



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 08:09 pm BST

PDB ID : 3TB9
Title : Structure of Yeast Ribonucleotide Reductase 1 Q288A with AMPPNP and CDP
Authors : Ahmad, M.F.; Kaushal, P.S.; Wan, Q.; Wijeratna, S.R.; Huang, M.; Dealwis, C.D.
Deposited on : 2011-08-05
Resolution : 2.53 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 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

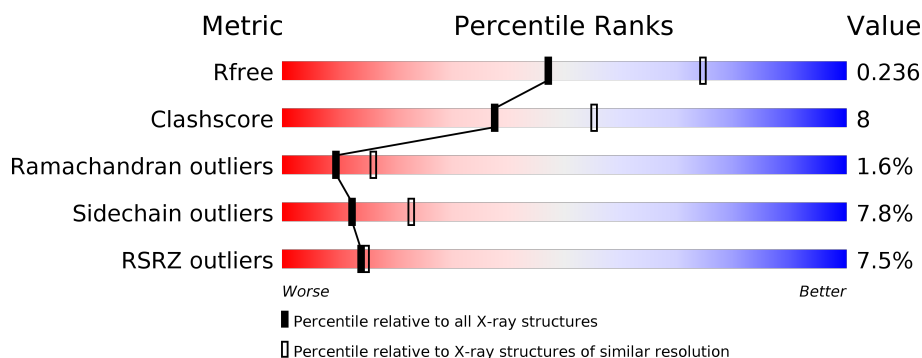
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.53 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	5743 (2.54-2.50)
Clashscore	141614	6463 (2.54-2.50)
Ramachandran outliers	138981	6335 (2.54-2.50)
Sidechain outliers	138945	6337 (2.54-2.50)
RSRZ outliers	127900	5630 (2.54-2.50)

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 ≥ 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>5%</div> <div>59%</div> <div>11%</div> <div>•</div> <div>28%</div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5278 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.

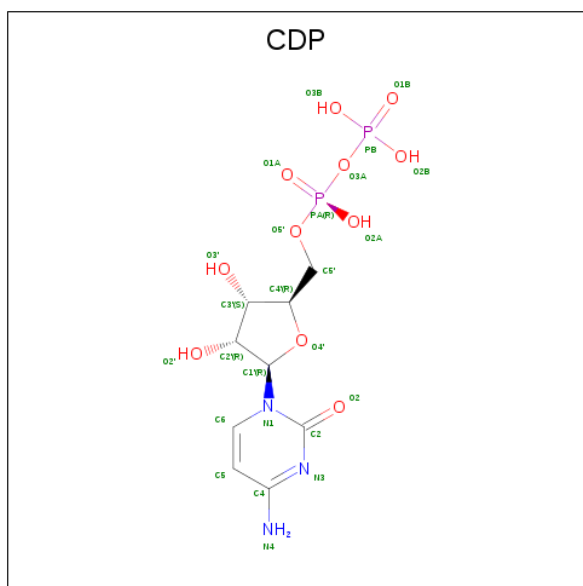
- Molecule 1 is a protein called Ribonucleoside-diphosphate reductase large chain 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	643	5107	3253	864	959	31	0	0	0

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 CYTIDINE-5'-DIPHOSPHATE (three-letter code: CDP) (formula: $C_9H_{15}N_3O_{11}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	25	9	3	11	2	0	0

