



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2017 – 09:18 PM EDT

PDB ID : 1XJE  
Title : Structural mechanism of allosteric substrate specificity in a ribonucleotide reductase: dTTP-GDP complex  
Authors : Larsson, K.-M.; Jordan, A.; Eliasson, R.; Reichard, P.; Logan, D.T.; Nordlund, P.  
Deposited on : unknown  
Resolution : 1.90 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

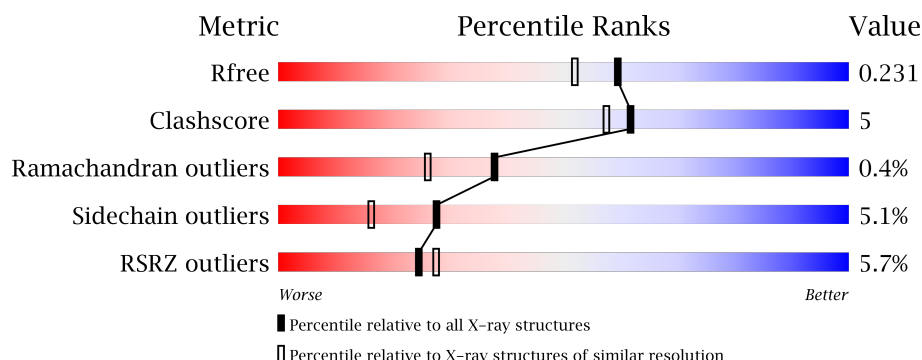
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
$R_{free}$	100719	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

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. 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	644	<div> <div>6%</div> <div> <div></div> <div>85%</div> <div>9%</div> <div>• •</div> </div> </div>
1	B	644	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>10%</div> <div>• •</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	GOL	B	1001	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10914 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 ribonucleotide reductase, B12-dependent.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	627	Total	C	N	O	S	0	0	0
			5035	3224	860	931	20			
1	B	618	Total	C	N	O	S	0	0	0
			4966	3183	849	914	20			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	SER	TYR	SEE REMARK 999	UNP O33839
B	205	SER	TYR	SEE REMARK 999	UNP O33839

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

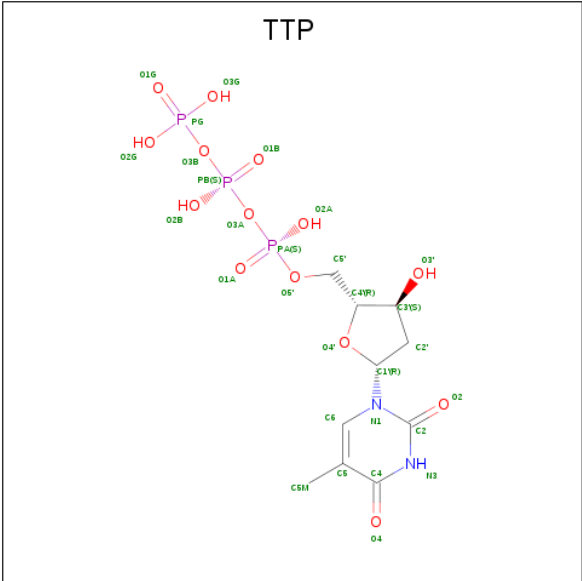
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
3	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 4 is THYMIDINE-5'-TRIPHOSPHATE (three-letter code: TTP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>2</sub>O<sub>14</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			29	10	2	14	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			29	10	2	14	3		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			6	3	3		

