



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 06:50 am BST

PDB ID : 3TBA  
Title : Structure of Yeast Ribonucleotide Reductase 1 Q288A with dGTP and ADP  
Authors : Ahmad, M.F.; Kaushal, P.S.; Wan, Q.; Wijeratna, S.R.; Huang, M.; Dealwis, C.  
Deposited on : 2011-08-05  
Resolution : 2.80 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
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)	:	2.11

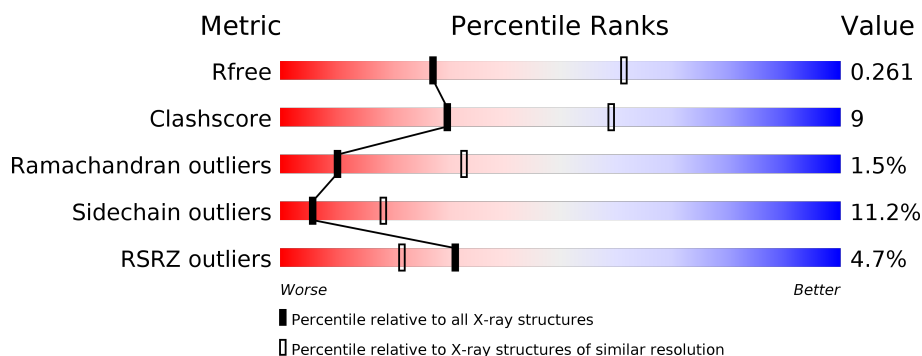
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	888	<div> <div>3%</div> <div>55%</div> <div>16%</div> <div>•</div> <div>26%</div> </div>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5354 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
1	A	660	Total	C	N	O	S	0	0	0
			5234	3331	889	983	31			

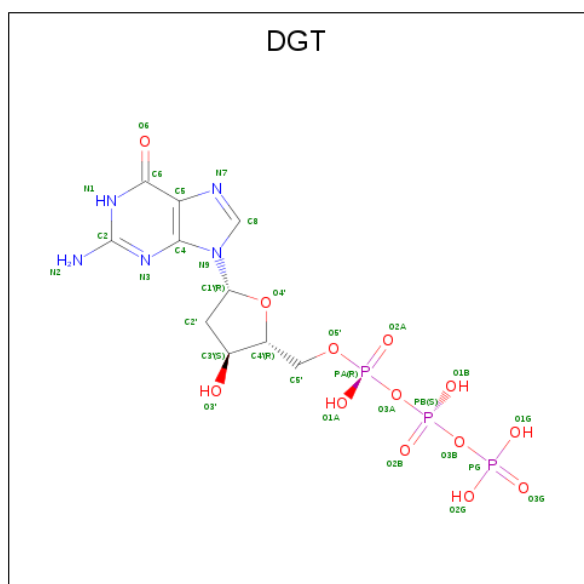
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	288	ALA	GLN	ENGINEERED MUTATION	UNP P21524

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

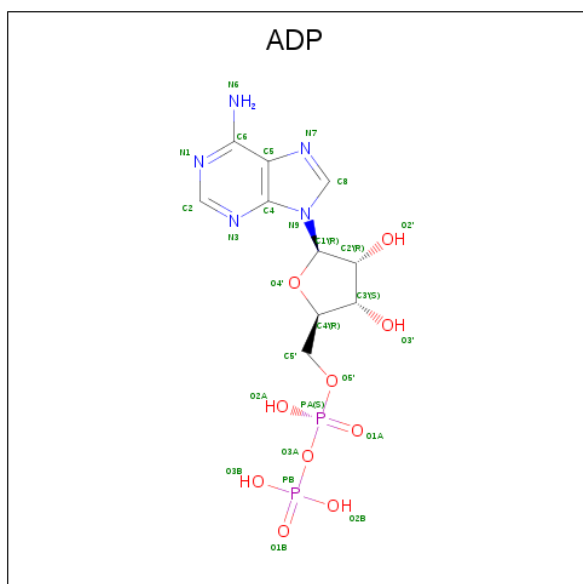
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (three-letter code: DGT) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



