



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:52 PM UTC

PDB ID : 3S8A / pdb_00003s8a
Title : Structure of Yeast Ribonucleotide Reductase R293A with dGTP
Authors : Ahmad, M.F.; Kaushal, P.S.; Wan, Q.; Wijeratna, S.R.; Huang, M.; Dealwis, C.D.
Deposited on : 2011-05-27
Resolution : 2.90 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

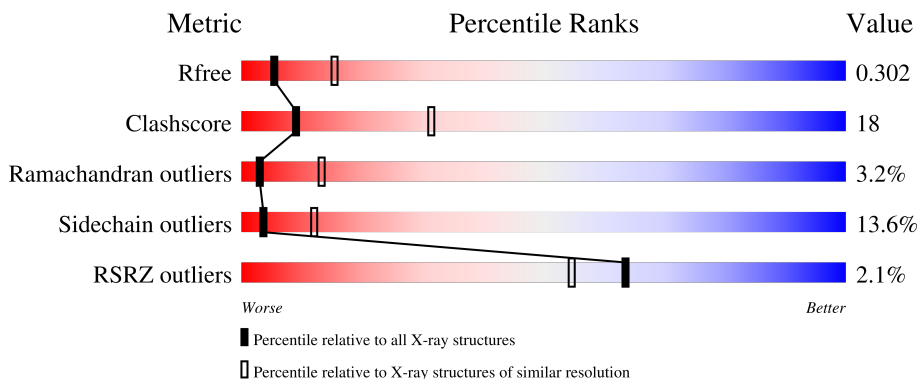
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	888	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5341 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 Ribonucleoside-diphosphate reductase large chain 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	664	5296	3373	899	993	31	0	0	0

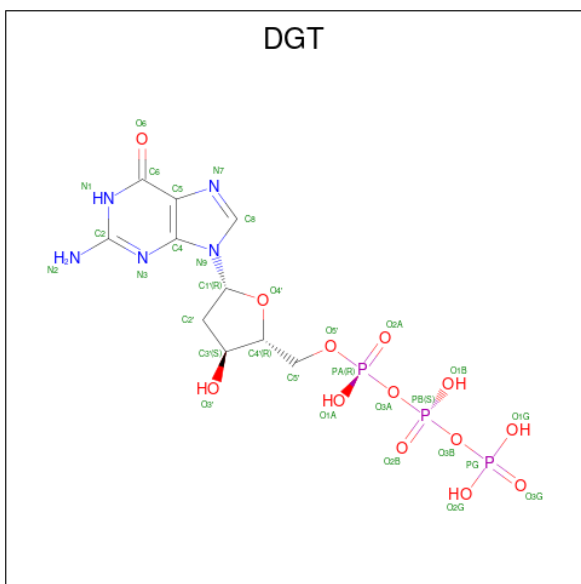
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	293	ALA	ARG	engineered mutation	UNP P21524

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (CCD ID: DGT) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	31	10	5	13	3	0	0

