



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 29, 2020 – 10:53 AM BST

PDB ID : 6YFD
Title : Virus-like particle of Beihai levi-like virus 14
Authors : Rumnieks, J.; Kalnins, G.; Sisovs, M.; Lieknina, I.; Tars, K.
Deposited on : 2020-03-26
Resolution : 3.30 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.13
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13

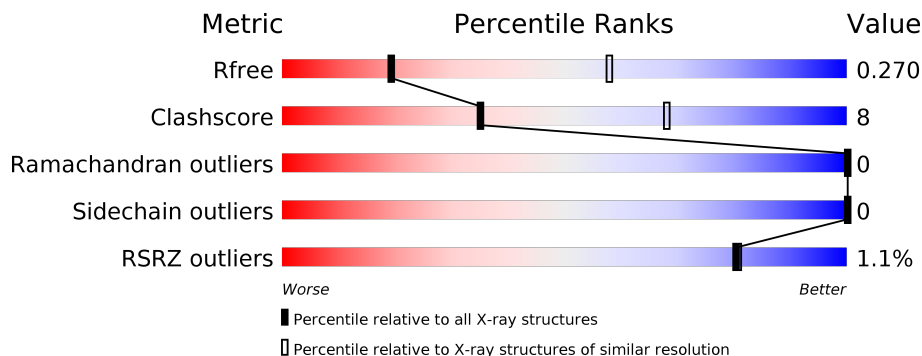
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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.













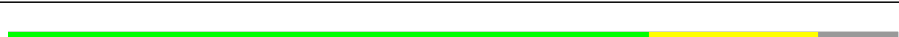


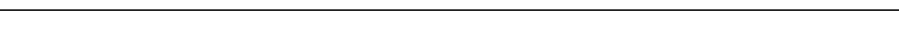











Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 on 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	208	
1	AB	208	
1	AC	208	
1	AD	208	
1	AE	208	
1	AF	208	

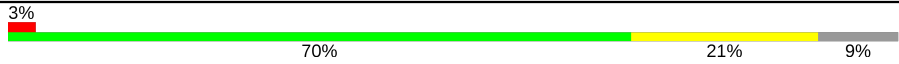



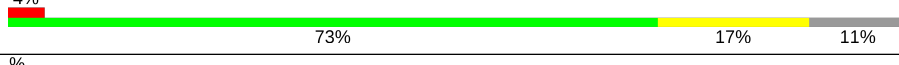
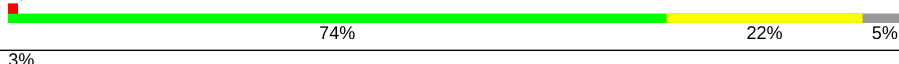
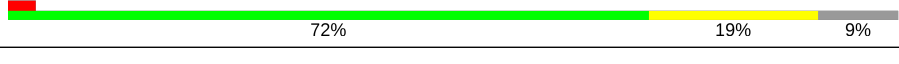

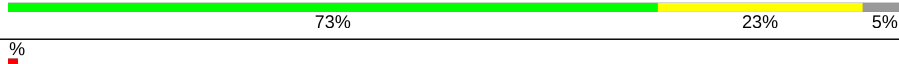


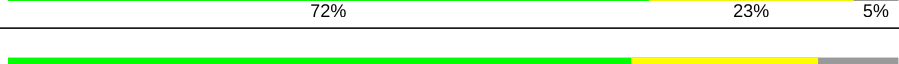

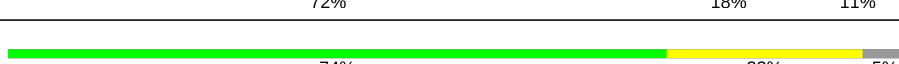

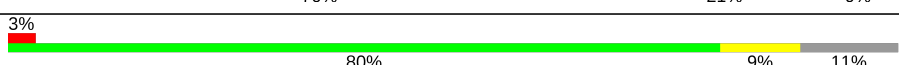
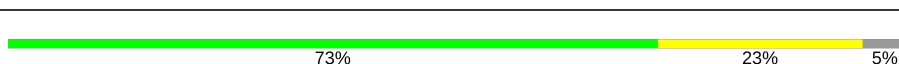
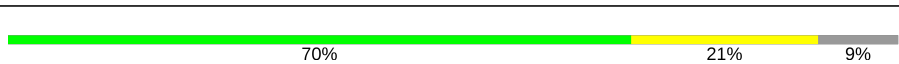
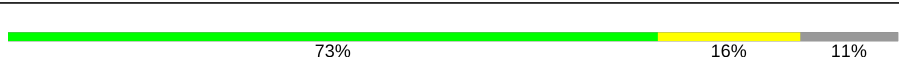


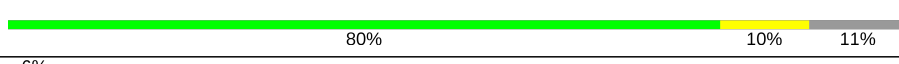
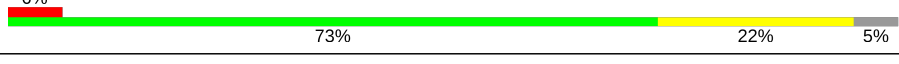


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Mol	Chain	Length	Quality of chain
1	AG	208	
1	AH	208	
1	AI	208	
1	AJ	208	
1	AK	208	
1	AL	208	
1	AM	208	
1	AN	208	
1	AO	208	
1	AP	208	
1	AQ	208	
1	AR	208	
1	AS	208	
1	AT	208	
1	AU	208	
1	AV	208	
1	AW	208	
1	AX	208	
1	AY	208	
1	AZ	208	
1	BA	208	
1	BB	208	
1	BC	208	
1	BD	208	
1	BE	208	





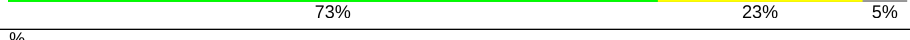
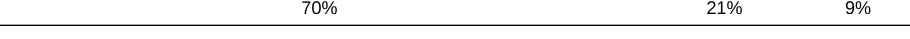
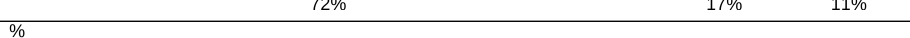
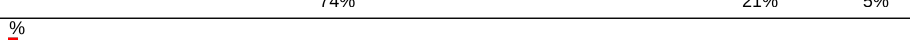
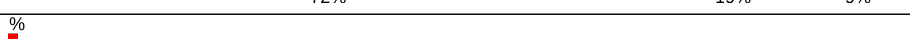
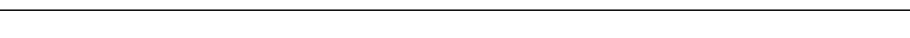















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Mol	Chain	Length	Quality of chain
1	BF	208	 3% 70% 21% 9%
1	BG	208	 3% 72% 17% 11%
1	BH	208	 2% 74% 22% 5%
1	BI	208	 % 71% 20% 9%
1	BJ	208	 4% 73% 17% 11%
1	BK	208	 % 74% 22% 5%
1	BL	208	 3% 72% 19% 9%
1	BM	208	 % 73% 16% 11%
1	BN	208	 % 73% 23% 5%
1	BO	208	 % 74% 17% 9%
1	BP	208	 % 73% 17% 11%
1	BQ	208	 % 72% 23% 5%
1	BR	208	 % 70% 21% 9%
1	BS	208	 % 72% 18% 11%
1	BT	208	 % 74% 22% 5%
1	BU	208	 % 70% 21% 9%
1	BV	208	 3% 80% 9% 11%
1	BW	208	 % 73% 23% 5%
1	BX	208	 % 70% 21% 9%
1	BY	208	 % 73% 16% 11%
1	BZ	208	 % 75% 20% 5%
1	CA	208	 % 71% 20% 9%
1	CB	208	 % 80% 10% 11%
1	CC	208	 6% 73% 22% 5%
1	CD	208	 % 70% 21% 9%




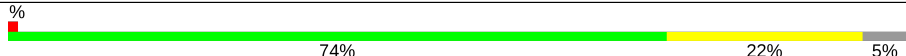
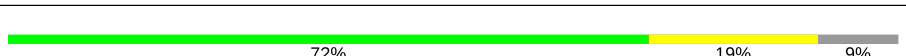
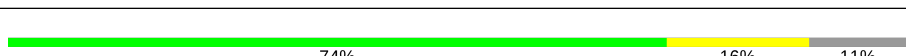
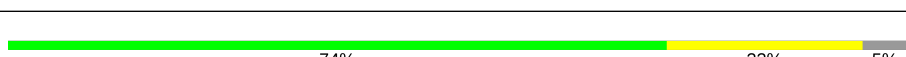
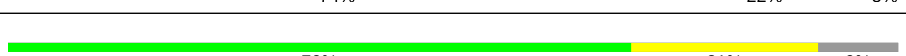

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Mol	Chain	Length	Quality of chain
1	CE	208	 73% 17% 11% 2%
1	CF	208	 74% 22% 5%
1	CG	208	 72% 19% 9%
1	CH	208	 78% 11% 11% 0%
1	CI	208	 73% 23% 5%
1	CJ	208	 70% 21% 9% 0%
1	CK	208	 72% 17% 11%
1	CL	208	 74% 21% 5% 0%
1	CM	208	 72% 19% 9% 0%
1	CN	208	 73% 17% 11% 0%
1	CO	208	 74% 22% 5%
1	CP	208	 68% 23% 9% 0%
1	CQ	208	 71% 19% 11%
1	CR	208	 75% 21% 5% 0%
1	CS	208	 72% 19% 9% 2%
1	CT	208	 74% 15% 11% 2%
1	CU	208	 71% 25% 5%
1	CV	208	 69% 22% 9%
1	CW	208	 72% 17% 11%
1	CX	208	 75% 21% 5% 2%
1	CY	208	 71% 20% 9% 0%
1	CZ	208	 73% 17% 11% 4%
1	DA	208	 73% 23% 5% 2%
1	DB	208	 71% 20% 9% 2%
1	DC	208	 73% 16% 11% 3%

