Full wwPDB X-ray Structure Validation Report (i)

Dec 12, 2023 – 03:41 pm GMT

PDB ID	:	4BMA
Title	:	structural of Aspergillus fumigatus UDP-N-acetylglucosamine pyrophosphorylase
Authors	:	Fang, W.; Raimi, O.G.; HurtadoGuerrero, R.; vanAalten, D.M.F.
Deposited on	:	2013-05-07
Resolution	:	2.08 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 (i) 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 (i)) were used in the production of this report:

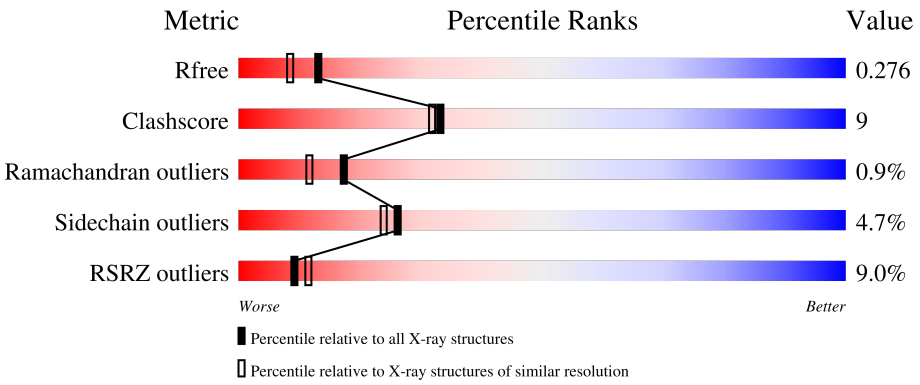
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.08 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	6189 (2.10-2.06)
Clashscore	141614	6738 (2.10-2.06)
Ramachandran outliers	138981	6663 (2.10-2.06)
Sidechain outliers	138945	6664 (2.10-2.06)
RSRZ outliers	127900	6057 (2.10-2.06)

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 <=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	509	10% 76% 13% • 9%
1	B	509	6% 71% 15% • 12%

2 Entry composition (i)

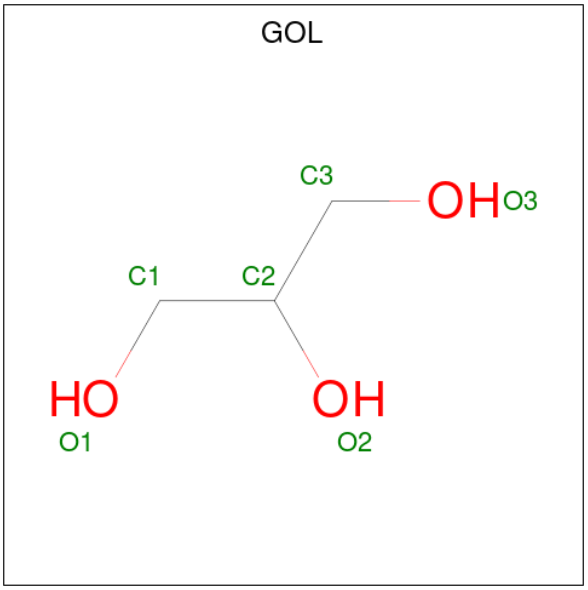
There are 3 unique types of molecules in this entry. The entry contains 7503 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	465	3651	2331	624	683	13	0	1	0
1	B	447	3522	2251	603	653	15	0	1	0

