



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 10, 2022 – 08:45 am GMT

PDB ID : 6YFM
Title : Virus-like particle of bacteriophage ESE021
Authors : Rumnieks, J.; Kalnins, G.; Sisovs, M.; Lieknina, I.; Tars, K.
Deposited on : 2020-03-26
Resolution : 2.76 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 2.26
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.26

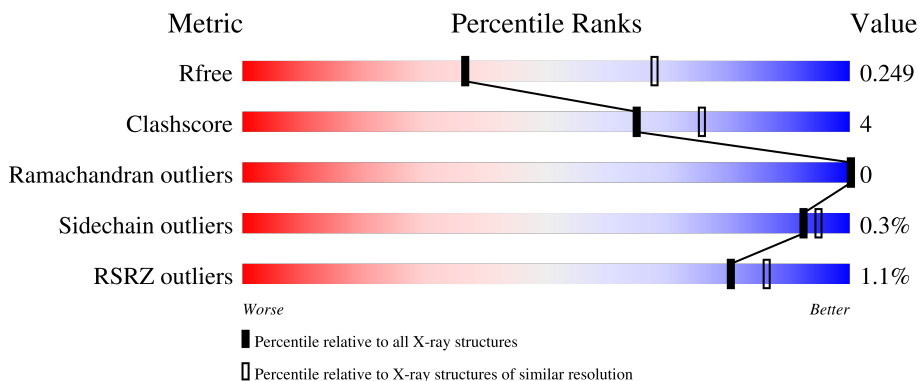
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

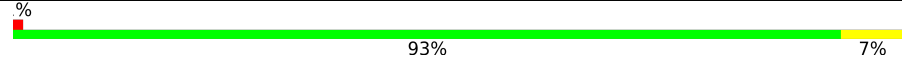
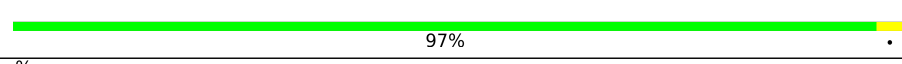

The reported resolution of this entry is 2.76 Å.

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.



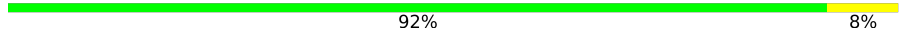
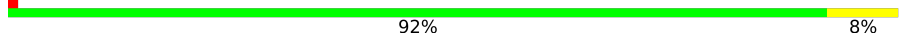




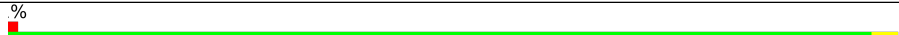
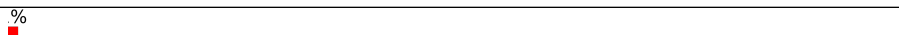
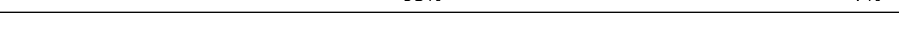
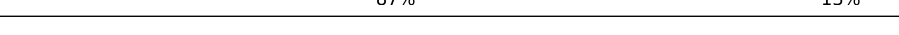
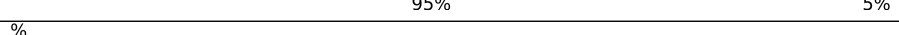
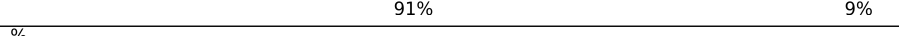

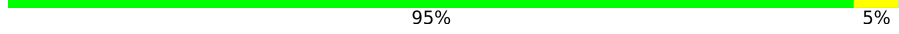
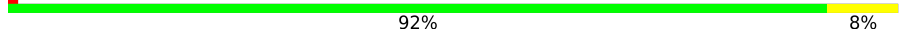








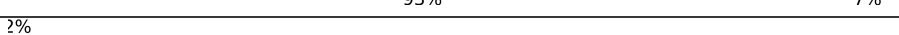

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	150	
1	AB	150	
1	AC	150	
1	AD	150	
1	AE	150	

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Mol	Chain	Length	Quality of chain
1	AF	150	 92% 8%
1	AG	150	 92% 8%
1	AH	150	 88% 12%
1	AI	150	 92% 8%
1	AJ	150	 89% 11%
1	AK	150	 87% 13%
1	AL	150	 97%
1	AM	150	 93% 7%
1	AN	150	 87% 13%
1	AO	150	 95% 5%
1	AP	150	 91% 9%
1	AQ	150	 89% 11%
1	AR	150	 95% 5%
1	AS	150	 92% 8%
1	AT	150	 85% 15%
1	AU	150	 91% 9%
1	AV	150	 88% 12%
1	AW	150	 88% 12%
1	AX	150	 93% 7%
1	AY	150	 91% 9%
1	AZ	150	 86% 14%
1	BA	150	 93% 7%
1	BB	150	 89% 11%
1	BC	150	 87% 13%
1	BD	150	 93% 7%

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Mol	Chain	Length	Quality of chain
1	BE	150	 92% 8%
1	BF	150	 86% 14% 2%
1	BG	150	 96%
1	BH	150	 91% 9% 3%
1	BI	150	 83% 17%
1	BJ	150	 91% 9%
1	BK	150	 83% 17% 3%
1	BL	150	 89% 11%
1	BM	150	 97%
1	BN	150	 87% 13%
1	BO	150	 89% 11%
1	BP	150	 94% 6% 2%
1	BQ	150	 89% 11%
1	BR	150	 86% 14%
1	BS	150	 91% 9%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ZN	AB	201	-	-	-	X
2	ZN	AT	201	-	-	-	X
2	ZN	AW	201	-	-	-	X
2	ZN	BF	201	-	-	-	X

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 50190 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	150	1114	700	193	219	2	0	0	0
1	AB	150	1114	700	193	219	2	0	0	0
1	AC	150	1114	700	193	219	2	0	0	0
1	AD	150	1114	700	193	219	2	0	0	0
1	AE	150	1114	700	193	219	2	0	0	0
1	AF	150	1114	700	193	219	2	0	0	0
1	AG	150	1114	700	193	219	2	0	0	0
1	AH	150	1114	700	193	219	2	0	0	0
1	AI	150	1114	700	193	219	2	0	0	0
1	AJ	150	1114	700	193	219	2	0	0	0
1	AK	150	1114	700	193	219	2	0	0	0
1	AL	150	1114	700	193	219	2	0	0	0
1	AM	150	1114	700	193	219	2	0	0	0
1	AN	150	1114	700	193	219	2	0	0	0
1	AO	150	1114	700	193	219	2	0	0	0
1	AP	150	1114	700	193	219	2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AQ	150	1114	700	193	219	2	0	0	0
1	AR	150	1114	700	193	219	2	0	0	0
1	AS	150	1114	700	193	219	2	0	0	0
1	AT	150	1114	700	193	219	2	0	0	0
1	AU	150	1114	700	193	219	2	0	0	0
1	AV	150	1114	700	193	219	2	0	0	0
1	AW	150	1114	700	193	219	2	0	0	0
1	AX	150	1114	700	193	219	2	0	0	0
1	AY	150	1114	700	193	219	2	0	0	0
1	AZ	150	1114	700	193	219	2	0	0	0
1	BA	150	1114	700	193	219	2	0	0	0
1	BB	150	1114	700	193	219	2	0	0	0
1	BC	150	1114	700	193	219	2	0	0	0
1	BD	150	1114	700	193	219	2	0	0	0
1	BE	150	1114	700	193	219	2	0	0	0
1	BF	150	1114	700	193	219	2	0	0	0
1	BG	150	1114	700	193	219	2	0	0	0
1	BH	150	1114	700	193	219	2	0	0	0
1	BI	150	1114	700	193	219	2	0	0	0
1	BJ	150	1114	700	193	219	2	0	0	0
1	BK	150	1114	700	193	219	2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BL	150	Total	C	N	O	S	0	0	0
			1114	700	193	219	2			
1	BM	150	Total	C	N	O	S	0	0	0
			1114	700	193	219	2			
1	BN	150	Total	C	N	O	S	0	0	0
			1114	700	193	219	2			
1	BO	150	Total	C	N	O	S	0	0	0
			1114	700	193	219	2			
1	BP	150	Total	C	N	O	S	0	0	0
			1114	700	193	219	2			
1	BQ	150	Total	C	N	O	S	0	0	0
			1114	700	193	219	2			
1	BR	150	Total	C	N	O	S	0	0	0
			1114	700	193	219	2			
1	BS	150	Total	C	N	O	S	0	0	0
			1114	700	193	219	2			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AA	2	Total	Zn	0	0
			2	2		
2	AB	1	Total	Zn	0	0
			1	1		
2	AC	1	Total	Zn	0	0
			1	1		
2	AD	2	Total	Zn	0	0
			2	2		
2	AE	1	Total	Zn	0	0
			1	1		
2	AF	1	Total	Zn	0	0
			1	1		
2	AG	2	Total	Zn	0	0
			2	2		
2	AH	1	Total	Zn	0	0
			1	1		
2	AI	1	Total	Zn	0	0
			1	1		
2	AJ	2	Total	Zn	0	0
			2	2		
2	AK	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AL	1	Total 1	Zn 1	0	0
2	AM	2	Total 2	Zn 2	0	0
2	AN	1	Total 1	Zn 1	0	0
2	AO	1	Total 1	Zn 1	0	0
2	AP	2	Total 2	Zn 2	0	0
2	AQ	1	Total 1	Zn 1	0	0
2	AR	1	Total 1	Zn 1	0	0
2	AS	2	Total 2	Zn 2	0	0
2	AT	1	Total 1	Zn 1	0	0
2	AU	1	Total 1	Zn 1	0	0
2	AV	2	Total 2	Zn 2	0	0
2	AW	1	Total 1	Zn 1	0	0
2	AX	1	Total 1	Zn 1	0	0
2	AY	2	Total 2	Zn 2	0	0
2	AZ	1	Total 1	Zn 1	0	0
2	BA	1	Total 1	Zn 1	0	0
2	BB	2	Total 2	Zn 2	0	0
2	BC	1	Total 1	Zn 1	0	0
2	BD	1	Total 1	Zn 1	0	0
2	BE	2	Total 2	Zn 2	0	0
2	BF	1	Total 1	Zn 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	BG	1	Total 1	Zn 1	0	0
2	BH	2	Total 2	Zn 2	0	0
2	BI	1	Total 1	Zn 1	0	0
2	BJ	1	Total 1	Zn 1	0	0
2	BK	2	Total 2	Zn 2	0	0
2	BL	1	Total 1	Zn 1	0	0
2	BM	1	Total 1	Zn 1	0	0
2	BN	2	Total 2	Zn 2	0	0
2	BO	1	Total 1	Zn 1	0	0
2	BP	1	Total 1	Zn 1	0	0
2	BQ	2	Total 2	Zn 2	0	0
2	BR	1	Total 1	Zn 1	0	0
2	BS	1	Total 1	Zn 1	0	0

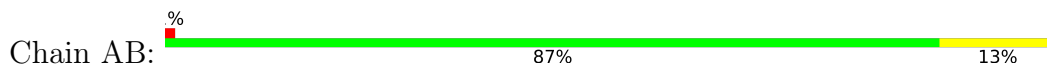
3 Residue-property plots [i](#)