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

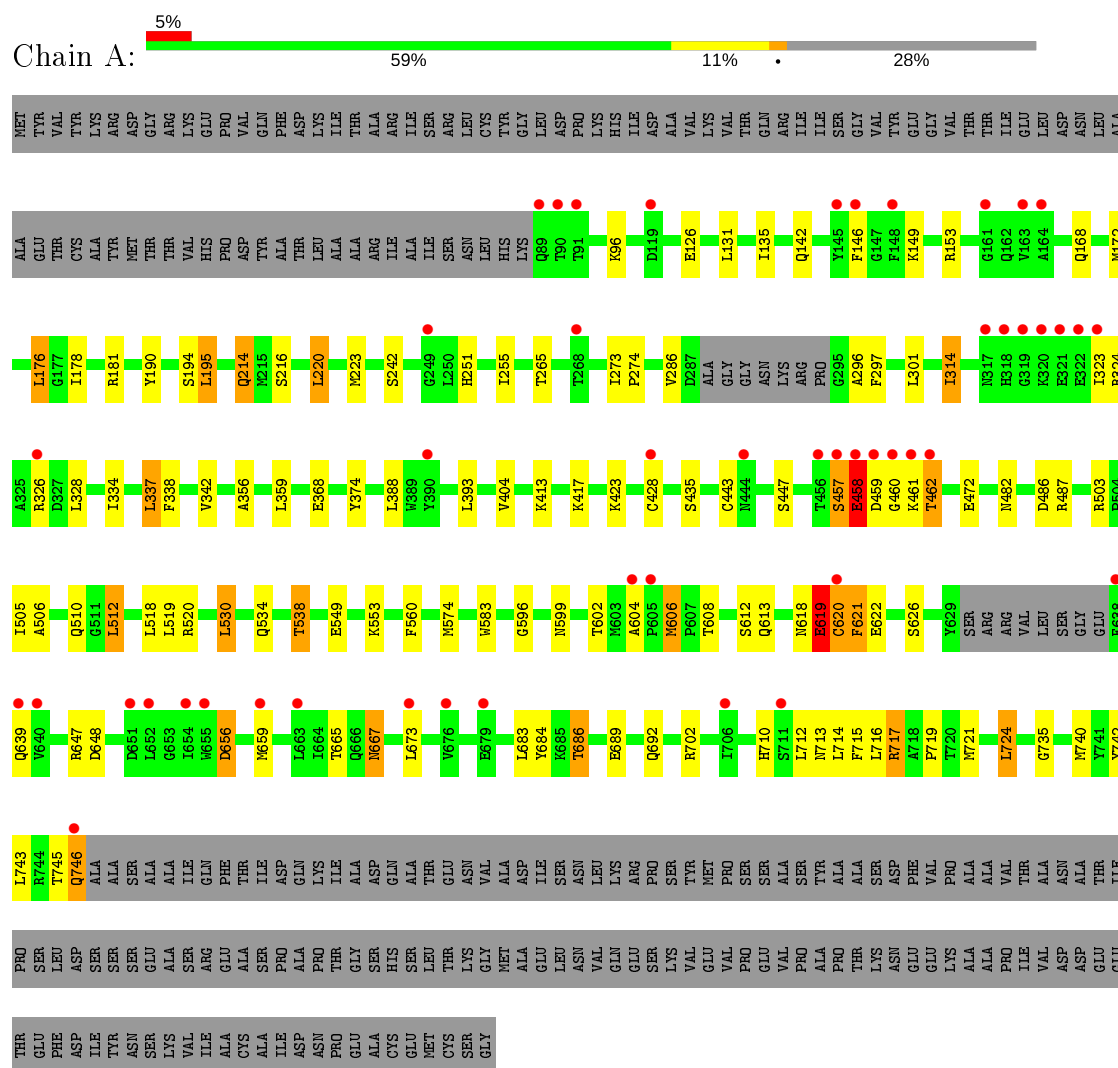
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	114	Total O 114 114	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, α , β , γ	107.89 Å 116.96 Å 64.33 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.48 – 2.53 43.27 – 2.53	Depositor EDS
% Data completeness (in resolution range)	99.9 (43.48-2.53) 99.9 (43.27-2.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.54 (at 2.54 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.199 , 0.237 0.199 , 0.236	Depositor DCC
R_{free} test set	2793 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	39.3	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 41.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5278	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% 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: CDP, MG, ANP

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	0.60	0/5223	0.70	1/7075 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	220	LEU	CA-CB-CG	5.21	127.28	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	5107	0	5013	78	0
2	A	25	0	12	1	0
3	A	31	0	13	0	0
4	A	1	0	0	0	0
5	A	114	0	0	1	0
All	All	5278	0	5038	78	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 8.

