



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:16 PM UTC

PDB ID : 7JRM / pdb_00007jrm
Title : The structure of CBM51-2 and INT domains from *Clostridium perfringens* ZmpB
Authors : Pluinage, B.; Boraston, A.B.
Deposited on : 2020-08-12
Resolution : 2.00 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 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

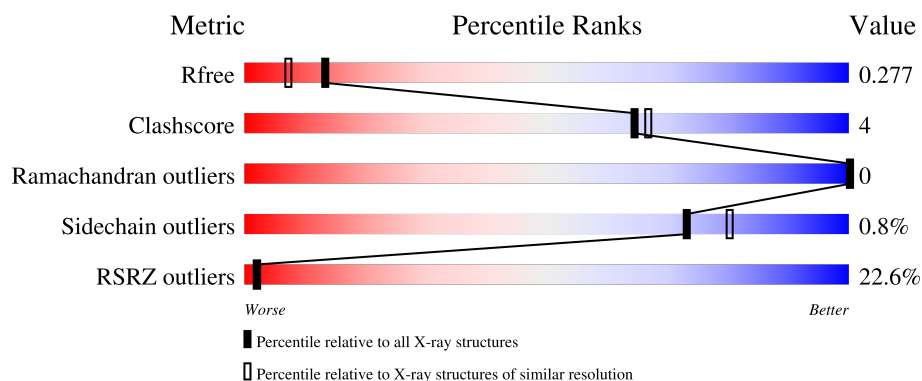
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	462	22% 89% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4000 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 F5/8 type C domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	455	Total	C	N	O	S	0	1	0
			3509	2192	585	724	8			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

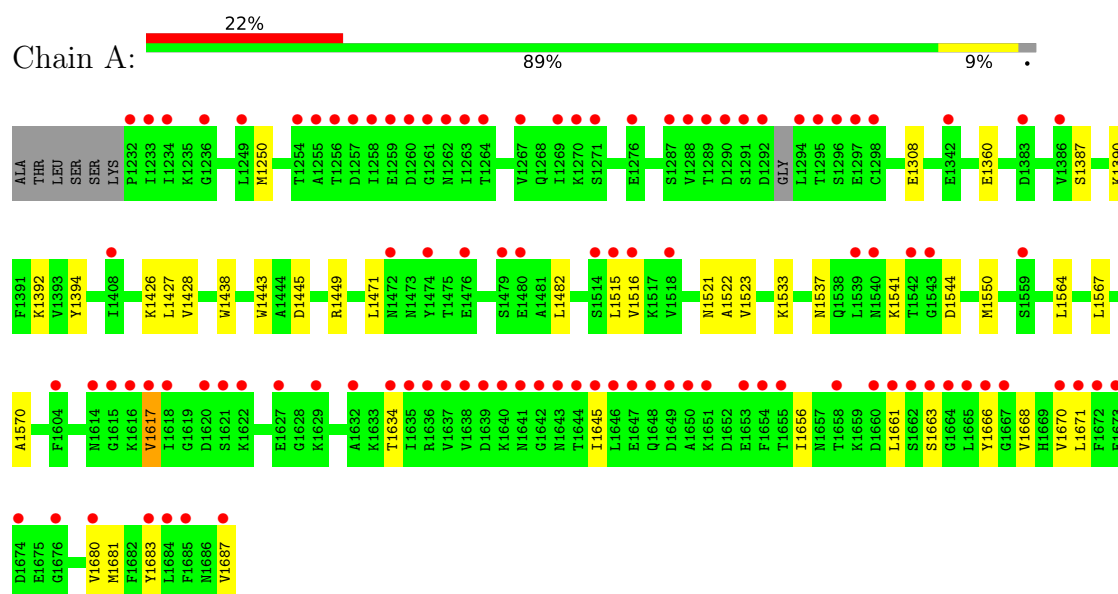
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	490	Total	O	0	0
			490	490		

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: F5/8 type C domain protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	151.05Å 49.16Å 78.50Å 90.00° 112.05° 90.00°	Depositor
Resolution (Å)	41.52 – 2.00 41.52 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.4 (41.52-2.00) 99.6 (41.52-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.64 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.18_3845	Depositor
R, R_{free}	0.248 , 0.272 0.252 , 0.277	Depositor DCC
R_{free} test set	1772 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	17.7	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	4000	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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: CA

