



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:46 PM UTC

PDB ID : 4L22 / pdb_00004l22
Title : Crystal structure of putative glycogen phosphorylase from *Streptococcus mutans*
Authors : Lihan, M.-Y.; Li, G.-L.; Li, L.-F.; Su, X.-D.
Deposited on : 2013-06-04
Resolution : 2.45 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

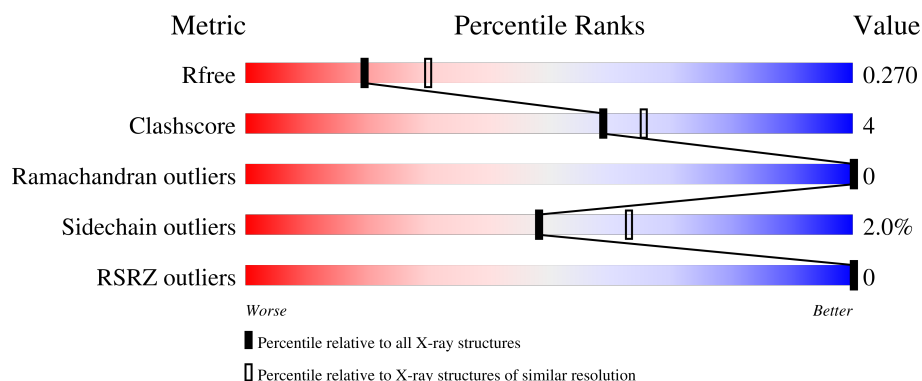
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	758	 87% 12% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6114 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 Phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	753	Total	C	N	O	S	0	0	0
			6086	3904	1000	1166	16			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	28	Total	O	0	0
			28	28		

- Molecule 1: Phosphorylase

Y511	P287	Met
I519	N310	Thr
A537	M311	Gln
	I312	Lys
L554	P337	Thr
S555	V340	K6
I558	E344	Q31
S585	V384	H34
P566	L397	F35
Y567	K398	P44
V570	P399	K63
M606	Y404	L64
M607	P405	L65
L611	E406	S86
	I415	M67
G632	T416	K76
M635	F417	T77
K641	R418	E96
I646	R419	C112
	W420	Q144
A665	L421	P149
V666	D427	R150
I667	L428	Y151
K684	I432	S165
K685	I436	R171
E689	Y440	S177
F701	L441	D190
W702	E442	L203
T703	D443	
	L450	I208
D706	I466	N222
L707		L223
D723	K482	V248
	G483	E258
M728	I484	B262
K729	R498	V276
I732	F499	Q276
F741	Y502	I277
L758	K503	T285
	R504	L296
	Q505	
	Q506	
	M507	

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	119.72Å 85.02Å 84.46Å 90.00° 93.30° 90.00°	Depositor
Resolution (Å)	84.32 – 2.45 84.32 – 2.45	Depositor EDS
% Data completeness (in resolution range)	88.3 (84.32-2.45) 88.3 (84.32-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.92 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.8.0069, PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.222 , 0.266 (Not available) , 0.270	Depositor DCC
R_{free} test set	1402 reflections (4.48%)	wwPDB-VP
Wilson B-factor (Å ²)	49.2	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 12.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6114	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.88% 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](#)

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	0.76	0/6204	0.82	0/8390

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	6086	0	6065	54	0
2	A	28	0	0	1	0
All	All	6114	0	6065	54	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 4.

