



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 11:30 PM GMT

PDB ID : 1XJK
Title : Structural mechanism of allosteric substrate specificity in a ribonucleotide reductase: dGTP-ADP complex
Authors : Larsson, K.-M.; Jordan, A.; Eliasson, R.; Reichard, P.; Logan, D.T.; Nordlund, P.
Deposited on : 2004-09-23
Resolution : 2.12 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at 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.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

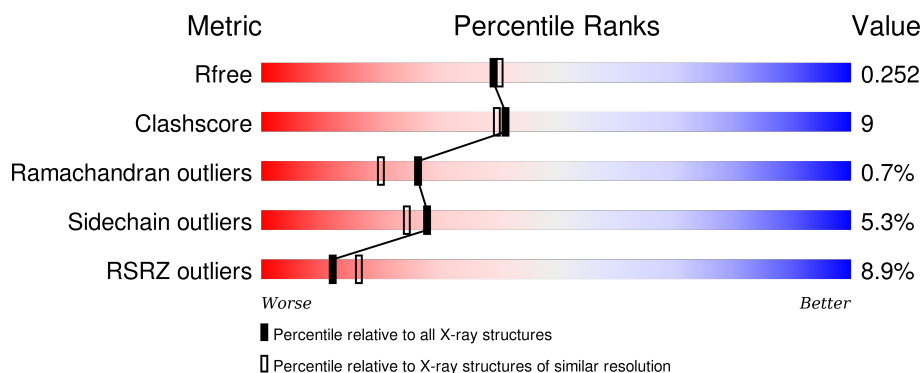
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.12 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}	91344	4587 (2.14-2.10)
Clashscore	102246	5132 (2.14-2.10)
Ramachandran outliers	100387	5080 (2.14-2.10)
Sidechain outliers	100360	5081 (2.14-2.10)
RSRZ outliers	91569	4597 (2.14-2.10)

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. 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>10%</div> <div>78%</div> <div>16%</div> <div>• •</div> </div>
1	B	644	<div> <div>7%</div> <div>73%</div> <div>20%</div> <div>• 6%</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
3	ADP	B	1002	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10248 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	624	Total	C	N	O	S	0	0	0
			5005	3208	848	929	20			
1	B	608	Total	C	N	O	S	0	0	0
			4878	3125	830	903	20			

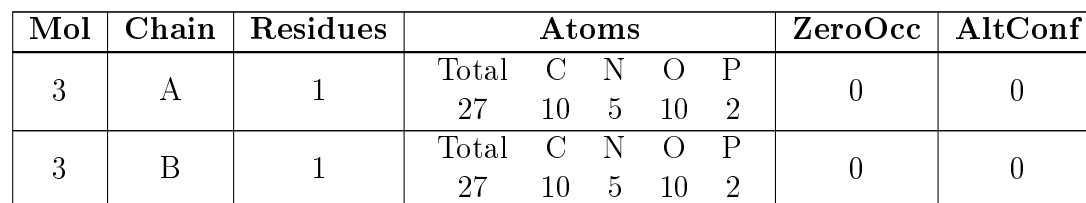
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	SER	TYR	SEE REMARK 999	UNP O33839
A	519	ASP	GLU	CONFLICT	UNP O33839
B	205	SER	TYR	SEE REMARK 999	UNP O33839
B	519	ASP	GLU	CONFLICT	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 ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



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- The chemical structure of dGTP (deoxythymine triphosphate) is shown. It consists of a thymine base (a pyrimidine ring with a methyl group at C5 and a carbonyl group at C4) attached to a deoxyribose sugar (a five-membered ring with a hydroxyl group at C3' and a phosphate group at C5'). The phosphate group is a triphosphate, consisting of three phosphate groups linked together. The atoms are labeled with their respective element symbols and numbers: N1, N3, N7, N9 for nitrogen; C2, C4, C5, C6, C8 for carbon; O1, O2, O3, O4, O5, O6 for oxygen; and P1, P2, P3 for phosphorus. The deoxyribose sugar is shown in a chair conformation, and the phosphate groups are shown in a zig-zag chain. The thymine base is shown in a planar conformation.

