



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2020 – 06:14 pm BST

PDB ID : 2XN0  
Title : Structure of alpha-galactosidase from Lactobacillus acidophilus NCFM, PtC14 derivative  
Authors : Fredslund, F.; Abou Hachem, M.; Larsen, R.J.; Sorensen, P.G.; Lo Leggio, L.; Svensson, B.  
Deposited on : 2010-07-30  
Resolution : 2.50 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](mailto: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.

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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

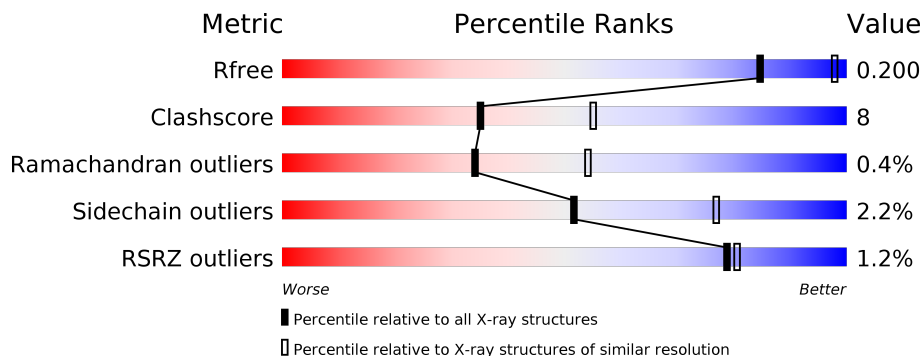
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


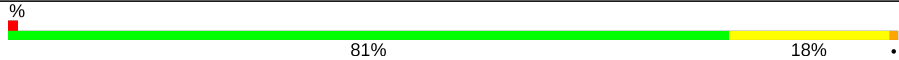
The reported resolution of this entry is 2.50 Å.

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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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  $\geq 3$ , 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	732	 81% 17%
1	B	732	 81% 18%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12849 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.

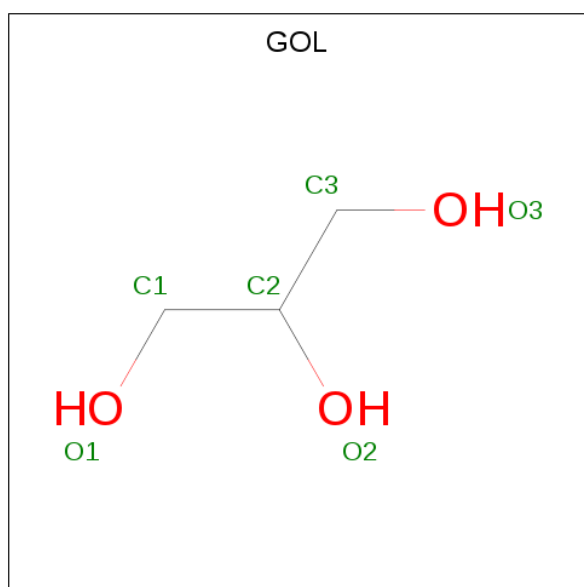
- Molecule 1 is a protein called ALPHA-GALACTOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	729	5936	3770	1008	1131	27	0	0	0
1	B	729	5936	3770	1008	1131	27	0	0	0

- Molecule 2 is PLATINUM (II) ION (three-letter code: PT) (formula: Pt).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	8	Total	Pt	0	0
			8	8		
2	A	9	Total	Pt	0	0
			9	9		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

