



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:04 PM GMT

PDB ID : 1RYF  
Title : Alternative Splicing of Rac1 Generates Rac1b, a Self-activating GTPase  
Authors : Ahmadian, M.R.; Fiegen, D.  
Deposited on : 2003-12-22  
Resolution : 1.75 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.

---

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

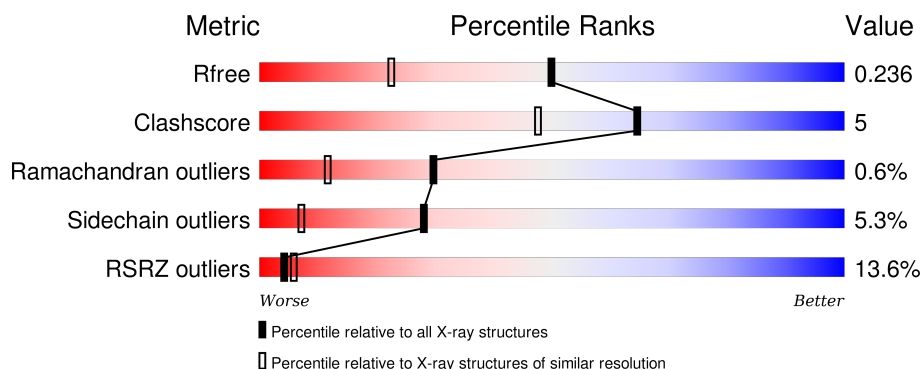
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.75 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	1609 (1.76-1.76)
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

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	203	<div> <div>12%</div> <div>73%</div> <div>9%</div> <div>16%</div> </div>
1	B	203	<div> <div>11%</div> <div>68%</div> <div>12%</div> <div>18%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2917 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 ras-related C3 botulinum toxin substrate 1 isoform Rac1b.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	170	Total	C	N	O	S	0	1	0
			1300	837	213	241	9			
1	B	167	Total	C	N	O	S	0	1	0
			1286	829	210	238	9			

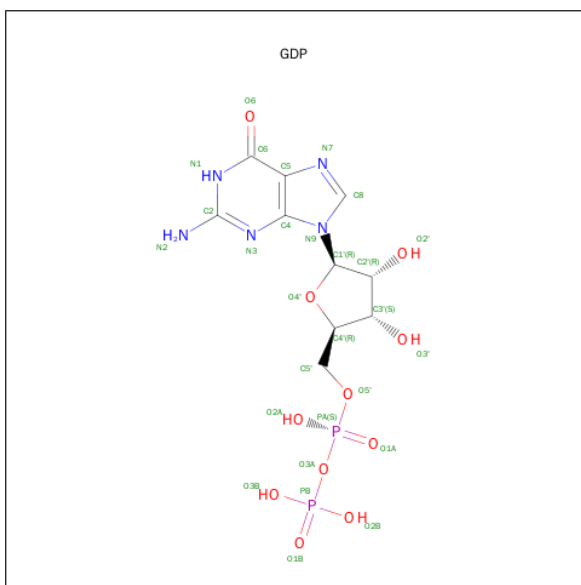
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1A	GLY	-	CLONING ARTIFACT	UNP P63000
A	2A	SER	-	CLONING ARTIFACT	UNP P63000
B	1A	GLY	-	CLONING ARTIFACT	UNP P63000
B	2A	SER	-	CLONING ARTIFACT	UNP P63000

- 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 28	C 10	N 5	O 11	P 2	0	0
3	B	1	Total 28	C 10	N 5	O 11	P 2	0	0

