



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2026 – 06:19 AM UTC

PDB ID : 6YFR / pdb_00006yfr
Title : Virus-like particle of bacteriophage NT-391
Authors : Rumnieks, J.; Kalnins, G.; Sisovs, M.; Lieknina, I.; Tars, K.
Deposited on : 2020-03-26
Resolution : 2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

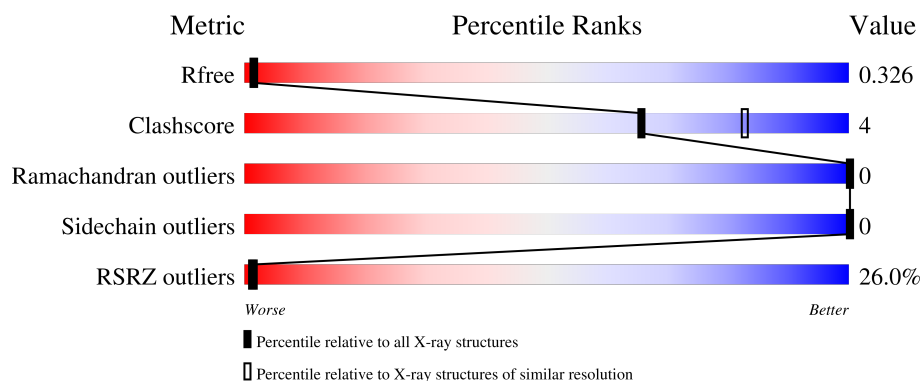
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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

Mol	Chain	Length	Quality of chain
1	AA	123	20% 91% 9%
1	AB	123	20% 85% 15%
1	AC	123	31% 91% 9%
1	AD	123	27% 93% 7%
1	AE	123	30% 89% 11%

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Mol	Chain	Length	Quality of chain		
1	AF	123	26%	89%	11%
1	AG	123	16%	86%	14%
1	AH	123	24%	89%	11%
1	AI	123	32%	89%	11%
1	AJ	123	31%	86%	14%
1	AK	123	33%	89%	11%
1	AL	123	28%	92%	8%
1	AM	123	15%	89%	11%
1	AN	123	24%	90%	10%
1	AO	123	30%	92%	8%
1	AP	123	28%	89%	11%
1	AQ	123	33%	89%	11%
1	AR	123	21%	90%	10%
1	AS	123	31%	90%	10%
1	AT	123	30%	89%	11%
1	AU	123	19%	85%	15%
1	AV	123	34%	92%	8%
1	AW	123	19%	91%	9%
1	AX	123	20%	89%	11%
1	AY	123	26%	87%	13%
1	AZ	123	23%	90%	10%
1	BA	123	24%	89%	11%
1	BB	123	24%	90%	10%
1	BC	123	28%	89%	11%
1	BD	123	20%	89%	11%

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Mol	Chain	Length	Quality of chain	
1	BE	123	31%	89% 11%
1	BF	123	21%	91% 9%
1	BG	123	27%	91% 9%
1	BH	123	31%	88% 12%
1	BI	123	24%	87% 13%
1	BJ	123	25%	89% 11%
1	BK	123	24%	89% 11%
1	BL	123	33%	90% 10%
1	BM	123	20%	89% 11%
1	BN	123	30%	89% 11%
1	BO	123	28%	88% 12%
1	BP	123	22%	88% 12%
1	BQ	123	25%	89% 11%
1	BR	123	25%	89% 11%
1	BS	123	29%	92% 8%
1	BT	123	28%	92% 8%
1	BU	123	30%	91% 9%
1	BV	123	26%	91% 9%
1	BW	123	26%	89% 11%
1	BX	123	24%	89% 11%
1	BY	123	28%	89% 11%
1	BZ	123	23%	89% 11%
1	CA	123	24%	87% 13%
1	CB	123	40%	89% 11%
1	CC	123	21%	85% 15%

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Mol	Chain	Length	Quality of chain
1	CD	123	
1	CE	123	
1	CF	123	
1	CG	123	
1	CH	123	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 56340 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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					ZeroOcc	AltConf	Trace
1	AA	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AB	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AC	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AD	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AE	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AF	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AG	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AH	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AI	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AJ	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AK	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AL	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AM	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AN	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AO	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	AP	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	AR	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	AS	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	AT	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	AU	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	AV	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	AW	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	AX	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	AY	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	AZ	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BA	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BB	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BC	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BD	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BE	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BF	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BG	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BH	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BI	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BJ	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BK	123	Total 939	C 591	N 157	O 186	S 5	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BL	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BM	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BN	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BO	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BP	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BQ	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BR	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BS	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BT	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BU	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BV	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BW	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BX	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BY	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	BZ	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	CA	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	CB	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	CC	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	CD	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	CE	123	Total 939	C 591	N 157	O 186	S 5	0	0	0
1	CF	123	Total 939	C 591	N 157	O 186	S 5	0	0	0

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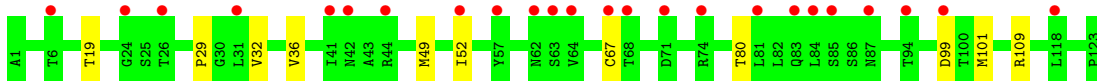
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CG	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			
1	CH	123	Total	C	N	O	S	0	0	0
			939	591	157	186	5			

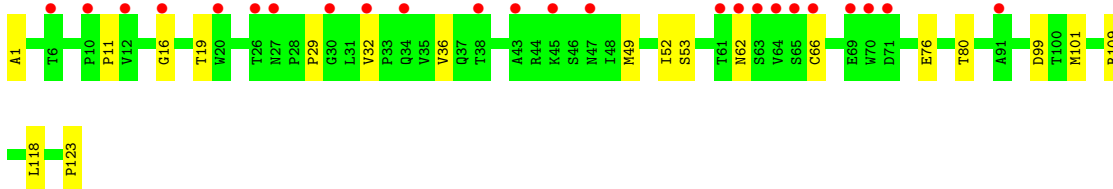
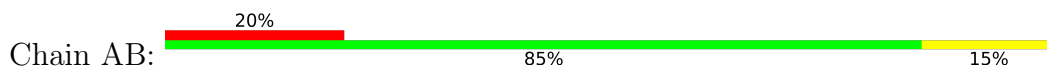
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

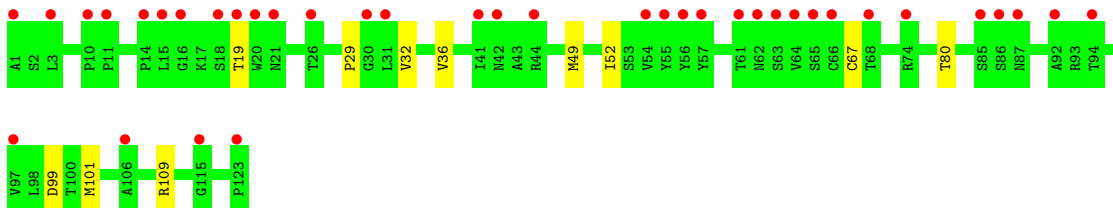
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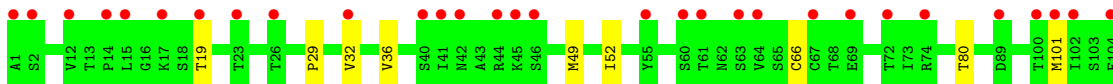
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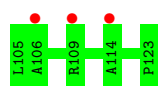


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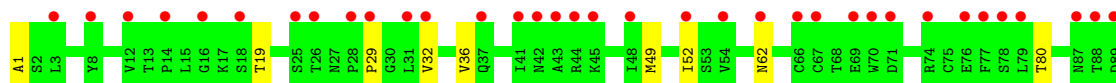
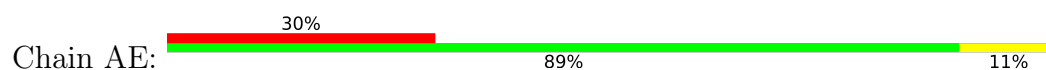


- Molecule 1: coat protein

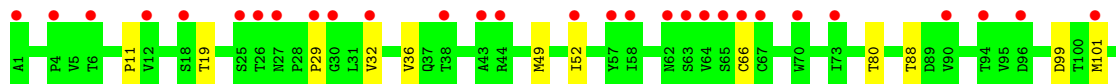
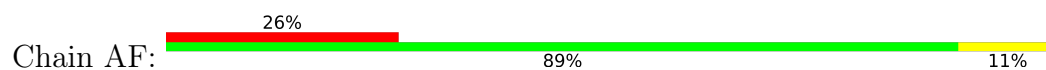




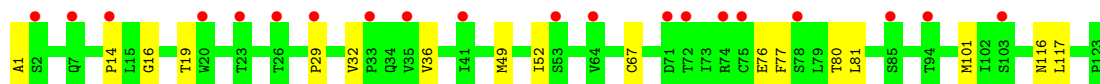
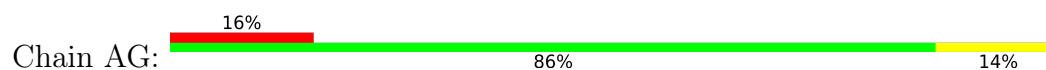
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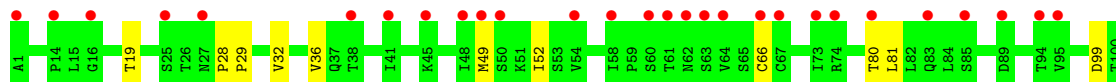
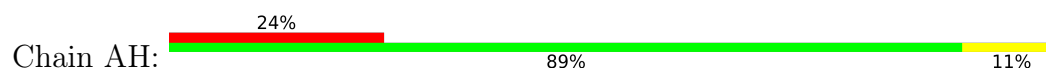
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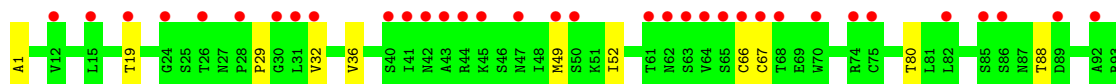
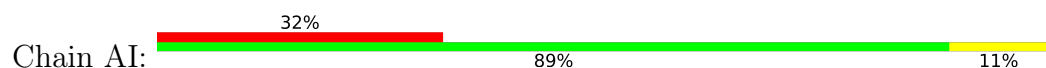
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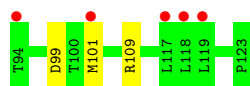


