



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:13 PM UTC

PDB ID : 1PYX / pdb_00001pyx
Title : GSK-3 Beta complexed with AMP-PNP
Authors : Bertrand, J.A.; Thieffine, S.; Vulpetti, A.; Cristiani, C.; Valsasina, B.; Knapp, S.; Kalisz, H.M.; Flocco, M.
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

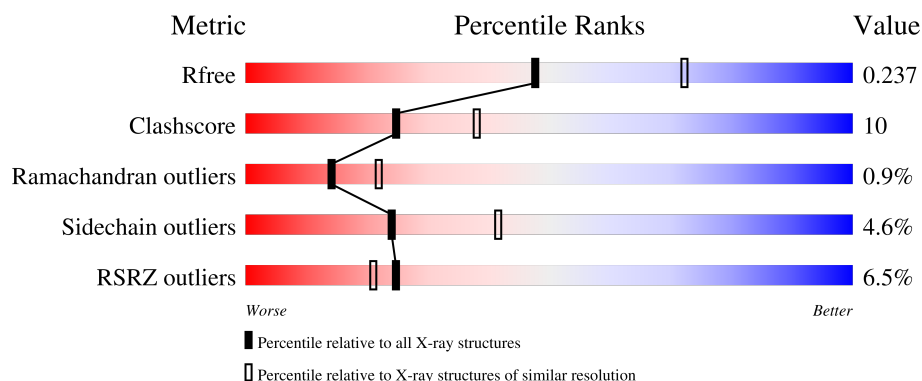
1 Overall quality at a glance

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}	180053	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	5% 63% 15% • 19%
1	B	422	5% 64% 14% • 20%

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 (CCD ID: MG) (formula: Mg).

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

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).

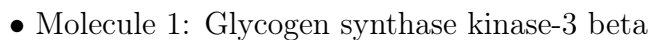


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 31	C 10	N 6	O 12	P 3	0	0
3	B	1	Total 31	C 10	N 6	O 12	P 3	0	0

- 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

- Molecule 1: Glycogen synthase kinase-3 beta



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 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.1 (19.92-2.40) 98.9 (19.92-2.40)	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	Depositor
R, R_{free}	0.206 , 0.233 (Not available) , 0.237	Depositor DCC
R_{free} test set	2468 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	0.468	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.61	0/2811	1.05	17/3823 (0.4%)
1	B	0.60	0/2773	1.03	19/3770 (0.5%)
All	All	0.60	0/5584	1.04	36/7593 (0.5%)

There are no bond length outliers.

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	309	THR	N-CA-C	-7.85	99.86	109.83
1	A	135	VAL	CA-C-N	7.65	127.54	119.05
1	A	135	VAL	C-N-CA	7.65	127.54	119.05
1	B	47	GLY	CA-C-N	7.62	127.38	119.76
1	B	47	GLY	C-N-CA	7.62	127.38	119.76
1	A	284	MET	N-CA-C	-7.36	103.34	111.36
1	B	135	VAL	CA-C-N	7.20	127.04	119.05
1	B	135	VAL	C-N-CA	7.20	127.04	119.05
1	A	285	ASN	N-CA-C	7.08	125.45	109.81
1	B	190	ASP	CA-C-N	6.97	127.27	119.32
1	B	190	ASP	C-N-CA	6.97	127.27	119.32
1	B	330	THR	N-CA-C	-6.76	101.30	110.36
1	A	190	ASP	CA-C-N	6.58	126.82	119.32
1	A	190	ASP	C-N-CA	6.58	126.82	119.32
1	B	277	THR	N-CA-C	-6.49	101.97	110.53
1	A	72	GLN	N-CA-C	-6.45	99.70	109.95
1	A	330	THR	N-CA-C	-6.32	101.90	110.36
1	B	76	CYS	N-CA-C	6.24	118.08	111.28
1	A	371	PRO	N-CA-C	6.22	118.28	110.70
1	B	293	PHE	CA-C-N	5.91	125.92	119.90
1	B	293	PHE	C-N-CA	5.91	125.92	119.90
1	A	91	LYS	N-CA-C	-5.63	105.51	112.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	368	SER	N-CA-C	5.62	118.95	111.75
1	A	137	GLU	N-CA-C	5.61	117.14	109.18
1	B	137	GLU	N-CA-C	5.55	117.06	109.18
1	B	307	PRO	N-CA-C	-5.55	102.41	111.68
1	B	345	ASP	CA-C-N	5.31	125.62	119.47
1	B	345	ASP	C-N-CA	5.31	125.62	119.47
1	A	376	ILE	CB-CA-C	-5.29	105.47	111.55
1	A	378	ILE	CA-C-N	5.19	123.45	119.66
1	A	378	ILE	C-N-CA	5.19	123.45	119.66
1	A	50	ARG	CA-C-N	5.18	125.18	119.90
1	A	50	ARG	C-N-CA	5.18	125.18	119.90
1	B	377	LEU	N-CA-C	5.13	117.61	111.71
1	B	149	ALA	N-CA-C	-5.07	100.01	110.80
1	B	371	PRO	N-CA-C	5.02	116.83	110.70

