



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 08:10 PM UTC

PDB ID : 4KCB / pdb_00004kcb
Title : Crystal Structure of Exo-1,5-alpha-L-arabinanase from Bovine Ruminal Metagenomic Library
Authors : Santos, C.R.; Polo, C.C.; Costa, M.C.M.F.; Nascimento, A.F.Z.; Wong, D.W.S.; Murakami, M.T.
Deposited on : 2013-04-24
Resolution : 2.90 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
Mogul : 2022.3.0, CSD as543be (2022)
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

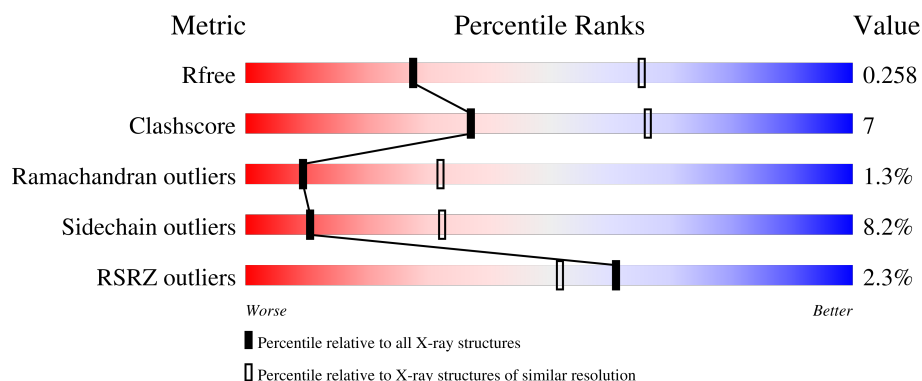
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	447	2% 51% 15% • 33%
1	B	447	% 54% 13% • 31%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4898 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 Arabinan endo-1,5-alpha-L-arabinosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	300	Total	C	N	O	S	0	0	0
			2404	1529	415	444	16			
1	B	307	Total	C	N	O	S	6	0	0
			2460	1559	430	455	16			

