



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Jan 12, 2017 – 09:16 AM EST

PDB ID : 5LQP
EMDB ID: : EMD-4098
Title : Cryo-EM reconstruction of bacteriophage AP205 virus-like particles
Authors : Diebolder, C.A.; Rumnieks, J.; Tars, K.; Koning, R.I.
Deposited on : 2016-08-17
Resolution : 6.00 Å(reported)

This is a wwPDB/EMDataBank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20028442

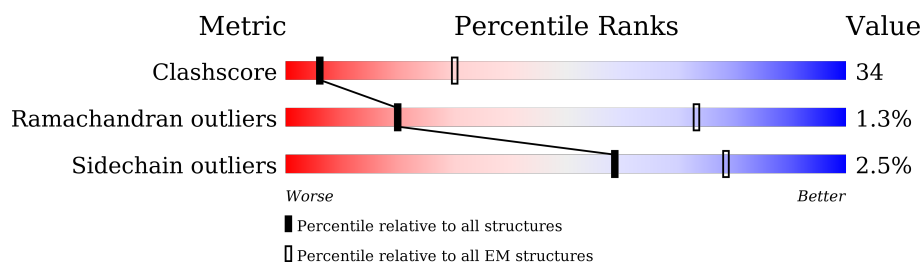
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 6.00 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	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	AB	129	
1	AC	129	
1	AD	129	
1	AE	129	
1	AF	129	
1	AG	129	
1	AH	129	
1	AI	129	
1	AJ	129	


























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Mol	Chain	Length	Quality of chain
1	AK	129	
1	AL	129	
1	AM	129	
1	AN	129	
1	AO	129	
1	AP	129	
1	AQ	129	
1	AR	129	
1	AS	129	
1	AT	129	
1	AU	129	
1	AV	129	
1	AW	129	
1	AX	129	
1	AY	129	
1	AZ	129	
1	BA	129	
1	BB	129	
1	BC	129	
1	BD	129	
1	BE	129	
1	BF	129	
1	BG	129	
1	BH	129	
1	BI	129	


























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Mol	Chain	Length	Quality of chain
1	BJ	129	 67%31%..
1	BK	129	 60%37%. .
1	BL	129	 63%34%..
1	BM	129	 67%31%..
1	BN	129	 60%36%. .
1	BO	129	 62%35%..
1	BP	129	 68%29%..
1	BQ	129	 62%35%. .
1	BR	129	 63%35%..
1	BS	129	 68%29%..
1	BT	129	 60%36%. .
1	BU	129	 63%34%..
1	BV	129	 67%31%..
1	BW	129	 60%36%. .
1	BX	129	 62%36%..
1	BY	129	 67%31%..
1	BZ	129	 60%37%. .
1	CA	129	 62%35%..
1	CB	129	 67%30%..
1	CC	129	 61%36%. .
1	CD	129	 62%35%..
1	CE	129	 68%29%..
1	CF	129	 59%38%. .
1	CG	129	 62%35%..
1	CH	129	 67%30%..


























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Mol	Chain	Length	Quality of chain
1	CI	129	
1	CJ	129	
1	CK	129	
1	CL	129	
1	CM	129	
1	CN	129	
1	CO	129	
1	CP	129	
1	CQ	129	
1	CR	129	
1	CS	129	
1	CT	129	
1	CU	129	
1	CV	129	
1	CW	129	
1	CX	129	
1	CY	129	
1	CZ	129	
1	DA	129	
1	DB	129	
1	DC	129	
1	DD	129	
1	DE	129	
1	DF	129	
1	DG	129	

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Mol	Chain	Length	Quality of chain
1	DH	129	
1	DI	129	
1	DJ	129	
1	DK	129	
1	DL	129	
1	DM	129	
1	DN	129	
1	DO	129	
1	DP	129	
1	DQ	129	
1	DR	129	
1	DS	129	
1	DT	129	
1	DU	129	
1	DV	129	
1	DW	129	
1	DX	129	
1	DY	129	
1	DZ	129	
1	EA	129	
1	EB	129	
1	EC	129	
1	ED	129	
1	EE	129	
1	EF	129	


























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Mol	Chain	Length	Quality of chain
1	EG	129	
1	EH	129	
1	EI	129	
1	EJ	129	
1	EK	129	
1	EL	129	
1	EM	129	
1	EN	129	
1	EO	129	
1	EP	129	
1	EQ	129	
1	ER	129	
1	ES	129	
1	ET	129	
1	EU	129	
1	EV	129	
1	EW	129	
1	EX	129	
1	EY	129	
1	EZ	129	
1	FA	129	
1	FB	129	
1	FC	129	
1	FD	129	
1	FE	129	









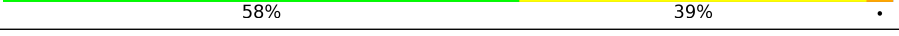
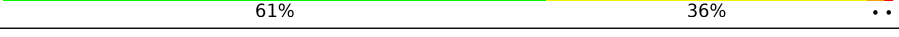
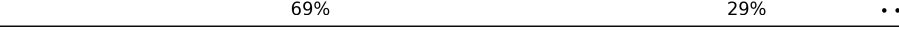

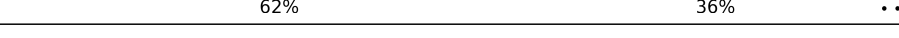
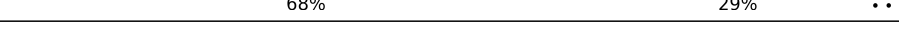
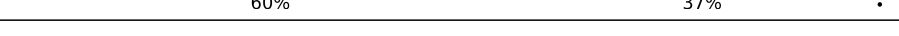


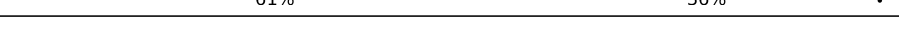
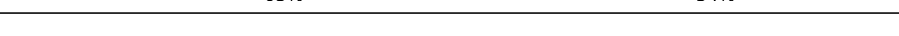


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Mol	Chain	Length	Quality of chain
1	FF	129	 61% 36% .
1	FG	129	 64% 34% ..
1	FH	129	 67% 30% ..
1	FI	129	 60% 36% .
1	FJ	129	 62% 35% ..
1	FK	129	 70% 28% ..
1	FL	129	 60% 37% .
1	FM	129	 63% 35% ..
1	FN	129	 67% 30% ..
1	FO	129	 60% 36% .
1	FP	129	 62% 35% ..
1	FQ	129	 67% 30% ..
1	FR	129	 59% 38% .
1	FS	129	 62% 36% ..
1	FT	129	 67% 30% ..
1	FU	129	 60% 37% .
1	FV	129	 62% 36% ..
1	FW	129	 67% 30% ..
1	FX	129	 60% 36% .
1	FY	129	 61% 36% ..
1	FZ	129	 67% 30% ..
1	GA	129	 60% 37% .
1	GB	129	 63% 35% ..
1	GC	129	 67% 30% ..
1	GD	129	 60% 36% .

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Mol	Chain	Length	Quality of chain
1	GE	129	 61%36%..
1	GF	129	 67%30%..
1	GG	129	 61%36%.
1	GH	129	 62%36%..
1	GI	129	 68%29%..
1	GJ	129	 60%37%.
1	GK	129	 63%35%..
1	GL	129	 67%30%..
1	GM	129	 58%39%.
1	GN	129	 61%36%..
1	GO	129	 69%29%..
1	GP	129	 60%36%.
1	GQ	129	 62%36%..
1	GR	129	 68%29%..
1	GS	129	 60%37%.
1	GT	129	 61%36%..
1	GU	129	 67%30%..
1	GV	129	 61%36%.
1	GW	129	 63%34%..
1	GX	129	 69%29%..
1	GY	129	 60%36%.

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 174240 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 Coat protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AB	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AC	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AD	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AE	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AF	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AG	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AH	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AI	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AJ	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AK	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AL	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AM	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AN	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AO	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AP	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AQ	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	AR	129	Total	C	N	O	S	0	0
			968	602	171	191	4		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	AS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	AZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BM	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	BN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	BZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CH	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	CI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	CZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DC	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DX	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	DY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	DZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	ED	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EN	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	ER	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	ES	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	ET	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	EZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FI	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FJ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FK	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FL	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FM	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FN	129	Total 968	C 602	N 171	O 191	S 4	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	FO	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FP	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FQ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FR	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FS	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FT	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FU	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FV	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FW	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FX	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FY	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	FZ	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GA	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GB	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GC	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GD	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GE	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GF	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GG	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GH	129	Total 968	C 602	N 171	O 191	S 4	0	0
1	GI	129	Total 968	C 602	N 171	O 191	S 4	0	0

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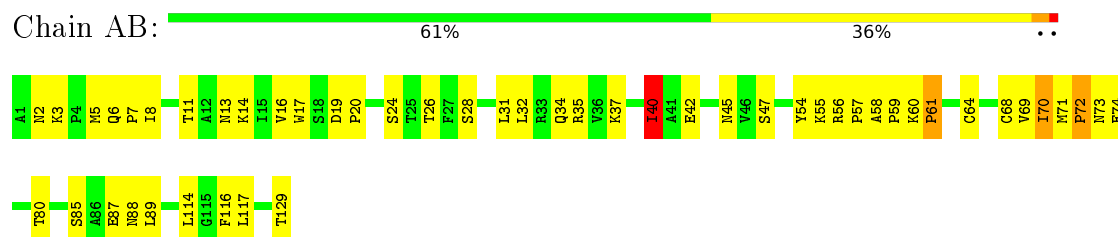
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	GJ	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GK	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GL	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GM	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GN	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GO	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GP	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GQ	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GR	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GS	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GT	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GU	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GV	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GW	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GX	129	Total	C	N	O	S	0	0
			968	602	171	191	4		
1	GY	129	Total	C	N	O	S	0	0
			968	602	171	191	4		

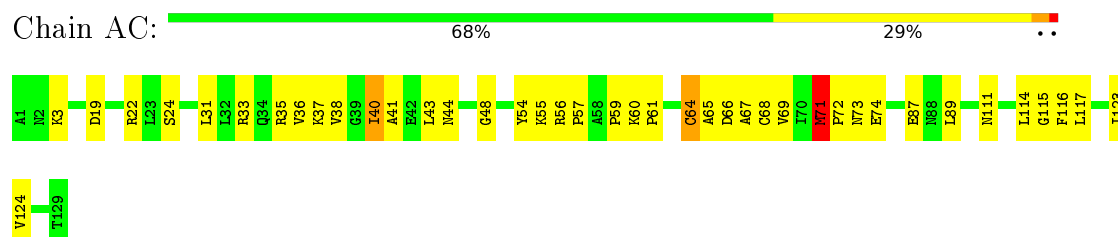
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

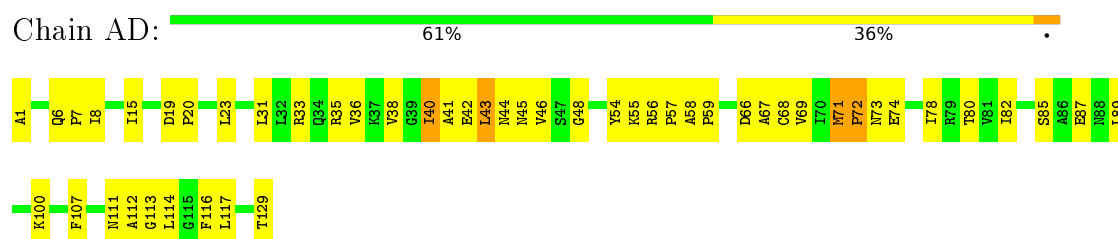
- Molecule 1: Coat protein



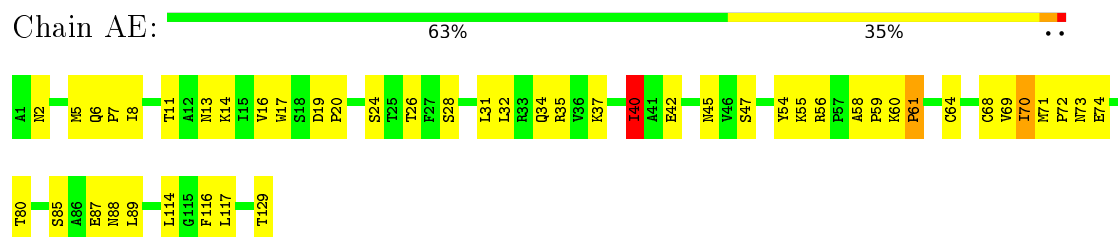
- Molecule 1: Coat protein



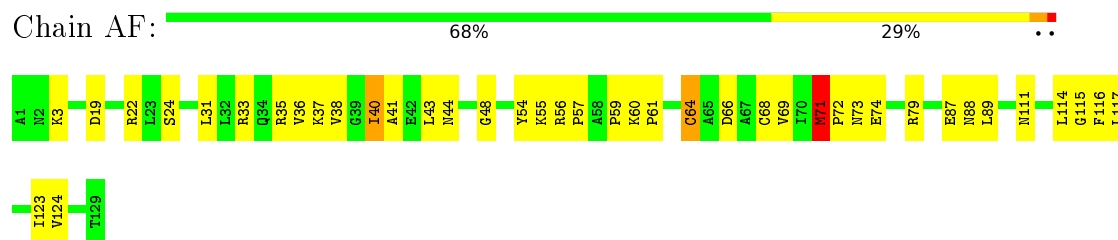
- Molecule 1: Coat protein



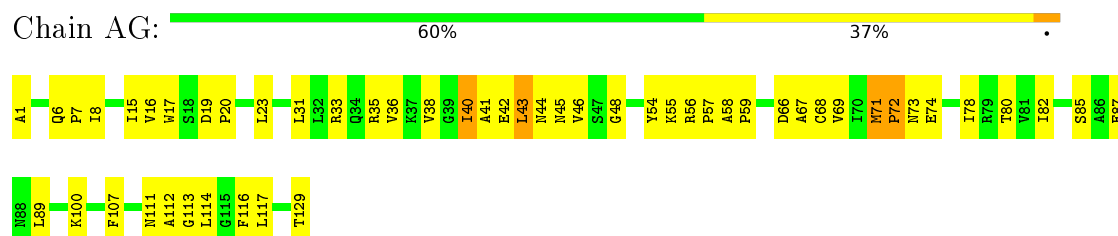
- Molecule 1: Coat protein



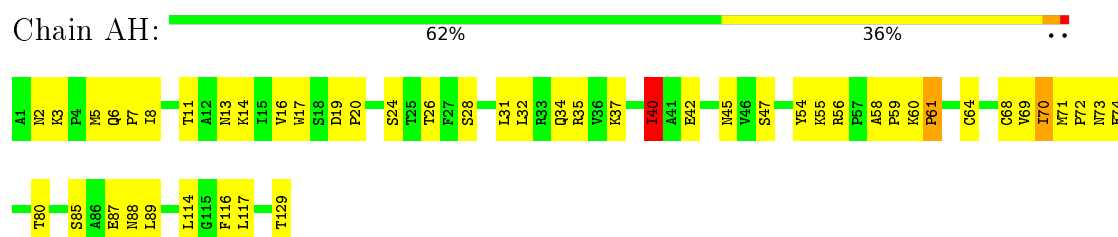
- Molecule 1: Coat protein



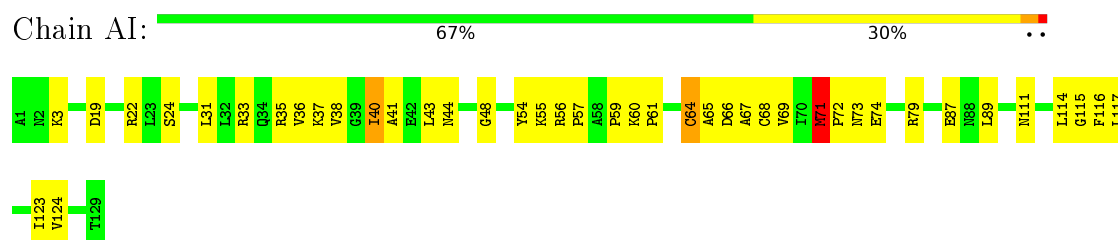
- Molecule 1: Coat protein



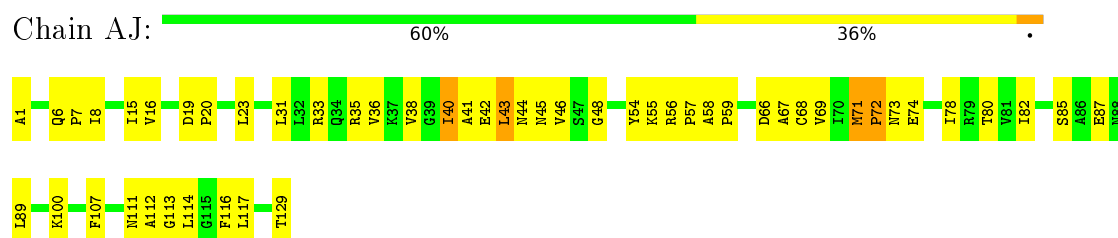
- Molecule 1: Coat protein



- Molecule 1: Coat protein

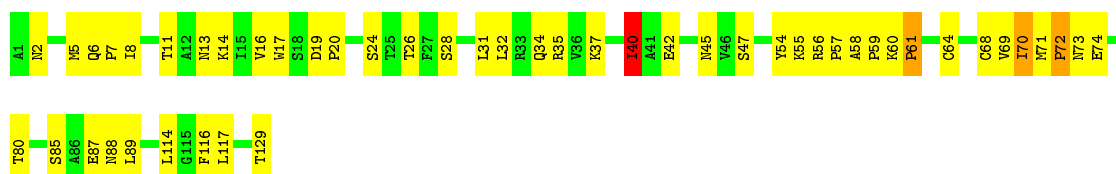


- Molecule 1: Coat protein



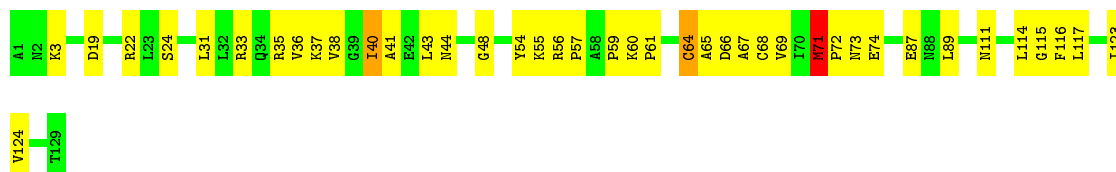
- Molecule 1: Coat protein





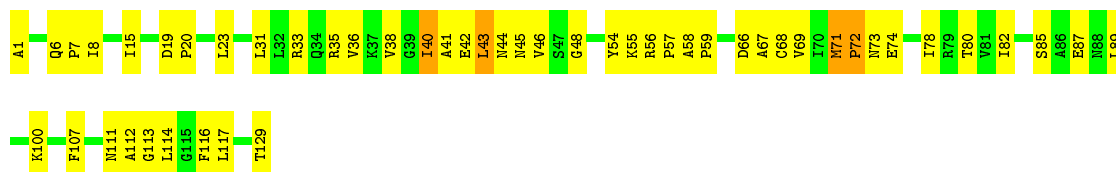
- Molecule 1: Coat protein

Chain AL: 68% 29% ..



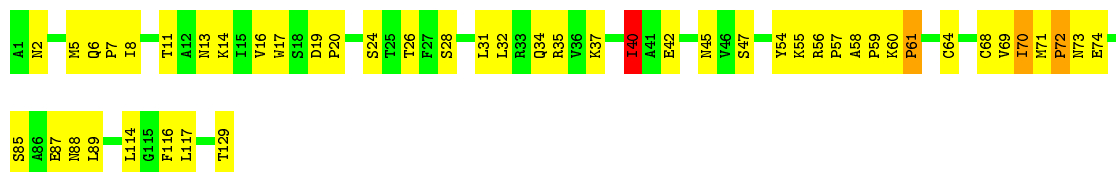
- Molecule 1: Coat protein

Chain AM: 61% 36% .



- Molecule 1: Coat protein

Chain AN: 63% 34% ..



