



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:37 PM GMT

PDB ID : 1PXO  
Title : HUMAN CYCLIN DEPENDENT KINASE 2 COMPLEXED WITH THE INHIBITOR [4-(2-Amino-4-methyl-thiazol-5-yl)-pyrimidin-2-yl]-(3-nitro-phenyl)-amine  
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Deposited on : 2003-07-04  
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 (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

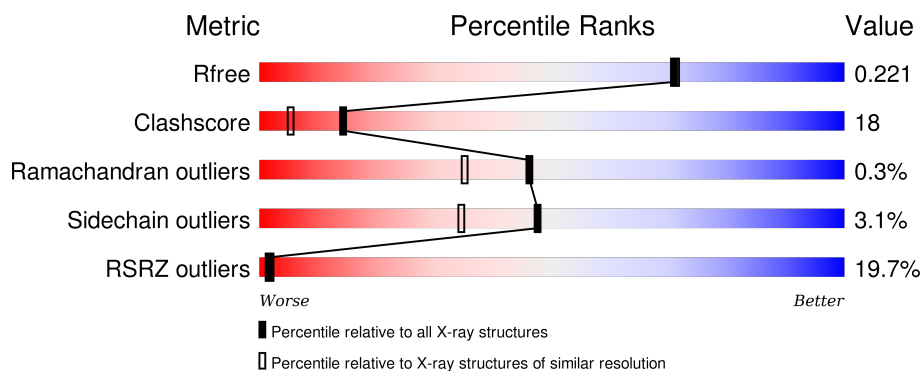
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


The reported resolution of this entry is 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))
$R_{free}$	91344	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (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	298	

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
2	CK7	A	500[C]	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CK7	A	500[D]	-	-	-	X

## 2 Entry composition [i](#)

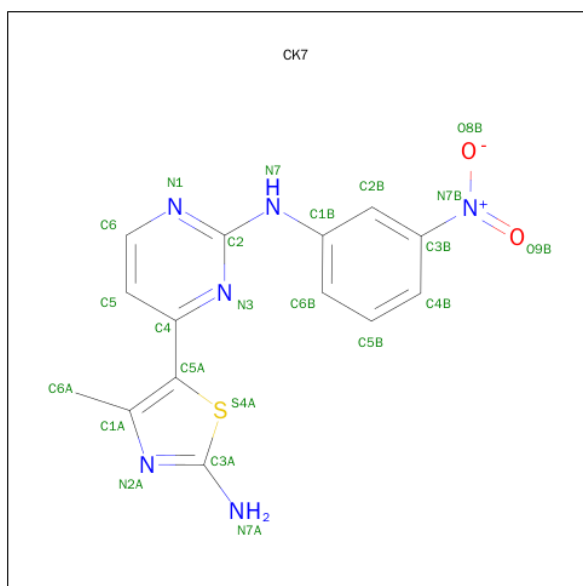
There are 3 unique types of molecules in this entry. The entry contains 2575 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Cell division protein kinase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	S	0	1	0
			2375	1546	406	415	8			

- Molecule 2 is [4-(2-AMINO-4-METHYL-THIAZOL-5-YL)-PYRIMIDIN-2-YL]-(3-NITRO-PHENYL)-AMINE (three-letter code: CK7) (formula: C<sub>14</sub>H<sub>12</sub>N<sub>6</sub>O<sub>2</sub>S).



