



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 04:08 AM UTC

PDB ID : 4NX0 / pdb_00004nx0
Title : Crystal structure of Abp-WT, a GH27-b-L-arabinopyranosidase from *Geobacillus stearothermophilus*
Authors : Lansky, S.; Solomon, H.V.; Salama, R.; Belrhali, H.; Shoham, Y.; Shoham, G.
Deposited on : 2013-12-08
Resolution : 2.28 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 ⓘ 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

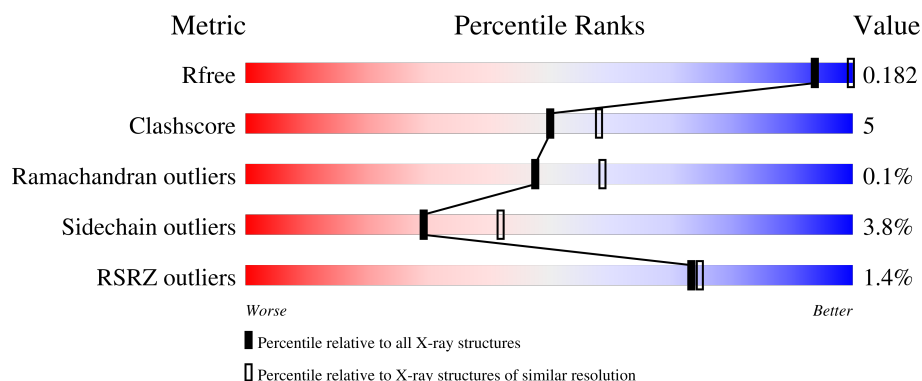
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	448	87% 8% ••
1	B	448	2% 83% 12% ••
1	C	448	2% 85% 10% •
1	D	448	88% 8% ••
1	E	448	87% 8% ••

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Mol	Chain	Length	Quality of chain
1	F	448	% 85% 9% ...
1	G	448	3% 82% 11% ...
1	H	448	2% 82% 11% ...

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	GOL	C	503	-	X	-	-
2	GOL	C	505	-	-	X	-
2	GOL	D	502	-	-	X	-
2	GOL	D	503	-	X	-	-
2	GOL	D	505	-	-	X	-
2	GOL	E	505	-	X	X	-
2	GOL	F	502	-	-	X	-
4	CIT	A	515	-	X	X	-
4	CIT	B	520	-	-	X	-
4	CIT	C	519	-	X	-	-
4	CIT	G	513	-	X	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 32820 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 Abp, a GH27 beta-L-arabinopyranosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	S	0	4	0
			3492	2233	598	636	25			
1	B	430	Total	C	N	O	S	0	4	0
			3496	2235	598	638	25			
1	C	431	Total	C	N	O	S	0	2	0
			3487	2230	598	634	25			
1	D	435	Total	C	N	O	S	0	1	0
			3506	2243	603	635	25			
1	E	430	Total	C	N	O	S	0	3	0
			3484	2228	597	634	25			
1	F	430	Total	C	N	O	S	0	0	0
			3470	2219	596	630	25			
1	G	430	Total	C	N	O	S	0	2	0
			3481	2226	596	634	25			
1	H	430	Total	C	N	O	S	0	0	0
			3470	2219	596	630	25			

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	A	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	B	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		

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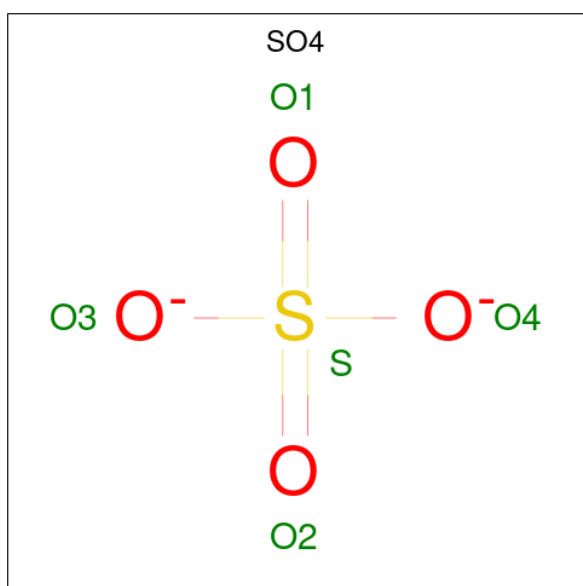
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	C	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	E	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	F	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	G	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		
2	H	1	Total	C	O	0	0
			6	3	3		
2	H	1	Total	C	O	0	0
			6	3	3		
2	H	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		

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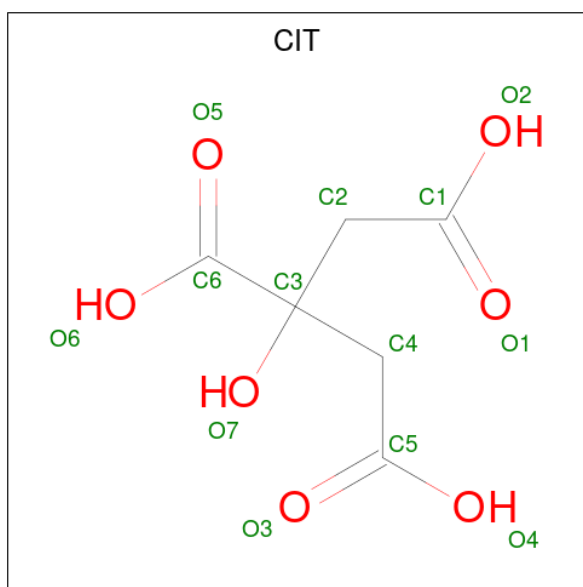
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	6	7		
4	B	1	Total	C	O	0	0
			13	6	7		
4	C	1	Total	C	O	0	0
			13	6	7		
4	E	1	Total	C	O	0	0
			13	6	7		
4	G	1	Total	C	O	0	0
			13	6	7		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	662	Total	O	0	0
			662	662		
5	B	625	Total	O	0	0
			625	625		
5	C	579	Total	O	0	0
			579	579		
5	D	536	Total	O	0	0
			536	536		
5	E	500	Total	O	0	0
			500	500		
5	F	495	Total	O	0	0
			495	495		
5	G	439	Total	O	0	0
			439	439		