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



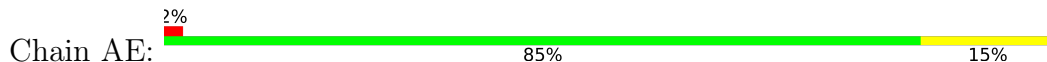
- Molecule 1: coat protein



- Molecule 1: coat protein

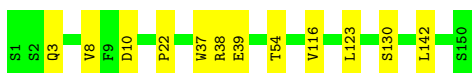


- Molecule 1: coat protein



- Molecule 1: coat protein

Chain AF:  92% 8%




● Molecule 1: coat protein

Chain AG:  92% 8%




● Molecule 1: coat protein

Chain AH:  88% 12%




● Molecule 1: coat protein

Chain AI:  92% 8%




● Molecule 1: coat protein

Chain AJ:  89% 11%



● Molecule 1: coat protein

Chain AK:  87% 13%

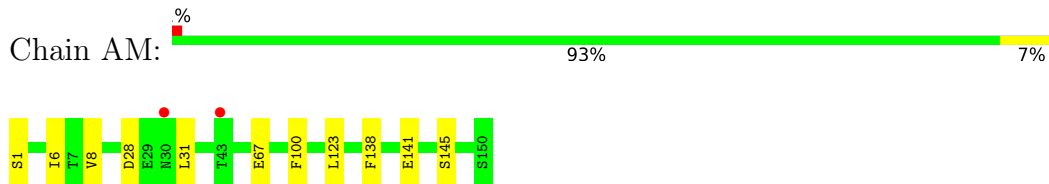


● Molecule 1: coat protein

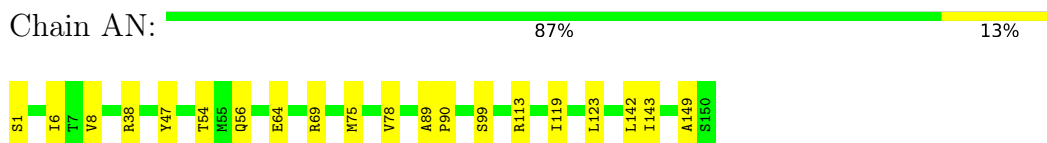
Chain AL:  97%



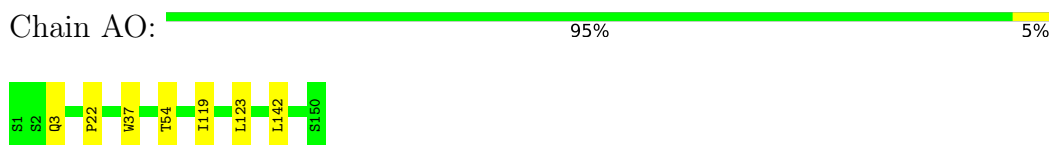
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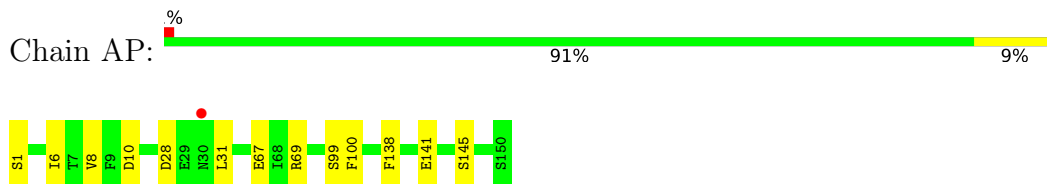
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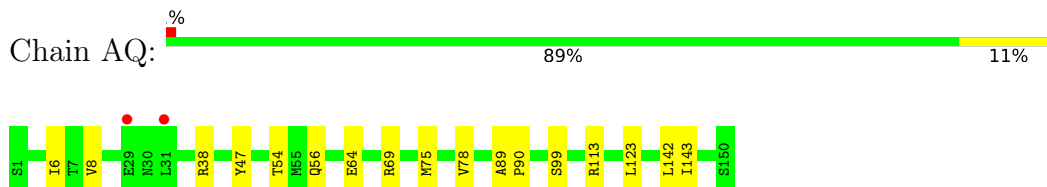
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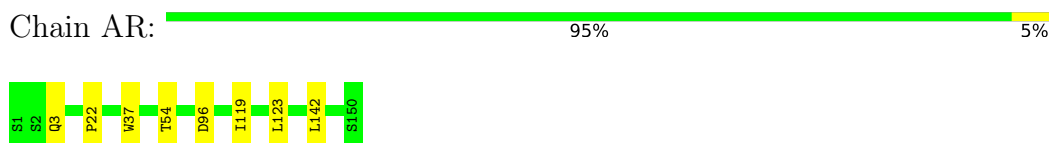
- Molecule 1: coat protein



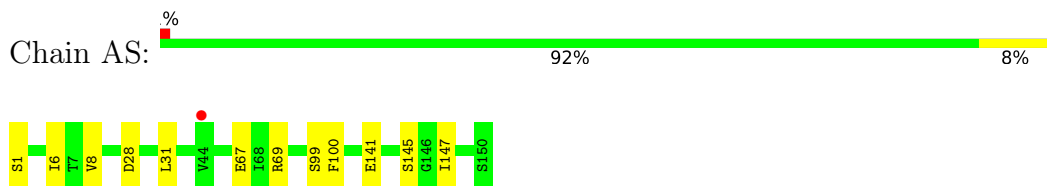
- Molecule 1: coat protein



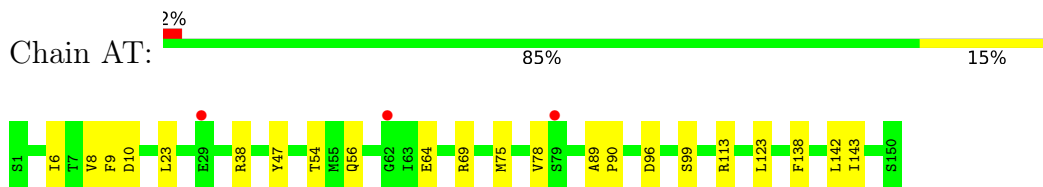
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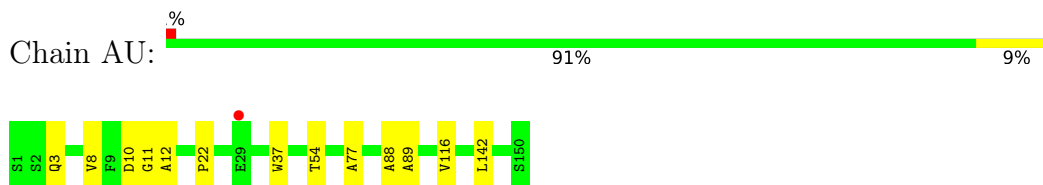
- Molecule 1: coat protein



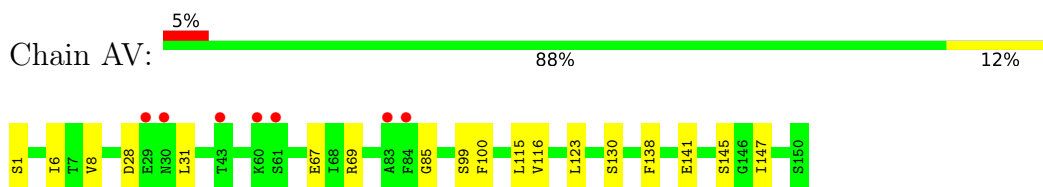
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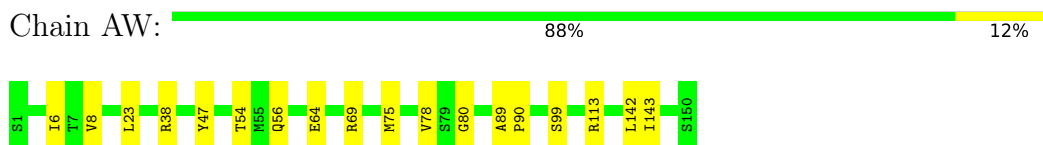
- Molecule 1: coat protein