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	155	155	155	0	0

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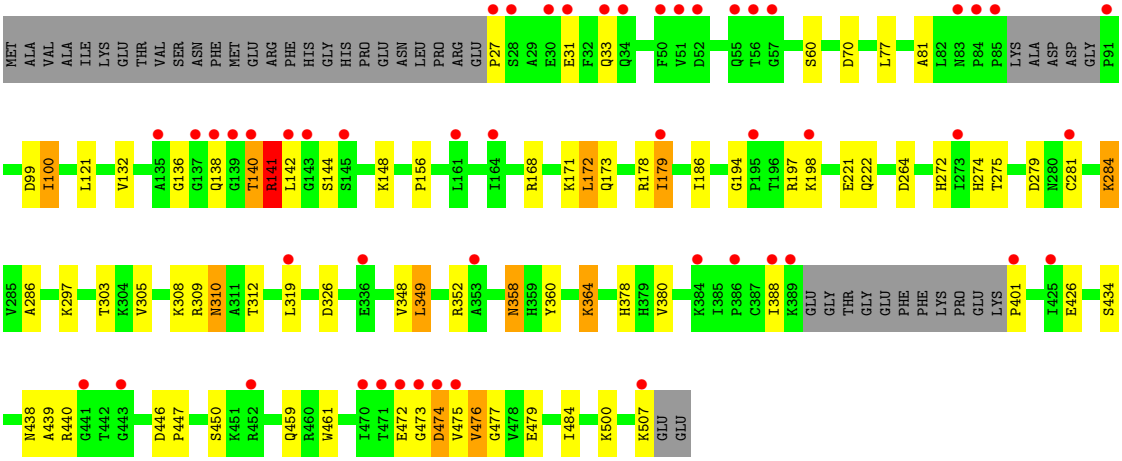
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	B	169	169	169	0	0

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.

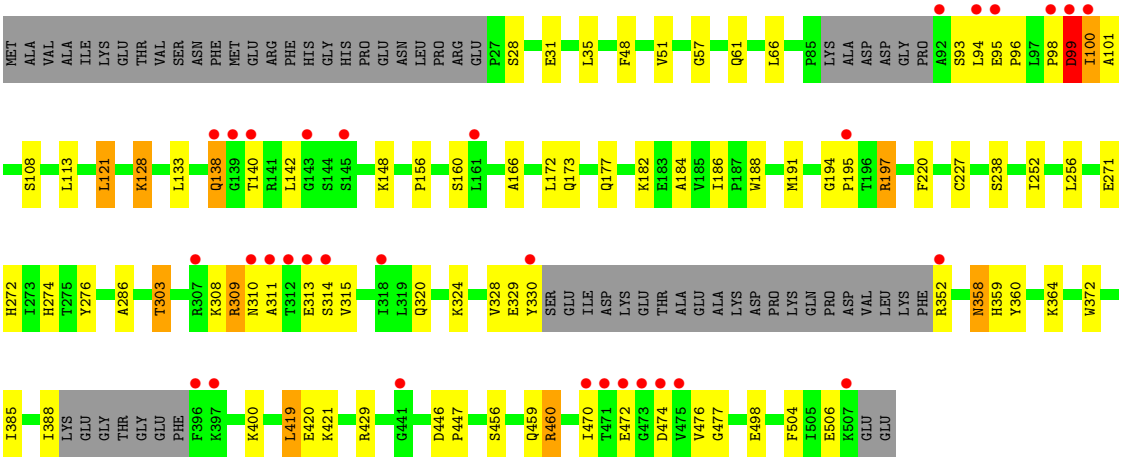
• Molecule 1: UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE

Chain A:



• Molecule 1: UDP-N-ACETYLGLUCOSAMINE PYROPHOSPHORYLASE

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	55.65Å 139.74Å 144.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.08 19.94 – 2.08	Depositor EDS
% Data completeness (in resolution range)	98.6 (40.00-2.08) 98.8 (19.94-2.08)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.98 (at 2.07Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.212 , 0.265 0.237 , 0.276	Depositor DCC
R_{free} test set	3453 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	26.1	Xtriage
Anisotropy	0.560	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 49.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.007 for -h,l,k	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	7503	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: GOL

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	0.87	1/3729 (0.0%)	0.93	9/5030 (0.2%)
1	B	0.96	2/3600 (0.1%)	0.99	4/4855 (0.1%)
All	All	0.92	3/7329 (0.0%)	0.96	13/9885 (0.1%)

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	461	TRP	CD2-CE2	5.38	1.47	1.41
1	B	160	SER	CB-OG	5.32	1.49	1.42
1	B	372	TRP	CD2-CE2	5.01	1.47	1.41

