



Full wwPDB EM Validation Report ⓘ

Jul 15, 2024 – 09:22 am BST

PDB ID : 7ZTS
EMDB ID : EMD-14963
Title : Saccharomyces cerevisiae L-BC virus, open particle, asymmetric reconstruction
Authors : Grybchuk, D.; Prochazkova, M.; Fuzik, T.; Konovalovas, A.; Serva, S.; Yurchenko, V.; Plevka, P.
Deposited on : 2022-05-11
Resolution : 16.00 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

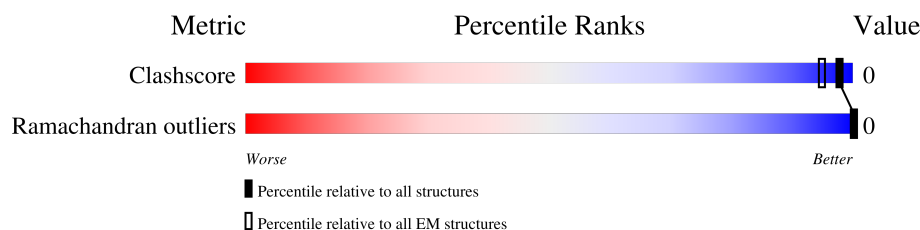
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

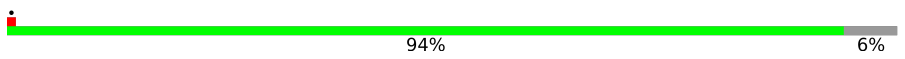
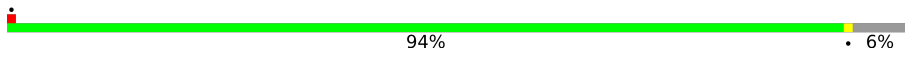
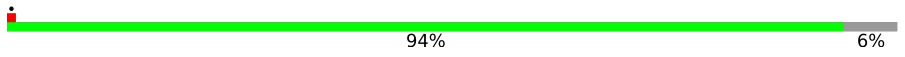
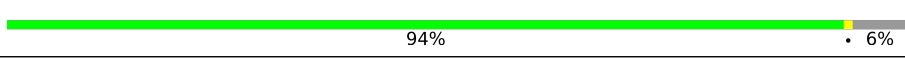
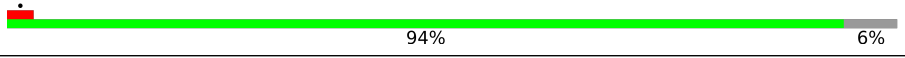
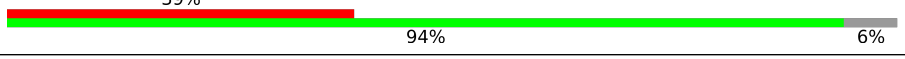

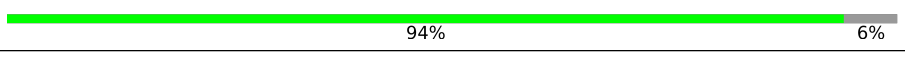
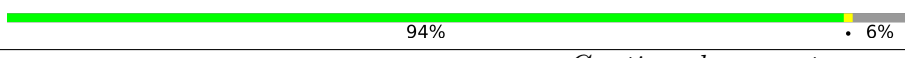
The reported resolution of this entry is 16.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023

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	AA	697	 94% 6%
1	AB	697	 94% • 6%
1	AC	697	 94% 6%
1	AD	697	 94% • 6%
1	AE	697	 94% 6%
1	AF	697	 39% 94% 6%
1	AG	697	 88% 12%
1	AH	697	 94% 6%
1	AI	697	 94% • 6%

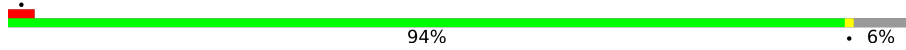
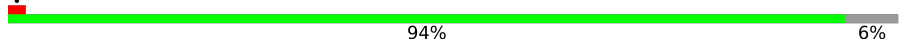
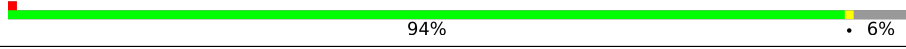
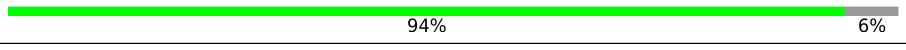
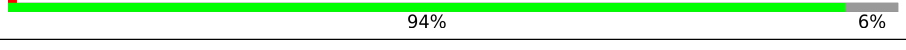
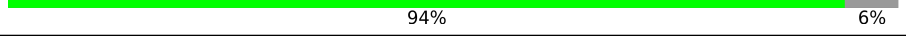
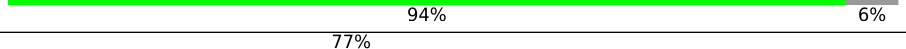
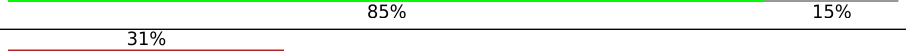

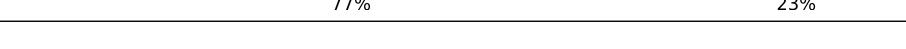
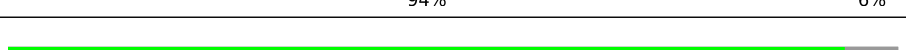
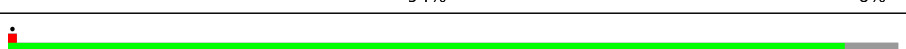
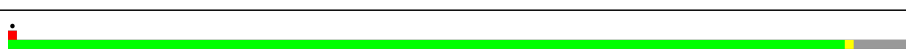
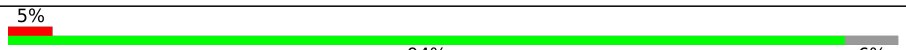
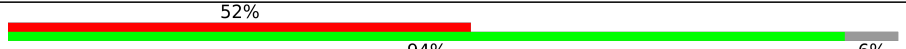

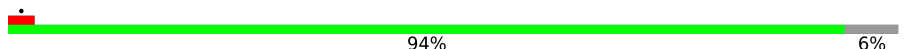
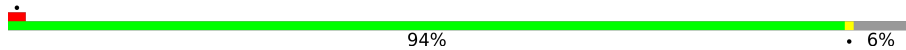
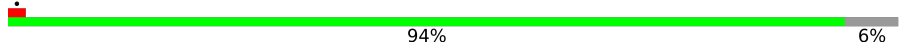
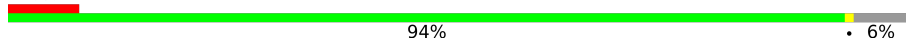
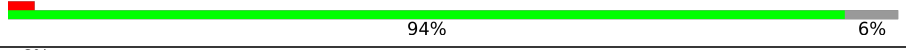
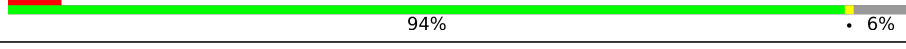
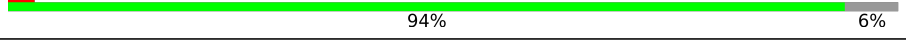
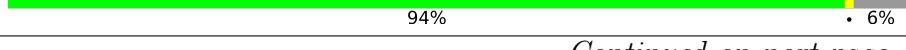

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Mol	Chain	Length	Quality of chain
1	AJ	697	
1	AK	697	
1	AL	697	
1	AM	697	
1	AN	697	
1	AO	697	
1	AP	697	
1	AQ	697	
1	AR	697	
1	AS	697	
1	AT	697	
1	AU	697	
1	AV	697	
1	AW	697	
1	AX	697	
1	AY	697	
1	AZ	697	
1	BA	697	
1	BB	697	
1	BC	697	
1	BD	697	
1	BE	697	
1	BF	697	
1	BG	697	
1	BH	697	

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Mol	Chain	Length	Quality of chain
1	BI	697	
1	BJ	697	
1	BK	697	
1	BL	697	
1	BM	697	
1	BN	697	
1	BO	697	
1	BP	697	
1	BQ	697	
1	BR	697	
1	BS	697	
1	BT	697	
1	BU	697	
1	BV	697	
1	BW	697	
1	BX	697	
1	BY	697	
1	BZ	697	
1	CA	697	
1	CB	697	
1	CC	697	
1	CD	697	
1	CE	697	
1	CF	697	
1	CG	697	

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Mol	Chain	Length	Quality of chain
1	CH	697	
1	CI	697	
1	CJ	697	
1	CK	697	
1	CL	697	
1	CM	697	
1	CN	697	
1	CO	697	
1	CP	697	
1	CQ	697	
1	CR	697	
1	CS	697	
1	CT	697	
1	CU	697	
1	CV	697	
1	CW	697	
1	CX	697	
1	CY	697	
1	CZ	697	
1	DA	697	
1	DB	697	
1	DC	697	
1	DD	697	
1	DE	697	
1	DF	697	

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Mol	Chain	Length	Quality of chain
1	DG	697	
1	DH	697	
1	DI	697	
1	DJ	697	
1	DK	697	
1	DL	697	
1	DM	697	
1	DN	697	
1	DO	697	
1	DP	697	
1	DQ	697	
1	DR	697	
1	DS	697	
1	DT	697	
1	DU	697	
1	DV	697	
1	DW	697	
1	DX	697	
1	DY	697	
1	DZ	697	
1	EA	697	
1	EB	697	
1	EC	697	
1	ED	697	
1	EE	697	

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Mol	Chain	Length	Quality of chain
1	EF	697	<div> <div>70%</div> <div>77%</div> <div>23%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 280400 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 Major capsid protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	AA	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AB	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	AC	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AD	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	AE	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AF	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	AG	613	Total	C	N	O	0	0
			2452	1226	613	613		
1	AH	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AI	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	AJ	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AK	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	AL	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AM	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	AN	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AO	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	AP	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AQ	658	Total	C	N	O	0	0
			2632	1316	658	658		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	AR	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AS	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	AT	593	Total	C	N	O	0	0
			2372	1186	593	593		
1	AU	422	Total	C	N	O	1	0
			1692	846	423	423		
1	AV	538	Total	C	N	O	0	0
			2152	1076	538	538		
1	AW	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AX	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	AY	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	AZ	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BA	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	BB	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BC	613	Total	C	N	O	0	0
			2452	1226	613	613		
1	BD	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	BE	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BF	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	BG	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BH	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	BI	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BJ	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	BK	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BL	658	Total	C	N	O	1	0
			2636	1318	659	659		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	BM	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BN	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	BO	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BP	593	Total	C	N	O	0	0
			2372	1186	593	593		
1	BQ	422	Total	C	N	O	1	0
			1692	846	423	423		
1	BR	538	Total	C	N	O	0	0
			2152	1076	538	538		
1	BS	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	BT	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BU	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	BV	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BW	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	BX	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	BY	613	Total	C	N	O	0	0
			2452	1226	613	613		
1	BZ	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CA	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	CB	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CC	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	CD	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CE	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	CF	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CG	658	Total	C	N	O	0	0
			2632	1316	658	658		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	CH	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CI	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	CJ	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CK	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	CL	593	Total	C	N	O	0	0
			2372	1186	593	593		
1	CM	422	Total	C	N	O	1	0
			1692	846	423	423		
1	CN	538	Total	C	N	O	0	0
			2152	1076	538	538		
1	CO	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CP	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	CQ	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CR	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	CS	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CT	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	CU	613	Total	C	N	O	0	0
			2452	1226	613	613		
1	CV	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CW	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	CX	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	CY	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	CZ	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	DA	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	DB	658	Total	C	N	O	1	0
			2636	1318	659	659		

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Mol	Chain	Residues	Atoms				AltConf	Trace
1	DC	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	DD	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	DE	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	DF	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	DG	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	DH	593	Total	C	N	O	0	0
			2372	1186	593	593		
1	DI	422	Total	C	N	O	1	0
			1692	846	423	423		
1	DJ	538	Total	C	N	O	0	0
			2152	1076	538	538		
1	DK	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	DL	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	DM	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	DN	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	DO	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	DP	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	DQ	613	Total	C	N	O	0	0
			2452	1226	613	613		
1	DR	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	DS	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	DT	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	DU	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	DV	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	DW	658	Total	C	N	O	0	0
			2632	1316	658	658		

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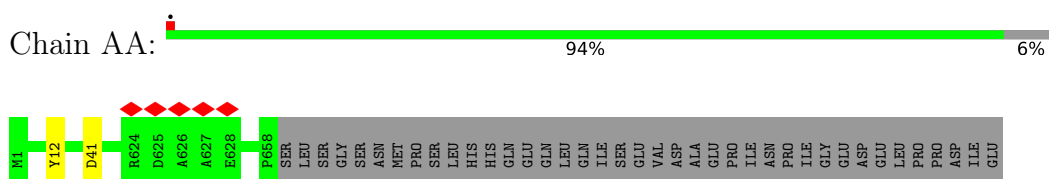
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Mol	Chain	Residues	Atoms				AltConf	Trace
1	DX	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	DY	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	DZ	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	EA	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	EB	658	Total	C	N	O	1	0
			2636	1318	659	659		
1	EC	658	Total	C	N	O	0	0
			2632	1316	658	658		
1	ED	593	Total	C	N	O	0	0
			2372	1186	593	593		
1	EE	422	Total	C	N	O	1	0
			1692	846	423	423		
1	EF	538	Total	C	N	O	0	0
			2152	1076	538	538		

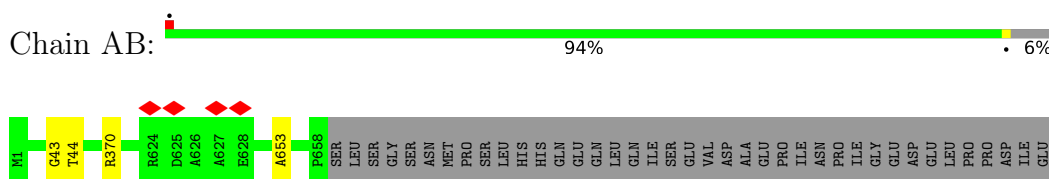
3 Residue-property plots

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.

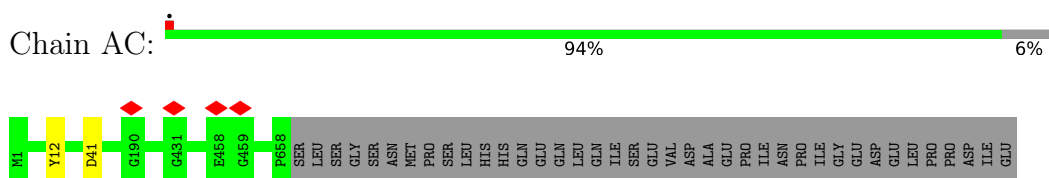
- Molecule 1: Major capsid protein



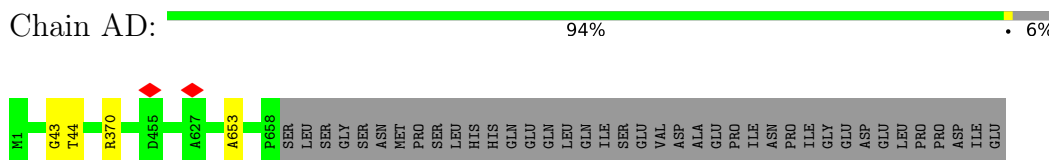
- Molecule 1: Major capsid protein



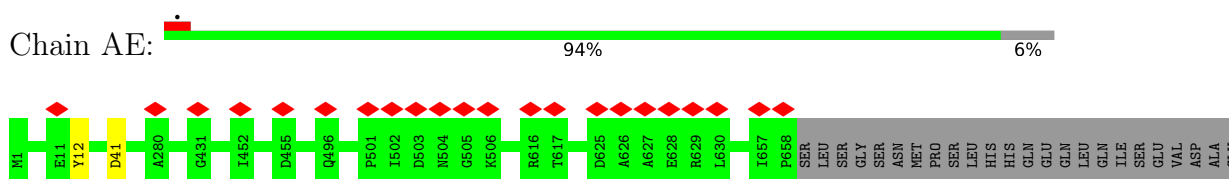
- Molecule 1: Major capsid protein



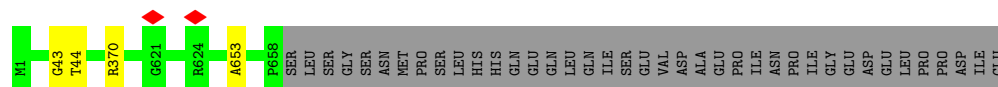
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

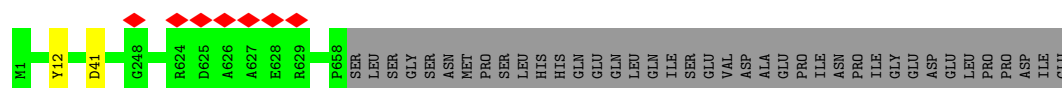


Chain AI:  94% 6%



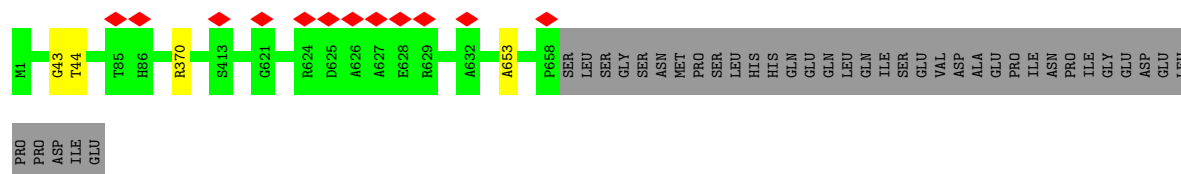
- Molecule 1: Major capsid protein

Chain AJ:  94% 6%



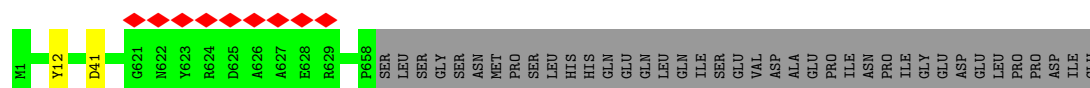
- Molecule 1: Major capsid protein

Chain AK:  94% 6%



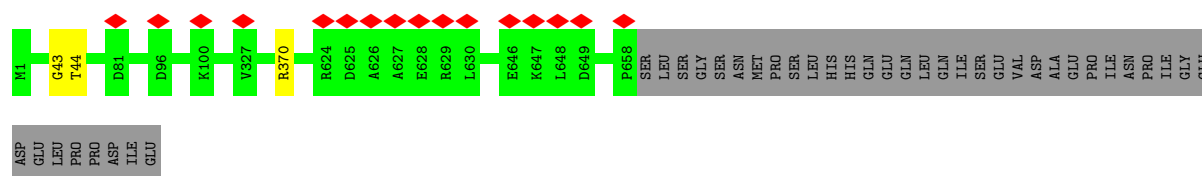
- Molecule 1: Major capsid protein

Chain AL:  94% 6%



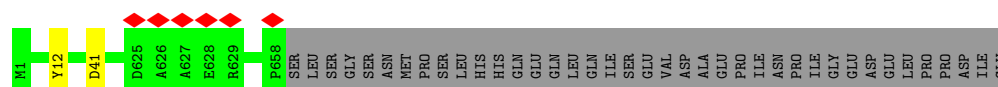
- Molecule 1: Major capsid protein

Chain AM:  94% 6%



- Molecule 1: Major capsid protein

Chain AN:  94% 6%



- Molecule 1: Major capsid protein

M1
 G43
 T44
 R370
 E628
 K647
 L648
 A653
 P658
 LEU
 SER
 GLY
 SER
 SER
 ASN
 MET
 PRO
 SER
 SER
 HIS
 HIS
 GLN
 GLU
 GLN
 LEU
 LEU
 GLN
 ILE
 SER
 SER
 GLU
 VAL
 ASP
 ALA
 ALA
 GLU
 GLU
 PRO
 PRO
 ILE
 ASN
 PRO
 PRO
 ILE
 GLY
 GLU
 ASP
 GLU
 LEU
 LEU
 PRO
 PRO
 ASP
 ASP
 ILE
 GLU

- Chain AP:  94% 6%

- Chain AQ:  94% • 6%

Amino Acid	Percentage (%)	Category
M1	~1	Red
G43	~1	Yellow
T44	~1	Yellow
R370	~1	Yellow
T620	~1	Red (with diamond)
G621	~1	Red (with diamond)
R624	~1	Red (with diamond)
E628	~1	Green (with diamond)
A632	~1	Red (with diamond)
A653	~1	Yellow
P658	~1	Green
SER	~1	Grey
LEU	~1	Grey
SER	~1	Grey
GLY	~1	Grey
SER	~1	Grey
ASN	~1	Grey
NET	~1	Grey
PRO	~1	Grey
SER	~1	Grey
LEU	~1	Grey
HIS	~1	Grey
HIS	~1	Grey
GLN	~1	Grey
GLU	~1	Grey
GLN	~1	Grey
LEU	~1	Grey
GLN	~1	Grey
ILE	~1	Grey
SER	~1	Grey
GLU	~1	Grey
VAL	~1	Grey
ASP	~1	Grey
ALA	~1	Grey
GLU	~1	Grey
PRO	~1	Grey
ILE	~1	Grey
ASN	~1	Grey
PRO	~1	Grey
ILE	~1	Grey
GLY	~1	Grey
GLU	~1	Grey
ASP	~1	Grey
GLU	~1	Grey
PRO	~1	Grey
PRO	~1	Grey
ASP	~1	Grey
ILE	~1	Grey
ILE	~1	Grey

