



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 17, 2024 – 07:46 AM EST

PDB ID : 3S8A
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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
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

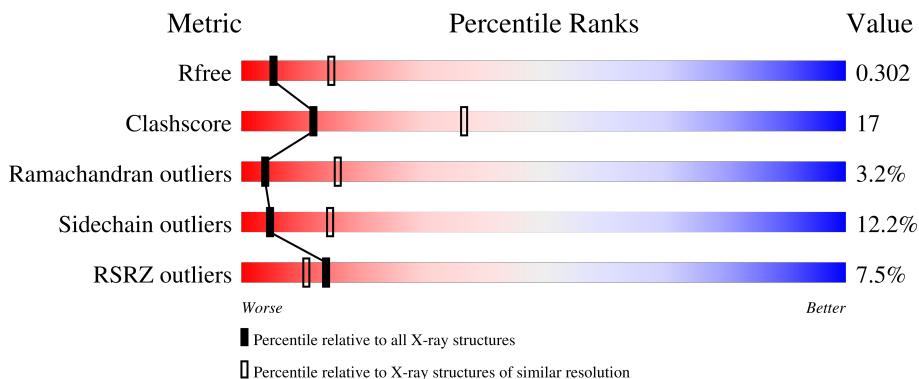
1 Overall quality at a glance

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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (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

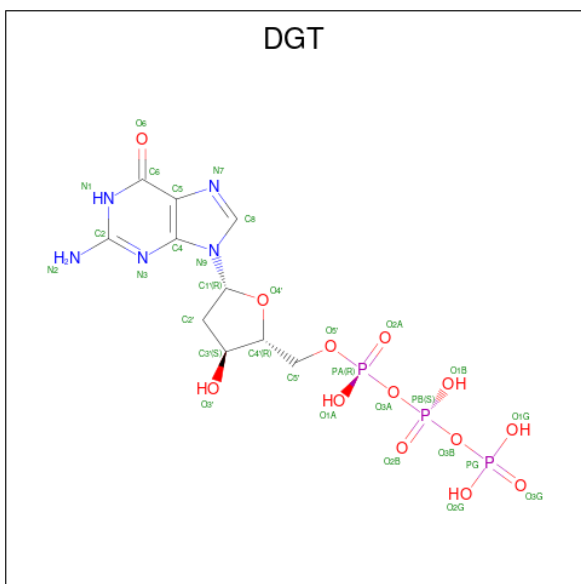
There is a discrepancy between the modelled and reference sequences:

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

- Molecule 2 is MAGNESIUM ION (three-letter code: 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 (three-letter code: 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		

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 19.94 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.5 (19.99-2.90) 96.5 (19.94-2.90)	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 (10.03%)	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	0.68	1/5418 (0.0%)	0.79	3/7337 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	620	CYS	CB-SG	-7.81	1.69	1.82

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	170	LEU	CA-CB-CG	7.22	131.91	115.30
1	A	244	THR	N-CA-C	-6.13	94.44	111.00
1	A	507	LEU	CA-CB-CG	5.57	128.11	115.30

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	183	0
2	A	1	0	0	0	0
3	A	31	0	12	0	0
4	A	13	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5341	0	5238	183	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 17.

All (183) 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	1.03
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:159:ILE:HG22	1:A:160:ASN:N	1.93	0.83
1:A:686:THR:HG21	1:A:688:TRP:HD1	1.43	0.83
1:A:460:GLY:O	1:A:462:THR:CG2	2.30	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:461:LYS:C	1:A:462:THR:CG2	2.46	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
1:A:245:ALA:HB1	1:A:288:GLN:CD	2.07	0.74
1:A:447:SER:HB3	1:A:606:MET:HE3	1.69	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:245:ALA:HB1	1:A:288:GLN:OE1	1.90	0.72
1:A:502:HIS:O	1:A:600:SER:HB3	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:H	1:A:666:GLN:CD	1.97	0.67
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:160:ASN:C	1:A:162:GLN:H	1.98	0.65
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:666:GLN:CD	1:A:666:GLN:N	2.53	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: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
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:447:SER:HB3	1:A:606:MET:HE1	1.87	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:422:ILE:HG21	1:A:432:VAL:HG23	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:ASN:N	1:A:207:ASN:HD22	2.05	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: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:245:ALA:CB	1:A:288:GLN:CD	2.75	0.53
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: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:384:LYS:O	1:A:385:ALA:C	2.49	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:243:LYS:O	1:A:243:LYS:HG2	2.08	0.51
1:A:139:ARG:HD3	1:A:194:SER:HB2	1.93	0.51
1:A:459:ASP:C	1:A:459:ASP:OD2	2.49	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:160:ASN:C	1:A:162:GLN:N	2.64	0.50
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
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:304:TRP:CE3	1:A:304:TRP:C	2.86	0.49
1:A:664:ILE:HG13	1:A:665:THR:H	1.78	0.49
1:A:246:GLY:C	1:A:247:GLY:O	2.50	0.48
1:A:329:PHE:CE1	1:A:742:TYR:OH	2.60	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:319:GLY:O	1:A:320:LYS:C	2.52	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:265:THR:O	1:A:266:ASN:C	2.54	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: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: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:243:LYS:C	1:A:244:THR:O	2.51	0.44
1:A:162:GLN:HG3	1:A:163:VAL:N	2.32	0.43
1:A:604:ALA:HB2	1:A:708:GLN:HB2	2.00	0.43
1:A:523:PHE:CE1	1:A:623:PRO:HG3	2.53	0.43
1:A:116:ILE:C	1:A:211:PRO:HD3	2.38	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:460:GLY:O	1:A:462:THR:HG22	2.16	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: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:671:GLN:O	1:A:672:GLY:C	2.59	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:N	1:A:445:LEU:HD23	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
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