All (54) 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:607:MET:HE3	1:A:741:PHE:HB3	1.63	0.80
1:A:555:SER:HB2	1:A:570:VAL:O	1.89	0.71
1:A:149:PRO:HB2	1:A:151:TYR:CE2	2.37	0.60
1:A:427:ASP:HB3	1:A:466:ILE:HD12	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:VAL:HG13	1:A:285:VAL:HA	1.85	0.57
1:A:165:SER:OG	1:A:177:SER:O	2.23	0.54
1:A:482:LYS:O	1:A:484:ILE:HG13	2.08	0.54
1:A:415:ILE:HG23	1:A:607:MET:HE2	1.90	0.54
1:A:112:CYS:SG	1:A:416:THR:HG22	2.48	0.54
1:A:641:LYS:HB2	1:A:646:ILE:CD1	2.39	0.53
1:A:685:LYS:O	1:A:689:GLU:HB2	2.09	0.53
1:A:723:ASP:OD2	1:A:723:ASP:C	2.54	0.51
1:A:684:LYS:HD2	1:A:684:LYS:N	2.26	0.50
1:A:428:LEU:O	1:A:432:ILE:HG12	2.12	0.49
1:A:222:ASN:O	1:A:223:LEU:C	2.55	0.48
1:A:499:PHE:HB2	1:A:537:ALA:HB2	1.96	0.48
1:A:421:LEU:HB2	1:A:611:LEU:HD21	1.96	0.48
1:A:277:ILE:HG13	1:A:277:ILE:O	2.14	0.47
1:A:258:GLU:O	1:A:262:ARG:HG3	2.13	0.47
1:A:504:ARG:HA	1:A:506:GLN:NE2	2.29	0.47
1:A:498:ARG:O	1:A:503:LYS:HD2	2.15	0.46
1:A:632:GLY:H	1:A:635:ASN:HD22	1.62	0.46
1:A:149:PRO:HG3	1:A:208:ILE:HG21	1.96	0.46
1:A:607:MET:HG2	1:A:741:PHE:CG	2.51	0.46
1:A:507:MET:CE	1:A:703:THR:O	2.64	0.45
1:A:286:ILE:HB	1:A:287:PRO:HD3	1.98	0.45
1:A:511:TYR:CD2	1:A:511:TYR:C	2.91	0.45
1:A:519:ILE:HD13	1:A:567:TYR:HB2	1.99	0.45
1:A:436:ILE:HD13	1:A:450:LEU:HG	1.98	0.45
1:A:440:TYR:HA	1:A:443:ASP:O	2.17	0.45
1:A:63:LYS:O	1:A:419:ARG:NH2	2.50	0.44
1:A:729:LYS:HE3	1:A:729:LYS:HB2	1.83	0.44
1:A:171:ARG:HB3	2:A:815:HOH:O	2.17	0.44
1:A:64:LEU:O	1:A:65:LEU:C	2.61	0.43
1:A:502:TYR:HB3	1:A:701:PHE:CD1	2.53	0.43
1:A:565:SER:HB2	1:A:566:PRO:HD3	2.01	0.43
1:A:275:VAL:HB	1:A:312:ILE:HD13	2.01	0.43
1:A:507:MET:HE1	1:A:706:ASP:HB2	2.00	0.43
1:A:665:ALA:O	1:A:666:VAL:C	2.61	0.42
1:A:554:LEU:O	1:A:558:ILE:HG12	2.19	0.42
1:A:398:LYS:HB3	1:A:399:PRO:HD3	2.01	0.42
1:A:728:ASN:O	1:A:732:ILE:HG13	2.19	0.42
1:A:398:LYS:N	1:A:399:PRO:CD	2.83	0.42
1:A:171:ARG:HG3	1:A:337:PRO:HG3	2.01	0.42
1:A:76:LYS:HG3	1:A:77:THR:N	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:607:MET:HG2	1:A:741:PHE:CD1	2.55	0.41
1:A:417:PHE:O	1:A:421:LEU:HB3	2.21	0.41
1:A:63:LYS:HE2	1:A:96:GLU:O	2.20	0.41
1:A:144:GLN:HE21	1:A:684:LYS:HD3	1.85	0.41
1:A:34:HIS:O	1:A:35:PHE:C	2.61	0.41
1:A:44:PRO:HD2	1:A:190:ASP:O	2.21	0.41
1:A:667:ILE:HG12	1:A:707:LEU:HD23	2.03	0.41
1:A:340:VAL:O	1:A:344:GLU:HG3	2.21	0.40
1:A:404:TYR:HA	1:A:406:GLU:OE1	2.22	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	751/758 (99%)	720 (96%)	31 (4%)	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	664/669 (99%)	651 (98%)	13 (2%)	48	63

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	GLN
1	A	67	ASN
1	A	203	LEU
1	A	248	VAL
1	A	310	ASN
1	A	384	VAL
1	A	397	LEU
1	A	406	GLU
1	A	442	GLU
1	A	606	ASN
1	A	666	VAL
1	A	684	LYS
1	A	689	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	ASN
1	A	144	GLN
1	A	243	GLN
1	A	244	GLN
1	A	612	ASN
1	A	664	ASN
1	A	725	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](#)

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	753/758 (99%)	-0.15	0 100 100	38, 52, 70, 82	0

There are no RSRZ outliers to report.

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.