



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 01:40 AM GMT

PDB ID : 1QW9  
Title : Crystal structure of a family 51 alpha-L-arabinofuranosidasein complex with 4-nitrophenyl-Ara  
Authors : Hoevel, K.; Shallom, D.; Niefind, K.; Belakhov, V.; Shoham, G.; Bassov, T.; Shoham, Y.; Schomburg, D.  
Deposited on : 2003-09-01  
Resolution : 1.20 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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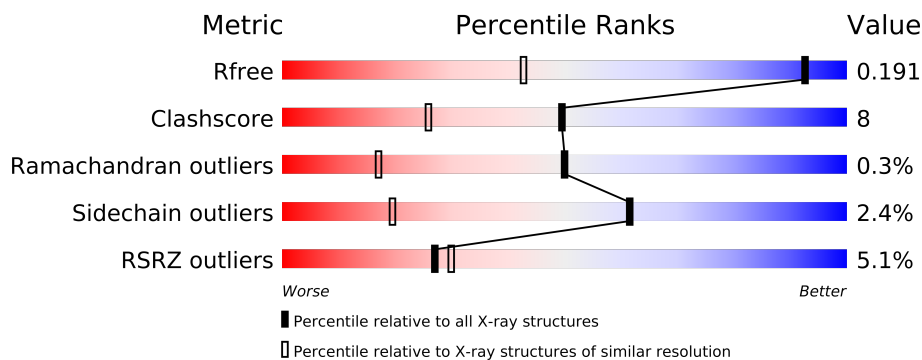
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 1.20 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))
$R_{free}$	66092	1038 (1.26-1.14)
Clashscore	79885	1158 (1.26-1.14)
Ramachandran outliers	78287	1106 (1.26-1.14)
Sidechain outliers	78261	1104 (1.26-1.14)
RSRZ outliers	66119	1038 (1.26-1.14)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	502	
1	B	502	

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 9598 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

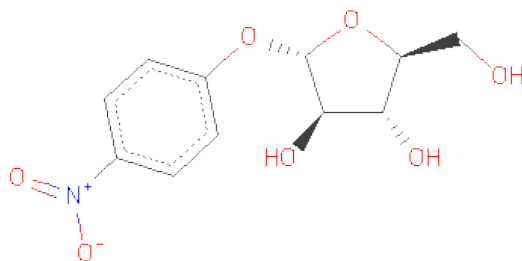
- Molecule 1 is a protein called Alpha-L-arabinofuranosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	0	0
			3986	2540	680	746	20			
1	B	497	Total	C	N	O	S	0	0	0
			3986	2540	680	746	20			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	175	ALA	GLU	ENGINEERED	UNP Q9XBQ3
B	175	ALA	GLU	ENGINEERED	UNP Q9XBQ3

- Molecule 2 is 2-HYDROXYMETHYL-5-(4-NITRO-PHENOXY)-TETRAHYDRO-FURAN-3,4-DIOL (three-letter code: KHP) (formula: C<sub>11</sub>H<sub>13</sub>NO<sub>7</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			19	11	1	7		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			19	11	1	7		

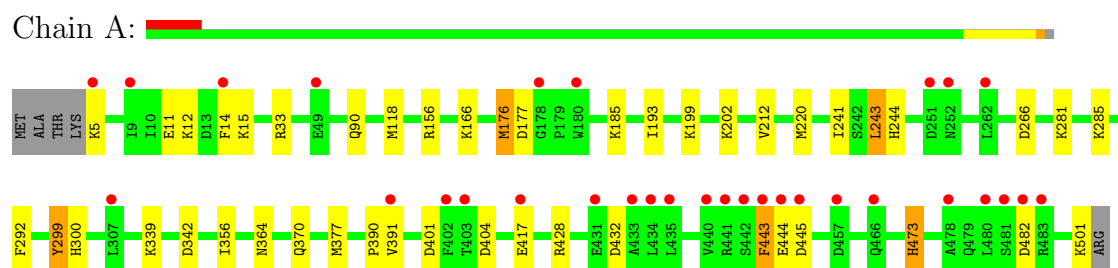
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	805	Total	O	0	0
			805	805		
3	B	783	Total	O	0	0
			783	783		

