



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:07 PM GMT

PDB ID : 4HA9
Title : Structural insights into the reduction mechanism of *Saccharomyces cerevisia*
Riboflavin Biosynthesis Reductase Rib7
Authors : Lv, Z.; Sun, J.; Liu, Y.
Deposited on : 2012-09-25
Resolution : 2.35 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

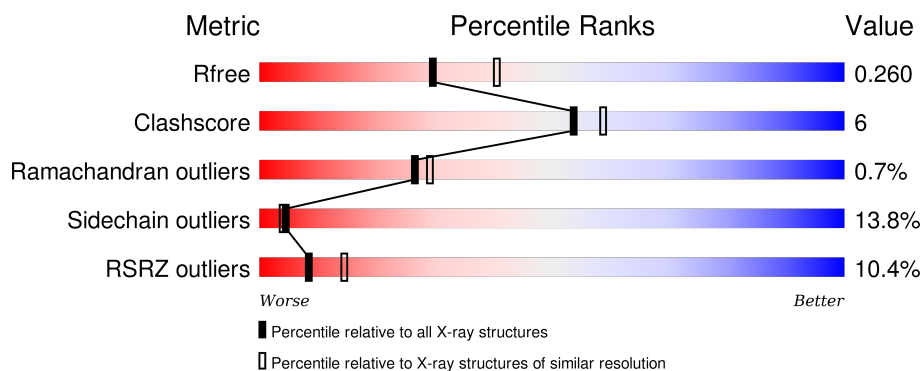
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

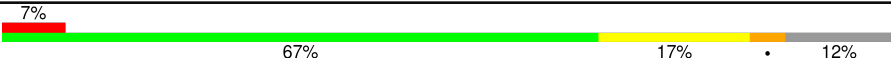
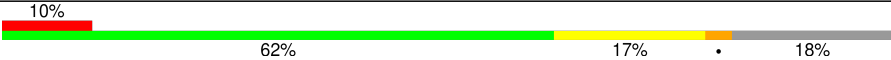
The reported resolution of this entry is 2.35 Å.

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	1352 (2.38-2.34)
Clashscore	102246	1456 (2.38-2.34)
Ramachandran outliers	100387	1435 (2.38-2.34)
Sidechain outliers	100360	1436 (2.38-2.34)
RSRZ outliers	91569	1358 (2.38-2.34)

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	249	
1	B	249	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3466 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 2,5-diamino-6-ribosylamino-4(3H)-pyrimidinone 5'-phosphate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1722	1098	297	320	7			
1	B	204	Total	C	N	O	S	0	0	0
			1626	1041	278	301	6			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	EXPRESSION TAG	UNP P33312
A	-3	PRO	-	EXPRESSION TAG	UNP P33312
A	-2	LEU	-	EXPRESSION TAG	UNP P33312
A	-1	GLY	-	EXPRESSION TAG	UNP P33312
A	0	SER	-	EXPRESSION TAG	UNP P33312
B	-4	GLY	-	EXPRESSION TAG	UNP P33312
B	-3	PRO	-	EXPRESSION TAG	UNP P33312
B	-2	LEU	-	EXPRESSION TAG	UNP P33312
B	-1	GLY	-	EXPRESSION TAG	UNP P33312
B	0	SER	-	EXPRESSION TAG	UNP P33312

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

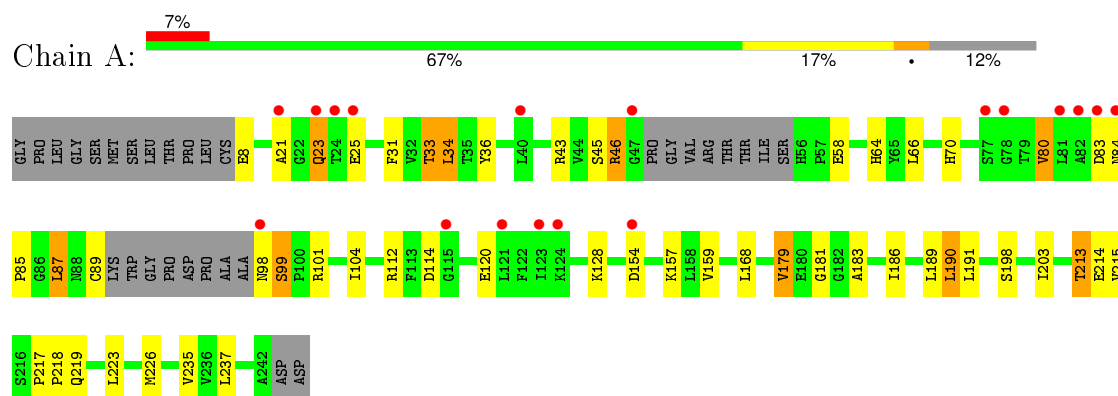
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	37	Total	O	0	0
			37	37		
3	B	33	Total	O	0	0
			33	33		