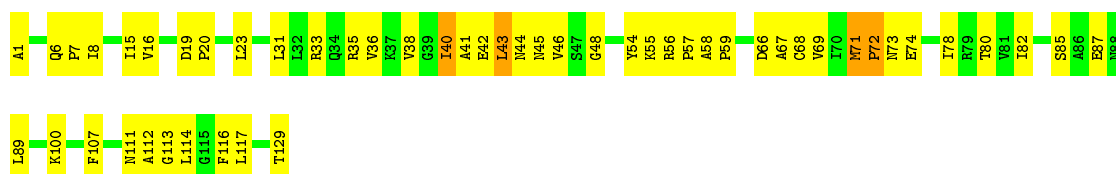
- Molecule 1: Coat protein

Chain AO: 68% 29% ..



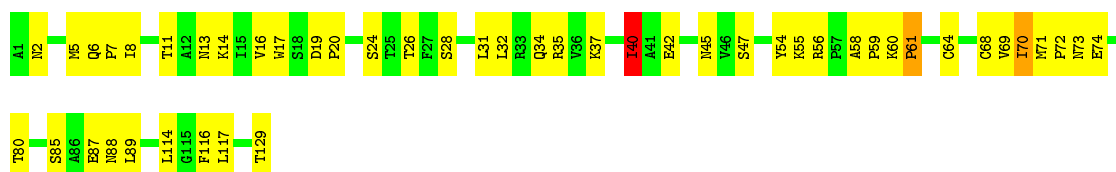
- Molecule 1: Coat protein

Chain AP: 60% 36% .



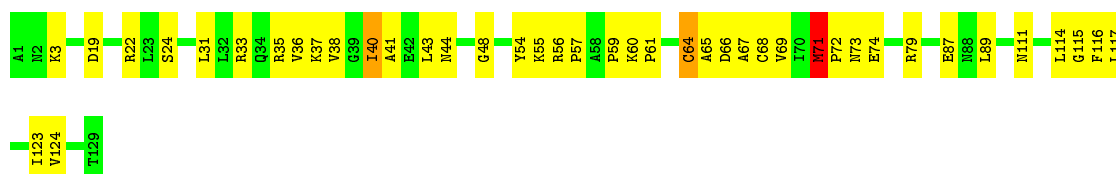
- Molecule 1: Coat protein

Chain AQ: 63% 35% ..



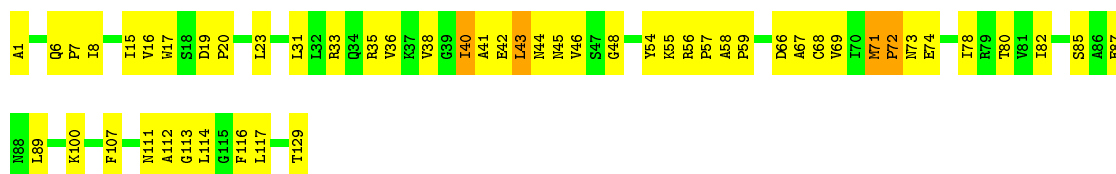
- Molecule 1: Coat protein

Chain AR: 67% 30% ..



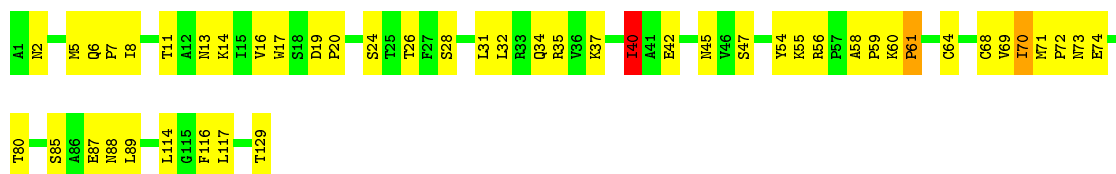
- Molecule 1: Coat protein

Chain AS: 60% 37% .



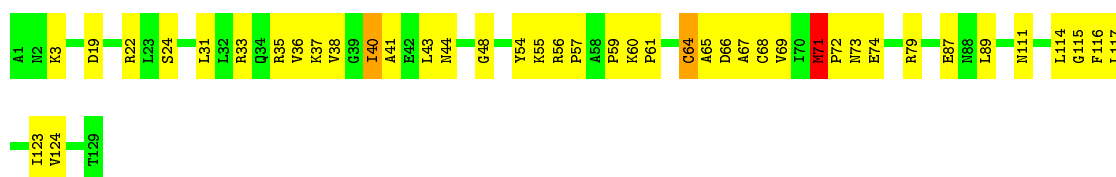
- Molecule 1: Coat protein

Chain AT: 63% 35% ..



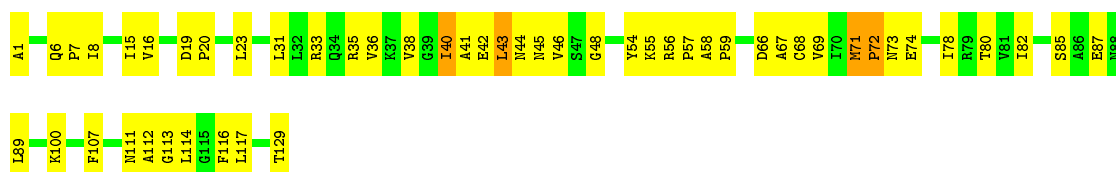
- Molecule 1: Coat protein

Chain AU: 67% 30% ..



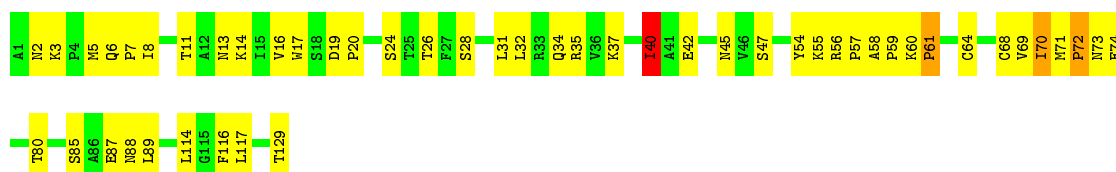
- Molecule 1: Coat protein

Chain AV: 60% 36%



- Molecule 1: Coat protein

Chain AW: 61% 36%



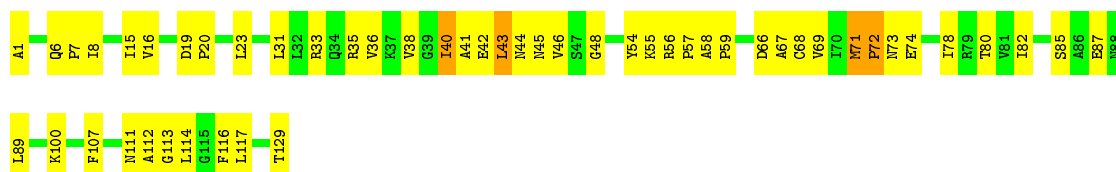
- Molecule 1: Coat protein

Chain AX: 67% 31%



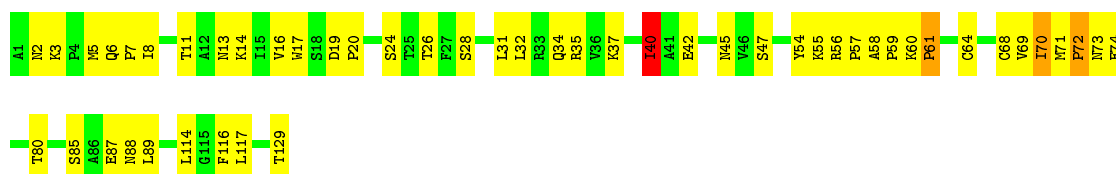
- Molecule 1: Coat protein

Chain AY: 60% 36%



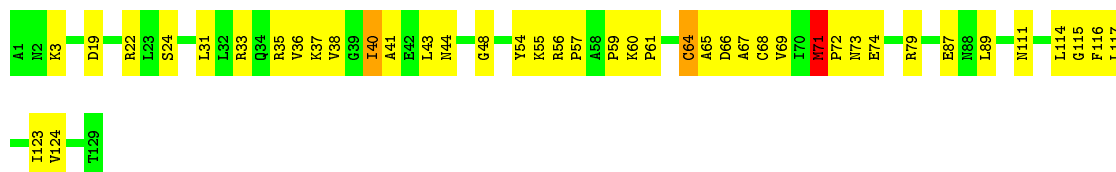
- Molecule 1: Coat protein

Chain AZ: 61% 36%



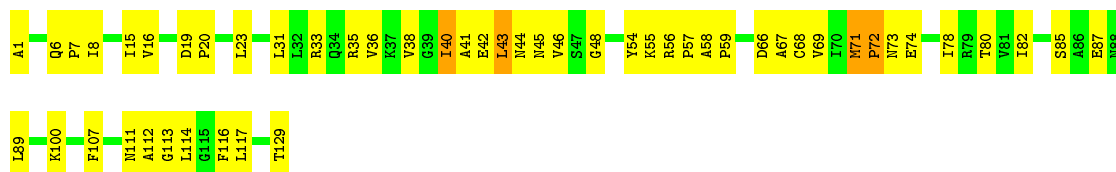
- Molecule 1: Coat protein

Chain BA: 67% 30% ..



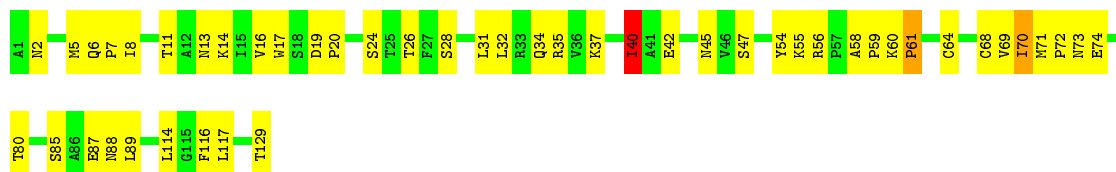
- Molecule 1: Coat protein

Chain BB: 60% 36% .



- Molecule 1: Coat protein

Chain BC: 63% 35% ..



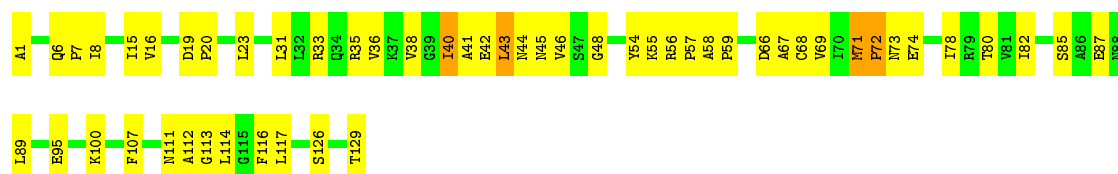
- Molecule 1: Coat protein

Chain BD: 67% 30% ..

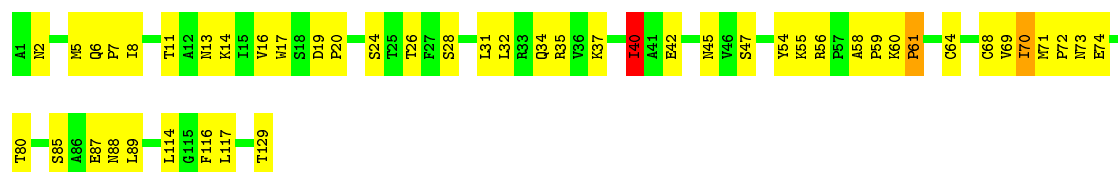


- Molecule 1: Coat protein

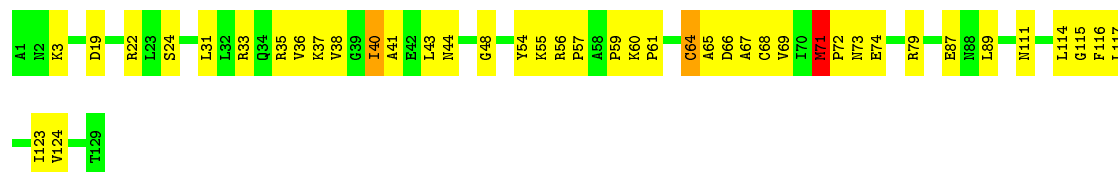
Chain BE: 59% 38% .



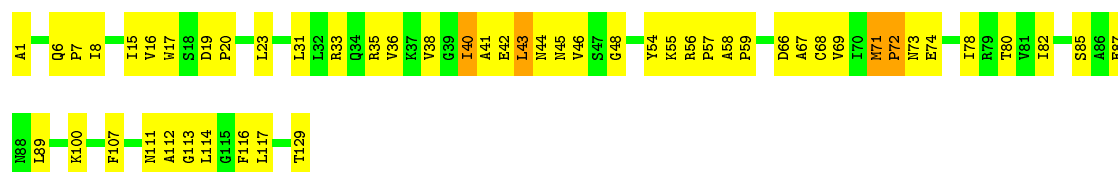
- Molecule 1: Coat protein



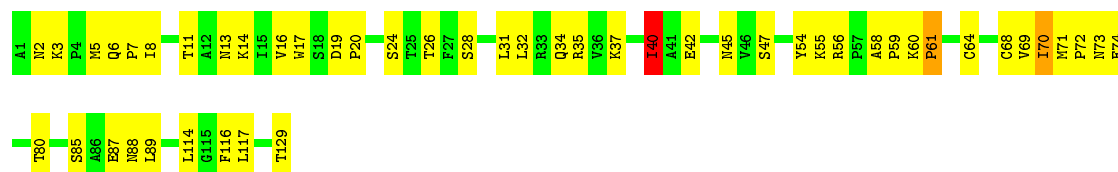
- Molecule 1: Coat protein



- Molecule 1: Coat protein

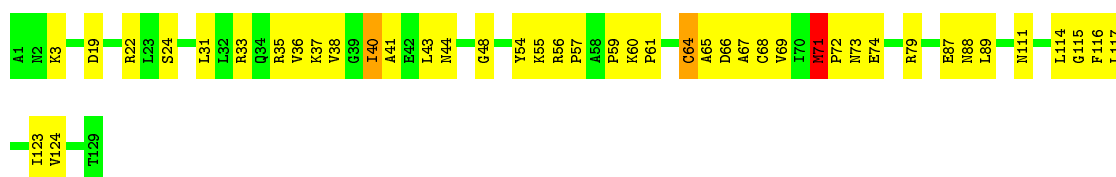


- Molecule 1: Coat protein



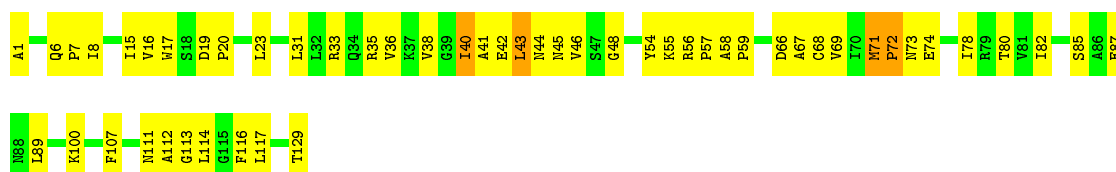
- Molecule 1: Coat protein





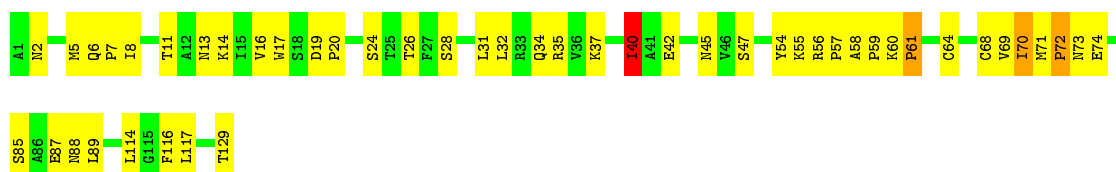
- Molecule 1: Coat protein

Chain BK: 60% 37%



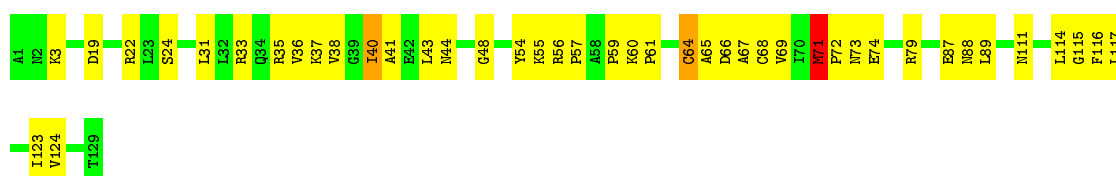
- Molecule 1: Coat protein

Chain BL: 63% 34%



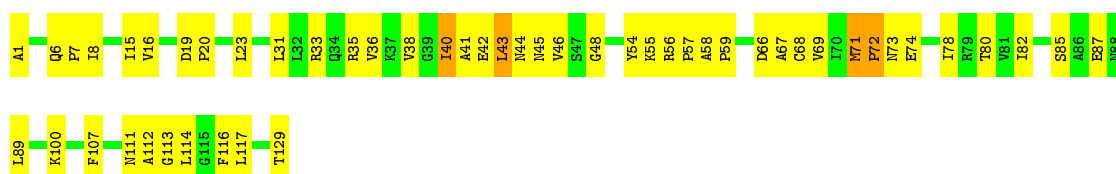
- Molecule 1: Coat protein

Chain BM: 67% 31%



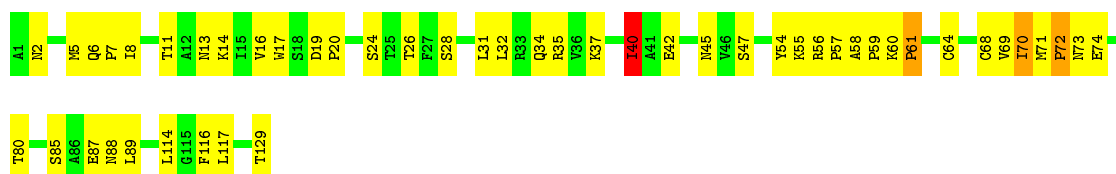
- Molecule 1: Coat protein

Chain BN: 60% 36%



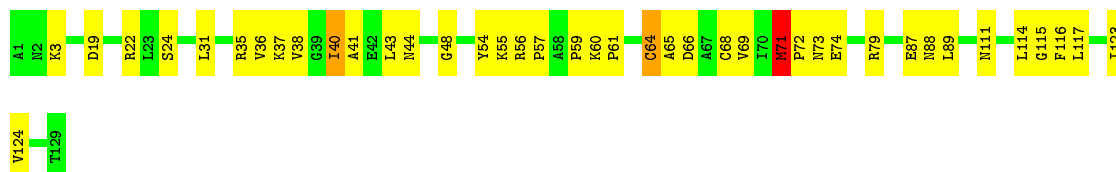
- Molecule 1: Coat protein

Chain BO: 62% 35%



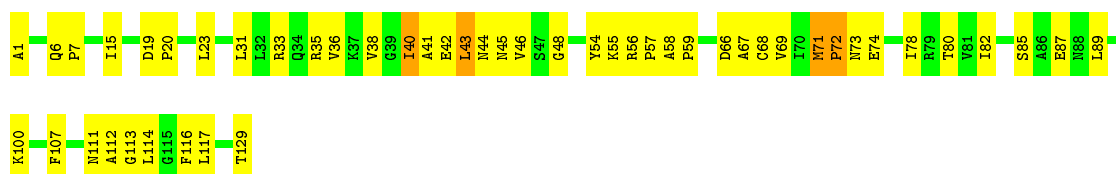
- Molecule 1: Coat protein

Chain BP: 68% 29% ..



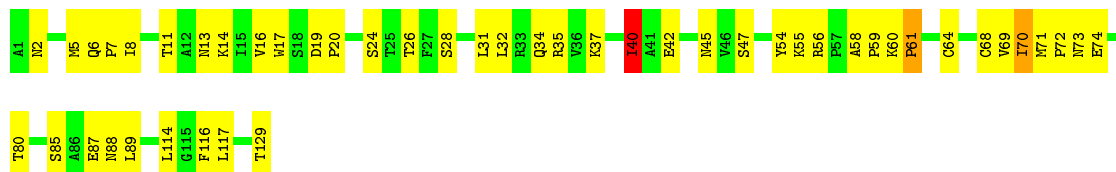
- Molecule 1: Coat protein

Chain BQ: 62% 35% .