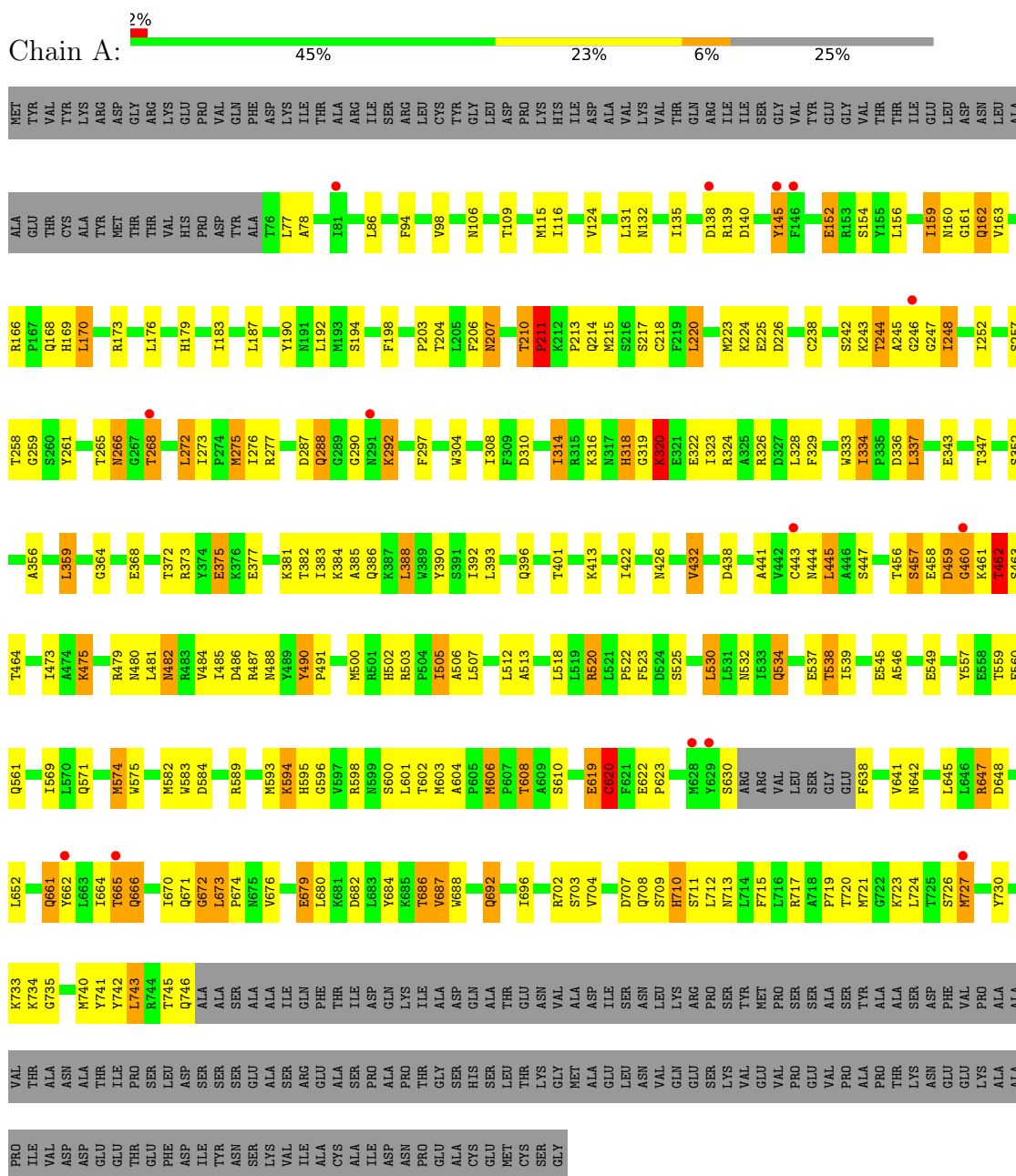
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	13	Total	O	0	0
			13	13		

3 Residue-property plots

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: Ribonucleoside-diphosphate reductase large chain 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	108.44Å 117.72Å 64.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.90 19.99 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.5 (19.99-2.90) 96.1 (19.99-2.90)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.14 (at 2.88Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.228 , 0.300 0.237 , 0.302	Depositor DCC
R_{free} test set	1834 reflections (9.68%)	wwPDB-VP
Wilson B-factor (Å ²)	61.0	Xtrriage
Anisotropy	0.286	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 62.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5341	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: DGT, MG

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	0.83	0/5418	1.09	14/7337 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	244	THR	N-CA-C	-7.68	94.44	110.80
1	A	490	TYR	CA-C-N	7.01	127.31	119.32
1	A	490	TYR	C-N-CA	7.01	127.31	119.32
1	A	482	ASN	N-CA-C	6.85	118.40	111.07
1	A	210	THR	CA-C-N	6.78	128.32	119.84
1	A	210	THR	C-N-CA	6.78	128.32	119.84
1	A	443	CYS	N-CA-C	6.21	118.86	109.23
1	A	710	HIS	N-CA-C	6.17	118.79	109.23
1	A	224	LYS	N-CA-C	6.11	118.74	111.71
1	A	218	CYS	N-CA-C	5.60	117.92	109.23
1	A	334	ILE	N-CA-C	5.59	113.08	107.55
1	A	179	HIS	N-CA-C	5.48	120.11	113.38
1	A	506	ALA	N-CA-C	5.17	119.31	107.48
1	A	308	ILE	N-CA-C	5.01	117.31	111.05

There are no chirality outliers.

There are no planarity outliers.

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	5296	0	5226	194	0
2	A	1	0	0	0	0
3	A	31	0	12	0	0
4	A	13	0	0	2	0
All	All	5341	0	5238	194	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 18.