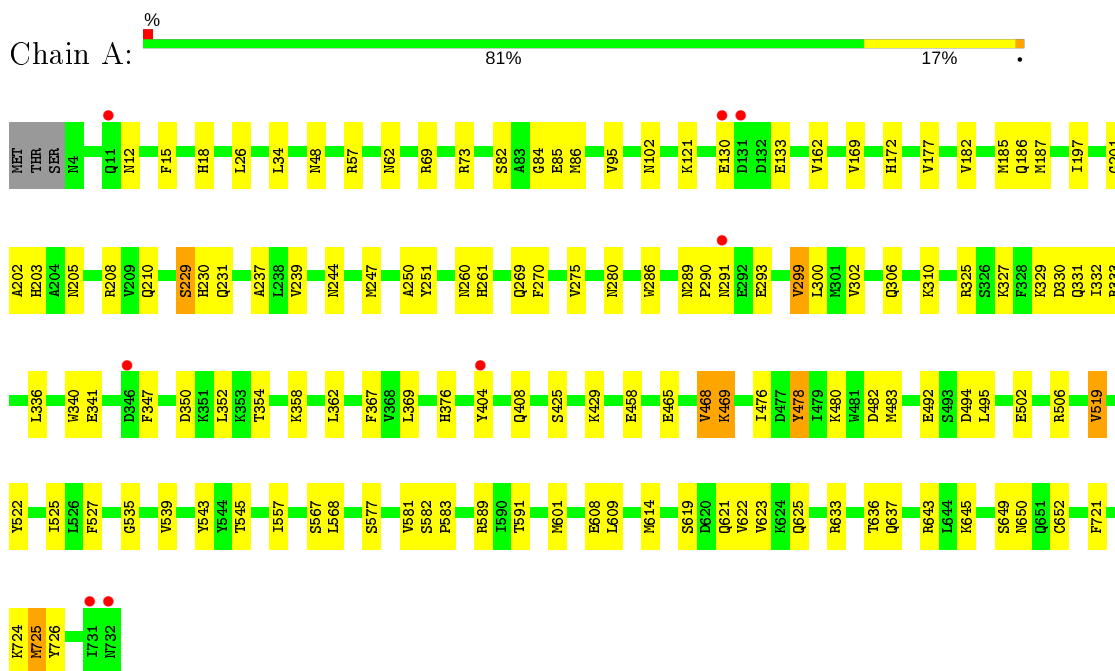
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	456	Total O 456 456	0	0
4	B	426	Total O 426 426	0	0

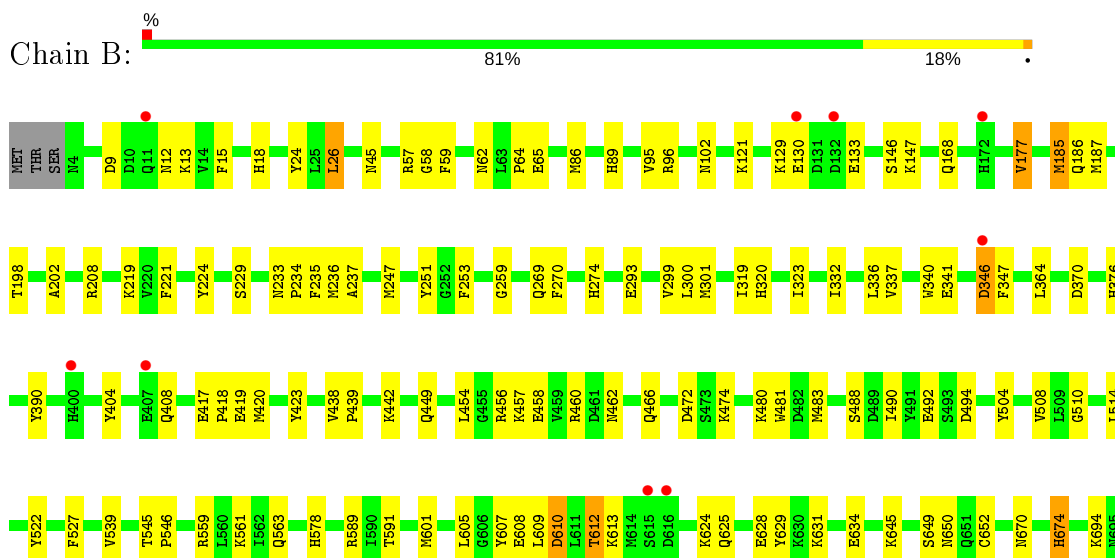
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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-GALACTOSIDASE



#### • Molecule 1: ALPHA-GALACTOSIDASE





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	126.37Å 149.58Å 90.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.84 – 2.50 29.84 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.84-2.50) 100.0 (29.84-2.50)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.62 (at 2.51Å)	Xtrriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.148 , 0.203 0.147 , 0.200	Depositor DCC
$R_{free}$ test set	2000 reflections (3.32%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.1	Xtrriage
Anisotropy	0.060	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 51.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	12849	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.99% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GOL, PT

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	0.39	0/6084	0.55	0/8220
1	B	0.40	0/6084	0.54	0/8220
All	All	0.40	0/12168	0.55	0/16440

There are no bond length outliers.

There are no bond angle outliers.

