



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 10:23 AM EDT

PDB ID : 5DKX
Title : Crystal structure of glucosidase II alpha subunit (Tris-bound from)
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Deposited on : 2015-09-04
Resolution : 1.40 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.37.1
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) : 2.37.1

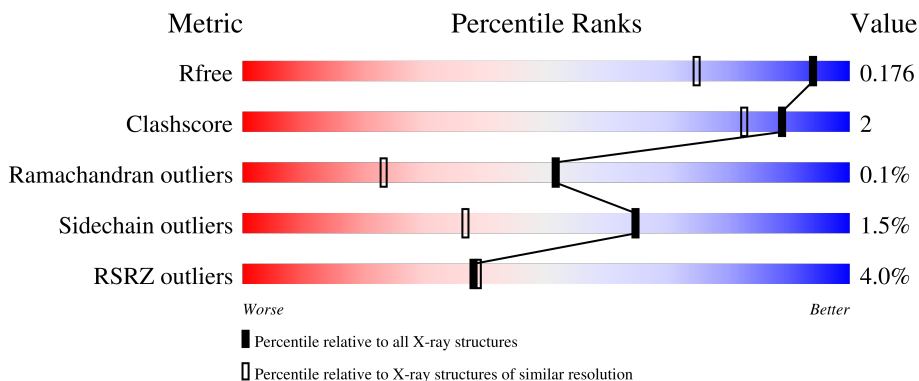
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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}	130704	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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 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	951	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8820 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.

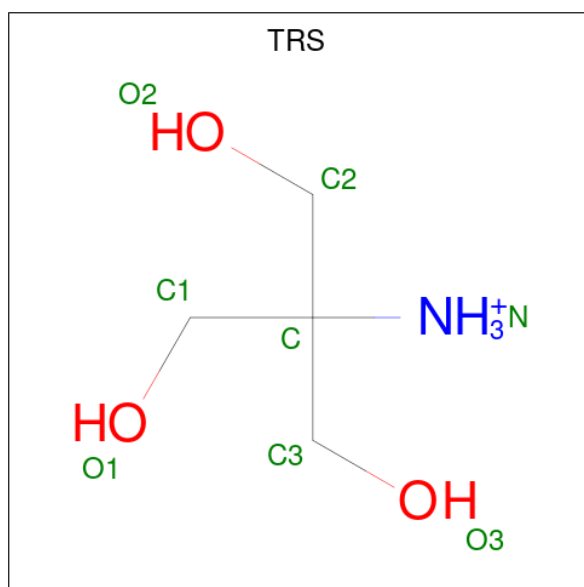
- Molecule 1 is a protein called Alpha glucosidase-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	925	7588	4854	1294	1415	25	0	15	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	GLY	-	expression tag	UNP G0SG42
A	28	SER	-	expression tag	UNP G0SG42
A	29	GLU	-	expression tag	UNP G0SG42
A	30	PHE	-	expression tag	UNP G0SG42

- Molecule 2 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	8	4	1	3	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total 2	Cl 2	0	0

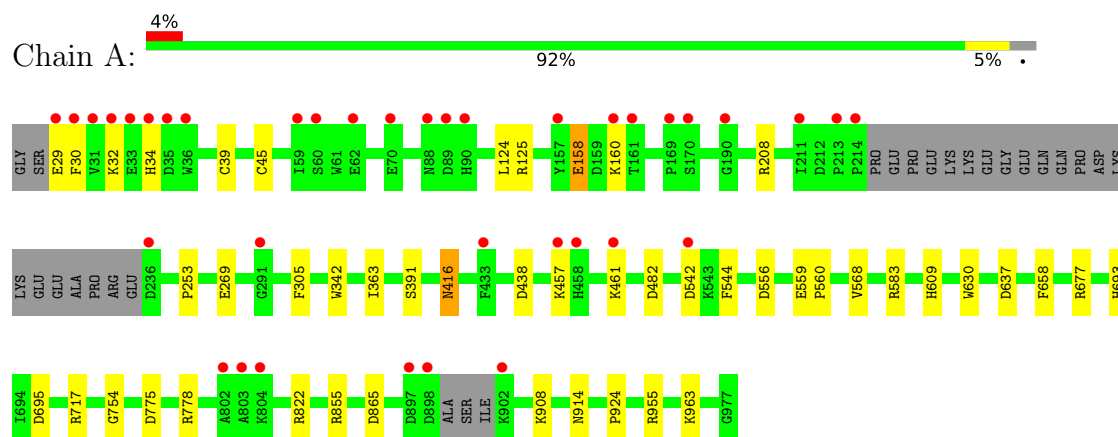
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1222	Total 1222	O 1222	0	0

3 Residue-property plots

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: Alpha glucosidase-like protein



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	189.03Å 189.03Å 157.18Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.40 19.84 – 1.40	Depositor EDS
% Data completeness (in resolution range)	99.6 (20.00-1.40) 99.6 (19.84-1.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.71 (at 1.40Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.154 , 0.175 0.155 , 0.176	Depositor DCC
R_{free} test set	10568 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	12.3	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	8820	wwPDB-VP
Average B, all atoms (Å ²)	16.0	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.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, TRS

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	0.53	0/7814	0.73	8/10587 (0.1%)

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	A	0	2

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	822	ARG	NE-CZ-NH1	7.22	123.91	120.30
1	A	677	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	A	125	ARG	NE-CZ-NH2	-5.82	117.39	120.30
1	A	637	ASP	CB-CG-OD1	5.64	123.38	118.30
1	A	482	ASP	CB-CG-OD2	-5.60	113.26	118.30
1	A	865	ASP	CB-CG-OD1	5.34	123.10	118.30
1	A	822	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	A	583	ARG	NE-CZ-NH1	5.11	122.86	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	416	ASN	Peptide
1	A	914	ASN	Peptide

