



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 3WOV / pdb_00003wov
Title : Crystal structure of the C-terminal globular domain of oligosaccharyltransferase (PaAglB-L, Q9V250_PYRAB, PAB2202) from *Pyrococcus abyssi*
Authors : Matsuoka, R.; Nyirenda, J.; Maita, N.; Kohda, D.
Deposited on : 2014-01-05
Resolution : 3.11 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
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

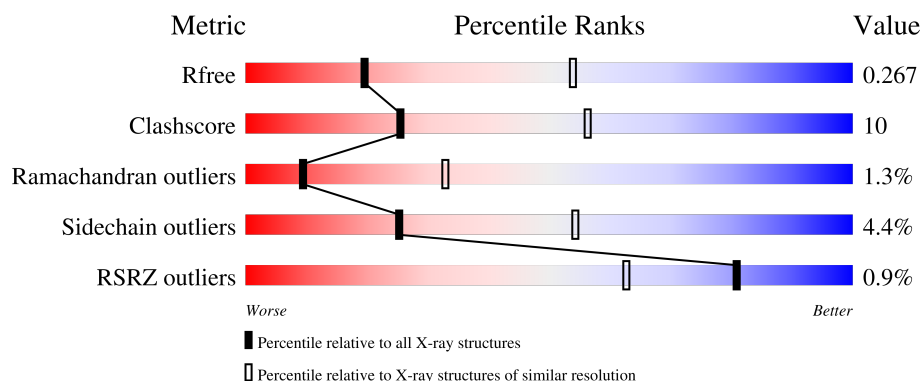
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.11 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	1816 (3.14-3.10)
Clashscore	190562	1906 (3.14-3.10)
Ramachandran outliers	187476	1802 (3.14-3.10)
Sidechain outliers	187428	1802 (3.14-3.10)
RSRZ outliers	180081	1816 (3.14-3.10)

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	512	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3650 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 Oligosaccharyl transferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	457	Total	C	N	O	S	0	0	0
			3649	2366	610	667	6			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	475	MET	-	expression tag	UNP Q9V250
A	977	HIS	-	expression tag	UNP Q9V250
A	978	HIS	-	expression tag	UNP Q9V250
A	979	HIS	-	expression tag	UNP Q9V250
A	980	HIS	-	expression tag	UNP Q9V250
A	981	HIS	-	expression tag	UNP Q9V250
A	982	HIS	-	expression tag	UNP Q9V250
A	983	HIS	-	expression tag	UNP Q9V250
A	984	HIS	-	expression tag	UNP Q9V250
A	985	HIS	-	expression tag	UNP Q9V250
A	986	HIS	-	expression tag	UNP Q9V250

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 1: Oligosaccharyl transferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	70.75Å 70.75Å 204.75Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	23.62 – 3.11 23.62 – 3.11	Depositor EDS
% Data completeness (in resolution range)	99.6 (23.62-3.11) 99.3 (23.62-3.11)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.15 (at 3.10Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.228 , 0.266 0.234 , 0.267	Depositor DCC
R_{free} test set	1124 reflections (9.95%)	wwPDB-VP
Wilson B-factor (Å ²)	102.8	Xtriage
Anisotropy	0.073	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 78.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.057 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	3650	wwPDB-VP
Average B, all atoms (Å ²)	116.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.01% 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: CA

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	0.30	0/3737	0.76	2/5068 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	641	ARG	N-CA-C	-5.72	105.60	112.58
1	A	664	GLY	N-CA-C	-5.60	107.52	115.30

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	3649	0	3660	70	0
2	A	1	0	0	0	0
All	All	3650	0	3660	70	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 10.

