



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 14, 2020 – 07:23 am BST

PDB ID : 1V4V  
Title : Crystal Structure Of UDP-N-Acetylglucosamine 2-Epimerase From Thermus  
Thermophilus HB8  
Authors : Bagautdinov, B.; Tahirov, T.H.; RIKEN Structural Genomics/Proteomics Ini-  
tiative (RSGI)  
Deposited on : 2003-11-19  
Resolution : 1.80 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

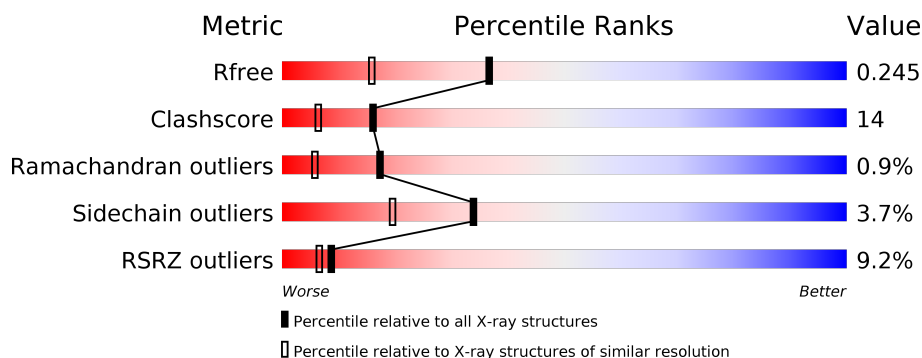
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	376	<div> <div>3%</div> <div>79%</div> <div>19%</div> <div>..</div> </div>
1	B	376	<div> <div>14%</div> <div>68%</div> <div>27%</div> <div>..</div> </div>

## 2 Entry composition [i](#)

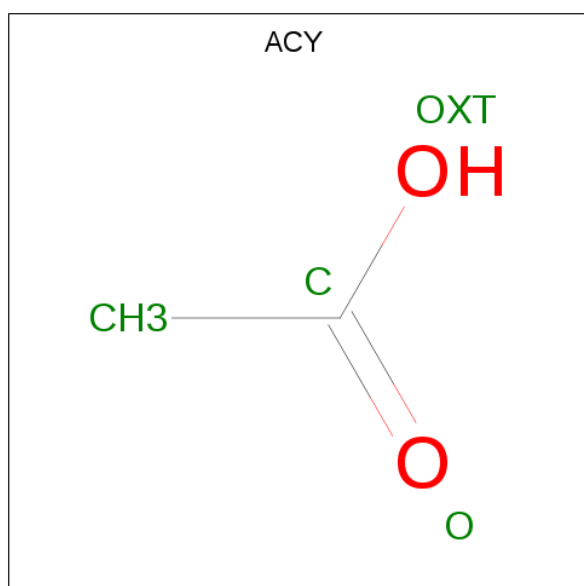
There are 4 unique types of molecules in this entry. The entry contains 6736 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 2-Epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	373	Total	C	N	O	Se	0	4	0
			2868	1834	511	513	10			
1	B	372	Total	C	N	O	Se	182	5	0
			2878	1841	512	516	9			

- Molecule 2 is ACETIC ACID (three-letter code: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		

- 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	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