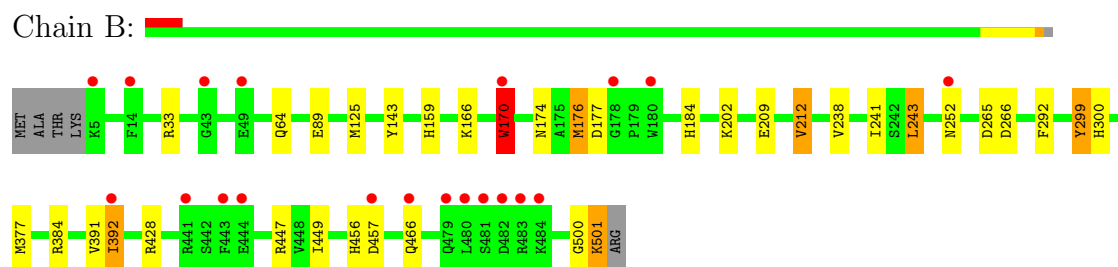
### 3 Residue-property plots i

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: Alpha-L-arabinofuranosidase



- Molecule 1: Alpha-L-arabinofuranosidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	179.31Å 179.31Å 100.40Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.20 44.83 – 1.20	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-1.20) 98.8 (44.83-1.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.65 (at 1.20Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, $R_{free}$	0.160 , 0.179 0.174 , 0.191	Depositor DCC
$R_{free}$ test set	18644 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	13.6	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 39.9	EDS
Estimated twinning fraction	0.008 for h,-h-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 370234 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9598	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.93% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 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: KHP

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	0.65	3/4087 (0.1%)	0.85	14/5553 (0.3%)
1	B	0.66	6/4087 (0.1%)	0.88	15/5553 (0.3%)
All	All	0.65	9/8174 (0.1%)	0.87	29/11106 (0.3%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	170	TRP	CB-CG	-10.08	1.32	1.50
1	B	176	MET	CB-CG	7.59	1.75	1.51
1	A	220	MET	SD-CE	-6.75	1.40	1.77
1	A	202	LYS	CD-CE	6.66	1.68	1.51
1	A	212	VAL	CB-CG1	-6.64	1.39	1.52
1	B	170	TRP	CG-CD2	6.57	1.54	1.43
1	B	212	VAL	CB-CG1	-6.31	1.39	1.52
1	B	209	GLU	CD-OE1	-6.09	1.19	1.25
1	B	89	GLU	CD-OE1	5.38	1.31	1.25

