



## wwPDB EM Validation Summary Report ⓘ

May 25, 2024 – 09:26 PM EDT

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

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.14 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	1	735	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 70%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%; margin-top: 5px;"> <span>8%</span> <span>70%</span> <span>•</span> <span>30%</span> </div>
1	2	735	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 70%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%; margin-top: 5px;"> <span>8%</span> <span>70%</span> <span>•</span> <span>30%</span> </div>
1	3	735	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 70%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%; margin-top: 5px;"> <span>8%</span> <span>70%</span> <span>•</span> <span>30%</span> </div>
1	4	735	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 70%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%; margin-top: 5px;"> <span>8%</span> <span>70%</span> <span>•</span> <span>30%</span> </div>
1	5	735	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 70%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%; margin-top: 5px;"> <span>8%</span> <span>70%</span> <span>•</span> <span>30%</span> </div>
1	6	735	<div style="display: flex; align-items: center;"> <div style="width: 9%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 70%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 16%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%; margin-top: 5px;"> <span>9%</span> <span>70%</span> <span>•</span> <span>30%</span> </div>
1	7	735	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 70%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%; margin-top: 5px;"> <span>8%</span> <span>70%</span> <span>•</span> <span>30%</span> </div>
1	8	735	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 70%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%; margin-top: 5px;"> <span>8%</span> <span>70%</span> <span>•</span> <span>30%</span> </div>
1	A	735	<div style="display: flex; align-items: center;"> <div style="width: 8%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 70%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 17%; height: 10px; background-color: grey;"></div> </div> <div style="display: flex; justify-content: space-between; width: 100%; margin-top: 5px;"> <span>8%</span> <span>70%</span> <span>•</span> <span>30%</span> </div>

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Mol	Chain	Length	Quality of chain		
1	B	735	8%	70%	30%
1	C	735	7%	70%	30%
1	D	735	8%	70%	30%
1	E	735	7%	70%	30%
1	F	735	8%	70%	30%
1	G	735	8%	70%	30%
1	H	735	8%	70%	30%
1	I	735	7%	70%	30%
1	J	735	8%	70%	30%
1	K	735	7%	70%	30%
1	L	735	8%	70%	30%
1	M	735	8%	70%	30%
1	N	735	8%	70%	30%
1	O	735	8%	70%	30%
1	P	735	9%	70%	30%
1	Q	735	8%	70%	30%
1	R	735	8%	70%	30%
1	S	735	8%	70%	30%
1	T	735	8%	70%	30%
1	U	735	8%	70%	30%
1	V	735	8%	70%	30%
1	W	735	8%	70%	30%
1	X	735	8%	70%	30%
1	Y	735	9%	70%	30%
1	Z	735	7%	70%	30%


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Mol	Chain	Length	Quality of chain		
1	a	735	8%	70%	30%
1	b	735	8%	70%	30%
1	c	735	8%	70%	30%
1	d	735	9%	70%	30%
1	e	735	9%	70%	30%
1	f	735	9%	70%	30%
1	g	735	8%	70%	30%
1	h	735	9%	70%	30%
1	i	735	9%	70%	30%
1	j	735	9%	70%	30%
1	k	735	9%	70%	30%
1	l	735	9%	70%	30%
1	m	735	8%	70%	30%
1	n	735	9%	70%	30%
1	o	735	8%	70%	30%
1	p	735	8%	70%	30%
1	q	735	9%	70%	30%
1	r	735	9%	70%	30%
1	s	735	8%	70%	30%
1	t	735	8%	70%	30%
1	u	735	8%	70%	30%
1	v	735	9%	70%	30%
1	w	735	9%	70%	30%
1	x	735	8%	70%	30%
1	y	735	9%	70%	30%

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Mol	Chain	Length	Quality of chain
1	z	735	 <p>A horizontal bar chart representing the quality of the chain. The bar is divided into three segments: a red segment on the left labeled '8%', a green segment in the middle labeled '70%', and a grey segment on the right labeled '30%'. A small black dot is located at the end of the green segment, which is approximately 78% of the way across the bar.</p>

## 2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 248580 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Capsid protein VP1.

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

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

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	m	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	n	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	o	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	p	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	q	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	r	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	s	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	t	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	u	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	v	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	w	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	x	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	y	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	z	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	1	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	2	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	3	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	4	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	5	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	6	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		
1	7	517	Total	C	N	O	S	0	0
			4143	2607	723	800	13		

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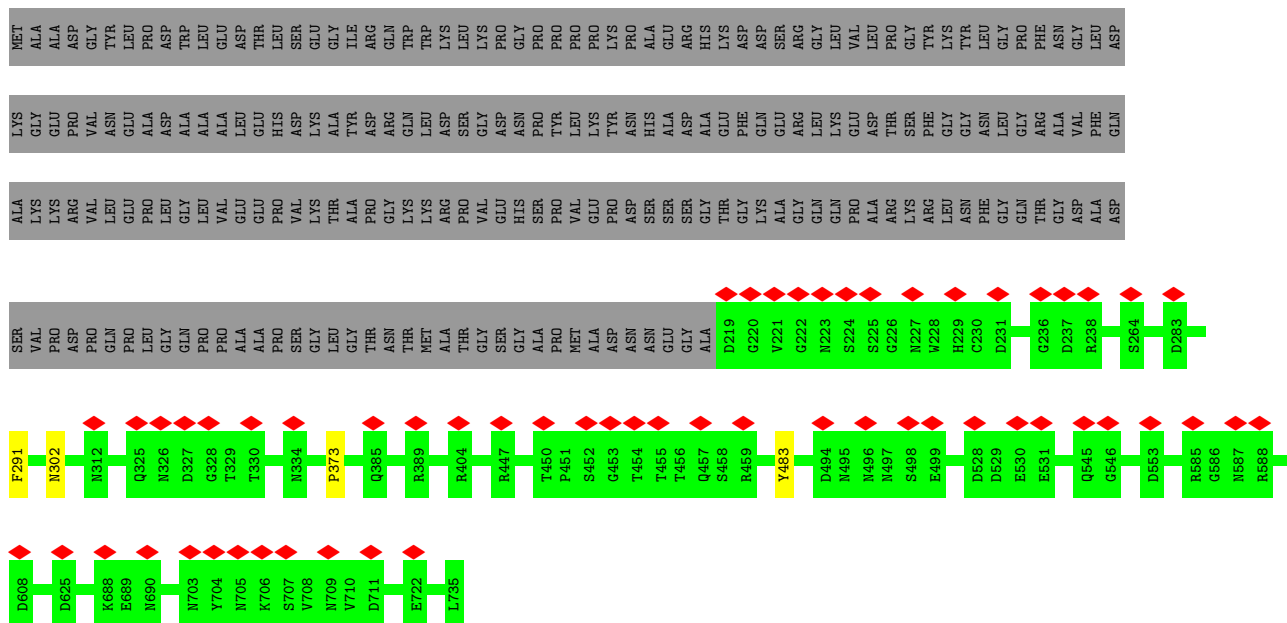
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Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	8	517	4143	2607	723	800	13	0	0