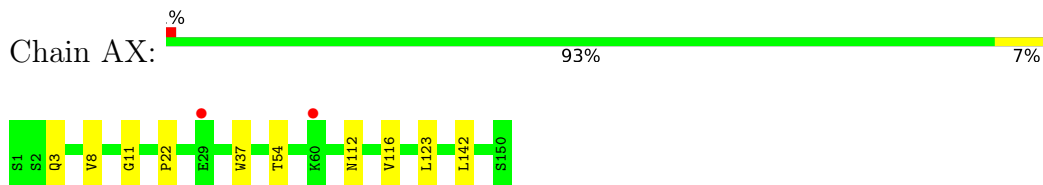
- Molecule 1: coat protein



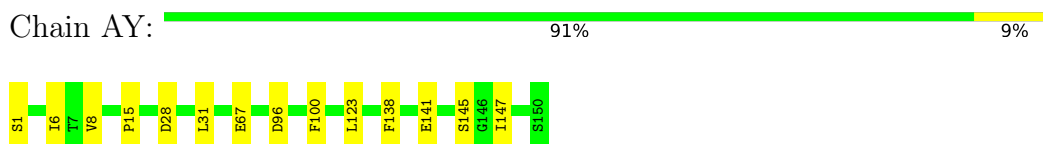
- Molecule 1: coat protein



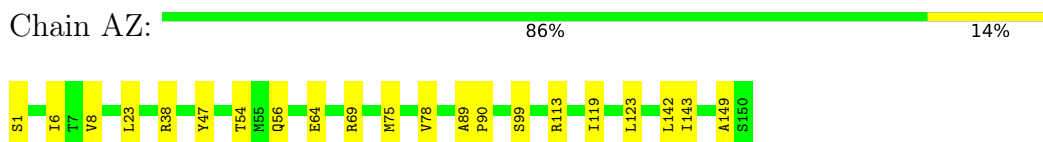
- Molecule 1: coat protein



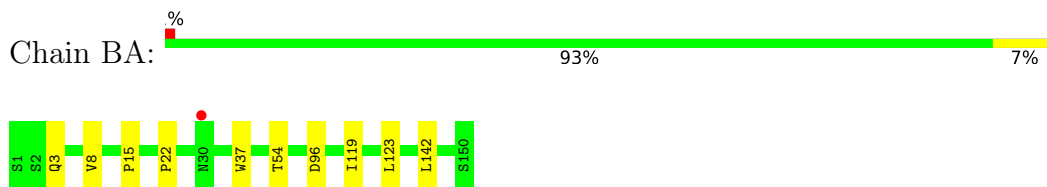
- Molecule 1: coat protein



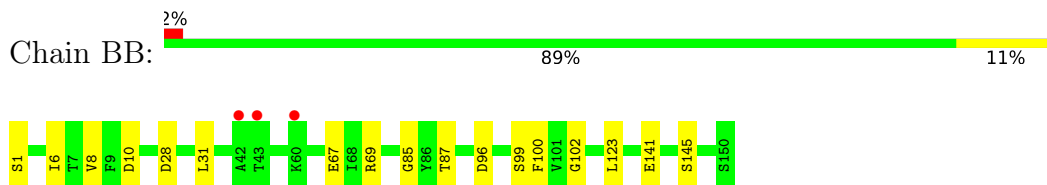
- Molecule 1: coat protein



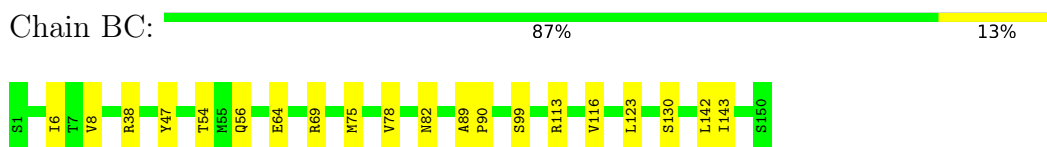
- Molecule 1: coat protein



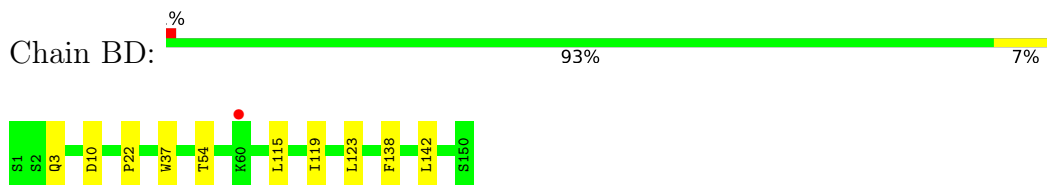
- Molecule 1: coat protein



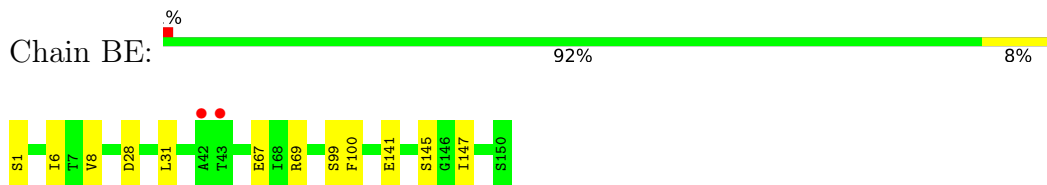
- Molecule 1: coat protein



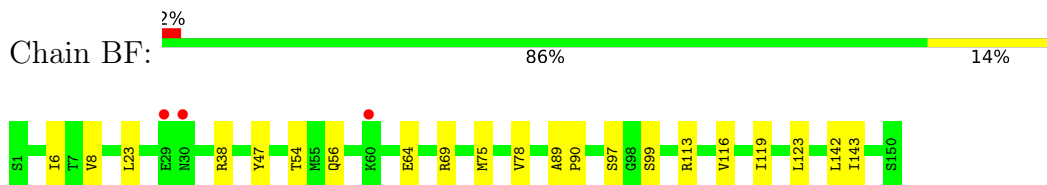
- Molecule 1: coat protein



- Molecule 1: coat protein

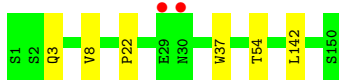


- Molecule 1: coat protein

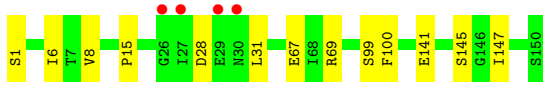
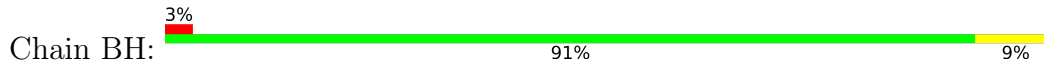


- Molecule 1: coat protein

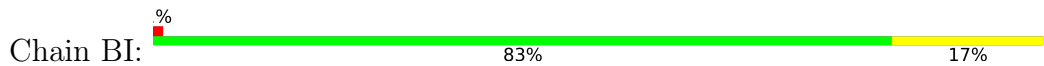




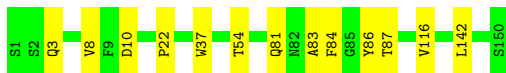
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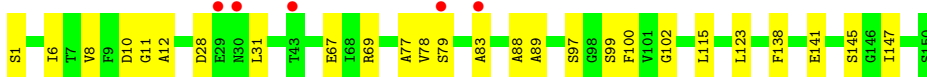
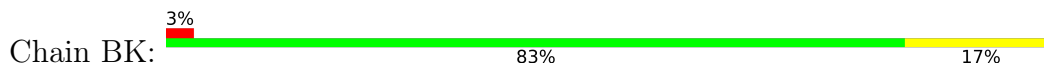
- Molecule 1: coat protein



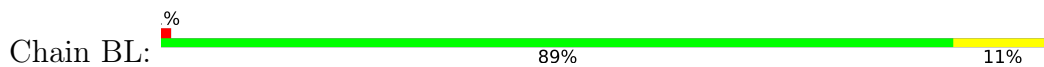
- Molecule 1: coat protein



- Molecule 1: coat protein



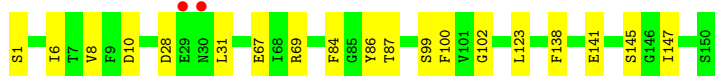
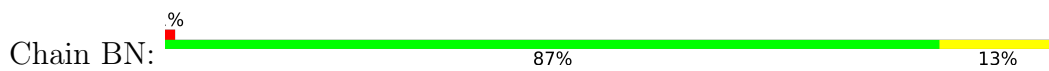
- Molecule 1: coat protein



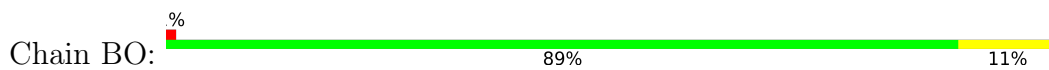
- Molecule 1: coat protein



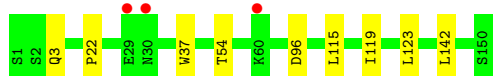
- Molecule 1: coat protein



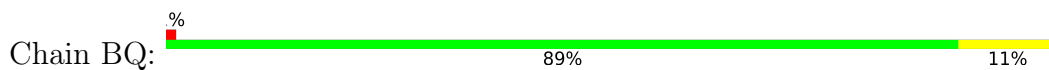
• Molecule 1: coat protein



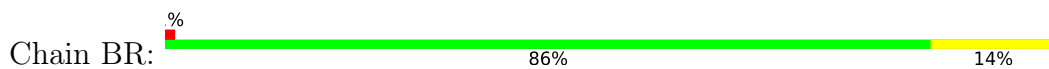
• Molecule 1: coat protein



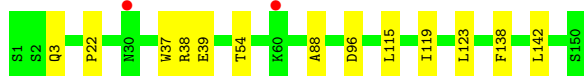
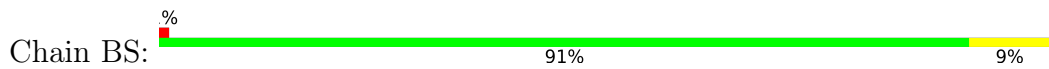
• Molecule 1: coat protein



• Molecule 1: coat protein



• Molecule 1: coat protein



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	282.02Å 302.81Å 352.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.08 – 2.76 60.08 – 2.76	Depositor EDS
% Data completeness (in resolution range)	99.3 (60.08-2.76) 99.3 (60.08-2.76)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.36	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.244 , 0.248 0.245 , 0.249	Depositor DCC
R_{free} test set	9971 reflections (2.63%)	wwPDB-VP
Wilson B-factor (Å ²)	36.1	Xtriage
Anisotropy	0.379	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	50190	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.84% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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	0.28	0/1131	0.48	0/1537
1	AB	0.29	0/1131	0.49	0/1537
1	AC	0.28	0/1131	0.47	0/1537
1	AD	0.28	0/1131	0.48	0/1537
1	AE	0.29	0/1131	0.48	0/1537
1	AF	0.28	0/1131	0.47	0/1537
1	AG	0.28	0/1131	0.48	0/1537
1	AH	0.29	0/1131	0.49	0/1537
1	AI	0.28	0/1131	0.47	0/1537
1	AJ	0.28	0/1131	0.49	0/1537
1	AK	0.29	0/1131	0.49	0/1537
1	AL	0.28	0/1131	0.47	0/1537
1	AM	0.28	0/1131	0.49	0/1537
1	AN	0.29	0/1131	0.49	0/1537
1	AO	0.28	0/1131	0.47	0/1537
1	AP	0.28	0/1131	0.48	0/1537
1	AQ	0.29	0/1131	0.49	0/1537
1	AR	0.28	0/1131	0.47	0/1537
1	AS	0.28	0/1131	0.48	0/1537
1	AT	0.29	0/1131	0.48	0/1537
1	AU	0.28	0/1131	0.47	0/1537
1	AV	0.28	0/1131	0.49	0/1537
1	AW	0.29	0/1131	0.49	0/1537
1	AX	0.28	0/1131	0.47	0/1537
1	AY	0.28	0/1131	0.49	0/1537
1	AZ	0.29	0/1131	0.49	0/1537
1	BA	0.28	0/1131	0.47	0/1537
1	BB	0.28	0/1131	0.49	0/1537
1	BC	0.29	0/1131	0.48	0/1537
1	BD	0.28	0/1131	0.47	0/1537
1	BE	0.28	0/1131	0.48	0/1537
1	BF	0.29	0/1131	0.49	0/1537

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	BG	0.28	0/1131	0.47	0/1537
1	BH	0.28	0/1131	0.49	0/1537
1	BI	0.29	0/1131	0.49	0/1537
1	BJ	0.28	0/1131	0.47	0/1537
1	BK	0.28	0/1131	0.49	0/1537
1	BL	0.29	0/1131	0.48	0/1537
1	BM	0.28	0/1131	0.47	0/1537
1	BN	0.28	0/1131	0.49	0/1537
1	BO	0.29	0/1131	0.49	0/1537
1	BP	0.28	0/1131	0.47	0/1537
1	BQ	0.28	0/1131	0.49	0/1537
1	BR	0.29	0/1131	0.49	0/1537
1	BS	0.28	0/1131	0.47	0/1537
All	All	0.28	0/50895	0.48	0/69165

