



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 08:39 pm BST

PDB ID : 2XIB
Title : CRYSTAL STRUCTURE OF AN ALPHA-L-FUCOSIDASE GH29 FROM BACTEROIDES THETA IOTA MICRON IN COMPLEX WITH DEOXY-FUCONOJIRIMYCIN
Authors : Lammerts van Bueren, A.; Popat, S.D.; Lin, C.H.; Davies, G.J.
Deposited on : 2010-06-28
Resolution : 2.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

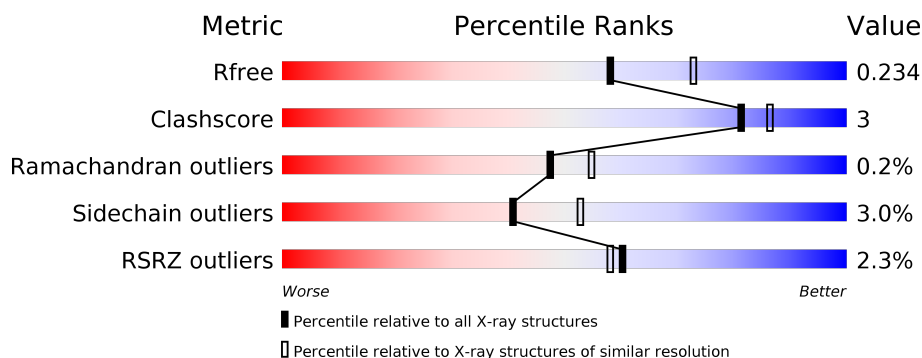
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 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	453	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>7%</div> <div>• •</div> </div> </div>
1	B	453	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>8%</div> <div>• •</div> </div> </div>
1	C	453	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>6%</div> <div>• •</div> </div> </div>
1	D	453	<div> <div>3%</div> <div> <div></div> <div>90%</div> <div>6%</div> <div>•</div> </div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	TRS	D	1474	-	X	-	-

2 Entry composition [i](#)

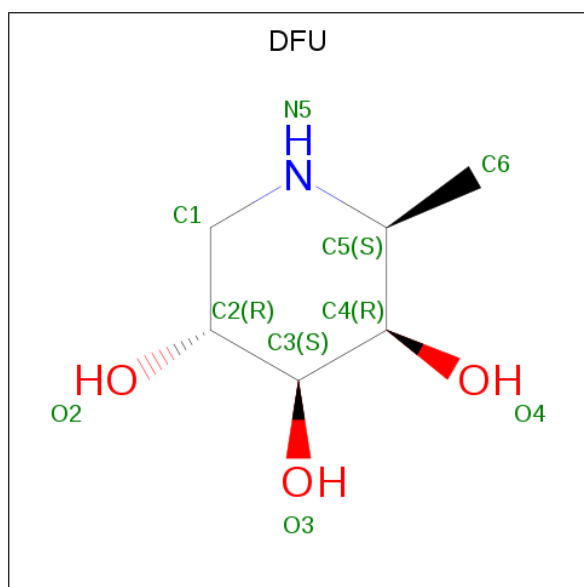
There are 6 unique types of molecules in this entry. The entry contains 15070 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called ALPHA-L-FUCOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	0	0	0
			3562	2290	601	655	16			
1	B	437	Total	C	N	O	S	0	0	0
			3562	2290	601	655	16			
1	C	437	Total	C	N	O	S	0	0	0
			3562	2290	601	655	16			
1	D	437	Total	C	N	O	S	0	0	0
			3562	2290	601	655	16			

- Molecule 2 is (2S,3R,4S,5R)-2-METHYLPYPERIDINE-3,4,5-TRIOL (three-letter code: DFU) (formula: C₆H₁₃NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			10	6	1	3		
2	B	1	Total	C	N	O	0	0
			10	6	1	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			10	6	1	3		
2	D	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 3 is SULFATE ION (three-letter code: 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	B	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		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	D	1	Total	C	N	O	0	0
			8	4	1	3		