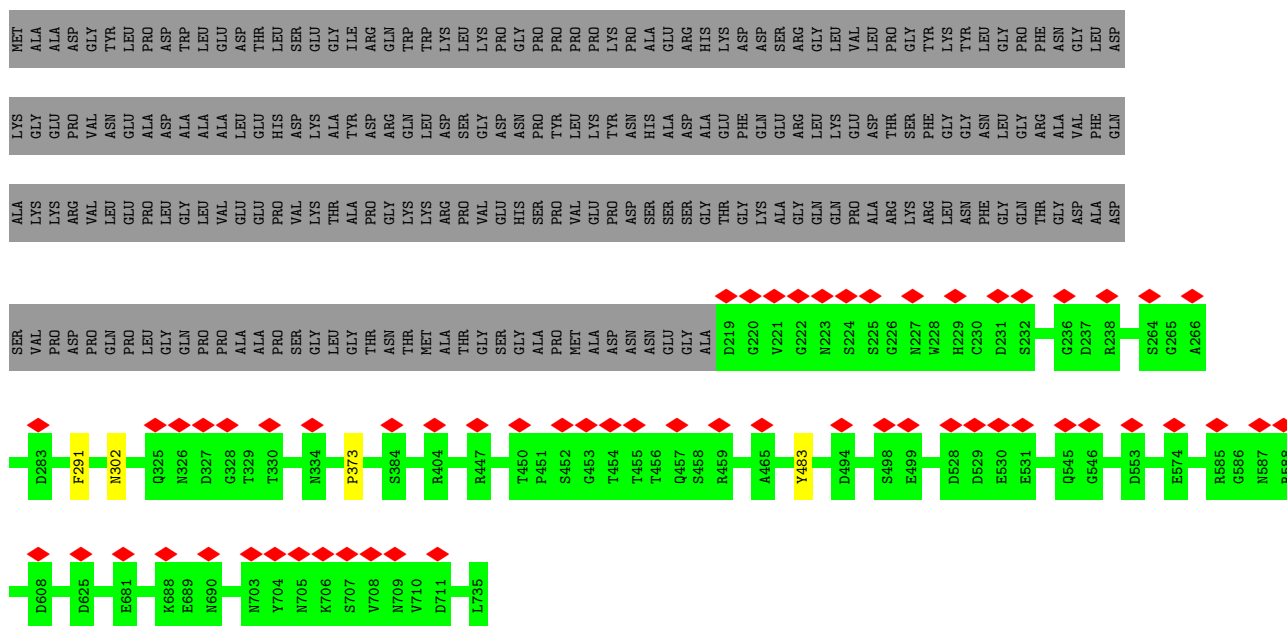




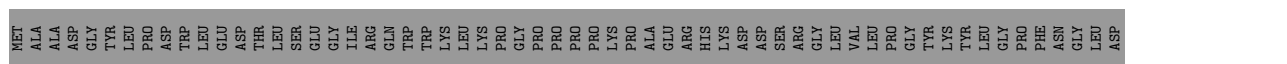


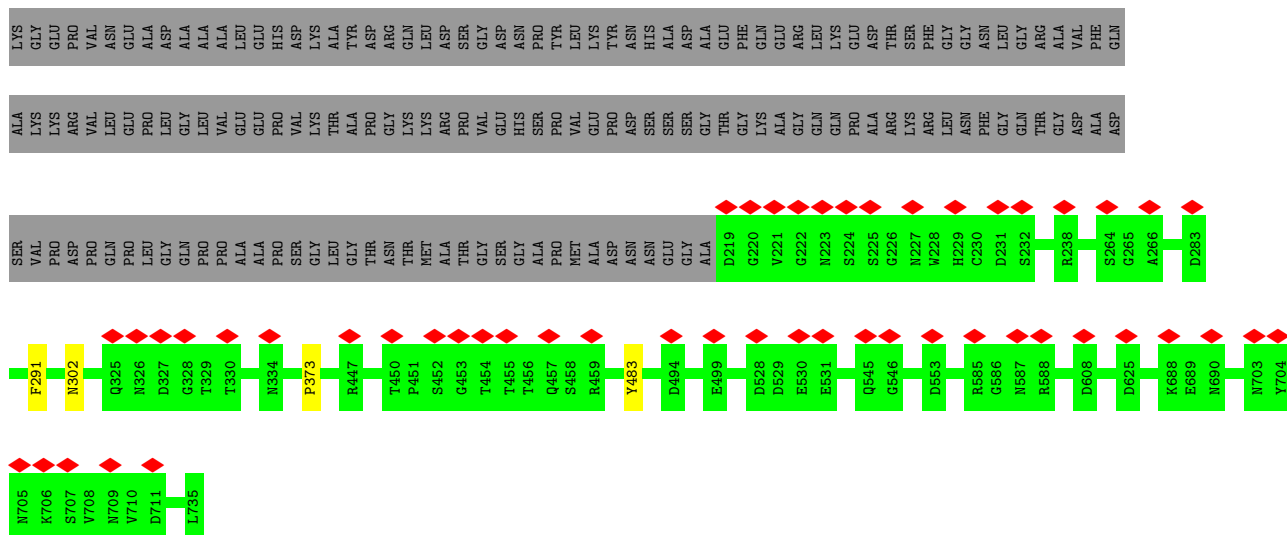


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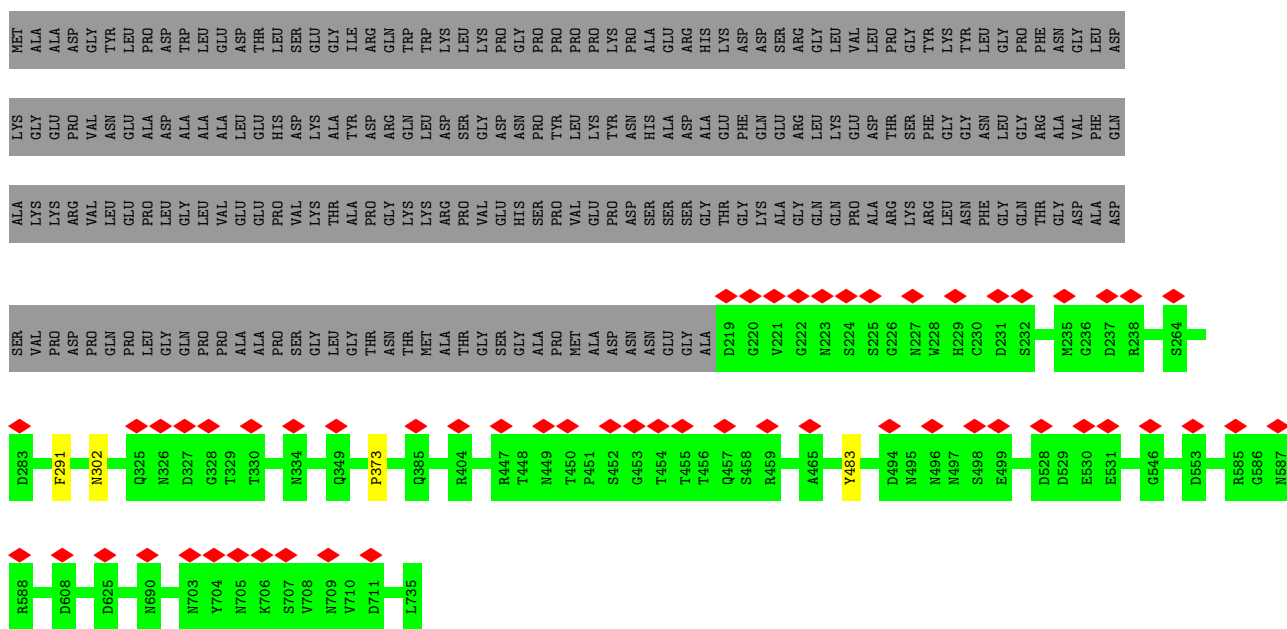


• Molecule 1: Capsid protein VP1

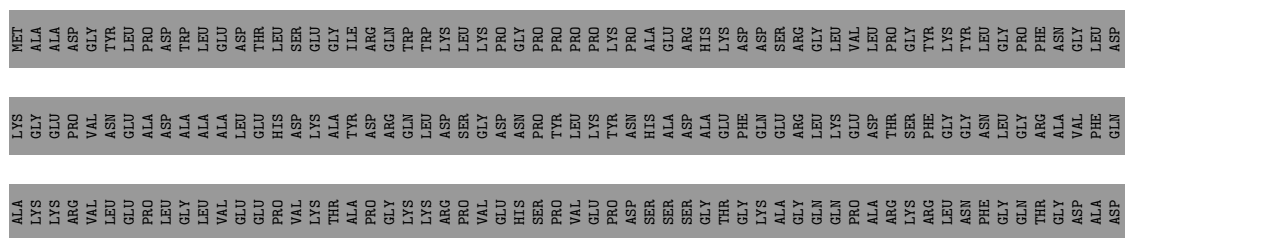


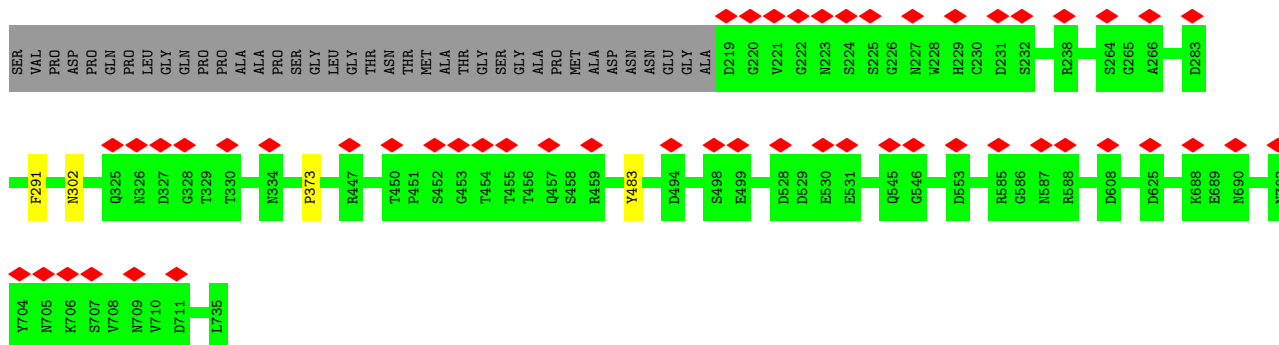


• Molecule 1: Capsid protein VP1

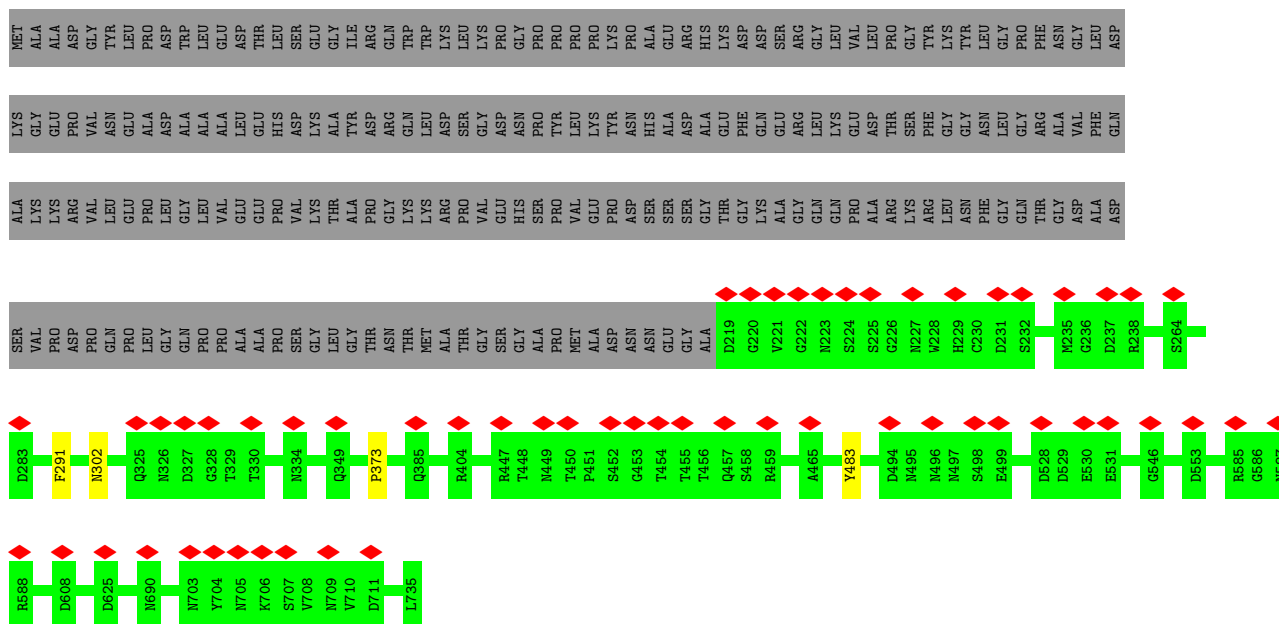


• Molecule 1: Capsid protein VP1

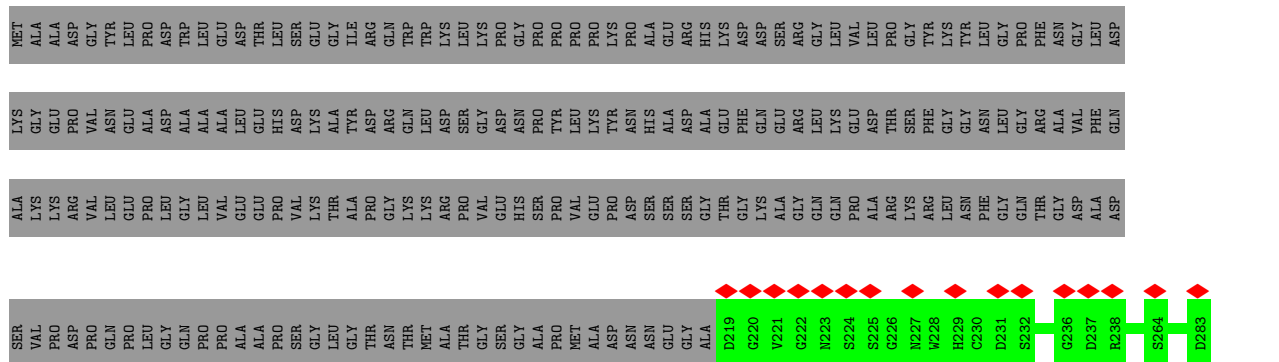




• Molecule 1: Capsid protein VP1



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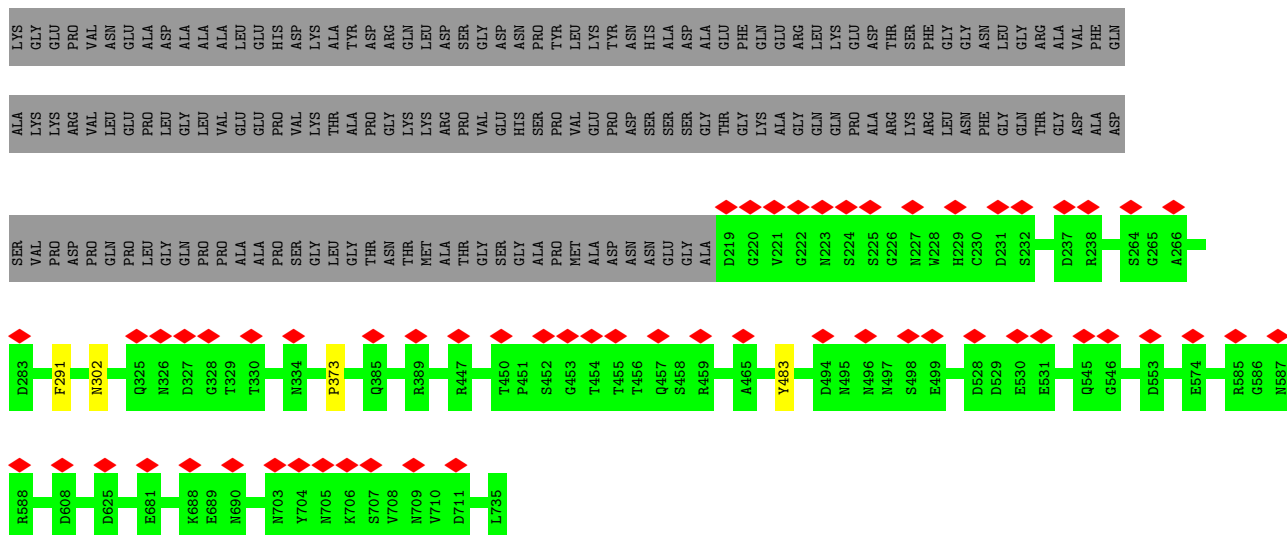