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

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

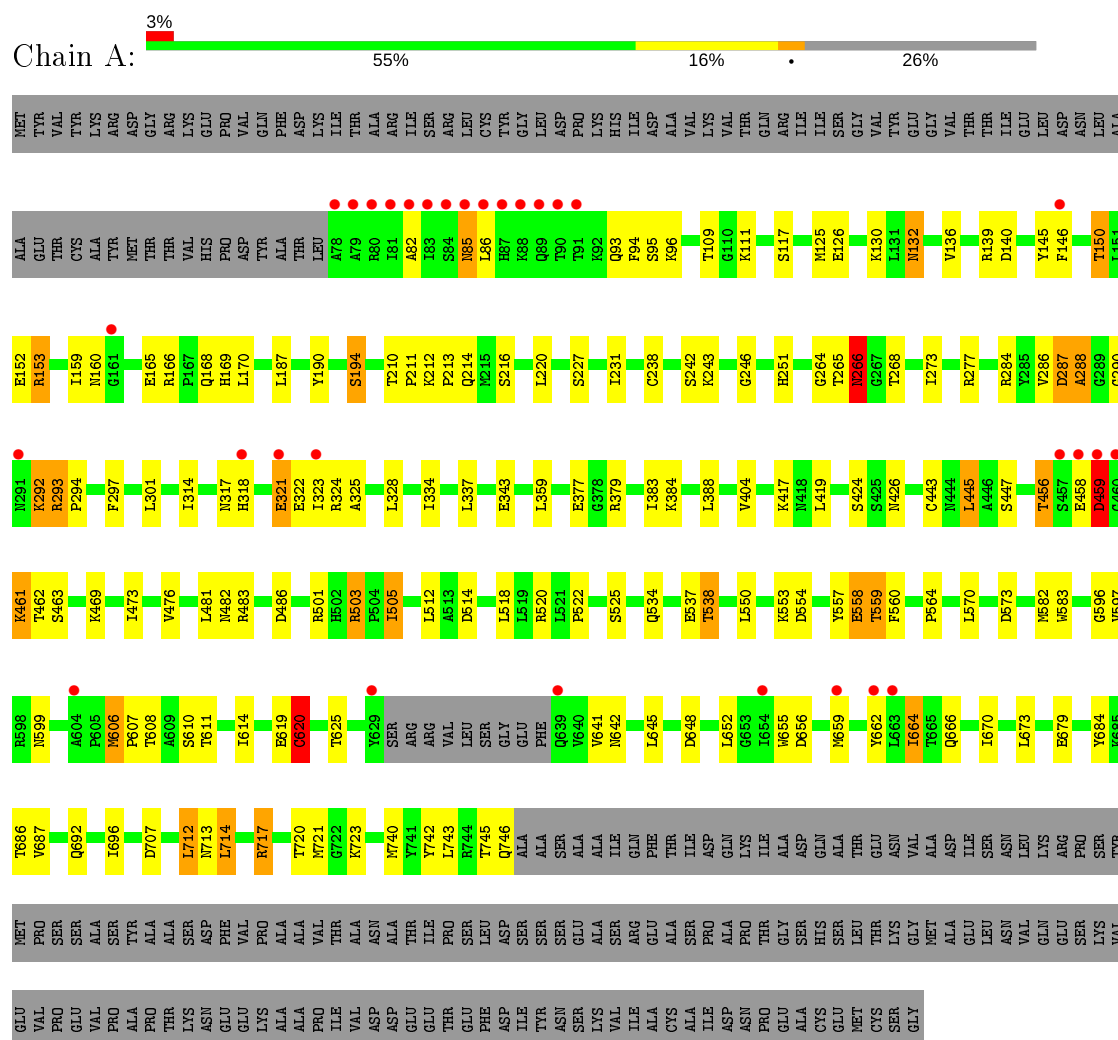
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	61	Total O 61 61	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 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, $\alpha$ , $\beta$ , $\gamma$	107.77 Å 118.09 Å 67.71 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.13 – 2.80 41.13 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.1 (41.13-2.80) 96.1 (41.13-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.49 (at 2.81 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.196 , 0.264 0.195 , 0.261	Depositor DCC
$R_{free}$ test set	2122 reflections (10.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	56.9	Xtriage
Anisotropy	0.241	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 34.6	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	0.94	EDS
Total number of atoms	5354	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.37% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	0.61	1/5354 (0.0%)	0.74	5/7255 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	620	CYS	CB-SG	-5.44	1.73	1.81

