



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 14, 2019 – 10:16 AM EST

PDB ID : 4X7R
Title : Crystal structure of S. aureus TarM G117R mutant in complex with Fondaparinux, alpha-GlcNAc-glycerol and UDP
Authors : Worrall, L.J.; Sobhanifar, S.; Strynadka, N.C.
Deposited on : 2014-12-09
Resolution : 2.15 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
Xtriage (Phenix)	:	1.13
EDS	:	2.4
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.4

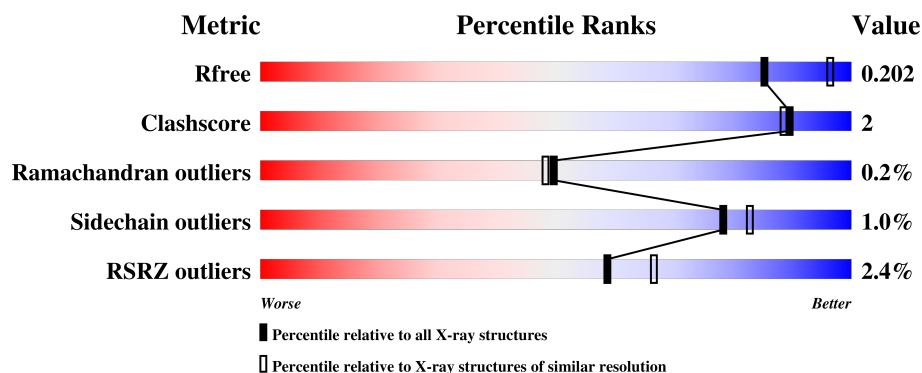
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	111664	1287 (2.16-2.16)
Clashscore	122126	1390 (2.16-2.16)
Ramachandran outliers	120053	1368 (2.16-2.16)
Sidechain outliers	120020	1367 (2.16-2.16)
RSRZ outliers	108989	1262 (2.16-2.16)

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 $\leq 5\%$. 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	493	
1	B	493	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8717 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.

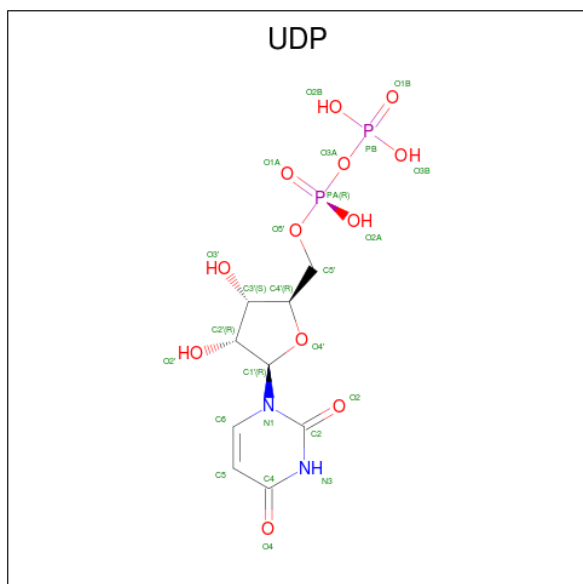
- Molecule 1 is a protein called TarM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	493	Total	C	N	O	S	0	0	0
			4040	2585	684	752	19			
1	B	493	Total	C	N	O	S	0	0	0
			4040	2585	684	752	19			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	117	ARG	GLY	engineered mutation	UNP H0AM96
B	117	ARG	GLY	engineered mutation	UNP H0AM96

- Molecule 2 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C₉H₁₄N₂O₁₂P₂).