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-93	MET	-	initiating methionine	UNP D2XML8
A	-92	SER	-	expression tag	UNP D2XML8
A	-91	ASP	-	expression tag	UNP D2XML8
A	-90	LYS	-	expression tag	UNP D2XML8
A	-89	ILE	-	expression tag	UNP D2XML8
A	-88	ILE	-	expression tag	UNP D2XML8
A	-87	HIS	-	expression tag	UNP D2XML8
A	-86	LEU	-	expression tag	UNP D2XML8
A	-85	THR	-	expression tag	UNP D2XML8
A	-84	ASP	-	expression tag	UNP D2XML8
A	-83	ASP	-	expression tag	UNP D2XML8
A	-82	SER	-	expression tag	UNP D2XML8
A	-81	PHE	-	expression tag	UNP D2XML8
A	-80	ASP	-	expression tag	UNP D2XML8
A	-79	THR	-	expression tag	UNP D2XML8
A	-78	ASP	-	expression tag	UNP D2XML8
A	-77	VAL	-	expression tag	UNP D2XML8
A	-76	LEU	-	expression tag	UNP D2XML8
A	-75	LYS	-	expression tag	UNP D2XML8
A	-74	ALA	-	expression tag	UNP D2XML8
A	-73	ASP	-	expression tag	UNP D2XML8
A	-72	GLY	-	expression tag	UNP D2XML8
A	-71	ALA	-	expression tag	UNP D2XML8
A	-70	ILE	-	expression tag	UNP D2XML8
A	-69	LEU	-	expression tag	UNP D2XML8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-68	VAL	-	expression tag	UNP D2XML8
A	-67	ASP	-	expression tag	UNP D2XML8
A	-66	PHE	-	expression tag	UNP D2XML8
A	-65	TRP	-	expression tag	UNP D2XML8
A	-64	ALA	-	expression tag	UNP D2XML8
A	-63	GLU	-	expression tag	UNP D2XML8
A	-62	TRP	-	expression tag	UNP D2XML8
A	-61	CYS	-	expression tag	UNP D2XML8
A	-60	GLY	-	expression tag	UNP D2XML8
A	-59	PRO	-	expression tag	UNP D2XML8
A	-58	CYS	-	expression tag	UNP D2XML8
A	-57	LYS	-	expression tag	UNP D2XML8
A	-56	MET	-	expression tag	UNP D2XML8
A	-55	ILE	-	expression tag	UNP D2XML8
A	-54	ALA	-	expression tag	UNP D2XML8
A	-53	PRO	-	expression tag	UNP D2XML8
A	-52	ILE	-	expression tag	UNP D2XML8
A	-51	LEU	-	expression tag	UNP D2XML8
A	-50	ASP	-	expression tag	UNP D2XML8
A	-49	GLU	-	expression tag	UNP D2XML8
A	-48	ILE	-	expression tag	UNP D2XML8
A	-47	ALA	-	expression tag	UNP D2XML8
A	-46	ASP	-	expression tag	UNP D2XML8
A	-45	GLU	-	expression tag	UNP D2XML8
A	-44	TYR	-	expression tag	UNP D2XML8
A	-43	GLN	-	expression tag	UNP D2XML8
A	-42	GLY	-	expression tag	UNP D2XML8
A	-41	LYS	-	expression tag	UNP D2XML8
A	-40	LEU	-	expression tag	UNP D2XML8
A	-39	THR	-	expression tag	UNP D2XML8
A	-38	VAL	-	expression tag	UNP D2XML8
A	-37	ALA	-	expression tag	UNP D2XML8
A	-36	LYS	-	expression tag	UNP D2XML8
A	-35	LEU	-	expression tag	UNP D2XML8
A	-34	ASN	-	expression tag	UNP D2XML8
A	-33	ILE	-	expression tag	UNP D2XML8
A	-32	ASP	-	expression tag	UNP D2XML8
A	-31	GLN	-	expression tag	UNP D2XML8
A	-30	ASN	-	expression tag	UNP D2XML8
A	-29	PRO	-	expression tag	UNP D2XML8
A	-28	GLY	-	expression tag	UNP D2XML8
A	-27	THR	-	expression tag	UNP D2XML8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-26	ALA	-	expression tag	UNP D2XML8
A	-25	PRO	-	expression tag	UNP D2XML8
A	-24	LYS	-	expression tag	UNP D2XML8
A	-23	TYR	-	expression tag	UNP D2XML8
A	-22	GLY	-	expression tag	UNP D2XML8
A	-21	ILE	-	expression tag	UNP D2XML8
A	-20	ARG	-	expression tag	UNP D2XML8
A	-19	GLY	-	expression tag	UNP D2XML8
A	-18	ILE	-	expression tag	UNP D2XML8
A	-17	PRO	-	expression tag	UNP D2XML8
A	-16	THR	-	expression tag	UNP D2XML8
A	-15	LEU	-	expression tag	UNP D2XML8
A	-14	LEU	-	expression tag	UNP D2XML8
A	-13	LEU	-	expression tag	UNP D2XML8
A	-12	PHE	-	expression tag	UNP D2XML8
A	-11	LYS	-	expression tag	UNP D2XML8
A	-10	ASN	-	expression tag	UNP D2XML8
A	-9	GLY	-	expression tag	UNP D2XML8
A	-8	GLU	-	expression tag	UNP D2XML8
A	-7	VAL	-	expression tag	UNP D2XML8
A	-6	ALA	-	expression tag	UNP D2XML8
A	-5	ALA	-	expression tag	UNP D2XML8
A	-4	THR	-	expression tag	UNP D2XML8
A	-3	LYS	-	expression tag	UNP D2XML8
A	-2	VAL	-	expression tag	UNP D2XML8
A	-1	GLY	-	expression tag	UNP D2XML8
A	0	ALA	-	expression tag	UNP D2XML8
A	1	LEU	-	expression tag	UNP D2XML8
A	2	SER	-	expression tag	UNP D2XML8
