



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:15 PM GMT

PDB ID : 1ESQ  
Title : CRYSTAL STRUCTURE OF THIAZOLE KINASE MUTANT (C198S)  
WITH ATP AND THIAZOLE PHOSPHATE.  
Authors : Campobasso, N.; Mathews, I.I.; Begley, T.P.; Ealick, S.E.  
Deposited on : 2000-04-10  
Resolution : 2.50 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

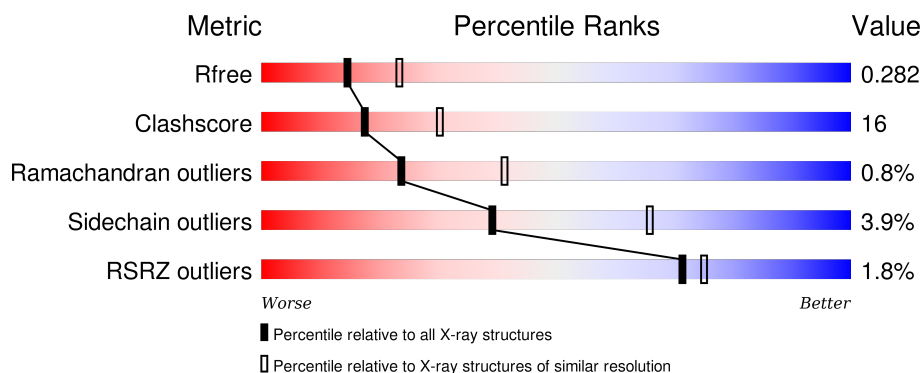
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	284	<div> <div>2%</div> <div> <div></div> <div>65%</div> <div>24%</div> <div>•</div> <div>9%</div> </div> </div>
1	B	284	<div> <div></div> <div> <div>67%</div> <div>22%</div> <div>•</div> <div>9%</div> </div> </div>
1	C	284	<div> <div>2%</div> <div> <div></div> <div>66%</div> <div>28%</div> <div>•</div> <div>•</div> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6061 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 HYDROXYETHYLTHIAZOLE KINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	0	0
			1881	1176	331	368	6			
1	B	258	Total	C	N	O	S	0	0	0
			1876	1174	331	365	6			
1	C	274	Total	C	N	O	S	0	0	0
			1982	1230	362	383	7			

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	EXPRESSION TAG	UNP P39593
A	-10	ARG	-	EXPRESSION TAG	UNP P39593
A	-9	GLY	-	EXPRESSION TAG	UNP P39593
A	-8	SER	-	EXPRESSION TAG	UNP P39593
A	-7	HIS	-	EXPRESSION TAG	UNP P39593
A	-6	HIS	-	EXPRESSION TAG	UNP P39593
A	-5	HIS	-	EXPRESSION TAG	UNP P39593
A	-4	HIS	-	EXPRESSION TAG	UNP P39593
A	-3	HIS	-	EXPRESSION TAG	UNP P39593
A	-2	HIS	-	EXPRESSION TAG	UNP P39593
A	-1	GLY	-	EXPRESSION TAG	UNP P39593
A	0	SER	-	EXPRESSION TAG	UNP P39593
A	198	SER	CYS	ENGINEERED	UNP P39593
B	-11	MET	-	EXPRESSION TAG	UNP P39593
B	-10	ARG	-	EXPRESSION TAG	UNP P39593
B	-9	GLY	-	EXPRESSION TAG	UNP P39593
B	-8	SER	-	EXPRESSION TAG	UNP P39593
B	-7	HIS	-	EXPRESSION TAG	UNP P39593
B	-6	HIS	-	EXPRESSION TAG	UNP P39593
B	-5	HIS	-	EXPRESSION TAG	UNP P39593
B	-4	HIS	-	EXPRESSION TAG	UNP P39593
B	-3	HIS	-	EXPRESSION TAG	UNP P39593
B	-2	HIS	-	EXPRESSION TAG	UNP P39593

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	EXPRESSION TAG	UNP P39593
B	0	SER	-	EXPRESSION TAG	UNP P39593
B	198	SER	CYS	ENGINEERED	UNP P39593
C	-11	MET	-	EXPRESSION TAG	UNP P39593
C	-10	ARG	-	EXPRESSION TAG	UNP P39593
C	-9	GLY	-	EXPRESSION TAG	UNP P39593
C	-8	SER	-	EXPRESSION TAG	UNP P39593
C	-7	HIS	-	EXPRESSION TAG	UNP P39593
C	-6	HIS	-	EXPRESSION TAG	UNP P39593
C	-5	HIS	-	EXPRESSION TAG	UNP P39593
C	-4	HIS	-	EXPRESSION TAG	UNP P39593
C	-3	HIS	-	EXPRESSION TAG	UNP P39593
C	-2	HIS	-	EXPRESSION TAG	UNP P39593
C	-1	GLY	-	EXPRESSION TAG	UNP P39593
C	0	SER	-	EXPRESSION TAG	UNP P39593
C	198	SER	CYS	ENGINEERED	UNP P39593