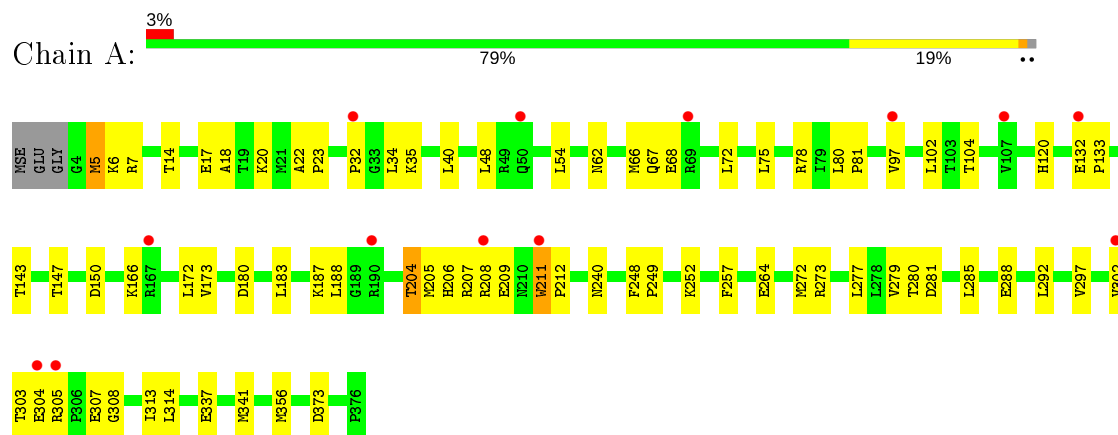
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	609	Total	O	0	0
			609	609		
4	B	365	Total	O	0	0
			365	365		

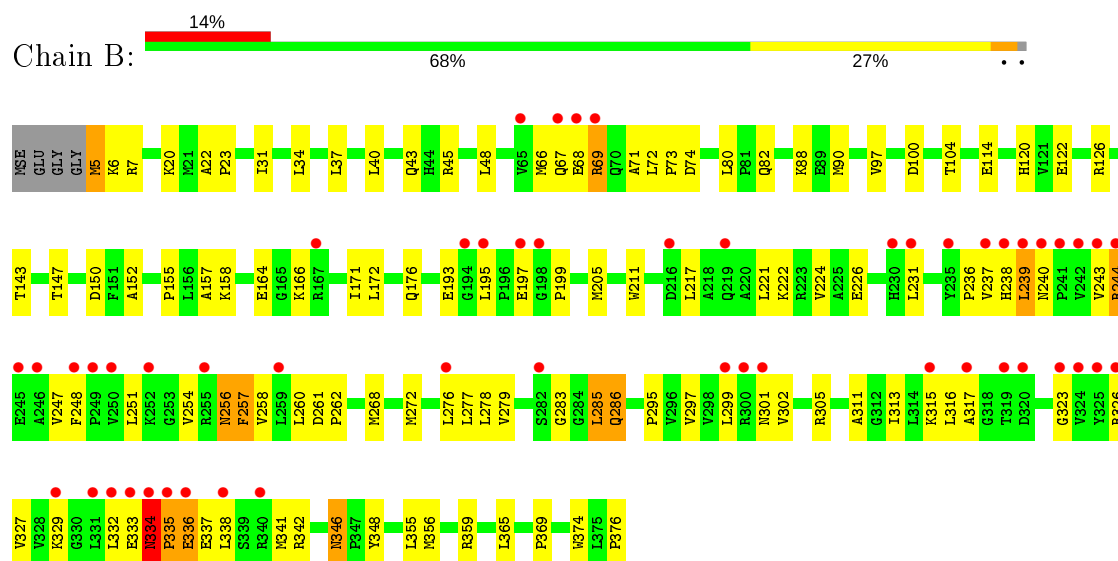
### 3 Residue-property plots [i](#)

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: UDP-N-Acetylglucosamine 2-Epimerase



#### • Molecule 1: UDP-N-Acetylglucosamine 2-Epimerase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	169.73Å 51.45Å 105.51Å 90.00° 104.20° 90.00°	Depositor
Resolution (Å)	40.00 – 1.80 34.65 – 1.80	Depositor EDS
% Data completeness (in resolution range)	95.8 (40.00-1.80) 98.1 (34.65-1.80)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 1.81Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.209 , 0.235 0.220 , 0.245	Depositor DCC
$R_{free}$ test set	7814 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.8	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 80.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6736	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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, ACY

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	0.29	0/2940	0.58	0/3977
1	B	0.28	0/2948	0.57	0/3992
All	All	0.28	0/5888	0.58	0/7969

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	2868	0	2968	70	0
1	B	2878	0	2980	95	0
2	A	4	0	3	0	0
3	A	6	0	8	0	0
3	B	6	0	8	3	0
4	A	609	0	0	17	0
4	B	365	0	0	14	0
All	All	6736	0	5967	165	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 14.