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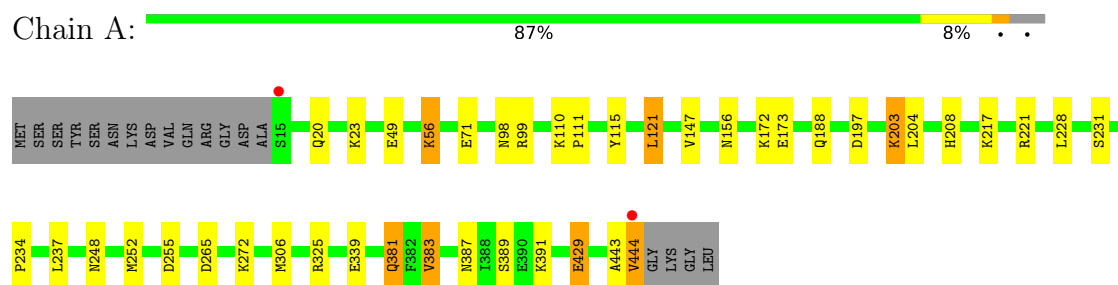
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	368	Total 368	O 368	0	0

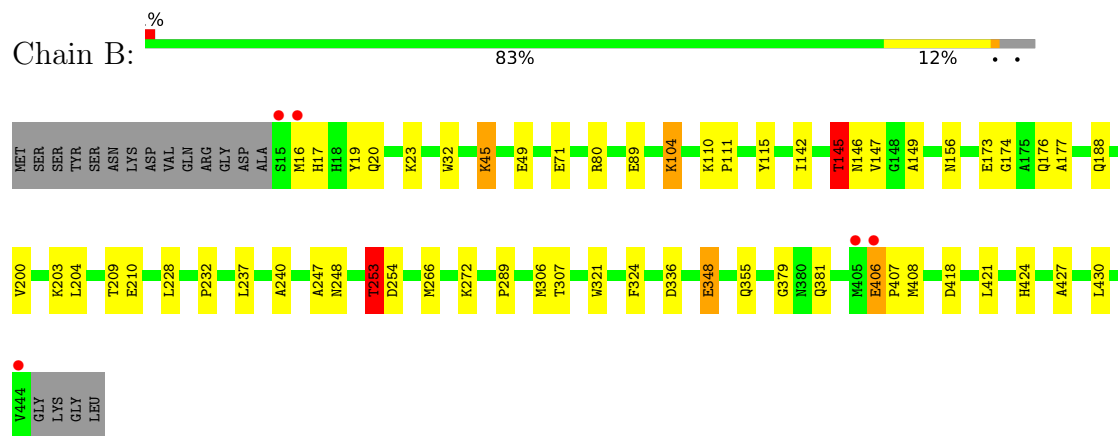
3 Residue-property plots [i](#)

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.

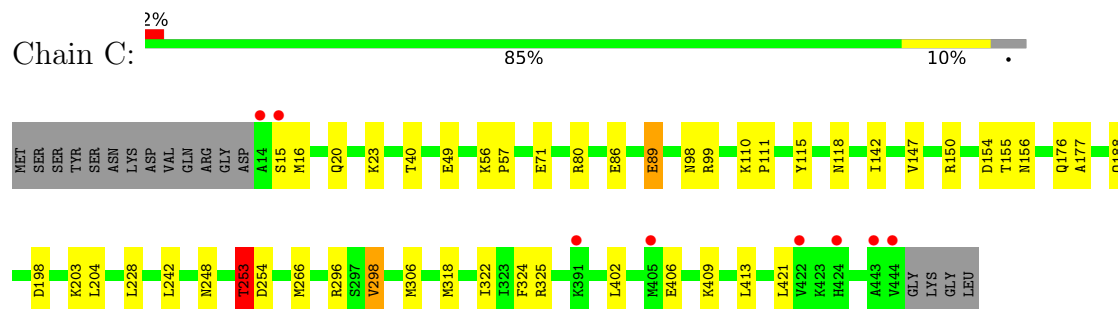
- Molecule 1: Abp, a GH27 beta-L-arabinopyranosidase



- Molecule 1: Abp, a GH27 beta-L-arabinopyranosidase

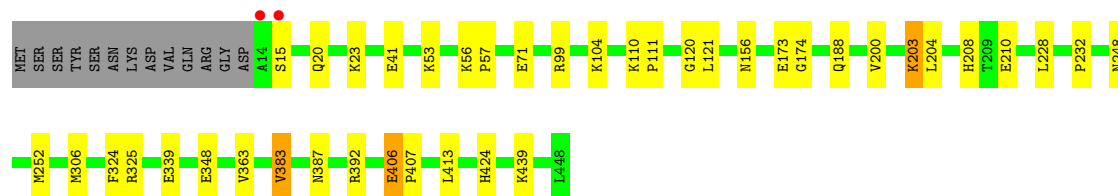


- Molecule 1: Abp, a GH27 beta-L-arabinopyranosidase



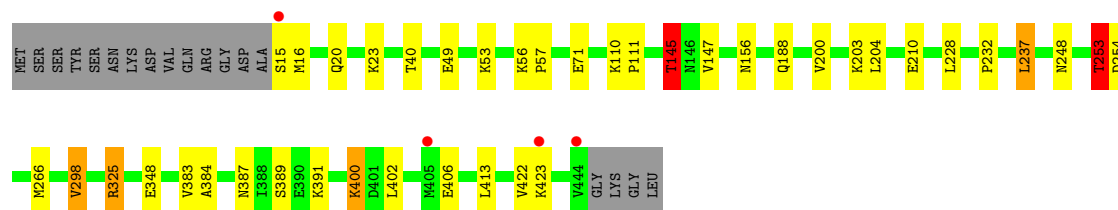
- Molecule 1: Abp, a GH27 beta-L-arabinopyranosidase

Chain D:  88% 8% . .