- Chain AR:  94% 6%

- Chain AS:  94% • 6%

- Chain AT: 85% 15%

M1	S2	S3	S4	L5	L6	M6	S7	L8	L9	P10	E11	Y12	F13	K14	P15	K16	T17	M18	L19	N20	T21	N22	A32	R33	I34	D35	M36	Q37	Y38	E39	D40	D41	S42	G43	T44	R45	K46	G47	S48	R49	P50	M51	A52	F53	M54	S55	A59	F60	I61	G62	N63	Y64	E65	G66	I6E	I6E	VAL	S6P
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D71	I72	P73	I74	L75	D76	A80	D81	I82	F83	D84	T85	H86	G87	D88	L89	D90	M91	G92	L93	V94	E95	D96	A97	L98	S99	K100	S101	T102	M103	I104	R105	R106	N107	V108	P109	THR	TYR	THR	ALA	TYR	ALA	ALA	SER	GLU	LEU	LEU	TYR	K121	R122	N123	D153	N154	G155	H156	A157	S178	I179
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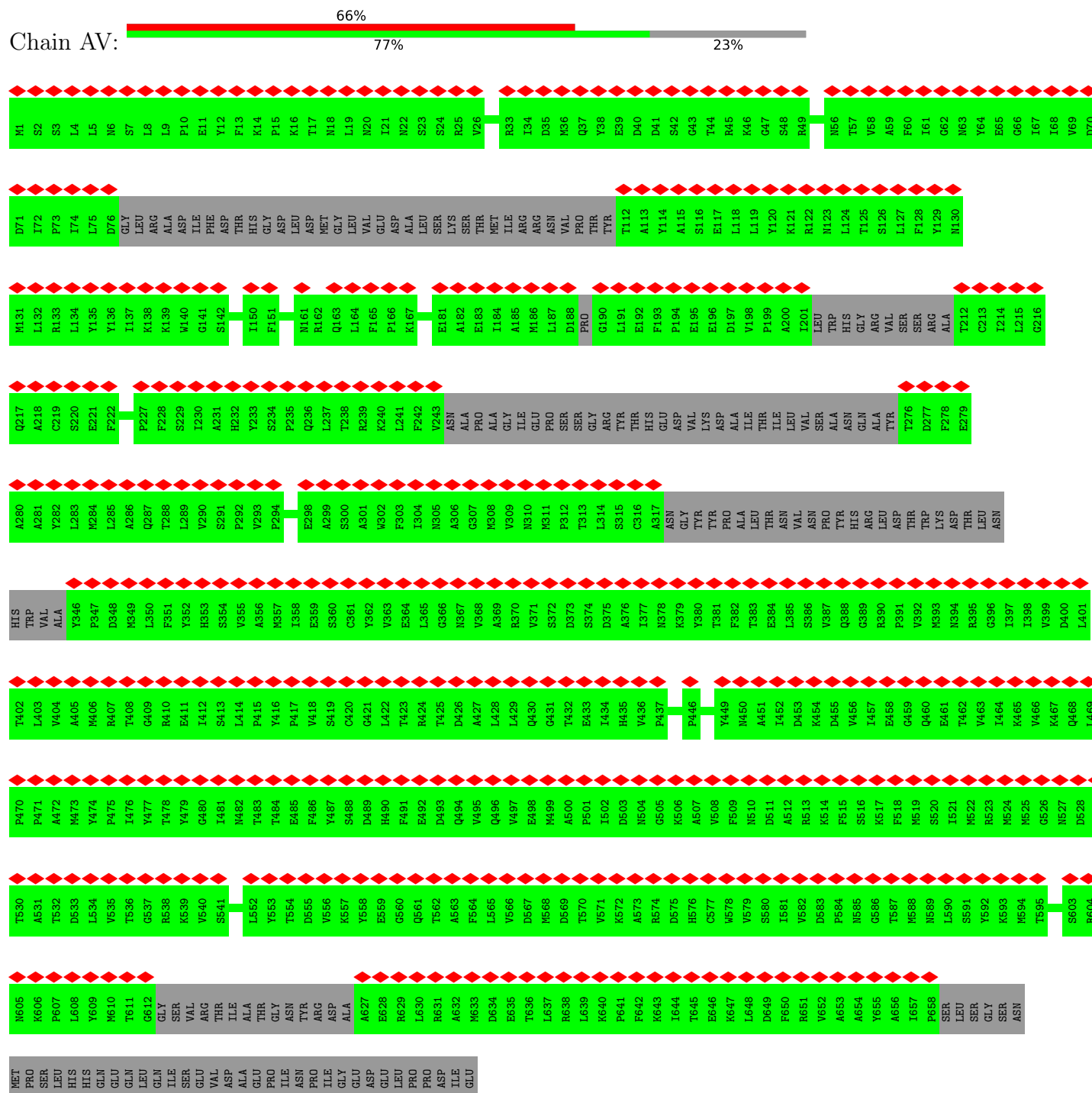
P180	E181	A182	E183		D188	P189	G190	L191	GLU	PHE	PRO	GLU	GLU	D197	V198	P199		W203	H204	G205	R206	V207	S208	S209	R210		P227	F228	S229		T238	R239	K240		A245	P246	A247	G248	I249	E250		R255	Y256	T257	H258	E259	D260	V261	K262	D263	A264	I265	T266	I267	L268	V269	S270	A271
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LEU LYS PRO PHE LYS LYS THR GLU LYS LEU ASP PHE ASP ARG VAL ALA ALA TYR THR ALA ALA ILE PRO SER SER SER GLY SER ASN MET PRO SER LEU HIS HIS GLN GLU GLN ILE SER GLU VAL ASP ALA ALA PRO ILE ASN ASN ILE GLY GLU ASP LEU LEU PRO ASP ILE GLU

• Molecule 1: Major capsid protein

Chain AV:

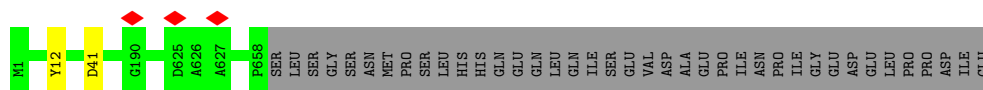


• Molecule 1: Major capsid protein

Chain AW:

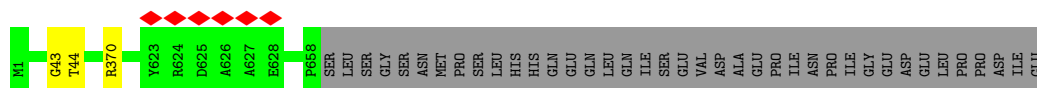
94%

6%



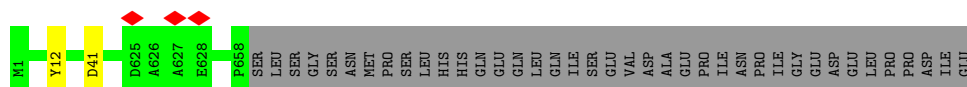
- Molecule 1: Major capsid protein

Chain AX: 94% 6%



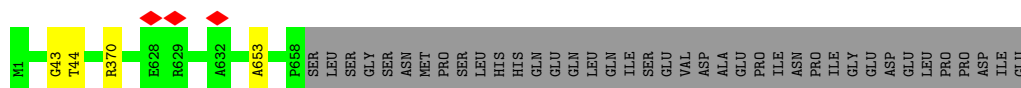
- Molecule 1: Major capsid protein

Chain AY: 94% 6%



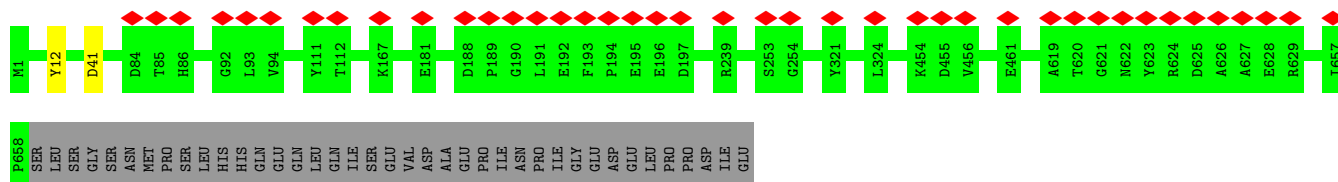
- Molecule 1: Major capsid protein

Chain AZ: 94% 6%



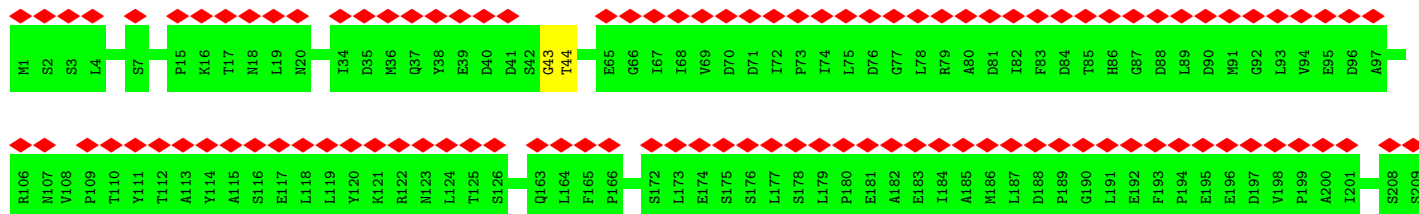
- Molecule 1: Major capsid protein

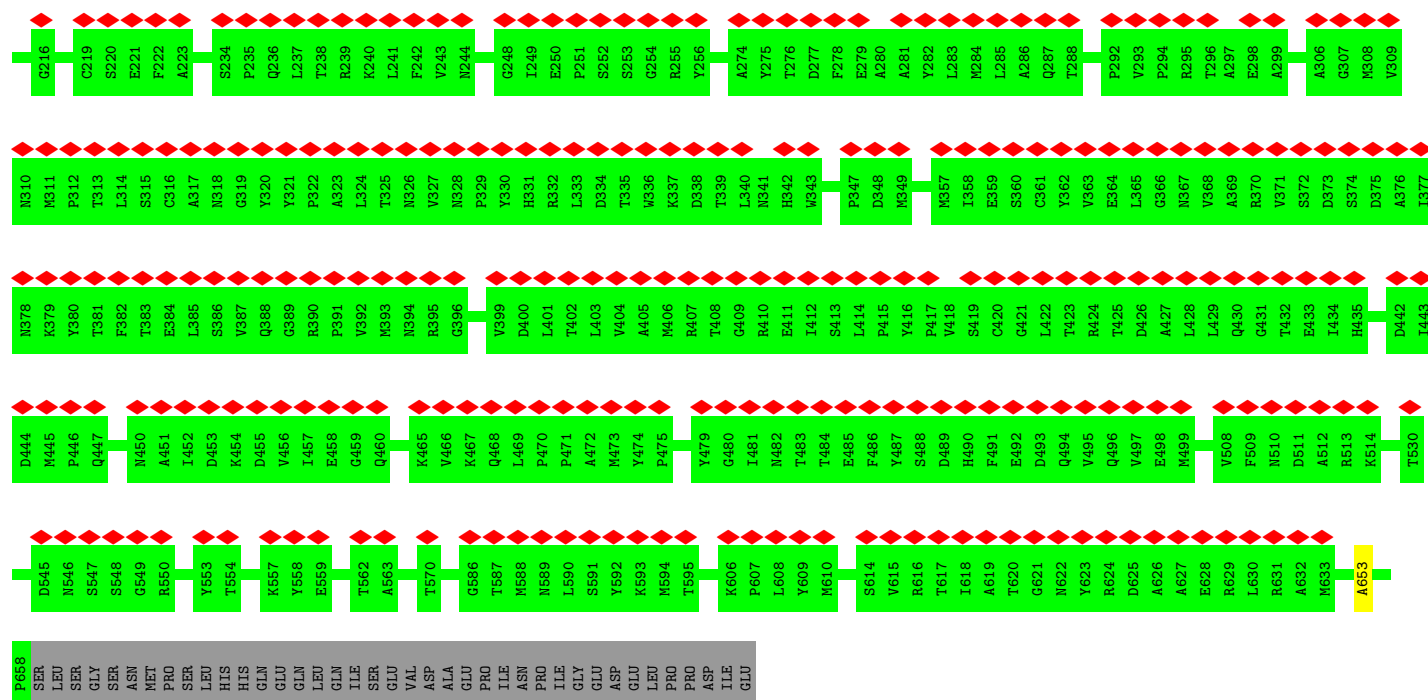
Chain BA: 94% 6%



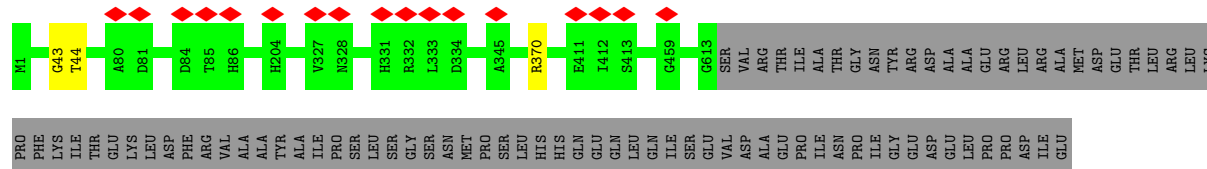
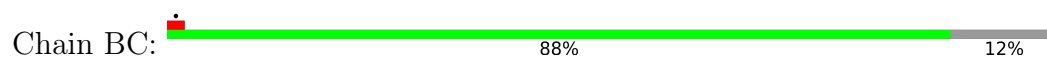
- Molecule 1: Major capsid protein

Chain BB: 54% 94% 6%

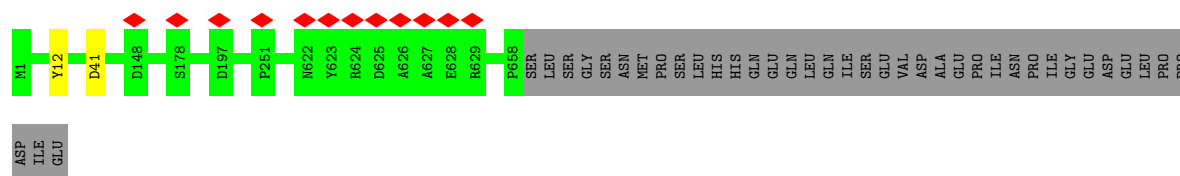




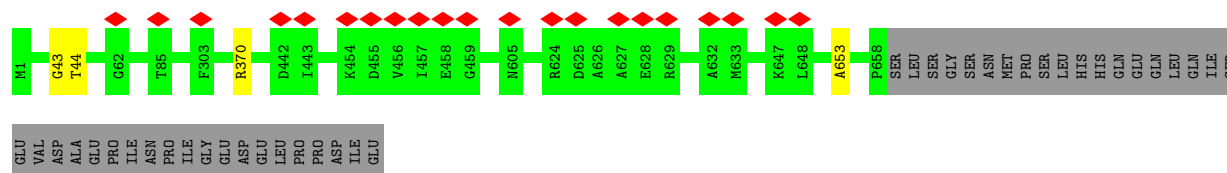
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

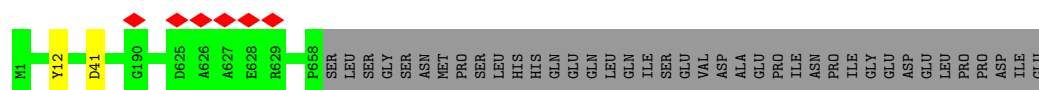


- Molecule 1: Major capsid protein



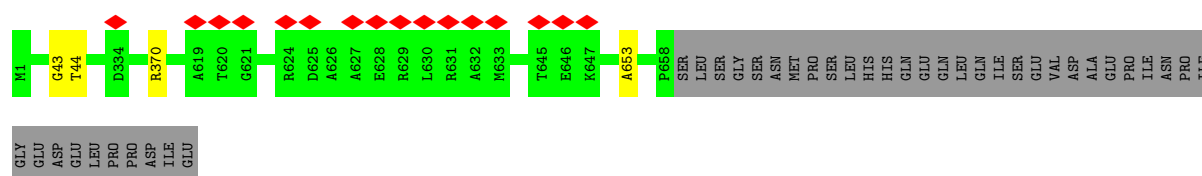
- Molecule 1: Major capsid protein

Chain BF:  94% 6%



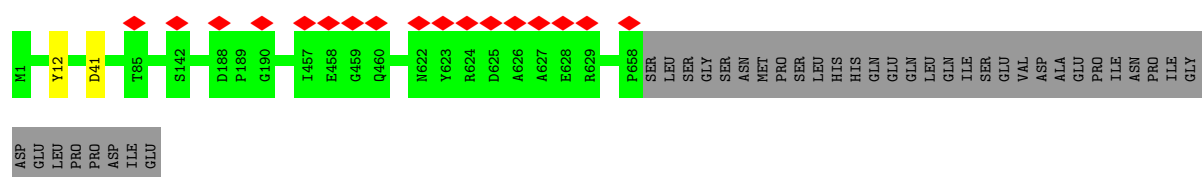
- Molecule 1: Major capsid protein

Chain BG:  94% 6%



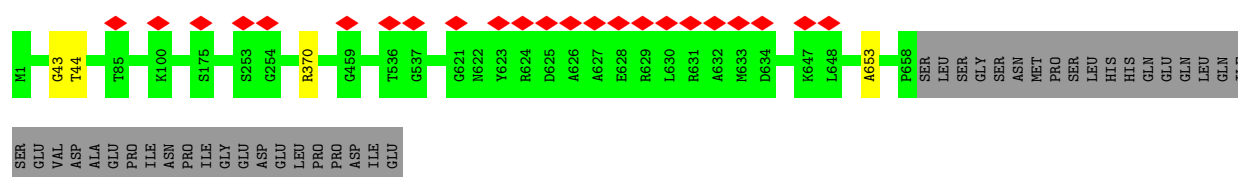
- Molecule 1: Major capsid protein

Chain BH:  94% 6%



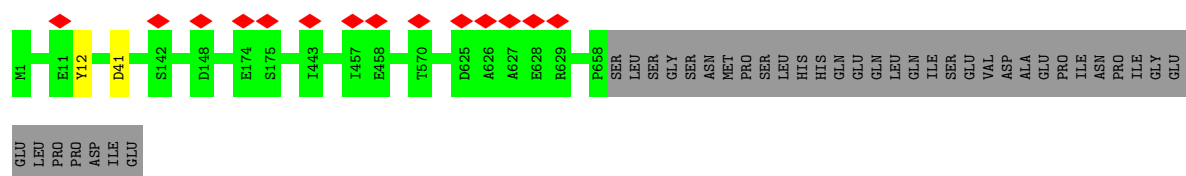
- Molecule 1: Major capsid protein

Chain BI:  94% 6%



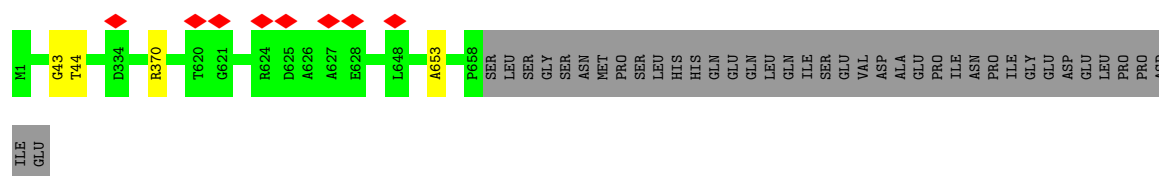
- Molecule 1: Major capsid protein

Chain BJ:  94% 6%



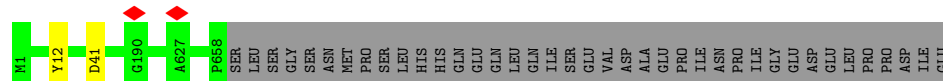
- Molecule 1: Major capsid protein

Chain BK:  94% 6%



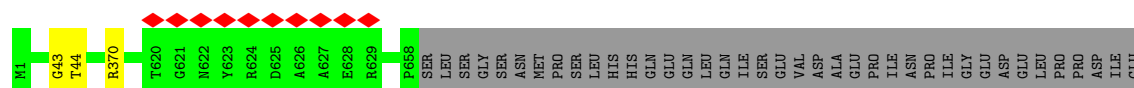
- Molecule 1: Major capsid protein

Chain BL:  94% 6%



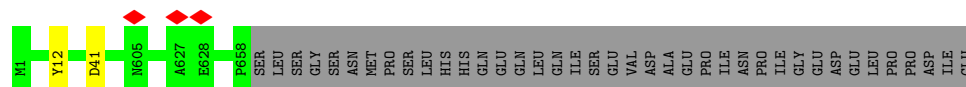
- Molecule 1: Major capsid protein

Chain BM:  94% 6%



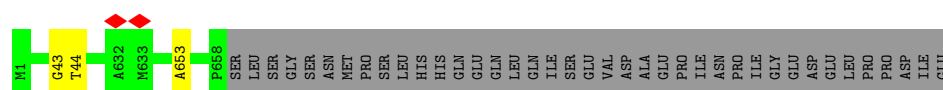
- Molecule 1: Major capsid protein

Chain BN:  94% 6%




- Molecule 1: Major capsid protein

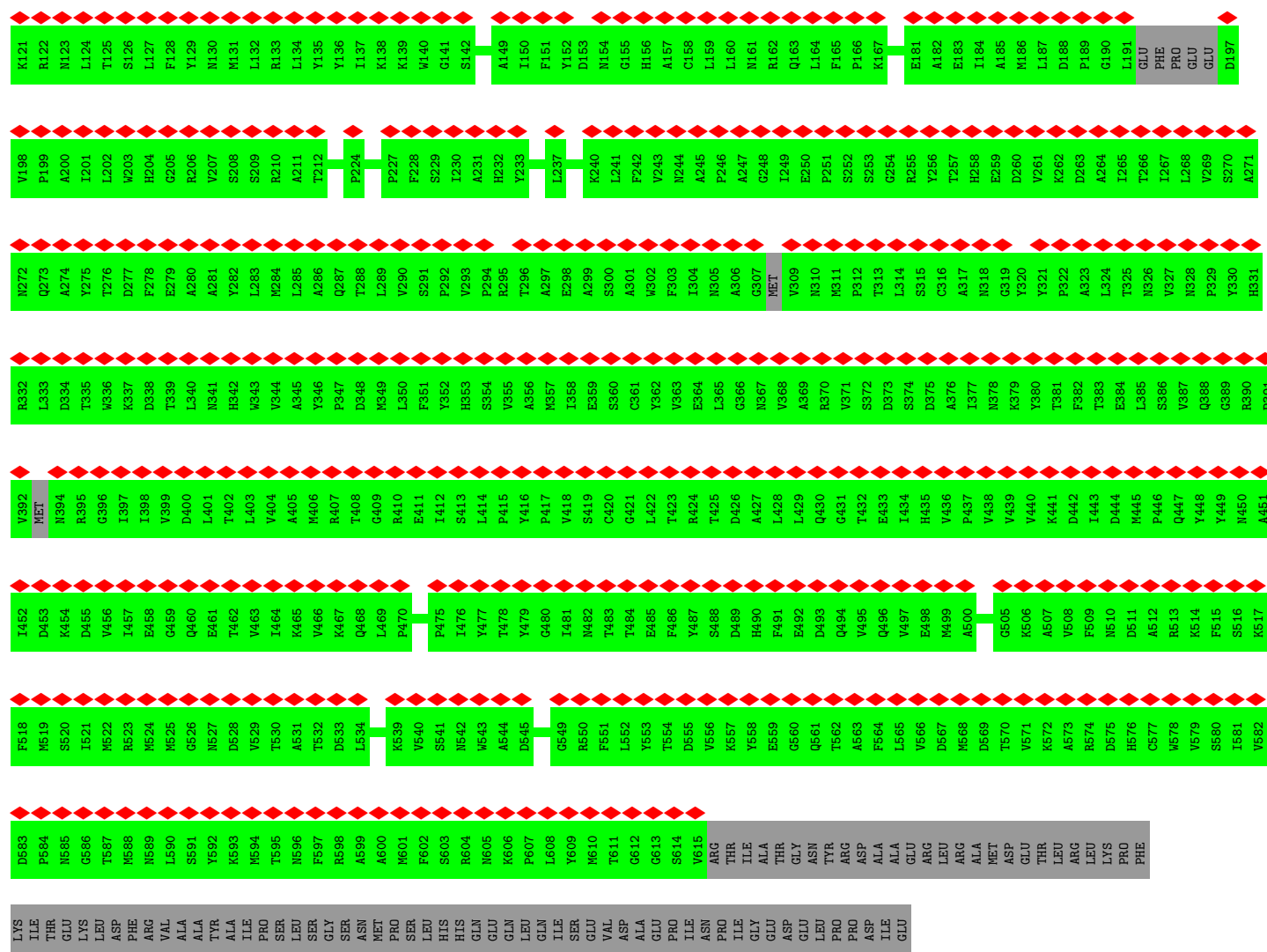
Chain BO:  94% 6%



- Molecule 1: Major capsid protein

Chain BP:  77% 85% 15%

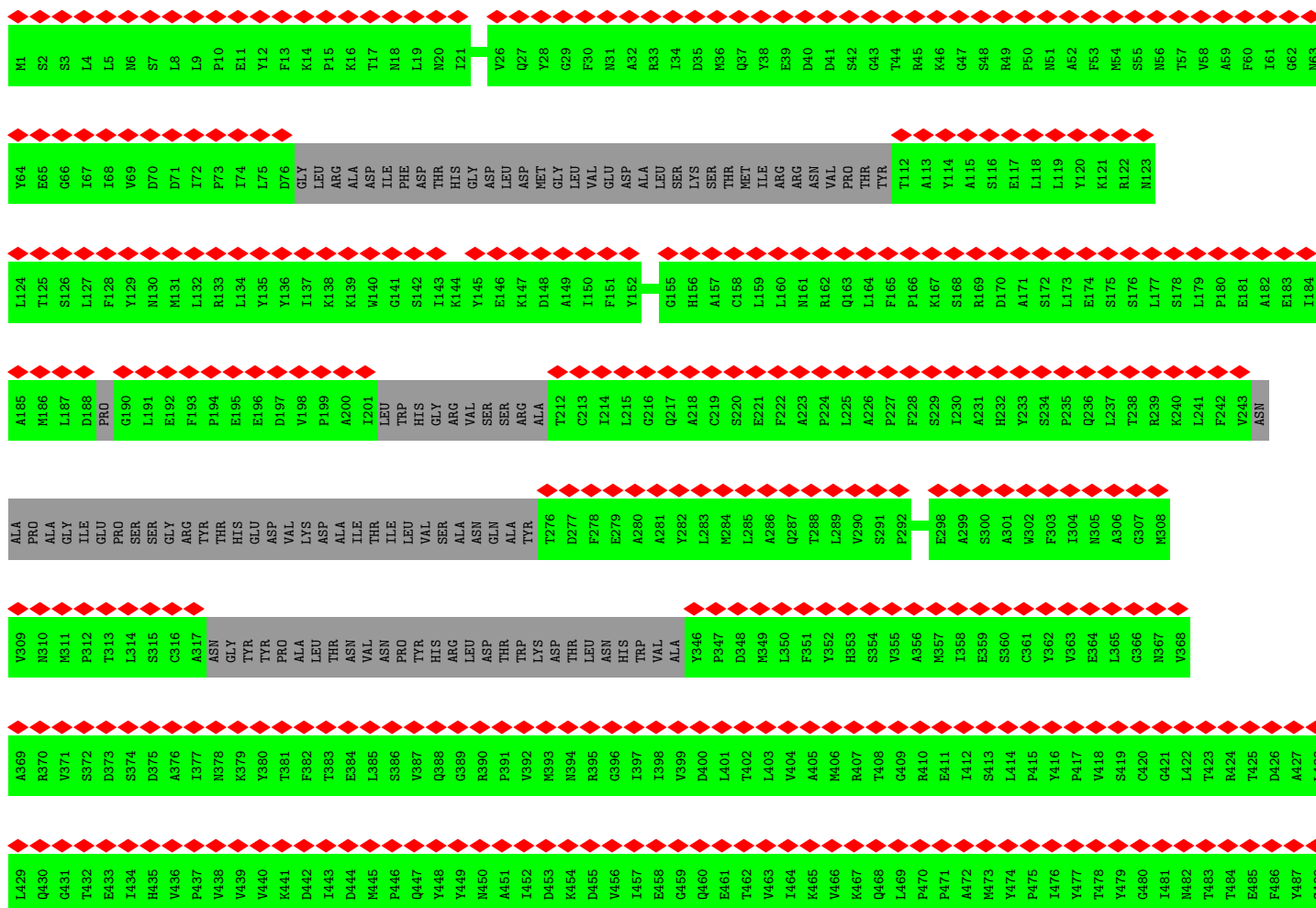
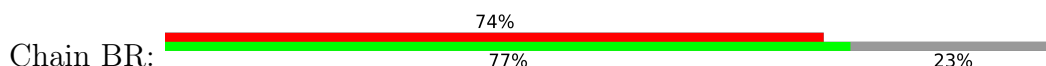


