



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 07:59 PM GMT

PDB ID : 4X3V  
Title : Crystal structure of human ribonucleotide reductase 1 bound to inhibitor  
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Deposited on : 2014-12-01  
Resolution : 3.70 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](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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
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) : rb-20026982

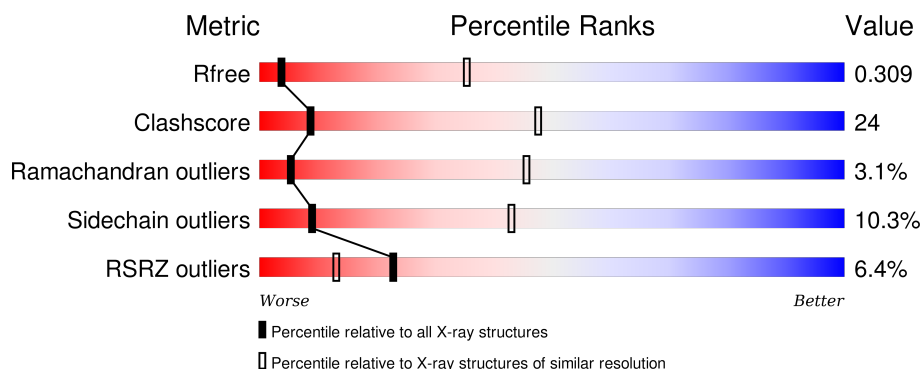
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*



The reported resolution of this entry is 3.70 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	1101 (3.90-3.50)
Clashscore	102246	1224 (3.90-3.50)
Ramachandran outliers	100387	1172 (3.90-3.50)
Sidechain outliers	100360	1170 (3.90-3.50)
RSRZ outliers	91569	1108 (3.90-3.50)

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  $\geq 3$ , 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	792	
1	B	792	

## 2 Entry composition [i](#)

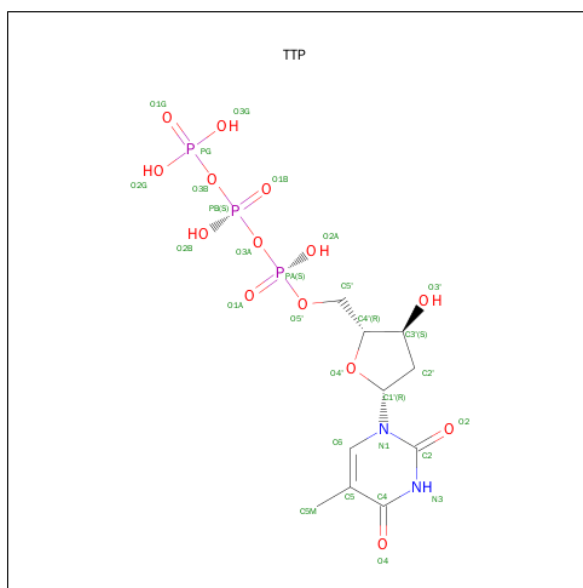
There are 3 unique types of molecules in this entry. The entry contains 11384 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	714	Total	C	N	O	S	7	0	0
			5545	3542	924	1047	32			
1	B	738	Total	C	N	O	S	0	0	0
			5751	3669	968	1080	34			

- Molecule 2 is THYMIDINE-5'-TRIPHOSPHATE (three-letter code: TTP) (formula:  $C_{10}H_{17}N_2O_{14}P_3$ ).