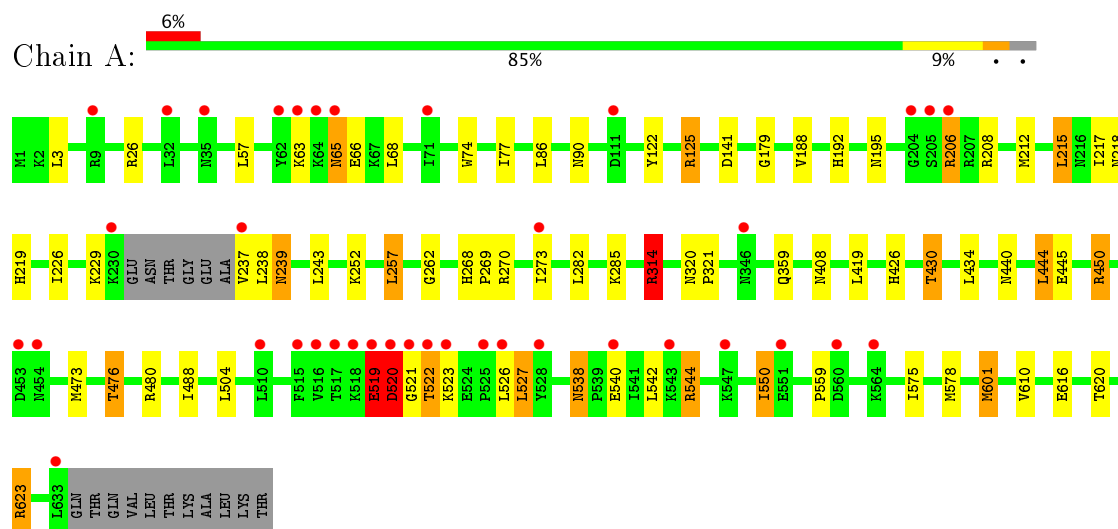
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	382	Total	O	0	0
			382	382		
6	B	409	Total	O	0	0
			409	409		

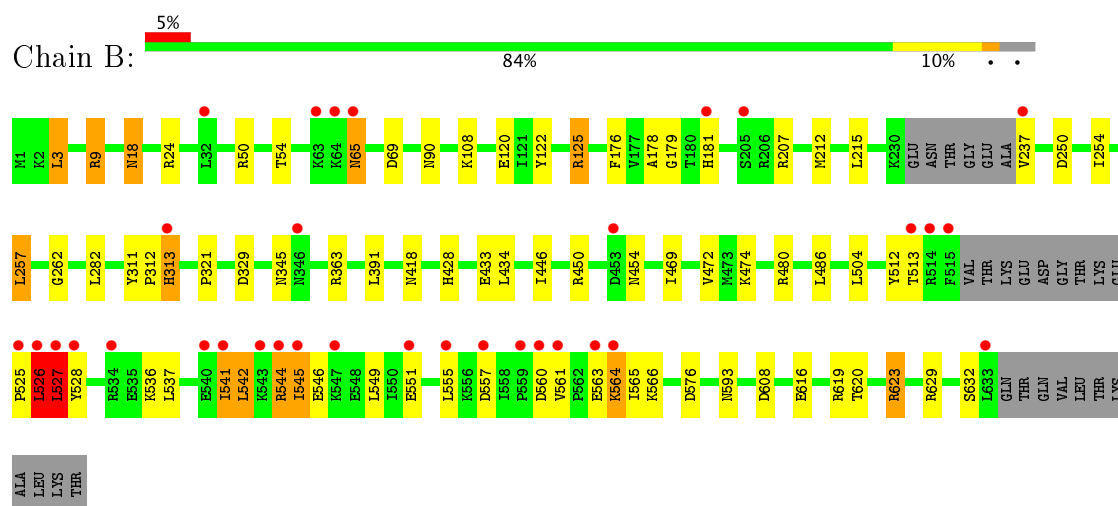
### 3 Residue-property plots

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: ribonucleotide reductase, B12-dependent



- Molecule 1: ribonucleotide reductase, B12-dependent



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	119.39Å 124.38Å 107.24Å 90.00° 103.68° 90.00°	Depositor
Resolution (Å)	18.00 – 1.90 17.82 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.2 (18.00-1.90) 97.2 (17.82-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.68 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.182 , 0.223 0.191 , 0.231	Depositor DCC
$R_{free}$ test set	5794 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.0	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 58.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10914	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% 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

### 5.1 Standard geometry

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

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	0.85	1/5135 (0.0%)	0.89	9/6931 (0.1%)
1	B	0.86	0/5065	0.95	17/6835 (0.2%)
All	All	0.85	1/10200 (0.0%)	0.92	26/13766 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	2
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	601	MET	CG-SD	-5.20	1.67	1.81