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

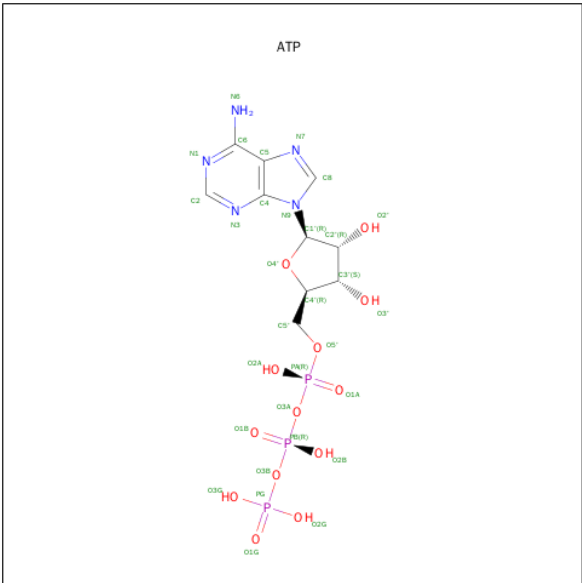
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Mg 2 2	0	0
2	A	2	Total Mg 2 2	0	0
2	C	2	Total Mg 2 2	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>).



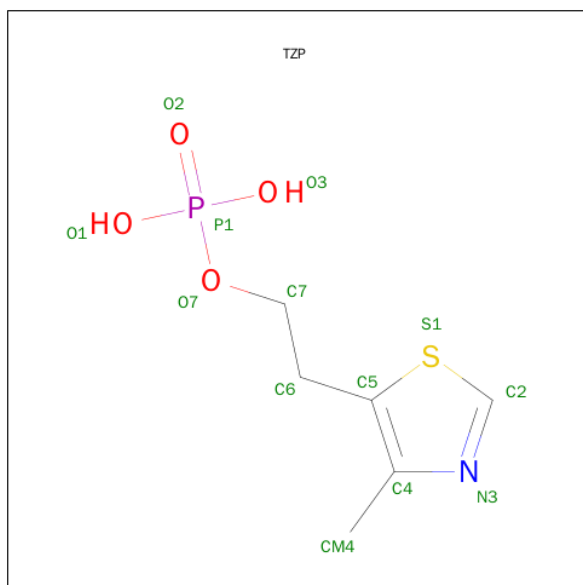
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
4	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 5 is 4-METHYL-5-HYDROXYETHYLTHIAZOLE PHOSPHATE (three-letter code: TZP) (formula: C<sub>6</sub>H<sub>10</sub>NO<sub>4</sub>PS).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	S	0	0
			13	6	1	4	1	1		
5	B	1	Total	C	N	O	P	S	0	0
			13	6	1	4	1	1		
5	C	1	Total	C	N	O	P	S	0	0
			13	6	1	4	1	1		

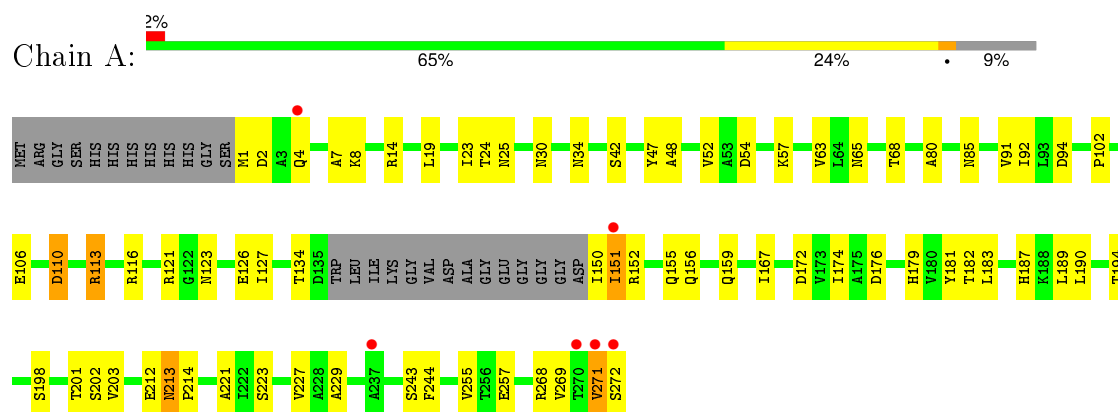
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	56	Total	O	0	0
			56	56		
6	B	73	Total	O	0	0
			73	73		
6	C	50	Total	O	0	0
			50	50		

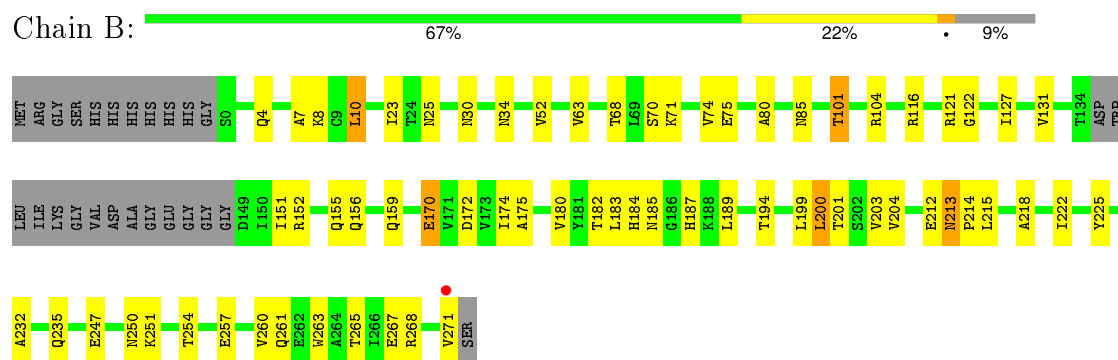
### 3 Residue-property plots [i](#)

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.