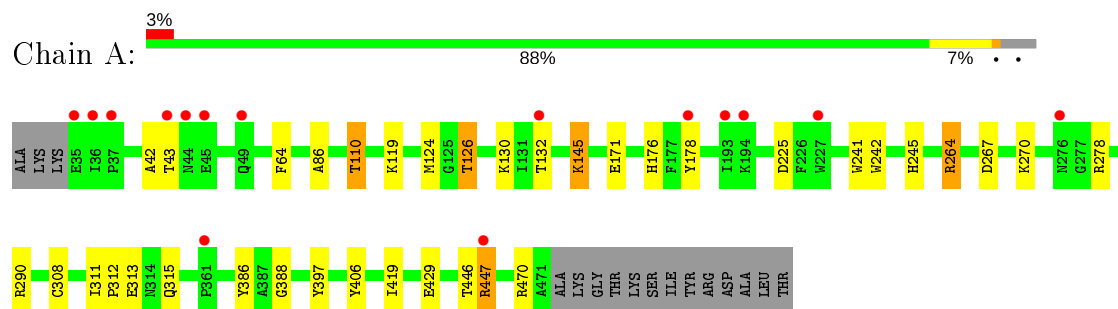
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	163	Total	O	0	0
			163	163		
6	B	203	Total	O	0	0
			203	203		
6	C	194	Total	O	0	0
			194	194		
6	D	159	Total	O	0	0
			159	159		

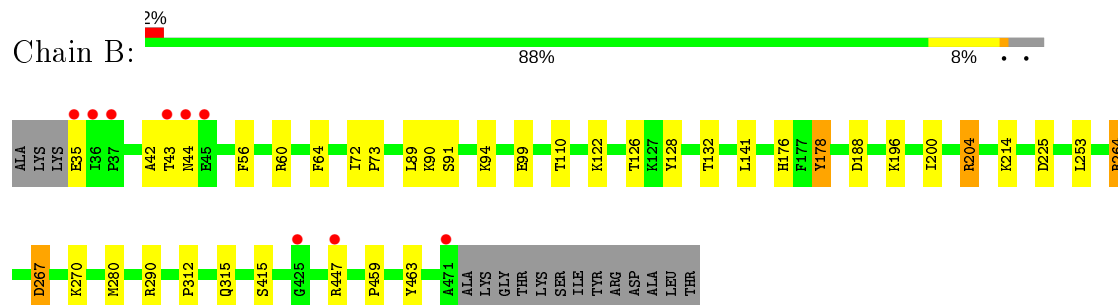
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