All (165) 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:244:ARG:HB3	1:B:244:ARG:HH11	1.21	1.00
1:B:40:LEU:HD22	1:B:48[A]:LEU:HD13	1.43	0.99
1:A:204:THR:HG21	1:A:285:LEU:HD12	1.49	0.93
1:A:204:THR:HG21	1:A:285:LEU:CD1	2.08	0.83
1:A:66:MSE:HE3	1:A:68:GLU:HG3	1.61	0.80
1:B:66:MSE:HE2	1:B:68:GLU:OE1	1.80	0.80
1:A:205[B]:MSE:HE1	1:A:281:ASP:HB3	1.64	0.79
1:A:6:LYS:HB2	1:A:34:LEU:HD23	1.70	0.72
1:A:172:LEU:HD12	1:A:373[A]:ASP:OD1	1.91	0.71
1:A:204:THR:O	1:A:205[B]:MSE:SE	2.59	0.70
1:B:150:ASP:OD2	1:B:166:LYS:HE2	1.91	0.69
1:B:238:HIS:C	1:B:239:LEU:HD23	2.14	0.68
1:B:334:ASN:N	1:B:335:PRO:HD3	2.08	0.68
1:A:66:MSE:HE3	1:A:68:GLU:CG	2.24	0.68
1:A:208:ARG:HH11	1:A:208:ARG:HG2	1.59	0.66
1:B:244:ARG:NH1	1:B:244:ARG:HB3	2.03	0.66
1:B:240:ASN:HD22	1:B:243:VAL:HG23	1.60	0.65
1:A:80:LEU:HB3	1:A:81:PRO:HD3	1.79	0.65
1:B:301:ASN:HA	1:B:316:LEU:HD23	1.78	0.64
1:B:283:GLY:O	1:B:286:GLN:HG3	1.97	0.64
1:B:205:MSE:HE2	1:B:299:LEU:HD11	1.80	0.63
1:B:334:ASN:N	1:B:335:PRO:CD	2.62	0.63
1:B:172:LEU:HD21	1:B:356:MSE:HG2	1.81	0.62
1:A:54:LEU:HD22	4:A:1803:HOH:O	2.00	0.61
1:B:20:LYS:HE3	4:B:1693:HOH:O	1.99	0.61
1:B:88:LYS:HD3	1:B:114:GLU:HB3	1.80	0.61
1:B:315:LYS:HG3	1:B:341:MSE:HE3	1.83	0.61
1:B:346:ASN:ND2	1:B:348:TYR:H	1.99	0.61
1:B:48[A]:LEU:HD12	4:B:1575:HOH:O	2.00	0.61
1:B:205:MSE:HE1	1:B:217:LEU:HB3	1.84	0.59
1:B:323:GLY:O	1:B:327:VAL:HG23	2.01	0.59
1:B:205:MSE:HE2	1:B:299:LEU:CD1	2.32	0.59
1:B:359:ARG:HG2	3:B:1501:GOL:H11	1.84	0.59
1:B:329:LYS:NZ	1:B:329:LYS:HB3	2.17	0.59
1:B:67:GLN:HB3	4:B:1855:HOH:O	2.03	0.59
1:B:315:LYS:HG3	1:B:341:MSE:CE	2.32	0.58
1:A:277:LEU:HD11	1:A:297[A]:VAL:HG23	1.84	0.58
1:B:143:THR:O	1:B:147[B]:THR:HG23	2.02	0.58
1:B:122:GLU:HG3	1:B:176:GLN:NE2	2.18	0.58
1:A:337:GLU:O	1:A:341:MSE:HG3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:THR:O	1:A:147:THR:HG23	2.03	0.58