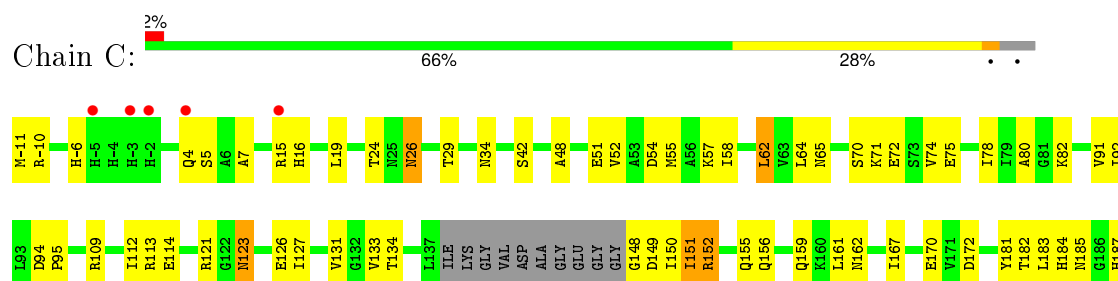
#### • Molecule 1: HYDROXYETHYLTHIAZOLE KINASE

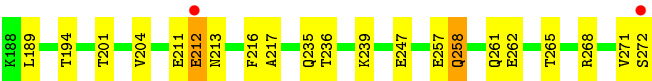


#### • Molecule 1: HYDROXYETHYLTHIAZOLE KINASE



#### • Molecule 1: HYDROXYETHYLTHIAZOLE KINASE







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.08 Å 100.84 Å 72.51 Å 90.00° 95.10° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 19.82 – 2.50	Depositor EDS
% Data completeness (in resolution range)	94.9 (20.00-2.50) 99.8 (19.82-2.50)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.16 (at 2.50 Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, $R_{free}$	0.209 , 0.282 0.210 , 0.282	Depositor DCC
$R_{free}$ test set	1300 reflections (4.85%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.0	Xtriage
Anisotropy	0.474	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 37.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 26794 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6061	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 5.28% 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: TZP, MG, SO4, ATP

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	0.36	0/1903	0.58	1/2589 (0.0%)
1	B	0.38	0/1898	0.59	1/2582 (0.0%)
1	C	0.36	0/2010	0.60	0/2727
All	All	0.37	0/5811	0.59	2/7898 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	ILE	N-CA-C	-5.33	96.60	111.00
1	B	23	ILE	N-CA-C	-5.31	96.66	111.00

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	1881	0	1921	73	0
1	B	1876	0	1913	53	0
1	C	1982	0	1980	70	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	5	0	0	0	0
4	A	31	0	12	0	0
4	B	31	0	12	0	0
4	C	31	0	12	1	0
5	A	13	0	8	1	0
5	B	13	0	8	0	0
5	C	13	0	8	0	0
6	A	56	0	0	4	0
6	B	73	0	0	2	0
6	C	50	0	0	1	0
All	All	6061	0	5874	188	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 16.