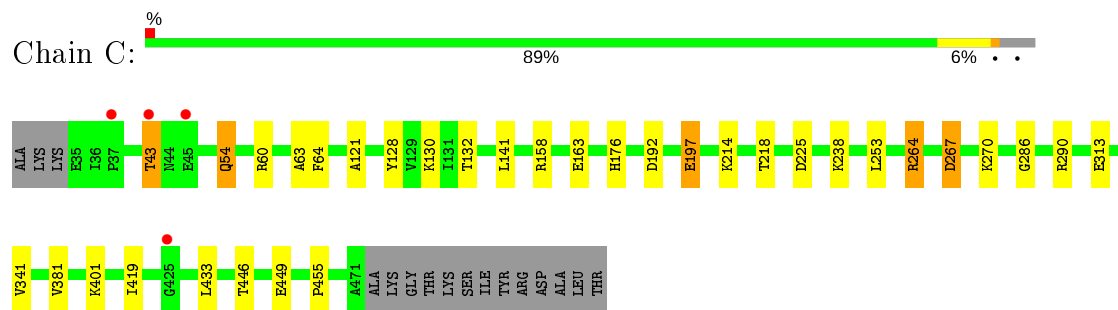
• Molecule 1: ALPHA-L-FUCOSIDASE



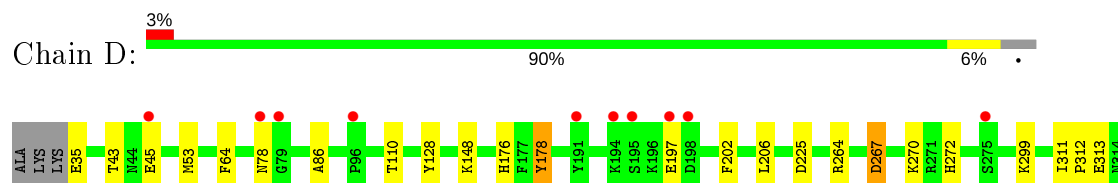
• Molecule 1: ALPHA-L-FUCOSIDASE



• Molecule 1: ALPHA-L-FUCOSIDASE



• Molecule 1: ALPHA-L-FUCOSIDASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.68 Å 185.99 Å 97.63 Å 90.00° 94.75° 90.00°	Depositor
Resolution (Å)	34.75 – 2.20 34.29 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.75-2.20) 100.0 (34.29-2.20)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 2.20 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.185 , 0.235 0.187 , 0.234	Depositor DCC
R_{free} test set	4927 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	27.6	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15070	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% 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: DFU, GOL, TRS, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.59	0/3669	0.66	1/4976 (0.0%)
1	B	0.61	0/3669	0.68	4/4976 (0.1%)
1	C	0.62	0/3669	0.69	2/4976 (0.0%)
1	D	0.58	0/3669	0.66	0/4976
All	All	0.60	0/14676	0.67	7/19904 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	264	ARG	NE-CZ-NH2	-7.75	116.42	120.30
1	B	264	ARG	NE-CZ-NH2	-7.33	116.64	120.30
1	C	264	ARG	NE-CZ-NH1	6.87	123.73	120.30
1	B	204	ARG	NE-CZ-NH1	6.83	123.72	120.30
1	B	264	ARG	NE-CZ-NH1	6.40	123.50	120.30
1	B	204	ARG	NE-CZ-NH2	-6.29	117.16	120.30
1	A	264	ARG	NE-CZ-NH2	-5.32	117.64	120.30

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	3562	0	3431	19	0
1	B	3562	0	3431	20	0
1	C	3562	0	3431	22	0
1	D	3562	0	3431	12	0
2	A	10	0	13	0	0
2	B	10	0	13	0	0
2	C	10	0	13	0	0
2	D	10	0	13	0	0
3	A	10	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
4	A	6	0	8	1	0
4	B	12	0	16	1	0
4	C	6	0	8	2	0
4	D	6	0	8	1	0
5	D	8	0	12	1	0
6	A	163	0	0	4	0
6	B	203	0	0	1	0
6	C	194	0	0	2	0
6	D	159	0	0	3	0
All	All	15070	0	13828	74	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 3.