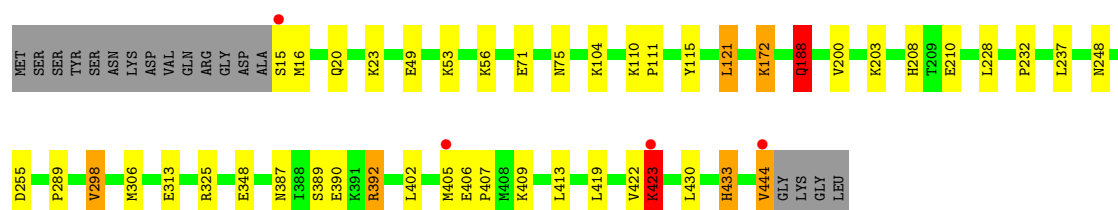
- Molecule 1: Abp, a GH27 beta-L-arabinopyranosidase

Chain E:  87% 8% . .



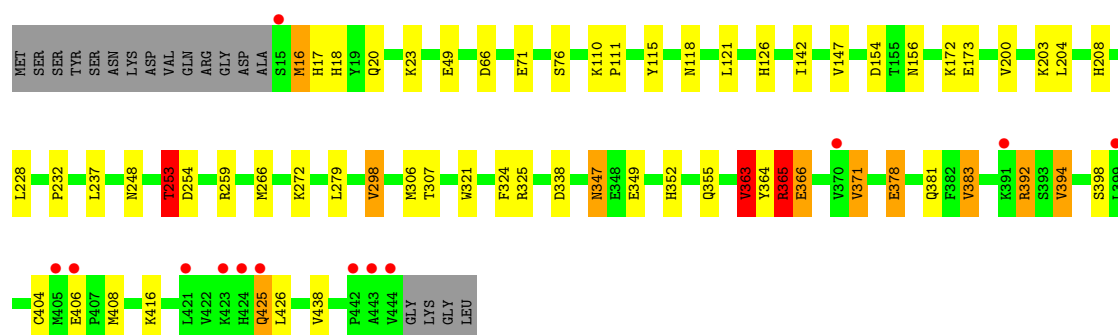
- Molecule 1: Abp, a GH27 beta-L-arabinopyranosidase

Chain F:  85% 9% . .



- Molecule 1: Abp, a GH27 beta-L-arabinopyranosidase

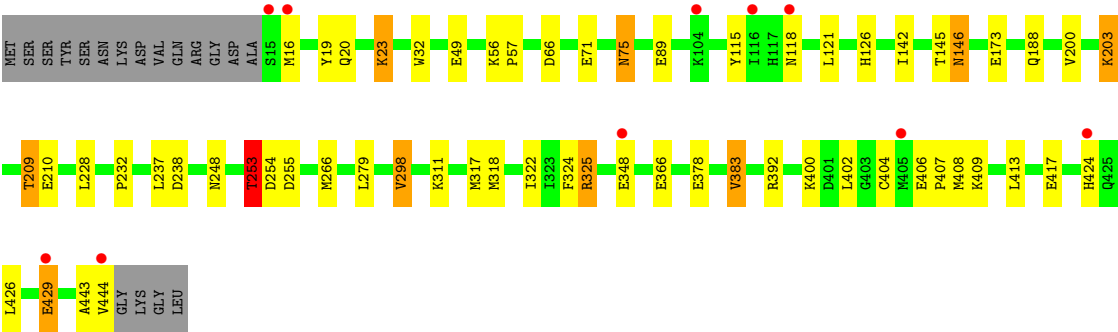
Chain G:  82% 11% . . .



- Molecule 1: Abp, a GH27 beta-L-arabinopyranosidase

Chain H:  82% 11% . .





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	107.71Å 202.16Å 287.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.90 – 2.28 29.90 – 2.28	Depositor EDS
% Data completeness (in resolution range)	96.8 (29.90-2.28) 96.8 (29.90-2.28)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.45 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.146 , 0.177 0.155 , 0.182	Depositor DCC
R_{free} test set	13899 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtriage
Anisotropy	0.206	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.9	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	0.96	EDS
Total number of atoms	32820	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.38% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CIT, GOL, 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	1.27	5/3606 (0.1%)	1.02	4/4895 (0.1%)
1	B	1.26	10/3607 (0.3%)	0.99	5/4896 (0.1%)
1	C	1.24	8/3595 (0.2%)	0.99	7/4880 (0.1%)
1	D	1.22	6/3611 (0.2%)	0.98	5/4899 (0.1%)
1	E	1.12	3/3595 (0.1%)	0.97	5/4881 (0.1%)
1	F	1.12	3/3572 (0.1%)	0.97	3/4849 (0.1%)
1	G	1.10	3/3589 (0.1%)	1.01	7/4872 (0.1%)
1	H	1.13	4/3572 (0.1%)	1.00	6/4849 (0.1%)
All	All	1.18	42/28747 (0.1%)	0.99	42/39021 (0.1%)

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	98	ASN	C-O	-7.23	1.15	1.24
1	C	98	ASN	C-O	-7.04	1.15	1.24
1	C	150	ARG	N-CA	-6.98	1.37	1.46
1	G	76	SER	C-O	-6.56	1.17	1.24
1	C	155	THR	C-O	-6.46	1.15	1.24

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	15	SER	N-CA-C	8.55	123.01	112.23
1	F	298	VAL	N-CA-CB	-7.43	98.97	111.23
1	E	298	VAL	N-CA-CB	-7.39	99.03	111.23
1	G	394	VAL	N-CA-CB	7.37	118.75	110.72
1	H	253	THR	N-CA-CB	-7.32	98.95	111.69

There are no chirality outliers.

There are no planarity outliers.

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	3492	0	3370	35	0
1	B	3496	0	3369	41	0
1	C	3487	0	3365	30	0
1	D	3506	0	3394	28	0
1	E	3484	0	3363	28	0
1	F	3470	0	3346	31	0
1	G	3481	0	3356	43	0
1	H	3470	0	3346	35	0
2	A	24	0	32	6	0
2	B	54	0	72	8	0
2	C	30	0	40	9	0
2	D	30	0	40	11	0
2	E	36	0	48	6	0
2	F	24	0	32	7	0
2	G	24	0	32	1	0
2	H	18	0	24	4	0
3	A	50	0	0	1	0
3	B	50	0	0	3	0
3	C	65	0	0	1	0
3	D	60	0	0	1	0
3	E	50	0	0	0	0
3	F	55	0	0	1	0
3	G	40	0	0	1	0
3	H	55	0	0	3	0
4	A	13	0	6	6	0
4	B	13	0	5	8	0
4	C	13	0	5	4	0
4	E	13	0	5	2	0
4	G	13	0	5	7	0
5	A	662	0	0	17	0
5	B	625	0	0	17	0
5	C	579	0	0	14	0
5	D	536	0	0	8	0
5	E	500	0	0	4	0
5	F	495	0	0	11	0
5	G	439	0	0	17	0
5	H	368	0	0	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	32820	0	27255	298	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 5.

