



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 02:52 am GMT

PDB ID : 2WAD
Title : PENICILLIN-BINDING PROTEIN 2B (PBP-2B) FROM STREPTOCOCCUS PNEUMONIAE (STRAIN 5204)
Authors : Contreras-Martel, C.; Dahout-Gonzalez, C.; Dos-Santos-Martins, A.; Kotnik, M.; Dessen, A.
Deposited on : 2009-02-05
Resolution : 2.18 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

<http://wwpdb.org/validation/2016/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)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

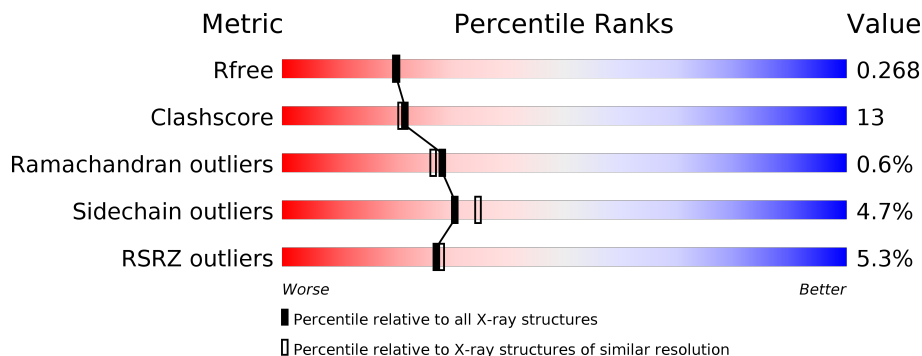
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.18 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}	100719	5526 (2.20-2.16)
Clashscore	112137	6386 (2.20-2.16)
Ramachandran outliers	110173	6282 (2.20-2.16)
Sidechain outliers	110143	6282 (2.20-2.16)
RSRZ outliers	101464	5562 (2.20-2.16)

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. 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	A	680	<div> <div>2%</div> <div> <div></div> <div>71%</div> <div>17%</div> <div>•</div> <div>11%</div> </div> </div>
1	B	680	<div> <div>9%</div> <div> <div></div> <div>69%</div> <div>19%</div> <div>•</div> <div>11%</div> </div> </div>
1	C	680	<div> <div>3%</div> <div> <div></div> <div>69%</div> <div>18%</div> <div>•</div> <div>11%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14408 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 PENICILLIN-BINDING PROTEIN 2B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	606	Total	C	N	O	S	0	2	0
			4622	2907	759	946	10			
1	B	605	Total	C	N	O	S	0	0	0
			4596	2893	755	938	10			
1	C	607	Total	C	N	O	S	0	0	0
			4611	2901	758	942	10			

There are 171 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	54	VAL	ILE	CONFLICT SEE REMARK 9	UNP P0A3M6
A	56	THR	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
A	96	ILE	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
A	130	THR	ILE	CONFLICT SEE REMARK 9	UNP P0A3M6
A	161	PRO	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	225	ILE	VAL	CONFLICT SEE REMARK 9	UNP P0A3M6
A	251	SER	ALA	CONFLICT SEE REMARK 9	UNP P0A3M6
A	275	VAL	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
A	281	PRO	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
A	290	HIS	TYR	CONFLICT SEE REMARK 9	UNP P0A3M6
A	292	ASP	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	297	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
A	298	ASN	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
A	306	LYS	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	333	GLY	GLU	CONFLICT SEE REMARK 9	UNP P0A3M6
A	351	GLN	LYS	CONFLICT SEE REMARK 9	UNP P0A3M6
A	361	LEU	ILE	CONFLICT SEE REMARK 9	UNP P0A3M6
A	412	PRO	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
A	422	TYR	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	426	LYS	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
A	427	LEU	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	438	GLU	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	446	ALA	THR	CONFLICT SEE REMARK 9	UNP P0A3M6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	448	VAL	MET	CONFLICT SEE REMARK 9	UNP P0A3M6
A	455	ILE	LEU	CONFLICT SEE REMARK 9	UNP P0A3M6
A	476	GLY	GLU	CONFLICT SEE REMARK 9	UNP P0A3M6
A	489	SER	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
A	502	LEU	PHE	CONFLICT SEE REMARK 9	UNP P0A3M6
A	508	ASN	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
A	512	PHE	TYR	CONFLICT SEE REMARK 9	UNP P0A3M6
A	542	LEU	VAL	CONFLICT SEE REMARK 9	UNP P0A3M6
A	545	HIS	ARG	CONFLICT SEE REMARK 9	UNP P0A3M6
A	552	ASP	GLY	CONFLICT SEE REMARK 9	UNP P0A3M6
A	561	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
A	565	ALA	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	566	ILE	LEU	CONFLICT SEE REMARK 9	UNP P0A3M6
A	567	ASP	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	568	THR	PRO	CONFLICT SEE REMARK 9	UNP P0A3M6
A	569	LYS	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
A	571	ILE	MET	CONFLICT SEE REMARK 9	UNP P0A3M6
A	578	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
A	582	ALA	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
A	592	SER	ALA	CONFLICT SEE REMARK 9	UNP P0A3M6
A	597	PRO	GLY	CONFLICT SEE REMARK 9	UNP P0A3M6
A	606	ASP	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	609	THR	LEU	CONFLICT SEE REMARK 9	UNP P0A3M6
A	619	GLY	ALA	CONFLICT SEE REMARK 9	UNP P0A3M6
A	625	GLY	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
A	628	GLU	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	640	THR	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
A	641	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
A	659	LYS	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	660	ASN	GLY	CONFLICT SEE REMARK 9	UNP P0A3M6
A	664	ALA	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
A	674	ASN	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
A	675	GLN	LYS	CONFLICT SEE REMARK 9	UNP P0A3M6
A	676	HIS	TYR	CONFLICT SEE REMARK 9	UNP P0A3M6
B	54	VAL	ILE	CONFLICT SEE REMARK 9	UNP P0A3M6
B	56	THR	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
B	96	ILE	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
B	130	THR	ILE	CONFLICT SEE REMARK 9	UNP P0A3M6
B	161	PRO	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	225	ILE	VAL	CONFLICT SEE REMARK 9	UNP P0A3M6
B	251	SER	ALA	CONFLICT SEE REMARK 9	UNP P0A3M6
B	275	VAL	THR	CONFLICT SEE REMARK 9	UNP P0A3M6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	281	PRO	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
B	290	HIS	TYR	CONFLICT SEE REMARK 9	UNP P0A3M6
B	292	ASP	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	297	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
B	298	ASN	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
B	306	LYS	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	333	GLY	GLU	CONFLICT SEE REMARK 9	UNP P0A3M6
B	351	GLN	LYS	CONFLICT SEE REMARK 9	UNP P0A3M6
B	361	LEU	ILE	CONFLICT SEE REMARK 9	UNP P0A3M6
B	412	PRO	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
B	422	TYR	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	426	LYS	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
B	427	LEU	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	438	GLU	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	446	ALA	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
B	448	VAL	MET	CONFLICT SEE REMARK 9	UNP P0A3M6
B	455	ILE	LEU	CONFLICT SEE REMARK 9	UNP P0A3M6
B	476	GLY	GLU	CONFLICT SEE REMARK 9	UNP P0A3M6
B	489	SER	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
B	502	LEU	PHE	CONFLICT SEE REMARK 9	UNP P0A3M6
B	508	ASN	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
B	512	PHE	TYR	CONFLICT SEE REMARK 9	UNP P0A3M6
B	542	LEU	VAL	CONFLICT SEE REMARK 9	UNP P0A3M6
B	545	HIS	ARG	CONFLICT SEE REMARK 9	UNP P0A3M6
B	552	ASP	GLY	CONFLICT SEE REMARK 9	UNP P0A3M6
B	561	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
B	565	ALA	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	566	ILE	LEU	CONFLICT SEE REMARK 9	UNP P0A3M6
B	567	ASP	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	568	THR	PRO	CONFLICT SEE REMARK 9	UNP P0A3M6
B	569	LYS	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
B	571	ILE	MET	CONFLICT SEE REMARK 9	UNP P0A3M6
B	578	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
B	582	ALA	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
B	592	SER	ALA	CONFLICT SEE REMARK 9	UNP P0A3M6
B	597	PRO	GLY	CONFLICT SEE REMARK 9	UNP P0A3M6
B	606	ASP	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	609	THR	LEU	CONFLICT SEE REMARK 9	UNP P0A3M6
B	619	GLY	ALA	CONFLICT SEE REMARK 9	UNP P0A3M6
B	625	GLY	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
B	628	GLU	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	640	THR	SER	CONFLICT SEE REMARK 9	UNP P0A3M6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	641	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
B	659	LYS	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	660	ASN	GLY	CONFLICT SEE REMARK 9	UNP P0A3M6
B	664	ALA	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
B	674	ASN	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
B	675	GLN	LYS	CONFLICT SEE REMARK 9	UNP P0A3M6
B	676	HIS	TYR	CONFLICT SEE REMARK 9	UNP P0A3M6
C	54	VAL	ILE	CONFLICT SEE REMARK 9	UNP P0A3M6
C	56	THR	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
C	96	ILE	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
C	130	THR	ILE	CONFLICT SEE REMARK 9	UNP P0A3M6
C	161	PRO	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	225	ILE	VAL	CONFLICT SEE REMARK 9	UNP P0A3M6
C	251	SER	ALA	CONFLICT SEE REMARK 9	UNP P0A3M6
C	275	VAL	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
C	281	PRO	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
C	290	HIS	TYR	CONFLICT SEE REMARK 9	UNP P0A3M6
C	292	ASP	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	297	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
C	298	ASN	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
C	306	LYS	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	333	GLY	GLU	CONFLICT SEE REMARK 9	UNP P0A3M6
C	351	GLN	LYS	CONFLICT SEE REMARK 9	UNP P0A3M6
C	361	LEU	ILE	CONFLICT SEE REMARK 9	UNP P0A3M6
C	412	PRO	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
C	422	TYR	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	426	LYS	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
C	427	LEU	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	438	GLU	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	446	ALA	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
C	448	VAL	MET	CONFLICT SEE REMARK 9	UNP P0A3M6
C	455	ILE	LEU	CONFLICT SEE REMARK 9	UNP P0A3M6
C	476	GLY	GLU	CONFLICT SEE REMARK 9	UNP P0A3M6
C	489	SER	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
C	502	LEU	PHE	CONFLICT SEE REMARK 9	UNP P0A3M6
C	508	ASN	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
C	512	PHE	TYR	CONFLICT SEE REMARK 9	UNP P0A3M6
C	542	LEU	VAL	CONFLICT SEE REMARK 9	UNP P0A3M6
C	545	HIS	ARG	CONFLICT SEE REMARK 9	UNP P0A3M6
C	552	ASP	GLY	CONFLICT SEE REMARK 9	UNP P0A3M6
C	561	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
C	565	ALA	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	566	ILE	LEU	CONFLICT SEE REMARK 9	UNP P0A3M6
C	567	ASP	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	568	THR	PRO	CONFLICT SEE REMARK 9	UNP P0A3M6
C	569	LYS	THR	CONFLICT SEE REMARK 9	UNP P0A3M6
C	571	ILE	MET	CONFLICT SEE REMARK 9	UNP P0A3M6
C	578	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
C	582	ALA	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
C	592	SER	ALA	CONFLICT SEE REMARK 9	UNP P0A3M6
C	597	PRO	GLY	CONFLICT SEE REMARK 9	UNP P0A3M6
C	606	ASP	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	609	THR	LEU	CONFLICT SEE REMARK 9	UNP P0A3M6
C	619	GLY	ALA	CONFLICT SEE REMARK 9	UNP P0A3M6
C	625	GLY	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
C	628	GLU	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	640	THR	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
C	641	GLU	ASP	CONFLICT SEE REMARK 9	UNP P0A3M6
C	659	LYS	ASN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	660	ASN	GLY	CONFLICT SEE REMARK 9	UNP P0A3M6
C	664	ALA	SER	CONFLICT SEE REMARK 9	UNP P0A3M6
C	674	ASN	GLN	CONFLICT SEE REMARK 9	UNP P0A3M6
C	675	GLN	LYS	CONFLICT SEE REMARK 9	UNP P0A3M6
C	676	HIS	TYR	CONFLICT SEE REMARK 9	UNP P0A3M6