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	460	ARG	NE-CZ-NH1	-11.94	114.33	120.30
1	B	128	LYS	CD-CE-NZ	-9.71	89.38	111.70
1	B	460	ARG	NE-CZ-NH2	8.19	124.39	120.30
1	A	349	LEU	CB-CG-CD1	6.80	122.57	111.00
1	A	264	ASP	CB-CG-OD2	6.09	123.78	118.30
1	A	326	ASP	CB-CG-OD1	6.08	123.77	118.30
1	B	197	ARG	NE-CZ-NH2	-5.86	117.37	120.30
1	A	168	ARG	NE-CZ-NH2	-5.76	117.42	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	284	LYS	CD-CE-NZ	5.66	124.73	111.70
1	A	172	LEU	CB-CG-CD2	5.40	120.18	111.00
1	A	309	ARG	NE-CZ-NH2	-5.36	117.62	120.30
1	A	326	ASP	CB-CG-OD2	-5.24	113.58	118.30
1	A	70	ASP	CB-CG-OD1	5.18	122.96	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	99	ASP	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	3651	0	3666	49	0
1	B	3522	0	3533	74	0
2	A	6	0	8	2	0
3	A	155	0	0	8	0
3	B	169	0	0	2	0
All	All	7503	0	7207	123	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 9.