A	3	LYS	-	expression tag	UNP D2XML8
A	4	GLY	-	expression tag	UNP D2XML8
A	5	GLN	-	expression tag	UNP D2XML8
A	6	LEU	-	expression tag	UNP D2XML8
A	7	LYS	-	expression tag	UNP D2XML8
A	8	GLU	-	expression tag	UNP D2XML8
A	9	PHE	-	expression tag	UNP D2XML8
A	10	LEU	-	expression tag	UNP D2XML8
A	11	ASP	-	expression tag	UNP D2XML8
A	12	ALA	-	expression tag	UNP D2XML8
A	13	ASN	-	expression tag	UNP D2XML8
A	14	LEU	-	expression tag	UNP D2XML8
A	15	ALA	-	expression tag	UNP D2XML8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	16	GLY	-	expression tag	UNP D2XML8
A	17	SER	-	expression tag	UNP D2XML8
A	18	GLY	-	expression tag	UNP D2XML8
A	19	SER	-	expression tag	UNP D2XML8
A	20	GLY	-	expression tag	UNP D2XML8
A	348	HIS	-	expression tag	UNP D2XML8
A	349	HIS	-	expression tag	UNP D2XML8
A	350	HIS	-	expression tag	UNP D2XML8
A	351	HIS	-	expression tag	UNP D2XML8
A	352	HIS	-	expression tag	UNP D2XML8
A	353	HIS	-	expression tag	UNP D2XML8
B	-93	MET	-	initiating methionine	UNP D2XML8
B	-92	SER	-	expression tag	UNP D2XML8
B	-91	ASP	-	expression tag	UNP D2XML8
B	-90	LYS	-	expression tag	UNP D2XML8
B	-89	ILE	-	expression tag	UNP D2XML8
B	-88	ILE	-	expression tag	UNP D2XML8
B	-87	HIS	-	expression tag	UNP D2XML8
B	-86	LEU	-	expression tag	UNP D2XML8
B	-85	THR	-	expression tag	UNP D2XML8
B	-84	ASP	-	expression tag	UNP D2XML8
B	-83	ASP	-	expression tag	UNP D2XML8
B	-82	SER	-	expression tag	UNP D2XML8
B	-81	PHE	-	expression tag	UNP D2XML8
B	-80	ASP	-	expression tag	UNP D2XML8
B	-79	THR	-	expression tag	UNP D2XML8
B	-78	ASP	-	expression tag	UNP D2XML8
B	-77	VAL	-	expression tag	UNP D2XML8
B	-76	LEU	-	expression tag	UNP D2XML8
B	-75	LYS	-	expression tag	UNP D2XML8
B	-74	ALA	-	expression tag	UNP D2XML8
B	-73	ASP	-	expression tag	UNP D2XML8
B	-72	GLY	-	expression tag	UNP D2XML8
B	-71	ALA	-	expression tag	UNP D2XML8
B	-70	ILE	-	expression tag	UNP D2XML8
B	-69	LEU	-	expression tag	UNP D2XML8
B	-68	VAL	-	expression tag	UNP D2XML8
B	-67	ASP	-	expression tag	UNP D2XML8
B	-66	PHE	-	expression tag	UNP D2XML8
B	-65	TRP	-	expression tag	UNP D2XML8
B	-64	ALA	-	expression tag	UNP D2XML8
B	-63	GLU	-	expression tag	UNP D2XML8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-62	TRP	-	expression tag	UNP D2XML8
B	-61	CYS	-	expression tag	UNP D2XML8
B	-60	GLY	-	expression tag	UNP D2XML8
B	-59	PRO	-	expression tag	UNP D2XML8
B	-58	CYS	-	expression tag	UNP D2XML8
B	-57	LYS	-	expression tag	UNP D2XML8
B	-56	MET	-	expression tag	UNP D2XML8
B	-55	ILE	-	expression tag	UNP D2XML8
B	-54	ALA	-	expression tag	UNP D2XML8
B	-53	PRO	-	expression tag	UNP D2XML8
B	-52	ILE	-	expression tag	UNP D2XML8
B	-51	LEU	-	expression tag	UNP D2XML8
B	-50	ASP	-	expression tag	UNP D2XML8
B	-49	GLU	-	expression tag	UNP D2XML8
B	-48	ILE	-	expression tag	UNP D2XML8
B	-47	ALA	-	expression tag	UNP D2XML8
B	-46	ASP	-	expression tag	UNP D2XML8
B	-45	GLU	-	expression tag	UNP D2XML8
B	-44	TYR	-	expression tag	UNP D2XML8
B	-43	GLN	-	expression tag	UNP D2XML8
B	-42	GLY	-	expression tag	UNP D2XML8
B	-41	LYS	-	expression tag	UNP D2XML8
B	-40	LEU	-	expression tag	UNP D2XML8
B	-39	THR	-	expression tag	UNP D2XML8
B	-38	VAL	-	expression tag	UNP D2XML8
B	-37	ALA	-	expression tag	UNP D2XML8
B	-36	LYS	-	expression tag	UNP D2XML8
B	-35	LEU	-	expression tag	UNP D2XML8
B	-34	ASN	-	expression tag	UNP D2XML8
B	-33	ILE	-	expression tag	UNP D2XML8
B	-32	ASP	-	expression tag	UNP D2XML8
B	-31	GLN	-	expression tag	UNP D2XML8
B	-30	ASN	-	expression tag	UNP D2XML8
B	-29	PRO	-	expression tag	UNP D2XML8
B	-28	GLY	-	expression tag	UNP D2XML8
B	-27	THR	-	expression tag	UNP D2XML8
B	-26	ALA	-	expression tag	UNP D2XML8
B	-25	PRO	-	expression tag	UNP D2XML8
B	-24	LYS	-	expression tag	UNP D2XML8
B	-23	TYR	-	expression tag	UNP D2XML8
B	-22	GLY	-	expression tag	UNP D2XML8
B	-21	ILE	-	expression tag	UNP D2XML8