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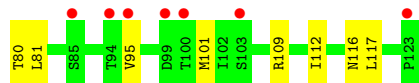
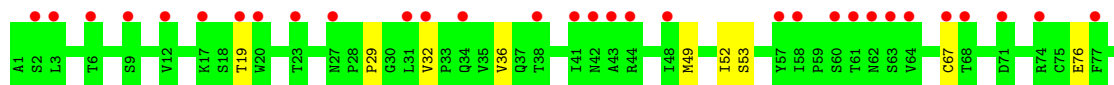
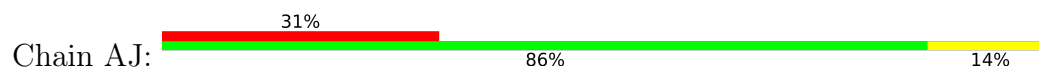


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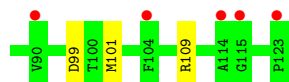
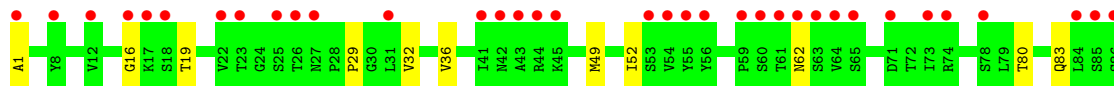
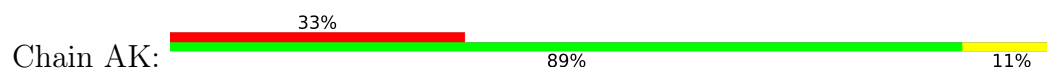




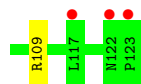
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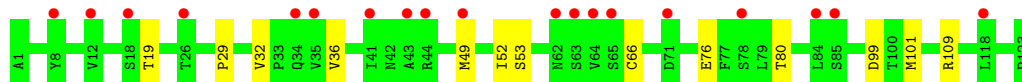
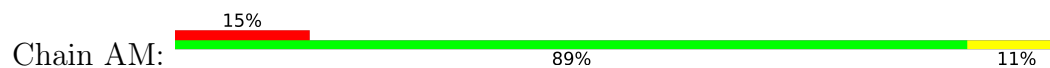
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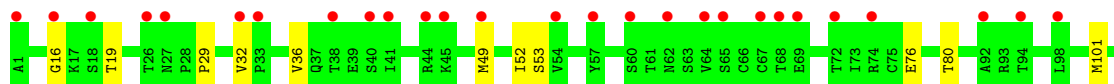
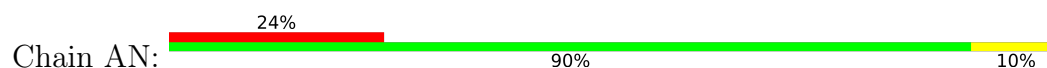
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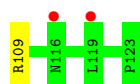


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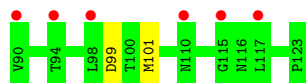
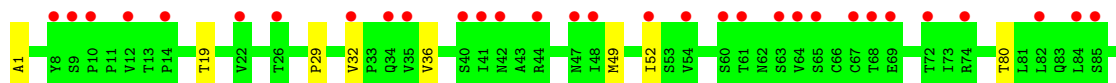


- Molecule 1: coat protein

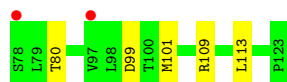
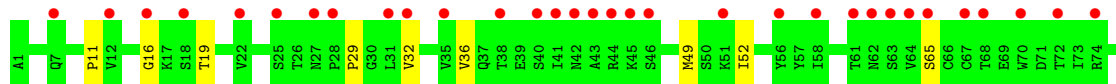
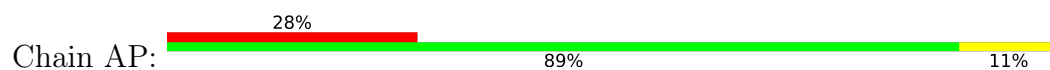




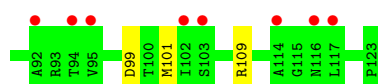
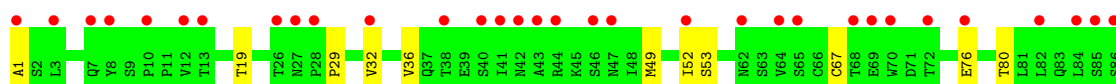
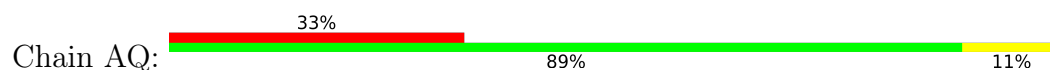
- Molecule 1: coat protein



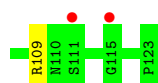
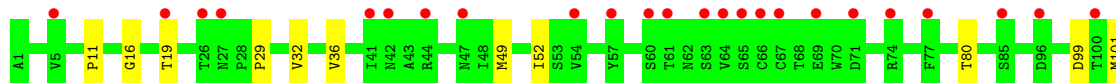
- Molecule 1: coat protein



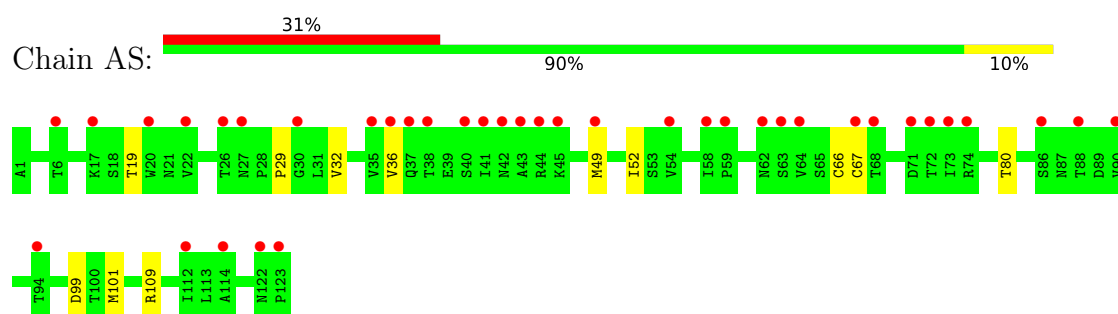
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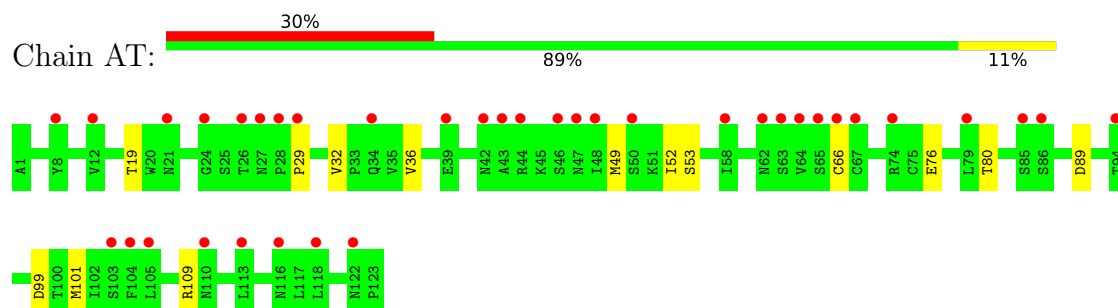
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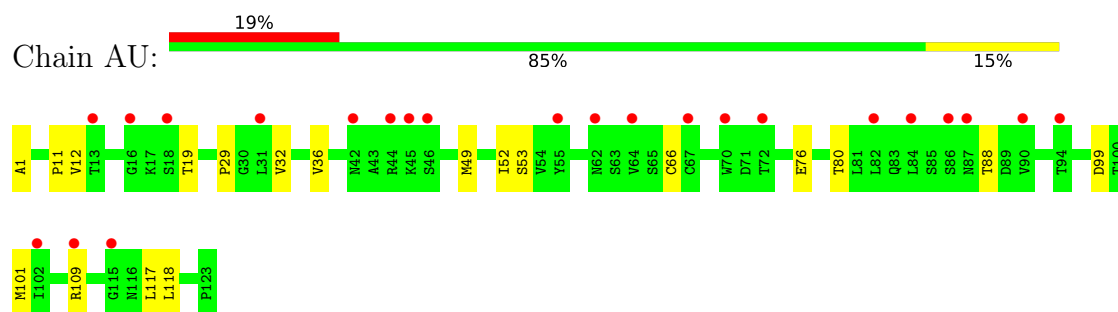
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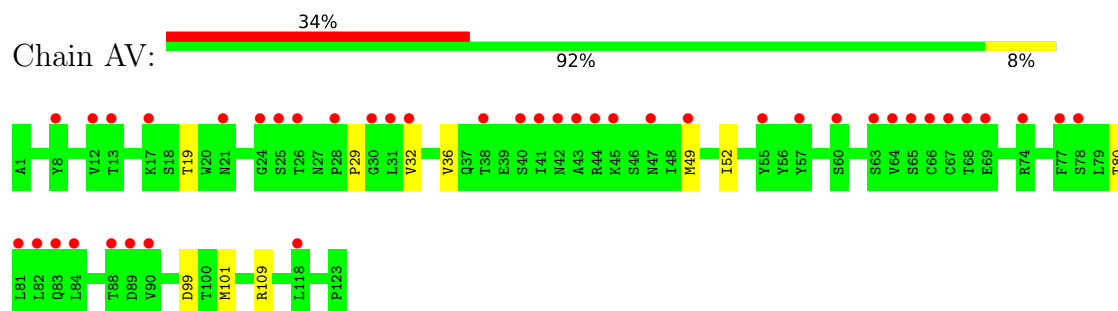
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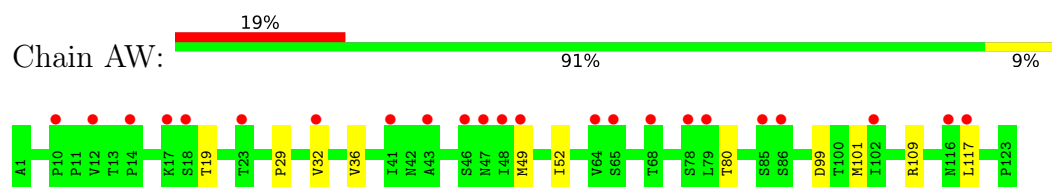
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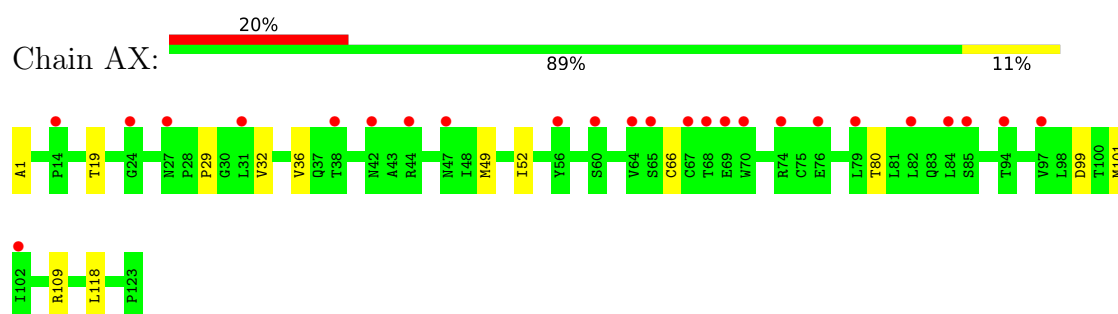
- Molecule 1: coat protein