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	3	Total Zn 3 3	0	0
2	A	3	Total Zn 3 3	0	0
2	C	3	Total Zn 3 3	0	0

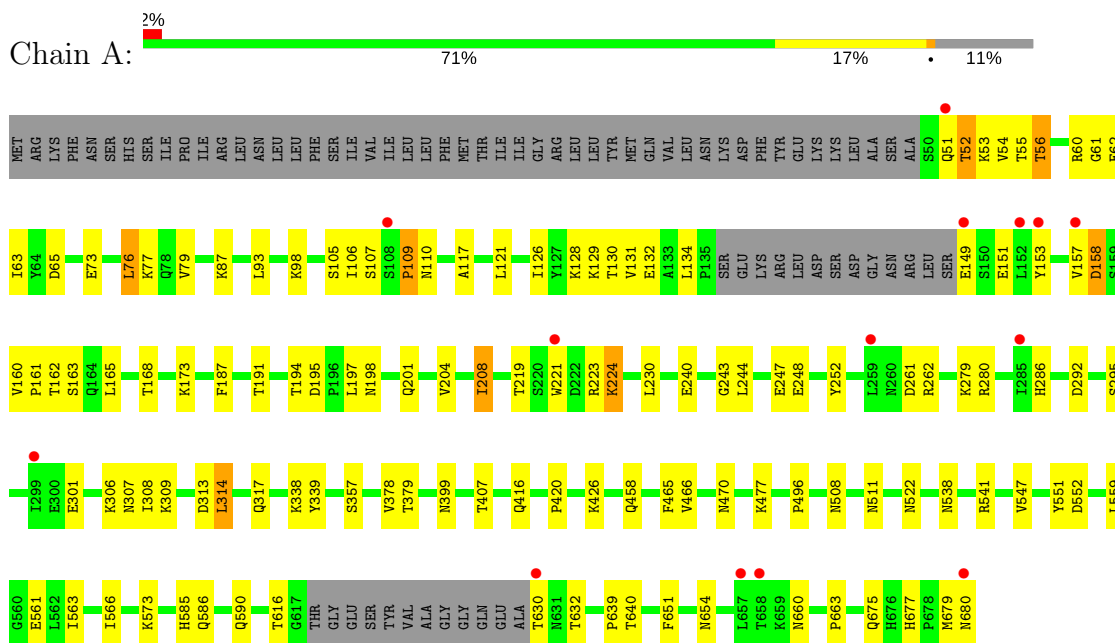
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	255	Total O 255 255	0	0
3	B	202	Total O 202 202	0	0
3	C	113	Total O 113 113	0	0