All (78) 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:447:SER:HB3	1:A:606:MET:CE	1.87	1.05
1:A:447:SER:HB3	1:A:606:MET:HE1	1.50	0.92
1:A:620:CYS:O	1:A:620:CYS:SG	2.33	0.85
1:A:608:THR:HG22	1:A:612:SER:HB3	1.65	0.78
1:A:447:SER:HB3	1:A:606:MET:HE3	1.67	0.77
1:A:417:LYS:HE3	1:A:574:MET:HE1	1.69	0.74
1:A:417:LYS:HE3	1:A:574:MET:CE	2.21	0.70
1:A:608:THR:CG2	1:A:612:SER:HB3	2.24	0.67
1:A:486:ASP:OD2	1:A:503:ARG:NH2	2.29	0.65
1:A:413:LYS:NZ	1:A:735:GLY:O	2.31	0.64
1:A:447:SER:CB	1:A:606:MET:HE1	2.25	0.64
1:A:538:THR:HB	1:A:583:TRP:NE1	2.13	0.64
1:A:745:THR:O	1:A:746:GLN:HB2	1.97	0.64
1:A:482:ASN:HD21	1:A:503:ARG:HH11	1.47	0.62
1:A:534:GLN:O	1:A:538:THR:HG23	2.00	0.61
1:A:457:SER:O	1:A:458:GLU:HB2	2.00	0.61
1:A:486:ASP:CG	1:A:503:ARG:HH22	2.03	0.61
1:A:620:CYS:O	1:A:622:GLU:N	2.34	0.61
1:A:618:ASN:O	1:A:619:GLU:CB	2.46	0.61
1:A:482:ASN:HD22	1:A:599:ASN:HD21	1.48	0.61
1:A:482:ASN:ND2	1:A:503:ARG:HH11	1.99	0.60
1:A:608:THR:O	1:A:608:THR:HG22	2.02	0.59
1:A:126:GLU:OE1	1:A:181:ARG:NH1	2.34	0.59
1:A:482:ASN:ND2	1:A:503:ARG:NH1	2.51	0.58
1:A:560:PHE:CZ	1:A:596:GLY:HA2	2.38	0.58
1:A:297:PHE:HB2	1:A:328:LEU:HD22	1.85	0.58
1:A:520:ARG:HH22	1:A:648:ASP:CG	2.07	0.58
1:A:618:ASN:O	1:A:619:GLU:HB2	2.04	0.57
1:A:168:GLN:NE2	1:A:190:TYR:OH	2.34	0.57
1:A:619:GLU:O	1:A:620:CYS:HB3	2.03	0.56
1:A:506:ALA:HB1	1:A:604:ALA:HB3	1.87	0.55
1:A:214:GLN:HE22	1:A:216:SER:HB2	1.71	0.55
1:A:428:CYS:SG	2:A:889:CDP:H3'	2.48	0.53
1:A:512:LEU:HD12	1:A:621:PHE:HA	1.89	0.53
1:A:168:GLN:HE22	1:A:194:SER:HB2	1.73	0.53
1:A:393:LEU:HD22	1:A:724:LEU:HD13	1.91	0.53
1:A:618:ASN:O	1:A:619:GLU:CD	2.48	0.51
1:A:286:VAL:HG13	1:A:286:VAL:O	2.10	0.51
1:A:724:LEU:HD21	1:A:740:MET:HE1	1.93	0.51
1:A:549:GLU:O	1:A:553:LYS:HG3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:LEU:O	1:A:534:GLN:HG3	2.11	0.50
1:A:692:GLN:NE2	1:A:715:PHE:H	2.09	0.50
1:A:510:GLN:HB3	1:A:608:THR:HG21	1.94	0.49
1:A:251:HIS:HE1	1:A:435:SER:OG	1.96	0.49
1:A:608:THR:HB	1:A:619:GLU:O	2.13	0.49
1:A:334:ILE:HD12	1:A:404:VAL:HG13	1.94	0.48
1:A:713:ASN:ND2	1:A:742:TYR:HB2	2.29	0.48
1:A:178:ILE:O	1:A:487:ARG:HD3	2.14	0.48
1:A:482:ASN:HD21	1:A:503:ARG:NH1	2.08	0.47
1:A:702:ARG:HH11	1:A:710:HIS:HE1	1.62	0.47
1:A:142:GLN:HE22	1:A:195:LEU:HD12	1.79	0.46
1:A:656:ASP:H	1:A:659:MET:HB2	1.80	0.46
1:A:538:THR:HB	1:A:583:TRP:HE1	1.78	0.46
1:A:608:THR:HG22	1:A:612:SER:CB	2.41	0.46
1:A:534:GLN:O	1:A:538:THR:CG2	2.63	0.45
1:A:510:GLN:OE1	1:A:612:SER:HA	2.16	0.45
1:A:338:PHE:O	1:A:342:VAL:HG23	2.16	0.45
1:A:457:SER:O	1:A:458:GLU:CB	2.65	0.45
1:A:460:GLY:O	1:A:462:THR:N	2.48	0.44
1:A:146:PHE:HE1	1:A:613:GLN:HE21	1.65	0.44
1:A:620:CYS:O	1:A:621:PHE:CG	2.71	0.44
1:A:683:LEU:HD23	1:A:684:TYR:CZ	2.51	0.44
1:A:273:ILE:HD12	1:A:314:ILE:HD11	2.00	0.44
1:A:519:LEU:O	1:A:520:ARG:HB2	2.18	0.43
1:A:172:MET:O	1:A:176:LEU:HD22	2.18	0.43
1:A:618:ASN:O	1:A:619:GLU:OE2	2.37	0.43
1:A:135:ILE:HG23	1:A:168:GLN:HB3	2.01	0.43
1:A:273:ILE:HB	1:A:274:PRO:HD3	2.01	0.43
1:A:337:LEU:HG	1:A:368:GLU:HG2	2.00	0.43
1:A:146:PHE:CE1	1:A:613:GLN:NE2	2.86	0.43
1:A:273:ILE:HG21	1:A:323:ILE:HA	2.01	0.42
1:A:505:ILE:HG13	1:A:602:THR:HA	2.01	0.41
1:A:686:THR:HB	1:A:689:GLU:OE1	2.20	0.41
1:A:356:ALA:HB1	1:A:374:TYR:CD1	2.55	0.41
1:A:487:ARG:HD2	5:A:997:HOH:O	2.20	0.41
1:A:717:ARG:O	1:A:719:PRO:HD3	2.20	0.41
1:A:223:MET:HG2	1:A:255:ILE:HD11	2.01	0.41
1:A:146:PHE:CZ	1:A:613:GLN:NE2	2.89	0.41