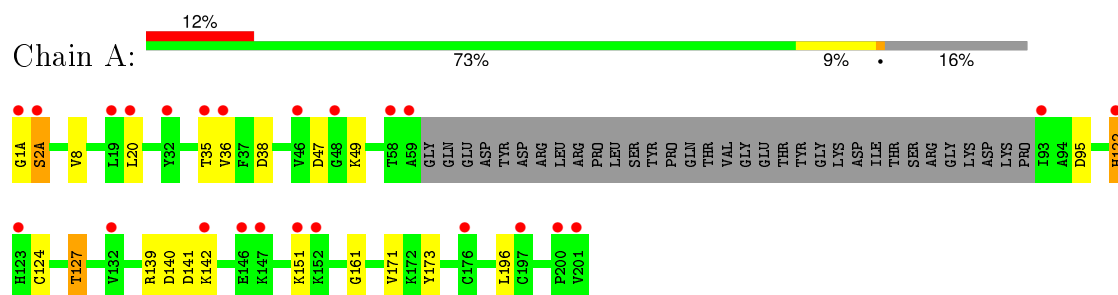
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	128	Total O 128 128	0	0
4	B	145	Total O 145 145	0	0

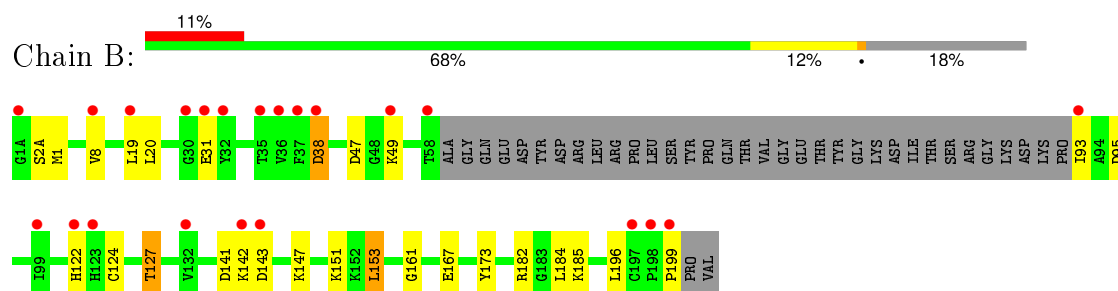
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: ras-related C3 botulinum toxin substrate 1 isoform Rac1b



- Molecule 1: ras-related C3 botulinum toxin substrate 1 isoform Rac1b



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	51.64Å 78.69Å 96.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.92 – 1.75 24.95 – 1.75	Depositor EDS
% Data completeness (in resolution range)	97.9 (24.92-1.75) 97.9 (24.95-1.75)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.96 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, $R_{free}$	0.188 , 0.223 0.206 , 0.236	Depositor DCC
$R_{free}$ test set	1956 reflections (4.93%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.6	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 50.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Outliers	0 of 39684 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2917	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 48.59 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 8.4239e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 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: GDP, MG

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	0.94	2/1332 (0.2%)	0.97	6/1814 (0.3%)
1	B	1.01	1/1317 (0.1%)	1.02	6/1792 (0.3%)
All	All	0.98	3/2649 (0.1%)	1.00	12/3606 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	171	VAL	CB-CG2	-6.18	1.39	1.52
1	A	139	ARG	CG-CD	-6.07	1.36	1.51
1	B	167	GLU	CD-OE1	5.64	1.31	1.25

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	182	ARG	NE-CZ-NH2	-9.62	115.49	120.30
1	A	140	ASP	CB-CG-OD2	8.57	126.01	118.30
1	A	47	ASP	CB-CG-OD2	7.85	125.36	118.30
1	B	47	ASP	CB-CG-OD2	7.58	125.12	118.30
1	A	141	ASP	CB-CG-OD2	6.92	124.52	118.30
1	B	38	ASP	CB-CG-OD2	6.90	124.51	118.30
1	B	143	ASP	CB-CG-OD2	6.57	124.21	118.30
1	B	95	ASP	CB-CG-OD2	6.46	124.11	118.30
1	A	95	ASP	CB-CG-OD2	6.39	124.05	118.30
1	A	139	ARG	NE-CZ-NH1	-5.76	117.42	120.30
1	A	38	ASP	CB-CG-OD2	5.31	123.08	118.30
1	B	141	ASP	CB-CG-OD2	5.28	123.06	118.30

There are no chirality outliers.

