



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 03:00 AM GMT

PDB ID : 2JKI  
Title : COMPLEX OF HSP90 N-TERMINAL AND SGT1 CS DOMAIN  
Authors : Zhang, M.; Pearl, L.H.  
Deposited on : 2008-08-28  
Resolution : 3.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

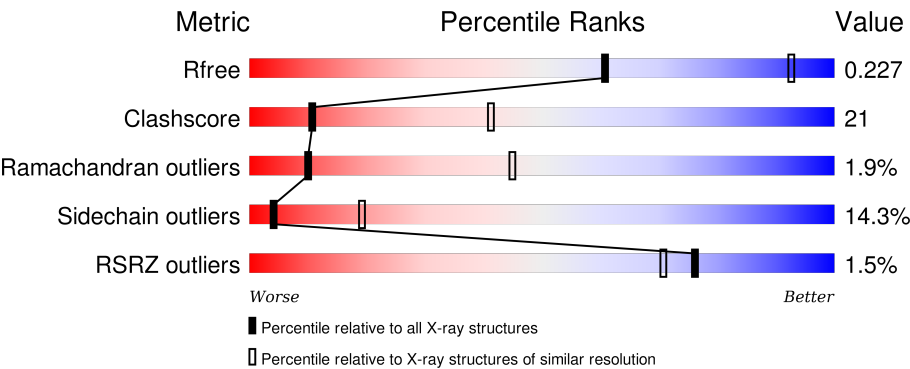
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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 <sub>free</sub>	91344	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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	223	<div><div>1%</div><div>56%30%10%.</div></div>
1	B	223	<div><div>2%</div><div>58%28%13%.</div></div>
1	C	223	<div><div>3%</div><div>56%30%9%..</div></div>
2	S	90	<div><div></div><div>64%28%7%.</div></div>
2	T	90	<div><div></div><div>67%27%6%.</div></div>

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Mol	Chain	Length	Quality of chain
2	U	90	<div><div><div>%</div><div><div></div></div><div>68%</div><div>26%</div><div>7%</div></div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7404 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 CYTOSOLIC HEAT SHOCK PROTEIN 90.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1686	1067	277	337	5			
1	B	223	Total	C	N	O	S	0	0	0
			1761	1112	296	347	6			
1	C	214	Total	C	N	O	S	0	0	0
			1686	1067	277	337	5			

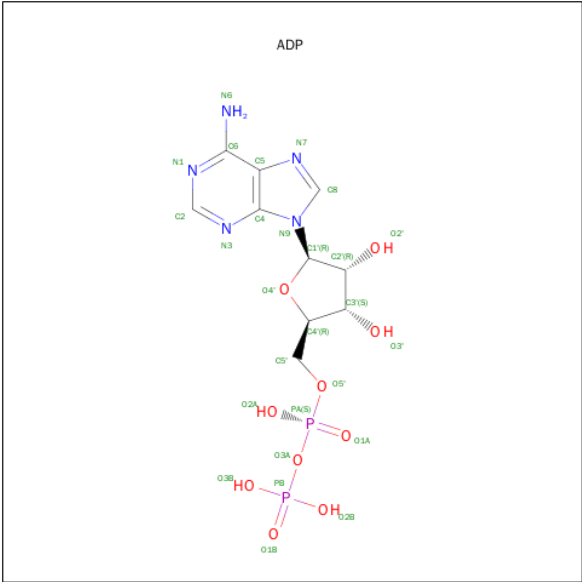
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	198	ARG	LYS	CONFLICT	UNP Q7XJ80
B	198	ARG	LYS	CONFLICT	UNP Q7XJ80
C	198	ARG	LYS	CONFLICT	UNP Q7XJ80

- Molecule 2 is a protein called SGT1-LIKE PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	S	90	Total	C	N	O	S	0	0	0
			730	477	116	135	2			
2	T	90	Total	C	N	O	S	0	0	0
			730	477	116	135	2			
2	U	90	Total	C	N	O	S	0	0	0
			730	477	116	135	2			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).