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	170	LEU	CA-CB-CG	6.79	130.92	115.30
1	A	620	CYS	CB-CA-C	-5.80	98.81	110.40
1	A	445	LEU	CA-CB-CG	5.68	128.37	115.30
1	A	503	ARG	NE-CZ-NH2	-5.21	117.69	120.30
1	A	712	LEU	CA-CB-CG	5.15	127.15	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	5234	0	5138	96	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	31	0	12	1	0
4	A	27	0	12	4	0
5	A	61	0	0	2	0
All	All	5354	0	5162	98	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 (98) 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:109:THR:CG2	1:A:111:LYS:HG2	1.99	0.93
1:A:557:TYR:HE1	1:A:559:THR:HG22	1.34	0.93
1:A:109:THR:HG22	1:A:111:LYS:HG2	1.55	0.88
1:A:717:ARG:HB2	5:A:934:HOH:O	1.73	0.87
1:A:557:TYR:CE1	1:A:559:THR:HG22	2.09	0.85
1:A:482:ASN:HD22	1:A:599:ASN:HD21	1.26	0.81
1:A:458:GLU:O	1:A:459:ASP:HB3	1.82	0.78
1:A:619:GLU:O	1:A:620:CYS:CB	2.33	0.77
1:A:481:LEU:HB3	1:A:505:ILE:HD12	1.66	0.77
1:A:153:ARG:HH11	1:A:153:ARG:HB2	1.50	0.76
1:A:619:GLU:O	1:A:620:CYS:HB2	1.83	0.76
1:A:109:THR:HG21	1:A:111:LYS:HG2	1.73	0.70
1:A:140:ASP:OD2	1:A:168:GLN:HG2	1.94	0.67
1:A:538:THR:HB	1:A:583:TRP:HE1	1.59	0.67
1:A:461:LYS:N	1:A:461:LYS:HE3	2.09	0.67
1:A:692:GLN:O	1:A:696:ILE:HD13	1.96	0.66
1:A:447:SER:HB3	1:A:606:MET:CE	2.26	0.66
4:A:891:ADP:H5'2	4:A:891:ADP:H8	1.61	0.65
1:A:287:ASP:HA	1:A:294:PRO:HA	1.80	0.62
1:A:538:THR:HB	1:A:583:TRP:NE1	2.15	0.62
1:A:159:ILE:HG23	1:A:160:ASN:H	1.65	0.62
1:A:159:ILE:HG23	1:A:160:ASN:N	2.14	0.62
1:A:534:GLN:O	1:A:538:THR:HG22	2.01	0.60
1:A:251:HIS:HB3	1:A:424:SER:HB3	1.84	0.59
1:A:288:ALA:O	1:A:292:LYS:HB2	2.02	0.59
1:A:277:ARG:NH2	1:A:322:GLU:HA	2.18	0.58
1:A:238:CYS:O	1:A:242:SER:HB2	2.03	0.57
1:A:745:THR:HG23	1:A:746:GLN:HG3	1.85	0.56
1:A:447:SER:HB3	1:A:606:MET:HE3	1.86	0.56
1:A:486:ASP:CG	1:A:503:ARG:HH22	2.10	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:ARG:HB2	1:A:169:HIS:ND1	2.22	0.55
1:A:447:SER:HB3	1:A:606:MET:HE1	1.89	0.54
1:A:655:TRP:HA	1:A:659:MET:HG3	1.89	0.54
1:A:277:ARG:NH2	1:A:321:GLU:O	2.41	0.53
1:A:456:THR:HA	1:A:463:SER:HA	1.90	0.52
1:A:220:LEU:HD21	1:A:426:ASN:HB3	1.91	0.52
1:A:286:VAL:O	1:A:286:VAL:HG12	2.08	0.52
1:A:220:LEU:CD2	1:A:426:ASN:HB3	2.40	0.52
1:A:662:TYR:CD1	1:A:673:LEU:HG	2.44	0.52
1:A:377:GLU:OE1	1:A:379:ARG:NH1	2.35	0.52
1:A:550:LEU:HD23	1:A:553:LYS:NZ	2.25	0.51
1:A:85:ASN:C	1:A:85:ASN:HD22	2.14	0.51
1:A:334:ILE:HD12	1:A:404:VAL:HG13	1.91	0.51
