



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 3, 2017 – 12:54 AM EDT

PDB ID : 1PR9  
Title : Human L-Xylulose Reductase Holoenzyme  
Authors : El-Kabbani, O.; Ishikura, S.; Darmanin, C.; Carbone, V.; Chung, R.P.-T.;  
Usami, N.; Hara, A.  
Deposited on : unknown  
Resolution : 1.96 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.

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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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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-20030345

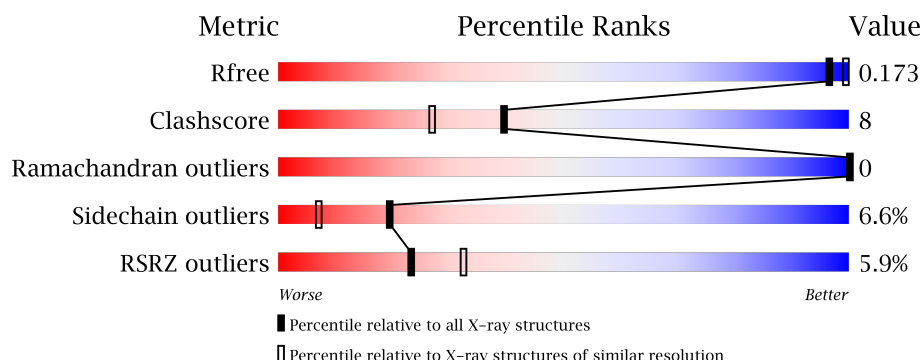
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.96 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))
$R_{free}$	100719	2004 (1.96-1.96)
Clashscore	112137	2136 (1.96-1.96)
Ramachandran outliers	110173	2117 (1.96-1.96)
Sidechain outliers	110143	2117 (1.96-1.96)
RSRZ outliers	101464	2018 (1.96-1.96)

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	244	<div> <div>7%</div> <div>80%</div> <div>16%</div> <div>.</div> </div>
1	B	244	<div> <div>5%</div> <div>84%</div> <div>12%</div> <div>.</div> </div>

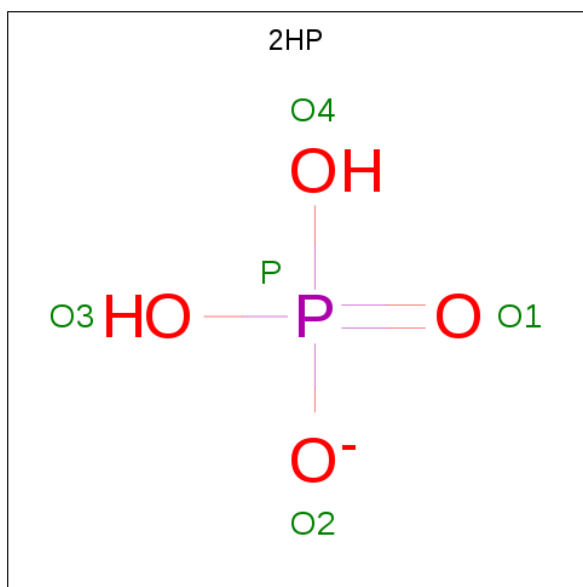
The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	2HP	A	247	-	-	-	X
4	2HP	B	1247	-	-	-	X



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

- Molecule 4 is DIHYDROGENPHOSPHATE ION (three-letter code: 2HP) (formula:  $\text{H}_2\text{O}_4\text{P}$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	B	1	Total	O	P	0	0
			5	4	1		