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	623	ARG	NE-CZ-NH1	16.47	128.53	120.30
1	B	623	ARG	NE-CZ-NH2	-12.98	113.81	120.30
1	A	623	ARG	NE-CZ-NH1	11.02	125.81	120.30
1	B	125	ARG	NE-CZ-NH2	-10.75	114.92	120.30
1	B	619	ARG	NE-CZ-NH2	-9.78	115.41	120.30
1	B	125	ARG	NE-CZ-NH1	9.51	125.06	120.30
1	B	629	ARG	NE-CZ-NH2	-8.25	116.18	120.30
1	A	623	ARG	NE-CZ-NH2	-7.28	116.66	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	526	LEU	CA-CB-CG	6.89	131.16	115.30
1	A	125	ARG	NE-CZ-NH1	6.73	123.67	120.30
1	B	623	ARG	CB-CG-CD	6.42	128.29	111.60
1	B	527	LEU	CA-CB-CG	6.37	129.95	115.30
1	B	576	ASP	CB-CG-OD1	6.30	123.97	118.30
1	B	363	ARG	NE-CZ-NH1	6.09	123.34	120.30
1	A	141	ASP	CB-CG-OD1	5.92	123.63	118.30
1	A	314	ARG	NE-CZ-NH1	5.70	123.15	120.30
1	B	619	ARG	NE-CZ-NH1	5.63	123.12	120.30
1	B	629	ARG	NE-CZ-NH1	5.55	123.08	120.30
1	B	623	ARG	CD-NE-CZ	5.50	131.30	123.60
1	A	450	ARG	NE-CZ-NH2	-5.49	117.55	120.30
1	B	3	LEU	CB-CG-CD2	5.36	120.10	111.00
1	B	329	ASP	CB-CG-OD2	5.35	123.11	118.30
1	B	24	ARG	NE-CZ-NH2	-5.35	117.63	120.30
1	A	125	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	A	544	ARG	NE-CZ-NH1	5.09	122.85	120.30
1	A	450	ARG	NE-CZ-NH1	5.03	122.81	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	522	THR	Peptide
1	B	526	LEU	Peptide
1	B	560	ASP	Peptide

## 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	5035	0	5096	50	0
1	B	4966	0	5028	54	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	28	0	12	0	0
3	B	28	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	29	0	13	1	0
4	B	29	0	13	1	0
5	B	6	0	8	0	0
6	A	382	0	0	7	0
6	B	409	0	0	9	0
All	All	10914	0	10182	104	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 5.