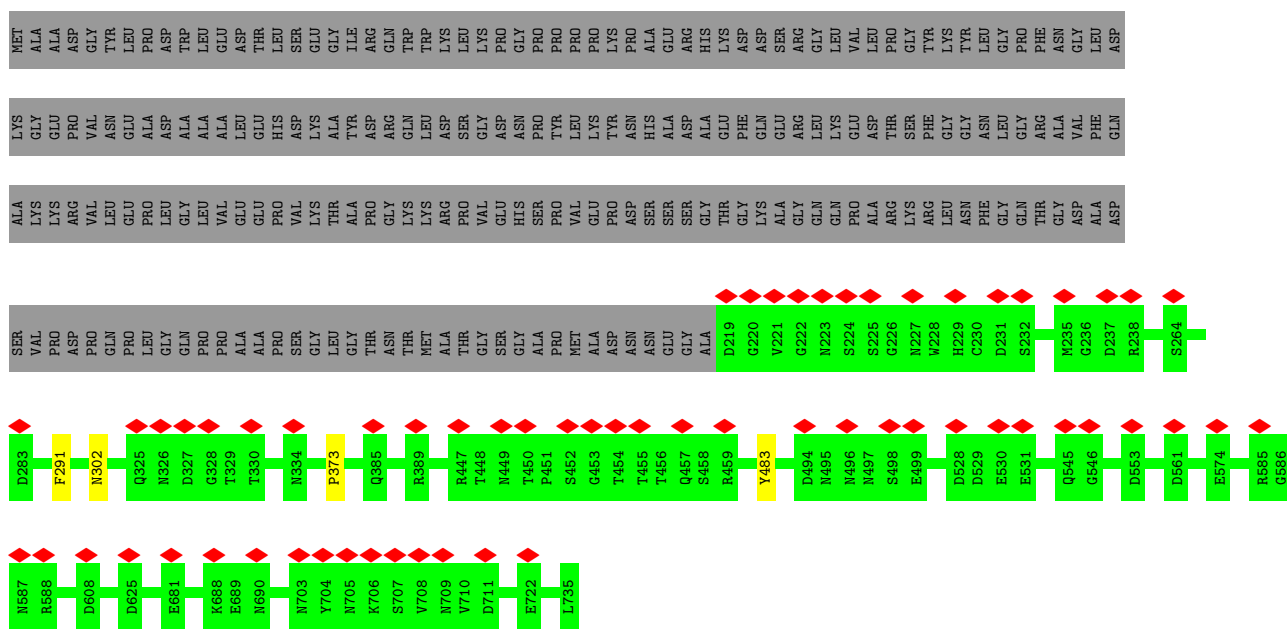




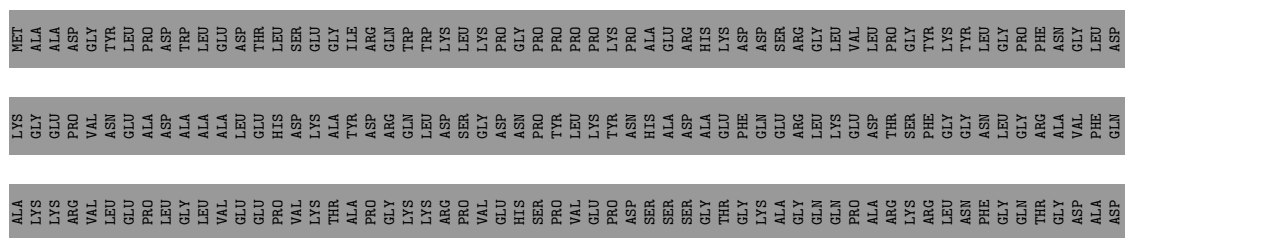


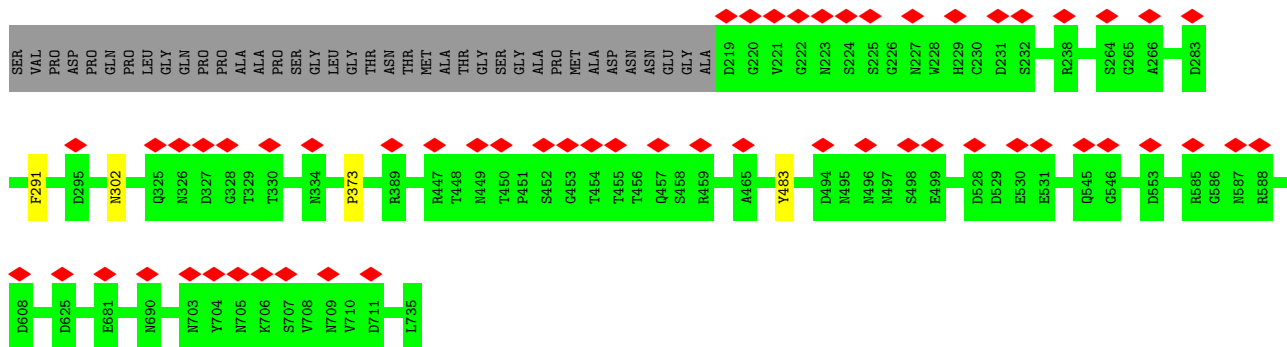


• Molecule 1: Capsid protein VP1

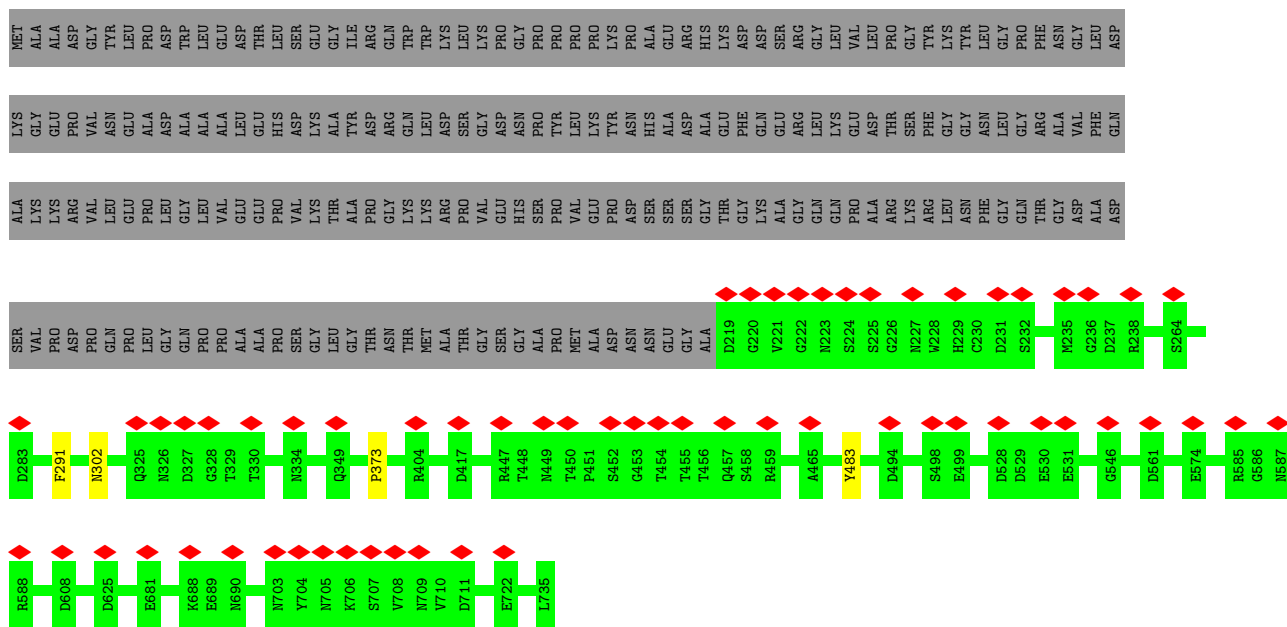


• Molecule 1: Capsid protein VP1

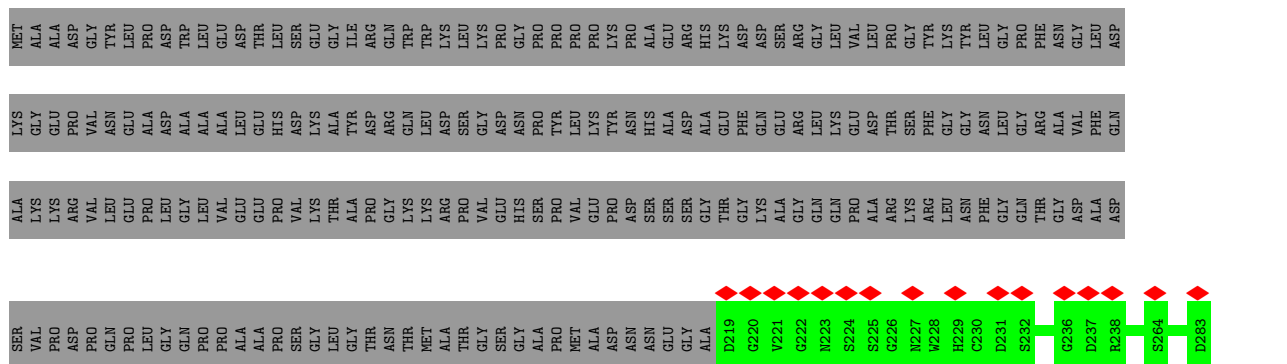




• Molecule 1: Capsid protein VP1

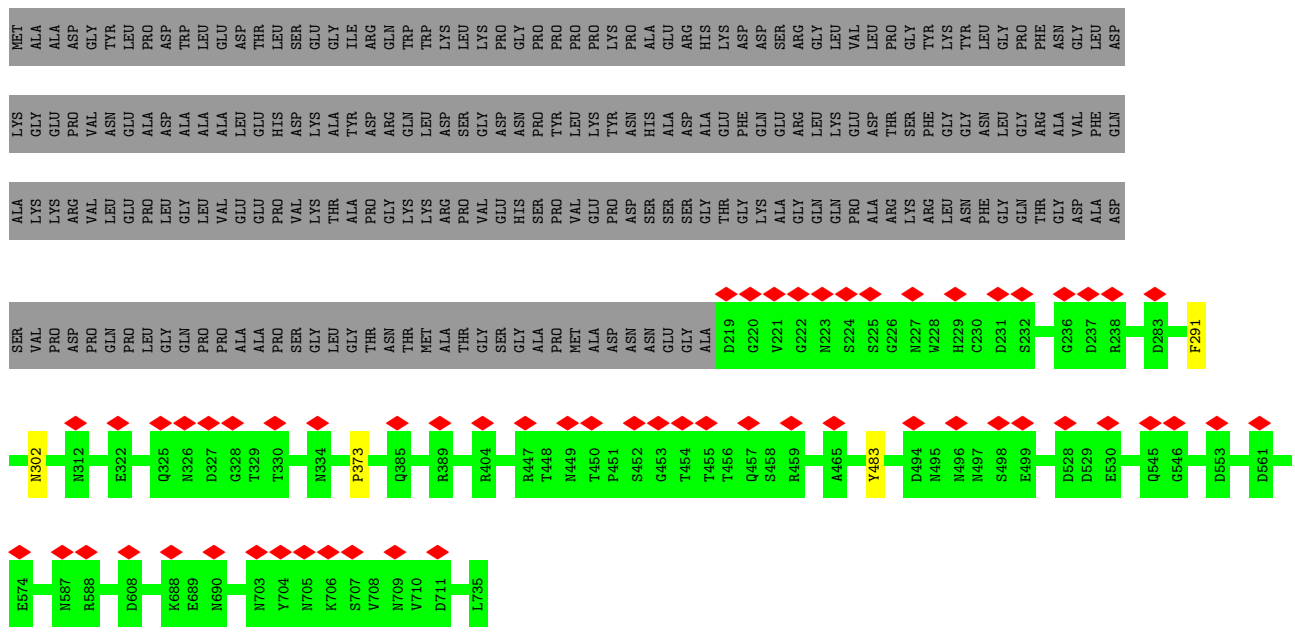


• Molecule 1: Capsid protein VP1

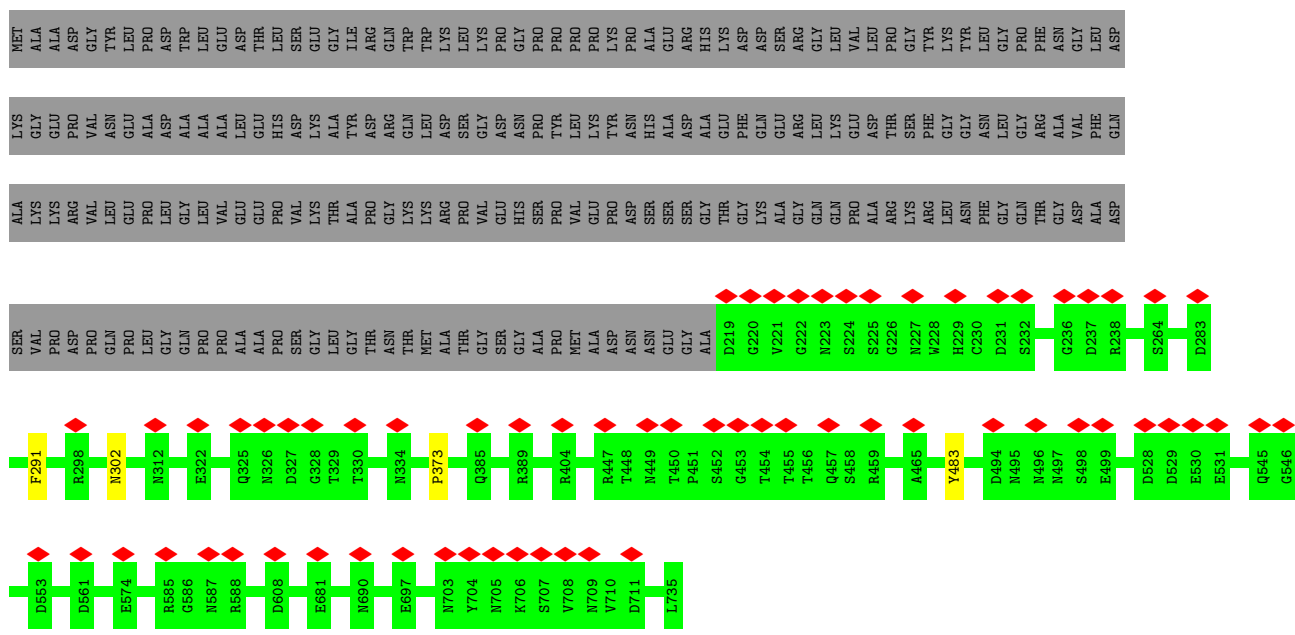




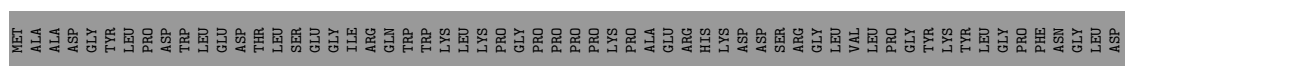


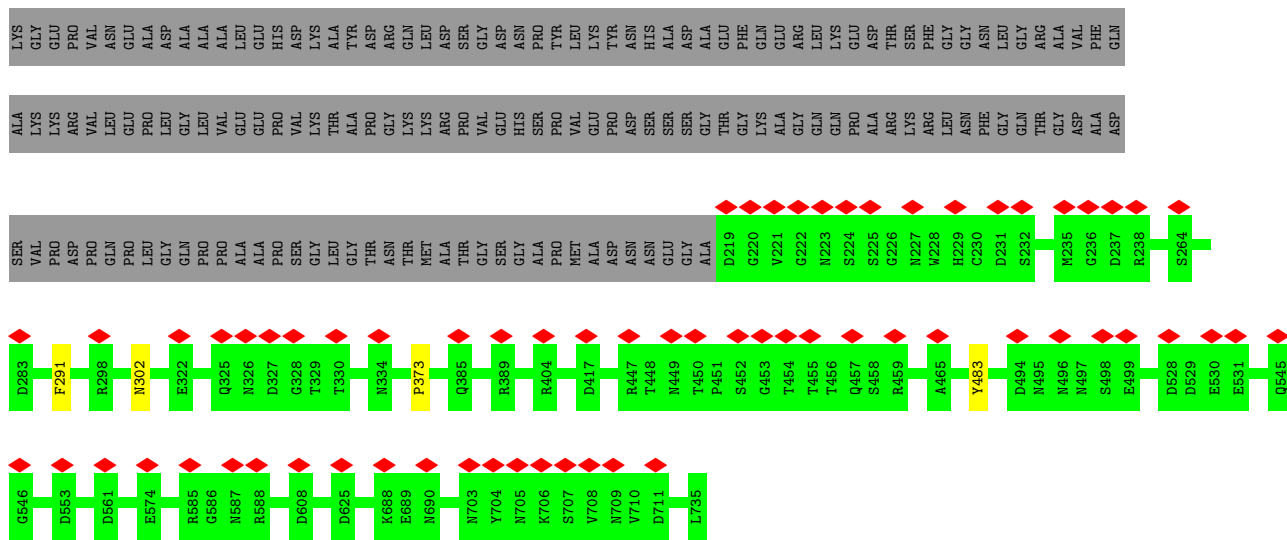


• Molecule 1: Capsid protein VP1

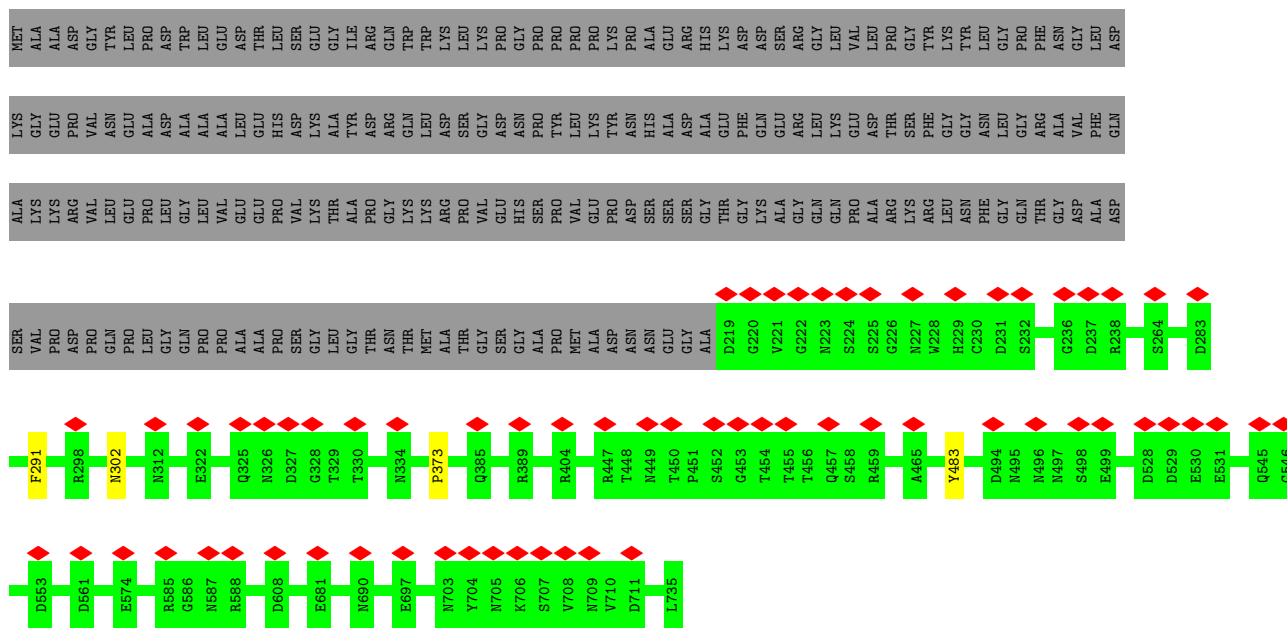


• Molecule 1: Capsid protein VP1





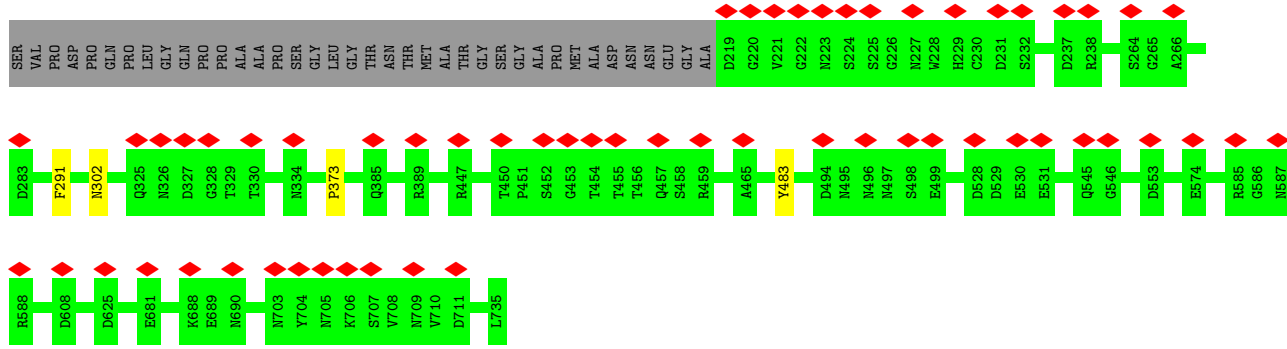
• Molecule 1: Capsid protein VP1



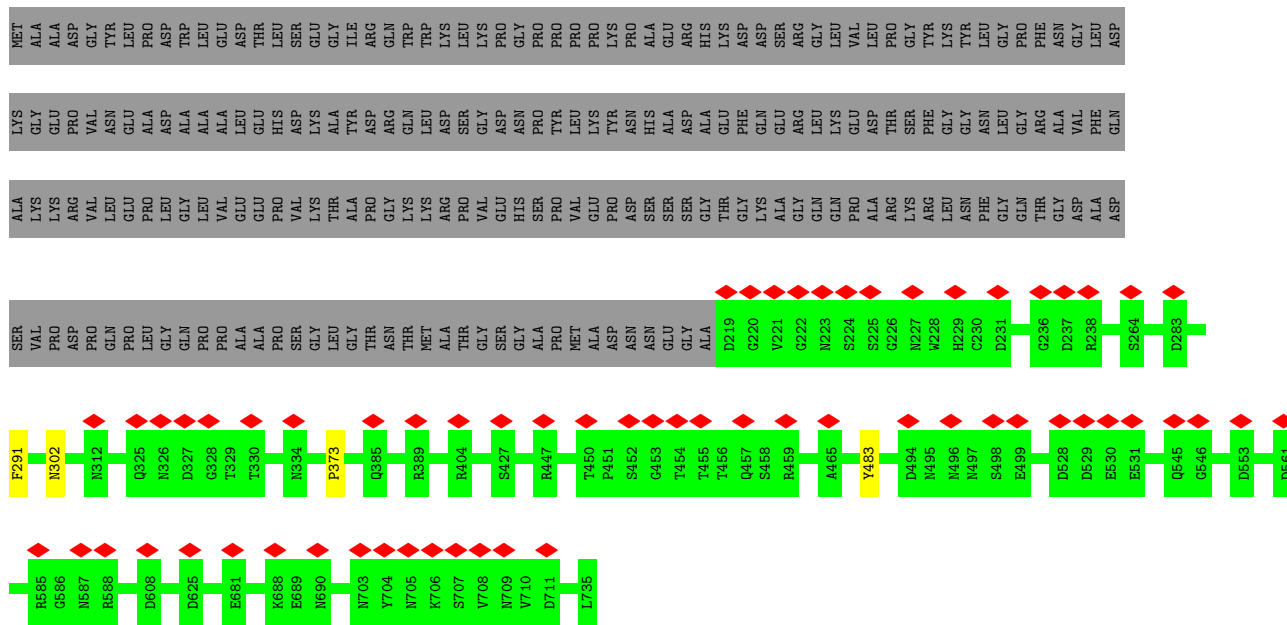
• Molecule 1: Capsid protein VP1



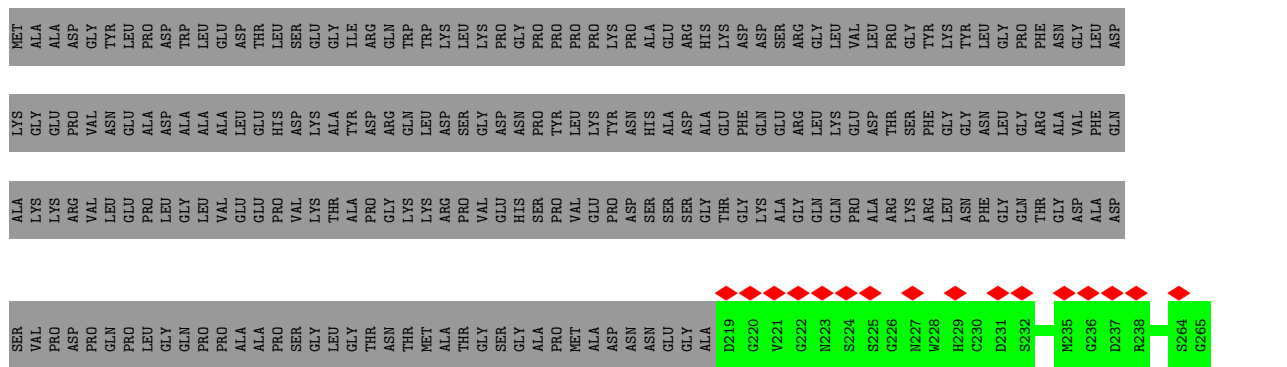




• Molecule 1: Capsid protein VP1



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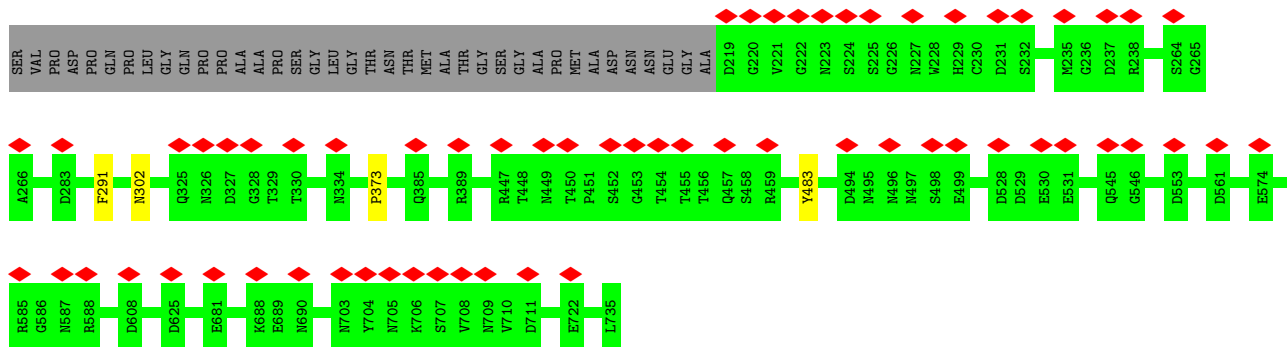




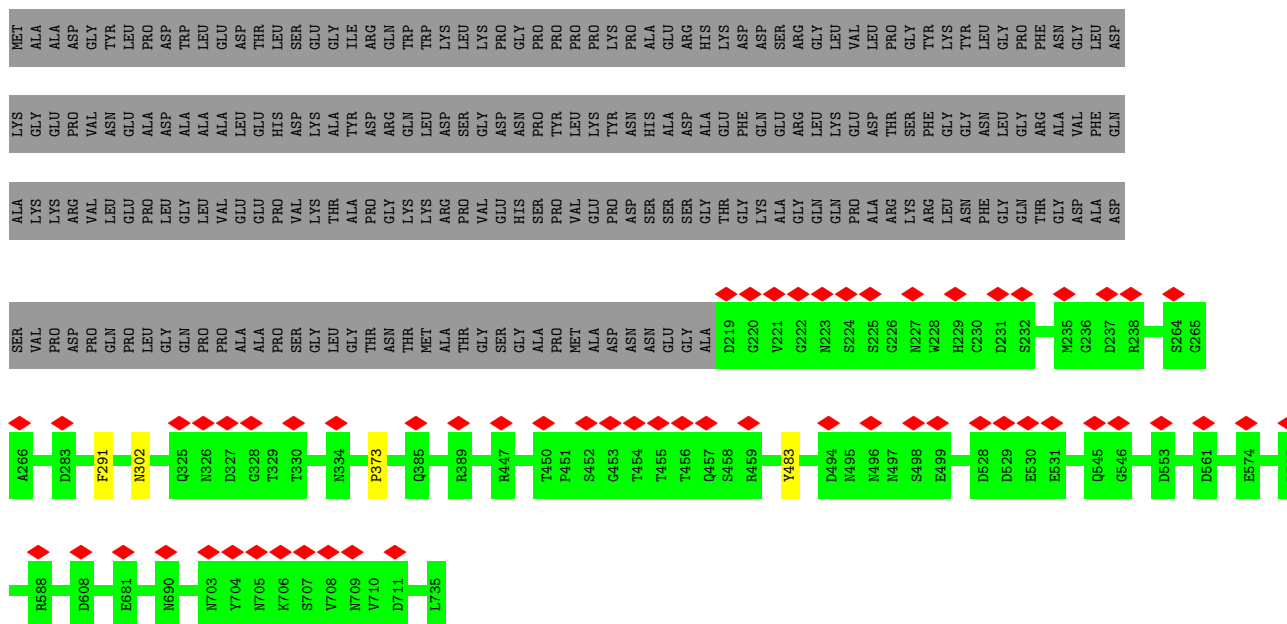




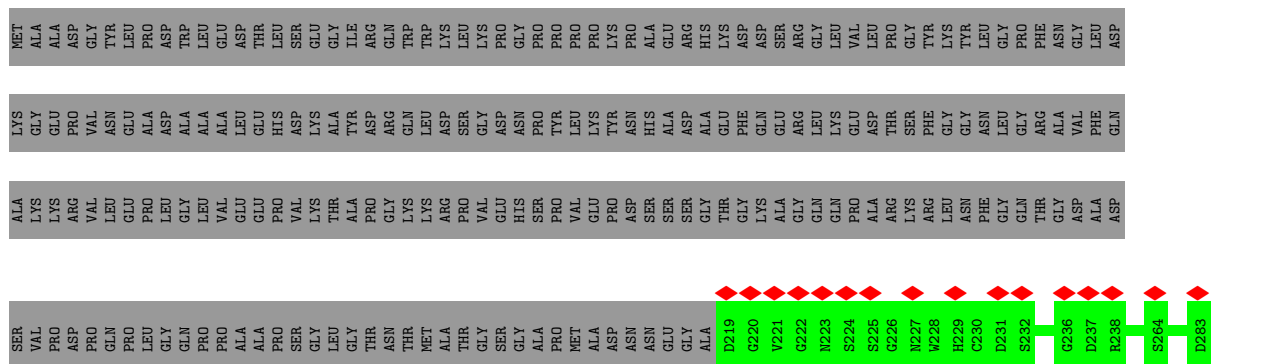




• Molecule 1: Capsid protein VP1



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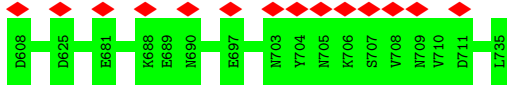












• Molecule 1: Capsid protein VP1



MET ALA  
ALA  
ASP  
GLY  
TYR  
LEU  
PRO  
ASP  
TRP  
LEU  
ALA  
GLU  
ASP  
THR

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

ALA  
LYS  
LYS  
ARG  
VAL  
LEU  
GLU  
PRO  
LEU  
GLY  
LEU  
LEU  
VAL  
GLU  
GLU  
PRO  
VAL  
SER  
VAL  
GLY  
LYS  
THR  
ALA  
PRO  
GLY  
LYS  
LYS  
LYS  
ARG  
PRO  
VAL  
GLY  
HIS  
SER  
PRO  
PRO  
TYR  
PRO  
SER  
VAL  
GLU  
GLU  
PRO  
ASP  
ASN  
SER  
SER  
SER  
GLY  
THR

SER  
VAL  
PRO  
ASP  
PRO  
GLM  