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	637/888 (72%)	613 (96%)	14 (2%)	10 (2%)	9	16

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	458	GLU
1	A	461	LYS
1	A	620	CYS
1	A	619	GLU
1	A	621	PHE
1	A	717	ARG
1	A	296	ALA
1	A	457	SER
1	A	639	GLN
1	A	667	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	550/760 (72%)	507 (92%)	43 (8%)	12	23

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	96	LYS

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Mol	Chain	Res	Type
1	A	131	LEU
1	A	149	LYS
1	A	153	ARG
1	A	176	LEU
1	A	195	LEU
1	A	214	GLN
1	A	220	LEU
1	A	242	SER
1	A	265	THR
1	A	301	LEU
1	A	314	ILE
1	A	324	ARG
1	A	326	ARG
1	A	337	LEU
1	A	359	LEU
1	A	388	LEU
1	A	423	LYS
1	A	443	CYS
1	A	458	GLU
1	A	459	ASP
1	A	462	THR
1	A	472	GLU
1	A	512	LEU
1	A	518	LEU
1	A	530	LEU
1	A	538	THR
1	A	606	MET
1	A	619	GLU
1	A	626	SER
1	A	647	ARG
1	A	656	ASP
1	A	665	THR
1	A	667	ASN
1	A	673	LEU
1	A	686	THR
1	A	712	LEU
1	A	714	LEU
1	A	716	LEU
1	A	721	MET
1	A	724	LEU
1	A	743	LEU
1	A	746	GLN

