



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 08:52 PM UTC

PDB ID : 2WAD / pdb_00002wad
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 wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

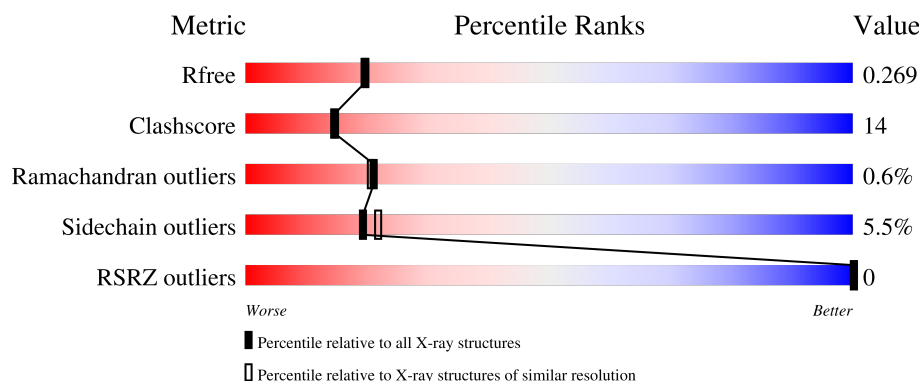
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.18 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}	180053	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (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 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	A	680	 70% 17% • 11%
1	B	680	 67% 20% • 11%
1	C	680	 68% 19% • 11%

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	UNP P0A3M6
A	56	THR	SER	conflict	UNP P0A3M6
A	96	ILE	THR	conflict	UNP P0A3M6
A	130	THR	ILE	conflict	UNP P0A3M6
A	161	PRO	GLN	conflict	UNP P0A3M6
A	225	ILE	VAL	conflict	UNP P0A3M6
A	251	SER	ALA	conflict	UNP P0A3M6
A	275	VAL	THR	conflict	UNP P0A3M6
A	281	PRO	SER	conflict	UNP P0A3M6
A	290	HIS	TYR	conflict	UNP P0A3M6
A	292	ASP	ASN	conflict	UNP P0A3M6
A	297	GLU	ASP	conflict	UNP P0A3M6
A	298	ASN	THR	conflict	UNP P0A3M6
A	306	LYS	ASN	conflict	UNP P0A3M6
A	333	GLY	GLU	conflict	UNP P0A3M6
A	351	GLN	LYS	conflict	UNP P0A3M6
A	361	LEU	ILE	conflict	UNP P0A3M6
A	412	PRO	SER	conflict	UNP P0A3M6
A	422	TYR	ASN	conflict	UNP P0A3M6
A	426	LYS	THR	conflict	UNP P0A3M6
A	427	LEU	GLN	conflict	UNP P0A3M6
A	438	GLU	GLN	conflict	UNP P0A3M6
A	446	ALA	THR	conflict	UNP P0A3M6

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

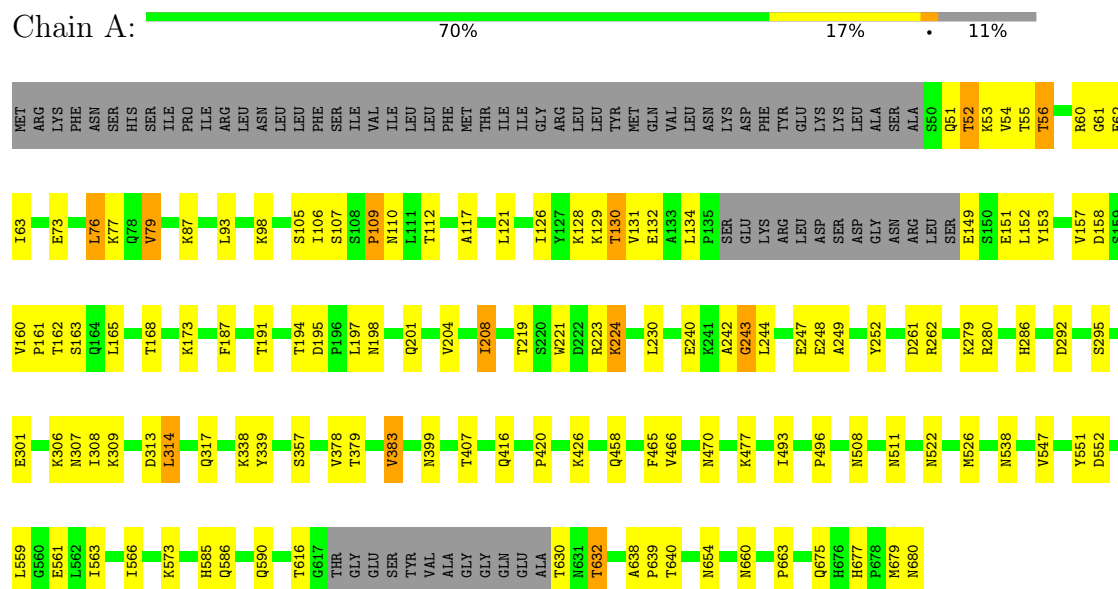
- Molecule 3 is water.