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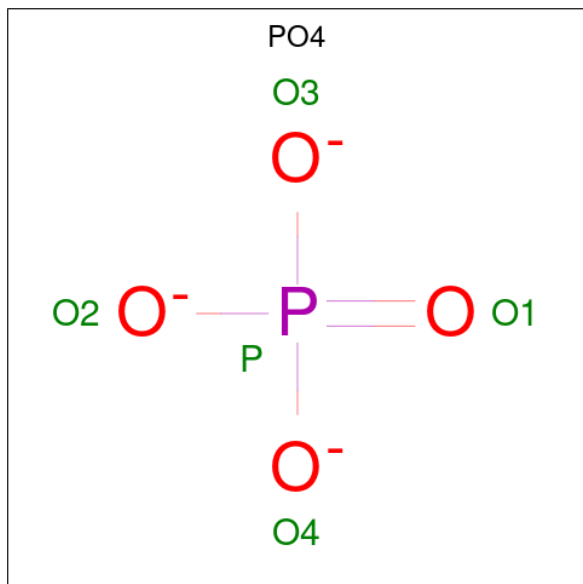
Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	ARG	-	expression tag	UNP D2XML8
B	-19	GLY	-	expression tag	UNP D2XML8
B	-18	ILE	-	expression tag	UNP D2XML8
B	-17	PRO	-	expression tag	UNP D2XML8
B	-16	THR	-	expression tag	UNP D2XML8
B	-15	LEU	-	expression tag	UNP D2XML8
B	-14	LEU	-	expression tag	UNP D2XML8
B	-13	LEU	-	expression tag	UNP D2XML8
B	-12	PHE	-	expression tag	UNP D2XML8
B	-11	LYS	-	expression tag	UNP D2XML8
B	-10	ASN	-	expression tag	UNP D2XML8
B	-9	GLY	-	expression tag	UNP D2XML8
B	-8	GLU	-	expression tag	UNP D2XML8
B	-7	VAL	-	expression tag	UNP D2XML8
B	-6	ALA	-	expression tag	UNP D2XML8
B	-5	ALA	-	expression tag	UNP D2XML8
B	-4	THR	-	expression tag	UNP D2XML8
B	-3	LYS	-	expression tag	UNP D2XML8
B	-2	VAL	-	expression tag	UNP D2XML8
B	-1	GLY	-	expression tag	UNP D2XML8
B	0	ALA	-	expression tag	UNP D2XML8
B	1	LEU	-	expression tag	UNP D2XML8
B	2	SER	-	expression tag	UNP D2XML8
B	3	LYS	-	expression tag	UNP D2XML8
B	4	GLY	-	expression tag	UNP D2XML8
B	5	GLN	-	expression tag	UNP D2XML8
B	6	LEU	-	expression tag	UNP D2XML8
B	7	LYS	-	expression tag	UNP D2XML8
B	8	GLU	-	expression tag	UNP D2XML8
B	9	PHE	-	expression tag	UNP D2XML8
B	10	LEU	-	expression tag	UNP D2XML8
B	11	ASP	-	expression tag	UNP D2XML8
B	12	ALA	-	expression tag	UNP D2XML8
B	13	ASN	-	expression tag	UNP D2XML8
B	14	LEU	-	expression tag	UNP D2XML8
B	15	ALA	-	expression tag	UNP D2XML8
B	16	GLY	-	expression tag	UNP D2XML8
B	17	SER	-	expression tag	UNP D2XML8
B	18	GLY	-	expression tag	UNP D2XML8
B	19	SER	-	expression tag	UNP D2XML8
B	20	GLY	-	expression tag	UNP D2XML8
B	348	HIS	-	expression tag	UNP D2XML8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	349	HIS	-	expression tag	UNP D2XML8
B	350	HIS	-	expression tag	UNP D2XML8
B	351	HIS	-	expression tag	UNP D2XML8
B	352	HIS	-	expression tag	UNP D2XML8
B	353	HIS	-	expression tag	UNP D2XML8

