



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 26, 2014 – 02:58 PM GMT

PDB ID : 2CVV  
Title : Structures of Yeast Ribonucleotide Reductase I  
Authors : Xu, H.; Faber, C.; Uchiki, T.; Fairman, J.W.; Racca, J.; Dealwis, C.  
Deposited on : 2005-06-14  
Resolution : 2.90 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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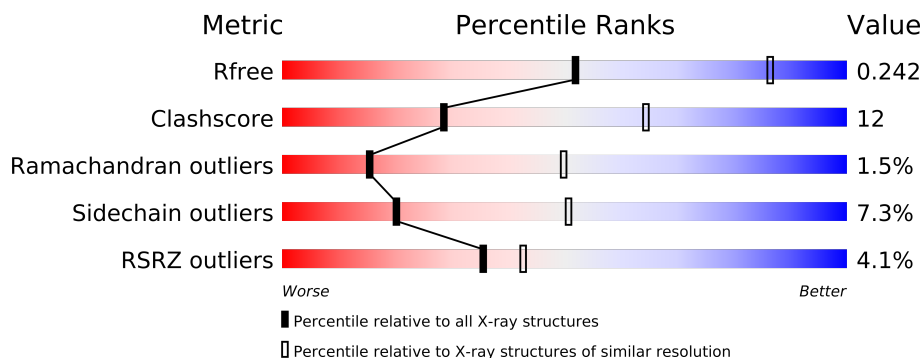
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

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))
$R_{free}$	66092	1053 (2.90-2.90)
Clashscore	79885	1326 (2.90-2.90)
Ramachandran outliers	78287	1290 (2.90-2.90)
Sidechain outliers	78261	1292 (2.90-2.90)
RSRZ outliers	66119	1054 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	888	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	UDP	A	1002	-	X

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 5403 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

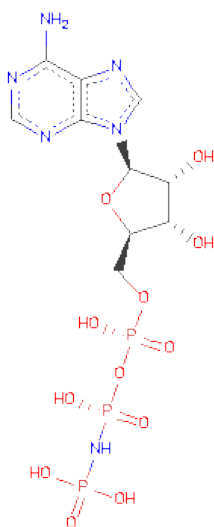
- Molecule 1 is a protein called Ribonucleoside-diphosphatereductase large chain 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	651	Total	C	N	O	S	0	0	0
			5208	3317	883	977	31			

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

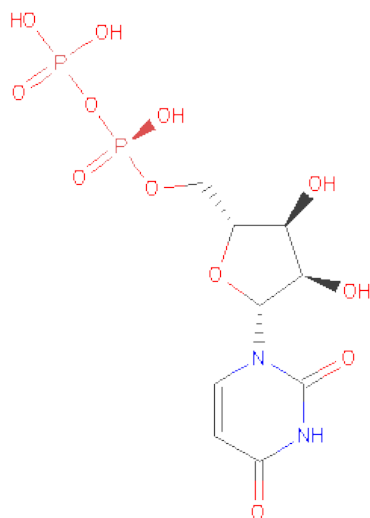
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PHOSPHOAMINOPHOSPHONICACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>12</sub>P<sub>3</sub>).



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

- Molecule 4 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula:  $C_9H_{14}N_2O_{12}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	138	Total	O	0	0
			138	138		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.87Å 117.59Å 64.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.90 25.99 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.0 (50.00-2.90) 97.8 (25.99-2.60)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	0.13	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.49 (at 2.60Å)	Xtriage
Refinement program	REFMAC 5.2.0007	Depositor
R, $R_{free}$	0.177 , 0.245 0.178 , 0.242	Depositor DCC
$R_{free}$ test set	1874 reflections (11.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.2	Xtriage
Anisotropy	0.688	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 21.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 25560 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5403	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.32% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.65	0/5329	0.85	18/7214 (0.2%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	100	ASP	CB-CG-OD2	7.18	124.76	118.30
1	A	310	ASP	CB-CG-OD2	6.84	124.46	118.30
1	A	233	ASP	CB-CG-OD2	6.66	124.30	118.30
1	A	182	ASP	CB-CG-OD2	6.53	124.18	118.30
1	A	682	ASP	CB-CG-OD2	6.06	123.75	118.30
1	A	138	ASP	CB-CG-OD2	5.99	123.69	118.30
1	A	140	ASP	CB-CG-OD2	5.94	123.65	118.30
1	A	226	ASP	CB-CG-OD2	5.70	123.43	118.30
1	A	586	ASP	CB-CG-OD2	5.61	123.35	118.30
1	A	459	ASP	CB-CG-OD2	5.54	123.29	118.30
1	A	287	ASP	CB-CG-OD2	5.46	123.21	118.30
1	A	438	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	503	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	A	327	ASP	CB-CG-OD2	5.09	122.88	118.30
1	A	701	ASP	CB-CG-OD2	5.08	122.88	118.30
1	A	129	ASP	CB-CG-OD2	5.06	122.85	118.30
1	A	365	ASP	CB-CG-OD2	5.05	122.84	118.30
1	A	361	ASP	CB-CG-OD2	5.03	122.83	118.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5208	0	5135	129	0
2	A	1	0	0	0	0
3	A	31	0	13	0	0
4	A	25	0	11	3	0
5	A	138	0	0	4	0
All	All	5403	0	5159	130	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