There are no planarity outliers.

## 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	1300	0	1317	13	0
1	B	1286	0	1312	14	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
4	A	128	0	0	3	0
4	B	145	0	0	3	0
All	All	2917	0	2653	27	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 (27) 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:124:CYS:HB3	1:A:127:THR:HG23	1.61	0.82
1:A:124:CYS:HB3	1:A:127:THR:CG2	2.11	0.81
1:B:49:LYS:HD3	1:B:196:LEU:HD13	1.64	0.80
1:B:124:CYS:HB3	1:B:127:THR:HG23	1.72	0.72
1:A:127:THR:HG21	4:A:596:HOH:O	1.94	0.67
1:A:124:CYS:CB	1:A:127:THR:HG23	2.27	0.65
1:B:127:THR:HG21	4:B:1568:HOH:O	1.97	0.65
1:A:1(A):GLY:HA2	1:A:2(A):SER:HB2	1.87	0.56
1:A:49:LYS:HD3	1:A:196:LEU:HD13	1.88	0.55
1:A:122:HIS:HD1	1:A:122:HIS:C	2.08	0.55
1:B:124:CYS:HB3	1:B:127:THR:CG2	2.38	0.54
1:B:199:PRO:C	4:B:1680:HOH:O	2.47	0.53
1:B:185:LYS:NZ	4:B:1634:HOH:O	2.39	0.50
1:B:49:LYS:CD	1:B:196:LEU:HD13	2.40	0.49
1:A:1(A):GLY:HA2	1:A:2(A):SER:CB	2.43	0.48
1:A:122:HIS:ND1	1:A:122:HIS:C	2.67	0.48
1:B:151:LYS:HB3	1:B:153:LEU:HD22	1.97	0.47
1:B:8:VAL:HG21	1:B:20:LEU:HD21	1.97	0.47
1:A:161:GLY:HA3	1:A:173:TYR:CZ	2.51	0.46

*Continued on next page...*



Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:THR:HG22	4:A:554:HOH:O	2.15	0.45
1:A:127:THR:HB	4:A:588:HOH:O	2.16	0.45
1:B:151:LYS:CB	1:B:153:LEU:HD22	2.49	0.43
1:B:161:GLY:HA3	1:B:173:TYR:CZ	2.54	0.42
1:B:19:LEU:HD12	1:B:184:LEU:CD1	2.48	0.42
1:B:151:LYS:O	1:B:153:LEU:HD13	2.19	0.42
1:A:8:VAL:HG21	1:A:20:LEU:HD21	2.03	0.41
1:B:124:CYS:CB	1:B:127:THR:HG23	2.47	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	167/203 (82%)	164 (98%)	1 (1%)	2 (1%)	16	3
1	B	164/203 (81%)	161 (98%)	3 (2%)	0	100	100
All	All	331/406 (82%)	325 (98%)	4 (1%)	2 (1%)	30	12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	VAL
1	A	2(A)	SER

### 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	143/174 (82%)	138 (96%)	5 (4%)	43	17
1	B	143/174 (82%)	133 (93%)	10 (7%)	19	3
All	All	286/348 (82%)	271 (95%)	15 (5%)	28	7

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	THR
1	A	122	HIS
1	A	127	THR
1	A	142	LYS
1	A	151	LYS
1	B	2(A)	SER
1	B	1	MET
1	B	31	GLU
1	B	38	ASP
1	B	93	ILE
1	B	122	HIS
1	B	127	THR
1	B	142	LYS
1	B	147	LYS
1	B	153	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	A	52	ASN
1	B	43	ASN
1	B	52	ASN
1	B	181	GLN