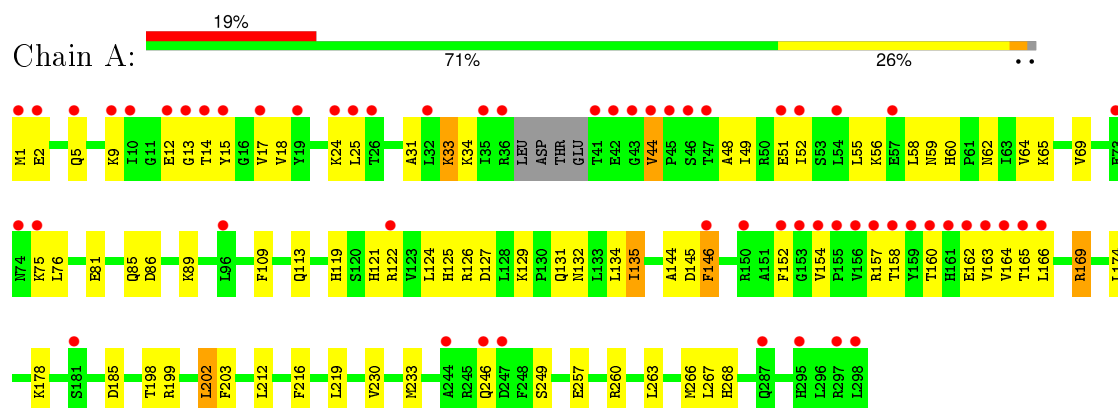
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	1
			32	20	7	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	168	Total	O	0	9
			168	168		



- Molecule 1: Cell division protein kinase 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.49Å 71.99Å 72.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.99 – 1.96 14.98 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.9 (14.99-1.96) 99.0 (14.98-1.95)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	8.29 (at 1.95Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.217 , 0.235 0.218 , 0.221	Depositor DCC
$R_{free}$ test set	1056 reflections (5.15%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.5	Xtriage
Anisotropy	0.628	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 76.9	EDS
Estimated twinning fraction	0.016 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 20574 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2575	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.90% 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: CK7

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	0.33	0/2436	0.62	3/3302 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	31	ALA	O-C-N	-8.41	109.24	122.70
1	A	34	LYS	C-N-CA	-6.22	106.15	121.70
1	A	31	ALA	CA-C-N	5.78	129.92	117.20

There are no chirality outliers.

There are no planarity outliers.

### 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	2375	0	2432	87	0
2	A	32	0	15	6	0
3	A	168	0	0	5	0
All	All	2575	0	2447	88	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 18.

