Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:37 AM GMT

PDB ID	:	3BJE
Title	:	Crystal structure of Trypanosoma brucei nucleoside phosphorylase shows uridine phosphorylase activity
Authors	:	Larson, E.T.; Merritt, E.A.; Structural Genomics of Pathogenic Protozoa Consortium (SGPP)
Deposited on	:	2007-12-03
Resolution	:	1.44 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
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:

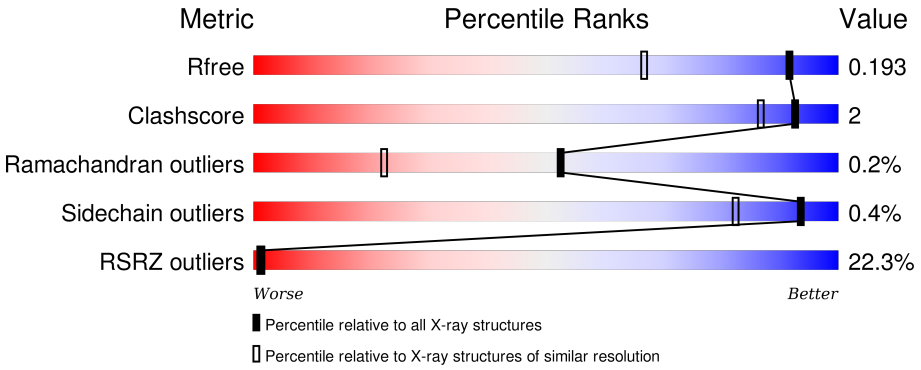
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.44 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	1164 (1.46-1.42)
Clashscore	102246	1219 (1.46-1.42)
Ramachandran outliers	100387	1200 (1.46-1.42)
Sidechain outliers	100360	1200 (1.46-1.42)
RSRZ outliers	91569	1166 (1.46-1.42)

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 <=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	349	23% 91% • 6%
1	B	349	19% 88% 6% 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5601 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.

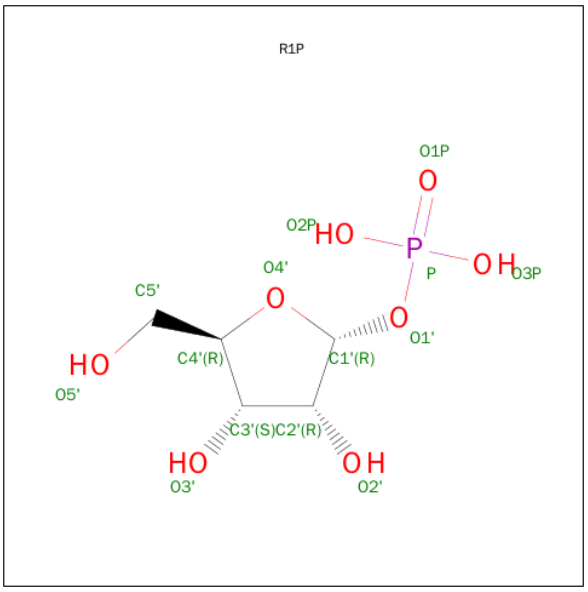
- Molecule 1 is a protein called Nucleoside phosphorylase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	5	0
			2521	1568	450	484	19			
1	B	327	Total	C	N	O	S	0	8	0
			2526	1573	444	489	20			

There are 16 discrepancies between the modelled and reference sequences:

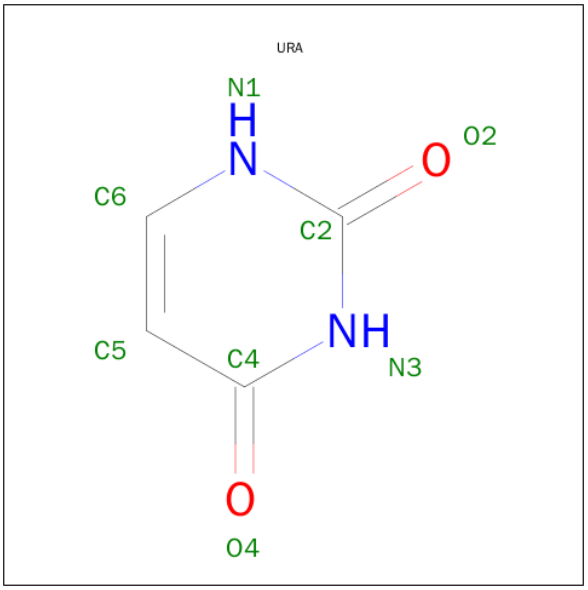
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	EXPRESSION TAG	UNP Q57VZ2
A	-6	ALA	-	EXPRESSION TAG	UNP Q57VZ2
A	-5	HIS	-	EXPRESSION TAG	UNP Q57VZ2
A	-4	HIS	-	EXPRESSION TAG	UNP Q57VZ2
A	-3	HIS	-	EXPRESSION TAG	UNP Q57VZ2
A	-2	HIS	-	EXPRESSION TAG	UNP Q57VZ2
A	-1	HIS	-	EXPRESSION TAG	UNP Q57VZ2
A	0	HIS	-	EXPRESSION TAG	UNP Q57VZ2
B	-7	MET	-	EXPRESSION TAG	UNP Q57VZ2
B	-6	ALA	-	EXPRESSION TAG	UNP Q57VZ2
B	-5	HIS	-	EXPRESSION TAG	UNP Q57VZ2
B	-4	HIS	-	EXPRESSION TAG	UNP Q57VZ2
B	-3	HIS	-	EXPRESSION TAG	UNP Q57VZ2
B	-2	HIS	-	EXPRESSION TAG	UNP Q57VZ2
B	-1	HIS	-	EXPRESSION TAG	UNP Q57VZ2
B	0	HIS	-	EXPRESSION TAG	UNP Q57VZ2

- Molecule 2 is SUGAR (RIBOSE-1-PHOSPHATE) (three-letter code: R1P) (formula: $C_5H_{11}O_8P$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O P 14 5 8 1	0	0
2	B	1	Total C O P 14 5 8 1	0	0

- Molecule 3 is URACIL (three-letter code: URA) (formula: $C_4H_4N_2O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 8 4 2 2	0	0
3	B	1	Total C N O 8 4 2 2	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Ca 1 1	0	0

- Molecule 5 is water.

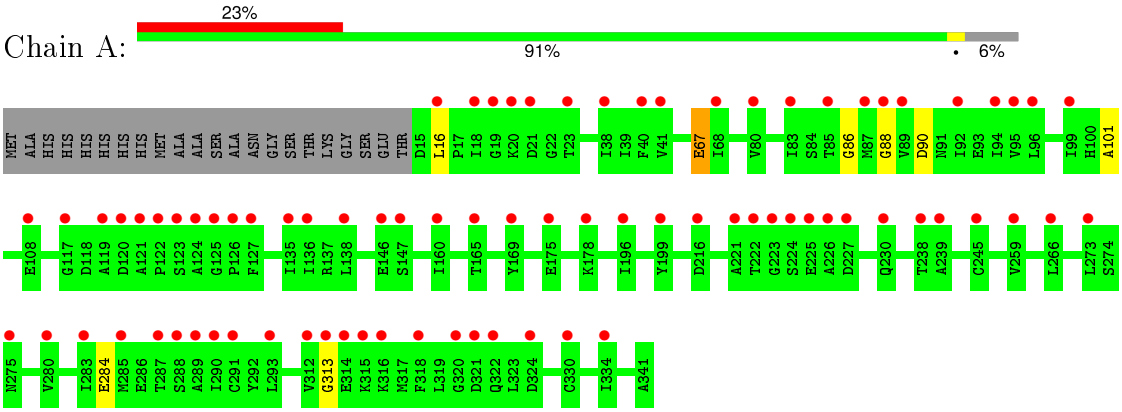
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	234	Total O 238 238	0	4
5	B	267	Total O 271 271	0	4

3 Residue-property plots (i)

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.

