



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:02 PM GMT

PDB ID : 4KCB
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

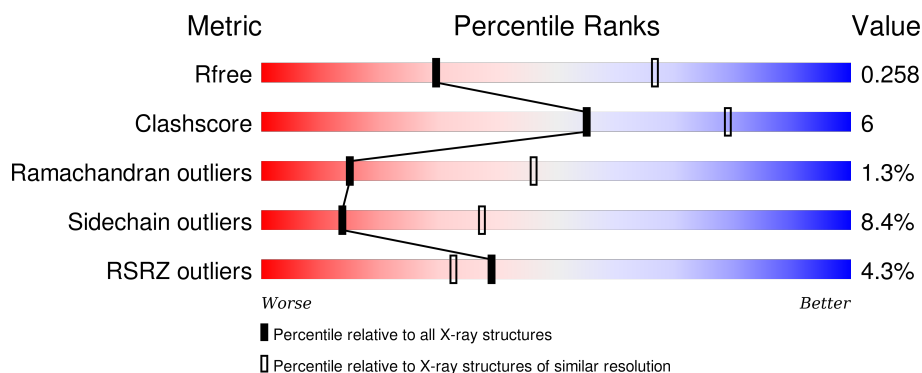
1 Overall quality at a glance

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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	
1	B	447	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	B	401	-	-	-	X

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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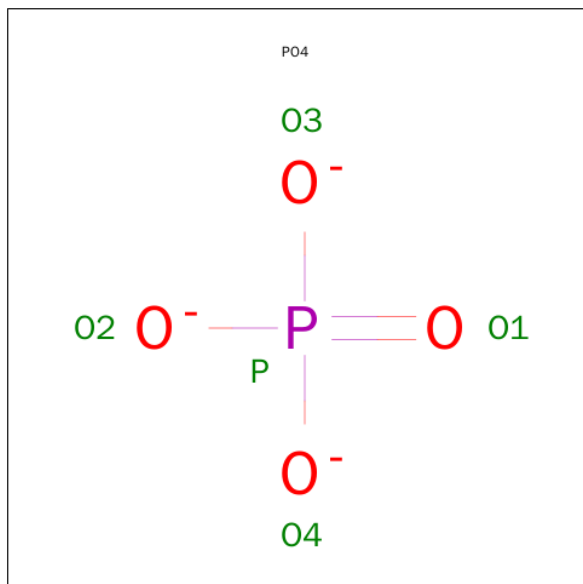
Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	ARG	-	EXPRESSION TAG	UNP D2XML8
B	-19	GLY	-	EXPRESSION TAG	UNP D2XML8
B	-18	ILE	-	EXPRESSION TAG	UNP D2XML8
B	-17	PRO	-	EXPRESSION TAG	UNP D2XML8
B	-16	THR	-	EXPRESSION TAG	UNP D2XML8
B	-15	LEU	-	EXPRESSION TAG	UNP D2XML8
B	-14	LEU	-	EXPRESSION TAG	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 (three-letter code: PO4) (formula: O₄P).



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

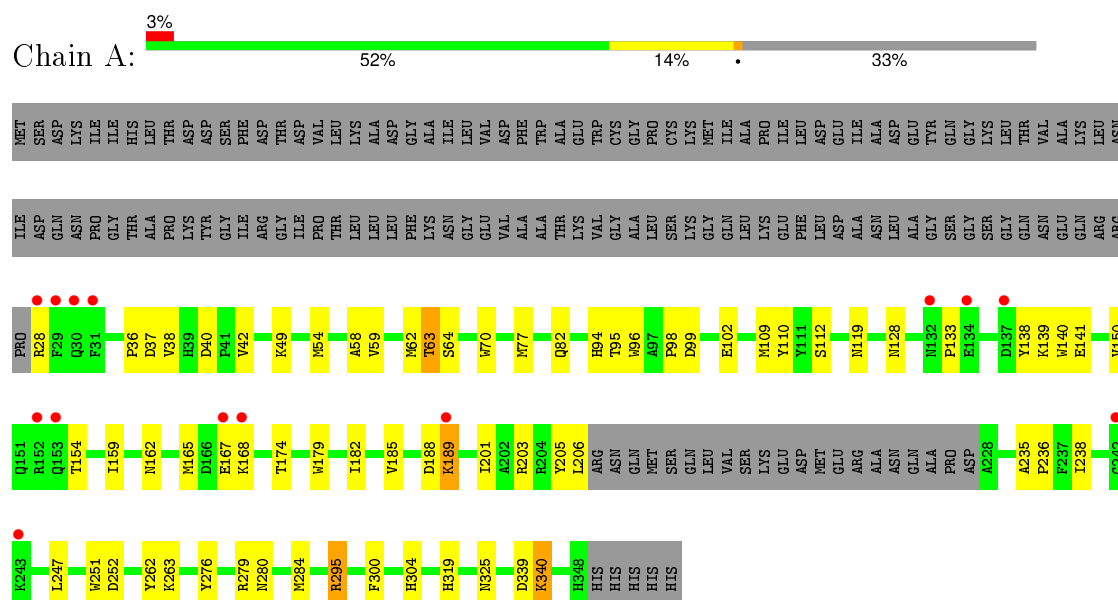
- Molecule 3 is water.