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	5936	0	5712	93	0
1	B	5936	0	5712	99	0
2	A	9	0	0	0	0
2	B	8	0	0	0	0
3	A	42	0	56	11	0
3	B	36	0	48	6	0
4	A	456	0	0	11	0
4	B	426	0	0	12	0
All	All	12849	0	11528	192	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 8.



All (192) 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:B:559:ARG:HH11	1:B:563:GLN:HE21	1.19	0.88
1:B:185:MET:HG2	1:B:299:VAL:HG11	1.60	0.83
1:A:84:GLY:H	3:A:1743:GOL:H12	1.49	0.77
1:A:341:GLU:HB2	1:A:608:GLU:HG2	1.67	0.76
1:B:300:LEU:HD11	1:B:539:VAL:HG11	1.68	0.76
1:B:610:ASP:OD1	1:B:612:THR:HB	1.86	0.75
1:A:130:GLU:O	1:A:133:GLU:HG2	1.90	0.72
1:B:460:ARG:HB3	3:B:1746:GOL:H2	1.70	0.72
1:B:121:LYS:HE2	4:B:2207:HOH:O	1.92	0.70
1:B:480:LYS:NZ	3:B:1741:GOL:H32	2.07	0.69
1:A:185:MET:HG2	1:A:299:VAL:HG11	1.76	0.67
3:A:1746:GOL:H12	4:A:2453:HOH:O	1.95	0.65
1:A:62:ASN:ND2	1:A:69:ARG:HA	2.12	0.65
1:A:519:VAL:HG13	3:A:1747:GOL:H31	1.80	0.64
1:A:480:LYS:HZ1	3:A:1741:GOL:H32	1.62	0.64
1:A:208:ARG:HB3	4:A:2147:HOH:O	1.99	0.62
1:A:12:ASN:HD22	1:A:48:ASN:ND2	1.99	0.61
1:A:325:ARG:HD3	1:A:543:TYR:CE1	2.35	0.61
1:A:57:ARG:HD3	1:A:270:PHE:CZ	2.35	0.61
4:A:2056:HOH:O	1:B:224:TYR:HD2	1.84	0.60
1:A:269:GLN:HB2	1:B:202:ALA:HB2	1.84	0.59
1:A:567:SER:OG	1:A:643:ARG:HD3	2.02	0.59
1:B:376:HIS:HD2	4:B:2238:HOH:O	1.84	0.59
1:B:492:GLU:HG2	1:B:494:ASP:OD1	2.03	0.59
1:B:527:PHE:HB3	1:B:545:THR:HG22	1.85	0.59
1:A:350:ASP:O	1:A:354:THR:HG23	2.04	0.58
1:B:480:LYS:HZ1	3:B:1741:GOL:H32	1.68	0.58
1:A:527:PHE:HB3	1:A:545:THR:HG22	1.85	0.58
1:B:86:MET:HG3	1:B:86:MET:O	2.03	0.57
1:B:130:GLU:O	1:B:133:GLU:HG2	2.03	0.57
1:B:474:LYS:HE2	1:B:522:TYR:HD1	1.70	0.57
1:B:121:LYS:HE3	4:B:2210:HOH:O	2.04	0.57
1:A:724:LYS:HD3	1:A:726:TYR:CZ	2.38	0.57
1:B:460:ARG:HG2	1:B:514:LEU:HB2	1.87	0.57
1:A:185:MET:CG	1:A:299:VAL:HG11	2.35	0.56
1:A:376:HIS:CD2	4:A:2251:HOH:O	2.58	0.56
1:B:601:MET:SD	1:B:725:MET:CE	2.94	0.56
1:A:341:GLU:HB2	1:A:608:GLU:CG	2.36	0.56
1:B:722:LYS:HE2	4:B:2068:HOH:O	2.05	0.56
1:B:609:LEU:N	1:B:609:LEU:HD23	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:ARG:HD3	1:A:543:TYR:CZ	2.42	0.55
1:A:330:ASP:HB2	4:A:2231:HOH:O	2.06	0.55
1:B:341:GLU:HG3	1:B:608:GLU:OE2	2.07	0.55