All (130) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:578:LYS:HE2	1:A:578:LYS:HA	1.46	0.95
1:A:505:ILE:HG22	1:A:602:THR:HA	1.51	0.92
1:A:393:LEU:HD22	1:A:724:LEU:HD13	1.48	0.92
1:A:482:ASN:HD22	1:A:599:ASN:HD21	1.18	0.89
1:A:214:GLN:HE22	1:A:216:SER:HB2	1.39	0.88
1:A:272:LEU:O	1:A:276:ILE:HG12	1.77	0.84
1:A:534:GLN:O	1:A:538:THR:HG22	1.82	0.80
1:A:415:ASN:HA	1:A:564:PRO:HG2	1.64	0.77
1:A:428:CYS:SG	4:A:1002:UDP:H3'	2.26	0.76
1:A:482:ASN:ND2	1:A:599:ASN:HD21	1.85	0.74
1:A:662:TYR:CZ	1:A:666:GLN:HG3	2.26	0.71
1:A:140:ASP:OD2	1:A:168:GLN:HG2	1.90	0.70
1:A:692:GLN:O	1:A:696:ILE:HG12	1.91	0.70
1:A:91:THR:HG21	1:A:96:LYS:HG2	1.75	0.69
1:A:288:GLN:HB3	1:A:293:ARG:NH2	2.08	0.68
1:A:106:ASN:OD1	1:A:109:THR:HG22	1.93	0.68
1:A:602:THR:N	1:A:707:ASP:OD2	2.29	0.65
1:A:693:LYS:H	1:A:693:LYS:HD2	1.62	0.64
1:A:109:THR:HG23	1:A:111:LYS:H	1.63	0.64
1:A:717:ARG:O	1:A:719:PRO:HD3	1.97	0.63
1:A:534:GLN:O	1:A:538:THR:CG2	2.47	0.63
1:A:456:THR:HA	1:A:463:SER:HA	1.79	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:475:LYS:HD2	1:A:546:ALA:HB2	1.80	0.63
1:A:481:LEU:CB	1:A:505:ILE:HG12	2.30	0.61
1:A:571:GLN:HA	1:A:571:GLN:HE21	1.65	0.61
1:A:142:GLN:HB3	1:A:196:LYS:HE2	1.82	0.61
1:A:393:LEU:CD2	1:A:724:LEU:HD13	2.29	0.60
1:A:661:GLN:HA	1:A:664:ILE:HD12	1.83	0.60
1:A:665:THR:HG22	1:A:666:GLN:HE21	1.67	0.59
1:A:317:ASN:OD1	1:A:326:ARG:NH1	2.36	0.59
1:A:225:GLU:HG3	5:A:2133:HOH:O	2.03	0.59
1:A:571:GLN:HA	1:A:571:GLN:NE2	2.19	0.58
1:A:481:LEU:HB3	1:A:505:ILE:HG12	1.85	0.58
1:A:373:ARG:HG2	1:A:377:GLU:OE2	2.04	0.58
1:A:165:GLU:HG2	1:A:169:HIS:HB2	1.86	0.57
1:A:214:GLN:HE21	1:A:488:ASN:HD21	1.53	0.56
1:A:220:LEU:HD22	1:A:426:ASN:HB3	1.88	0.55
1:A:538:THR:HB	1:A:583:TRP:NE1	2.22	0.55
1:A:713:ASN:ND2	1:A:742:TYR:H	2.05	0.54
1:A:665:THR:HG22	1:A:666:GLN:NE2	2.22	0.54
1:A:446:ALA:HB3	1:A:477:VAL:CG1	2.37	0.54
1:A:306:ALA:HA	1:A:350:LEU:HB3	1.89	0.54
1:A:146:PHE:CZ	1:A:640:VAL:HG21	2.43	0.54