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

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

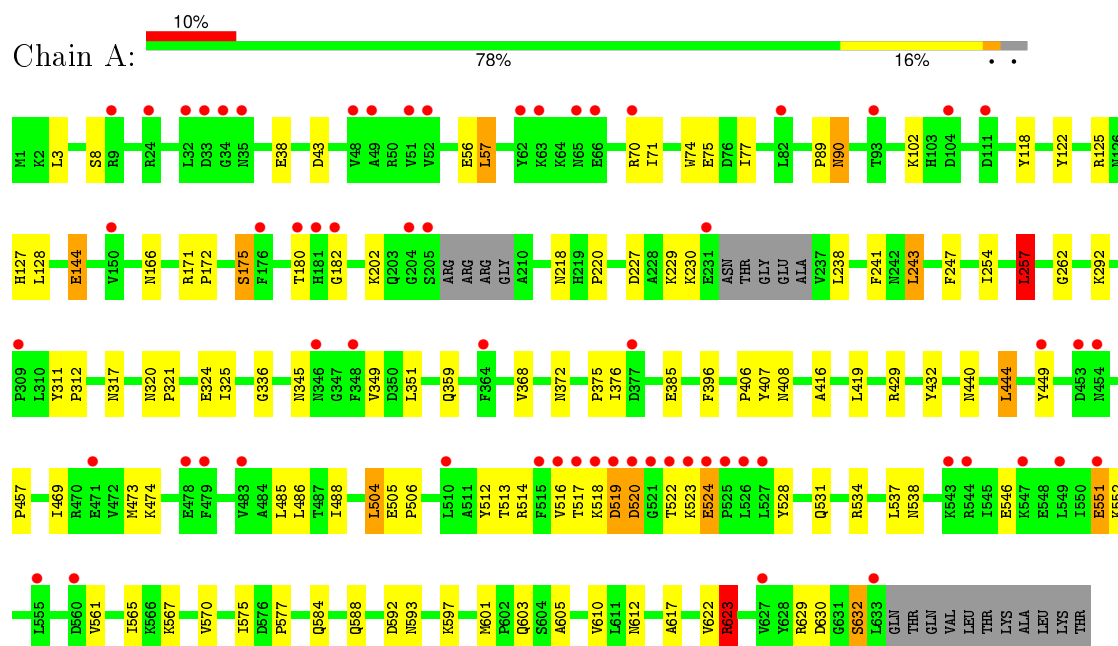
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	139	Total	O	0	0
			139	139		
5	B	108	Total	O	0	0
			108	108		

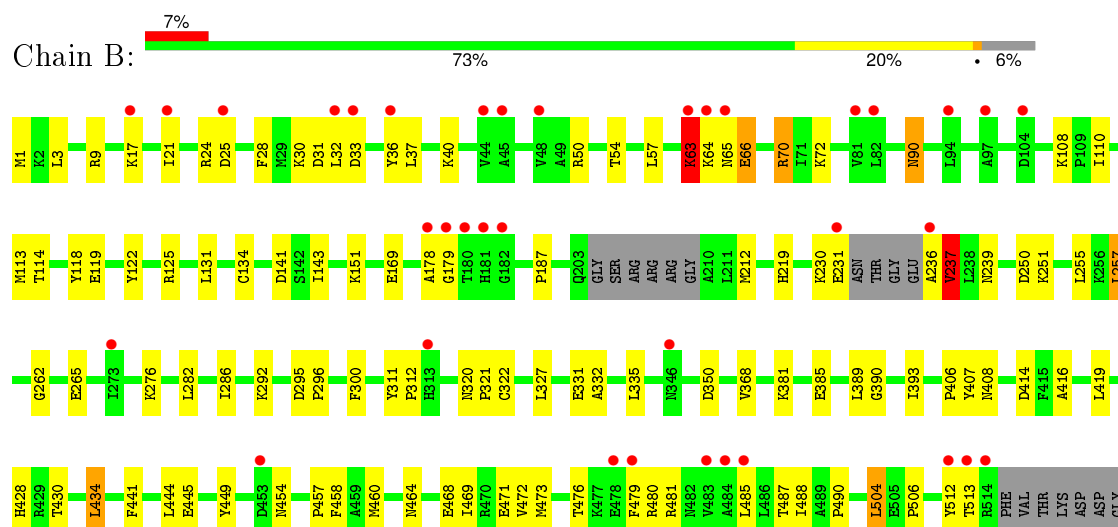
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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, α , β , γ	118.12Å 122.86Å 106.06Å 90.00° 103.46° 90.00°	Depositor
Resolution (Å)	22.70 – 2.12 22.68 – 2.12	Depositor EDS
% Data completeness (in resolution range)	97.0 (22.70-2.12) 97.0 (22.68-2.12)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 2.11Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.205 , 0.256 0.203 , 0.252	Depositor DCC
R_{free} test set	4113 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	38.9	Xtriage
Anisotropy	0.354	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 51.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 80741 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10248	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	0.85	3/5104 (0.1%)	0.88	3/6890 (0.0%)
1	B	0.82	0/4973	0.85	1/6711 (0.0%)
All	All	0.84	3/10077 (0.0%)	0.86	4/13601 (0.0%)