1:A:208:ARG:NH1	1:A:208:ARG:HG2	2.19	0.55
1:B:295:PRO:HD3	1:B:342:ARG:HG2	1.87	0.55
1:B:268:MSE:HE2	1:B:285:LEU:HD21	1.89	0.55
1:A:205[B]:MSE:CE	1:A:281:ASP:HB3	2.37	0.54
1:B:254:VAL:HB	1:B:257:PHE:HB2	1.88	0.54
1:B:82:GLN:HG3	4:B:1754:HOH:O	2.07	0.54
1:B:244:ARG:CB	1:B:244:ARG:HH11	2.09	0.54
1:A:211:TRP:CE3	1:A:211:TRP:HA	2.42	0.54
1:B:236:PRO:HA	1:B:260:LEU:O	2.08	0.54
1:A:206:HIS:HA	1:A:211:TRP:HZ3	1.73	0.54
1:B:68:GLU:N	1:B:68:GLU:OE2	2.40	0.54
1:B:205:MSE:HE3	1:B:221:LEU:HD11	1.90	0.53
1:B:268:MSE:O	1:B:272:MSE:HG3	2.08	0.53
1:B:199:PRO:HB3	1:B:276:LEU:HD23	1.91	0.53
1:A:14:THR:OG1	1:A:17:GLU:HG3	2.08	0.53
1:B:97:VAL:HB	1:B:104:THR:HG23	1.89	0.53
1:B:222:LYS:O	1:B:226:GLU:HG3	2.07	0.53
1:B:43[A]:GLN:HG2	1:B:66:MSE:O	2.08	0.53
1:A:303:THR:HA	4:A:1883:HOH:O	2.09	0.53
1:A:279:VAL:HG22	1:A:297[B]:VAL:CG1	2.39	0.53
1:B:277:LEU:HD11	1:B:297:VAL:HG13	1.91	0.53
1:A:150:ASP:OD1	1:A:166:LYS:HE2	2.09	0.53
1:A:314:LEU:HD12	1:A:314:LEU:C	2.30	0.53
1:A:40:LEU:HD12	1:A:62:ASN:ND2	2.24	0.52
1:A:75:LEU:HD23	1:A:102:LEU:HD23	1.91	0.52
1:B:238:HIS:O	1:B:239:LEU:HD23	2.10	0.52
1:A:211:TRP:HE3	1:A:211:TRP:HA	1.74	0.52
1:A:304:GLU:O	1:A:304:GLU:HG2	2.10	0.52
1:A:72:LEU:HD22	1:A:102:LEU:HD22	1.90	0.52
1:A:173:VAL:O	1:A:356:MSE:HE1	2.10	0.52
1:A:22:ALA:HB3	1:A:23:PRO:HD3	1.92	0.51
1:B:301:ASN:CA	1:B:316:LEU:HD23	2.41	0.51
1:A:40:LEU:HD12	1:A:62:ASN:HD21	1.76	0.51
1:B:297:VAL:O	1:B:297:VAL:HG23	2.10	0.50
1:B:6:LYS:HB2	1:B:34:LEU:HD23	1.94	0.50
1:B:279:VAL:HG22	1:B:297:VAL:HG21	1.94	0.50
1:B:317:ALA:HA	1:B:327:VAL:HG21	1.92	0.50
1:A:7:ARG:HG2	1:A:7:ARG:HH11	1.77	0.49
1:A:40:LEU:HD22	1:A:48:LEU:HD23	1.93	0.49
1:B:329:LYS:HZ3	1:B:329:LYS:HB3	1.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:THR:O	1:A:280:THR:HA	2.12	0.49
1:B:237:VAL:O	1:B:262:PRO:HD3	2.13	0.49
1:B:7:ARG:NE	1:B:90:MSE:O	2.39	0.49