1:A:578:LYS:HA	1:A:578:LYS:CE	2.31	0.54
1:A:691:SER:HB2	1:A:693:LYS:HD3	1.89	0.54
1:A:606:MET:HB2	1:A:607:PRO:CD	2.38	0.54
1:A:270:ASN:HB3	1:A:274:PRO:HG2	1.90	0.54
1:A:475:LYS:O	1:A:479:ARG:HG3	2.09	0.53
1:A:214:GLN:HE22	1:A:216:SER:CB	2.15	0.53
1:A:723:LYS:HG2	5:A:2115:HOH:O	2.08	0.53
1:A:447:SER:HB3	1:A:606:MET:HE3	1.90	0.52
1:A:560:PHE:CZ	1:A:596:GLY:HA2	2.45	0.52
1:A:655:TRP:CZ2	1:A:660:LYS:HG2	2.45	0.52
1:A:538:THR:HB	1:A:583:TRP:HE1	1.75	0.51
1:A:436:ALA:HB1	1:A:437:PRO:CD	2.41	0.50
1:A:288:GLN:O	1:A:291:ASN:ND2	2.45	0.49
1:A:654:ILE:O	1:A:659:MET:HG3	2.13	0.49
1:A:304:TRP:CZ2	1:A:359:LEU:HB3	2.48	0.49
1:A:481:LEU:HB2	1:A:505:ILE:HG12	1.94	0.48
1:A:450:LEU:HD22	1:A:535:ILE:HG21	1.95	0.48
1:A:693:LYS:H	1:A:693:LYS:CD	2.26	0.48
1:A:94:PHE:HB3	1:A:132:ASN:OD1	2.14	0.48
1:A:298:ALA:HB2	1:A:427:LEU:HD12	1.94	0.48
1:A:139:ARG:HD3	1:A:194:SER:HB2	1.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:482:ASN:HD21	1:A:503:ARG:HH11	1.61	0.48
1:A:168:GLN:NE2	1:A:190:TYR:OH	2.43	0.48
1:A:334:ILE:HD12	1:A:404:VAL:HG13	1.97	0.47
1:A:251:HIS:HB3	1:A:424:SER:HB3	1.96	0.47
1:A:168:GLN:HE22	1:A:194:SER:HB3	1.80	0.47
1:A:220:LEU:N	1:A:220:LEU:HD23	2.30	0.46
1:A:673:LEU:HD22	1:A:676:VAL:HG23	1.98	0.46
1:A:625:THR:HA	1:A:687:VAL:HG12	1.97	0.46
1:A:482:ASN:ND2	1:A:503:ARG:HH11	2.13	0.46
1:A:288:GLN:HB3	1:A:293:ARG:HH21	1.77	0.46
1:A:520:ARG:HH22	1:A:648:ASP:CG	2.18	0.46
1:A:606:MET:HE3	1:A:608:THR:HG22	1.98	0.46
1:A:740:MET:SD	1:A:743:LEU:HB2	2.56	0.46
1:A:557:TYR:HB3	1:A:598:ARG:O	2.17	0.45
1:A:311:PHE:HA	1:A:314:ILE:HD13	1.98	0.45
1:A:444:ASN:C	1:A:445:LEU:HD12	2.37	0.45
1:A:458:GLU:OE1	1:A:462:THR:HB	2.16	0.45
1:A:104:TYR:CD1	1:A:159:ILE:HG23	2.52	0.45
1:A:483:ARG:HH22	1:A:487:ARG:HD2	1.82	0.45
1:A:512:LEU:HB2	1:A:621:PHE:HA	2.00	0.44
1:A:288:GLN:C	1:A:290:GLY:H	2.20	0.44
1:A:662:TYR:CE1	1:A:666:GLN:HG3	2.51	0.44
1:A:428:CYS:HB2	1:A:430:GLU:OE2	2.17	0.44
1:A:412:ARG:O	1:A:417:LYS:NZ	2.37	0.44