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	1114	0	1130	8	0
1	AB	1114	0	1130	16	0
1	AC	1114	0	1130	3	0
1	AD	1114	0	1130	6	0
1	AE	1114	0	1130	19	0
1	AF	1114	0	1130	11	0
1	AG	1114	0	1130	7	0
1	AH	1114	0	1130	12	0
1	AI	1114	0	1130	11	0
1	AJ	1114	0	1130	13	0
1	AK	1114	0	1130	13	0
1	AL	1114	0	1130	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AM	1114	0	1130	9	0
1	AN	1114	0	1130	15	0
1	AO	1114	0	1130	5	0
1	AP	1114	0	1130	11	0
1	AQ	1114	0	1130	14	0
1	AR	1114	0	1130	9	0
1	AS	1114	0	1130	7	0
1	AT	1114	0	1130	22	0
1	AU	1114	0	1130	17	0
1	AV	1114	0	1130	18	0
1	AW	1114	0	1130	12	0
1	AX	1114	0	1130	12	0
1	AY	1114	0	1130	12	0
1	AZ	1114	0	1130	17	0
1	BA	1114	0	1130	10	0
1	BB	1114	0	1130	14	0
1	BC	1114	0	1130	17	0
1	BD	1114	0	1130	9	0
1	BE	1114	0	1130	7	0
1	BF	1114	0	1130	18	0
1	BG	1114	0	1130	5	0
1	BH	1114	0	1130	8	0
1	BI	1114	0	1130	27	0
1	BJ	1114	0	1130	16	0
1	BK	1114	0	1130	30	0
1	BL	1114	0	1130	11	0
1	BM	1114	0	1130	3	0
1	BN	1114	0	1130	17	0
1	BO	1114	0	1130	11	0
1	BP	1114	0	1130	13	0
1	BQ	1114	0	1130	13	0
1	BR	1114	0	1130	17	0
1	BS	1114	0	1130	14	0
2	AA	2	0	0	0	0
2	AB	1	0	0	0	0
2	AC	1	0	0	0	0
2	AD	2	0	0	0	0
2	AE	1	0	0	0	0
2	AF	1	0	0	0	0
2	AG	2	0	0	0	0
2	AH	1	0	0	0	0
2	AI	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	AJ	2	0	0	0	0
2	AK	1	0	0	0	0
2	AL	1	0	0	0	0
2	AM	2	0	0	0	0
2	AN	1	0	0	0	0
2	AO	1	0	0	0	0
2	AP	2	0	0	0	0
2	AQ	1	0	0	0	0
2	AR	1	0	0	0	0
2	AS	2	0	0	0	0
2	AT	1	0	0	0	0
2	AU	1	0	0	0	0
2	AV	2	0	0	0	0
2	AW	1	0	0	0	0
2	AX	1	0	0	0	0
2	AY	2	0	0	0	0
2	AZ	1	0	0	0	0
2	BA	1	0	0	0	0
2	BB	2	0	0	0	0
2	BC	1	0	0	0	0
2	BD	1	0	0	0	0
2	BE	2	0	0	0	0
2	BF	1	0	0	0	0
2	BG	1	0	0	0	0
2	BH	2	0	0	0	0
2	BI	1	0	0	0	0
2	BJ	1	0	0	0	0
2	BK	2	0	0	0	0
2	BL	1	0	0	0	0
2	BM	1	0	0	0	0
2	BN	2	0	0	0	0
2	BO	1	0	0	0	0
2	BP	1	0	0	0	0
2	BQ	2	0	0	0	0
2	BR	1	0	0	0	0
2	BS	1	0	0	0	0
All	All	50190	0	50850	411	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (411) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AZ:64:GLU:OE1	1:AZ:113:ARG:NH2	2.13	0.82
1:AN:64:GLU:OE1	1:AN:113:ARG:NH2	2.13	0.82
1:BF:64:GLU:OE1	1:BF:113:ARG:NH2	2.13	0.82
1:AB:64:GLU:OE1	1:AB:113:ARG:NH2	2.13	0.82
1:AQ:64:GLU:OE1	1:AQ:113:ARG:NH2	2.13	0.82
1:AH:64:GLU:OE1	1:AH:113:ARG:NH2	2.13	0.81
1:AK:64:GLU:OE1	1:AK:113:ARG:NH2	2.13	0.81
1:AT:64:GLU:OE1	1:AT:113:ARG:NH2	2.13	0.81
1:BO:64:GLU:OE1	1:BO:113:ARG:NH2	2.13	0.81
1:AE:64:GLU:OE1	1:AE:113:ARG:NH2	2.13	0.81
1:BR:64:GLU:OE1	1:BR:113:ARG:NH2	2.13	0.81
1:BC:64:GLU:OE1	1:BC:113:ARG:NH2	2.13	0.81
1:BI:64:GLU:OE1	1:BI:113:ARG:NH2	2.13	0.81
1:BL:64:GLU:OE1	1:BL:113:ARG:NH2	2.13	0.81
1:BJ:86:TYR:OH	1:BK:89:ALA:O	1.98	0.80
1:AW:64:GLU:OE1	1:AW:113:ARG:NH2	2.13	0.80
1:BR:75:MET:HE1	1:BR:89:ALA:HB1	1.66	0.76
1:AQ:75:MET:HE1	1:AQ:89:ALA:HB1	1.71	0.72
1:AB:75:MET:HE1	1:AB:89:ALA:HB1	1.75	0.68
1:AT:113:ARG:NH1	1:AT:143:ILE:O	2.27	0.68
1:BO:113:ARG:NH1	1:BO:143:ILE:O	2.27	0.68
1:AE:113:ARG:NH1	1:AE:143:ILE:O	2.27	0.67
1:AQ:113:ARG:NH1	1:AQ:143:ILE:O	2.27	0.67
1:AW:113:ARG:NH1	1:AW:143:ILE:O	2.27	0.67
1:BF:113:ARG:NH1	1:BF:143:ILE:O	2.27	0.67
1:BL:113:ARG:NH1	1:BL:143:ILE:O	2.27	0.67
1:AN:113:ARG:NH1	1:AN:143:ILE:O	2.27	0.66
1:AK:113:ARG:NH1	1:AK:143:ILE:O	2.27	0.66
1:BL:75:MET:HE1	1:BL:89:ALA:HB1	1.76	0.66
1:AH:113:ARG:NH1	1:AH:143:ILE:O	2.27	0.66
1:BR:113:ARG:NH1	1:BR:143:ILE:O	2.27	0.66
1:AZ:113:ARG:NH1	1:AZ:143:ILE:O	2.27	0.66
1:BI:113:ARG:NH1	1:BI:143:ILE:O	2.27	0.66
1:BJ:87:THR:HB	1:BK:77:ALA:HB3	1.78	0.66
1:BC:113:ARG:NH1	1:BC:143:ILE:O	2.27	0.66
1:AB:113:ARG:NH1	1:AB:143:ILE:O	2.27	0.65
1:AH:56:GLN:NE2	1:AH:64:GLU:OE2	2.30	0.65
1:AQ:56:GLN:NE2	1:AQ:64:GLU:OE2	2.30	0.65
1:AT:56:GLN:NE2	1:AT:64:GLU:OE2	2.30	0.65
1:AB:56:GLN:NE2	1:AB:64:GLU:OE2	2.30	0.64
1:AE:56:GLN:NE2	1:AE:64:GLU:OE2	2.30	0.64
1:AK:56:GLN:NE2	1:AK:64:GLU:OE2	2.30	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:56:GLN:NE2	1:BC:64:GLU:OE2	2.30	0.64
1:BF:75:MET:HE1	1:BF:89:ALA:HB1	1.78	0.64
1:BR:56:GLN:NE2	1:BR:64:GLU:OE2	2.30	0.64
1:BL:56:GLN:NE2	1:BL:64:GLU:OE2	2.30	0.64
1:AH:75:MET:HE1	1:AH:89:ALA:HB1	1.78	0.64
1:BI:56:GLN:NE2	1:BI:64:GLU:OE2	2.30	0.63
1:AT:75:MET:HE1	1:AT:89:ALA:HB1	1.80	0.63
1:BO:56:GLN:NE2	1:BO:64:GLU:OE2	2.30	0.63
1:AN:56:GLN:NE2	1:AN:64:GLU:OE2	2.30	0.63
1:BF:56:GLN:NE2	1:BF:64:GLU:OE2	2.30	0.63
1:AW:56:GLN:NE2	1:AW:64:GLU:OE2	2.30	0.62
1:AZ:56:GLN:NE2	1:AZ:64:GLU:OE2	2.30	0.61
1:AU:8:VAL:HG11	1:BP:119:ILE:HG23	1.82	0.61
1:BH:145:SER:O	1:BI:38:ARG:NH2	2.31	0.59
1:AW:75:MET:HE1	1:AW:89:ALA:HB1	1.83	0.59
1:AP:145:SER:O	1:AQ:38:ARG:NH2	2.31	0.59
1:AV:145:SER:O	1:AW:38:ARG:NH2	2.31	0.58
1:AX:112:ASN:HB3	1:BS:96:ASP:OD2	2.02	0.58
1:BB:145:SER:O	1:BC:38:ARG:NH2	2.31	0.58
1:BN:145:SER:O	1:BO:38:ARG:NH2	2.31	0.58
1:AI:10:ASP:HB2	1:BD:115:LEU:HG	1.86	0.58
1:BC:75:MET:HE1	1:BC:89:ALA:HB1	1.85	0.58
1:AR:123:LEU:CD2	1:BJ:8:VAL:HG21	2.34	0.57
1:AS:145:SER:O	1:AT:38:ARG:NH2	2.31	0.57
1:BJ:84:PHE:O	1:BK:88:ALA:HB2	2.04	0.57
1:BQ:145:SER:O	1:BR:38:ARG:NH2	2.31	0.57
1:AY:145:SER:O	1:AZ:38:ARG:NH2	2.31	0.57
1:AZ:75:MET:HE1	1:AZ:89:ALA:HB1	1.87	0.57
1:BI:119:ILE:HG23	1:BK:8:VAL:HG11	1.87	0.56
1:AA:145:SER:O	1:AB:38:ARG:NH2	2.31	0.56
1:AM:145:SER:O	1:AN:38:ARG:NH2	2.31	0.56
1:AU:8:VAL:HG21	1:BP:123:LEU:CD2	2.36	0.56
1:AJ:145:SER:O	1:AK:38:ARG:NH2	2.31	0.56
1:AU:88:ALA:HB2	1:BN:84:PHE:O	2.06	0.55
1:BO:75:MET:HE1	1:BO:89:ALA:HB1	1.87	0.55
1:AX:123:LEU:HD22	1:BS:138:PHE:CE2	2.42	0.55
1:AI:8:VAL:HG11	1:BD:119:ILE:HG23	1.90	0.54
1:AK:75:MET:HE1	1:AK:89:ALA:HB1	1.90	0.54
1:AD:145:SER:O	1:AE:38:ARG:NH2	2.31	0.54
1:AX:123:LEU:HD22	1:BS:138:PHE:CZ	2.42	0.54
1:BD:54:THR:HB	1:BD:142:LEU:HD22	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BP:54:THR:HB	1:BP:142:LEU:HD22	1.91	0.53
1:AF:8:VAL:HG21	1:BA:123:LEU:CD2	2.38	0.53
1:BG:54:THR:HB	1:BG:142:LEU:HD22	1.91	0.53
1:BI:123:LEU:HD22	1:BK:138:PHE:HE2	1.71	0.53
1:AT:138:PHE:CE2	1:AV:123:LEU:HD22	2.43	0.53
1:AU:11:GLY:CA	1:BP:115:LEU:HA	2.38	0.53
1:BI:115:LEU:HA	1:BK:11:GLY:CA	2.38	0.53
1:BJ:54:THR:HB	1:BJ:142:LEU:HD22	1.91	0.53
1:AI:54:THR:HB	1:AI:142:LEU:HD22	1.91	0.53
1:AU:77:ALA:HB3	1:BN:87:THR:HB	1.91	0.53
1:BK:145:SER:O	1:BL:38:ARG:NH2	2.31	0.53
1:BM:54:THR:HB	1:BM:142:LEU:HD22	1.91	0.53
1:AF:54:THR:HB	1:AF:142:LEU:HD22	1.91	0.53
1:AL:54:THR:HB	1:AL:142:LEU:HD22	1.91	0.53
1:AI:138:PHE:CE2	1:BD:123:LEU:HD22	2.43	0.53
1:AX:54:THR:HB	1:AX:142:LEU:HD22	1.91	0.53
1:AB:123:LEU:HD21	1:BQ:8:VAL:HG21	1.91	0.52
1:AO:54:THR:HB	1:AO:142:LEU:HD22	1.91	0.52
1:AB:8:VAL:HG21	1:BQ:123:LEU:HD21	1.92	0.52
1:AX:116:VAL:HG21	1:BS:96:ASP:HB2	1.91	0.52
1:AX:8:VAL:HG21	1:BS:123:LEU:CD2	2.39	0.52
1:AC:54:THR:HB	1:AC:142:LEU:HD22	1.91	0.52
1:BI:123:LEU:HD22	1:BK:138:PHE:CE2	2.45	0.52
1:BS:54:THR:HB	1:BS:142:LEU:HD22	1.91	0.52
1:BA:54:THR:HB	1:BA:142:LEU:HD22	1.91	0.52
1:BE:145:SER:O	1:BF:38:ARG:NH2	2.31	0.52
1:AI:77:ALA:HB3	1:BB:87:THR:HB	1.91	0.52
1:AR:54:THR:HB	1:AR:142:LEU:HD22	1.91	0.52
1:AU:54:THR:HB	1:AU:142:LEU:HD22	1.91	0.52
1:AB:119:ILE:HG12	1:BQ:10:ASP:HA	1.92	0.52
1:BI:123:LEU:HD21	1:BK:8:VAL:HG21	1.91	0.51
1:AK:69:ARG:HA	1:AK:99:SER:HB3	1.93	0.51
1:AQ:69:ARG:HA	1:AQ:99:SER:HB3	1.93	0.51
1:AY:15:PRO:HG2	1:BR:130:SER:OG	2.09	0.51
1:AE:69:ARG:HA	1:AE:99:SER:HB3	1.93	0.51
1:AG:145:SER:O	1:AH:38:ARG:NH2	2.31	0.51
1:BC:69:ARG:HA	1:BC:99:SER:HB3	1.93	0.51
1:BL:69:ARG:HA	1:BL:99:SER:HB3	1.93	0.51
1:AY:123:LEU:HD21	1:BR:8:VAL:HG21	1.92	0.51
1:BI:138:PHE:CE2	1:BK:123:LEU:HD22	2.45	0.50
1:AR:96:ASP:HB2	1:BJ:116:VAL:HG21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AH:69:ARG:HA	1:AH:99:SER:HB3	1.93	0.50
1:AU:8:VAL:HG21	1:BP:123:LEU:HD21	1.93	0.50
1:BF:69:ARG:HA	1:BF:99:SER:HB3	1.93	0.50
1:AB:69:ARG:HA	1:AB:99:SER:HB3	1.93	0.50
1:AT:69:ARG:HA	1:AT:99:SER:HB3	1.93	0.50
1:AZ:69:ARG:HA	1:AZ:99:SER:HB3	1.93	0.50
1:BI:69:ARG:HA	1:BI:99:SER:HB3	1.93	0.50
1:AN:69:ARG:HA	1:AN:99:SER:HB3	1.93	0.50
1:BO:69:ARG:HA	1:BO:99:SER:HB3	1.93	0.49
1:BR:69:ARG:HA	1:BR:99:SER:HB3	1.93	0.49
1:AW:75:MET:CE	1:AW:89:ALA:HB1	2.43	0.49
1:BC:6:ILE:HG22	1:BC:8:VAL:HG23	1.95	0.49
1:BE:1:SER:HA	1:BE:141:GLU:OE1	2.13	0.49
1:AB:6:ILE:HG22	1:AB:8:VAL:HG23	1.95	0.49
1:AS:1:SER:HA	1:AS:141:GLU:OE1	2.13	0.49
1:AJ:1:SER:HA	1:AJ:141:GLU:OE1	2.13	0.49
1:AM:1:SER:HA	1:AM:141:GLU:OE1	2.13	0.49
1:AP:1:SER:HA	1:AP:141:GLU:OE1	2.13	0.49
1:AW:6:ILE:HG22	1:AW:8:VAL:HG23	1.95	0.49
1:AW:69:ARG:HA	1:AW:99:SER:HB3	1.93	0.49
1:BB:8:VAL:HG21	1:BF:123:LEU:CD2	2.43	0.49
1:BH:1:SER:HA	1:BH:141:GLU:OE1	2.13	0.49
1:AA:1:SER:HA	1:AA:141:GLU:OE1	2.13	0.49
1:AF:116:VAL:HG21	1:BA:96:ASP:HB2	1.94	0.49
1:AH:6:ILE:HG22	1:AH:8:VAL:HG23	1.95	0.49
1:BF:6:ILE:HG22	1:BF:8:VAL:HG23	1.95	0.49
1:BQ:1:SER:HA	1:BQ:141:GLU:OE1	2.13	0.49
1:BK:1:SER:HA	1:BK:141:GLU:OE1	2.13	0.49
1:BR:6:ILE:HG22	1:BR:8:VAL:HG23	1.95	0.49
1:AT:6:ILE:HG22	1:AT:8:VAL:HG23	1.95	0.49
1:AE:75:MET:CE	1:AE:89:ALA:HB1	2.43	0.49
1:AI:3:GLN:HG3	1:AI:37:TRP:CZ2	2.48	0.49
1:AZ:75:MET:CE	1:AZ:89:ALA:HB1	2.43	0.49
1:BL:6:ILE:HG22	1:BL:8:VAL:HG23	1.95	0.49
1:AD:1:SER:HA	1:AD:141:GLU:OE1	2.13	0.49
1:AG:1:SER:HA	1:AG:141:GLU:OE1	2.13	0.49
1:AN:75:MET:CE	1:AN:89:ALA:HB1	2.43	0.49
1:AO:3:GLN:HG3	1:AO:37:TRP:CZ2	2.48	0.49
1:AY:1:SER:HA	1:AY:141:GLU:OE1	2.13	0.49
1:BB:1:SER:HA	1:BB:141:GLU:OE1	2.13	0.49
1:BD:3:GLN:HG3	1:BD:37:TRP:CZ2	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:54:THR:HB	1:AE:142:LEU:HD22	1.95	0.48
1:AN:6:ILE:HG22	1:AN:8:VAL:HG23	1.95	0.48
1:AH:75:MET:CE	1:AH:89:ALA:HB1	2.43	0.48
1:AK:54:THR:HB	1:AK:142:LEU:HD22	1.95	0.48
1:BA:3:GLN:HG3	1:BA:37:TRP:CZ2	2.48	0.48
1:BI:75:MET:CE	1:BI:89:ALA:HB1	2.43	0.48
1:AT:123:LEU:HD22	1:AV:138:PHE:CE2	2.48	0.48
1:BJ:86:TYR:HA	1:BK:77:ALA:O	2.13	0.48
1:BM:3:GLN:HG3	1:BM:37:TRP:CZ2	2.48	0.48
1:BP:3:GLN:HG3	1:BP:37:TRP:CZ2	2.48	0.48
1:AL:3:GLN:HG3	1:AL:37:TRP:CZ2	2.48	0.48
1:AQ:6:ILE:HG22	1:AQ:8:VAL:HG23	1.95	0.48
1:AR:3:GLN:HG3	1:AR:37:TRP:CZ2	2.48	0.48
1:AT:54:THR:HB	1:AT:142:LEU:HD22	1.95	0.48
1:AZ:6:ILE:HG22	1:AZ:8:VAL:HG23	1.95	0.48
1:BI:6:ILE:HG22	1:BI:8:VAL:HG23	1.95	0.48
1:BI:54:THR:HB	1:BI:142:LEU:HD22	1.95	0.48
1:BJ:3:GLN:HG3	1:BJ:37:TRP:CZ2	2.48	0.48
1:BO:54:THR:HB	1:BO:142:LEU:HD22	1.95	0.48
1:AT:9:PHE:CG	1:AV:130:SER:HA	2.48	0.48
1:AU:3:GLN:HG3	1:AU:37:TRP:CZ2	2.48	0.48
1:AU:89:ALA:O	1:BN:86:TYR:OH	2.21	0.48
1:AW:54:THR:HB	1:AW:142:LEU:HD22	1.96	0.48
1:AX:3:GLN:HG3	1:AX:37:TRP:CZ2	2.48	0.48
1:AX:8:VAL:HG11	1:BS:119:ILE:HG23	1.96	0.48
1:BG:3:GLN:HG3	1:BG:37:TRP:CZ2	2.48	0.48
1:BN:1:SER:HA	1:BN:141:GLU:OE1	2.13	0.48
1:AC:3:GLN:HG3	1:AC:37:TRP:CZ2	2.48	0.48
1:BI:123:LEU:CD2	1:BK:8:VAL:HG21	2.43	0.48
1:BL:54:THR:HB	1:BL:142:LEU:HD22	1.95	0.48
1:BO:6:ILE:HG22	1:BO:8:VAL:HG23	1.95	0.48
1:AI:123:LEU:HD22	1:BD:138:PHE:CE2	2.48	0.48
1:AU:12:ALA:HB2	1:BP:115:LEU:HD12	1.94	0.48
1:AY:96:ASP:HB2	1:BR:116:VAL:HG21	1.94	0.48
1:BJ:81:GLN:HG3	1:BK:79:SER:O	2.13	0.48
1:BR:54:THR:HB	1:BR:142:LEU:HD22	1.96	0.48
1:AF:3:GLN:HG3	1:AF:37:TRP:CZ2	2.48	0.48
1:AT:9:PHE:CE1	1:AV:130:SER:HB2	2.49	0.48
1:AU:77:ALA:O	1:BN:86:TYR:HA	2.14	0.48
1:BB:123:LEU:HD21	1:BF:8:VAL:HG21	1.94	0.48
1:BC:54:THR:HB	1:BC:142:LEU:HD22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:6:ILE:HG22	1:AE:8:VAL:HG23	1.95	0.48
1:AK:6:ILE:HG22	1:AK:8:VAL:HG23	1.95	0.48
1:AV:1:SER:HA	1:AV:141:GLU:OE1	2.13	0.48
1:BC:75:MET:CE	1:BC:89:ALA:HB1	2.43	0.48
1:AK:75:MET:CE	1:AK:89:ALA:HB1	2.43	0.48
1:BF:54:THR:HB	1:BF:142:LEU:HD22	1.96	0.48
1:AP:10:ASP:HA	1:AZ:119:ILE:HG12	1.96	0.47
1:AU:10:ASP:HA	1:BP:119:ILE:HG12	1.96	0.47
1:AB:54:THR:HB	1:AB:142:LEU:HD22	1.95	0.47
1:BO:75:MET:CE	1:BO:89:ALA:HB1	2.43	0.47
1:BS:3:GLN:HG3	1:BS:37:TRP:CZ2	2.48	0.47
1:AT:75:MET:CE	1:AT:89:ALA:HB1	2.43	0.47
1:BI:119:ILE:HG12	1:BK:10:ASP:HA	1.95	0.47
1:AB:123:LEU:CD2	1:BQ:8:VAL:HG21	2.44	0.47
1:AQ:54:THR:HB	1:AQ:142:LEU:HD22	1.95	0.47
1:AP:8:VAL:HG21	1:AZ:123:LEU:HD21	1.95	0.47
1:BI:97:SER:O	1:BK:102:GLY:HA2	2.14	0.47
1:BI:138:PHE:HE2	1:BK:123:LEU:HD22	1.80	0.47
1:AH:54:THR:HB	1:AH:142:LEU:HD22	1.95	0.47
1:AN:54:THR:HB	1:AN:142:LEU:HD22	1.95	0.47
1:AE:123:LEU:HD21	1:BN:8:VAL:HG21	1.96	0.46
1:AZ:54:THR:HB	1:AZ:142:LEU:HD22	1.95	0.46
1:AJ:138:PHE:CE2	1:BC:123:LEU:HD22	2.49	0.46
1:BL:75:MET:CE	1:BL:89:ALA:HB1	2.43	0.46
1:AU:10:ASP:HA	1:BP:119:ILE:CG1	2.45	0.46
1:AY:96:ASP:CB	1:BR:116:VAL:HG21	2.45	0.46
1:BF:75:MET:CE	1:BF:89:ALA:HB1	2.43	0.46
1:BN:28:ASP:HB3	1:BN:31:LEU:HB2	1.98	0.46
1:AE:123:LEU:CD2	1:BN:8:VAL:HG21	2.46	0.46
1:AJ:28:ASP:HB3	1:AJ:31:LEU:HB2	1.98	0.46
1:AQ:75:MET:CE	1:AQ:89:ALA:HB1	2.43	0.46
1:BJ:86:TYR:CE1	1:BK:78:VAL:HG22	2.50	0.46
1:BQ:28:ASP:HB3	1:BQ:31:LEU:HB2	1.98	0.46