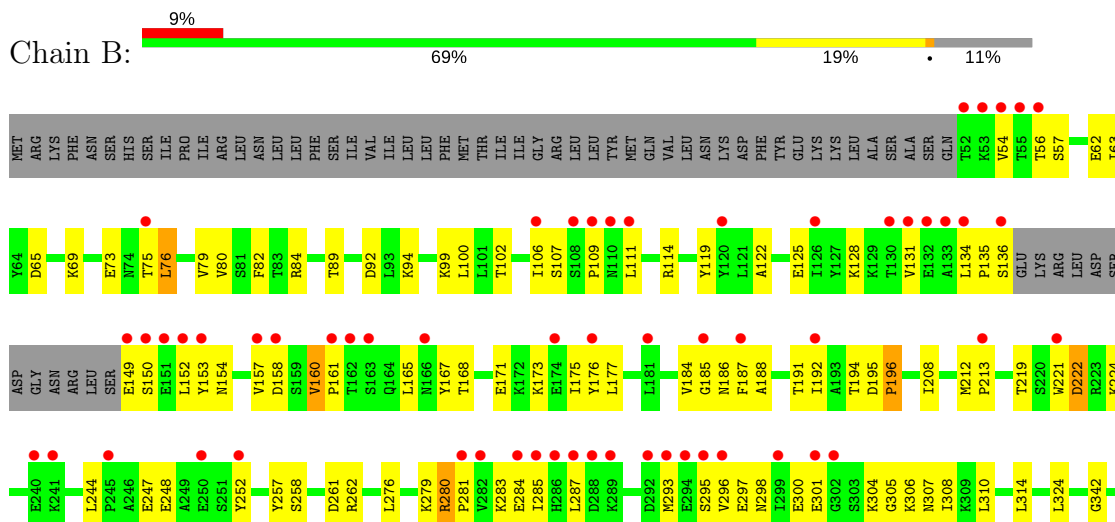
3 Residue-property plots

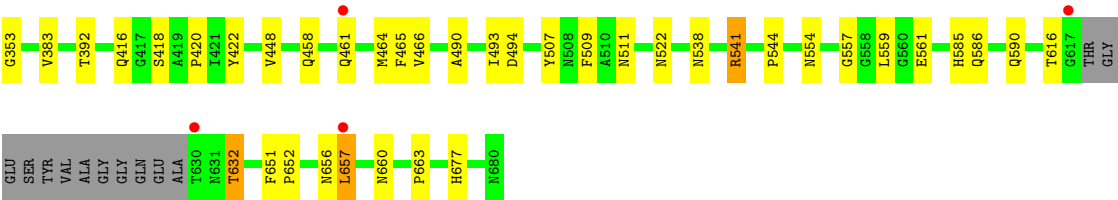
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: PENICILLIN-BINDING PROTEIN 2B

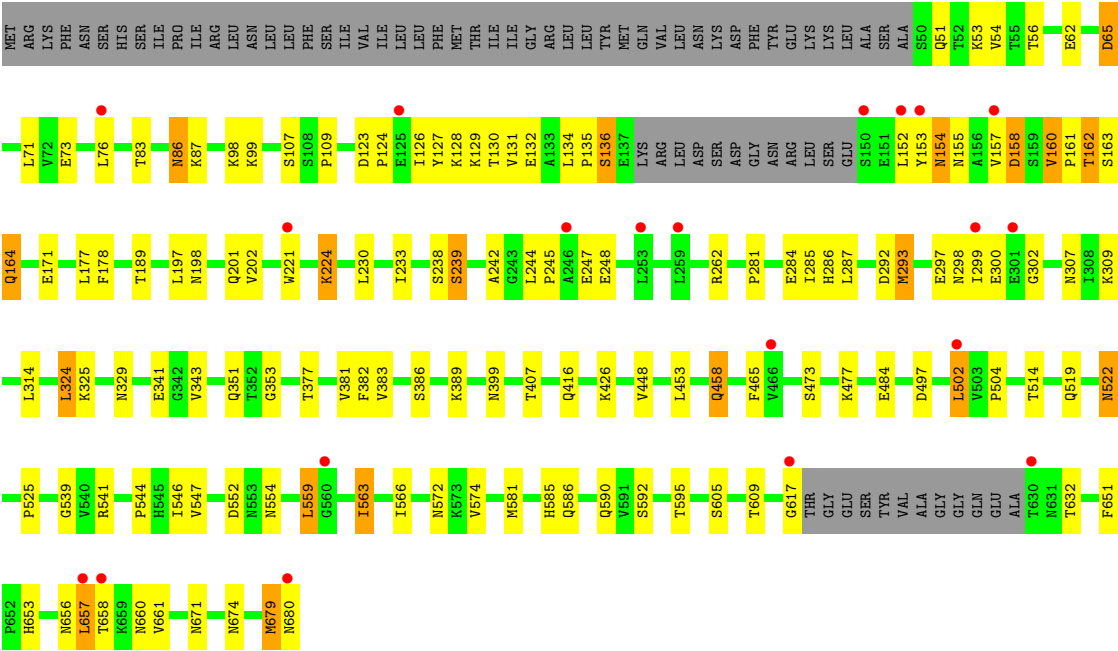


• Molecule 1: PENICILLIN-BINDING PROTEIN 2B





● Molecule 1: PENICILLIN-BINDING PROTEIN 2B



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	128.79Å 128.79Å 123.14Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.50 – 2.18 44.50 – 2.18	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.50-2.18) 98.3 (44.50-2.18)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.5.0070	Depositor
R, R_{free}	0.211 , 0.261 0.219 , 0.268	Depositor DCC
R_{free} test set	5889 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	36.6	Xtriage
Anisotropy	0.208	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 51.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l 0.127 for h,-h-k,-l 0.030 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14408	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.08% 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	A	0.42	0/4706	0.70	1/6394 (0.0%)
1	B	0.39	0/4680	0.68	2/6359 (0.0%)
1	C	0.33	0/4695	0.63	0/6379
All	All	0.38	0/14081	0.67	3/19132 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	541	ARG	NE-CZ-NH2	-11.72	114.44	120.30
1	B	541	ARG	NE-CZ-NH1	8.93	124.77	120.30
1	A	541	ARG	NE-CZ-NH2	-5.79	117.40	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	A	4622	0	4533	97	0
1	B	4596	0	4517	133	0
1	C	4611	0	4530	142	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	3	0	0	0	0
3	A	255	0	0	19	0
3	B	202	0	0	19	0
3	C	113	0	0	18	0
All	All	14408	0	13580	367	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 13.

