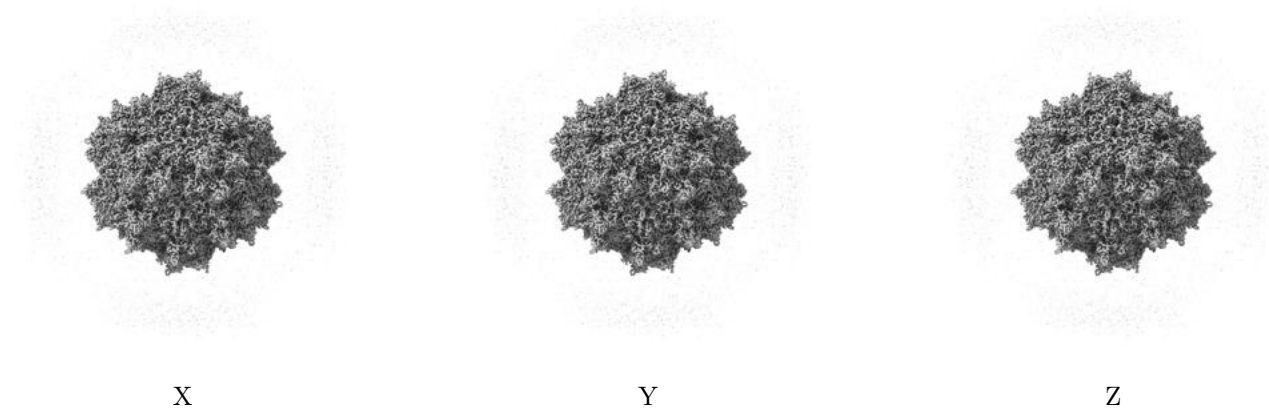


Z

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

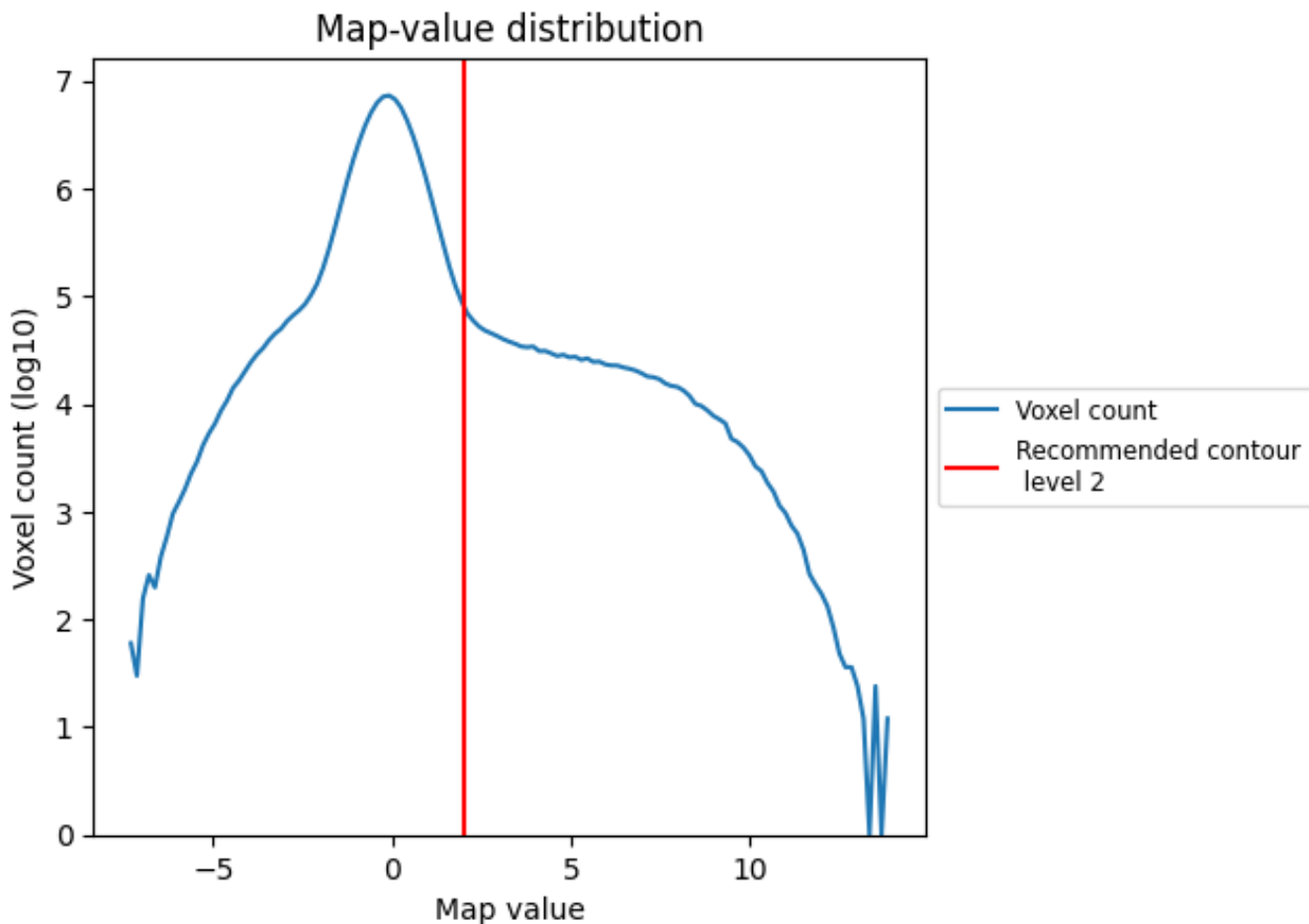
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