There are no chirality outliers.

There are no planarity outliers.

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	2743	0	2777	62	0
1	B	2706	0	2740	49	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
All	All	5682	0	5543	108	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 10.

All (108) 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:HG2	1:A:220:ARG:HH11	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:HG2	1:B:220:ARG:HH11	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:370:ASN:HD22	1:A:370:ASN:C	2.04	0.64
1:A:91:LYS:HE2	1:A:126:VAL:HG23	1.79	0.62
1:B:291:PHE:CE2	1:B:293:PHE:HB2	2.35	0.61
1:B:307:PRO:O	1:B:308:ARG:HB2	2.00	0.60
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: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:A:349:LYS:HE2	1:A:355:ASP:OD1	2.04	0.58
1:B:307:PRO:O	1:B:308:ARG:CB	2.50	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
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:A:285:ASN:HB3	1:A:286:PRO:HD3	1.86	0.56
1:B:370:ASN:ND2	1:B:372:PRO:HD2	2.18	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:B:370:ASN:HD22	1:B:370:ASN:C	2.18	0.51
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:A:196:LEU:C	1:A:196:LEU:HD23	2.37	0.49
1:B:369:SER:O	1:B:370:ASN:HB2	2.12	0.49
1:A:276:PRO:HG3	1:A:323:TYR:CZ	2.48	0.48
1:B:220:ARG:O	1:B:223:ARG:HG3	2.14	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:80:GLU:CD	1:B:113:ARG:HH22	2.23	0.47
1:A:279:GLU:HG3	1:A:282:ARG:HH12	1.79	0.46
1:A:285:ASN:HB3	1:A:286:PRO:HD2	1.96	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:153:LEU:H	1:A:153:LEU:CD2	2.26	0.46
1:A:220:ARG:HD3	1:A:221:TYR:CD2	2.50	0.46
1:B:196:LEU:C	1:B:196:LEU:HD23	2.41	0.46
1:A:193:THR:O	1:A:357:PRO:HG3	2.15	0.46
1:A:370:ASN:ND2	1:A:370:ASN:C	2.73	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:A:112:LEU:HA	1:A:132:LEU:HD23	1.97	0.45
1:B:88:LEU:HD11	1:B:125:GLU:OE1	2.16	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
1:B:281:ILE:HA	1:B:284:MET:HE3	1.99	0.44
1:A:371:PRO:HB2	1:A:372:PRO:HD3	1.98	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:92:ARG:C	1:A:93:PHE:CD1	2.98	0.42
1:A:195:VAL:HG22	1:A:357:PRO:HB3	2.01	0.42
1:A:250:LEU:HD12	1:A:250:LEU:HA	1.87	0.42
1:B:115:PHE:HA	1:B:129:ASN:O	2.19	0.42
1:A:65:GLY:HA3	3:A:1001:ANP:O1B	2.20	0.42
1:A:316:LEU:HD22	1:A:320:LEU:CD2	2.49	0.42
1:B:249:GLU:HG3	1:B:254:GLN:C	2.45	0.42
1:B:211:GLU:HA	1:B:212:PRO:HD3	1.92	0.42
1:B:135:VAL:HA	1:B:136:PRO:HD3	1.76	0.42
1:A:379:PRO:HA	1:A:380:PRO:HD3	1.93	0.41
1:B:220:ARG:HD3	1:B:221:TYR:CD2	2.55	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:A:351:PRO:C	1:A:353:GLY:H	2.29	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:A:266:LEU:HD12	1:A:266:LEU:HA	1.84	0.41
1:B:60:LYS:O	1:B:62:ILE:HG23	2.20	0.41
1:B:267:VAL:HG12	1:B:271:LYS:HE3	2.03	0.40
1:A:90:ASP:C	1:A:92:ARG:N	2.76	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%)	10 16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	332/422 (79%)	315 (95%)	15 (4%)	2 (1%)	21	32
All	All	669/844 (79%)	637 (95%)	26 (4%)	6 (1%)	14	22