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



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

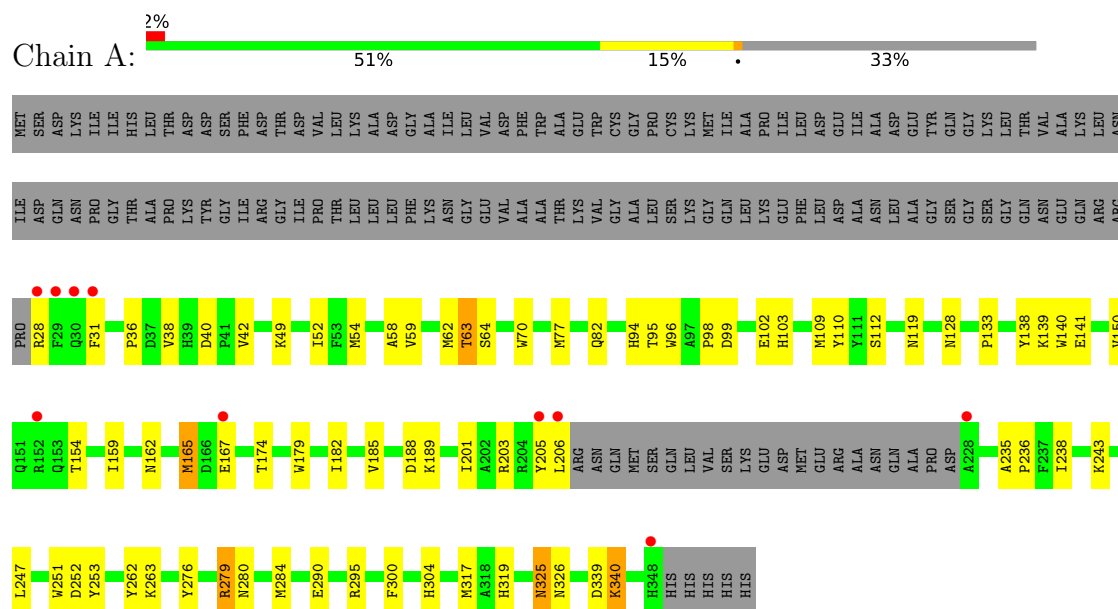
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	13	Total	O	0	0
			13	13		
3	B	6	Total	O	0	0
			6	6		