All (367) 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:C:131:VAL:HG23	1:C:153:TYR:CE2	1.68	1.27
1:C:158:ASP:O	1:C:161:PRO:CD	1.90	1.17
1:A:110:ASN:HB3	3:A:2015:HOH:O	1.45	1.16
1:B:283:LYS:HD3	1:B:296:VAL:CG1	1.76	1.15
1:C:128:LYS:O	1:C:132:GLU:HG2	1.43	1.14
1:B:56:THR:O	1:B:281:PRO:HD2	1.45	1.12
1:B:135:PRO:HA	3:B:2012:HOH:O	1.48	1.11
1:A:126:ILE:O	1:A:130:THR:HG23	1.47	1.11
1:C:158:ASP:O	1:C:161:PRO:HD2	1.47	1.10
1:B:106:ILE:O	1:B:173:LYS:HE2	1.51	1.10
1:C:99:LYS:HB3	3:C:2012:HOH:O	1.54	1.06
1:B:283:LYS:HD3	1:B:296:VAL:HG11	1.10	1.05
1:C:131:VAL:CG2	1:C:153:TYR:CE2	2.42	1.03
1:A:261:ASP:OD2	1:A:280:ARG:NH2	1.92	1.03
1:C:99:LYS:HE3	3:C:2012:HOH:O	1.57	1.02
1:B:657:LEU:H	1:B:657:LEU:HD12	1.27	1.00
1:C:632:THR:HG21	3:C:2110:HOH:O	1.60	0.99
1:C:131:VAL:HG23	1:C:153:TYR:CZ	1.99	0.98
1:C:679:MET:O	1:C:680:ASN:HB2	1.65	0.96
1:C:221:TRP:HB2	3:C:2034:HOH:O	1.64	0.95
1:B:416:GLN:HE22	1:C:407:THR:H	0.96	0.94
1:B:285:ILE:HG13	1:B:296:VAL:HG13	1.49	0.94
1:C:586:GLN:HE21	1:C:590:GLN:HE21	1.16	0.93
1:C:62:GLU:H	1:C:307:ASN:HD22	1.05	0.93
1:B:149:GLU:HG2	1:B:150:SER:H	1.33	0.93
1:A:134:LEU:CD2	1:A:160:VAL:HG21	1.98	0.93
1:A:586:GLN:HE21	1:A:590:GLN:HE21	1.06	0.92
1:C:107:SER:O	1:C:109:PRO:HD3	1.69	0.92
1:B:586:GLN:HE21	1:B:590:GLN:HE21	1.19	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:420:PRO:HB2	3:B:2095:HOH:O	1.69	0.91
1:C:56:THR:HG23	1:C:281:PRO:HG2	1.52	0.90
1:B:125:GLU:HG3	3:B:2010:HOH:O	1.71	0.89
1:C:62:GLU:H	1:C:307:ASN:ND2	1.70	0.89
1:C:134:LEU:HD12	1:C:153:TYR:CE1	2.08	0.88
1:C:158:ASP:O	1:C:161:PRO:HD3	1.72	0.88
1:C:134:LEU:CD1	1:C:153:TYR:CE1	2.57	0.88
1:C:154:ASN:O	1:C:157:VAL:HG22	1.74	0.87
1:A:62:GLU:H	1:A:307:ASN:HD22	1.23	0.86
1:C:131:VAL:CG2	1:C:153:TYR:HE2	1.85	0.86
1:C:164:GLN:O	1:C:164:GLN:HG3	1.75	0.85
1:A:407:THR:H	1:C:416:GLN:HE22	1.20	0.85
1:A:547:VAL:HG12	1:A:566:ILE:HD12	1.59	0.85
1:C:155:ASN:HA	1:C:158:ASP:HB2	1.59	0.85
1:B:461:GLN:NE2	1:B:464:MET:HB3	1.92	0.84
1:B:106:ILE:O	1:B:173:LYS:CE	2.24	0.84
1:C:134:LEU:CD1	1:C:153:TYR:HE1	1.89	0.84
1:A:132:GLU:HB3	3:A:2020:HOH:O	1.77	0.84
1:B:284:GLU:O	1:B:297:GLU:HG2	1.78	0.83
1:B:416:GLN:NE2	1:C:407:THR:H	1.75	0.83
1:C:131:VAL:HG23	1:C:153:TYR:HE2	1.38	0.83
1:B:107:SER:O	1:B:109:PRO:HD3	1.78	0.83
1:B:248:GLU:HB3	1:B:252:TYR:CE2	2.14	0.83
1:A:134:LEU:HD21	1:A:160:VAL:HG21	1.60	0.82
1:B:285:ILE:HG21	1:B:293:MET:SD	2.20	0.82
1:B:221:TRP:O	1:B:262:ARG:NH1	2.13	0.82
1:C:136:SER:HA	3:C:2016:HOH:O	1.78	0.82
1:A:552:ASP:HB2	1:A:563:ILE:HD11	1.62	0.81
1:A:106:ILE:O	1:A:173:LYS:HE2	1.80	0.81
1:C:632:THR:HB	1:C:660:ASN:OD1	1.80	0.81
1:C:134:LEU:HD12	1:C:153:TYR:CZ	2.17	0.80
1:B:416:GLN:HE22	1:C:407:THR:N	1.79	0.80
1:B:422:TYR:CE2	3:B:2095:HOH:O	2.33	0.80
1:A:107:SER:O	1:A:109:PRO:HD3	1.81	0.79
1:B:656:ASN:HB3	3:B:2191:HOH:O	1.83	0.79
1:C:484:GLU:HB3	1:C:574:VAL:HG12	1.64	0.79
1:B:283:LYS:CD	1:B:296:VAL:HG11	2.04	0.78
1:A:158:ASP:O	1:A:161:PRO:HD2	1.83	0.78
1:C:157:VAL:O	1:C:160:VAL:HG12	1.84	0.77
1:C:127:TYR:O	1:C:131:VAL:HG12	1.83	0.77
1:C:128:LYS:O	1:C:131:VAL:HG13	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:GLU:H	1:B:307:ASN:HD22	1.33	0.76
1:A:128:LYS:O	1:A:132:GLU:HG2	1.87	0.74
1:C:134:LEU:HD12	1:C:153:TYR:OH	1.86	0.74
1:C:134:LEU:HD13	1:C:153:TYR:HE1	1.52	0.73
1:B:616:THR:HG22	1:B:663:PRO:HG3	1.68	0.73
1:B:422:TYR:HE2	3:B:2095:HOH:O	1.70	0.73
1:A:286:HIS:HB2	1:A:295:SER:HB3	1.71	0.73
1:B:79:VAL:HG12	1:B:80:VAL:N	2.03	0.72
1:C:129:LYS:HA	1:C:132:GLU:HG3	1.70	0.72
1:A:313:ASP:HB2	3:A:2076:HOH:O	1.88	0.72
1:A:149:GLU:N	1:A:153:TYR:HH	1.86	0.72
1:A:52:THR:HG21	1:A:187:PHE:CE1	2.25	0.72
1:B:416:GLN:HG3	3:B:2092:HOH:O	1.89	0.72
1:A:420:PRO:HG2	3:A:2119:HOH:O	1.90	0.71
1:A:158:ASP:O	1:A:161:PRO:CD	2.38	0.71
1:C:671:ASN:HB3	3:C:2111:HOH:O	1.90	0.71
1:B:195:ASP:O	1:B:196:PRO:O	2.09	0.70
1:B:257:TYR:HD1	1:B:280:ARG:HH22	1.37	0.70
1:B:279:LYS:NZ	1:B:300:GLU:HB3	2.07	0.70
1:C:399:ASN:OD1	1:C:477:LYS:HD3	1.91	0.70
1:C:386:SER:HB2	1:C:617:GLY:HA2	1.74	0.69
1:C:54:VAL:HG22	1:C:285:ILE:CD1	2.22	0.68