PRO  
LEU  
GLY  
GLM  
PRO  
PRO  
ALA  
ALA  
SER  
SER  
LEU  
GLY  
THR  
THR  
ASN  
MET  
THR  
ALA  
THR  
GLY  
SER  
GLY  
D219  
G220  
V221  
G222  
N223  
S224  
S225  
G226  
N227  
W228  
H229  
C230  
D231  
G236  
D237  
R238  
S264  
D283

F291  
N302  
N312  
Q325  
N326  
D327  
G328  
T329  
T330  
N334  
P373  
Q385  
R389  
R404  
R447  
T450  
P451  
G452  
G453  
T454  
T455  
T456  
Q457  
S458  
R459  
Y483  
D494  
N495  
N496  
N497  
S498  
E499  
D528  
D529  
E530  
E531  
Q545  
G546  
D553  
R585  
G586  
N587  
R588



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	291	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	34	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	30.997	Depositor
Minimum map value	-13.154	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	5.0	Depositor
Map size ( $\text{\AA}$ )	821.76, 821.76, 821.76	wwPDB
Map dimensions	768, 768, 768	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.07, 1.07, 1.07	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	1	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	2	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	3	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	4	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	5	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	6	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	7	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	8	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	A	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	B	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	C	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	D	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	E	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	F	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	G	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	H	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	I	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	J	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	K	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	L	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	M	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	N	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	O	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	P	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	Q	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	R	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	S	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	T	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	U	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	V	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	W	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	X	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	Y	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)
1	Z	0.55	2/4266 (0.0%)	0.67	2/5815 (0.0%)

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

The worst 5 of 120 bond length outliers are listed below:

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

The worst 5 of 120 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	302	ASN	N-CA-C	5.94	127.04	111.00
1	J	302	ASN	N-CA-C	5.94	127.04	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	302	ASN	N-CA-C	5.94	127.04	111.00
1	R	302	ASN	N-CA-C	5.94	127.04	111.00
1	S	302	ASN	N-CA-C	5.94	127.04	111.00

There are no chirality outliers.