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	B	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	605	ALA	CA-CB	5.54	1.64	1.52
1	A	247	PHE	CD2-CE2	5.33	1.50	1.39
1	A	385	GLU	CG-CD	5.14	1.59	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	623	ARG	NE-CZ-NH1	9.30	124.95	120.30
1	A	623	ARG	NE-CZ-NH2	-7.25	116.67	120.30
1	B	414	ASP	CB-CG-OD1	6.50	124.15	118.30
1	A	257	LEU	CA-CB-CG	5.34	127.59	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	63	LYS	Peptide

5.2 Too-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 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	5005	0	5057	70	0
1	B	4878	0	4929	104	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	27	0	12	2	0
3	B	27	0	12	4	0
4	A	31	0	12	0	0
4	B	31	0	12	0	0
5	A	139	0	0	1	0
5	B	108	0	0	2	0
All	All	10248	0	10034	171	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.

The worst 5 of 171 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:230:LYS:CA	1:B:231:GLU:HB2	1.72	1.19
1:B:230:LYS:HA	1:B:231:GLU:CB	1.84	1.06
1:B:428:HIS:CD2	1:B:480:ARG:HH22	1.83	0.96
1:B:428:HIS:HD2	1:B:480:ARG:HH22	0.91	0.90
1:B:449:TYR:HE1	1:B:473:MET:CE	1.85	0.90

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	618/644 (96%)	578 (94%)	36 (6%)	4 (1%)	30	24
1	B	600/644 (93%)	562 (94%)	33 (6%)	5 (1%)	24	17
All	All	1218/1288 (95%)	1140 (94%)	69 (6%)	9 (1%)	26	20

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	66	GLU
1	A	519	ASP
1	A	523	LYS
1	A	630	ASP
1	B	32	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	550/566 (97%)	519 (94%)	31 (6%)	26	22
1	B	535/566 (94%)	509 (95%)	26 (5%)	31	27
All	All	1085/1132 (96%)	1028 (95%)	57 (5%)	28	25

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	561	VAL

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Mol	Chain	Res	Type
1	B	3	LEU
1	B	504	LEU
1	A	570	VAL
1	A	603	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	600	ASN
1	A	603	GLN
1	B	346	ASN
1	A	531	GLN
1	A	538	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	ADP	A	1001	-	22,29,29	1.25	2 (9%)	27,45,45	2.89	8 (29%)
4	DGT	A	1003	2	25,33,33	1.89	5 (20%)	35,52,52	1.61	7 (20%)
3	ADP	B	1002	-	22,29,29	1.79	5 (22%)	27,45,45	3.37	9 (33%)
4	DGT	B	1004	2	25,33,33	1.36	3 (12%)	35,52,52	2.37	10 (28%)

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	ADP	A	1001	-	-	0/12/32/32	0/3/3/3
4	DGT	A	1003	2	-	0/18/34/34	0/3/3/3
3	ADP	B	1002	-	-	0/12/32/32	0/3/3/3
4	DGT	B	1004	2	-	0/18/34/34	0/3/3/3

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1003	DGT	PG-O1G	-2.42	1.46	1.54
4	B	1004	DGT	PA-O1A	-2.33	1.45	1.54
4	B	1004	DGT	PG-O1G	-2.09	1.47	1.54
4	A	1003	DGT	O4'-C1'	-2.04	1.37	1.42
3	B	1002	ADP	O4'-C4'	2.21	1.50	1.45

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1002	ADP	N3-C2-N1	-9.88	121.33	128.89
3	B	1002	ADP	O3A-PA-O5'	-9.04	78.96	102.94
3	A	1001	ADP	N3-C2-N1	-8.51	122.38	128.89
4	B	1004	DGT	N3-C2-N1	-7.16	116.54	127.44
3	B	1002	ADP	O2A-PA-O5'	-6.48	75.81	108.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1001	ADP	2	0
3	B	1002	ADP	4	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	624/644 (96%)	0.51	62 (9%) 9 13	24, 41, 72, 104	0
1	B	608/644 (94%)	0.46	48 (7%) 15 21	27, 43, 73, 91	0
All	All	1232/1288 (95%)	0.49	110 (8%) 12 16	24, 42, 73, 104	0

The worst 5 of 110 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	521	GLY	7.6
1	B	236	ALA	7.4
1	B	513	THR	6.8
1	A	517	THR	6.6
1	A	518	LYS	6.4

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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	ADP	B	1002	27/27	0.91	0.19	3.50	38,56,66,66	0
3	ADP	A	1001	27/27	0.95	0.15	1.28	41,60,65,65	0
4	DGT	B	1004	31/31	0.94	0.10	-0.86	24,31,52,52	0
4	DGT	A	1003	31/31	0.96	0.08	-1.10	32,36,49,52	0
2	MG	B	1006	1/1	0.94	0.08	-	44,44,44,44	0
2	MG	A	1005	1/1	0.97	0.07	-	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.