1:A:262:ARG:HD2	3:A:2059:HOH:O	1.94	0.68
1:C:581:MET:O	1:C:585:HIS:HD2	1.77	0.68
1:B:248:GLU:HB3	1:B:252:TYR:HE2	1.58	0.68
1:B:632:THR:HG21	3:B:2190:HOH:O	1.94	0.68
1:C:53:LYS:HB3	1:C:284:GLU:HG2	1.76	0.67
1:B:89:THR:HG23	1:B:92:ASP:H	1.59	0.67
1:B:279:LYS:HZ1	1:B:300:GLU:HB3	1.58	0.67
1:A:248:GLU:CB	1:A:252:TYR:HE2	2.07	0.67
1:C:416:GLN:HG2	1:C:465:PHE:CE1	2.29	0.67
1:B:632:THR:HB	1:B:660:ASN:OD1	1.95	0.67
1:C:87:LYS:HD3	1:C:292:ASP:OD1	1.94	0.67
1:B:248:GLU:CB	1:B:252:TYR:HE2	2.07	0.66
1:C:245:PRO:HA	3:C:2033:HOH:O	1.95	0.66
1:A:197:LEU:HD23	1:A:201:GLN:NE2	2.11	0.66
1:B:656:ASN:CG	3:B:2191:HOH:O	2.34	0.66
1:B:656:ASN:CB	3:B:2191:HOH:O	2.42	0.65
1:A:149:GLU:N	1:A:153:TYR:CZ	2.64	0.65
1:B:262:ARG:HD2	3:B:2032:HOH:O	1.96	0.65
1:B:89:THR:HG22	1:B:92:ASP:CG	2.17	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:420:PRO:CB	3:B:2095:HOH:O	2.36	0.65
1:B:306:LYS:HE2	3:B:2041:HOH:O	1.96	0.65
1:C:128:LYS:O	1:C:132:GLU:CG	2.35	0.65
1:B:79:VAL:CG1	1:B:80:VAL:N	2.59	0.65
1:B:63:ILE:HD12	1:B:308:ILE:HD11	1.79	0.65
1:C:83:THR:HG1	1:C:189:THR:HG1	1.43	0.64
1:A:632:THR:HG21	3:A:2238:HOH:O	1.96	0.64
1:C:158:ASP:C	1:C:161:PRO:HD3	2.16	0.64
1:C:381:VAL:HG21	1:C:502:LEU:HG	1.78	0.64
1:A:248:GLU:HB2	1:A:252:TYR:HE2	1.63	0.64
1:A:675:GLN:HG3	3:A:2248:HOH:O	1.97	0.64
1:A:87:LYS:HD3	1:A:292:ASP:OD1	1.98	0.63
1:A:62:GLU:H	1:A:307:ASN:ND2	1.95	0.63
1:B:154:ASN:O	1:B:158:ASP:HB2	1.98	0.63
1:B:244:LEU:HD11	1:B:261:ASP:HB2	1.81	0.62
1:B:131:VAL:HB	1:B:157:VAL:HG11	1.80	0.62
1:A:130:THR:OG1	1:A:157:VAL:HG13	2.00	0.62
1:C:129:LYS:HA	1:C:132:GLU:CG	2.29	0.62
1:B:149:GLU:HG2	1:B:150:SER:N	2.10	0.62
1:C:62:GLU:N	1:C:307:ASN:HD22	1.88	0.62
1:A:244:LEU:HD13	1:A:252:TYR:HB2	1.82	0.62
1:C:154:ASN:O	1:C:157:VAL:CG2	2.44	0.62
1:A:52:THR:HG21	1:A:187:PHE:HE1	1.62	0.62
1:B:461:GLN:HE21	1:B:464:MET:HB3	1.63	0.62
1:B:257:TYR:CD1	1:B:280:ARG:NH2	2.68	0.61
1:B:461:GLN:NE2	1:B:464:MET:CB	2.63	0.61
1:A:221:TRP:HB2	1:A:262:ARG:HH22	1.66	0.61
1:B:57:SER:OG	1:B:261:ASP:OD1	2.19	0.61
1:C:547:VAL:HG12	1:C:566:ILE:HD12	1.82	0.61
1:B:75:THR:HG23	1:B:222:ASP:CB	2.30	0.60
1:C:299:ILE:HG22	1:C:300:GLU:N	2.15	0.60
1:B:657:LEU:HD12	1:B:657:LEU:N	2.08	0.60
1:B:538:ASN:OD1	1:B:585:HIS:HE1	1.85	0.59
1:A:157:VAL:O	1:A:161:PRO:HD3	2.01	0.59
1:A:547:VAL:HG12	1:A:566:ILE:CD1	2.30	0.58
1:C:353:GLY:O	1:C:544:PRO:HA	2.03	0.58
1:A:240:GLU:N	1:A:262:ARG:HD3	2.19	0.58
1:B:75:THR:HG23	1:B:222:ASP:HB3	1.85	0.58
1:C:473:SER:O	1:C:477:LYS:HG3	2.04	0.58
1:B:656:ASN:ND2	3:B:2191:HOH:O	2.36	0.58
1:A:130:THR:OG1	1:A:157:VAL:CG1	2.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:281:PRO:HD3	1:C:302:GLY:HA3	1.84	0.57
1:C:128:LYS:HA	1:C:131:VAL:CG1	2.34	0.57
1:A:561:GLU:HG3	3:A:2198:HOH:O	2.04	0.57
1:C:128:LYS:O	1:C:131:VAL:CG1	2.52	0.57
1:B:100:LEU:HD23	1:B:177:LEU:HD22	1.86	0.57
1:A:470:ASN:HB2	3:A:2153:HOH:O	2.06	0.56
1:B:76:LEU:HD23	1:B:219:THR:HB	1.87	0.56
1:B:677:HIS:CD2	1:B:677:HIS:O	2.58	0.56
1:C:126:ILE:O	1:C:130:THR:HG23	2.03	0.56
1:A:76:LEU:HD23	1:A:219:THR:HB	1.86	0.56
1:A:680:ASN:HA	3:A:2252:HOH:O	2.05	0.56
1:A:616:THR:HG22	1:A:663:PRO:HG3	1.88	0.56
1:C:197:LEU:HA	1:C:201:GLN:NE2	2.20	0.56
1:B:420:PRO:CG	3:B:2095:HOH:O	2.54	0.56
1:A:61:GLY:HA3	1:A:306:LYS:O	2.06	0.56
1:B:79:VAL:HG11	1:B:191:THR:HG23	1.88	0.56
1:C:484:GLU:CB	1:C:574:VAL:HG12	2.35	0.56
1:B:157:VAL:O	1:B:161:PRO:HD3	2.06	0.55
1:B:416:GLN:HG2	1:B:465:PHE:CE1	2.41	0.55
1:A:204:VAL:O	1:A:208:ILE:HD13	2.07	0.55
1:C:632:THR:CG2	3:C:2110:HOH:O	2.36	0.55
1:B:65:ASP:OD1	1:B:314:LEU:HB2	2.06	0.55
1:A:160:VAL:N	1:A:161:PRO:CD	2.70	0.55
1:A:160:VAL:N	1:A:161:PRO:HD3	2.22	0.54
1:C:547:VAL:HG12	1:C:566:ILE:CD1	2.38	0.54
1:C:453:LEU:HG	1:C:458:GLN:HB3	1.89	0.54
1:B:261:ASP:OD2	1:B:280:ARG:NH1	2.41	0.54
1:B:56:THR:HG22	1:B:281:PRO:HB2	1.89	0.54
1:C:157:VAL:O	1:C:161:PRO:HD3	2.08	0.54
1:A:632:THR:HG23	1:A:654:ASN:HB3	1.88	0.54
1:B:65:ASP:HB2	1:B:69:LYS:HB2	1.90	0.54
1:A:679:MET:O	1:A:680:ASN:HB2	2.08	0.53
1:C:341:GLU:OE1	1:C:653:HIS:HD2	1.91	0.53