All (194) 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:A:461:LYS:O	1:A:462:THR:HG22	1.50	1.11
1:A:461:LYS:C	1:A:462:THR:HG22	1.76	1.08
1:A:159:ILE:HG22	1:A:160:ASN:H	1.20	1.02
1:A:337:LEU:HG	1:A:368:GLU:HG2	1.46	0.94
1:A:686:THR:CG2	1:A:688:TRP:HD1	1.82	0.93
1:A:571:GLN:HE21	1:A:571:GLN:HA	1.37	0.88
1:A:502:HIS:ND1	1:A:559:THR:HG21	1.87	0.88
1:A:481:LEU:HB3	1:A:505:ILE:HG13	1.57	0.87
1:A:447:SER:HB3	1:A:606:MET:CE	2.05	0.86
1:A:460:GLY:O	1:A:462:THR:HG23	1.72	0.86
1:A:485:ILE:HD11	1:A:505:ILE:HD13	1.57	0.86
1:A:686:THR:HG21	1:A:688:TRP:HD1	1.43	0.83
1:A:461:LYS:C	1:A:462:THR:CG2	2.46	0.82
1:A:159:ILE:HG22	1:A:160:ASN:N	1.93	0.81
1:A:460:GLY:O	1:A:462:THR:CG2	2.30	0.79
1:A:245:ALA:HB1	1:A:288:GLN:CD	2.07	0.79
1:A:661:GLN:HG2	1:A:664:ILE:HD11	1.62	0.79
1:A:166:ARG:HB2	1:A:169:HIS:ND1	1.97	0.79
1:A:461:LYS:O	1:A:462:THR:CG2	2.30	0.78
1:A:140:ASP:OD2	1:A:168:GLN:HG2	1.83	0.78
1:A:662:TYR:O	1:A:662:TYR:CD1	2.37	0.77
1:A:686:THR:CG2	1:A:688:TRP:CD1	2.67	0.77
1:A:297:PHE:HB2	1:A:328:LEU:HD22	1.65	0.76
1:A:388:LEU:O	1:A:392:ILE:HG13	1.86	0.76
1:A:557:TYR:HE1	1:A:559:THR:HG23	1.48	0.76
1:A:94:PHE:HD1	1:A:169:HIS:HD2	1.32	0.75
1:A:571:GLN:HA	1:A:571:GLN:NE2	2.02	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:447:SER:HB3	1:A:606:MET:HE3	1.68	0.74
1:A:220:LEU:HB2	1:A:441:ALA:HB3	1.69	0.73
1:A:94:PHE:HD1	1:A:169:HIS:CD2	2.05	0.73
1:A:539:ILE:HG22	1:A:603:MET:SD	2.30	0.72
1:A:666:GLN:H	1:A:666:GLN:CD	1.97	0.72
1:A:245:ALA:HB1	1:A:288:GLN:OE1	1.90	0.71
1:A:502:HIS:O	1:A:600:SER:HB3	1.90	0.71
1:A:220:LEU:HD21	1:A:426:ASN:HB3	1.73	0.70
1:A:390:TYR:HE1	4:A:896:HOH:O	1.75	0.70
1:A:160:ASN:C	1:A:162:GLN:H	1.98	0.70
1:A:538:THR:HB	1:A:583:TRP:NE1	2.07	0.69
1:A:661:GLN:HG2	1:A:664:ILE:CD1	2.21	0.69
1:A:538:THR:HB	1:A:583:TRP:HE1	1.57	0.68
1:A:662:TYR:O	1:A:662:TYR:HD1	1.75	0.68
1:A:482:ASN:OD1	1:A:503:ARG:NH1	2.27	0.67
1:A:666:GLN:CD	1:A:666:GLN:N	2.53	0.66
1:A:168:GLN:NE2	1:A:190:TYR:OH	2.28	0.66
1:A:557:TYR:CE1	1:A:559:THR:HG23	2.31	0.66
1:A:686:THR:HG22	1:A:688:TRP:H	1.61	0.65
1:A:106:ASN:OD1	1:A:109:THR:HG22	1.97	0.64
1:A:619:GLU:O	1:A:620:CYS:CB	2.46	0.64
1:A:152:GLU:HA	1:A:156:LEU:HD12	1.81	0.63
1:A:244:THR:OG1	1:A:245:ALA:N	2.30	0.63
1:A:94:PHE:HB3	1:A:132:ASN:OD1	1.99	0.62
1:A:481:LEU:HB3	1:A:505:ILE:CG1	2.28	0.62
1:A:213:PRO:HB2	1:A:215:MET:HE2	1.80	0.62
1:A:475:LYS:HD2	1:A:546:ALA:HB2	1.82	0.61
1:A:522:PRO:HG2	1:A:525:SER:HB3	1.82	0.61
1:A:589:ARG:O	1:A:593:MET:HG3	2.01	0.61
1:A:272:LEU:O	1:A:276:ILE:HG12	2.00	0.61
1:A:560:PHE:CZ	1:A:596:GLY:HA2	2.35	0.61
1:A:475:LYS:O	1:A:479:ARG:HG3	2.01	0.61
1:A:692:GLN:O	1:A:696:ILE:HG12	2.00	0.61
1:A:709:SER:OG	1:A:710:HIS:N	2.34	0.60
1:A:288:GLN:O	1:A:292:LYS:HD2	2.02	0.60
1:A:619:GLU:O	1:A:620:CYS:HB2	2.02	0.58
1:A:620:CYS:HB3	1:A:622:GLU:H	1.68	0.58
1:A:245:ALA:CB	1:A:288:GLN:CD	2.75	0.58