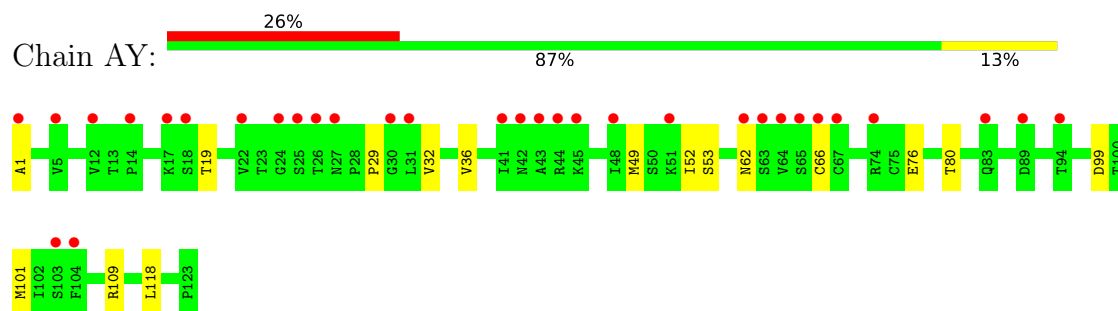
- Molecule 1: coat protein



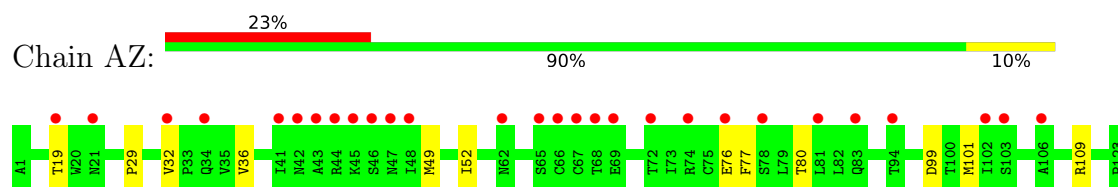
- Molecule 1: coat protein



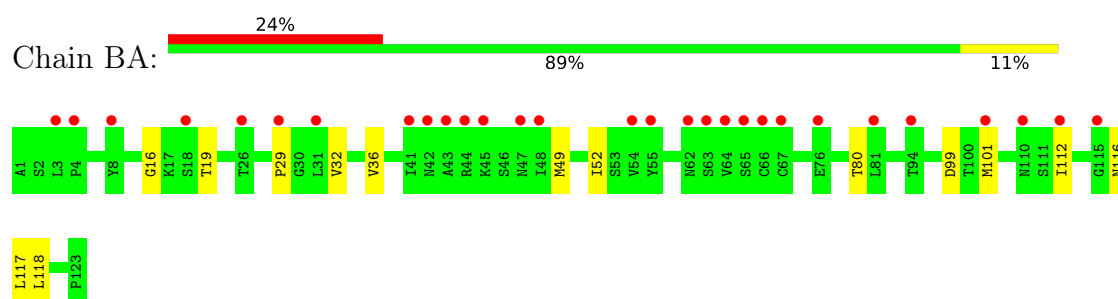
- Molecule 1: coat protein



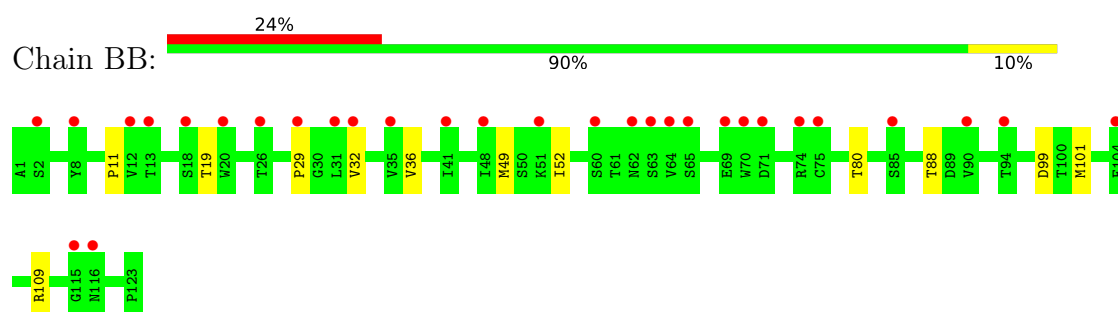
- Molecule 1: coat protein



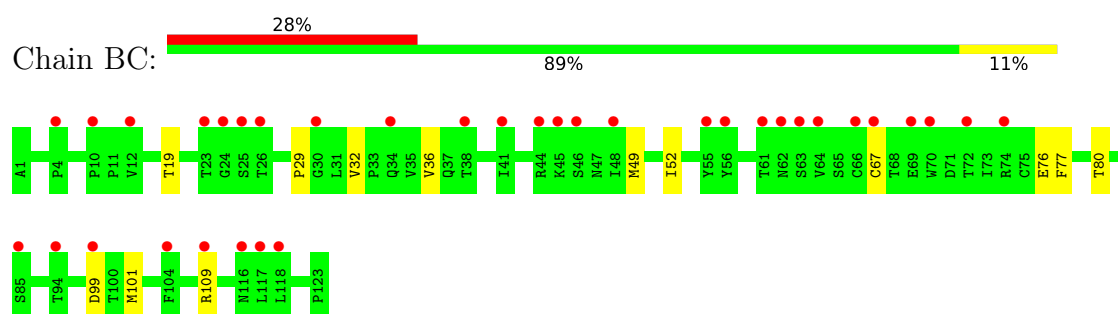
- Molecule 1: coat protein



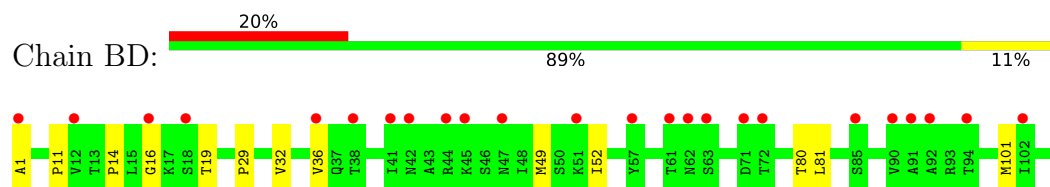
- Molecule 1: coat protein



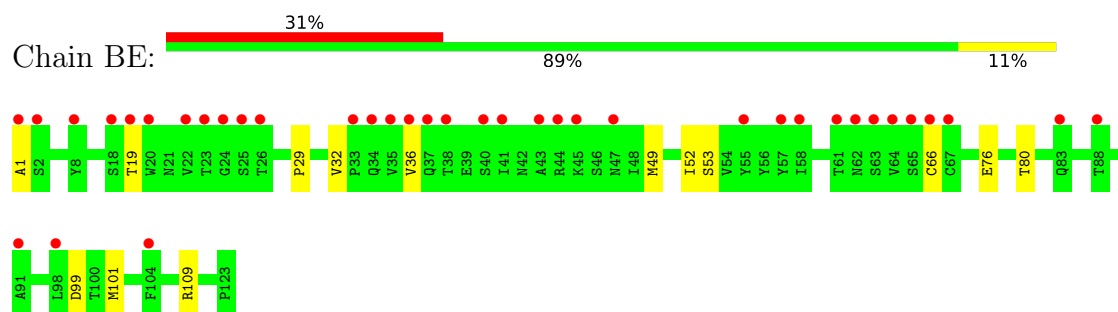
- Molecule 1: coat protein



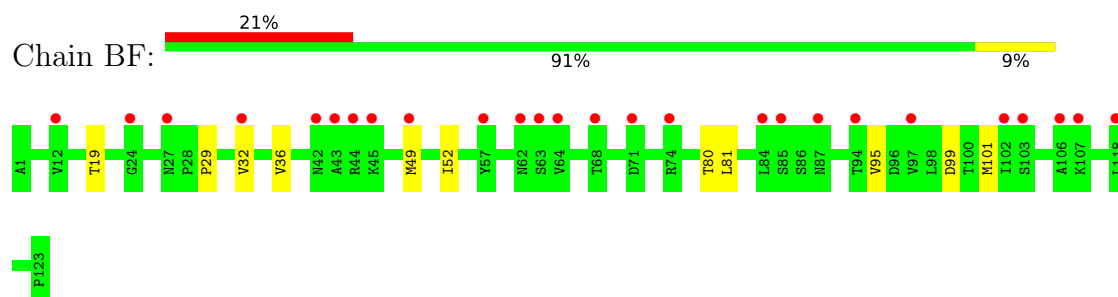
- Molecule 1: coat protein



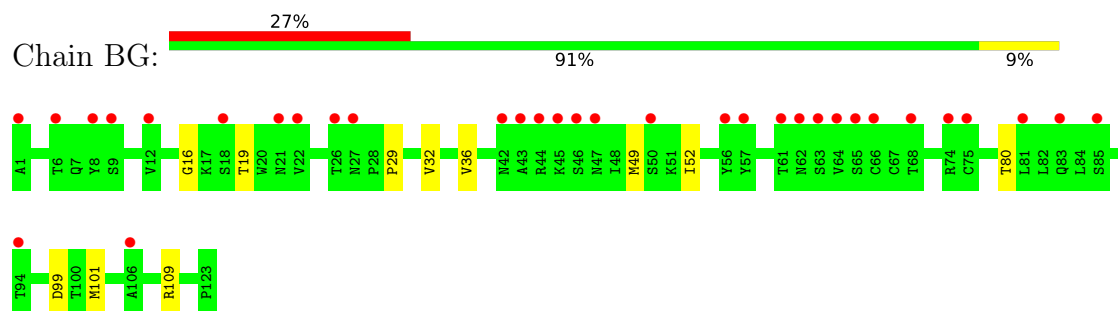
- Molecule 1: coat protein



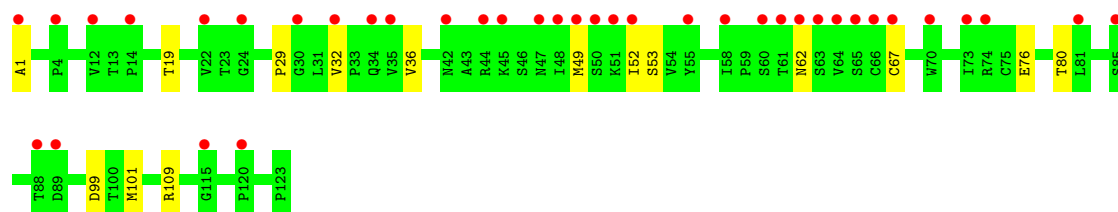
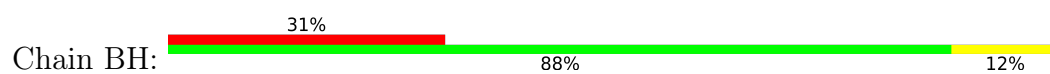
- Molecule 1: coat protein



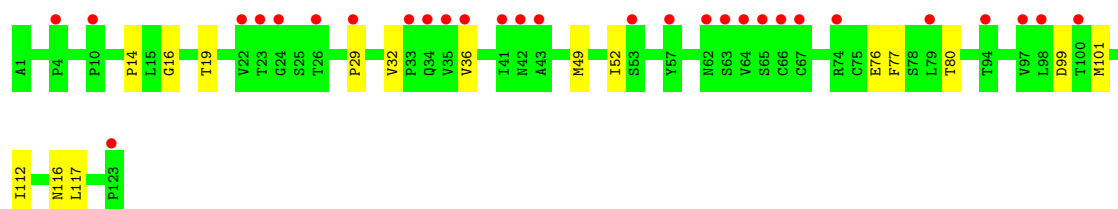