All (188) 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:C:185:ASN:HD21	1:C:265:THR:H	1.14	0.90
1:A:190:LEU:HD21	1:A:229:ALA:HB1	1.57	0.86
1:B:127:ILE:O	1:B:131:VAL:HG12	1.78	0.84
1:A:271:VAL:HG12	1:A:272:SER:H	1.46	0.80
1:C:71:LYS:O	1:C:75:GLU:HG2	1.82	0.80
1:A:187:HIS:HD2	1:A:189:LEU:HB2	1.48	0.77
1:B:170:GLU:H	1:B:170:GLU:CD	1.87	0.75
1:C:-11:MET:HB2	1:C:16:HIS:ND1	2.02	0.75
1:B:182:THR:HG22	1:B:267:GLU:HB3	1.67	0.74
1:C:123:ASN:HD21	1:C:126:GLU:HG3	1.52	0.73
1:C:123:ASN:C	1:C:123:ASN:HD22	1.92	0.73
1:C:187:HIS:HD2	1:C:189:LEU:H	1.37	0.72
1:A:94:ASP:HB2	1:A:201:THR:HG21	1.70	0.71
1:A:34:ASN:HD21	1:C:194:THR:H	1.39	0.70
1:A:151:ILE:HD11	1:A:152:ARG:NH1	2.05	0.70
1:A:243:SER:H	1:B:250:ASN:HD21	1.39	0.70
1:B:172:ASP:HB2	1:B:183:LEU:HB2	1.72	0.70
1:B:71:LYS:O	1:B:75:GLU:HG3	1.93	0.69
1:C:156:GLN:HA	1:C:159:GLN:HE21	1.57	0.69
1:A:34:ASN:ND2	1:C:194:THR:H	1.90	0.68
1:C:187:HIS:CD2	1:C:189:LEU:H	2.10	0.68
1:C:123:ASN:ND2	1:C:126:GLU:H	1.90	0.68
1:A:187:HIS:CD2	1:A:189:LEU:HB2	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:101:THR:HG21	1:C:51:GLU:OE1	1.94	0.67
1:B:185:ASN:HD21	1:B:265:THR:H	1.41	0.67
1:C:172:ASP:O	1:C:182:THR:HA	1.94	0.66
1:A:187:HIS:HD2	1:A:189:LEU:H	1.42	0.66
1:A:151:ILE:HG12	1:A:152:ARG:N	2.10	0.66
1:B:52:VAL:HB	1:B:80:ALA:HB2	1.78	0.65
1:A:187:HIS:CD2	1:A:189:LEU:H	2.14	0.65
1:B:199:LEU:O	1:B:203:VAL:HG23	1.95	0.65
1:B:7:ALA:HB2	1:B:260:VAL:HB	1.79	0.65
1:A:151:ILE:HG12	1:A:152:ARG:H	1.60	0.65
1:C:271:VAL:HG22	1:C:272:SER:N	2.12	0.65
1:B:182:THR:HG23	1:B:184:HIS:NE2	2.12	0.65
1:B:101:THR:HG22	1:B:104:ARG:H	1.61	0.65
1:B:4:GLN:HA	1:B:261:GLN:HG2	1.79	0.64
1:A:85:ASN:HD21	1:A:116:ARG:H	1.43	0.64
1:C:123:ASN:ND2	1:C:126:GLU:HG3	2.12	0.64
1:C:55:MET:CE	1:C:58:ILE:HD11	2.27	0.64
1:A:91:VAL:C	1:A:92:ILE:HD12	2.18	0.64
1:B:213:ASN:HD22	1:B:213:ASN:C	2.00	0.64
1:A:212:GLU:HG2	6:A:453:HOH:O	1.97	0.64
1:B:7:ALA:HB1	1:B:257:GLU:HG2	1.80	0.63
1:B:4:GLN:O	1:B:8:LYS:HG2	1.98	0.63
1:A:172:ASP:O	1:A:182:THR:HA	1.98	0.63
1:B:187:HIS:HD2	1:B:189:LEU:H	1.47	0.63
1:B:152:ARG:CG	1:B:156:GLN:HE21	2.12	0.63
1:B:213:ASN:HD22	1:B:214:PRO:N	1.97	0.63
1:A:85:ASN:ND2	1:A:116:ARG:H	1.97	0.62
1:A:123:ASN:OD1	1:A:126:GLU:HG3	1.99	0.62
1:A:172:ASP:HB2	1:A:183:LEU:HB2	1.81	0.61
1:C:123:ASN:HD21	1:C:126:GLU:H	1.48	0.61
1:A:174:ILE:HD12	1:A:174:ILE:N	2.15	0.61
1:B:174:ILE:HD11	1:B:222:ILE:HD12	1.82	0.61
1:A:213:ASN:HD22	1:A:213:ASN:C	2.04	0.61
1:C:185:ASN:ND2	1:C:265:THR:H	1.92	0.60
1:B:30:ASN:ND2	6:B:539:HOH:O	2.32	0.59
1:B:85:ASN:HD21	1:B:116:ARG:H	1.49	0.59
1:B:121:ARG:HD2	1:B:122:GLY:N	2.18	0.59
1:C:127:ILE:HG13	1:C:167:ILE:HG12	1.84	0.59
1:A:190:LEU:HD21	1:A:229:ALA:CB	2.31	0.59
1:C:161:LEU:N	1:C:161:LEU:HD12	2.18	0.59