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%)	4 16

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
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%)	503 (88%)	70 (12%)	5 15

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	77	LEU
1	A	115	MET
1	A	119	ASP
1	A	131	LEU
1	A	138	ASP
1	A	145	TYR
1	A	146	PHE
1	A	154	SER
1	A	162	GLN
1	A	170	LEU
1	A	176	LEU
1	A	183	ILE
1	A	207	ASN
1	A	211	PRO
1	A	214	GLN
1	A	220	LEU
1	A	266	ASN
1	A	272	LEU
1	A	275	MET
1	A	314	ILE
1	A	317	ASN
1	A	318	HIS
1	A	320	LYS
1	A	322	GLU
1	A	323	ILE
1	A	326	ARG
1	A	333	TRP
1	A	337	LEU
1	A	359	LEU
1	A	383	ILE
1	A	388	LEU
1	A	401	THR
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

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Mol	Chain	Res	Type
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	620	CYS
1	A	621	PHE
1	A	638	PHE
1	A	647	ARG
1	A	652	LEU
1	A	661	GLN
1	A	665	THR
1	A	666	GLN
1	A	673	LEU
1	A	679	GLU
1	A	686	THR
1	A	692	GLN
1	A	712	LEU
1	A	720	THR
1	A	721	MET
1	A	726	SER
1	A	743	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	ASN
1	A	162	GLN
1	A	168	GLN
1	A	207	ASN
1	A	214	GLN
1	A	251	HIS
1	A	266	ASN
1	A	270	ASN
1	A	317	ASN
1	A	534	GLN
1	A	561	GLN

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Mol	Chain	Res	Type
1	A	567	GLN
1	A	571	GLN
1	A	613	GLN
1	A	666	GLN
1	A	713	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 monosaccharides 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	26,33,33	1.35	6 (23%)	32,52,52	1.57	8 (25%)

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	DGT	A	1001	2	-	1/18/34/34	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	DGT	C8-N7	3.09	1.40	1.35
3	A	1001	DGT	C2-N3	2.63	1.39	1.33
3	A	1001	DGT	C2-N2	2.45	1.40	1.34
3	A	1001	DGT	C5-C4	2.27	1.48	1.43
3	A	1001	DGT	PG-O3G	2.21	1.57	1.50
3	A	1001	DGT	O6-C6	2.07	1.27	1.23

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	DGT	PA-O3A-PB	-3.96	119.25	132.83
3	A	1001	DGT	C8-N7-C5	2.90	108.51	102.99
3	A	1001	DGT	O3B-PG-O3G	-2.52	97.22	111.19
3	A	1001	DGT	PB-O3B-PG	-2.35	124.76	132.83
3	A	1001	DGT	O2G-PG-O3G	2.30	119.68	110.68
3	A	1001	DGT	C5-C6-N1	2.29	117.99	113.95
3	A	1001	DGT	O1A-PA-O5'	2.28	118.33	107.75
3	A	1001	DGT	PA-O5'-C5'	-2.25	108.51	121.68

There are no chirality outliers.