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

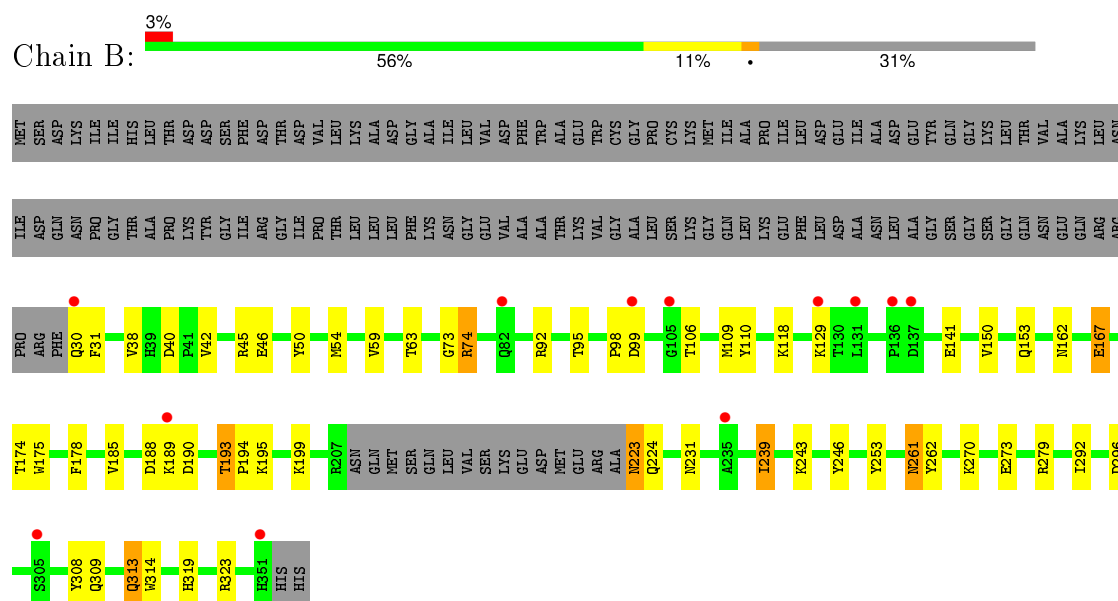
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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) 97.0 (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	1543 reflections (7.98%)	DCC
Wilson B-factor (Å ²)	55.0	Xtriage
Anisotropy	0.018	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 23.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 20617 reflections	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, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	0.40	0/2478	0.56	0/3355
1	B	0.40	0/2537	0.57	0/3437
All	All	0.40	0/5015	0.56	0/6792

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.

There are no bond angle outliers.

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 [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	2404	0	2265	31	0
1	B	2460	0	2306	30	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	59	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 6.

