



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 26, 2026 – 03:32 AM EDT

PDB ID : 7JRD / pdb_00007jrd
Title : The crystal structure of lactoferrin binding protein B (LbpB) from *Neisseria meningitidis* in complex with human lactoferrin
Authors : Yadav, R.; Noinaj, N.
Deposited on : 2020-08-12
Resolution : 2.85 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

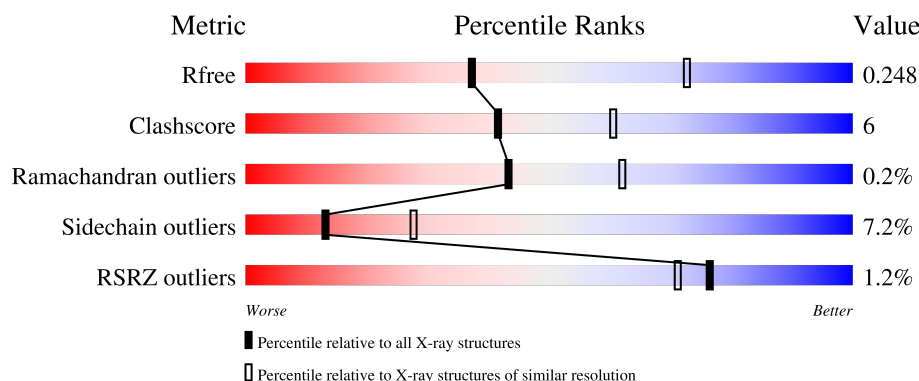
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	722	 2% 61% 16% 22%
2	B	692	 83% 15% ..

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
3	SO4	B	714	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9547 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 Lactoferrin-binding protein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	566	Total	C	N	O	S	0	1	0
			4234	2657	741	830	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q9JYK4
A	-2	ALA	-	expression tag	UNP Q9JYK4
A	-1	MET	-	expression tag	UNP Q9JYK4
A	0	GLY	-	expression tag	UNP Q9JYK4

- Molecule 2 is a protein called Lactotransferrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	688	Total	C	N	O	S	0	0	0
			5225	3272	926	990	37			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	11	ALA	THR	conflict	UNP W8QEY1

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

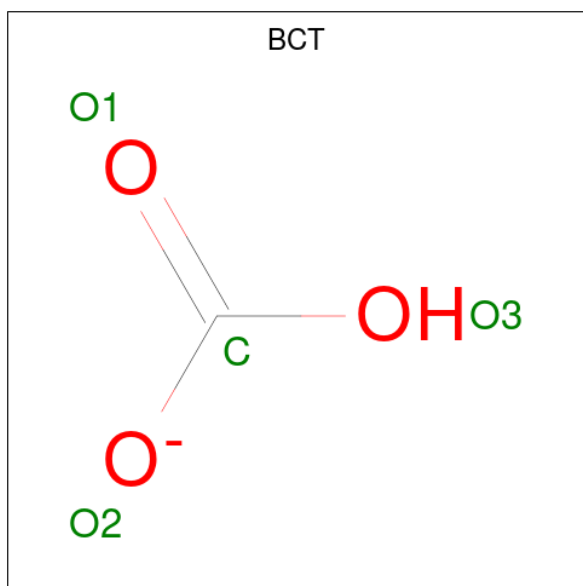


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Fe	0	0
			2	2		

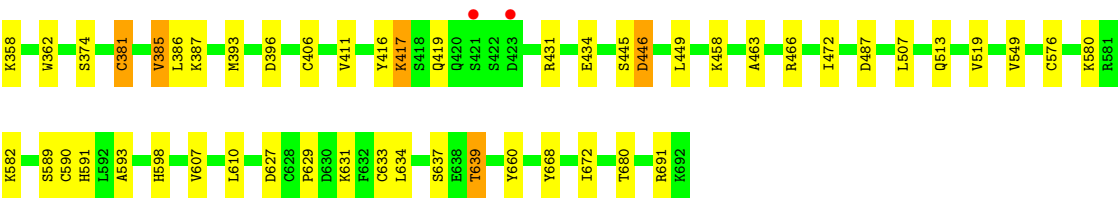
- Molecule 5 is BICARBONATE ION (CCD ID: BCT) (formula: CHO_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			4	1	3		
5	B	1	Total	C	O	0	0
			4	1	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	10	Total	O	0	0
			10	10		
6	B	3	Total	O	0	0
			3	3		



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	120.39Å 120.39Å 207.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.78 – 2.85 47.78 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.78-2.85) 99.9 (47.78-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.67 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.201 , 0.251 0.200 , 0.248	Depositor DCC
R_{free} test set	2000 reflections (5.53%)	wwPDB-VP
Wilson B-factor (Å ²)	77.5	Xtriage
Anisotropy	0.001	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 81.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9547	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% 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: BCT, SO4, FE

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	0.12	0/4316	0.36	0/5839
2	B	0.11	0/5339	0.35	0/7241
All	All	0.12	0/9655	0.35	0/13080

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	426	CYS	Peptide
2	B	292	SER	Peptide

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	4234	0	3904	63	0
2	B	5225	0	5000	56	0
3	A	15	0	0	1	0
3	B	50	0	0	6	0
4	B	2	0	0	0	0
5	B	8	0	0	1	0
6	A	10	0	0	0	0
6	B	3	0	0	0	0
All	All	9547	0	8904	118	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 6.