The worst 5 of 298 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)
2:C:505:GOL:O3	2:C:505:GOL:C3	1.67	1.40
4:A:515:CIT:O5	4:A:515:CIT:C5	1.75	1.20
1:H:146:ASN:HB3	5:H:917:HOH:O	1.40	1.18
4:C:519:CIT:O4	4:C:519:CIT:H21	1.47	1.11
1:C:49:GLU:HG2	5:C:1111:HOH:O	1.53	1.09

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	432/448 (96%)	418 (97%)	14 (3%)	0	100	100
1	B	432/448 (96%)	413 (96%)	19 (4%)	0	100	100
1	C	431/448 (96%)	416 (96%)	15 (4%)	0	100	100
1	D	434/448 (97%)	419 (96%)	15 (4%)	0	100	100
1	E	431/448 (96%)	416 (96%)	15 (4%)	0	100	100
1	F	428/448 (96%)	413 (96%)	14 (3%)	1 (0%)	43	53
1	G	430/448 (96%)	415 (96%)	15 (4%)	0	100	100
1	H	428/448 (96%)	410 (96%)	17 (4%)	1 (0%)	43	53
All	All	3446/3584 (96%)	3320 (96%)	124 (4%)	2 (0%)	48	59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	325	ARG
1	F	325	ARG

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	373/383 (97%)	363 (97%)	10 (3%)	39	55
1	B	373/383 (97%)	362 (97%)	11 (3%)	37	52
1	C	371/383 (97%)	361 (97%)	10 (3%)	39	55
1	D	372/383 (97%)	365 (98%)	7 (2%)	50	66
1	E	372/383 (97%)	359 (96%)	13 (4%)	32	45
1	F	369/383 (96%)	351 (95%)	18 (5%)	22	31
1	G	371/383 (97%)	348 (94%)	23 (6%)	16	21
1	H	369/383 (96%)	348 (94%)	21 (6%)	18	25
All	All	2970/3064 (97%)	2857 (96%)	113 (4%)	29	42

5 of 113 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	237	LEU
1	H	413	LEU
1	G	118	ASN
1	H	409	LYS
1	H	203	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	248	ASN
1	H	20	GLN
1	E	138	GLN

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Mol	Chain	Res	Type
1	G	387	ASN
1	H	248	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 ⓘ