1:A:181:ARG:O	1:A:183:ILE:HD12	2.18	0.44
1:A:692:GLN:NE2	1:A:715:PHE:H	2.15	0.44
1:A:604:ALA:HB2	1:A:708:GLN:HB2	2.00	0.43
1:A:136:VAL:HB	1:A:139:ARG:HD2	2.00	0.43
1:A:671:GLN:O	1:A:672:GLY:C	2.56	0.43
1:A:507:LEU:HD12	1:A:602:THR:O	2.19	0.43
1:A:436:ALA:HB1	1:A:437:PRO:HD2	2.01	0.43
1:A:120:VAL:HG21	1:A:209:GLY:HA2	2.01	0.43
1:A:601:LEU:HA	1:A:707:ASP:OD2	2.19	0.42
1:A:164:ALA:HB3	5:A:2071:HOH:O	2.18	0.42
1:A:109:THR:OG1	1:A:111:LYS:HG3	2.19	0.42
1:A:442:VAL:HG12	1:A:443:CYS:N	2.34	0.42
1:A:401:THR:HB	1:A:402:PRO:HA	2.02	0.42
4:A:1002:UDP:H6	4:A:1002:UDP:O5'	2.02	0.42
1:A:446:ALA:HB3	1:A:477:VAL:HG11	2.00	0.42
1:A:577:GLN:HB3	5:A:2106:HOH:O	2.19	0.42
1:A:509:VAL:O	1:A:620:CYS:HA	2.20	0.42
1:A:413:LYS:HE3	1:A:575:TRP:CE2	2.55	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:518:LEU:HA	1:A:518:LEU:HD12	1.94	0.41
1:A:628:MET:HE2	1:A:664:ILE:HG12	2.02	0.41
1:A:450:LEU:HD22	1:A:535:ILE:HD13	2.01	0.41
1:A:131:LEU:HD12	1:A:131:LEU:HA	1.82	0.41
1:A:455:GLU:C	1:A:457:SER:H	2.24	0.41
1:A:91:THR:HG21	1:A:96:LYS:CG	2.47	0.41
1:A:127:ASN:HB2	1:A:131:LEU:HD22	2.02	0.41
1:A:482:ASN:ND2	1:A:503:ARG:NH1	2.69	0.41
1:A:293:ARG:HA	1:A:294:PRO:HD3	1.82	0.41
1:A:426:ASN:ND2	4:A:1002:UDP:O3'	2.53	0.41
1:A:659:MET:CE	1:A:673:LEU:HD11	2.51	0.41
1:A:673:LEU:HD22	1:A:676:VAL:CG2	2.50	0.41
1:A:256:ARG:HG2	1:A:260:SER:HB2	2.03	0.41
1:A:484:VAL:O	1:A:488:ASN:HB2	2.21	0.41
1:A:259:GLY:HA2	1:A:268:THR:HG23	2.02	0.41
1:A:170:LEU:C	1:A:170:LEU:HD23	2.41	0.41
1:A:220:LEU:HD21	1:A:431:ILE:HG21	2.01	0.41
1:A:713:ASN:HD22	1:A:742:TYR:H	1.69	0.41
1:A:702:ARG:O	1:A:706:ILE:HG13	2.20	0.41
1:A:588:LEU:O	1:A:592:ILE:HG13	2.21	0.41
1:A:713:ASN:ND2	1:A:742:TYR:HB2	2.36	0.40
1:A:537:GLU:OE2	1:A:582:MET:HB3	2.21	0.40
1:A:578:LYS:HE2	1:A:578:LYS:CA	2.32	0.40
1:A:656:ASP:OD1	1:A:658:GLY:N	2.51	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	647/888 (73%)	591 (91%)	46 (7%)	10 (2%)	15 50