All (123) 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:308:LYS:HA	1:B:309:ARG:CB	1.73	1.17
1:B:108:SER:HB2	3:B:2029:HOH:O	0.99	1.16
1:B:313:GLU:HG2	1:B:330:TYR:HB2	1.27	1.14
1:B:313:GLU:HB3	1:B:314:SER:HA	1.33	1.07
1:A:222:GLN:OE1	2:A:1508:GOL:H32	1.53	1.06
1:B:308:LYS:CA	1:B:309:ARG:HB3	1.85	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:HIS:HD2	1:A:286:ALA:H	1.06	1.02
1:B:310:ASN:HB2	1:B:311:ALA:HB3	1.41	0.99
1:B:308:LYS:HA	1:B:309:ARG:HB3	1.00	0.97
1:B:274:HIS:HD2	1:B:286:ALA:H	1.15	0.93
1:A:274:HIS:CD2	1:A:286:ALA:H	1.88	0.91
1:A:173:GLN:HE21	1:A:186:ILE:H	1.20	0.90
1:B:274:HIS:CD2	1:B:286:ALA:H	1.91	0.88
1:A:378:HIS:HD2	3:A:2123:HOH:O	1.58	0.85
1:B:313:GLU:CB	1:B:314:SER:HA	2.07	0.85
1:A:140:THR:HA	1:A:144:SER:O	1.77	0.85
1:B:313:GLU:HG2	1:B:330:TYR:CB	2.06	0.85
1:B:177:GLN:HE21	1:B:184:ALA:H	1.24	0.83
1:B:313:GLU:HB3	1:B:314:SER:CA	2.08	0.83
1:A:197:ARG:HH11	1:A:221:GLU:HG3	1.43	0.82
1:B:310:ASN:H	1:B:311:ALA:C	1.82	0.82
1:A:484:ILE:HD11	1:A:507:LYS:HA	1.64	0.79
1:A:310:ASN:HD22	1:A:312:THR:H	1.31	0.76
1:B:173:GLN:HE21	1:B:186:ILE:H	1.36	0.72
1:B:272:HIS:HD2	1:B:360:TYR:OH	1.72	0.71
1:A:173:GLN:NE2	1:A:186:ILE:H	1.90	0.70
1:B:98:PRO:HB2	1:B:100:ILE:HB	1.75	0.68
1:B:456:SER:OG	1:B:460:ARG:NH1	2.27	0.67
1:A:27:PRO:HA	1:A:31:GLU:OE2	1.94	0.67
1:A:136:GLY:N	2:A:1508:GOL:O1	2.26	0.67
1:B:309:ARG:HA	1:B:310:ASN:ND2	2.11	0.66
1:B:310:ASN:N	1:B:311:ALA:C	2.51	0.65
1:A:274:HIS:HE1	1:A:358:ASN:HD21	1.43	0.64
1:B:274:HIS:HE1	1:B:358:ASN:ND2	1.96	0.64
1:B:98:PRO:C	1:B:100:ILE:HB	2.19	0.64
1:A:100:ILE:O	1:A:297:LYS:HE2	1.97	0.63
1:A:148:LYS:HD3	1:A:279:ASP:HB3	1.80	0.63
1:B:98:PRO:O	1:B:101:ALA:N	2.28	0.62
1:A:284:LYS:HG2	3:A:2150:HOH:O	1.99	0.62
1:B:308:LYS:HG2	1:B:309:ARG:O	1.99	0.62
1:B:310:ASN:CB	1:B:311:ALA:HB3	2.24	0.61
1:B:308:LYS:CA	1:B:309:ARG:CB	2.56	0.60
1:A:459:GLN:HE21	1:A:477:GLY:HA2	1.67	0.60
1:A:310:ASN:ND2	1:A:312:THR:H	1.99	0.60
1:B:98:PRO:HB2	1:B:100:ILE:CB	2.32	0.60
1:B:303:THR:OG1	1:B:359:HIS:HD2	1.84	0.60
1:B:320:GLN:HE21	1:B:419:LEU:HD21	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:MET:HB2	1:B:220:PHE:CZ	2.39	0.58
1:A:171:LYS:NZ	3:A:2061:HOH:O	2.37	0.57
1:A:272:HIS:HD2	1:A:360:TYR:OH	1.88	0.57
1:A:274:HIS:HD2	1:A:286:ALA:N	1.89	0.56
1:A:274:HIS:HE1	1:A:358:ASN:ND2	2.04	0.56
1:A:364:LYS:HG3	3:A:2121:HOH:O	2.05	0.56
1:B:113:LEU:HD21	3:B:2029:HOH:O	2.04	0.56
1:B:309:ARG:HG2	1:B:315:VAL:HG21	1.87	0.56
1:A:77:LEU:HD22	1:A:378:HIS:CD2	2.41	0.55
1:B:313:GLU:CG	1:B:330:TYR:CB	2.82	0.55
1:A:99:ASP:O	3:A:2023:HOH:O	2.18	0.54
1:B:99:ASP:N	1:B:100:ILE:HB	2.22	0.54
1:B:309:ARG:HB2	1:B:429:ARG:NH2	2.23	0.54
1:B:470:ILE:HD11	1:B:498:GLU:HG2	1.89	0.54
1:B:274:HIS:HE1	1:B:358:ASN:HD21	1.52	0.54
1:B:313:GLU:CG	1:B:330:TYR:HB2	2.19	0.54
1:A:274:HIS:CD2	1:A:286:ALA:N	2.68	0.54
1:A:378:HIS:CD2	3:A:2123:HOH:O	2.43	0.54
1:B:173:GLN:NE2	1:B:186:ILE:H	2.05	0.54
1:B:310:ASN:H	1:B:311:ALA:CA	2.21	0.53
1:B:48:PHE:HD1	1:B:51:VAL:HG21	1.74	0.53
1:A:446:ASP:HB2	1:A:447:PRO:CD	2.39	0.53
1:B:177:GLN:HG2	1:B:182:LYS:O	2.10	0.52
1:A:438:ASN:O	1:A:447:PRO:HD3	2.10	0.51
1:B:328:VAL:HG23	1:B:328:VAL:O	2.11	0.51
1:B:313:GLU:CB	1:B:314:SER:CA	2.80	0.51
1:A:148:LYS:CD	1:A:279:ASP:HB3	2.40	0.51
1:B:142:LEU:HD11	1:B:148:LYS:HE2	1.94	0.50
1:B:35:LEU:HD21	1:B:66:LEU:HB2	1.94	0.49
1:B:142:LEU:HD12	1:B:142:LEU:N	2.28	0.49
1:A:281[B]:CYS:SG	1:A:434:SER:HB3	2.54	0.48
1:A:474:ASP:O	1:A:476:VAL:HG13	2.14	0.48
1:B:99:ASP:H	1:B:100:ILE:HG12	1.78	0.48
1:A:140:THR:C	1:A:142:LEU:H	2.18	0.47
1:B:166:ALA:HB2	1:B:188:TRP:CZ3	2.50	0.46
1:B:194:GLY:N	1:B:195:PRO:HD2	2.31	0.46
1:B:274:HIS:CD2	1:B:286:ALA:N	2.73	0.46
1:B:308:LYS:HB2	1:B:352:ARG:O	2.16	0.45
1:B:98:PRO:HB2	1:B:100:ILE:CG2	2.47	0.45
1:A:281[B]:CYS:SG	1:A:450:SER:HB3	2.56	0.45
1:B:156:PRO:HB2	1:B:504:PHE:HB2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:VAL:O	1:A:275:THR:HG23	2.16	0.45
1:B:446:ASP:HB2	1:B:447:PRO:CD	2.47	0.45
1:A:472:GLU:OE1	1:A:500:LYS:HD3	2.17	0.44
1:B:252:ILE:O	1:B:256:LEU:HG	2.17	0.44
1:A:305:VAL:HG23	1:A:426:GLU:HA	2.00	0.44
1:A:173:GLN:HE21	1:A:186:ILE:N	2.02	0.44
1:A:360:TYR:CD1	1:A:360:TYR:C	2.91	0.43
1:B:138:GLN:CG	1:B:140:THR:HG23	2.49	0.43
1:B:421:LYS:HD3	1:B:421:LYS:HA	1.84	0.43
1:A:473:GLY:O	1:A:475:VAL:N	2.51	0.43
1:B:313:GLU:HG3	1:B:315:VAL:H	1.84	0.43
1:A:308:LYS:HB3	1:A:352:ARG:HA	2.01	0.43
1:B:57:GLY:O	1:B:61:GLN:HG3	2.18	0.43
1:B:309:ARG:H	1:B:310:ASN:HA	1.84	0.43
1:A:440:ARG:HG3	1:A:447:PRO:HG2	2.00	0.43
1:B:459:GLN:HE21	1:B:477:GLY:HA2	1.84	0.43
1:A:348:VAL:HG13	1:A:352:ARG:HD3	2.00	0.42
1:B:504:PHE:CZ	1:B:506:GLU:HB2	2.55	0.42
1:A:171:LYS:CE	3:A:2060:HOH:O	2.68	0.42
1:B:313:GLU:HA	1:B:315:VAL:H	1.85	0.42
1:B:28:SER:OG	1:B:31:GLU:HG2	2.20	0.42
1:B:238:SER:HA	1:B:388:ILE:HD11	2.02	0.42
1:A:156:PRO:HD2	1:A:479:GLU:OE1	2.20	0.41
1:A:274:HIS:CE1	1:A:358:ASN:HD21	2.30	0.41
1:A:141:ARG:O	1:A:439:ALA:HB2	2.21	0.41
1:B:320:GLN:HA	1:B:324:LYS:O	2.20	0.41
1:A:81:ALA:HB1	1:A:380:VAL:HG23	2.03	0.41
1:B:128:LYS:HE2	1:B:271:GLU:OE2	2.21	0.41
1:B:133:LEU:HD13	1:B:276:TYR:CE2	2.56	0.41
1:B:272:HIS:CD2	1:B:360:TYR:OH	2.62	0.41
1:A:179:ILE:HD11	3:A:2031:HOH:O	2.20	0.41
1:B:227:CYS:HB3	1:B:385:ILE:HD13	2.03	0.41
1:B:138:GLN:HG2	1:B:140:THR:HG23	2.03	0.40
1:B:121:LEU:HD23	1:B:121:LEU:HA	1.78	0.40
1:B:310:ASN:HB2	1:B:311:ALA:CB	2.29	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	460/509 (90%)	438 (95%)	18 (4%)	4 (1%)	17	12
1	B	442/509 (87%)	423 (96%)	15 (3%)	4 (1%)	17	12
All	All	902/1018 (89%)	861 (96%)	33 (4%)	8 (1%)	17	12