130 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	$\# Z > 2$
3	SO4	C	511	-	4,4,4	0.55	0	6,6,6	0.64	0
2	GOL	E	502	-	5,5,5	0.62	0	5,5,5	0.46	0
2	GOL	D	505	-	5,5,5	0.98	0	5,5,5	1.54	1 (20%)
3	SO4	B	511	-	4,4,4	0.79	0	6,6,6	0.60	0
2	GOL	A	502	-	5,5,5	0.62	0	5,5,5	0.36	0
3	SO4	A	513	-	4,4,4	0.52	0	6,6,6	0.63	0
3	SO4	C	509	-	4,4,4	0.51	0	6,6,6	0.15	0
2	GOL	A	504	-	5,5,5	0.48	0	5,5,5	0.68	0
3	SO4	G	505	-	4,4,4	0.45	0	6,6,6	0.65	0
3	SO4	D	506	-	4,4,4	0.52	0	6,6,6	0.64	0
2	GOL	F	502	-	5,5,5	0.51	0	5,5,5	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CIT	C	519	-	12,12,12	3.07	7 (58%)	17,17,17	3.61	9 (52%)
2	GOL	G	504	-	5,5,5	0.51	0	5,5,5	0.95	0
2	GOL	E	506	-	5,5,5	0.39	0	5,5,5	0.31	0
3	SO4	E	509	-	4,4,4	0.75	0	6,6,6	1.34	1 (16%)
3	SO4	F	512	-	4,4,4	0.69	0	6,6,6	0.81	0
3	SO4	H	504	-	4,4,4	0.61	0	6,6,6	0.56	0
3	SO4	C	510	-	4,4,4	0.87	0	6,6,6	0.42	0
3	SO4	F	509	-	4,4,4	0.61	0	6,6,6	0.78	0
3	SO4	C	508	-	4,4,4	0.59	0	6,6,6	0.53	0
3	SO4	C	518	-	4,4,4	0.57	0	6,6,6	0.37	0
3	SO4	E	507	-	4,4,4	0.58	0	6,6,6	0.63	0
3	SO4	D	513	-	4,4,4	0.69	0	6,6,6	0.80	0
2	GOL	B	505	-	5,5,5	1.15	0	5,5,5	0.77	0
3	SO4	F	507	-	4,4,4	0.63	0	6,6,6	0.35	0
3	SO4	F	514	-	4,4,4	0.81	0	6,6,6	0.46	0
3	SO4	C	512	-	4,4,4	0.63	0	6,6,6	0.72	0
3	SO4	F	506	-	4,4,4	0.62	0	6,6,6	0.25	0
3	SO4	C	515	-	4,4,4	0.79	0	6,6,6	1.30	1 (16%)
3	SO4	E	515	-	4,4,4	0.85	0	6,6,6	0.69	0
3	SO4	F	510	-	4,4,4	0.70	0	6,6,6	0.58	0
3	SO4	F	508	-	4,4,4	1.00	0	6,6,6	0.91	0
3	SO4	H	513	-	4,4,4	0.50	0	6,6,6	0.62	0
3	SO4	A	511	-	4,4,4	0.74	0	6,6,6	0.79	0
2	GOL	B	501	-	5,5,5	0.63	0	5,5,5	1.21	1 (20%)
3	SO4	B	518	-	4,4,4	0.58	0	6,6,6	0.22	0
2	GOL	E	501	-	5,5,5	0.55	0	5,5,5	0.25	0
2	GOL	B	506	-	5,5,5	0.74	0	5,5,5	0.54	0
2	GOL	H	502	-	5,5,5	0.43	0	5,5,5	0.99	0
3	SO4	A	505	-	4,4,4	1.27	0	6,6,6	1.08	0
3	SO4	D	514	-	4,4,4	0.62	0	6,6,6	0.38	0
3	SO4	D	510	-	4,4,4	0.66	0	6,6,6	0.54	0
2	GOL	A	503	-	5,5,5	0.84	0	5,5,5	2.28	2 (40%)
2	GOL	F	503	-	5,5,5	0.71	0	5,5,5	0.35	0
3	SO4	C	507	-	4,4,4	0.79	0	6,6,6	0.67	0
2	GOL	H	501	-	5,5,5	0.65	0	5,5,5	0.55	0
3	SO4	A	509	-	4,4,4	0.57	0	6,6,6	1.13	1 (16%)
3	SO4	H	511	-	4,4,4	0.50	0	6,6,6	0.43	0
3	SO4	D	515	-	4,4,4	0.62	0	6,6,6	0.47	0
2	GOL	D	503	-	5,5,5	0.57	0	5,5,5	1.89	3 (60%)
3	SO4	H	514	-	4,4,4	0.27	0	6,6,6	0.42	0
3	SO4	H	510	-	4,4,4	0.61	0	6,6,6	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	G	512	-	4,4,4	0.60	0	6,6,6	0.38	0
3	SO4	E	508	-	4,4,4	0.82	0	6,6,6	1.05	0
3	SO4	F	513	-	4,4,4	0.75	0	6,6,6	1.14	1 (16%)
3	SO4	A	506	-	4,4,4	0.56	0	6,6,6	0.48	0
3	SO4	D	516	-	4,4,4	0.64	0	6,6,6	0.82	0
2	GOL	B	508	-	5,5,5	0.76	0	5,5,5	0.93	0
2	GOL	B	509	-	5,5,5	0.68	0	5,5,5	0.85	0
3	SO4	C	514	-	4,4,4	0.55	0	6,6,6	0.37	0
3	SO4	G	507	-	4,4,4	0.76	0	6,6,6	0.51	0
3	SO4	H	507	-	4,4,4	0.29	0	6,6,6	0.37	0
2	GOL	C	503	-	5,5,5	2.32	3 (60%)	5,5,5	2.29	3 (60%)
3	SO4	G	506	-	4,4,4	0.79	0	6,6,6	0.90	0
3	SO4	H	508	-	4,4,4	0.60	0	6,6,6	0.45	0
3	SO4	B	514	-	4,4,4	0.59	0	6,6,6	0.60	0
3	SO4	E	514	-	4,4,4	1.15	0	6,6,6	1.09	0
2	GOL	B	503	-	5,5,5	0.93	0	5,5,5	1.53	1 (20%)
4	CIT	A	515	-	12,12,12	1.79	4 (33%)	17,17,17	4.53	13 (76%)
3	SO4	G	508	-	4,4,4	0.26	0	6,6,6	0.31	0
3	SO4	B	510	-	4,4,4	0.55	0	6,6,6	0.67	0
2	GOL	C	502	-	5,5,5	0.60	0	5,5,5	0.60	0
2	GOL	H	503	-	5,5,5	0.86	0	5,5,5	0.93	0
2	GOL	D	501	-	5,5,5	0.84	0	5,5,5	0.57	0
3	SO4	D	517	-	4,4,4	0.56	0	6,6,6	0.72	0
3	SO4	F	515	-	4,4,4	0.58	0	6,6,6	0.47	0
2	GOL	G	503	-	5,5,5	0.54	0	5,5,5	1.21	1 (20%)
3	SO4	B	515	-	4,4,4	0.81	0	6,6,6	0.82	0
3	SO4	H	512	-	4,4,4	0.51	0	6,6,6	0.70	0
2	GOL	E	503	-	5,5,5	0.69	0	5,5,5	1.86	2 (40%)
