



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:43 PM UTC

PDB ID : 2C1I / pdb_00002c1i
Title : Structure of Streptococcus pneumoniae peptidoglycan deacetylase (SpPgdA)
D 275 N Mutant.
Authors : Blair, D.E.; Schuttelkopf, A.W.; MacRae, J.I.; van Aalten, D.M.F.
Deposited on : 2005-09-15
Resolution : 1.35 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
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

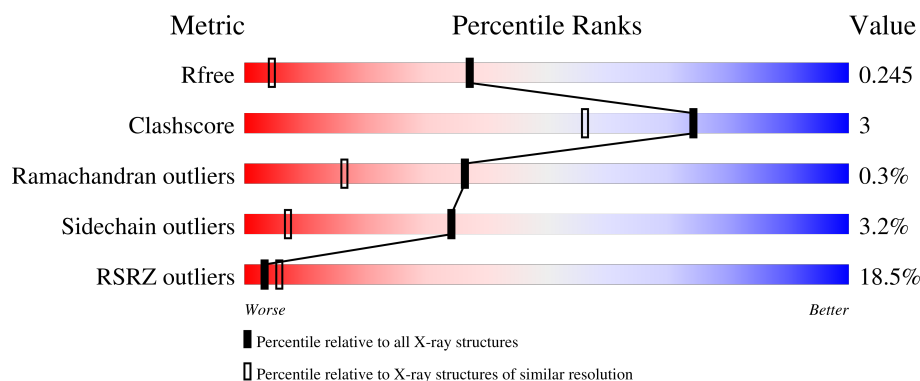
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.35 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	1216 (1.36-1.36)
Clashscore	190562	1232 (1.36-1.36)
Ramachandran outliers	187476	1220 (1.36-1.36)
Sidechain outliers	187428	1220 (1.36-1.36)
RSRZ outliers	180081	1214 (1.36-1.36)

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	431	16% 81% 6% • 11%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3315 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.

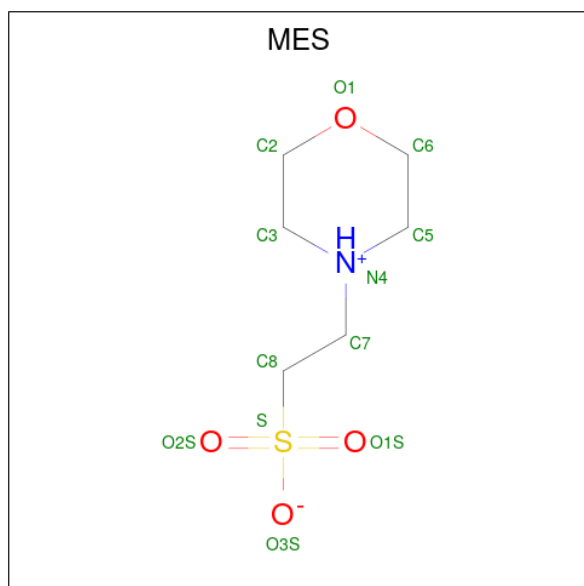
- Molecule 1 is a protein called PEPTIDOGLYCAN GLCNAC DEACETYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	383	3085	1961	507	613	4	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	275	ASN	ASP	engineered mutation	UNP Q8DP63

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).