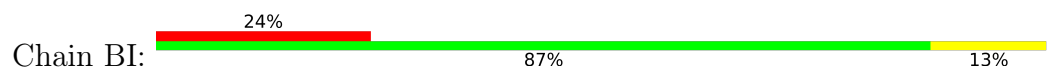
- Molecule 1: coat protein



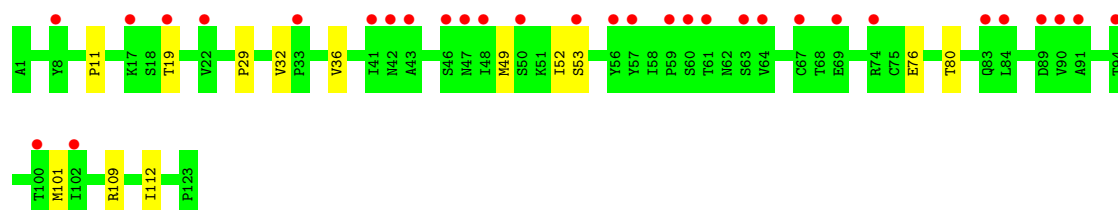
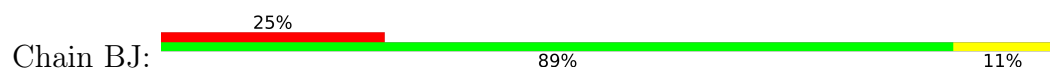
- Molecule 1: coat protein



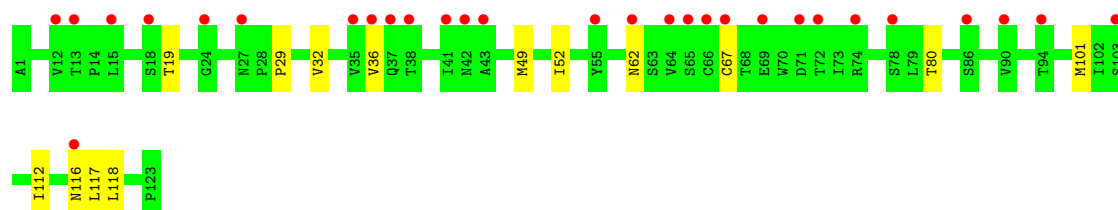
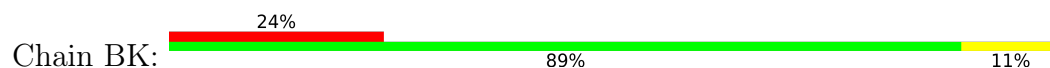
- Molecule 1: coat protein



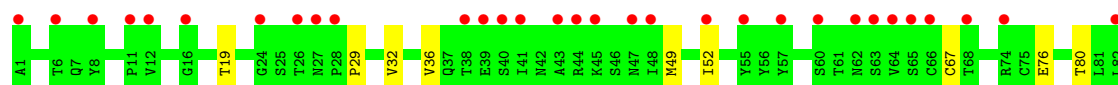
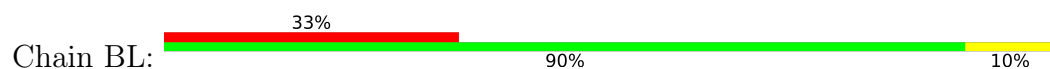
- Molecule 1: coat protein

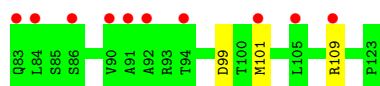


- Molecule 1: coat protein

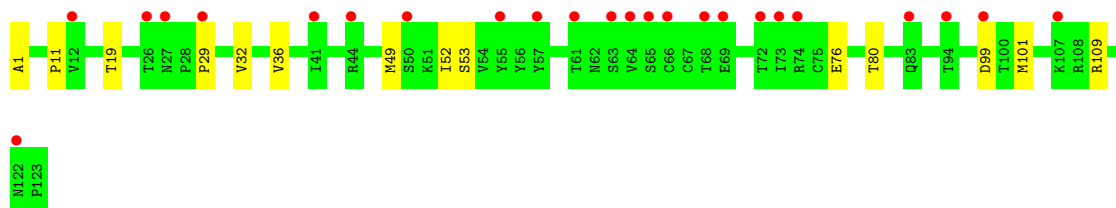
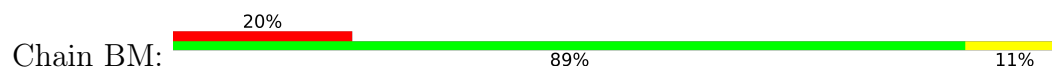


- Molecule 1: coat protein

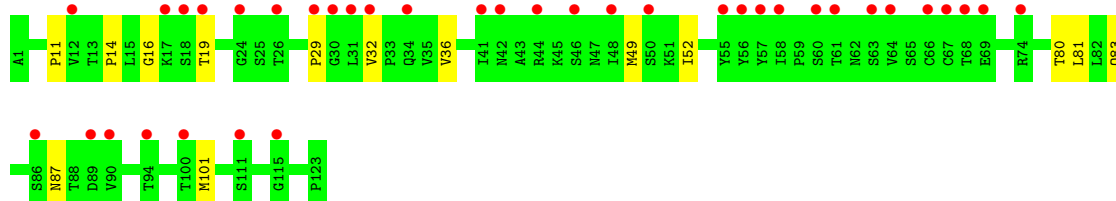
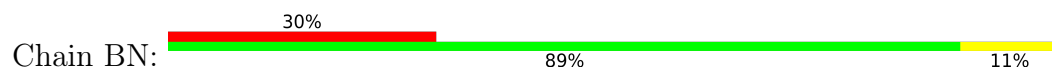




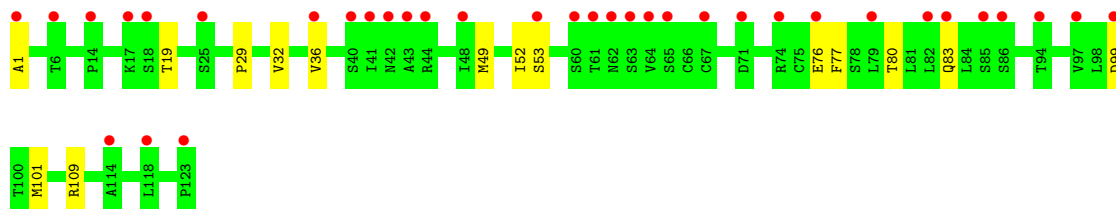
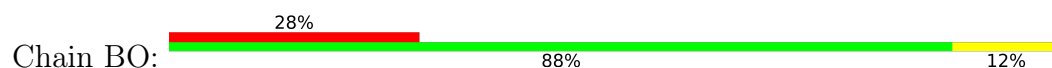
- Molecule 1: coat protein