1:A:484:VAL:O	1:A:488:ASN:HB2	2.04	0.58
1:A:261:TYR:OH	1:A:266:ASN:ND2	2.37	0.58
1:A:717:ARG:O	1:A:719:PRO:HD3	2.02	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:665:THR:H	1:A:666:GLN:NE2	2.02	0.58
1:A:481:LEU:CB	1:A:505:ILE:HG13	2.32	0.57
1:A:384:LYS:O	1:A:385:ALA:C	2.49	0.56
1:A:94:PHE:CD1	1:A:169:HIS:HD2	2.18	0.56
1:A:557:TYR:CD1	1:A:559:THR:HG22	2.41	0.56
1:A:159:ILE:CG2	1:A:160:ASN:N	2.65	0.56
1:A:645:LEU:HD13	1:A:684:TYR:CD1	2.41	0.56
1:A:459:ASP:C	1:A:459:ASP:OD2	2.49	0.55
1:A:422:ILE:HG21	1:A:432:VAL:HG23	1.88	0.55
1:A:207:ASN:N	1:A:207:ASN:HD22	2.05	0.55
1:A:447:SER:HB3	1:A:606:MET:HE1	1.88	0.55
1:A:245:ALA:CB	1:A:288:GLN:OE1	2.55	0.55
1:A:665:THR:H	1:A:666:GLN:HE22	1.54	0.55
1:A:630:SER:HB2	1:A:638:PHE:O	2.07	0.55
1:A:557:TYR:HB3	1:A:598:ARG:O	2.07	0.54
1:A:304:TRP:CE3	1:A:304:TRP:C	2.86	0.54
1:A:713:ASN:HD21	1:A:741:TYR:HD2	1.55	0.54
1:A:713:ASN:ND2	1:A:741:TYR:CD2	2.76	0.54
1:A:356:ALA:HB1	1:A:359:LEU:CD2	2.39	0.53
1:A:458:GLU:O	1:A:459:ASP:HB3	2.09	0.53
1:A:246:GLY:C	1:A:247:GLY:O	2.50	0.53
1:A:520:ARG:NH2	1:A:648:ASP:OD2	2.42	0.53
1:A:480:ASN:O	1:A:484:VAL:HG23	2.08	0.52
1:A:413:LYS:NZ	1:A:735:GLY:O	2.42	0.52
1:A:730:TYR:O	1:A:734:LYS:HG2	2.09	0.52
1:A:557:TYR:CE1	1:A:559:THR:CG2	2.91	0.52
1:A:723:LYS:O	1:A:727:MET:HG2	2.09	0.52
1:A:545:GLU:O	1:A:549:GLU:HG3	2.09	0.52
1:A:557:TYR:HD1	1:A:559:THR:HG22	1.73	0.52
1:A:686:THR:HG21	1:A:688:TRP:CD1	2.35	0.52
1:A:623:PRO:HD2	1:A:687:VAL:HG23	1.93	0.51
1:A:670:ILE:HA	1:A:673:LEU:HD12	1.92	0.51
1:A:670:ILE:HD11	1:A:684:TYR:HB2	1.93	0.51
1:A:319:GLY:O	1:A:320:LYS:C	2.52	0.51
1:A:243:LYS:O	1:A:243:LYS:HG2	2.08	0.51
1:A:265:THR:O	1:A:266:ASN:C	2.54	0.51
1:A:139:ARG:HD3	1:A:194:SER:HB2	1.93	0.51
1:A:204:THR:HA	1:A:215:MET:HG2	1.92	0.51
1:A:666:GLN:H	1:A:666:GLN:NE2	2.09	0.51
1:A:459:ASP:OD2	1:A:459:ASP:O	2.30	0.50
1:A:713:ASN:ND2	1:A:741:TYR:HD2	2.08	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:ASN:C	1:A:162:GLN:N	2.64	0.50
1:A:459:ASP:O	1:A:460:GLY:O	2.30	0.50
1:A:381:LYS:HE2	4:A:893:HOH:O	2.11	0.50
1:A:505:ILE:HG22	1:A:602:THR:HA	1.93	0.50
1:A:461:LYS:O	1:A:462:THR:CB	2.58	0.49
1:A:487:ARG:HH11	1:A:487:ARG:HG2	1.78	0.49
1:A:373:ARG:O	1:A:377:GLU:HG3	2.12	0.49
1:A:116:ILE:C	1:A:211:PRO:HD3	2.38	0.49
1:A:243:LYS:C	1:A:244:THR:O	2.51	0.49
1:A:664:ILE:HG13	1:A:665:THR:H	1.78	0.49
1:A:329:PHE:CE1	1:A:742:TYR:OH	2.60	0.48
1:A:160:ASN:O	1:A:162:GLN:N	2.46	0.48
1:A:745:THR:OG1	1:A:746:GLN:N	2.46	0.47
1:A:203:PRO:HG2	1:A:217:SER:HA	1.97	0.47
1:A:259:GLY:HA2	1:A:268:THR:HG23	1.96	0.47
1:A:530:LEU:HD22	1:A:534:GLN:NE2	2.29	0.47
1:A:210:THR:HB	1:A:211:PRO:HD2	1.96	0.47
1:A:569:ILE:CG2	1:A:574:MET:HG2	2.45	0.47
1:A:247:GLY:O	1:A:248:ILE:HG12	2.15	0.47
1:A:413:LYS:HE2	1:A:575:TRP:CE2	2.50	0.47
1:A:575:TRP:CZ2	1:A:703:SER:HB3	2.50	0.47
1:A:347:THR:HB	1:A:382:THR:CG2	2.45	0.47