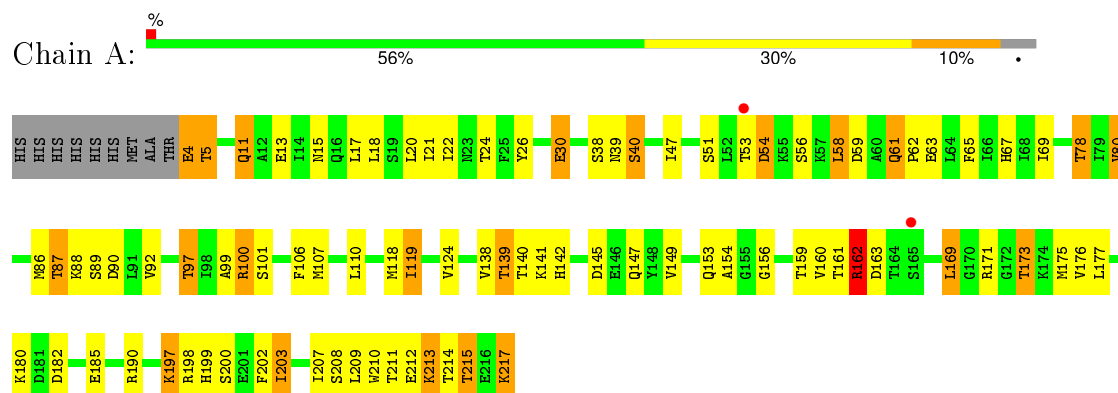


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

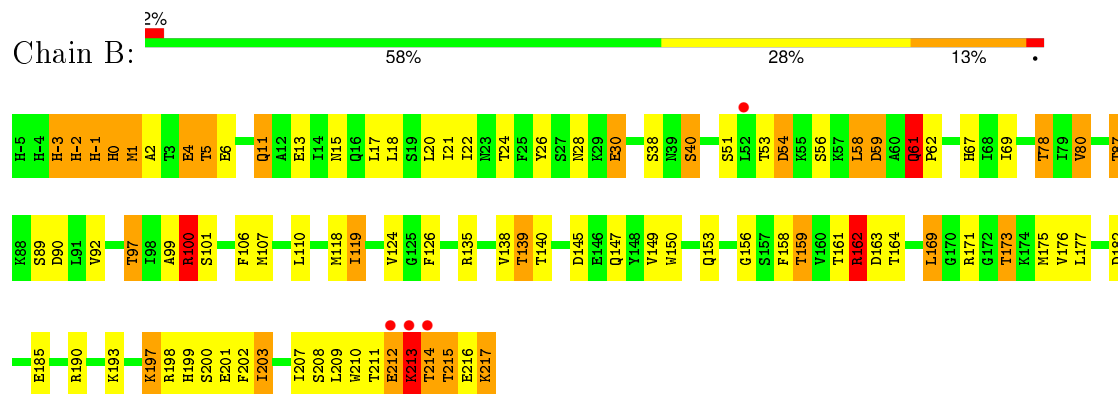
### 3 Residue-property plots [i](#)

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.

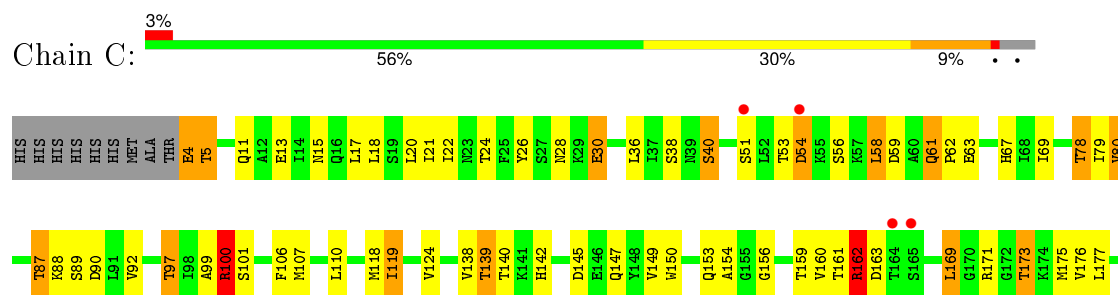
#### • Molecule 1: CYTOSOLIC HEAT SHOCK PROTEIN 90