All (74) 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:C:54:GLN:HE22	1:C:401:LYS:NZ	1.60	0.98
1:C:54:GLN:HE22	1:C:401:LYS:HZ2	1.01	0.93
5:D:1474:TRS:N	4:D:1475:GOL:O2	2.07	0.87
1:A:245:HIS:ND1	6:A:2076:HOH:O	2.22	0.72
1:A:308:CYS:HB3	6:A:2097:HOH:O	1.90	0.71
1:D:402:ASN:HB3	6:D:2127:HOH:O	1.90	0.70
1:C:158:ARG:HD2	1:C:163:GLU:OE2	1.93	0.68
1:D:86:ALA:H	1:D:315:GLN:HE22	1.46	0.64
1:C:176:HIS:CG	1:C:225:ASP:HB3	2.34	0.63
1:C:63:ALA:CB	4:C:1474:GOL:H11	2.30	0.61
1:C:197:GLU:HB2	6:C:2075:HOH:O	2.00	0.61
1:B:91:SER:O	1:B:94:LYS:HD2	2.00	0.61
1:C:54:GLN:NE2	1:C:401:LYS:NZ	2.42	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:214:LYS:O	1:C:218:THR:HG23	2.03	0.58
1:A:119:LYS:HD3	1:A:171:GLU:OE2	2.04	0.57
1:C:446:THR:HG22	1:C:449:GLU:HB3	1.87	0.57
1:D:267:ASP:OD2	1:D:267:ASP:N	2.37	0.57
1:B:35:GLU:N	6:B:2001:HOH:O	2.37	0.56
1:B:188:ASP:OD2	1:B:204:ARG:HD2	2.06	0.56
1:C:267:ASP:OD2	1:C:267:ASP:N	2.38	0.56
1:C:132:THR:O	1:C:141:LEU:HD12	2.06	0.56
1:B:415:SER:HB3	4:B:1474:GOL:H32	1.88	0.53
1:A:311:ILE:HB	1:A:312:PRO:HD3	1.91	0.53
1:B:214:LYS:HG2	1:B:253:LEU:HD11	1.91	0.53
1:D:86:ALA:H	1:D:315:GLN:NE2	2.07	0.53
1:D:311:ILE:HB	1:D:312:PRO:HD3	1.93	0.51
1:A:429:GLU:OE2	1:A:470:ARG:CB	2.58	0.51
1:B:312:PRO:HG2	1:B:315:GLN:HB2	1.93	0.51
1:A:176:HIS:CG	1:A:225:ASP:HB3	2.46	0.50
1:D:176:HIS:CG	1:D:225:ASP:HB3	2.46	0.50
1:A:145:LYS:HD2	6:A:2067:HOH:O	2.11	0.50
1:D:202:PHE:CE2	1:D:206:LEU:HD21	2.46	0.50
1:B:176:HIS:CG	1:B:225:ASP:HB3	2.46	0.49
1:B:196:LYS:NZ	1:B:200:ILE:HD11	2.28	0.49
1:C:341:VAL:HG21	1:C:381:VAL:HG13	1.94	0.49
1:C:121:ALA:HB2	4:C:1474:GOL:H31	1.96	0.48
1:A:42:ALA:HB3	1:A:278:ARG:HE	1.78	0.47
1:B:72:ILE:HB	1:B:73:PRO:HD3	1.97	0.47
1:D:35:GLU:N	6:D:2002:HOH:O	2.46	0.47
1:A:446:THR:OG1	1:A:447:ARG:N	2.46	0.47
1:A:86:ALA:H	1:A:315:GLN:NE2	2.13	0.46
1:A:397:TYR:HA	1:A:406:TYR:O	2.15	0.46
1:A:42:ALA:HB2	1:A:278:ARG:HB2	1.96	0.46
1:C:214:LYS:HG2	1:C:253:LEU:HD11	1.96	0.46
1:B:56:PHE:CD2	1:B:56:PHE:C	2.89	0.46
1:D:386:TYR:CZ	1:D:388:GLY:HA2	2.51	0.46
1:D:53:MET:HE2	6:D:2072:HOH:O	2.15	0.45
1:A:110:THR:HG22	6:A:2030:HOH:O	2.17	0.45
1:B:42:ALA:HA	1:B:280:MET:HG2	1.99	0.45
1:A:132:THR:HA	1:A:178:TYR:HB3	1.98	0.44
1:C:54:GLN:NE2	1:C:401:LYS:HZ2	1.86	0.44
1:B:267:ASP:OD2	1:B:267:ASP:N	2.51	0.44
1:C:128:TYR:CD1	1:C:176:HIS:CE1	3.06	0.44
1:D:128:TYR:CD1	1:D:176:HIS:CE1	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:459:PRO:HG2	1:B:463:TYR:CD1	2.54	0.43
1:C:43:THR:HG21	6:C:2099:HOH:O	2.17	0.43
1:A:241:TRP:CD2	1:A:242:TRP:N	2.87	0.43
1:A:386:TYR:CZ	1:A:388:GLY:HA2	2.54	0.43
1:A:419:ILE:HD11	4:A:1475:GOL:H11	2.00	0.43
1:B:196:LYS:HZ1	1:B:200:ILE:HD11	1.83	0.42
1:A:124:MET:HB3	1:A:126:THR:HG23	2.00	0.42
1:B:128:TYR:CD1	1:B:176:HIS:CE1	3.07	0.42
1:A:130:LYS:HG2	1:A:176:HIS:HB2	2.02	0.42
1:C:192:ASP:OD1	1:C:238:LYS:NZ	2.47	0.42
1:B:132:THR:O	1:B:141:LEU:HD12	2.19	0.42
1:B:89:LEU:O	1:B:90:LYS:C	2.58	0.42
1:D:178:TYR:C	1:D:178:TYR:CD2	2.94	0.42
1:C:130:LYS:HG2	1:C:176:HIS:HB2	2.02	0.41
1:C:433:LEU:HD13	1:C:455:PRO:HG3	2.02	0.41
1:B:178:TYR:CD2	1:B:178:TYR:C	2.94	0.41
1:C:286:GLY:O	1:C:290:ARG:NH1	2.53	0.41
1:B:132:THR:HA	1:B:178:TYR:HB3	2.02	0.41
1:C:419:ILE:HD13	1:C:419:ILE:HG21	1.91	0.40
1:B:459:PRO:HG2	1:B:463:TYR:CG	2.57	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	435/453 (96%)	419 (96%)	16 (4%)	0	100	100
1	B	435/453 (96%)	420 (97%)	14 (3%)	1 (0%)	47	55
1	C	435/453 (96%)	419 (96%)	15 (3%)	1 (0%)	47	55
1	D	435/453 (96%)	410 (94%)	23 (5%)	2 (0%)	29	31
All	All	1740/1812 (96%)	1668 (96%)	68 (4%)	4 (0%)	47	55

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	60	ARG
1	D	45	GLU
1	C	60	ARG
1	D	272	HIS

