wwPDB X-ray Structure Validation Summary Report (i)

Feb 3, 2024 – 09:23 AM EST

PDB ID	:	1LF6
Title	:	CRYSTAL STRUCTURE OF BACTERIAL GLUCOAMYLASE
Authors	:	Aleshin, A.E.; Feng, P.-H.; Honzatko, R.B.; Reilly, P.J.
Deposited on	:	2002-04-10
Resolution	:	2.10 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

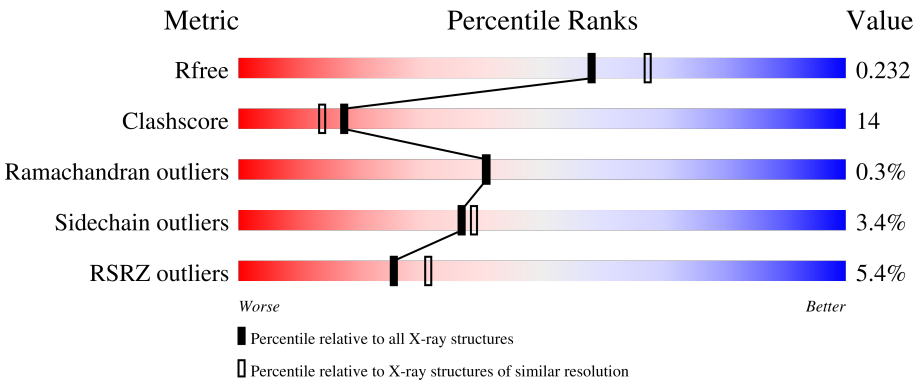
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 <=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	684	7% 74% 24% ••
1	B	684	4% 74% 22% ••

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 11584 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.

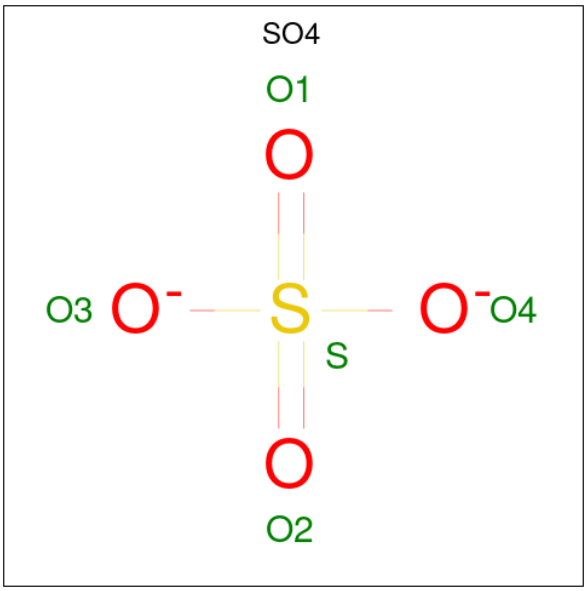
- Molecule 1 is a protein called glucoamylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	674	5333	3385	881	1052	15	0	0	0
1	B	674	5333	3385	881	1052	15	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	125	PHE	-	SEE REMARK 999	UNP O85672
A	252	GLN	GLY	conflict	UNP O85672
A	680	LYS	-	SEE REMARK 999	UNP O85672
A	681	ARG	-	SEE REMARK 999	UNP O85672
A	682	TYR	-	SEE REMARK 999	UNP O85672
A	683	VAL	-	SEE REMARK 999	UNP O85672
A	684	ALA	-	SEE REMARK 999	UNP O85672
B	125	PHE	-	SEE REMARK 999	UNP O85672
B	252	GLN	GLY	conflict	UNP O85672
B	680	LYS	-	SEE REMARK 999	UNP O85672
B	681	ARG	-	SEE REMARK 999	UNP O85672
B	682	TYR	-	SEE REMARK 999	UNP O85672
B	683	VAL	-	SEE REMARK 999	UNP O85672
B	684	ALA	-	SEE REMARK 999	UNP O85672

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is water.