All (70) 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:519:TYR:HA	1:A:522:GLU:HB3	1.62	0.80
1:A:846:ILE:HD11	1:A:871:LEU:HD21	1.64	0.78
1:A:941:GLY:HA3	1:A:943:LYS:H	1.50	0.77
1:A:600:ARG:HH11	1:A:601:GLY:H	1.37	0.72
1:A:500:TRP:HD1	1:A:501:LEU:HD12	1.57	0.68
1:A:771:ASP:OD1	1:A:799:HIS:ND1	2.30	0.64
1:A:820:VAL:HG12	1:A:962:VAL:HA	1.78	0.64
1:A:654:ILE:HD11	1:A:702:ILE:HG23	1.80	0.63
1:A:941:GLY:HA3	1:A:942:ASP:HB3	1.83	0.60
1:A:686:THR:HG21	1:A:696:ILE:HD11	1.84	0.60
1:A:652:LEU:HD22	1:A:704:ILE:HD12	1.84	0.58
1:A:666:CYS:SG	1:A:667:SER:N	2.76	0.58
1:A:648:PRO:HB3	1:A:676:LEU:HD13	1.87	0.56
1:A:547:LEU:HD12	1:A:551:ARG:HG3	1.88	0.56
1:A:791:ILE:HB	1:A:807:VAL:HG21	1.87	0.55
1:A:755:THR:O	1:A:759:HIS:NE2	2.41	0.54
1:A:616:TYR:CE2	1:A:678:LEU:HG	2.43	0.54
1:A:779:VAL:HG22	1:A:819:LEU:HG	1.91	0.52
1:A:854:THR:HA	1:A:921:GLU:HB3	1.90	0.52
1:A:813:LYS:HD2	1:A:813:LYS:H	1.74	0.52
1:A:925:PRO:HB2	1:A:928:VAL:HG23	1.91	0.51
1:A:741:GLU:HG2	1:A:750:ALA:HA	1.92	0.51
1:A:859:VAL:HG21	1:A:955:PHE:CE1	2.46	0.51
1:A:571:TYR:CE2	1:A:573:ASN:HB2	2.46	0.50
1:A:842:ASN:HD21	1:A:844:ILE:HG12	1.77	0.49
1:A:608:PRO:O	1:A:618:ASN:ND2	2.41	0.49
1:A:697:LYS:HD2	1:A:714:LEU:HD22	1.94	0.49
1:A:570:ILE:HD11	1:A:728:ILE:HD12	1.94	0.49
1:A:501:LEU:HA	1:A:505:THR:HG23	1.95	0.48
1:A:826:PRO:O	1:A:959:LYS:NZ	2.27	0.48
1:A:839:GLU:HG3	1:A:854:THR:O	2.13	0.48
1:A:932:TYR:HA	1:A:935:LYS:HB2	1.95	0.48
1:A:653:LEU:O	1:A:657:ASN:N	2.45	0.48
1:A:737:ILE:HD13	1:A:763:LEU:HD22	1.95	0.48
1:A:570:ILE:HG12	1:A:730:TYR:HE1	1.79	0.48
1:A:941:GLY:CA	1:A:943:LYS:H	2.25	0.48
1:A:570:ILE:HD13	1:A:699:ALA:HA	1.96	0.47
1:A:941:GLY:HA3	1:A:943:LYS:N	2.26	0.46
1:A:744:ILE:HB	1:A:749:LYS:HD2	1.98	0.46
1:A:909:ILE:HD13	1:A:918:VAL:HG11	1.96	0.46
1:A:846:ILE:HD13	1:A:953:PRO:HD3	1.98	0.46
1:A:605:THR:HB	1:A:690:VAL:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:855:LEU:HB2	1:A:920:ALA:O	2.16	0.46
1:A:902:ILE:HD13	1:A:924:MET:HE1	1.98	0.46
1:A:909:ILE:HD13	1:A:918:VAL:HG21	1.99	0.45
1:A:651:THR:HG21	1:A:678:LEU:HD22	2.00	0.44
1:A:702:ILE:HG22	1:A:704:ILE:HG22	2.00	0.44
1:A:842:ASN:ND2	1:A:844:ILE:HG12	2.33	0.43
1:A:609:LEU:HD11	1:A:685:ILE:HG13	2.00	0.43
1:A:709:GLY:O	1:A:713:LYS:HG3	2.19	0.43
1:A:840:ILE:HG23	1:A:841:ALA:H	1.82	0.43
1:A:650:TYR:CD1	1:A:659:LYS:HD3	2.54	0.43
1:A:849:GLU:OE2	1:A:929:ILE:HG13	2.19	0.43
1:A:923:ASN:OD1	1:A:924:MET:N	2.52	0.43
1:A:591:ARG:HA	1:A:595:GLY:HA2	2.01	0.43
1:A:852:LYS:HE3	1:A:923:ASN:HB2	2.00	0.43
1:A:679:ALA:HB1	1:A:680:PRO:HD2	2.00	0.43
1:A:860:GLY:HA2	1:A:914:GLY:O	2.19	0.42
1:A:898:ASP:OD2	1:A:932:TYR:OH	2.38	0.42
1:A:645:GLU:O	1:A:667:SER:N	2.53	0.42
1:A:630:SER:OG	1:A:631:ASN:N	2.51	0.41
1:A:645:GLU:H	1:A:667:SER:HB2	1.85	0.41
1:A:613:GLY:HA2	1:A:614:GLY:HA2	1.53	0.41
1:A:641:ARG:HG3	1:A:641:ARG:O	2.21	0.41
1:A:780:TYR:HB2	1:A:818:ARG:HB3	2.03	0.41
1:A:500:TRP:O	1:A:501:LEU:HB2	2.21	0.40
1:A:845:ARG:HH21	1:A:949:ILE:HG21	1.86	0.40
1:A:816:LYS:HB2	1:A:816:LYS:HE3	1.87	0.40
1:A:609:LEU:HD23	1:A:618:ASN:HB2	2.03	0.40
1:A:733:ARG:HA	1:A:734:PRO:HD2	1.95	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	449/512 (88%)	410 (91%)	33 (7%)	6 (1%)	9	33

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	600	ARG
1	A	840	ILE
1	A	855	LEU
1	A	920	ALA
1	A	629	GLN
1	A	928	VAL

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	388/433 (90%)	371 (96%)	17 (4%)	25	54

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

Mol	Chain	Res	Type
1	A	497	VAL
1	A	519	TYR
1	A	579	ASN
1	A	617	VAL
1	A	657	ASN
1	A	678	LEU
1	A	716	SER
1	A	771	ASP
1	A	800	LEU
1	A	809	VAL
1	A	821	LEU
1	A	849	GLU
1	A	903	THR
1	A	912	HIS
1	A	929	ILE

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Mol	Chain	Res	Type
1	A	939	GLU
1	A	944	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	502	ASN
1	A	602	GLN
1	A	896	HIS
1	A	916	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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	457/512 (89%)	-0.12	4 (0%) 81 63	66, 110, 186, 230	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	504	ASN	4.0
1	A	924	MET	3.2
1	A	520	TRP	2.9
1	A	596	ASP	2.5

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(Å ²)	Q<0.9
2	CA	A	1001	1/1	0.99	0.10	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.