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

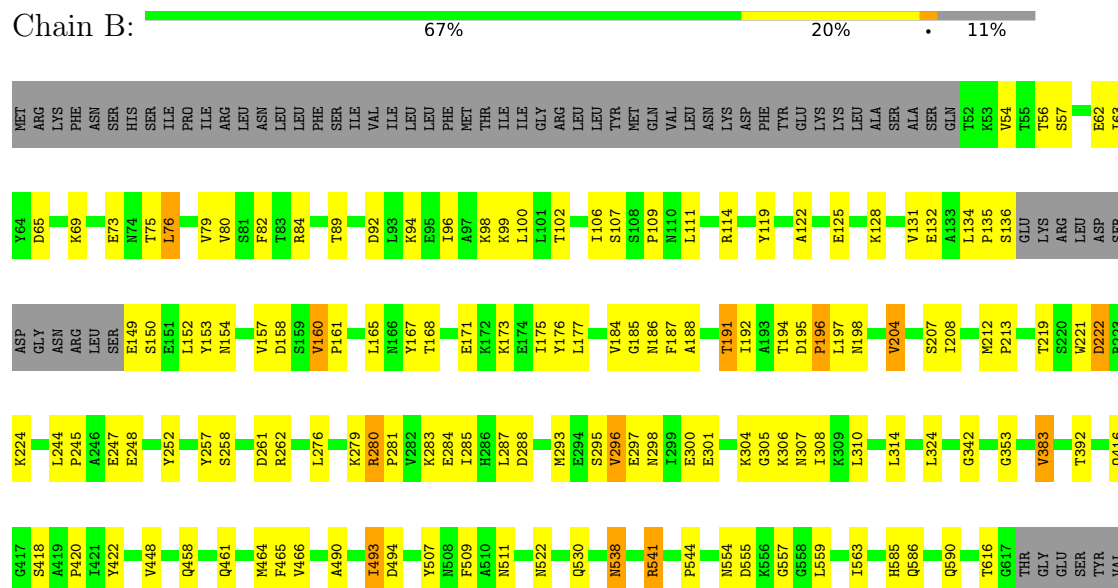
3 Residue-property plots

These plots are drawn for all protein, RNA, 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: PENICILLIN-BINDING PROTEIN 2B