1:A:714:LEU:HD22	1:A:740:MET:HG3	1.93	0.51
1:A:251:HIS:HD2	5:A:894:HOH:O	1.93	0.50
1:A:95:SER:H	1:A:132:ASN:HD21	1.60	0.49
1:A:159:ILE:CG2	1:A:160:ASN:H	2.24	0.49
1:A:168:GLN:NE2	1:A:190:TYR:OH	2.43	0.49
1:A:560:PHE:CZ	1:A:596:GLY:HA2	2.48	0.48
1:A:277:ARG:HH21	1:A:322:GLU:HA	1.79	0.48
1:A:461:LYS:HE3	1:A:461:LYS:H	1.78	0.48
1:A:642:ASN:HB3	1:A:645:LEU:HB3	1.95	0.48
1:A:159:ILE:CG2	1:A:160:ASN:N	2.77	0.48
1:A:625:THR:HA	1:A:687:VAL:HG12	1.96	0.48
1:A:94:PHE:HD1	1:A:169:HIS:HD2	1.60	0.47
1:A:606:MET:HB2	1:A:607:PRO:CD	2.45	0.47
1:A:656:ASP:H	1:A:659:MET:HB2	1.79	0.47
1:A:662:TYR:CZ	1:A:666:GLN:HG3	2.50	0.47
1:A:570:LEU:O	1:A:573:ASP:HB2	2.14	0.47
1:A:662:TYR:CZ	1:A:666:GLN:CG	2.98	0.47
1:A:292:LYS:C	1:A:293:ARG:HG3	2.35	0.47
1:A:93:GLN:HG3	1:A:132:ASN:OD1	2.14	0.47
1:A:648:ASP:O	1:A:652:LEU:HD23	2.14	0.47
1:A:662:TYR:CD1	1:A:662:TYR:O	2.68	0.47
1:A:264:GLY:HA3	3:A:890:DGT:O2B	2.15	0.47
1:A:117:SER:HB3	1:A:211:PRO:HA	1.97	0.46
1:A:537:GLU:OE1	1:A:582:MET:HB2	2.16	0.46
1:A:419:LEU:HD21	1:A:559:THR:HG21	1.98	0.46
4:A:891:ADP:C8	4:A:891:ADP:H5'2	2.47	0.46
1:A:227:SER:O	1:A:231:ILE:HG13	2.16	0.45
1:A:611:THR:HA	1:A:614:ILE:HD12	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:THR:N	4:A:891:ADP:O2A	2.51	0.44
1:A:740:MET:HE1	1:A:743:LEU:HD23	2.00	0.44
1:A:417:LYS:HD2	1:A:564:PRO:HG3	1.98	0.44
1:A:501:ARG:HA	1:A:558:GLU:OE1	2.17	0.43
1:A:165:GLU:HG2	1:A:169:HIS:HB2	2.00	0.43
1:A:383:ILE:HA	1:A:383:ILE:HD12	1.86	0.43
1:A:212:LYS:HA	1:A:213:PRO:HD3	1.62	0.43
1:A:82:ALA:HA	1:A:85:ASN:OD1	2.19	0.42
1:A:550:LEU:HD23	1:A:553:LYS:HZ1	1.85	0.42
1:A:210:THR:HB	1:A:211:PRO:CD	2.50	0.42
1:A:740:MET:CE	1:A:743:LEU:HD23	2.49	0.42
1:A:318:HIS:O	1:A:324:ARG:NH1	2.53	0.42
1:A:210:THR:HB	1:A:211:PRO:HD2	2.02	0.41
1:A:713:ASN:HD22	1:A:742:TYR:H	1.68	0.41
1:A:146:PHE:O	1:A:150:THR:OG1	2.38	0.41
1:A:265:THR:O	1:A:266:ASN:C	2.59	0.41
1:A:419:LEU:HD21	1:A:559:THR:CG2	2.50	0.41
1:A:664:ILE:HG13	1:A:664:ILE:H	1.72	0.41
1:A:190:TYR:O	1:A:194:SER:OG	2.39	0.41
1:A:522:PRO:HG2	1:A:525:SER:HB3	2.02	0.41
1:A:670:ILE:HD11	1:A:684:TYR:HB2	2.02	0.41
1:A:608:THR:HA	4:A:891:ADP:O2A	2.21	0.41
1:A:136:VAL:HB	1:A:139:ARG:HD2	2.03	0.40
1:A:297:PHE:HB2	1:A:328:LEU:HD22	2.01	0.40
1:A:266:ASN:HA	1:A:266:ASN:HD22	1.73	0.40
1:A:287:ASP:O	1:A:288:ALA:C	2.60	0.40
1:A:85:ASN:ND2	1:A:86:LEU:N	2.70	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	656/888 (74%)	602 (92%)	44 (7%)	10 (2%)	10	33