The worst 5 of 118 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:426:CYS:SG	1:A:427:CYS:N	2.43	0.88
2:B:14:GLN:HG2	2:B:15:PRO:HD3	1.56	0.85
1:A:181:TYR:HB2	1:A:235:TYR:HB2	1.67	0.76
1:A:56:ARG:NH1	1:A:73:GLN:OE1	2.18	0.76
1:A:396:LYS:O	1:A:535:LYS:NZ	2.18	0.75

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	555/722 (77%)	503 (91%)	49 (9%)	3 (0%)	24	42
2	B	686/692 (99%)	646 (94%)	40 (6%)	0	100	100
All	All	1241/1414 (88%)	1149 (93%)	89 (7%)	3 (0%)	43	62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	653	GLN
1	A	447	PRO
1	A	652	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	408/599 (68%)	378 (93%)	30 (7%)	13	26
2	B	548/575 (95%)	509 (93%)	39 (7%)	13	28
All	All	956/1174 (81%)	887 (93%)	69 (7%)	13	28

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	385	VAL
2	B	445	SER
2	B	576	CYS
1	A	632	SER
1	A	619	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	24	GLN
2	B	360	ASN
1	A	565	GLN
1	A	569	GLN
1	A	642	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 2 are monoatomic - leaving 15 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	B	710	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	B	711	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	B	712	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	B	706	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	B	714	-	4,4,4	0.23	0	6,6,6	0.09	0
3	SO4	B	713	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	B	705	-	4,4,4	0.24	0	6,6,6	0.07	0
5	BCT	B	703	4	3,3,3	0.75	0	2,3,3	0.03	0
3	SO4	B	709	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	B	707	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	A	802	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	A	803	-	4,4,4	0.23	0	6,6,6	0.11	0
3	SO4	B	708	-	4,4,4	0.23	0	6,6,6	0.06	0
5	BCT	B	704	4	3,3,3	0.82	0	2,3,3	0.34	0
3	SO4	A	801	-	4,4,4	0.24	0	6,6,6	0.08	0

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.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	710	SO4	1	0
3	B	714	SO4	4	0
3	B	709	SO4	1	0
3	A	803	SO4	1	0
5	B	704	BCT	1	0

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	566/722 (78%)	0.03	13 (2%) 61 52	49, 91, 184, 248	1 (0%)
2	B	688/692 (99%)	-0.27	2 (0%) 90 89	48, 73, 121, 225	0
All	All	1254/1414 (88%)	-0.14	15 (1%) 76 71	48, 78, 160, 248	1 (0%)

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	34	GLY	3.3
2	B	421	SER	3.1
1	A	68	ILE	2.7
1	A	357	SER	2.7
1	A	35	SER	2.5

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($\text{\AA}^2$)	Q<0.9
3	SO4	A	803	5/5	0.28	0.09	203,204,227,309	0
3	SO4	B	706	5/5	0.56	0.09	120,129,145,160	0
3	SO4	B	705	5/5	0.57	0.09	122,138,148,155	0
3	SO4	B	711	5/5	0.57	0.09	125,134,147,161	0
3	SO4	B	709	5/5	0.59	0.09	111,112,143,149	0
3	SO4	A	801	5/5	0.62	0.11	164,165,171,176	0
3	SO4	B	712	5/5	0.70	0.11	126,126,129,154	0
3	SO4	B	713	5/5	0.76	0.12	120,121,124,139	0
3	SO4	B	714	5/5	0.76	0.08	153,153,171,262	0
3	SO4	B	710	5/5	0.77	0.25	88,106,117,129	0
3	SO4	A	802	5/5	0.79	0.09	119,126,153,230	0
3	SO4	B	707	5/5	0.79	0.19	98,101,119,121	0
5	BCT	B	704	4/4	0.89	0.10	65,65,73,76	0
3	SO4	B	708	5/5	0.90	0.07	90,100,113,116	0
5	BCT	B	703	4/4	0.96	0.05	43,59,60,66	0
4	FE	B	702	1/1	0.98	0.07	72,72,72,72	0
4	FE	B	701	1/1	0.99	0.05	68,68,68,68	0

6.5 Other polymers [i](#)

There are no such residues in this entry.