



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:38 PM GMT

PDB ID : 1PYX
Title : GSK-3 Beta complexed with AMP-PNP
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Deposited on : 2003-07-09
Resolution : 2.40 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
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

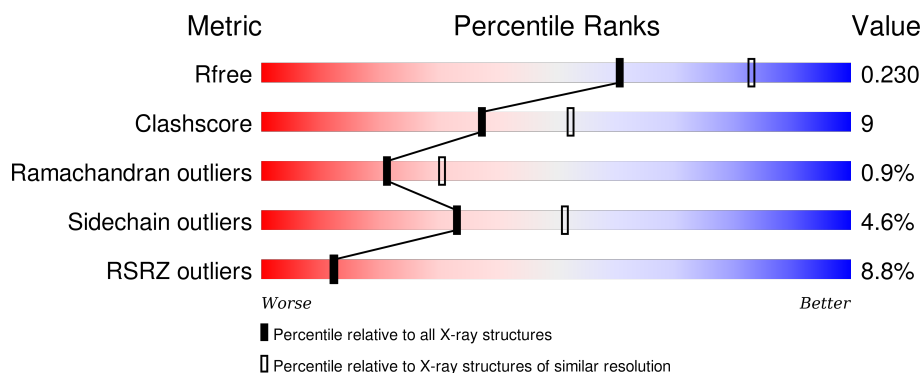
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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 ≥ 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	422	<div> <div>8%</div> <div>65%</div> <div>14%</div> <div>•</div> <div>19%</div> </div>
1	B	422	<div> <div>6%</div> <div>67%</div> <div>11%</div> <div>•</div> <div>20%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5682 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 Glycogen synthase kinase-3 beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	S	0	0	0
			2743	1767	472	493	11			
1	B	338	Total	C	N	O	S	0	0	0
			2706	1744	465	486	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	CLONING ARTIFACT	UNP P49841
A	0	PRO	-	CLONING ARTIFACT	UNP P49841
B	-1	GLY	-	CLONING ARTIFACT	UNP P49841
B	0	PRO	-	CLONING ARTIFACT	UNP P49841

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

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

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



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	85	Total O 85 85	0	0
4	B	82	Total O 82 82	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.69Å 85.21Å 178.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.92 – 2.40 19.92 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.1 (19.92-2.40) 98.7 (19.92-2.39)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.38Å)	Xtriage
Refinement program	CNX 2002 (ACCELRYN)	Depositor
R, R_{free}	0.206 , 0.233 0.203 , 0.230	Depositor DCC
R_{free} test set	2468 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	0.468	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 51.5	EDS
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 49993 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5682	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: 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	0.52	0/2811	0.70	1/3823 (0.0%)
1	B	0.49	0/2773	0.68	0/3770
All	All	0.50	0/5584	0.69	1/7593 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	285	ASN	N-CA-C	5.35	125.45	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	2743	0	2777	59	0
1	B	2706	0	2740	47	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	31	0	13	1	0
3	B	31	0	13	0	0
4	A	85	0	0	0	0
4	B	82	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5682	0	5543	103	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 9.