1:A:306:GLN:CG	1:A:310:LYS:HD2	2.38	0.54
1:A:476:ILE:N	1:A:476:ILE:HD12	2.22	0.54
1:A:203:HIS:CE1	3:A:1746:GOL:H11	2.44	0.53
1:B:185:MET:HE1	1:B:187:MET:HE3	1.89	0.53
1:A:327:LYS:HG2	1:A:327:LYS:O	2.08	0.53
1:A:86:MET:HG3	1:A:86:MET:O	2.08	0.53
1:A:121:LYS:HE2	4:A:2214:HOH:O	2.08	0.52
1:A:332:ILE:HD13	1:A:633:ARG:HG3	1.91	0.52
1:A:306:GLN:HG2	1:A:310:LYS:HD2	1.91	0.52
1:A:601:MET:SD	1:A:725:MET:HE1	2.50	0.52
1:B:185:MET:CG	1:B:299:VAL:HG11	2.38	0.52
1:A:519:VAL:HG13	3:A:1747:GOL:C3	2.40	0.52
1:A:601:MET:SD	1:A:725:MET:CE	2.98	0.52
1:B:253:PHE:CD1	1:B:301:MET:HG2	2.45	0.52
1:B:15:PHE:HB2	1:B:26:LEU:HG	1.91	0.52
1:B:337:VAL:HB	1:B:364:LEU:HD13	1.92	0.52
1:A:12:ASN:HD22	1:A:48:ASN:HD21	1.59	0.51
1:A:582:SER:HA	1:A:583:PRO:C	2.31	0.51
1:A:609:LEU:HD11	1:A:614:MET:CE	2.41	0.51
1:B:601:MET:SD	1:B:725:MET:HE1	2.51	0.51
1:B:320:HIS:ND1	3:B:1745:GOL:H32	2.26	0.51
1:B:607:TYR:OH	1:B:625:GLN:NE2	2.42	0.51
1:B:696:LEU:HD11	1:B:729:LYS:HE2	1.92	0.51
1:A:197:ILE:HA	1:A:210:GLN:O	2.11	0.51
1:B:419:GLU:HG2	1:B:454:LEU:HD11	1.92	0.51
1:B:420:MET:HG3	1:B:449:GLN:NE2	2.26	0.51
1:B:62:ASN:HB3	4:B:2065:HOH:O	2.10	0.51
1:B:480:LYS:HZ3	3:B:1741:GOL:H32	1.76	0.50
1:B:418:PRO:HG2	1:B:481:TRP:CZ2	2.46	0.50
1:B:613:LYS:O	1:B:613:LYS:HG3	2.11	0.50
1:B:332:ILE:HD11	1:B:634:GLU:OE1	2.12	0.49
1:A:482:ASP:OD2	3:A:1741:GOL:H31	2.13	0.49
1:A:289:ASN:HB3	1:A:290:PRO:HD2	1.94	0.49
1:A:203:HIS:ND1	3:A:1746:GOL:H11	2.27	0.49
1:B:233:ASN:CG	1:B:234:PRO:HD2	2.33	0.49
1:B:186:GLN:CD	1:B:274:HIS:HE1	2.16	0.49
1:A:286:TRP:CE3	1:A:502:GLU:HG2	2.48	0.48
1:A:202:ALA:HB2	1:B:269:GLN:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:LEU:HD11	1:A:506:ARG:HD2	1.94	0.48
1:B:460:ARG:HD2	1:B:510:GLY:O	2.13	0.48
1:A:340:TRP:HB3	1:A:608:GLU:OE2	2.12	0.48
1:B:237:ALA:HA	1:B:251:TYR:O	2.14	0.48
1:B:208:ARG:NH2	4:B:2152:HOH:O	2.47	0.48
1:B:628:GLU:OE1	1:B:631:LYS:HD2	2.14	0.48
1:B:698:THR:O	1:B:699:ASP:HB2	2.14	0.48
1:B:64:PRO:O	1:B:65:GLU:HB2	2.14	0.47
1:A:468:VAL:HG22	1:A:522:TYR:OH	2.15	0.47
1:A:352:LEU:HD22	1:A:367:PHE:HZ	1.79	0.47
1:B:605:LEU:HB3	1:B:629:TYR:CE2	2.49	0.47
1:A:465:GLU:O	1:A:469:LYS:HD2	2.14	0.47
1:A:480:LYS:NZ	3:A:1741:GOL:H32	2.27	0.47
