



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 26, 2014 – 09:15 PM GMT

PDB ID : 1V25  
Title : Crystal structure of tt0168 from *Thermus thermophilus* HB8  
Authors : Hisanaga, Y.; Ago, H.; Nakatsu, T.; Hamada, K.; Ida, K.; Kanda, H.; Yamamoto, M.; Hori, T.; Arii, Y.; Sugahara, M.; Kuramitsu, S.; Yokoyama, S.; Miyano, M.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2003-10-07  
Resolution : 2.30 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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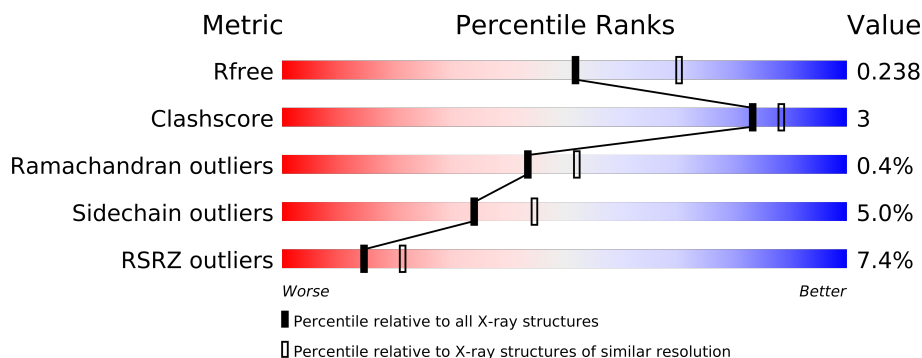
The following versions of software and data (see [references](#)) were used in the production of this report:

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 2.30 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))
$R_{free}$	66092	2929 (2.30-2.30)
Clashscore	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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	541	
1	B	541	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 8236 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.

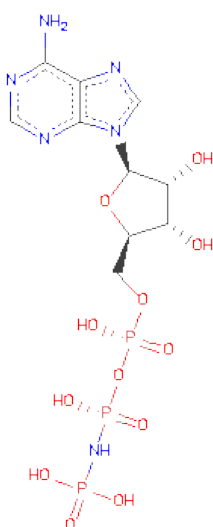
- Molecule 1 is a protein called long-chain-fatty-acid-CoAsynthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	0	0	0
			3812	2441	663	698	10			
1	B	507	Total	C	N	O	S	0	0	0
			3939	2525	686	717	11			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PHOSPHOAMINOPHOSPHONICACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 31	C 10	N 6	O 12	P 3	0	0
3	B	1	Total 31	C 10	N 6	O 12	P 3	0	0

- Molecule 4 is water.

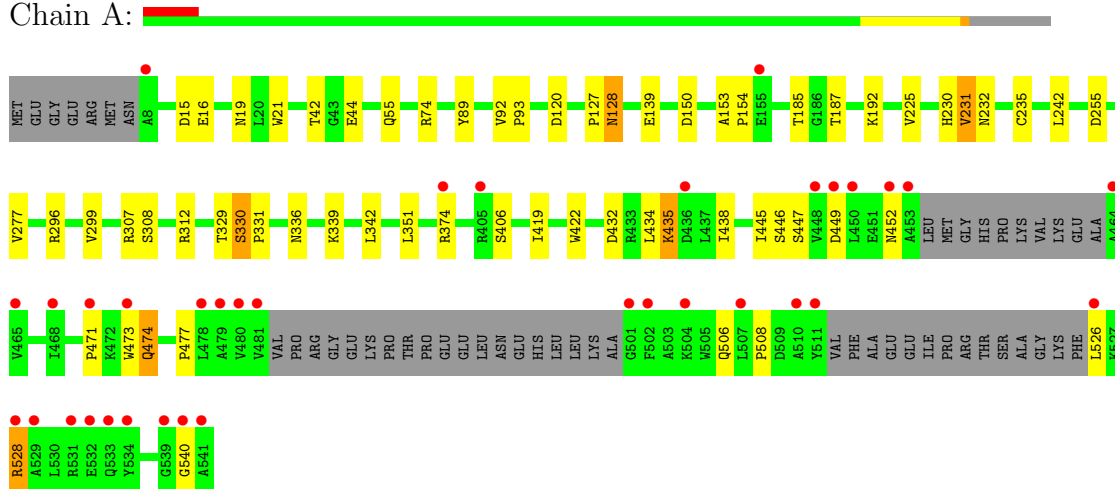
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	225	Total 225	O 225	0	0
4	B	196	Total 196	O 196	0	0

### 3 Residue-property plots

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.

