



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2024 – 10:15 am BST

PDB ID : 2XTL
Title : Structure of the major pilus backbone protein from *Streptococcus Agalactiae*
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Deposited on : 2010-10-11
Resolution : 1.75 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	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

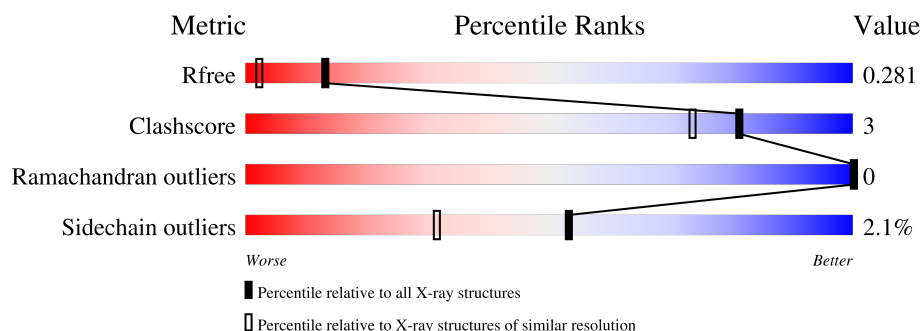
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	452	 93% 6% •
1	B	452	 92% 7% •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7974 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 CELL WALL SURFACE ANCHOR FAMILY PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	449	Total	C	N	O	S	0	12	0
			3502	2198	580	723	1			
1	B	452	Total	C	N	O	S	0	21	0
			3574	2246	588	739	1			

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	K	0	0
			2	2		
2	B	1	Total	K	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	454	Total	O	0	0
			454	454		
3	B	441	Total	O	0	0
			441	441		

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. 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. 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.

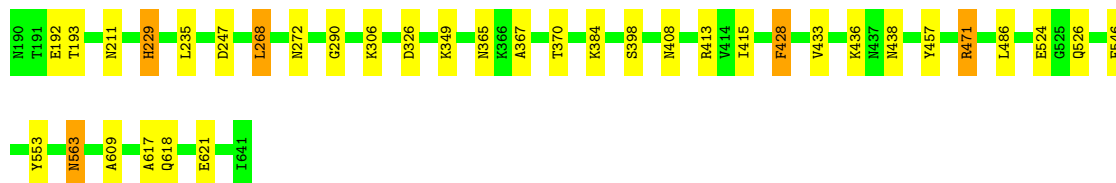
• Molecule 1: CELL WALL SURFACE ANCHOR FAMILY PROTEIN

Chain A: 



• Molecule 1: CELL WALL SURFACE ANCHOR FAMILY PROTEIN

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.86Å 104.68Å 159.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.75 38.03 – 1.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (40.00-1.75) 100.0 (38.03-1.75)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.26 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.185 , 0.216 0.250 , 0.281	Depositor DCC
R_{free} test set	5403 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	17.6	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7974	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.82% 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: K

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	0.36	0/3588	0.54	0/4850
1	B	0.38	1/3687 (0.0%)	0.54	0/4979
All	All	0.37	1/7275 (0.0%)	0.54	0/9829

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	524	GLU	CD-OE2	6.80	1.33	1.25

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	3502	0	3509	17	0
1	B	3574	0	3602	22	0
2	A	2	0	0	0	0
2	B	1	0	0	0	0
3	A	454	0	0	0	0
3	B	441	0	0	2	0
All	All	7974	0	7111	37	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 3.