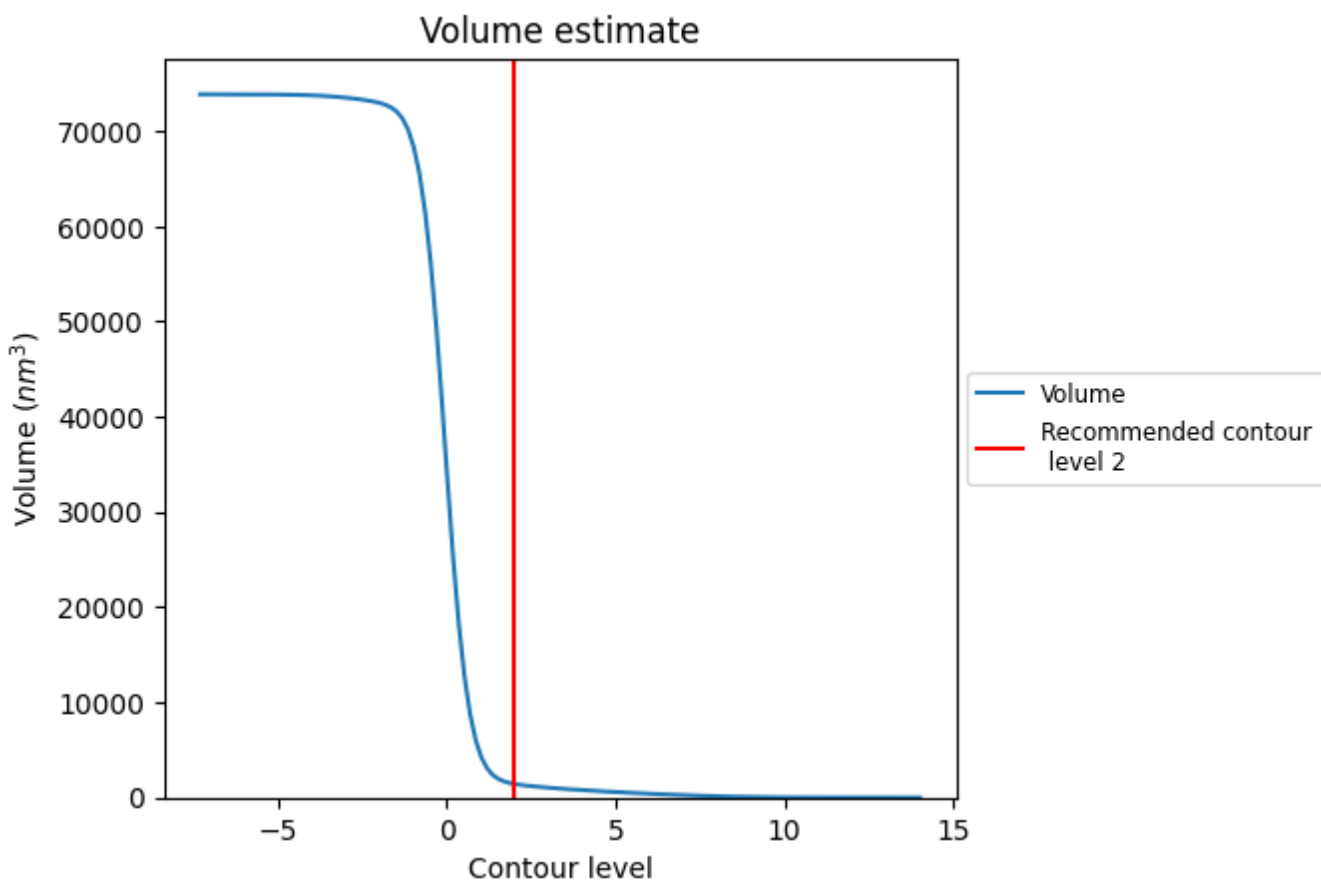
This section contains the results of statistical analysis of the map.