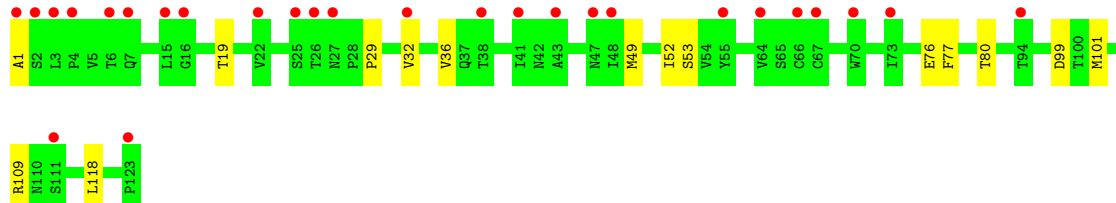
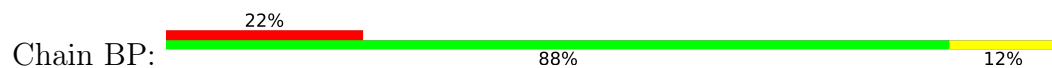
- Molecule 1: coat protein



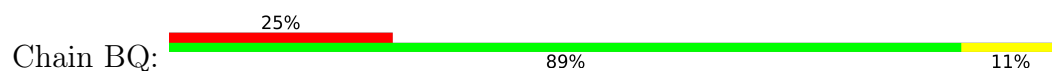
- Molecule 1: coat protein

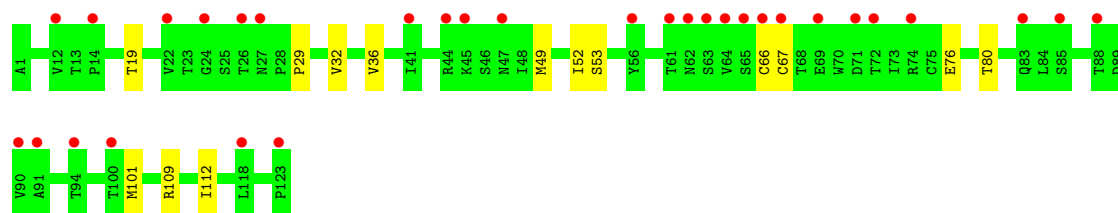


- Molecule 1: coat protein

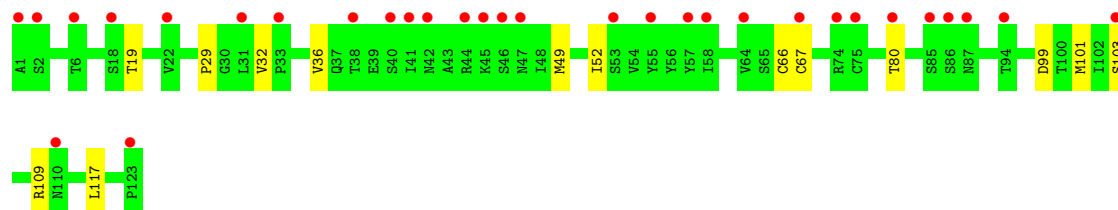
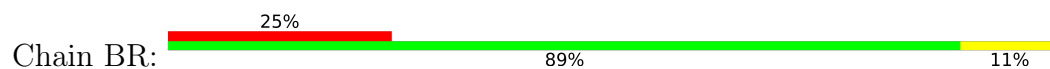


- Molecule 1: coat protein

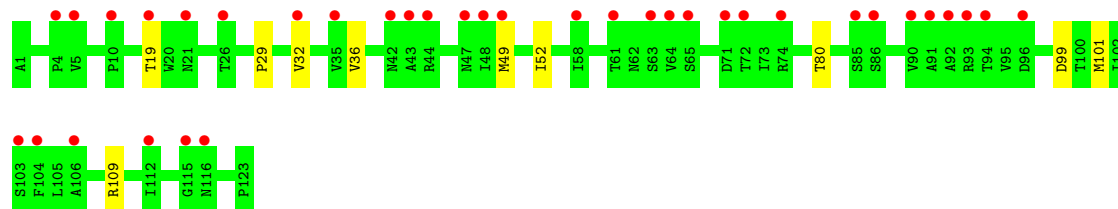
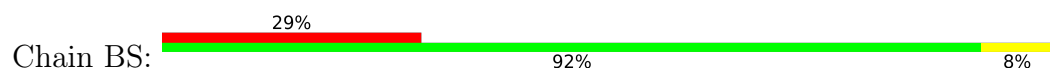




