



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 09:20 am BST

PDB ID : 5HL8
Title : 1.93 Angstrom resolution crystal structure of a pullulanase-specific type II secretion system integral cytoplasmic membrane protein GspL (C-terminal fragment; residues 309-397) from *Klebsiella pneumoniae* subsp. *pneumoniae* NTUH-K2044
Authors : Halavaty, A.S.; Minasov, G.; Kiryukhina, O.; Grimshaw, S.; Light, S.; Dubrovskaya, I.; Shuvalova, L.; Kwon, K.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2016-01-14
Resolution : 1.93 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

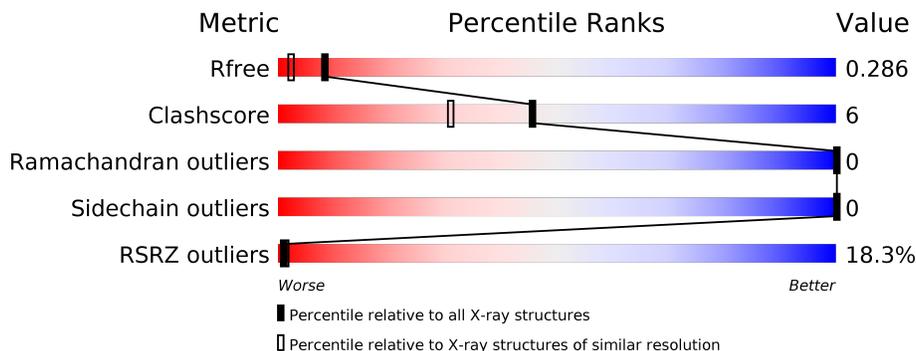
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.93 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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 on 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	92	
1	B	92	
1	C	92	
1	D	92	

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 2582 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 Type II secretion system protein L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	Se			
1	A	81	Total 640	C 396	N 122	O 120	Se 2	0	1	0
1	B	81	Total 655	C 404	N 125	O 124	Se 2	0	3	0
1	C	79	Total 656	C 403	N 123	O 128	Se 2	0	6	0
1	D	68	Total 541	C 337	N 105	O 99		0	1	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	306	SER	-	expression tag	UNP A0A060VDE2
A	307	ASN	-	expression tag	UNP A0A060VDE2
A	308	ALA	-	expression tag	UNP A0A060VDE2
B	306	SER	-	expression tag	UNP A0A060VDE2
B	307	ASN	-	expression tag	UNP A0A060VDE2
B	308	ALA	-	expression tag	UNP A0A060VDE2
C	306	SER	-	expression tag	UNP A0A060VDE2
C	307	ASN	-	expression tag	UNP A0A060VDE2
C	308	ALA	-	expression tag	UNP A0A060VDE2
D	306	SER	-	expression tag	UNP A0A060VDE2
D	307	ASN	-	expression tag	UNP A0A060VDE2
D	308	ALA	-	expression tag	UNP A0A060VDE2

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	39	Total 39	O 39	0	0
2	B	23	Total 23	O 23	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	21	Total	O	0	1
			22	22		
2	D	6	Total	O	0	0
			6	6		

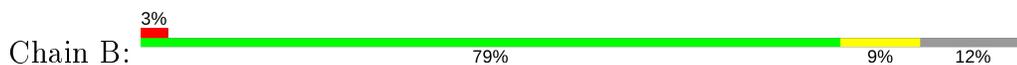
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Type II secretion system protein L



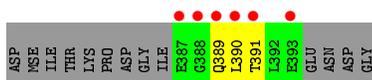
- Molecule 1: Type II secretion system protein L



- Molecule 1: Type II secretion system protein L



- Molecule 1: Type II secretion system protein L



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.38Å 51.28Å 117.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.44 – 1.93 26.43 – 1.93	Depositor EDS
% Data completeness (in resolution range)	99.8 (26.44-1.93) 99.8 (26.43-1.93)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.26 (at 1.93Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.226 , 0.281 0.231 , 0.286	Depositor DCC
R_{free} test set	1203 reflections (5.15%)	wwPDB-VP
Wilson B-factor (Å ²)	29.8	Xtrriage
Anisotropy	0.598	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.021 for k,h,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2582	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical 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

5.1 Standard geometry

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	0.58	0/648	0.84	0/875
1	B	0.52	0/663	0.81	0/895
1	C	0.56	0/661	0.90	0/888
1	D	0.42	0/547	0.87	0/738
All	All	0.53	0/2519	0.86	0/3396

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

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	640	0	648	11	0
1	B	655	0	659	8	0
1	C	656	0	661	9	0
1	D	541	0	557	15	0
2	A	39	0	0	0	0
2	B	23	0	0	2	0
2	C	22	0	0	1	0
2	D	6	0	0	0	0
All	All	2582	0	2525	32	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.