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.

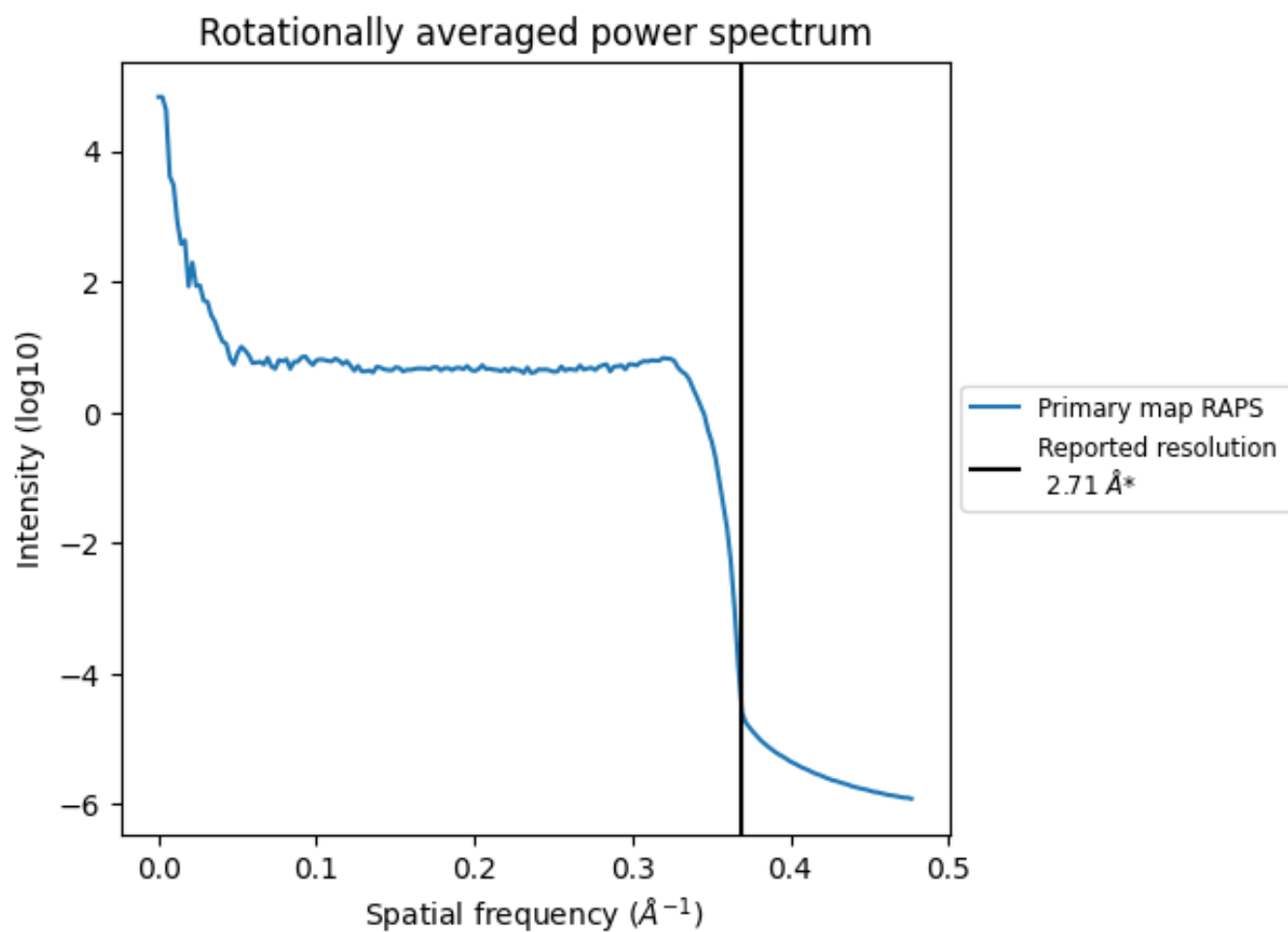
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1432 nm³; this corresponds to an approximate mass of 1293 kDa.