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	93	GLN
1	A	142	GLN
1	A	168	GLN
1	A	214	GLN
1	A	251	HIS
1	A	444	ASN
1	A	482	ASN
1	A	666	GLN
1	A	692	GLN
1	A	710	HIS
1	A	713	ASN
1	A	746	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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
2	CDP	A	889	-	21,26,26	0.76	1 (4%)	28,40,40	1.37	2 (7%)
3	ANP	A	890	4	29,33,33	1.98	6 (20%)	31,52,52	1.89	7 (22%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CDP	A	889	-	-	1/14/32/32	0/2/2/2
3	ANP	A	890	4	-	3/14/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	890	ANP	PB-N3B	4.93	1.76	1.63
3	A	890	ANP	PG-N3B	4.64	1.75	1.63
3	A	890	ANP	PB-O1B	4.24	1.52	1.46
3	A	890	ANP	PG-O1G	3.41	1.51	1.46
3	A	890	ANP	PB-O3A	2.86	1.62	1.59
3	A	890	ANP	C5-C4	2.68	1.48	1.40
2	A	889	CDP	O4'-C1'	2.53	1.44	1.41

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	889	CDP	C2-N3-C4	5.01	121.42	116.34
3	A	890	ANP	O2B-PB-O1B	4.58	119.52	109.92
3	A	890	ANP	O1G-PG-N3B	-4.29	105.45	111.77
3	A	890	ANP	N3-C2-N1	-4.16	122.17	128.68
3	A	890	ANP	O3G-PG-O2G	3.59	117.21	107.64
3	A	890	ANP	O1B-PB-N3B	-2.80	107.64	111.77
3	A	890	ANP	C2-N1-C6	2.68	123.34	118.75
2	A	889	CDP	N4-C4-N3	2.61	120.61	116.49
3	A	890	ANP	C3'-C2'-C1'	2.21	104.31	100.98

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	889	CDP	PA-O3A-PB-O3B

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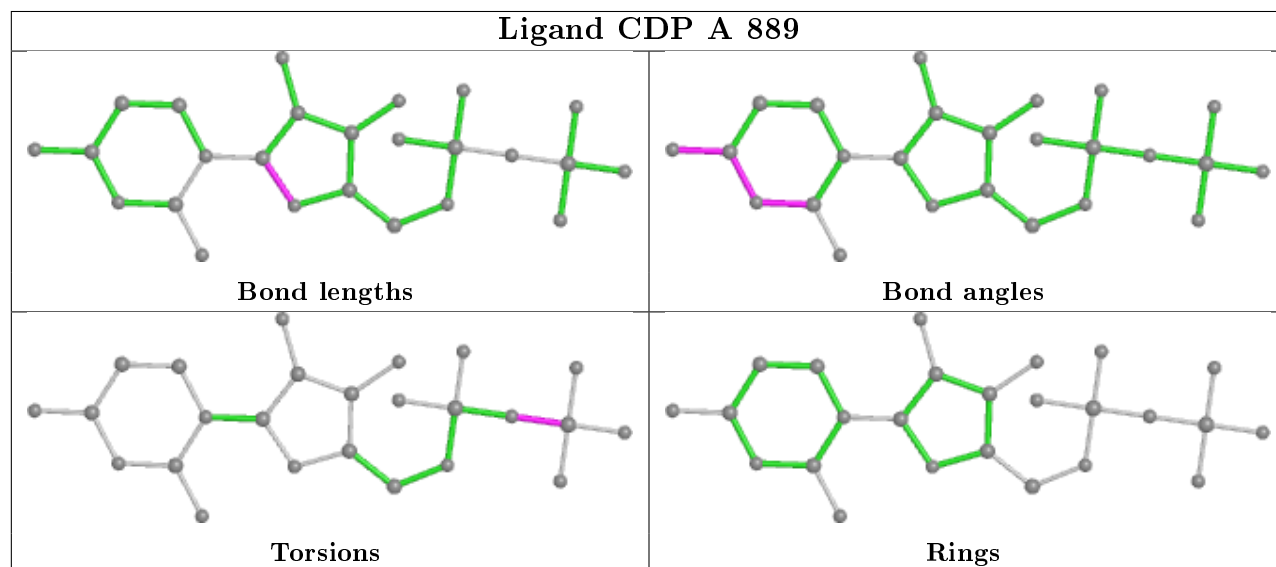
Mol	Chain	Res	Type	Atoms
3	A	890	ANP	PG-N3B-PB-O3A
3	A	890	ANP	PA-O3A-PB-O1B
3	A	890	ANP	PA-O3A-PB-O2B