3	SO4	C	506	-	4,4,4	0.54	0	6,6,6	0.48	0
2	GOL	G	502	-	5,5,5	0.37	0	5,5,5	0.49	0
2	GOL	F	501	-	5,5,5	0.86	0	5,5,5	0.34	0
3	SO4	D	509	-	4,4,4	0.90	0	6,6,6	1.59	1 (16%)
2	GOL	B	502	-	5,5,5	0.54	0	5,5,5	0.70	0
2	GOL	C	504	-	5,5,5	0.66	0	5,5,5	0.99	1 (20%)
3	SO4	B	519	-	4,4,4	0.64	0	6,6,6	0.63	0
4	CIT	E	517	-	12,12,12	1.47	2 (16%)	17,17,17	1.86	5 (29%)
3	SO4	A	514	-	4,4,4	0.87	0	6,6,6	0.73	0
4	CIT	G	513	-	12,12,12	2.07	5 (41%)	17,17,17	3.89	10 (58%)
2	GOL	B	504	-	5,5,5	0.69	0	5,5,5	1.27	1 (20%)
3	SO4	F	505	-	4,4,4	0.64	0	6,6,6	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	B	517	-	4,4,4	0.94	0	6,6,6	1.06	0
4	CIT	B	520	-	12,12,12	2.28	3 (25%)	17,17,17	1.70	4 (23%)
2	GOL	B	507	-	5,5,5	0.36	0	5,5,5	1.58	1 (20%)
3	SO4	C	516	-	4,4,4	0.67	0	6,6,6	0.76	0
3	SO4	A	512	-	4,4,4	1.11	0	6,6,6	1.36	1 (16%)
3	SO4	E	510	-	4,4,4	0.67	0	6,6,6	0.35	0
3	SO4	B	516	-	4,4,4	0.81	0	6,6,6	1.21	0
3	SO4	G	510	-	4,4,4	0.59	0	6,6,6	0.23	0
3	SO4	A	510	-	4,4,4	0.73	0	6,6,6	0.86	0
3	SO4	E	511	-	4,4,4	0.62	0	6,6,6	1.28	1 (16%)
3	SO4	H	506	-	4,4,4	0.78	0	6,6,6	0.74	0
3	SO4	D	512	-	4,4,4	0.62	0	6,6,6	1.18	0
2	GOL	C	505	-	5,5,5	2.78	1 (20%)	5,5,5	1.77	2 (40%)
3	SO4	A	507	-	4,4,4	0.73	0	6,6,6	0.71	0
3	SO4	G	511	-	4,4,4	0.24	0	6,6,6	0.58	0
2	GOL	C	501	-	5,5,5	0.26	0	5,5,5	0.73	0
2	GOL	E	505	-	5,5,5	1.52	1 (20%)	5,5,5	2.67	4 (80%)
3	SO4	H	509	-	4,4,4	0.76	0	6,6,6	0.85	0
3	SO4	A	508	-	4,4,4	0.62	0	6,6,6	0.43	0
3	SO4	D	507	-	4,4,4	0.63	0	6,6,6	0.30	0
2	GOL	D	502	-	5,5,5	0.93	0	5,5,5	1.68	2 (40%)
2	GOL	F	504	-	5,5,5	0.26	0	5,5,5	0.54	0
2	GOL	D	504	-	5,5,5	0.68	0	5,5,5	1.41	1 (20%)
3	SO4	B	512	-	4,4,4	0.77	0	6,6,6	1.09	0
3	SO4	E	512	-	4,4,4	0.66	0	6,6,6	0.74	0
3	SO4	E	516	-	4,4,4	0.62	0	6,6,6	0.36	0
3	SO4	C	513	-	4,4,4	0.80	0	6,6,6	1.32	1 (16%)
3	SO4	G	509	-	4,4,4	0.45	0	6,6,6	0.55	0
2	GOL	E	504	-	5,5,5	0.76	0	5,5,5	0.87	0
2	GOL	G	501	-	5,5,5	0.64	0	5,5,5	0.91	0
3	SO4	B	513	-	4,4,4	0.48	0	6,6,6	0.53	0
2	GOL	A	501	-	5,5,5	0.64	0	5,5,5	0.53	0
3	SO4	D	508	-	4,4,4	1.18	0	6,6,6	0.55	0
3	SO4	E	513	-	4,4,4	0.67	0	6,6,6	0.83	0
3	SO4	C	517	-	4,4,4	0.75	0	6,6,6	0.39	0
3	SO4	D	511	-	4,4,4	0.75	0	6,6,6	1.85	1 (16%)
3	SO4	H	505	-	4,4,4	0.51	0	6,6,6	0.42	0
3	SO4	F	511	-	4,4,4	0.76	0	6,6,6	0.80	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	GOL	B	504	-	-	2/4/4/4	-
2	GOL	B	501	-	-	0/4/4/4	-
2	GOL	C	502	-	-	2/4/4/4	-
2	GOL	E	502	-	-	2/4/4/4	-
2	GOL	E	501	-	-	2/4/4/4	-
2	GOL	B	506	-	-	4/4/4/4	-
2	GOL	H	502	-	-	4/4/4/4	-
2	GOL	B	507	-	-	1/4/4/4	-
4	CIT	B	520	-	-	10/16/16/16	-
2	GOL	D	505	-	-	4/4/4/4	-
2	GOL	A	502	-	-	2/4/4/4	-
2	GOL	H	503	-	-	4/4/4/4	-
2	GOL	A	504	-	-	0/4/4/4	-
2	GOL	D	501	-	-	0/4/4/4	-
2	GOL	A	503	-	-	1/4/4/4	-
2	GOL	F	502	-	-	4/4/4/4	-
2	GOL	F	503	-	-	0/4/4/4	-
2	GOL	E	506	-	-	2/4/4/4	-
2	GOL	G	504	-	-	2/4/4/4	-
4	CIT	C	519	-	-	8/16/16/16	-
2	GOL	H	501	-	-	2/4/4/4	-
2	GOL	G	503	-	-	2/4/4/4	-
2	GOL	C	505	-	-	2/4/4/4	-
2	GOL	C	501	-	-	1/4/4/4	-
2	GOL	E	503	-	-	2/4/4/4	-
2	GOL	E	505	-	-	2/4/4/4	-
2	GOL	D	503	-	-	3/4/4/4	-
2	GOL	B	505	-	-	0/4/4/4	-
2	GOL	G	502	-	-	4/4/4/4	-
2	GOL	D	502	-	-	0/4/4/4	-
2	GOL	F	504	-	-	3/4/4/4	-
2	GOL	D	504	-	-	0/4/4/4	-
2	GOL	B	508	-	-	0/4/4/4	-
2	GOL	B	509	-	-	2/4/4/4	-
2	GOL	F	501	-	-	0/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	C	503	-	-	4/4/4/4	-
2	GOL	E	504	-	-	2/4/4/4	-
2	GOL	G	501	-	-	0/4/4/4	-
2	GOL	A	501	-	-	4/4/4/4	-
2	GOL	B	502	-	-	2/4/4/4	-
2	GOL	B	503	-	-	1/4/4/4	-
2	GOL	C	504	-	-	0/4/4/4	-
4	CIT	A	515	-	-	6/16/16/16	-
4	CIT	E	517	-	-	7/16/16/16	-
4	CIT	G	513	-	-	7/16/16/16	-