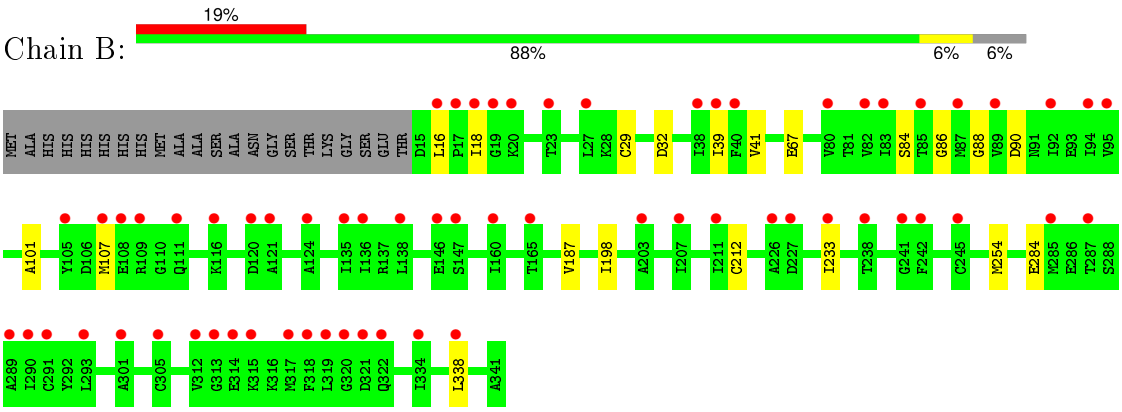
- Molecule 1: Nucleoside phosphorylase, putative

Chain A:



- Molecule 1: Nucleoside phosphorylase, putative

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	63.02Å 95.39Å 63.48Å 90.00° 105.91° 90.00°	Depositor
Resolution (Å)	35.38 – 1.44 35.38 – 1.44	Depositor EDS
% Data completeness (in resolution range)	94.7 (35.38-1.44) 94.7 (35.38-1.44)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 1.44Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.155 , 0.184 0.164 , 0.193	Depositor DCC
R_{free} test set	6072 reflections (5.31%)	DCC
Wilson B-factor (Å^2)	14.8	Xtriage
Anisotropy	0.314	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 44.7	EDS
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 123193 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5601	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: CA, URA, R1P

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	0.48	1/2572 (0.0%)	0.66	0/3468
1	B	0.50	1/2589 (0.0%)	0.68	0/3492
All	All	0.49	2/5161 (0.0%)	0.67	0/6960

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	67	GLU	CD-OE2	6.14	1.32	1.25
1	B	29	CYS	CB-SG	-5.04	1.73	1.81

There are no bond angle outliers.

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	2521	0	2537	7	0
1	B	2526	0	2542	16	0
2	A	14	0	9	0	0
2	B	14	0	9	0	0
3	A	8	0	3	0	0
3	B	8	0	3	0	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	238	0	0	0	0
5	B	271	0	0	2	0
All	All	5601	0	5103	20	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 2.

All (20) 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:32[A]:ASP:OD1	5:B:753:HOH:O	1.95	0.84
1:B:254[B]:MET:HE3	5:B:739:HOH:O	1.79	0.82
1:B:16:LEU:HD21	1:B:101:ALA:CB	2.14	0.77
1:A:67:GLU:HG3	1:A:86:GLY:HA3	1.74	0.69
1:B:16:LEU:HD21	1:B:101:ALA:HB1	1.73	0.69
1:B:67:GLU:HG3	1:B:86:GLY:HA3	1.80	0.63
1:A:67:GLU:HB3	1:B:67:GLU:HB3	1.81	0.62
1:B:16:LEU:HD21	1:B:101:ALA:HB2	1.82	0.61
1:A:16:LEU:HD21	1:A:101:ALA:CB	2.32	0.59
1:B:187:VAL:HG11	1:B:198:ILE:CD1	2.34	0.58
1:A:16:LEU:HD21	1:A:101:ALA:HB2	1.87	0.56
1:B:187:VAL:HG11	1:B:198:ILE:HD13	1.93	0.51
1:B:18:ILE:HG21	1:B:107:MET:HE3	1.95	0.49
1:B:212:CYS:SG	1:B:233:ILE:HD11	2.57	0.45
1:A:90:ASP:OD2	1:B:88:GLY:HA3	2.19	0.43
1:A:16:LEU:HD21	1:A:101:ALA:HB1	2.00	0.42
1:A:88:GLY:HA3	1:B:90:ASP:OD2	2.20	0.41
1:B:39:ILE:HG13	1:B:338:LEU:HD22	2.03	0.41
1:B:41:VAL:O	1:B:84:SER:HA	2.21	0.41
1:B:187:VAL:CG1	1:B:198:ILE:CD1	3.00	0.40