1:A:692:GLN:HE21	1:A:715:PHE:H	1.63	0.47
1:A:287:ASP:OD2	1:A:290:GLY:HA2	2.15	0.47
1:A:275:MET:HE2	1:A:275:MET:HB3	1.79	0.46
1:A:316:LYS:HD3	1:A:318:HIS:CE1	2.50	0.46
1:A:393:LEU:HD22	1:A:724:LEU:HB3	1.97	0.46
1:A:686:THR:HG23	1:A:688:TRP:CD1	2.46	0.46
1:A:604:ALA:HB2	1:A:708:GLN:HG3	1.97	0.46
1:A:606:MET:HG2	1:A:608:THR:HG22	1.97	0.46
1:A:273:ILE:HD11	1:A:310:ASP:HB3	1.97	0.46
1:A:679:GLU:HG3	1:A:680:LEU:N	2.31	0.46
1:A:594:LYS:HG2	1:A:595:HIS:CE1	2.51	0.46
1:A:671:GLN:O	1:A:672:GLY:C	2.59	0.45
1:A:98:VAL:HG21	1:A:124:VAL:HG21	1.98	0.45
1:A:490:TYR:HA	1:A:491:PRO:HD2	1.73	0.45
1:A:168:GLN:HE22	1:A:194:SER:HB3	1.81	0.45
1:A:246:GLY:O	1:A:247:GLY:O	2.35	0.45
1:A:456:THR:O	1:A:457:SER:O	2.35	0.45
1:A:740:MET:SD	1:A:743:LEU:HB2	2.57	0.45
1:A:140:ASP:CG	1:A:168:GLN:HG2	2.40	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:MET:HE2	1:A:252:ILE:HG22	1.98	0.45
1:A:206:PHE:CB	1:A:207:ASN:HD22	2.30	0.44
1:A:392:ILE:O	1:A:396:GLN:HG3	2.17	0.44
1:A:534:GLN:O	1:A:538:THR:CG2	2.65	0.44
1:A:630:SER:CB	1:A:638:PHE:O	2.65	0.44
1:A:713:ASN:HD22	1:A:741:TYR:HB3	1.82	0.44
1:A:106:ASN:CG	1:A:109:THR:HG22	2.43	0.43
1:A:604:ALA:HB2	1:A:708:GLN:HB2	2.00	0.43
1:A:336:ASP:O	1:A:337:LEU:C	2.61	0.43
1:A:523:PHE:CE1	1:A:623:PRO:HG3	2.53	0.43
1:A:170:LEU:HD22	1:A:173:ARG:NH2	2.34	0.43
1:A:664:ILE:HG13	1:A:665:THR:N	2.34	0.43
1:A:606:MET:O	1:A:608:THR:HG23	2.19	0.43
1:A:333:TRP:HA	1:A:333:TRP:CE3	2.53	0.43
1:A:513:ALA:HB2	1:A:623:PRO:HA	2.00	0.43
1:A:665:THR:N	1:A:666:GLN:NE2	2.66	0.43
1:A:257:SER:O	1:A:258:THR:C	2.61	0.43
1:A:192:LEU:HB2	1:A:198:PHE:HE1	1.84	0.42
1:A:356:ALA:HB1	1:A:359:LEU:HD21	2.01	0.42
1:A:162:GLN:HG3	1:A:163:VAL:N	2.32	0.42
1:A:460:GLY:O	1:A:462:THR:HG22	2.16	0.42
1:A:384:LYS:C	1:A:386:GLN:N	2.77	0.42
1:A:641:VAL:O	1:A:642:ASN:C	2.62	0.42
1:A:225:GLU:HG2	1:A:226:ASP:N	2.34	0.42
1:A:372:THR:O	1:A:375:GLU:HB3	2.19	0.42
1:A:444:ASN:C	1:A:445:LEU:HD23	2.45	0.42
1:A:505:ILE:HD12	1:A:505:ILE:HA	1.53	0.42
1:A:532:ASN:HD21	1:A:702:ARG:HB3	1.85	0.42
1:A:661:GLN:O	1:A:664:ILE:HG12	2.19	0.42
1:A:238:CYS:O	1:A:242:SER:HB2	2.20	0.41
1:A:569:ILE:HG22	1:A:574:MET:HG2	2.02	0.41
1:A:623:PRO:HD2	1:A:687:VAL:CG2	2.50	0.41
1:A:257:SER:OG	1:A:352:SER:HB2	2.21	0.41
1:A:601:LEU:HA	1:A:707:ASP:OD2	2.21	0.41
1:A:647:ARG:HE	1:A:647:ARG:HB2	1.66	0.41
1:A:537:GLU:OE2	1:A:582:MET:HB3	2.21	0.40
1:A:220:LEU:HD22	1:A:426:ASN:HA	2.04	0.40
1:A:343:GLU:OE2	1:A:733:LYS:NZ	2.45	0.40
1:A:445:LEU:HD23	1:A:445:LEU:N	2.37	0.40
1:A:522:PRO:HB3	1:A:682:ASP:O	2.20	0.40
1:A:571:GLN:NE2	1:A:571:GLN:CA	2.74	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:604:ALA:HB2	1:A:708:GLN:CG	2.51	0.40
1:A:106:ASN:HB3	1:A:109:THR:CG2	2.51	0.40
1:A:486:ASP:OD2	1:A:500:MET:HE1	2.21	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	660/888 (74%)	587 (89%)	52 (8%)	21 (3%)	3 13