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	519	CIT	C3-C6	6.28	1.60	1.53
2	C	505	GOL	O3-C3	6.01	1.67	1.42
4	B	520	CIT	O7-C3	5.50	1.53	1.43
4	C	519	CIT	O7-C3	4.96	1.52	1.43
4	C	519	CIT	C4-C3	3.57	1.58	1.54

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	515	CIT	O5-C6-C3	-11.49	99.83	122.09
4	G	513	CIT	O5-C6-C3	-10.25	102.24	122.09
4	A	515	CIT	O6-C6-C3	8.09	128.67	113.14
4	G	513	CIT	O6-C6-C3	8.00	128.50	113.14
4	C	519	CIT	O2-C1-O1	7.39	142.34	123.33

There are no chirality outliers.

5 of 110 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	O1-C1-C2-C3
2	A	501	GOL	C1-C2-C3-O3
2	A	501	GOL	O2-C2-C3-O3
2	B	502	GOL	O1-C1-C2-C3
2	B	506	GOL	O1-C1-C2-O2

There are no ring outliers.

37 monomers are involved in 89 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	505	GOL	4	0
3	B	511	SO4	1	0
2	A	502	GOL	2	0
2	F	502	GOL	5	0
4	C	519	CIT	4	0
3	C	508	SO4	1	0
2	B	505	GOL	1	0
3	F	506	SO4	1	0
2	H	502	GOL	2	0
2	A	503	GOL	1	0
2	H	501	GOL	1	0
2	D	503	GOL	2	0
2	C	503	GOL	3	0
3	H	508	SO4	1	0
3	B	514	SO4	1	0
2	B	503	GOL	3	0
4	A	515	CIT	6	0
2	H	503	GOL	1	0
2	G	502	GOL	1	0
2	B	502	GOL	1	0
2	C	504	GOL	2	0
4	E	517	CIT	2	0
4	G	513	CIT	7	0
2	B	504	GOL	3	0
4	B	520	CIT	8	0
3	G	510	SO4	1	0
3	A	510	SO4	1	0
3	D	512	SO4	1	0
2	C	505	GOL	4	0
2	E	505	GOL	5	0
3	H	509	SO4	1	0
2	D	502	GOL	5	0
2	F	504	GOL	2	0
2	E	504	GOL	1	0
3	B	513	SO4	1	0
2	A	501	GOL	3	0
3	H	505	SO4	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	430/448 (95%)	-0.80	2 (0%) 87 88	8, 13, 35, 96	4 (0%)
1	B	430/448 (95%)	-0.68	5 (1%) 76 78	9, 17, 36, 91	4 (0%)
1	C	431/448 (96%)	-0.58	8 (1%) 66 68	9, 18, 50, 107	2 (0%)
1	D	435/448 (97%)	-0.51	2 (0%) 87 88	10, 22, 45, 88	1 (0%)
1	E	430/448 (95%)	-0.43	4 (0%) 81 82	11, 23, 56, 114	3 (0%)
1	F	430/448 (95%)	-0.29	4 (0%) 81 82	16, 27, 53, 116	0
1	G	430/448 (95%)	0.12	13 (3%) 52 54	11, 32, 61, 111	3 (0%)
1	H	430/448 (95%)	0.38	10 (2%) 61 63	22, 37, 61, 115	0
All	All	3446/3584 (96%)	-0.35	48 (1%) 73 75	8, 23, 53, 116	17 (0%)

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	444	VAL	8.0
1	G	444	VAL	7.9
1	A	444	VAL	7.6
1	E	444	VAL	7.4
1	C	14	ALA	7.3