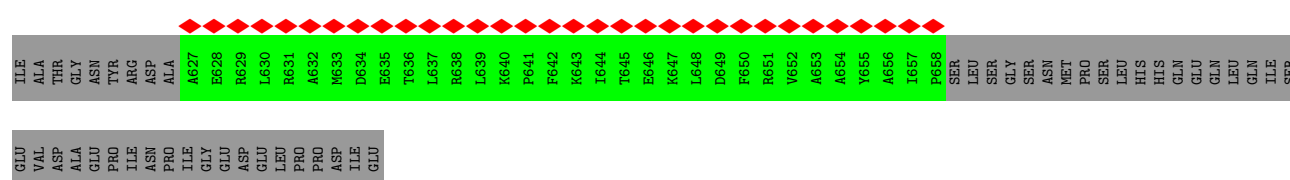


• Molecule 1: Major capsid protein



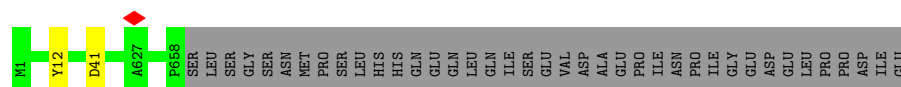
- Molecule 1: Major capsid protein





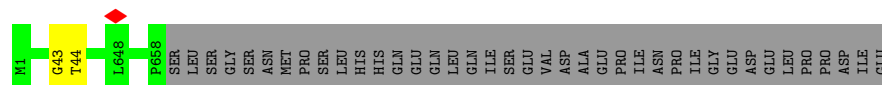
• Molecule 1: Major capsid protein

Chain BS: 94% (green bar), 6% (grey bar)



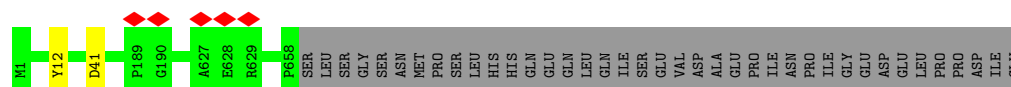
• Molecule 1: Major capsid protein

Chain BT: 94% (green bar), 6% (grey bar)



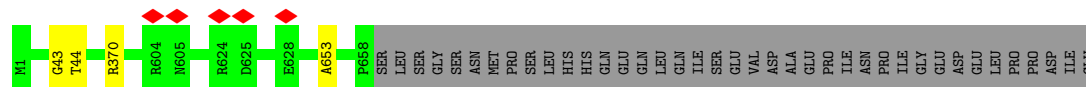
• Molecule 1: Major capsid protein

Chain BU: 94% (green bar), 6% (grey bar)



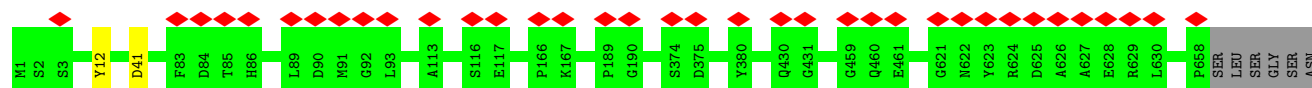
• Molecule 1: Major capsid protein

Chain BV: 94% (green bar), 6% (grey bar)

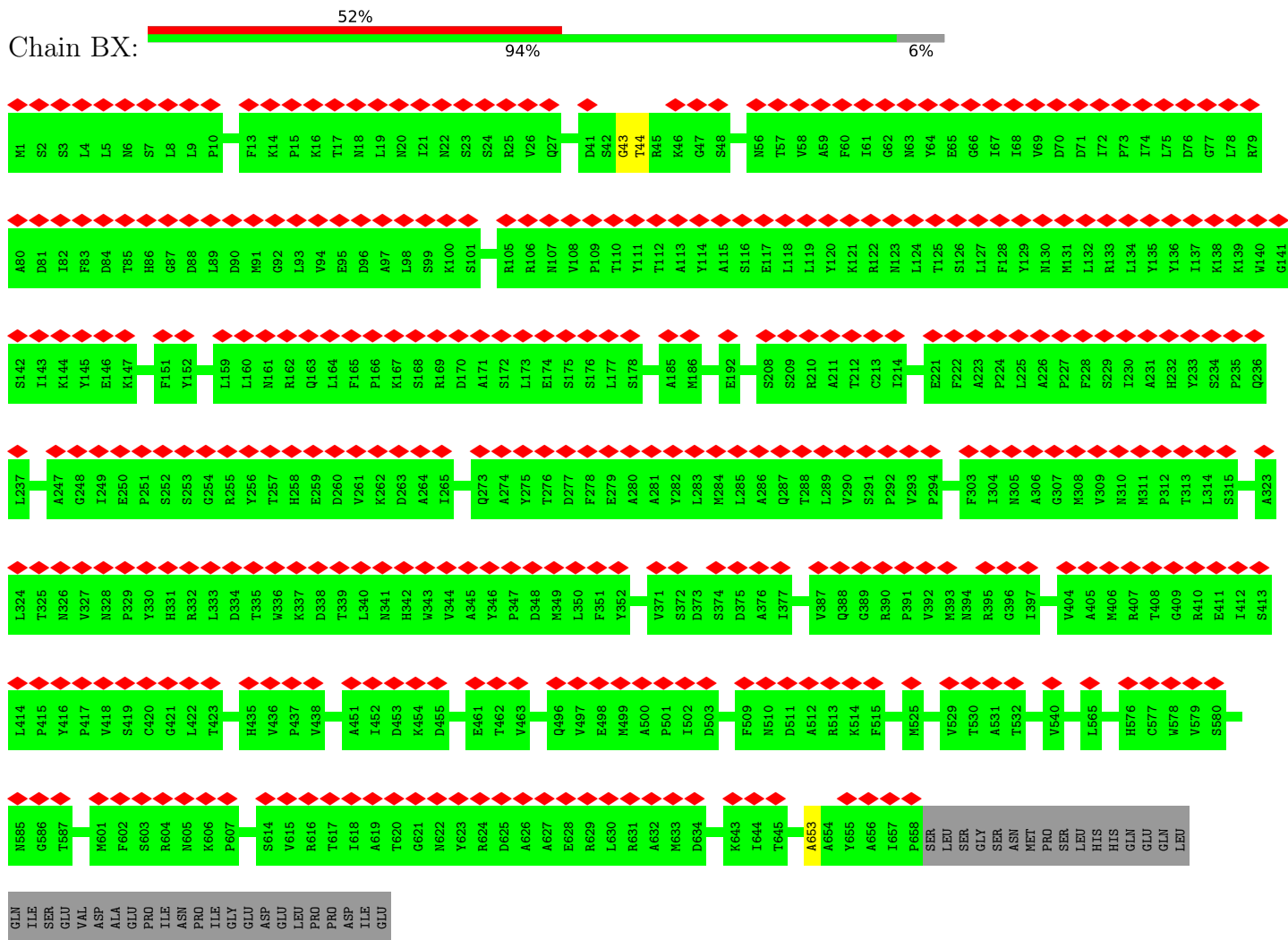


• Molecule 1: Major capsid protein

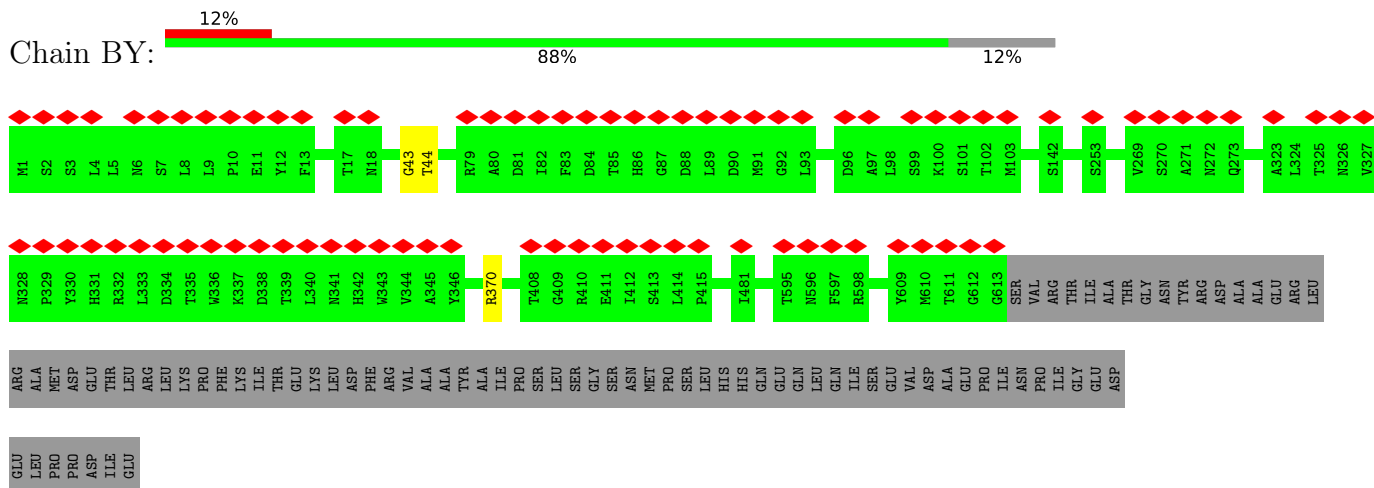
Chain BW: 5% (red bar), 94% (green bar), 6% (grey bar)



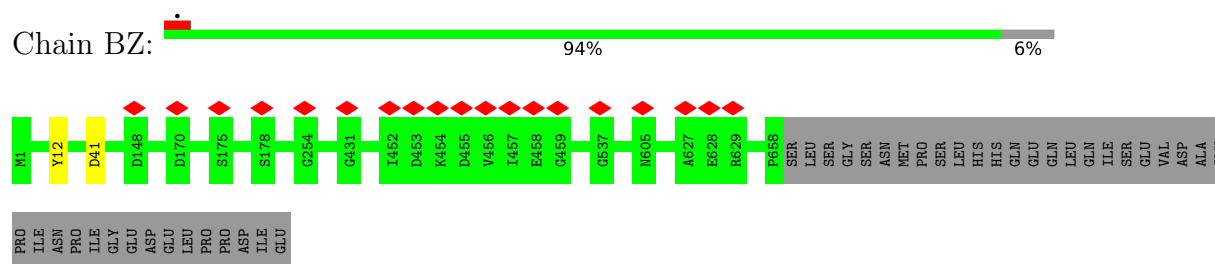
- Molecule 1: Major capsid protein



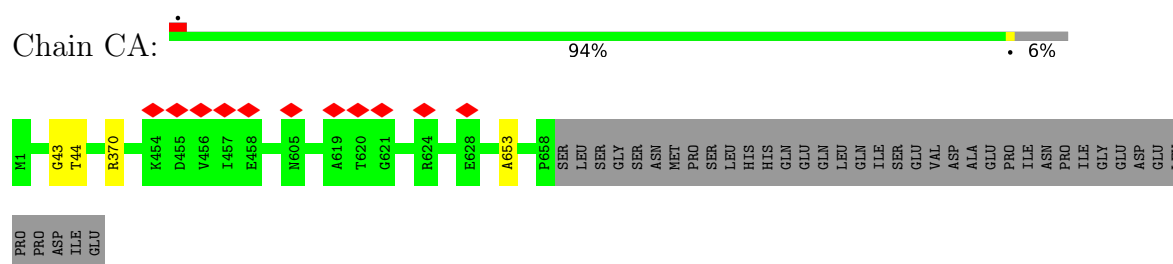
- Molecule 1: Major capsid protein



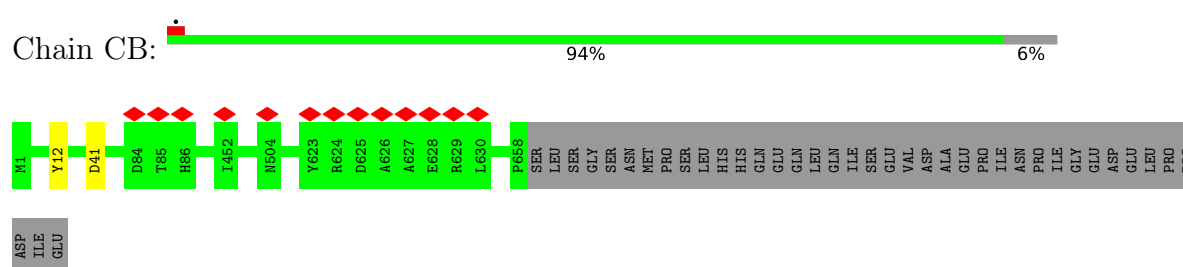
- Molecule 1: Major capsid protein



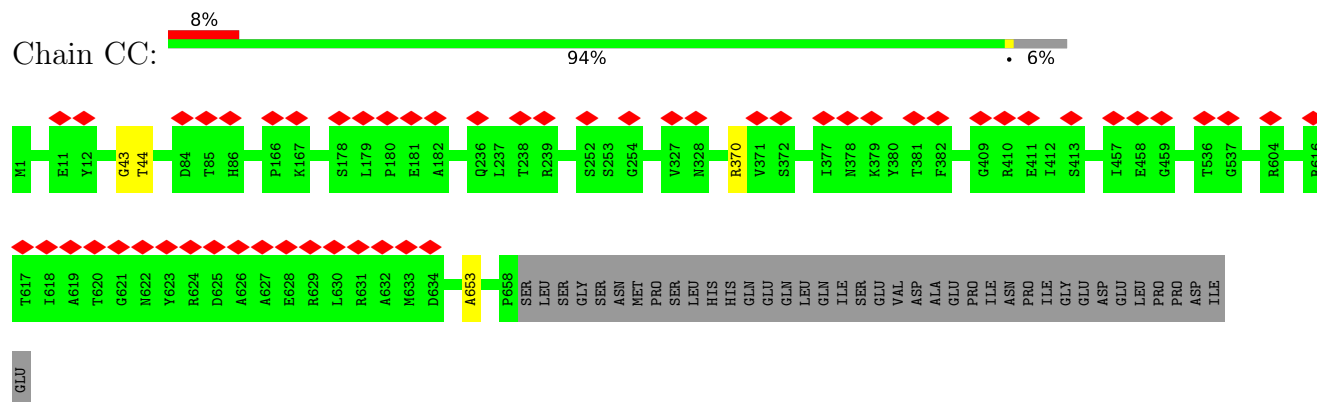
- Molecule 1: Major capsid protein



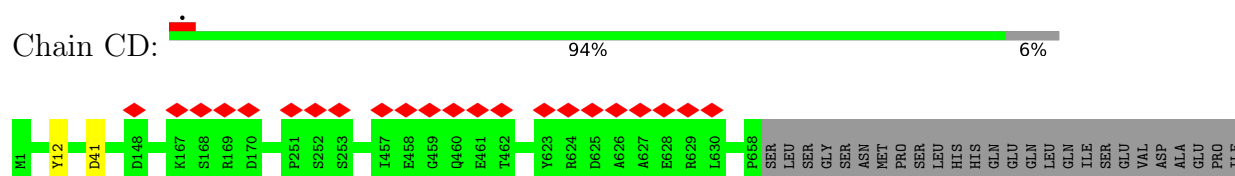
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein



ASN
PRO
ILE
GLY
GLU
ASP
GLU
LEU
PRO
PRO
ASP
ILE
GLU

- Molecule 1: Major capsid protein

Chain CE:  94% 6%

HI G43 T44 A80 D81 D84 T85 H86 N326 V327 N328 D334 T335 R370 E458 G459 T617 I618 A619 T620 G621 N622 Y623 R624 D625 A626 A627 E628 R629 L630 R631 A632 M633 D634 E635 T636 L637 R638 L639 K640 P641 A653 A656 I657 P658 SER LEU SER GLY SER

ASN
MET
PRO
SER
LEU
HIS
HIS
GLN
GLU
GLN
LEU
GLN
ILE
SER
VAL
VAL
ASP
ALA
GLU
PRO
ILE
ASN
PRO
ILE
GLY
GLU
ASP
LEU
PRO
PRO
ASP
ILE
GLU

- Molecule 1: Major capsid protein

Chain CF:  94% 6%

HI Y12 D41 D148 A149 I150 F151 Y152 D153 D170 K454 D455 V456 I457 E458 D625 A626 E628 R629 L630 P658 SER LEU SER GLY SER ASN MET PRO SER LEU HIS HIS GLN GLU GLN LEU ILE SER VAL ASP ALA GLU PRO ASN ILE PRO ILE GLU

ASP
GLU
LEU
PRO
PRO
ASP
ILE
GLU

- Molecule 1: Major capsid protein

Chain CG:  94% 6%

HI G43 T44 T85 H86 R370 R504 D569 G621 R624 D625 A626 A627 E628 R629 L630 A632 H633 A653 I657 P658 SER LEU SER GLY SER ASN MET PRO SER LEU HIS HIS GLN GLN LEU ILE SER VAL ASP ALA GLU PRO ASN ILE PRO ILE GLU

GLY
GLU
ASP
GLU
LEU
PRO
PRO
ASP
ASP
ILE
GLU

- Molecule 1: Major capsid protein

Chain CH:  94% 6%

HI Y12 D41 G190 A627 E628 P658 SER LEU SER GLY SER ASN MET PRO GLY SER LEU HIS HIS GLN GLN LEU ILE SER VAL ASP ALA GLU PRO ILE ILE ASN ASP PRO PRO ASP ILE GLU

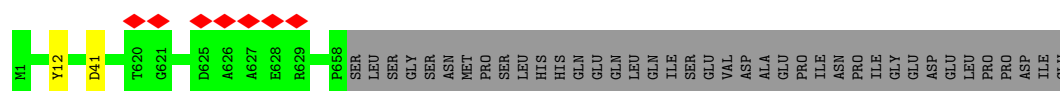
- Molecule 1: Major capsid protein

Chain CI:  94% 6%

HI G43 T44 R370 R624 A627 E628 R629 A653 P658 SER LEU SER GLY SER ASN MET PRO SER LEU HIS HIS GLN GLN LEU ILE SER VAL ASP ALA GLU PRO ILE ILE ASN ASP PRO PRO ASP ILE GLU

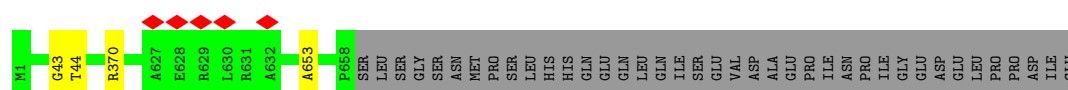
- Molecule 1: Major capsid protein

Chain CJ:  94% 6%




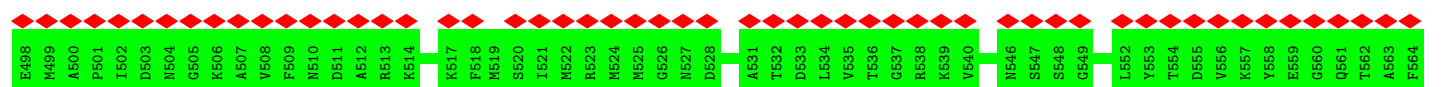
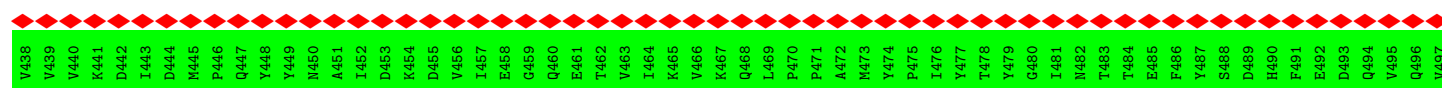
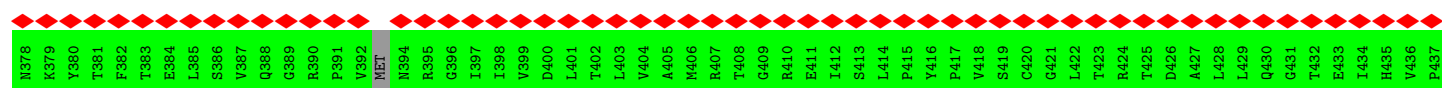
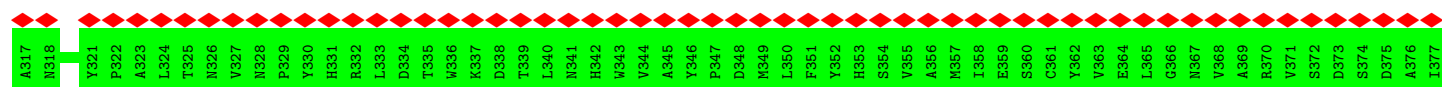
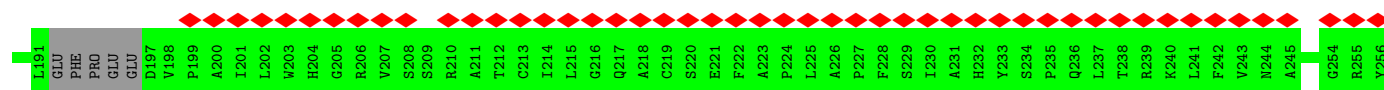
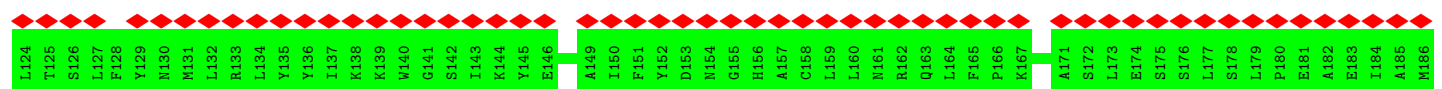
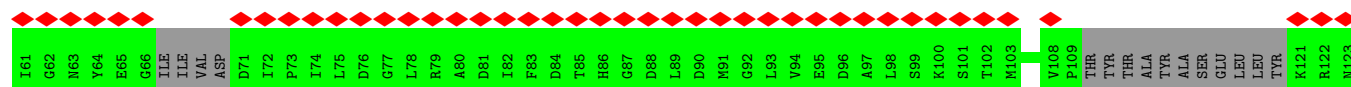
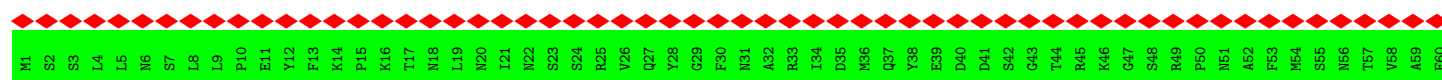
- Molecule 1: Major capsid protein