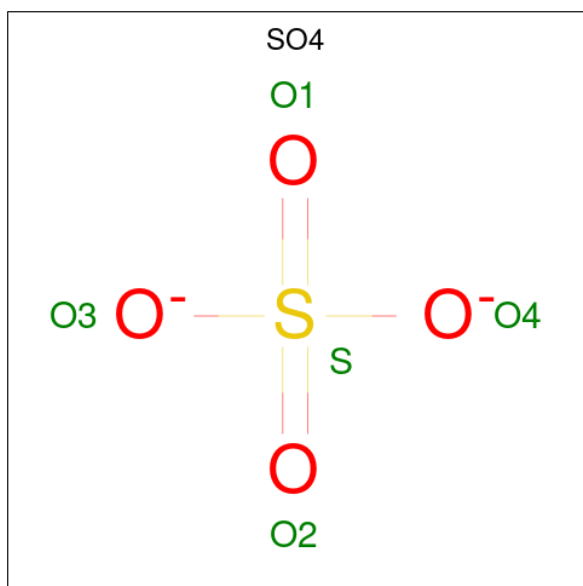


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	12	6	1	4	1	0	0

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

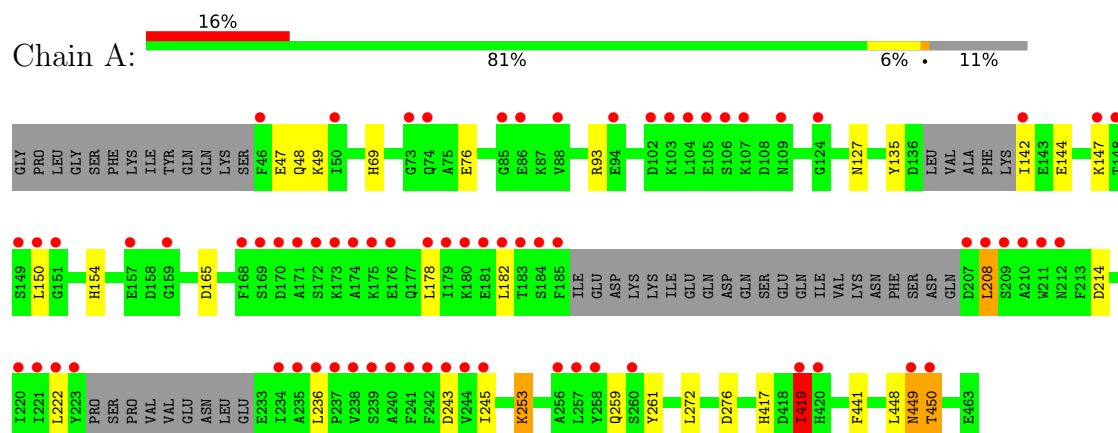
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	211	Total	O	0	0
			211	211		

3 Residue-property plots [i](#)

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: PEPTIDOGLYCAN GLCNAC DEACETYLASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.27Å 79.24Å 100.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.35 15.00 – 1.35	Depositor EDS
% Data completeness (in resolution range)	94.2 (15.00-1.35) 94.1 (15.00-1.35)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 1.35Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.188 , 0.225 0.209 , 0.245	Depositor DCC
R_{free} test set	1840 reflections (1.97%)	wwPDB-VP
Wilson B-factor (Å ²)	16.2	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3315	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.26% 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: MES, ZN, SO4

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	0.86	1/3142 (0.0%)	0.90	1/4245 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	450	THR	CA-CB	5.49	1.61	1.53

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	419	ILE	CB-CA-C	5.31	116.36	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	3085	0	3046	19	0
2	A	12	0	13	0	0
3	A	2	0	0	0	0
4	A	5	0	0	0	0
5	A	211	0	0	1	0
All	All	3315	0	3059	19	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 (19) 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:417:HIS:HB3	1:A:419:ILE:HD11	1.52	0.91
1:A:276:ASP:HB2	1:A:419:ILE:HD12	1.69	0.73
1:A:417:HIS:HB3	1:A:419:ILE:CD1	2.20	0.70
1:A:69:HIS:HE1	1:A:76:GLU:OE2	1.79	0.66
1:A:182:LEU:HD13	1:A:222:LEU:HD22	1.77	0.65
1:A:178:LEU:O	1:A:182:LEU:HB2	1.97	0.64
1:A:222:LEU:HD13	1:A:236:LEU:HD13	1.84	0.60
1:A:165:ASP:HA	1:A:208:LEU:HD12	1.94	0.50
1:A:449:ASN:OD1	1:A:450:THR:HG22	2.12	0.49
1:A:127:ASN:ND2	1:A:154:HIS:ND1	2.61	0.48
1:A:93:ARG:HH11	1:A:93:ARG:HG2	1.78	0.48
1:A:272:LEU:HG	1:A:441:PHE:CE2	2.51	0.46
1:A:243:ASP:OD1	1:A:261:TYR:OH	2.26	0.46
1:A:222:LEU:HD13	1:A:236:LEU:CD1	2.46	0.45
1:A:253:LYS:HA	1:A:253:LYS:HD2	1.77	0.45
1:A:448:LEU:O	1:A:449:ASN:C	2.62	0.43
1:A:69:HIS:CE1	1:A:76:GLU:OE2	2.66	0.42
1:A:135:TYR:CD1	1:A:144:GLU:HB3	2.54	0.42
1:A:47:GLU:HG3	5:A:2001:HOH:O	2.21	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	375/431 (87%)	365 (97%)	9 (2%)	1 (0%)	36 16