1:A:80:LEU:HD22	4:A:1892:HOH:O	2.11	0.49
1:A:264:GLU:HG2	4:A:2029:HOH:O	2.11	0.49
1:A:18:ALA:HB2	1:A:48:LEU:HD11	1.94	0.49
1:A:187:LYS:HE3	4:A:1937:HOH:O	2.13	0.48
1:B:279:VAL:HA	1:B:297:VAL:HG23	1.95	0.48
1:B:34:LEU:HD21	1:B:365:LEU:HD12	1.96	0.48
1:A:307:GLU:CD	1:A:307:GLU:H	2.16	0.48
1:B:31:ILE:HG23	3:B:1501:GOL:H32	1.96	0.48
1:A:54:LEU:O	1:A:188:LEU:HD13	2.13	0.48
1:B:279:VAL:HG22	1:B:297:VAL:CG2	2.44	0.47
1:B:376:PRO:HD3	4:B:1860:HOH:O	2.13	0.47
1:A:120:HIS:HB2	1:A:147:THR:HG21	1.95	0.47
1:B:120:HIS:HB2	1:B:147[B]:THR:HG21	1.97	0.47
1:B:338:LEU:O	1:B:342:ARG:HG3	2.14	0.47
1:B:71:ALA:HB3	1:B:74:ASP:OD2	2.15	0.47
1:A:206:HIS:HA	1:A:211:TRP:CZ3	2.51	0.46
1:B:45:ARG:HA	4:B:1588:HOH:O	2.15	0.46
1:B:222:LYS:NZ	1:B:254:VAL:HG22	2.31	0.46
1:A:20:LYS:HE3	4:A:1750:HOH:O	2.14	0.46
1:B:334:ASN:H	1:B:335:PRO:HD3	1.77	0.46
1:B:48[A]:LEU:HD12	4:B:1588:HOH:O	2.16	0.46
1:B:195:LEU:HD23	1:B:258:VAL:HG11	1.97	0.46
1:B:48[A]:LEU:CD1	4:B:1575:HOH:O	2.59	0.46
1:A:273:ARG:HG3	4:A:1560:HOH:O	2.16	0.45
1:B:197:GLU:HG3	4:B:1792:HOH:O	2.16	0.45
1:B:279:VAL:HA	1:B:297:VAL:CG2	2.47	0.45
1:B:5:MSE:N	4:B:1850:HOH:O	2.48	0.45
1:A:207:ARG:HG2	1:A:209:GLU:HG2	1.98	0.45
1:B:329:LYS:O	1:B:333:GLU:HG3	2.17	0.45
1:A:32:PRO:HG3	4:A:1964:HOH:O	2.15	0.45
1:B:332:LEU:C	1:B:335:PRO:HD3	2.37	0.45
1:B:69:ARG:H	1:B:69:ARG:HD3	1.82	0.44
1:A:272:MSE:HE1	1:A:288:GLU:HB3	1.99	0.44
1:A:240:ASN:HB3	4:A:1578:HOH:O	2.17	0.44
1:A:304:GLU:O	1:A:305:ARG:HG3	2.17	0.44
1:A:183:LEU:HD23	1:A:292:LEU:HD23	1.99	0.44
1:A:7:ARG:NH1	1:A:35:LYS:HE2	2.33	0.44
1:B:247:VAL:HG23	1:B:248:PHE:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:356:MSE:HE1	1:B:374:TRP:HB2	1.99	0.44
1:B:72:LEU:HB2	1:B:73:PRO:HD3	2.00	0.44
1:A:5:MSE:SE	1:A:6:LYS:HG2	2.68	0.43
1:A:132:GLU:HA	1:A:133:PRO:HA	1.87	0.43
1:B:126:ARG:NE	1:B:164:GLU:OE1	2.42	0.43