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	370/385 (96%)	359 (97%)	11 (3%)	41	53
1	B	370/385 (96%)	357 (96%)	13 (4%)	36	46
1	C	370/385 (96%)	362 (98%)	8 (2%)	52	65
1	D	370/385 (96%)	358 (97%)	12 (3%)	39	50
All	All	1480/1540 (96%)	1436 (97%)	44 (3%)	41	53

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	THR
1	A	64	PHE
1	A	110	THR
1	A	126	THR
1	A	145	LYS
1	A	264	ARG
1	A	267	ASP
1	A	270	LYS
1	A	290	ARG
1	A	313	GLU
1	A	447	ARG
1	B	43	THR
1	B	44	ASN
1	B	64	PHE
1	B	99	GLU
1	B	110	THR

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Mol	Chain	Res	Type
1	B	122	LYS
1	B	126	THR
1	B	178	TYR
1	B	264	ARG
1	B	267	ASP
1	B	270	LYS
1	B	290	ARG
1	B	447	ARG
1	C	43	THR
1	C	54	GLN
1	C	64	PHE
1	C	197	GLU
1	C	264	ARG
1	C	267	ASP
1	C	270	LYS
1	C	313	GLU
1	D	43	THR
1	D	64	PHE
1	D	78	ASN
1	D	110	THR
1	D	148	LYS
1	D	178	TYR
1	D	197	GLU
1	D	264	ARG
1	D	267	ASP
1	D	270	LYS
1	D	299	LYS
1	D	313	GLU

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	315	GLN
1	B	44	ASN
1	B	49	GLN
1	B	54	GLN
1	B	354	GLN
1	C	49	GLN
1	C	54	GLN
1	C	78	ASN
1	C	402	ASN
1	C	466	GLN

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Mol	Chain	Res	Type
1	D	49	GLN
1	D	54	GLN
1	D	78	ASN
1	D	315	GLN
1	D	402	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

15 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	D	1473	-	4,4,4	0.17	0	6,6,6	0.21	0
3	SO4	B	1473	-	4,4,4	0.19	0	6,6,6	0.28	0
4	GOL	B	1475	-	5,5,5	0.37	0	5,5,5	0.42	0
5	TRS	D	1474	-	7,7,7	1.02	0	9,9,9	2.08	4 (44%)
4	GOL	C	1474	-	5,5,5	0.45	0	5,5,5	0.79	0
2	DFU	D	1472	-	10,10,10	0.86	0	12,14,14	0.89	1 (8%)
3	SO4	A	1473	-	4,4,4	0.13	0	6,6,6	0.38	0
3	SO4	C	1473	-	4,4,4	0.12	0	6,6,6	0.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	1474	-	4,4,4	0.18	0	6,6,6	0.19	0
2	DFU	C	1472	-	10,10,10	1.05	1 (10%)	12,14,14	0.87	0
2	DFU	B	1472	-	10,10,10	0.93	0	12,14,14	1.07	1 (8%)
2	DFU	A	1472	-	10,10,10	0.75	0	12,14,14	0.76	0
4	GOL	B	1474	-	5,5,5	0.93	0	5,5,5	1.22	0
4	GOL	D	1475	-	5,5,5	0.32	0	5,5,5	0.35	0
4	GOL	A	1475	-	5,5,5	0.41	0	5,5,5	0.59	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
4	GOL	B	1475	-	-	2/4/4/4	-
5	TRS	D	1474	-	-	9/9/9/9	-
4	GOL	C	1474	-	-	4/4/4/4	-
2	DFU	D	1472	-	-	-	0/1/1/1
4	GOL	B	1474	-	-	4/4/4/4	-
4	GOL	A	1475	-	-	0/4/4/4	-
2	DFU	C	1472	-	-	-	0/1/1/1
2	DFU	B	1472	-	-	-	0/1/1/1
2	DFU	A	1472	-	-	-	0/1/1/1
4	GOL	D	1475	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1472	DFU	C1-C2	2.18	1.54	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	1474	TRS	O3-C3-C	3.03	120.61	111.00
5	D	1474	TRS	O1-C1-C	2.90	120.19	111.00
2	B	1472	DFU	C2-C3-C4	-2.77	106.09	110.89
5	D	1474	TRS	O2-C2-C	2.65	119.41	111.00
2	D	1472	DFU	C1-N5-C5	2.22	115.24	109.57
5	D	1474	TRS	C2-C-C1	2.09	117.28	110.81