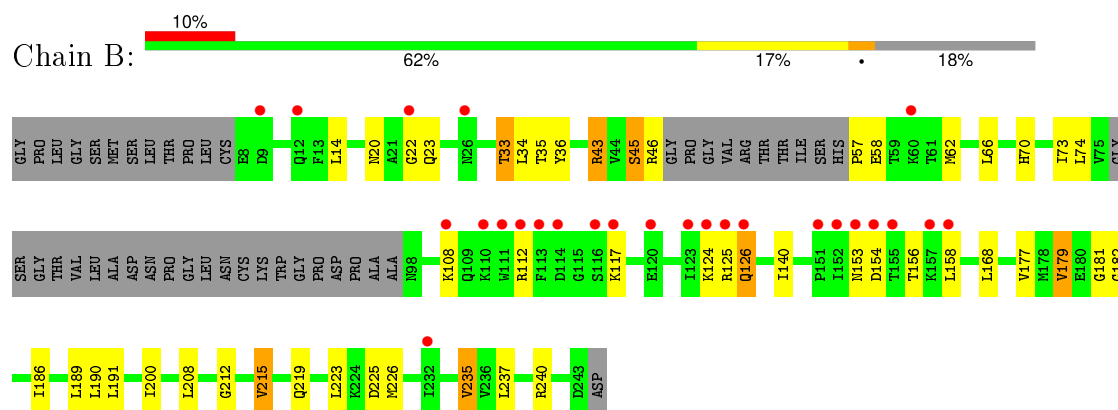
3 Residue-property plots [i](#)

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: 2,5-diamino-6-ribosylamino-4(3H)-pyrimidinone 5'-phosphate reductase



- Molecule 1: 2,5-diamino-6-ribosylamino-4(3H)-pyrimidinone 5'-phosphate reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	45.98 Å 68.87 Å 150.34 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.43 – 2.35 34.43 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.3 (34.43-2.35) 99.3 (34.43-2.35)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.18 (at 2.34 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.205 , 0.265 0.190 , 0.260	Depositor DCC
R_{free} test set	1050 reflections (5.13%)	DCC
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 20490 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3466	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.89% 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: NDP

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	0.41	0/1757	0.64	0/2386
1	B	0.39	0/1659	0.65	0/2251
All	All	0.40	0/3416	0.64	0/4637

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	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	181	GLY	Peptide
1	B	181	GLY	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	1722	0	1745	27	0
1	B	1626	0	1655	18	0
2	A	48	0	25	5	0
3	A	37	0	0	2	0
3	B	33	0	0	0	0
All	All	3466	0	3425	44	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 6.