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Mol	Chain	Length	Quality of chain
1	DD	208	 74% 22% 5%
1	DE	208	 2% 72% 19% 9%
1	DF	208	 4% 73% 16% 11%
1	DG	208	 1% 74% 22% 5%
1	DH	208	 72% 19% 9%
1	DI	208	 74% 16% 11%
1	DJ	208	 74% 22% 5%
1	DK	208	 70% 21% 9%
1	DL	208	 1% 71% 19% 11%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 126960 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
			Total	C	N	O	S			
1	AA	198	1463	910	261	286	6	0	0	0
1	AB	189	1396	869	249	273	5	0	0	0
1	AC	186	1373	854	245	269	5	0	0	0
1	AD	198	1463	910	261	286	6	0	0	0
1	AE	189	1396	869	249	273	5	0	0	0
1	AF	186	1373	854	245	269	5	0	0	0
1	AG	198	1463	910	261	286	6	0	0	0
1	AH	189	1396	869	249	273	5	0	0	0
1	AI	186	1373	854	245	269	5	0	0	0
1	AJ	198	1463	910	261	286	6	0	0	0
1	AK	189	1396	869	249	273	5	0	0	0
1	AL	186	1373	854	245	269	5	0	0	0
1	AM	198	1463	910	261	286	6	0	0	0
1	AN	189	1396	869	249	273	5	0	0	0
1	AO	186	1373	854	245	269	5	0	0	0
1	AP	198	1463	910	261	286	6	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AQ	189	1396	869	249	273	5	0	0	0
1	AR	186	1373	854	245	269	5	0	0	0
1	AS	198	1463	910	261	286	6	0	0	0
1	AT	189	1396	869	249	273	5	0	0	0
1	AU	186	1373	854	245	269	5	0	0	0
1	AV	198	1463	910	261	286	6	0	0	0
1	AW	189	1396	869	249	273	5	0	0	0
1	AX	186	1373	854	245	269	5	0	0	0
1	AY	198	1463	910	261	286	6	0	0	0
1	AZ	189	1396	869	249	273	5	0	0	0
1	BA	186	1373	854	245	269	5	0	0	0
1	BB	198	1463	910	261	286	6	0	0	0
1	BC	189	1396	869	249	273	5	0	0	0
1	BD	186	1373	854	245	269	5	0	0	0
1	BE	198	1463	910	261	286	6	0	0	0
1	BF	189	1396	869	249	273	5	0	0	0
1	BG	186	1373	854	245	269	5	0	0	0
1	BH	198	1463	910	261	286	6	0	0	0
1	BI	189	1396	869	249	273	5	0	0	0
1	BJ	186	1373	854	245	269	5	0	0	0
1	BK	198	1463	910	261	286	6	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	BL	189	1396	869	249	273	5	0	0	0
1	BM	186	1373	854	245	269	5	0	0	0
1	BN	198	1463	910	261	286	6	0	0	0
1	BO	189	1396	869	249	273	5	0	0	0
1	BP	186	1373	854	245	269	5	0	0	0
1	BQ	198	1463	910	261	286	6	0	0	0
1	BR	189	1396	869	249	273	5	0	0	0
1	BS	186	1373	854	245	269	5	0	0	0
1	BT	198	1463	910	261	286	6	0	0	0
1	BU	189	1396	869	249	273	5	0	0	0
1	BV	186	1373	854	245	269	5	0	0	0
1	BW	198	1463	910	261	286	6	0	0	0
1	BX	189	1396	869	249	273	5	0	0	0
1	BY	186	1373	854	245	269	5	0	0	0
1	BZ	198	1463	910	261	286	6	0	0	0
1	CA	189	1396	869	249	273	5	0	0	0
1	CB	186	1373	854	245	269	5	0	0	0
1	CC	198	1463	910	261	286	6	0	0	0
1	CD	189	1396	869	249	273	5	0	0	0
1	CE	186	1373	854	245	269	5	0	0	0
1	CF	198	1463	910	261	286	6	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	CG	189	1396	869	249	273	5	0	0	0
1	CH	186	1373	854	245	269	5	0	0	0
1	CI	198	1463	910	261	286	6	0	0	0
1	CJ	189	1396	869	249	273	5	0	0	0
1	CK	186	1373	854	245	269	5	0	0	0
1	CL	198	1463	910	261	286	6	0	0	0
1	CM	189	1396	869	249	273	5	0	0	0
1	CN	186	1373	854	245	269	5	0	0	0
1	CO	198	1463	910	261	286	6	0	0	0
1	CP	189	1396	869	249	273	5	0	0	0
1	CQ	186	1373	854	245	269	5	0	0	0
1	CR	198	1463	910	261	286	6	0	0	0
1	CS	189	1396	869	249	273	5	0	0	0
1	CT	186	1373	854	245	269	5	0	0	0
1	CU	198	1463	910	261	286	6	0	0	0
1	CV	189	1396	869	249	273	5	0	0	0
1	CW	186	1373	854	245	269	5	0	0	0
1	CX	198	1463	910	261	286	6	0	0	0
1	CY	189	1396	869	249	273	5	0	0	0
1	CZ	186	1373	854	245	269	5	0	0	0
1	DA	198	1463	910	261	286	6	0	0	0

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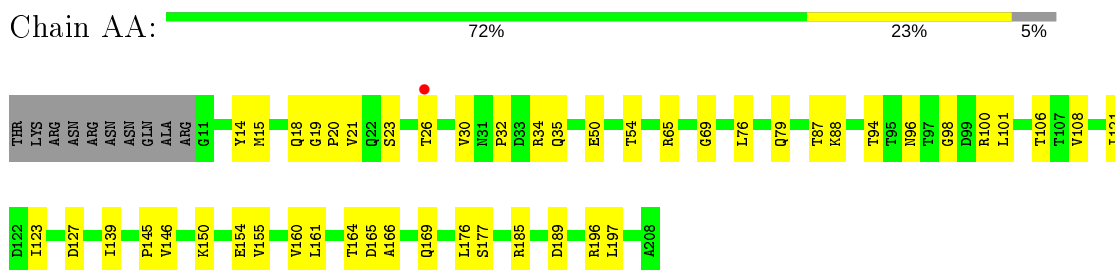
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DB	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	DC	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	DD	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	DE	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	DF	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	DG	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	DH	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	DI	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			
1	DJ	198	Total	C	N	O	S	0	0	0
			1463	910	261	286	6			
1	DK	189	Total	C	N	O	S	0	0	0
			1396	869	249	273	5			
1	DL	186	Total	C	N	O	S	0	0	0
			1373	854	245	269	5			

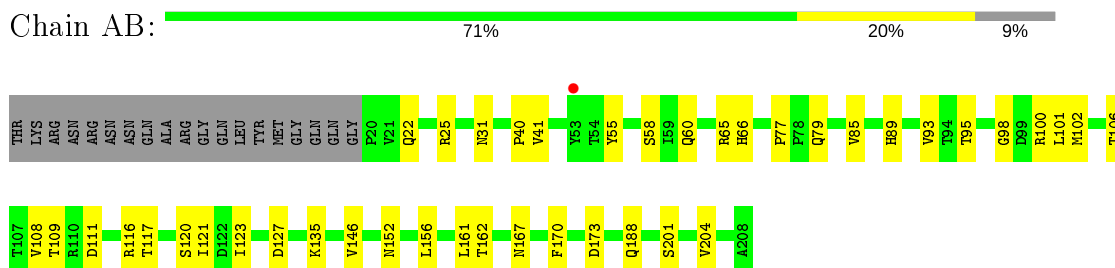
3 Residue-property plots [i](#)

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.

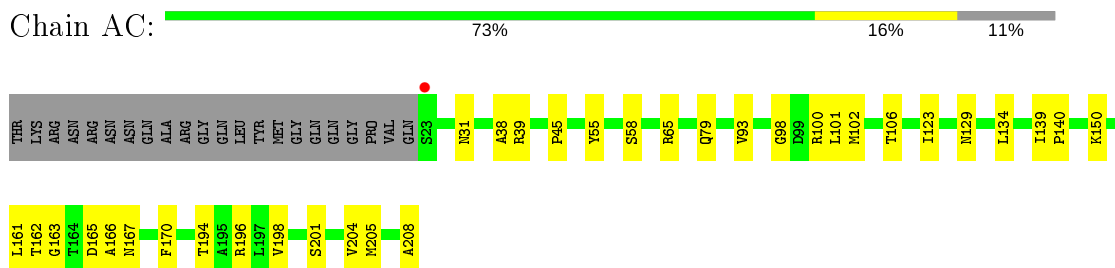
- Molecule 1: coat protein



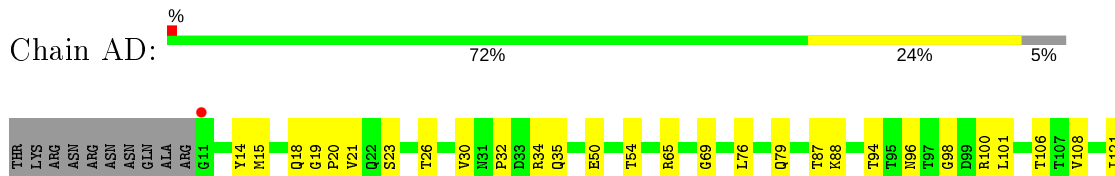
- Molecule 1: coat protein



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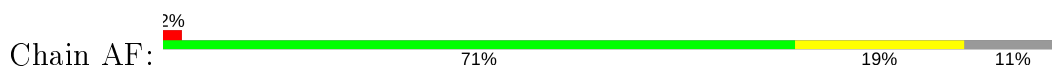




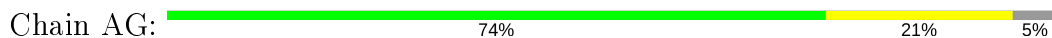
- Molecule 1: coat protein



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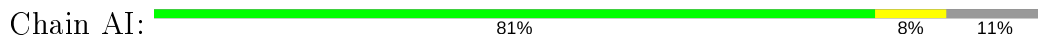
- Molecule 1: coat protein



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- Molecule 1: coat protein





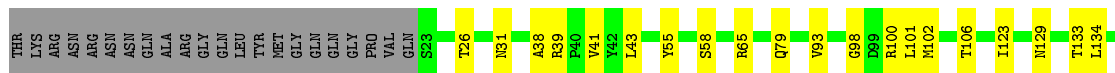
- Molecule 1: coat protein



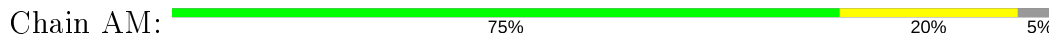
- Molecule 1: coat protein



- Molecule 1: coat protein

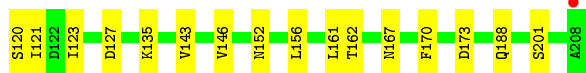


- Molecule 1: coat protein

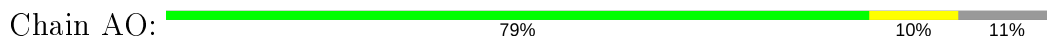


- Molecule 1: coat protein

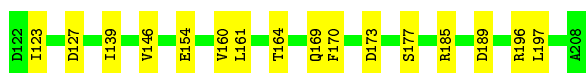
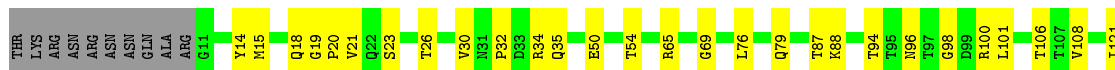




- Molecule 1: coat protein



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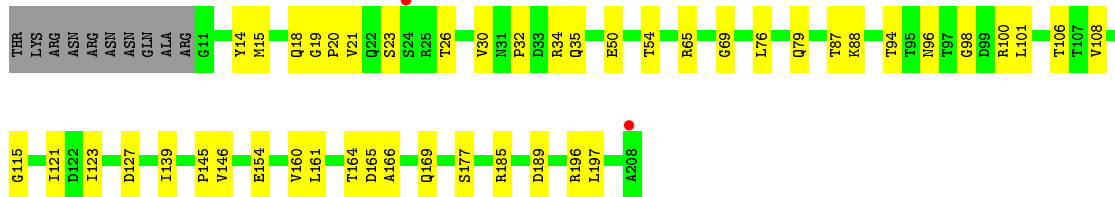
- Molecule 1: coat protein