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

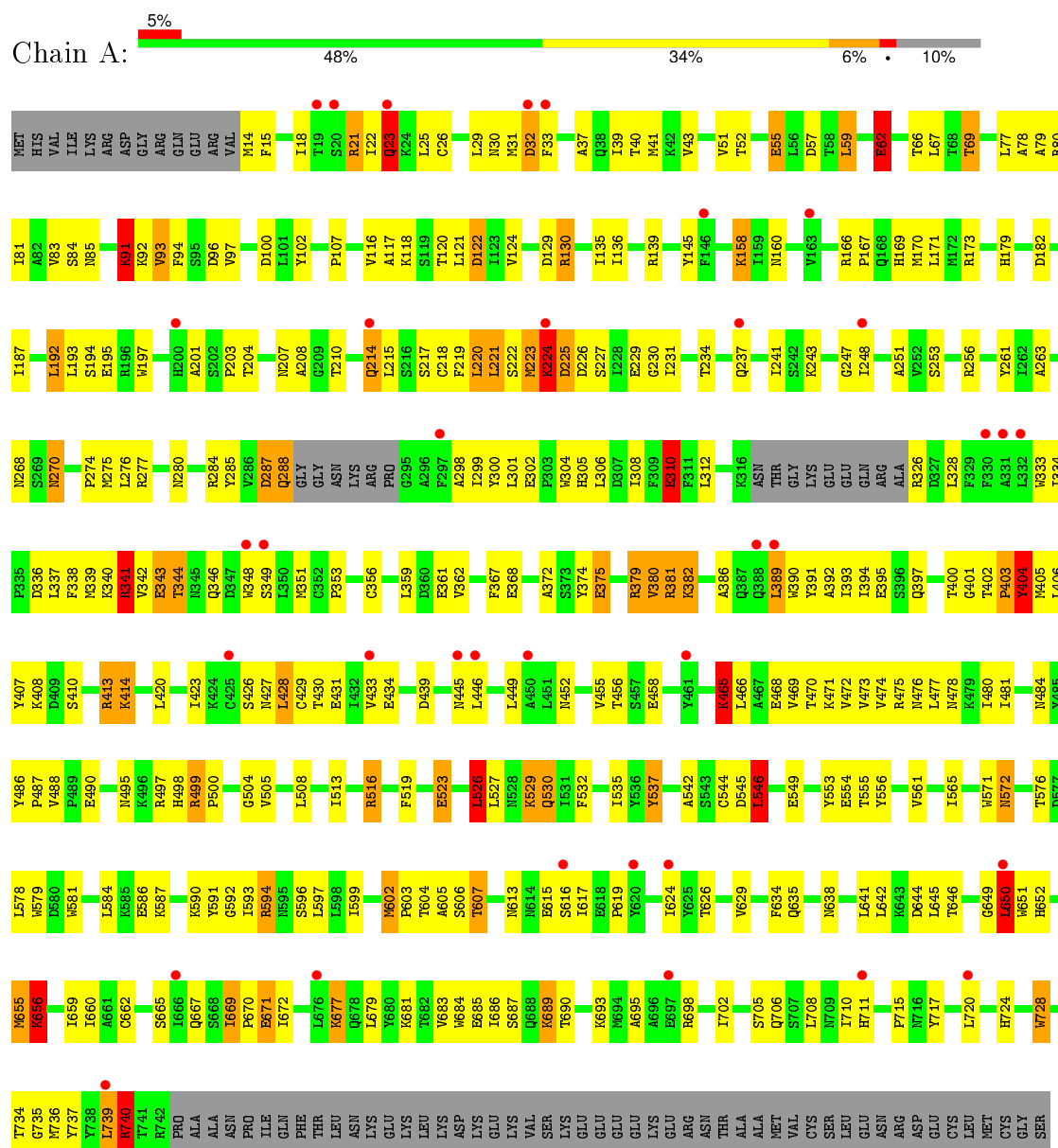
- Molecule 3 is N 6 -{N-[(1,3-dioxo-1,3-dihydro-2H-isoindol-2-yl)acetyl]-2-methyl-D-alanyl}-D-lysine (three-letter code: 3X4) (formula:  $C_{20}H_{26}N_4O_6$ ).