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 ⓘ

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
3	SO4	E	516	5/5	0.55	0.14	91,102,118,122	0
3	SO4	G	508	5/5	0.61	0.16	96,103,128,136	0
3	SO4	H	514	5/5	0.61	0.13	101,112,123,125	0
3	SO4	H	507	5/5	0.64	0.13	104,110,115,123	0
3	SO4	G	510	5/5	0.71	0.14	90,99,107,116	0
3	SO4	H	505	5/5	0.71	0.13	75,97,102,103	0
3	SO4	D	516	5/5	0.72	0.15	75,76,93,95	0
3	SO4	F	515	5/5	0.73	0.12	90,102,112,113	0
3	SO4	E	507	5/5	0.73	0.17	78,97,117,120	0
3	SO4	C	518	5/5	0.73	0.14	83,92,120,127	0
3	SO4	A	513	5/5	0.74	0.14	74,76,86,93	0
3	SO4	D	513	5/5	0.76	0.14	71,82,108,108	0
3	SO4	D	515	5/5	0.77	0.13	76,91,101,105	0
3	SO4	F	508	5/5	0.78	0.20	54,67,89,95	0
3	SO4	F	511	5/5	0.78	0.19	54,74,86,91	0
3	SO4	E	510	5/5	0.78	0.15	84,91,94,107	0
3	SO4	H	512	5/5	0.78	0.12	81,83,96,96	0
3	SO4	C	507	5/5	0.78	0.17	72,81,101,102	0
3	SO4	D	511	5/5	0.79	0.17	49,62,78,78	0
3	SO4	H	509	5/5	0.80	0.18	43,46,66,74	5
3	SO4	H	510	5/5	0.80	0.17	78,82,95,96	0
2	GOL	G	502	6/6	0.80	0.18	56,68,77,82	0
3	SO4	H	508	5/5	0.80	0.13	69,71,88,94	0
3	SO4	F	506	5/5	0.81	0.13	86,87,108,111	0
3	SO4	C	506	5/5	0.81	0.10	76,77,94,94	0
3	SO4	G	512	5/5	0.81	0.14	80,91,99,104	0
3	SO4	D	507	5/5	0.81	0.13	78,96,97,105	0
3	SO4	B	518	5/5	0.81	0.13	102,103,116,122	0
3	SO4	E	509	5/5	0.82	0.22	46,60,77,91	5
2	GOL	C	505	6/6	0.82	0.20	21,27,34,43	0
3	SO4	E	513	5/5	0.82	0.14	75,76,88,92	0
2	GOL	B	505	6/6	0.82	0.20	43,54,65,67	0
3	SO4	D	514	5/5	0.82	0.14	62,91,99,102	0
3	SO4	G	511	5/5	0.82	0.12	82,101,104,113	0
3	SO4	F	507	5/5	0.82	0.15	71,88,91,99	5
2	GOL	D	503	6/6	0.83	0.16	43,49,54,62	0
3	SO4	B	519	5/5	0.83	0.14	56,73,88,106	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GOL	G	504	6/6	0.83	0.20	52,58,67,71	0
2	GOL	F	503	6/6	0.83	0.18	59,67,71,72	0
3	SO4	H	504	5/5	0.84	0.11	73,79,92,107	0
3	SO4	B	513	5/5	0.84	0.14	79,94,112,117	0
3	SO4	D	510	5/5	0.84	0.14	66,78,95,97	0
3	SO4	G	505	5/5	0.84	0.19	71,98,113,117	0
3	SO4	F	505	5/5	0.84	0.12	72,75,85,96	0
2	GOL	B	508	6/6	0.84	0.17	63,65,68,70	0
3	SO4	C	509	5/5	0.84	0.12	104,108,116,118	0
2	GOL	E	506	6/6	0.84	0.18	58,72,74,75	0
3	SO4	A	514	5/5	0.85	0.15	48,62,67,83	0
3	SO4	C	508	5/5	0.85	0.12	74,75,79,82	0
3	SO4	F	510	5/5	0.85	0.19	62,74,79,88	0
3	SO4	C	514	5/5	0.86	0.12	65,79,88,91	0
3	SO4	E	515	5/5	0.86	0.18	52,70,82,84	0
3	SO4	F	513	5/5	0.86	0.19	56,60,79,90	0
3	SO4	H	506	5/5	0.86	0.16	59,63,68,77	0
3	SO4	F	514	5/5	0.86	0.21	59,70,77,89	0
2	GOL	B	503	6/6	0.86	0.15	29,31,43,48	0
2	GOL	H	502	6/6	0.86	0.20	52,62,74,81	0
3	SO4	B	516	5/5	0.86	0.19	51,67,68,72	0
3	SO4	H	511	5/5	0.86	0.11	70,92,95,103	0
3	SO4	B	517	5/5	0.86	0.17	39,41,60,63	0
2	GOL	B	507	6/6	0.86	0.17	54,64,72,76	0
4	CIT	E	517	13/13	0.86	0.16	35,64,73,87	0
2	GOL	D	505	6/6	0.87	0.16	32,36,39,50	0
2	GOL	C	503	6/6	0.87	0.19	18,24,28,33	6
2	GOL	H	503	6/6	0.87	0.15	38,42,49,53	0
2	GOL	F	502	6/6	0.87	0.14	40,47,49,56	0
3	SO4	G	506	5/5	0.87	0.15	45,80,86,98	0
2	GOL	A	502	6/6	0.87	0.17	54,66,71,72	0
3	SO4	B	511	5/5	0.87	0.17	45,58,66,67	5
2	GOL	B	506	6/6	0.87	0.16	56,67,71,71	0
3	SO4	E	514	5/5	0.87	0.19	41,52,66,79	0
3	SO4	F	512	5/5	0.87	0.15	64,69,90,96	0
2	GOL	C	504	6/6	0.88	0.13	36,38,44,56	0
3	SO4	D	508	5/5	0.88	0.22	48,59,67,81	0
2	GOL	F	504	6/6	0.88	0.16	50,57,62,66	0
3	SO4	F	509	5/5	0.88	0.17	56,75,85,85	0
2	GOL	B	509	6/6	0.88	0.15	50,58,65,66	0
3	SO4	B	512	5/5	0.88	0.21	44,48,51,65	5
3	SO4	C	515	5/5	0.88	0.15	49,58,72,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	A	507	5/5	0.88	0.15	39,52,60,70	5
4	CIT	C	519	13/13	0.88	0.13	26,45,62,62	0
3	SO4	D	506	5/5	0.88	0.11	72,74,85,96	0
3	SO4	D	509	5/5	0.89	0.17	45,56,68,71	0
3	SO4	E	512	5/5	0.89	0.15	50,66,84,88	0
3	SO4	B	514	5/5	0.89	0.20	61,66,79,82	5
3	SO4	C	517	5/5	0.89	0.20	56,64,78,90	0
3	SO4	D	512	5/5	0.89	0.17	60,73,82,87	0
3	SO4	E	508	5/5	0.89	0.14	39,43,56,60	5
3	SO4	A	512	5/5	0.89	0.19	41,41,58,59	0
2	GOL	E	505	6/6	0.90	0.20	32,45,48,49	0
3	SO4	A	506	5/5	0.90	0.17	66,66,86,88	0
4	CIT	B	520	13/13	0.90	0.12	31,46,59,64	0
2	GOL	E	503	6/6	0.90	0.14	50,57,62,65	0
3	SO4	A	508	5/5	0.90	0.24	62,73,75,86	0
3	SO4	C	511	5/5	0.91	0.13	67,67,82,88	0
2	GOL	H	501	6/6	0.91	0.12	32,43,45,48	0
3	SO4	G	507	5/5	0.91	0.12	40,46,60,61	5
3	SO4	C	510	5/5	0.91	0.20	51,60,76,78	0
3	SO4	A	509	5/5	0.92	0.15	55,62,69,75	0
3	SO4	A	511	5/5	0.92	0.18	39,53,58,69	0
2	GOL	E	504	6/6	0.92	0.17	37,56,61,63	0
2	GOL	G	503	6/6	0.92	0.11	29,36,38,44	0
3	SO4	C	513	5/5	0.92	0.16	43,45,49,62	0
2	GOL	A	504	6/6	0.92	0.12	38,45,53,54	0
4	CIT	G	513	13/13	0.92	0.11	35,44,66,66	0
2	GOL	G	501	6/6	0.93	0.11	40,49,64,65	0
4	CIT	A	515	13/13	0.93	0.12	15,29,39,49	13
2	GOL	D	504	6/6	0.93	0.10	31,37,44,54	0
2	GOL	D	502	6/6	0.93	0.10	31,35,39,41	0
3	SO4	B	510	5/5	0.93	0.16	68,70,76,86	0
2	GOL	C	502	6/6	0.93	0.11	31,38,49,63	0
2	GOL	B	502	6/6	0.94	0.09	32,37,45,57	0
2	GOL	E	501	6/6	0.94	0.10	35,49,58,64	0
3	SO4	A	505	5/5	0.94	0.14	32,35,47,64	0
2	GOL	A	501	6/6	0.94	0.10	28,38,48,60	0
3	SO4	C	516	5/5	0.94	0.15	40,58,64,72	0
2	GOL	F	501	6/6	0.94	0.09	25,32,35,37	0
3	SO4	D	517	5/5	0.94	0.12	34,35,49,51	5
2	GOL	B	504	6/6	0.95	0.10	30,35,38,40	0
2	GOL	D	501	6/6	0.96	0.07	18,22,23,24	0
3	SO4	E	511	5/5	0.96	0.13	39,41,44,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GOL	A	503	6/6	0.96	0.08	14,18,19,24	0
2	GOL	C	501	6/6	0.96	0.05	18,20,21,22	0
2	GOL	E	502	6/6	0.96	0.07	22,26,27,32	0
3	SO4	C	512	5/5	0.97	0.12	40,46,54,54	0
2	GOL	B	501	6/6	0.97	0.08	18,25,27,34	0
3	SO4	H	513	5/5	0.97	0.11	53,53,57,60	0
3	SO4	B	515	5/5	0.98	0.09	23,35,38,39	0
3	SO4	G	509	5/5	0.99	0.04	24,25,28,29	0
3	SO4	A	510	5/5	0.99	0.05	23,24,26,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.