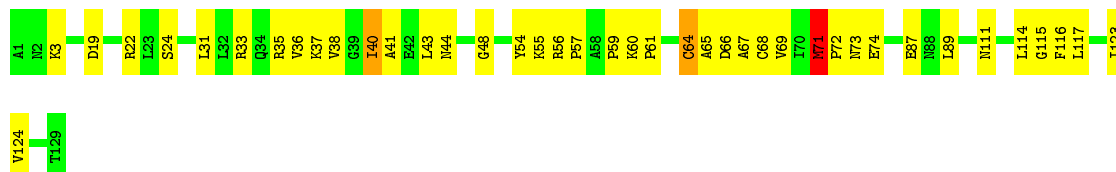
- Molecule 1: Coat protein

Chain BR: 63% 35% ..



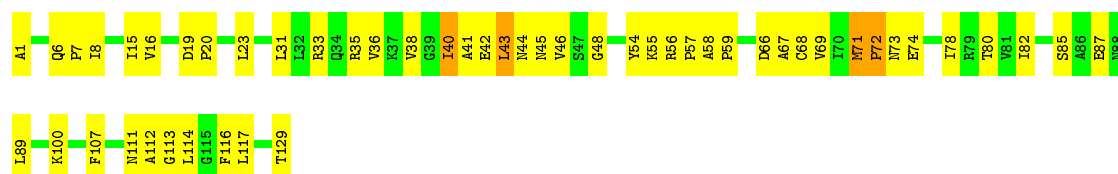
- Molecule 1: Coat protein

Chain BS: 68% 29% ..

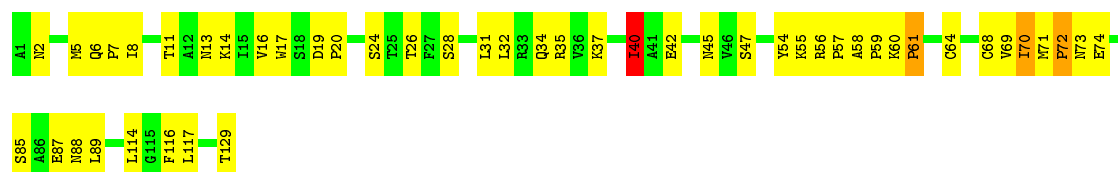


- Molecule 1: Coat protein

Chain BT: 60% 36% .



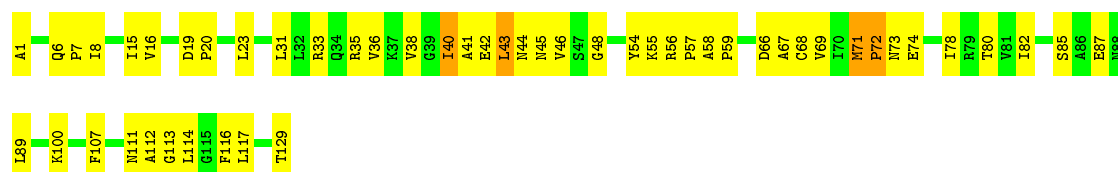
- Molecule 1: Coat protein



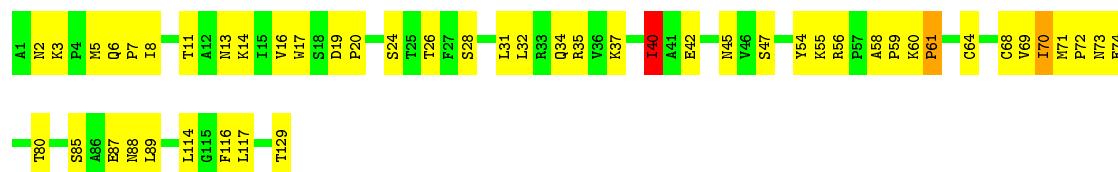
- Molecule 1: Coat protein



- Molecule 1: Coat protein



- Molecule 1: Coat protein



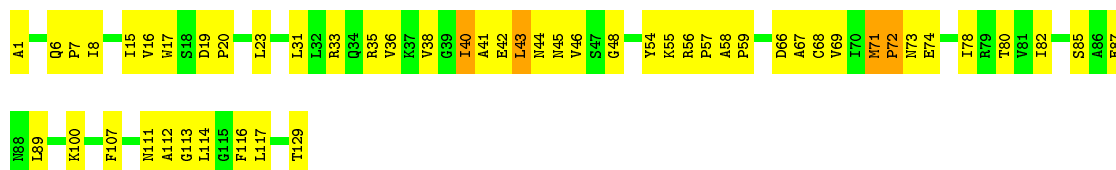
- Molecule 1: Coat protein





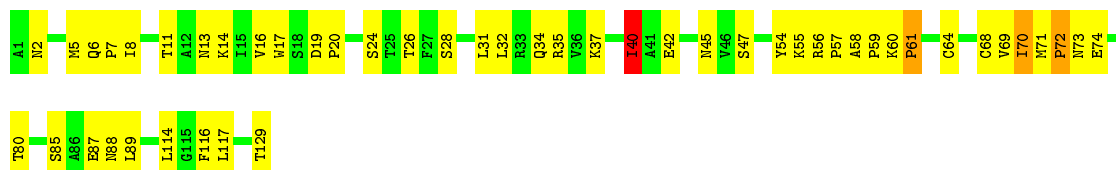
- Molecule 1: Coat protein

Chain BZ: 60% 37% .



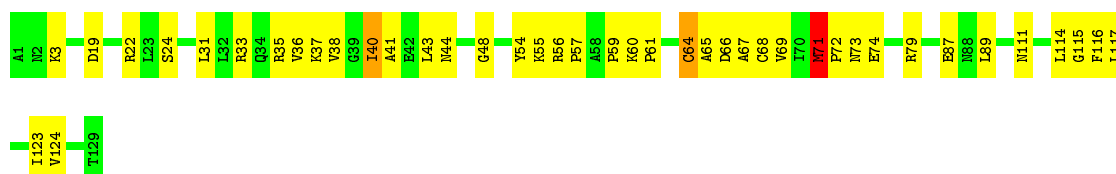
- Molecule 1: Coat protein

Chain CA: 62% 35% ..



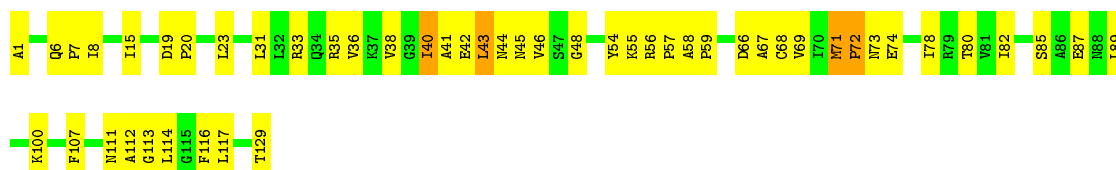
- Molecule 1: Coat protein

Chain CB: 67% 30% ..



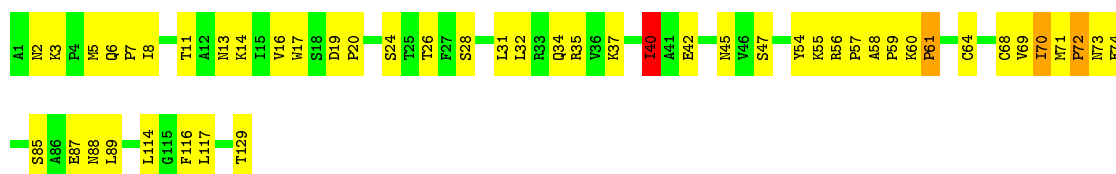
- Molecule 1: Coat protein

Chain CC: 61% 36% .



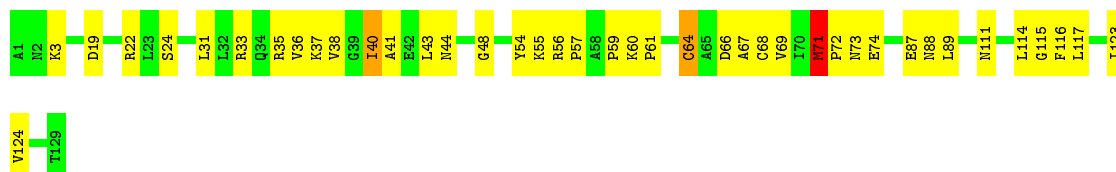
- Molecule 1: Coat protein

Chain CD: 62% 35% ..



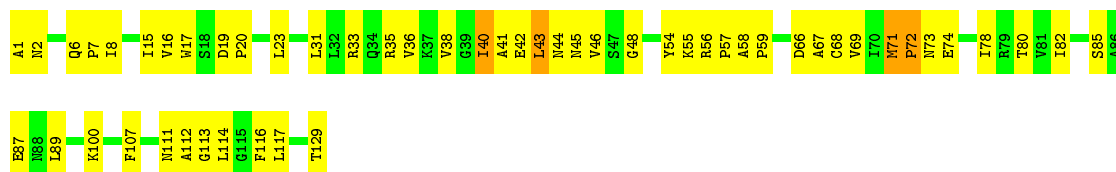
- Molecule 1: Coat protein

Chain CE: 68% 29% ..



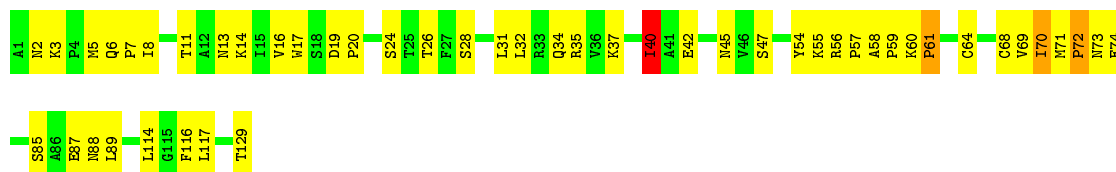
- Molecule 1: Coat protein

Chain CF: 59% 38% .



- Molecule 1: Coat protein

Chain CG: 62% 35% ..



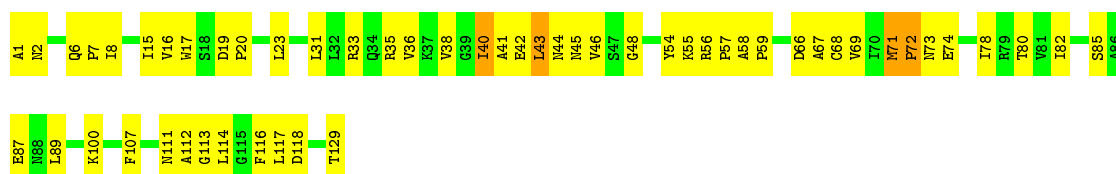
- Molecule 1: Coat protein

Chain CH: 67% 30% ..



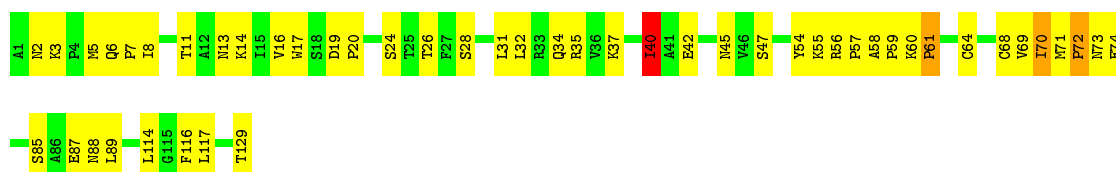
- Molecule 1: Coat protein

Chain CI: 58% 39% .



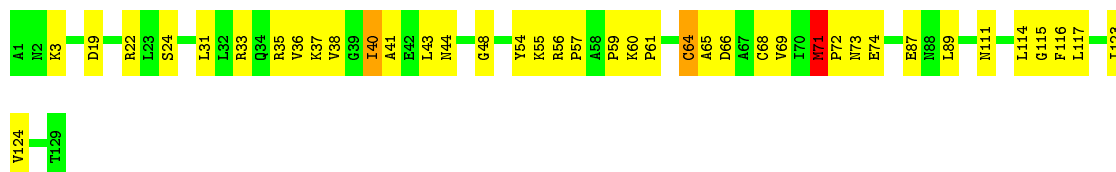
- Molecule 1: Coat protein

Chain CJ: 62% 35% ..



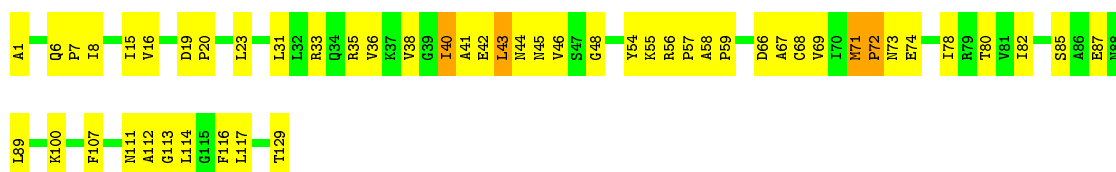
- Molecule 1: Coat protein

Chain CK: 69% 29% ..



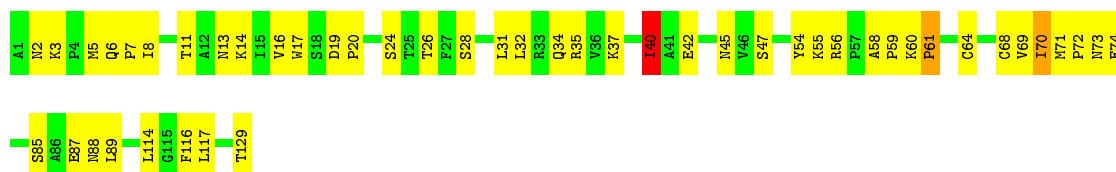
- Molecule 1: Coat protein

Chain CL: 60% 36% .



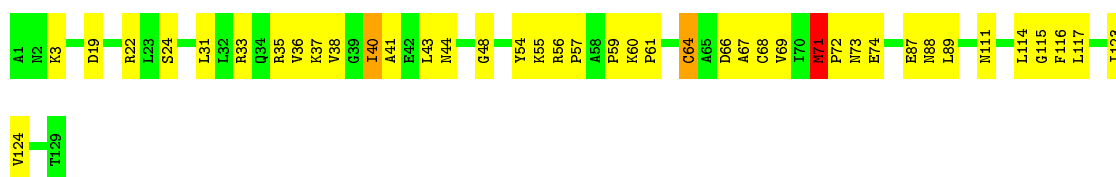
- Molecule 1: Coat protein

Chain CM: 63% 35% ..



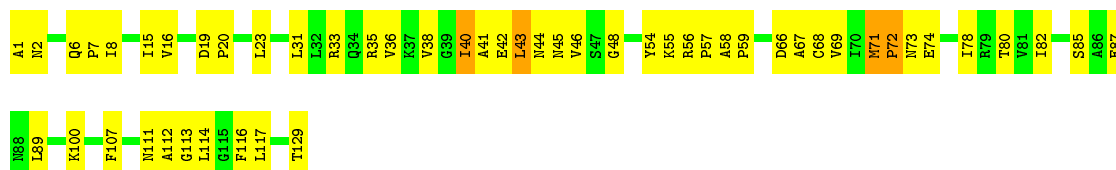
- Molecule 1: Coat protein

Chain CN: 68% 29% ..



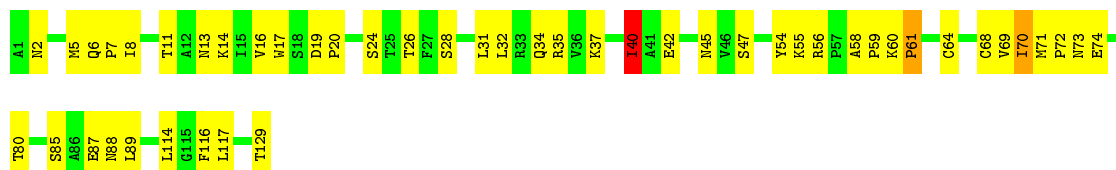
- Molecule 1: Coat protein

Chain CO: 60% 37%



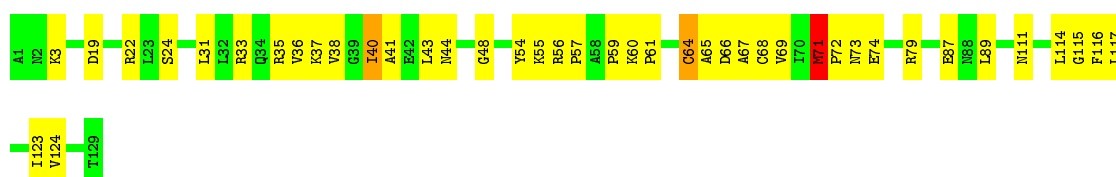
- Molecule 1: Coat protein

Chain CP: 63% 35%



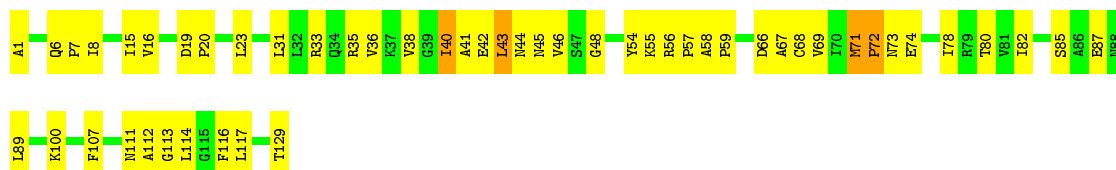
- Molecule 1: Coat protein

Chain CQ: 67% 30%



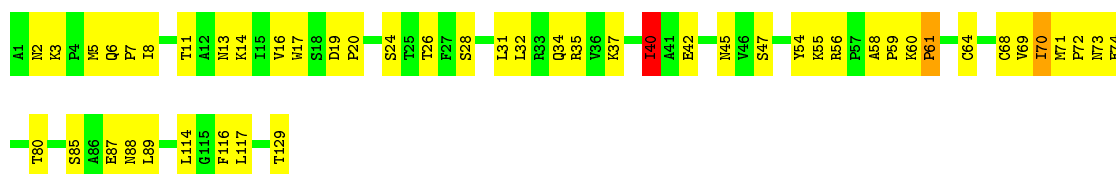
- Molecule 1: Coat protein

Chain CR: 60% 36%



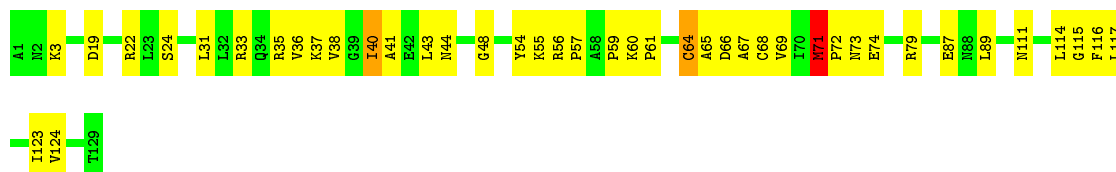
- Molecule 1: Coat protein

Chain CS: 62% 36%



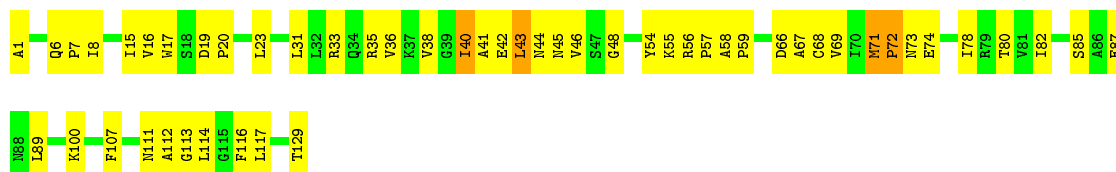
- Molecule 1: Coat protein

Chain CT: 67% 30% ..