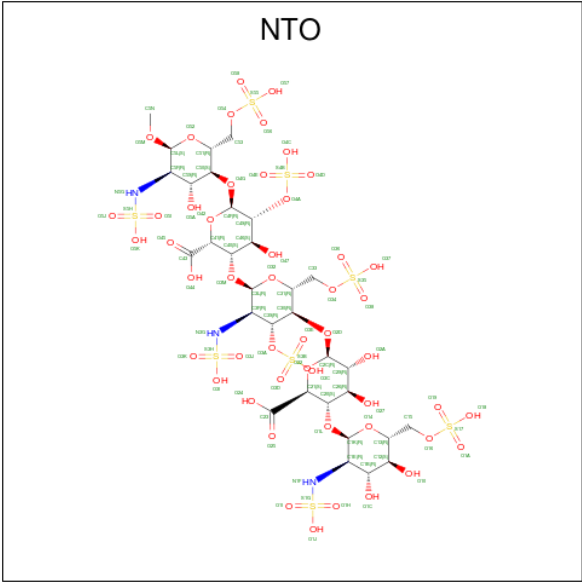
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

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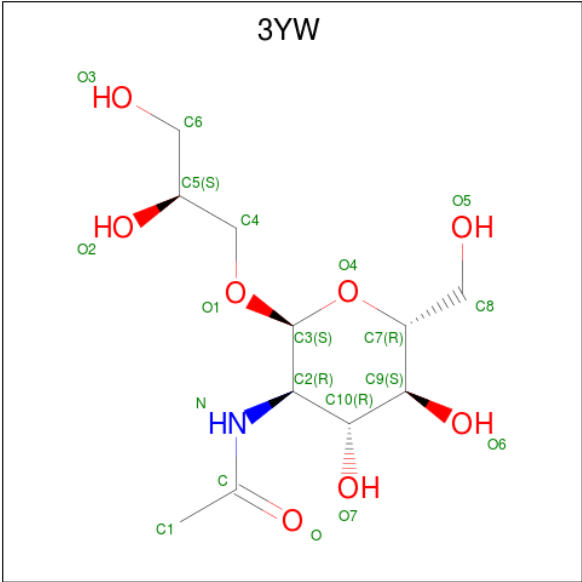
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 3 is TRISULFOAMINO HEPARIN PENTASACCHARIDE (three-letter code: NTO) (formula: C₃₁H₅₃N₃O₄₉S₈).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			91	31	3	49	8		
3	B	1	Total	C	N	O	S	0	0
			91	31	3	49	8		

- Molecule 4 is (2S)-2,3-dihydroxypropyl 2-(acetlamino)-2-deoxy-alpha-D-glucopyranoside (three-letter code: 3YW) (formula: C₁₁H₂₁NO₈).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			20	11	1	8		
4	B	1	Total	C	N	O	0	0
			20	11	1	8		

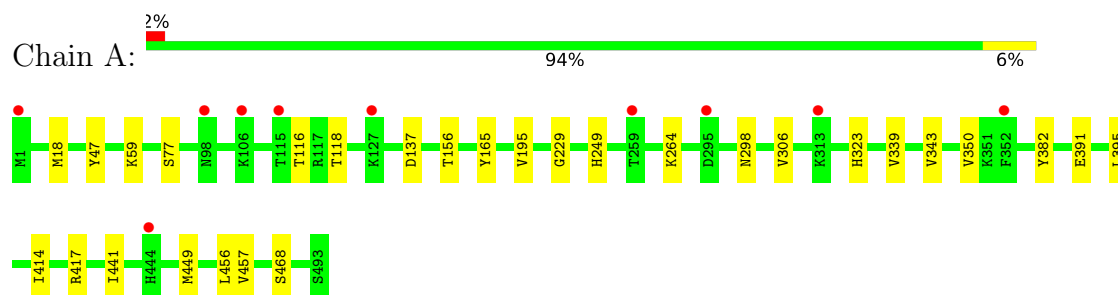
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	183	Total	O	0	0
			183	183		
5	B	182	Total	O	0	0
			182	182		