There are no planarity outliers.

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

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

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	2	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	3	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	4	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	5	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	6	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	7	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	8	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	A	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	B	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	C	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	D	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	E	515/735 (70%)	506 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	G	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	H	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	I	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	J	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	K	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	L	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	M	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	N	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	O	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	P	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	Q	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	R	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	S	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	T	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	U	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	V	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	W	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	X	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	Y	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	Z	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	a	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	b	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	c	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	d	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	e	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	f	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	g	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	h	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	i	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	j	515/735 (70%)	506 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	k	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	l	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	m	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	n	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	o	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	p	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	q	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	r	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	s	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	t	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	u	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	v	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	w	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	x	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	y	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
1	z	515/735 (70%)	506 (98%)	9 (2%)	0	100	100
All	All	30900/44100 (70%)	30360 (98%)	540 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [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	459/630 (73%)	459 (100%)	0	100	100
1	2	459/630 (73%)	459 (100%)	0	100	100
1	3	459/630 (73%)	459 (100%)	0	100	100
1	4	459/630 (73%)	459 (100%)	0	100	100
1	5	459/630 (73%)	459 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	6	459/630 (73%)	459 (100%)	0	100	100
1	7	459/630 (73%)	459 (100%)	0	100	100
1	8	459/630 (73%)	459 (100%)	0	100	100
1	A	459/630 (73%)	459 (100%)	0	100	100
1	B	459/630 (73%)	459 (100%)	0	100	100
1	C	459/630 (73%)	459 (100%)	0	100	100
1	D	459/630 (73%)	459 (100%)	0	100	100
1	E	459/630 (73%)	459 (100%)	0	100	100
1	F	459/630 (73%)	459 (100%)	0	100	100
1	G	459/630 (73%)	459 (100%)	0	100	100
1	H	459/630 (73%)	459 (100%)	0	100	100
1	I	459/630 (73%)	459 (100%)	0	100	100
1	J	459/630 (73%)	459 (100%)	0	100	100
1	K	459/630 (73%)	459 (100%)	0	100	100
1	L	459/630 (73%)	459 (100%)	0	100	100
1	M	459/630 (73%)	459 (100%)	0	100	100
1	N	459/630 (73%)	459 (100%)	0	100	100
1	O	459/630 (73%)	459 (100%)	0	100	100
1	P	459/630 (73%)	459 (100%)	0	100	100
1	Q	459/630 (73%)	459 (100%)	0	100	100
1	R	459/630 (73%)	459 (100%)	0	100	100
1	S	459/630 (73%)	459 (100%)	0	100	100
1	T	459/630 (73%)	459 (100%)	0	100	100
1	U	459/630 (73%)	459 (100%)	0	100	100
1	V	459/630 (73%)	459 (100%)	0	100	100
1	W	459/630 (73%)	459 (100%)	0	100	100
1	X	459/630 (73%)	459 (100%)	0	100	100
1	Y	459/630 (73%)	459 (100%)	0	100	100
1	Z	459/630 (73%)	459 (100%)	0	100	100
1	a	459/630 (73%)	459 (100%)	0	100	100
1	b	459/630 (73%)	459 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	c	459/630 (73%)	459 (100%)	0	100	100
1	d	459/630 (73%)	459 (100%)	0	100	100
1	e	459/630 (73%)	459 (100%)	0	100	100
1	f	459/630 (73%)	459 (100%)	0	100	100
1	g	459/630 (73%)	459 (100%)	0	100	100
1	h	459/630 (73%)	459 (100%)	0	100	100
1	i	459/630 (73%)	459 (100%)	0	100	100
1	j	459/630 (73%)	459 (100%)	0	100	100
1	k	459/630 (73%)	459 (100%)	0	100	100
1	l	459/630 (73%)	459 (100%)	0	100	100
1	m	459/630 (73%)	459 (100%)	0	100	100
1	n	459/630 (73%)	459 (100%)	0	100	100
1	o	459/630 (73%)	459 (100%)	0	100	100
1	p	459/630 (73%)	459 (100%)	0	100	100
1	q	459/630 (73%)	459 (100%)	0	100	100
1	r	459/630 (73%)	459 (100%)	0	100	100
1	s	459/630 (73%)	459 (100%)	0	100	100
1	t	459/630 (73%)	459 (100%)	0	100	100
1	u	459/630 (73%)	459 (100%)	0	100	100
1	v	459/630 (73%)	459 (100%)	0	100	100
1	w	459/630 (73%)	459 (100%)	0	100	100
1	x	459/630 (73%)	459 (100%)	0	100	100
1	y	459/630 (73%)	459 (100%)	0	100	100
1	z	459/630 (73%)	459 (100%)	0	100	100
All	All	27540/37800 (73%)	27540 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 1020 such sidechains are listed below:

Mol	Chain	Res	Type
1	b	334	ASN
1	1	297	GLN

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Mol	Chain	Res	Type
1	h	623	HIS
1	z	536	GLN
1	4	598	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

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

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

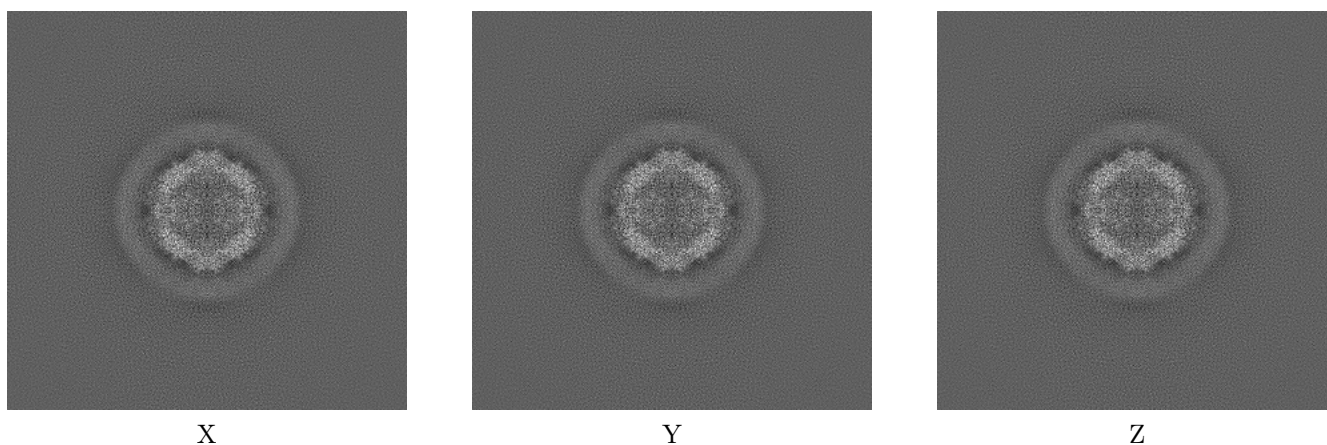
## 6 Map visualisation [i](#)

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

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

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

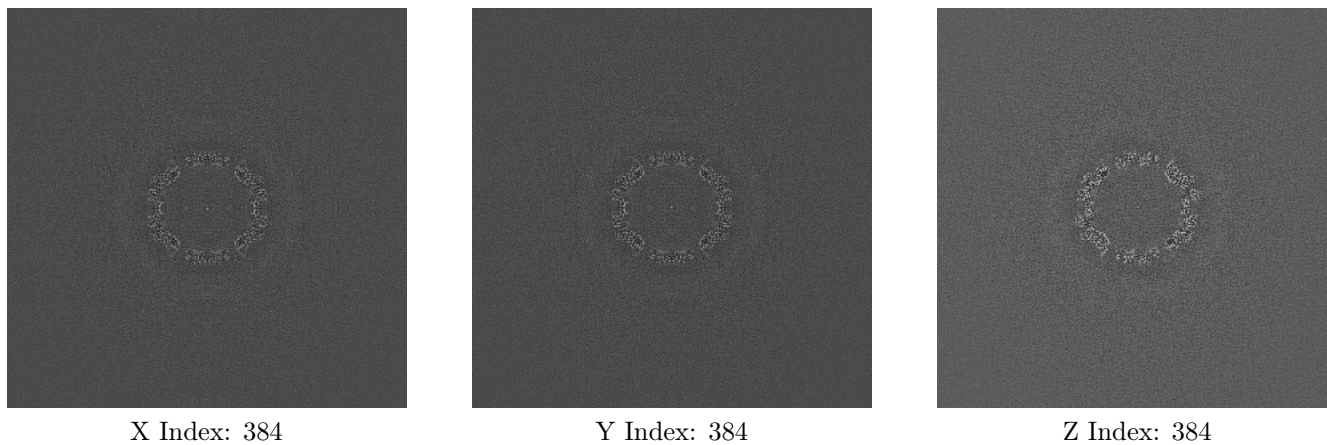
#### 6.1.1 Primary map



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

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

#### 6.2.1 Primary map

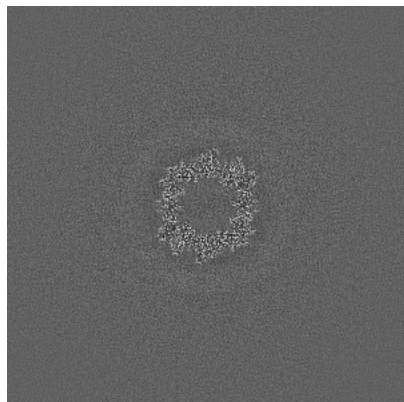




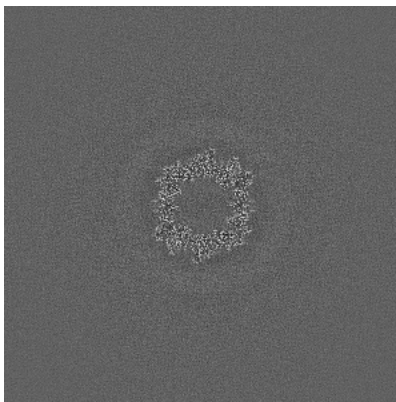
The images above show central slices of the map in three orthogonal directions.