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

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.369\AA^{-1}

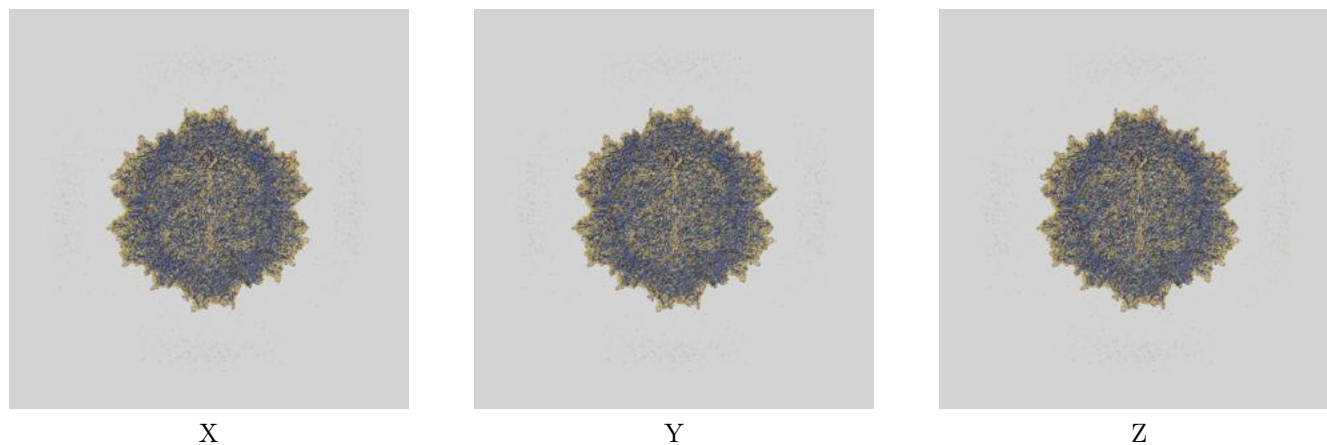
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