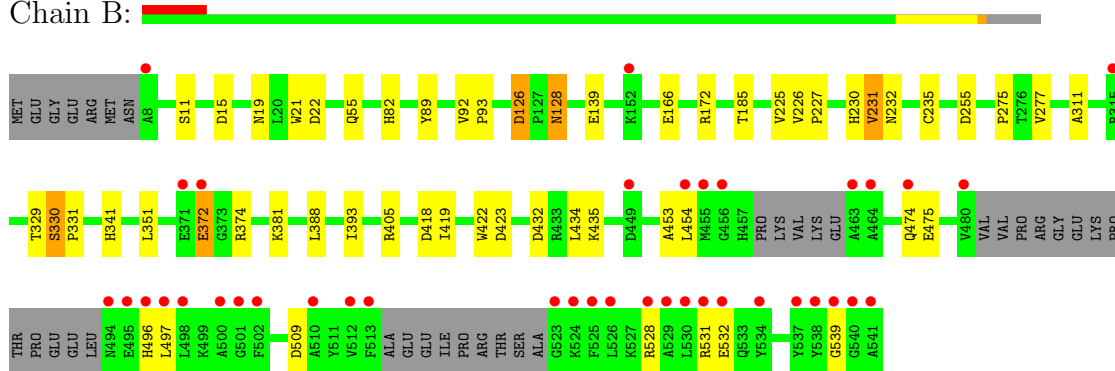
- Molecule 1: long-chain-fatty-acid-CoAsynthetase

Chain A:



- Molecule 1: long-chain-fatty-acid-CoAsynthetase

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.52Å 101.15Å 176.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.60 – 2.30 48.62 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.60-2.30) 99.1 (48.62-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.99 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.204 , 0.240 0.203 , 0.238	Depositor DCC
$R_{free}$ test set	5205 reflections (11.21%)	DCC
Wilson B-factor (Å <sup>2</sup> )	18.4	Xtriage
Anisotropy	0.358	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 14.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 51622 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	8236	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ANP

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	0.34	0/3900	0.63	4/5297 (0.1%)
1	B	0.33	0/4031	0.62	7/5471 (0.1%)
All	All	0.33	0/7931	0.62	11/10768 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	432	ASP	CB-CG-OD2	6.19	123.87	118.30
1	B	432	ASP	CB-CG-OD2	5.97	123.67	118.30
1	B	255	ASP	CB-CG-OD2	5.28	123.05	118.30
1	B	126	ASP	CB-CG-OD2	5.27	123.04	118.30
1	A	120	ASP	CB-CG-OD2	5.15	122.94	118.30
1	A	255	ASP	CB-CG-OD2	5.15	122.93	118.30
1	A	15	ASP	CB-CG-OD2	5.15	122.93	118.30
1	B	15	ASP	CB-CG-OD2	5.12	122.91	118.30
1	B	22	ASP	CB-CG-OD2	5.08	122.88	118.30
1	B	418	ASP	CB-CG-OD2	5.08	122.88	118.30
1	B	423	ASP	CB-CG-OD2	5.06	122.85	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	3812	0	3822	26	0
1	B	3939	0	3950	21	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	31	0	13	2	0
3	B	31	0	13	2	0
4	A	225	0	0	3	0
4	B	196	0	0	0	0
All	All	8236	0	7798	47	0

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 3.