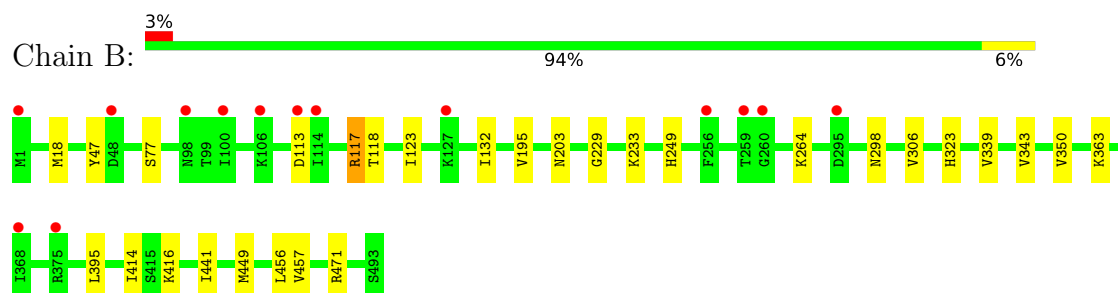
3 Residue-property plots [i](#)

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: TarM



• Molecule 1: TarM



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	43.47Å 92.14Å 96.11Å 65.89° 83.66° 84.12°	Depositor
Resolution (Å)	87.48 – 2.15 87.48 – 2.15	Depositor EDS
% Data completeness (in resolution range)	97.9 (87.48-2.15) 97.9 (87.48-2.15)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.14Å)	Xtriage
Refinement program	BUSTER	Depositor
R, R_{free}	0.179 , 0.200 0.181 , 0.202	Depositor DCC
R_{free} test set	3707 reflections (5.16%)	wwPDB-VP
Wilson B-factor (Å ²)	38.4	Xtriage
Anisotropy	0.351	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 55.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.106 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8717	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.28% 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: UDP, 3YW, NTO

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	0.49	0/4117	0.66	0/5525
1	B	0.49	0/4117	0.66	0/5525
All	All	0.49	0/8234	0.66	0/11050

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 [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	4040	0	4067	16	0
1	B	4040	0	4067	17	0
2	A	25	0	11	1	0
2	B	25	0	11	0	0
3	A	91	0	51	1	0
3	B	91	0	51	2	0
4	A	20	0	21	3	0
4	B	20	0	21	2	0
5	A	183	0	0	1	0
5	B	182	0	0	2	0
All	All	8717	0	8300	34	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 2.

All (34) 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:339:VAL:HG21	1:B:449:MET:HE2	1.57	0.87
1:A:339:VAL:HG21	1:A:449:MET:HE2	1.57	0.87
1:A:343:VAL:HG12	1:A:350:VAL:HG11	1.72	0.71
1:B:343:VAL:HG12	1:B:350:VAL:HG11	1.72	0.69
1:B:18:MET:HB2	4:B:503:3YW:H2	1.79	0.63
1:B:306:VAL:CG2	1:B:414:ILE:HD11	2.29	0.63
1:A:306:VAL:CG2	1:A:414:ILE:HD11	2.31	0.60
1:B:395:LEU:HD22	1:B:456:LEU:HB3	1.89	0.54
1:A:395:LEU:HD22	1:A:456:LEU:HB3	1.89	0.53
1:B:249:HIS:O	4:B:503:3YW:H19	2.09	0.53
1:A:229:GLY:HA3	3:A:502:NTO:O3D	2.11	0.51
1:B:395:LEU:HD21	1:B:457:VAL:HG13	1.95	0.49
1:A:395:LEU:HD21	1:A:457:VAL:HG13	1.94	0.48
1:B:123:ILE:HG12	1:B:132:ILE:HG12	1.98	0.46
1:A:323:HIS:HE1	5:A:610:HOH:O	1.99	0.45
1:A:18:MET:HB2	4:A:503:3YW:C4	2.47	0.45
1:B:229:GLY:HA3	3:B:502:NTO:O3D	2.17	0.44
1:B:323:HIS:HE1	5:B:619:HOH:O	2.00	0.44
1:B:306:VAL:HG22	1:B:414:ILE:HD11	2.00	0.44
1:B:416:LYS:HE3	1:B:471:ARG:HD2	1.99	0.43
1:A:441:ILE:HG21	1:A:449:MET:HB2	2.01	0.43
1:A:249:HIS:O	4:A:503:3YW:H19	2.18	0.43
1:B:113:ASP:O	1:B:117:ARG:HA	2.19	0.43
1:B:77:SER:HB2	1:B:195:VAL:HG11	1.99	0.43
1:A:77:SER:HB2	1:A:195:VAL:HG11	2.01	0.42
1:B:233:LYS:NZ	5:B:604:HOH:O	2.52	0.42
1:B:441:ILE:HG21	1:B:449:MET:HB2	2.01	0.42
1:A:156:THR:HB	1:A:165:TYR:HB3	2.00	0.42
1:A:306:VAL:HG22	1:A:414:ILE:HD11	1.99	0.42
1:A:391:GLU:HA	1:A:417:ARG:HH21	1.85	0.42
1:A:116:THR:HG23	1:A:118:THR:HG22	2.02	0.42
2:A:501:UDP:O1B	4:A:503:3YW:O1	2.39	0.41
1:B:203:ASN:HB3	3:B:502:NTO:O4E	2.20	0.41
1:A:59:LYS:NZ	1:A:382:TYR:OH	2.53	0.41