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	243	LEU	CA-CB-CG	10.63	139.74	115.30
1	B	177	ASP	CB-CG-OD2	9.56	126.90	118.30
1	A	33	ARG	NE-CZ-NH1	8.23	124.42	120.30
1	B	33	ARG	NE-CZ-NH2	-8.22	116.19	120.30
1	B	170	TRP	CB-CG-CD1	-7.95	116.67	127.00
1	B	176	MET	CG-SD-CE	-7.72	87.84	100.20
1	B	170	TRP	CB-CG-CD2	7.69	136.60	126.60
1	B	170	TRP	CG-CD2-CE3	7.44	140.59	133.90
1	B	33	ARG	NE-CZ-NH1	7.42	124.01	120.30
1	B	170	TRP	CE2-CD2-CG	-6.87	101.81	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	457	ASP	CB-CG-OD2	6.67	124.30	118.30
1	B	384	ARG	NE-CZ-NH1	6.59	123.60	120.30
1	B	176	MET	CA-CB-CG	6.46	124.29	113.30
1	A	177	ASP	CB-CG-OD1	6.37	124.03	118.30
1	A	281	LYS	CD-CE-NZ	-6.19	97.45	111.70
1	B	428	ARG	NE-CZ-NH1	5.99	123.29	120.30
1	B	428	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	B	265	ASP	CB-CG-OD2	5.93	123.64	118.30
1	A	33	ARG	NE-CZ-NH2	-5.90	117.35	120.30
1	A	445	ASP	CB-CG-OD2	5.76	123.48	118.30
1	A	342	ASP	CB-CG-OD1	5.68	123.41	118.30
1	A	482	ASP	CB-CG-OD2	5.50	123.25	118.30
1	A	432	ASP	CB-CG-OD2	5.36	123.12	118.30
1	A	243	LEU	CB-CA-C	-5.23	100.26	110.20
1	A	404	ASP	CB-CG-OD2	5.23	123.00	118.30
1	A	428	ARG	NE-CZ-NH2	-5.18	117.71	120.30
1	A	266	ASP	CB-CG-OD2	5.16	122.94	118.30
1	A	156	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	A	401	ASP	CB-CG-OD2	5.02	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3986	0	0	31	0
1	B	3986	0	0	32	0
2	A	19	0	0	0	0
2	B	19	0	0	0	0
3	A	805	0	0	23	0
3	B	783	0	0	21	1
All	All	9598	0	0	61	1



Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 8.