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%)	291 (95%)	14 (5%)	24	41
1	B	301/365 (82%)	287 (95%)	14 (5%)	23	41
All	All	606/730 (83%)	578 (95%)	28 (5%)	24	41

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	153	LEU
1	A	169	LEU
1	A	217	ILE
1	A	220	ARG
1	A	227	LEU
1	A	232	THR
1	A	250	LEU
1	A	266	LEU

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Mol	Chain	Res	Type
1	A	286	PRO
1	A	295	GLN
1	A	316	LEU
1	A	320	LEU
1	B	49	ASP
1	B	91	LYS
1	B	151	GLN
1	B	169	LEU
1	B	217	ILE
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	375	THR

Sometimes 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	106	HIS
1	B	108	ASN
1	B	299	HIS
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 oligosaccharides 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	33,33,33	2.15	7 (21%)	45,52,52	2.01	14 (31%)
3	ANP	B	2001	2	33,33,33	2.33	7 (21%)	45,52,52	2.04	15 (33%)

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	-	3/18/38/38	0/3/3/3
3	ANP	B	2001	2	-	3/18/38/38	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2001	ANP	PG-O1G	8.31	1.58	1.46
3	A	1001	ANP	PG-O1G	7.28	1.57	1.46
3	B	2001	ANP	C5-C4	5.60	1.49	1.39
3	B	2001	ANP	PB-O1B	4.92	1.53	1.46
3	A	1001	ANP	C5-C4	4.75	1.47	1.39
3	A	1001	ANP	PB-O1B	4.71	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	ANP	PA-O3A	4.20	1.64	1.59
3	B	2001	ANP	C4-N3	3.90	1.41	1.34
3	A	1001	ANP	C4-N3	3.38	1.40	1.34
3	B	2001	ANP	PG-N3B	-2.63	1.56	1.63
3	B	2001	ANP	C6-N6	2.60	1.40	1.34
3	A	1001	ANP	C8-N7	2.33	1.36	1.31
3	A	1001	ANP	PG-N3B	-2.11	1.57	1.63
3	B	2001	ANP	PA-O3A	2.10	1.61	1.59