All (88) 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:85:GLN:HG3	1:A:89:LYS:HE3	1.62	0.81
1:A:1:MET:HG2	1:A:2:GLU:H	1.47	0.79
1:A:14:THR:HA	1:A:158:THR:HG22	1.66	0.77
1:A:1:MET:HG2	1:A:2:GLU:N	2.06	0.70
1:A:64:VAL:HG21	1:A:134:LEU:HD12	1.73	0.70
1:A:129:LYS:HG2	1:A:132:ASN:ND2	2.06	0.70
1:A:249:SER:HB3	1:A:260:ARG:NH1	2.07	0.69
1:A:125:HIS:HD2	1:A:127:ASP:H	1.39	0.69
1:A:263:LEU:O	1:A:267:LEU:HD13	1.94	0.68
1:A:126:ARG:HH22	1:A:154:VAL:HB	1.58	0.68
1:A:126:ARG:HH12	1:A:154:VAL:HB	1.61	0.65
1:A:18:VAL:HG22	1:A:33[A]:LYS:HG2	1.80	0.64
1:A:85:GLN:O	1:A:135:ILE:HD13	1.98	0.63
1:A:135:ILE:HD13	1:A:135:ILE:H	1.63	0.62
1:A:5:GLN:HB2	1:A:24:LYS:NZ	2.15	0.61
1:A:60:HIS:CD2	1:A:62:ASN:H	2.18	0.61
1:A:60:HIS:HD2	1:A:62:ASN:H	1.49	0.61
1:A:126:ARG:NH2	1:A:154:VAL:HB	2.15	0.60
1:A:126:ARG:NH1	1:A:154:VAL:HB	2.17	0.60
1:A:146:PHE:HB2	3:A:551:HOH:O	2.00	0.60
1:A:164:VAL:HG12	1:A:165:THR:H	1.66	0.60
1:A:164:VAL:HG12	1:A:165:THR:N	2.16	0.59
1:A:125:HIS:HE1	1:A:144:ALA:O	1.85	0.59
1:A:124:LEU:HD23	3:A:532:HOH:O	2.02	0.59
1:A:124:LEU:HD23	1:A:124:LEU:H	1.67	0.58
1:A:75:LYS:HE2	1:A:75:LYS:HA	1.83	0.58
1:A:81:GLU:O	2:A:500[A]:CK7:H6	2.04	0.58
1:A:121:HIS:HA	1:A:122:ARG:HH21	1.69	0.57
1:A:230:VAL:O	1:A:233:MET:HG3	2.04	0.57
1:A:55:LEU:HA	1:A:58:LEU:HD13	1.87	0.57
1:A:9:LYS:HD3	1:A:12:GLU:CD	2.26	0.56
1:A:129:LYS:HE2	1:A:165:THR:HG22	1.89	0.55
1:A:48:ALA:O	1:A:52:ILE:HG13	2.06	0.54
1:A:212:LEU:HG	1:A:216:PHE:CZ	2.44	0.53
1:A:56:LYS:HE2	1:A:69:VAL:HG23	1.91	0.53
1:A:202:LEU:HD13	1:A:203:PHE:CE2	2.44	0.52
1:A:14:THR:CA	1:A:158:THR:HG22	2.38	0.52
1:A:158:THR:HG23	1:A:162:GLU:O	2.10	0.52
1:A:89:LYS:NZ	2:A:500[C]:CK7:H5B	2.26	0.51
1:A:2:GLU:H	1:A:2:GLU:CD	2.14	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:HIS:HD2	3:A:512:HOH:O	1.94	0.51
1:A:9:LYS:HE2	1:A:17:VAL:HG11	1.92	0.50
1:A:268:HIS:HE1	3:A:585:HOH:O	1.94	0.50
1:A:121:HIS:C	1:A:122:ARG:HE	2.15	0.49
1:A:52:ILE:CD1	1:A:76:LEU:HD21	2.43	0.49
1:A:165:THR:O	1:A:165:THR:HG23	2.13	0.49
1:A:166:LEU:N	1:A:166:LEU:HD12	2.28	0.48
1:A:178:LYS:HG2	3:A:594:HOH:O	2.12	0.48
1:A:169:ARG:HG3	1:A:169:ARG:HH11	1.78	0.48
1:A:126:ARG:CZ	1:A:154:VAL:HB	2.44	0.48
1:A:109:PHE:O	1:A:113:GLN:HG3	2.13	0.48
1:A:129:LYS:HG2	1:A:132:ASN:HD21	1.77	0.47
1:A:15:TYR:HB2	1:A:33[A]:LYS:HE3	1.97	0.46
1:A:125:HIS:HD2	1:A:127:ASP:N	2.10	0.46
1:A:129:LYS:HB3	1:A:165:THR:HG21	1.98	0.46
1:A:135:ILE:N	1:A:135:ILE:HD13	2.30	0.46
1:A:154:VAL:HG13	1:A:154:VAL:O	2.15	0.45
1:A:59:ASN:HD21	1:A:65:LYS:HE3	1.81	0.45
1:A:52:ILE:HD11	1:A:152:PHE:CE1	2.51	0.45
1:A:52:ILE:HD11	1:A:152:PHE:CZ	2.51	0.45
1:A:160:THR:O	1:A:160:THR:HG22	2.16	0.45
1:A:157:ARG:HG2	1:A:158:THR:H	1.82	0.45
1:A:131:GLN:O	2:A:500[C]:CK7:O8B	2.34	0.45
1:A:257:GLU:OE1	1:A:260:ARG:NH2	2.50	0.45
1:A:267:LEU:HD12	1:A:267:LEU:N	2.32	0.45
1:A:119:HIS:HE1	1:A:185:ASP:OD2	2.00	0.44
1:A:169:ARG:NH1	1:A:169:ARG:HG3	2.32	0.44
1:A:144:ALA:O	1:A:145:ASP:HB2	2.18	0.44
1:A:5:GLN:HB2	1:A:24:LYS:HZ2	1.82	0.44
1:A:64:VAL:CG2	1:A:134:LEU:HD12	2.45	0.44
1:A:246:GLN:HA	1:A:246:GLN:HE21	1.83	0.44
1:A:125:HIS:CD2	1:A:127:ASP:H	2.27	0.43
1:A:86:ASP:OD2	2:A:500[C]:CK7:H4B	2.18	0.43
1:A:13:GLY:O	1:A:158:THR:HB	2.19	0.42
1:A:163:VAL:HG12	1:A:164:VAL:N	2.33	0.42
1:A:144:ALA:HB1	2:A:500[A]:CK7:H6A2	2.01	0.42
1:A:44:VAL:HG11	1:A:49:ILE:HD11	2.01	0.42
1:A:25:LEU:C	1:A:25:LEU:HD23	2.40	0.42
1:A:157:ARG:HG2	1:A:162:GLU:O	2.20	0.41
1:A:58:LEU:C	1:A:59:ASN:HD22	2.22	0.41
1:A:166:LEU:CD1	1:A:166:LEU:H	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:MET:C	1:A:267:LEU:HD12	2.41	0.41
1:A:12:GLU:OE1	1:A:17:VAL:HG13	2.21	0.41
2:A:500[A]:CK7:H6A1	2:A:500[A]:CK7:H5	2.02	0.41
1:A:58:LEU:N	1:A:58:LEU:HD12	2.35	0.41
1:A:198:THR:O	1:A:199:ARG:HB2	2.21	0.41
1:A:166:LEU:H	1:A:166:LEU:HD12	1.86	0.41
1:A:5:GLN:HB2	1:A:24:LYS:HZ1	1.84	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	291/298 (98%)	277 (95%)	13 (4%)	1 (0%)	46 35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	VAL