Chain CK:  94% 6%

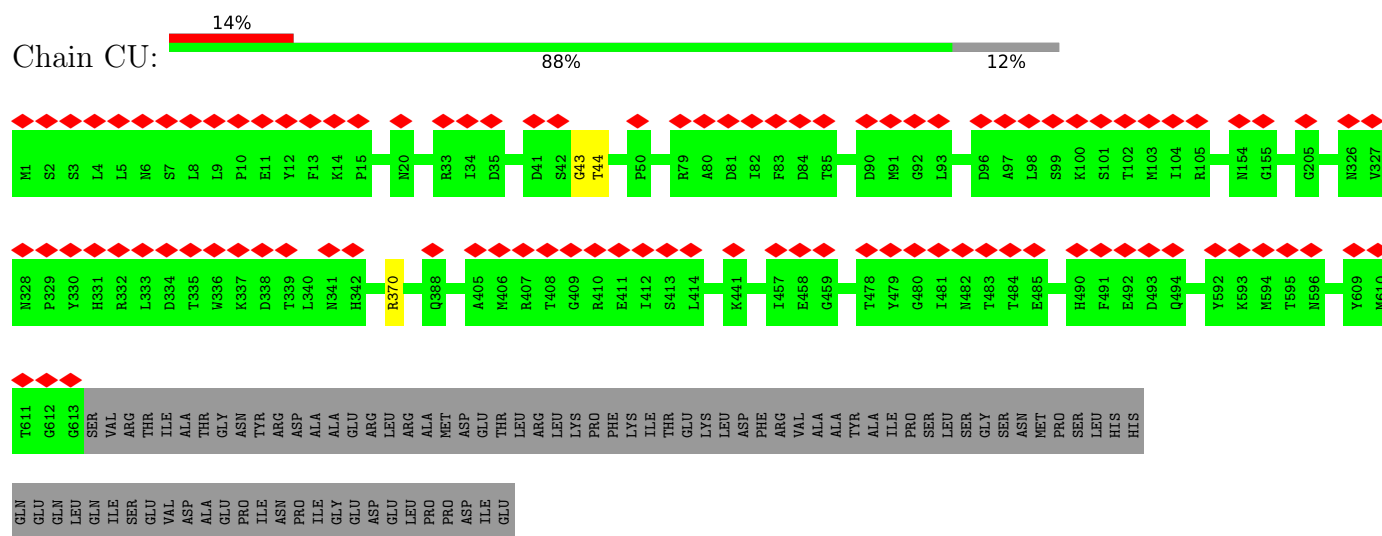


- Molecule 1: Major capsid protein

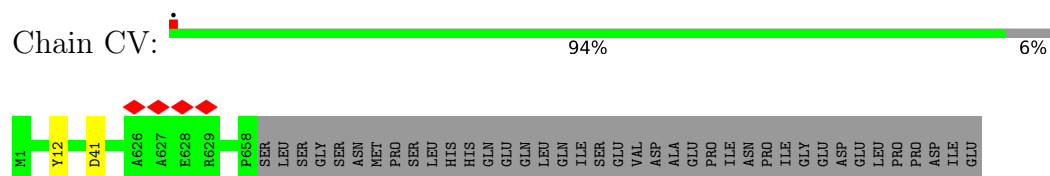
Chain CL:  79% 85% 15%



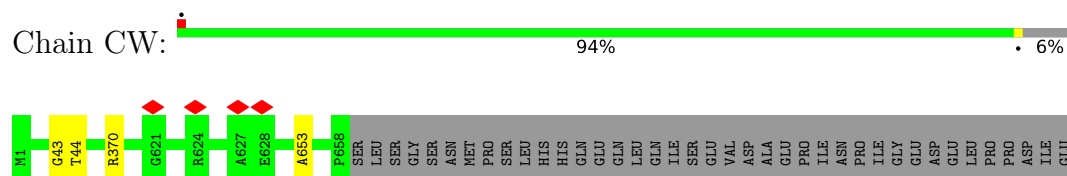
● Molecule 1: Major capsid protein



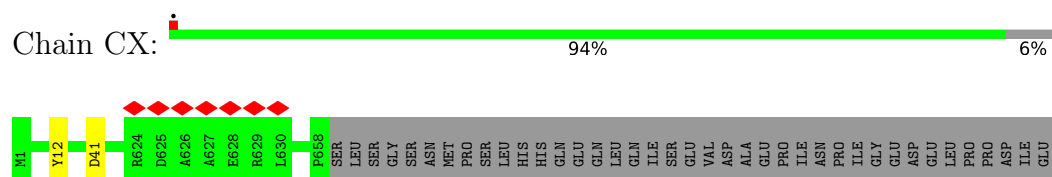
● Molecule 1: Major capsid protein



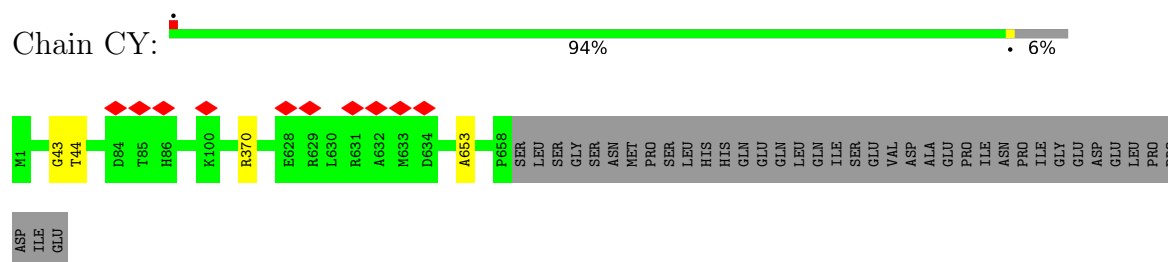
● Molecule 1: Major capsid protein



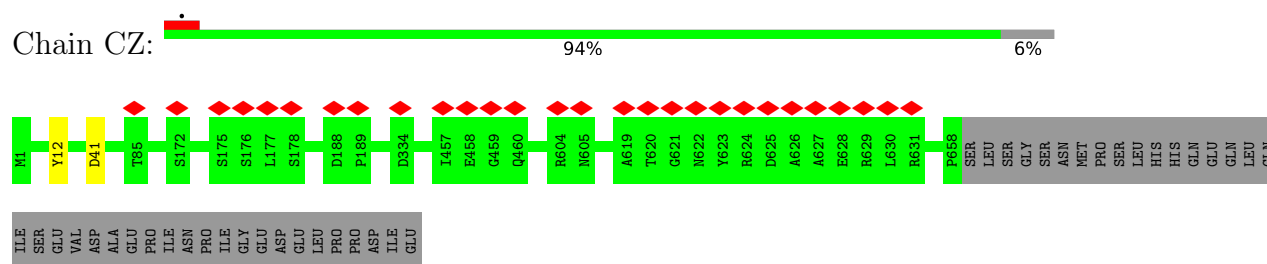
● Molecule 1: Major capsid protein



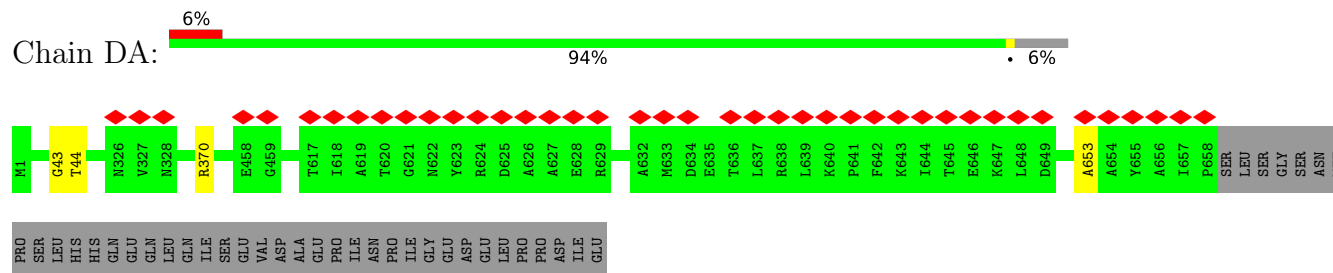
● Molecule 1: Major capsid protein



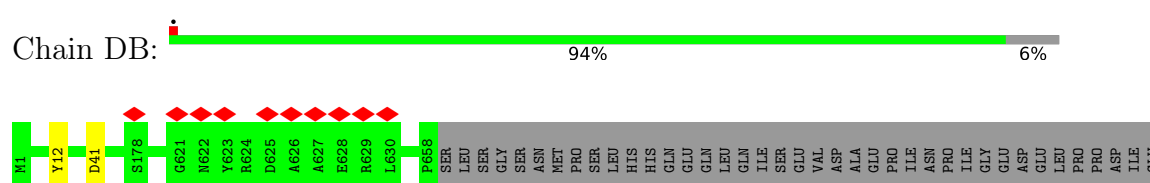
- Molecule 1: Major capsid protein



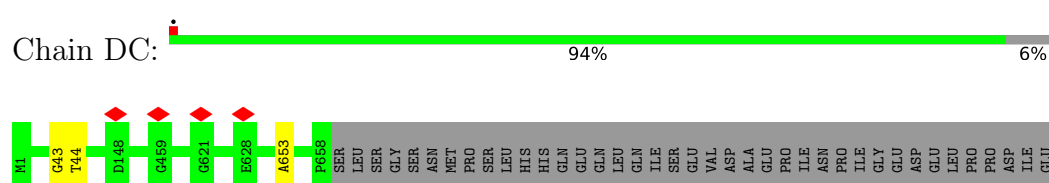
- Molecule 1: Major capsid protein



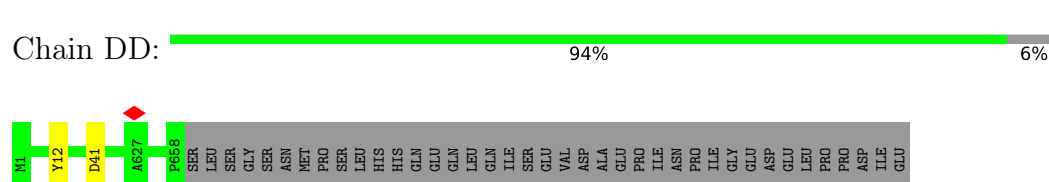
- Molecule 1: Major capsid protein



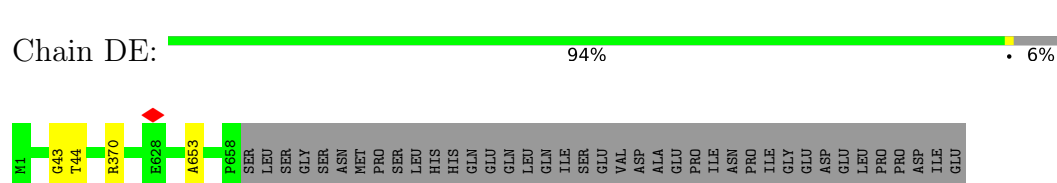
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein

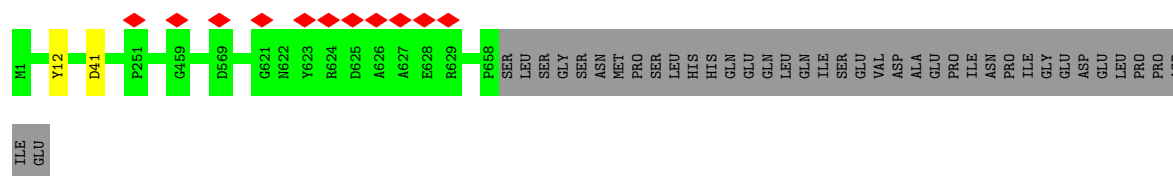


- Molecule 1: Major capsid protein



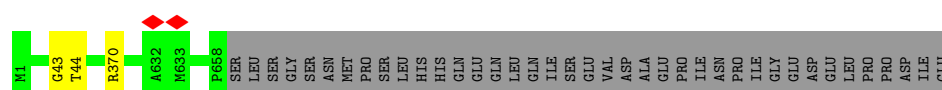
- Molecule 1: Major capsid protein

Chain DF:  94% 6%




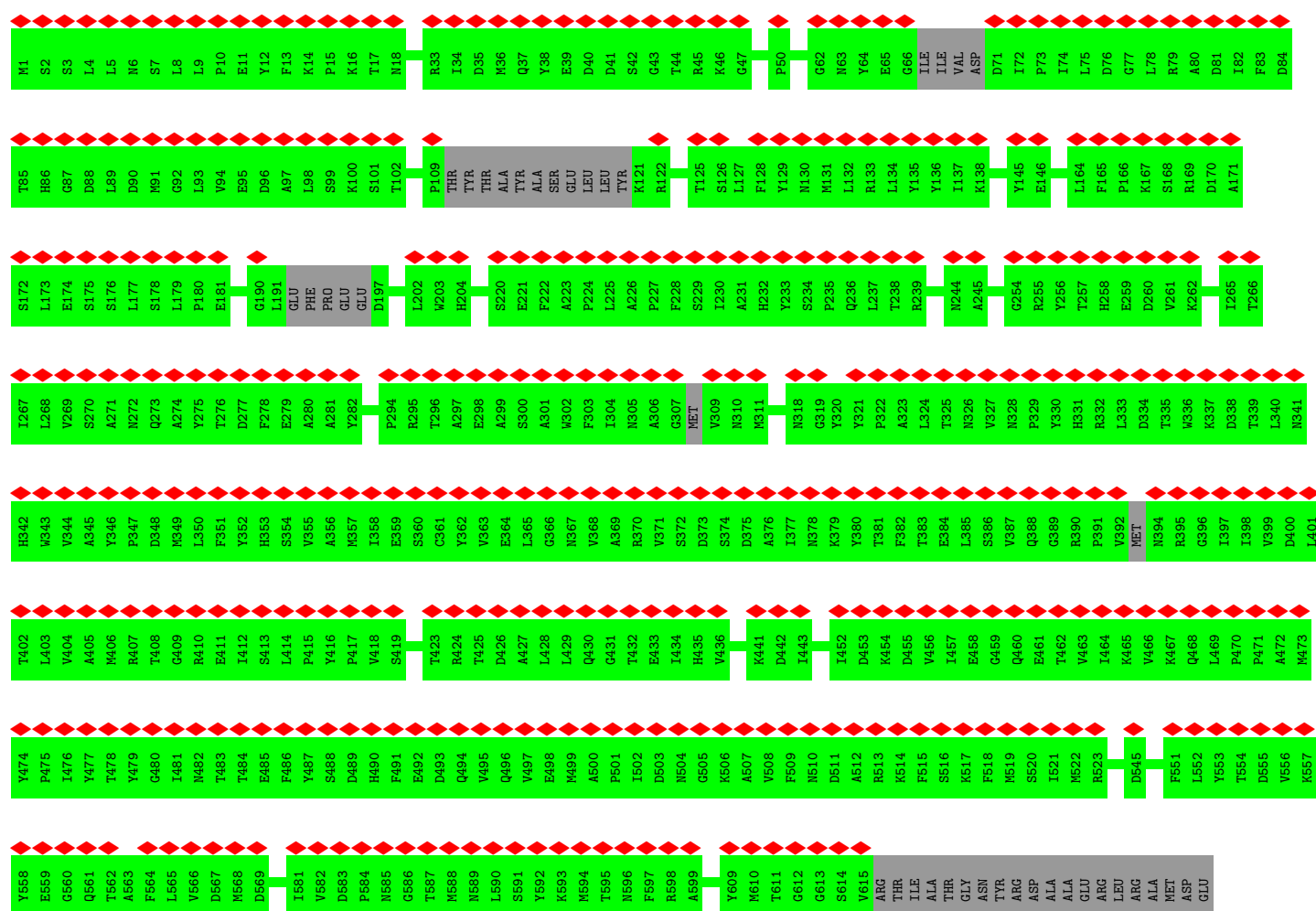
- Molecule 1: Major capsid protein

Chain DG:  94% 6%



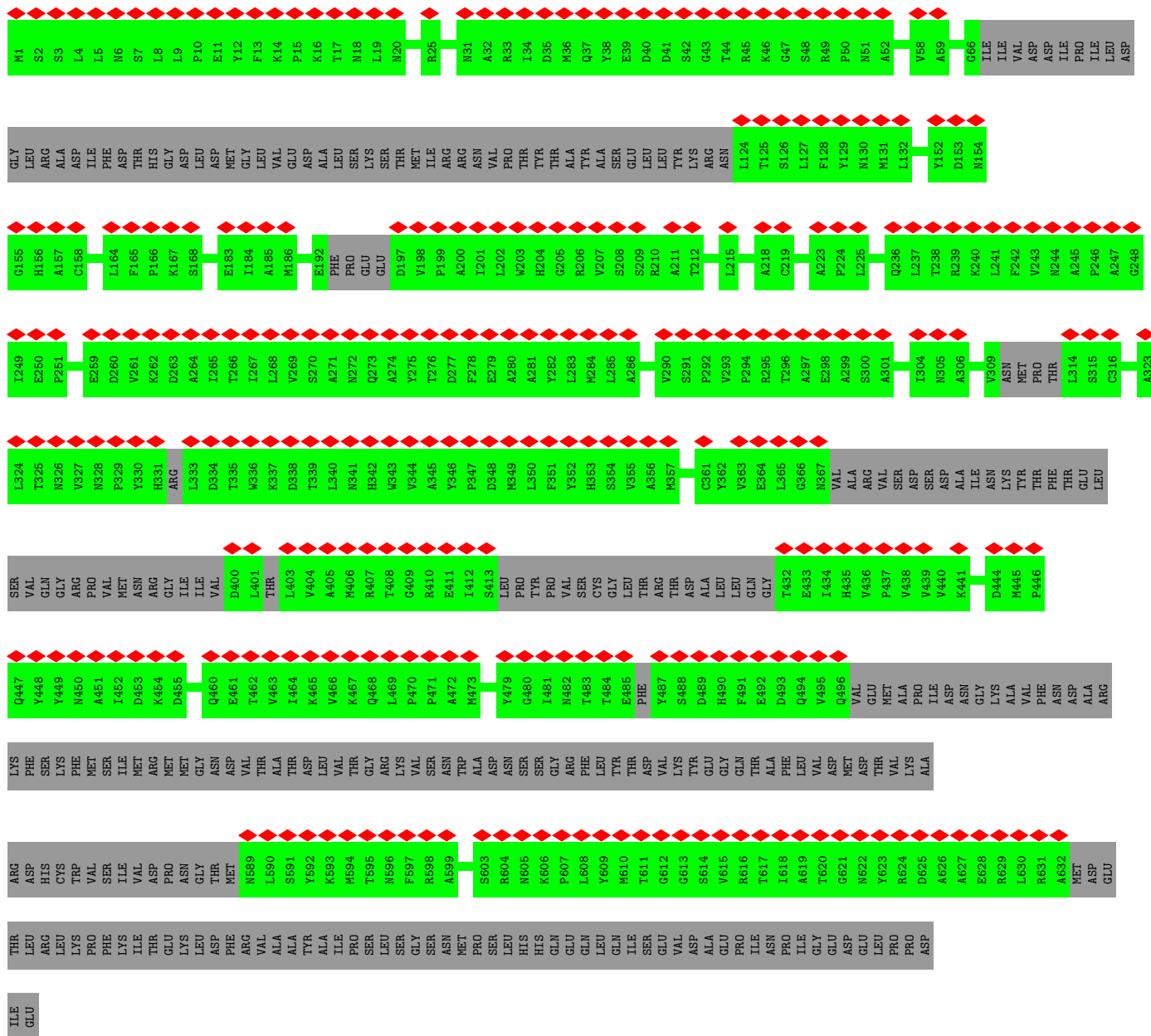
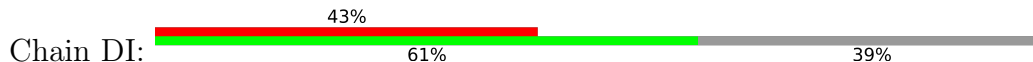
- Molecule 1: Major capsid protein

Chain DH:  59% 85% 15%

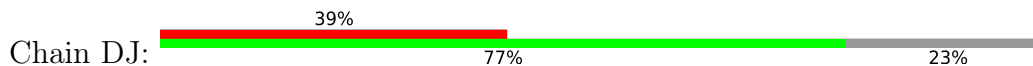


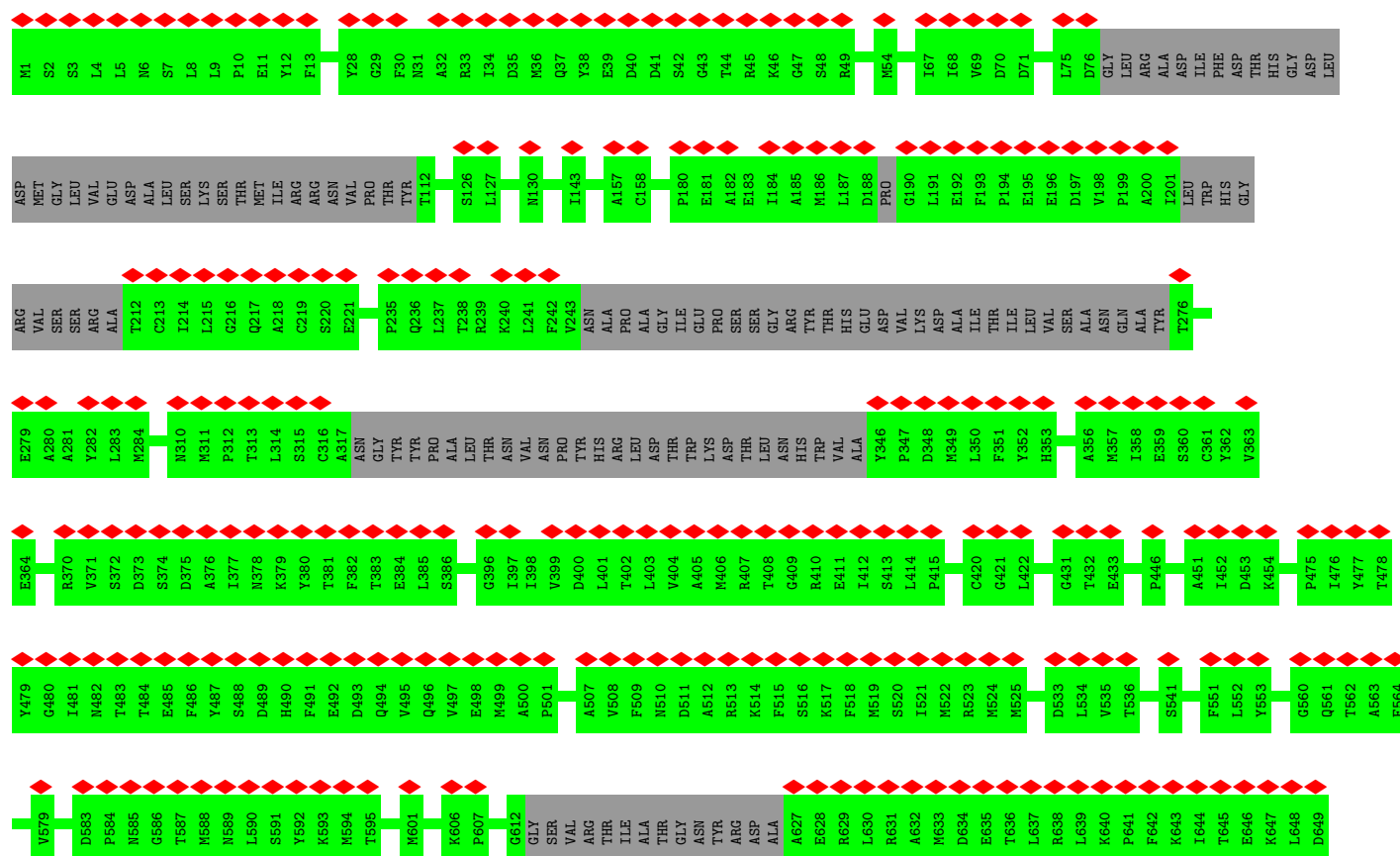
[illegible]