All (47) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:230:HIS:HA	3:B:1666:ANP:O1G	1.86	0.76
1:A:231:VAL:HG22	3:A:666:ANP:O2G	1.86	0.73
1:A:330:SER:N	1:A:331:PRO:HA	2.08	0.69
1:B:330:SER:N	1:B:331:PRO:HA	2.08	0.69
1:B:231:VAL:HG23	3:B:1666:ANP:HNB1	1.64	0.63
1:A:42:THR:OG1	1:A:44:GLU:HG2	2.00	0.61
1:A:308:SER:O	1:A:312:ARG:HG3	2.00	0.61
1:A:296:ARG:HG2	4:A:1133:HOH:O	2.00	0.60
1:B:225:VAL:HG11	1:B:277:VAL:HG11	1.83	0.60
1:B:275:PRO:HB2	1:B:474:GLN:OE1	2.02	0.59
1:B:19:ASN:HD22	1:B:21:TRP:H	1.50	0.58
1:B:92:VAL:HB	1:B:93:PRO:HD3	1.86	0.57
1:A:474:GLN:NE2	4:A:1154:HOH:O	2.36	0.57
1:A:128:ASN:HD22	1:A:128:ASN:H	1.53	0.57
1:A:307:ARG:NH1	1:A:351:LEU:HD23	2.20	0.56
1:A:89:TYR:OH	1:A:232:ASN:HA	2.07	0.55
1:A:230:HIS:HA	3:A:666:ANP:O1G	2.07	0.55
1:A:438:ILE:HD13	1:A:477:PRO:HG3	1.87	0.54
1:A:445:ILE:HG12	1:A:506:GLN:HG2	1.90	0.53
1:A:471:PRO:HG3	1:A:540:GLY:HA2	1.91	0.53
1:B:329:THR:C	1:B:331:PRO:HA	2.30	0.51
1:A:92:VAL:HB	1:A:93:PRO:HD3	1.92	0.51
1:A:225:VAL:HG11	1:A:277:VAL:HG11	1.93	0.50
1:A:19:ASN:HD22	1:A:21:TRP:H	1.59	0.50
1:B:454:LEU:HG	1:B:497:LEU:HD21	1.93	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:477:PRO:HB2	1:A:508:PRO:HA	1.93	0.49
1:B:128:ASN:HD22	1:B:128:ASN:H	1.60	0.49
1:A:127:PRO:HG3	1:A:150:ASP:HB2	1.95	0.49
1:A:329:THR:C	1:A:331:PRO:HA	2.33	0.49
1:B:419:ILE:HD11	1:B:434:LEU:HG	1.95	0.47
4:A:1222:HOH:O	1:B:341:HIS:HD2	1.97	0.47
1:B:311:ALA:HB2	1:B:351:LEU:HD21	1.97	0.46
1:B:388:LEU:HB3	1:B:393:ILE:HD13	1.97	0.45
1:A:128:ASN:H	1:A:128:ASN:ND2	2.14	0.45
1:B:474:GLN:O	1:B:475:GLU:HG3	2.18	0.43
1:B:82:HIS:HE1	1:B:126:ASP:OD1	2.01	0.43
1:B:372:GLU:HG3	1:B:374:ARG:NH1	2.34	0.43
1:B:128:ASN:ND2	1:B:128:ASN:H	2.17	0.43
1:A:528:ARG:H	1:A:528:ARG:HG2	1.65	0.43
1:B:453:ALA:O	1:B:496:HIS:HE1	2.02	0.43
1:A:419:ILE:HD11	1:A:434:LEU:HG	2.00	0.42
1:A:435:LYS:H	1:A:435:LYS:HG3	1.57	0.41
1:B:89:TYR:OH	1:B:232:ASN:HA	2.21	0.41
1:A:153:ALA:HA	1:A:154:PRO:HD3	1.94	0.41
1:B:226:VAL:HA	1:B:227:PRO:HD3	1.89	0.41
1:A:187:THR:HG21	1:A:192:LYS:HD2	2.03	0.41
1:A:339:LYS:HB2	1:A:342:LEU:HD12	2.03	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	483/541 (89%)	465 (96%)	16 (3%)	2 (0%)	43	52
1	B	499/541 (92%)	488 (98%)	9 (2%)	2 (0%)	43	52
All	All	982/1082 (91%)	953 (97%)	25 (2%)	4 (0%)	43	52