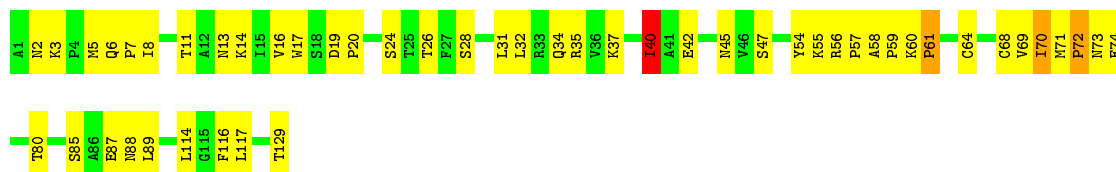
- Molecule 1: Coat protein

Chain CU: 60% 37% .



- Molecule 1: Coat protein

Chain CV: 61% 36% ..



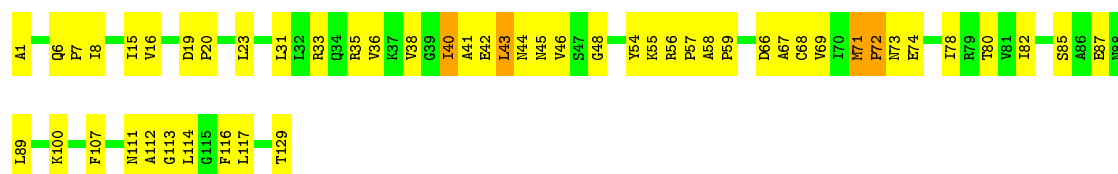
- Molecule 1: Coat protein

Chain CW: 67% 30% ..

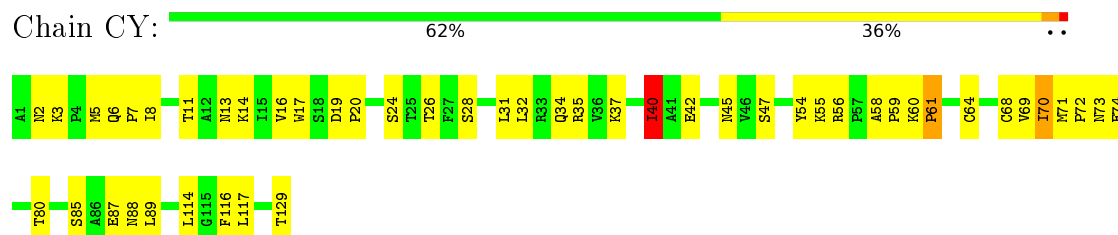


- Molecule 1: Coat protein

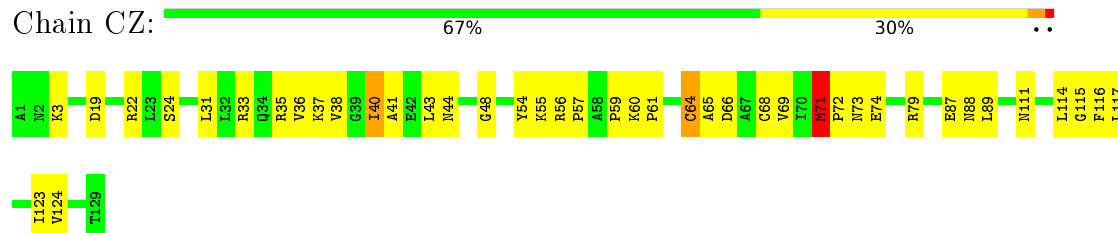
Chain CX: 60% 36% .



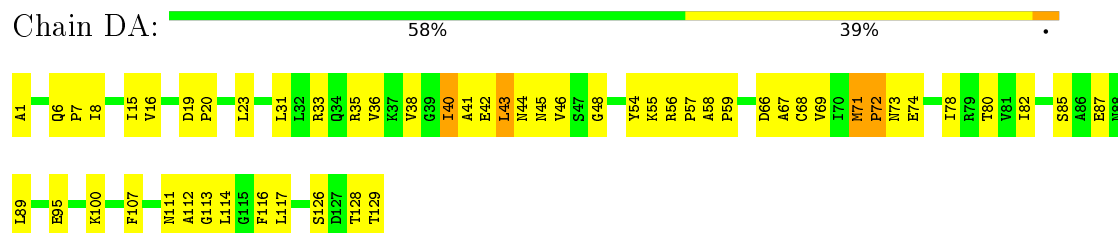
- Molecule 1: Coat protein



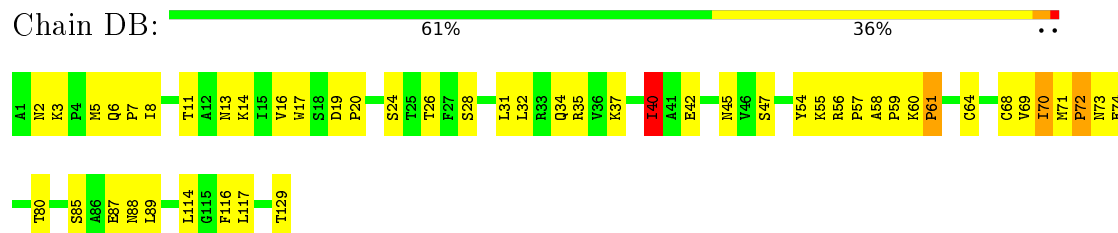
- Molecule 1: Coat protein



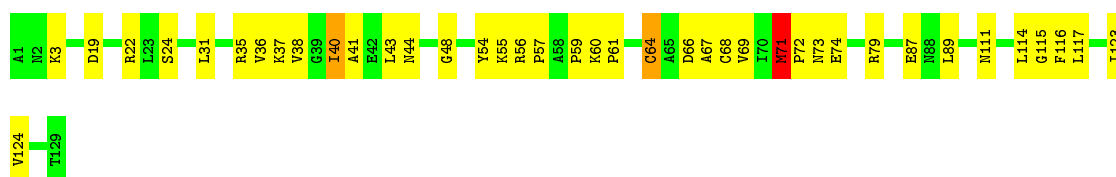
- Molecule 1: Coat protein



- Molecule 1: Coat protein

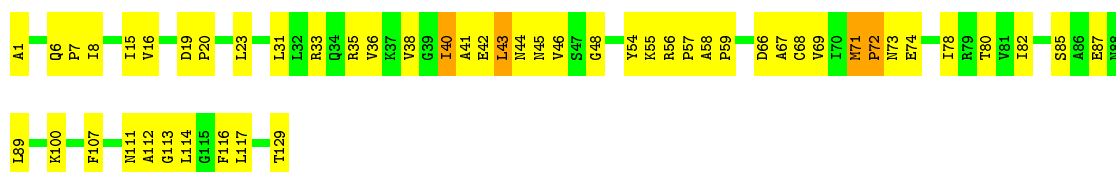


- Molecule 1: Coat protein



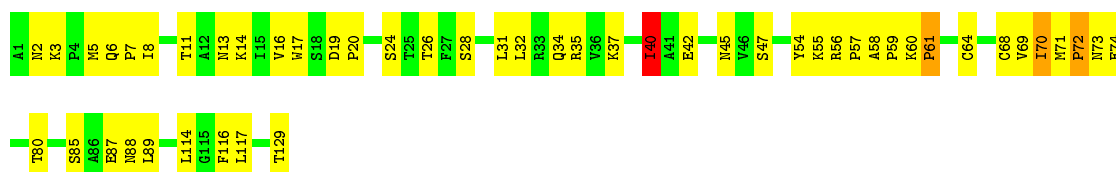
- Molecule 1: Coat protein

Chain DD: 60% 36%



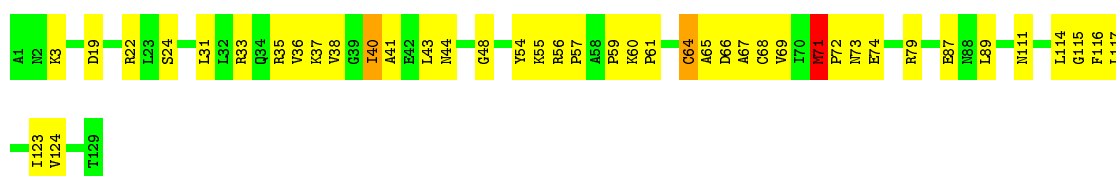
- Molecule 1: Coat protein

Chain DE: 61% 36%



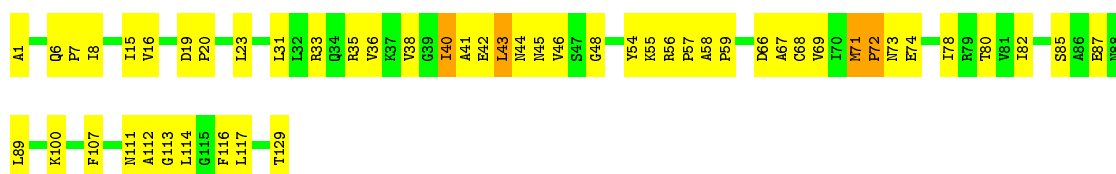
- Molecule 1: Coat protein

Chain DF: 67% 30%



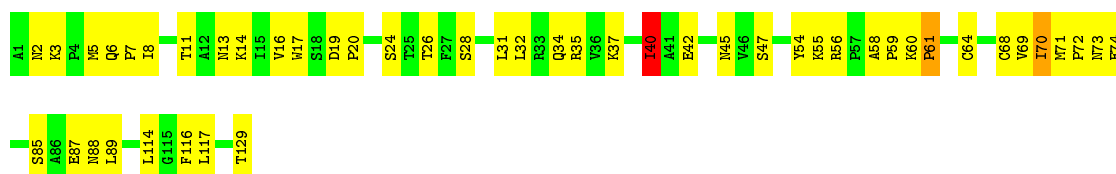
- Molecule 1: Coat protein

Chain DG: 60% 36%



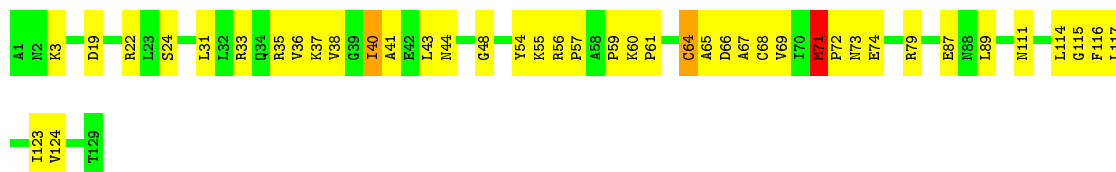
- Molecule 1: Coat protein

Chain DH: 63% 35%



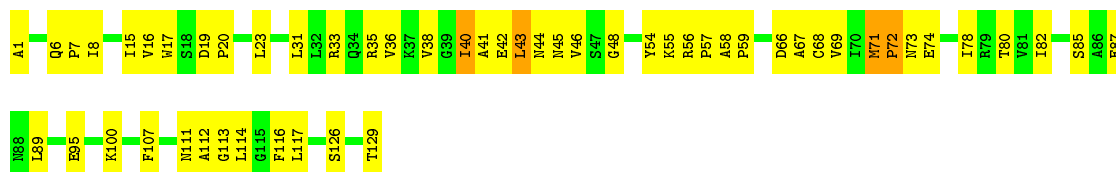
- Molecule 1: Coat protein

Chain DI: 67% 30% ..



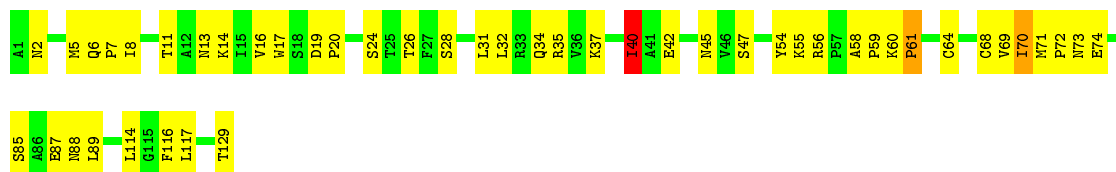
- Molecule 1: Coat protein

Chain DJ: 58% 39% .



- Molecule 1: Coat protein

Chain DK: 64% 34% ..



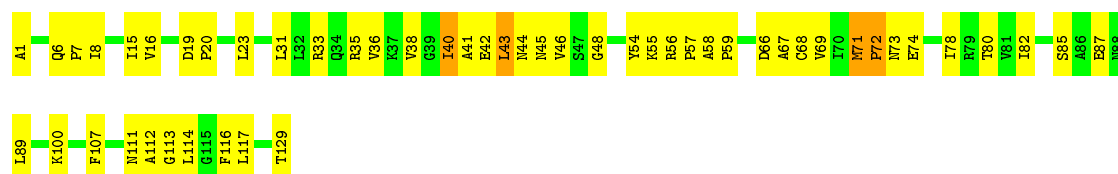
- Molecule 1: Coat protein

Chain DL: 68% 29% ..



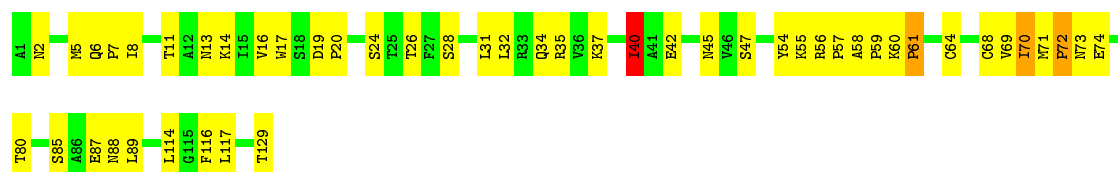
- Molecule 1: Coat protein

Chain DM: 60% 36% .



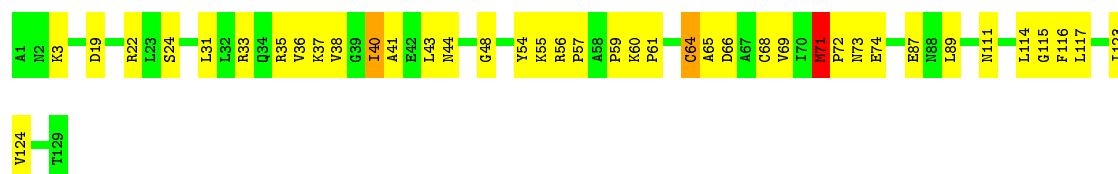
- Molecule 1: Coat protein

Chain DN: 62% 35%



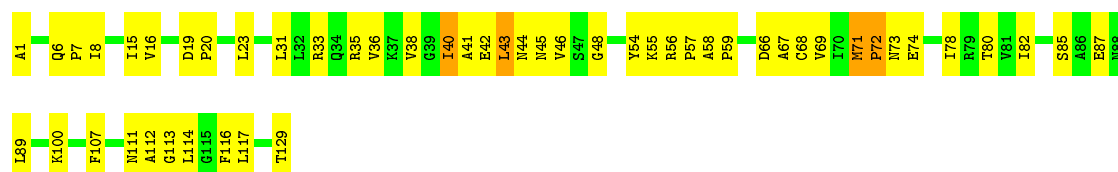
- Molecule 1: Coat protein

Chain DO: 69% 29%



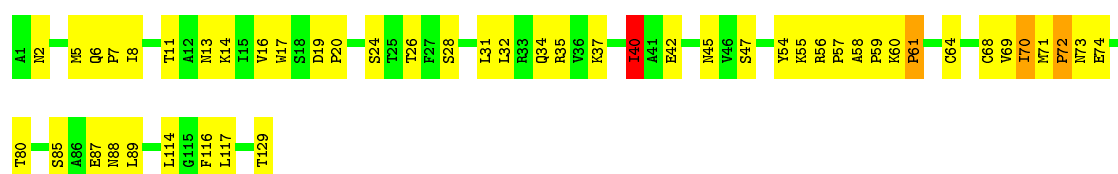
- Molecule 1: Coat protein

Chain DP: 60% 36%



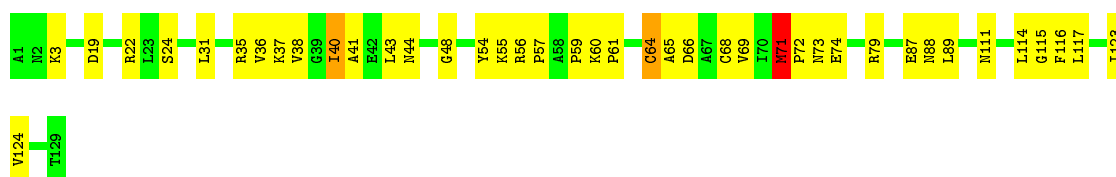
- Molecule 1: Coat protein

Chain DQ: 62% 35%



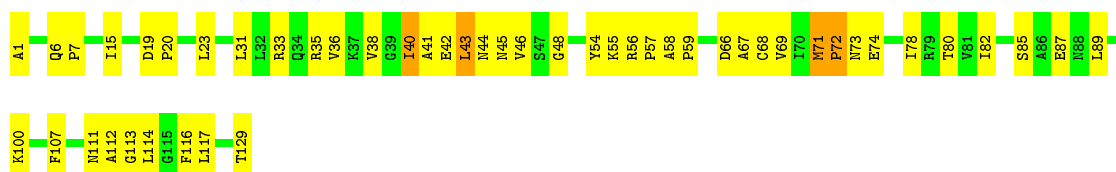
- Molecule 1: Coat protein

Chain DR: 68% 29%



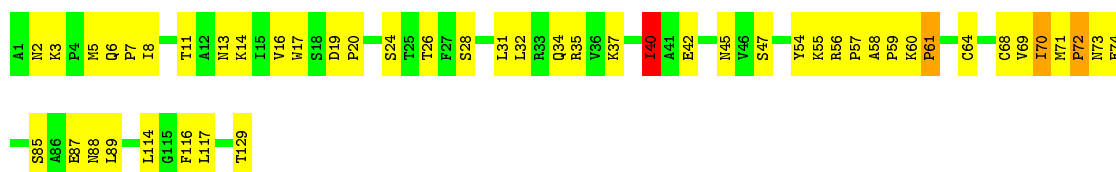
- Molecule 1: Coat protein

Chain DS: 62% 35% .



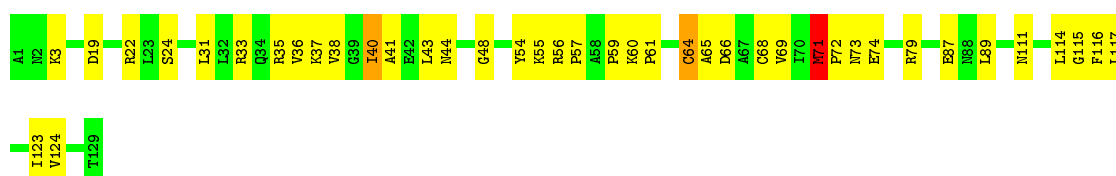
- Molecule 1: Coat protein

Chain DT: 62% 35% ..



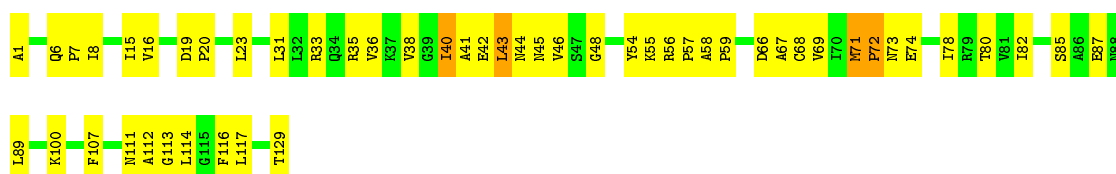
- Molecule 1: Coat protein

Chain DU: 68% 29% ..



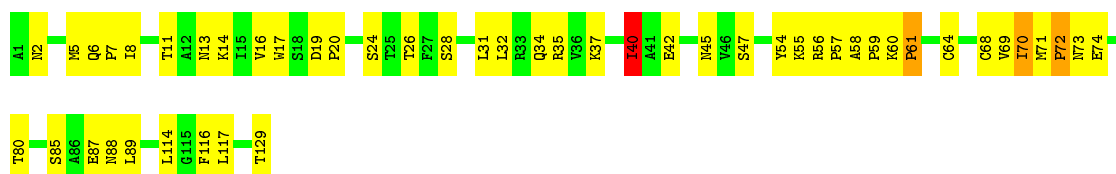
- Molecule 1: Coat protein

Chain DV: 60% 36% .