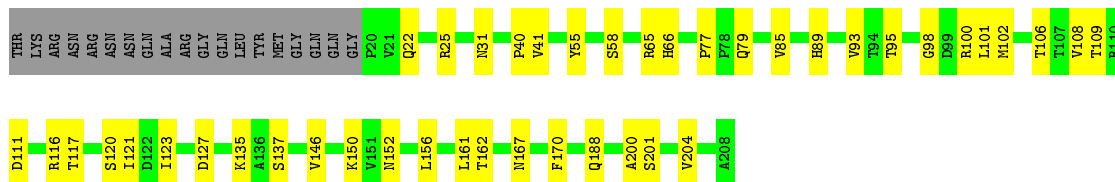
- Molecule 1: coat protein



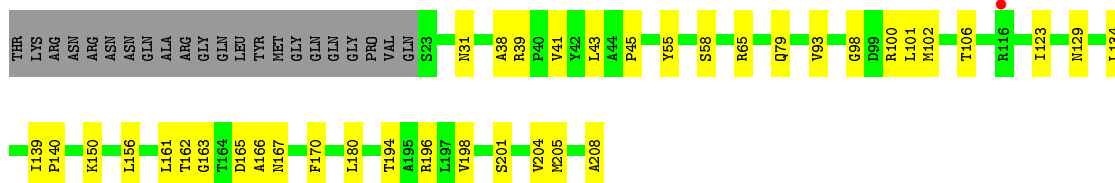
- Molecule 1: coat protein



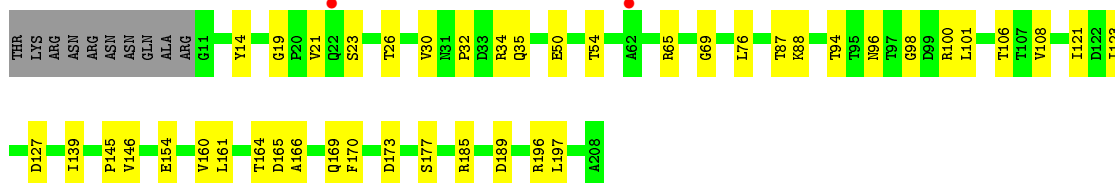
• Molecule 1: coat protein



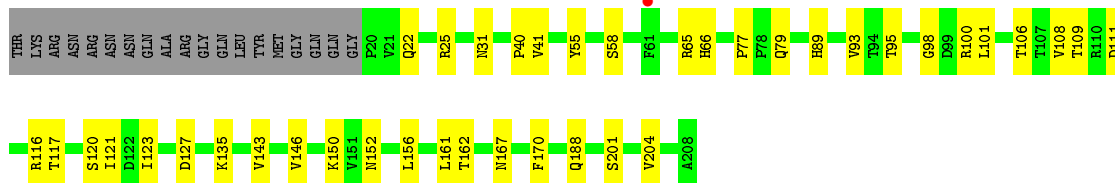
• Molecule 1: coat protein




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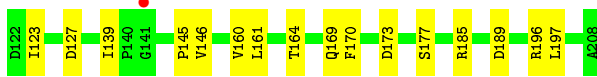
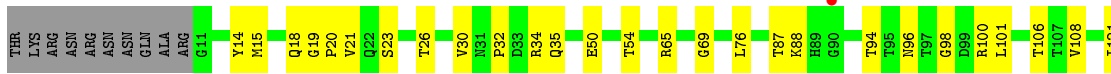
- Molecule 1: coat protein

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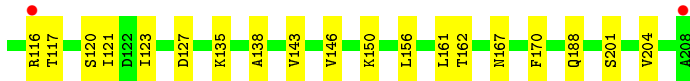
- Molecule 1: coat protein

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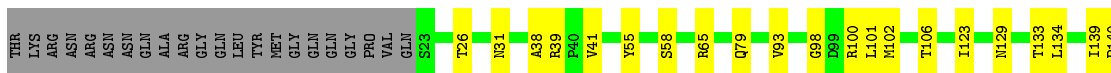
- Molecule 1: coat protein

Chain AZ: 




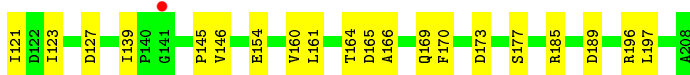
- Molecule 1: coat protein

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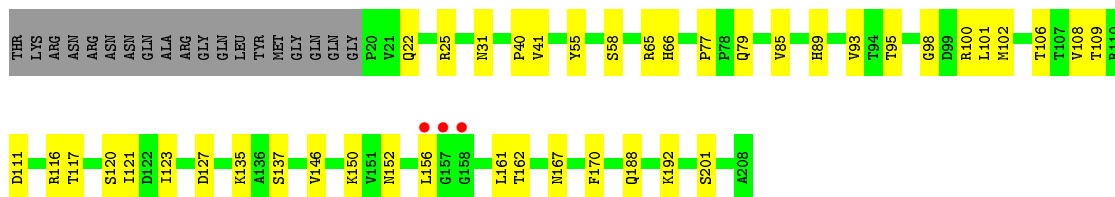
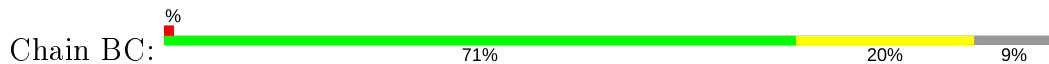


- Molecule 1: coat protein

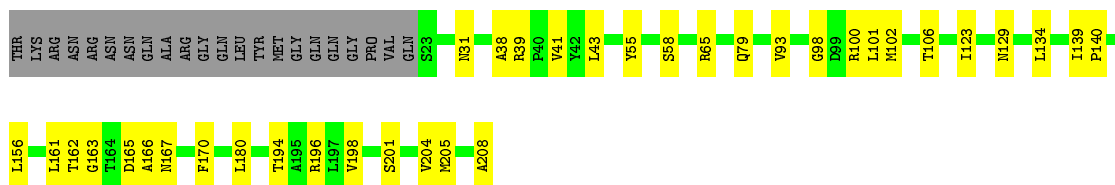
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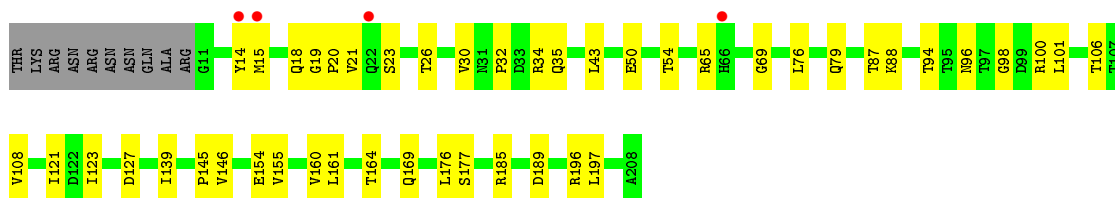
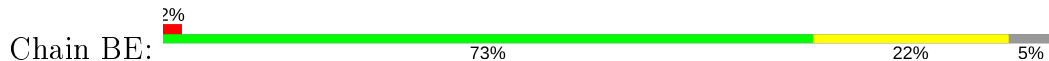
• Molecule 1: coat protein



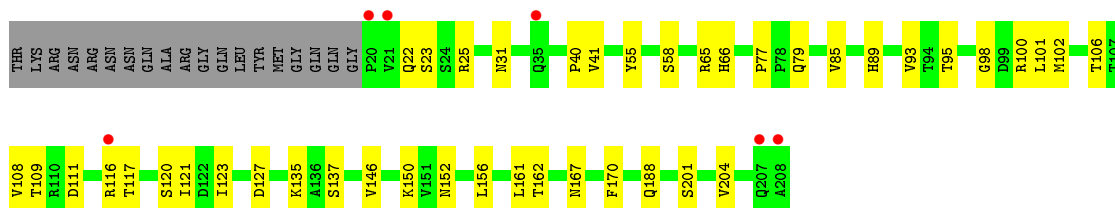
• Molecule 1: coat protein



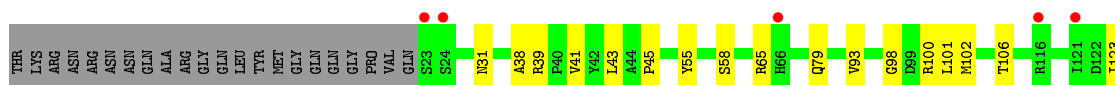
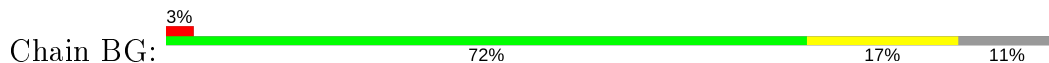
• Molecule 1: coat protein



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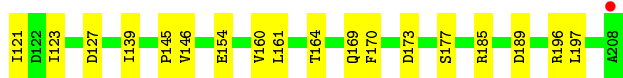
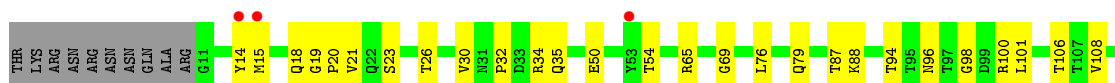
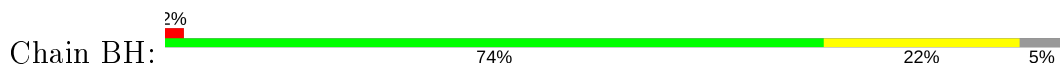


• Molecule 1: coat protein





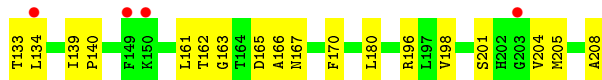
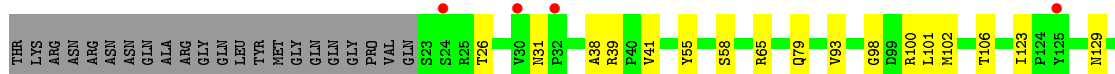
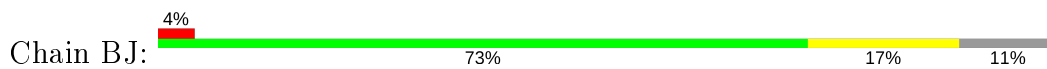
- Molecule 1: coat protein



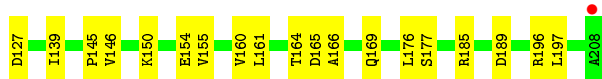
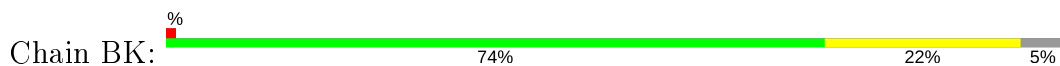
- Molecule 1: coat protein



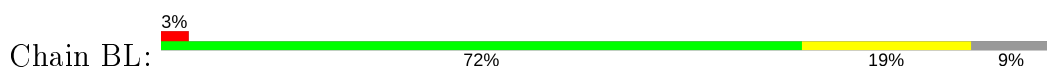
- Molecule 1: coat protein



- Molecule 1: coat protein

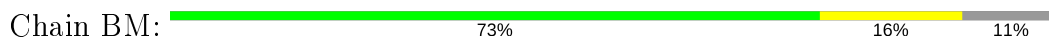


- Molecule 1: coat protein

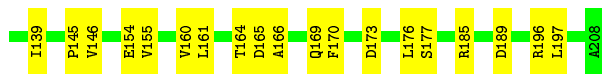




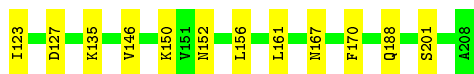
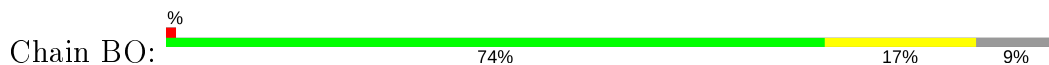
• Molecule 1: coat protein



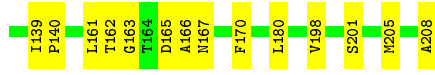
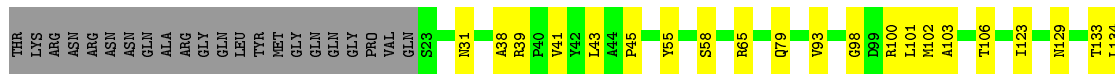
• Molecule 1: coat protein