All (37) 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:B:349:LYS:H	1:B:408:ASN:HD21	1.28	0.80
1:A:349:LYS:H	1:A:408:ASN:HD21	1.27	0.79
1:A:401:HIS:HD2	1:B:367:ALA:H	1.31	0.78
1:B:436:LYS:HE3	1:B:438:ASN:HD21	1.58	0.68
1:A:401:HIS:CD2	1:B:367:ALA:H	2.13	0.67
1:B:563:ASN:HD22	1:B:563:ASN:H	1.41	0.67
1:A:561:ALA:HB3	1:A:564[B]:VAL:HG23	1.77	0.66
1:B:370[B]:THR:HG22	3:B:2229:HOH:O	1.99	0.63
1:A:561:ALA:HB3	1:A:564[A]:VAL:HG13	1.80	0.62
1:B:365:ASN:HD22	1:B:398:SER:H	1.46	0.60
1:B:384[A]:LYS:NZ	3:B:2246:HOH:O	2.36	0.58
1:A:247:ASP:HA	1:A:326:ASP:O	2.03	0.57
1:A:436:LYS:HE2	1:A:438:ASN:HD21	1.70	0.55
1:A:384:LYS:HE3	1:A:386:VAL:HG22	1.89	0.54
1:A:365:ASN:HD22	1:A:398:SER:H	1.56	0.53
1:B:247:ASP:HA	1:B:326:ASP:O	2.09	0.52
1:B:365:ASN:ND2	1:B:398:SER:H	2.09	0.50
1:B:193:THR:HB	1:B:235:LEU:HD12	1.95	0.49
1:A:478:LEU:HD22	1:A:564[B]:VAL:HG11	1.95	0.49
1:B:563:ASN:HD22	1:B:563:ASN:N	2.11	0.49
1:A:457:TYR:CE1	1:A:609:ALA:HA	2.49	0.48
1:B:413:ARG:CZ	1:B:415:ILE:HD11	2.43	0.48
1:B:617:ALA:O	1:B:618:GLN:HB2	2.16	0.46
1:B:272:ASN:HD22	1:B:290:GLY:HA2	1.81	0.46
1:A:428:PHE:CD2	1:A:433:VAL:HG22	2.51	0.46
1:B:268:LEU:HD22	1:B:272:ASN:CG	2.36	0.45
1:B:229:HIS:HD2	1:B:306:LYS:NZ	2.14	0.45
1:B:486:LEU:HD11	1:B:553:TYR:CG	2.52	0.45
1:A:561:ALA:HB3	1:A:564[B]:VAL:CG2	2.46	0.45
1:A:457:TYR:HB2	1:A:607:VAL:CG1	2.48	0.42
1:A:365:ASN:ND2	1:A:398:SER:H	2.17	0.42
1:B:457:TYR:CE1	1:B:609:ALA:HA	2.54	0.42
1:A:548:LYS:N	1:A:548:LYS:HD3	2.35	0.42
1:B:428:PHE:CD2	1:B:433:VAL:HG22	2.55	0.41
1:A:475:ALA:HB2	1:A:593:PRO:HG3	2.03	0.41
1:B:471:ARG:NH2	1:B:621:GLU:O	2.54	0.41
1:B:229:HIS:HD2	1:B:306:LYS:HZ1	1.70	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	459/452 (102%)	456 (99%)	3 (1%)	0	100	100
1	B	471/452 (104%)	465 (99%)	6 (1%)	0	100	100
All	All	930/904 (103%)	921 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	388/379 (102%)	381 (98%)	7 (2%)	59	40
1	B	400/379 (106%)	390 (98%)	10 (2%)	47	25
All	All	788/758 (104%)	771 (98%)	17 (2%)	53	29

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	229	HIS
1	A	366	LYS
1	A	380	LYS
1	A	428	PHE
1	A	526	GLN

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Mol	Chain	Res	Type
1	A	546	PHE
1	A	548	LYS
1	B	192	GLU
1	B	211	ASN
1	B	229	HIS
1	B	268	LEU
1	B	428	PHE
1	B	471	ARG
1	B	526[A]	GLN
1	B	526[B]	GLN
1	B	546	PHE
1	B	563	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	365	ASN
1	A	401	HIS
1	A	408	ASN
1	A	438	ASN
1	A	442	ASN
1	B	211	ASN
1	B	229	HIS
1	B	272	ASN
1	B	334	ASN
1	B	365	ASN
1	B	408	ASN
1	B	438	ASN
1	B	563	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.