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	449	ASN

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	348/393 (88%)	337 (97%)	11 (3%)	34 7

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	GLN
1	A	49	LYS
1	A	142	ILE
1	A	147	LYS
1	A	150	LEU
1	A	208	LEU
1	A	214	ASP
1	A	245	ILE
1	A	253	LYS
1	A	259	GLN
1	A	419	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	HIS
1	A	109	ASN
1	A	127	ASN
1	A	129	ASN
1	A	177	GLN
1	A	285	GLN
1	A	309	ASN
1	A	407	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
2	MES	A	1464	-	12,12,12	1.49	1 (8%)	15,16,16	1.55	3 (20%)
4	SO4	A	1467	3	4,4,4	0.95	0	6,6,6	0.67	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MES	A	1464	-	-	0/6/14/14	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1464	MES	C8-S	4.34	1.83	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	1464	MES	O2S-S-C8	2.93	111.15	106.73
2	A	1464	MES	O1-C6-C5	-2.08	107.29	111.77
2	A	1464	MES	O1S-S-C8	2.05	109.83	106.73

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	383/431 (88%)	1.04	71 (18%) 3 6	11, 18, 35, 49	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	148	THR	6.6
1	A	450	THR	5.7
1	A	182	LEU	5.7
1	A	183	THR	5.3
1	A	236	LEU	5.2
1	A	185	PHE	4.6
1	A	149	SER	4.6
1	A	211	TRP	4.4
1	A	46	PHE	4.4
1	A	109	ASN	4.4
1	A	234	ILE	4.0
1	A	106	SER	3.9
1	A	222	LEU	3.8
1	A	244	VAL	3.7
1	A	150	LEU	3.7
1	A	104	LEU	3.7
1	A	179	ILE	3.6
1	A	223	TYR	3.6
1	A	210	ALA	3.4
1	A	173	LYS	3.3
1	A	168	PHE	3.3
1	A	171	ALA	3.3
1	A	419	ILE	3.3
1	A	151	GLY	3.3
1	A	208	LEU	3.3
1	A	243	ASP	3.2
1	A	176	GLU	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	174	ALA	3.2
1	A	175	LYS	3.2
1	A	184	SER	3.2
1	A	170	ASP	3.1
1	A	107	LYS	3.1
1	A	221	ILE	3.0
1	A	207	ASP	3.0
1	A	142	ILE	3.0
1	A	180	LYS	3.0
1	A	245	ILE	3.0
1	A	420	HIS	3.0
1	A	240	ALA	2.8
1	A	242	PHE	2.8
1	A	209	SER	2.8
1	A	212	ASN	2.7
1	A	239	SER	2.7
1	A	50	ILE	2.7
1	A	220	ILE	2.6
1	A	147	LYS	2.6
1	A	102	ASP	2.5
1	A	103	LYS	2.5
1	A	169	SER	2.4
1	A	172	SER	2.4
1	A	178	LEU	2.4
1	A	235	ALA	2.4
1	A	85	GLY	2.4
1	A	124	GLY	2.4
1	A	94	GLU	2.3
1	A	449	ASN	2.3
1	A	88	VAL	2.3
1	A	105	GLU	2.3
1	A	238	VAL	2.3
1	A	159	GLY	2.2
1	A	258	TYR	2.2
1	A	157	GLU	2.2
1	A	241	PHE	2.2
1	A	73	GLY	2.2
1	A	74	GLN	2.2
1	A	257	LEU	2.1
1	A	237	PRO	2.1
1	A	86	GLU	2.1
1	A	256	ALA	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	260	SER	2.0
1	A	181	GLU	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 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	MES	A	1464	12/12	0.84	0.13	23,26,38,38	0
4	SO4	A	1467	5/5	0.99	0.04	14,15,16,17	0
3	ZN	A	1466	1/1	1.00	0.10	16,16,16,16	0
3	ZN	A	1465	1/1	1.00	0.01	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.