All (61) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:176:MET:CB	1:B:176:MET:CG	1.75	1.64
1:A:118:MET:CG	3:A:2484:HOH:O	1.78	1.28
1:B:377:MET:CG	3:B:2459:HOH:O	1.83	1.22
1:A:377:MET:CG	3:A:2482:HOH:O	1.84	1.21
1:A:176:MET:CE	3:A:2486:HOH:O	1.85	1.19
1:A:118:MET:SD	3:A:2484:HOH:O	2.03	1.14
1:A:176:MET:SD	3:A:2486:HOH:O	2.05	1.14
1:A:377:MET:SD	3:A:2482:HOH:O	2.16	1.01
1:B:170:TRP:CE3	3:B:2458:HOH:O	2.13	1.01
1:A:243:LEU:CD1	3:A:2487:HOH:O	2.09	1.00
1:B:377:MET:SD	3:B:2459:HOH:O	2.17	0.98
1:A:176:MET:CG	3:A:2283:HOH:O	2.11	0.97
1:B:501:LYS:CA	3:B:2350:HOH:O	2.09	0.97
1:A:377:MET:CE	3:A:2482:HOH:O	2.23	0.86
1:B:377:MET:CE	3:B:2459:HOH:O	2.26	0.84
1:B:176:MET:CB	1:B:176:MET:SD	2.67	0.83
1:B:170:TRP:CD2	3:B:2458:HOH:O	2.31	0.82
1:A:166:LYS:NZ	3:A:2534:HOH:O	2.13	0.80
1:A:176:MET:CG	3:A:2486:HOH:O	2.25	0.80
1:A:244:HIS:CE1	3:A:1931:HOH:O	2.41	0.74
1:B:170:TRP:CB	3:B:2458:HOH:O	2.36	0.73
1:B:166:LYS:CG	3:B:2351:HOH:O	2.35	0.73
1:B:501:LYS:CB	3:B:2350:HOH:O	2.37	0.72
1:B:170:TRP:CG	3:B:2458:HOH:O	2.45	0.68
1:A:443:PHE:CE2	3:A:2231:HOH:O	2.48	0.67
1:A:364:ASN:CG	3:A:2136:HOH:O	2.33	0.67
1:A:443:PHE:CD2	3:A:2231:HOH:O	2.48	0.66
1:B:266:ASP:OD2	3:B:2344:HOH:O	2.15	0.65
1:A:90:GLN:NE2	3:A:2221:HOH:O	2.30	0.65
1:A:299:TYR:CZ	1:A:300:HIS:CE1	2.86	0.63
1:A:243:LEU:CG	3:A:2487:HOH:O	2.44	0.62
1:A:14:PHE:CE2	1:B:391:VAL:CG2	2.82	0.61
1:A:299:TYR:CE1	1:A:300:HIS:CE1	2.92	0.57
1:A:166:LYS:CG	3:A:2290:HOH:O	2.53	0.55
1:A:14:PHE:CZ	1:B:391:VAL:CG2	2.89	0.55
1:B:456:HIS:CD2	3:B:2189:HOH:O	2.60	0.54
1:A:199:LYS:NZ	3:A:1759:HOH:O	2.41	0.54
1:A:243:LEU:CB	3:A:2487:HOH:O	2.56	0.53
1:B:500:GLY:O	1:B:501:LYS:CB	2.57	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:391:VAL:N	3:A:2318:HOH:O	2.41	0.52
1:B:143:TYR:OH	1:B:159:HIS:CD2	2.65	0.50
1:B:64:GLN:NE2	3:B:2424:HOH:O	2.45	0.49
1:A:185:LYS:NZ	1:A:193:ILE:CD1	2.77	0.48
1:B:392:ILE:CG2	3:B:2465:HOH:O	2.62	0.47
1:B:125:MET:O	1:B:170:TRP:CD1	2.68	0.47
1:B:202:LYS:CD	3:B:2208:HOH:O	2.64	0.46
1:B:166:LYS:NZ	3:B:2052:HOH:O	2.48	0.46
1:B:449:ILE:CD1	3:B:2437:HOH:O	2.64	0.45
1:B:392:ILE:CD1	3:B:2039:HOH:O	2.65	0.45
1:B:176:MET:O	1:B:184:HIS:CD2	2.71	0.43
1:A:390:PRO:O	3:A:2513:HOH:O	2.21	0.43
1:B:501:LYS:CG	3:B:2350:HOH:O	2.65	0.42
1:A:11:GLU:CG	1:A:14:PHE:CD1	3.03	0.42
1:B:212:VAL:CG1	1:B:238:VAL:CG1	2.98	0.42
1:B:202:LYS:NZ	3:B:2391:HOH:O	2.51	0.42
1:A:243:LEU:CD2	3:A:2487:HOH:O	2.68	0.42
1:B:174:ASN:O	1:B:176:MET:CG	2.69	0.41
1:A:473:HIS:C	1:A:473:HIS:CD2	2.94	0.41
1:B:299:TYR:CZ	1:B:300:HIS:CE1	3.09	0.40
1:A:12:LYS:O	1:A:15:LYS:NZ	2.55	0.40
1:B:64:GLN:NE2	3:B:1847:HOH:O	2.54	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:B:1871:HOH:O	3:B:2530:HOH:O[2.655]	1.77	0.43

## 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	495/502 (99%)	478 (97%)	15 (3%)	2 (0%)	43	12
1	B	495/502 (99%)	479 (97%)	15 (3%)	1 (0%)	56	20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	990/1004 (99%)	957 (97%)	30 (3%)	3 (0%)	50 17

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	299	TYR
1	A	299	TYR
1	A	356	ILE

### 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	429/433 (99%)	417 (97%)	12 (3%)	56 14
1	B	429/433 (99%)	420 (98%)	9 (2%)	66 24
All	All	858/866 (99%)	837 (98%)	21 (2%)	61 19

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LYS
1	A	176	MET
1	A	241	ILE
1	A	285	LYS
1	A	292	PHE
1	A	339	LYS
1	A	370	GLN
1	A	417	GLU
1	A	443	PHE
1	A	444	GLU
1	A	473	HIS
1	A	501	LYS
1	B	170	TRP
1	B	241	ILE
1	B	243	LEU
1	B	252	ASN

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Mol	Chain	Res	Type
1	B	292	PHE
1	B	392	ILE
1	B	447	ARG
1	B	466	GLN
1	B	501	LYS

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 chains 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 ⓘ