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	330/349 (95%)	322 (98%)	7 (2%)	1 (0%)	46 18
1	B	333/349 (95%)	325 (98%)	8 (2%)	0	100 100
All	All	663/698 (95%)	647 (98%)	15 (2%)	1 (0%)	52 22

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	313	GLY

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	273/284 (96%)	272 (100%)	1 (0%)	93 82
1	B	276/284 (97%)	275 (100%)	1 (0%)	93 82
All	All	549/568 (97%)	547 (100%)	2 (0%)	93 82

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	284	GLU
1	B	284	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 5 ligands modelled in this entry, 1 is 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	$\#\|Z\| > 2$
2	R1P	A	401	-	13,14,14	0.74	0	18,21,21	1.72	4 (22%)
3	URA	A	501	-	4,8,8	0.56	0	6,10,10	8.59	4 (66%)
2	R1P	B	401	-	13,14,14	0.74	0	18,21,21	1.94	3 (16%)
3	URA	B	501	-	4,8,8	0.68	0	6,10,10	8.13	4 (66%)

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	R1P	A	401	-	-	0/6/23/23	0/1/1/1
3	URA	A	501	-	-	0/0/0/0	0/1/1/1
2	R1P	B	401	-	-	0/6/23/23	0/1/1/1
3	URA	B	501	-	-	0/0/0/0	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	501	URA	N1-C2-N3	-13.44	119.76	128.33
3	B	501	URA	N1-C2-N3	-12.52	120.35	128.33
3	A	501	URA	C5-C6-N1	-3.67	119.71	123.90
3	B	501	URA	C5-C6-N1	-3.44	119.97	123.90
2	B	401	R1P	O1'-P-O1P	-3.21	99.10	107.11
2	A	401	R1P	O1'-P-O1P	-2.94	99.77	107.11
2	A	401	R1P	O3P-P-O2P	2.18	115.67	107.38
2	A	401	R1P	O4'-C1'-O1'	2.29	113.63	108.90
2	B	401	R1P	O4'-C1'-O1'	2.30	113.66	108.90
2	A	401	R1P	O1'-C1'-C2'	4.64	114.95	106.67
2	B	401	R1P	O1'-C1'-C2'	5.57	116.60	106.67
3	B	501	URA	C4-N3-C2	6.79	120.87	114.14
3	A	501	URA	C4-N3-C2	7.27	121.35	114.14
3	B	501	URA	C6-N1-C2	13.37	120.98	114.40
3	A	501	URA	C6-N1-C2	13.94	121.26	114.40

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^{th} 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	327/349 (93%)	1.47	81 (24%) 1 1	14, 20, 35, 51	0
1	B	327/349 (93%)	1.34	65 (19%) 1 2	11, 17, 33, 48	0
All	All	654/698 (93%)	1.40	146 (22%) 1 1	11, 19, 34, 51	0