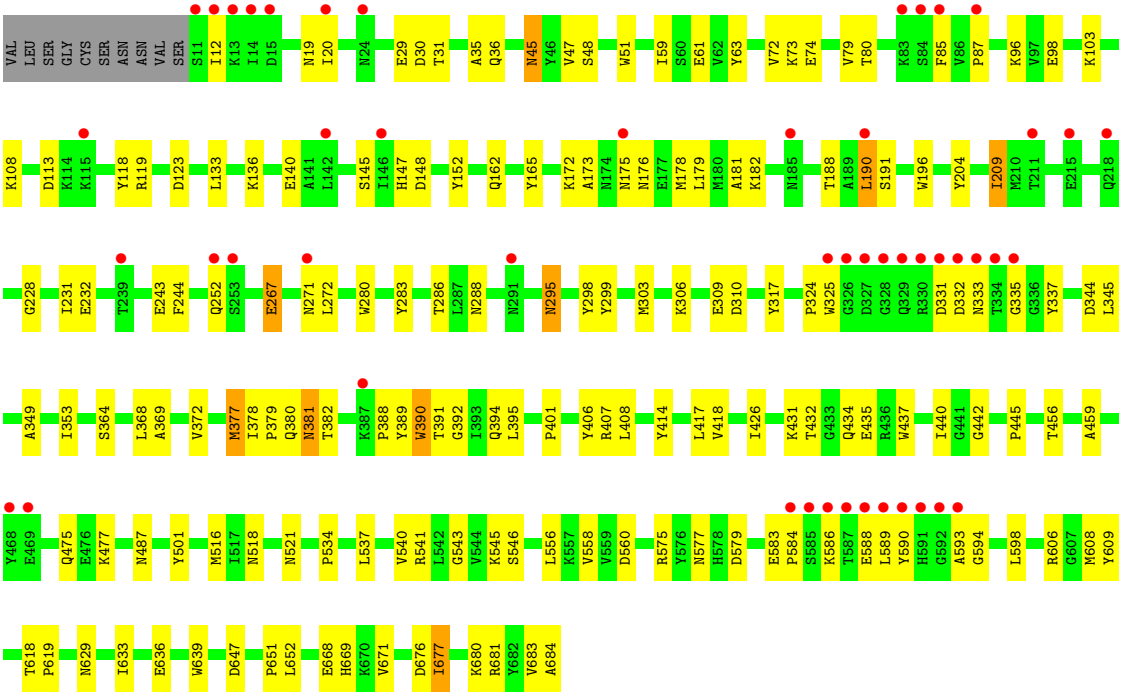
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	397	Total O 397 397	0	0
3	B	511	Total O 511 511	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

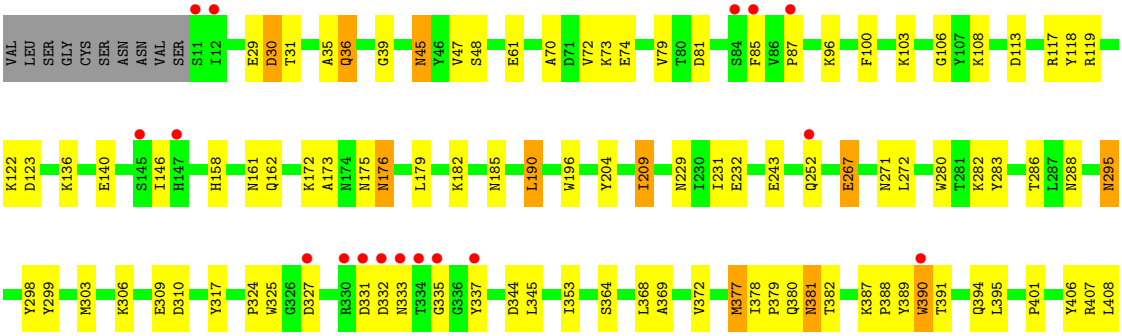
- Molecule 1: glucoamylase

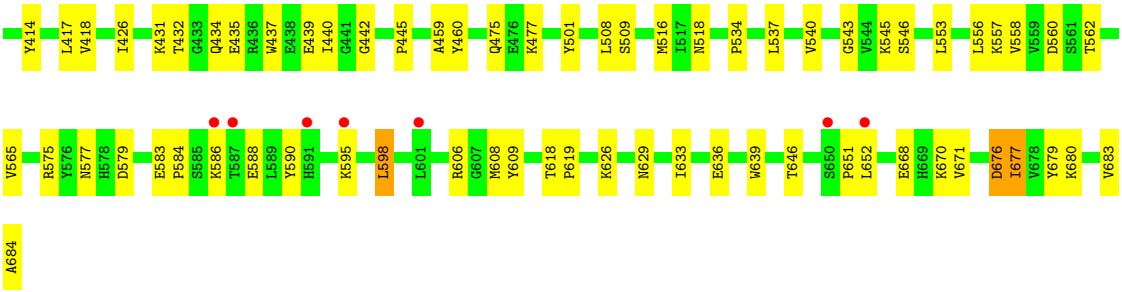
Chain A:



- Molecule 1: glucoamylase

Chain B:




Y414
L417
V418
I426
K431
T432
G433
Q434
E435
R436
W437
E438
E439
I440
G441
G442
P445
A459
Y460
Q475
E476
K477
Y501
L508
S509
M516
I517
N518
P534
L537
V540
G543
V544
K545
S546
L553
L556
K557
V558
V559
D560
S561
T562
V565
R575
Y576
N577
H578
D579
E583
P584
S585
K586
T587
E588
L589
Y590
H591
K595
L598
L601
R606
G607
M608
Y609
T618
P619
K626
N629
I633
E636
W639
T646
S650
P651
L652
E668
H669
K670
V671
D676
I677
V678
Y679
K680
V683
A684

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	81.19Å 102.51Å 164.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.69 – 2.10 29.69 – 2.10	Depositor EDS
% Data completeness (in resolution range)	93.2 (29.69-2.10) 93.2 (29.69-2.10)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	20.27 (at 2.10Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.194 , 0.232 0.194 , 0.232	Depositor DCC
R_{free} test set	5360 reflections (7.11%)	wwPDB-VP
Wilson B-factor (Å^2)	21.7	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 57.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11584	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: SO4

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	0.32	0/5453	0.56	1/7391 (0.0%)
1	B	0.33	0/5453	0.59	2/7391 (0.0%)
All	All	0.32	0/10906	0.57	3/14782 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	30	ASP	CB-CG-OD1	9.57	126.92	118.30
1	A	30	ASP	CB-CG-OD1	8.68	126.11	118.30
1	B	676	ASP	CB-CG-OD2	8.28	125.75	118.30

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	5333	0	5172	147	0
1	B	5333	0	5172	148	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	397	0	0	25	0
3	B	511	0	0	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	11584	0	10344	290	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 14.

The worst 5 of 290 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:516:MET:H	1:B:518:ASN:HD21	1.11	0.94
1:A:518:ASN:HD21	1:B:516:MET:H	1.18	0.88
1:B:280:TRP:HB3	1:B:303:MET:HE1	1.55	0.87
1:B:353:ILE:HD11	1:B:408:LEU:HD21	1.55	0.86
1:A:353:ILE:HD11	1:A:408:LEU:HD21	1.56	0.85

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	672/684 (98%)	631 (94%)	39 (6%)	2 (0%)	41	41
1	B	672/684 (98%)	633 (94%)	37 (6%)	2 (0%)	41	41
All	All	1344/1368 (98%)	1264 (94%)	76 (6%)	4 (0%)	41	41

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	333	ASN
1	B	333	ASN
1	A	335	GLY
1	B	335	GLY

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	566/575 (98%)	547 (97%)	19 (3%)	37	39
1	B	566/575 (98%)	547 (97%)	19 (3%)	37	39
All	All	1132/1150 (98%)	1094 (97%)	38 (3%)	37	39

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	332	ASP
1	B	577	ASN
1	B	344	ASP
1	B	390	TRP
1	B	677	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	45	ASN
1	B	218	GLN
1	B	518	ASN
1	B	161	ASN
1	B	229	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	SO4	A	950	-	4,4,4	0.31	0	6,6,6	0.06	0
2	SO4	B	951	-	4,4,4	0.28	0	6,6,6	0.07	0

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	674/684 (98%)	0.26	49 (7%)	15	19	11, 24, 50, 66	0
1	B	674/684 (98%)	-0.05	24 (3%)	42	49	11, 20, 41, 64	0
All	All	1348/1368 (98%)	0.10	73 (5%)	25	31	11, 22, 46, 66	0

The worst 5 of 73 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	333	ASN	10.9
1	B	333	ASN	10.6
1	A	593	ALA	7.7
1	A	591	HIS	6.6
1	A	334	THR	6.5

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 monosaccharides 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	SO4	A	950	5/5	0.92	0.23	54,54,55,56	0
2	SO4	B	951	5/5	0.97	0.15	50,51,52,52	0

6.5 Other polymers (i)

There are no such residues in this entry.