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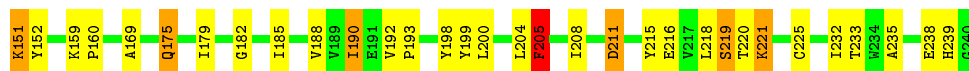


#### • Molecule 1: CYTOSOLIC HEAT SHOCK PROTEIN 90

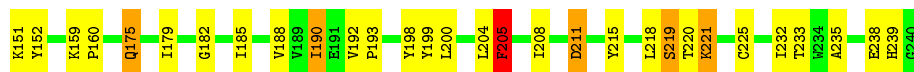




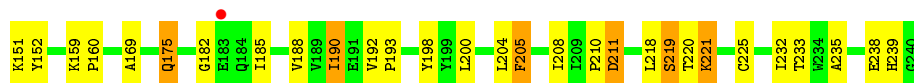
• Molecule 2: SGT1-LIKE PROTEIN



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• Molecule 2: SGT1-LIKE PROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.27Å 129.65Å 136.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.07 – 3.30 38.07 – 3.30	Depositor EDS
% Data completeness (in resolution range)	98.2 (38.07-3.30) 99.2 (38.07-3.30)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 3.32Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.199 , 0.238 0.187 , 0.227	Depositor DCC
$R_{free}$ test set	1389 reflections (5.13%)	DCC
Wilson B-factor (Å <sup>2</sup> )	61.2	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 70.7	EDS
Estimated twinning fraction	0.032 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 27124 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	7404	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.00% 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: ADP

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	2.18	1/1712 (0.1%)	0.81	3/2310 (0.1%)
1	B	1.78	1/1792 (0.1%)	0.83	4/2419 (0.2%)
1	C	1.85	1/1712 (0.1%)	0.90	5/2310 (0.2%)
2	S	0.64	1/747 (0.1%)	0.72	0/1011
2	T	0.62	1/747 (0.1%)	0.72	0/1011
2	U	0.61	1/747 (0.1%)	0.71	0/1011
All	All	1.66	6/7457 (0.1%)	0.81	12/10072 (0.1%)

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	2
All	All	0	3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4	GLU	C-O	87.35	2.89	1.23
1	C	4	GLU	C-O	73.37	2.62	1.23
1	B	4	GLU	C-O	71.52	2.59	1.23
2	S	225	CYS	CB-SG	7.73	1.95	1.82
2	T	225	CYS	CB-SG	7.45	1.95	1.82

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	GLU	CA-C-O	-17.24	83.90	120.10
1	C	162	ARG	NE-CZ-NH1	-17.22	111.69	120.30
1	C	162	ARG	NE-CZ-NH2	16.39	128.50	120.30
1	B	4	GLU	CA-C-O	-15.86	86.79	120.10
1	C	4	GLU	CA-C-O	-11.43	96.11	120.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	213	LYS	Peptide
1	B	-1	HIS	Peptide
1	B	213	LYS	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	1686	0	1658	84	0
1	B	1761	0	1719	87	0
1	C	1686	0	1658	80	0
2	S	730	0	739	23	0
2	T	730	0	739	23	0
2	U	730	0	739	18	0
3	A	27	0	12	5	0
3	B	27	0	12	2	0
3	C	27	0	12	1	0
All	All	7404	0	7288	311	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 21.