- Molecule 1: Major capsid protein



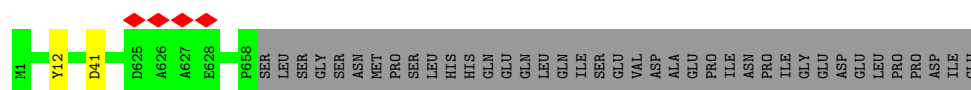
- Molecule 1: Major capsid protein





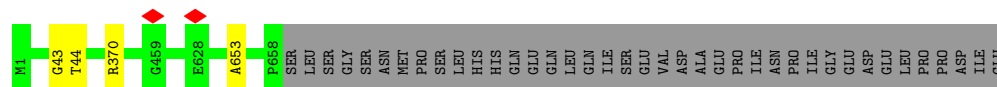
- Molecule 1: Major capsid protein

Chain DK: 94% 6%



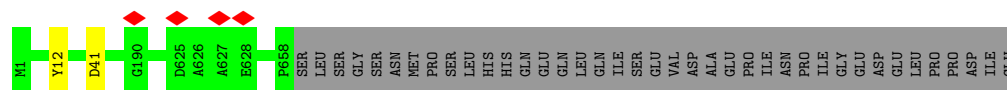
- Molecule 1: Major capsid protein

Chain DL: 94% 6%

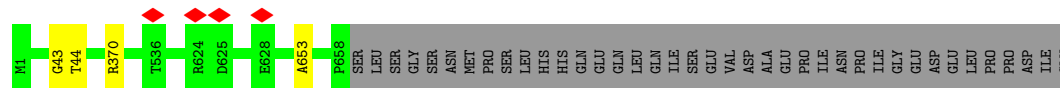


- Molecule 1: Major capsid protein

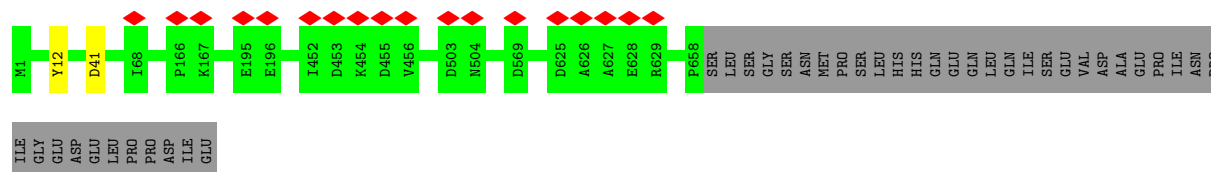
Chain DM: 94% 6%



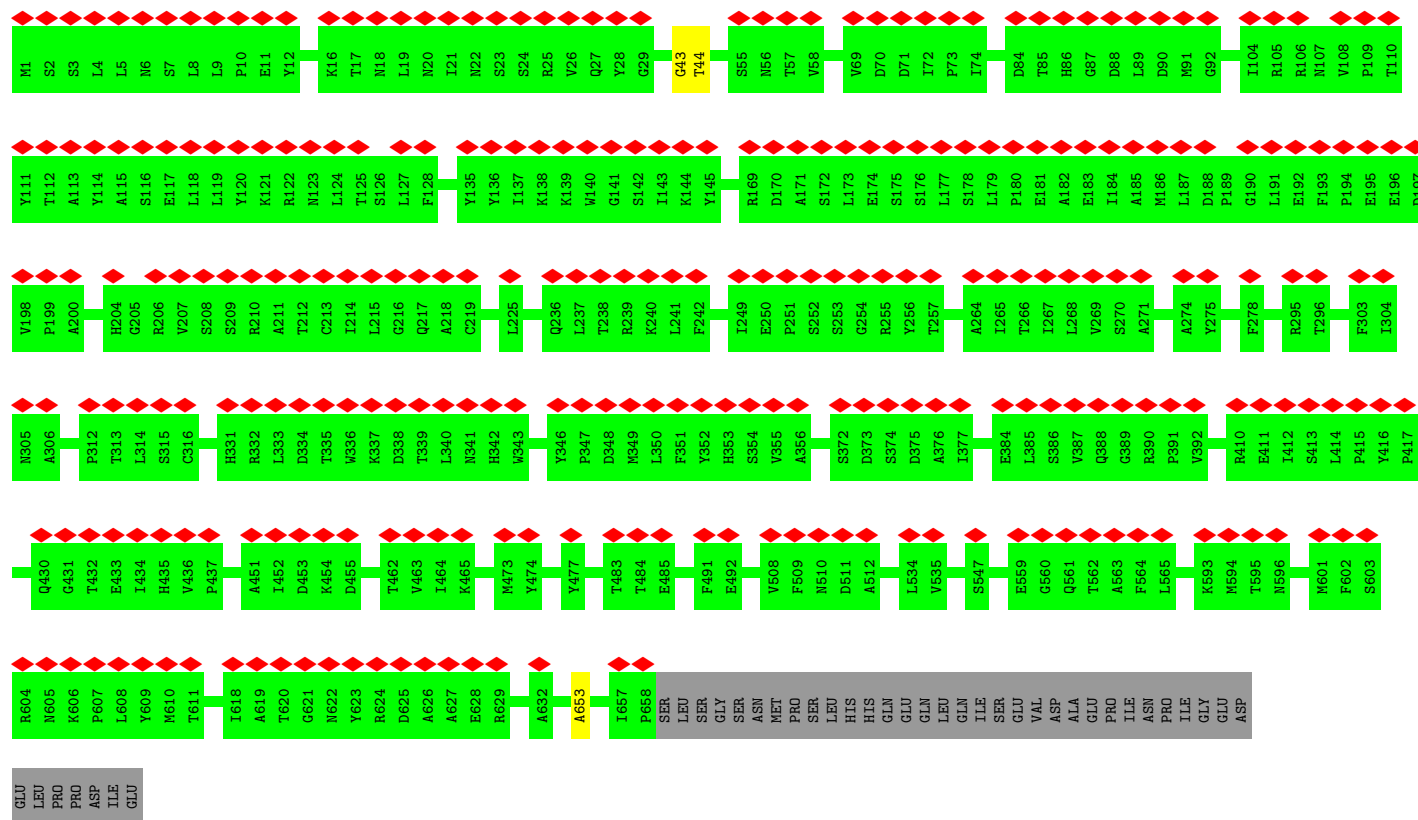
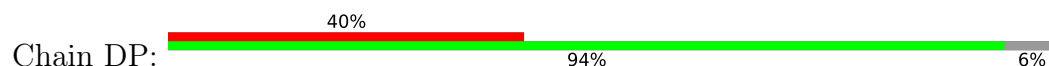
- Molecule 1: Major capsid protein



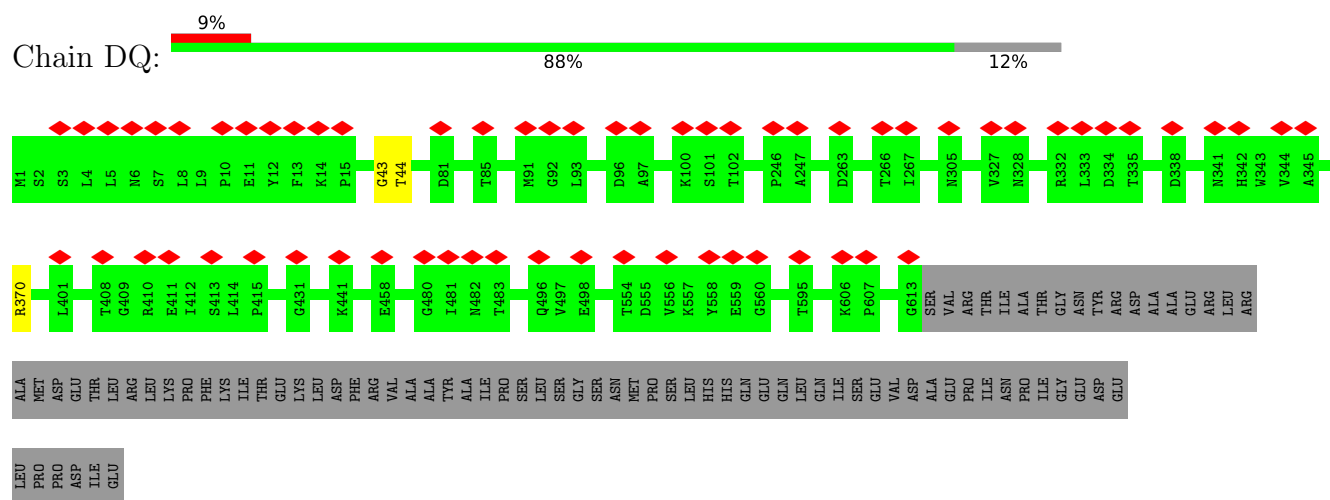
- Molecule 1: Major capsid protein



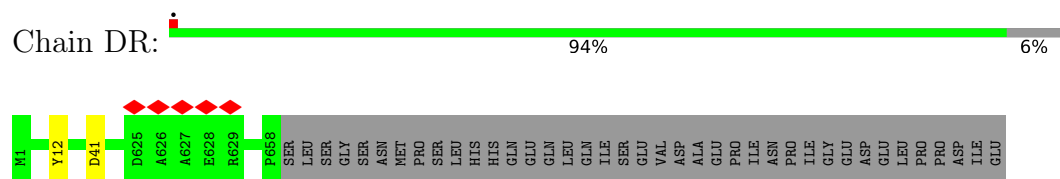
- Molecule 1: Major capsid protein



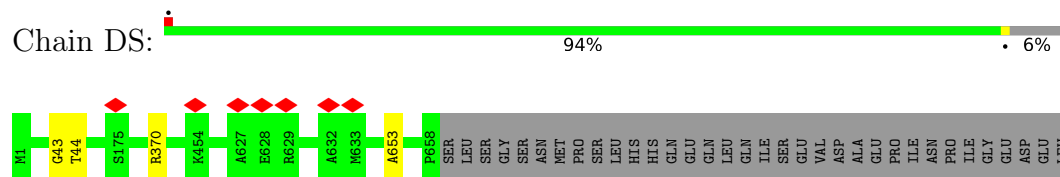
- Molecule 1: Major capsid protein



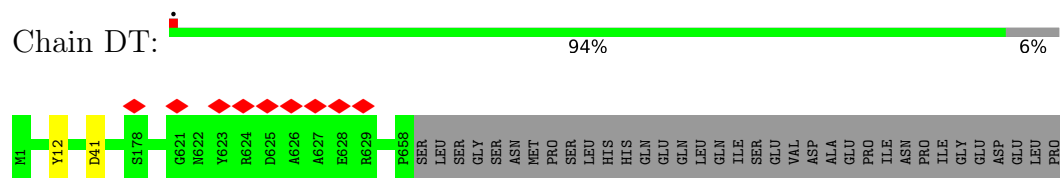
- Molecule 1: Major capsid protein



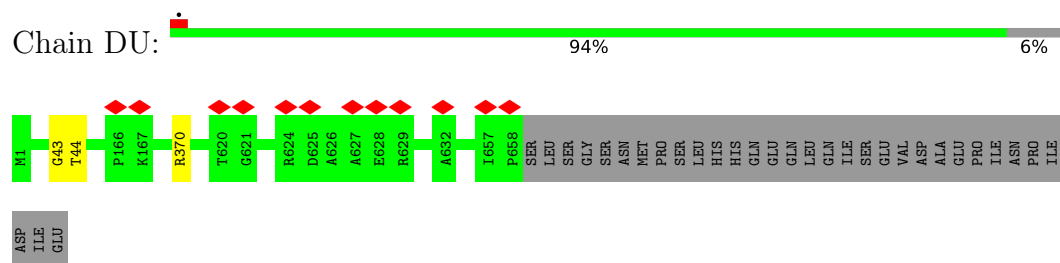
- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein