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	491/493 (100%)	473 (96%)	17 (4%)	1 (0%)	49	48
1	B	491/493 (100%)	473 (96%)	17 (4%)	1 (0%)	49	48
All	All	982/986 (100%)	946 (96%)	34 (4%)	2 (0%)	49	48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	298	ASN
1	A	298	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	450/450 (100%)	446 (99%)	4 (1%)	81	85
1	B	450/450 (100%)	445 (99%)	5 (1%)	76	80
All	All	900/900 (100%)	891 (99%)	9 (1%)	78	83

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	TYR
1	A	137	ASP
1	A	264	LYS
1	A	468	SER

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Mol	Chain	Res	Type
1	B	47	TYR
1	B	117	ARG
1	B	118	THR
1	B	264	LYS
1	B	363	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	HIS
1	A	203	ASN
1	B	203	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

6 ligands are modelled in this entry.

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

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	493/493 (100%)	0.26	10 (2%) 65 72	31, 54, 93, 118	0
1	B	493/493 (100%)	0.26	14 (2%) 53 61	32, 54, 95, 132	0
All	All	986/986 (100%)	0.26	24 (2%) 59 66	31, 54, 95, 132	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	295	ASP	4.8
1	B	368	ILE	4.2
1	B	1	MET	3.9
1	B	259	THR	3.7
1	B	295	ASP	3.5
1	A	1	MET	3.5
1	B	114	ILE	3.2
1	A	127	LYS	3.2
1	B	260	GLY	3.1
1	A	115	THR	3.1
1	A	98	ASN	2.8
1	B	375	ARG	2.7
1	B	127	LYS	2.6
1	A	313	LYS	2.5
1	A	106	LYS	2.4
1	B	100	ILE	2.4
1	A	444	HIS	2.3
1	B	106	LYS	2.2
1	B	98	ASN	2.2
1	B	256	PHE	2.2
1	B	113	ASP	2.2
1	B	48	ASP	2.1
1	A	352	PHE	2.1
1	A	259	THR	2.1

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. 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(\AA^2)	Q<0.9
4	3YW	B	503	20/20	0.81	0.20	37,52,63,67	20
4	3YW	A	503	20/20	0.88	0.20	36,51,55,57	20
3	NTO	B	502	91/91	0.95	0.14	40,52,75,87	91
3	NTO	A	502	91/91	0.95	0.13	41,51,76,89	91
2	UDP	A	501	25/25	0.97	0.11	45,50,55,57	0
2	UDP	B	501	25/25	0.97	0.12	46,50,56,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.