1:AD:28:ASP:HB3	1:AD:31:LEU:HB2	1.98	0.46
1:BE:28:ASP:HB3	1:BE:31:LEU:HB2	1.98	0.46
1:AI:88:ALA:HB2	1:BB:85:GLY:HA3	1.98	0.45
1:AR:123:LEU:HD21	1:BJ:8:VAL:HG21	1.98	0.45
1:AS:28:ASP:HB3	1:AS:31:LEU:HB2	1.98	0.45
1:BH:28:ASP:HB3	1:BH:31:LEU:HB2	1.98	0.45
1:AM:28:ASP:HB3	1:AM:31:LEU:HB2	1.98	0.45
1:AV:28:ASP:HB3	1:AV:31:LEU:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:82:ASN:OD1	1:BF:78:VAL:HG23	2.16	0.45
1:AU:10:ASP:HB2	1:BP:115:LEU:HG	1.99	0.45
1:AX:116:VAL:HG21	1:BS:96:ASP:CB	2.46	0.45
1:AE:119:ILE:HG12	1:BN:10:ASP:HA	1.97	0.45
1:AM:138:PHE:CE2	1:AQ:123:LEU:HD22	2.52	0.45
1:BD:3:GLN:HG2	1:BD:22:PRO:HB3	1.99	0.45
1:BP:3:GLN:HG2	1:BP:22:PRO:HB3	1.99	0.45
1:AE:8:VAL:HG21	1:BN:123:LEU:HD21	1.98	0.45
1:BG:3:GLN:HG2	1:BG:22:PRO:HB3	1.99	0.45
1:AI:138:PHE:HE2	1:BD:123:LEU:HD22	1.81	0.45
1:AA:28:ASP:HB3	1:AA:31:LEU:HB2	1.98	0.45
1:AP:28:ASP:HB3	1:AP:31:LEU:HB2	1.98	0.45
1:AU:3:GLN:HG2	1:AU:22:PRO:HB3	1.99	0.45
1:BB:10:ASP:HA	1:BF:119:ILE:HG12	1.98	0.45
1:AF:3:GLN:HG2	1:AF:22:PRO:HB3	1.99	0.45
1:AG:28:ASP:HB3	1:AG:31:LEU:HB2	1.98	0.45
1:AF:116:VAL:HG21	1:BA:96:ASP:CB	2.48	0.44
1:AF:130:SER:OG	1:BA:15:PRO:HG2	2.17	0.44
1:AL:3:GLN:HG2	1:AL:22:PRO:HB3	1.99	0.44
1:AX:3:GLN:HG2	1:AX:22:PRO:HB3	1.99	0.44
1:BB:8:VAL:HG21	1:BF:123:LEU:HD21	1.97	0.44
1:BI:75:MET:HE1	1:BI:89:ALA:HB1	1.99	0.44
1:AI:3:GLN:HG2	1:AI:22:PRO:HB3	1.99	0.44
1:BB:28:ASP:HB3	1:BB:31:LEU:HB2	1.98	0.44
1:BR:75:MET:CE	1:BR:89:ALA:HB1	2.43	0.44
1:BI:103:TYR:HB2	1:BK:97:SER:HB3	1.98	0.44
1:AU:11:GLY:C	1:BP:115:LEU:HA	2.37	0.44
1:AQ:78:VAL:HG22	1:AQ:90:PRO:HD3	2.00	0.44
1:AY:28:ASP:HB3	1:AY:31:LEU:HB2	1.98	0.44
1:BI:115:LEU:HD12	1:BK:12:ALA:HB2	1.99	0.44
1:BJ:83:ALA:O	1:BK:83:ALA:N	2.50	0.44
1:BK:28:ASP:HB3	1:BK:31:LEU:HB2	1.98	0.44
1:BO:78:VAL:HG22	1:BO:90:PRO:HD3	2.00	0.44
1:BS:3:GLN:HG2	1:BS:22:PRO:HB3	1.99	0.44
1:AB:75:MET:CE	1:AB:89:ALA:HB1	2.43	0.44
1:AC:3:GLN:HG2	1:AC:22:PRO:HB3	1.99	0.44
1:AD:6:ILE:HG22	1:AD:8:VAL:HG23	2.00	0.44
1:AO:3:GLN:HG2	1:AO:22:PRO:HB3	1.99	0.44
1:AW:78:VAL:HG22	1:AW:90:PRO:HD3	2.00	0.44
1:BF:78:VAL:HG22	1:BF:90:PRO:HD3	2.00	0.44
1:BI:115:LEU:HG	1:BK:10:ASP:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BJ:3:GLN:HG2	1:BJ:22:PRO:HB3	1.99	0.44
1:BN:6:ILE:HG22	1:BN:8:VAL:HG23	2.00	0.44
1:AO:119:ILE:HG23	1:BG:8:VAL:HG11	2.00	0.44
1:AV:6:ILE:HG22	1:AV:8:VAL:HG23	2.00	0.44
1:BA:3:GLN:HG2	1:BA:22:PRO:HB3	1.99	0.44
1:AR:3:GLN:HG2	1:AR:22:PRO:HB3	1.99	0.43
1:AR:119:ILE:HG23	1:BJ:8:VAL:HG11	2.00	0.43
1:BE:6:ILE:HG22	1:BE:8:VAL:HG23	2.00	0.43
1:BL:78:VAL:HG22	1:BL:90:PRO:HD3	2.00	0.43
1:BM:3:GLN:HG2	1:BM:22:PRO:HB3	1.99	0.43
1:BQ:6:ILE:HG22	1:BQ:8:VAL:HG23	2.00	0.43
1:BR:78:VAL:HG22	1:BR:90:PRO:HD3	2.00	0.43
1:AA:123:LEU:HD21	1:AN:8:VAL:HG21	1.99	0.43
1:AF:8:VAL:HG21	1:BA:123:LEU:HD21	2.00	0.43
1:AI:115:LEU:HG	1:BD:10:ASP:HB2	2.00	0.43
1:AM:6:ILE:HG22	1:AM:8:VAL:HG23	2.00	0.43
1:BC:78:VAL:HG22	1:BC:90:PRO:HD3	2.00	0.43
1:AA:8:VAL:HG21	1:AN:123:LEU:HD21	1.99	0.43
1:AR:119:ILE:HG12	1:BJ:10:ASP:HA	2.00	0.43
1:BH:6:ILE:HG22	1:BH:8:VAL:HG23	2.00	0.43
1:AG:6:ILE:HG22	1:AG:8:VAL:HG23	2.00	0.43
1:AT:78:VAL:HG22	1:AT:90:PRO:HD3	2.00	0.43
1:AZ:78:VAL:HG22	1:AZ:90:PRO:HD3	2.00	0.43
1:AJ:6:ILE:HG22	1:AJ:8:VAL:HG23	2.00	0.43
1:AM:123:LEU:HD21	1:AQ:8:VAL:HG21	2.00	0.43
1:AK:78:VAL:HG22	1:AK:90:PRO:HD3	2.00	0.43
1:AN:78:VAL:HG22	1:AN:90:PRO:HD3	2.00	0.43
1:AA:10:ASP:HA	1:AN:119:ILE:HG12	2.01	0.43
1:AJ:119:ILE:HG23	1:BC:8:VAL:HG11	2.00	0.43
1:AO:123:LEU:CD2	1:BG:8:VAL:HG21	2.48	0.43
1:AP:138:PHE:CE2	1:AZ:123:LEU:HD22	2.53	0.43
1:AH:78:VAL:HG22	1:AH:90:PRO:HD3	2.00	0.43
1:AE:78:VAL:HG22	1:AE:90:PRO:HD3	2.00	0.43
1:AS:6:ILE:HG22	1:AS:8:VAL:HG23	2.00	0.43
1:AT:138:PHE:CZ	1:AV:123:LEU:HD22	2.53	0.43
1:AV:85:GLY:HA3	1:BS:88:ALA:HB2	2.00	0.43
1:BB:102:GLY:HA2	1:BF:97:SER:O	2.18	0.43
1:BI:78:VAL:HG22	1:BI:90:PRO:HD3	2.00	0.42
1:BI:102:GLY:HA2	1:BK:97:SER:O	2.19	0.42
1:BK:6:ILE:HG22	1:BK:8:VAL:HG23	2.00	0.42
1:AA:6:ILE:HG22	1:AA:8:VAL:HG23	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AB:78:VAL:HG22	1:AB:90:PRO:HD3	2.00	0.42
1:BB:6:ILE:HG22	1:BB:8:VAL:HG23	2.00	0.42
1:BI:10:ASP:HB2	1:BK:115:LEU:HG	2.00	0.42
1:AT:78:VAL:O	1:AW:80:GLY:HA3	2.20	0.42
1:AU:116:VAL:HG21	1:BP:96:ASP:HB2	2.02	0.42
1:AE:97:SER:O	1:BN:102:GLY:HA2	2.20	0.42
1:AK:75:MET:HB3	1:AK:75:MET:HE2	1.91	0.42
1:AR:96:ASP:CB	1:BJ:116:VAL:HG21	2.49	0.42
1:AX:11:GLY:CA	1:BS:115:LEU:HA	2.50	0.42
1:AP:6:ILE:HG22	1:AP:8:VAL:HG23	2.00	0.42
1:AY:6:ILE:HG22	1:AY:8:VAL:HG23	2.00	0.42
1:AY:67:GLU:HA	1:AY:100:PHE:O	2.20	0.42
1:AP:67:GLU:HA	1:AP:100:PHE:O	2.20	0.41
1:AP:138:PHE:HE2	1:AZ:123:LEU:HD22	1.84	0.41
1:AT:96:ASP:CB	1:AV:116:VAL:HG21	2.50	0.41
1:BB:96:ASP:HB2	1:BF:116:VAL:HG21	2.02	0.41
1:AJ:67:GLU:HA	1:AJ:100:PHE:O	2.20	0.41
1:AJ:123:LEU:HD21	1:BC:8:VAL:HG21	2.01	0.41
1:AS:69:ARG:HA	1:AS:99:SER:HB3	2.02	0.41
1:AY:138:PHE:CE2	1:BR:123:LEU:HD22	2.55	0.41
1:BI:119:ILE:CG1	1:BK:10:ASP:HA	2.50	0.41
1:BN:67:GLU:HA	1:BN:100:PHE:O	2.20	0.41
1:BQ:67:GLU:HA	1:BQ:100:PHE:O	2.20	0.41
1:AG:67:GLU:HA	1:AG:100:PHE:O	2.20	0.41
1:AG:147:ILE:HG12	1:AH:23:LEU:HD23	2.03	0.41
1:AJ:147:ILE:HG12	1:AK:23:LEU:HD23	2.03	0.41
1:AV:67:GLU:HA	1:AV:100:PHE:O	2.20	0.41
1:AV:69:ARG:HA	1:AV:99:SER:HB3	2.02	0.41
1:AY:96:ASP:OD2	1:BR:112:ASN:HB3	2.20	0.41
1:BB:67:GLU:HA	1:BB:100:PHE:O	2.20	0.41
1:AD:147:ILE:HG12	1:AE:23:LEU:HD23	2.03	0.41
1:AF:123:LEU:CD2	1:BA:8:VAL:HG21	2.50	0.41
1:AN:75:MET:HE1	1:AN:89:ALA:HB1	2.02	0.41
1:BE:69:ARG:HA	1:BE:99:SER:HB3	2.03	0.41
1:AM:67:GLU:HA	1:AM:100:PHE:O	2.20	0.41
1:AP:8:VAL:HG21	1:AZ:123:LEU:CD2	2.50	0.41
1:AP:69:ARG:HA	1:AP:99:SER:HB3	2.02	0.41
1:AV:147:ILE:HG12	1:AW:23:LEU:HD23	2.03	0.41
1:AY:147:ILE:HG12	1:AZ:23:LEU:HD23	2.03	0.41
1:BH:69:ARG:HA	1:BH:99:SER:HB3	2.03	0.41
1:AS:67:GLU:HA	1:AS:100:PHE:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BH:147:ILE:HG12	1:BI:23:LEU:HD23	2.03	0.41
1:BK:67:GLU:HA	1:BK:100:PHE:O	2.20	0.41
1:BN:69:ARG:HA	1:BN:99:SER:HB3	2.03	0.41
1:BN:147:ILE:HG12	1:BO:23:LEU:HD23	2.03	0.41
1:AA:69:ARG:HA	1:AA:99:SER:HB3	2.03	0.41
1:AJ:15:PRO:HG2	1:BC:130:SER:OG	2.21	0.41
1:BE:147:ILE:HG12	1:BF:23:LEU:HD23	2.03	0.41
1:AD:67:GLU:HA	1:AD:100:PHE:O	2.20	0.41
1:AT:96:ASP:HB2	1:AV:116:VAL:HG21	2.02	0.41
1:BK:69:ARG:HA	1:BK:99:SER:HB3	2.03	0.41
1:BK:147:ILE:HG12	1:BL:23:LEU:HD23	2.03	0.41
1:AB:97:SER:O	1:BQ:102:GLY:HA2	2.21	0.41
1:AT:123:LEU:HD22	1:AV:138:PHE:HE2	1.85	0.41
1:AJ:96:ASP:HB2	1:BC:116:VAL:HG21	2.03	0.41
1:BB:69:ARG:HA	1:BB:99:SER:HB3	2.03	0.41
1:BH:67:GLU:HA	1:BH:100:PHE:O	2.20	0.41
1:AE:75:MET:HE1	1:AE:89:ALA:HB1	2.03	0.40
1:AF:38:ARG:HG2	1:AF:39:GLU:O	2.22	0.40
1:AG:69:ARG:HA	1:AG:99:SER:HB3	2.02	0.40
1:AS:147:ILE:HG12	1:AT:23:LEU:HD23	2.03	0.40
1:AT:10:ASP:HB2	1:AV:115:LEU:HG	2.02	0.40
1:AE:75:MET:HE3	1:AE:89:ALA:HB1	2.02	0.40
1:AH:130:SER:OG	1:BH:15:PRO:HG2	2.20	0.40
1:AM:138:PHE:HE2	1:AQ:123:LEU:HD22	1.86	0.40
1:AT:138:PHE:HE2	1:AV:123:LEU:HD22	1.85	0.40
1:AB:10:ASP:HA	1:BQ:119:ILE:HG12	2.03	0.40
1:AF:10:ASP:HA	1:BA:119:ILE:HG12	2.03	0.40
1:AM:8:VAL:HG21	1:AQ:123:LEU:CD2	2.52	0.40
1:AJ:69:ARG:HA	1:AJ:99:SER:HB3	2.02	0.40
1:AJ:138:PHE:HE2	1:BC:123:LEU:HD22	1.87	0.40
1:AN:75:MET:HB3	1:AN:75:MET:HE2	1.84	0.40
1:BQ:69:ARG:HA	1:BQ:99:SER:HB3	2.03	0.40
1:AE:1:SER:O	1:AE:149:ALA:HA	2.22	0.40
1:AE:123:LEU:HD22	1:BN:138:PHE:CE2	2.56	0.40
1:AK:1:SER:O	1:AK:149:ALA:HA	2.22	0.40
1:AN:1:SER:O	1:AN:149:ALA:HA	2.22	0.40
1:AX:8:VAL:HG21	1:BS:123:LEU:HD21	2.03	0.40
1:AZ:1:SER:O	1:AZ:149:ALA:HA	2.22	0.40
1:BE:67:GLU:HA	1:BE:100:PHE:O	2.20	0.40
1:BQ:147:ILE:HG12	1:BR:23:LEU:HD23	2.03	0.40
1:BS:38:ARG:HG2	1:BS:39:GLU:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AB	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	AC	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AD	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AE	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	AF	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AG	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AH	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	AI	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AJ	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AK	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	AL	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AM	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AN	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	AO	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AP	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AQ	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	AR	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AS	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AT	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	AU	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AV	148/150 (99%)	147 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AW	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	AX	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AY	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	AZ	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	BA	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BB	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BC	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	BD	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BE	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BF	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	BG	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BH	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BI	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	BJ	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BK	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BL	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	BM	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BN	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BO	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	BP	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BQ	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
1	BR	148/150 (99%)	145 (98%)	3 (2%)	0	100	100
1	BS	148/150 (99%)	147 (99%)	1 (1%)	0	100	100
All	All	6660/6750 (99%)	6585 (99%)	75 (1%)	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	122/122 (100%)	122 (100%)	0	100	100
1	AB	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	AC	122/122 (100%)	122 (100%)	0	100	100
1	AD	122/122 (100%)	122 (100%)	0	100	100
1	AE	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	AF	122/122 (100%)	122 (100%)	0	100	100
1	AG	122/122 (100%)	122 (100%)	0	100	100
1	AH	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	AI	122/122 (100%)	122 (100%)	0	100	100
1	AJ	122/122 (100%)	122 (100%)	0	100	100
1	AK	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	AL	122/122 (100%)	122 (100%)	0	100	100
1	AM	122/122 (100%)	122 (100%)	0	100	100
1	AN	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	AO	122/122 (100%)	122 (100%)	0	100	100
1	AP	122/122 (100%)	122 (100%)	0	100	100
1	AQ	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	AR	122/122 (100%)	122 (100%)	0	100	100
1	AS	122/122 (100%)	122 (100%)	0	100	100
1	AT	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	AU	122/122 (100%)	122 (100%)	0	100	100
1	AV	122/122 (100%)	122 (100%)	0	100	100
1	AW	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	AX	122/122 (100%)	122 (100%)	0	100	100
1	AY	122/122 (100%)	122 (100%)	0	100	100
1	AZ	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	BA	122/122 (100%)	122 (100%)	0	100	100
1	BB	122/122 (100%)	122 (100%)	0	100	100
1	BC	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	BD	122/122 (100%)	122 (100%)	0	100	100
1	BE	122/122 (100%)	122 (100%)	0	100	100
1	BF	122/122 (100%)	121 (99%)	1 (1%)	81	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	BG	122/122 (100%)	122 (100%)	0	100	100
1	BH	122/122 (100%)	122 (100%)	0	100	100
1	BI	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	BJ	122/122 (100%)	122 (100%)	0	100	100
1	BK	122/122 (100%)	122 (100%)	0	100	100
1	BL	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	BM	122/122 (100%)	122 (100%)	0	100	100
1	BN	122/122 (100%)	122 (100%)	0	100	100
1	BO	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	BP	122/122 (100%)	122 (100%)	0	100	100
1	BQ	122/122 (100%)	122 (100%)	0	100	100
1	BR	122/122 (100%)	121 (99%)	1 (1%)	81	88
1	BS	122/122 (100%)	122 (100%)	0	100	100
All	All	5490/5490 (100%)	5475 (100%)	15 (0%)	92	95