All (103) 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:220:ARG:CD	1:A:221:TYR:H	1.65	1.09
1:B:220:ARG:CD	1:B:221:TYR:H	1.66	1.08
1:B:220:ARG:HD3	1:B:221:TYR:H	1.19	1.07
1:A:220:ARG:HD3	1:A:221:TYR:H	1.20	1.05
1:A:370:ASN:HD22	1:A:372:PRO:HD2	1.41	0.83
1:B:106:HIS:HD2	1:B:108:ASN:H	1.24	0.82
1:A:106:HIS:CD2	1:A:108:ASN:H	1.98	0.81
1:A:106:HIS:HD2	1:A:108:ASN:H	1.24	0.81
1:B:106:HIS:CD2	1:B:108:ASN:H	1.99	0.80
1:B:220:ARG:CD	1:B:221:TYR:N	2.47	0.77
1:B:370:ASN:HD22	1:B:372:PRO:HD2	1.51	0.76
1:A:370:ASN:ND2	1:A:372:PRO:HD2	2.01	0.75
1:A:220:ARG:CD	1:A:221:TYR:N	2.46	0.75
1:A:285:ASN:HB3	1:A:286:PRO:CD	2.16	0.75
1:A:220:ARG:HH11	1:A:220:ARG:HG2	1.56	0.71
1:B:220:ARG:HD2	1:B:221:TYR:H	1.56	0.70
1:A:220:ARG:HD2	1:A:221:TYR:H	1.54	0.68
1:B:220:ARG:HH11	1:B:220:ARG:HG2	1.58	0.68
1:A:220:ARG:HD3	1:A:221:TYR:CG	2.33	0.64
1:A:60:LYS:HE2	1:A:72:GLN:NE2	2.13	0.64
1:A:91:LYS:HE2	1:A:126:VAL:HG23	1.79	0.62
1:B:307:PRO:O	1:B:308:ARG:HB2	2.00	0.61
1:B:291:PHE:CE2	1:B:293:PHE:HB2	2.35	0.61
1:B:279:GLU:O	1:B:283:GLU:HG2	2.00	0.60
1:A:153:LEU:HD23	1:A:153:LEU:H	1.65	0.60
1:A:370:ASN:C	1:A:370:ASN:HD22	2.04	0.59
1:B:220:ARG:HD2	1:B:221:TYR:N	2.14	0.59
1:A:220:ARG:HD2	1:A:221:TYR:N	2.13	0.59
1:B:220:ARG:HD3	1:B:221:TYR:CG	2.38	0.59
1:B:307:PRO:O	1:B:308:ARG:CB	2.50	0.58
1:A:349:LYS:HE2	1:A:355:ASP:OD1	2.04	0.58
1:A:220:ARG:HD3	1:A:221:TYR:N	2.05	0.58
1:B:91:LYS:O	1:B:91:LYS:HD3	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:ILE:HD11	1:B:67:PHE:CE1	2.40	0.57
1:A:98:LEU:O	1:A:102:ARG:HG3	2.05	0.57
1:B:212:PRO:HB3	1:B:232:THR:HG23	1.88	0.56
1:A:285:ASN:CB	1:A:286:PRO:CD	2.82	0.56
1:B:370:ASN:ND2	1:B:372:PRO:HD2	2.18	0.56
1:A:285:ASN:HB3	1:A:286:PRO:HD3	1.86	0.56
1:B:98:LEU:O	1:B:102:ARG:HG3	2.06	0.55
1:B:316:LEU:HD22	1:B:320:LEU:HD22	1.89	0.55
1:B:220:ARG:HD3	1:B:221:TYR:N	2.04	0.54
1:A:144:ARG:HD2	1:A:148:ARG:NH2	2.23	0.54
1:B:212:PRO:HB3	1:B:232:THR:CG2	2.39	0.53
1:A:91:LYS:HE2	1:A:126:VAL:CG2	2.39	0.53
1:B:62:ILE:HG21	1:B:72:GLN:HB2	1.90	0.52
1:A:316:LEU:HD22	1:A:320:LEU:HD22	1.91	0.51
1:A:106:HIS:HD2	1:A:108:ASN:N	2.01	0.51
1:B:106:HIS:HD2	1:B:108:ASN:N	2.00	0.51
1:B:137:GLU:HG3	1:B:191:PRO:HG3	1.94	0.50
1:B:276:PRO:HB2	1:B:281:ILE:HG13	1.93	0.50
1:A:137:GLU:HG3	1:A:191:PRO:HG3	1.93	0.50
1:A:294:PRO:HG2	1:B:67:PHE:CE2	2.47	0.49
1:B:369:SER:O	1:B:370:ASN:HB2	2.12	0.49
1:B:220:ARG:O	1:B:223:ARG:HG3	2.14	0.48
1:A:276:PRO:HG3	1:A:323:TYR:CZ	2.48	0.48
1:A:220:ARG:O	1:A:223:ARG:HG3	2.13	0.48
1:A:296:ILE:HD11	1:B:67:PHE:CZ	2.50	0.47
1:A:38:THR:O	1:A:55:SER:HA	2.15	0.47
1:B:370:ASN:C	1:B:370:ASN:HD22	2.18	0.46
1:A:285:ASN:HB3	1:A:286:PRO:HD2	1.96	0.46
1:A:279:GLU:HG3	1:A:282:ARG:HH12	1.79	0.46
1:A:153:LEU:HD23	1:A:153:LEU:N	2.31	0.46
1:A:305:PHE:CD2	1:A:314:ILE:HG12	2.51	0.46
1:A:220:ARG:HD3	1:A:221:TYR:CD2	2.50	0.46
1:A:153:LEU:H	1:A:153:LEU:CD2	2.26	0.46
1:A:193:THR:O	1:A:357:PRO:HG3	2.15	0.46
1:B:344:ARG:HG2	1:B:379:PRO:HG3	1.96	0.45
1:B:106:HIS:HE1	1:B:366:GLU:OE1	1.98	0.45
1:B:88:LEU:HD11	1:B:125:GLU:OE1	2.16	0.45
1:A:112:LEU:HA	1:A:132:LEU:HD23	1.97	0.45
1:A:46:GLN:HE21	1:A:46:GLN:HB3	1.55	0.45
1:A:135:VAL:HA	1:A:136:PRO:HD3	1.75	0.45
1:A:225:PRO:HB2	1:A:284:MET:SD	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:PRO:HB2	1:A:372:PRO:HD3	1.98	0.44
1:A:196:LEU:HD23	1:A:196:LEU:C	2.37	0.44
1:B:316:LEU:HD22	1:B:320:LEU:CD2	2.47	0.44
1:A:92:ARG:O	1:A:93:PHE:CD1	2.71	0.44
1:B:220:ARG:HH11	1:B:220:ARG:CG	2.29	0.43
1:B:64:ASN:HB3	1:B:65:GLY:H	1.54	0.43
1:A:94:LYS:HD2	1:A:99:GLN:NE2	2.34	0.42
1:A:195:VAL:HG22	1:A:357:PRO:HB3	2.01	0.42
1:A:250:LEU:HA	1:A:250:LEU:HD12	1.87	0.42
1:B:115:PHE:HA	1:B:129:ASN:O	2.19	0.42
1:A:316:LEU:HD22	1:A:320:LEU:CD2	2.49	0.42
1:A:65:GLY:HA3	3:A:1001:ANP:O1B	2.20	0.42
1:B:211:GLU:HA	1:B:212:PRO:HD3	1.92	0.42
1:B:80:GLU:CD	1:B:113:ARG:HH22	2.23	0.42
1:B:135:VAL:HA	1:B:136:PRO:HD3	1.76	0.42
1:B:220:ARG:HD3	1:B:221:TYR:CD2	2.55	0.41
1:A:379:PRO:HA	1:A:380:PRO:HD3	1.93	0.41
1:A:52:GLN:NE2	1:A:114:TYR:HE2	2.17	0.41
1:A:267:VAL:HG12	1:A:271:LYS:HE3	2.02	0.41
1:B:196:LEU:HD23	1:B:196:LEU:C	2.41	0.41
1:A:91:LYS:HE2	1:A:126:VAL:CB	2.51	0.41
1:A:301:TRP:O	1:A:304:VAL:HB	2.21	0.41
1:B:93:PHE:CD1	1:B:93:PHE:N	2.89	0.41
1:B:60:LYS:O	1:B:62:ILE:HG23	2.20	0.41
1:A:266:LEU:HA	1:A:266:LEU:HD12	1.84	0.41
1:A:370:ASN:C	1:A:370:ASN:ND2	2.73	0.40
1:B:267:VAL:HG12	1:B:271:LYS:HE3	2.03	0.40
1:B:193:THR:O	1:B:194:ALA:HB3	2.21	0.40
1:A:293:PHE:HA	1:A:294:PRO:HD3	1.94	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	337/422 (80%)	322 (96%)	11 (3%)	4 (1%)	16	23
1	B	332/422 (79%)	315 (95%)	15 (4%)	2 (1%)	30	43
All	All	669/844 (79%)	637 (95%)	26 (4%)	6 (1%)	21	30