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2001	ANP	C4-N9-C8	5.18	111.18	105.74
3	A	1001	ANP	C4-N9-C8	4.98	110.96	105.74
3	B	2001	ANP	O3G-PG-O1G	-3.91	103.65	113.45
3	A	1001	ANP	O3G-PG-O1G	-3.84	103.83	113.45
3	A	1001	ANP	N9-C8-N7	-3.41	109.11	113.94
3	A	1001	ANP	O4'-C1'-N9	3.39	114.59	108.09
3	B	2001	ANP	N9-C8-N7	-3.38	109.14	113.94
3	A	1001	ANP	N3-C2-N1	-3.32	123.55	128.58
3	A	1001	ANP	N3-C4-N9	3.25	132.69	127.17
3	B	2001	ANP	O2B-PB-O3A	3.22	115.39	104.64
3	A	1001	ANP	C6-C5-N7	3.22	138.29	132.09
3	B	2001	ANP	N3-C4-N9	3.20	132.61	127.17
3	A	1001	ANP	O2A-PA-O1A	-3.16	97.73	112.44
3	B	2001	ANP	N3-C2-N1	-3.14	123.83	128.58
3	B	2001	ANP	O2A-PA-O1A	-3.10	98.03	112.44
3	B	2001	ANP	C6-C5-N7	3.10	138.06	132.09
3	A	1001	ANP	C5-N7-C8	3.07	108.28	103.45
3	B	2001	ANP	C6-C5-C4	-3.00	113.08	117.18
3	B	2001	ANP	C5-N7-C8	2.98	108.14	103.45
3	B	2001	ANP	C2-N1-C6	2.97	123.62	118.73
3	A	1001	ANP	C6-C5-C4	-2.95	113.15	117.18
3	A	1001	ANP	O2A-PA-O3A	2.95	115.25	107.27
3	B	2001	ANP	O4'-C1'-N9	2.94	113.74	108.09
3	B	2001	ANP	C5-C4-N9	-2.89	102.66	105.81
3	A	1001	ANP	O2B-PB-O3A	2.87	114.22	104.64
3	B	2001	ANP	O2A-PA-O3A	2.81	114.87	107.27
3	A	1001	ANP	C5-C4-N9	-2.50	103.08	105.81
3	A	1001	ANP	C2-N1-C6	2.50	122.83	118.73
3	B	2001	ANP	O1G-PG-N3B	-2.47	108.13	111.77

There are no chirality outliers.

All (6) torsion outliers are listed below:

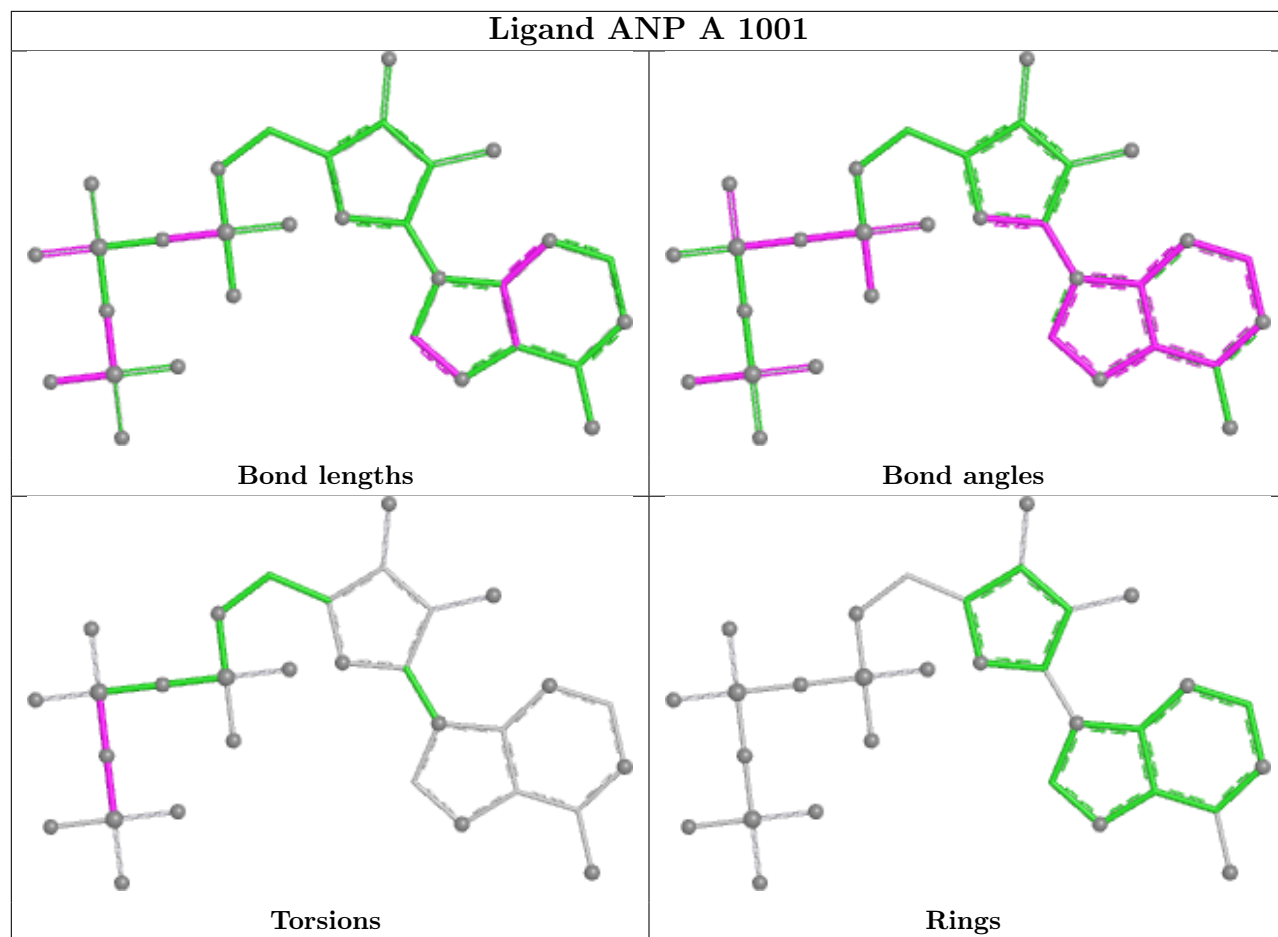
Mol	Chain	Res	Type	Atoms
3	A	1001	ANP	PB-N3B-PG-O1G
3	A	1001	ANP	PG-N3B-PB-O1B
3	A	1001	ANP	PG-N3B-PB-O3A
3	B	2001	ANP	PB-N3B-PG-O1G
3	B	2001	ANP	PG-N3B-PB-O1B
3	B	2001	ANP	PG-N3B-PB-O3A