2 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	KHP	A	1750	-	20,20,20	2.38	6 (30%)	28,28,28	1.17	3 (10%)
2	KHP	B	1751	-	20,20,20	2.40	6 (30%)	28,28,28	1.10	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	KHP	A	1750	-	-	0/10/26/26	0/2/2/2
2	KHP	B	1751	-	-	0/10/26/26	0/2/2/2

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1751	KHP	C4'-N1'	-7.96	1.34	1.46
2	A	1750	KHP	C4'-N1'	-7.67	1.34	1.46
2	A	1750	KHP	O1'-C1'	3.52	1.44	1.38
2	B	1751	KHP	O1'-C1'	3.20	1.44	1.38
2	A	1750	KHP	O5'-C5B	-3.11	1.28	1.42
2	B	1751	KHP	O5'-C5B	-2.80	1.30	1.42
2	A	1750	KHP	O1'-C1B	2.43	1.45	1.41
2	B	1751	KHP	C3'-C4'	-2.33	1.34	1.38
2	B	1751	KHP	C3'-C2'	-2.16	1.34	1.38
2	B	1751	KHP	C6'-C5'	-2.14	1.34	1.38
2	A	1750	KHP	C3'-C4'	-2.10	1.34	1.38
2	A	1750	KHP	C3'-C2'	-2.05	1.34	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1750	KHP	O3'-N1'-C4'	3.26	120.68	114.42
2	B	1751	KHP	O3'-N1'-C4'	3.25	120.67	114.42
2	A	1750	KHP	C1B-C2B-C3B	2.70	105.88	102.32
2	B	1751	KHP	O5'-C5B-C4B	2.24	119.06	111.36
2	A	1750	KHP	O5'-C5B-C4B	2.13	118.69	111.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	497/502 (99%)	0.50	31 (6%)	20 22	8, 15, 30, 50	0
1	B	497/502 (99%)	0.18	20 (4%)	36 38	9, 15, 28, 38	0
All	All	994/1004 (99%)	0.34	51 (5%)	27 30	8, 15, 29, 50	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	441	ARG	6.1
1	A	443	PHE	6.0
1	A	482	ASP	5.9
1	A	444	GLU	5.2
1	A	14	PHE	4.7
1	A	417	GLU	4.6
1	A	178	GLY	4.3
1	A	445	ASP	4.2
1	A	252	ASN	4.1
1	A	391	VAL	3.9
1	B	480	LEU	3.8
1	A	433	ALA	3.7
1	B	482	ASP	3.7
1	B	14	PHE	3.6
1	B	441	ARG	3.5
1	B	49	GLU	3.4
1	A	457	ASP	3.4
1	B	180	TRP	3.4
1	A	180	TRP	3.2
1	A	483	ARG	3.0
1	B	43	GLY	3.0
1	B	444	GLU	3.0
1	A	434	LEU	3.0
1	B	457	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	178	GLY	2.9
1	B	170	TRP	2.9
1	A	251	ASP	2.8
1	A	402	PHE	2.8
1	A	481	SER	2.7
1	B	252	ASN	2.7
1	A	5	LYS	2.6
1	A	466	GLN	2.6
1	A	442	SER	2.6
1	A	440	VAL	2.6
1	A	435	LEU	2.6
1	B	481	SER	2.6
1	B	466	GLN	2.6
1	A	480	LEU	2.5
1	A	307	LEU	2.5
1	B	5	LYS	2.5
1	B	392	ILE	2.3
1	A	49	GLU	2.3
1	A	403	THR	2.2
1	A	9	ILE	2.2
1	A	431	GLU	2.2
1	B	443	PHE	2.1
1	A	478	ALA	2.1
1	B	483	ARG	2.1
1	B	484	LYS	2.0
1	A	262	LEU	2.0
1	B	479	GLN	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	KHP	A	1750	19/19	0.14	1.79	10,13,42,43	0
2	KHP	B	1751	19/19	0.13	1.44	11,14,42,43	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.