The worst 5 of 311 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:-3:HIS:O	1:B:-2:HIS:HB2	1.52	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:GLU:C	1:B:5:THR:N	2.14	1.00
1:C:11:GLN:HG2	1:C:99:ALA:HB2	1.46	0.95
1:A:11:GLN:HG2	1:A:99:ALA:HB2	1.51	0.92
1:B:197:LYS:NZ	1:B:217:LYS:HG2	1.84	0.92

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	211/223 (95%)	184 (87%)	25 (12%)	2 (1%)	21	60
1	B	219/223 (98%)	184 (84%)	27 (12%)	8 (4%)	4	27
1	C	211/223 (95%)	183 (87%)	26 (12%)	2 (1%)	21	60
2	S	88/90 (98%)	81 (92%)	5 (6%)	2 (2%)	8	39
2	T	88/90 (98%)	80 (91%)	6 (7%)	2 (2%)	8	39
2	U	88/90 (98%)	80 (91%)	7 (8%)	1 (1%)	17	57
All	All	905/939 (96%)	792 (88%)	96 (11%)	17 (2%)	10	45

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	54	ASP
1	B	54	ASP
1	C	54	ASP
1	B	-2	HIS
1	B	1	MET

### 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	185/196 (94%)	157 (85%)	28 (15%)	3	16
1	B	192/196 (98%)	162 (84%)	30 (16%)	3	16
1	C	185/196 (94%)	158 (85%)	27 (15%)	4	18
2	S	80/80 (100%)	70 (88%)	10 (12%)	6	24
2	T	80/80 (100%)	70 (88%)	10 (12%)	6	24
2	U	80/80 (100%)	70 (88%)	10 (12%)	6	24
All	All	802/828 (97%)	687 (86%)	115 (14%)	4	19

5 of 115 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	202	PHE
1	C	78	THR
2	U	175	GLN
1	B	203	ILE
1	C	5	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	147	GLN
1	B	183	GLN
1	C	183	GLN
1	B	94	ASN
2	S	178	ASN

### 5.3.3 RNA [i](#)

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$
3	ADP	A	1218	-	22,29,29	0.99	1 (4%)	27,45,45	1.74	5 (18%)
3	ADP	B	1218	-	22,29,29	1.06	1 (4%)	27,45,45	2.31	8 (29%)
3	ADP	C	1218	-	22,29,29	1.13	2 (9%)	27,45,45	2.10	8 (29%)

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	ADP	A	1218	-	-	0/12/32/32	0/3/3/3
3	ADP	B	1218	-	-	0/12/32/32	0/3/3/3
3	ADP	C	1218	-	-	0/12/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1218	ADP	O4'-C1'	2.62	1.44	1.41
3	A	1218	ADP	C5-C4	3.12	1.47	1.40
3	B	1218	ADP	C5-C4	3.21	1.47	1.40
3	C	1218	ADP	C5-C4	3.35	1.48	1.40

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1218	ADP	N3-C2-N1	-6.13	124.20	128.89
3	B	1218	ADP	C2'-C1'-N9	-5.41	106.03	114.29
3	C	1218	ADP	C2'-C1'-N9	-4.80	106.95	114.29
3	C	1218	ADP	N3-C2-N1	-4.73	125.27	128.89
3	A	1218	ADP	N3-C2-N1	-4.59	125.38	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1218	ADP	5	0
3	B	1218	ADP	2	0
3	C	1218	ADP	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	214/223 (95%)	-0.17	2 (0%) 85 82	31, 48, 90, 139	0
1	B	223/223 (100%)	-0.24	4 (1%) 71 65	30, 49, 88, 140	0
1	C	214/223 (95%)	-0.18	7 (3%) 50 43	30, 50, 92, 140	0
2	S	90/90 (100%)	-0.20	0 100 100	29, 44, 69, 95	0
2	T	90/90 (100%)	-0.22	0 100 100	29, 45, 74, 96	0
2	U	90/90 (100%)	-0.28	1 (1%) 82 78	28, 45, 73, 94	0
All	All	921/939 (98%)	-0.21	14 (1%) 76 71	28, 48, 84, 140	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	165	SER	4.4
1	A	165	SER	3.0
1	C	214	THR	3.0
1	A	53	THR	2.9
1	B	52	LEU	2.8

### 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( $\text{\AA}^2$ )	Q<0.9
3	ADP	C	1218	27/27	0.93	0.21	1.17	6,49,77,89	0
3	ADP	A	1218	27/27	0.97	0.21	0.53	17,38,55,57	0
3	ADP	B	1218	27/27	0.96	0.17	0.17	1,47,73,93	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.