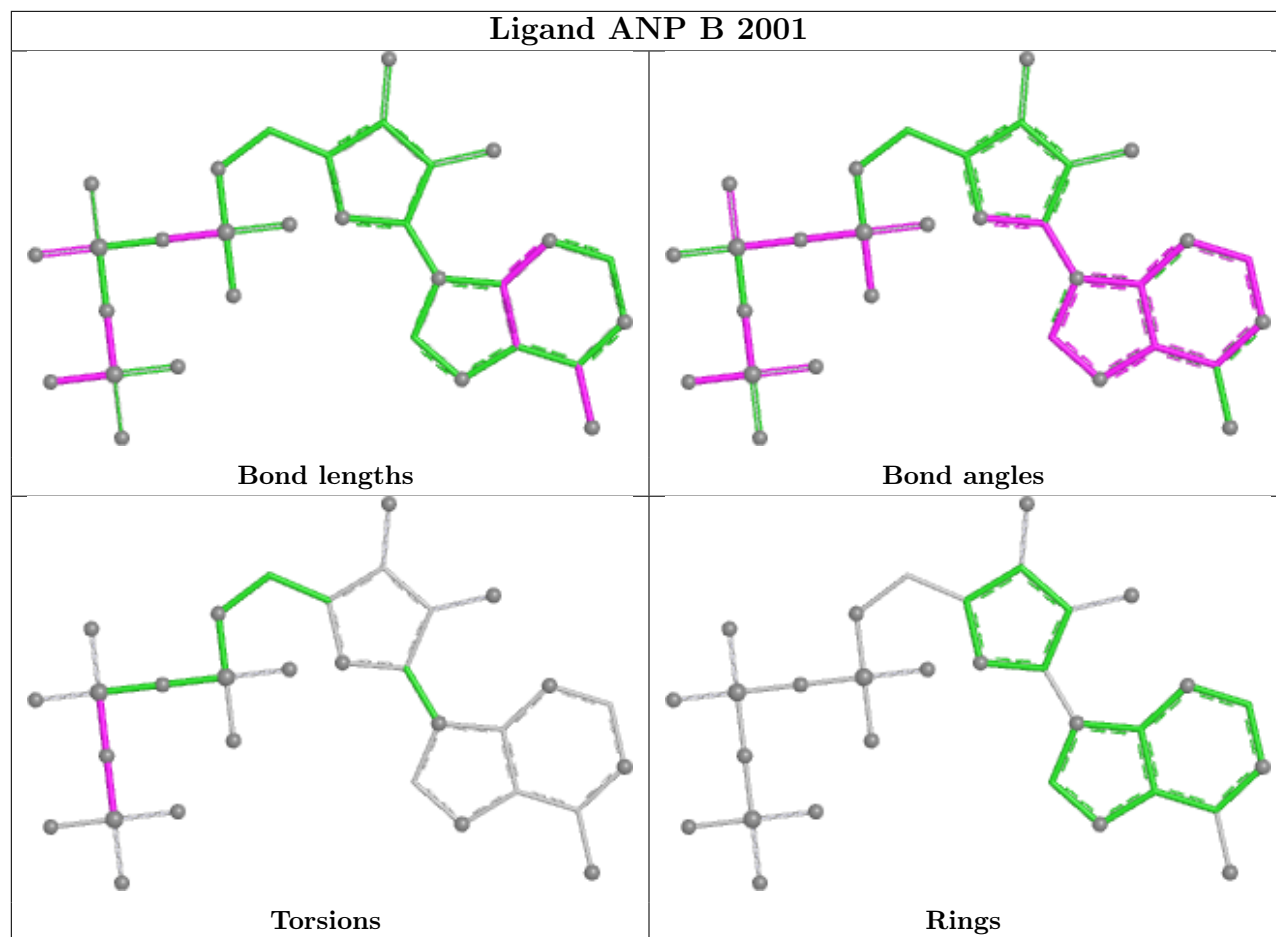
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1001	ANP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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

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%)	0.08	23 (6%) 24 20	25, 40, 74, 91	0
1	B	338/422 (80%)	0.01	21 (6%) 26 23	24, 38, 69, 95	0
All	All	681/844 (80%)	0.05	44 (6%) 25 21	24, 39, 72, 95	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	386	ALA	6.1
1	A	286	PRO	4.3
1	A	35	SER	4.3
1	A	295	GLN	3.8
1	B	35	SER	3.7
1	A	93	PHE	3.7
1	B	65	GLY	3.6
1	A	282	ARG	3.5
1	A	91	LYS	3.4
1	B	125	GLU	3.3
1	A	119	SER	3.2
1	A	152	THR	3.2
1	A	285	ASN	3.1
1	B	279	GLU	3.0
1	A	291	PHE	3.0
1	A	77	ASP	3.0
1	B	119	SER	3.0
1	A	125	GLU	2.9
1	A	90	ASP	2.8
1	B	292	LYS	2.8
1	B	64	ASN	2.8
1	A	94	LYS	2.8
1	B	66	SER	2.8
1	B	67	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	92	ARG	2.7
1	B	306	ARG	2.6
1	B	383	ARG	2.6
1	B	291	PHE	2.6
1	B	282	ARG	2.6
1	B	91	LYS	2.5
1	B	93	PHE	2.5
1	A	294	PRO	2.5
1	B	295	GLN	2.5
1	A	303	LYS	2.3
1	B	293	PHE	2.3
1	A	66	SER	2.3
1	A	293	PHE	2.2
1	A	151	GLN	2.2
1	B	148	ARG	2.1
1	B	278	ARG	2.1
1	B	92	ARG	2.1
1	A	46	GLN	2.0
1	B	220	ARG	2.0
1	A	114	TYR	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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	A	1002	1/1	0.94	0.05	44,44,44,44	0
2	MG	B	2002	1/1	0.97	0.05	59,59,59,59	0
3	ANP	A	1001	31/31	0.97	0.06	27,34,42,43	0