All (59) 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: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:A:276:TYR:HB3	1:A:284:MET:HE2	1.82	0.62
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:A:36:PRO:HB2	1:A:62:MET:HE1	1.87	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:49:LYS:HE2	1:A:63:THR:HG23	1.89	0.55
1:B:73:GLY:HA2	1:B:74:ARG:HB2	1.89	0.53
1:A:276:TYR:HB3	1:A:284:MET:CE	2.39	0.53
1:A:112:SER:HB3	1:A:159:ILE:HG22	1.91	0.53
1:B:188:ASP:O	1:B:190:ASP:N	2.42	0.52
1:B:223:ASN:N	1:B:223:ASN:HD22	2.07	0.52
1:A:182:ILE:HD12	1:A:236:PRO:HG3	1.93	0.51
1:A:247:LEU:HB3	1:A:284:MET:HE1	1.93	0.51
1:B:253:TYR:H	1:B:261:ASN:ND2	2.09	0.51
1:A:247:LEU:HD23	1:A:284:MET:HE3	1.94	0.50
1:B:178:PHE:HA	1:B:231:ASN:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:B:162:ASN:HB3	1:B:174:THR:CG2	2.45	0.47
1:B:99:ASP:O	1:B:109:MET:HA	2.15	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: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: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: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:A:133:PRO:HA	1:A:138:TYR:CG	2.56	0.41
1:B:239:ILE:HA	1:B:239:ILE:HD12	1.91	0.41
1:A:42:VAL:HG21	1:A:99:ASP:HA	2.02	0.41
1:A:247:LEU:HB3	1:A:284:MET:CE	2.51	0.40
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
1:B:175:TRP:HZ3	1:B:185:VAL:HG12	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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%)	26	63
1	B	303/447 (68%)	276 (91%)	21 (7%)	6 (2%)	9	33
All	All	599/894 (67%)	550 (92%)	41 (7%)	8 (1%)	15	46

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 ⓘ

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%)	223 (91%)	23 (9%)	11	32
1	B	252/367 (69%)	233 (92%)	19 (8%)	17	44
All	All	498/734 (68%)	456 (92%)	42 (8%)	14	37

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	ASP
1	A	63	THR
1	A	82	GLN
1	A	95	THR
1	A	102	GLU

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Mol	Chain	Res	Type
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	168	LYS
1	A	174	THR
1	A	185	VAL
1	A	189	LYS
1	A	201	ILE
1	A	203	ARG
1	A	262	TYR
1	A	279	ARG
1	A	280	ASN
1	A	295	ARG
1	A	325	ASN
1	A	340	LYS
1	B	30	GLN
1	B	63	THR
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	153	GLN
1	B	167	GLU
1	B	223	ASN
1	B	224	GLN
1	B	239	ILE
1	B	261	ASN
1	B	262	TYR
1	B	273	GLU
1	B	279	ARG
1	B	292	ILE
1	B	313	GLN

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

Mol	Chain	Res	Type
1	A	35	ASN

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Mol	Chain	Res	Type
1	A	94	HIS
1	A	162	ASN
1	A	298	ASN
1	A	313	GLN
1	A	319	HIS
1	A	325	ASN
1	A	326	ASN
1	A	337	ASN
1	B	35	ASN
1	B	153	GLN
1	B	261	ASN
1	B	313	GLN
1	B	319	HIS
1	B	325	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 carbohydrates 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	A	401	-	4,4,4	0.43	0	6,6,6	0.27	0
2	PO4	B	401	-	4,4,4	0.39	0	6,6,6	0.27	0
2	PO4	B	402	-	4,4,4	0.47	0	6,6,6	0.28	0

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	PO4	A	401	-	-	0/0/0/0	0/0/0/0
2	PO4	B	401	-	-	0/0/0/0	0/0/0/0
2	PO4	B	402	-	-	0/0/0/0	0/0/0/0

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 ⓘ

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	300/447 (67%)	0.00	14 (4%) 35 29	40, 54, 69, 83	4 (1%)
1	B	307/447 (68%)	0.11	12 (3%) 43 36	35, 53, 71, 77	6 (1%)
All	All	607/894 (67%)	0.06	26 (4%) 39 32	35, 54, 70, 83	10 (1%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	29	PHE	4.7
1	A	134	GLU	4.7
1	B	30	GLN	3.9
1	B	82	GLN	3.8
1	A	152	ARG	3.5
1	A	243	LYS	3.4
1	B	137	ASP	3.2
1	B	189	LYS	2.8
1	B	136	PRO	2.8
1	A	153	GLN	2.8
1	B	105	GLY	2.8
1	A	30	GLN	2.8
1	A	168	LYS	2.7
1	B	129	LYS	2.7
1	A	242	GLY	2.6
1	A	28	ARG	2.5
1	A	167	GLU	2.5
1	B	351	HIS	2.4
1	B	99	ASP	2.4
1	B	131	LEU	2.3
1	A	132	ASN	2.2
1	B	235	ALA	2.2
1	A	189	LYS	2.1
1	A	31	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	305	SER	2.1
1	A	137	ASP	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	PO4	B	401	5/5	0.87	0.39	2.59	102,102,102,102	0
2	PO4	A	401	5/5	0.87	0.21	0.77	123,123,124,124	0
2	PO4	B	402	5/5	0.95	0.27	0.45	75,75,75,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.