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1475	GOL	O1-C1-C2-O2
4	B	1475	GOL	O1-C1-C2-C3
5	D	1474	TRS	C2-C-C1-O1
5	D	1474	TRS	N-C-C1-O1
5	D	1474	TRS	C1-C-C2-O2
5	D	1474	TRS	C1-C-C3-O3
5	D	1474	TRS	C2-C-C3-O3
5	D	1474	TRS	N-C-C3-O3
4	B	1474	GOL	O1-C1-C2-C3
4	B	1474	GOL	C1-C2-C3-O3
4	B	1474	GOL	O2-C2-C3-O3
4	C	1474	GOL	O1-C1-C2-C3
4	C	1474	GOL	C1-C2-C3-O3
4	C	1474	GOL	O2-C2-C3-O3
4	B	1474	GOL	O1-C1-C2-O2
5	D	1474	TRS	C3-C-C2-O2
4	C	1474	GOL	O1-C1-C2-O2
5	D	1474	TRS	N-C-C2-O2
5	D	1474	TRS	C3-C-C1-O1

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	1474	TRS	1	0
4	C	1474	GOL	2	0
4	B	1474	GOL	1	0
4	D	1475	GOL	1	0
4	A	1475	GOL	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	437/453 (96%)	-0.07	15 (3%) 45 43	14, 25, 43, 58	0
1	B	437/453 (96%)	-0.15	9 (2%) 63 61	13, 24, 38, 56	0
1	C	437/453 (96%)	-0.30	4 (0%) 84 83	12, 23, 37, 47	0
1	D	437/453 (96%)	-0.02	12 (2%) 54 52	15, 30, 52, 65	0
All	All	1748/1812 (96%)	-0.13	40 (2%) 60 58	12, 25, 43, 65	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	79	GLY	5.8
1	B	44	ASN	4.7
1	B	45	GLU	4.7
1	B	43	THR	4.5
1	C	45	GLU	4.1
1	D	78	ASN	3.7
1	D	45	GLU	3.7
1	A	36	ILE	3.7
1	B	35	GLU	3.5
1	A	43	THR	3.4
1	D	194	LYS	3.4
1	A	45	GLU	3.4
1	B	471	ALA	3.3
1	A	44	ASN	3.1
1	B	37	PRO	3.0
1	D	96	PRO	3.0
1	C	43	THR	2.8
1	A	193	ILE	2.8
1	A	35	GLU	2.8
1	D	195	SER	2.8
1	D	191	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	198	ASP	2.6
1	D	197	GLU	2.5
1	A	178	TYR	2.5
1	A	37	PRO	2.5
1	B	425	GLY	2.4
1	D	402	ASN	2.4
1	D	447	ARG	2.4
1	A	276	ASN	2.4
1	B	447	ARG	2.3
1	A	227	TRP	2.3
1	A	194	LYS	2.2
1	D	275	SER	2.2
1	C	37	PRO	2.2
1	B	36	ILE	2.1
1	A	132	THR	2.1
1	A	361	PRO	2.1
1	C	425	GLY	2.1
1	A	49	GLN	2.0
1	A	447	ARG	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 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. 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
5	TRS	D	1474	8/8	0.76	0.28	32,35,36,37	0
3	SO4	A	1473	5/5	0.77	0.29	92,92,93,93	0
4	GOL	B	1475	6/6	0.82	0.16	50,53,53,54	0
4	GOL	B	1474	6/6	0.85	0.20	26,32,35,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	GOL	C	1474	6/6	0.88	0.17	26,32,33,35	0
4	GOL	A	1475	6/6	0.90	0.18	29,32,34,35	0
4	GOL	D	1475	6/6	0.91	0.15	16,28,29,30	0
3	SO4	B	1473	5/5	0.94	0.24	62,64,65,65	0
3	SO4	C	1473	5/5	0.95	0.21	51,51,53,53	0
3	SO4	D	1473	5/5	0.95	0.21	66,67,67,68	0
3	SO4	A	1474	5/5	0.96	0.13	53,54,56,57	0
2	DFU	D	1472	10/10	0.96	0.15	22,24,25,27	0
2	DFU	A	1472	10/10	0.97	0.21	17,18,19,21	0
2	DFU	C	1472	10/10	0.98	0.14	12,17,19,22	0
2	DFU	B	1472	10/10	0.98	0.08	12,14,15,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.