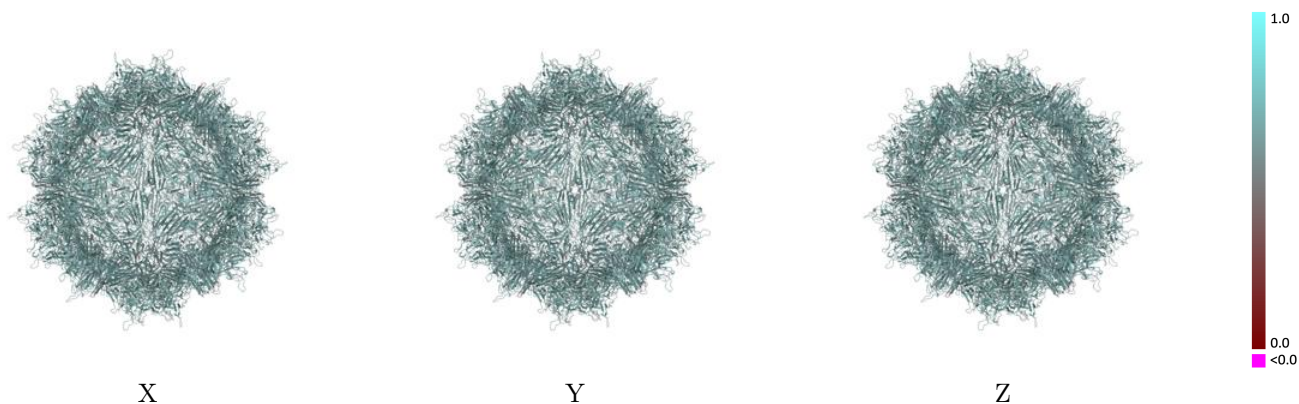
This section contains information regarding the fit between EMDB map EMD-24513 and PDB model 7RL1. Per-residue inclusion information can be found in section [3](#) on page [29](#).

9.1 Map-model overlay [i](#)



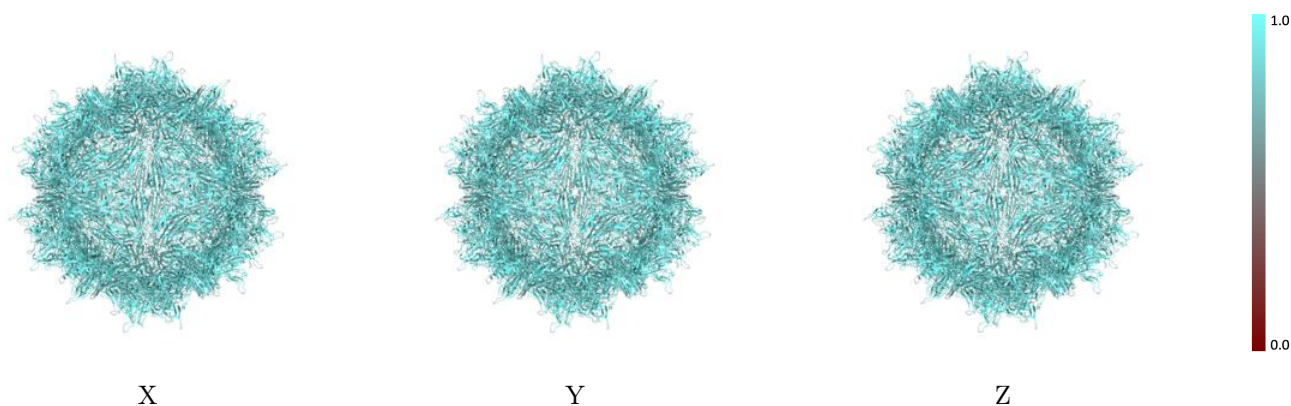
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