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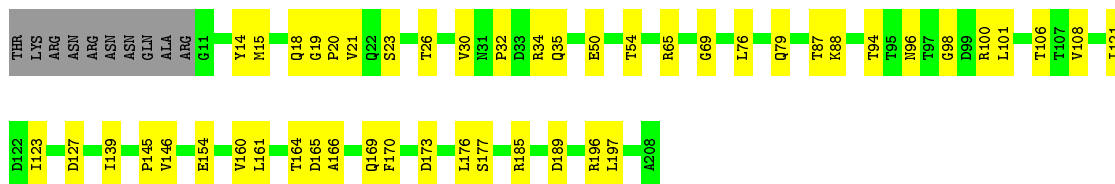


• Molecule 1: coat protein



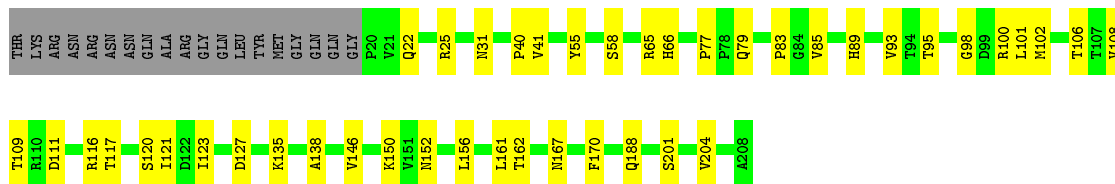
• Molecule 1: coat protein

Chain BQ:  72% 23% 5%



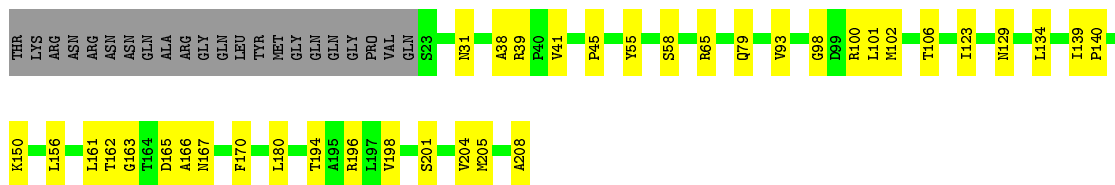
• Molecule 1: coat protein

Chain BR:  70% 21% 9%



• Molecule 1: coat protein

Chain BS:  72% 18% 11%



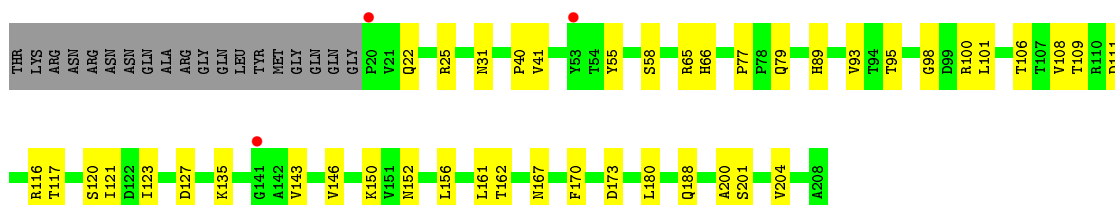
• Molecule 1: coat protein

Chain BT:  74% 22% 5%




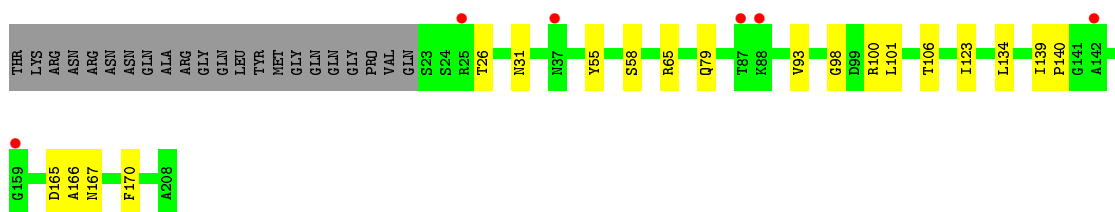
• Molecule 1: coat protein

Chain BU:  70% 21% 9%



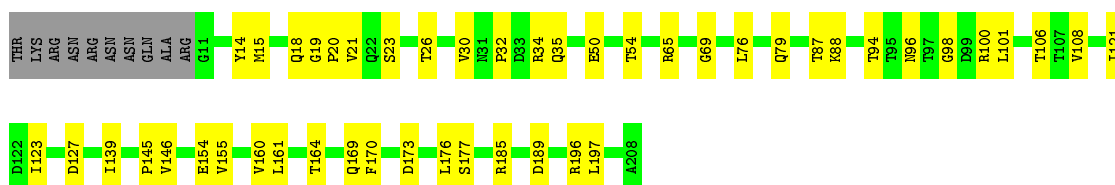
- Molecule 1: coat protein

Chain BV: 



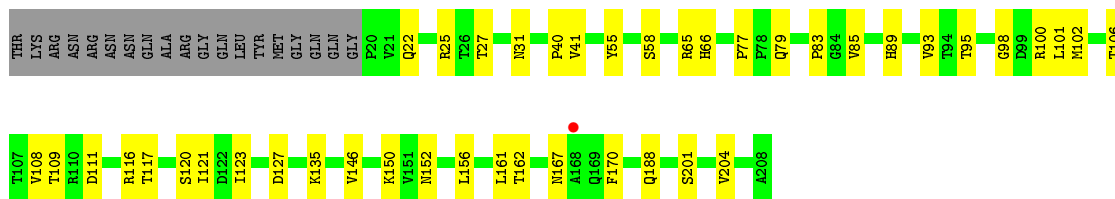
- Molecule 1: coat protein

Chain BW: 



- Molecule 1: coat protein

Chain BX: 




- Molecule 1: coat protein

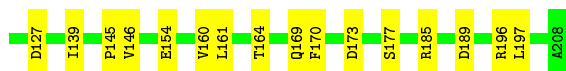
Chain BY: 



- Molecule 1: coat protein

Chain BZ: 

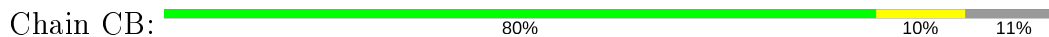




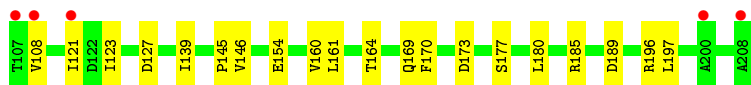
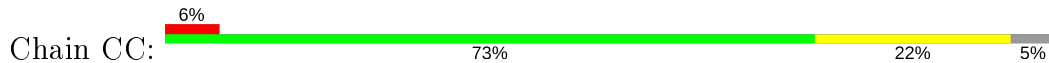
• Molecule 1: coat protein



• Molecule 1: coat protein



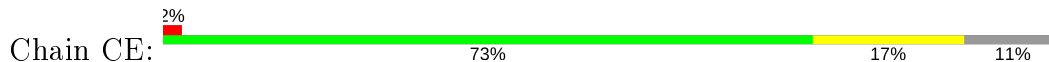
• Molecule 1: coat protein

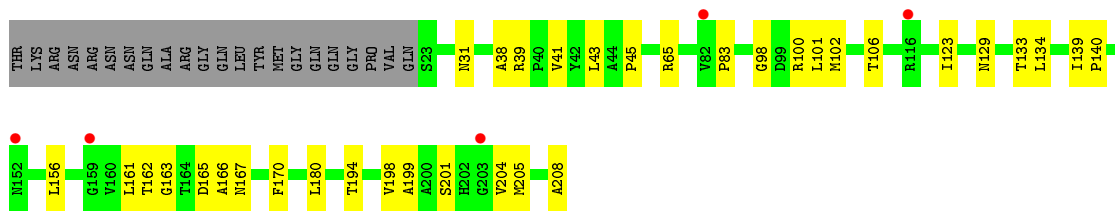


• Molecule 1: coat protein

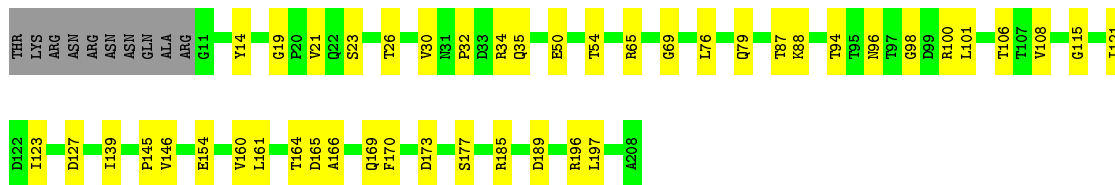


• Molecule 1: coat protein

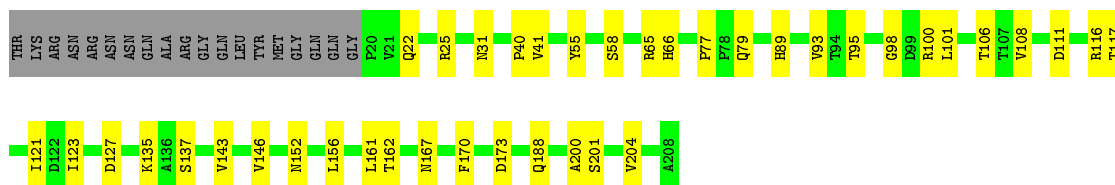




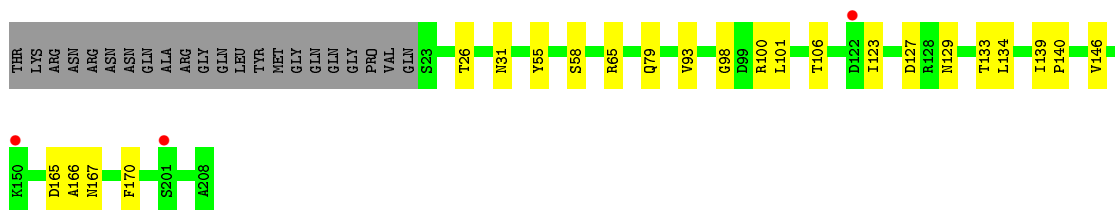
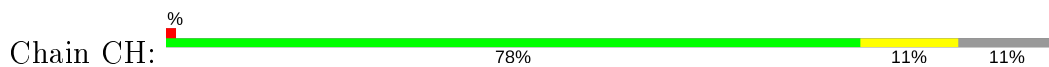
• Molecule 1: coat protein