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	459	ASP
1	A	287	ASP
1	A	288	ALA
1	A	290	GLY
1	A	145	TYR
1	A	246	GLY
1	A	266	ASN
1	A	620	CYS
1	A	325	ALA
1	A	717	ARG

### 5.3.2 Protein sidechains ⓘ

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	562/760 (74%)	499 (89%)	63 (11%)	6	18

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	96	LYS
1	A	125	MET
1	A	126	GLU
1	A	130	LYS
1	A	132	ASN
1	A	150	THR
1	A	152	GLU
1	A	153	ARG
1	A	187	LEU
1	A	194	SER

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Mol	Chain	Res	Type
1	A	214	GLN
1	A	216	SER
1	A	243	LYS
1	A	266	ASN
1	A	268	THR
1	A	273	ILE
1	A	284	ARG
1	A	292	LYS
1	A	293	ARG
1	A	301	LEU
1	A	314	ILE
1	A	317	ASN
1	A	321	GLU
1	A	323	ILE
1	A	337	LEU
1	A	343	GLU
1	A	359	LEU
1	A	384	LYS
1	A	388	LEU
1	A	443	CYS
1	A	445	LEU
1	A	456	THR
1	A	459	ASP
1	A	461	LYS
1	A	462	THR
1	A	469	LYS
1	A	473	ILE
1	A	476	VAL
1	A	483	ARG
1	A	505	ILE
1	A	512	LEU
1	A	514	ASP
1	A	518	LEU
1	A	520	ARG
1	A	538	THR
1	A	554	ASP
1	A	558	GLU
1	A	559	THR
1	A	597	VAL
1	A	606	MET
1	A	610	SER
1	A	620	CYS

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Mol	Chain	Res	Type
1	A	641	VAL
1	A	664	ILE
1	A	679	GLU
1	A	686	THR
1	A	707	ASP
1	A	712	LEU
1	A	714	LEU
1	A	720	THR
1	A	721	MET
1	A	723	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	168	GLN
1	A	214	GLN
1	A	251	HIS
1	A	266	ASN
1	A	270	ASN
1	A	482	ASN
1	A	613	GLN
1	A	675	ASN
1	A	692	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 ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	890	2	26,33,33	1.28	2 (7%)	32,52,52	1.91	10 (31%)
4	ADP	A	891	-	24,29,29	1.11	2 (8%)	29,45,45	1.34	3 (10%)

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	890	2	-	4/18/34/34	0/3/3/3
4	ADP	A	891	-	-	5/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	890	DGT	C6-C5	4.94	1.49	1.41
4	A	891	ADP	C5-C4	2.88	1.48	1.40
3	A	890	DGT	C5-C4	2.60	1.47	1.40
4	A	891	ADP	C2-N3	2.27	1.35	1.32

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	890	DGT	C2-N3-C4	4.53	120.54	115.36
4	A	891	ADP	N3-C2-N1	-3.86	122.65	128.68
3	A	890	DGT	C5-C6-N1	-3.80	118.23	123.43
3	A	890	DGT	C6-N1-C2	3.65	121.73	115.93
3	A	890	DGT	C6-C5-C4	-3.48	117.47	120.80
3	A	890	DGT	C2'-C1'-N9	-2.90	107.57	114.27
4	A	891	ADP	C3'-C2'-C1'	2.90	105.34	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	890	DGT	N3-C2-N1	-2.84	123.43	127.22
3	A	890	DGT	C4-C5-N7	-2.62	106.67	109.40
3	A	890	DGT	PA-O3A-PB	-2.49	124.29	132.83
4	A	891	ADP	C4-C5-N7	-2.32	106.99	109.40
3	A	890	DGT	PB-O3B-PG	-2.25	125.10	132.83
3	A	890	DGT	O3B-PG-O3G	-2.03	99.95	111.19

There are no chirality outliers.