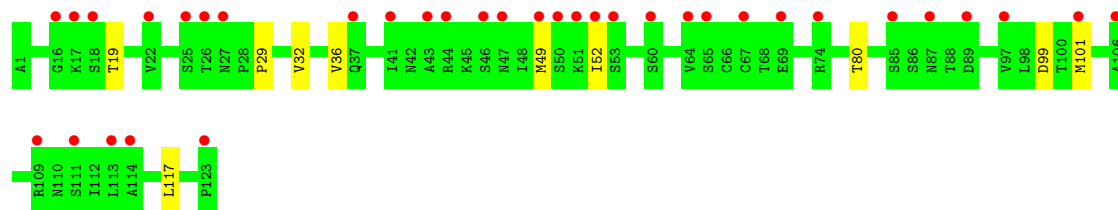
• Molecule 1: coat protein



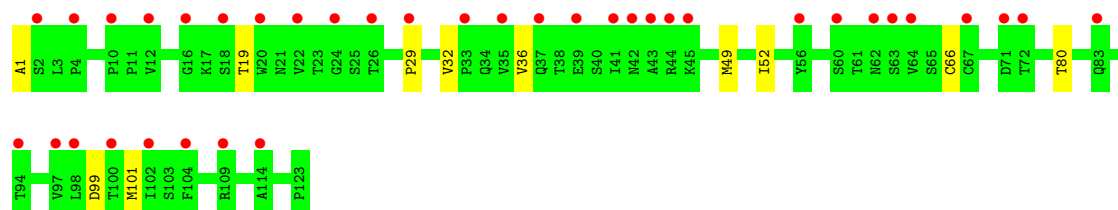
• Molecule 1: coat protein



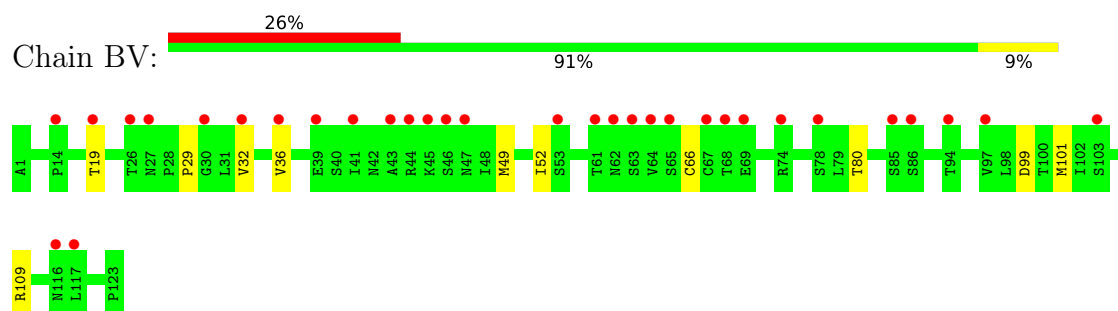
• Molecule 1: coat protein



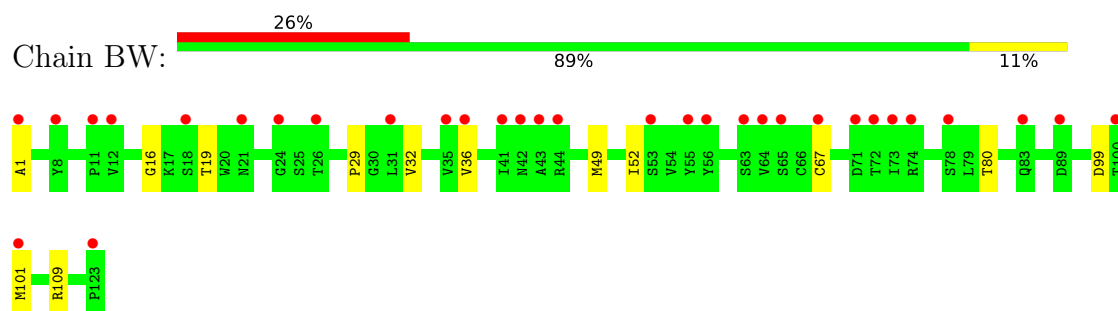
• Molecule 1: coat protein



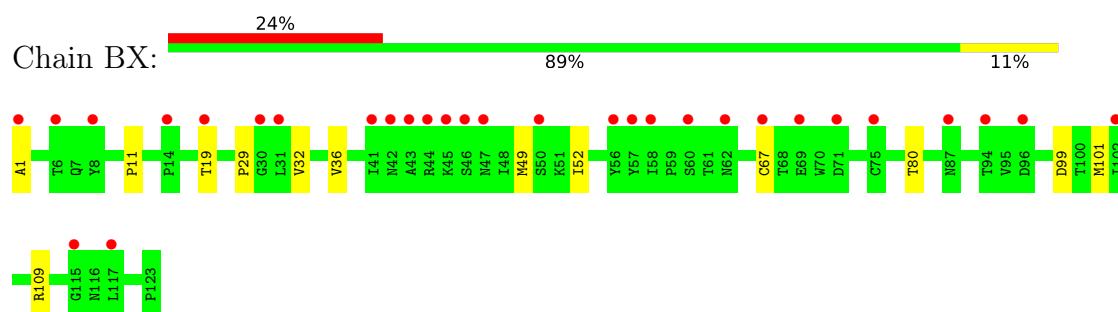
- Molecule 1: coat protein



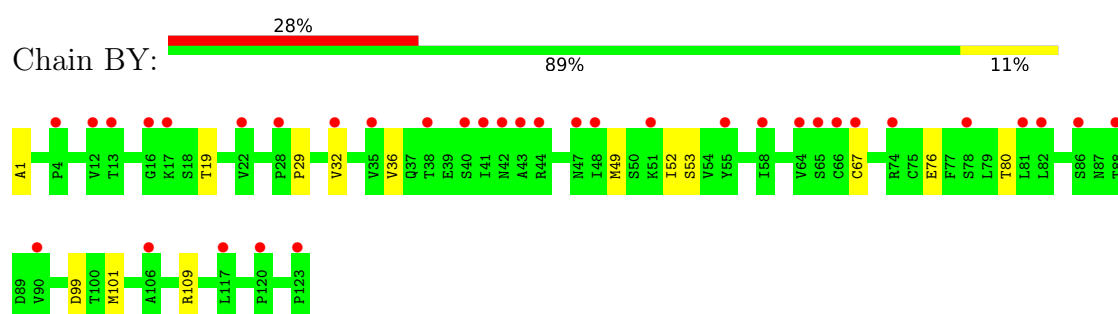
- Molecule 1: coat protein



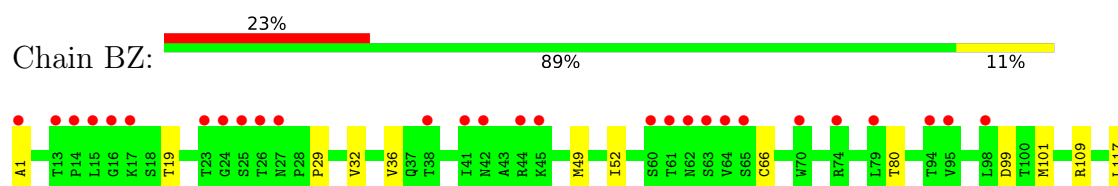
- Molecule 1: coat protein



- Molecule 1: coat protein

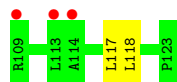
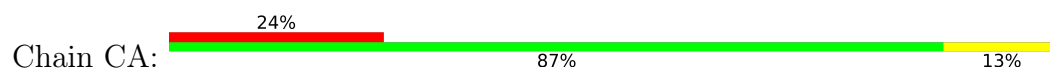


- Molecule 1: coat protein

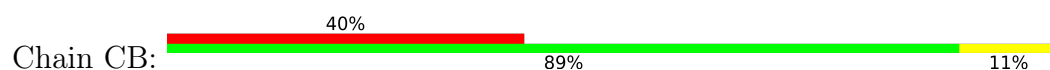




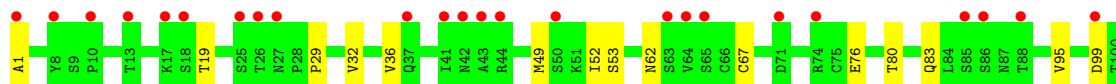
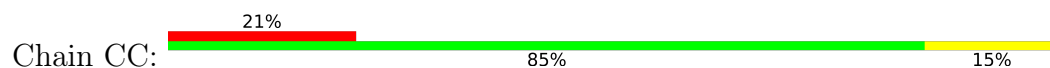
- Molecule 1: coat protein



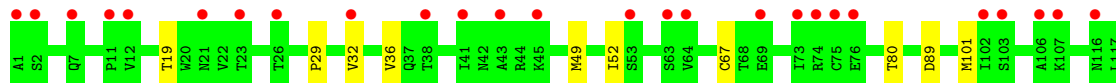
- Molecule 1: coat protein



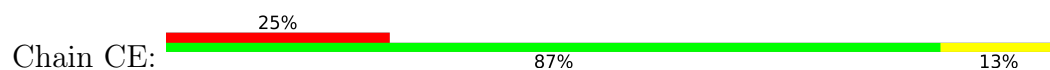
- Molecule 1: coat protein

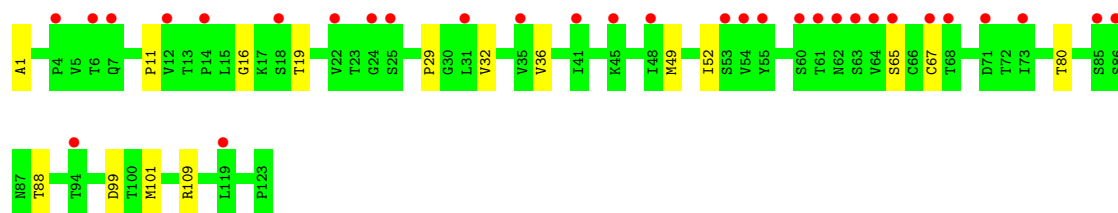


- Molecule 1: coat protein

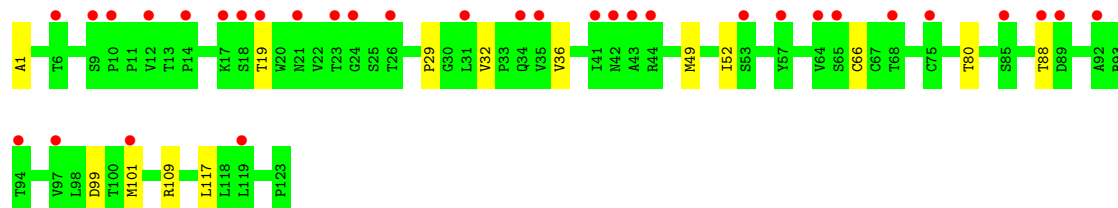
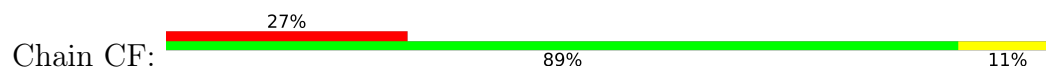


- Molecule 1: coat protein

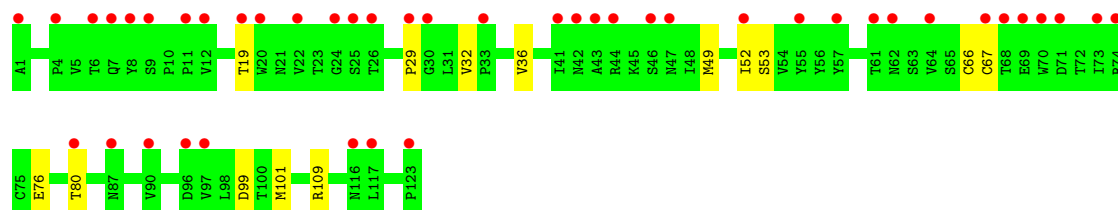
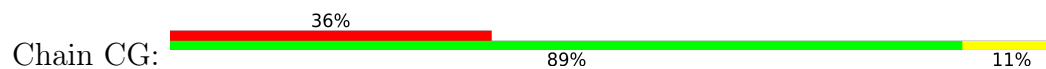




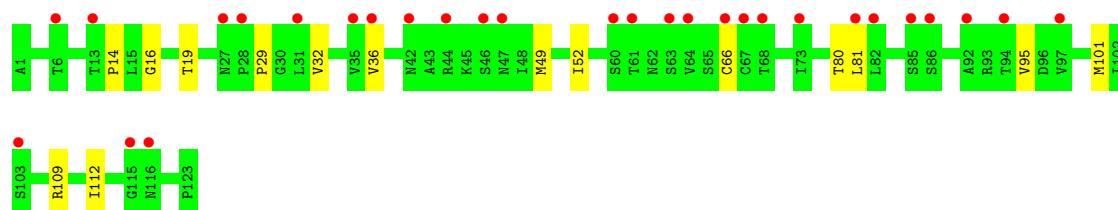
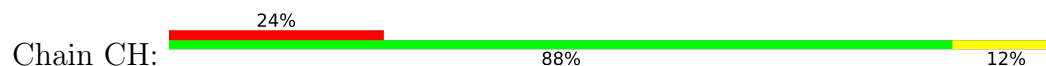
● Molecule 1: coat protein



● Molecule 1: coat protein



● Molecule 1: coat protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	161.92Å 162.07Å 162.98Å 71.16° 66.67° 66.83°	Depositor
Resolution (Å)	51.88 – 2.60 51.88 – 2.60	Depositor EDS
% Data completeness (in resolution range)	68.0 (51.88-2.60) 69.4 (51.88-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.24	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.318 , 0.323 0.320 , 0.326	Depositor DCC
R_{free} test set	9929 reflections (3.38%)	wwPDB-VP
Wilson B-factor (Å ²)	41.0	Xtriage
Anisotropy	0.467	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.028 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	56340	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	0.15	0/958	0.35	0/1313
1	AB	0.15	0/958	0.35	0/1313
1	AC	0.15	0/958	0.35	0/1313
1	AD	0.15	0/958	0.35	0/1313
1	AE	0.15	0/958	0.35	0/1313
1	AF	0.15	0/958	0.35	0/1313
1	AG	0.15	0/958	0.35	0/1313
1	AH	0.15	0/958	0.35	0/1313
1	AI	0.15	0/958	0.35	0/1313
1	AJ	0.15	0/958	0.35	0/1313
1	AK	0.15	0/958	0.35	0/1313
1	AL	0.15	0/958	0.35	0/1313
1	AM	0.15	0/958	0.35	0/1313
1	AN	0.15	0/958	0.35	0/1313
1	AO	0.15	0/958	0.35	0/1313
1	AP	0.15	0/958	0.35	0/1313
1	AQ	0.15	0/958	0.35	0/1313
1	AR	0.15	0/958	0.35	0/1313
1	AS	0.15	0/958	0.35	0/1313
1	AT	0.15	0/958	0.35	0/1313
1	AU	0.15	0/958	0.35	0/1313
1	AV	0.15	0/958	0.35	0/1313
1	AW	0.15	0/958	0.35	0/1313
1	AX	0.15	0/958	0.35	0/1313
1	AY	0.15	0/958	0.35	0/1313
1	AZ	0.16	0/958	0.35	0/1313
1	BA	0.15	0/958	0.35	0/1313
1	BB	0.15	0/958	0.35	0/1313
1	BC	0.15	0/958	0.35	0/1313
1	BD	0.15	0/958	0.35	0/1313
1	BE	0.16	0/958	0.35	0/1313
1	BF	0.15	0/958	0.35	0/1313
1	BG	0.15	0/958	0.35	0/1313
1	BH	0.15	0/958	0.35	0/1313