All (44) 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:225:ASP:OD1	1:B:240:ARG:NH1	2.15	0.79
1:B:35:THR:HG23	1:B:200:ILE:HB	1.72	0.72
1:A:235:VAL:HG21	1:B:235:VAL:HG21	1.73	0.71
1:B:20:ASN:ND2	1:B:22:GLY:O	2.28	0.66
1:B:36:TYR:CE1	1:B:215:VAL:HG11	2.31	0.64
1:A:186:ILE:HG22	1:A:190:LEU:HD22	1.82	0.62
1:B:14:LEU:HD11	1:B:62:MET:HG3	1.83	0.61
1:A:99:SER:O	1:A:128:LYS:NZ	2.25	0.61
1:B:46:ARG:HG2	1:B:212:GLY:HA2	1.84	0.60
1:A:21:ALA:O	1:A:23:GLN:NE2	2.38	0.57
1:A:159:VAL:HG12	2:A:301:NDP:C6A	2.34	0.57
1:A:45:SER:HB3	1:A:213:THR:HG23	1.87	0.56
1:A:80:VAL:HG11	1:A:104:ILE:HD12	1.88	0.55
1:A:214:GLU:O	3:A:419:HOH:O	2.18	0.54
1:A:83:ASP:O	1:A:85:PRO:HD3	2.08	0.54
1:A:183:ALA:H	2:A:301:NDP:H51N	1.72	0.54
1:A:34:LEU:HD23	1:A:179:VAL:HG22	1.90	0.53
1:B:182:GLY:O	1:B:186:ILE:HG12	2.09	0.52
1:B:35:THR:HA	1:B:200:ILE:O	2.13	0.49
1:A:89:CYS:HB3	1:A:99:SER:HB2	1.94	0.49
1:A:31:PHE:HE1	1:A:33:THR:HG22	1.78	0.48
1:B:57:PRO:HA	1:B:58:GLU:HA	1.70	0.47
1:A:85:PRO:HB2	1:A:87:LEU:HD13	1.98	0.46
1:A:85:PRO:HG2	1:A:87:LEU:HD21	1.97	0.46
1:A:64:HIS:CE1	1:A:89:CYS:HA	2.51	0.46
1:A:31:PHE:CE1	1:A:33:THR:HG22	2.51	0.46
1:A:36:TYR:HB2	2:A:301:NDP:H41N	1.99	0.45
1:A:33:THR:HG23	1:A:70:HIS:NE2	2.32	0.45
1:B:43:ARG:HG2	1:B:212:GLY:C	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:VAL:HG12	2:A:301:NDP:N6A	2.32	0.45
1:B:124:LYS:NZ	1:B:126:GLN:OE1	2.51	0.43
1:B:45:SER:OG	1:B:46:ARG:N	2.48	0.43
1:A:45:SER:OG	1:A:46:ARG:N	2.51	0.43
1:A:33:THR:HB	1:A:198:SER:HB2	2.01	0.43
1:A:159:VAL:HG12	2:A:301:NDP:N1A	2.35	0.42
1:A:83:ASP:OD1	1:A:84:ASN:N	2.52	0.42
1:B:33:THR:HG23	1:B:70:HIS:NE2	2.34	0.42
1:A:203:ILE:HB	1:A:235:VAL:HG12	2.02	0.41
1:B:153:ASN:HB3	1:B:156:THR:OG1	2.19	0.41
1:B:208:LEU:HA	1:B:208:LEU:HD23	1.90	0.41
1:B:74:LEU:HB3	1:B:179:VAL:HB	2.02	0.41
1:A:217:PRO:HA	1:A:218:PRO:HD3	1.87	0.41
1:A:8:GLU:N	3:A:420:HOH:O	2.53	0.41
1:B:36:TYR:HE1	1:B:215:VAL:HG11	1.84	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	213/249 (86%)	201 (94%)	10 (5%)	2 (1%)	21	22
1	B	198/249 (80%)	189 (96%)	8 (4%)	1 (0%)	34	39
All	All	411/498 (82%)	390 (95%)	18 (4%)	3 (1%)	26	29

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	23	GLN
1	A	23	GLN
1	A	58	GLU

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	197/221 (89%)	170 (86%)	27 (14%)	4	4
1	B	187/221 (85%)	161 (86%)	26 (14%)	4	4
All	All	384/442 (87%)	331 (86%)	53 (14%)	4	4

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	GLU
1	A	33	THR
1	A	34	LEU
1	A	43	ARG
1	A	46	ARG
1	A	66	LEU
1	A	80	VAL
1	A	87	LEU
1	A	98	ASN
1	A	99	SER
1	A	101	ARG
1	A	112	ARG
1	A	114	ASP
1	A	120	GLU
1	A	154	ASP
1	A	157	LYS
1	A	168	LEU
1	A	179	VAL
1	A	189	LEU
1	A	190	LEU
1	A	191	LEU
1	A	213	THR
1	A	215	VAL
1	A	219	GLN
1	A	223	LEU
1	A	226	MET
1	A	237	LEU