All (1) torsion outliers are listed below:

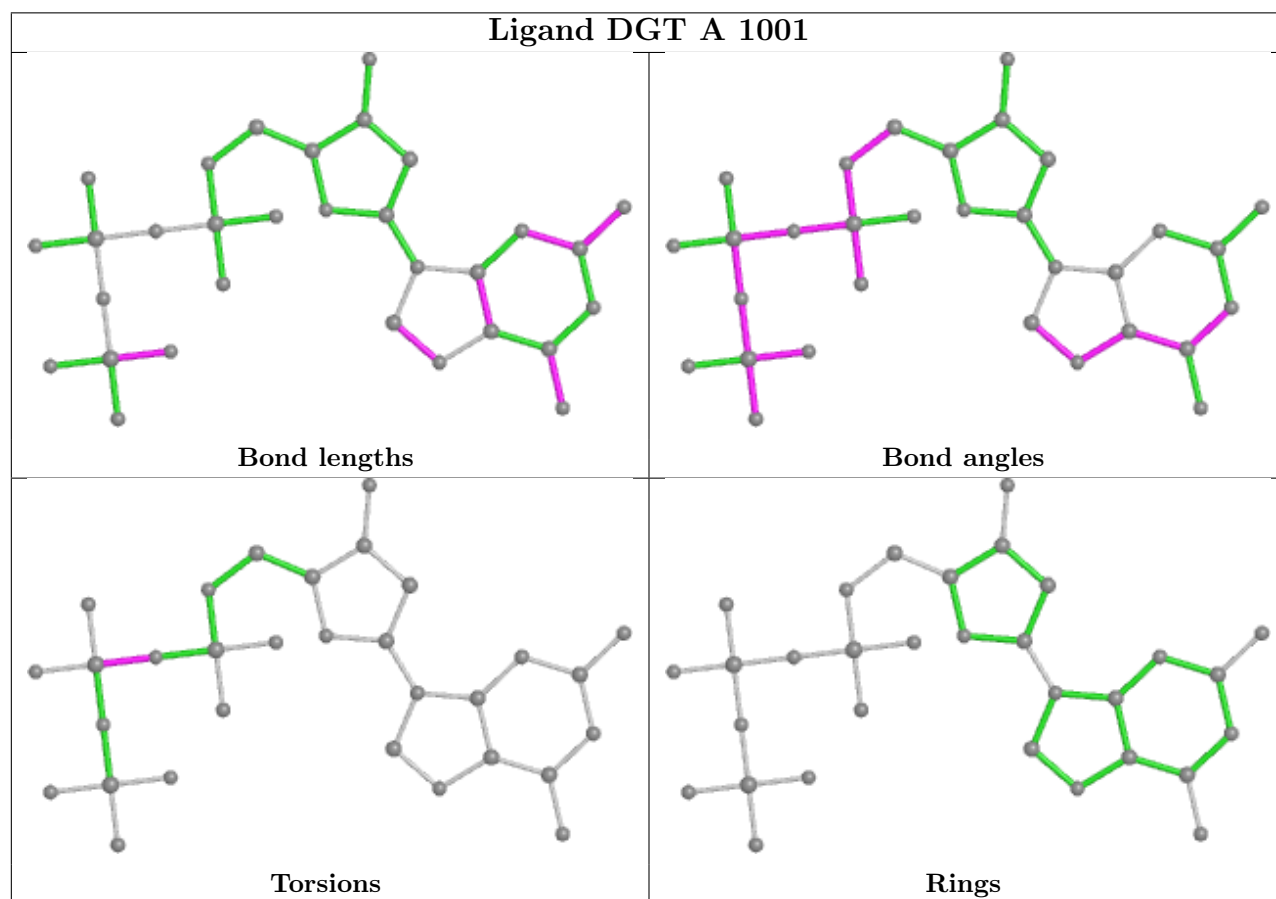
Mol	Chain	Res	Type	Atoms
3	A	1001	DGT	PA-O3A-PB-O1B

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

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	664/888 (74%)	0.19	50 (7%) 14 11	57, 71, 108, 132	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	665	THR	7.9
1	A	291	ASN	7.1
1	A	638	PHE	5.6
1	A	318	HIS	4.9
1	A	138	ASP	4.9
1	A	319	GLY	4.8
1	A	461	LYS	4.5
1	A	77	LEU	4.4
1	A	629	TYR	4.1
1	A	81	ILE	3.9
1	A	321	GLU	3.9
1	A	320	LYS	3.8
1	A	293	ALA	3.8
1	A	145	TYR	3.6
1	A	462	THR	3.5
1	A	322	GLU	3.3
1	A	460	GLY	3.3
1	A	662	TYR	3.2
1	A	456	THR	3.2
1	A	457	SER	3.1
1	A	89	GLN	3.1
1	A	647	ARG	3.1
1	A	718	ALA	3.0
1	A	746	GLN	2.9
1	A	80	ARG	2.9
1	A	78	ALA	2.9
1	A	459	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	129	ASP	2.8
1	A	390	TYR	2.8
1	A	610	SER	2.7
1	A	88	LYS	2.7
1	A	458	GLU	2.7
1	A	717	ARG	2.6
1	A	294	PRO	2.5
1	A	133	SER	2.4
1	A	153	ARG	2.4
1	A	594	LYS	2.3
1	A	657	GLU	2.3
1	A	76	THR	2.3
1	A	292	LYS	2.2
1	A	146	PHE	2.2
1	A	630	SER	2.2
1	A	264	GLY	2.2
1	A	268	THR	2.2
1	A	553	LYS	2.1
1	A	85	ASN	2.1
1	A	160	ASN	2.1
1	A	468	LYS	2.1
1	A	733	LYS	2.1
1	A	162	GLN	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](#)