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	474	ASP
1	B	96	PRO
1	B	309	ARG
1	A	194	GLY
1	B	100	ILE
1	A	141	ARG
1	B	95	GLU
1	A	179	ILE

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	395/431 (92%)	376 (95%)	19 (5%)	25	23
1	B	381/431 (88%)	364 (96%)	17 (4%)	27	26
All	All	776/862 (90%)	740 (95%)	36 (5%)	26	25

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	60	SER
1	A	100	ILE
1	A	121	LEU
1	A	138	GLN
1	A	140	THR
1	A	141	ARG
1	A	172	LEU
1	A	178	ARG
1	A	198	LYS
1	A	303	THR
1	A	310	ASN
1	A	319	LEU
1	A	349	LEU
1	A	358	ASN
1	A	364	LYS
1	A	388	ILE
1	A	401	PRO
1	A	476	VAL
1	B	93	SER
1	B	94	LEU
1	B	99	ASP
1	B	121	LEU
1	B	138	GLN
1	B	172	LEU
1	B	197	ARG
1	B	303	THR
1	B	329	GLU
1	B	358	ASN
1	B	364	LYS
1	B	400	LYS
1	B	419	LEU
1	B	420	GLU
1	B	472	GLU
1	B	474	ASP
1	B	476	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	ASN
1	A	163	GLN
1	A	173	GLN