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	296	ALA
1	A	459	ASP
1	A	460	GLY
1	A	629	TYR
1	A	639	GLN
1	A	707	ASP
1	A	256	ARG
1	A	314	ILE
1	A	741	TYR
1	A	161	GLY

### 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	565/761 (74%)	524 (93%)	41 (7%)	20	51

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	119	ASP
1	A	126	GLU
1	A	131	LEU
1	A	146	PHE
1	A	162	GLN
1	A	176	LEU
1	A	183	ILE
1	A	195	LEU
1	A	212	LYS
1	A	214	GLN
1	A	220	LEU
1	A	243	LYS
1	A	268	THR
1	A	292	LYS
1	A	293	ARG
1	A	301	LEU
1	A	314	ILE
1	A	321	GLU

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Mol	Chain	Res	Type
1	A	326	ARG
1	A	337	LEU
1	A	359	LEU
1	A	388	LEU
1	A	443	CYS
1	A	456	THR
1	A	459	ASP
1	A	462	THR
1	A	503	ARG
1	A	505	ILE
1	A	512	LEU
1	A	518	LEU
1	A	520	ARG
1	A	530	LEU
1	A	538	THR
1	A	606	MET
1	A	610	SER
1	A	638	PHE
1	A	639	GLN
1	A	659	MET
1	A	712	LEU
1	A	720	THR
1	A	746	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	168	GLN
1	A	214	GLN
1	A	444	ASN
1	A	482	ASN
1	A	613	GLN
1	A	666	GLN
1	A	692	GLN
1	A	710	HIS
1	A	713	ASN
1	A	746	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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	ANP	A	1001	2	33,33,33	1.43	3 (9%)	51,52,52	2.32	17 (33%)
4	UDP	A	1002	-	26,26,26	1.11	1 (3%)	36,40,40	1.67	4 (11%)

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	ANP	A	1001	2	-	0/18/38/38	0/1/3/3
4	UDP	A	1002	-	-	0/14/32/32	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	ANP	C5-C4	4.12	1.49	1.40
3	A	1001	ANP	PG-O1G	4.05	1.51	1.46
3	A	1001	ANP	PB-O1B	3.44	1.50	1.46
4	A	1002	UDP	C2-N1	2.69	1.41	1.38

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1002	UDP	C2-N1-C1'	7.53	122.93	118.21
3	A	1001	ANP	O1G-PG-N3B	-6.73	101.67	111.83
3	A	1001	ANP	N3-C4-N9	5.24	134.90	125.43
3	A	1001	ANP	N3-C2-N1	-4.96	124.56	128.71
3	A	1001	ANP	C3'-C2'-C1'	4.74	108.32	100.91
3	A	1001	ANP	C4-C5-N7	-4.14	105.98	109.52
3	A	1001	ANP	O1B-PB-N3B	-3.92	105.90	111.83
3	A	1001	ANP	PB-N3B-PG	-3.70	123.84	130.07
3	A	1001	ANP	C5-C4-N3	-3.57	117.93	125.70
3	A	1001	ANP	O2B-PB-O1B	3.33	117.57	109.89
3	A	1001	ANP	O3A-PB-N3B	-3.30	97.43	106.59
3	A	1001	ANP	O2B-PB-N3B	3.22	115.36	106.61
4	A	1002	UDP	C5-C6-N1	3.19	124.82	121.21
4	A	1002	UDP	N3-C2-N1	3.00	118.48	115.97
3	A	1001	ANP	C4'-O4'-C1'	2.72	112.70	109.75
3	A	1001	ANP	O4'-C1'-C2'	-2.47	102.98	106.77
4	A	1002	UDP	C4'-O4'-C1'	2.35	112.31	109.75
3	A	1001	ANP	C2-N3-C4	2.25	120.42	114.01
3	A	1001	ANP	PA-O3A-PB	-2.25	124.13	131.81
3	A	1001	ANP	C2-N1-C6	2.24	122.82	118.77
3	A	1001	ANP	O2A-PA-O1A	2.08	123.86	112.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	651/888 (73%)	-0.29	27 (4%) 35 43	12, 24, 57, 69	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	458	GLU	5.8
1	A	457	SER	5.6
1	A	294	PRO	5.0
1	A	629	TYR	4.8
1	A	459	ASP	4.4
1	A	292	LYS	4.3
1	A	89	GLN	4.3
1	A	718	ALA	4.1
1	A	638	PHE	3.8
1	A	293	ARG	3.5
1	A	456	THR	3.4
1	A	746	GLN	3.4
1	A	320	LYS	3.3
1	A	461	LYS	3.2
1	A	460	GLY	3.2
1	A	319	GLY	3.1
1	A	323	ILE	3.0
1	A	317	ASN	2.9
1	A	717	ARG	2.7
1	A	91	THR	2.6
1	A	667	ASN	2.5
1	A	90	THR	2.4
1	A	661	GLN	2.3
1	A	462	THR	2.3
1	A	145	TYR	2.2
1	A	639	GLN	2.0
1	A	290	GLY	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	UDP	A	1002	25/25	0.24	2.24	40,54,58,58	0
3	ANP	A	1001	31/31	0.09	-1.54	14,18,20,26	0
2	MG	A	2001	1/1	0.07	-2.34	16,16,16,16	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.