1:C:185:ASN:HD21	1:C:265:THR:N	1.94	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:ILE:HD13	1:A:151:ILE:N	2.18	0.59
1:B:218:ALA:O	1:B:222:ILE:HG13	2.04	0.58
1:C:24:THR:HA	1:C:65:ASN:HB3	1.83	0.58
1:C:72:GLU:CD	1:C:72:GLU:H	2.06	0.58
1:C:183:LEU:HB3	6:C:416:HOH:O	2.04	0.58
1:A:7:ALA:HB1	1:A:257:GLU:HG2	1.85	0.57
1:B:187:HIS:CD2	1:B:189:LEU:H	2.22	0.57
1:B:213:ASN:HD22	1:B:214:PRO:CD	2.17	0.57
1:B:194:THR:H	1:C:34:ASN:ND2	2.02	0.56
1:A:271:VAL:HG12	1:A:272:SER:N	2.18	0.56
1:C:48:ALA:O	1:C:52:VAL:HG13	2.06	0.55
1:B:194:THR:H	1:C:34:ASN:HD21	1.55	0.55
1:B:194:THR:HA	6:B:574:HOH:O	2.07	0.55
1:C:271:VAL:HG22	1:C:272:SER:H	1.72	0.55
1:C:4:GLN:HA	1:C:261:GLN:HG3	1.90	0.54
1:A:151:ILE:H	1:A:151:ILE:HD13	1.73	0.54
1:A:213:ASN:HD22	1:A:214:PRO:N	2.04	0.54
1:B:200:LEU:HG	1:B:225:TYR:CD2	2.43	0.54
1:A:194:THR:H	1:B:34:ASN:ND2	2.06	0.54
1:C:156:GLN:HA	1:C:159:GLN:NE2	2.23	0.54
1:B:152:ARG:HG3	1:B:156:GLN:HE21	1.73	0.54
1:C:94:ASP:HB2	1:C:201:THR:HG21	1.90	0.54
1:A:30:ASN:HB3	6:A:401:HOH:O	2.08	0.54
1:C:258:GLN:H	1:C:258:GLN:HE21	1.57	0.53
1:C:92:ILE:N	1:C:92:ILE:HD12	2.24	0.53
1:C:26:ASN:C	1:C:26:ASN:HD22	2.09	0.53
1:C:91:VAL:C	1:C:92:ILE:HD12	2.29	0.53
1:A:85:ASN:HD21	1:A:116:ARG:N	2.05	0.53
1:C:62:LEU:HD11	1:C:64:LEU:HD21	1.90	0.53
1:A:127:ILE:HG13	1:A:167:ILE:HG12	1.91	0.53
1:C:149:ASP:O	1:C:151:ILE:N	2.36	0.52
1:B:70:SER:O	1:B:74:VAL:HG23	2.11	0.51
1:A:181:TYR:CZ	1:A:268:ARG:HD3	2.44	0.51
1:C:7:ALA:HB1	1:C:257:GLU:HB2	1.92	0.51
1:A:194:THR:H	1:B:34:ASN:HD21	1.57	0.51
1:C:62:LEU:CD1	1:C:64:LEU:HD21	2.41	0.51
1:A:54:ASP:HA	1:A:57:LYS:HE3	1.92	0.51
1:B:213:ASN:C	1:B:213:ASN:ND2	2.65	0.50
1:A:183:LEU:HB3	6:A:405:HOH:O	2.11	0.50
1:B:232:ALA:HB1	1:B:247:GLU:HB3	1.93	0.50
1:A:203:VAL:HG12	1:A:221:ALA:HB1	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:THR:HG23	1:A:269:VAL:CG2	2.42	0.50
1:B:263:TRP:O	1:B:265:THR:HG23	2.12	0.49
1:B:174:ILE:CD1	1:B:222:ILE:HD12	2.41	0.49
1:A:110:ASP:O	1:A:113:ARG:HG2	2.12	0.49
1:C:155:GLN:OE1	1:C:271:VAL:HG21	2.11	0.49
1:A:2:ASP:OD2	1:A:4:GLN:HG2	2.13	0.49
1:A:187:HIS:O	1:A:190:LEU:HD23	2.12	0.49
1:A:52:VAL:HB	1:A:80:ALA:HB2	1.94	0.49
1:A:223:SER:O	1:A:227:VAL:HG13	2.13	0.48
1:C:236:THR:HG22	1:C:239:LYS:HD2	1.94	0.48
1:B:235:GLN:HG2	1:B:247:GLU:OE2	2.14	0.48
1:C:26:ASN:ND2	1:C:26:ASN:C	2.66	0.48
1:C:55:MET:HE3	1:C:58:ILE:HD11	1.95	0.47
1:A:198:SER:N	5:A:320:TZP:O3	2.44	0.47
1:C:109:ARG:O	1:C:113:ARG:HG3	2.15	0.47
1:A:102:PRO:O	1:A:106:GLU:HG3	2.15	0.47
1:A:189:LEU:HD23	1:A:244:PHE:CG	2.49	0.47
1:A:151:ILE:HD11	1:A:152:ARG:HH12	1.77	0.47
1:B:10:LEU:HD12	1:B:260:VAL:HG21	1.96	0.47
1:A:268:ARG:HG2	1:A:268:ARG:HH11	1.80	0.47
1:C:95:PRO:HD2	1:C:121:ARG:O	2.14	0.47
1:A:48:ALA:O	1:A:52:VAL:HG13	2.15	0.47
1:A:155:GLN:O	1:A:159:GLN:HG3	2.15	0.46
1:B:213:ASN:HD22	1:B:214:PRO:HD2	1.80	0.46