All (104) 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:B:537:LEU:HD11	1:B:541:ILE:HD11	1.48	0.94
1:B:418:ASN:OD1	6:B:1364:HOH:O	1.85	0.93
1:B:9:ARG:HD3	1:B:9:ARG:O	1.75	0.86
1:A:521:GLY:O	1:A:522:THR:OG1	1.94	0.85
1:B:525:PRO:O	1:B:526:LEU:HD12	1.75	0.85
1:A:473:MET:O	1:A:476:THR:HG22	1.77	0.84
1:B:454:ASN:OD1	1:B:474:LYS:NZ	2.12	0.82
1:A:522:THR:HA	1:A:523:LYS:HG2	1.62	0.81
1:A:476:THR:HG21	1:A:480:ARG:HH21	1.52	0.74
1:B:544:ARG:O	1:B:545:ILE:HG12	1.89	0.72
1:A:122:TYR:O	1:A:125:ARG:HD3	1.91	0.71
1:B:525:PRO:O	1:B:526:LEU:CD1	2.39	0.70
1:B:428:HIS:HD2	1:B:480:ARG:HH22	1.39	0.70
1:B:526:LEU:HD13	1:B:527:LEU:HD12	1.74	0.68
1:A:237:VAL:HG13	1:A:238:LEU:H	1.59	0.67
1:B:18:ASN:ND2	1:B:528:TYR:OH	2.28	0.67
1:A:359:GLN:HA	1:A:430:THR:HG21	1.77	0.67
1:B:541:ILE:HD13	1:B:561:VAL:H	1.59	0.66
1:B:526:LEU:HD13	1:B:527:LEU:CD1	2.27	0.65
1:B:525:PRO:O	1:B:526:LEU:CG	2.45	0.65
1:B:69:ASP:OD1	6:B:1353:HOH:O	2.15	0.64
1:B:623:ARG:HD2	6:B:1013:HOH:O	1.98	0.64
1:A:26:ARG:HB2	1:A:206:ARG:HG3	1.79	0.63
1:B:537:LEU:HD23	1:B:542:LEU:HD22	1.79	0.63
1:A:273:ILE:O	1:A:273:ILE:HD12	1.98	0.63
1:B:537:LEU:HD23	1:B:542:LEU:CD2	2.28	0.62
1:B:541:ILE:HD12	1:B:541:ILE:O	1.99	0.62
1:B:257:LEU:HD22	1:B:262:GLY:HA3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:9:ARG:CD	1:B:9:ARG:O	2.47	0.62
1:A:601:MET:HE1	1:A:610:VAL:HG22	1.82	0.60
1:A:314:ARG:CG	1:A:314:ARG:HH11	2.13	0.60
1:B:418:ASN:CG	6:B:1364:HOH:O	2.34	0.59
1:B:526:LEU:HB2	1:B:527:LEU:HG	1.82	0.59
1:A:314:ARG:HG3	1:A:314:ARG:HH11	1.68	0.58
1:B:313:HIS:HE1	1:B:446:ILE:O	1.86	0.58
1:B:50:ARG:O	1:B:54:THR:HG23	2.04	0.57
1:B:525:PRO:O	1:B:526:LEU:HG	2.04	0.57
1:A:226:ILE:HG21	1:A:285:LYS:HG2	1.86	0.56
1:A:239:ASN:HD22	1:A:239:ASN:H	1.54	0.56
1:B:418:ASN:CB	6:B:1364:HOH:O	2.53	0.56
1:A:522:THR:HB	1:A:523:LYS:O	2.05	0.56
1:B:433:GLU:HG2	6:B:1351:HOH:O	2.06	0.55
1:A:623:ARG:HD2	6:A:1012:HOH:O	2.06	0.55
1:B:526:LEU:HB2	1:B:527:LEU:CB	2.37	0.55
1:B:212:MET:HB2	1:B:321:PRO:HA	1.89	0.54
1:A:544:ARG:NH2	1:A:559:PRO:O	2.36	0.54
1:A:252:LYS:CB	1:A:252:LYS:NZ	2.73	0.52
1:B:179:GLY:HA3	4:B:1004:TTP:O1B	2.10	0.52
1:A:538:ASN:HD22	1:A:540:GLU:H	1.58	0.52
1:B:469:ILE:O	1:B:472:VAL:HG12	2.09	0.52
1:A:179:GLY:HA3	4:A:1005:TTP:O1B	2.10	0.51
1:A:578:MET:HB3	6:A:1306:HOH:O	2.10	0.51
1:B:122:TYR:O	1:B:125:ARG:HD3	2.10	0.51
1:B:18:ASN:ND2	1:B:528:TYR:CZ	2.79	0.50
1:B:608:ASP:OD2	6:B:1213:HOH:O	2.19	0.50
1:A:445:GLU:HG3	6:A:1136:HOH:O	2.11	0.50
1:A:601:MET:CE	1:A:610:VAL:HG22	2.40	0.50
1:A:229:LYS:HE2	6:A:1296:HOH:O	2.13	0.48
1:A:522:THR:HA	1:A:523:LYS:CG	2.36	0.48
1:B:549:LEU:HD13	1:B:555:LEU:HD23	1.94	0.48
1:A:257:LEU:HD22	1:A:262:GLY:HA3	1.94	0.48
1:A:526:LEU:O	1:A:527:LEU:HB3	2.13	0.48
1:B:65:ASN:OD1	1:B:65:ASN:C	2.51	0.48
1:A:616:GLU:O	1:A:620:THR:HG23	2.13	0.48
1:B:428:HIS:CD2	1:B:480:ARG:HH22	2.27	0.48
1:B:526:LEU:HD22	1:B:527:LEU:HG	1.95	0.48
1:B:9:ARG:C	1:B:9:ARG:CD	2.82	0.47
1:A:63:LYS:O	1:A:66:GLU:HG2	2.14	0.47
1:B:526:LEU:HB2	1:B:527:LEU:CG	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:120:GLU:HG3	6:B:1298:HOH:O	2.14	0.47
1:B:542:LEU:O	1:B:546:GLU:HG3	2.14	0.47
1:B:311:TYR:CD1	1:B:312:PRO:HA	2.49	0.46
1:A:268:HIS:CG	1:A:269:PRO:HD2	2.51	0.46
1:B:537:LEU:HD13	1:B:565:ILE:HG21	1.97	0.46
1:B:561:VAL:HG12	1:B:566:LYS:HG3	1.97	0.46
1:B:313:HIS:H	1:B:313:HIS:CD2	2.35	0.45
1:A:527:LEU:CD1	1:A:550:ILE:HD11	2.47	0.45
1:B:418:ASN:HB2	6:B:1364:HOH:O	2.14	0.45
1:A:314:ARG:HD3	6:A:1126:HOH:O	2.15	0.45
1:A:229:LYS:HE3	1:A:238:LEU:O	2.18	0.44
1:A:426:HIS:O	1:A:430:THR:CG2	2.66	0.44
1:A:195:ASN:HD21	1:A:239:ASN:ND2	2.16	0.43
1:A:408:ASN:HB3	1:A:575:ILE:HG23	2.00	0.43
1:B:512:TYR:CZ	1:B:528:TYR:HB2	2.53	0.43
1:A:74:TRP:HA	1:A:77:ILE:HG22	2.00	0.43
1:A:519:GLU:O	1:A:520:ASP:HB3	2.19	0.43
1:B:616:GLU:O	1:B:620:THR:HG23	2.19	0.43
1:A:215:LEU:HD13	1:A:219:HIS:HB3	2.00	0.43
1:B:486:LEU:O	1:B:593:ASN:HB2	2.19	0.43
1:A:192:HIS:HE1	1:A:237:VAL:HG23	1.84	0.42
1:A:578:MET:CG	6:A:1306:HOH:O	2.66	0.42
1:A:578:MET:SD	6:A:1306:HOH:O	2.62	0.42
1:B:513:THR:HG22	1:B:527:LEU:HB3	2.01	0.42
1:B:563:GLU:O	1:B:564:LYS:HB2	2.19	0.42
1:A:522:THR:HG22	1:A:523:LYS:CG	2.49	0.42
1:B:176:PHE:CE1	1:B:178:ALA:HA	2.55	0.42
1:A:212:MET:HB2	1:A:321:PRO:HA	2.02	0.41
1:A:440:ASN:ND2	1:A:444:LEU:HD12	2.35	0.41
1:A:217:ILE:HD11	1:A:282:LEU:HD23	2.03	0.41
1:A:320:ASN:HB2	1:A:321:PRO:HD2	2.03	0.41
1:A:63:LYS:HE2	1:A:65:ASN:OD1	2.20	0.41
1:A:188:VAL:O	1:A:192:HIS:HD2	2.04	0.41
1:B:50:ARG:NH2	1:B:108:LYS:O	2.51	0.40
1:A:314:ARG:CG	1:A:314:ARG:NH1	2.77	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	623/644 (97%)	606 (97%)	14 (2%)	3 (0%)	32	20
1	B	612/644 (95%)	593 (97%)	17 (3%)	2 (0%)	44	34
All	All	1235/1288 (96%)	1199 (97%)	31 (2%)	5 (0%)	38	26