1:B:247:MET:HE2	4:B:2180:HOH:O	2.15	0.47
1:B:527:PHE:O	1:B:546:PRO:HD2	2.15	0.47
1:A:162:VAL:HG22	1:A:302:VAL:HG22	1.97	0.47
1:A:332:ILE:HG23	1:A:633:ARG:HD2	1.97	0.47
1:A:73:ARG:NH1	1:A:85:GLU:OE1	2.46	0.47
1:A:300:LEU:HD11	1:A:539:VAL:HG11	1.96	0.46
1:B:9:ASP:CG	1:B:12:ASN:HD22	2.16	0.46
1:A:261:HIS:HB3	4:A:2188:HOH:O	2.16	0.46
1:A:589:ARG:HG2	1:A:591:THR:HG23	1.97	0.46
1:A:15:PHE:HB2	1:A:26:LEU:CD2	2.45	0.46
1:B:24:TYR:HE2	1:B:187:MET:HE1	1.81	0.46
1:B:86:MET:O	1:B:86:MET:CG	2.64	0.46
1:A:237:ALA:HA	1:A:251:TYR:O	2.16	0.46
1:A:425:SER:O	1:A:429:LYS:HG3	2.16	0.46
1:B:187:MET:HE3	1:B:301:MET:SD	2.55	0.46
1:B:57:ARG:HD3	1:B:270:PHE:CE1	2.51	0.46
1:B:674:HIS:N	1:B:674:HIS:ND1	2.63	0.46
1:B:168:GLN:NE2	1:B:293:GLU:OE2	2.49	0.46
1:B:601:MET:SD	1:B:725:MET:HE3	2.55	0.45
1:B:716:ILE:N	1:B:716:ILE:HD12	2.31	0.45
1:A:609:LEU:HD11	1:A:614:MET:HE2	1.97	0.45
1:B:198:THR:HG21	1:B:221:PHE:CE2	2.52	0.45
1:B:457:LYS:HG3	3:B:1746:GOL:O1	2.16	0.45
1:A:522:TYR:HB3	1:A:525:ILE:HD12	1.97	0.45
1:A:362:LEU:HD13	1:A:622:VAL:HG11	1.98	0.45
1:A:327:LYS:HE2	1:A:331:GLN:OE1	2.17	0.45
1:A:244:ASN:OD1	1:A:247:MET:HG2	2.17	0.45
1:A:329:LYS:HA	1:A:333:ARG:NH2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:GLN:HA	1:A:275:VAL:O	2.17	0.45
1:B:480:LYS:HE3	4:B:2286:HOH:O	2.17	0.45
1:A:336:LEU:HD12	1:A:336:LEU:C	2.37	0.45
1:B:624:LYS:O	1:B:628:GLU:HG2	2.17	0.45
1:B:670:ASN:HB3	4:B:2394:HOH:O	2.17	0.45
1:B:89:HIS:CD2	4:B:2192:HOH:O	2.69	0.45
1:B:376:HIS:CD2	4:B:2238:HOH:O	2.66	0.44
1:A:458:GLU:HG2	4:A:2287:HOH:O	2.17	0.44
1:A:633:ARG:HA	1:A:636:THR:OG1	2.17	0.44
1:B:336:LEU:HD12	1:B:336:LEU:C	2.38	0.44
1:B:589:ARG:HG2	1:B:591:THR:HG23	1.99	0.44
3:A:1743:GOL:H31	1:B:488:SER:HA	1.99	0.44
1:A:169:VAL:O	1:A:293:GLU:HA	2.17	0.44
1:A:34:LEU:HD12	1:A:34:LEU:HA	1.77	0.44
1:A:260:ASN:HB3	1:A:280:ASN:HB3	2.00	0.44
1:A:187:MET:HE3	1:A:187:MET:HB2	1.82	0.44
1:B:649:SER:O	1:B:650:ASN:HB3	2.17	0.44
1:A:649:SER:O	1:A:650:ASN:HB3	2.18	0.43
1:B:559:ARG:HH11	1:B:563:GLN:NE2	2.01	0.43
1:B:259:GLY:HA3	1:B:508:VAL:HG21	1.99	0.43
1:B:129:LYS:N	1:B:133:GLU:OE1	2.44	0.43
1:A:404:TYR:O	1:A:408:GLN:HG2	2.19	0.43
1:B:418:PRO:HG2	1:B:481:TRP:CE2	2.54	0.43