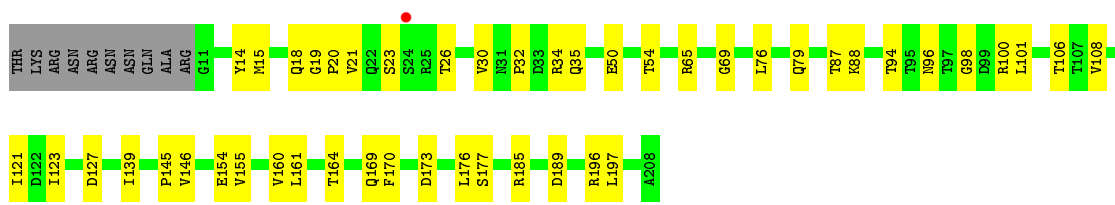
• Molecule 1: coat protein



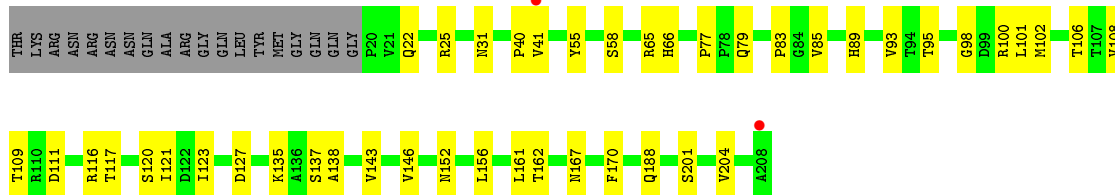
• Molecule 1: coat protein



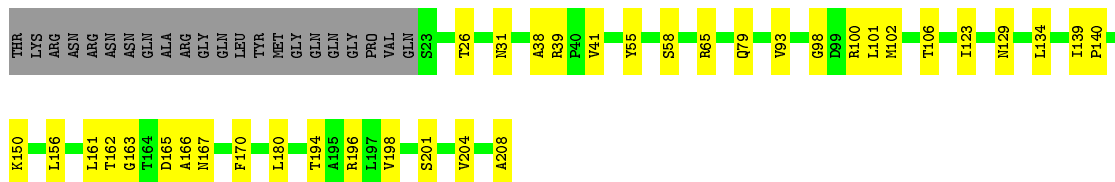
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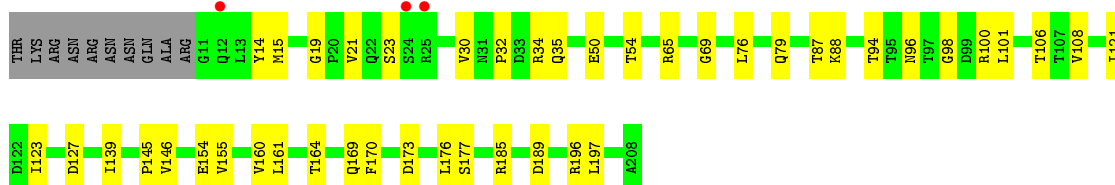
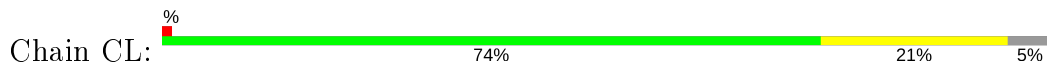
• Molecule 1: coat protein



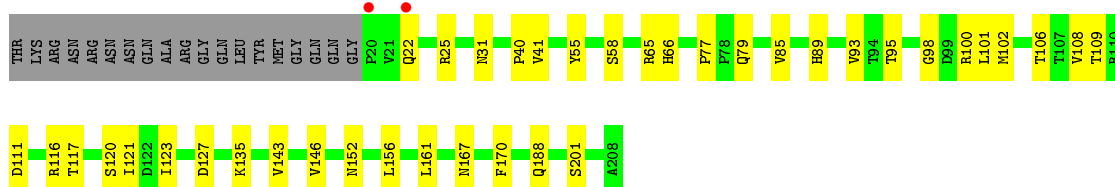
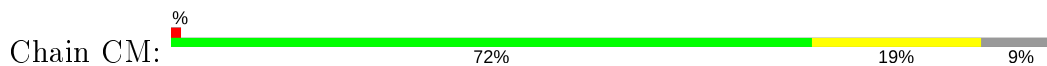
- Molecule 1: coat protein



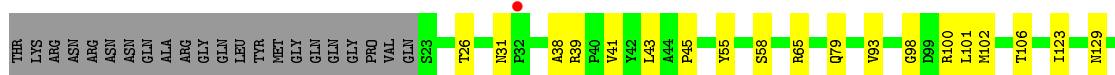
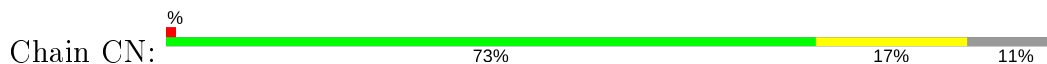
- Molecule 1: coat protein



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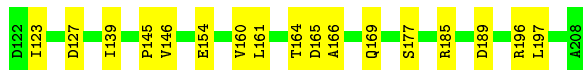
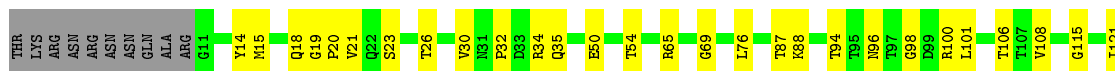
- Molecule 1: coat protein





- Molecule 1: coat protein

Chain CO: 74% 22% 5%



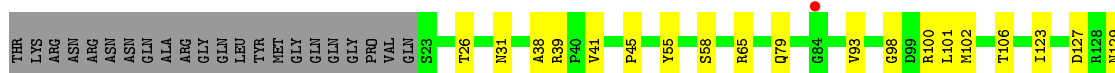
- Molecule 1: coat protein

Chain CP: 68% 23% 9%



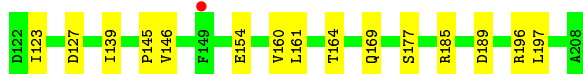
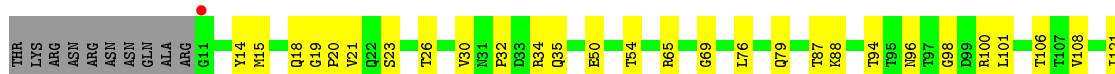
- Molecule 1: coat protein

Chain CQ: 71% 19% 11%



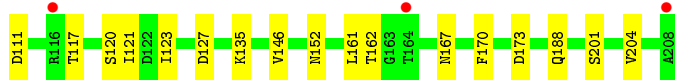
- Molecule 1: coat protein

Chain CR: 75% 21% 5%

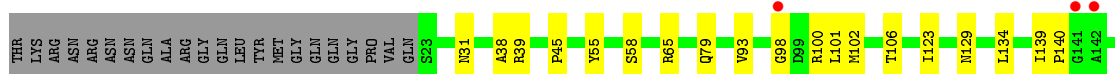
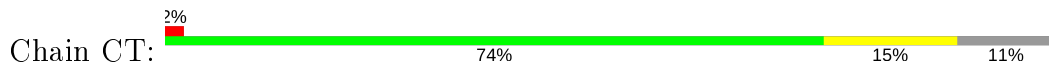


- Molecule 1: coat protein

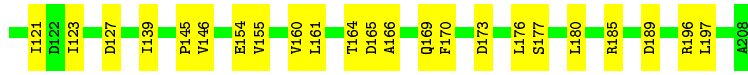
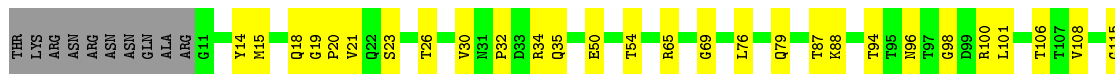
Chain CS: 72% 19% 9%



• Molecule 1: coat protein



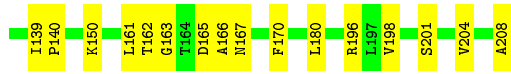
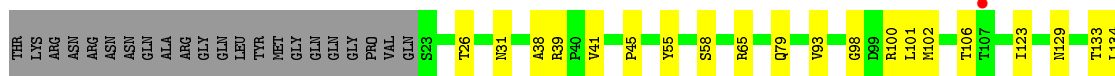
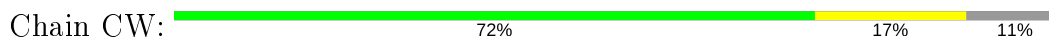
• Molecule 1: coat protein



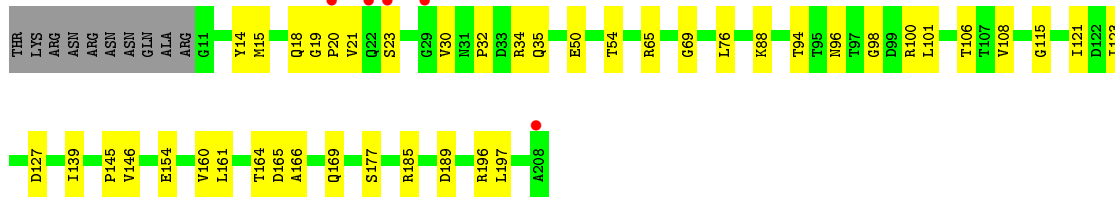
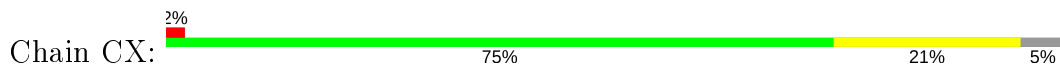
• Molecule 1: coat protein



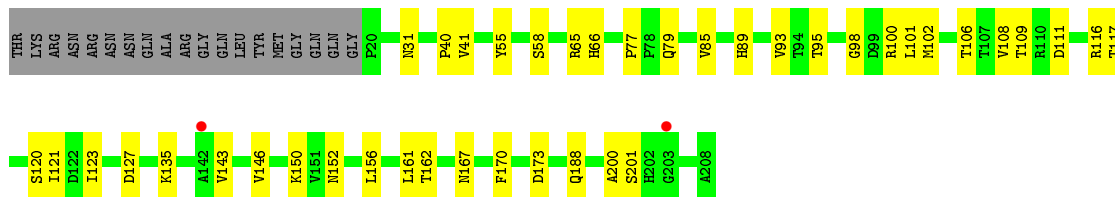
• Molecule 1: coat protein



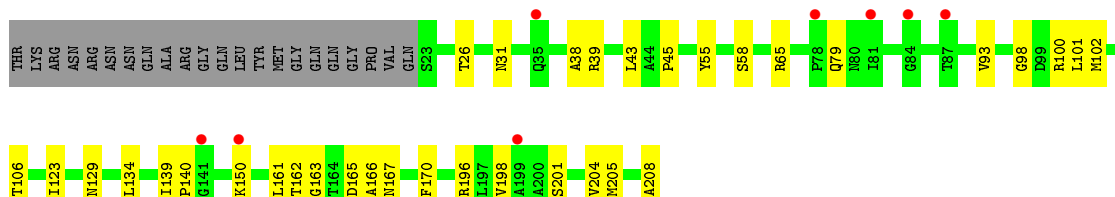
• Molecule 1: coat protein



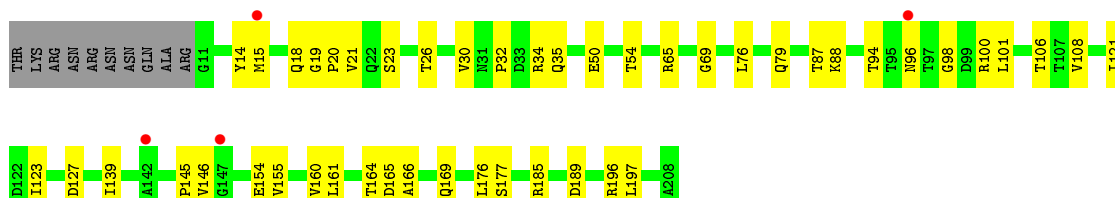
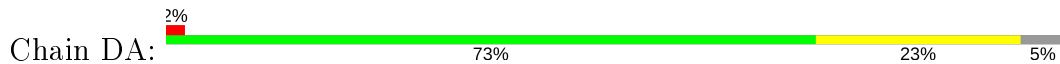
• Molecule 1: coat protein