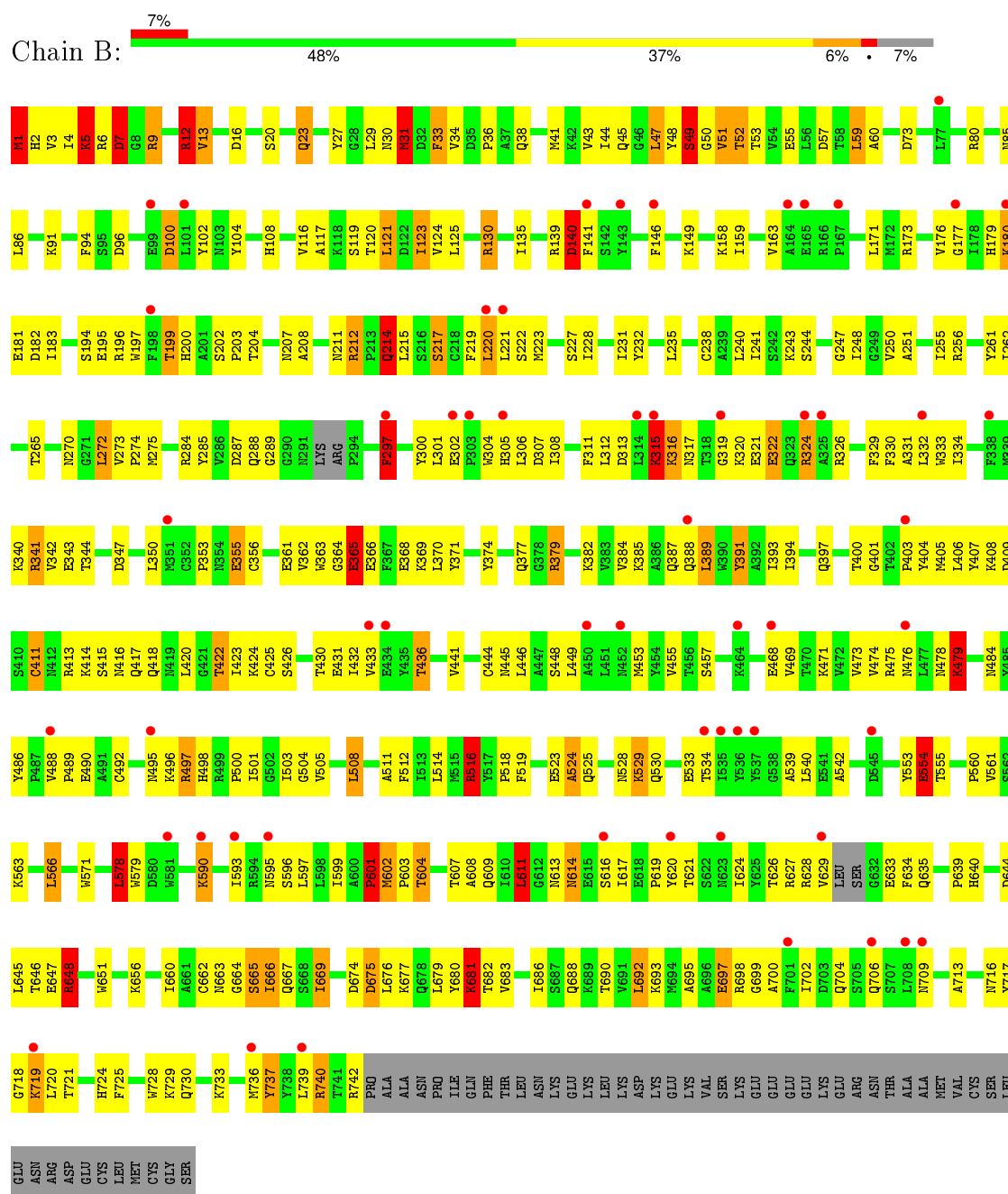


### 3 Residue-property plots

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: Ribonucleoside-diphosphate reductase large subunit





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.88Å 110.50Å 216.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	108.36 – 3.70 108.36 – 3.55	Depositor EDS
% Data completeness (in resolution range)	95.8 (108.36-3.70) 85.5 (108.36-3.55)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.25 (at 3.58Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.232 , 0.289 0.265 , 0.309	Depositor DCC
$R_{free}$ test set	1834 reflections (11.81%)	DCC
Wilson B-factor (Å <sup>2</sup> )	109.2	Xtriage
Anisotropy	0.253	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 64.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	1 of 19866 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	11384	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	121.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% 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, 0.375 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: TTP, 3X4

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	0.46	1/5666 (0.0%)	0.84	20/7709 (0.3%)
1	B	0.45	1/5877 (0.0%)	0.89	29/7989 (0.4%)
All	All	0.46	2/11543 (0.0%)	0.87	49/15698 (0.3%)

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	6
1	B	0	8
All	All	0	14

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	361	GLU	CD-OE1	7.08	1.33	1.25
1	B	692	LEU	C-O	5.05	1.32	1.23

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	526	LEU	CA-CB-CG	15.65	151.29	115.30
1	B	590	LYS	CA-CB-CG	9.49	134.28	113.40
1	B	578	LEU	CA-CB-CG	9.40	136.91	115.30
1	A	656	LYS	CD-CE-NZ	8.93	132.24	111.70
1	B	648	ARG	CG-CD-NE	-7.65	95.74	111.80

There are no chirality outliers.