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Mol	Chain	Res	Type
1	A	272	HIS
1	A	274	HIS
1	A	310	ASN
1	A	358	ASN
1	A	359	HIS
1	A	378	HIS
1	A	459	GLN
1	B	83	ASN
1	B	163	GLN
1	B	173	GLN
1	B	177	GLN
1	B	272	HIS
1	B	274	HIS
1	B	358	ASN
1	B	359	HIS
1	B	459	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	GOL	A	1508	-	5,5,5	0.27	0	5,5,5	1.02	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	A	1508	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1508	GOL	O1-C1-C2-C3
2	A	1508	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1508	GOL	2	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, 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	465/509 (91%)	0.61	50 (10%) 5 7	8, 19, 37, 79	0
1	B	447/509 (87%)	0.38	32 (7%) 15 19	3, 16, 38, 65	0
All	All	912/1018 (89%)	0.50	82 (8%) 9 11	3, 18, 38, 79	0

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	143	GLY	7.3
1	A	139	GLY	7.1
1	B	474	ASP	6.6
1	B	475	VAL	5.8
1	A	475	VAL	5.2
1	B	472	GLU	4.7
1	A	472	GLU	4.7
1	B	311	ALA	4.5
1	B	396	PHE	4.5
1	B	100	ILE	4.3
1	A	140	THR	4.2
1	A	52	ASP	4.2
1	B	310	ASN	4.1
1	B	471	THR	4.1
1	A	473	GLY	4.0
1	B	473	GLY	4.0
1	A	33	GLN	3.8
1	B	98	PRO	3.8
1	B	313	GLU	3.7
1	B	95	GLU	3.6
1	A	56	THR	3.6
1	B	312	THR	3.5
1	B	330	TYR	3.5
1	A	452	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	28	SER	3.5
1	B	397	LYS	3.4
1	A	161	LEU	3.4
1	A	84	PRO	3.4
1	A	138	GLN	3.3
1	A	55	GLN	3.3
1	A	388	ILE	3.3
1	B	138	GLN	3.1
1	A	85	PRO	3.1
1	A	389	LYS	3.1
1	A	441	GLY	3.0
1	B	99	ASP	3.0
1	A	142	LEU	3.0
1	B	352	ARG	3.0
1	A	386	PRO	3.0
1	A	30	GLU	2.9
1	A	474	ASP	2.9
1	A	443	GLY	2.9
1	B	470	ILE	2.9
1	A	401	PRO	2.9
1	A	471	THR	2.8
1	B	140	THR	2.8
1	A	195	PRO	2.8
1	A	470	ILE	2.8
1	B	145	SER	2.8
1	B	139	GLY	2.8
1	B	143	GLY	2.7
1	A	27	PRO	2.7
1	A	507	LYS	2.5
1	B	507	LYS	2.5
1	B	307	ARG	2.5
1	A	198	LYS	2.5
1	A	145	SER	2.4
1	A	384	LYS	2.4
1	A	281[A]	CYS	2.4
1	A	135	ALA	2.4
1	B	94	LEU	2.3
1	B	318	ILE	2.3
1	B	441	GLY	2.3
1	A	50	PHE	2.3
1	A	34	GLN	2.2
1	A	83	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	319	LEU	2.2
1	A	91	PRO	2.2
1	A	57	GLY	2.2
1	A	353	ALA	2.1
1	A	164	ILE	2.1
1	A	31	GLU	2.1
1	A	179	ILE	2.1
1	A	273	ILE	2.1
1	A	51	VAL	2.1
1	B	161	LEU	2.1
1	B	92	ALA	2.1
1	A	425	ILE	2.0
1	B	314	SER	2.0
1	A	336	GLU	2.0
1	B	195	PRO	2.0
1	A	137	GLY	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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GOL	A	1508	6/6	0.89	0.17	36,42,44,44	0

6.5 Other polymers (i)

There are no such residues in this entry.