• Molecule 1: coat protein

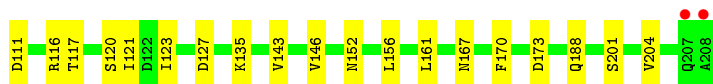


• Molecule 1: coat protein

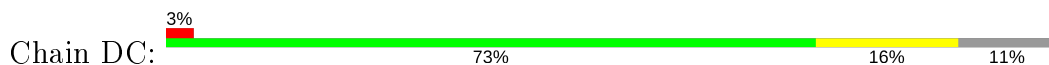


• Molecule 1: coat protein

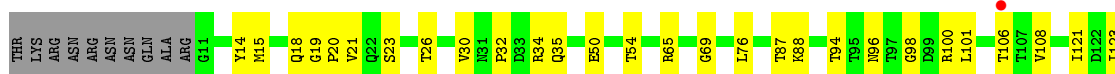




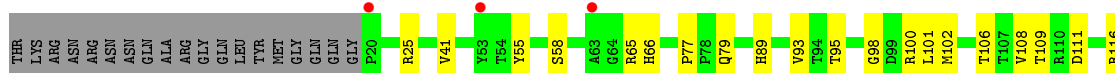
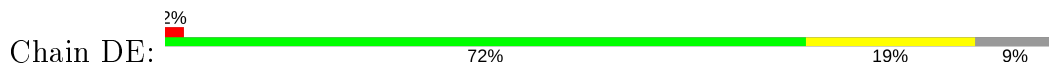
• Molecule 1: coat protein



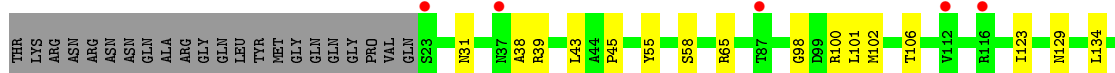
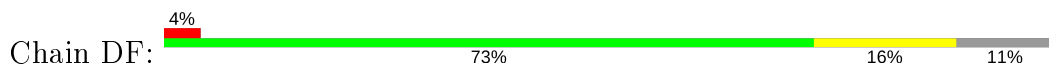
• Molecule 1: coat protein



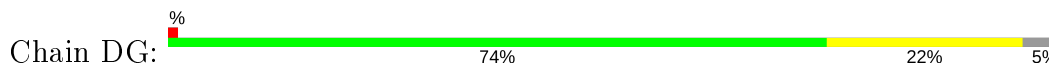
• Molecule 1: coat protein

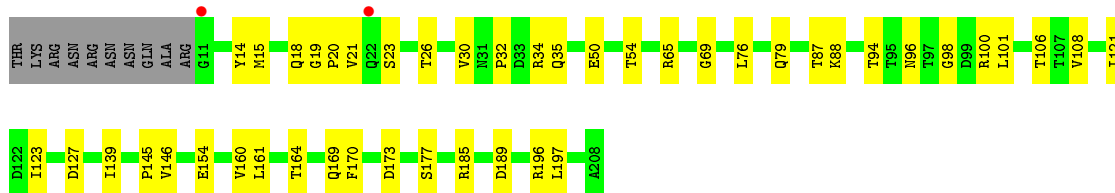


• Molecule 1: coat protein

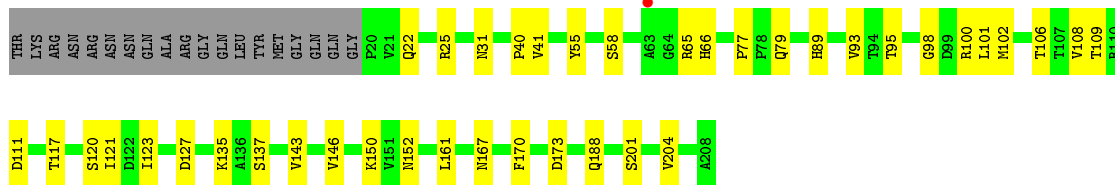


• Molecule 1: coat protein

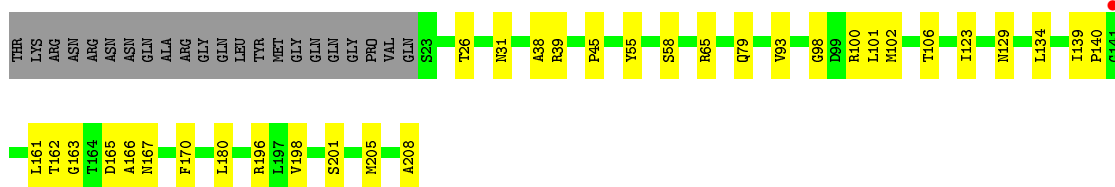




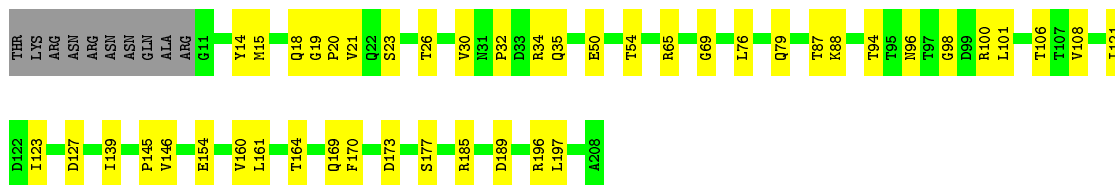
• Molecule 1: coat protein



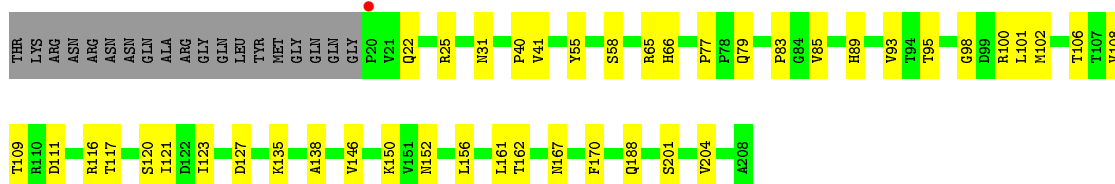
• Molecule 1: coat protein



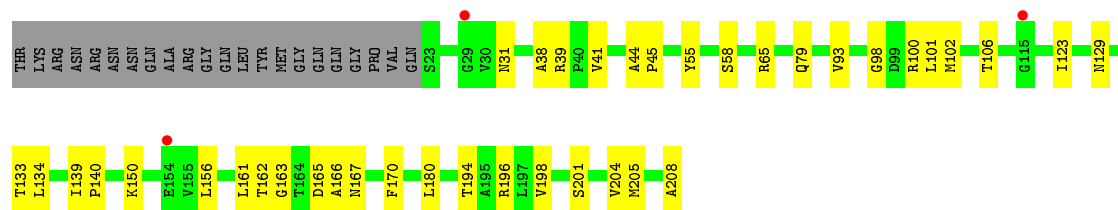
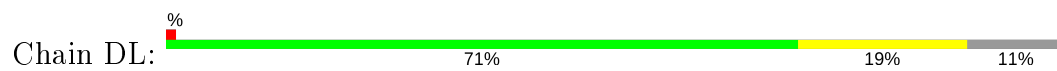
• Molecule 1: coat protein



• Molecule 1: coat protein



• Molecule 1: coat protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	328.67Å 373.71Å 310.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.33 – 3.30 49.33 – 3.30	Depositor EDS
% Data completeness (in resolution range)	92.6 (49.33-3.30) 94.4 (49.33-3.30)	Depositor EDS
R_{merge}	0.65	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.03 (at 3.33Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.265 , 0.267 0.268 , 0.270	Depositor DCC
R_{free} test set	10025 reflections (1.87%)	wwPDB-VP
Wilson B-factor (Å ²)	97.5	Xtrriage
Anisotropy	0.183	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 50.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.22$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	126960	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.55% 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	0.33	0/1492	0.54	0/2035
1	AB	0.33	0/1424	0.55	0/1944
1	AC	0.34	0/1400	0.56	0/1911
1	AD	0.33	0/1492	0.54	0/2035
1	AE	0.33	0/1424	0.55	0/1944
1	AF	0.34	0/1400	0.56	0/1911
1	AG	0.33	0/1492	0.54	0/2035
1	AH	0.33	0/1424	0.55	0/1944
1	AI	0.34	0/1400	0.56	0/1911
1	AJ	0.33	0/1492	0.54	0/2035
1	AK	0.33	0/1424	0.55	0/1944
1	AL	0.34	0/1400	0.56	0/1911
1	AM	0.33	0/1492	0.54	0/2035
1	AN	0.34	0/1424	0.55	0/1944
1	AO	0.34	0/1400	0.56	0/1911
1	AP	0.33	0/1492	0.54	0/2035
1	AQ	0.33	0/1424	0.55	0/1944
1	AR	0.34	0/1400	0.56	0/1911
1	AS	0.33	0/1492	0.54	0/2035
1	AT	0.34	0/1424	0.55	0/1944
1	AU	0.34	0/1400	0.56	0/1911
1	AV	0.33	0/1492	0.54	0/2035
1	AW	0.33	0/1424	0.55	0/1944
1	AX	0.34	0/1400	0.56	0/1911
1	AY	0.33	0/1492	0.54	0/2035
1	AZ	0.33	0/1424	0.55	0/1944
1	BA	0.34	0/1400	0.56	0/1911
1	BB	0.33	0/1492	0.54	0/2035
1	BC	0.33	0/1424	0.55	0/1944
1	BD	0.34	0/1400	0.56	0/1911
1	BE	0.33	0/1492	0.54	0/2035
1	BF	0.33	0/1424	0.55	0/1944
1	BG	0.34	0/1400	0.56	0/1911
1	BH	0.33	0/1492	0.54	0/2035

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BI	0.34	0/1424	0.55	0/1944
1	BJ	0.34	0/1400	0.56	0/1911
1	BK	0.33	0/1492	0.54	0/2035
1	BL	0.33	0/1424	0.55	0/1944
1	BM	0.34	0/1400	0.56	0/1911
1	BN	0.33	0/1492	0.54	0/2035
1	BO	0.33	0/1424	0.55	0/1944
1	BP	0.34	0/1400	0.56	0/1911
1	BQ	0.33	0/1492	0.54	0/2035
1	BR	0.33	0/1424	0.55	0/1944
1	BS	0.34	0/1400	0.56	0/1911
1	BT	0.33	0/1492	0.54	0/2035
1	BU	0.34	0/1424	0.55	0/1944
1	BV	0.34	0/1400	0.56	0/1911
1	BW	0.33	0/1492	0.54	0/2035
1	BX	0.33	0/1424	0.55	0/1944
1	BY	0.34	0/1400	0.56	0/1911
1	BZ	0.33	0/1492	0.54	0/2035
1	CA	0.33	0/1424	0.55	0/1944
1	CB	0.34	0/1400	0.56	0/1911
1	CC	0.33	0/1492	0.54	0/2035
1	CD	0.33	0/1424	0.55	0/1944
1	CE	0.34	0/1400	0.56	0/1911
1	CF	0.33	0/1492	0.54	0/2035
1	CG	0.33	0/1424	0.55	0/1944
1	CH	0.34	0/1400	0.56	0/1911
1	CI	0.33	0/1492	0.54	0/2035
1	CJ	0.33	0/1424	0.55	0/1944
1	CK	0.34	0/1400	0.56	0/1911
1	CL	0.33	0/1492	0.54	0/2035
1	CM	0.34	0/1424	0.55	0/1944
1	CN	0.34	0/1400	0.56	0/1911
1	CO	0.33	0/1492	0.54	0/2035
1	CP	0.33	0/1424	0.55	0/1944
1	CQ	0.34	0/1400	0.56	0/1911
1	CR	0.33	0/1492	0.54	0/2035
1	CS	0.33	0/1424	0.55	0/1944
1	CT	0.34	0/1400	0.56	0/1911
1	CU	0.33	0/1492	0.54	0/2035
1	CV	0.33	0/1424	0.55	0/1944
1	CW	0.34	0/1400	0.56	0/1911
1	CX	0.33	0/1492	0.54	0/2035
1	CY	0.33	0/1424	0.55	0/1944