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	520	ASP
1	B	564	LYS
1	B	545	ILE
1	A	519	GLU
1	A	527	LEU

### 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	552/566 (98%)	524 (95%)	28 (5%)	28	16
1	B	544/566 (96%)	516 (95%)	28 (5%)	28	16
All	All	1096/1132 (97%)	1040 (95%)	56 (5%)	28	16

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU

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Mol	Chain	Res	Type
1	A	57	LEU
1	A	65	ASN
1	A	68	LEU
1	A	86	LEU
1	A	90	ASN
1	A	206	ARG
1	A	208	ARG
1	A	215	LEU
1	A	218	ASN
1	A	239	ASN
1	A	243	LEU
1	A	257	LEU
1	A	270	ARG
1	A	314	ARG
1	A	419	LEU
1	A	430	THR
1	A	434	LEU
1	A	444	LEU
1	A	450	ARG
1	A	476	THR
1	A	488	ILE
1	A	504	LEU
1	A	519	GLU
1	A	520	ASP
1	A	538	ASN
1	A	542	LEU
1	A	550	ILE
1	B	3	LEU
1	B	9	ARG
1	B	18	ASN
1	B	65	ASN
1	B	90	ASN
1	B	181	HIS
1	B	207	ARG
1	B	215	LEU
1	B	237	VAL
1	B	250	ASP
1	B	254	ILE
1	B	257	LEU
1	B	282	LEU
1	B	313	HIS
1	B	345	ASN

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Mol	Chain	Res	Type
1	B	391	LEU
1	B	434	LEU
1	B	450	ARG
1	B	504	LEU
1	B	526	LEU
1	B	527	LEU
1	B	536	LYS
1	B	541	ILE
1	B	542	LEU
1	B	544	ARG
1	B	551	GLU
1	B	557	ASP
1	B	632	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	192	HIS
1	A	239	ASN
1	A	313	HIS
1	A	454	ASN
1	A	538	ASN
1	A	603	GLN
1	A	612	ASN
1	B	18	ASN
1	B	192	HIS
1	B	203	GLN
1	B	289	ASN
1	B	313	HIS
1	B	345	ASN
1	B	346	ASN
1	B	428	HIS
1	B	496	ASN
1	B	531	GLN
1	B	584	GLN
1	B	603	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.