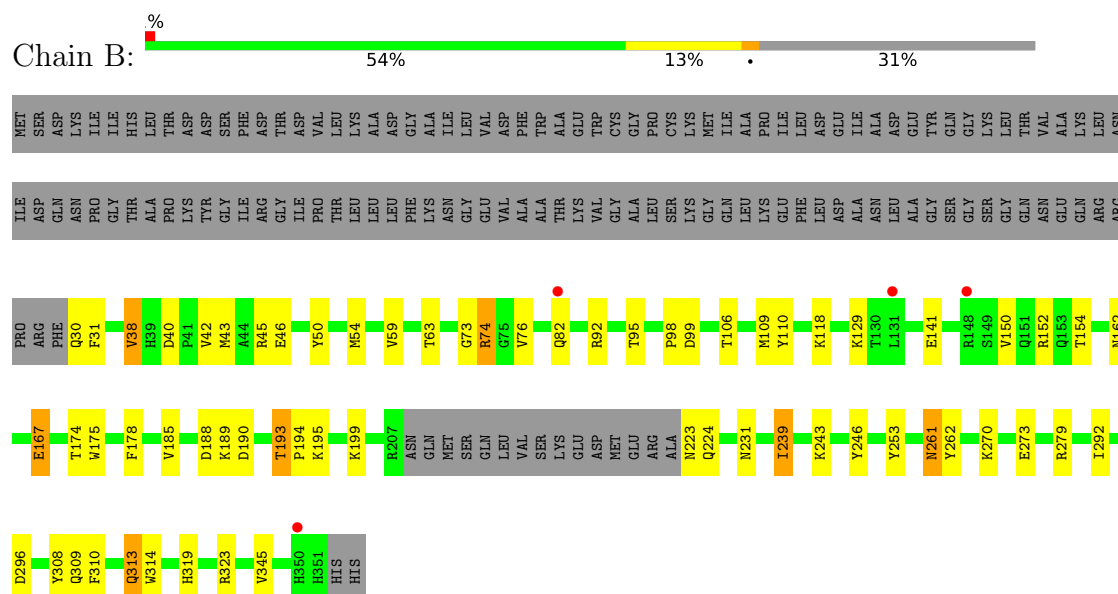
3 Residue-property plots

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: Arabinan endo-1,5- α -L-arabinosidase



- Molecule 1: Arabinan endo-1,5- α -L-arabinosidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	140.12Å 140.12Å 159.01Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.03 – 2.90 35.03 – 2.90	Depositor EDS
% Data completeness (in resolution range)	97.7 (35.03-2.90) 96.9 (35.03-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.98 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.217 , 0.267 0.209 , 0.258	Depositor DCC
R_{free} test set	1545 reflections (7.32%)	wwPDB-VP
Wilson B-factor (Å ²)	55.0	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 20.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4898	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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: PO4

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	0.47	0/2478	0.77	1/3355 (0.0%)
1	B	0.48	0/2537	0.82	1/3437 (0.0%)
All	All	0.48	0/5015	0.80	2/6792 (0.0%)

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	B	0	1

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	B	76	VAL	N-CA-C	6.99	117.10	110.53
1	A	253	TYR	N-CA-C	5.23	117.24	107.99

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	46	GLU	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	2404	0	2265	36	0
1	B	2460	0	2306	33	0
2	A	5	0	0	0	0
2	B	10	0	0	0	0
3	A	13	0	0	0	0
3	B	6	0	0	0	0
All	All	4898	0	4571	67	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 7.