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	ILE
1	A	320	LYS
1	A	457	SER
1	A	459	ASP
1	A	674	PRO
1	A	145	TYR
1	A	161	GLY
1	A	288	GLN
1	A	460	GLY
1	A	462	THR
1	A	687	VAL
1	A	375	GLU
1	A	584	ASP
1	A	620	CYS
1	A	672	GLY
1	A	211	PRO
1	A	314	ILE
1	A	78	ALA

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	292	LYS
1	A	135	ILE
1	A	364	GLY

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	573/760 (75%)	495 (86%)	78 (14%)	3 12

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	77	LEU
1	A	86	LEU
1	A	115	MET
1	A	131	LEU
1	A	138	ASP
1	A	145	TYR
1	A	152	GLU
1	A	154	SER
1	A	162	GLN
1	A	170	LEU
1	A	176	LEU
1	A	183	ILE
1	A	187	LEU
1	A	207	ASN
1	A	211	PRO
1	A	214	GLN
1	A	220	LEU
1	A	248	ILE
1	A	266	ASN
1	A	268	THR
1	A	272	LEU
1	A	275	MET
1	A	277	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	314	ILE
1	A	318	HIS
1	A	320	LYS
1	A	322	GLU
1	A	323	ILE
1	A	324	ARG
1	A	326	ARG
1	A	334	ILE
1	A	337	LEU
1	A	359	LEU
1	A	383	ILE
1	A	388	LEU
1	A	401	THR
1	A	432	VAL
1	A	438	ASP
1	A	445	LEU
1	A	462	THR
1	A	463	SER
1	A	464	THR
1	A	473	ILE
1	A	475	LYS
1	A	505	ILE
1	A	507	LEU
1	A	512	LEU
1	A	518	LEU
1	A	520	ARG
1	A	530	LEU
1	A	534	GLN
1	A	538	THR
1	A	561	GLN
1	A	574	MET
1	A	594	LYS
1	A	606	MET
1	A	608	THR
1	A	610	SER
1	A	619	GLU
1	A	620	CYS
1	A	647	ARG
1	A	652	LEU
1	A	661	GLN
1	A	665	THR
1	A	666	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	673	LEU
1	A	676	VAL
1	A	679	GLU
1	A	686	THR
1	A	692	GLN
1	A	704	VAL
1	A	711	SER
1	A	712	LEU
1	A	720	THR
1	A	721	MET
1	A	726	SER
1	A	727	MET
1	A	743	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	142	GLN
1	A	162	GLN
1	A	168	GLN
1	A	207	ASN
1	A	251	HIS
1	A	266	ASN
1	A	270	ASN
1	A	291	ASN
1	A	317	ASN
1	A	534	GLN
1	A	552	GLN
1	A	561	GLN
1	A	567	GLN
1	A	595	HIS
1	A	618	ASN
1	A	666	GLN
1	A	713	ASN

5.3.3 RNA

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	DGT	A	1001	2	32,33,33	1.68	9 (28%)	48,52,52	2.03	16 (33%)

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DGT	A	1001	2	-	1/22/34/34	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	DGT	C5-C4	3.69	1.48	1.38
3	A	1001	DGT	PB-O3B	3.64	1.63	1.59
3	A	1001	DGT	PB-O3A	3.56	1.63	1.59
3	A	1001	DGT	C8-N7	2.76	1.40	1.32
3	A	1001	DGT	C2-N3	2.63	1.39	1.33
3	A	1001	DGT	C2-N2	2.50	1.40	1.34
3	A	1001	DGT	PA-O3A	2.48	1.62	1.59
3	A	1001	DGT	PG-O3G	2.31	1.57	1.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	DGT	O6-C6	2.08	1.27	1.23