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AB	47	TYR
1	AE	47	TYR
1	AH	47	TYR
1	AK	47	TYR
1	AN	47	TYR
1	AQ	47	TYR
1	AT	47	TYR
1	AW	47	TYR
1	AZ	47	TYR
1	BC	47	TYR
1	BF	47	TYR
1	BI	47	TYR
1	BL	47	TYR
1	BO	47	TYR
1	BR	47	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

Of 60 ligands modelled in this entry, 60 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	150/150 (100%)	-0.08	2 (1%) 77 84	23, 34, 58, 81	0
1	AB	150/150 (100%)	-0.14	1 (0%) 87 91	23, 33, 57, 86	0
1	AC	150/150 (100%)	-0.17	0 100 100	23, 34, 51, 77	0
1	AD	150/150 (100%)	0.07	2 (1%) 77 84	23, 34, 58, 81	0
1	AE	150/150 (100%)	0.05	3 (2%) 65 73	23, 33, 57, 86	0
1	AF	150/150 (100%)	-0.10	0 100 100	23, 34, 51, 77	0
1	AG	150/150 (100%)	-0.08	2 (1%) 77 84	23, 34, 58, 81	0
1	AH	150/150 (100%)	-0.03	2 (1%) 77 84	23, 33, 57, 86	0
1	AI	150/150 (100%)	-0.01	1 (0%) 87 91	23, 34, 51, 77	0
1	AJ	150/150 (100%)	-0.13	2 (1%) 77 84	23, 34, 58, 81	0
1	AK	150/150 (100%)	-0.05	1 (0%) 87 91	23, 33, 57, 86	0
1	AL	150/150 (100%)	-0.20	2 (1%) 77 84	23, 34, 51, 77	0
1	AM	150/150 (100%)	-0.14	2 (1%) 77 84	23, 34, 58, 81	0
1	AN	150/150 (100%)	-0.22	0 100 100	23, 33, 57, 86	0
1	AO	150/150 (100%)	-0.22	0 100 100	23, 34, 51, 77	0
1	AP	150/150 (100%)	-0.14	1 (0%) 87 91	23, 34, 58, 81	0
1	AQ	150/150 (100%)	-0.09	2 (1%) 77 84	23, 33, 57, 86	0
1	AR	150/150 (100%)	-0.18	0 100 100	23, 34, 51, 77	0
1	AS	150/150 (100%)	-0.04	1 (0%) 87 91	23, 34, 58, 81	0
1	AT	150/150 (100%)	0.01	3 (2%) 65 73	23, 33, 57, 86	0
1	AU	150/150 (100%)	-0.03	1 (0%) 87 91	23, 34, 51, 77	0
1	AV	150/150 (100%)	0.12	7 (4%) 31 37	23, 34, 58, 81	0
1	AW	150/150 (100%)	-0.01	0 100 100	23, 33, 57, 86	0
1	AX	150/150 (100%)	-0.05	2 (1%) 77 84	23, 34, 51, 77	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	150/150 (100%)	-0.11	0 100 100	23, 34, 58, 81	0
1	AZ	150/150 (100%)	-0.19	0 100 100	23, 33, 57, 86	0
1	BA	150/150 (100%)	-0.14	1 (0%) 87 91	23, 34, 51, 77	0
1	BB	150/150 (100%)	-0.02	3 (2%) 65 73	23, 34, 58, 81	0
1	BC	150/150 (100%)	-0.02	0 100 100	23, 33, 57, 86	0
1	BD	150/150 (100%)	-0.04	1 (0%) 87 91	23, 34, 51, 77	0
1	BE	150/150 (100%)	0.08	2 (1%) 77 84	23, 34, 58, 81	0
1	BF	150/150 (100%)	-0.05	3 (2%) 65 73	23, 33, 57, 86	0
1	BG	150/150 (100%)	-0.12	2 (1%) 77 84	23, 34, 51, 77	0
1	BH	150/150 (100%)	0.12	4 (2%) 54 63	23, 34, 58, 81	0
1	BI	150/150 (100%)	0.08	2 (1%) 77 84	23, 33, 57, 86	0
1	BJ	150/150 (100%)	-0.08	0 100 100	23, 34, 51, 77	0
1	BK	150/150 (100%)	-0.01	5 (3%) 46 54	23, 34, 58, 81	0
1	BL	150/150 (100%)	-0.03	2 (1%) 77 84	23, 33, 57, 86	0
1	BM	150/150 (100%)	0.15	3 (2%) 65 73	23, 34, 51, 77	0
1	BN	150/150 (100%)	-0.07	2 (1%) 77 84	23, 34, 58, 81	0
1	BO	150/150 (100%)	-0.03	2 (1%) 77 84	23, 33, 57, 86	0
1	BP	150/150 (100%)	-0.09	3 (2%) 65 73	23, 34, 51, 77	0
1	BQ	150/150 (100%)	-0.13	1 (0%) 87 91	23, 34, 58, 81	0
1	BR	150/150 (100%)	-0.01	2 (1%) 77 84	23, 33, 57, 86	0
1	BS	150/150 (100%)	-0.00	2 (1%) 77 84	23, 34, 51, 77	0
All	All	6750/6750 (100%)	-0.06	77 (1%) 80 86	23, 34, 57, 86	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AV	83	ALA	4.1
1	AE	29	GLU	4.0
1	BH	30	ASN	3.8
1	AD	43	THR	3.7
1	BI	29	GLU	3.5
1	BH	26	GLY	3.4
1	AL	60	LYS	3.3
1	AM	43	THR	3.3
1	AE	79	SER	3.2