1:C:56:THR:O	1:C:281:PRO:HD2	2.08	0.53
1:B:56:THR:CG2	1:B:281:PRO:HB2	2.39	0.53
1:C:221:TRP:CB	3:C:2034:HOH:O	2.39	0.53
1:C:514:THR:HB	1:C:519:GLN:HB2	1.91	0.53
1:C:86:ASN:N	1:C:86:ASN:OD1	2.40	0.53
1:A:87:LYS:CD	1:A:292:ASP:OD1	2.57	0.53
1:C:131:VAL:HG21	1:C:153:TYR:CE2	2.41	0.53
1:C:389:LYS:HG2	1:C:448:VAL:HG11	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:586:GLN:HE21	1:A:590:GLN:NE2	1.91	0.53
1:C:325:LYS:HE2	1:C:329:ASN:HD21	1.74	0.52
1:B:62:GLU:H	1:B:307:ASN:ND2	2.02	0.52
1:B:89:THR:CG2	1:B:92:ASP:H	2.22	0.52
1:C:54:VAL:CG2	1:C:285:ILE:HD11	2.39	0.52
1:C:299:ILE:HG22	1:C:300:GLU:HG3	1.91	0.52
1:A:128:LYS:O	1:A:131:VAL:HG12	2.10	0.52
1:B:466:VAL:HG21	1:B:509:PHE:CE1	2.44	0.52
1:A:248:GLU:HB3	1:A:252:TYR:HE2	1.74	0.52
1:A:56:THR:O	1:A:280:ARG:HB3	2.10	0.52
1:B:149:GLU:O	1:B:153:TYR:CG	2.62	0.52
1:B:160:VAL:N	1:B:161:PRO:CD	2.73	0.52
1:C:541:ARG:NH1	1:C:572:ASN:OD1	2.41	0.52
1:A:63:ILE:HD12	1:A:308:ILE:HD11	1.92	0.52
1:C:154:ASN:C	1:C:157:VAL:HG22	2.30	0.52
1:A:248:GLU:HB3	1:A:252:TYR:CE2	2.45	0.52
1:B:283:LYS:HD3	1:B:296:VAL:HG12	1.79	0.52
1:C:131:VAL:HG23	1:C:153:TYR:OH	2.10	0.51
1:B:276:LEU:O	1:B:305:GLY:HA3	2.10	0.51
1:B:657:LEU:H	1:B:657:LEU:CD1	2.08	0.51
1:B:168:THR:OG1	1:B:171:GLU:HB2	2.10	0.51
1:B:285:ILE:CG1	1:B:296:VAL:HG13	2.31	0.51
1:A:632:THR:CG2	3:A:2238:HOH:O	2.58	0.51
1:A:458:GLN:OE1	1:A:466:VAL:HG13	2.11	0.51
1:B:195:ASP:O	1:B:196:PRO:C	2.47	0.51
1:B:56:THR:O	1:B:281:PRO:CD	2.38	0.51
1:C:546:ILE:HG22	1:C:546:ILE:O	2.11	0.51
1:B:106:ILE:O	1:B:173:LYS:NZ	2.43	0.51
1:B:304:LYS:NZ	1:B:557:GLY:O	2.36	0.51
1:B:285:ILE:H	1:B:285:ILE:HD12	1.74	0.51
1:B:418:SER:HA	3:B:2093:HOH:O	2.10	0.51
1:B:677:HIS:HD2	1:B:677:HIS:O	1.94	0.51
1:B:149:GLU:O	1:B:153:TYR:CD2	2.65	0.50
1:C:554:ASN:OD1	1:C:554:ASN:C	2.50	0.50
1:B:466:VAL:HG21	1:B:509:PHE:CZ	2.47	0.50
1:C:51:GLN:HG2	1:C:286:HIS:ND1	2.26	0.50
1:C:502:LEU:HB2	1:C:522:ASN:HB2	1.92	0.50
1:A:73:GLU:HB3	1:A:224:LYS:HG2	1.93	0.50
1:A:547:VAL:CG1	1:A:566:ILE:CD1	2.89	0.50
1:A:117:ALA:O	1:A:121:LEU:HG	2.12	0.50
1:A:198:ASN:C	1:A:198:ASN:OD1	2.50	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:TYR:HA	1:B:280:ARG:HH12	1.76	0.49
1:B:149:GLU:HB3	1:B:152:LEU:HB2	1.94	0.49
1:A:677:HIS:CD2	1:A:677:HIS:O	2.65	0.49
1:B:89:THR:O	1:B:92:ASP:HB2	2.12	0.49
1:A:221:TRP:O	1:A:262:ARG:NH1	2.45	0.49
1:A:51:GLN:HG2	3:A:2003:HOH:O	2.12	0.49
1:B:538:ASN:OD1	1:B:585:HIS:CE1	2.66	0.49
1:C:239:SER:HB2	1:C:242:ALA:H	1.77	0.49
1:C:54:VAL:HG22	1:C:285:ILE:HD13	1.95	0.49
1:C:552:ASP:HB2	1:C:563:ILE:HD11	1.95	0.49
1:A:230:LEU:HD12	1:A:314:LEU:CD1	2.42	0.49
1:A:573:LYS:NZ	3:A:2207:HOH:O	2.45	0.49
1:B:493:ILE:HG13	1:B:494:ASP:N	2.27	0.49
1:C:65:ASP:OD1	1:C:314:LEU:HB2	2.13	0.49
1:C:99:LYS:CE	3:C:2012:HOH:O	2.36	0.49
1:C:324:LEU:HG	1:C:343:VAL:HG13	1.95	0.48
1:B:82:PHE:HB3	1:B:192:ILE:HD11	1.96	0.48
1:C:54:VAL:HG22	1:C:285:ILE:HD11	1.93	0.48
1:B:160:VAL:N	1:B:161:PRO:HD3	2.27	0.48
1:C:153:TYR:O	1:C:153:TYR:CD1	2.66	0.48
1:C:54:VAL:CG2	1:C:285:ILE:CD1	2.91	0.48
1:B:63:ILE:HD12	1:B:308:ILE:CD1	2.44	0.48
1:B:94:LYS:HE3	1:B:122:ALA:HB3	1.96	0.48
1:C:285:ILE:N	1:C:285:ILE:HD12	2.29	0.47
1:B:134:LEU:CD1	1:B:157:VAL:HG12	2.44	0.47
1:B:285:ILE:CG2	1:B:293:MET:HB2	2.44	0.47
1:B:111:LEU:HD21	1:B:176:TYR:HA	1.97	0.47
1:C:502:LEU:O	1:C:504:PRO:HD3	2.15	0.47
1:C:157:VAL:HG23	1:C:158:ASP:N	2.29	0.47
1:C:73:GLU:N	1:C:224:LYS:O	2.48	0.47
1:C:661:VAL:HG22	3:C:2042:HOH:O	2.15	0.47
1:C:160:VAL:N	1:C:161:PRO:CD	2.78	0.46
1:C:287:LEU:HD23	1:C:293:MET:HA	1.98	0.46
1:A:538:ASN:OD1	1:A:585:HIS:HE1	1.98	0.46
1:C:123:ASP:HA	1:C:124:PRO:HD3	1.78	0.46
1:B:79:VAL:CG1	1:B:80:VAL:H	2.27	0.46
1:A:134:LEU:HD23	1:A:160:VAL:HG21	1.89	0.46
1:B:186:ASN:C	1:B:188:ALA:H	2.19	0.46
1:B:212:MET:O	1:B:213:PRO:C	2.53	0.46
1:B:420:PRO:HD2	3:B:2095:HOH:O	2.16	0.46
1:C:154:ASN:HA	1:C:157:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:135:PRO:O	1:B:136:SER:C	2.52	0.46
1:C:609:THR:OG1	1:C:674:ASN:ND2	2.43	0.46
1:A:632:THR:CG2	1:A:654:ASN:HB3	2.46	0.45
1:C:238:SER:OG	1:C:262:ARG:HA	2.16	0.45