### 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	260/263 (99%)	251 (96%)	9 (4%)	43 29

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33[A]	LYS
1	A	33[B]	LYS
1	A	51	GLU
1	A	135	ILE
1	A	146	PHE
1	A	169	ARG
1	A	174	LEU
1	A	202	LEU
1	A	219	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	59	ASN
1	A	60	HIS
1	A	85	GLN
1	A	113	GLN
1	A	119	HIS
1	A	125	HIS
1	A	246	GLN
1	A	268	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 ⓘ

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	CK7	A	500[A]	-	11,15,25	2.52	4 (36%)	11,21,35	5.66	8 (72%)
2	CK7	A	500[C]	-	7,9,25	1.89	3 (42%)	9,11,35	3.58	4 (44%)
2	CK7	A	500[D]	-	7,9,25	1.90	3 (42%)	9,11,35	3.93	4 (44%)

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	CK7	A	500[A]	-	-	0/0/4/12	0/2/2/3
2	CK7	A	500[C]	-	-	2/4/4/12	0/1/1/3
2	CK7	A	500[D]	-	-	0/4/4/12	0/1/1/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500[A]	CK7	C2-N1	-2.43	1.32	1.35
2	A	500[A]	CK7	C4-N3	2.08	1.37	1.34
2	A	500[C]	CK7	C5B-C6B	2.18	1.43	1.38
2	A	500[D]	CK7	C5B-C6B	2.20	1.43	1.38
2	A	500[C]	CK7	C1B-C2B	2.33	1.43	1.38
2	A	500[D]	CK7	C1B-C2B	2.43	1.43	1.38
2	A	500[D]	CK7	C2B-C3B	2.46	1.43	1.38
2	A	500[C]	CK7	C2B-C3B	2.50	1.43	1.38
2	A	500[A]	CK7	C3A-N7A	5.05	1.49	1.35
2	A	500[A]	CK7	C5A-C1A	5.52	1.53	1.37