- Molecule 1: Major capsid protein



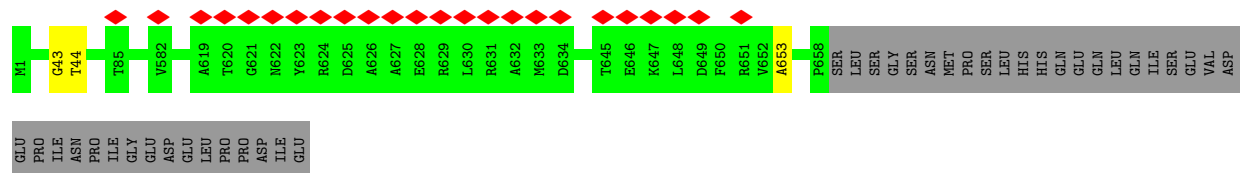
- Molecule 1: Major capsid protein





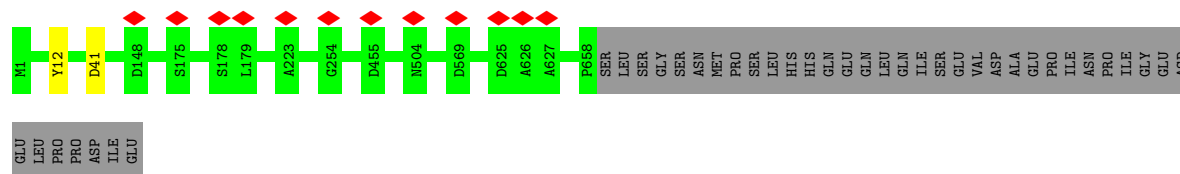
- Molecule 1: Major capsid protein

Chain DW: 94% 6%



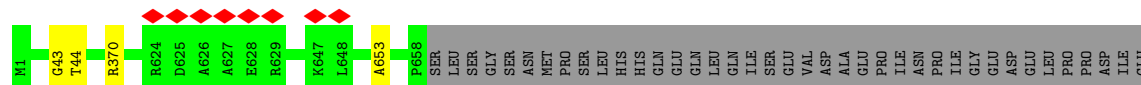
- Molecule 1: Major capsid protein

Chain DX: 94% 6%



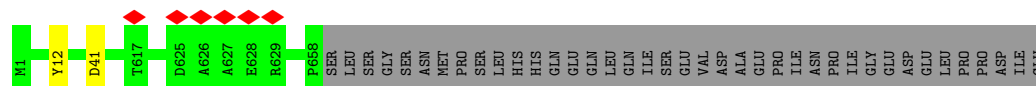
- Molecule 1: Major capsid protein

Chain DY: 94% 6%



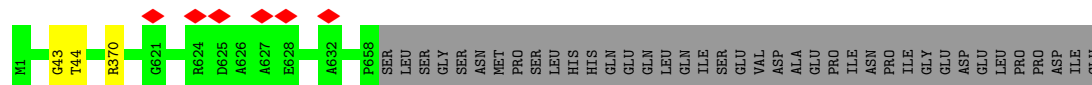
- Molecule 1: Major capsid protein

Chain DZ: 94% 6%



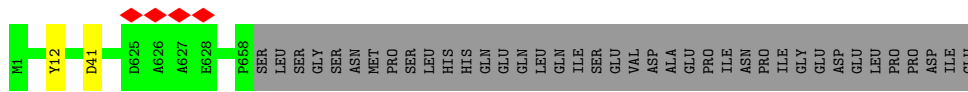
- Molecule 1: Major capsid protein

Chain EA: 94% 6%



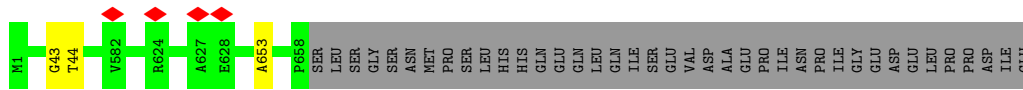
- Molecule 1: Major capsid protein

Chain EB:  94% 6%




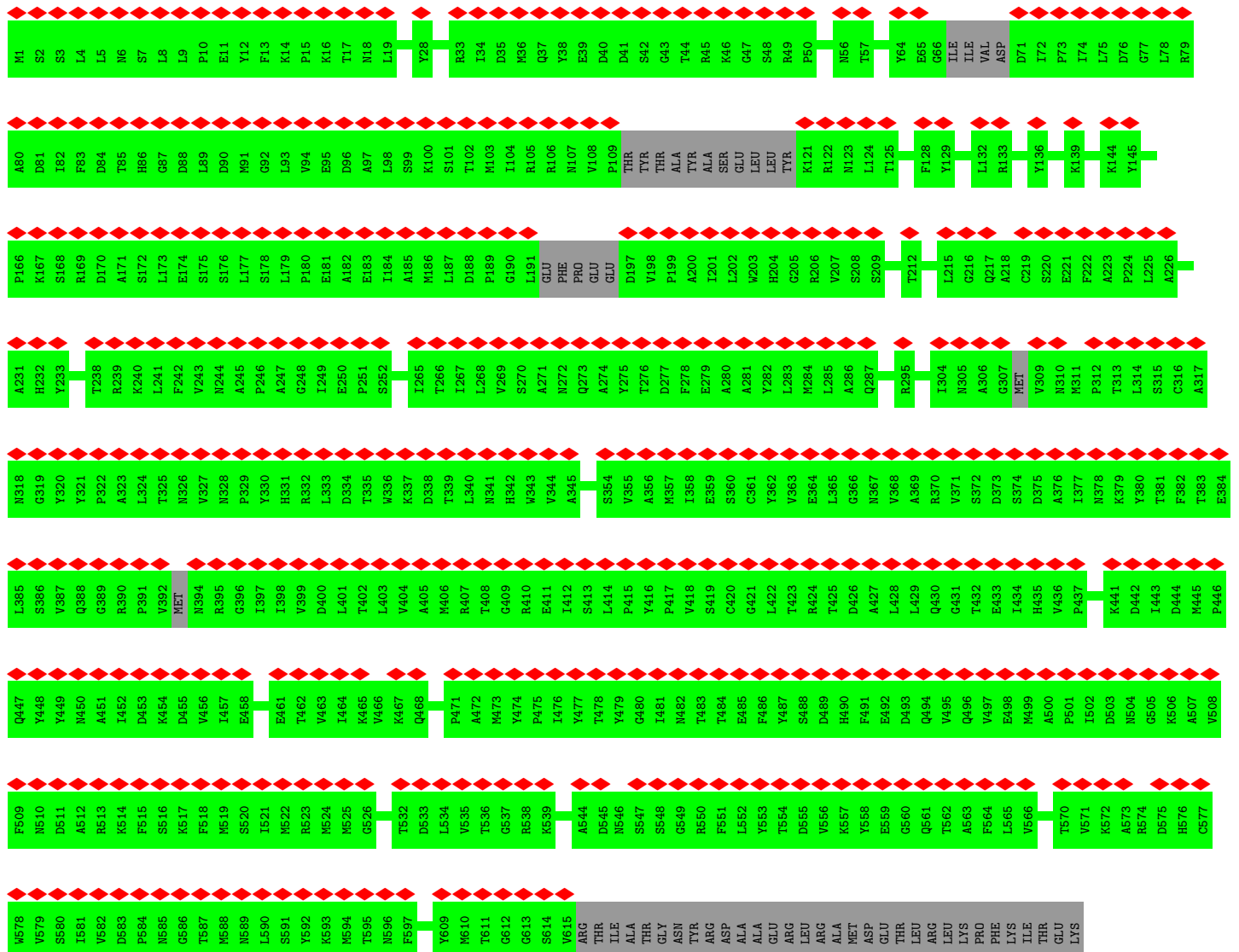
- Molecule 1: Major capsid protein

Chain EC:  94% 6%



- Molecule 1: Major capsid protein

Chain ED:  65% 85% 15%



ILE GLU	T636 L637 R638 L639 R640 P641 F642 R643 I644 T645 E646 R647 L648 D649 F650 R651 V652 A653 A654 Y655 A656 T657 F658	D583 P584 N585 G586 T587 N588 L590 S591 Y592 K593 N594 T595 N596 F597 R598 A599 A600 M601 F602 S603 M604 N605 K606 P607 L608 Y609 M610 T611 G612	GLY SER GLU VAL ASP ALA GLU PRO ASN PRO ILE GLY ASN PRO ILE GLY ASP ALA	R574 D575 H576 C577 W578 V579	D583 P584 N585 G586 T587 N588 L590 S591 Y592 K593 N594 T595 N596 F597 R598 A599 A600 M601 F602 S603 M604 N605 K606 P607 L608 Y609 M610 T611 G612	GLY SER GLU VAL ASP ALA GLU PRO ASN PRO ILE GLY ASN PRO ILE GLY ASP ALA	R574 D575 H576 C577 W578 V579	A512 R513 K514 F515 S516 K517 F518 M519 S520 I521 N522 R523 M524	D528 V529 T530 A531 T532 D533 L534 V535 T536 G537 R538 K539 V540 S541 N542 K543 A544 D545 N546 S547 S548 G549 R550 F551 L552 T553 T554 D555 V556 K557 Y558 E559 G560 Q561 T562 A563 F564 L565 V566 D567 N568 D569 T570 V571 K572 A573	I452 D453 K454 D455 V456 T457 E458 G459 Q460 E461 T462 V463 I464 A465 V466 K467 Q468 L469 P470 P471 A472 M473 Y474 P475 I476 Y477 T478 Y479 G480 T481 M482 T483 T484 E485 F486 Y487 S488 D489 H490 F491 E492 D493 Q494 V495 Q496 V497 E498 M499 A500 P501 I502 D503 N504 G505 K506 A507 V508 F509 N510 D511	V392 M393 N394 R395 G396 I397 I398 V399 D400 L401 T402 L403 V404 A405 M406 R407 T408 G409 R410 E411 I412 S413 L414 P415 Y416 P417 V418 S419 C420 G421 L422 T423 R424 T425 D426 A427 L428 L429 Q430 G431 T432 E433 I434 H435 V436 P437 V438 V439 V440 K441 D442 T443 D444 M445 P446 Q447 Y448 Y449 M450 A451	ARG LEU ASP THR LYS ASP THR LEU ASN HIS TRP VAL ALA	V346 F347 D348 M349 L350 F351 Y352 H353 S354 V355 A356 M357 I358 E359 S360 C361 V362 V363 E364 L365 G366 N367 V368 A369 R370 V371 S372 D373 D375 I377 N378 K379 Y380 T381 F382 T383 E384 L385 S386 V387 Q388 G389 R390 P391	SER ALA ASN GLN ALA TYR T276 D277 F278 E279 A280 A281 Y282 L283 M284 L285 A286 Q287 T288 L289 V290 S291 P292 V293 P294 R295 T296 A297 E298 A299 S300 A301 W302 F303 I304 N305 A306 G307 M308 V309 N310 M311 F312 T313	ASN GLY TYR TRP PRO ALA THR LEU ASN VAL ASP LYS ASP ALA ILE THR HIS GLU ASP VAL	D197 V198 P199 A200 I201	TRP HIS GLY ARG VAL SER ARG ALA T212	F222 A223 P224 L225 A226 P227 F228 S229 I230 A231	T238 R239 K240 L241 F242 V243	ASN ALA PRO ALA GLY ILE GLU PRO SER GLY ARG N310 M311 F312 T313	ASN GLY TYR TRP PRO ALA THR LEU ASN VAL ASP LYS ASP ALA ILE THR HIS GLU ASP VAL	E183 I184 A185 M186 L187 D188 PRO	G190 L191 E192 F193 P194 E195 E196	L134 Y135 Y136 I137 K138 K139 W140 G141 S142 I143 K144 Y145 E146 K147 D148 A149 I150 F151 Y152 D153 N154 G155 H156 A157 C158 L159 L160 M161 R162 Q163 L164 F165 P166 K167 S168 R169 D170 A171 S172 L173 E174 S175 S176 L177 S178	E183 I184 A185 M186 L187 D188 PRO	G190 L191 E192 F193 P194 E195 E196
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1120	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 ($e^-/\text{\AA}^2$)	36	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	130000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	8.764	Depositor
Minimum map value	-3.432	Depositor
Average map value	-0.238	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.0	Depositor
Map size (\AA)	603.97125, 603.97125, 603.97125	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07852, 1.07852, 1.07852	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.93	0/2635	0.94	0/3292
1	AB	0.93	0/2631	0.94	0/3287
1	AC	0.93	0/2635	0.94	0/3292
1	AD	0.93	0/2631	0.94	0/3287
1	AE	0.93	0/2635	0.94	0/3292
1	AF	0.93	0/2631	0.94	0/3287
1	AG	0.93	0/2451	0.94	0/3062
1	AH	0.93	0/2635	0.94	0/3292
1	AI	0.93	0/2631	0.94	0/3287
1	AJ	0.93	0/2635	0.94	0/3292
1	AK	0.93	0/2631	0.94	0/3287
1	AL	0.93	0/2635	0.94	0/3292
1	AM	0.93	0/2631	0.94	0/3287
1	AN	0.93	0/2635	0.94	0/3292
1	AO	0.93	0/2631	0.94	0/3287
1	AP	0.93	0/2635	0.94	0/3292
1	AQ	0.93	0/2631	0.94	0/3287
1	AR	0.93	0/2635	0.94	0/3292
1	AS	0.93	0/2631	0.94	0/3287
1	AT	0.93	0/2366	0.94	0/2947
1	AU	0.92	0/1682	0.94	0/2085
1	AV	0.93	0/2145	0.94	0/2669
1	AW	0.93	0/2635	0.94	0/3292
1	AX	0.93	0/2631	0.94	0/3287
1	AY	0.93	0/2635	0.94	0/3292
1	AZ	0.93	0/2631	0.94	0/3287
1	BA	0.93	0/2635	0.94	0/3292
1	BB	0.93	0/2631	0.94	0/3287
1	BC	0.93	0/2451	0.94	0/3062
1	BD	0.93	0/2635	0.94	0/3292
1	BE	0.93	0/2631	0.94	0/3287
1	BF	0.93	0/2635	0.94	0/3292
1	BG	0.93	0/2631	0.94	0/3287
1	BH	0.93	0/2635	0.94	0/3292

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.93	0/2631	0.94	0/3287
1	BJ	0.93	0/2635	0.94	0/3292
1	BK	0.93	0/2631	0.94	0/3287
1	BL	0.93	0/2635	0.94	0/3292
1	BM	0.93	0/2631	0.94	0/3287
1	BN	0.93	0/2635	0.94	0/3292
1	BO	0.93	0/2631	0.94	0/3287
1	BP	0.93	0/2366	0.94	0/2947
1	BQ	0.92	0/1682	0.94	0/2085
1	BR	0.93	0/2145	0.94	0/2669
1	BS	0.93	0/2635	0.94	0/3292
1	BT	0.93	0/2631	0.94	0/3287
1	BU	0.93	0/2635	0.94	0/3292
1	BV	0.93	0/2631	0.94	0/3287
1	BW	0.93	0/2635	0.94	0/3292
1	BX	0.93	0/2631	0.94	0/3287
1	BY	0.93	0/2451	0.94	0/3062
1	BZ	0.93	0/2635	0.94	0/3292
1	CA	0.93	0/2631	0.94	0/3287
1	CB	0.93	0/2635	0.94	0/3292
1	CC	0.93	0/2631	0.94	0/3287
1	CD	0.93	0/2635	0.94	0/3292
1	CE	0.93	0/2631	0.94	0/3287
1	CF	0.93	0/2635	0.94	0/3292
1	CG	0.93	0/2631	0.94	0/3287
1	CH	0.93	0/2635	0.94	0/3292
1	CI	0.93	0/2631	0.94	0/3287
1	CJ	0.93	0/2635	0.94	0/3292
1	CK	0.93	0/2631	0.94	0/3287
1	CL	0.93	0/2366	0.94	0/2947
1	CM	0.92	0/1682	0.94	0/2085
1	CN	0.93	0/2145	0.94	0/2669
1	CO	0.93	0/2635	0.94	0/3292
1	CP	0.93	0/2631	0.94	0/3287
1	CQ	0.93	0/2635	0.94	0/3292
1	CR	0.93	0/2631	0.94	0/3287
1	CS	0.93	0/2635	0.94	0/3292
1	CT	0.93	0/2631	0.94	0/3287
1	CU	0.93	0/2451	0.94	0/3062
1	CV	0.93	0/2635	0.94	0/3292
1	CW	0.93	0/2631	0.94	0/3287
1	CX	0.93	0/2635	0.94	0/3292
1	CY	0.93	0/2631	0.94	0/3287

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CZ	0.93	0/2635	0.94	0/3292
1	DA	0.93	0/2631	0.94	0/3287
1	DB	0.93	0/2635	0.94	0/3292
1	DC	0.93	0/2631	0.94	0/3287
1	DD	0.93	0/2635	0.94	0/3292
1	DE	0.93	0/2631	0.94	0/3287
1	DF	0.93	0/2635	0.94	0/3292
1	DG	0.93	0/2631	0.94	0/3287
1	DH	0.93	0/2366	0.94	0/2947
1	DI	0.92	0/1682	0.94	0/2085
1	DJ	0.93	0/2145	0.94	0/2669
1	DK	0.92	0/2635	0.94	0/3292
1	DL	0.93	0/2631	0.94	0/3287
1	DM	0.93	0/2635	0.94	0/3292
1	DN	0.93	0/2631	0.94	0/3287
1	DO	0.93	0/2635	0.94	0/3292
1	DP	0.93	0/2631	0.94	0/3287
1	DQ	0.93	0/2451	0.94	0/3062
1	DR	0.93	0/2635	0.94	0/3292
1	DS	0.93	0/2631	0.94	0/3287
1	DT	0.93	0/2635	0.94	0/3292
1	DU	0.93	0/2631	0.94	0/3287
1	DV	0.93	0/2635	0.94	0/3292
1	DW	0.93	0/2631	0.94	0/3287
1	DX	0.93	0/2635	0.94	0/3292
1	DY	0.93	0/2631	0.94	0/3287
1	DZ	0.93	0/2635	0.94	0/3292
1	EA	0.93	0/2631	0.94	0/3287
1	EB	0.93	0/2635	0.94	0/3292
1	EC	0.93	0/2631	0.94	0/3287
1	ED	0.93	0/2366	0.94	0/2947
1	EE	0.92	0/1682	0.94	0/2085
1	EF	0.93	0/2145	0.94	0/2669
All	All	0.93	0/280190	0.94	0/349870

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

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	AA	2636	0	696	2	0
1	AB	2632	0	694	4	0
1	AC	2636	0	696	2	0
1	AD	2632	0	694	4	0
1	AE	2636	0	696	2	0
1	AF	2632	0	694	3	0
1	AG	2452	0	649	2	0
1	AH	2636	0	696	2	0
1	AI	2632	0	694	4	0
1	AJ	2636	0	696	2	0
1	AK	2632	0	694	4	0
1	AL	2636	0	696	2	0
1	AM	2632	0	694	3	0
1	AN	2636	0	696	2	0
1	AO	2632	0	694	4	0
1	AP	2636	0	696	2	0
1	AQ	2632	0	694	4	0
1	AR	2636	0	696	2	0
1	AS	2632	0	694	4	0
1	AT	2372	0	625	0	0
1	AU	1692	0	436	0	0
1	AV	2152	0	556	0	0
1	AW	2636	0	696	2	0
1	AX	2632	0	694	3	0
1	AY	2636	0	696	2	0
1	AZ	2632	0	694	4	0
1	BA	2636	0	696	2	0
1	BB	2632	0	694	3	0
1	BC	2452	0	649	3	0
1	BD	2636	0	696	2	0
1	BE	2632	0	694	4	0
1	BF	2636	0	696	2	0
1	BG	2632	0	694	4	0
1	BH	2636	0	696	2	0
1	BI	2632	0	694	4	0
1	BJ	2636	0	696	2	0
1	BK	2632	0	694	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BL	2636	0	696	2	0
1	BM	2632	0	694	3	0
1	BN	2636	0	696	2	0
1	BO	2632	0	694	3	0
1	BP	2372	0	625	0	0
1	BQ	1692	0	436	0	0
1	BR	2152	0	556	0	0
1	BS	2636	0	696	2	0
1	BT	2632	0	694	2	0
1	BU	2636	0	696	2	0
1	BV	2632	0	694	4	0
1	BW	2636	0	696	2	0
1	BX	2632	0	694	3	0
1	BY	2452	0	649	3	0
1	BZ	2636	0	696	2	0
1	CA	2632	0	694	4	0
1	CB	2636	0	696	2	0
1	CC	2632	0	694	4	0
1	CD	2636	0	696	2	0
1	CE	2632	0	694	4	0
1	CF	2636	0	696	2	0
1	CG	2632	0	694	4	0
1	CH	2636	0	696	2	0
1	CI	2632	0	694	4	0
1	CJ	2636	0	696	2	0
1	CK	2632	0	694	4	0
1	CL	2372	0	625	0	0
1	CM	1692	0	436	0	0
1	CN	2152	0	556	0	0
1	CO	2636	0	696	2	0
1	CP	2632	0	694	3	0
1	CQ	2636	0	696	2	0
1	CR	2632	0	694	4	0
1	CS	2636	0	696	2	0
1	CT	2632	0	694	3	0
1	CU	2452	0	649	3	0
1	CV	2636	0	696	2	0
1	CW	2632	0	694	4	0
1	CX	2636	0	696	2	0
1	CY	2632	0	694	4	0
1	CZ	2636	0	696	2	0
1	DA	2632	0	694	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DB	2636	0	696	2	0
1	DC	2632	0	694	3	0
1	DD	2636	0	696	2	0
1	DE	2632	0	694	4	0
1	DF	2636	0	696	2	0
1	DG	2632	0	694	3	0
1	DH	2372	0	625	0	0
1	DI	1692	0	436	0	0
1	DJ	2152	0	556	0	0
1	DK	2636	0	696	2	0
1	DL	2632	0	694	4	0
1	DM	2636	0	696	2	0
1	DN	2632	0	694	4	0
1	DO	2636	0	696	2	0
1	DP	2632	0	694	3	0
1	DQ	2452	0	649	3	0
1	DR	2636	0	696	2	0
1	DS	2632	0	694	4	0
1	DT	2636	0	696	2	0
1	DU	2632	0	694	3	0
1	DV	2636	0	696	2	0
1	DW	2632	0	694	3	0
1	DX	2636	0	696	2	0
1	DY	2632	0	694	4	0
1	DZ	2636	0	696	2	0
1	EA	2632	0	694	3	0
1	EB	2636	0	696	2	0
1	EC	2632	0	694	3	0
1	ED	2372	0	625	0	0
1	EE	1692	0	436	0	0
1	EF	2152	0	556	0	0
All	All	280400	0	73880	133	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 0.

All (133) 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:AZ:43:GLY:HA3	1:CK:44:THR:O	2.04	0.58
1:AK:43:GLY:HA3	1:AO:44:THR:O	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AS:44:THR:O	1:CR:43:GLY:HA3	2.04	0.57
1:BC:43:GLY:HA3	1:DP:44:THR:O	2.04	0.57
1:DL:43:GLY:HA3	1:EA:44:THR:O	2.04	0.57
1:AB:43:GLY:HA3	1:AQ:44:THR:O	2.04	0.57
1:AF:43:GLY:HA3	1:DQ:44:THR:O	2.04	0.57
1:AI:44:THR:O	1:DW:43:GLY:HA3	2.05	0.57
1:AK:44:THR:O	1:AO:43:GLY:HA3	2.05	0.57
1:AX:44:THR:O	1:BM:43:GLY:HA3	2.04	0.57
1:AZ:44:THR:O	1:CK:43:GLY:HA3	2.05	0.57
1:CA:44:THR:O	1:DA:43:GLY:HA3	2.05	0.57
1:AI:43:GLY:HA3	1:DW:44:THR:O	2.05	0.57
1:BE:43:GLY:HA3	1:CE:44:THR:O	2.05	0.57
1:BI:43:GLY:HA3	1:DS:44:THR:O	2.04	0.57
1:BX:43:GLY:HA3	1:CU:44:THR:O	2.05	0.57
1:BO:43:GLY:HA3	1:DN:44:THR:O	2.05	0.57
1:BV:44:THR:O	1:DG:43:GLY:HA3	2.05	0.57
1:AG:43:GLY:HA3	1:CT:44:THR:O	2.04	0.57
1:AX:43:GLY:HA3	1:BM:44:THR:O	2.05	0.57
1:BB:44:THR:O	1:BY:43:GLY:HA3	2.04	0.57
1:BI:44:THR:O	1:DS:43:GLY:HA3	2.04	0.57
1:BT:44:THR:O	1:CI:43:GLY:HA3	2.05	0.57
1:CA:43:GLY:HA3	1:DA:44:THR:O	2.04	0.57
1:AD:44:THR:O	1:EC:43:GLY:HA3	2.04	0.57
1:AM:44:THR:O	1:CW:43:GLY:HA3	2.04	0.57
1:BX:44:THR:O	1:CU:43:GLY:HA3	2.04	0.57
1:CC:44:THR:O	1:CG:43:GLY:HA3	2.05	0.57
1:CP:43:GLY:HA3	1:DE:44:THR:O	2.04	0.57
1:DU:43:GLY:HA3	1:DY:44:THR:O	2.05	0.57
1:DU:44:THR:O	1:DY:43:GLY:HA3	2.04	0.57
1:AG:44:THR:O	1:CT:43:GLY:HA3	2.05	0.57
1:BC:44:THR:O	1:DP:43:GLY:HA3	2.04	0.57
1:BV:43:GLY:HA3	1:DG:44:THR:O	2.04	0.57
1:BG:43:GLY:HA3	1:BK:44:THR:O	2.05	0.56
1:AM:43:GLY:HA3	1:CW:44:THR:O	2.04	0.56
1:AS:43:GLY:HA3	1:CR:44:THR:O	2.05	0.56
1:BO:44:THR:O	1:DN:43:GLY:HA3	2.04	0.56
1:BT:43:GLY:HA3	1:CI:44:THR:O	2.04	0.56
1:AB:44:THR:O	1:AQ:43:GLY:HA3	2.04	0.56
1:BE:44:THR:O	1:CE:43:GLY:HA3	2.05	0.56
1:CC:43:GLY:HA3	1:CG:44:THR:O	2.05	0.56
1:CP:44:THR:O	1:DE:43:GLY:HA3	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DL:44:THR:O	1:EA:43:GLY:HA3	2.04	0.56
1:CY:44:THR:O	1:DC:43:GLY:HA3	2.05	0.56
1:AF:44:THR:O	1:DQ:43:GLY:HA3	2.04	0.56
1:BB:43:GLY:HA3	1:BY:44:THR:O	2.04	0.56
1:CY:43:GLY:HA3	1:DC:44:THR:O	2.05	0.56
1:AD:43:GLY:HA3	1:EC:44:THR:O	2.04	0.56
1:BG:44:THR:O	1:BK:43:GLY:HA3	2.05	0.56
1:CG:370:ARG:O	1:CK:653:ALA:N	2.44	0.47
1:AO:370:ARG:O	1:AS:653:ALA:N	2.44	0.47
1:CF:12:TYR:O	1:CZ:41:ASP:O	2.34	0.46
1:AA:12:TYR:O	1:DZ:41:ASP:O	2.34	0.46
1:AH:12:TYR:O	1:EB:41:ASP:O	2.34	0.46
1:AB:370:ARG:O	1:CP:653:ALA:N	2.44	0.46
1:AE:41:ASP:O	1:DV:12:TYR:O	2.34	0.46
1:CS:12:TYR:O	1:DB:41:ASP:O	2.34	0.46
1:AE:12:TYR:O	1:AN:41:ASP:O	2.34	0.46
1:AP:41:ASP:O	1:CO:12:TYR:O	2.34	0.46
1:BF:12:TYR:O	1:DR:41:ASP:O	2.34	0.46
1:BX:653:ALA:N	1:CC:370:ARG:O	2.44	0.46
1:DT:41:ASP:O	1:EB:12:TYR:O	2.34	0.46
1:AA:41:ASP:O	1:AC:12:TYR:O	2.34	0.46
1:BF:41:ASP:O	1:BN:12:TYR:O	2.34	0.46
1:AC:41:ASP:O	1:DZ:12:TYR:O	2.34	0.46
1:BN:41:ASP:O	1:DR:12:TYR:O	2.34	0.46
1:DK:41:ASP:O	1:DM:12:TYR:O	2.34	0.46
1:BJ:12:TYR:O	1:CD:41:ASP:O	2.34	0.46
1:AD:370:ARG:O	1:AI:653:ALA:N	2.44	0.46
1:AL:41:ASP:O	1:DB:12:TYR:O	2.34	0.46
1:BD:41:ASP:O	1:CB:12:TYR:O	2.34	0.46
1:BL:41:ASP:O	1:DK:12:TYR:O	2.34	0.46
1:BU:41:ASP:O	1:DD:12:TYR:O	2.34	0.46
1:AJ:41:ASP:O	1:AR:12:TYR:O	2.34	0.46
1:AP:12:TYR:O	1:CQ:41:ASP:O	2.34	0.46
1:AY:41:ASP:O	1:CH:12:TYR:O	2.34	0.46
1:BW:12:TYR:O	1:CF:41:ASP:O	2.34	0.46
1:BW:41:ASP:O	1:CZ:12:TYR:O	2.34	0.46
1:CW:370:ARG:O	1:DC:653:ALA:N	2.44	0.46
1:DO:12:TYR:O	1:DX:41:ASP:O	2.33	0.46
1:AX:370:ARG:O	1:DL:653:ALA:N	2.44	0.45
1:AK:653:ALA:N	1:AM:370:ARG:O	2.44	0.45
1:AL:12:TYR:O	1:CS:41:ASP:O	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BD:12:TYR:O	1:CJ:41:ASP:O	2.34	0.45
1:BL:12:TYR:O	1:DM:41:ASP:O	2.34	0.45
1:BY:370:ARG:O	1:CE:653:ALA:N	2.44	0.45
1:DN:370:ARG:O	1:DS:653:ALA:N	2.44	0.45
1:AH:41:ASP:O	1:DT:12:TYR:O	2.34	0.45
1:AI:370:ARG:O	1:AO:653:ALA:N	2.44	0.45
1:BA:12:TYR:O	1:BJ:41:ASP:O	2.34	0.45
1:AJ:12:TYR:O	1:CV:41:ASP:O	2.34	0.45
1:AW:41:ASP:O	1:AY:12:TYR:O	2.34	0.45
1:AZ:653:ALA:N	1:BM:370:ARG:O	2.44	0.45
1:BS:12:TYR:O	1:DD:41:ASP:O	2.34	0.45
1:CB:41:ASP:O	1:CJ:12:TYR:O	2.34	0.45
1:CU:370:ARG:O	1:DA:653:ALA:N	2.44	0.45
1:CX:41:ASP:O	1:DF:12:TYR:O	2.34	0.45
1:AD:653:ALA:N	1:AQ:370:ARG:O	2.44	0.45
1:BH:12:TYR:O	1:DO:41:ASP:O	2.34	0.45
1:BS:41:ASP:O	1:BU:12:TYR:O	2.34	0.45
1:BZ:12:TYR:O	1:DF:41:ASP:O	2.34	0.45
1:AW:12:TYR:O	1:CH:41:ASP:O	2.34	0.45
1:BH:41:ASP:O	1:DX:12:TYR:O	2.34	0.45
1:CO:41:ASP:O	1:CQ:12:TYR:O	2.34	0.45
1:AR:41:ASP:O	1:CV:12:TYR:O	2.34	0.45
1:BZ:41:ASP:O	1:CX:12:TYR:O	2.34	0.45
1:DP:653:ALA:N	1:DU:370:ARG:O	2.44	0.45
1:BA:41:ASP:O	1:CD:12:TYR:O	2.34	0.44
1:BV:653:ALA:N	1:CI:370:ARG:O	2.44	0.44
1:CY:653:ALA:N	1:DA:370:ARG:O	2.44	0.44
1:DE:653:ALA:N	1:DG:370:ARG:O	2.44	0.44
1:BG:653:ALA:N	1:BI:370:ARG:O	2.44	0.44
1:BK:370:ARG:O	1:BO:653:ALA:N	2.44	0.44
1:CT:653:ALA:N	1:CY:370:ARG:O	2.44	0.44
1:AF:653:ALA:N	1:AK:370:ARG:O	2.44	0.44
1:AB:653:ALA:N	1:DL:370:ARG:O	2.44	0.44
1:CI:653:ALA:N	1:CK:370:ARG:O	2.44	0.44
1:AN:12:TYR:O	1:DV:41:ASP:O	2.34	0.44
1:BC:370:ARG:O	1:BI:653:ALA:N	2.44	0.44
1:CC:653:ALA:N	1:CE:370:ARG:O	2.44	0.43
1:AQ:653:ALA:N	1:AS:370:ARG:O	2.44	0.43
1:DS:370:ARG:O	1:DY:653:ALA:N	2.44	0.43
1:DY:370:ARG:O	1:EC:653:ALA:N	2.44	0.43
1:DQ:370:ARG:O	1:DW:653:ALA:N	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CR:370:ARG:O	1:CW:653:ALA:N	2.44	0.42
1:BV:370:ARG:O	1:CA:653:ALA:N	2.44	0.42
1:CR:653:ALA:N	1:DE:370:ARG:O	2.44	0.42
1:BE:370:ARG:O	1:BK:653:ALA:N	2.44	0.42
1:DN:653:ALA:N	1:EA:370:ARG:O	2.44	0.41
1:AZ:370:ARG:O	1:BE:653:ALA:N	2.44	0.41
1:CA:370:ARG:O	1:CG:653:ALA:N	2.44	0.40
1:BB:653:ALA:N	1:BG:370:ARG:O	2.44	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AB	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	AC	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AD	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	AE	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AF	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	AG	611/697 (88%)	566 (93%)	45 (7%)	0	100	100
1	AH	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AI	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	AJ	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AK	656/697 (94%)	604 (92%)	52 (8%)	0	100	100
1	AL	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AM	656/697 (94%)	603 (92%)	53 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AN	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AO	656/697 (94%)	604 (92%)	52 (8%)	0	100	100
1	AP	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AQ	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	AR	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AS	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	AT	581/697 (83%)	538 (93%)	43 (7%)	0	100	100
1	AU	403/697 (58%)	376 (93%)	27 (7%)	0	100	100
1	AV	524/697 (75%)	489 (93%)	35 (7%)	0	100	100
1	AW	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AX	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	AY	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	AZ	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	BA	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	BB	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	BC	611/697 (88%)	566 (93%)	45 (7%)	0	100	100
1	BD	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	BE	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	BF	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	BG	656/697 (94%)	604 (92%)	52 (8%)	0	100	100
1	BH	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	BI	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	BJ	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	BK	656/697 (94%)	604 (92%)	52 (8%)	0	100	100
1	BL	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	BM	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	BN	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	BO	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	BP	581/697 (83%)	538 (93%)	43 (7%)	0	100	100
1	BQ	403/697 (58%)	376 (93%)	27 (7%)	0	100	100
1	BR	524/697 (75%)	489 (93%)	35 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BS	657/697 (94%)	613 (93%)	44 (7%)	0	100	100
1	BT	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	BU	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	BV	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	BW	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	BX	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	BY	611/697 (88%)	566 (93%)	45 (7%)	0	100	100
1	BZ	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	CA	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	CB	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	CC	656/697 (94%)	604 (92%)	52 (8%)	0	100	100
1	CD	657/697 (94%)	613 (93%)	44 (7%)	0	100	100
1	CE	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	CF	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	CG	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	CH	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	CI	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	CJ	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	CK	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	CL	581/697 (83%)	538 (93%)	43 (7%)	0	100	100
1	CM	403/697 (58%)	376 (93%)	27 (7%)	0	100	100
1	CN	524/697 (75%)	489 (93%)	35 (7%)	0	100	100
1	CO	657/697 (94%)	613 (93%)	44 (7%)	0	100	100
1	CP	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	CQ	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	CR	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	CS	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	CT	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	CU	611/697 (88%)	566 (93%)	45 (7%)	0	100	100
1	CV	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	CW	656/697 (94%)	603 (92%)	53 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CX	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	CY	656/697 (94%)	604 (92%)	52 (8%)	0	100	100
1	CZ	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DA	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	DB	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DC	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	DD	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DE	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	DF	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DG	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	DH	581/697 (83%)	538 (93%)	43 (7%)	0	100	100
1	DI	403/697 (58%)	376 (93%)	27 (7%)	0	100	100
1	DJ	524/697 (75%)	489 (93%)	35 (7%)	0	100	100
1	DK	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DL	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	DM	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DN	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	DO	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DP	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	DQ	611/697 (88%)	566 (93%)	45 (7%)	0	100	100
1	DR	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DS	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	DT	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DU	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	DV	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DW	656/697 (94%)	604 (92%)	52 (8%)	0	100	100
1	DX	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	DY	656/697 (94%)	604 (92%)	52 (8%)	0	100	100
1	DZ	657/697 (94%)	614 (94%)	43 (6%)	0	100	100
1	EA	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	EB	657/697 (94%)	614 (94%)	43 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EC	656/697 (94%)	603 (92%)	53 (8%)	0	100	100
1	ED	581/697 (83%)	538 (93%)	43 (7%)	0	100	100
1	EE	403/697 (58%)	376 (93%)	27 (7%)	0	100	100
1	EF	524/697 (75%)	489 (93%)	35 (7%)	0	100	100
All	All	69680/76670 (91%)	64615 (93%)	5065 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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.