1:C:78:ILE:HG22	1:C:82:LYS:HE2	1.98	0.46
1:C:236:THR:CG2	1:C:247:GLU:HG3	2.46	0.46
1:B:271:VAL:HG12	1:B:271:VAL:O	2.15	0.46
1:A:187:HIS:H	1:A:190:LEU:HD23	1.81	0.45
1:B:182:THR:HG22	1:B:267:GLU:CB	2.40	0.45
1:C:112:ILE:HD13	1:C:161:LEU:HD23	1.97	0.45
1:A:151:ILE:CD1	1:A:151:ILE:H	2.28	0.45
1:B:201:THR:O	1:B:204:VAL:HB	2.15	0.45
1:A:150:ILE:CA	6:A:467:HOH:O	2.64	0.45
1:B:175:ALA:CB	1:B:180:VAL:HG22	2.46	0.45
1:C:271:VAL:CG2	1:C:272:SER:N	2.78	0.45
1:C:123:ASN:C	1:C:123:ASN:ND2	2.65	0.45
1:C:15:ARG:HG2	1:C:16:HIS:CD2	2.52	0.44
1:C:258:GLN:H	1:C:258:GLN:NE2	2.15	0.44
1:C:70:SER:O	1:C:74:VAL:HG23	2.17	0.44
1:C:-6:HIS:HD2	1:C:5:SER:OG	2.00	0.44
1:C:54:ASP:HA	1:C:57:LYS:HE2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:ASN:HB2	1:A:68:THR:HG23	2.00	0.44
1:C:149:ASP:C	1:C:151:ILE:H	2.20	0.44
1:A:151:ILE:CG1	1:A:152:ARG:H	2.30	0.43
1:C:26:ASN:HA	1:C:29:THR:HG23	2.00	0.43
1:A:19:LEU:HA	1:A:42:SER:O	2.18	0.43
1:A:92:ILE:N	1:A:92:ILE:HD12	2.33	0.43
1:C:201:THR:O	1:C:204:VAL:HB	2.18	0.43
1:A:268:ARG:HG2	1:A:268:ARG:NH1	2.34	0.43
1:B:151:ILE:HG23	1:B:180:VAL:HG11	2.01	0.43
1:A:113:ARG:HH11	1:A:113:ARG:CB	2.32	0.42
1:A:113:ARG:HB3	1:A:113:ARG:NH1	2.34	0.42
1:C:211:GLU:HB3	1:C:217:ALA:HB2	2.01	0.42
1:A:2:ASP:CG	1:A:4:GLN:HG2	2.39	0.42
1:A:63:VAL:HG21	1:A:202:SER:HA	2.01	0.42
1:A:176:ASP:OD1	1:A:179:HIS:N	2.48	0.42
1:C:52:VAL:HB	1:C:80:ALA:HB2	2.00	0.42
1:A:8:LYS:HA	1:A:8:LYS:HD2	1.84	0.42
1:A:151:ILE:CG1	1:A:152:ARG:N	2.80	0.42
1:A:179:HIS:ND1	1:A:268:ARG:NH2	2.68	0.42
1:B:155:GLN:HE21	1:B:159:GLN:CD	2.23	0.41
1:A:34:ASN:HD22	1:A:34:ASN:HA	1.67	0.41
1:A:151:ILE:CD1	1:A:151:ILE:N	2.83	0.41
1:A:152:ARG:O	1:A:156:GLN:HG3	2.20	0.41
1:B:175:ALA:HB2	1:B:180:VAL:HG13	2.03	0.41
1:A:271:VAL:CG1	1:A:272:SER:H	2.17	0.41
1:C:213:ASN:HB3	1:C:216:PHE:CD1	2.55	0.41
1:C:19:LEU:HA	1:C:42:SER:HB2	2.02	0.41
1:B:212:GLU:OE2	1:B:212:GLU:N	2.41	0.41
1:B:213:ASN:ND2	1:B:215:LEU:H	2.19	0.41
1:C:161:LEU:H	1:C:161:LEU:HD12	1.84	0.41
1:C:181:TYR:CZ	1:C:268:ARG:HD3	2.56	0.41
1:C:184:HIS:HB2	1:C:265:THR:OG1	2.19	0.40
1:C:-10:ARG:HG2	1:C:212:GLU:OE1	2.21	0.40
1:A:14:ARG:HH22	1:A:255:VAL:HG12	1.86	0.40
1:C:170:GLU:HA	4:C:310:ATP:C6	2.56	0.40
1:C:148:GLY:O	1:C:152:ARG:HB2	2.20	0.40
1:C:131:VAL:HG12	1:C:161:LEU:HD21	2.03	0.40
1:A:24:THR:HA	1:A:65:ASN:HB3	2.03	0.40
1:B:25:ASN:HB2	1:B:68:THR:HG23	2.03	0.40
1:A:189:LEU:HD23	1:A:244:PHE:CD1	2.57	0.40
1:C:161:LEU:O	1:C:162:ASN:C	2.60	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:251:LYS:HA	1:B:254:THR:HB	2.03	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	254/284 (89%)	243 (96%)	9 (4%)	2 (1%)	24	41
1	B	254/284 (89%)	242 (95%)	12 (5%)	0	100	100
1	C	270/284 (95%)	254 (94%)	12 (4%)	4 (2%)	13	22
All	All	778/852 (91%)	739 (95%)	33 (4%)	6 (1%)	24	41