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Mol	Chain	Res	Type	RSRZ
1	BE	43	THR	3.2
1	BF	29	GLU	3.2
1	BG	29	GLU	3.0
1	BK	83	ALA	2.9
1	AL	29	GLU	2.9
1	AV	43	THR	2.8
1	BS	30	ASN	2.8
1	AU	29	GLU	2.8
1	BH	27	ILE	2.8
1	BK	29	GLU	2.8
1	BB	43	THR	2.7
1	BG	30	ASN	2.6
1	AE	30	ASN	2.6
1	BM	29	GLU	2.6
1	AV	61	SER	2.6
1	AT	29	GLU	2.6
1	BL	60	LYS	2.6
1	BI	30	ASN	2.6
1	AH	79	SER	2.6
1	BN	30	ASN	2.5
1	AX	29	GLU	2.5
1	AT	62	GLY	2.5
1	AJ	29	GLU	2.5
1	AV	84	PHE	2.4
1	AQ	29	GLU	2.4
1	BE	42	ALA	2.4
1	BK	30	ASN	2.4
1	AV	60	LYS	2.4
1	AD	44	VAL	2.4
1	AT	79	SER	2.3
1	BS	60	LYS	2.3
1	BR	29	GLU	2.3
1	BP	30	ASN	2.3
1	BA	30	ASN	2.3
1	AG	30	ASN	2.3
1	BM	43	THR	2.3
1	BL	84	PHE	2.3
1	AB	29	GLU	2.3
1	BQ	43	THR	2.2
1	BB	60	LYS	2.2
1	BB	42	ALA	2.2
1	BP	29	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	BK	43	THR	2.1
1	AJ	30	ASN	2.1
1	AM	30	ASN	2.1
1	AQ	31	LEU	2.1
1	BD	60	LYS	2.1
1	BH	29	GLU	2.1
1	AG	43	THR	2.1
1	AX	60	LYS	2.1
1	AP	30	ASN	2.1
1	AA	42	ALA	2.1
1	AK	79	SER	2.1
1	AS	44	VAL	2.1
1	BM	60	LYS	2.1
1	AV	29	GLU	2.1
1	BK	79	SER	2.1
1	AV	30	ASN	2.0
1	BF	30	ASN	2.0
1	BN	29	GLU	2.0
1	BO	80	GLY	2.0
1	BF	60	LYS	2.0
1	AA	30	ASN	2.0
1	BR	60	LYS	2.0
1	AH	29	GLU	2.0
1	AI	29	GLU	2.0
1	BO	60	LYS	2.0
1	BP	60	LYS	2.0