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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 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	GDP	A	1002	-	25,30,30	1.52	2 (8%)	26,47,47	2.56	8 (30%)
4	TTP	A	1005	2	22,30,30	1.98	7 (31%)	25,47,47	2.35	7 (28%)
5	GOL	B	1001	-	5,5,5	0.51	0	5,5,5	0.48	0
3	GDP	B	1003	-	25,30,30	1.44	5 (20%)	26,47,47	2.37	8 (30%)
4	TTP	B	1004	2	22,30,30	2.07	4 (18%)	25,47,47	2.30	8 (32%)

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	GDP	A	1002	-	-	0/12/32/32	0/3/3/3
4	TTP	A	1005	2	-	0/18/34/34	0/2/2/2
5	GOL	B	1001	-	-	0/4/4/4	0/0/0/0
3	GDP	B	1003	-	-	0/12/32/32	0/3/3/3
4	TTP	B	1004	2	-	0/18/34/34	0/2/2/2

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1004	TTP	C5M-C5	-6.33	1.39	1.51
4	A	1005	TTP	C5M-C5	-4.60	1.42	1.51
4	B	1004	TTP	C2-N3	-3.02	1.32	1.38
4	B	1004	TTP	O4'-C4'	-2.06	1.40	1.45
4	A	1005	TTP	O4'-C4'	-2.04	1.40	1.45
4	A	1005	TTP	C4-N3	2.04	1.36	1.33
4	A	1005	TTP	O4'-C1'	2.12	1.47	1.42
3	B	1003	GDP	C3'-C4'	2.20	1.58	1.53
3	B	1003	GDP	O4'-C1'	2.20	1.44	1.41
4	A	1005	TTP	C2'-C1'	2.44	1.59	1.52
3	B	1003	GDP	C2-N1	2.61	1.40	1.35
4	A	1005	TTP	PG-O3G	2.87	1.66	1.54
3	B	1003	GDP	C2'-C1'	2.96	1.58	1.53
3	B	1003	GDP	PB-O3A	3.62	1.65	1.60
4	B	1004	TTP	O4-C4	3.97	1.34	1.24
3	A	1002	GDP	C6-N1	4.35	1.40	1.33
4	A	1005	TTP	O4-C4	4.51	1.35	1.24
3	A	1002	GDP	O4'-C1'	4.54	1.47	1.41

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1002	GDP	N3-C2-N1	-6.15	118.48	127.46
3	B	1003	GDP	N3-C2-N1	-6.11	118.54	127.46
3	A	1002	GDP	C5-C6-N1	-4.29	117.38	123.48
4	A	1005	TTP	C5-C4-N3	-4.20	120.60	125.24
3	A	1002	GDP	C4'-O4'-C1'	-4.01	105.50	109.77
3	B	1003	GDP	C5-C6-N1	-3.97	117.84	123.48
4	B	1004	TTP	C5-C4-N3	-3.58	121.29	125.24
3	A	1002	GDP	C6-C5-C4	-3.42	117.44	120.84
4	B	1004	TTP	O4'-C1'-C2'	-3.32	99.89	106.25
3	B	1003	GDP	C4'-O4'-C1'	-3.02	106.56	109.77
4	A	1005	TTP	C2'-C1'-N1	-2.81	107.59	114.23
4	B	1004	TTP	C2'-C1'-N1	-2.77	107.69	114.23
4	A	1005	TTP	O4'-C1'-C2'	-2.68	101.10	106.25
3	B	1003	GDP	C6-C5-C4	-2.44	118.42	120.84
3	A	1002	GDP	C5'-C4'-C3'	-2.37	106.26	115.29
4	B	1004	TTP	O5'-PA-O1A	-2.02	101.11	109.25
4	B	1004	TTP	C5-C6-N1	-2.00	119.98	122.15
4	B	1004	TTP	C5M-C5-C6	2.14	122.94	118.67
4	A	1005	TTP	O5'-C5'-C4'	2.18	116.72	109.00
4	A	1005	TTP	O4'-C1'-N1	2.37	111.78	107.78
4	A	1005	TTP	O2G-PG-O1G	2.63	120.78	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1004	TTP	O2G-PG-O1G	2.73	121.19	110.50
3	B	1003	GDP	O3B-PB-O2B	2.74	118.65	107.61
3	B	1003	GDP	N2-C2-N3	2.89	123.08	117.75
3	A	1002	GDP	N2-C2-N3	2.94	123.17	117.75
3	B	1003	GDP	C2-N3-C4	3.84	119.64	115.16
3	A	1002	GDP	C2-N3-C4	4.87	120.84	115.16
3	A	1002	GDP	C6-N1-C2	4.95	123.18	116.06
3	B	1003	GDP	C6-N1-C2	5.31	123.69	116.06
4	B	1004	TTP	C4-N3-C2	8.17	122.31	115.16
4	A	1005	TTP	C4-N3-C2	8.89	122.93	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1005	TTP	1	0
4	B	1004	TTP	1	0