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

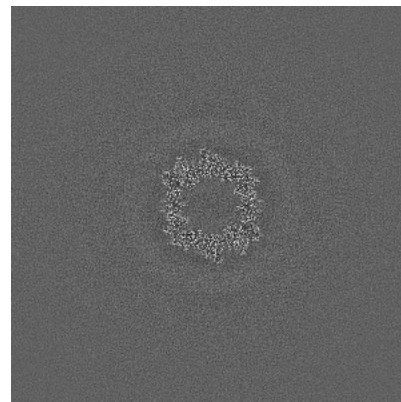
### 6.3.1 Primary map



X Index: 446



Y Index: 446

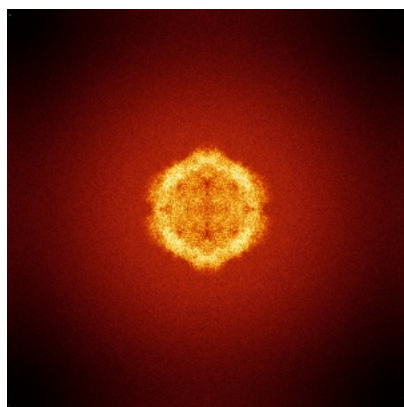


Z Index: 321

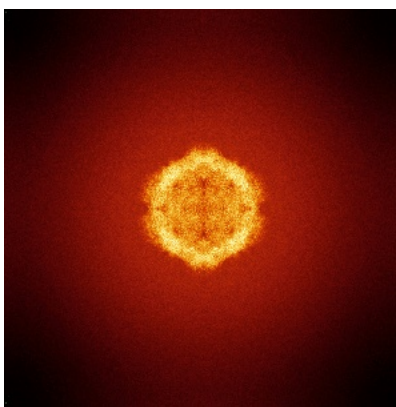
The images above show the largest variance slices of the map in three orthogonal directions.

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

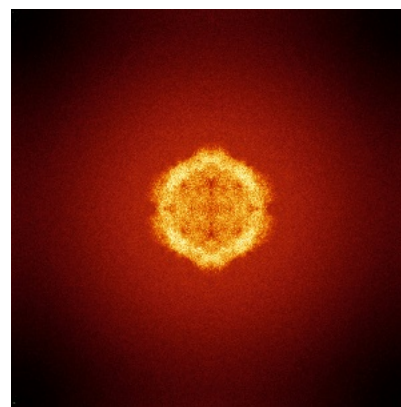
### 6.4.1 Primary map



X



Y



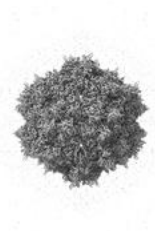
Z

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



## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

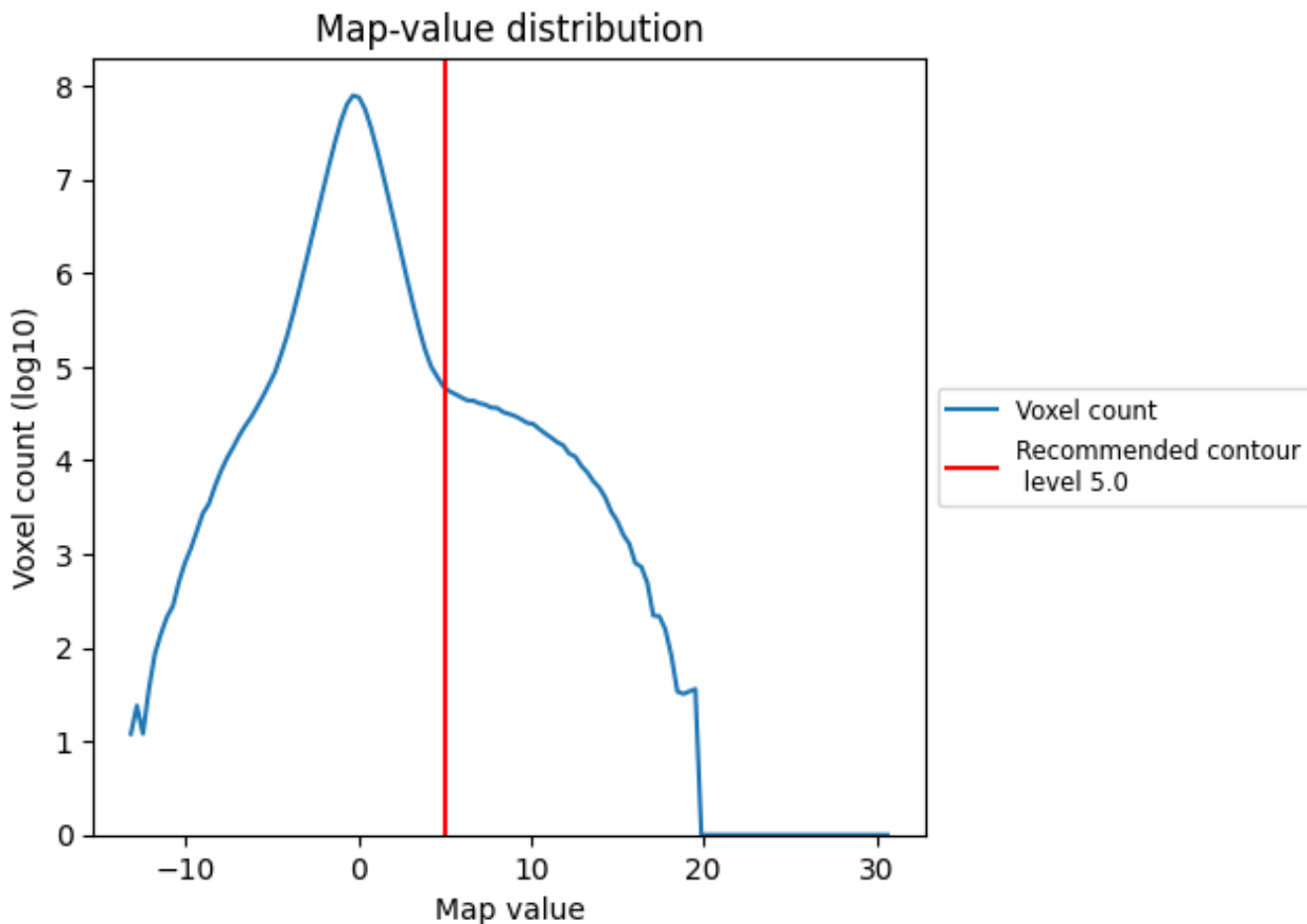
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

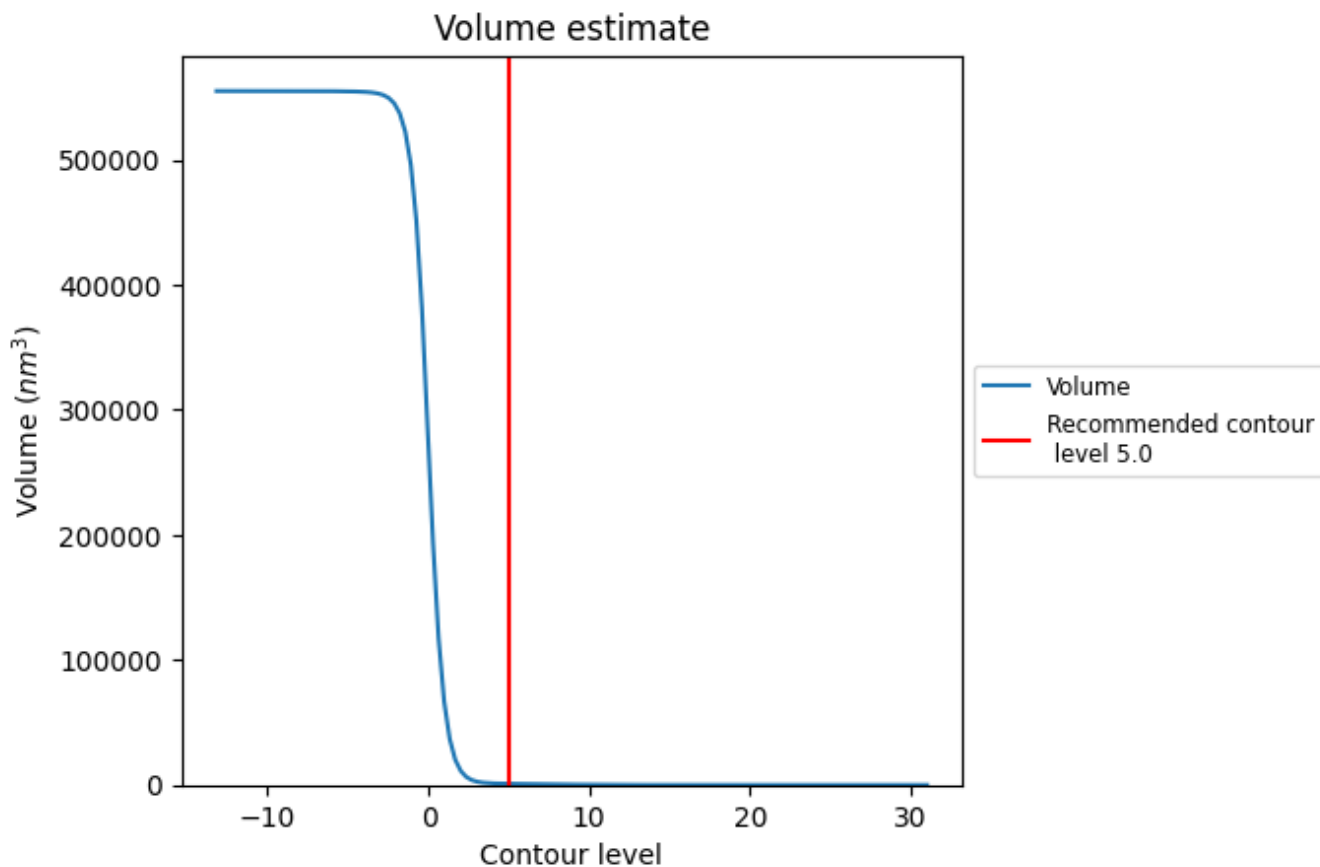
This section contains the results of statistical analysis of the map.

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



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

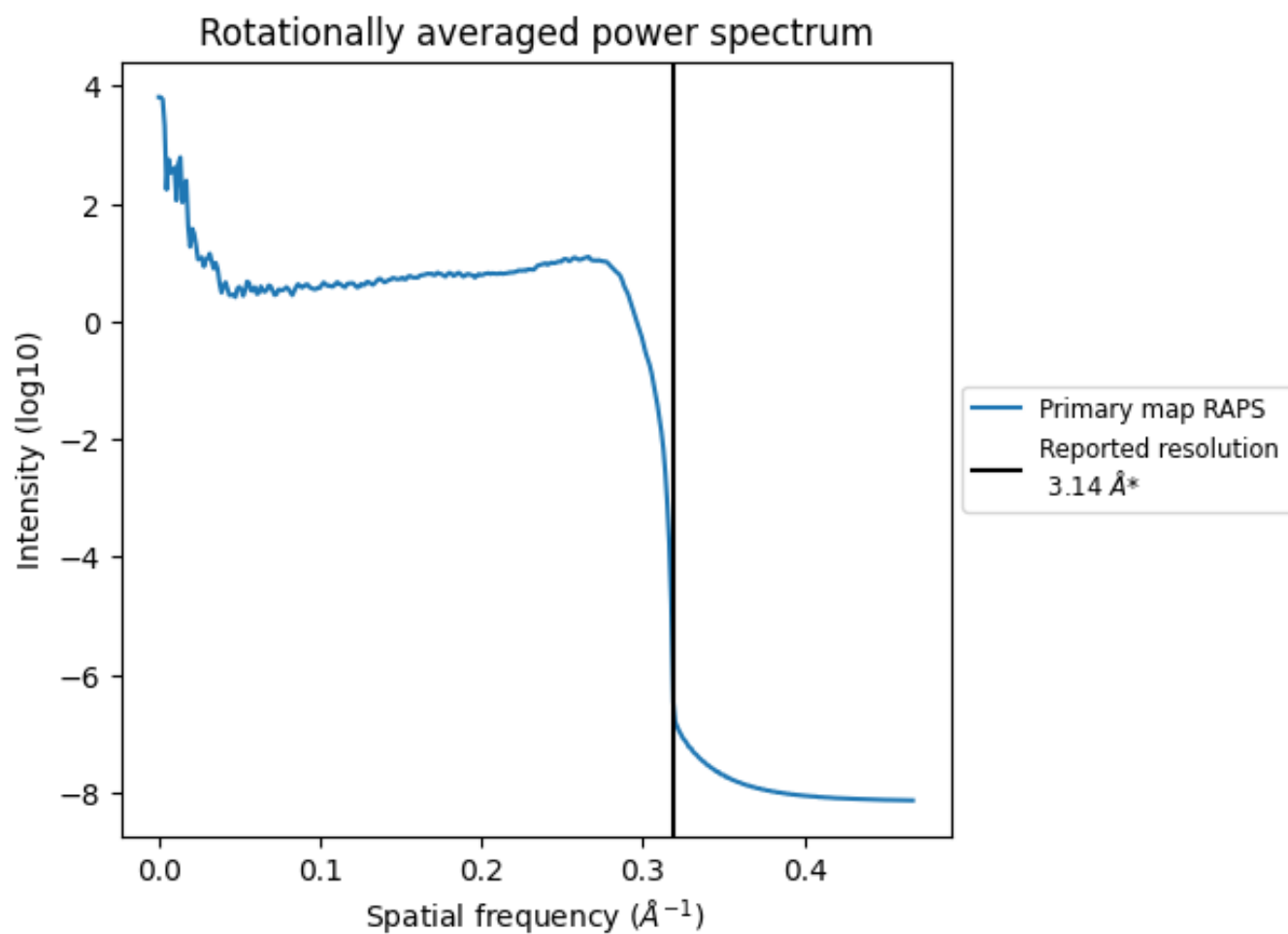
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 938  $\text{nm}^3$ ; this corresponds to an approximate mass of 847 kDa.