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 [\(i\)](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ZN	AH	201	1/1	0.54	0.32	273,273,273,273	0
2	ZN	AE	201	1/1	0.58	0.35	273,273,273,273	0
2	ZN	AN	201	1/1	0.59	0.29	273,273,273,273	0
2	ZN	AW	201	1/1	0.62	0.59	273,273,273,273	0
2	ZN	BM	201	1/1	0.63	0.14	160,160,160,160	0
2	ZN	BF	201	1/1	0.65	0.54	273,273,273,273	0
2	ZN	AT	201	1/1	0.66	0.51	273,273,273,273	0
2	ZN	AZ	201	1/1	0.68	0.34	273,273,273,273	0
2	ZN	AQ	201	1/1	0.69	0.37	273,273,273,273	0
2	ZN	AB	201	1/1	0.69	0.59	273,273,273,273	0
2	ZN	BL	201	1/1	0.72	0.32	273,273,273,273	0
2	ZN	AO	201	1/1	0.72	0.27	160,160,160,160	0
2	ZN	BR	201	1/1	0.72	0.34	273,273,273,273	0
2	ZN	AL	201	1/1	0.76	0.29	160,160,160,160	0
2	ZN	BP	201	1/1	0.77	0.19	160,160,160,160	0
2	ZN	BJ	201	1/1	0.77	0.14	160,160,160,160	0
2	ZN	BG	201	1/1	0.78	0.31	160,160,160,160	0
2	ZN	BO	201	1/1	0.78	0.37	273,273,273,273	0
2	ZN	BS	201	1/1	0.79	0.29	160,160,160,160	0
2	ZN	BA	201	1/1	0.82	0.19	160,160,160,160	0
2	ZN	AK	201	1/1	0.83	0.24	273,273,273,273	0
2	ZN	BK	201	1/1	0.84	0.19	117,117,117,117	0
2	ZN	BQ	201	1/1	0.84	0.22	117,117,117,117	0
2	ZN	BD	201	1/1	0.85	0.23	160,160,160,160	0
2	ZN	AR	201	1/1	0.85	0.33	160,160,160,160	0
2	ZN	AX	201	1/1	0.85	0.31	160,160,160,160	0
2	ZN	BI	201	1/1	0.86	0.29	273,273,273,273	0
2	ZN	AP	201	1/1	0.88	0.22	117,117,117,117	0
2	ZN	AS	201	1/1	0.89	0.12	117,117,117,117	0
2	ZN	BE	201	1/1	0.89	0.19	117,117,117,117	0
2	ZN	BC	201	1/1	0.90	0.42	273,273,273,273	0
2	ZN	AC	201	1/1	0.90	0.24	160,160,160,160	0
2	ZN	AF	201	1/1	0.90	0.38	160,160,160,160	0
2	ZN	AM	202	1/1	0.91	0.13	65,65,65,65	0
2	ZN	AU	201	1/1	0.91	0.32	160,160,160,160	0
2	ZN	BN	201	1/1	0.91	0.18	117,117,117,117	0
2	ZN	AV	201	1/1	0.91	0.22	117,117,117,117	0
2	ZN	BH	201	1/1	0.92	0.19	117,117,117,117	0
2	ZN	AY	201	1/1	0.92	0.14	117,117,117,117	0
2	ZN	AI	201	1/1	0.92	0.32	160,160,160,160	0
2	ZN	BB	201	1/1	0.93	0.27	117,117,117,117	0
2	ZN	AJ	201	1/1	0.93	0.18	117,117,117,117	0
2	ZN	AY	202	1/1	0.93	0.15	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ZN	BK	202	1/1	0.94	0.16	65,65,65,65	0
2	ZN	AA	202	1/1	0.95	0.10	65,65,65,65	0
2	ZN	AA	201	1/1	0.95	0.14	117,117,117,117	0
2	ZN	BN	202	1/1	0.95	0.16	65,65,65,65	0
2	ZN	AV	202	1/1	0.95	0.12	65,65,65,65	0
2	ZN	AG	201	1/1	0.96	0.19	117,117,117,117	0
2	ZN	AJ	202	1/1	0.97	0.15	65,65,65,65	0
2	ZN	BE	202	1/1	0.97	0.16	65,65,65,65	0
2	ZN	AG	202	1/1	0.97	0.13	65,65,65,65	0
2	ZN	BB	202	1/1	0.97	0.13	65,65,65,65	0
2	ZN	AD	202	1/1	0.97	0.11	65,65,65,65	0
2	ZN	AM	201	1/1	0.97	0.19	117,117,117,117	0
2	ZN	AS	202	1/1	0.98	0.14	65,65,65,65	0
2	ZN	AP	202	1/1	0.98	0.10	65,65,65,65	0
2	ZN	BQ	202	1/1	0.98	0.14	65,65,65,65	0
2	ZN	BH	202	1/1	0.98	0.14	65,65,65,65	0
2	ZN	AD	201	1/1	0.98	0.11	117,117,117,117	0

6.5 Other polymers [i](#)

There are no such residues in this entry.