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	0.07	0/3550	0.24	0/4793

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 [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	3509	0	3430	27	0
2	A	1	0	0	0	0
3	A	490	0	0	4	0
All	All	4000	0	3430	27	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 (27) 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:A:1668:VAL:HB	1:A:1683:TYR:HB2	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1663:SER:HA	1:A:1687:VAL:HG12	1.81	0.63
1:A:1670:VAL:HB	1:A:1681:MET:HB3	1.81	0.62
1:A:1645:ILE:HD12	1:A:1661:LEU:HD21	1.82	0.60
1:A:1390:LYS:HD2	1:A:1392:LYS:HE2	1.87	0.56
1:A:1482:LEU:HD22	1:A:1515:LEU:HD11	1.88	0.56
1:A:1390:LYS:NZ	3:A:1814:HOH:O	2.37	0.56
1:A:1617:VAL:HG12	1:A:1656:ILE:HB	1.90	0.53
1:A:1308:GLU:HG2	1:A:1449:ARG:HG2	1.91	0.53
1:A:1521:ASN:ND2	3:A:1824:HOH:O	2.39	0.52
1:A:1550:MET:HE3	1:A:1570:ALA:HB2	1.94	0.50
1:A:1394:TYR:HB2	1:A:1426:LYS:HB3	1.93	0.50
1:A:1360:GLU:HG2	1:A:1428:VAL:HG22	1.94	0.49
1:A:1522:ALA:O	3:A:1801:HOH:O	2.20	0.46
1:A:1427:LEU:HB3	1:A:1443:TRP:CZ2	2.51	0.45
1:A:1387:SER:OG	1:A:1438:TRP:O	2.30	0.45
1:A:1661:LEU:HD22	1:A:1666:TYR:CZ	2.51	0.44
1:A:1471:LEU:HD22	1:A:1471:LEU:H	1.83	0.44
1:A:1522:ALA:N	3:A:1801:HOH:O	2.52	0.43
1:A:1671:LEU:HD22	1:A:1680:VAL:HG22	2.01	0.43
1:A:1533:LYS:HE2	1:A:1537:ASN:HD21	1.83	0.43
1:A:1541:LYS:HE3	1:A:1541:LYS:HB2	1.78	0.42
1:A:1523:VAL:HG23	1:A:1544:ASP:HB3	2.01	0.42
1:A:1250:MET:HE3	1:A:1250:MET:HB3	1.91	0.41
1:A:1564:LEU:HD22	1:A:1567:LEU:HD12	2.02	0.41
1:A:1390:LYS:HB2	1:A:1390:LYS:HE3	1.87	0.40
1:A:1634:THR:HB	1:A:1671:LEU:HB2	2.03	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	452/462 (98%)	441 (98%)	11 (2%)	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	A	383/405 (95%)	380 (99%)	3 (1%)	73	80

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1445	ASP
1	A	1516	VAL
1	A	1617	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1310	GLN
1	A	1513	ASN
1	A	1521	ASN
1	A	1537	ASN
1	A	1686	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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 ⓘ

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	455/462 (98%)	1.26	103 (22%) 2 2	11, 26, 48, 60	1 (0%)

All (103) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1289	THR	6.6
1	A	1634	THR	5.9
1	A	1294	LEU	5.2
1	A	1638	VAL	5.2
1	A	1642	GLY	5.0
1	A	1650	ALA	4.9
1	A	1232	PRO	4.7
1	A	1295	THR	4.6
1	A	1663	SER	4.5
1	A	1233	ILE	4.4
1	A	1292	ASP	4.3
1	A	1687	VAL	4.2
1	A	1635	ILE	4.0
1	A	1543	GLY	3.9
1	A	1661	LEU	3.9
1	A	1641	ASN	3.8
1	A	1644	THR	3.8
1	A	1260	ASP	3.8
1	A	1632	ALA	3.8
1	A	1257	ASP	3.8
1	A	1476	GLU	3.7
1	A	1263	ILE	3.7
1	A	1261	GLY	3.7
1	A	1664	GLY	3.7
1	A	1645	ILE	3.7
1	A	1288	VAL	3.6
1	A	1258	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	1270	LYS	3.6
1	A	1539	LEU	3.5
1	A	1271	SER	3.3
1	A	1667	GLY	3.3
1	A	1639	ASP	3.3
1	A	1291	SER	3.2
1	A	1684	LEU	3.2
1	A	1383	ASP	3.1
1	A	1665	LEU	3.1
1	A	1647	GLU	3.1
1	A	1262	ASN	3.1
1	A	1479	SER	3.1
1	A	1515	LEU	3.0
1	A	1636	ARG	3.0
1	A	1666	TYR	3.0
1	A	1259	GLU	3.0
1	A	1296	SER	3.0
1	A	1472	ASN	3.0
1	A	1643	ASN	2.9
1	A	1646	LEU	2.9
1	A	1256	THR	2.9
1	A	1658	THR	2.8
1	A	1614	ASN	2.8
1	A	1683	TYR	2.8
1	A	1637	VAL	2.8
1	A	1516	VAL	2.7
1	A	1621	SER	2.7
1	A	1671	LEU	2.6
1	A	1651	LYS	2.6
1	A	1234	ILE	2.6
1	A	1680	VAL	2.6
1	A	1276	GLU	2.6
1	A	1615	GLY	2.6
1	A	1654	PHE	2.6
1	A	1408	ILE	2.6
1	A	1542	THR	2.6
1	A	1297	GLU	2.5
1	A	1673	GLU	2.5
1	A	1290	ASP	2.5
1	A	1264	THR	2.5
1	A	1662	SER	2.5
1	A	1676	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1540	ASN	2.5
1	A	1648	GLN	2.5
1	A	1287	SER	2.5
1	A	1269	ILE	2.4
1	A	1255	ALA	2.4
1	A	1616	LYS	2.4
1	A	1655	THR	2.4
1	A	1670	VAL	2.3
1	A	1480	GLU	2.3
1	A	1649	ASP	2.3
1	A	1559	SER	2.3
1	A	1685	PHE	2.3
1	A	1267	VAL	2.3
1	A	1640	LYS	2.3
1	A	1514	SER	2.2
1	A	1604	PHE	2.2
1	A	1629	LYS	2.2
1	A	1627	GLU	2.2
1	A	1672	PHE	2.1
1	A	1653	GLU	2.1
1	A	1236	GLY	2.1
1	A	1249	LEU	2.1
1	A	1342	GLU	2.1
1	A	1660	ASP	2.1
1	A	1674	ASP	2.1
1	A	1618	ILE	2.1
1	A	1617	VAL	2.1
1	A	1386	VAL	2.1
1	A	1518	VAL	2.1
1	A	1620	ASP	2.0
1	A	1254	THR	2.0
1	A	1474	TYR	2.0
1	A	1298	CYS	2.0
1	A	1622	LYS	2.0

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

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($\text{\AA}^2$)	Q<0.9
2	CA	A	1701	1/1	0.98	0.07	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.