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	133	VAL
1	C	134	THR
1	C	150	ILE
1	C	151	ILE
1	A	134	THR
1	A	271	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	197/216 (91%)	190 (96%)	7 (4%)	42	69
1	B	195/216 (90%)	188 (96%)	7 (4%)	42	69
1	C	203/216 (94%)	194 (96%)	9 (4%)	35	60
All	All	595/648 (92%)	572 (96%)	23 (4%)	39	66

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	47	TYR
1	A	110	ASP
1	A	113	ARG
1	A	121	ARG
1	A	151	ILE
1	A	213	ASN
1	B	10	LEU
1	B	63	VAL
1	B	101	THR
1	B	170	GLU
1	B	200	LEU
1	B	213	ASN
1	B	268	ARG
1	C	26	ASN
1	C	62	LEU
1	C	114	GLU
1	C	123	ASN
1	C	152	ARG
1	C	212	GLU
1	C	235	GLN
1	C	258	GLN
1	C	262	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	ASN
1	A	85	ASN
1	A	187	HIS
1	A	213	ASN
1	A	261	GLN
1	B	34	ASN

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Mol	Chain	Res	Type
1	B	85	ASN
1	B	155	GLN
1	B	156	GLN
1	B	159	GLN
1	B	185	ASN
1	B	187	HIS
1	B	213	ASN
1	B	230	GLN
1	B	235	GLN
1	B	250	ASN
1	B	261	GLN
1	C	-6	HIS
1	C	4	GLN
1	C	26	ASN
1	C	34	ASN
1	C	123	ASN
1	C	156	GLN
1	C	159	GLN
1	C	185	ASN
1	C	187	HIS
1	C	234	GLN
1	C	258	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 6 are monoatomic - leaving 7 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
4	ATP	A	300	2	24,33,33	1.91	8 (33%)	31,52,52	2.10	10 (32%)
5	TZP	A	320	2	9,13,13	2.72	4 (44%)	9,18,18	2.67	4 (44%)
4	ATP	B	305	2	24,33,33	1.93	6 (25%)	31,52,52	2.22	10 (32%)
5	TZP	B	325	2	9,13,13	2.63	4 (44%)	9,18,18	2.95	4 (44%)
3	SO4	B	370	-	4,4,4	0.16	0	6,6,6	0.13	0
4	ATP	C	310	2	24,33,33	1.92	7 (29%)	31,52,52	2.21	10 (32%)
5	TZP	C	330	2	9,13,13	2.80	4 (44%)	9,18,18	2.80	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
4	ATP	A	300	2	-	0/18/38/38	0/3/3/3
5	TZP	A	320	2	-	0/6/7/7	0/1/1/1
4	ATP	B	305	2	-	0/18/38/38	0/3/3/3
5	TZP	B	325	2	-	0/6/7/7	0/1/1/1
3	SO4	B	370	-	-	0/0/0/0	0/0/0/0
4	ATP	C	310	2	-	0/18/38/38	0/3/3/3
5	TZP	C	330	2	-	0/6/7/7	0/1/1/1

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	330	TZP	P1-O7	-5.63	1.41	1.60
5	B	325	TZP	P1-O7	-5.09	1.43	1.60
5	A	320	TZP	P1-O7	-5.07	1.43	1.60
5	A	320	TZP	C5-C4	-3.14	1.36	1.42
5	C	330	TZP	C5-C4	-3.04	1.36	1.42
5	B	325	TZP	C5-C4	-2.49	1.37	1.42
4	C	310	ATP	PG-O2G	-2.33	1.46	1.54
4	A	300	ATP	PG-O2G	-2.29	1.46	1.54
4	B	305	ATP	PG-O2G	-2.26	1.46	1.54
4	C	310	ATP	C8-N7	-2.04	1.30	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	305	ATP	C2-N1	2.35	1.38	1.33
4	A	300	ATP	C2-N1	2.36	1.38	1.33
5	A	320	TZP	C2-S1	2.39	1.76	1.68
4	C	310	ATP	C2-N1	2.42	1.38	1.33
4	A	300	ATP	C5'-C4'	2.47	1.59	1.51
4	A	300	ATP	O4'-C1'	2.51	1.44	1.41
5	B	325	TZP	C2-S1	2.55	1.77	1.68
5	C	330	TZP	C2-S1	2.64	1.77	1.68
4	A	300	ATP	C2-N3	2.80	1.37	1.32
4	B	305	ATP	C2-N3	2.88	1.37	1.32
4	B	305	ATP	PA-O1A	2.99	1.62	1.51
4	A	300	ATP	PA-O1A	3.02	1.62	1.51
4	C	310	ATP	PA-O1A	3.05	1.62	1.51
4	C	310	ATP	C2-N3	3.31	1.38	1.32
5	C	330	TZP	P1-O3	3.63	1.67	1.54
5	A	320	TZP	P1-O3	3.77	1.68	1.54
5	B	325	TZP	P1-O3	3.78	1.68	1.54
4	C	310	ATP	PG-O3G	3.81	1.68	1.54
4	A	300	ATP	PG-O3G	3.84	1.68	1.54
4	B	305	ATP	PG-O3G	4.07	1.69	1.54
4	A	300	ATP	C4-N3	4.69	1.42	1.35
4	C	310	ATP	C4-N3	5.04	1.43	1.35
4	B	305	ATP	C4-N3	5.34	1.43	1.35