1:C:552:ASP:CB	1:C:563:ILE:HD11	2.46	0.45
1:A:53:LYS:HB3	3:A:2003:HOH:O	2.16	0.45
1:A:338:LYS:HE2	1:A:339:TYR:OH	2.17	0.45
1:A:630:THR:HB	3:A:2234:HOH:O	2.16	0.45
1:C:162:THR:OG1	1:C:164:GLN:HG2	2.15	0.45
1:A:77:LYS:O	1:A:219:THR:HA	2.17	0.45
1:A:496:PRO:HG2	3:A:2062:HOH:O	2.16	0.45
1:B:490:ALA:O	1:B:541:ARG:NH2	2.50	0.45
1:B:353:GLY:O	1:B:544:PRO:HA	2.17	0.45
1:C:198:ASN:H	1:C:201:GLN:NE2	2.15	0.45
1:C:87:LYS:CE	1:C:292:ASP:OD1	2.65	0.45
1:C:73:GLU:HB3	1:C:224:LYS:HG2	1.99	0.45
1:B:102:THR:O	1:B:102:THR:HG22	2.17	0.44
1:C:595:THR:HB	3:C:2103:HOH:O	2.16	0.44
1:B:392:THR:HG21	1:B:448:VAL:HB	1.99	0.44
1:B:420:PRO:CD	3:B:2095:HOH:O	2.66	0.44
1:C:224:LYS:NZ	3:C:2029:HOH:O	2.50	0.44
1:C:87:LYS:CD	1:C:292:ASP:OD1	2.62	0.44
1:C:377:THR:HA	1:C:525:PRO:HG2	1.98	0.44
1:C:547:VAL:CG1	1:C:566:ILE:CD1	2.96	0.44
1:B:194:THR:OG1	1:B:195:ASP:N	2.51	0.44
1:C:198:ASN:O	1:C:202:VAL:HG23	2.18	0.44
1:A:60:ARG:HD3	1:A:223:ARG:CZ	2.48	0.44
1:B:160:VAL:H	1:B:161:PRO:HD3	1.82	0.44
1:A:221:TRP:HB2	1:A:262:ARG:NH2	2.32	0.44
1:C:65:ASP:O	1:C:309:LYS:HG3	2.17	0.44
1:A:399:ASN:OD1	1:A:477:LYS:HD3	2.17	0.43
1:A:508:ASN:H	1:A:511:ASN:ND2	2.16	0.43
1:A:160:VAL:CG1	1:A:160:VAL:O	2.66	0.43
1:C:426:LYS:HB2	3:C:2060:HOH:O	2.18	0.43
1:A:55:THR:CG2	1:A:280:ARG:HD2	2.48	0.43
1:C:230:LEU:HA	3:C:2032:HOH:O	2.18	0.43
1:A:129:LYS:HB3	1:A:129:LYS:HE2	1.76	0.43
1:A:248:GLU:CB	1:A:252:TYR:CE2	2.95	0.43
1:C:233:ILE:HD12	3:C:2032:HOH:O	2.18	0.43
1:A:194:THR:HG23	1:A:195:ASP:O	2.18	0.43
1:B:310:LEU:HD23	1:B:310:LEU:N	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:GLU:CB	1:B:252:TYR:CE2	2.86	0.43
1:C:56:THR:CG2	1:C:281:PRO:HG2	2.36	0.43
1:C:87:LYS:NZ	1:C:292:ASP:OD1	2.52	0.43
1:C:539:GLY:HA3	3:C:2098:HOH:O	2.19	0.43
1:A:416:GLN:HG3	1:A:465:PHE:CG	2.54	0.42
1:B:461:GLN:HE21	1:B:464:MET:CB	2.27	0.42
1:C:324:LEU:HA	1:C:324:LEU:HD12	1.81	0.42
1:C:65:ASP:HB3	1:C:71:LEU:HD21	2.01	0.42
1:A:151:GLU:HB3	3:A:2023:HOH:O	2.19	0.42
1:C:153:TYR:O	1:C:157:VAL:HG13	2.18	0.42
1:B:208:ILE:C	1:B:208:ILE:HD12	2.40	0.42
1:B:165:LEU:HD13	1:B:167:TYR:CE2	2.53	0.42
1:B:554:ASN:C	1:B:554:ASN:OD1	2.57	0.42
1:C:155:ASN:HA	1:C:158:ASP:CB	2.41	0.42
1:B:244:LEU:CD1	1:B:261:ASP:HB2	2.47	0.42
1:C:353:GLY:HA2	3:C:2043:HOH:O	2.19	0.42
1:B:99:LYS:HG2	3:B:2007:HOH:O	2.19	0.42
1:A:426:LYS:HB2	3:A:2127:HOH:O	2.20	0.42
1:A:168:THR:HG21	3:A:2029:HOH:O	2.19	0.42
1:A:407:THR:H	1:C:416:GLN:NE2	2.01	0.42
1:B:128:LYS:O	1:B:131:VAL:HG12	2.20	0.42
1:B:185:GLY:O	1:B:188:ALA:HB3	2.20	0.42
1:C:679:MET:O	1:C:680:ASN:CB	2.47	0.42
1:A:317:GLN:OE1	1:A:357:SER:HB2	2.19	0.41
1:B:119:TYR:CD1	1:B:175:ILE:HG12	2.55	0.41
1:C:157:VAL:CG2	1:C:158:ASP:N	2.83	0.41
1:B:131:VAL:CB	1:B:157:VAL:HG11	2.49	0.41
1:A:279:LYS:NZ	1:A:301:GLU:O	2.53	0.41
1:B:342:GLY:O	1:B:652:PRO:HD2	2.20	0.41
1:C:177:LEU:HD23	1:C:177:LEU:HA	1.78	0.41
1:C:178:PHE:C	1:C:178:PHE:CD2	2.94	0.41
1:A:309:LYS:HE2	1:A:551:TYR:OH	2.20	0.41
1:C:129:LYS:HE2	1:C:129:LYS:HB3	1.78	0.41
1:C:131:VAL:HG23	1:C:153:TYR:HH	1.83	0.41
1:C:382:PHE:CD2	1:C:382:PHE:N	2.87	0.41
1:A:639:PRO:O	1:A:640:THR:C	2.59	0.41
1:B:298:ASN:ND2	1:B:301:GLU:HG2	2.36	0.41
1:B:507:TYR:HA	1:B:511:ASN:HD22	1.86	0.41
1:C:592:SER:O	1:C:605:SER:OG	2.35	0.41
1:A:378:VAL:HG23	1:A:379:THR:HG23	2.02	0.41
1:B:84:ARG:HD2	1:B:184:VAL:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:PHE:CB	1:B:192:ILE:HD11	2.51	0.41
1:C:299:ILE:CG2	1:C:300:GLU:N	2.84	0.41
1:A:52:THR:CG2	1:A:187:PHE:CE1	2.99	0.41
1:C:160:VAL:N	1:C:161:PRO:HD3	2.36	0.41
1:B:298:ASN:HD21	1:B:301:GLU:HG2	1.85	0.40
1:C:293:MET:HG3	1:C:293:MET:O	2.22	0.40
1:A:79:VAL:HG13	1:A:191:THR:HG23	2.03	0.40
1:C:657:LEU:HG	1:C:657:LEU:H	1.64	0.40
1:B:257:TYR:HA	1:B:280:ARG:NH1	2.36	0.40
1:A:632:THR:HB	1:A:660:ASN:OD1	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	A	602/680 (88%)	576 (96%)	23 (4%)	3 (0%)	32	32
1	B	599/680 (88%)	574 (96%)	23 (4%)	2 (0%)	44	47
1	C	601/680 (88%)	563 (94%)	33 (6%)	5 (1%)	22	19
All	All	1802/2040 (88%)	1713 (95%)	79 (4%)	10 (1%)	28	27