5.2 Too-close contacts ⓘ

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	7588	0	7308	28	1
2	A	8	0	12	1	0
3	A	2	0	0	0	0
4	A	1222	0	0	8	0
All	All	8820	0	7320	28	1

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 (28) 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:45[B]:CYS:SG	1:A:342:TRP:NE1	2.05	1.29
1:A:45[B]:CYS:SG	1:A:342:TRP:CD1	2.48	1.06
1:A:542:ASP:HB3	4:A:1988:HOH:O	1.66	0.94
1:A:45[B]:CYS:SG	1:A:342:TRP:CE2	2.77	0.75
1:A:39[B]:CYS:SG	4:A:1949:HOH:O	1.93	0.74
1:A:775:ASP:HB2	1:A:778:ARG:HG3	1.70	0.73
1:A:457:LYS:O	1:A:461:LYS:HG2	1.98	0.64
1:A:45[B]:CYS:HG	1:A:342:TRP:NE1	1.37	0.63
1:A:269[A]:GLU:HG2	1:A:363:ILE:HB	1.82	0.62
1:A:693:HIS:CD2	1:A:695:ASP:H	2.25	0.54
1:A:391[C]:SER:OG	4:A:1101:HOH:O	2.19	0.53
1:A:124[B]:LEU:HD23	1:A:253:PRO:HB2	1.91	0.52
1:A:158[A]:GLU:O	1:A:158[A]:GLU:HG3	2.08	0.50
1:A:363:ILE:HD11	4:A:2186:HOH:O	2.13	0.48
1:A:775:ASP:HB2	1:A:778:ARG:CG	2.40	0.47
1:A:609:HIS:HD2	4:A:2144:HOH:O	1.98	0.47
1:A:717:ARG:NH1	4:A:1102:HOH:O	2.23	0.47
1:A:556:ASP:OD2	2:A:1001:TRS:H11	2.15	0.46
1:A:855:ARG:HD3	1:A:924:PRO:HB3	1.96	0.46
1:A:34:HIS:CE1	1:A:305:PHE:CB	2.99	0.46
1:A:34:HIS:CE1	1:A:305:PHE:HB3	2.51	0.46
1:A:39[B]:CYS:SG	1:A:45[B]:CYS:HB3	2.56	0.46
1:A:39[A]:CYS:HB2	1:A:45[A]:CYS:SG	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:559:GLU:N	1:A:560:PRO:HA	2.33	0.43
1:A:754:GLY:HA3	4:A:1620:HOH:O	2.17	0.43
1:A:39[A]:CYS:HB2	4:A:1949:HOH:O	2.17	0.43
1:A:29:GLU:OE2	1:A:693:HIS:HE1	2.02	0.42
1:A:457:LYS:O	1:A:461:LYS:CG	2.65	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:PHE:CZ	1:A:30:PHE:CZ[12_555]	2.05	0.15

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	936/951 (98%)	915 (98%)	20 (2%)	1 (0%)	51 23

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	568	VAL

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	805/810 (99%)	792 (98%)	13 (2%)	62 33

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

Mol	Chain	Res	Type
1	A	32	LYS
1	A	158[A]	GLU
1	A	158[B]	GLU
1	A	160	LYS
1	A	208	ARG
1	A	416	ASN
1	A	438	ASP
1	A	544	PHE
1	A	630	TRP
1	A	658	PHE
1	A	908	LYS
1	A	955	ARG
1	A	963	LYS

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	579	ASN
1	A	599	HIS
1	A	609	HIS
1	A	693	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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	TRS	A	1001	-	7,7,7	1.20	1 (14%)	9,9,9	1.35	1 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TRS	A	1001	-	-	4/9/9/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	TRS	O1-C1	2.00	1.48	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	TRS	O3-C3-C	2.48	118.84	111.00

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	TRS	N-C-C2-O2
2	A	1001	TRS	C1-C-C3-O3
2	A	1001	TRS	C2-C-C3-O3
2	A	1001	TRS	N-C-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	TRS	1	0

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	925/951 (97%)	0.07	37 (4%) 38 39	7, 13, 28, 55	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	31	VAL	7.0
1	A	30	PHE	6.6
1	A	457	LYS	6.3
1	A	90	HIS	6.0
1	A	160	LYS	5.5
1	A	34	HIS	5.4
1	A	157	TYR	5.0
1	A	897	ASP	5.0
1	A	803	ALA	4.8
1	A	32	LYS	4.8
1	A	190	GLY	4.7
1	A	89	ASP	4.5
1	A	902	LYS	4.4
1	A	802	ALA	4.3
1	A	60	SER	3.9
1	A	804	LYS	3.7
1	A	213	PRO	3.6
1	A	214	PRO	3.6
1	A	36	TRP	3.4
1	A	236	ASP	3.4
1	A	898	ASP	3.3
1	A	169	PRO	3.1
1	A	29	GLU	3.1
1	A	33	GLU	2.9
1	A	458	HIS	2.9
1	A	211	ILE	2.8
1	A	291	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	433	PHE	2.7
1	A	161	THR	2.5
1	A	461	LYS	2.5
1	A	59	ILE	2.5
1	A	35	ASP	2.5
1	A	542	ASP	2.3
1	A	88	ASN	2.2
1	A	170	SER	2.1
1	A	62	GLU	2.1
1	A	70	GLU	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 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(\AA^2)	Q<0.9
2	TRS	A	1001	8/8	0.92	0.11	13,15,16,16	0
3	CL	A	1002	1/1	0.94	0.13	29,29,29,29	0
3	CL	A	1003	1/1	0.96	0.08	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.