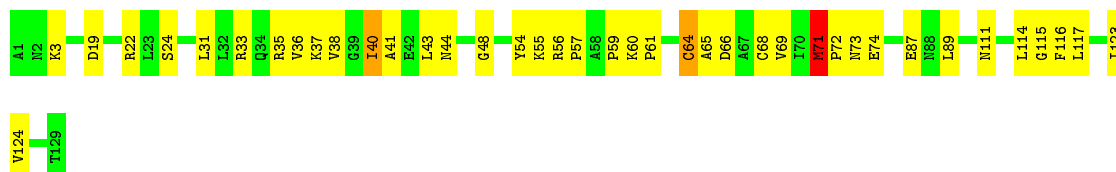
- Molecule 1: Coat protein

Chain DW: 62% 35% ..



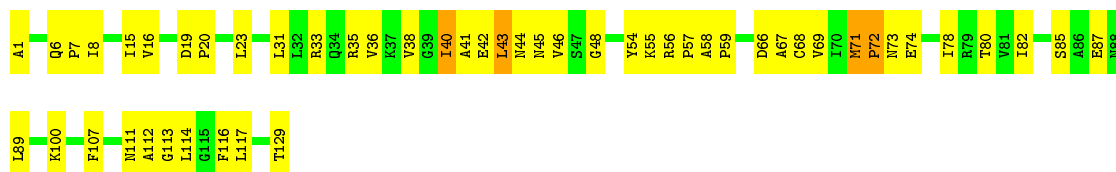
- Molecule 1: Coat protein

Chain DX: 69% 29% ..



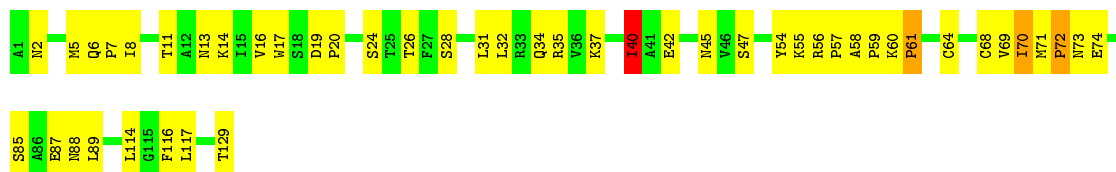
- Molecule 1: Coat protein

Chain DY: 60% 36% .



- Molecule 1: Coat protein

Chain DZ: 63% 34% ..



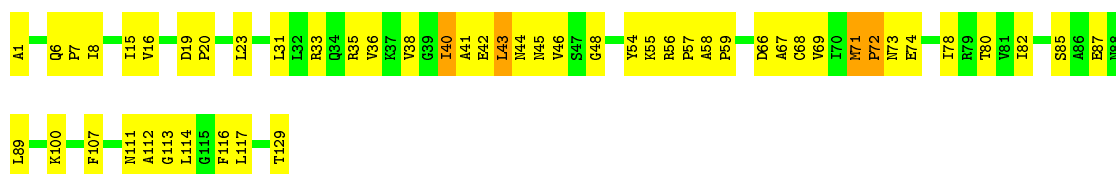
- Molecule 1: Coat protein

Chain EA: 67% 30% ..



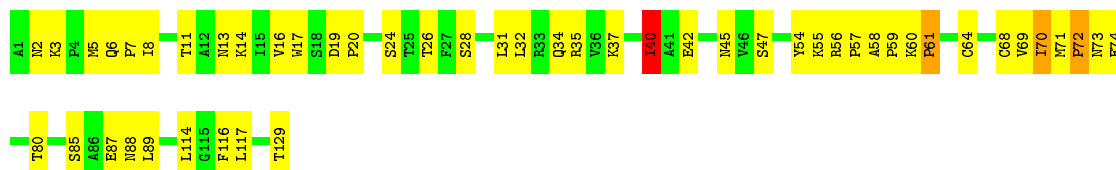
- Molecule 1: Coat protein

Chain EB: 60% 36% .



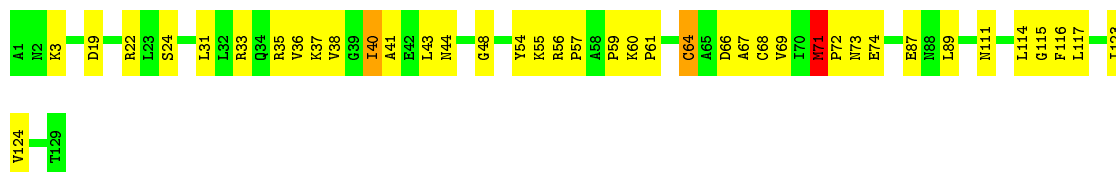
- Molecule 1: Coat protein

Chain EC: 61% 36% ..



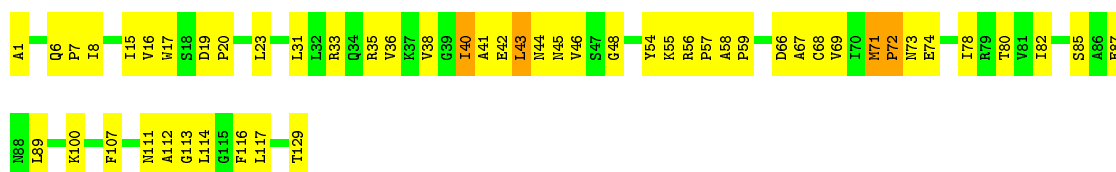
- Molecule 1: Coat protein

Chain ED: 69% 29% ..



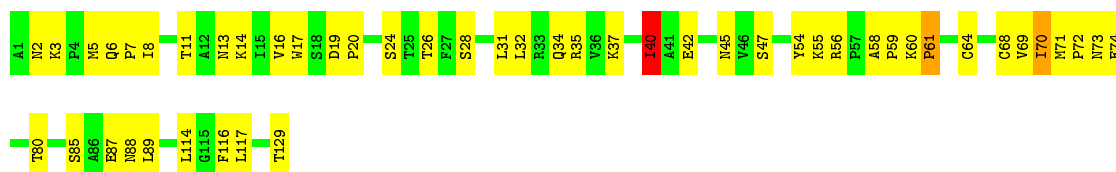
- Molecule 1: Coat protein

Chain EE: 60% 37% .



- Molecule 1: Coat protein

Chain EF: 62% 36% ..



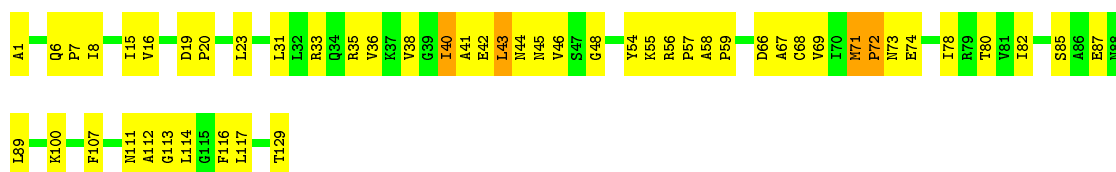
- Molecule 1: Coat protein

Chain EG: 67% 30% ..



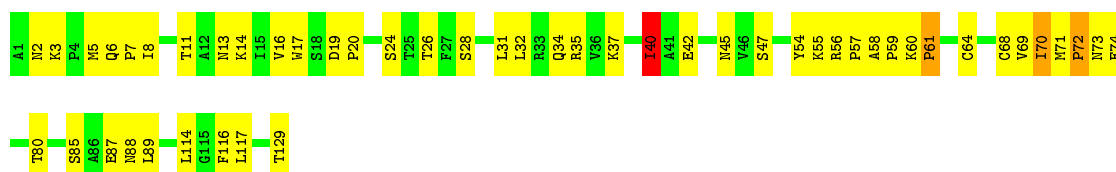
- Molecule 1: Coat protein

Chain EH: 60% 36% .



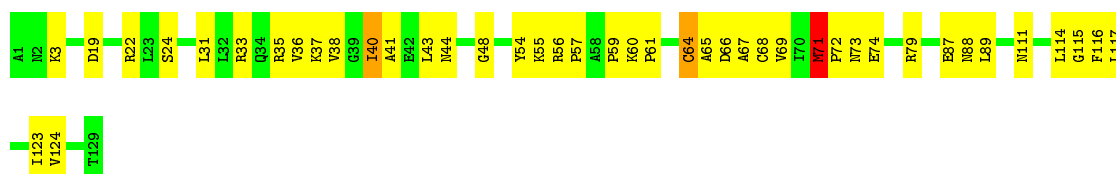
- Molecule 1: Coat protein

Chain EI: 61% 36% ..



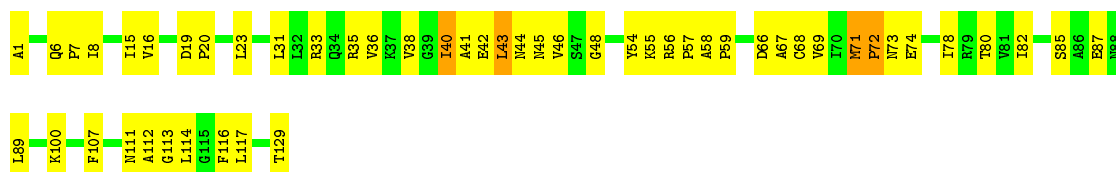
- Molecule 1: Coat protein

Chain EJ: 67% 31% ..



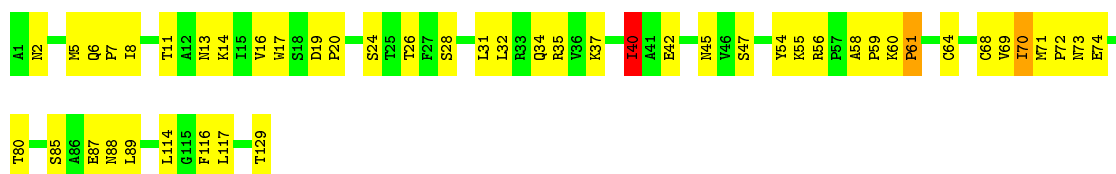
- Molecule 1: Coat protein

Chain EK: 60% 36% .



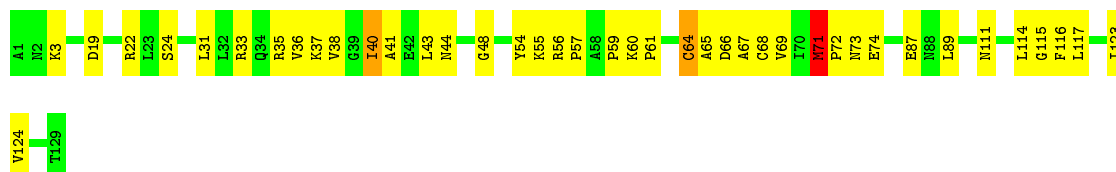
- Molecule 1: Coat protein

Chain EL: 63% 35% ..



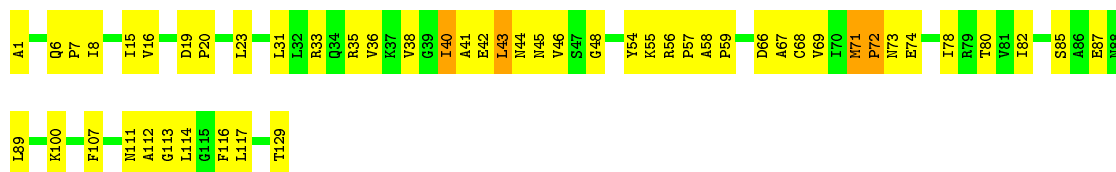
- Molecule 1: Coat protein

Chain EM: 68% 29% ..



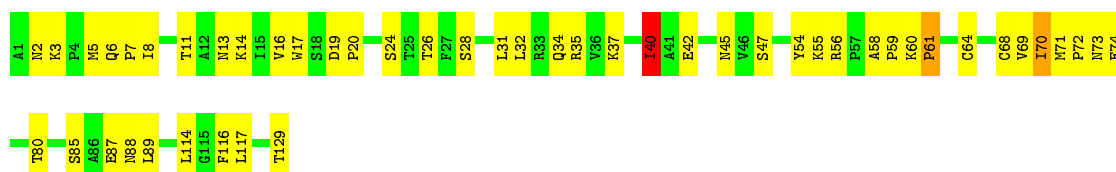
- Molecule 1: Coat protein

Chain EN: 60% 36% .



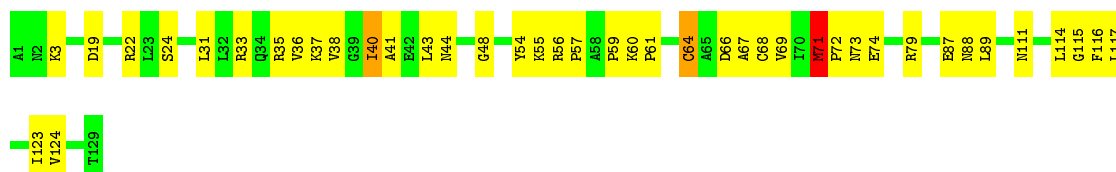
- Molecule 1: Coat protein

Chain EO: 62% 36% ..



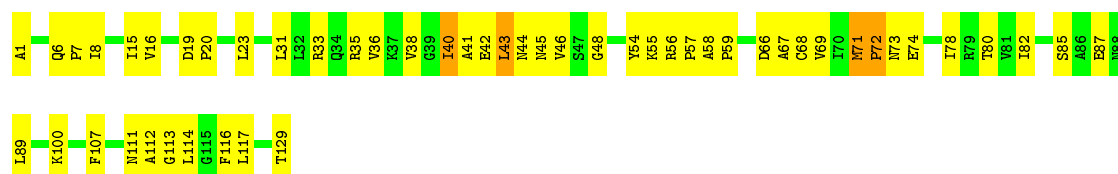
- Molecule 1: Coat protein

Chain EP: 67% 30% ..

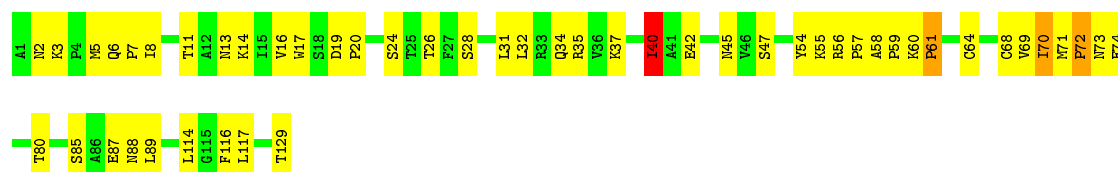


- Molecule 1: Coat protein

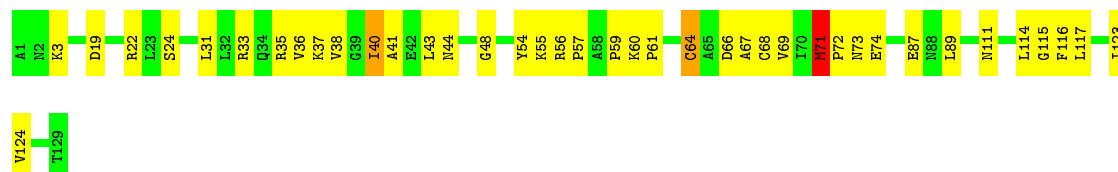
Chain EQ: 60% 36% .



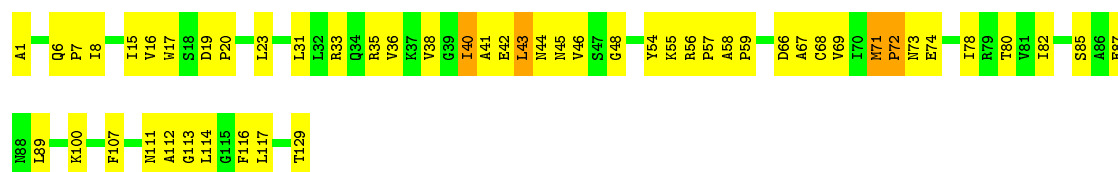
- Molecule 1: Coat protein



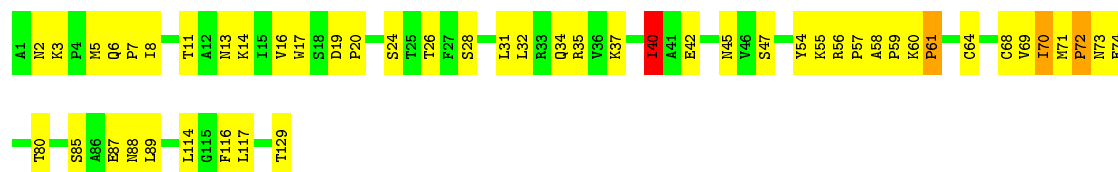
- Molecule 1: Coat protein



- Molecule 1: Coat protein

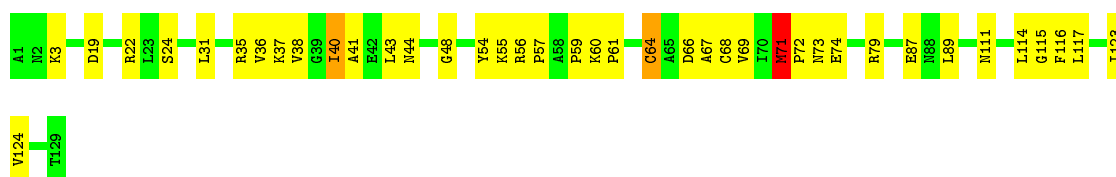


- Molecule 1: Coat protein



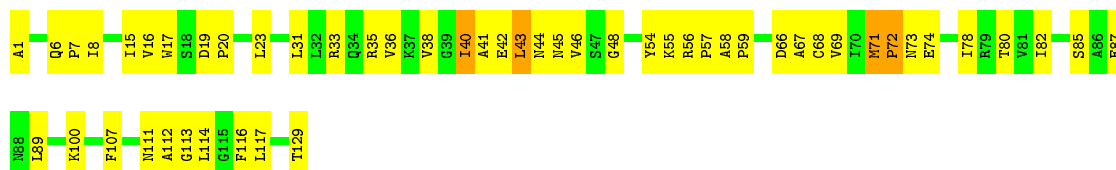
- Molecule 1: Coat protein





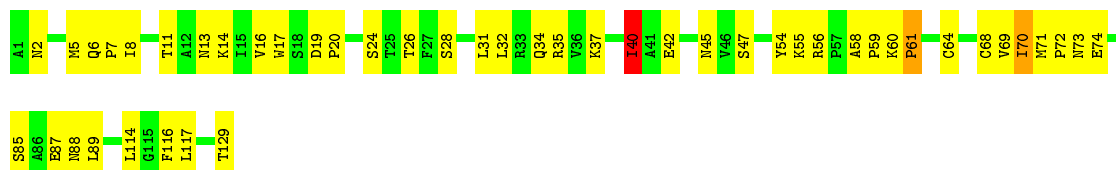
- Molecule 1: Coat protein

Chain EW: 60% 37%



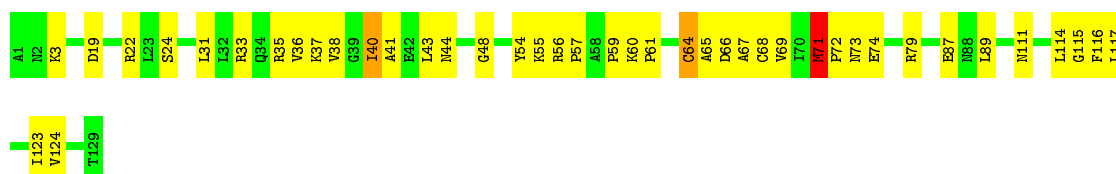
- Molecule 1: Coat protein

Chain EX: 64% 34%



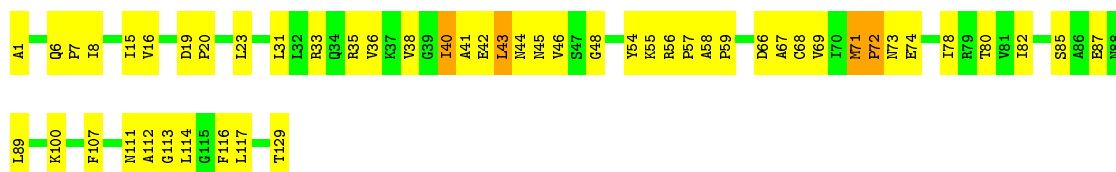
- Molecule 1: Coat protein

Chain EY: 67% 30%



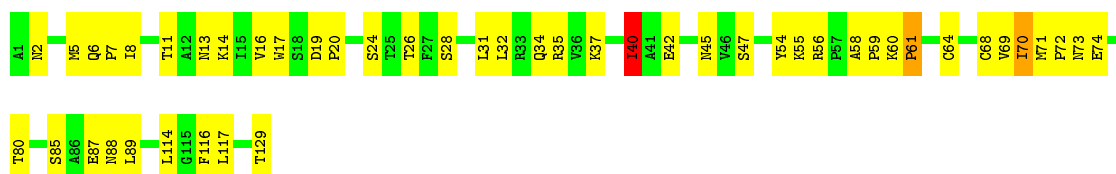
- Molecule 1: Coat protein

Chain EZ: 60% 36%



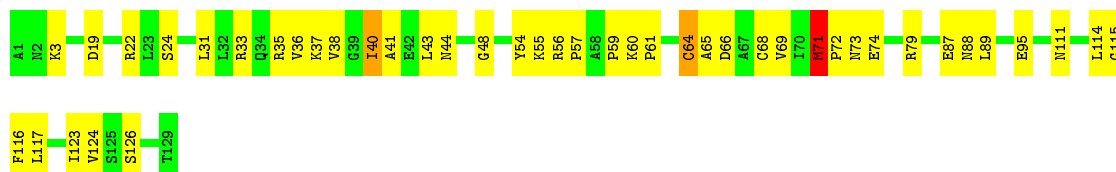
- Molecule 1: Coat protein

Chain FA: 63% 35%



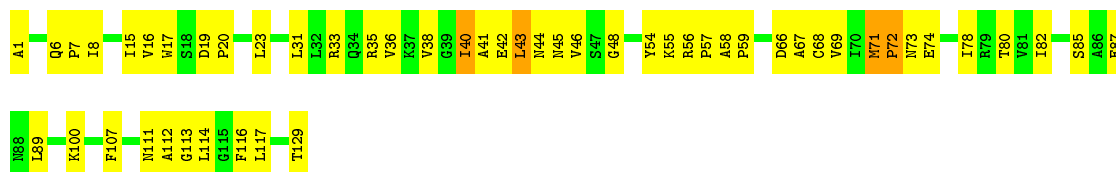
- Molecule 1: Coat protein

Chain FB: 66% 32% ..