### 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 4 ligands modelled in this entry, 2 are 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	GDP	A	538	2	23,30,30	1.18	1 (4%)	30,47,47	1.67	5 (16%)
3	GDP	B	1538	2	23,30,30	1.11	1 (4%)	30,47,47	2.17	8 (26%)

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	538	2	-	0/12/32/32	0/3/3/3
3	GDP	B	1538	2	-	0/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	538	GDP	C6-N1	3.60	1.39	1.33
3	B	1538	GDP	C6-N1	4.19	1.40	1.33

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
3	B	1538	GDP	N3-C2-N1	-5.79	118.63	127.44
3	B	1538	GDP	C5-C6-N1	-5.00	116.75	123.59
3	A	538	GDP	N3-C2-N1	-4.61	120.42	127.44
3	A	538	GDP	C5-C6-N1	-3.11	119.34	123.59
3	B	1538	GDP	C6-C5-C4	-2.71	117.66	120.90
3	B	1538	GDP	PA-O3A-PB	-2.65	123.78	132.67
3	A	538	GDP	C6-C5-C4	-2.60	117.79	120.90
3	B	1538	GDP	C4-C5-N7	-2.06	107.58	109.48
3	B	1538	GDP	O3B-PB-O1B	2.41	118.33	110.58
3	A	538	GDP	N2-C2-N1	3.08	122.30	117.20
3	B	1538	GDP	N2-C2-N1	3.11	122.36	117.20
3	A	538	GDP	C6-N1-C2	3.65	121.01	115.94
3	B	1538	GDP	C6-N1-C2	5.38	123.40	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	170/203 (83%)	0.77	24 (14%) <b>4</b> <b>5</b>	13, 19, 40, 50	0
1	B	167/203 (82%)	0.70	22 (13%) <b>4</b> <b>6</b>	14, 19, 36, 44	0
All	All	337/406 (83%)	0.74	46 (13%) <b>4</b> <b>6</b>	13, 19, 38, 50	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	35	THR	10.2
1	B	93	ILE	7.4
1	A	36	VAL	7.4
1	B	36	VAL	7.1
1	A	59	ALA	6.2
1	A	1(A)	GLY	6.0
1	A	201	VAL	5.9
1	B	35	THR	5.6
1	B	199	PRO	5.0
1	A	93	ILE	4.8
1	B	123	HIS	4.7
1	B	32	TYR	4.6
1	A	58	THR	4.4
1	A	32	TYR	4.4
1	A	123	HIS	4.4
1	B	198	PRO	3.2
1	B	30	GLY	3.1
1	A	19	LEU	3.0
1	B	58	THR	3.0
1	B	143	ASP	3.0
1	B	99	ILE	2.9
1	A	197	CYS	2.9
1	B	132	VAL	2.9
1	A	2(A)	SER	2.8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	48	GLY	2.8
1	B	19	LEU	2.7
1	A	132	VAL	2.7
1	B	1(A)	GLY	2.7
1	B	8	VAL	2.6
1	A	152	LYS	2.6
1	B	197	CYS	2.4
1	B	38	ASP	2.4
1	A	122	HIS	2.3
1	A	142	LYS	2.3
1	A	176	CYS	2.2
1	A	46	VAL	2.2
1	B	31	GLU	2.2
1	B	142	LYS	2.2
1	A	20	LEU	2.2
1	A	146	GLU	2.1
1	A	147	LYS	2.1
1	A	200	PRO	2.0
1	B	122	HIS	2.0
1	B	49	LYS	2.0
1	B	37	PHE	2.0
1	A	151	LYS	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. 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( $\text{\AA}^2$ )	Q<0.9
3	GDP	B	1538	28/28	0.95	0.12	0.52	13,15,17,18	0
3	GDP	A	538	28/28	0.96	0.11	-0.02	12,15,17,18	0
2	MG	A	539	1/1	0.97	0.17	-	16,16,16,16	0
2	MG	B	1539	1/1	0.99	0.19	-	15,15,15,15	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.