All (67) 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:40:ASP:H	1:A:319:HIS:HD2	1.17	0.90
1:A:38:VAL:HG23	1:A:54:MET:SD	2.16	0.85
1:B:73:GLY:CA	1:B:74:ARG:HB2	2.05	0.85
1:B:73:GLY:HA3	1:B:74:ARG:HB2	1.60	0.82
1:A:36:PRO:HB2	1:A:62:MET:HE1	1.64	0.77
1:B:40:ASP:H	1:B:319:HIS:CD2	2.05	0.74
1:A:340:LYS:H	1:A:340:LYS:HD3	1.53	0.72
1:A:40:ASP:H	1:A:319:HIS:CD2	2.06	0.69
1:A:205:TYR:O	1:A:206:LEU:HG	1.95	0.67
1:B:40:ASP:H	1:B:319:HIS:HD2	1.42	0.65
1:B:239:ILE:HG22	1:B:246:TYR:HB2	1.78	0.63
1:B:73:GLY:CA	1:B:74:ARG:CB	2.77	0.60
1:B:296:ASP:O	1:B:323:ARG:NH1	2.36	0.58
1:B:38:VAL:HG22	1:B:54:MET:SD	2.45	0.57
1:B:43:MET:HE3	1:B:310:PHE:HE2	1.70	0.57
1:B:188:ASP:HB3	1:B:195:LYS:HE3	1.88	0.56
1:A:162:ASN:ND2	1:A:238:ILE:H	2.04	0.56
1:A:103:HIS:CE1	1:A:165:MET:HE3	2.41	0.55
1:A:49:LYS:HE2	1:A:63:THR:HG23	1.89	0.55
1:A:247:LEU:HB3	1:A:284:MET:HE1	1.89	0.54
1:A:276:TYR:HB3	1:A:284:MET:HE2	1.91	0.53
1:A:276:TYR:HB3	1:A:284:MET:CE	2.39	0.53
1:B:73:GLY:HA2	1:B:74:ARG:HB2	1.89	0.53
1:A:112:SER:HB3	1:A:159:ILE:HG22	1.91	0.53
1:A:31:PHE:HZ	1:A:62:MET:HE2	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:ASP:O	1:B:190:ASP:N	2.42	0.52
1:B:223:ASN:HD22	1:B:223:ASN:N	2.07	0.52
1:A:182:ILE:HD12	1:A:236:PRO:HG3	1.93	0.51
1:B:253:TYR:H	1:B:261:ASN:ND2	2.09	0.51
1:B:178:PHE:HA	1:B:231:ASN:O	2.13	0.49
1:A:188:ASP:OD1	1:A:189:LYS:N	2.45	0.49
1:A:99:ASP:O	1:A:109:MET:HA	2.12	0.49
1:B:43:MET:HE3	1:B:310:PHE:CE2	2.48	0.48
1:A:295:ARG:HD2	1:A:300:PHE:HA	1.95	0.47
1:A:339:ASP:HB2	1:A:340:LYS:HD3	1.96	0.47
1:A:31:PHE:CZ	1:A:62:MET:HE2	2.49	0.47
1:B:99:ASP:O	1:B:109:MET:HA	2.15	0.47
1:B:162:ASN:HB3	1:B:174:THR:CG2	2.45	0.47
1:A:119:ASN:HB3	1:A:179:TRP:CH2	2.50	0.46
1:B:243:LYS:HE3	1:B:270:LYS:HE2	1.98	0.45
1:B:45:ARG:HD3	1:B:50:TYR:CE1	2.52	0.45
1:A:98:PRO:HA	1:A:110:TYR:O	2.17	0.45
1:B:253:TYR:H	1:B:261:ASN:HD21	1.65	0.44
1:B:98:PRO:HA	1:B:110:TYR:O	2.16	0.44
1:A:94:HIS:CE1	1:B:150:VAL:HG21	2.53	0.44
1:A:235:ALA:HB2	1:A:304:HIS:CD2	2.53	0.44
1:B:309:GLN:HA	1:B:313:GLN:O	2.17	0.44
1:B:239:ILE:HG13	1:B:314:TRP:CH2	2.53	0.43
1:A:251:TRP:HB2	1:A:263:LYS:HG3	2.00	0.43
1:B:152:ARG:C	1:B:154:THR:H	2.27	0.43
1:A:247:LEU:HD23	1:A:284:MET:HE3	2.01	0.43
1:A:325:ASN:O	1:A:326:ASN:C	2.62	0.43
1:B:73:GLY:HA2	1:B:74:ARG:CB	2.47	0.42
1:A:58:ALA:HB1	1:A:77:MET:HB2	2.00	0.42
1:A:96:TRP:HB2	1:A:112:SER:HB2	2.00	0.42
1:A:42:VAL:C	1:A:317:MET:HE1	2.44	0.42
1:A:279:ARG:HB2	1:A:290:GLU:CD	2.45	0.42
1:B:42:VAL:HG22	1:B:308:TYR:OH	2.19	0.41
1:A:64:SER:HB2	1:A:70:TRP:CD2	2.56	0.41
1:A:133:PRO:HA	1:A:138:TYR:CG	2.56	0.41
1:B:42:VAL:HG21	1:B:99:ASP:HA	2.01	0.41
1:B:193:THR:HA	1:B:194:PRO:HD2	1.95	0.41
1:B:239:ILE:HD12	1:B:239:ILE:HA	1.91	0.41
1:A:42:VAL:HG21	1:A:99:ASP:HA	2.02	0.41
1:A:28:ARG:HH21	1:B:199:LYS:HE3	1.86	0.40
1:A:128:ASN:HB2	1:A:140:TRP:CE3	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:175:TRP:HZ3	1:B:185:VAL:HG12	1.86	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	296/447 (66%)	274 (93%)	20 (7%)	2 (1%)	18	48
1	B	303/447 (68%)	276 (91%)	21 (7%)	6 (2%)	6	22
All	All	599/894 (67%)	550 (92%)	41 (7%)	8 (1%)	9	32

