wwPDB X-ray Structure Validation Summary Report (i)

Feb 22, 2017 – 10:56 AM EST

PDB ID	:	5GVW
Title	:	Crystal structure of the apo-form glycosyltransferase GlyE in Streptococcus pneumoniae TIGR4
Authors	:	Jiang, Y.L.; Jin, H.; Zhao, R.L.; Yang, H.B.; Chen, Y.; Zhou, C.Z.
Deposited on	:	2016-09-07
Resolution	:	2.40 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

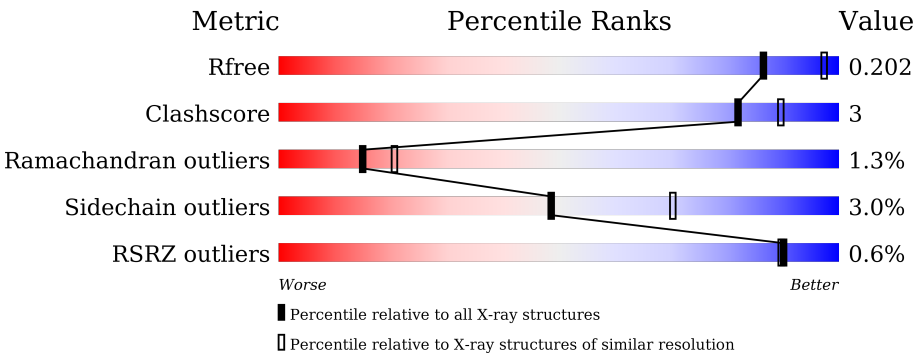
MolProbity	:	4.02b-467
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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. 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 <=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	406	89% 5% • •
1	B	406	.% 88% 6% • •
1	C	406	89% 7% • •
1	D	406	.% 87% 8% • •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 13300 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 Glycosyl transferase family 8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	C	391	3212	2082	516	598	16	0	0	0
1	A	390	3204	2078	514	596	16	0	0	0
1	B	389	3197	2074	513	594	16	0	0	0
1	D	389	3196	2073	513	595	15	0	0	0

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mn		
2	B	1	1	1	0	0
2	A	1	1	1	0	0
2	D	1	1	1	0	0
2	C	1	1	1	0	0

- Molecule 3 is water.

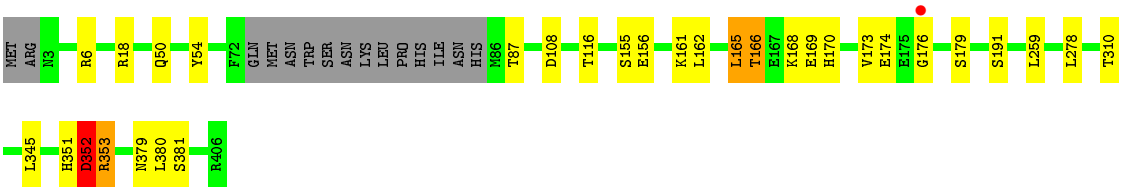
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	C	127	127	127	0	0
3	A	136	136	136	0	0
3	B	121	121	121	0	0
3	D	103	103	103	0	0

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 errors 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.

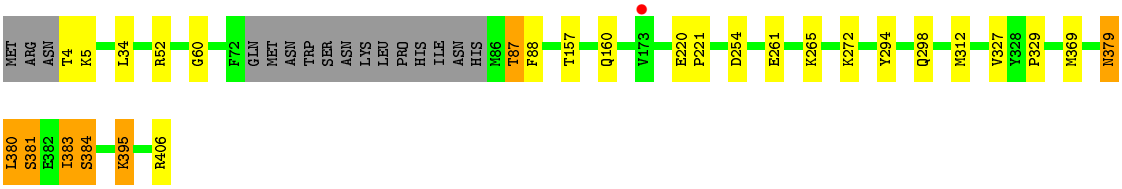
- Molecule 1: Glycosyl transferase family 8

Chain C:



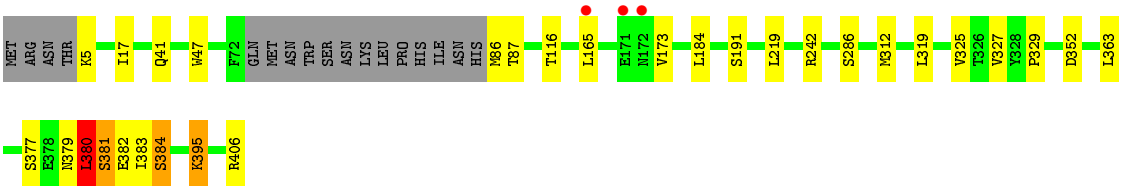
- Molecule 1: Glycosyl transferase family 8

Chain A:



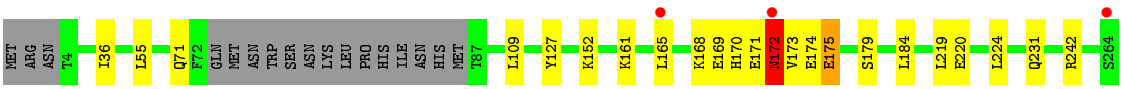
- Molecule 1: Glycosyl transferase family 8

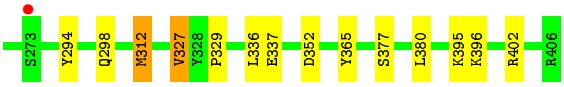
Chain B:



- Molecule 1: Glycosyl transferase family 8

Chain D:




S273
Y294
Q298
N312
V327
Y328
P329
L336
E337
D352
Y365
S377
L380
K395
K396
R402
R406

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	89.12Å 84.21Å 130.11Å 90.00° 89.97° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 44.57 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.0 (50.00-2.40) 95.6 (44.57-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.95 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.198 , 0.255 0.198 , 0.202	Depositor DCC
R_{free} test set	3638 reflections (5.30%)	DCC
Wilson B-factor (Å^2)	33.1	Xtriage
Anisotropy	1.369	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 20.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.118 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	13300	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.33 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 8.8898e-03.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: MN

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	0.63	0/3284	0.78	3/4452 (0.1%)
1	B	0.63	0/3277	0.79	0/4442
1	C	0.60	0/3292	0.76	2/4463 (0.0%)
1	D	0.62	0/3276	0.77	2/4442 (0.0%)
All	All	0.62	0/13129	0.77	7/17799 (0.0%)

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	C	0	1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	402	ARG	NE-CZ-NH1	6.58	123.59	120.30
1	C	108	ASP	CB-CG-OD1	5.92	123.63	118.30
1	A	254	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	D	109	LEU	CA-CB-CG	5.60	128.19	115.30
1	A	254	ASP	CB-CG-OD1	5.37	123.14	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	352	ASP	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	3204	0	3142	13	0
1	B	3197	0	3135	18	0
1	C	3212	0	3148	18	0
1	D	3196	0	3133	33	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	136	0	0	1	0
3	B	121	0	0	2	0
3	C	127	0	0	1	0
3	D	103	0	0	0	0
All	All	13300	0	12558	82	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.

The worst 5 of 82 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:D:165:LEU:CD1	1:D:184:LEU:HD13	1.44	1.44
1:D:165:LEU:HD11	1:D:184:LEU:CD1	1.47	1.42
1:C:173:VAL:HG11	1:C:179:SER:CB	1.54	1.37
1:C:173:VAL:CG1	1:C:179:SER:CB	2.23	1.15
1:D:165:LEU:HD12	1:D:184:LEU:HD13	1.28	1.08

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	386/406 (95%)	366 (95%)	14 (4%)	6 (2%)	12	16
1	B	385/406 (95%)	367 (95%)	13 (3%)	5 (1%)	15	21
1	C	387/406 (95%)	369 (95%)	13 (3%)	5 (1%)	15	21
1	D	385/406 (95%)	362 (94%)	19 (5%)	4 (1%)	19	28
All	All	1543/1624 (95%)	1464 (95%)	59 (4%)	20 (1%)	15	21

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	352	ASP
1	A	381	SER
1	B	379	ASN
1	D	172	ASN
1	D	175	GLU

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	353/369 (96%)	345 (98%)	8 (2%)	58	78
1	B	352/369 (95%)	340 (97%)	12 (3%)	44	65
1	C	354/369 (96%)	342 (97%)	12 (3%)	44	65
1	D	352/369 (95%)	342 (97%)	10 (3%)	51	72
All	All	1411/1476 (96%)	1369 (97%)	42 (3%)	48	70

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	395	LYS
1	B	191	SER
1	D	327	VAL

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Mol	Chain	Res	Type
1	A	406	ARG
1	B	116	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	274	GLN

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)

Of 4 ligands modelled in this entry, 4 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)

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	390/406 (96%)	-0.69	1 (0%)	94	94	26, 39, 83, 120	0
1	B	389/406 (95%)	-0.73	3 (0%)	87	87	26, 38, 77, 133	0
1	C	391/406 (96%)	-0.64	1 (0%)	94	94	28, 44, 85, 112	0
1	D	389/406 (95%)	-0.60	4 (1%)	84	83	32, 46, 82, 146	0
All	All	1559/1624 (95%)	-0.66	9 (0%)	90	90	26, 42, 83, 146	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	173	VAL	3.6
1	B	172	ASN	3.5
1	D	273	SER	3.0
1	B	165	LEU	2.8
1	D	165	LEU	2.8

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
2	MN	B	501	1/1	0.92	0.04	-	65,65,65,65	0
2	MN	D	501	1/1	0.97	0.06	-	66,66,66,66	0
2	MN	A	501	1/1	0.90	0.04	-	70,70,70,70	0
2	MN	C	501	1/1	0.91	0.06	-	79,79,79,79	0

6.5 Other polymers (i)

There are no such residues in this entry.