5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	287	ASP	Peptide
1	A	403	PRO	Peptide
1	A	546	LEU	Peptide
1	A	571	TRP	Peptide
1	A	91	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	5545	0	5342	250	0
1	B	5751	0	5586	281	0
2	A	29	0	13	5	0
2	B	29	0	13	4	0
3	A	30	0	25	3	0
All	All	11384	0	10979	527	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 24.

The worst 5 of 527 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:497:ARG:HG3	1:B:554:GLU:HG2	1.30	1.14
1:A:667:GLN:HE21	1:A:677:LYS:HB2	1.26	0.97
1:B:1:MET:H2	1:B:12:ARG:HE	1.10	0.95
1:B:624:ILE:HD11	1:B:635:GLN:HE21	1.32	0.95
1:B:363:TRP:HD1	1:B:422:THR:HG23	1.31	0.93

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	708/792 (89%)	607 (86%)	82 (12%)	19 (3%)	6	48
1	B	732/792 (92%)	619 (85%)	88 (12%)	25 (3%)	5	43
All	All	1440/1584 (91%)	1226 (85%)	170 (12%)	44 (3%)	5	45

5 of 44 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	218	CYS
1	A	219	PHE
1	A	263	ALA
1	A	615	GLU
1	A	656	LYS

### 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	581/693 (84%)	518 (89%)	63 (11%)	8	41
1	B	607/693 (88%)	548 (90%)	59 (10%)	10	46
All	All	1188/1386 (86%)	1066 (90%)	122 (10%)	9	43

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	669	ILE

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Mol	Chain	Res	Type
1	B	31	MET
1	B	604	THR
1	A	671	GLU
1	A	739	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 18 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	200	HIS
1	B	214	GLN
1	B	476	ASN
1	B	2	HIS
1	B	85	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](#)

3 ligands are modelled in this entry.

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	TTP	A	801	-	21,30,30	0.67	0	26,47,47	2.26	2 (7%)
3	3X4	A	802	-	28,31,31	2.25	5 (17%)	38,44,44	2.30	7 (18%)
2	TTP	B	801	-	21,30,30	0.65	0	26,47,47	2.06	2 (7%)

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	TTP	A	801	-	-	0/18/34/34	0/2/2/2
3	3X4	A	802	-	-	0/23/43/43	0/2/2/2
2	TTP	B	801	-	-	0/18/34/34	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	802	3X4	C11-C12	-5.53	1.39	1.48
3	A	802	3X4	C6-C5	-3.47	1.43	1.48
3	A	802	3X4	C4-C3	2.93	1.56	1.52
3	A	802	3X4	O1-C12	6.26	1.35	1.22
3	A	802	3X4	O2-C5	6.31	1.35	1.22

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	TTP	C5-C4-N3	-8.40	118.29	125.35
3	A	802	3X4	C5-N1-C12	-7.18	106.63	111.93
2	B	801	TTP	C5-C4-N3	-7.04	119.44	125.35
3	A	802	3X4	O1-C12-N1	-5.17	120.18	124.77
3	A	802	3X4	O2-C5-N1	-4.08	121.15	124.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	TTP	5	0
3	A	802	3X4	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	801	TTP	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, 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	714/792 (90%)	0.47	36 (5%)	32 21	87, 115, 140, 165	2 (0%)
1	B	738/792 (93%)	0.54	57 (7%)	16 10	90, 125, 154, 173	0
All	All	1452/1584 (91%)	0.50	93 (6%)	23 13	87, 119, 148, 173	2 (0%)

The worst 5 of 93 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	165	GLU	5.4
1	A	666	ILE	4.2
1	B	198	PHE	4.1
1	A	433	VAL	3.9
1	B	434	GLU	3.6

### 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
2	TTP	A	801	29/29	0.78	0.27	-0.07	101,127,159,165	0
3	3X4	A	802	30/30	0.78	0.24	-0.31	103,119,126,129	0
2	TTP	B	801	29/29	0.90	0.21	-0.48	93,111,129,132	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.