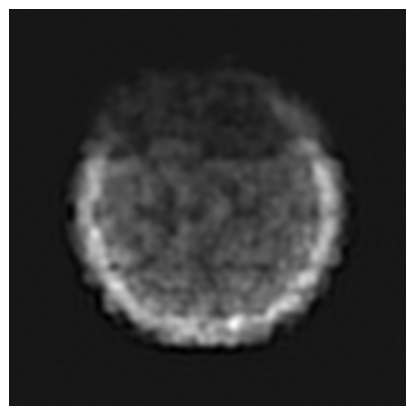
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-14963. These allow visual inspection of the internal detail of the map and identification of artifacts.

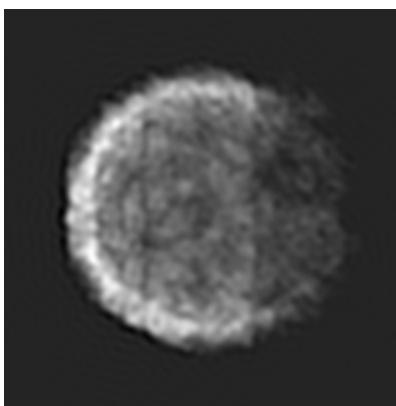
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

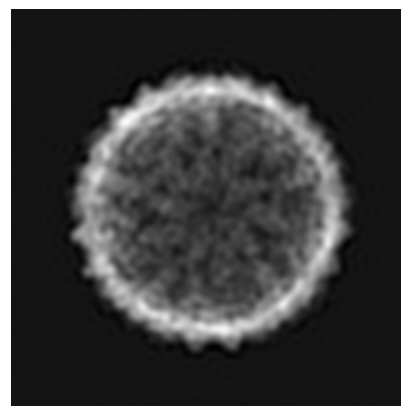
6.1.1 Primary map



X

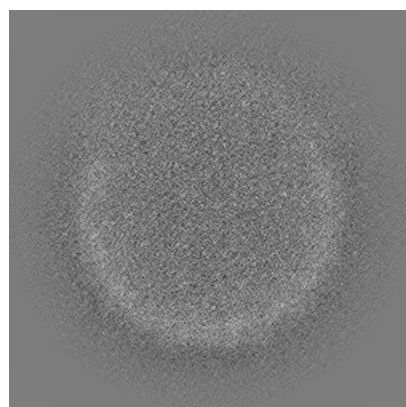


Y

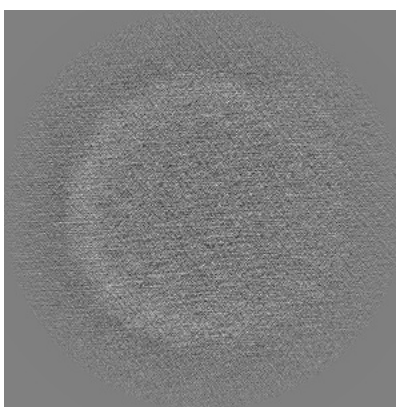


Z

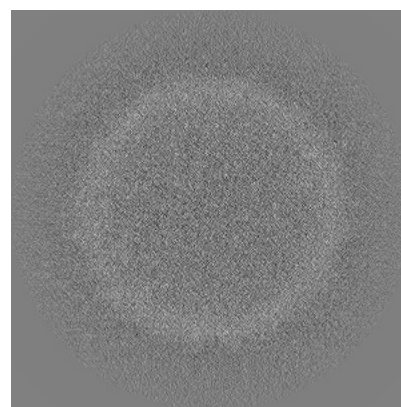
6.1.2 Raw map



X



Y



Z

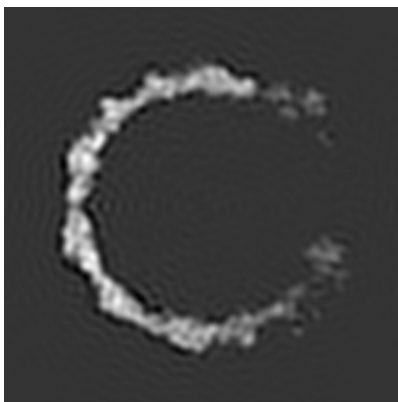
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 280

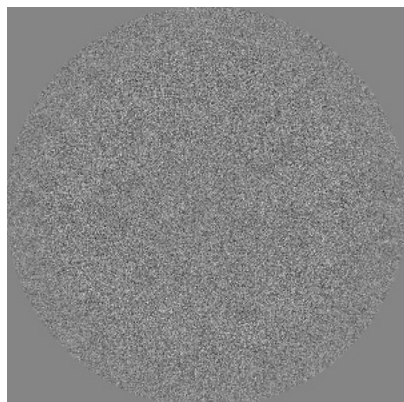


Y Index: 280

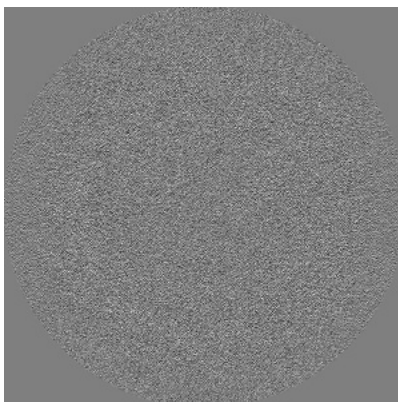


Z Index: 280

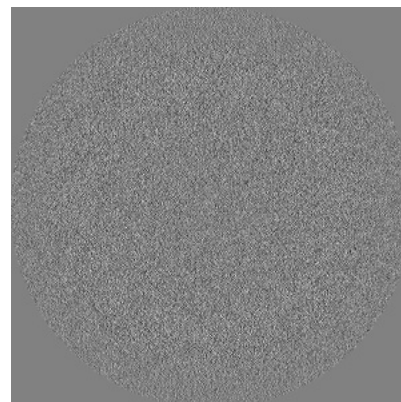
6.2.2 Raw map



X Index: 280



Y Index: 280

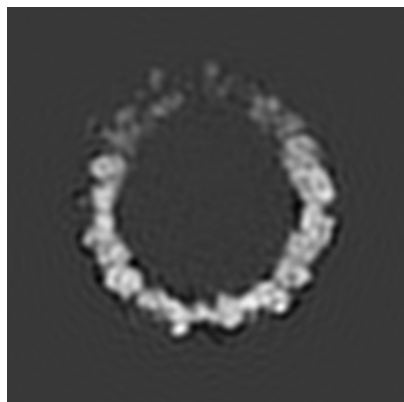


Z Index: 280

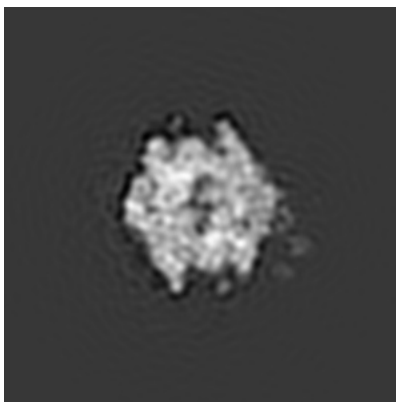
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 185

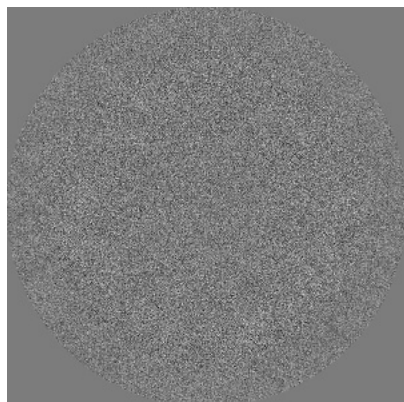


Y Index: 116

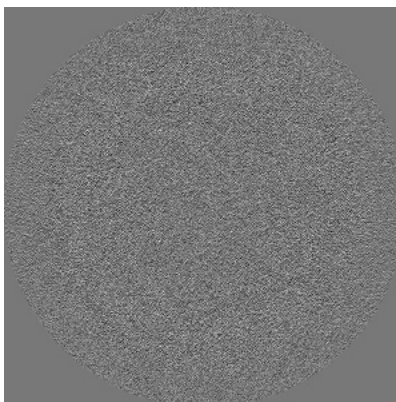


Z Index: 144

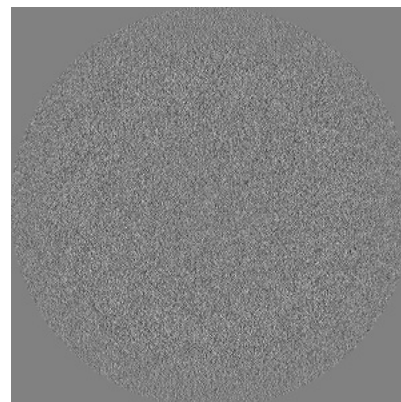
6.3.2 Raw map



X Index: 300



Y Index: 272

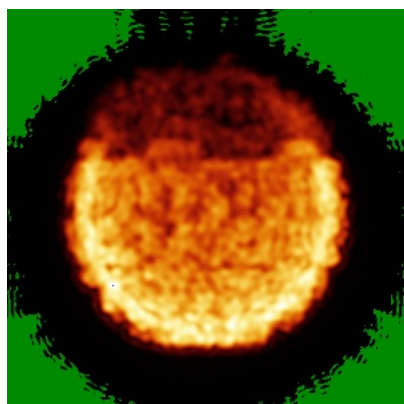


Z Index: 280

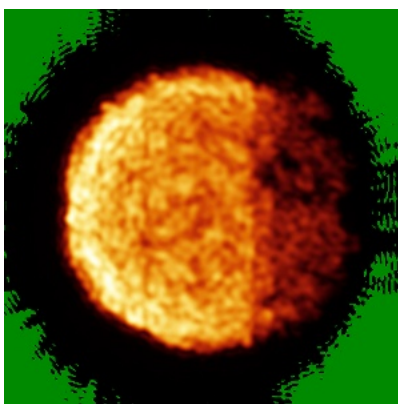
The images above show the largest variance slices of the map in three orthogonal directions.

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

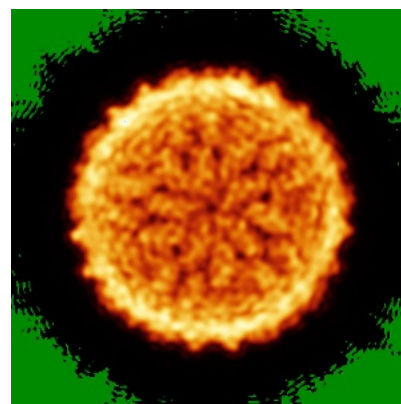
6.4.1 Primary map



X

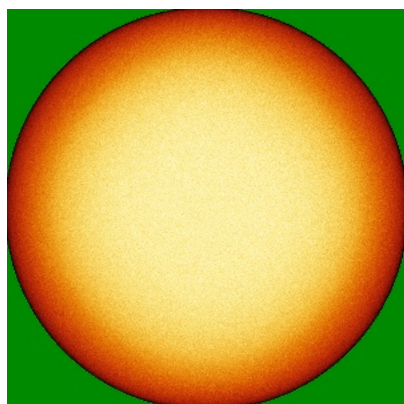


Y

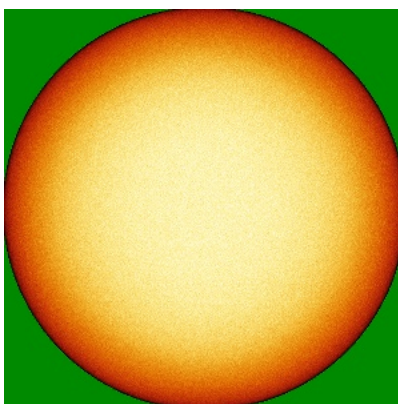


Z

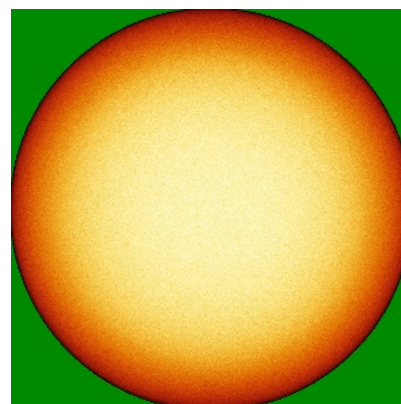
6.4.2 Raw map



X



Y

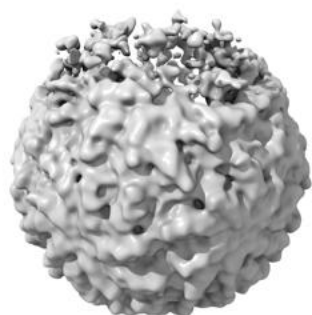


Z

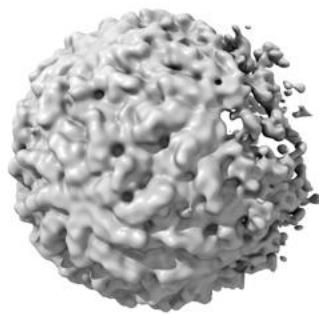
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

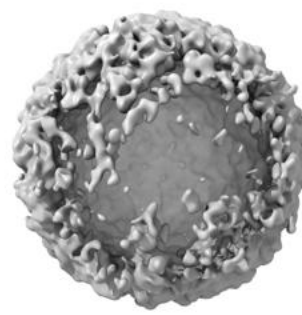
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

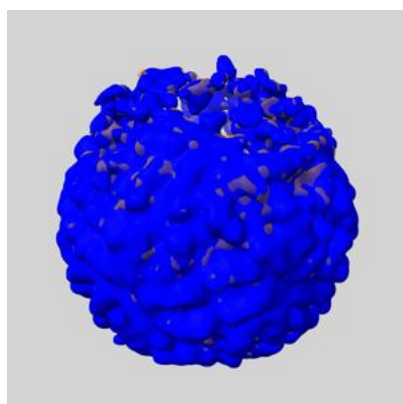
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

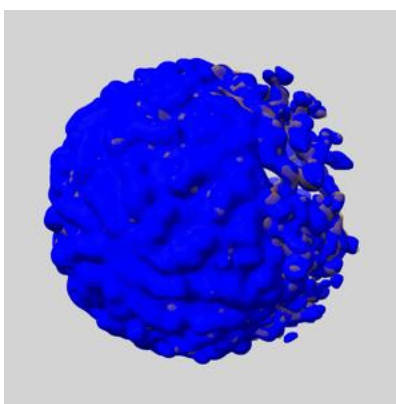
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

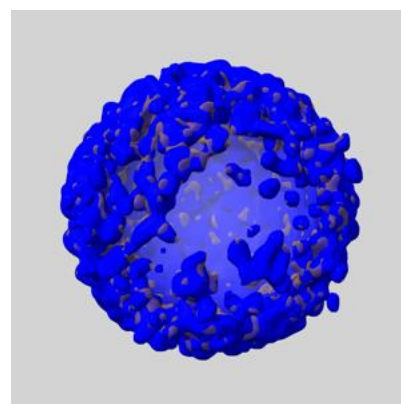
6.6.1 emd_14963_msk_1.map [i](#)



X



Y

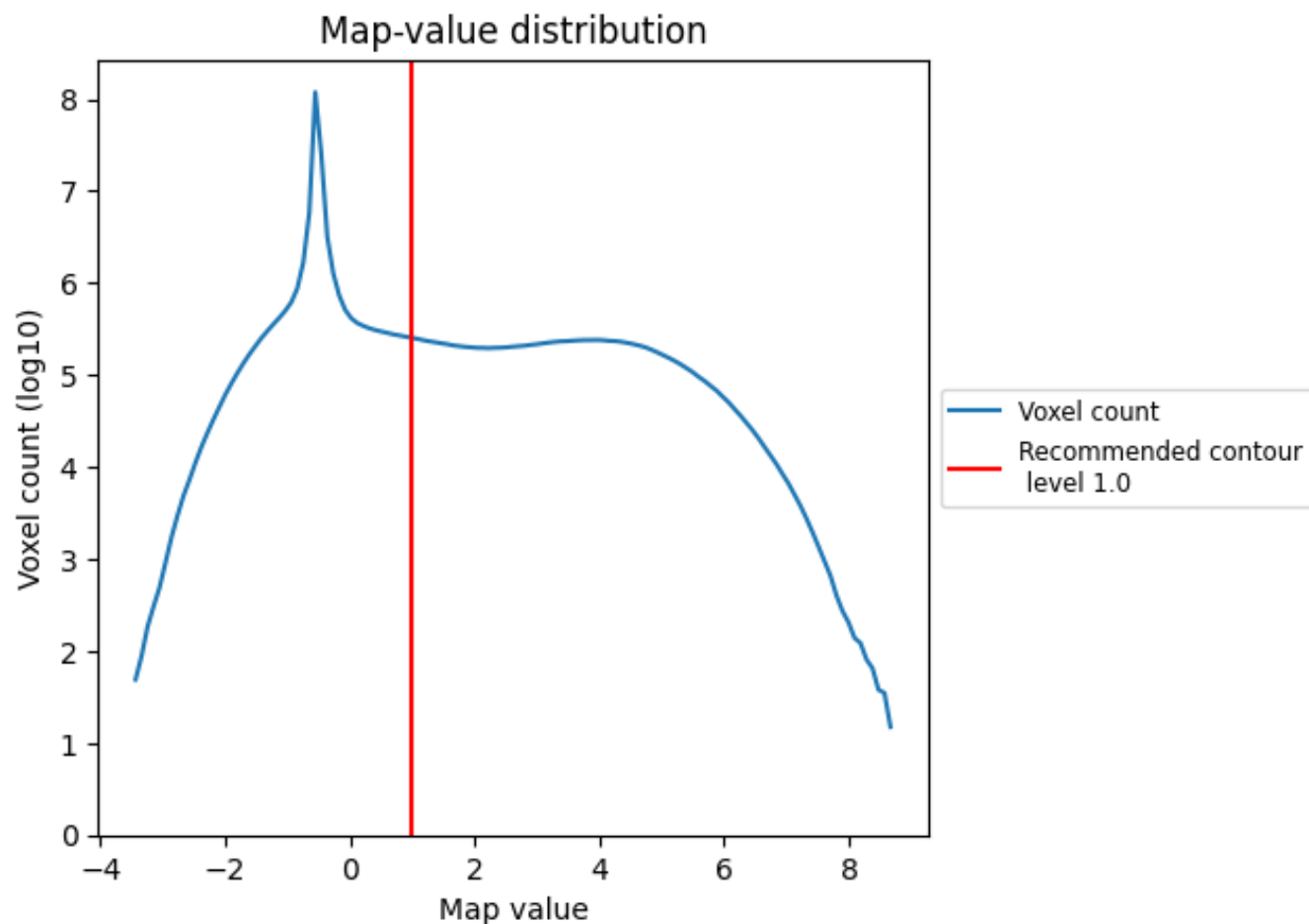


Z

7 Map analysis [i](#)

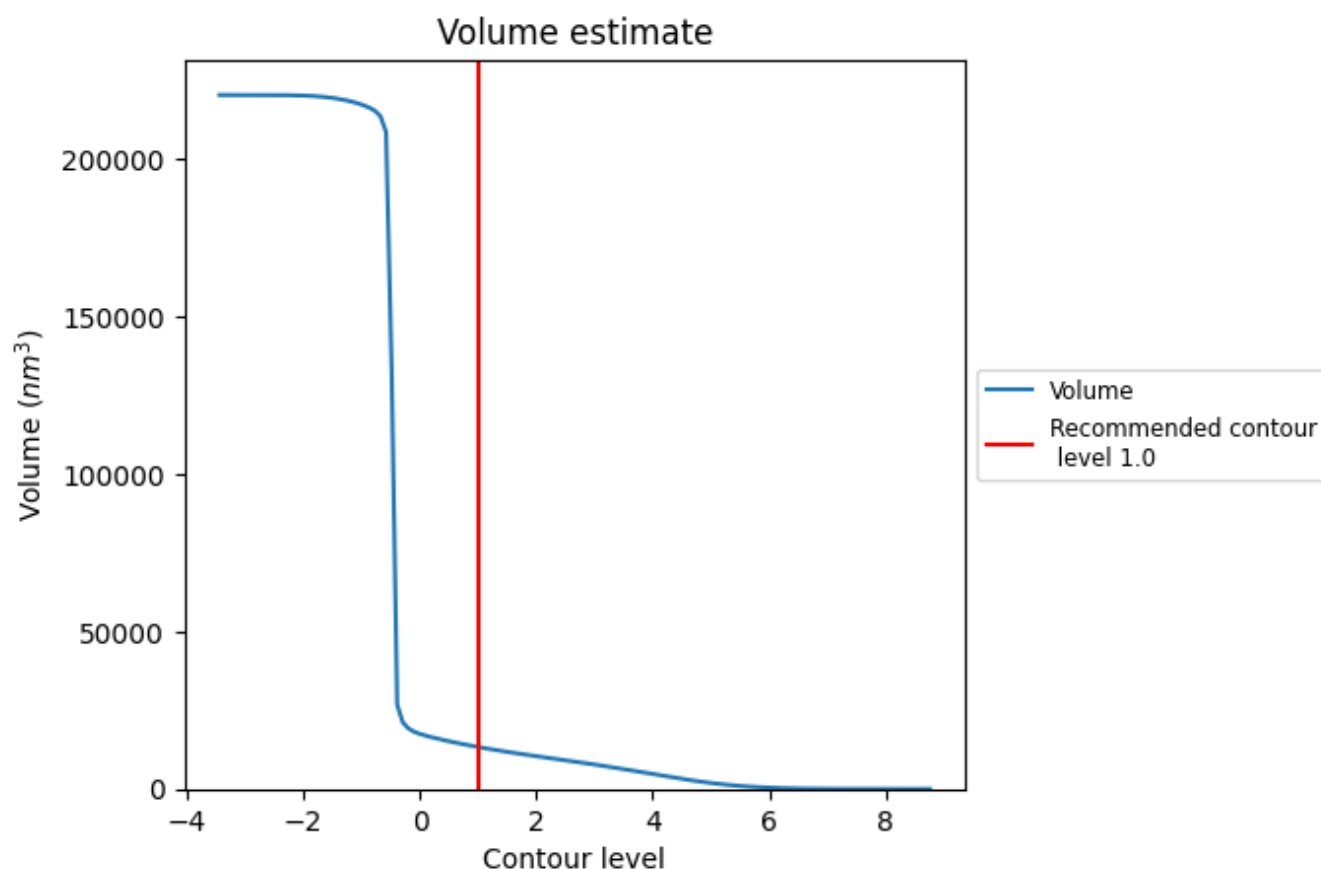
This section contains the results of statistical analysis of the map.