1:A:347:PHE:CD2	1:A:347:PHE:C	2.92	0.43
1:A:492:GLU:HG2	1:A:494:ASP:OD1	2.19	0.43
1:A:557:ILE:HG13	1:A:721:PHE:CD1	2.54	0.43
1:A:478:TYR:CD1	1:A:478:TYR:C	2.92	0.43
1:B:301:MET:HE3	1:B:301:MET:HB2	1.91	0.43
1:B:96:ARG:O	1:B:177:VAL:HG22	2.19	0.42
1:B:235:PHE:CG	1:B:236:MET:N	2.86	0.42
1:B:578:HIS:ND1	1:B:608:GLU:HG3	2.33	0.42
1:A:230:HIS:CE1	1:A:535:GLY:HA3	2.53	0.42
1:A:82:SER:O	1:A:85:GLU:HG2	2.19	0.42
1:A:621:GLN:O	1:A:625:GLN:HG3	2.19	0.42
1:B:198:THR:HG21	1:B:221:PHE:CD2	2.53	0.42
1:B:185:MET:HE1	1:B:187:MET:CE	2.49	0.42
1:B:404:TYR:CZ	1:B:408:GLN:NE2	2.81	0.42
1:B:442:LYS:HA	1:B:442:LYS:HD3	1.79	0.42
1:A:185:MET:HG2	1:A:299:VAL:CG1	2.47	0.42
1:B:146:SER:O	1:B:147:LYS:HB2	2.18	0.42
1:B:462:ASN:O	1:B:466:GLN:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:490:ILE:HG13	1:B:504:TYR:CZ	2.54	0.42
1:B:561:LYS:HD2	4:B:2331:HOH:O	2.20	0.42
1:B:645:LYS:O	1:B:652:CYS:HA	2.20	0.42
1:B:95:VAL:O	1:B:102:ASN:HA	2.19	0.42
1:A:95:VAL:O	1:A:102:ASN:HA	2.20	0.42
1:A:633:ARG:O	1:A:637:GLN:HB2	2.20	0.42
1:B:319:ILE:HA	1:B:323:ILE:HD12	2.01	0.41
1:B:731:ILE:C	1:B:731:ILE:HD12	2.40	0.41
1:A:352:LEU:CD1	1:A:369:LEU:HD13	2.51	0.41
1:B:219:LYS:HA	1:B:219:LYS:HD2	1.77	0.41
1:A:336:LEU:HD21	4:A:2347:HOH:O	2.19	0.41
1:B:694:LYS:HD3	1:B:699:ASP:OD1	2.20	0.41
1:B:346:ASP:O	1:B:347:PHE:HB3	2.20	0.41
1:B:454:LEU:O	1:B:460:ARG:HD3	2.20	0.41
1:A:172:HIS:HE1	4:A:2114:HOH:O	2.04	0.41
1:A:239:VAL:HG12	1:A:250:ALA:HA	2.02	0.41
1:A:568:LEU:HD12	1:A:568:LEU:HA	1.72	0.41
1:A:619:SER:O	1:A:623:VAL:HG23	2.21	0.41
1:A:201:GLY:O	1:A:231:GLN:HA	2.21	0.41
1:B:456:ARG:HH21	1:B:458:GLU:CD	2.24	0.41
1:A:645:LYS:O	1:A:652:CYS:HA	2.21	0.41
1:A:358:LYS:O	1:A:362:LEU:HG	2.21	0.40
3:A:1745:GOL:H11	4:A:2345:HOH:O	2.20	0.40
1:B:438:VAL:O	1:B:439:PRO:C	2.59	0.40
1:B:58:GLY:O	1:B:59:PHE:HB2	2.21	0.40
1:A:306:GLN:HG2	1:A:310:LYS:CD	2.52	0.40
1:A:581:VAL:HG22	1:A:582:SER:N	2.36	0.40
1:B:417:GLU:OE2	1:B:420:MET:HG3	2.21	0.40
1:B:9:ASP:O	1:B:13:LYS:N	2.54	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	727/732 (99%)	698 (96%)	27 (4%)	2 (0%)	41	61
1	B	727/732 (99%)	691 (95%)	32 (4%)	4 (1%)	25	43
All	All	1454/1464 (99%)	1389 (96%)	59 (4%)	6 (0%)	34	54