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

### 7.3 Rotationally averaged power spectrum i



\*Reported resolution corresponds to spatial frequency of 0.318 Å<sup>-1</sup>

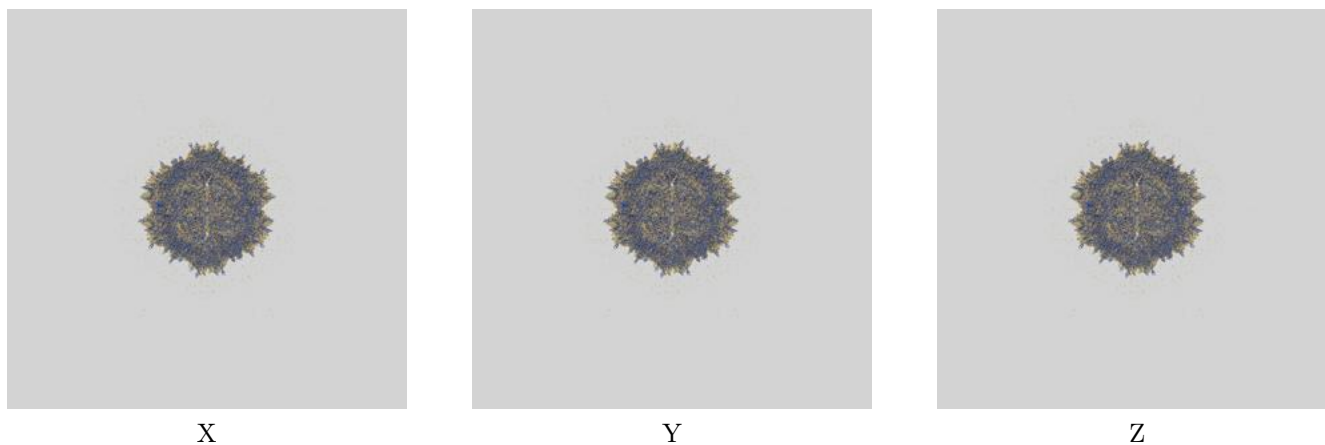
## 8 Fourier-Shell correlation

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

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

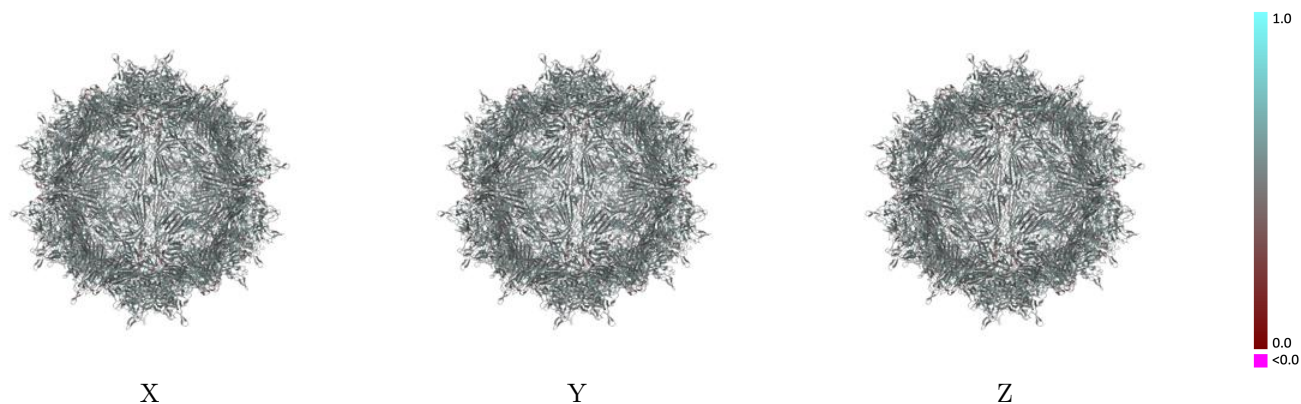
This section contains information regarding the fit between EMDB map EMD-24718 and PDB model 7RWL. Per-residue inclusion information can be found in section [3](#) on page [10](#).

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



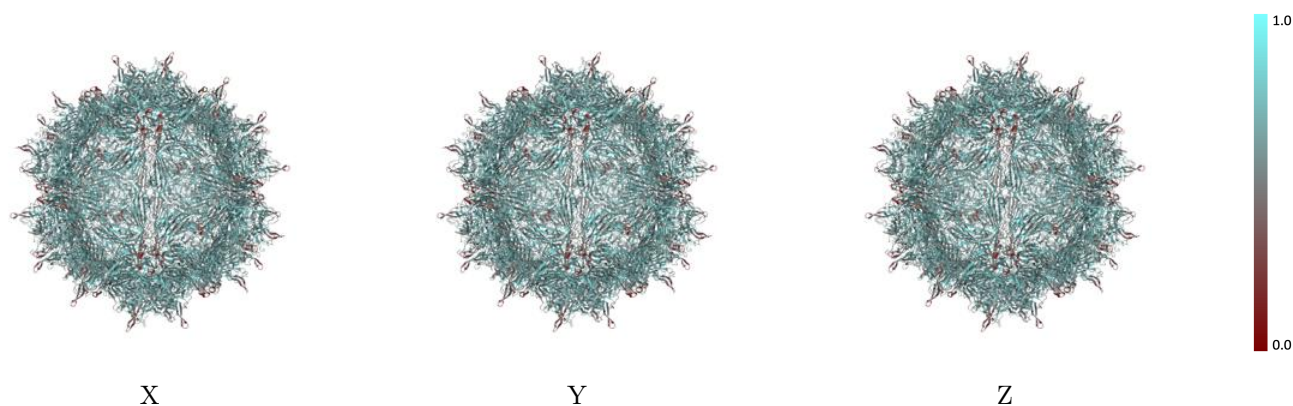
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



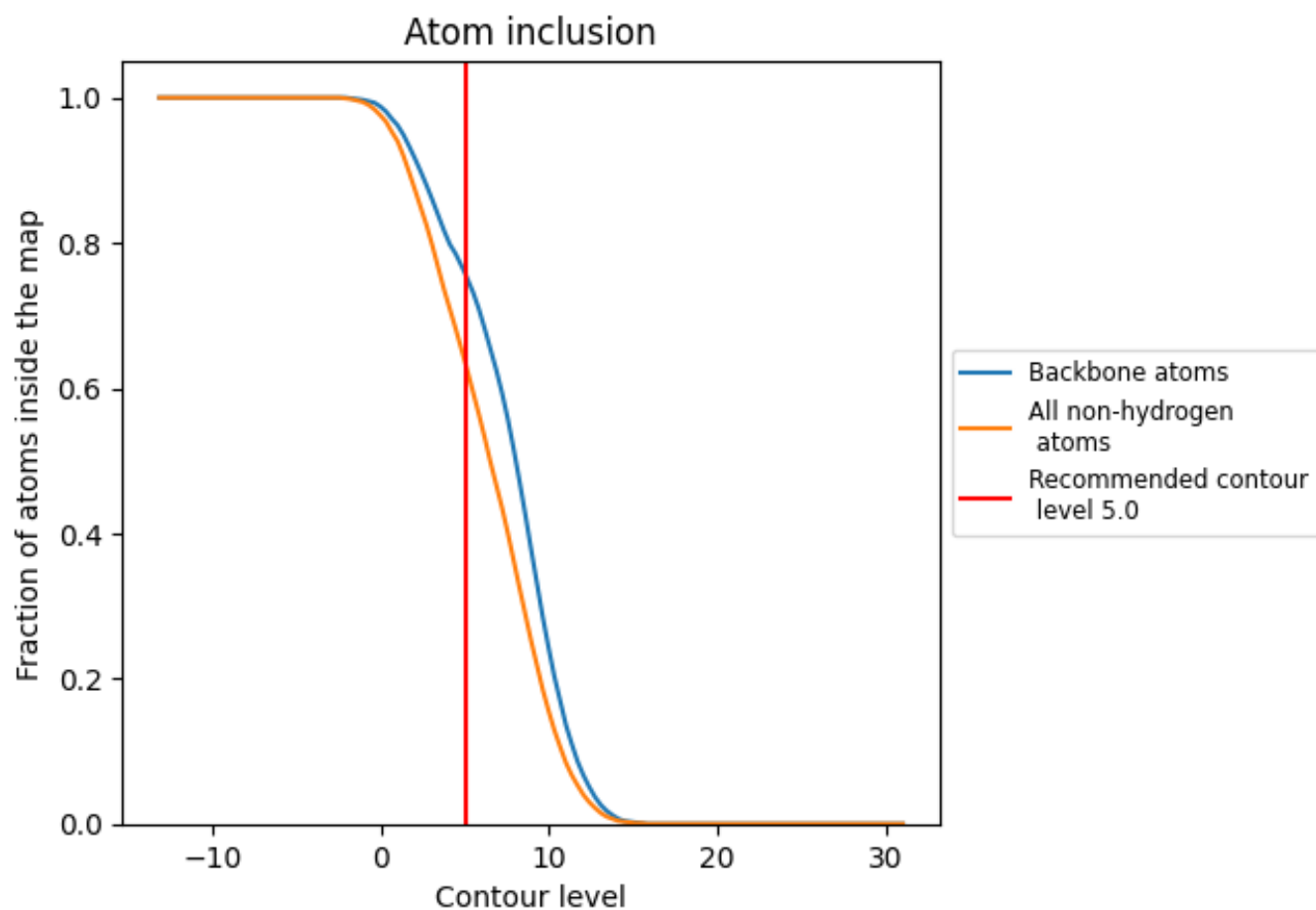
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (5.0).

## 9.4 Atom inclusion [i](#)









































































At the recommended contour level, 76% of all backbone atoms, 64% of all non-hydrogen atoms, are inside the map.



## 9.5 Map-model fit summary





















































The table lists the average atom inclusion at the recommended contour level (5.0) and Q-score for the entire model and for each chain.

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



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