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	330	SER
1	B	330	SER
1	B	539	GLY
1	A	473	TRP

### 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	395/437 (90%)	373 (94%)	22 (6%)	30	38
1	B	407/437 (93%)	389 (96%)	18 (4%)	39	51
All	All	802/874 (92%)	762 (95%)	40 (5%)	34	45

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	GLU
1	A	55	GLN
1	A	74	ARG
1	A	128	ASN
1	A	139	GLU
1	A	185	THR
1	A	231	VAL
1	A	235	CYS
1	A	242	LEU
1	A	299	VAL
1	A	336	ASN
1	A	374	ARG
1	A	406	SER
1	A	422	TRP
1	A	435	LYS
1	A	446	SER
1	A	447	SER
1	A	449	ASP
1	A	452	ASN
1	A	474	GLN
1	A	526	LEU
1	A	528	ARG

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Mol	Chain	Res	Type
1	B	11	SER
1	B	55	GLN
1	B	128	ASN
1	B	139	GLU
1	B	166	GLU
1	B	172	ARG
1	B	185	THR
1	B	231	VAL
1	B	235	CYS
1	B	372	GLU
1	B	381	LYS
1	B	405	ARG
1	B	422	TRP
1	B	435	LYS
1	B	509	ASP
1	B	528	ARG
1	B	531	ARG
1	B	532	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	ASN
1	A	41	HIS
1	A	55	GLN
1	A	82	HIS
1	A	128	ASN
1	A	145	HIS
1	A	232	ASN
1	A	290	HIS
1	A	335	GLN
1	A	336	ASN
1	B	19	ASN
1	B	41	HIS
1	B	82	HIS
1	B	128	ASN
1	B	232	ASN
1	B	290	HIS
1	B	322	GLN
1	B	335	GLN
1	B	336	ASN
1	B	341	HIS

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Mol	Chain	Res	Type
1	B	496	HIS

### 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 ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	ANP	A	666	2	33,33,33	1.59	6 (18%)	51,52,52	2.15	10 (19%)
3	ANP	B	1666	2	33,33,33	1.58	6 (18%)	51,52,52	2.01	10 (19%)

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	ANP	A	666	2	-	0/18/38/38	0/1/3/3
3	ANP	B	1666	2	-	0/18/38/38	0/1/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1666	ANP	PG-O1G	4.75	1.52	1.46
3	A	666	ANP	PG-O1G	4.50	1.51	1.46
3	B	1666	ANP	PB-O1B	4.47	1.51	1.46
3	A	666	ANP	PB-O1B	3.85	1.50	1.46
3	B	1666	ANP	O4'-C1'	3.10	1.46	1.41
3	A	666	ANP	PG-N3B	3.06	1.67	1.64
3	A	666	ANP	C4-N9	-3.01	1.33	1.37
3	A	666	ANP	O4'-C1'	2.98	1.45	1.41
3	A	666	ANP	PB-N3B	2.87	1.66	1.64
3	B	1666	ANP	C4-N9	-2.83	1.33	1.37
3	B	1666	ANP	PG-N3B	2.34	1.66	1.64
3	B	1666	ANP	PB-N3B	2.25	1.66	1.64