1:A:7:ARG:NH1	1:A:35:LYS:CE	2.82	0.43
1:B:335:PRO:O	1:B:336:GLU:HB2	2.19	0.43
1:A:305:ARG:HB3	1:A:307:GLU:OE1	2.17	0.43
1:A:356:MSE:HG3	4:A:1898:HOH:O	2.18	0.43
1:A:252:LYS:NZ	4:A:1692:HOH:O	2.51	0.43
1:B:316:LEU:N	1:B:316:LEU:HD12	2.33	0.43
1:B:122:GLU:HG3	1:B:176:GLN:HE22	1.84	0.43
1:B:152:ALA:HB1	1:B:157:ALA:HB3	2.00	0.42
1:B:158:LYS:HG3	1:B:171:ILE:HG21	2.00	0.42
1:B:238:HIS:HA	1:B:262:PRO:HG3	2.01	0.42
1:A:248:PHE:N	1:A:249:PRO:HD2	2.35	0.42
1:B:251:LEU:HD13	1:B:257:PHE:CE2	2.54	0.42
1:A:211:TRP:HB2	1:A:212:PRO:HD3	2.02	0.42
1:A:5:MSE:HE1	4:A:1826:HOH:O	2.19	0.42
1:B:276:LEU:HD23	4:B:1543:HOH:O	2.19	0.42
1:A:97:VAL:HB	1:A:104:THR:HG23	2.02	0.42
1:B:369:PRO:HD2	3:B:1501:GOL:O1	2.20	0.41
1:A:308:GLY:HA2	1:A:313:ILE:HD11	2.02	0.41
1:B:205:MSE:CE	1:B:217:LEU:HB3	2.47	0.41
1:A:17:GLU:HG2	4:A:1567:HOH:O	2.21	0.41
1:B:155:PRO:HD2	4:B:1733:HOH:O	2.20	0.41
1:A:264:GLU:HG3	4:A:1630:HOH:O	2.20	0.41
1:A:272:MSE:HE1	1:A:288:GLU:OE1	2.21	0.41
1:B:7:ARG:CZ	1:B:37:LEU:HD11	2.51	0.41
1:B:22:ALA:HB3	1:B:23:PRO:HD3	2.03	0.41
1:B:346:ASN:C	1:B:346:ASN:HD22	2.23	0.41
1:B:355:LEU:HD21	1:B:359:ARG:NH1	2.35	0.41
1:B:88:LYS:HE3	4:B:1859:HOH:O	2.21	0.41
1:A:279:VAL:HG22	1:A:297[B]:VAL:HG11	2.02	0.41
1:A:279:VAL:HA	1:A:297[B]:VAL:HG13	2.03	0.41
1:A:303:THR:HG22	4:A:1883:HOH:O	2.20	0.41
1:B:221:LEU:HA	1:B:224:VAL:HG22	2.03	0.40
1:B:326:ARG:HA	1:B:329:LYS:NZ	2.36	0.40
1:B:88:LYS:HG3	4:B:1859:HOH:O	2.21	0.40
1:A:302:VAL:HG23	4:A:1724:HOH:O	2.19	0.40
1:A:78:ARG:HD2	4:A:1555:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:277:LEU:HD12	1:B:278:LEU:H	1.87	0.40
1:B:231:LEU:O	1:B:256:ASN:ND2	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	375/376 (100%)	370 (99%)	5 (1%)	0	100	100
1	B	375/376 (100%)	352 (94%)	16 (4%)	7 (2%)	8	1
All	All	750/752 (100%)	722 (96%)	21 (3%)	7 (1%)	17	6