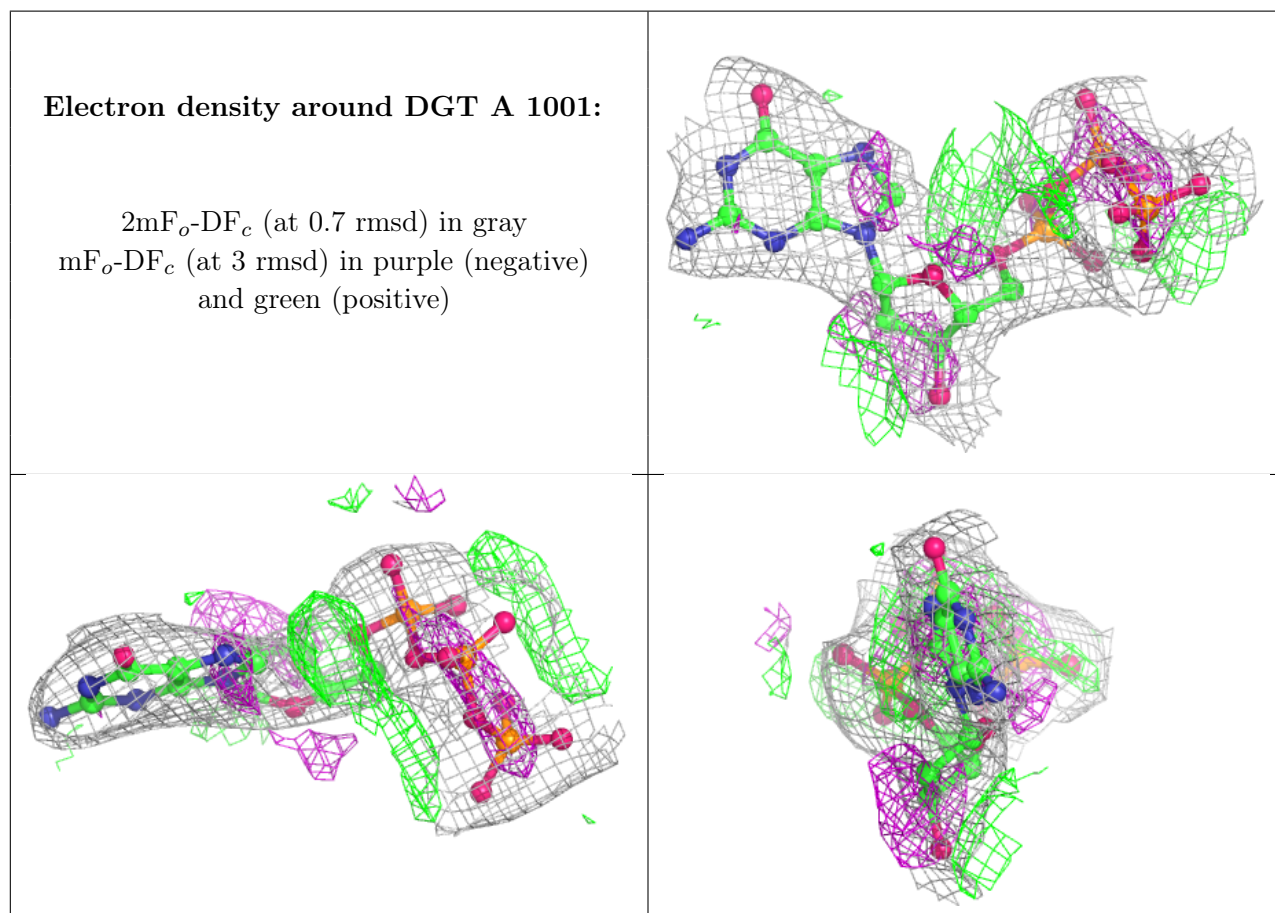
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	DGT	A	1001	31/31	0.92	0.17	40,43,49,52	0
2	MG	A	2001	1/1	0.94	0.22	64,64,64,64	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.