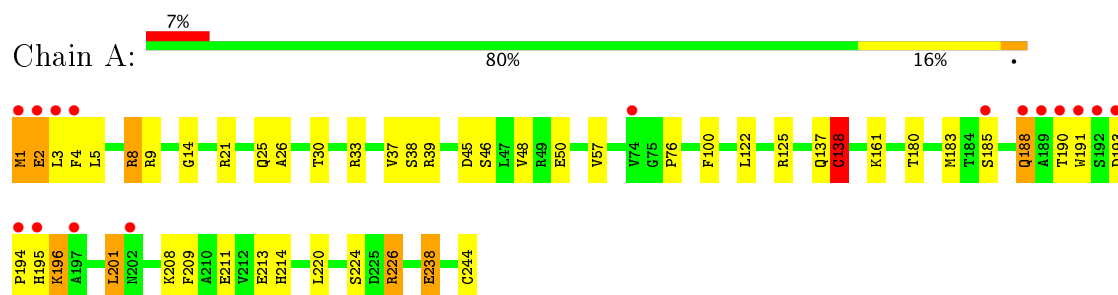
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	102	Total	O	0	0
			102	102		
5	B	70	Total	O	0	0
			70	70		

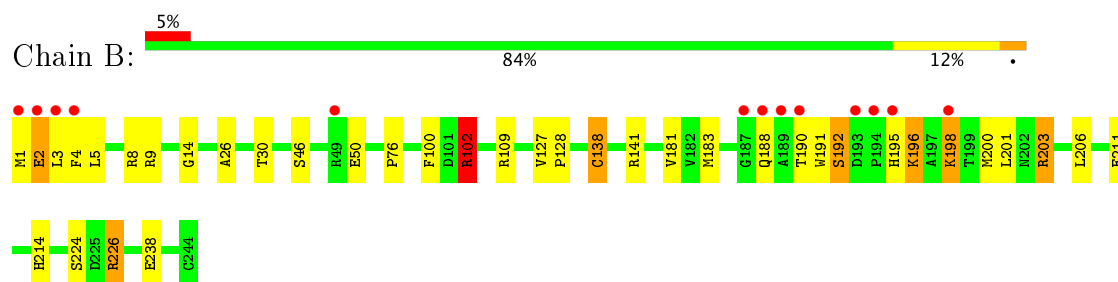
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: L-XYLULOSE REDUCTASE



#### • Molecule 1: L-XYLULOSE REDUCTASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.11Å 87.94Å 72.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 1.96 19.92 – 1.96	Depositor EDS
% Data completeness (in resolution range)	99.6 (10.00-1.96) 99.6 (19.92-1.96)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.74 (at 1.96Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.178 , 0.227 0.159 , 0.173	Depositor DCC
$R_{free}$ test set	1749 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	16.7	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 76.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.007 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3910	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	21.0	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 24.08 % 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 4.1063e-03. 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, 0.333 respectively for untwinned datasets, and 0.375, 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: 2HP, K, NAP

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	0.44	1/1843 (0.1%)	0.95	4/2503 (0.2%)
1	B	0.35	0/1843	1.00	7/2503 (0.3%)
All	All	0.40	1/3686 (0.0%)	0.97	11/5006 (0.2%)

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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	244	CYS	C-OXT	-12.56	0.99	1.23

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	203	ARG	NE-CZ-NH2	-8.21	116.20	120.30
1	B	100	PHE	CB-CG-CD2	7.20	125.84	120.80
1	B	102	ARG	NE-CZ-NH2	-7.10	116.75	120.30
1	A	244	CYS	CA-C-O	-6.35	106.77	120.10
1	B	203	ARG	CD-NE-CZ	5.96	131.95	123.60
1	A	100	PHE	CB-CG-CD2	5.70	124.79	120.80
1	A	39	ARG	NE-CZ-NH2	5.67	123.13	120.30
1	B	141	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	B	109	ARG	NE-CZ-NH2	-5.29	117.66	120.30
1	A	138	CYS	CA-CB-SG	5.15	123.28	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	203	ARG	NE-CZ-NH1	5.15	122.88	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	102	ARG	Sidechain

## 5.2 Too-close contacts [i](#)

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	1815	0	1865	32	0
1	B	1815	0	1865	31	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	48	0	25	1	0
3	B	48	0	25	1	0
4	A	5	0	0	1	0
4	B	5	0	0	1	0
5	A	102	0	0	2	0
5	B	70	0	0	4	0
All	All	3910	0	3780	63	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 8.