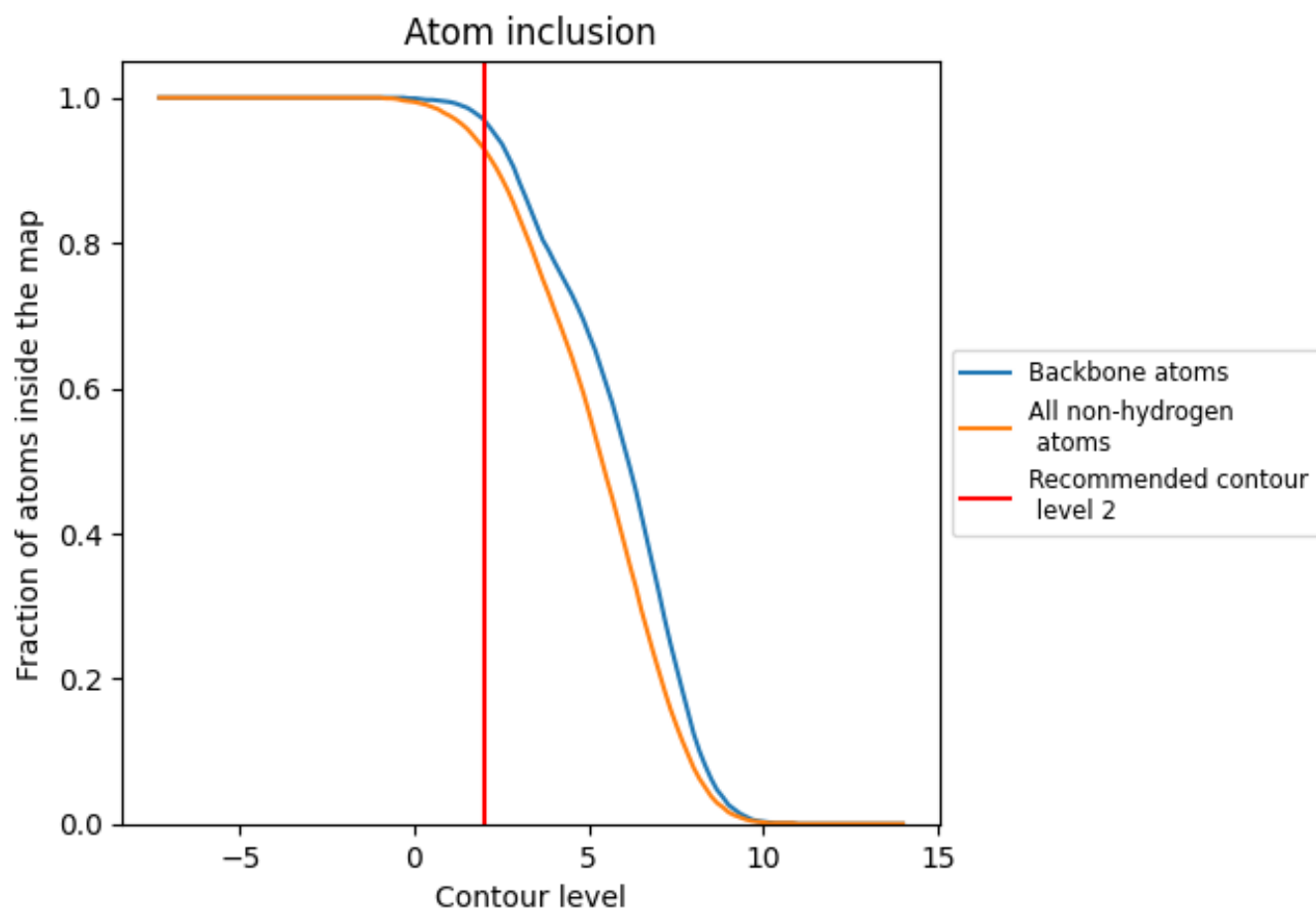
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 93% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9300	 0.6270
0	 0.6220	 0.4820
0A	 0.6220	 0.4730
1	 0.9330	 0.6310
1A	 0.5680	 0.4700
2	 0.9330	 0.6290
2A	 0.5950	 0.4840
3	 0.9340	 0.6280
3A	 0.5950	 0.4630
4	 0.9310	 0.6290
4A	 0.5680	 0.4780
5	 0.9340	 0.6290
5A	 0.5950	 0.4770
6	 0.9340	 0.6290
7	 0.9340	 0.6280
8	 0.9330	 0.6300
9	 0.5680	 0.4730
A	 0.9340	 0.6290
AA	 0.5680	 0.4710
B	 0.9330	 0.6300
BA	 0.5680	 0.4640
C	 0.9310	 0.6290
CA	 0.5950	 0.4650
D	 0.9340	 0.6280
DA	 0.6220	 0.4890
E	 0.9330	 0.6290
EA	 0.5950	 0.4740
F	 0.9340	 0.6290
FA	 0.5950	 0.4730
G	 0.9330	 0.6280
GA	 0.5680	 0.4740
H	 0.9340	 0.6290
HA	 0.5680	 0.4670
I	 0.9310	 0.6290
IA	 0.5680	 0.4750























































