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	285	ASN
1	A	220	ARG
1	B	220	ARG
1	B	308	ARG
1	A	77	ASP
1	A	218	CYS

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	305/365 (84%)	292 (96%)	13 (4%)	35	55
1	B	301/365 (82%)	286 (95%)	15 (5%)	30	48
All	All	606/730 (83%)	578 (95%)	28 (5%)	33	51

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	77	ASP
1	A	169	LEU
1	A	220	ARG
1	A	227	LEU
1	A	232	THR
1	A	250	LEU
1	A	266	LEU
1	A	286	PRO
1	A	295	GLN

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Mol	Chain	Res	Type
1	A	316	LEU
1	A	320	LEU
1	A	370	ASN
1	B	49	ASP
1	B	67	PHE
1	B	91	LYS
1	B	151	GLN
1	B	169	LEU
1	B	220	ARG
1	B	227	LEU
1	B	232	THR
1	B	250	LEU
1	B	266	LEU
1	B	279	GLU
1	B	316	LEU
1	B	320	LEU
1	B	370	ASN
1	B	383	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	72	GLN
1	A	99	GLN
1	A	106	HIS
1	A	108	ASN
1	A	365	GLN
1	A	370	ASN
1	B	72	GLN
1	B	106	HIS
1	B	108	ASN
1	B	365	GLN
1	B	370	ASN

5.3.3 RNA ⓘ

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 6 ligands modelled in this entry, 4 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	1001	2	27,33,33	2.52	5 (18%)	30,52,52	2.11	8 (26%)
3	ANP	B	2001	2	27,33,33	2.84	5 (18%)	30,52,52	2.05	9 (30%)

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	1001	2	-	0/12/38/38	0/3/3/3
3	ANP	B	2001	2	-	0/12/38/38	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2001	ANP	PG-N3B	-2.58	1.56	1.63
3	A	1001	ANP	PG-N3B	-2.07	1.57	1.63
3	A	1001	ANP	C5-C4	3.13	1.47	1.40
3	A	1001	ANP	C4-N3	3.47	1.40	1.35
3	B	2001	ANP	C5-C4	3.80	1.49	1.40
3	B	2001	ANP	C4-N3	4.12	1.41	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	ANP	PB-O1B	6.27	1.53	1.46
3	B	2001	ANP	PB-O1B	6.55	1.53	1.46
3	A	1001	ANP	PG-O1G	9.62	1.57	1.46
3	B	2001	ANP	PG-O1G	10.96	1.58	1.46