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	74	ARG
1	B	189	LYS
1	B	167	GLU
1	B	31	PHE
1	A	59	VAL
1	A	252	ASP
1	B	59	VAL
1	B	193	THR

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	246/367 (67%)	225 (92%)	21 (8%)	10	31
1	B	252/367 (69%)	232 (92%)	20 (8%)	11	34
All	All	498/734 (68%)	457 (92%)	41 (8%)	10	32

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	ILE
1	A	63	THR
1	A	82	GLN
1	A	95	THR
1	A	102	GLU
1	A	139	LYS
1	A	141	GLU
1	A	150	VAL
1	A	154	THR
1	A	165	MET
1	A	167	GLU
1	A	174	THR
1	A	185	VAL
1	A	201	ILE
1	A	203	ARG
1	A	243	LYS
1	A	262	TYR
1	A	279	ARG
1	A	280	ASN
1	A	325	ASN
1	A	340	LYS
1	B	30	GLN
1	B	38	VAL
1	B	63	THR
1	B	82	GLN
1	B	92	ARG
1	B	95	THR
1	B	106	THR
1	B	118	LYS
1	B	129	LYS
1	B	141	GLU
1	B	167	GLU
1	B	224	GLN
1	B	239	ILE
1	B	261	ASN

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Mol	Chain	Res	Type
1	B	262	TYR
1	B	273	GLU
1	B	279	ARG
1	B	292	ILE
1	B	313	GLN
1	B	345	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	35	ASN
1	A	94	HIS
1	A	103	HIS
1	A	104	ASN
1	A	162	ASN
1	A	298	ASN
1	A	319	HIS
1	A	326	ASN
1	B	153	GLN
1	B	261	ASN
1	B	294	GLN
1	B	313	GLN
1	B	319	HIS
1	B	337	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	PO4	B	402	-	4,4,4	0.95	0	6,6,6	0.57	0
2	PO4	B	401	-	4,4,4	0.90	0	6,6,6	0.45	0
2	PO4	A	401	-	4,4,4	0.91	0	6,6,6	0.52	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	300/447 (67%)	0.07	10 (3%) 49 40	40, 54, 67, 82	4 (1%)
1	B	307/447 (68%)	0.04	4 (1%) 75 67	30, 53, 71, 77	6 (1%)
All	All	607/894 (67%)	0.06	14 (2%) 61 52	30, 54, 70, 82	10 (1%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	28	ARG	5.8
1	A	29	PHE	5.7
1	B	148	ARG	3.3
1	B	350	HIS	3.1
1	A	206	LEU	2.7
1	A	348	HIS	2.6
1	B	82	GLN	2.6
1	A	228	ALA	2.3
1	B	131	LEU	2.3
1	A	31	PHE	2.2
1	A	152	ARG	2.1
1	A	205	TYR	2.1
1	A	167	GLU	2.1
1	A	30	GLN	2.0

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	PO4	A	401	5/5	0.78	0.12	123,123,124,124	0
2	PO4	B	401	5/5	0.78	0.22	102,102,102,102	0
2	PO4	B	402	5/5	0.93	0.17	75,75,75,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.