All (9) torsion outliers are listed below:

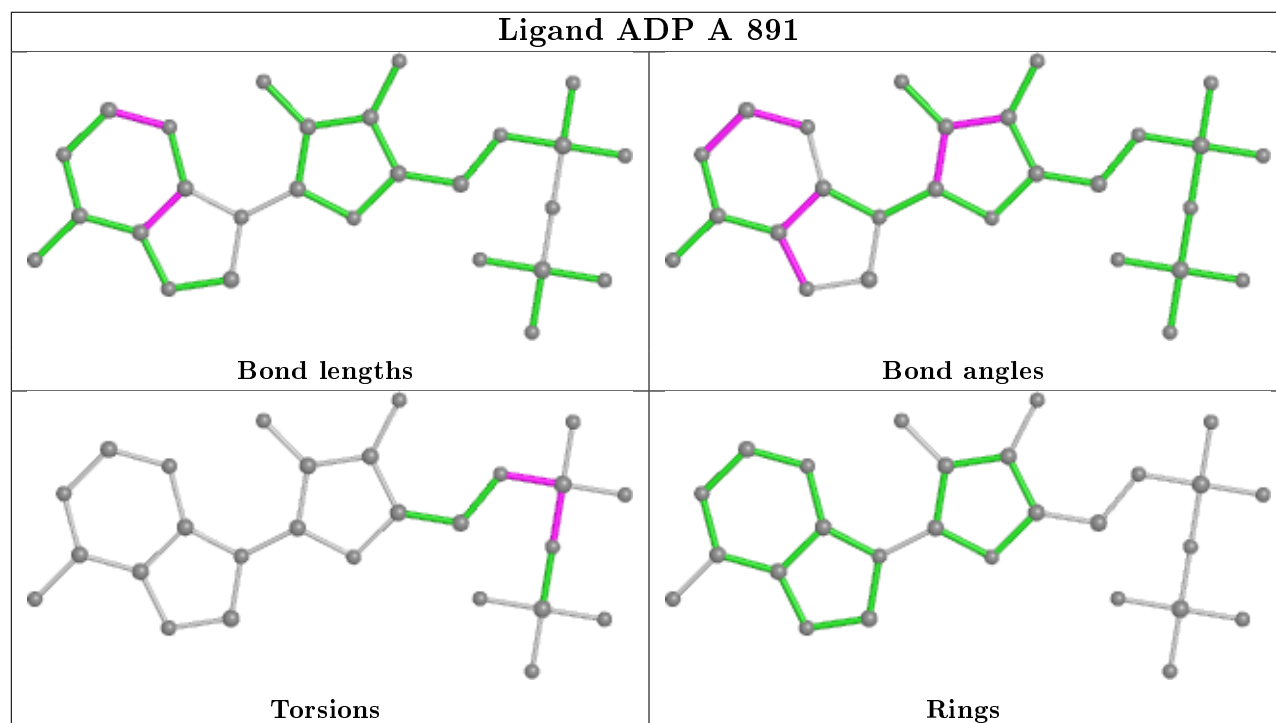
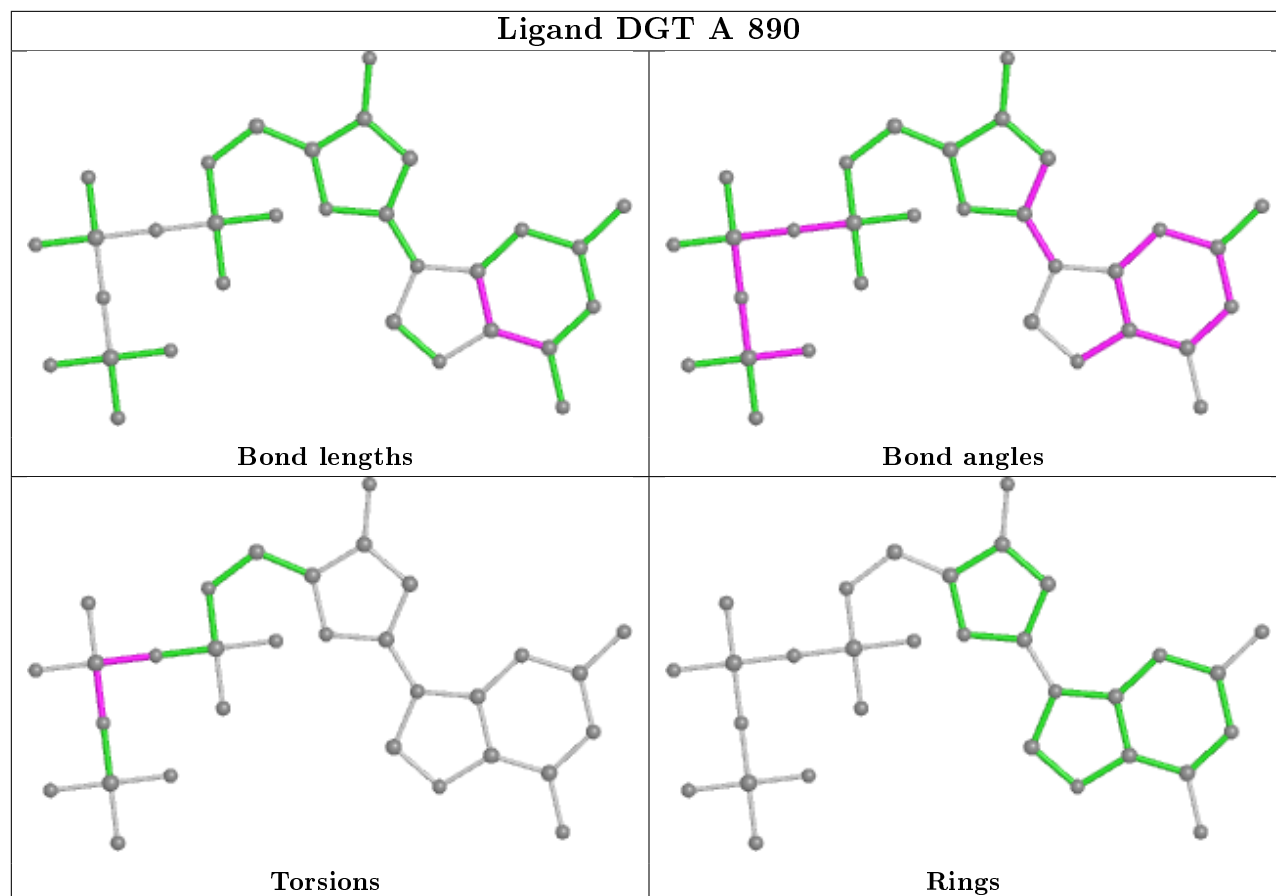
Mol	Chain	Res	Type	Atoms
4	A	891	ADP	C5'-O5'-PA-O1A
3	A	890	DGT	PG-O3B-PB-O2B
4	A	891	ADP	C5'-O5'-PA-O3A
4	A	891	ADP	PB-O3A-PA-O2A
4	A	891	ADP	C5'-O5'-PA-O2A
3	A	890	DGT	PG-O3B-PB-O1B
3	A	890	DGT	PA-O3A-PB-O1B
3	A	890	DGT	PA-O3A-PB-O2B
4	A	891	ADP	PB-O3A-PA-O1A