## 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, 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	627/644 (97%)	0.13	38 (6%)	22 25	23, 33, 56, 79	0
1	B	618/644 (95%)	-0.01	33 (5%)	27 31	21, 31, 58, 73	0
All	All	1245/1288 (96%)	0.06	71 (5%)	24 28	21, 32, 56, 79	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	515	PHE	8.9
1	A	522	THR	8.7
1	A	526	LEU	7.2
1	A	521	GLY	5.9
1	A	523	LYS	5.7
1	A	516	VAL	5.6
1	B	525	PRO	5.5
1	A	517	THR	4.7
1	A	520	ASP	4.7
1	A	204	GLY	4.7
1	B	633	LEU	4.5
1	A	32	LEU	4.4
1	A	205	SER	4.0
1	A	230	LYS	4.0
1	A	518	LYS	4.0
1	A	519	GLU	4.0
1	A	65	ASN	3.9
1	B	515	PHE	3.8
1	B	513	THR	3.8
1	B	514	ARG	3.6
1	B	559	PRO	3.6
1	B	63	LYS	3.5
1	B	563	GLU	3.5
1	A	237	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	557	ASP	3.3
1	A	540	GLU	3.3
1	B	541	ILE	3.2
1	B	551	GLU	3.2
1	A	633	LEU	3.2
1	B	453	ASP	3.2
1	A	547	LYS	3.1
1	B	526	LEU	3.1
1	B	64	LYS	2.9
1	B	540	GLU	2.9
1	B	527	LEU	2.9
1	B	543	LYS	2.9
1	B	205	SER	2.9
1	B	237	VAL	2.9
1	A	525	PRO	2.9
1	B	547	LYS	2.9
1	A	62	TYR	2.8
1	A	206	ARG	2.8
1	B	560	ASP	2.8
1	B	32	LEU	2.8
1	A	71	ILE	2.8
1	A	551	GLU	2.7
1	B	313	HIS	2.6
1	A	510	LEU	2.6
1	A	64	LYS	2.6
1	A	564	LYS	2.6
1	A	9	ARG	2.6
1	B	528	TYR	2.5
1	B	346	ASN	2.5
1	A	453	ASP	2.4
1	B	555	LEU	2.4
1	A	543	LYS	2.4
1	A	528	TYR	2.4
1	A	454	ASN	2.4
1	B	545	ILE	2.3
1	B	561	VAL	2.3
1	A	111	ASP	2.3
1	A	560	ASP	2.3
1	B	544	ARG	2.3
1	A	35	ASN	2.2
1	A	273	ILE	2.2
1	A	63	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	346	ASN	2.2
1	B	564	LYS	2.1
1	B	534	ARG	2.1
1	B	181	HIS	2.1
1	B	65	ASN	2.1

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

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

## 6.3 Carbohydrates [i](#)

There are no 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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
5	GOL	B	1001	6/6	0.68	0.30	6.35	61,66,66,66	0
4	TTP	B	1004	29/29	0.89	0.13	0.58	26,29,56,60	0
4	TTP	A	1005	29/29	0.95	0.10	-0.22	23,28,36,39	0
3	GDP	A	1002	28/28	0.96	0.07	-0.63	27,30,32,33	0
3	GDP	B	1003	28/28	0.98	0.06	-0.99	21,25,27,31	0
2	MG	B	1007	1/1	0.87	0.20	-	41,41,41,41	0
2	MG	A	1006	1/1	0.99	0.03	-	34,34,34,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.