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.

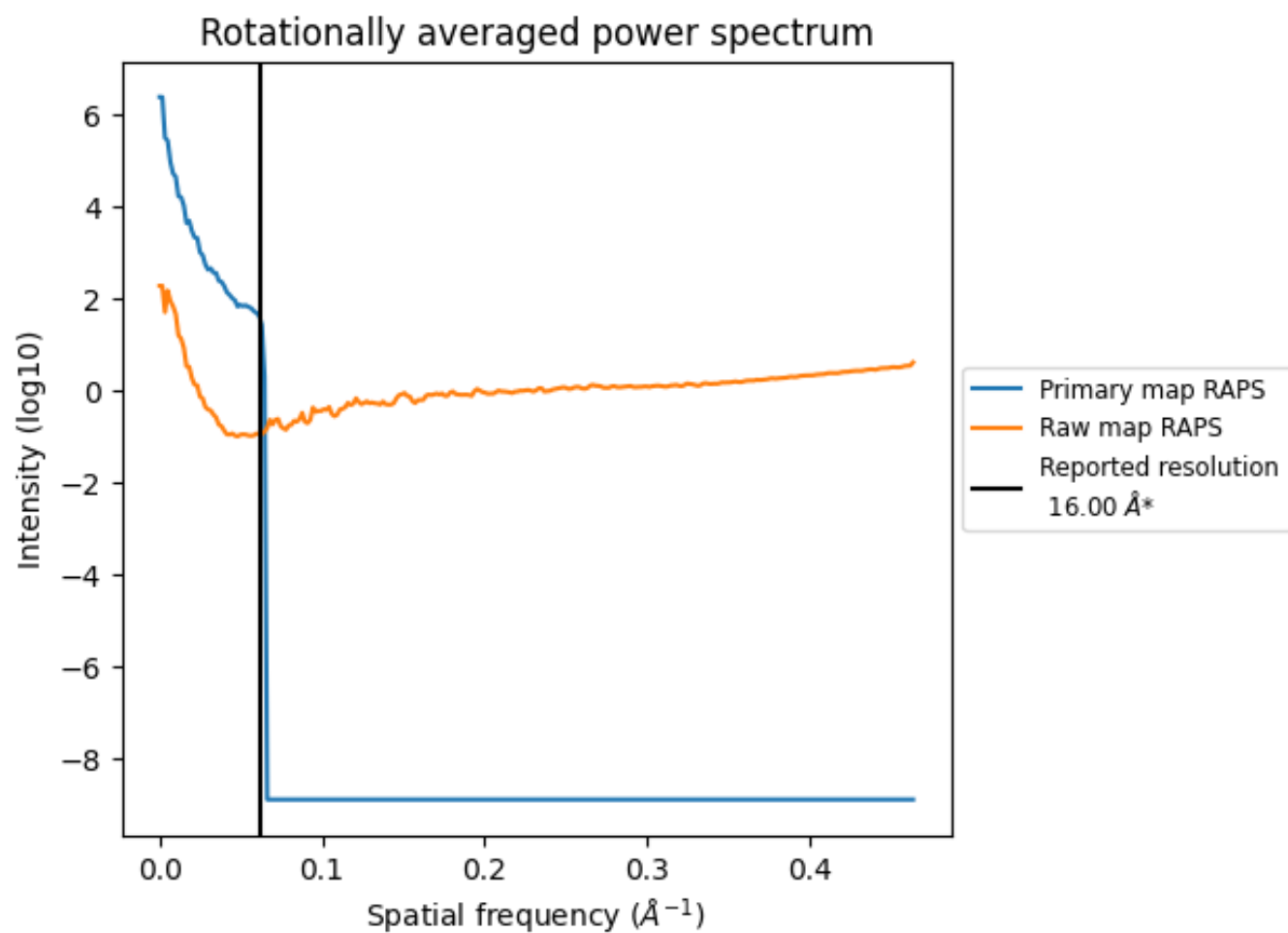
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 13348 nm^3 ; this corresponds to an approximate mass of 12058 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

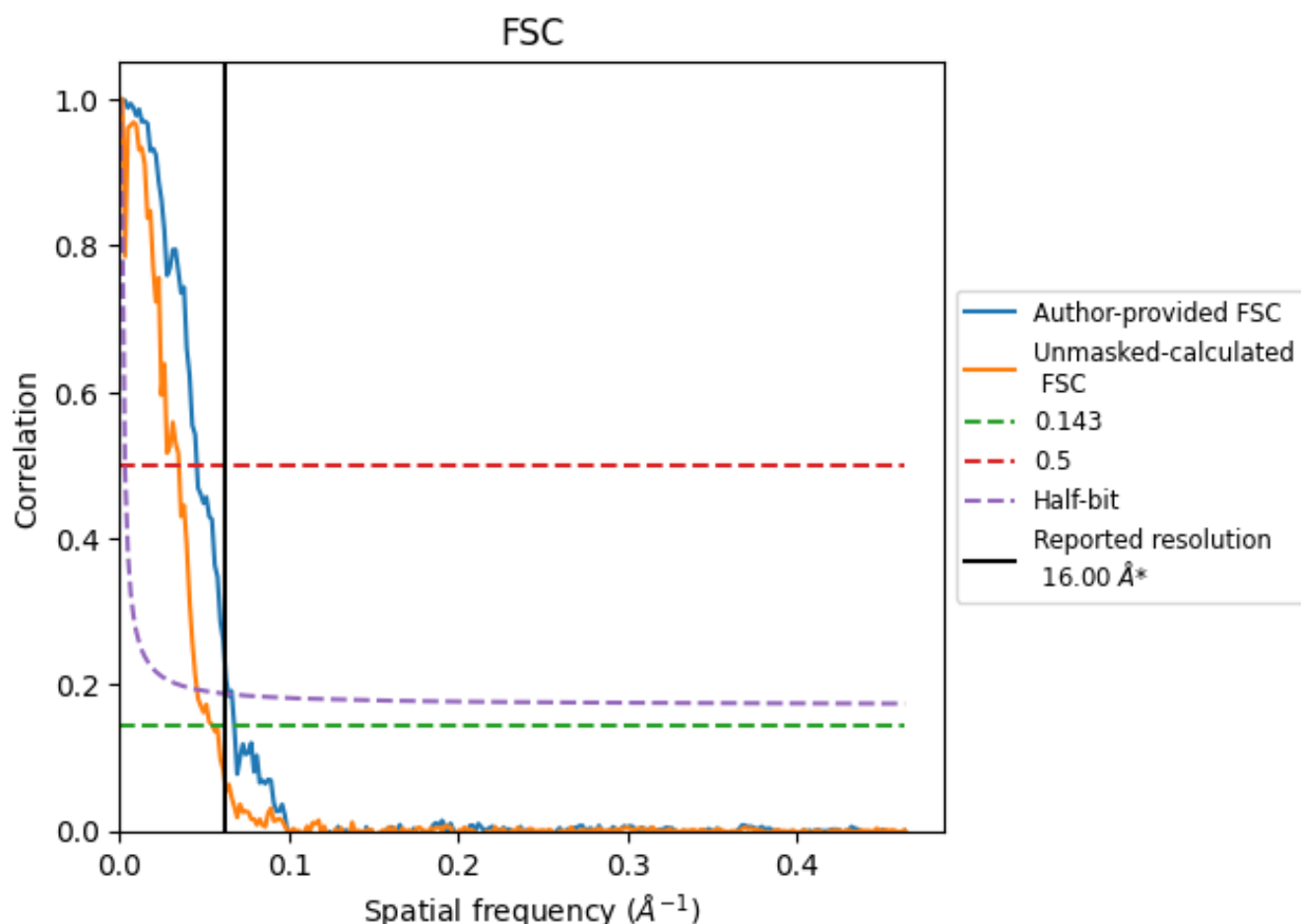


*Reported resolution corresponds to spatial frequency of 0.062 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.062 Å⁻¹

8.2 Resolution estimates [i](#)

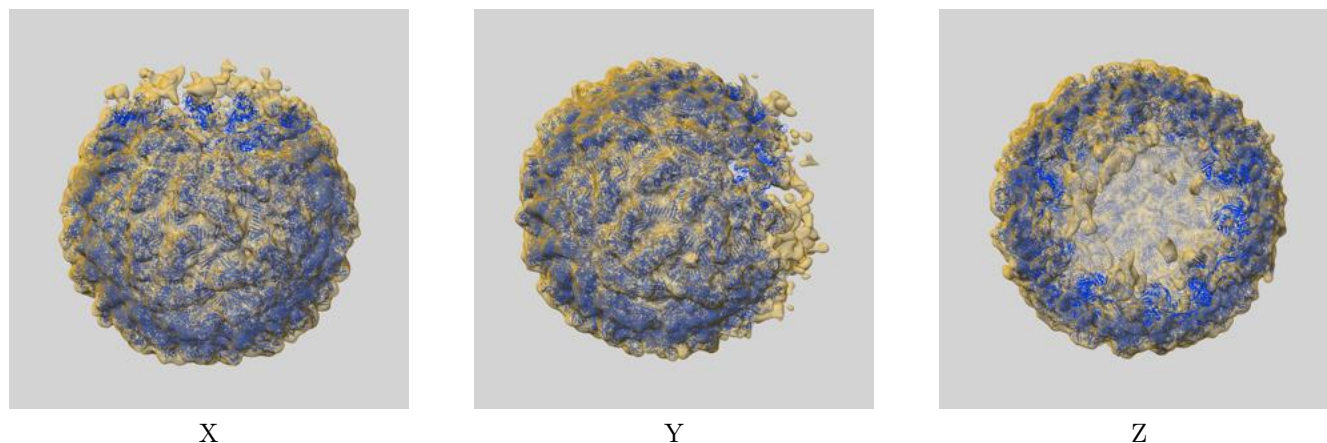
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	16.00	-	-
Author-provided FSC curve	14.75	21.93	15.53
Unmasked-calculated*	18.18	28.49	21.88

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 18.18 differs from the reported value 16.0 by more than 10 %

9 Map-model fit [i](#)

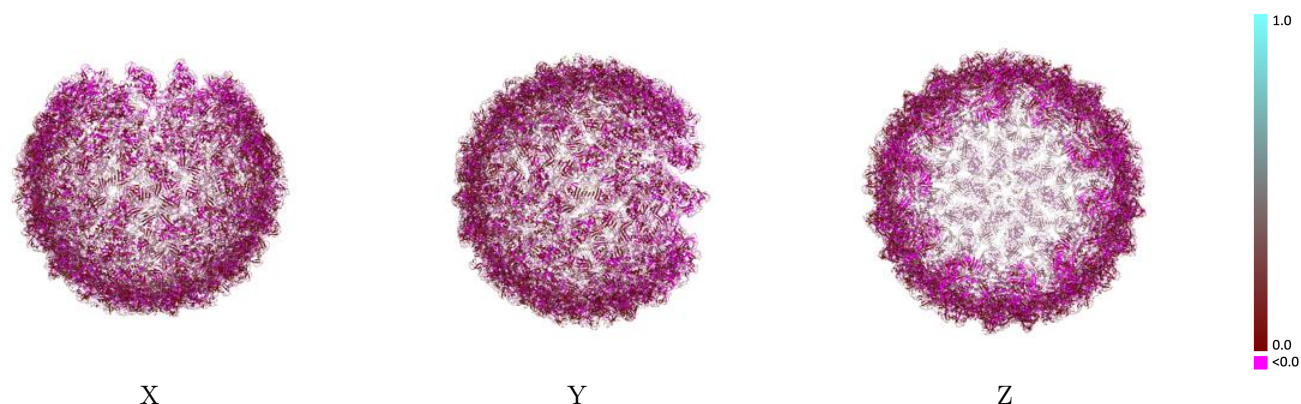
This section contains information regarding the fit between EMDB map EMD-14963 and PDB model 7ZTS. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



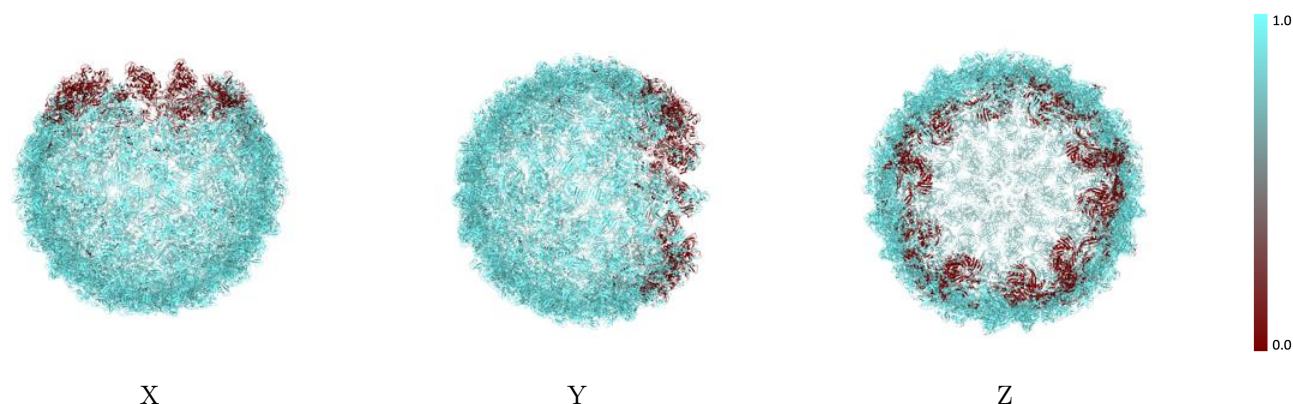
The images above show the 3D surface view of the map at the recommended contour level 1.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



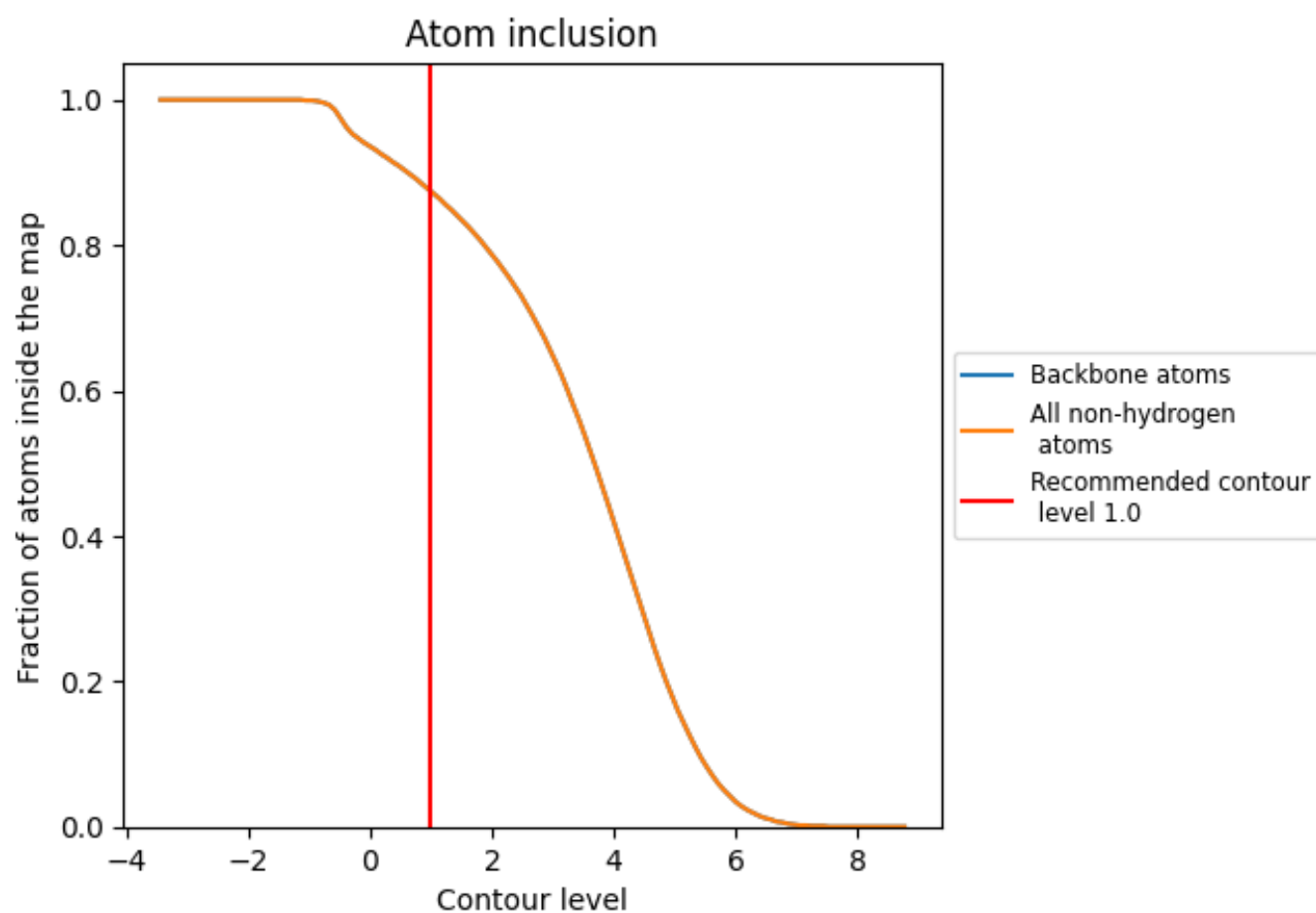
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.0).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 87% of all backbone atoms, 87% 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 (1.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8740	 0.0510
AA	 0.9900	 0.0730
AB	 0.9880	 0.0650
AC	 0.9900	 0.0690
AD	 0.9950	 0.0690
AE	 0.9580	 0.0620
AF	 0.5660	 0.0250
AG	 0.9580	 0.0540
AH	 0.9920	 0.0690
AI	 0.9930	 0.0550
AJ	 0.9850	 0.0620
AK	 0.9760	 0.0520
AL	 0.9820	 0.0540
AM	 0.9680	 0.0550
AN	 0.9880	 0.0590
AO	 0.9920	 0.0580
AP	 0.9930	 0.0740
AQ	 0.9900	 0.0640
AR	 0.9970	 0.0670
AS	 0.9960	 0.0660
AT	 0.2820	 0.0010
AU	 0.5750	 0.0060
AV	 0.1310	 -0.0140
AW	 0.9940	 0.0630
AX	 0.9880	 0.0600
AY	 0.9940	 0.0650
AZ	 0.9940	 0.0580
BA	 0.9240	 0.0520
BB	 0.4040	 0.0220
BC	 0.9630	 0.0480
BD	 0.9770	 0.0520
BE	 0.9590	 0.0600
BF	 0.9880	 0.0610
BG	 0.9750	 0.0490
BH	 0.9680	 0.0590







































































Continued on next page...

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Chain	Atom inclusion	Q-score
BI	 0.9590	 0.0480
BJ	 0.9730	 0.0600
BK	 0.9840	 0.0530
BL	 0.9950	 0.0620
BM	 0.9840	 0.0660
BN	 0.9940	 0.0660
BO	 0.9960	 0.0590
BP	 0.0900	 -0.0120
BQ	 0.4760	 -0.0080
BR	 0.0400	 -0.0050
BS	 0.9970	 0.0620
BT	 0.9960	 0.0620
BU	 0.9910	 0.0640
BV	 0.9880	 0.0540
BW	 0.9320	 0.0460
BX	 0.4290	 0.0190
BY	 0.8510	 0.0390
BZ	 0.9640	 0.0610
CA	 0.9720	 0.0500
CB	 0.9760	 0.0560
CC	 0.8990	 0.0460
CD	 0.9570	 0.0480
CE	 0.9310	 0.0570
CF	 0.9650	 0.0620
CG	 0.9710	 0.0450
CH	 0.9940	 0.0660
CI	 0.9920	 0.0570
CJ	 0.9810	 0.0590
CK	 0.9880	 0.0610
CL	 0.0620	 -0.0090
CM	 0.3090	 0.0010
CN	 0.0600	 0.0030
CO	 0.9950	 0.0690
CP	 0.9990	 0.0700
CQ	 0.9920	 0.0670
CR	 0.9910	 0.0560
CS	 0.9820	 0.0540
CT	 0.7330	 0.0260
CU	 0.8270	 0.0360
CV	 0.9930	 0.0600
CW	 0.9910	 0.0630
CX	 0.9860	 0.0590

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Chain	Atom inclusion	Q-score
CY	 0.9770	 0.0530
CZ	 0.9500	 0.0560
DA	 0.9300	 0.0450
DB	 0.9820	 0.0540
DC	 0.9930	 0.0560
DD	 0.9960	 0.0680
DE	 0.9970	 0.0690
DF	 0.9790	 0.0610
DG	 0.9960	 0.0670
DH	 0.2900	 0.0100
DI	 0.2650	 0.0130
DJ	 0.4750	 -0.0070
DK	 0.9920	 0.0670
DL	 0.9960	 0.0690
DM	 0.9910	 0.0750
DN	 0.9920	 0.0650
DO	 0.9720	 0.0670
DP	 0.5430	 0.0300
DQ	 0.8780	 0.0400
DR	 0.9900	 0.0630
DS	 0.9850	 0.0590
DT	 0.9830	 0.0700
DU	 0.9790	 0.0520
DV	 0.9610	 0.0490
DW	 0.9620	 0.0580
DX	 0.9740	 0.0580
DY	 0.9840	 0.0530
DZ	 0.9880	 0.0720
EA	 0.9900	 0.0630
EB	 0.9920	 0.0620
EC	 0.9910	 0.0650
ED	 0.2210	 0.0030
EE	 0.4950	 0.0160
EF	 0.0890	 0.0020