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	243	GLY
1	A	163	SER
1	B	196	PRO
1	C	656	ASN
1	A	109	PRO
1	C	163	SER
1	C	164	GLN

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Mol	Chain	Res	Type
1	C	559	LEU
1	B	187	PHE
1	C	135	PRO

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	A	510/573 (89%)	492 (96%)	18 (4%)	41	48
1	B	507/573 (88%)	486 (96%)	21 (4%)	35	41
1	C	509/573 (89%)	477 (94%)	32 (6%)	21	21
All	All	1526/1719 (89%)	1455 (95%)	71 (5%)	30	35

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	THR
1	A	54	VAL
1	A	56	THR
1	A	65	ASP
1	A	76	LEU
1	A	93	LEU
1	A	98	LYS
1	A	105	SER
1	A	158	ASP
1	A	162	THR
1	A	165	LEU
1	A	208	ILE
1	A	224	LYS
1	A	247	GLU
1	A	314	LEU
1	A	522	ASN
1	A	559	LEU
1	A	651	PHE
1	B	54	VAL

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Mol	Chain	Res	Type
1	B	73	GLU
1	B	76	LEU
1	B	114	ARG
1	B	160	VAL
1	B	222	ASP
1	B	224	LYS
1	B	247	GLU
1	B	258	SER
1	B	280	ARG
1	B	287	LEU
1	B	295	SER
1	B	324	LEU
1	B	383	VAL
1	B	458	GLN
1	B	522	ASN
1	B	559	LEU
1	B	561	GLU
1	B	632	THR
1	B	651	PHE
1	B	657	LEU
1	C	65	ASP
1	C	76	LEU
1	C	86	ASN
1	C	98	LYS
1	C	136	SER
1	C	152	LEU
1	C	154	ASN
1	C	158	ASP
1	C	160	VAL
1	C	162	THR
1	C	171	GLU
1	C	224	LYS
1	C	239	SER
1	C	244	LEU
1	C	247	GLU
1	C	248	GLU
1	C	293	MET
1	C	297	GLU
1	C	298	ASN
1	C	324	LEU
1	C	351	GLN
1	C	383	VAL

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Mol	Chain	Res	Type
1	C	458	GLN
1	C	497	ASP
1	C	502	LEU
1	C	522	ASN
1	C	559	LEU
1	C	563	ILE
1	C	651	PHE
1	C	657	LEU
1	C	658	THR
1	C	679	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	201	GLN
1	A	271	GLN
1	A	277	GLN
1	A	286	HIS
1	A	307	ASN
1	A	380	ASN
1	A	511	ASN
1	A	522	ASN
1	A	553	ASN
1	A	585	HIS
1	A	590	GLN
1	A	677	HIS
1	B	180	GLN
1	B	271	GLN
1	B	277	GLN
1	B	307	ASN
1	B	416	GLN
1	B	461	GLN
1	B	511	ASN
1	B	519	GLN
1	B	522	ASN
1	B	553	ASN
1	B	585	HIS
1	B	590	GLN
1	B	677	HIS
1	C	201	GLN
1	C	271	GLN
1	C	307	ASN

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Mol	Chain	Res	Type
1	C	329	ASN
1	C	416	GLN
1	C	511	ASN
1	C	522	ASN
1	C	553	ASN
1	C	585	HIS
1	C	590	GLN
1	C	677	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 9 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 ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	606/680 (89%)	0.01	14 (2%) 61 61	28, 42, 72, 91	0
1	B	605/680 (88%)	0.42	63 (10%) 7 7	31, 46, 81, 99	0
1	C	607/680 (89%)	0.16	20 (3%) 47 47	30, 48, 74, 93	0
All	All	1818/2040 (89%)	0.20	97 (5%) 27 28	28, 46, 77, 99	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	285	ILE	13.5
1	B	287	LEU	10.3
1	B	293	MET	8.0
1	B	157	VAL	7.8
1	B	55	THR	7.7
1	C	153	TYR	7.6
1	B	295	SER	6.8
1	B	299	ILE	6.8
1	B	108	SER	6.4
1	B	54	VAL	6.1
1	A	657	LEU	5.8
1	A	153	TYR	5.7
1	B	132	GLU	5.6
1	B	630	THR	5.5
1	C	630	THR	5.4
1	C	657	LEU	5.2
1	B	133	ALA	5.1
1	B	153	TYR	4.9
1	B	617	GLY	4.9
1	A	108	SER	4.8
1	B	149	GLU	4.7
1	A	157	VAL	4.6
1	B	282	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	221	TRP	4.3
1	C	221	TRP	4.2
1	B	286	HIS	4.1
1	C	658	THR	4.1
1	B	162	THR	4.0
1	B	187	PHE	3.9
1	B	288	ASP	3.8
1	A	658	THR	3.8
1	B	52	THR	3.8
1	B	134	LEU	3.8
1	B	296	VAL	3.8
1	B	109	PRO	3.7
1	B	53	LYS	3.7
1	B	152	LEU	3.7
1	C	157	VAL	3.6
1	B	284	GLU	3.5
1	C	617	GLY	3.5
1	B	126	ILE	3.4
1	B	301	GLU	3.4
1	B	289	LYS	3.3
1	C	259	LEU	3.3
1	B	110	ASN	3.3
1	B	111	LEU	3.2
1	C	150	SER	3.1
1	C	502	LEU	3.1
1	A	630	THR	3.0
1	B	56	THR	3.0
1	A	259	LEU	3.0
1	B	302	GLY	3.0
1	C	466	VAL	3.0
1	A	152	LEU	2.9
1	A	680	ASN	2.8
1	B	136	SER	2.8
1	B	657	LEU	2.7
1	B	292	ASP	2.6
1	B	294	GLU	2.6
1	B	161	PRO	2.6
1	B	120	TYR	2.6
1	B	181	LEU	2.6
1	B	241	LYS	2.6
1	C	560	GLY	2.4
1	C	680	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	245	PRO	2.4
1	C	76	LEU	2.4
1	B	150	SER	2.4
1	C	301	GLU	2.3
1	B	240	GLU	2.3
1	B	221	TRP	2.3
1	B	163	SER	2.3
1	B	192	ILE	2.3
1	B	176	TYR	2.3
1	B	151	GLU	2.3
1	C	125	GLU	2.2
1	B	106	ILE	2.2
1	B	130	THR	2.2
1	B	131	VAL	2.2
1	A	299	ILE	2.2
1	A	149	GLU	2.2
1	B	166	ASN	2.2
1	B	174	GLU	2.2
1	B	250	GLU	2.2
1	C	246	ALA	2.2
1	B	158	ASP	2.1
1	B	213	PRO	2.1
1	C	253	LEU	2.1
1	A	285	ILE	2.1
1	C	299	ILE	2.1
1	C	152	LEU	2.1
1	B	75	THR	2.1
1	B	185	GLY	2.1
1	B	252	TYR	2.0
1	B	281	PRO	2.0
1	A	51	GLN	2.0
1	B	461	GLN	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 carbohydrates in this entry.

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	ZN	A	701	1/1	0.99	0.10	-1.19	57,57,57,57	0
2	ZN	B	700	1/1	0.64	0.06	-1.50	116,116,116,116	0
2	ZN	C	701	1/1	0.97	0.07	-1.90	82,82,82,82	0
2	ZN	B	701	1/1	1.00	0.08	-2.01	70,70,70,70	0
2	ZN	A	700	1/1	0.99	0.09	-	61,61,61,61	0
2	ZN	A	702	1/1	0.89	0.14	-	99,99,99,99	0
2	ZN	B	702	1/1	0.92	0.06	-	109,109,109,109	0
2	ZN	C	702	1/1	0.93	0.06	-	101,101,101,101	0
2	ZN	C	700	1/1	0.99	0.07	-	69,69,69,69	0

6.5 Other polymers

There are no such residues in this entry.