All (63) 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:211:GLU:H	1:A:214:HIS:HD2	1.24	0.85
1:B:211:GLU:H	1:B:214:HIS:HD2	1.24	0.83
1:B:138:CYS:HB3	4:B:1247:2HP:O2	1.81	0.79
1:B:203:ARG:HD2	5:B:348:HOH:O	1.84	0.78
1:A:46:SER:O	1:A:50:GLU:HG3	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ALA:O	1:A:30:THR:HG23	1.86	0.74
1:B:2:GLU:HA	1:B:2:GLU:OE2	1.90	0.70
1:B:26:ALA:O	1:B:30:THR:HG23	1.91	0.69
1:A:183:MET:HB2	5:A:432:HOH:O	1.95	0.66
1:B:3:LEU:HD23	1:B:226:ARG:HG2	1.78	0.64
1:B:5:LEU:HA	1:B:8:ARG:HG3	1.80	0.64
1:A:1:MET:SD	1:A:226:ARG:HG3	2.39	0.63
1:B:46:SER:O	1:B:50:GLU:HG3	1.98	0.63
1:A:193:ASP:HB3	1:A:196:LYS:HG2	1.81	0.63
1:A:5:LEU:O	1:A:8:ARG:HG2	1.98	0.62
1:B:2:GLU:HB3	1:B:4:PHE:CE1	2.34	0.61
1:A:45:ASP:O	1:A:48:VAL:HG22	2.01	0.60
1:A:193:ASP:HB3	1:A:196:LYS:CG	2.32	0.60
1:A:2:GLU:HG3	1:A:4:PHE:CD1	2.37	0.59
1:A:211:GLU:H	1:A:214:HIS:CD2	2.14	0.58
1:A:21:ARG:O	1:A:25:GLN:HG3	2.04	0.58
1:A:3:LEU:HB3	1:A:224:SER:CB	2.34	0.57
1:B:183:MET:SD	1:B:188:GLN:HG3	2.44	0.57
1:B:190:THR:HG21	5:B:469:HOH:O	2.04	0.57
1:B:196:LYS:HE3	5:B:447:HOH:O	2.05	0.56
1:B:3:LEU:CD2	1:B:226:ARG:HG2	2.37	0.54
1:B:102:ARG:HD3	5:B:366:HOH:O	2.08	0.53
1:B:211:GLU:H	1:B:214:HIS:CD2	2.15	0.53
1:A:138:CYS:HB3	4:A:247:2HP:O2	2.08	0.53
1:A:201:LEU:HD22	1:A:209:PHE:CZ	2.45	0.51
1:B:1:MET:CE	1:B:226:ARG:HG3	2.41	0.50
1:A:193:ASP:OD1	1:A:194:PRO:HD2	2.12	0.50
1:B:1:MET:SD	1:B:226:ARG:HG3	2.52	0.50
1:A:122:LEU:HD23	1:A:125:ARG:NH2	2.25	0.50
1:B:9:ARG:HD3	1:B:76:PRO:O	2.12	0.50
1:B:3:LEU:HB3	1:B:224:SER:CB	2.42	0.50
1:B:183:MET:HE1	1:B:191:TRP:HB2	1.95	0.49
1:A:190:THR:HB	1:A:191:TRP:CD1	2.49	0.47
1:A:161:LYS:HE2	5:A:431:HOH:O	2.14	0.47
1:A:193:ASP:O	1:A:196:LYS:HB2	2.15	0.47
1:A:3:LEU:HB3	1:A:224:SER:HB2	1.98	0.46
1:B:138:CYS:O	1:B:138:CYS:SG	2.74	0.46
1:A:14:GLY:HA2	3:A:245:NAP:H1B	1.97	0.46
1:A:224:SER:OG	1:A:226:ARG:HB2	2.16	0.45
1:B:102:ARG:O	1:B:102:ARG:HG3	2.15	0.45
1:B:3:LEU:O	1:B:224:SER:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:VAL:HG22	1:A:57:VAL:HB	1.98	0.45
1:A:21:ARG:HH11	1:A:50:GLU:CD	2.19	0.45
1:A:21:ARG:NH1	1:A:50:GLU:OE1	2.50	0.43
1:A:8:ARG:H	1:A:8:ARG:HG2	1.67	0.43
1:A:2:GLU:HB3	1:A:4:PHE:CE1	2.54	0.43
1:B:188:GLN:O	1:B:192:SER:OG	2.29	0.43
1:B:14:GLY:HA2	3:B:1245:NAP:H1B	2.02	0.41
1:B:198:LYS:HD3	1:B:198:LYS:HA	1.48	0.41
1:B:181:VAL:HG23	1:B:200:MET:HE3	2.01	0.41
1:B:127:VAL:HB	1:B:128:PRO:HD2	2.03	0.41
1:B:3:LEU:HB3	1:B:224:SER:HB2	2.03	0.41
1:A:180:THR:HB	1:A:238:GLU:HA	2.02	0.41
1:A:183:MET:HB3	1:A:188:GLN:NE2	2.35	0.41
1:A:5:LEU:CD1	1:A:220:LEU:HD22	2.51	0.41
1:A:9:ARG:HD3	1:A:76:PRO:O	2.21	0.40
1:B:1:MET:O	1:B:3:LEU:HG	2.21	0.40
1:B:206:LEU:HA	1:B:206:LEU:HD23	1.93	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	242/244 (99%)	236 (98%)	6 (2%)	0	100	100
1	B	242/244 (99%)	234 (97%)	8 (3%)	0	100	100
All	All	484/488 (99%)	470 (97%)	14 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	196/196 (100%)	180 (92%)	16 (8%)	13	4
1	B	196/196 (100%)	186 (95%)	10 (5%)	28	13
All	All	392/392 (100%)	366 (93%)	26 (7%)	19	7