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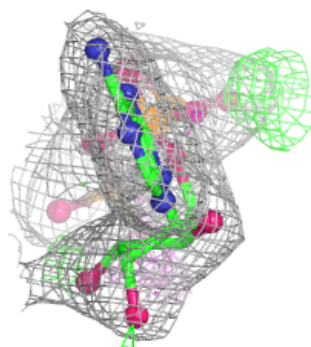
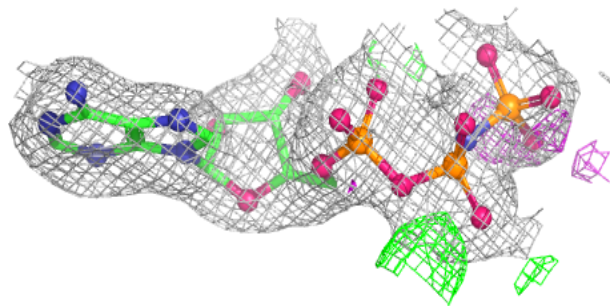
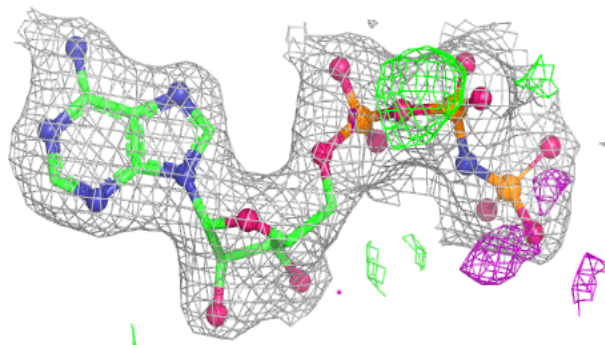
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ANP	B	2001	31/31	0.97	0.07	34,40,51,52	0
2	MG	A	1003	1/1	0.98	0.03	35,35,35,35	0
2	MG	B	2003	1/1	0.98	0.05	46,46,46,46	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

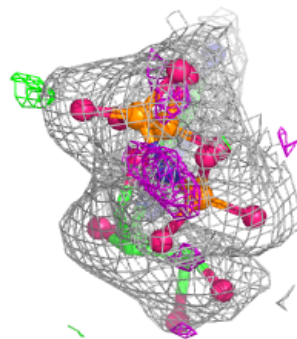
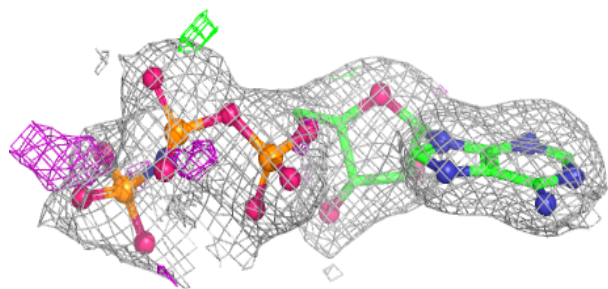
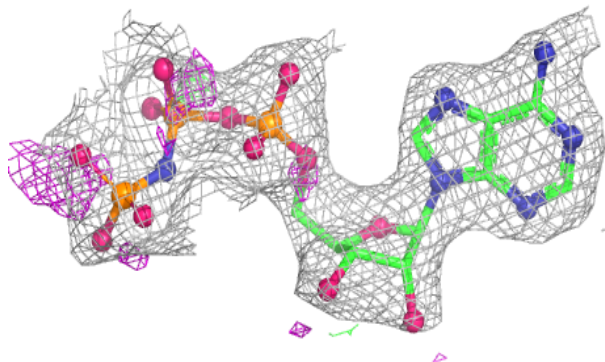
Electron density around ANP A 1001:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ANP B 2001:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.