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	ANP	N3-C2-N1	-6.98	123.55	128.89
3	B	2001	ANP	N3-C2-N1	-6.62	123.83	128.89
3	A	1001	ANP	PA-O3A-PB	-4.51	117.54	132.67
3	B	2001	ANP	PA-O3A-PB	-3.79	119.95	132.67
3	B	2001	ANP	O3G-PG-O1G	-3.70	103.65	113.49
3	A	1001	ANP	O3G-PG-O1G	-3.63	103.83	113.49
3	A	1001	ANP	O2A-PA-O1A	-2.73	97.73	112.53
3	B	2001	ANP	O2A-PA-O1A	-2.67	98.03	112.53
3	B	2001	ANP	O1G-PG-N3B	-2.46	108.13	111.90
3	A	1001	ANP	O2B-PB-O3A	2.01	114.22	105.09
3	B	2001	ANP	O2A-PA-O3A	2.15	114.87	105.09
3	A	1001	ANP	O2A-PA-O3A	2.24	115.25	105.09
3	B	2001	ANP	O2B-PB-O3A	2.27	115.39	105.09
3	A	1001	ANP	C2-N1-C6	2.28	122.83	118.77
3	B	2001	ANP	O4'-C1'-N9	2.70	113.74	108.10
3	B	2001	ANP	C2-N1-C6	2.71	123.62	118.77
3	A	1001	ANP	O4'-C1'-N9	3.10	114.59	108.10

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1001	ANP	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, 95th 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 ²)	Q<0.9
1	A	343/422 (81%)	0.22	34 (9%) 9 9	25, 40, 74, 91	0
1	B	338/422 (80%)	0.12	26 (7%) 16 16	24, 38, 69, 95	0
All	All	681/844 (80%)	0.17	60 (8%) 12 12	24, 39, 72, 95	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	93	PHE	7.2
1	A	35	SER	6.8
1	B	35	SER	6.6
1	A	386	ALA	6.4
1	A	119	SER	5.1
1	A	92	ARG	4.8
1	B	92	ARG	4.6
1	A	278	ARG	4.6
1	A	77	ASP	4.5
1	A	282	ARG	4.0
1	B	65	GLY	3.8
1	B	282	ARG	3.8
1	A	285	ASN	3.7
1	A	90	ASP	3.5
1	B	278	ARG	3.5
1	B	93	PHE	3.4
1	B	308	ARG	3.4
1	A	47	GLY	3.3
1	A	148	ARG	3.3
1	B	148	ARG	3.2
1	A	295	GLN	3.2
1	B	125	GLU	3.2
1	A	91	LYS	3.1
1	A	36	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	126	VAL	3.0
1	A	125	GLU	3.0
1	B	279	GLU	3.0
1	A	210	GLY	2.9
1	B	119	SER	2.9
1	B	209	ARG	2.9
1	A	385	GLN	2.9
1	A	303	LYS	2.9
1	B	36	LYS	2.9
1	A	292	LYS	2.8
1	A	209	ARG	2.8
1	A	308	ARG	2.8
1	B	307	PRO	2.8
1	B	91	LYS	2.7
1	B	295	GLN	2.7
1	B	64	ASN	2.6
1	A	48	PRO	2.6
1	A	130	LEU	2.5
1	B	130	LEU	2.5
1	B	131	VAL	2.5
1	A	297	LYS	2.5
1	A	300	PRO	2.4
1	A	152	THR	2.4
1	B	77	ASP	2.3
1	A	83	ALA	2.2
1	B	94	LYS	2.2
1	B	303	LYS	2.2
1	B	300	PRO	2.2
1	A	46	GLN	2.1
1	B	66	SER	2.1
1	A	132	LEU	2.1
1	A	212	PRO	2.1
1	A	84	ILE	2.1
1	B	78	SER	2.0
1	A	211	GLU	2.0
1	B	208	VAL	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 [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, 95th 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(\AA^2)	Q<0.9
3	ANP	A	1001	31/31	0.96	0.11	-0.73	27,34,42,43	0
3	ANP	B	2001	31/31	0.95	0.12	-0.78	34,40,51,52	0
2	MG	B	2003	1/1	0.90	0.07	-1.12	46,46,46,46	0
2	MG	A	1003	1/1	0.96	0.04	-2.07	35,35,35,35	0
2	MG	A	1002	1/1	0.84	0.06	-	44,44,44,44	0
2	MG	B	2002	1/1	0.97	0.08	-	59,59,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.