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	2	GLU
1	A	8	ARG
1	A	33	ARG
1	A	38	SER
1	A	137	GLN
1	A	138	CYS
1	A	185	SER
1	A	188	GLN
1	A	195	HIS
1	A	196	LYS
1	A	201	LEU
1	A	208	LYS
1	A	213	GLU
1	A	226	ARG
1	A	238	GLU
1	B	2	GLU
1	B	102	ARG
1	B	138	CYS
1	B	192	SER
1	B	195	HIS
1	B	196	LYS
1	B	198	LYS
1	B	201	LEU
1	B	226	ARG
1	B	238	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	ASN
1	A	137	GLN
1	A	188	GLN
1	A	214	HIS
1	B	137	GLN
1	B	214	HIS

### 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 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	NAP	A	245	-	44,52,52	1.04	2 (4%)	51,80,80	2.15	10 (19%)
4	2HP	A	247	2	4,4,4	2.06	1 (25%)	6,6,6	1.30	1 (16%)
3	NAP	B	1245	-	44,52,52	1.07	1 (2%)	51,80,80	2.03	8 (15%)
4	2HP	B	1247	2	4,4,4	2.04	1 (25%)	6,6,6	1.66	2 (33%)

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	NAP	A	245	-	-	0/27/67/67	0/5/5/5
4	2HP	A	247	2	-	0/0/0/0	0/0/0/0
3	NAP	B	1245	-	-	0/27/67/67	0/5/5/5
4	2HP	B	1247	2	-	0/0/0/0	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	245	NAP	O4D-C1D	2.02	1.44	1.41
3	B	1245	NAP	C6N-N1N	3.55	1.44	1.35
3	A	245	NAP	C6N-N1N	3.66	1.44	1.35
4	B	1247	2HP	P-O1	3.74	1.58	1.50
4	A	247	2HP	P-O1	3.96	1.59	1.50