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	890	DGT	1	0
4	A	891	ADP	4	0

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	660/888 (74%)	-0.04	31 (4%) 31 22	35, 51, 87, 118	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	81	ILE	6.2
1	A	82	ALA	5.3
1	A	78	ALA	5.2
1	A	87	HIS	4.5
1	A	659	MET	4.1
1	A	662	TYR	4.1
1	A	79	ALA	3.7
1	A	85	ASN	3.7
1	A	291	ASN	3.6
1	A	86	LEU	3.5
1	A	460	GLY	3.3
1	A	83	ILE	3.2
1	A	89	GLN	2.9
1	A	459	ASP	2.7
1	A	663	LEU	2.7
1	A	90	THR	2.6
1	A	161	GLY	2.6
1	A	323	ILE	2.6
1	A	88	LYS	2.6
1	A	457	SER	2.5
1	A	84	SER	2.5
1	A	639	GLN	2.5
1	A	146	PHE	2.4
1	A	80	ARG	2.3
1	A	91	THR	2.2
1	A	604	ALA	2.2
1	A	318	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	629	TYR	2.2
1	A	654	ILE	2.1
1	A	321	GLU	2.1
1	A	458	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](#)

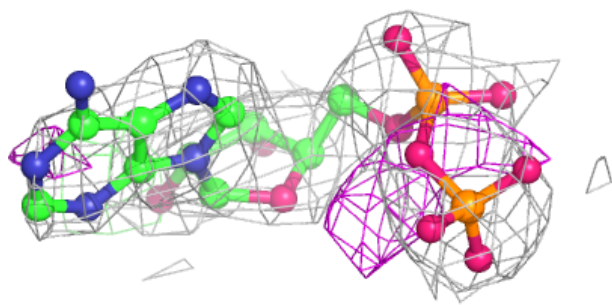
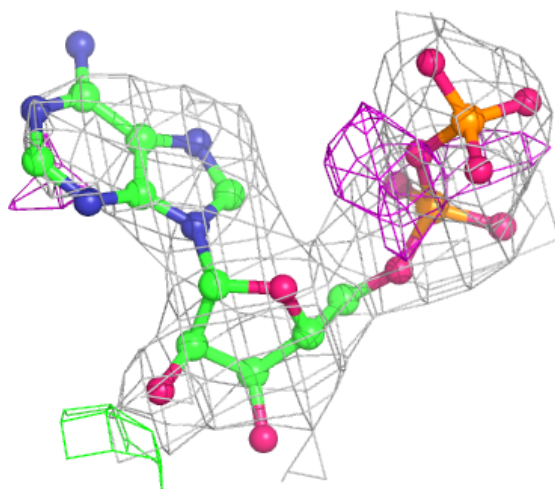
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