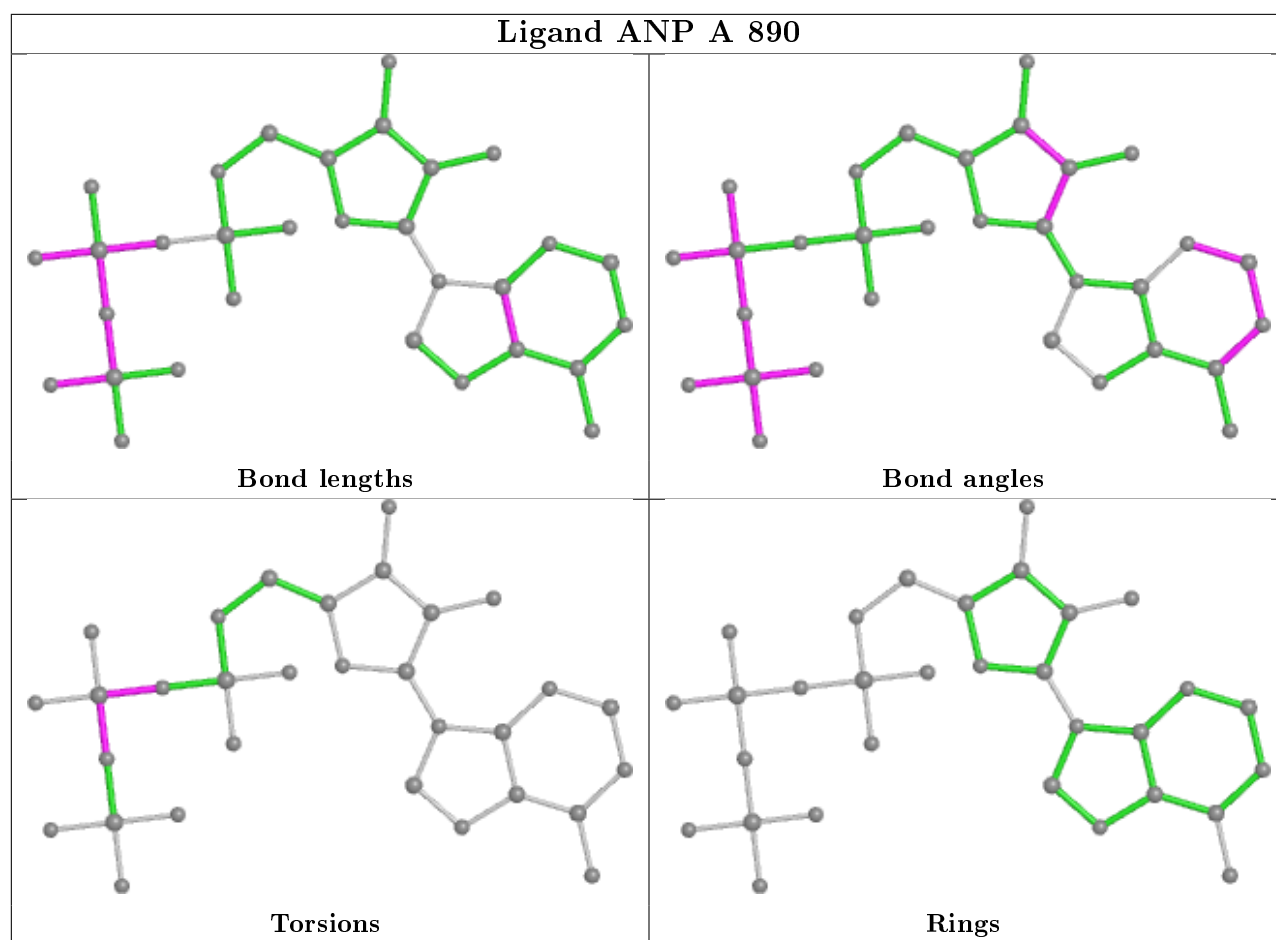
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	889	CDP	1	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 [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	643/888 (72%)	0.35	48 (7%) 14 15	22, 37, 64, 78	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	638	PHE	7.3
1	A	318	HIS	5.6
1	A	457	SER	4.7
1	A	91	THR	4.4
1	A	654	ILE	4.4
1	A	319	GLY	4.4
1	A	321	GLU	4.4
1	A	639	GLN	4.2
1	A	323	ILE	4.1
1	A	460	GLY	4.0
1	A	163	VAL	3.9
1	A	317	ASN	3.9
1	A	459	ASP	3.6
1	A	322	GLU	3.6
1	A	390	TYR	3.4
1	A	462	THR	3.4
1	A	145	TYR	3.4
1	A	620	CYS	3.4
1	A	663	LEU	3.2
1	A	652	LEU	3.2
1	A	461	LYS	3.1
1	A	89	GLN	3.0
1	A	746	GLN	3.0
1	A	659	MET	2.9
1	A	119	ASP	2.8
1	A	456	THR	2.7
1	A	320	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	640	VAL	2.5
1	A	326	ARG	2.5
1	A	655	TRP	2.5
1	A	90	THR	2.5
1	A	161	GLY	2.5
1	A	428	CYS	2.4
1	A	605	PRO	2.4
1	A	604	ALA	2.3
1	A	458	GLU	2.3
1	A	148	PHE	2.2
1	A	676	VAL	2.2
1	A	651	ASP	2.2
1	A	711	SER	2.2
1	A	146	PHE	2.1
1	A	706	ILE	2.1
1	A	679	GLU	2.1
1	A	249	GLY	2.1
1	A	164	ALA	2.0
1	A	673	LEU	2.0
1	A	268	THR	2.0
1	A	444	ASN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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.