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	340	TRP
1	B	610	ASP
1	A	205	ASN
1	A	229	SER
1	B	229	SER
1	B	612	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	645/648 (100%)	632 (98%)	13 (2%)	55	79
1	B	645/648 (100%)	630 (98%)	15 (2%)	50	76
All	All	1290/1296 (100%)	1262 (98%)	28 (2%)	52	77

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	177	VAL
1	A	182	VAL
1	A	229	SER
1	A	291	ASN
1	A	299	VAL
1	A	468	VAL
1	A	469	LYS
1	A	478	TYR
1	A	483	MET

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Mol	Chain	Res	Type
1	A	519	VAL
1	A	577	SER
1	A	725	MET
1	B	18	HIS
1	B	26	LEU
1	B	45	ASN
1	B	177	VAL
1	B	185	MET
1	B	346	ASP
1	B	370	ASP
1	B	390	TYR
1	B	423	TYR
1	B	472	ASP
1	B	483	MET
1	B	674	HIS
1	B	718	ARG
1	B	725	MET
1	B	729	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	48	ASN
1	A	205	ASN
1	A	376	HIS
1	A	625	GLN
1	B	205	ASN
1	B	272	GLN
1	B	306	GLN
1	B	376	HIS
1	B	563	GLN
1	B	625	GLN

### 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](#)

Of 30 ligands modelled in this entry, 17 are monoatomic - leaving 13 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GOL	A	1744	-	5,5,5	0.39	0	5,5,5	0.39	0
3	GOL	B	1742	-	5,5,5	0.33	0	5,5,5	0.38	0
3	GOL	A	1747	-	5,5,5	0.35	0	5,5,5	0.30	0
3	GOL	A	1743	-	5,5,5	0.37	0	5,5,5	0.35	0
3	GOL	B	1743	-	5,5,5	0.33	0	5,5,5	0.51	0
3	GOL	B	1744	-	5,5,5	0.27	0	5,5,5	0.62	0
3	GOL	A	1746	-	5,5,5	0.39	0	5,5,5	0.37	0
3	GOL	A	1745	-	5,5,5	0.33	0	5,5,5	0.38	0
3	GOL	A	1742	-	5,5,5	0.40	0	5,5,5	0.31	0
3	GOL	A	1741	-	5,5,5	0.33	0	5,5,5	0.73	0
3	GOL	B	1745	-	5,5,5	0.38	0	5,5,5	0.17	0
3	GOL	B	1746	-	5,5,5	0.39	0	5,5,5	0.26	0
3	GOL	B	1741	-	5,5,5	0.34	0	5,5,5	0.30	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
3	GOL	A	1744	-	-	2/4/4/4	-
3	GOL	B	1742	-	-	2/4/4/4	-
3	GOL	A	1747	-	-	3/4/4/4	-
3	GOL	A	1743	-	-	4/4/4/4	-
3	GOL	B	1743	-	-	4/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	1744	-	-	4/4/4/4	-
3	GOL	A	1746	-	-	4/4/4/4	-
3	GOL	A	1745	-	-	2/4/4/4	-
3	GOL	A	1742	-	-	2/4/4/4	-
3	GOL	A	1741	-	-	3/4/4/4	-
3	GOL	B	1745	-	-	2/4/4/4	-
3	GOL	B	1746	-	-	4/4/4/4	-
3	GOL	B	1741	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1746	GOL	O1-C1-C2-C3
3	A	1742	GOL	C1-C2-C3-O3
3	A	1741	GOL	O1-C1-C2-C3
3	A	1747	GOL	C1-C2-C3-O3
3	A	1743	GOL	O1-C1-C2-C3
3	B	1746	GOL	O1-C1-C2-O2
3	B	1746	GOL	O1-C1-C2-C3
3	B	1741	GOL	O1-C1-C2-C3
3	A	1743	GOL	O1-C1-C2-O2
3	B	1743	GOL	O2-C2-C3-O3
3	A	1744	GOL	C1-C2-C3-O3
3	B	1742	GOL	C1-C2-C3-O3
3	A	1746	GOL	C1-C2-C3-O3
3	B	1745	GOL	C1-C2-C3-O3
3	A	1745	GOL	C1-C2-C3-O3
3	A	1743	GOL	C1-C2-C3-O3
3	B	1743	GOL	O1-C1-C2-C3
3	B	1743	GOL	C1-C2-C3-O3
3	B	1746	GOL	C1-C2-C3-O3
3	B	1744	GOL	O1-C1-C2-C3
3	B	1744	GOL	C1-C2-C3-O3
3	A	1746	GOL	O1-C1-C2-O2
3	A	1742	GOL	O2-C2-C3-O3
3	A	1747	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	A	1743	GOL	O2-C2-C3-O3
3	B	1743	GOL	O1-C1-C2-O2
3	B	1744	GOL	O1-C1-C2-O2
3	B	1742	GOL	O2-C2-C3-O3
3	A	1746	GOL	O2-C2-C3-O3
3	B	1745	GOL	O2-C2-C3-O3
3	A	1745	GOL	O2-C2-C3-O3
3	B	1746	GOL	O2-C2-C3-O3
3	B	1741	GOL	O1-C1-C2-O2
3	A	1744	GOL	O2-C2-C3-O3
3	A	1741	GOL	O1-C1-C2-O2
3	B	1744	GOL	O2-C2-C3-O3
3	A	1747	GOL	O1-C1-C2-C3
3	A	1741	GOL	C1-C2-C3-O3