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	325	TZP	C6-C5-S1	-5.39	112.69	120.24
4	C	310	ATP	O4'-C4'-C5'	-5.02	91.37	109.32
5	C	330	TZP	C6-C5-S1	-4.98	113.28	120.24
4	B	305	ATP	O4'-C4'-C5'	-4.87	91.91	109.32
4	C	310	ATP	N3-C2-N1	-4.72	125.28	128.89
4	A	300	ATP	O4'-C4'-C5'	-4.63	92.75	109.32
5	A	320	TZP	C6-C5-S1	-4.47	113.98	120.24
4	B	305	ATP	N3-C2-N1	-4.20	125.68	128.89
4	A	300	ATP	N3-C2-N1	-3.84	125.95	128.89
5	A	320	TZP	O3-P1-O2	-3.50	99.32	110.58
5	C	330	TZP	O3-P1-O2	-3.49	99.34	110.58
5	B	325	TZP	O3-P1-O2	-3.23	100.17	110.58
4	B	305	ATP	O4'-C1'-N9	-2.85	102.12	108.10
4	C	310	ATP	O4'-C1'-N9	-2.67	102.51	108.10
4	A	300	ATP	O4'-C1'-N9	-2.57	102.73	108.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	300	ATP	O3G-PG-O2G	-2.22	98.91	107.38
4	B	305	ATP	O3G-PG-O2G	-2.11	99.35	107.38
4	C	310	ATP	O3G-PG-O2G	-2.08	99.48	107.38
4	A	300	ATP	O3G-PG-O1G	2.17	117.56	110.58
4	A	300	ATP	O2A-PA-O3A	2.20	115.06	105.09
4	C	310	ATP	O2A-PA-O3A	2.29	115.46	105.09
4	C	310	ATP	O3G-PG-O1G	2.30	117.99	110.58
4	A	300	ATP	C4-C5-N7	2.36	111.65	109.48
4	B	305	ATP	O3G-PG-O1G	2.39	118.29	110.58
4	B	305	ATP	O2A-PA-O3A	2.41	116.03	105.09
4	B	305	ATP	C4-C5-N7	2.49	111.77	109.48
4	C	310	ATP	C4-C5-N7	2.64	111.91	109.48
5	A	320	TZP	C6-C5-C4	3.32	130.54	127.56
5	C	330	TZP	O3-P1-O7	3.37	116.26	106.56
5	B	325	TZP	O3-P1-O7	3.50	116.65	106.56
4	C	310	ATP	C2'-C1'-N9	3.57	119.75	114.29
5	C	330	TZP	C6-C5-C4	3.98	131.13	127.56
5	A	320	TZP	O3-P1-O7	4.01	118.10	106.56
4	A	300	ATP	PA-O3A-PB	4.33	144.89	132.73
4	C	310	ATP	C5'-C4'-C3'	4.42	132.75	115.21
4	B	305	ATP	C5'-C4'-C3'	4.45	132.87	115.21
4	A	300	ATP	C5'-C4'-C3'	4.45	132.87	115.21
4	A	300	ATP	C2'-C1'-N9	4.48	121.14	114.29
5	B	325	TZP	C6-C5-C4	4.53	131.62	127.56
4	B	305	ATP	C2'-C1'-N9	4.54	121.23	114.29
4	B	305	ATP	PA-O3A-PB	4.91	146.52	132.73
4	C	310	ATP	PA-O3A-PB	4.99	146.75	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	320	TZP	1	0
4	C	310	ATP	1	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	258/284 (90%)	-0.17	6 (2%) 64 67	16, 30, 49, 88	0
1	B	258/284 (90%)	-0.23	1 (0%) 93 93	15, 29, 50, 66	0
1	C	274/284 (96%)	-0.17	7 (2%) 59 63	14, 30, 54, 63	0
All	All	790/852 (92%)	-0.19	14 (1%) 71 75	14, 29, 51, 88	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	272	SER	7.0
1	A	271	VAL	5.2
1	B	271	VAL	3.7
1	A	270	THR	3.4
1	C	272	SER	3.4
1	C	-3	HIS	3.2
1	C	-2	HIS	2.8
1	A	237	ALA	2.3
1	C	-5	HIS	2.2
1	C	4	GLN	2.2
1	C	212	GLU	2.2
1	A	151	ILE	2.1
1	C	15	ARG	2.1
1	A	4	GLN	2.1

### 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 [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
2	MG	A	340	1/1	0.90	0.12	0.54	32,32,32,32	0
4	ATP	C	310	31/31	0.95	0.13	0.13	27,31,33,35	0
4	ATP	B	305	31/31	0.93	0.14	-0.03	28,36,42,42	0
4	ATP	A	300	31/31	0.94	0.14	-0.19	35,40,44,47	0
2	MG	C	350	1/1	0.93	0.10	-0.29	41,41,41,41	0
5	TZP	B	325	13/13	0.97	0.09	-0.77	17,22,34,35	0
5	TZP	C	330	13/13	0.98	0.09	-0.94	20,22,31,32	0
5	TZP	A	320	13/13	0.98	0.08	-1.43	17,20,33,33	0
2	MG	A	365	1/1	0.90	0.17	-	46,46,46,46	0
2	MG	B	360	1/1	0.75	0.14	-	48,48,48,48	0
3	SO4	B	370	5/5	0.99	0.09	-	32,32,34,35	0
2	MG	B	345	1/1	0.91	0.12	-	22,22,22,22	0
2	MG	C	355	1/1	0.55	0.15	-	40,40,40,40	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.