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500[A]	CK7	N1-C2-N3	-7.76	117.67	125.78
2	A	500[D]	CK7	C4B-C3B-N7B	-6.48	114.26	119.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	500[C]	CK7	C4B-C3B-N7B	-5.23	115.27	119.48
2	A	500[A]	CK7	C5-C6-N1	-2.82	120.68	123.90
2	A	500[C]	CK7	C6B-C1B-C2B	-2.77	116.12	120.19
2	A	500[D]	CK7	C6B-C1B-C2B	-2.74	116.17	120.19
2	A	500[A]	CK7	N7-C2-N1	-2.44	115.20	117.39
2	A	500[A]	CK7	C6-C5-C4	-2.00	115.34	117.26
2	A	500[D]	CK7	C1B-C2B-C3B	2.66	123.29	119.41
2	A	500[C]	CK7	C1B-C2B-C3B	2.98	123.76	119.41
2	A	500[A]	CK7	N7-C2-N3	5.97	127.09	117.20
2	A	500[A]	CK7	C6-N1-C2	7.78	123.32	116.32
2	A	500[C]	CK7	C2B-C3B-N7B	8.31	126.18	119.48
2	A	500[D]	CK7	C2B-C3B-N7B	9.01	126.75	119.48
2	A	500[A]	CK7	N7A-C3A-N2A	9.25	135.03	122.92
2	A	500[A]	CK7	C4-N3-C2	9.53	121.51	116.34

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	500[C]	CK7	C2B-C3B-N7B-O9B
2	A	500[C]	CK7	C4B-C3B-N7B-O9B

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500[A]	CK7	3	0
2	A	500[C]	CK7	3	0

## 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	294/298 (98%)	1.19	58 (19%) 1 2	10, 23, 74, 152	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	164	VAL	20.7
1	A	155	PRO	20.0
1	A	158	THR	19.5
1	A	160	THR	15.7
1	A	159	TYR	11.0
1	A	156	VAL	10.5
1	A	25	LEU	9.2
1	A	161	HIS	8.4
1	A	163	VAL	7.0
1	A	41	THR	6.8
1	A	157	ARG	6.2
1	A	165	THR	5.9
1	A	154	VAL	5.8
1	A	14	THR	5.3
1	A	73	GLU	4.9
1	A	42	GLU	4.9
1	A	12	GLU	4.8
1	A	96	LEU	4.8
1	A	43	GLY	4.7
1	A	15	TYR	4.3
1	A	26	THR	4.2
1	A	297	ARG	3.9
1	A	166	LEU	3.7
1	A	36	ARG	3.6
1	A	1	MET	3.6
1	A	13	GLY	3.6
1	A	162	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	19	TYR	3.4
1	A	44	VAL	3.2
1	A	295	HIS	3.2
1	A	246	GLN	3.1
1	A	45	PRO	3.0
1	A	54	LEU	3.0
1	A	146	PHE	2.9
1	A	24	LYS	2.9
1	A	2	GLU	2.7
1	A	32	LEU	2.7
1	A	17	VAL	2.6
1	A	46	SER	2.6
1	A	153	GLY	2.5
1	A	9	LYS	2.5
1	A	10	ILE	2.4
1	A	74	ASN	2.3
1	A	298	LEU	2.3
1	A	150	ARG	2.2
1	A	247	ASP	2.2
1	A	75	LYS	2.2
1	A	47	THR	2.2
1	A	51	GLU	2.2
1	A	287	GLN	2.2
1	A	152	PHE	2.2
1	A	35	ILE	2.1
1	A	122	ARG	2.1
1	A	5	GLN	2.1
1	A	244	ALA	2.0
1	A	52	ILE	2.0
1	A	181	SER	2.0
1	A	57	GLU	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
2	CK7	A	500[D]	9/23	0.76	0.25	2.36	35,36,37,37	9
2	CK7	A	500[C]	9/23	0.76	0.25	2.22	35,37,37,38	9
2	CK7	A	500[A]	14/23	0.76	0.25	1.92	38,39,42,42	14

## 6.5 Other polymers [i](#)

There are no such residues in this entry.