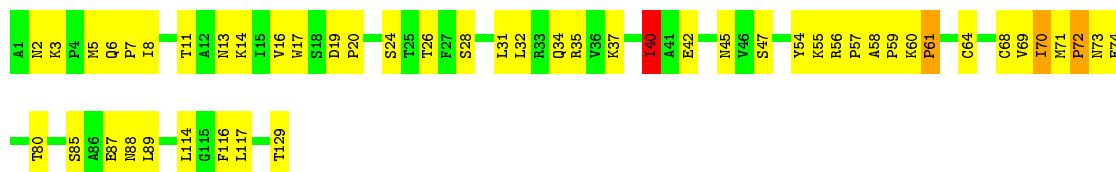
- Molecule 1: Coat protein

Chain FC: 60% 37% .



- Molecule 1: Coat protein

Chain FD: 61% 36% ..



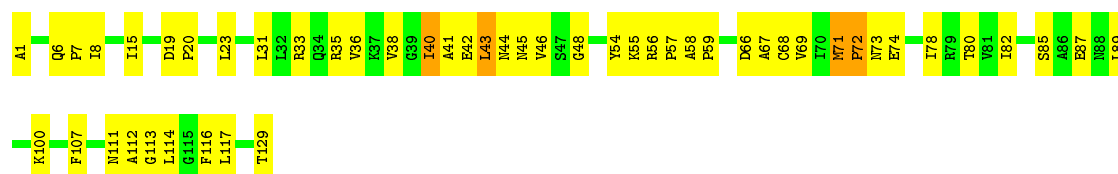
- Molecule 1: Coat protein

Chain FE: 67% 31% ..



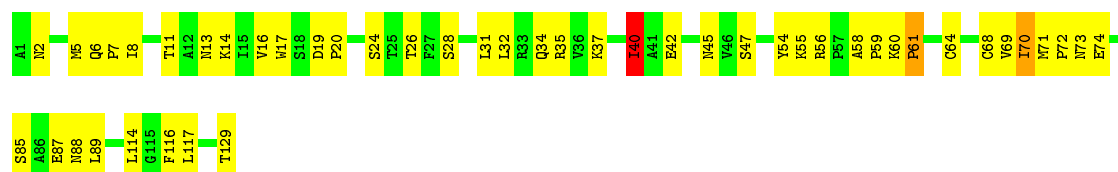
- Molecule 1: Coat protein

Chain FF: 61% 36% .



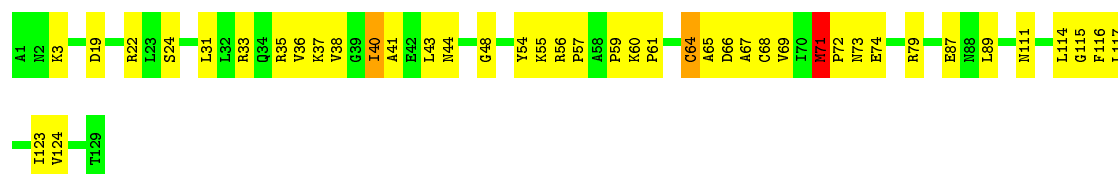
- Molecule 1: Coat protein

Chain FG: 64% 34% ..



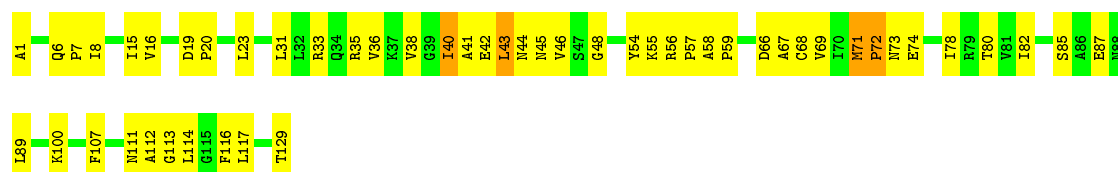
- Molecule 1: Coat protein

Chain FH: 67% 30% ..



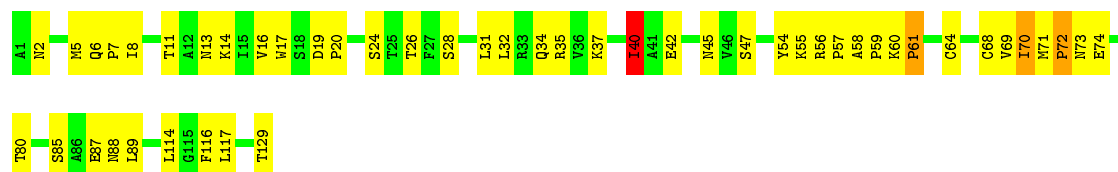
- Molecule 1: Coat protein

Chain FI: 60% 36% .



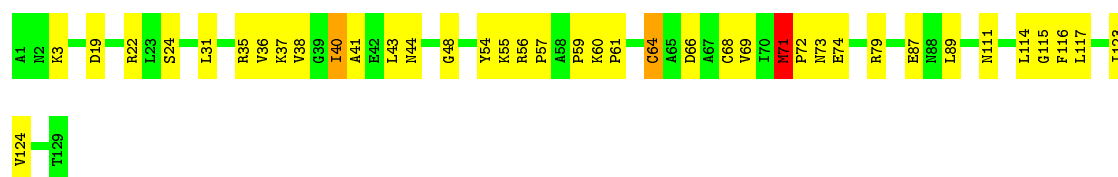
- Molecule 1: Coat protein

Chain FJ: 62% 35% ..

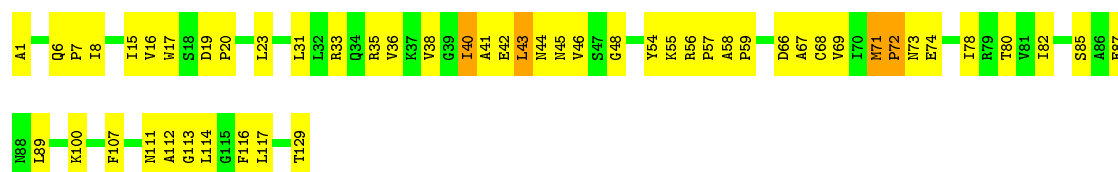


- Molecule 1: Coat protein

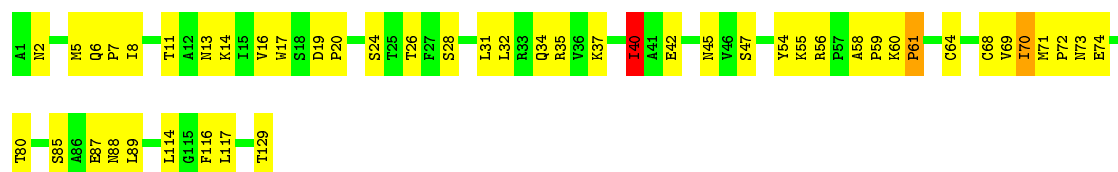
Chain FK: 70% 28% ..



- Molecule 1: Coat protein



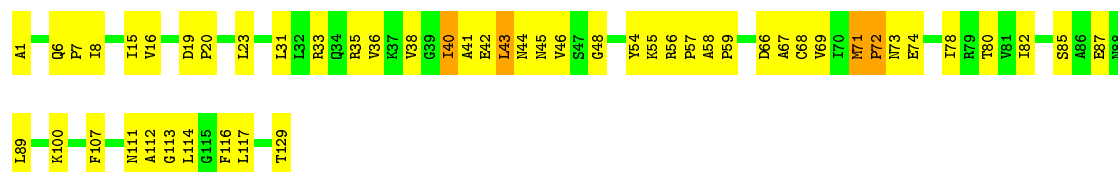
- Molecule 1: Coat protein



- Molecule 1: Coat protein

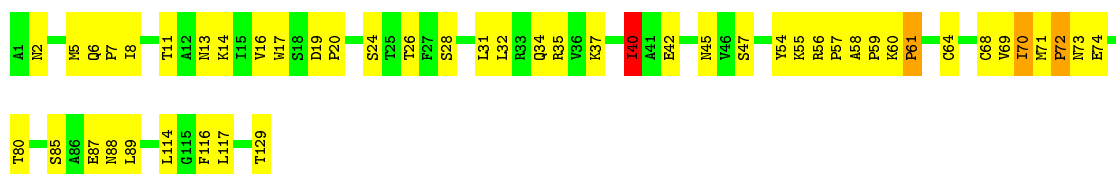


- Molecule 1: Coat protein



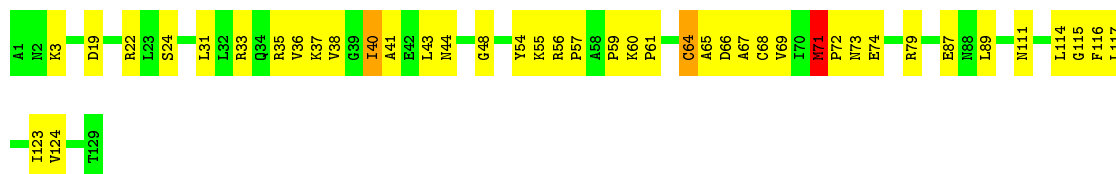
- Molecule 1: Coat protein





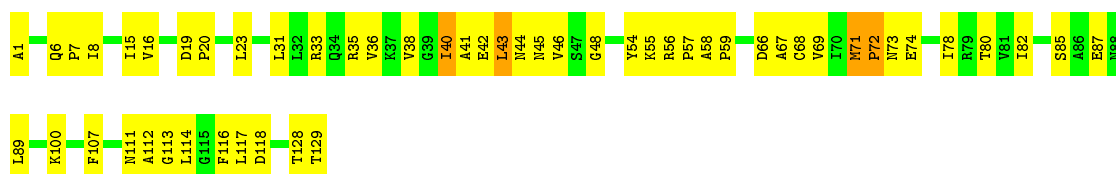
- Molecule 1: Coat protein

Chain FQ: 67% 30% ..



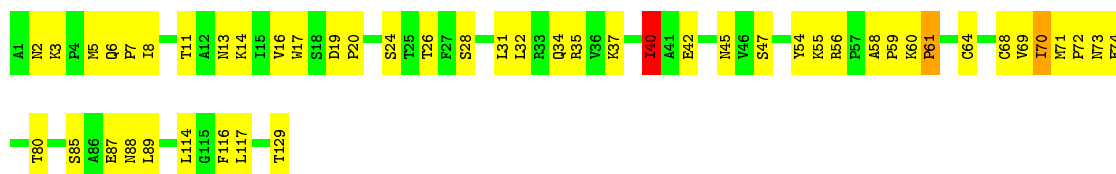
- Molecule 1: Coat protein

Chain FR: 59% 38% .



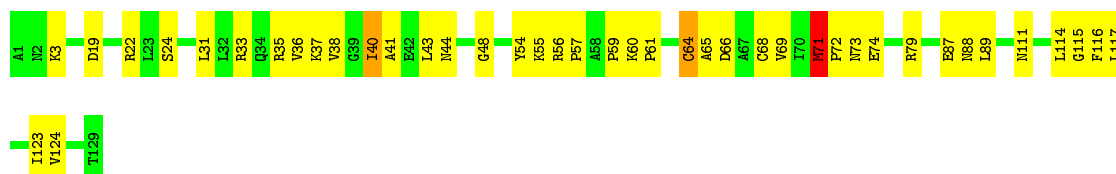
- Molecule 1: Coat protein

Chain FS: 62% 36% ..



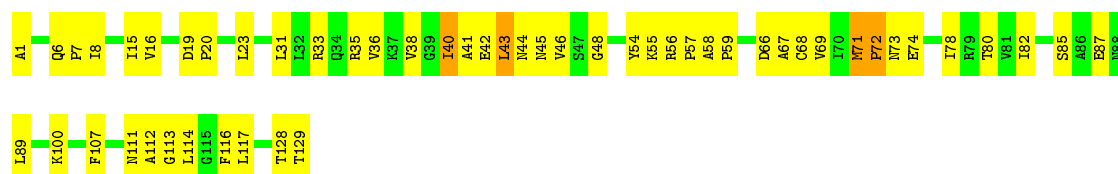
- Molecule 1: Coat protein

Chain FT: 67% 30% ..



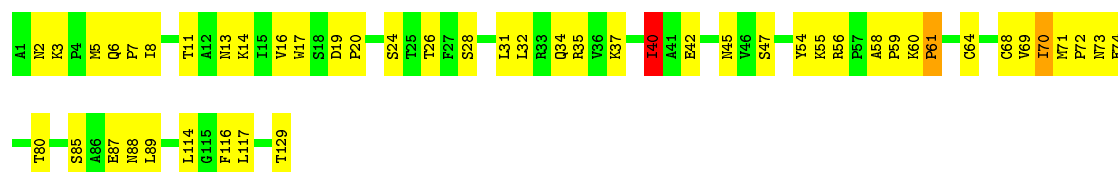
- Molecule 1: Coat protein

Chain FU: 60% 37% .



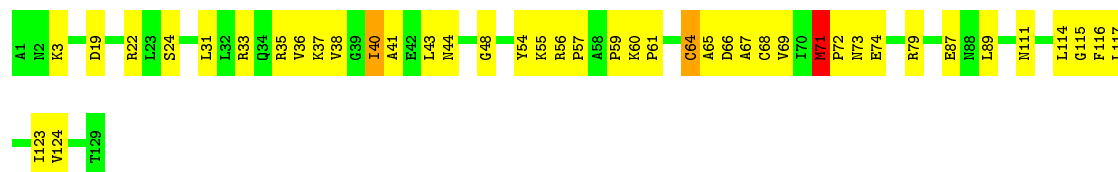
- Molecule 1: Coat protein

Chain FV: 62% 36% ..



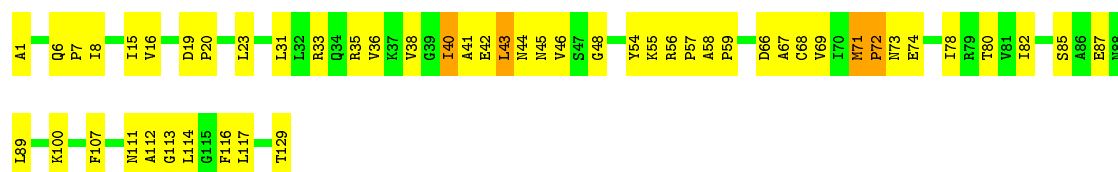
- Molecule 1: Coat protein

Chain FW: 67% 30% ..



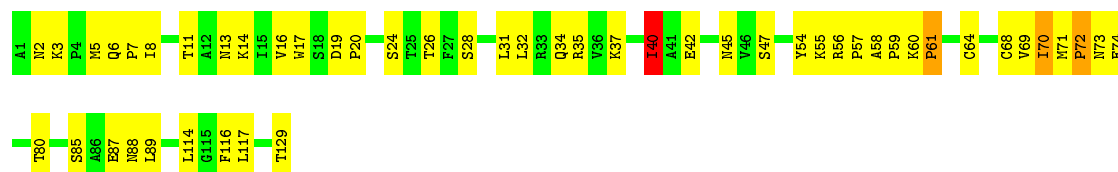
- Molecule 1: Coat protein

Chain FX: 60% 36% .



- Molecule 1: Coat protein

Chain FY: 61% 36% ..



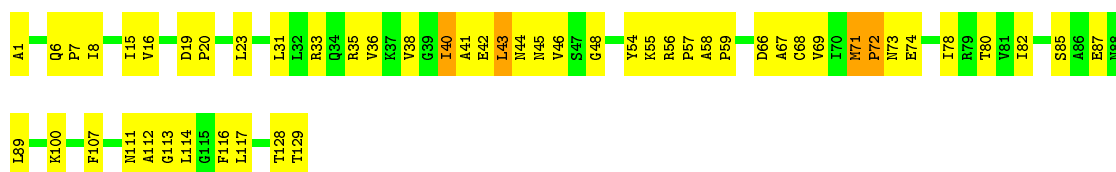
- Molecule 1: Coat protein

Chain FZ: 67% 30% ..