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Chain	Atom inclusion	Q-score
J	 0.9330	 0.6290
JA	 0.5680	 0.4650
K	 0.9310	 0.6280
KA	 0.5950	 0.4660
L	 0.9330	 0.6300
LA	 0.5950	 0.4670
M	 0.9330	 0.6290
MA	 0.5950	 0.4760
N	 0.9340	 0.6280
NA	 0.5680	 0.4720
O	 0.9330	 0.6290
OA	 0.5680	 0.4780
P	 0.9340	 0.6280
PA	 0.5680	 0.4690
Q	 0.9310	 0.6280
QA	 0.5680	 0.4700
R	 0.9330	 0.6290
RA	 0.5680	 0.4780
S	 0.9330	 0.6290
SA	 0.5680	 0.4700
T	 0.9310	 0.6290
TA	 0.5680	 0.4850
U	 0.9330	 0.6290
UA	 0.5950	 0.4720
V	 0.9310	 0.6280
VA	 0.5950	 0.4790
W	 0.9340	 0.6290
WA	 0.5680	 0.4610
X	 0.9330	 0.6290
XA	 0.5950	 0.4710
Y	 0.9340	 0.6280
YA	 0.6220	 0.4740
Z	 0.9330	 0.6300
ZA	 0.6220	 0.4820
a	 0.9340	 0.6280
aA	 0.6220	 0.4820
b	 0.9340	 0.6290
bA	 0.6220	 0.4770
c	 0.9340	 0.6290
cA	 0.6220	 0.4820
d	 0.9340	 0.6290
dA	 0.6220	 0.4770


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Chain	Atom inclusion	Q-score
e	 0.9340	 0.6290
eA	 0.5680	 0.4790
f	 0.9340	 0.6290
fA	 0.5950	 0.4810
g	 0.9310	 0.6280
gA	 0.5680	 0.4550
h	 0.9330	 0.6300
hA	 0.5950	 0.4780
i	 0.9340	 0.6290
iA	 0.5950	 0.4790
j	 0.9340	 0.6290
jA	 0.5950	 0.4680
k	 0.9340	 0.6290
kA	 0.5680	 0.4790
l	 0.9330	 0.6290
lA	 0.6220	 0.4840
m	 0.9310	 0.6280
mA	 0.5950	 0.4690
n	 0.9340	 0.6290
nA	 0.5680	 0.4830
o	 0.9330	 0.6290
oA	 0.5680	 0.4660
p	 0.9310	 0.6290
pA	 0.5680	 0.4760
q	 0.9330	 0.6280
qA	 0.5680	 0.4640
r	 0.9330	 0.6290
rA	 0.5950	 0.4700
s	 0.9330	 0.6300
sA	 0.5680	 0.4870
t	 0.9330	 0.6290
tA	 0.6220	 0.4850
u	 0.9310	 0.6280
uA	 0.5950	 0.4720
v	 0.9340	 0.6290
vA	 0.5680	 0.4730
w	 0.9330	 0.6290
wA	 0.6220	 0.4790
x	 0.9310	 0.6280
xA	 0.5680	 0.4710
y	 0.9340	 0.6290
yA	 0.5680	 0.4770

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Chain	Atom inclusion	Q-score
z	 0.9330	 0.6290
zA	 0.5680	 0.4710