All (146) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	313	GLY	9.9
1	A	119	ALA	8.0
1	A	122	PRO	7.3
1	B	16	LEU	6.1
1	A	221	ALA	5.9
1	A	318	PHE	5.7
1	B	108	GLU	5.7
1	B	315	LYS	5.6
1	A	20	LYS	5.5
1	A	92	ILE	5.3
1	B	107	MET	5.2
1	B	318	PHE	5.2
1	B	19	GLY	5.1
1	B	20	LYS	5.1
1	A	321	ASP	5.0
1	B	109	ARG	4.9
1	A	123	SER	4.9
1	A	226	ALA	4.8
1	B	319	LEU	4.8
1	A	117	GLY	4.8
1	A	89	VAL	4.6
1	A	320	GLY	4.6
1	B	18	ILE	4.3
1	A	94	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	222	THR	4.3
1	A	224	SER	4.3
1	A	120	ASP	4.2
1	B	314	GLU	4.2
1	B	111	GLN	4.0
1	A	127	PHE	4.0
1	A	18	ILE	3.9
1	A	293	LEU	3.9
1	B	92	ILE	3.8
1	A	96	LEU	3.8
1	B	89	VAL	3.8
1	A	290	ILE	3.7
1	B	226	ALA	3.7
1	A	146	GLU	3.6
1	A	316	LYS	3.6
1	A	313	GLY	3.6
1	A	125	GLY	3.5
1	A	136	ILE	3.5
1	B	320	GLY	3.5
1	A	95	VAL	3.4
1	B	321	ASP	3.4
1	A	121	ALA	3.3
1	A	314	GLU	3.3
1	A	135	ILE	3.2
1	B	135	ILE	3.2
1	B	290	ILE	3.2
1	A	175	GLU	3.1
1	A	275	ASN	3.1
1	B	242	PHE	3.1
1	B	17	PRO	3.1
1	A	124	ALA	3.0
1	A	312	VAL	3.0
1	A	216	ASP	3.0
1	B	38	ILE	3.0
1	A	223	GLY	3.0
1	A	23	THR	3.0
1	A	315	LYS	3.0
1	B	83	ILE	3.0
1	A	165	THR	2.9
1	B	105	TYR	2.9
1	B	23	THR	2.8
1	A	19	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	88	GLY	2.8
1	A	16	LEU	2.8
1	B	312	VAL	2.8
1	A	196	ILE	2.8
1	B	95	VAL	2.8
1	B	338	LEU	2.8
1	B	136	ILE	2.7
1	A	324	ASP	2.7
1	A	289	ALA	2.7
1	A	83	ILE	2.7
1	B	203	ALA	2.7
1	A	227	ASP	2.6
1	A	126	PRO	2.6
1	B	39	ILE	2.6
1	B	207	ILE	2.6
1	A	273	LEU	2.6
1	A	160	ILE	2.6
1	B	233	ILE	2.6
1	A	225	GLU	2.6
1	A	138	LEU	2.6
1	B	147	SER	2.5
1	A	80[A]	VAL	2.5
1	A	285	MET	2.5
1	B	87	MET	2.5
1	A	21	ASP	2.5
1	A	283	ILE	2.5
1	A	334	ILE	2.5
1	B	94	ILE	2.5
1	A	230	GLN	2.5
1	B	289	ALA	2.5
1	B	317	MET	2.5
1	B	245	CYS	2.5
1	A	147	SER	2.4
1	B	165	THR	2.4
1	B	227	ASP	2.4
1	A	38	ILE	2.4
1	A	287	THR	2.4
1	A	199	TYR	2.3
1	A	291	CYS	2.3
1	B	238	THR	2.3
1	A	178	LYS	2.3
1	B	293	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	238	THR	2.3
1	B	291	CYS	2.3
1	A	239	ALA	2.3
1	A	266	LEU	2.3
1	B	287	THR	2.3
1	B	116	LYS	2.2
1	A	41	VAL	2.2
1	A	245	CYS	2.2
1	B	138	LEU	2.2
1	A	87	MET	2.2
1	B	301	ALA	2.2
1	A	85	THR	2.2
1	B	40	PHE	2.2
1	B	80[A]	VAL	2.2
1	B	160	ILE	2.2
1	B	211	ILE	2.2
1	B	334	ILE	2.2
1	B	241	GLY	2.1
1	B	85	THR	2.1
1	A	288	SER	2.1
1	A	259	VAL	2.1
1	A	280	VAL	2.1
1	B	121	ALA	2.1
1	B	146	GLU	2.1
1	A	322	GLN	2.1
1	B	82	VAL	2.1
1	B	27	LEU	2.1
1	A	99	ILE	2.1
1	A	108	GLU	2.1
1	B	120	ASP	2.1
1	B	305	CYS	2.0
1	A	68	ILE	2.0
1	A	40	PHE	2.0
1	A	169	TYR	2.0
1	B	124	ALA	2.0
1	A	330	CYS	2.0
1	B	285	MET	2.0
1	B	322	GLN	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^{th} 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^2)	Q<0.9
2	R1P	B	401	14/14	0.93	0.19	1.13	19,24,28,31	0
2	R1P	A	401	14/14	0.91	0.18	0.64	19,24,27,28	0
3	URA	B	501	8/8	0.98	0.12	-1.09	14,17,20,20	0
3	URA	A	501	8/8	0.96	0.10	-1.11	16,19,22,23	0
4	CA	B	402	1/1	1.00	0.02	-14.33	13,13,13,13	0

6.5 Other polymers (i)

There are no such residues in this entry.