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Mol	Chain	Res	Type
1	B	33	THR
1	B	34	LEU
1	B	43	ARG
1	B	45	SER
1	B	66	LEU
1	B	73	ILE
1	B	108	LYS
1	B	112	ARG
1	B	117	LYS
1	B	125	ARG
1	B	126	GLN
1	B	140	ILE
1	B	154	ASP
1	B	158	LEU
1	B	168	LEU
1	B	177	VAL
1	B	179	VAL
1	B	189	LEU
1	B	190	LEU
1	B	191	LEU
1	B	215	VAL
1	B	219	GLN
1	B	223	LEU
1	B	226	MET
1	B	235	VAL
1	B	237	LEU

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

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

1 ligand is 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	NDP	A	301	-	42,52,52	1.90	11 (26%)	55,80,80	2.23	10 (18%)

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	NDP	A	301	-	-	0/30/77/77	0/5/5/5

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	NDP	C4N-C5N	-4.81	1.38	1.49
2	A	301	NDP	C3B-C4B	-3.86	1.42	1.53
2	A	301	NDP	C3D-C4D	-3.22	1.44	1.53
2	A	301	NDP	O2D-C2D	-3.21	1.35	1.43
2	A	301	NDP	C2D-C3D	-3.15	1.44	1.53
2	A	301	NDP	C3B-C2B	-2.78	1.46	1.53
2	A	301	NDP	PN-O1N	2.22	1.59	1.51
2	A	301	NDP	PA-O1A	2.67	1.60	1.51
2	A	301	NDP	C6N-C5N	2.93	1.39	1.33
2	A	301	NDP	C6A-N6A	3.51	1.45	1.34
2	A	301	NDP	C7N-N7N	4.11	1.45	1.33

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	NDP	N3A-C2A-N1A	-12.45	119.36	128.89
2	A	301	NDP	C1B-N9A-C4A	-4.73	119.80	126.94
2	A	301	NDP	C4A-C5A-N7A	-2.67	107.02	109.48

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	301	NDP	C4B-O4B-C1B	-2.66	106.80	109.72
2	A	301	NDP	C2A-N1A-C6A	2.05	122.43	118.77
2	A	301	NDP	C5N-C4N-C3N	2.47	119.33	112.52
2	A	301	NDP	O4D-C1D-N1N	2.53	113.42	108.07
2	A	301	NDP	O4B-C1B-N9A	2.62	113.57	108.10
2	A	301	NDP	O5D-C5D-C4D	2.76	119.30	109.12
2	A	301	NDP	O3-PN-O5D	3.96	113.45	102.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	NDP	5	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, 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	219/249 (87%)	0.42	18 (8%) 14 23	26, 46, 86, 103	0
1	B	204/249 (81%)	0.60	26 (12%) 5 9	28, 48, 98, 116	0
All	All	423/498 (84%)	0.50	44 (10%) 8 14	26, 47, 94, 116	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	155	THR	6.7
1	B	125	ARG	5.2
1	A	24	THR	5.1
1	B	9	ASP	4.9
1	A	83	ASP	4.5
1	B	113	PHE	4.0
1	B	124	LYS	3.7
1	B	152	ILE	3.6
1	B	114	ASP	3.5
1	B	153	ASN	3.4
1	B	126	GLN	3.4
1	B	151	PRO	3.4
1	A	81	LEU	3.3
1	B	154	ASP	3.3
1	A	77	SER	3.3
1	B	108	LYS	3.2
1	A	115	GLY	3.1
1	B	116	SER	3.1
1	A	98	ASN	3.1
1	B	158	LEU	3.1
1	A	25	GLU	3.1
1	B	26	ASN	3.0
1	A	124	LYS	2.9
1	B	110	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	23	GLN	2.8
1	B	117	LYS	2.8
1	A	47	GLY	2.8
1	A	84	ASN	2.7
1	A	78	GLY	2.7
1	B	111	TRP	2.7
1	B	120	GLU	2.6
1	B	22	GLY	2.6
1	A	82	ALA	2.6
1	B	12	GLN	2.5
1	A	154	ASP	2.4
1	B	112	ARG	2.4
1	B	60	LYS	2.4
1	B	232	ILE	2.3
1	A	121	LEU	2.3
1	A	123	ILE	2.3
1	B	123	ILE	2.3
1	B	157	LYS	2.2
1	A	40	LEU	2.1
1	A	21	ALA	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, 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(Å ²)	Q<0.9
2	NDP	A	301	48/48	0.88	0.28	1.95	39,77,123,130	0

6.5 Other polymers [i](#)

There are no such residues in this entry.