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	CZ	0.34	0/1400	0.56	0/1911
1	DA	0.33	0/1492	0.54	0/2035
1	DB	0.33	0/1424	0.55	0/1944
1	DC	0.34	0/1400	0.56	0/1911
1	DD	0.33	0/1492	0.54	0/2035
1	DE	0.33	0/1424	0.55	0/1944
1	DF	0.34	0/1400	0.56	0/1911
1	DG	0.33	0/1492	0.54	0/2035
1	DH	0.33	0/1424	0.55	0/1944
1	DI	0.34	0/1400	0.56	0/1911
1	DJ	0.33	0/1492	0.54	0/2035
1	DK	0.33	0/1424	0.55	0/1944
1	DL	0.34	0/1400	0.56	0/1911
All	All	0.33	0/129480	0.55	0/176700

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	1463	0	1446	35	0
1	AB	1396	0	1385	32	1
1	AC	1373	0	1360	34	0
1	AD	1463	0	1446	35	0
1	AE	1396	0	1385	39	0
1	AF	1373	0	1360	44	0
1	AG	1463	0	1446	29	0
1	AH	1396	0	1385	28	0
1	AI	1373	0	1360	10	2
1	AJ	1463	0	1446	33	0
1	AK	1396	0	1385	34	0
1	AL	1373	0	1360	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AM	1463	0	1446	29	0
1	AN	1396	0	1385	28	0
1	AO	1373	0	1360	14	1
1	AP	1463	0	1446	32	0
1	AQ	1396	0	1385	29	0
1	AR	1373	0	1360	37	0
1	AS	1463	0	1446	33	0
1	AT	1396	0	1385	35	0
1	AU	1373	0	1360	41	0
1	AV	1463	0	1446	31	0
1	AW	1396	0	1385	30	0
1	AX	1373	0	1360	12	2
1	AY	1463	0	1446	31	0
1	AZ	1396	0	1385	34	0
1	BA	1373	0	1360	34	0
1	BB	1463	0	1446	33	0
1	BC	1396	0	1385	33	1
1	BD	1373	0	1360	40	0
1	BE	1463	0	1446	36	0
1	BF	1396	0	1385	34	0
1	BG	1373	0	1360	35	0
1	BH	1463	0	1446	34	0
1	BI	1396	0	1385	34	0
1	BJ	1373	0	1360	36	0
1	BK	1463	0	1446	32	0
1	BL	1396	0	1385	31	0
1	BM	1373	0	1360	32	0
1	BN	1463	0	1446	32	0
1	BO	1396	0	1385	25	0
1	BP	1373	0	1360	35	0
1	BQ	1463	0	1446	34	0
1	BR	1396	0	1385	36	0
1	BS	1373	0	1360	42	0
1	BT	1463	0	1446	31	0
1	BU	1396	0	1385	33	0
1	BV	1373	0	1360	11	1
1	BW	1463	0	1446	34	0
1	BX	1396	0	1385	33	0
1	BY	1373	0	1360	33	0
1	BZ	1463	0	1446	29	0
1	CA	1396	0	1385	32	0
1	CB	1373	0	1360	12	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CC	1463	0	1446	35	0
1	CD	1396	0	1385	35	0
1	CE	1373	0	1360	42	0
1	CF	1463	0	1446	31	0
1	CG	1396	0	1385	31	0
1	CH	1373	0	1360	13	2
1	CI	1463	0	1446	35	0
1	CJ	1396	0	1385	38	0
1	CK	1373	0	1360	38	0
1	CL	1463	0	1446	31	0
1	CM	1396	0	1385	30	0
1	CN	1373	0	1360	34	0
1	CO	1463	0	1446	33	0
1	CP	1396	0	1385	40	0
1	CQ	1373	0	1360	39	0
1	CR	1463	0	1446	32	0
1	CS	1396	0	1385	32	0
1	CT	1373	0	1360	33	0
1	CU	1463	0	1446	37	0
1	CV	1396	0	1385	38	0
1	CW	1373	0	1360	37	0
1	CX	1463	0	1446	30	0
1	CY	1396	0	1385	31	0
1	CZ	1373	0	1360	37	0
1	DA	1463	0	1446	35	0
1	DB	1396	0	1385	31	0
1	DC	1373	0	1360	35	0
1	DD	1463	0	1446	32	0
1	DE	1396	0	1385	28	0
1	DF	1373	0	1360	33	0
1	DG	1463	0	1446	34	0
1	DH	1396	0	1385	31	0
1	DI	1373	0	1360	33	0
1	DJ	1463	0	1446	34	0
1	DK	1396	0	1385	35	0
1	DL	1373	0	1360	43	0
All	All	126960	0	125730	2072	7

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 8.

The worst 5 of 2072 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:BM:31:ASN:O	1:DF:65:ARG:NH1	2.04	0.90
1:BG:31:ASN:O	1:CZ:65:ARG:NH1	2.04	0.90
1:AL:31:ASN:O	1:CK:65:ARG:NH1	2.05	0.89
1:AL:65:ARG:NH1	1:CK:31:ASN:O	2.09	0.85
1:BP:65:ARG:NH1	1:DI:31:ASN:O	2.09	0.85

The worst 5 of 7 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:60:GLN:OE1	1:BC:192:LYS:NZ[4_556]	1.89	0.31
1:AI:65:ARG:NH1	1:AX:31:ASN:O[2_555]	2.09	0.11
1:BV:31:ASN:O	1:BV:65:ARG:NH1[2_555]	2.13	0.07
1:AO:31:ASN:O	1:AO:65:ARG:NH1[2_555]	2.16	0.04
1:AI:31:ASN:O	1:AX:65:ARG:NH1[2_555]	2.17	0.03

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 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	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AB	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AC	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AD	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AE	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AF	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AG	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AH	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AI	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AJ	196/208 (94%)	191 (97%)	5 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AK	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AL	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AM	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AN	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AO	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AP	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AQ	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AR	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AS	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AT	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AU	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AV	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AW	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	AX	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	AY	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	AZ	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BA	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BB	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BC	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BD	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BE	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BF	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BG	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BH	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BI	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BJ	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BK	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BL	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BM	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BN	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BO	187/208 (90%)	183 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	BP	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BQ	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BR	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BS	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BT	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BU	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BV	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BW	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	BX	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	BY	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	BZ	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CA	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CB	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CC	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CD	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CE	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CF	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CG	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CH	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CI	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CJ	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CK	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CL	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CM	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CN	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CO	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CP	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CQ	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CR	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CS	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CT	184/208 (88%)	182 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CU	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CV	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CW	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	CX	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	CY	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	CZ	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	DA	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	DB	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	DC	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	DD	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	DE	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	DF	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	DG	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	DH	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	DI	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
1	DJ	196/208 (94%)	191 (97%)	5 (3%)	0	100	100
1	DK	187/208 (90%)	183 (98%)	4 (2%)	0	100	100
1	DL	184/208 (88%)	182 (99%)	2 (1%)	0	100	100
All	All	17010/18720 (91%)	16680 (98%)	330 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	155/164 (94%)	155 (100%)	0	100	100
1	AB	149/164 (91%)	149 (100%)	0	100	100
1	AC	146/164 (89%)	146 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AD	155/164 (94%)	155 (100%)	0	100	100
1	AE	149/164 (91%)	149 (100%)	0	100	100
1	AF	146/164 (89%)	146 (100%)	0	100	100
1	AG	155/164 (94%)	155 (100%)	0	100	100
1	AH	149/164 (91%)	149 (100%)	0	100	100
1	AI	146/164 (89%)	146 (100%)	0	100	100
1	AJ	155/164 (94%)	155 (100%)	0	100	100
1	AK	149/164 (91%)	149 (100%)	0	100	100
1	AL	146/164 (89%)	146 (100%)	0	100	100
1	AM	155/164 (94%)	155 (100%)	0	100	100
1	AN	149/164 (91%)	149 (100%)	0	100	100
1	AO	146/164 (89%)	146 (100%)	0	100	100
1	AP	155/164 (94%)	155 (100%)	0	100	100
1	AQ	149/164 (91%)	149 (100%)	0	100	100
1	AR	146/164 (89%)	146 (100%)	0	100	100
1	AS	155/164 (94%)	155 (100%)	0	100	100
1	AT	149/164 (91%)	149 (100%)	0	100	100
1	AU	146/164 (89%)	146 (100%)	0	100	100
1	AV	155/164 (94%)	155 (100%)	0	100	100
1	AW	149/164 (91%)	149 (100%)	0	100	100
1	AX	146/164 (89%)	146 (100%)	0	100	100
1	AY	155/164 (94%)	155 (100%)	0	100	100
1	AZ	149/164 (91%)	149 (100%)	0	100	100
1	BA	146/164 (89%)	146 (100%)	0	100	100
1	BB	155/164 (94%)	155 (100%)	0	100	100
1	BC	149/164 (91%)	149 (100%)	0	100	100
1	BD	146/164 (89%)	146 (100%)	0	100	100
1	BE	155/164 (94%)	155 (100%)	0	100	100
1	BF	149/164 (91%)	149 (100%)	0	100	100
1	BG	146/164 (89%)	146 (100%)	0	100	100
1	BH	155/164 (94%)	155 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BI	149/164 (91%)	149 (100%)	0	100	100
1	BJ	146/164 (89%)	146 (100%)	0	100	100
1	BK	155/164 (94%)	155 (100%)	0	100	100
1	BL	149/164 (91%)	149 (100%)	0	100	100
1	BM	146/164 (89%)	146 (100%)	0	100	100
1	BN	155/164 (94%)	155 (100%)	0	100	100
1	BO	149/164 (91%)	149 (100%)	0	100	100
1	BP	146/164 (89%)	146 (100%)	0	100	100
1	BQ	155/164 (94%)	155 (100%)	0	100	100
1	BR	149/164 (91%)	149 (100%)	0	100	100
1	BS	146/164 (89%)	146 (100%)	0	100	100
1	BT	155/164 (94%)	155 (100%)	0	100	100
1	BU	149/164 (91%)	149 (100%)	0	100	100
1	BV	146/164 (89%)	146 (100%)	0	100	100
1	BW	155/164 (94%)	155 (100%)	0	100	100
1	BX	149/164 (91%)	149 (100%)	0	100	100
1	BY	146/164 (89%)	146 (100%)	0	100	100
1	BZ	155/164 (94%)	155 (100%)	0	100	100
1	CA	149/164 (91%)	149 (100%)	0	100	100
1	CB	146/164 (89%)	146 (100%)	0	100	100
1	CC	155/164 (94%)	155 (100%)	0	100	100
1	CD	149/164 (91%)	149 (100%)	0	100	100
1	CE	146/164 (89%)	146 (100%)	0	100	100
1	CF	155/164 (94%)	155 (100%)	0	100	100
1	CG	149/164 (91%)	149 (100%)	0	100	100
1	CH	146/164 (89%)	146 (100%)	0	100	100
1	CI	155/164 (94%)	155 (100%)	0	100	100
1	CJ	149/164 (91%)	149 (100%)	0	100	100
1	CK	146/164 (89%)	146 (100%)	0	100	100
1	CL	155/164 (94%)	155 (100%)	0	100	100
1	CM	149/164 (91%)	149 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CN	146/164 (89%)	146 (100%)	0	100	100
1	CO	155/164 (94%)	155 (100%)	0	100	100
1	CP	149/164 (91%)	149 (100%)	0	100	100
1	CQ	146/164 (89%)	146 (100%)	0	100	100
1	CR	155/164 (94%)	155 (100%)	0	100	100
1	CS	149/164 (91%)	149 (100%)	0	100	100
1	CT	146/164 (89%)	146 (100%)	0	100	100
1	CU	155/164 (94%)	155 (100%)	0	100	100
1	CV	149/164 (91%)	149 (100%)	0	100	100
1	CW	146/164 (89%)	146 (100%)	0	100	100
1	CX	155/164 (94%)	155 (100%)	0	100	100
1	CY	149/164 (91%)	149 (100%)	0	100	100
1	CZ	146/164 (89%)	146 (100%)	0	100	100
1	DA	155/164 (94%)	155 (100%)	0	100	100
1	DB	149/164 (91%)	149 (100%)	0	100	100
1	DC	146/164 (89%)	146 (100%)	0	100	100
1	DD	155/164 (94%)	155 (100%)	0	100	100
1	DE	149/164 (91%)	149 (100%)	0	100	100
1	DF	146/164 (89%)	146 (100%)	0	100	100
1	DG	155/164 (94%)	155 (100%)	0	100	100
1	DH	149/164 (91%)	149 (100%)	0	100	100
1	DI	146/164 (89%)	146 (100%)	0	100	100
1	DJ	155/164 (94%)	155 (100%)	0	100	100
1	DK	149/164 (91%)	149 (100%)	0	100	100
1	DL	146/164 (89%)	146 (100%)	0	100	100
All	All	13500/14760 (92%)	13500 (100%)	0	100	100