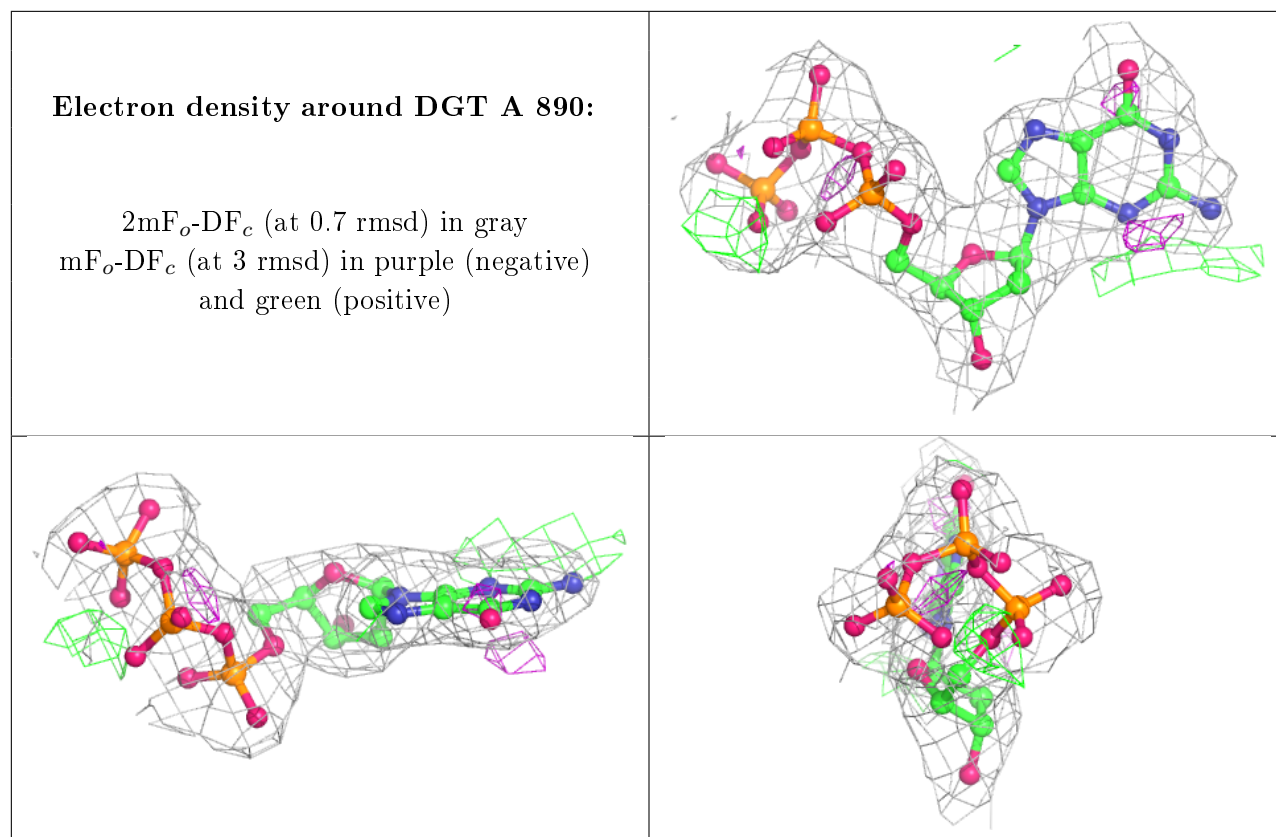
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MG	A	889	1/1	0.84	0.22	69,69,69,69	0
4	ADP	A	891	27/27	0.91	0.21	78,83,84,84	0
3	DGT	A	890	31/31	0.95	0.12	44,49,60,62	0

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.

**Electron density around ADP A 891:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.