There are no ring outliers.

8 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1747	GOL	2	0
3	A	1743	GOL	2	0
3	A	1746	GOL	3	0
3	A	1745	GOL	1	0
3	A	1741	GOL	3	0
3	B	1745	GOL	1	0
3	B	1746	GOL	2	0
3	B	1741	GOL	3	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	729/732 (99%)	-0.48	8 (1%) 80 82	7, 18, 39, 76	0
1	B	729/732 (99%)	-0.44	10 (1%) 75 77	8, 19, 44, 84	0
All	All	1458/1464 (99%)	-0.46	18 (1%) 79 80	7, 19, 41, 84	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	732	ASN	4.2
1	B	732	ASN	3.5
1	B	615	SER	3.3
1	B	616	ASP	3.3
1	A	11	GLN	3.2
1	A	731	ILE	3.0
1	A	130	GLU	2.6
1	B	11	GLN	2.5
1	B	346	ASP	2.4
1	B	130	GLU	2.4
1	A	131	ASP	2.4
1	B	407	GLU	2.4
1	A	404	TYR	2.4
1	A	291	ASN	2.3
1	B	132	ASP	2.2
1	B	172	HIS	2.2
1	B	400	HIS	2.1
1	A	346	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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
2	PT	B	1735	1/1	0.80	0.16	77,77,77,77	1
3	GOL	B	1746	6/6	0.86	0.27	50,50,51,53	0
3	GOL	A	1747	6/6	0.86	0.25	56,58,59,60	0
3	GOL	A	1743	6/6	0.88	0.24	34,48,50,51	0
3	GOL	B	1745	6/6	0.88	0.18	49,52,52,53	0
3	GOL	A	1744	6/6	0.88	0.25	44,46,48,49	0
3	GOL	B	1744	6/6	0.91	0.20	42,45,48,50	0
3	GOL	A	1745	6/6	0.92	0.15	40,42,45,47	0
3	GOL	A	1746	6/6	0.92	0.23	37,40,43,45	0
3	GOL	B	1742	6/6	0.92	0.35	49,51,53,54	0
3	GOL	B	1741	6/6	0.93	0.28	39,41,45,46	0
3	GOL	B	1743	6/6	0.94	0.19	42,45,46,47	0
2	PT	B	1738	1/1	0.96	0.06	55,55,55,55	1
2	PT	A	1734	1/1	0.96	0.13	44,44,44,44	1
3	GOL	A	1741	6/6	0.96	0.25	28,30,33,33	0
3	GOL	A	1742	6/6	0.96	0.34	38,39,43,45	0
2	PT	B	1736	1/1	0.96	0.10	57,57,57,57	1
2	PT	A	1735	1/1	0.98	0.14	56,56,56,56	1
2	PT	A	1733	1/1	0.98	0.04	48,48,48,48	1
2	PT	B	1734	1/1	0.98	0.03	64,64,64,64	0
2	PT	A	1737	1/1	0.98	0.10	47,47,47,47	1
2	PT	B	1737	1/1	0.99	0.03	37,37,37,37	1
2	PT	B	1739	1/1	0.99	0.05	40,40,40,40	1
2	PT	B	1740	1/1	0.99	0.03	44,44,44,44	1
2	PT	B	1733	1/1	0.99	0.03	36,36,36,36	1
2	PT	A	1738	1/1	0.99	0.05	41,41,41,41	1
2	PT	A	1748	1/1	0.99	0.08	51,51,51,51	1
2	PT	A	1740	1/1	0.99	0.02	33,33,33,33	1
2	PT	A	1739	1/1	0.99	0.03	46,46,46,46	0
2	PT	A	1736	1/1	1.00	0.03	33,33,33,33	1

## 6.5 Other polymers

There are no such residues in this entry.