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.15	0/958	0.35	0/1313
1	BJ	0.15	0/958	0.35	0/1313
1	BK	0.15	0/958	0.35	0/1313
1	BL	0.15	0/958	0.35	0/1313
1	BM	0.15	0/958	0.35	0/1313
1	BN	0.16	0/958	0.35	0/1313
1	BO	0.15	0/958	0.35	0/1313
1	BP	0.16	0/958	0.35	0/1313
1	BQ	0.15	0/958	0.35	0/1313
1	BR	0.15	0/958	0.35	0/1313
1	BS	0.15	0/958	0.35	0/1313
1	BT	0.15	0/958	0.35	0/1313
1	BU	0.15	0/958	0.35	0/1313
1	BV	0.15	0/958	0.35	0/1313
1	BW	0.15	0/958	0.35	0/1313
1	BX	0.16	0/958	0.35	0/1313
1	BY	0.15	0/958	0.35	0/1313
1	BZ	0.15	0/958	0.35	0/1313
1	CA	0.15	0/958	0.35	0/1313
1	CB	0.15	0/958	0.35	0/1313
1	CC	0.16	0/958	0.35	0/1313
1	CD	0.15	0/958	0.35	0/1313
1	CE	0.15	0/958	0.35	0/1313
1	CF	0.15	0/958	0.35	0/1313
1	CG	0.15	0/958	0.35	0/1313
1	CH	0.15	0/958	0.35	0/1313
All	All	0.15	0/57480	0.35	0/78780

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	939	0	950	9	0
1	AB	939	0	950	15	1
1	AC	939	0	950	11	0
1	AD	939	0	950	6	0
1	AE	939	0	950	12	0
1	AF	939	0	950	13	0
1	AG	939	0	950	16	0
1	AH	939	0	951	10	0
1	AI	939	0	951	14	0
1	AJ	939	0	950	13	0
1	AK	939	0	950	13	0
1	AL	939	0	950	9	0
1	AM	939	0	950	9	0
1	AN	939	0	950	8	0
1	AO	939	0	950	7	0
1	AP	939	0	950	11	0
1	AQ	939	0	950	10	0
1	AR	939	0	950	10	0
1	AS	939	0	950	10	0
1	AT	939	0	951	14	1
1	AU	939	0	950	16	0
1	AV	939	0	950	8	0
1	AW	939	0	950	9	0
1	AX	939	0	951	11	0
1	AY	939	0	950	13	0
1	AZ	939	0	950	9	0
1	BA	939	0	950	11	0
1	BB	939	0	951	11	0
1	BC	939	0	950	10	0
1	BD	939	0	950	11	0
1	BE	939	0	950	10	0
1	BF	939	0	950	8	0
1	BG	939	0	950	9	0
1	BH	939	0	950	12	0
1	BI	939	0	950	15	0
1	BJ	939	0	950	9	0
1	BK	939	0	950	11	0
1	BL	939	0	951	11	0
1	BM	939	0	950	12	0
1	BN	939	0	950	11	0
1	BO	939	0	950	11	0
1	BP	939	0	950	12	0
1	BQ	939	0	950	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	BR	939	0	950	10	1
1	BS	939	0	951	8	0
1	BT	939	0	950	7	0
1	BU	939	0	950	8	0
1	BV	939	0	950	8	0
1	BW	939	0	950	10	1
1	BX	939	0	950	11	0
1	BY	939	0	950	11	0
1	BZ	939	0	950	11	1
1	CA	939	0	950	12	0
1	CB	939	0	950	12	0
1	CC	939	0	950	15	0
1	CD	939	0	950	6	1
1	CE	939	0	951	17	0
1	CF	939	0	950	13	0
1	CG	939	0	950	12	0
1	CH	939	0	950	12	0
All	All	56340	0	57008	427	3

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 4.

The worst 5 of 427 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:AD:66:CYS:SG	1:AQ:67:CYS:N	2.45	0.90
1:AC:67:CYS:SG	1:CB:66:CYS:HA	2.17	0.85
1:AB:66:CYS:SG	1:AJ:67:CYS:N	2.62	0.73
1:AG:52:ILE:HB	1:BI:101:MET:HE1	1.71	0.71
1:AF:66:CYS:SG	1:AP:65:SER:HB2	2.31	0.70

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:123:PRO:OXT	1:BR:103:SER:OG[1_654]	1.65	0.55
1:AT:89:ASP:OD1	1:BW:1:ALA:CB[1_556]	2.06	0.14
1:BZ:1:ALA:CB	1:CD:89:ASP:OD1[1_556]	2.14	0.06

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	121/123 (98%)	121 (100%)	0	0	100	100
1	AB	121/123 (98%)	121 (100%)	0	0	100	100
1	AC	121/123 (98%)	121 (100%)	0	0	100	100
1	AD	121/123 (98%)	121 (100%)	0	0	100	100
1	AE	121/123 (98%)	121 (100%)	0	0	100	100
1	AF	121/123 (98%)	121 (100%)	0	0	100	100
1	AG	121/123 (98%)	121 (100%)	0	0	100	100
1	AH	121/123 (98%)	121 (100%)	0	0	100	100
1	AI	121/123 (98%)	121 (100%)	0	0	100	100
1	AJ	121/123 (98%)	121 (100%)	0	0	100	100
1	AK	121/123 (98%)	121 (100%)	0	0	100	100
1	AL	121/123 (98%)	121 (100%)	0	0	100	100
1	AM	121/123 (98%)	121 (100%)	0	0	100	100
1	AN	121/123 (98%)	121 (100%)	0	0	100	100
1	AO	121/123 (98%)	121 (100%)	0	0	100	100
1	AP	121/123 (98%)	121 (100%)	0	0	100	100
1	AQ	121/123 (98%)	121 (100%)	0	0	100	100
1	AR	121/123 (98%)	121 (100%)	0	0	100	100
1	AS	121/123 (98%)	121 (100%)	0	0	100	100
1	AT	121/123 (98%)	121 (100%)	0	0	100	100
1	AU	121/123 (98%)	121 (100%)	0	0	100	100
1	AV	121/123 (98%)	121 (100%)	0	0	100	100
1	AW	121/123 (98%)	121 (100%)	0	0	100	100
1	AX	121/123 (98%)	121 (100%)	0	0	100	100
1	AY	121/123 (98%)	121 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AZ	121/123 (98%)	121 (100%)	0	0	100	100
1	BA	121/123 (98%)	121 (100%)	0	0	100	100
1	BB	121/123 (98%)	121 (100%)	0	0	100	100
1	BC	121/123 (98%)	121 (100%)	0	0	100	100
1	BD	121/123 (98%)	121 (100%)	0	0	100	100
1	BE	121/123 (98%)	121 (100%)	0	0	100	100
1	BF	121/123 (98%)	121 (100%)	0	0	100	100
1	BG	121/123 (98%)	121 (100%)	0	0	100	100
1	BH	121/123 (98%)	121 (100%)	0	0	100	100
1	BI	121/123 (98%)	121 (100%)	0	0	100	100
1	BJ	121/123 (98%)	121 (100%)	0	0	100	100
1	BK	121/123 (98%)	121 (100%)	0	0	100	100
1	BL	121/123 (98%)	121 (100%)	0	0	100	100
1	BM	121/123 (98%)	121 (100%)	0	0	100	100
1	BN	121/123 (98%)	121 (100%)	0	0	100	100
1	BO	121/123 (98%)	121 (100%)	0	0	100	100
1	BP	121/123 (98%)	121 (100%)	0	0	100	100
1	BQ	121/123 (98%)	121 (100%)	0	0	100	100
1	BR	121/123 (98%)	121 (100%)	0	0	100	100
1	BS	121/123 (98%)	121 (100%)	0	0	100	100
1	BT	121/123 (98%)	121 (100%)	0	0	100	100
1	BU	121/123 (98%)	121 (100%)	0	0	100	100
1	BV	121/123 (98%)	121 (100%)	0	0	100	100
1	BW	121/123 (98%)	121 (100%)	0	0	100	100
1	BX	121/123 (98%)	121 (100%)	0	0	100	100
1	BY	121/123 (98%)	121 (100%)	0	0	100	100
1	BZ	121/123 (98%)	121 (100%)	0	0	100	100
1	CA	121/123 (98%)	121 (100%)	0	0	100	100
1	CB	121/123 (98%)	121 (100%)	0	0	100	100
1	CC	121/123 (98%)	121 (100%)	0	0	100	100
1	CD	121/123 (98%)	121 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CE	121/123 (98%)	121 (100%)	0	0	100	100
1	CF	121/123 (98%)	121 (100%)	0	0	100	100
1	CG	121/123 (98%)	121 (100%)	0	0	100	100
1	CH	121/123 (98%)	121 (100%)	0	0	100	100
All	All	7260/7380 (98%)	7260 (100%)	0	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	AA	113/113 (100%)	113 (100%)	0	100	100
1	AB	113/113 (100%)	113 (100%)	0	100	100
1	AC	113/113 (100%)	113 (100%)	0	100	100
1	AD	113/113 (100%)	113 (100%)	0	100	100
1	AE	113/113 (100%)	113 (100%)	0	100	100
1	AF	113/113 (100%)	113 (100%)	0	100	100
1	AG	113/113 (100%)	113 (100%)	0	100	100
1	AH	113/113 (100%)	113 (100%)	0	100	100
1	AI	113/113 (100%)	113 (100%)	0	100	100
1	AJ	113/113 (100%)	113 (100%)	0	100	100
1	AK	113/113 (100%)	113 (100%)	0	100	100
1	AL	113/113 (100%)	113 (100%)	0	100	100
1	AM	113/113 (100%)	113 (100%)	0	100	100
1	AN	113/113 (100%)	113 (100%)	0	100	100
1	AO	113/113 (100%)	113 (100%)	0	100	100
1	AP	113/113 (100%)	113 (100%)	0	100	100
1	AQ	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AR	113/113 (100%)	113 (100%)	0	100	100
1	AS	113/113 (100%)	113 (100%)	0	100	100
1	AT	113/113 (100%)	113 (100%)	0	100	100
1	AU	113/113 (100%)	113 (100%)	0	100	100
1	AV	113/113 (100%)	113 (100%)	0	100	100
1	AW	113/113 (100%)	113 (100%)	0	100	100
1	AX	113/113 (100%)	113 (100%)	0	100	100
1	AY	113/113 (100%)	113 (100%)	0	100	100
1	AZ	113/113 (100%)	113 (100%)	0	100	100
1	BA	113/113 (100%)	113 (100%)	0	100	100
1	BB	113/113 (100%)	113 (100%)	0	100	100
1	BC	113/113 (100%)	113 (100%)	0	100	100
1	BD	113/113 (100%)	113 (100%)	0	100	100
1	BE	113/113 (100%)	113 (100%)	0	100	100
1	BF	113/113 (100%)	113 (100%)	0	100	100
1	BG	113/113 (100%)	113 (100%)	0	100	100
1	BH	113/113 (100%)	113 (100%)	0	100	100
1	BI	113/113 (100%)	113 (100%)	0	100	100
1	BJ	113/113 (100%)	113 (100%)	0	100	100
1	BK	113/113 (100%)	113 (100%)	0	100	100
1	BL	113/113 (100%)	113 (100%)	0	100	100
1	BM	113/113 (100%)	113 (100%)	0	100	100
1	BN	113/113 (100%)	113 (100%)	0	100	100
1	BO	113/113 (100%)	113 (100%)	0	100	100
1	BP	113/113 (100%)	113 (100%)	0	100	100
1	BQ	113/113 (100%)	113 (100%)	0	100	100
1	BR	113/113 (100%)	113 (100%)	0	100	100
1	BS	113/113 (100%)	113 (100%)	0	100	100
1	BT	113/113 (100%)	113 (100%)	0	100	100
1	BU	113/113 (100%)	113 (100%)	0	100	100
1	BV	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BW	113/113 (100%)	113 (100%)	0	100	100
1	BX	113/113 (100%)	113 (100%)	0	100	100
1	BY	113/113 (100%)	113 (100%)	0	100	100
1	BZ	113/113 (100%)	113 (100%)	0	100	100
1	CA	113/113 (100%)	113 (100%)	0	100	100
1	CB	113/113 (100%)	113 (100%)	0	100	100
1	CC	113/113 (100%)	113 (100%)	0	100	100
1	CD	113/113 (100%)	113 (100%)	0	100	100
1	CE	113/113 (100%)	113 (100%)	0	100	100
1	CF	113/113 (100%)	113 (100%)	0	100	100
1	CG	113/113 (100%)	113 (100%)	0	100	100
1	CH	113/113 (100%)	113 (100%)	0	100	100
All	All	6780/6780 (100%)	6780 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 103 such sidechains are listed below:

Mol	Chain	Res	Type
1	BI	7	GLN
1	BQ	7	GLN
1	CG	7	GLN
1	BJ	7	GLN
1	BM	7	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AA	123/123 (100%)	1.41	24 (19%) 3 2	29, 44, 98, 126	0
1	AB	123/123 (100%)	1.25	24 (19%) 3 2	29, 44, 98, 126	0
1	AC	123/123 (100%)	1.61	38 (30%) 1 1	29, 44, 98, 126	0
1	AD	123/123 (100%)	1.55	33 (26%) 1 1	29, 44, 98, 126	0
1	AE	123/123 (100%)	1.62	37 (30%) 1 1	29, 44, 98, 126	0
1	AF	123/123 (100%)	1.38	32 (26%) 1 1	29, 44, 98, 126	0
1	AG	123/123 (100%)	1.20	20 (16%) 4 3	29, 44, 98, 126	0
1	AH	123/123 (100%)	1.40	29 (23%) 2 1	29, 44, 98, 126	0
1	AI	123/123 (100%)	1.73	39 (31%) 1 1	29, 44, 98, 126	0
1	AJ	123/123 (100%)	1.49	38 (30%) 1 1	29, 44, 98, 126	0
1	AK	123/123 (100%)	1.57	40 (32%) 1 1	29, 44, 98, 126	0
1	AL	123/123 (100%)	1.61	34 (27%) 1 1	29, 44, 98, 126	0
1	AM	123/123 (100%)	1.20	19 (15%) 5 4	29, 44, 98, 126	0
1	AN	123/123 (100%)	1.43	29 (23%) 2 1	29, 44, 98, 126	0
1	AO	123/123 (100%)	1.54	37 (30%) 1 1	29, 44, 98, 126	0
1	AP	123/123 (100%)	1.52	34 (27%) 1 1	29, 44, 98, 126	0
1	AQ	123/123 (100%)	1.55	40 (32%) 1 1	29, 44, 98, 126	0
1	AR	123/123 (100%)	1.32	26 (21%) 2 2	29, 44, 98, 126	0
1	AS	123/123 (100%)	1.58	38 (30%) 1 1	29, 44, 98, 126	0
1	AT	123/123 (100%)	1.59	37 (30%) 1 1	29, 44, 98, 126	0
1	AU	123/123 (100%)	1.16	23 (18%) 3 2	29, 44, 98, 126	0
1	AV	123/123 (100%)	1.70	42 (34%) 1 1	29, 44, 98, 126	0
1	AW	123/123 (100%)	1.18	23 (18%) 3 2	29, 44, 98, 126	0
1	AX	123/123 (100%)	1.40	25 (20%) 3 2	29, 44, 98, 126	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	123/123 (100%)	1.44	32 (26%) 1 1	29, 44, 98, 126	0
1	AZ	123/123 (100%)	1.36	28 (22%) 2 2	29, 44, 98, 126	0
1	BA	123/123 (100%)	1.39	29 (23%) 2 1	29, 44, 98, 126	0
1	BB	123/123 (100%)	1.32	30 (24%) 2 1	29, 44, 98, 126	0
1	BC	123/123 (100%)	1.46	35 (28%) 1 1	29, 44, 98, 126	0
1	BD	123/123 (100%)	1.22	24 (19%) 3 2	29, 44, 98, 126	0
1	BE	123/123 (100%)	1.71	38 (30%) 1 1	29, 44, 98, 126	0
1	BF	123/123 (100%)	1.24	26 (21%) 2 2	29, 44, 98, 126	0
1	BG	123/123 (100%)	1.37	33 (26%) 1 1	29, 44, 98, 126	0
1	BH	123/123 (100%)	1.61	38 (30%) 1 1	29, 44, 98, 126	0
1	BI	123/123 (100%)	1.37	29 (23%) 2 1	29, 44, 98, 126	0
1	BJ	123/123 (100%)	1.48	31 (25%) 1 1	29, 44, 98, 126	0
1	BK	123/123 (100%)	1.38	29 (23%) 2 1	29, 44, 98, 126	0
1	BL	123/123 (100%)	1.66	41 (33%) 1 1	29, 44, 98, 126	0
1	BM	123/123 (100%)	1.26	24 (19%) 3 2	29, 44, 98, 126	0
1	BN	123/123 (100%)	1.57	37 (30%) 1 1	29, 44, 98, 126	0
1	BO	123/123 (100%)	1.50	35 (28%) 1 1	29, 44, 98, 126	0
1	BP	123/123 (100%)	1.36	27 (21%) 2 2	29, 44, 98, 126	0
1	BQ	123/123 (100%)	1.46	31 (25%) 1 1	29, 44, 98, 126	0
1	BR	123/123 (100%)	1.35	31 (25%) 1 1	29, 44, 98, 126	0
1	BS	123/123 (100%)	1.53	36 (29%) 1 1	29, 44, 98, 126	0
1	BT	123/123 (100%)	1.60	35 (28%) 1 1	29, 44, 98, 126	0
1	BU	123/123 (100%)	1.60	37 (30%) 1 1	29, 44, 98, 126	0
1	BV	123/123 (100%)	1.41	32 (26%) 1 1	29, 44, 98, 126	0
1	BW	123/123 (100%)	1.51	32 (26%) 1 1	29, 44, 98, 126	0
1	BX	123/123 (100%)	1.49	30 (24%) 2 1	29, 44, 98, 126	0
1	BY	123/123 (100%)	1.51	35 (28%) 1 1	29, 44, 98, 126	0
1	BZ	123/123 (100%)	1.44	28 (22%) 2 2	29, 44, 98, 126	0
1	CA	123/123 (100%)	1.51	29 (23%) 2 1	29, 44, 98, 126	0
1	CB	123/123 (100%)	1.83	49 (39%) 1 0	29, 44, 98, 126	0
1	CC	123/123 (100%)	1.25	26 (21%) 2 2	29, 44, 98, 126	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	CD	123/123 (100%)	1.46	27 (21%) 2 2	29, 44, 98, 126	0
1	CE	123/123 (100%)	1.48	31 (25%) 1 1	29, 44, 98, 126	0
1	CF	123/123 (100%)	1.52	33 (26%) 1 1	29, 44, 98, 126	0
1	CG	123/123 (100%)	1.70	44 (35%) 1 1	29, 44, 98, 126	0
1	CH	123/123 (100%)	1.43	29 (23%) 2 1	29, 44, 98, 126	0
All	All	7380/7380 (100%)	1.46	1922 (26%) 1 1	29, 44, 99, 126	0

The worst 5 of 1922 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BS	43	ALA	11.2
1	CE	63	SER	7.1
1	CB	64	VAL	7.1
1	AS	58	ILE	6.6
1	AX	67	CYS	6.5

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.