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	DGT	C5-C4-N3	-5.93	118.96	128.39
3	A	1001	DGT	C2-N3-C4	5.33	121.48	112.30
3	A	1001	DGT	N9-C4-N3	4.28	134.52	125.95
3	A	1001	DGT	O1B-PB-O3B	3.43	116.53	107.27
3	A	1001	DGT	C6-C5-N7	3.25	136.20	130.29
3	A	1001	DGT	O3B-PB-O2B	-3.06	101.49	110.70
3	A	1001	DGT	C4-C5-N7	-2.64	106.48	110.67
3	A	1001	DGT	O3B-PG-O3G	-2.63	97.22	111.04
3	A	1001	DGT	N9-C8-N7	-2.49	108.78	113.40
3	A	1001	DGT	O4'-C1'-N9	-2.40	103.60	107.86
3	A	1001	DGT	C8-N7-C5	2.38	108.51	104.26
3	A	1001	DGT	O1A-PA-O5'	2.38	118.33	107.57
3	A	1001	DGT	O2G-PG-O3G	2.27	119.68	110.83
3	A	1001	DGT	PA-O5'-C5'	-2.24	108.51	121.35
3	A	1001	DGT	C3'-C2'-C1'	2.02	107.54	102.60
3	A	1001	DGT	O6-C6-C5	-2.01	121.22	126.53

There are no chirality outliers.

All (1) torsion outliers are listed below:

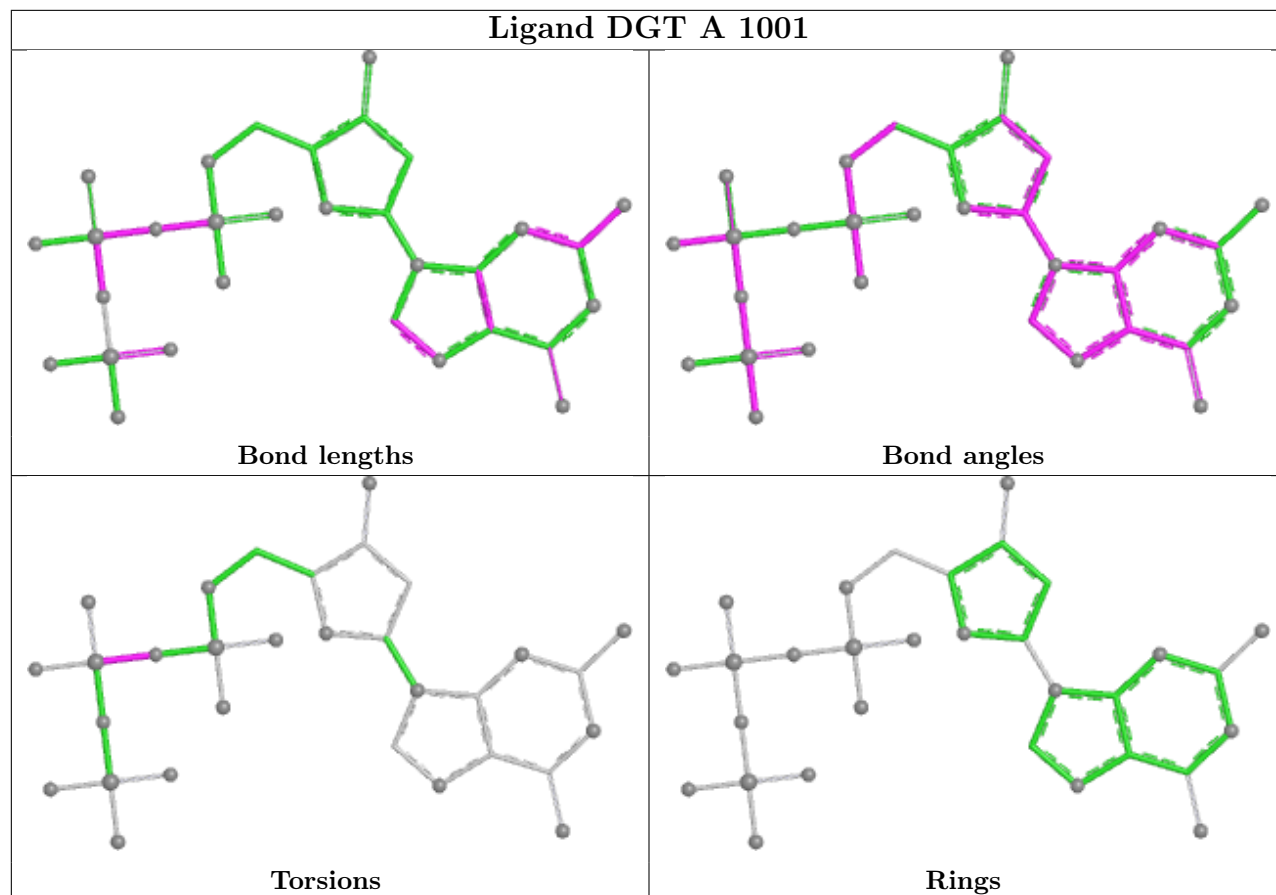
Mol	Chain	Res	Type	Atoms
3	A	1001	DGT	PA-O3A-PB-O1B

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

equivalents in the CSD to analyse the geometry.