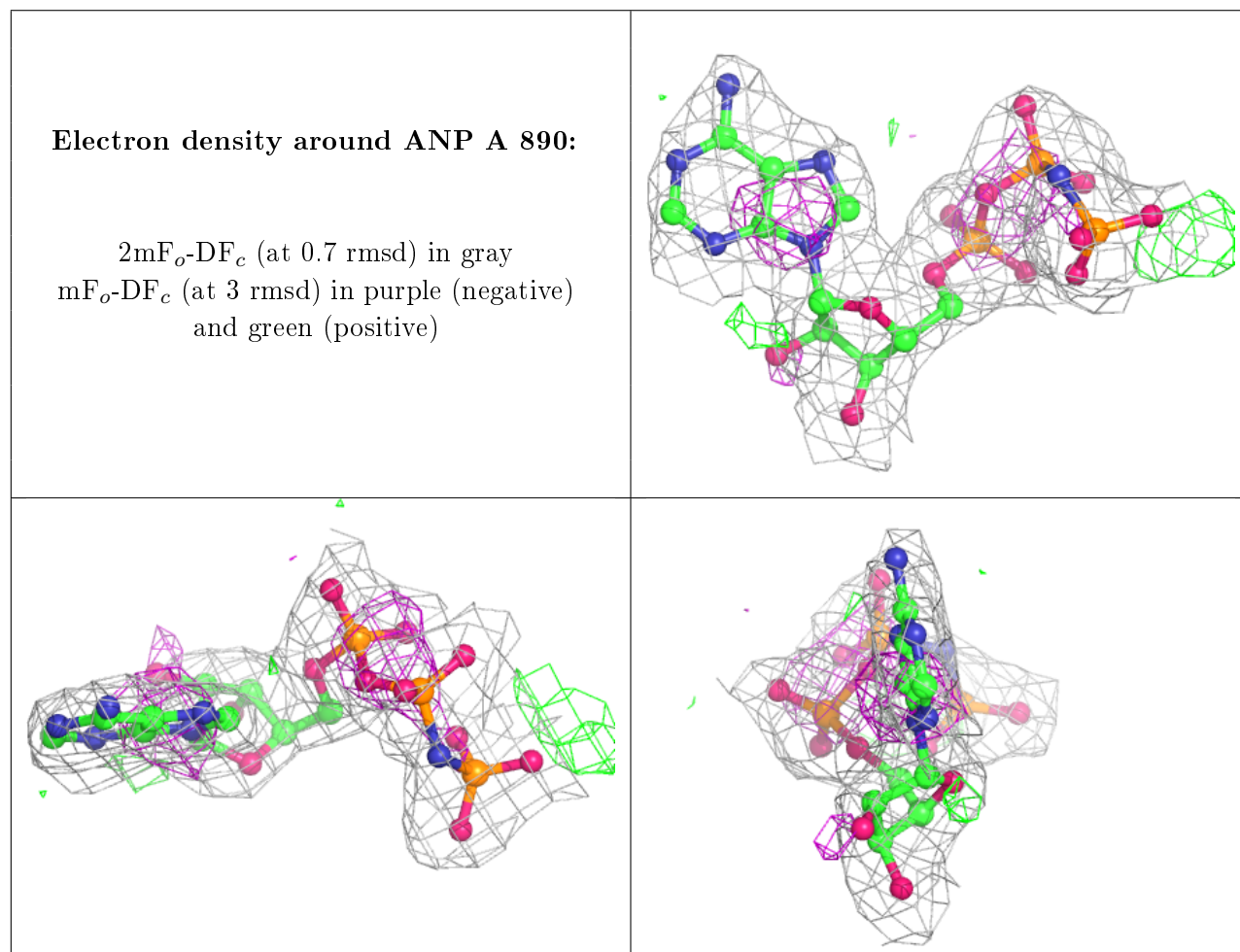
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	ANP	A	890	31/31	0.90	0.18	43,45,50,51	0
2	CDP	A	889	25/25	0.93	0.15	42,47,55,56	0