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

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	BL	31	ASN

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Mol	Chain	Res	Type
1	BX	31	ASN
1	DH	31	ASN
1	BP	129	ASN
1	BY	129	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	198/208 (95%)	-0.03	1 (0%) 91 91	67, 89, 121, 184	0
1	AB	189/208 (90%)	-0.15	1 (0%) 91 91	60, 89, 124, 186	0
1	AC	186/208 (89%)	-0.09	1 (0%) 91 91	65, 88, 115, 141	0
1	AD	198/208 (95%)	-0.23	2 (1%) 82 82	67, 89, 121, 184	0
1	AE	189/208 (90%)	-0.14	2 (1%) 80 81	60, 89, 124, 186	0
1	AF	186/208 (89%)	0.10	5 (2%) 54 52	65, 88, 115, 141	0
1	AG	198/208 (95%)	-0.26	0 100 100	67, 89, 121, 184	0
1	AH	189/208 (90%)	-0.16	1 (0%) 91 91	60, 89, 124, 186	0
1	AI	186/208 (89%)	-0.19	1 (0%) 91 91	65, 88, 115, 141	0
1	AJ	198/208 (95%)	-0.14	1 (0%) 91 91	67, 89, 121, 184	0
1	AK	189/208 (90%)	-0.13	1 (0%) 91 91	60, 89, 124, 186	0
1	AL	186/208 (89%)	0.02	0 100 100	65, 88, 115, 141	0
1	AM	198/208 (95%)	-0.21	0 100 100	67, 89, 121, 184	0
1	AN	189/208 (90%)	-0.07	1 (0%) 91 91	60, 89, 124, 186	0
1	AO	186/208 (89%)	-0.13	0 100 100	65, 88, 115, 141	0
1	AP	198/208 (95%)	-0.25	0 100 100	67, 89, 121, 184	0
1	AQ	189/208 (90%)	-0.26	1 (0%) 91 91	60, 89, 124, 186	0
1	AR	186/208 (89%)	-0.17	1 (0%) 91 91	65, 88, 115, 141	0
1	AS	198/208 (95%)	0.01	2 (1%) 82 82	67, 89, 121, 184	0
1	AT	189/208 (90%)	-0.09	0 100 100	60, 89, 124, 186	0
1	AU	186/208 (89%)	-0.00	1 (0%) 91 91	65, 88, 115, 141	0
1	AV	198/208 (95%)	-0.20	2 (1%) 82 82	67, 89, 121, 184	0
1	AW	189/208 (90%)	-0.17	1 (0%) 91 91	60, 89, 124, 186	0
1	AX	186/208 (89%)	-0.11	0 100 100	65, 88, 115, 141	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	198/208 (95%)	-0.06	2 (1%) 82 82	67, 89, 121, 184	0
1	AZ	189/208 (90%)	-0.08	2 (1%) 80 81	60, 89, 124, 186	0
1	BA	186/208 (89%)	-0.00	2 (1%) 80 81	65, 88, 115, 141	0
1	BB	198/208 (95%)	0.03	3 (1%) 73 72	67, 89, 121, 184	0
1	BC	189/208 (90%)	-0.06	3 (1%) 72 70	60, 89, 124, 186	0
1	BD	186/208 (89%)	-0.01	0 100 100	65, 88, 115, 141	0
1	BE	198/208 (95%)	-0.01	4 (2%) 65 64	67, 89, 121, 184	0
1	BF	189/208 (90%)	0.20	6 (3%) 47 46	60, 89, 124, 186	0
1	BG	186/208 (89%)	0.23	7 (3%) 40 37	65, 88, 115, 141	0
1	BH	198/208 (95%)	-0.04	4 (2%) 65 64	67, 89, 121, 184	0
1	BI	189/208 (90%)	-0.00	2 (1%) 80 81	60, 89, 124, 186	0
1	BJ	186/208 (89%)	0.26	8 (4%) 35 34	65, 88, 115, 141	0
1	BK	198/208 (95%)	-0.04	2 (1%) 82 82	67, 89, 121, 184	0
1	BL	189/208 (90%)	0.04	7 (3%) 41 38	60, 89, 124, 186	0
1	BM	186/208 (89%)	0.03	1 (0%) 91 91	65, 88, 115, 141	0
1	BN	198/208 (95%)	-0.21	1 (0%) 91 91	67, 89, 121, 184	0
1	BO	189/208 (90%)	-0.28	2 (1%) 80 81	60, 89, 124, 186	0
1	BP	186/208 (89%)	-0.06	0 100 100	65, 88, 115, 141	0
1	BQ	198/208 (95%)	-0.10	0 100 100	67, 89, 121, 184	0
1	BR	189/208 (90%)	-0.20	0 100 100	60, 89, 124, 186	0
1	BS	186/208 (89%)	-0.21	0 100 100	65, 88, 115, 141	0
1	BT	198/208 (95%)	-0.11	1 (0%) 91 91	67, 89, 121, 184	0
1	BU	189/208 (90%)	-0.15	3 (1%) 72 70	60, 89, 124, 186	0
1	BV	186/208 (89%)	0.25	6 (3%) 47 46	65, 88, 115, 141	0
1	BW	198/208 (95%)	-0.18	0 100 100	67, 89, 121, 184	0
1	BX	189/208 (90%)	-0.24	1 (0%) 91 91	60, 89, 124, 186	0
1	BY	186/208 (89%)	-0.04	1 (0%) 91 91	65, 88, 115, 141	0
1	BZ	198/208 (95%)	-0.06	1 (0%) 91 91	67, 89, 121, 184	0
1	CA	189/208 (90%)	-0.15	0 100 100	60, 89, 124, 186	0
1	CB	186/208 (89%)	-0.07	0 100 100	65, 88, 115, 141	0
1	CC	198/208 (95%)	0.31	13 (6%) 18 18	67, 89, 121, 184	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	CD	189/208 (90%)	-0.09	1 (0%) 91 91	60, 89, 124, 186	0
1	CE	186/208 (89%)	0.05	5 (2%) 54 52	65, 88, 115, 141	0
1	CF	198/208 (95%)	-0.17	0 100 100	67, 89, 121, 184	0
1	CG	189/208 (90%)	-0.18	0 100 100	60, 89, 124, 186	0
1	CH	186/208 (89%)	0.10	3 (1%) 72 70	65, 88, 115, 141	0
1	CI	198/208 (95%)	0.03	1 (0%) 91 91	67, 89, 121, 184	0
1	CJ	189/208 (90%)	0.03	2 (1%) 80 81	60, 89, 124, 186	0
1	CK	186/208 (89%)	-0.05	0 100 100	65, 88, 115, 141	0
1	CL	198/208 (95%)	-0.15	3 (1%) 73 72	67, 89, 121, 184	0
1	CM	189/208 (90%)	-0.21	2 (1%) 80 81	60, 89, 124, 186	0
1	CN	186/208 (89%)	-0.12	2 (1%) 80 81	65, 88, 115, 141	0
1	CO	198/208 (95%)	-0.20	0 100 100	67, 89, 121, 184	0
1	CP	189/208 (90%)	-0.24	3 (1%) 72 70	60, 89, 124, 186	0
1	CQ	186/208 (89%)	0.03	1 (0%) 91 91	65, 88, 115, 141	0
1	CR	198/208 (95%)	-0.06	2 (1%) 82 82	67, 89, 121, 184	0
1	CS	189/208 (90%)	0.10	4 (2%) 63 62	60, 89, 124, 186	0
1	CT	186/208 (89%)	-0.05	4 (2%) 62 60	65, 88, 115, 141	0
1	CU	198/208 (95%)	-0.13	0 100 100	67, 89, 121, 184	0
1	CV	189/208 (90%)	-0.18	1 (0%) 91 91	60, 89, 124, 186	0
1	CW	186/208 (89%)	0.05	1 (0%) 91 91	65, 88, 115, 141	0
1	CX	198/208 (95%)	-0.14	5 (2%) 57 54	67, 89, 121, 184	0
1	CY	189/208 (90%)	-0.07	2 (1%) 80 81	60, 89, 124, 186	0
1	CZ	186/208 (89%)	0.27	8 (4%) 35 34	65, 88, 115, 141	0
1	DA	198/208 (95%)	0.10	4 (2%) 65 64	67, 89, 121, 184	0
1	DB	189/208 (90%)	-0.01	4 (2%) 63 62	60, 89, 124, 186	0
1	DC	186/208 (89%)	0.07	6 (3%) 47 46	65, 88, 115, 141	0
1	DD	198/208 (95%)	-0.11	1 (0%) 91 91	67, 89, 121, 184	0
1	DE	189/208 (90%)	0.07	5 (2%) 56 53	60, 89, 124, 186	0
1	DF	186/208 (89%)	0.16	9 (4%) 30 28	65, 88, 115, 141	0
1	DG	198/208 (95%)	-0.14	2 (1%) 82 82	67, 89, 121, 184	0
1	DH	189/208 (90%)	-0.09	1 (0%) 91 91	60, 89, 124, 186	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	DI	186/208 (89%)	-0.17	1 (0%) 91 91	65, 88, 115, 141	0
1	DJ	198/208 (95%)	-0.11	0 100 100	67, 89, 121, 184	0
1	DK	189/208 (90%)	-0.24	1 (0%) 91 91	60, 89, 124, 186	0
1	DL	186/208 (89%)	-0.08	3 (1%) 72 70	65, 88, 115, 141	0
All	All	17190/18720 (91%)	-0.07	194 (1%) 80 81	60, 89, 120, 186	0

The worst 5 of 194 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AY	141	GLY	7.2
1	BO	20	PRO	6.7
1	BL	20	PRO	6.0
1	DE	208	ALA	5.4
1	AQ	20	PRO	4.6

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 monosaccharides 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.