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	664/888 (74%)	-0.01	14 (2%) 63 54	57, 71, 108, 132	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	665	THR	4.9
1	A	629	TYR	3.0
1	A	138	ASP	3.0
1	A	246	GLY	3.0
1	A	145	TYR	2.9
1	A	460	GLY	2.7
1	A	443	CYS	2.6
1	A	727	MET	2.5
1	A	662	TYR	2.4
1	A	291	ASN	2.3
1	A	81	ILE	2.3
1	A	146	PHE	2.3
1	A	628	MET	2.1
1	A	268	THR	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](#)

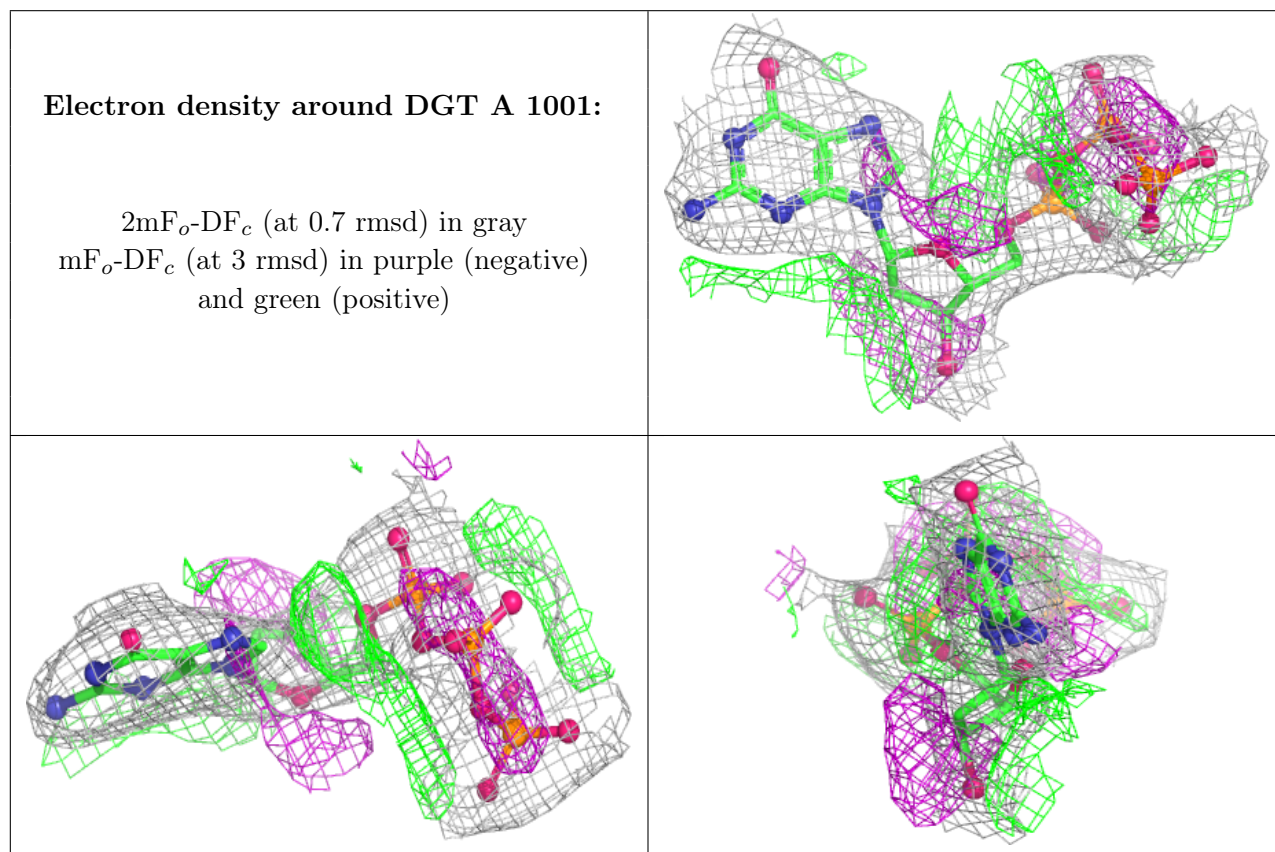
There are no oligosaccharides in this entry.

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	MG	A	2001	1/1	0.50	0.21	64,64,64,64	0
3	DGT	A	1001	31/31	0.85	0.12	40,43,49,52	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers [i](#)

There are no such residues in this entry.