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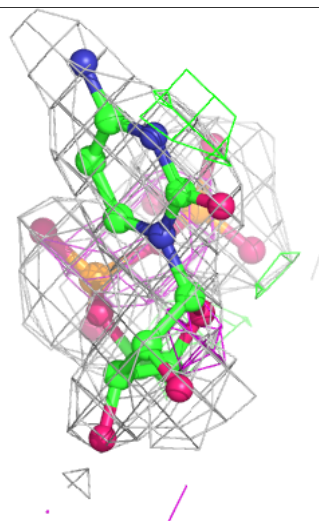
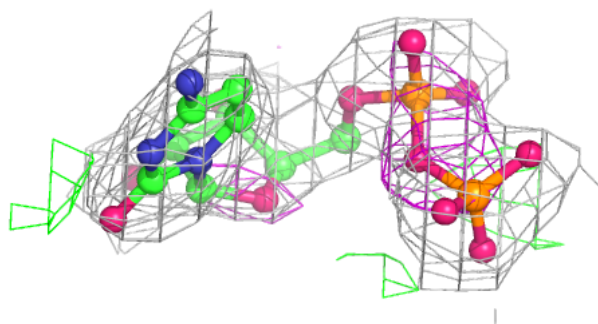
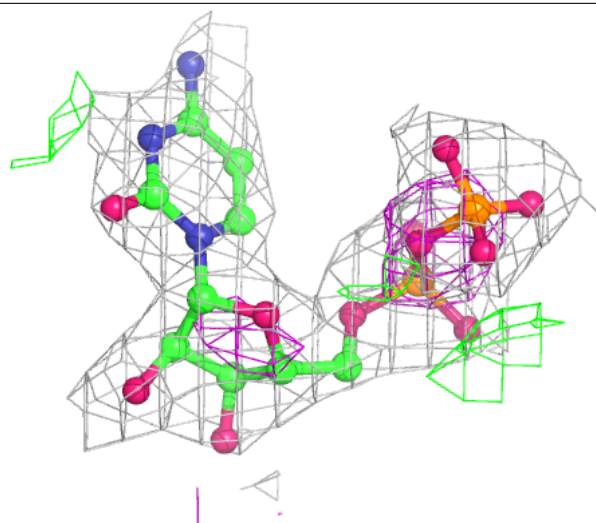
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MG	A	891	1/1	0.96	0.15	57,57,57,57	0

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 CDP A 889:

$2mF_o-DF_c$ (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.