All (32) 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:332[B]:THR:HG22	2:C:404:HOH:O	1.75	0.86
1:A:322:LEU:HB3	1:D:319:VAL:HG22	1.63	0.80
1:D:374:VAL:CG1	1:D:390[B]:LEU:HD11	2.17	0.74
1:D:348:ARG:HD3	1:D:391:THR:HG21	1.72	0.72
1:B:326:GLN:CG	1:C:319:VAL:HG13	2.21	0.70
1:A:322:LEU:HD12	1:D:322:LEU:HD23	1.73	0.69
1:A:322:LEU:HD12	1:D:322:LEU:CD2	2.28	0.63
1:A:379[A]:MSE:SE	1:A:388:GLY:HA3	2.49	0.62
1:B:326:GLN:HG3	1:C:319:VAL:HG13	1.79	0.62
1:D:350:GLN:NE2	1:D:389:GLN:OE1	2.35	0.60
1:A:353:ILE:HD11	1:A:361:LEU:CD1	2.32	0.59
1:C:373:ARG:NH1	1:C:393:GLU:OE1	2.35	0.59
1:A:322:LEU:HD11	1:D:322:LEU:HD22	1.84	0.58
1:B:350[A]:GLN:NE2	1:B:389:GLN:OE1	2.34	0.58
1:D:374:VAL:HG12	1:D:390[B]:LEU:HD11	1.84	0.58
1:B:394:GLU:HG3	2:B:413:HOH:O	2.05	0.57
1:A:322:LEU:CD1	1:D:322:LEU:HD22	2.35	0.56
1:B:328:ILE:O	1:B:332:THR:HG23	2.08	0.53
1:A:322:LEU:CD1	1:D:322:LEU:CD2	2.86	0.53
1:D:348:ARG:HD3	1:D:391:THR:CG2	2.39	0.52
1:A:319:VAL:CG2	1:D:326:GLN:HG3	2.41	0.51
1:D:374:VAL:HG13	1:D:390[B]:LEU:HD11	1.90	0.51
1:D:326:GLN:HA	1:D:326:GLN:OE1	2.13	0.48
1:B:337:LEU:HB3	1:C:318:LEU:HD21	1.98	0.46
1:C:358:SER:O	1:C:362:GLU:HG3	2.15	0.46
1:D:374:VAL:HG13	1:D:390[B]:LEU:HD21	1.98	0.46
1:C:332[B]:THR:CG2	1:C:335:ILE:HB	2.46	0.45
1:C:332[B]:THR:O	1:C:332[B]:THR:HG23	2.16	0.45
1:A:371:ARG:HH22	1:A:394:GLU:HG2	1.81	0.44
1:C:372:PHE:CE2	1:C:394:GLU:HG2	2.52	0.44
1:A:356:VAL:HG13	1:B:370:PRO:HB2	2.00	0.42
1:B:389:GLN:HG2	2:B:418:HOH:O	2.20	0.41

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	80/92 (87%)	80 (100%)	0	0	100	100
1	B	82/92 (89%)	82 (100%)	0	0	100	100
1	C	81/92 (88%)	81 (100%)	0	0	100	100
1	D	65/92 (71%)	65 (100%)	0	0	100	100
All	All	308/368 (84%)	308 (100%)	0	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	68/74 (92%)	68 (100%)	0	100	100
1	B	70/74 (95%)	70 (100%)	0	100	100
1	C	71/74 (96%)	71 (100%)	0	100	100
1	D	57/74 (77%)	57 (100%)	0	100	100
All	All	266/296 (90%)	266 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	80/92 (86%)	0.63	2 (2%) 57 64	21, 30, 50, 66	0
1	B	80/92 (86%)	0.57	3 (3%) 40 48	18, 36, 57, 88	0
1	C	78/92 (84%)	0.91	12 (15%) 2 3	23, 41, 64, 89	0
1	D	68/92 (73%)	2.74	39 (57%) 0 0	32, 67, 96, 124	0
All	All	306/368 (83%)	1.15	56 (18%) 1 1	18, 41, 82, 124	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	356	VAL	8.2
1	D	360	ALA	8.1
1	D	359	ARG	8.0
1	C	397	GLY	7.7
1	D	363	GLN	7.4
1	D	355	ALA	7.0
1	D	364	PHE	6.7
1	D	361	LEU	6.4
1	D	335	ILE	5.3
1	D	367	ARG	5.0
1	D	357	SER	5.0
1	D	370	PRO	4.8
1	D	371	ARG	4.8
1	A	315	HIS	4.4
1	D	390[A]	LEU	4.4
1	D	376	PRO	4.4
1	D	387	GLU	4.1
1	D	334	GLY	4.0
1	D	388	GLY	4.0
1	D	333	PRO	3.9
1	D	369	GLN	3.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	389	GLN	3.9
1	C	380	ILE	3.8
1	D	332	THR	3.6
1	C	332[A]	THR	3.5
1	C	370	PRO	3.5
1	D	375	ARG	3.4
1	D	317	PRO	3.3
1	C	378	ASP	3.3
1	D	331	GLU	3.3
1	D	362	GLU	3.1
1	C	381	THR	3.1
1	D	377	GLY	3.0
1	C	330[A]	SER	3.0
1	B	375	ARG	2.9
1	D	365	THR	2.8
1	B	378	ASP	2.8
1	A	329	LEU	2.8
1	D	328	ILE	2.7
1	C	371	ARG	2.7
1	C	353	ILE	2.6
1	D	372	PHE	2.6
1	D	393	GLU	2.5
1	C	331	GLU	2.5
1	B	384	ASP	2.5
1	D	325	LEU	2.5
1	D	366	GLN	2.4
1	D	345	ALA	2.4
1	C	358	SER	2.4
1	D	358	SER	2.3
1	D	373	ARG	2.2
1	D	319	VAL	2.2
1	C	386	ILE	2.1
1	D	353	ILE	2.1
1	D	352	ASP	2.1
1	D	391	THR	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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.