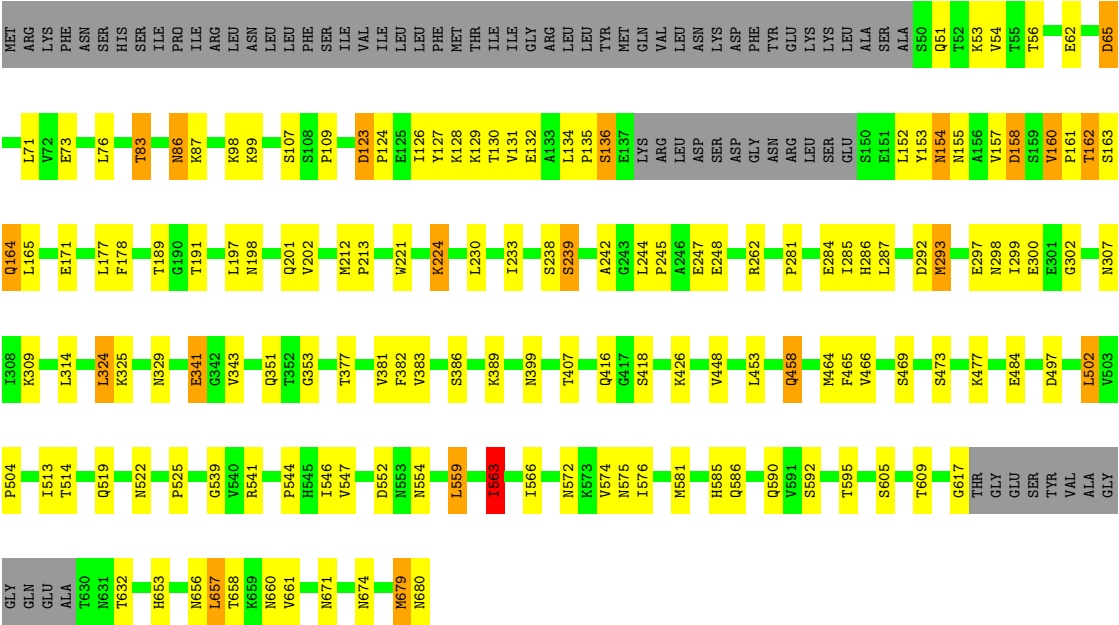


• Molecule 1: PENICILLIN-BINDING PROTEIN 2B





● 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) 98.4 (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 , 0.269	Depositor DCC
R_{free} test set	5889 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	36.6	Xtriage
Anisotropy	0.208	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.4	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	0.96	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	0.52	0/4706	0.95	1/6394 (0.0%)
1	B	0.49	0/4680	0.95	7/6359 (0.1%)
1	C	0.43	0/4695	0.94	5/6379 (0.1%)
All	All	0.48	0/14081	0.95	13/19132 (0.1%)

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	530	GLN	N-CA-C	-6.82	103.91	111.82
1	C	123	ASP	CA-C-N	6.63	126.88	119.32
1	C	123	ASP	C-N-CA	6.63	126.88	119.32
1	B	383	VAL	N-CA-CB	6.22	117.08	110.17
1	C	513	ILE	N-CA-C	5.67	116.41	110.62

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	101	0
1	B	4596	0	4517	139	0
1	C	4611	0	4530	145	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	3	0	0	0	0
2	B	3	0	0	0	0
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	380	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 14.

The worst 5 of 380 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

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%)	24	25
1	B	599/680 (88%)	574 (96%)	23 (4%)	2 (0%)	36	39
1	C	601/680 (88%)	563 (94%)	33 (6%)	5 (1%)	16	14
All	All	1802/2040 (88%)	1713 (95%)	79 (4%)	10 (1%)	21	20

5 of 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

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%)	489 (96%)	21 (4%)	27	33
1	B	507/573 (88%)	480 (95%)	27 (5%)	20	23
1	C	509/573 (89%)	473 (93%)	36 (7%)	13	14
All	All	1526/1719 (89%)	1442 (94%)	84 (6%)	19	22

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	160	VAL
1	C	341	GLU
1	C	165	LEU
1	C	247	GLU
1	C	458	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	277	GLN
1	C	553	ASN
1	C	307	ASN
1	C	463	ASN
1	C	590	GLN

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 oligosaccharides 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 [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	A	606/680 (89%)	-0.99	0 100 100	25, 42, 72, 91	2 (0%)
1	B	605/680 (88%)	-0.99	0 100 100	31, 46, 81, 99	0
1	C	607/680 (89%)	-0.97	0 100 100	30, 48, 74, 93	0
All	All	1818/2040 (89%)	-0.98	0 100 100	25, 46, 77, 99	2 (0%)

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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	B	700	1/1	0.97	0.06	116,116,116,116	0
2	ZN	A	702	1/1	0.98	0.05	99,99,99,99	0
2	ZN	B	702	1/1	0.99	0.04	109,109,109,109	0
2	ZN	C	701	1/1	0.99	0.04	82,82,82,82	0
2	ZN	C	702	1/1	0.99	0.04	101,101,101,101	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	A	700	1/1	1.00	0.03	61,61,61,61	0
2	ZN	C	700	1/1	1.00	0.03	69,69,69,69	0
2	ZN	A	701	1/1	1.00	0.03	57,57,57,57	0
2	ZN	B	701	1/1	1.00	0.03	70,70,70,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.