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	336	GLU
1	B	239	LEU
1	B	313	ILE
1	B	302	VAL
1	B	335	PRO
1	B	311	ALA
1	B	334	ASN

### 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	301/289 (104%)	295 (98%)	6 (2%)	55	44
1	B	302/289 (104%)	285 (94%)	17 (6%)	21	8
All	All	603/578 (104%)	580 (96%)	23 (4%)	34	18

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	MSE
1	A	67	GLN
1	A	180	ASP
1	A	204	THR
1	A	211	TRP
1	A	257	PHE
1	B	5	MSE
1	B	69	ARG
1	B	80	LEU
1	B	100[A]	ASP
1	B	100[B]	ASP
1	B	193	GLU
1	B	211	TRP
1	B	244	ARG
1	B	256	ASN
1	B	257	PHE
1	B	261	ASP
1	B	285	LEU
1	B	286	GLN
1	B	305	ARG
1	B	334	ASN
1	B	337	GLU
1	B	346	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	58	GLN
1	A	62	ASN
1	A	67	GLN
1	A	176	GLN
1	B	58	GLN
1	B	67	GLN
1	B	160	ASN

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Mol	Chain	Res	Type
1	B	240	ASN
1	B	256	ASN
1	B	286	GLN
1	B	334	ASN
1	B	346	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	ACY	A	1400	-	1,3,3	2.40	1 (100%)	0,3,3	0.00	-
3	GOL	B	1501	-	5,5,5	0.55	0	5,5,5	0.27	0
3	GOL	A	1500	-	5,5,5	0.53	0	5,5,5	0.28	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	1500	-	-	4/4/4/4	-
3	GOL	B	1501	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1400	ACY	CH3-C	2.40	1.51	1.48

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1501	GOL	O1-C1-C2-C3
3	A	1500	GOL	O1-C1-C2-C3
3	B	1501	GOL	O1-C1-C2-O2
3	A	1500	GOL	O1-C1-C2-O2
3	A	1500	GOL	C1-C2-C3-O3
3	A	1500	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1501	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

### 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, 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	364/376 (96%)	0.08	13 (3%) 42 37	17, 29, 51, 70	0
1	B	341/376 (90%)	0.60	52 (15%) 2 1	17, 34, 86, 93	0
All	All	705/752 (93%)	0.33	65 (9%) 9 6	17, 30, 81, 93	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	335	PRO	9.5
1	B	245	GLU	6.1
1	B	239	LEU	5.9
1	B	241	PRO	5.5
1	B	301	ASN	5.2
1	B	68	GLU	5.1
1	B	242	VAL	4.9
1	B	282	SER	4.9
1	A	305	ARG	4.8
1	B	69	ARG	4.8
1	B	246	ALA	4.7
1	B	65	VAL	4.2
1	B	238	HIS	4.0
1	B	248	PHE	4.0
1	B	319	THR	3.8
1	B	300	ARG	3.7
1	B	340	ARG	3.7
1	B	244	ARG	3.7
1	B	325	TYR	3.6
1	B	338	LEU	3.6
1	B	230	HIS	3.5
1	B	240	ASN	3.4
1	B	243	VAL	3.3
1	A	69	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	324	VAL	3.2
1	B	276	LEU	3.2
1	B	194	GLY	3.1
1	B	315	LYS	3.1
1	B	333	GLU	3.0
1	B	198	GLY	3.0
1	B	336	GLU	2.9
1	B	320	ASP	2.9
1	B	259	LEU	2.9
1	A	50	GLN	2.8
1	B	67	GLN	2.7
1	B	255	ARG	2.7
1	A	211	TRP	2.7
1	A	208	ARG	2.7
1	B	331	LEU	2.7
1	B	329	LYS	2.6
1	B	216	ASP	2.6
1	B	250	VAL	2.6
1	B	334	ASN	2.6
1	B	249	PRO	2.6
1	B	332	LEU	2.5
1	B	252	LYS	2.5
1	B	197	GLU	2.4
1	A	32	PRO	2.3
1	A	302	VAL	2.3
1	B	323	GLY	2.3
1	B	299	LEU	2.3
1	A	190	ARG	2.3
1	B	219	GLN	2.2
1	B	326	ARG	2.2
1	B	231	LEU	2.1
1	B	235	TYR	2.1
1	A	97	VAL	2.1
1	B	317	ALA	2.1
1	B	195	LEU	2.1
1	A	304	GLU	2.1
1	B	237	VAL	2.1
1	A	167	ARG	2.0
1	B	167	ARG	2.0
1	A	107	VAL	2.0
1	A	132	GLU	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, 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	ACY	A	1400	4/4	0.52	0.29	55,55,55,55	0
3	GOL	B	1501	6/6	0.74	0.18	69,69,70,70	0
3	GOL	A	1500	6/6	0.93	0.12	42,44,45,46	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.