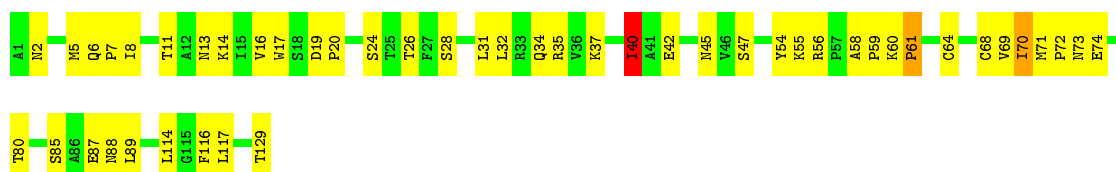
- Molecule 1: Coat protein

Chain GA: 60% 37%



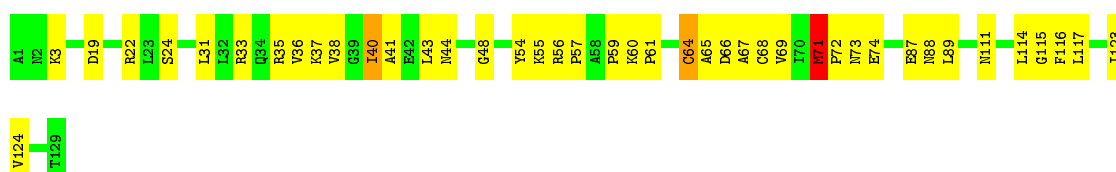
- Molecule 1: Coat protein

Chain GB: 63% 35%



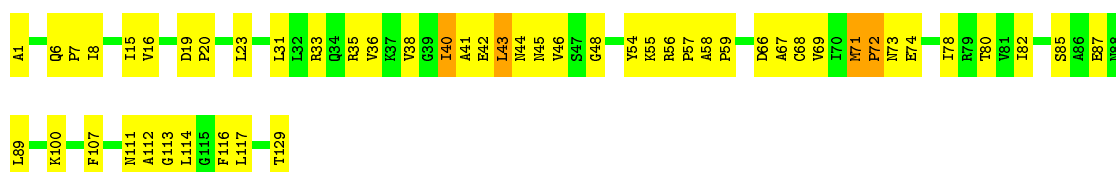
- Molecule 1: Coat protein

Chain GC: 67% 30%



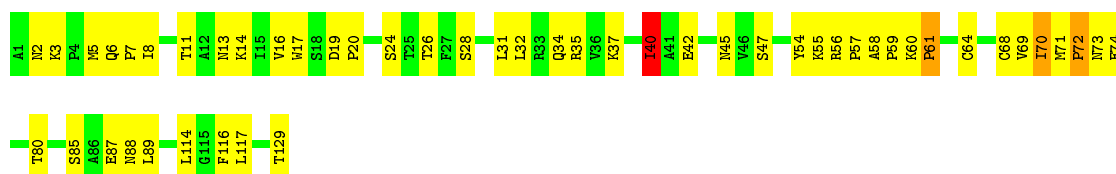
- Molecule 1: Coat protein

Chain GD: 60% 36%



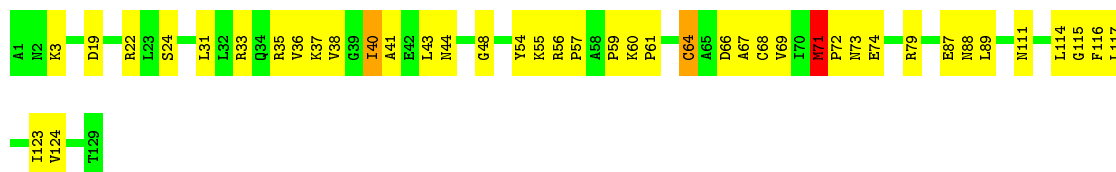
- Molecule 1: Coat protein

Chain GE: 61% 36%



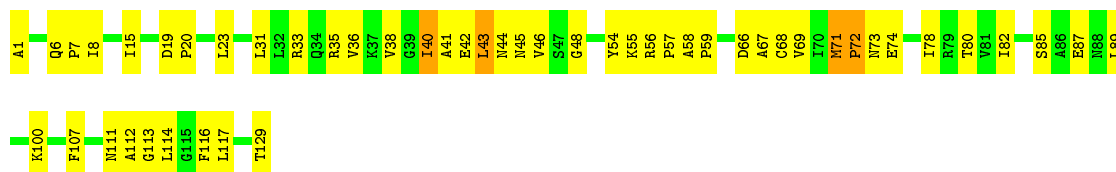
- Molecule 1: Coat protein

Chain GF: 67% 30% ..



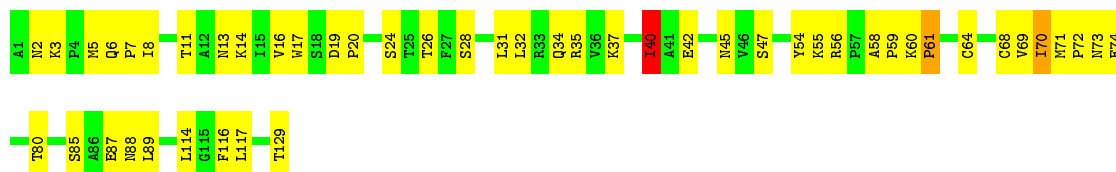
- Molecule 1: Coat protein

Chain GG: 61% 36% .



- Molecule 1: Coat protein

Chain GH: 62% 36% ..



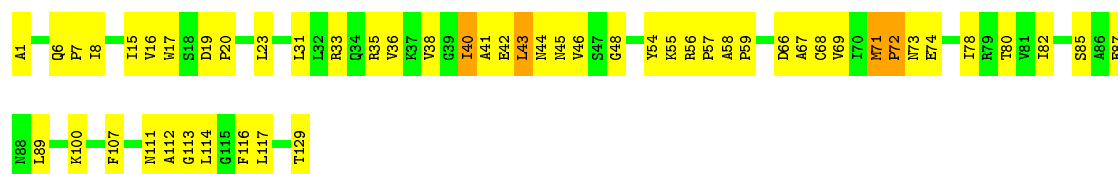
- Molecule 1: Coat protein

Chain GI: 68% 29% ..



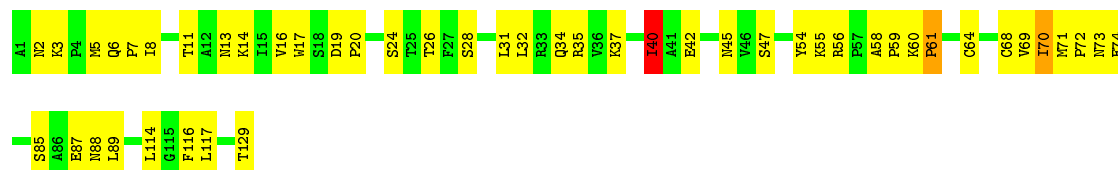
- Molecule 1: Coat protein

Chain GJ: 60% 37% .



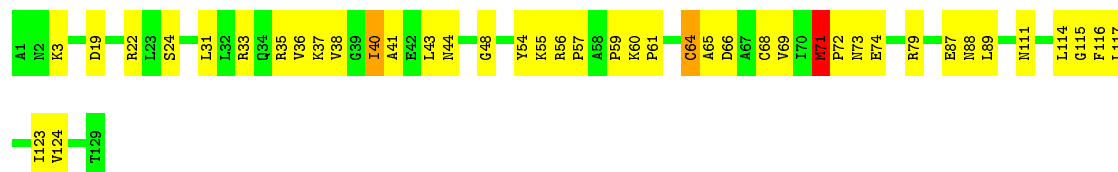
- Molecule 1: Coat protein

Chain GK: 63% 35% ..



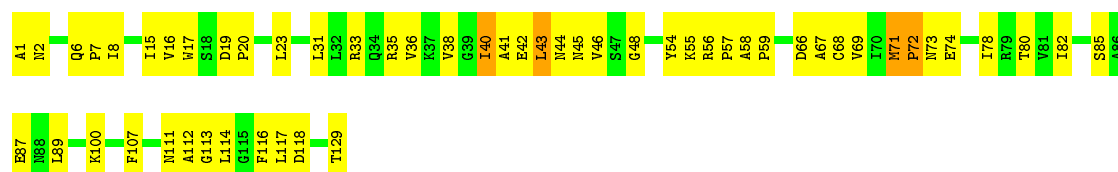
- Molecule 1: Coat protein

Chain GL: 67% 30% ..



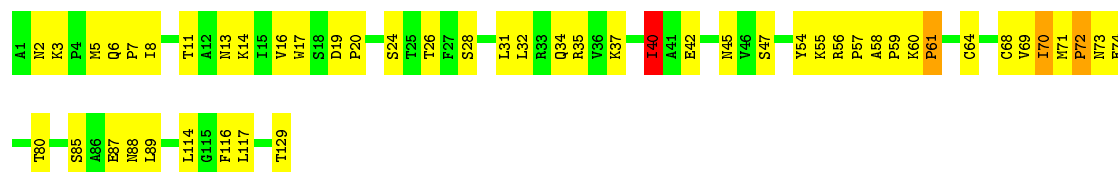
- Molecule 1: Coat protein

Chain GM: 58% 39% .



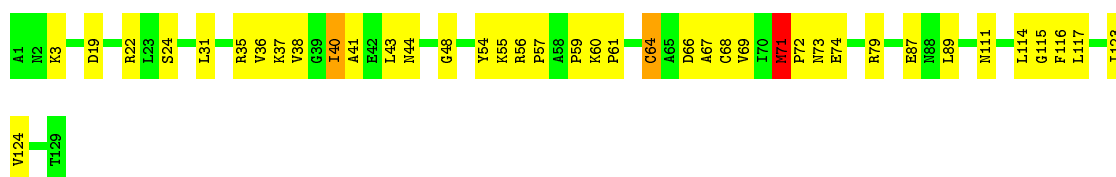
- Molecule 1: Coat protein

Chain GN: 61% 36% ..



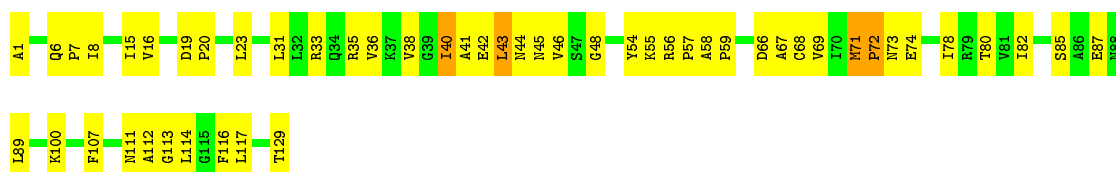
- Molecule 1: Coat protein

Chain GO: 69% 29% ..



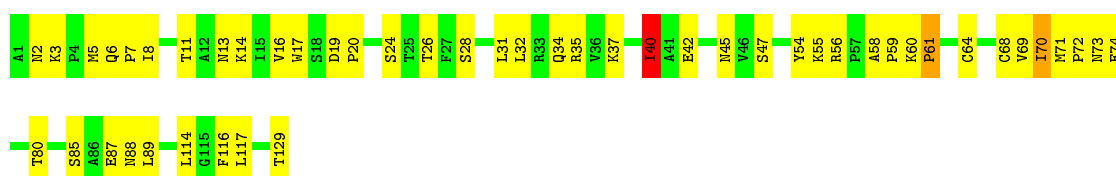
- Molecule 1: Coat protein

Chain GP: 60% 36%



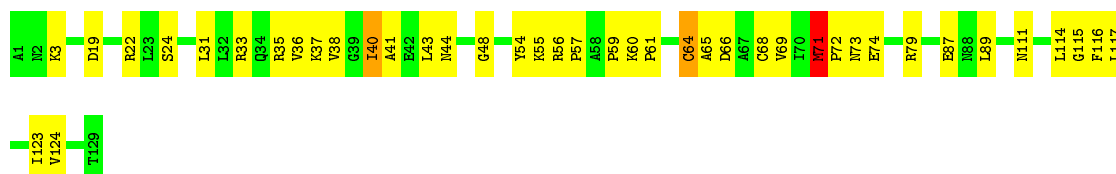
- Molecule 1: Coat protein

Chain GQ: 62% 36%



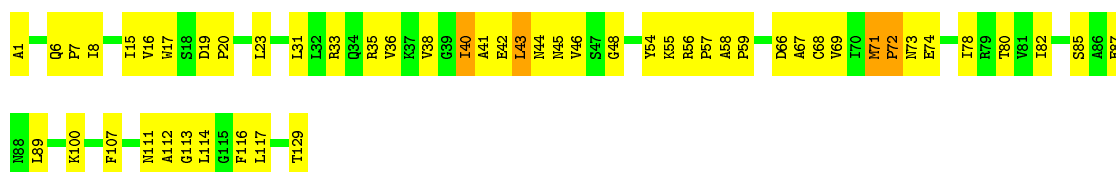
- Molecule 1: Coat protein

Chain GR: 68% 29%



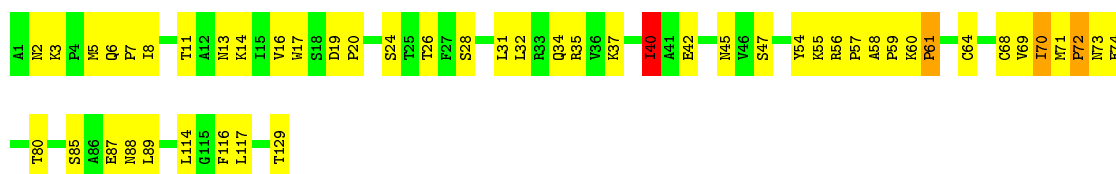
- Molecule 1: Coat protein

Chain GS: 60% 37%



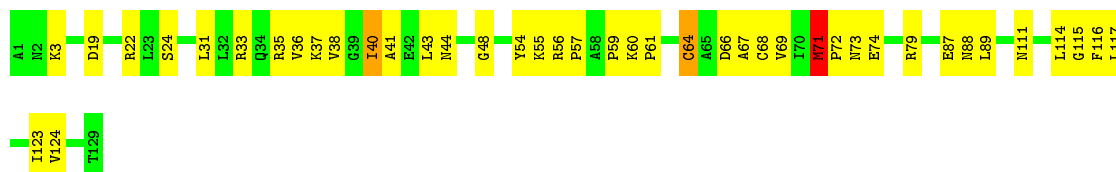
- Molecule 1: Coat protein

Chain GT: 61% 36%



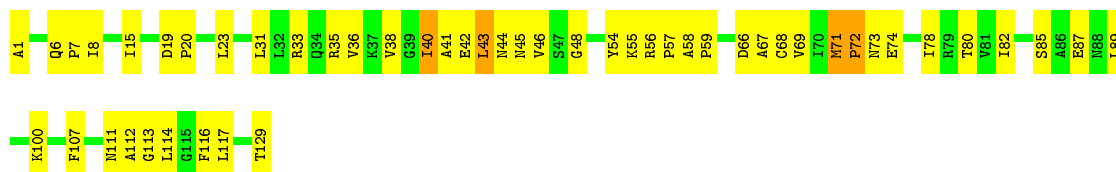
- Molecule 1: Coat protein

Chain GU: 67% 30% ..



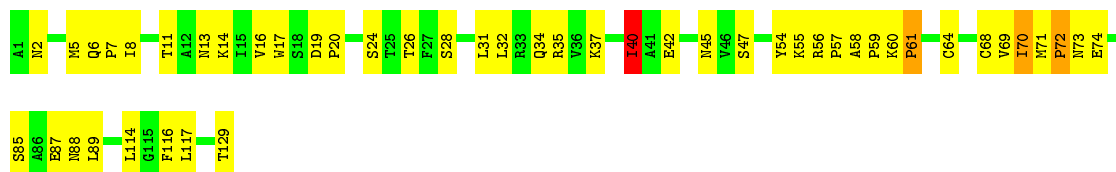
- Molecule 1: Coat protein

Chain GV: 61% 36% .



- Molecule 1: Coat protein

Chain GW: 63% 34% ..



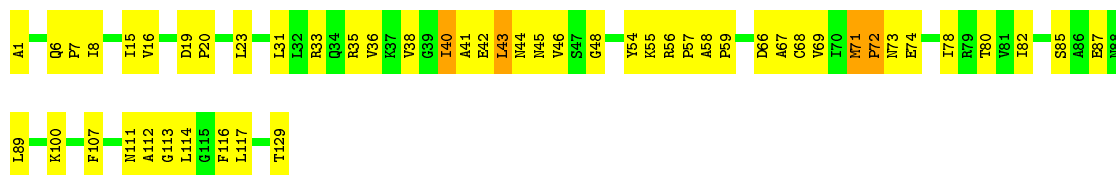
- Molecule 1: Coat protein

Chain GX: 69% 29% ..



- Molecule 1: Coat protein

Chain GY: 60% 36% .



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	2215	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	59000	Depositor
Image detector	Not provided	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 >2	RMSZ	# Z >2
1	AB	0.48	0/985	0.71	1/1342 (0.1%)
1	AC	0.44	0/985	0.69	1/1342 (0.1%)
1	AD	0.51	0/985	0.65	0/1342
1	AE	0.48	0/985	0.71	1/1342 (0.1%)
1	AF	0.44	0/985	0.70	1/1342 (0.1%)
1	AG	0.51	0/985	0.65	0/1342
1	AH	0.48	0/985	0.71	1/1342 (0.1%)
1	AI	0.44	0/985	0.70	1/1342 (0.1%)
1	AJ	0.51	0/985	0.65	0/1342
1	AK	0.48	0/985	0.71	1/1342 (0.1%)
1	AL	0.44	0/985	0.69	1/1342 (0.1%)
1	AM	0.51	0/985	0.65	0/1342
1	AN	0.47	0/985	0.71	1/1342 (0.1%)
1	AO	0.44	0/985	0.69	1/1342 (0.1%)
1	AP	0.51	0/985	0.65	0/1342
1	AQ	0.48	0/985	0.71	1/1342 (0.1%)
1	AR	0.44	0/985	0.69	1/1342 (0.1%)
1	AS	0.51	0/985	0.65	0/1342
1	AT	0.48	0/985	0.71	1/1342 (0.1%)
1	AU	0.44	0/985	0.70	1/1342 (0.1%)
1	AV	0.51	0/985	0.65	0/1342
1	AW	0.48	0/985	0.71	1/1342 (0.1%)
1	AX	0.44	0/985	0.69	1/1342 (0.1%)
1	AY	0.51	0/985	0.65	0/1342
1	AZ	0.47	0/985	0.71	1/1342 (0.1%)
1	BA	0.44	0/985	0.69	1/1342 (0.1%)
1	BB	0.51	0/985	0.65	0/1342
1	BC	0.48	0/985	0.71	1/1342 (0.1%)
1	BD	0.44	0/985	0.70	1/1342 (0.1%)
1	BE	0.51	0/985	0.65	0/1342
1	BF	0.48	0/985	0.71	1/1342 (0.1%)
1	BG	0.44	0/985	0.69	1/1342 (0.1%)
1	BH	0.51	0/985	0.65	0/1342
1	BI	0.48	0/985	0.71	1/1342 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	BJ	0.44	0/985	0.70	1/1342 (0.1%)
1	BK	0.51	0/985	0.65	0/1342
1	BL	0.47	0/985	0.71	1/1342 (0.1%)
1	BM	0.44	0/985	0.69	1/1342 (0.1%)
1	BN	0.51	0/985	0.65	0/1342
1	BO	0.48	0/985	0.71	1/1342 (0.1%)
1	BP	0.44	0/985	0.70	1/1342 (0.1%)
1	BQ	0.51	0/985	0.65	0/1342
1	BR	0.48	0/985	0.71	1/1342 (0.1%)
1	BS	0.44	0/985	0.69	1/1342 (0.1%)
1	BT	0.51	0/985	0.65	0/1342
1	BU	0.47	0/985	0.71	1/1342 (0.1%)
1	BV	0.44	0/985	0.69	1/1342 (0.1%)
1	BW	0.51	0/985	0.65	0/1342
1	BX	0.48	0/985	0.71	1/1342 (0.1%)
1	BY	0.44	0/985	0.70	1/1342 (0.1%)
1	BZ	0.51	0/985	0.65	0/1342
1	CA	0.48	0/985	0.71	1/1342 (0.1%)
1	CB	0.44	0/985	0.69	1/1342 (0.1%)
1	CC	0.51	0/985	0.65	0/1342
1	CD	0.48	0/985	0.71	1/1342 (0.1%)
1	CE	0.44	0/985	0.69	1/1342 (0.1%)
1	CF	0.51	0/985	0.65	0/1342
1	CG	0.47	0/985	0.71	1/1342 (0.1%)
1	CH	0.44	0/985	0.69	1/1342 (0.1%)
1	CI	0.51	0/985	0.65	0/1342
1	CJ	0.48	0/985	0.71	1/1342 (0.1%)
1	CK	0.44	0/985	0.70	1/1342 (0.1%)
1	CL	0.51	0/985	0.65	0/1342
1	CM	0.48	0/985	0.71	1/1342 (0.1%)
1	CN	0.44	0/985	0.69	1/1342 (0.1%)
1	CO	0.51	0/985	0.65	0/1342
1	CP	0.48	0/985	0.71	1/1342 (0.1%)
1	CQ	0.44	0/985	0.69	1/1342 (0.1%)
1	CR	0.51	0/985	0.65	0/1342
1	CS	0.48	0/985	0.71	1/1342 (0.1%)
1	CT	0.44	0/985	0.70	1/1342 (0.1%)
1	CU	0.51	0/985	0.65	0/1342
1	CV	0.48	0/985	0.71	1/1342 (0.1%)
1	CW	0.44	0/985	0.70	1/1342 (0.1%)
1	CX	0.51	0/985	0.65	0/1342
1	CY	0.48	0/985	0.71	1/1342 (0.1%)
1	CZ	0.44	0/985	0.69	1/1342 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	DA	0.51	0/985	0.65	0/1342
1	DB	0.48	0/985	0.71	1/1342 (0.1%)
1	DC	0.44	0/985	0.69	1/1342 (0.1%)
1	DD	0.51	0/985	0.65	0/1342
1	DE	0.48	0/985	0.71	1/1342 (0.1%)
1	DF	0.44	0/985	0.70	1/1342 (0.1%)
1	DG	0.51	0/985	0.65	0/1342
1	DH	0.48	0/985	0.71	1/1342 (0.1%)
1	DI	0.44	0/985	0.70	1/1342 (0.1%)
1	DJ	0.51	0/985	0.65	0/1342
1	DK	0.47	0/985	0.71	1/1342 (0.1%)
1	DL	0.44	0/985	0.69	1/1342 (0.1%)
1	DM	0.51	0/985	0.65	0/1342
1	DN	0.48	0/985	0.71	1/1342 (0.1%)
1	DO	0.44	0/985	0.69	1/1342 (0.1%)
1	DP	0.51	0/985	0.65	0/1342
1	DQ	0.48	0/985	0.71	1/1342 (0.1%)
1	DR	0.44	0/985	0.70	1/1342 (0.1%)
1	DS	0.51	0/985	0.65	0/1342
1	DT	0.48	0/985	0.71	1/1342 (0.1%)
1	DU	0.44	0/985	0.70	1/1342 (0.1%)
1	DV	0.51	0/985	0.65	0/1342
1	DW	0.48	0/985	0.71	1/1342 (0.1%)
1	DX	0.44	0/985	0.69	1/1342 (0.1%)
1	DY	0.51	0/985	0.65	0/1342
1	DZ	0.48	0/985	0.71	1/1342 (0.1%)
1	EA	0.44	0/985	0.69	1/1342 (0.1%)
1	EB	0.51	0/985	0.65	0/1342
1	EC	0.47	0/985	0.71	1/1342 (0.1%)
1	ED	0.44	0/985	0.69	1/1342 (0.1%)
1	EE	0.51	0/985	0.65	0/1342
1	EF	0.48	0/985	0.71	1/1342 (0.1%)
1	EG	0.44	0/985	0.70	1/1342 (0.1%)
1	EH	0.51	0/985	0.65	0/1342
1	EI	0.48	0/985	0.71	1/1342 (0.1%)
1	EJ	0.44	0/985	0.69	1/1342 (0.1%)
1	EK	0.51	0/985	0.65	0/1342
1	EL	0.48	0/985	0.71	1/1342 (0.1%)
1	EM	0.44	0/985	0.69	1/1342 (0.1%)
1	EN	0.51	0/985	0.65	0/1342
1	EO	0.48	0/985	0.71	1/1342 (0.1%)
1	EP	0.44	0/985	0.70	1/1342 (0.1%)
1	EQ	0.51	0/985	0.65	0/1342