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	666	ANP	N3-C2-N1	-8.83	121.33	128.71
3	B	1666	ANP	N3-C2-N1	-8.59	121.53	128.71
3	A	666	ANP	PB-N3B-PG	-6.45	119.23	130.07
3	A	666	ANP	C8-N9-C4	5.52	111.11	106.90
3	B	1666	ANP	PB-N3B-PG	-5.17	121.37	130.07
3	B	1666	ANP	C8-N9-C4	4.95	110.68	106.90
3	A	666	ANP	N3-C4-N9	4.66	133.85	125.43
3	B	1666	ANP	N3-C4-N9	4.50	133.56	125.43
3	B	1666	ANP	O2G-PG-O1G	-2.66	106.76	113.60
3	B	1666	ANP	C5-C4-N3	-2.58	120.07	125.70
3	A	666	ANP	C5-C4-N3	-2.57	120.10	125.70
3	B	1666	ANP	C4-C5-N7	-2.51	107.37	109.52
3	A	666	ANP	N7-C8-N9	-2.36	107.68	114.36
3	A	666	ANP	PA-O3A-PB	-2.36	123.75	131.81
3	B	1666	ANP	N7-C8-N9	-2.30	107.86	114.36
3	A	666	ANP	C4-C5-N7	-2.27	107.58	109.52
3	A	666	ANP	O3G-PG-O1G	-2.18	108.00	113.60
3	A	666	ANP	C2-N3-C4	2.13	120.07	114.01
3	B	1666	ANP	PA-O3A-PB	-2.12	124.58	131.81
3	B	1666	ANP	C2-N3-C4	2.06	119.86	114.01

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	491/541 (90%)	0.22	35 (7%)	16 23	7, 16, 58, 98	0
1	B	507/541 (93%)	0.15	39 (7%)	13 20	7, 16, 72, 96	0
All	All	998/1082 (92%)	0.18	74 (7%)	14 21	7, 16, 65, 98	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	541	ALA	9.3
1	B	523	GLY	9.0
1	A	540	GLY	8.4
1	B	526	LEU	7.7
1	B	539	GLY	7.4
1	A	481	VAL	6.9
1	A	526	LEU	6.5
1	B	525	PHE	6.2
1	B	529	ALA	6.1
1	A	529	ALA	5.9
1	B	454	LEU	5.7
1	A	532	GLU	5.4
1	B	513	PHE	5.2
1	B	464	ALA	5.1
1	B	512	VAL	5.1
1	B	463	ALA	5.1
1	A	534	TYR	5.0
1	B	456	GLY	5.0
1	B	497	LEU	5.0
1	A	528	ARG	4.9
1	B	500	ALA	4.7
1	B	528	ARG	4.7
1	A	480	VAL	4.7
1	A	502	PHE	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	531	ARG	4.6
1	A	473	TRP	4.5
1	A	450	LEU	4.3
1	B	501	GLY	3.8
1	B	8	ALA	3.6
1	A	478	LEU	3.5
1	B	480	VAL	3.5
1	A	501	GLY	3.4
1	A	539	GLY	3.4
1	A	510	ALA	3.4
1	B	371	GLU	3.4
1	A	453	ALA	3.4
1	B	524	LYS	3.3
1	B	455	MET	3.2
1	A	468	ILE	3.1
1	B	532	GLU	3.1
1	B	540	GLY	3.1
1	B	530	LEU	3.0
1	A	504	LYS	2.9
1	B	531	ARG	2.9
1	B	495	GLU	2.9
1	B	474	GLN	2.9
1	A	533	GLN	2.8
1	A	448	VAL	2.8
1	A	511	TYR	2.8
1	B	494	ASN	2.8
1	A	479	ALA	2.8
1	A	436	ASP	2.7
1	A	8	ALA	2.6
1	B	534	TYR	2.6
1	A	464	ALA	2.5
1	B	538	TYR	2.5
1	B	537	TYR	2.5
1	B	498	LEU	2.4
1	A	449	ASP	2.4
1	A	374	ARG	2.3
1	A	471	PRO	2.3
1	B	449	ASP	2.3
1	A	507	LEU	2.3
1	A	465	VAL	2.2
1	A	405	ARG	2.2
1	A	155	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	496	HIS	2.1
1	A	452	ASN	2.1
1	B	541	ALA	2.1
1	B	510	ALA	2.1
1	B	152	LYS	2.0
1	B	502	PHE	2.0
1	B	315	ARG	2.0
1	B	372	GLU	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
3	ANP	B	1666	31/31	0.17	1.63	15,16,41,41	0
3	ANP	A	666	31/31	0.17	1.09	10,11,40,42	0
2	MG	A	1001	1/1	0.15	0.23	23,23,23,23	0
2	MG	B	1002	1/1	0.06	-3.64	17,17,17,17	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.