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	245	NAP	N3A-C2A-N1A	-10.73	119.51	128.86
3	B	1245	NAP	N3A-C2A-N1A	-9.76	120.35	128.86
3	A	245	NAP	C6N-C5N-C4N	-3.25	114.54	119.44
3	B	1245	NAP	C6N-C5N-C4N	-3.00	114.91	119.44
3	A	245	NAP	C3N-C2N-N1N	-2.63	117.78	120.43
3	A	245	NAP	C4B-O4B-C1B	-2.10	107.53	109.77
3	A	245	NAP	C4D-O4D-C1D	-2.02	107.61	109.77
3	B	1245	NAP	O2A-PA-O1A	2.01	122.69	112.28
3	B	1245	NAP	O3X-P2B-O2X	2.02	115.76	107.61
3	B	1245	NAP	C2A-N1A-C6A	2.02	122.31	118.77
3	A	245	NAP	O3D-C3D-C2D	2.09	118.51	111.83
4	B	1247	2HP	O4-P-O3	2.10	115.61	107.90
4	A	247	2HP	O4-P-O2	2.10	115.61	107.90
3	A	245	NAP	O2A-PA-O1A	2.17	123.53	112.28
4	B	1247	2HP	O4-P-O2	2.54	117.24	107.90
3	B	1245	NAP	C4A-C5A-N7A	2.70	112.02	109.41
3	B	1245	NAP	O3D-C3D-C2D	2.84	120.91	111.83
3	A	245	NAP	C2A-N1A-C6A	3.31	124.56	118.77
3	A	245	NAP	C4A-C5A-N7A	3.45	112.75	109.41
3	A	245	NAP	C5N-C4N-C3N	5.05	126.29	120.35
3	B	1245	NAP	C5N-C4N-C3N	6.01	127.42	120.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	245	NAP	1	0
4	A	247	2HP	1	0
3	B	1245	NAP	1	0
4	B	1247	2HP	1	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, 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	244/244 (100%)	-0.01	16 (6%)	19 28	7, 15, 59, 60	0
1	B	244/244 (100%)	0.03	13 (5%)	27 37	7, 16, 59, 60	0
All	All	488/488 (100%)	0.01	29 (5%)	23 32	7, 15, 59, 60	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	4	PHE	7.1
1	A	194	PRO	6.8
1	B	195	HIS	6.7
1	A	189	ALA	6.1
1	B	194	PRO	5.6
1	A	195	HIS	5.3
1	A	4	PHE	5.1
1	B	1	MET	4.8
1	A	192	SER	4.4
1	B	3	LEU	4.0
1	B	189	ALA	3.9
1	A	2	GLU	3.8
1	A	188	GLN	3.8
1	A	3	LEU	3.7
1	B	190	THR	3.6
1	B	2	GLU	3.3
1	A	190	THR	3.3
1	A	193	ASP	3.0
1	A	191	TRP	2.8
1	A	197	ALA	2.7
1	A	1	MET	2.7
1	B	198	LYS	2.5
1	B	49	ARG	2.4
1	B	188	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	193	ASP	2.3
1	A	185	SER	2.2
1	A	74	VAL	2.1
1	B	187	GLY	2.1
1	A	202	ASN	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(Å <sup>2</sup> )	Q<0.9
4	2HP	B	1247	5/5	0.68	0.32	8.55	26,45,50,60	0
4	2HP	A	247	5/5	0.69	0.34	5.73	24,32,37,39	0
3	NAP	B	1245	48/48	0.97	0.08	-0.39	8,15,21,26	0
3	NAP	A	245	48/48	0.97	0.08	-0.58	7,17,22,28	0
2	K	B	1246	1/1	0.91	0.13	-	54,54,54,54	0
2	K	A	246	1/1	0.93	0.18	-	47,47,47,47	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.