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	ER	0.47	0/985	0.71	1/1342 (0.1%)
1	ES	0.44	0/985	0.69	1/1342 (0.1%)
1	ET	0.51	0/985	0.65	0/1342
1	EU	0.48	0/985	0.71	1/1342 (0.1%)
1	EV	0.44	0/985	0.70	1/1342 (0.1%)
1	EW	0.51	0/985	0.65	0/1342
1	EX	0.48	0/985	0.71	1/1342 (0.1%)
1	EY	0.44	0/985	0.69	1/1342 (0.1%)
1	EZ	0.51	0/985	0.65	0/1342
1	FA	0.48	0/985	0.71	1/1342 (0.1%)
1	FB	0.44	0/985	0.70	1/1342 (0.1%)
1	FC	0.51	0/985	0.65	0/1342
1	FD	0.47	0/985	0.71	1/1342 (0.1%)
1	FE	0.44	0/985	0.69	1/1342 (0.1%)
1	FF	0.51	0/985	0.65	0/1342
1	FG	0.48	0/985	0.71	1/1342 (0.1%)
1	FH	0.44	0/985	0.69	1/1342 (0.1%)
1	FI	0.51	0/985	0.65	0/1342
1	FJ	0.48	0/985	0.71	1/1342 (0.1%)
1	FK	0.44	0/985	0.70	1/1342 (0.1%)
1	FL	0.51	0/985	0.65	0/1342
1	FM	0.48	0/985	0.71	1/1342 (0.1%)
1	FN	0.44	0/985	0.69	1/1342 (0.1%)
1	FO	0.51	0/985	0.65	0/1342
1	FP	0.47	0/985	0.71	1/1342 (0.1%)
1	FQ	0.44	0/985	0.69	1/1342 (0.1%)
1	FR	0.51	0/985	0.65	0/1342
1	FS	0.48	0/985	0.71	1/1342 (0.1%)
1	FT	0.44	0/985	0.69	1/1342 (0.1%)
1	FU	0.51	0/985	0.65	0/1342
1	FV	0.48	0/985	0.71	1/1342 (0.1%)
1	FW	0.44	0/985	0.70	1/1342 (0.1%)
1	FX	0.51	0/985	0.65	0/1342
1	FY	0.47	0/985	0.71	1/1342 (0.1%)
1	FZ	0.44	0/985	0.69	1/1342 (0.1%)
1	GA	0.51	0/985	0.65	0/1342
1	GB	0.48	0/985	0.71	1/1342 (0.1%)
1	GC	0.44	0/985	0.69	1/1342 (0.1%)
1	GD	0.51	0/985	0.65	0/1342
1	GE	0.48	0/985	0.71	1/1342 (0.1%)
1	GF	0.44	0/985	0.70	1/1342 (0.1%)
1	GG	0.51	0/985	0.65	0/1342
1	GH	0.48	0/985	0.71	1/1342 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >2	RMSZ	# Z >2
1	GI	0.44	0/985	0.70	1/1342 (0.1%)
1	GJ	0.51	0/985	0.65	0/1342
1	GK	0.47	0/985	0.71	1/1342 (0.1%)
1	GL	0.44	0/985	0.69	1/1342 (0.1%)
1	GM	0.51	0/985	0.65	0/1342
1	GN	0.48	0/985	0.71	1/1342 (0.1%)
1	GO	0.44	0/985	0.69	1/1342 (0.1%)
1	GP	0.51	0/985	0.65	0/1342
1	GQ	0.48	0/985	0.71	1/1342 (0.1%)
1	GR	0.44	0/985	0.70	1/1342 (0.1%)
1	GS	0.51	0/985	0.65	0/1342
1	GT	0.48	0/985	0.71	1/1342 (0.1%)
1	GU	0.44	0/985	0.70	1/1342 (0.1%)
1	GV	0.51	0/985	0.65	0/1342
1	GW	0.48	0/985	0.71	1/1342 (0.1%)
1	GX	0.44	0/985	0.69	1/1342 (0.1%)
1	GY	0.51	0/985	0.65	0/1342
All	All	0.48	0/177300	0.69	120/241560 (0.0%)

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AN	61	PRO	N-CA-C	-6.76	94.53	112.10
1	AZ	61	PRO	N-CA-C	-6.76	94.53	112.10
1	BL	61	PRO	N-CA-C	-6.76	94.53	112.10
1	BU	61	PRO	N-CA-C	-6.76	94.53	112.10
1	CG	61	PRO	N-CA-C	-6.76	94.53	112.10

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	AB	968	0	973	79	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AC	968	0	973	64	0
1	AD	968	0	973	95	0
1	AE	968	0	973	78	0
1	AF	968	0	973	65	0
1	AG	968	0	973	99	0
1	AH	968	0	973	78	0
1	AI	968	0	973	65	0
1	AJ	968	0	973	98	0
1	AK	968	0	973	78	0
1	AL	968	0	973	65	0
1	AM	968	0	973	94	0
1	AN	968	0	973	76	0
1	AO	968	0	973	66	0
1	AP	968	0	973	97	0
1	AQ	968	0	973	78	0
1	AR	968	0	973	67	0
1	AS	968	0	973	98	0
1	AT	968	0	973	78	0
1	AU	968	0	973	67	0
1	AV	968	0	973	98	0
1	AW	968	0	973	79	0
1	AX	968	0	973	67	0
1	AY	968	0	973	99	0
1	AZ	968	0	973	79	0
1	BA	968	0	973	68	0
1	BB	968	0	973	99	0
1	BC	968	0	973	78	0
1	BD	968	0	973	66	0
1	BE	968	0	973	98	0
1	BF	968	0	973	78	0
1	BG	968	0	973	67	0
1	BH	968	0	973	97	0
1	BI	968	0	973	80	0
1	BJ	968	0	973	68	0
1	BK	968	0	973	99	0
1	BL	968	0	973	75	0
1	BM	968	0	973	68	0
1	BN	968	0	973	96	0
1	BO	968	0	973	79	0
1	BP	968	0	973	68	0
1	BQ	968	0	973	97	0
1	BR	968	0	973	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BS	968	0	973	64	0
1	BT	968	0	973	97	0
1	BU	968	0	973	75	0
1	BV	968	0	973	68	0
1	BW	968	0	973	96	0
1	BX	968	0	973	80	0
1	BY	968	0	973	68	0
1	BZ	968	0	973	99	0
1	CA	968	0	973	78	0
1	CB	968	0	973	66	0
1	CC	968	0	973	98	0
1	CD	968	0	973	78	0
1	CE	968	0	973	65	0
1	CF	968	0	973	96	0
1	CG	968	0	973	79	0
1	CH	968	0	973	68	0
1	CI	968	0	973	101	0
1	CJ	968	0	973	77	0
1	CK	968	0	973	66	0
1	CL	968	0	973	100	0
1	CM	968	0	973	77	0
1	CN	968	0	973	65	0
1	CO	968	0	973	96	0
1	CP	968	0	973	77	0
1	CQ	968	0	973	66	0
1	CR	968	0	973	99	0
1	CS	968	0	973	78	0
1	CT	968	0	973	66	0
1	CU	968	0	973	98	0
1	CV	968	0	973	80	0
1	CW	968	0	973	68	0
1	CX	968	0	973	97	0
1	CY	968	0	973	79	0
1	CZ	968	0	973	67	0
1	DA	968	0	973	99	0
1	DB	968	0	973	79	0
1	DC	968	0	973	66	0
1	DD	968	0	973	98	0
1	DE	968	0	973	80	0
1	DF	968	0	973	68	0
1	DG	968	0	973	98	0
1	DH	968	0	973	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	DI	968	0	973	68	0
1	DJ	968	0	973	99	0
1	DK	968	0	973	75	0
1	DL	968	0	973	66	0
1	DM	968	0	973	97	0
1	DN	968	0	973	78	0
1	DO	968	0	973	64	0
1	DP	968	0	973	95	0
1	DQ	968	0	973	80	0
1	DR	968	0	973	68	0
1	DS	968	0	973	97	0
1	DT	968	0	973	77	0
1	DU	968	0	973	67	0
1	DV	968	0	973	100	0
1	DW	968	0	973	77	0
1	DX	968	0	973	64	0
1	DY	968	0	973	95	0
1	DZ	968	0	973	79	0
1	EA	968	0	973	68	0
1	EB	968	0	973	98	0
1	EC	968	0	973	78	0
1	ED	968	0	973	66	0
1	EE	968	0	973	97	0
1	EF	968	0	973	77	0
1	EG	968	0	973	66	0
1	EH	968	0	973	99	0
1	EI	968	0	973	80	0
1	EJ	968	0	973	67	0
1	EK	968	0	973	99	0
1	EL	968	0	973	78	0
1	EM	968	0	973	64	0
1	EN	968	0	973	96	0
1	EO	968	0	973	78	0
1	EP	968	0	973	66	0
1	EQ	968	0	973	98	0
1	ER	968	0	973	77	0
1	ES	968	0	973	66	0
1	ET	968	0	973	98	0
1	EU	968	0	973	81	0
1	EV	968	0	973	64	0
1	EW	968	0	973	98	0
1	EX	968	0	973	77	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	EY	968	0	973	67	0
1	EZ	968	0	973	97	0
1	FA	968	0	973	78	0
1	FB	968	0	973	68	0
1	FC	968	0	973	99	0
1	FD	968	0	973	80	0
1	FE	968	0	973	69	0
1	FF	968	0	973	98	0
1	FG	968	0	973	76	0
1	FH	968	0	973	67	0
1	FI	968	0	973	97	0
1	FJ	968	0	973	80	0
1	FK	968	0	973	64	0
1	FL	968	0	973	97	0
1	FM	968	0	973	78	0
1	FN	968	0	973	66	0
1	FO	968	0	973	101	0
1	FP	968	0	973	80	0
1	FQ	968	0	973	66	0
1	FR	968	0	973	98	0
1	FS	968	0	973	79	0
1	FT	968	0	973	68	0
1	FU	968	0	973	99	0
1	FV	968	0	973	78	0
1	FW	968	0	973	65	0
1	FX	968	0	973	97	0
1	FY	968	0	973	81	0
1	FZ	968	0	973	66	0
1	GA	968	0	973	98	0
1	GB	968	0	973	78	0
1	GC	968	0	973	66	0
1	GD	968	0	973	101	0
1	GE	968	0	973	79	0
1	GF	968	0	973	67	0
1	GG	968	0	973	95	0
1	GH	968	0	973	79	0
1	GI	968	0	973	67	0
1	GJ	968	0	973	99	0
1	GK	968	0	973	78	0
1	GL	968	0	973	67	0
1	GM	968	0	973	102	0
1	GN	968	0	973	79	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	GO	968	0	973	66	0
1	GP	968	0	973	98	0
1	GQ	968	0	973	79	0
1	GR	968	0	973	67	0
1	GS	968	0	973	100	0
1	GT	968	0	973	79	0
1	GU	968	0	973	67	0
1	GV	968	0	973	97	0
1	GW	968	0	973	78	0
1	GX	968	0	973	67	0
1	GY	968	0	973	97	0
All	All	174240	0	175140	11770	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 34.

The worst 5 of 11770 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:DG:107:PHE:HA	1:DG:112:ALA:CB	1.43	1.49
1:CX:107:PHE:HA	1:CX:112:ALA:CB	1.43	1.49
1:BE:107:PHE:HA	1:BE:112:ALA:CB	1.43	1.48
1:BW:107:PHE:HA	1:BW:112:ALA:CB	1.43	1.48
1:FR:107:PHE:HA	1:FR:112:ALA:CB	1.43	1.48

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	AB	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7 47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AC	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	AD	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	AE	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	AF	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	AG	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	AH	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	AI	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	AJ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	AK	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	AL	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	AM	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	AN	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	AO	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	AP	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	AQ	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	AR	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	AS	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	AT	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	AU	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	AV	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	AW	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	AX	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	AY	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	AZ	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	BA	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	BB	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	BC	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	BD	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	BE	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	BF	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	BG	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BH	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	BI	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	BJ	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	BK	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	BL	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	BM	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	BN	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	BO	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	BP	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	BQ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	BR	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	BS	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	BT	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	BU	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	BV	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	BW	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	BX	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	BY	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	BZ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	CA	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	CB	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	CC	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	CD	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	CE	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	CF	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	CG	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	CH	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	CI	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	CJ	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	CK	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	CL	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CM	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	CN	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	CO	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	CP	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	CQ	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	CR	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	CS	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	CT	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	CU	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	CV	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	CW	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	CX	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	CY	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	CZ	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	DA	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	DB	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	DC	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	DD	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	DE	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	DF	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	DG	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	DH	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	DI	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	DJ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	DK	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	DL	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	DM	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	DN	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	DO	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	DP	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	DQ	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	DR	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	DS	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	DT	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	DU	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	DV	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	DW	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	DX	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	DY	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	DZ	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	EA	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	EB	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	EC	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	ED	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	EE	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	EF	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	EG	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	EH	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	EI	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	EJ	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	EK	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	EL	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	EM	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	EN	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	EO	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	EP	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	EQ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	ER	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	ES	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	ET	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	EU	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	EV	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	EW	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	EX	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	EY	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	EZ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	FA	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	FB	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	FC	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	FD	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	FE	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	FF	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	FG	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	FH	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	FI	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	FJ	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	FK	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	FL	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	FM	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	FN	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	FO	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	FP	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	FQ	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	FR	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	FS	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	FT	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	FU	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	FV	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	FW	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	FX	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	FY	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	FZ	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	GA	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	GB	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	GC	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	GD	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	GE	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	GF	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	GG	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	GH	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	GI	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	GJ	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	GK	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	GL	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	GM	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	GN	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	GO	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	GP	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	GQ	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	GR	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	GS	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	GT	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	GU	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	GV	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
1	GW	127/129 (98%)	116 (91%)	8 (6%)	3 (2%)	7	47
1	GX	127/129 (98%)	122 (96%)	4 (3%)	1 (1%)	24	69
1	GY	127/129 (98%)	119 (94%)	7 (6%)	1 (1%)	24	69
All	All	22860/23220 (98%)	21420 (94%)	1140 (5%)	300 (1%)	20	59

5 of 300 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AB	40	ILE
1	AE	40	ILE
1	AH	40	ILE
1	AK	40	ILE
1	AN	40	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AB	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	AC	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	AD	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	AE	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	AF	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	AG	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	AH	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	AI	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	AJ	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	AK	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	AL	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	AM	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	AN	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	AO	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	AP	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	AQ	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	AR	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	AS	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	AT	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	AU	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	AV	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	AW	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	AX	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	AY	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	AZ	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	BA	108/108 (100%)	104 (96%)	4 (4%)	41	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BB	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	BC	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	BD	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	BE	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	BF	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	BG	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	BH	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	BI	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	BJ	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	BK	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	BL	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	BM	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	BN	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	BO	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	BP	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	BQ	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	BR	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	BS	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	BT	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	BU	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	BV	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	BW	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	BX	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	BY	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	BZ	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	CA	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	CB	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	CC	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	CD	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	CE	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	CF	108/108 (100%)	105 (97%)	3 (3%)	51	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CG	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	CH	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	CI	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	CJ	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	CK	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	CL	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	CM	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	CN	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	CO	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	CP	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	CQ	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	CR	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	CS	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	CT	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	CU	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	CV	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	CW	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	CX	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	CY	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	CZ	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	DA	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	DB	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	DC	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	DD	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	DE	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	DF	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	DG	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	DH	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	DI	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	DJ	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	DK	108/108 (100%)	107 (99%)	1 (1%)	84	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	DL	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	DM	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	DN	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	DO	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	DP	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	DQ	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	DR	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	DS	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	DT	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	DU	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	DV	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	DW	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	DX	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	DY	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	DZ	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	EA	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	EB	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	EC	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	ED	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	EE	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	EF	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	EG	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	EH	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	EI	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	EJ	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	EK	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	EL	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	EM	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	EN	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	EO	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	EP	108/108 (100%)	104 (96%)	4 (4%)	41	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	EQ	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	ER	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	ES	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	ET	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	EU	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	EV	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	EW	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	EX	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	EY	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	EZ	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	FA	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	FB	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	FC	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	FD	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	FE	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	FF	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	FG	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	FH	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	FI	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	FJ	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	FK	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	FL	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	FM	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	FN	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	FO	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	FP	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	FQ	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	FR	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	FS	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	FT	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	FU	108/108 (100%)	105 (97%)	3 (3%)	51	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	FV	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	FW	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	FX	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	FY	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	FZ	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	GA	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	GB	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	GC	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	GD	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	GE	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	GF	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	GG	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	GH	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	GI	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	GJ	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	GK	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	GL	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	GM	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	GN	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	GO	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	GP	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	GQ	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	GR	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	GS	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	GT	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	GU	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	GV	108/108 (100%)	105 (97%)	3 (3%)	51	78
1	GW	108/108 (100%)	107 (99%)	1 (1%)	84	93
1	GX	108/108 (100%)	104 (96%)	4 (4%)	41	73
1	GY	108/108 (100%)	105 (97%)	3 (3%)	51	78
All	All	19440/19440 (100%)	18960 (98%)	480 (2%)	59	81

5 of 480 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	DF	40	ILE
1	DX	71	MET
1	GL	69	VAL
1	DG	71	MET
1	DO	69	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 540 such sidechains are listed below:

Mol	Chain	Res	Type
1	DE	34	GLN
1	DX	45	ASN
1	GL	2	ASN
1	DG	111	ASN
1	DO	2	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.