



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 03:24 AM UTC

PDB ID : 1Y64 / pdb_00001y64
Title : Bni1p Formin Homology 2 Domain complexed with ATP-actin
Authors : Otomo, T.; Tomchick, D.R.; Otomo, C.; Panchal, S.C.; Machius, M.; Rosen, M.K.
Deposited on : 2004-12-03
Resolution : 3.05 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

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

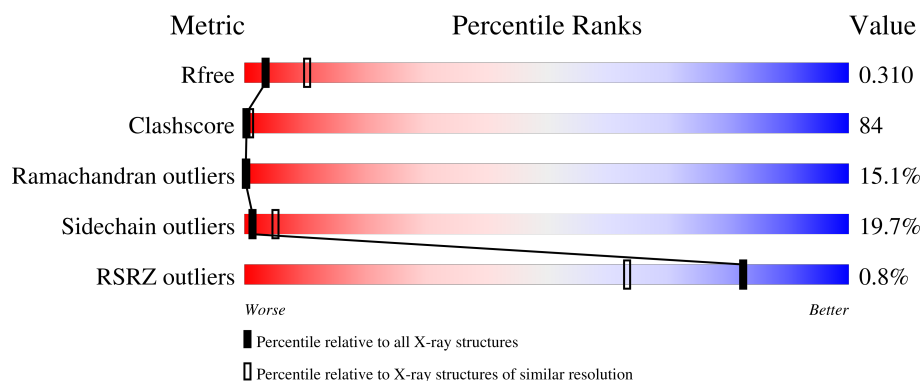
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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	375	
2	B	443	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ATP	A	2000	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6162 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 Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	0	0
			2795	1772	469	536	18			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	73	HIC	HIS	modified residue	UNP P68135

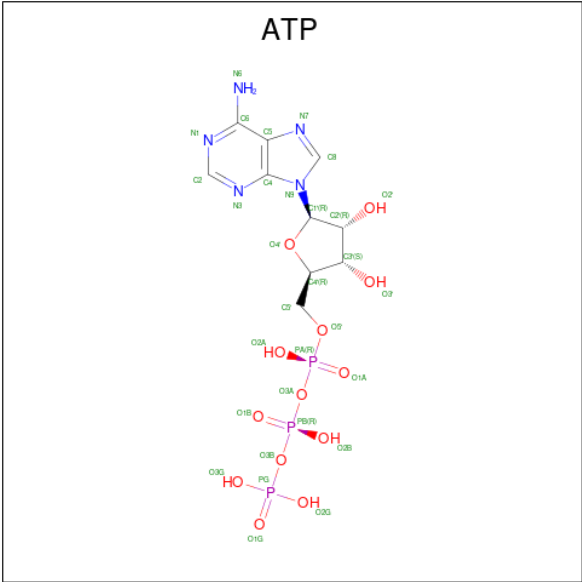
- Molecule 2 is a protein called BNI1 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	411	Total	C	N	O	S	7	0	0
			3335	2124	560	641	10			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca	0	0
			1	1		

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).

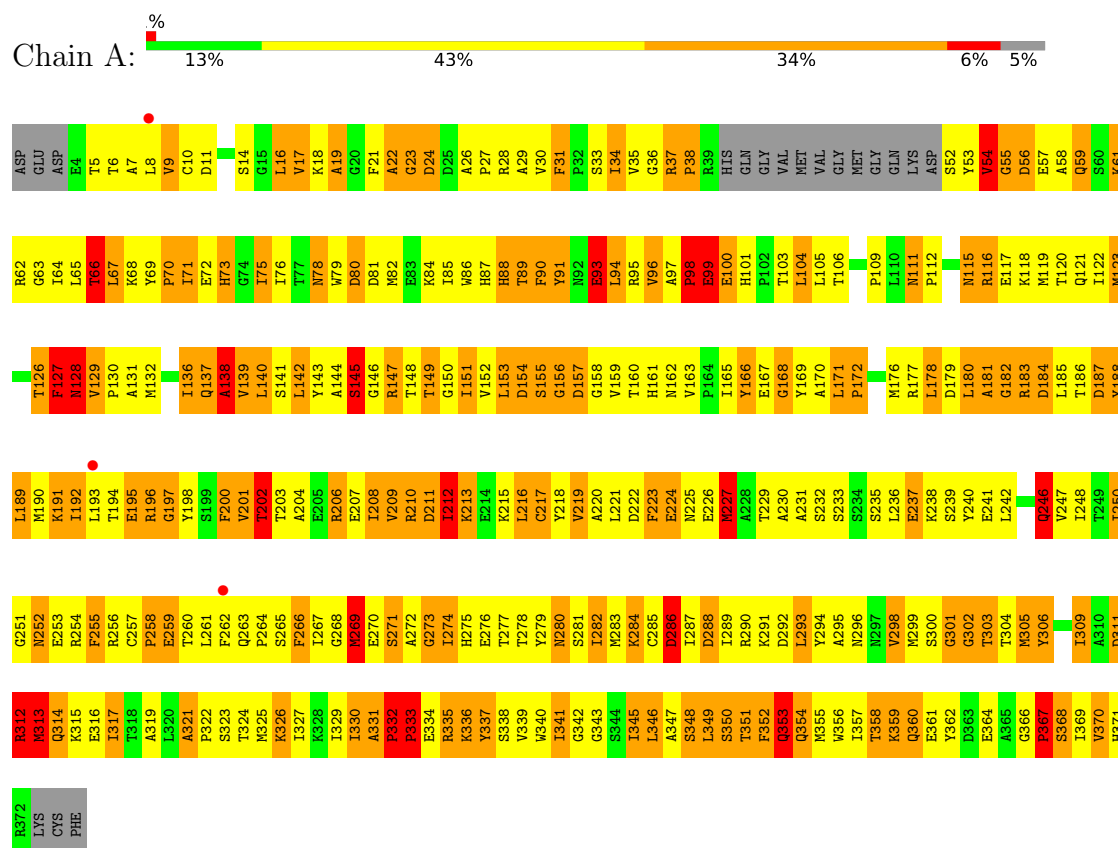


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

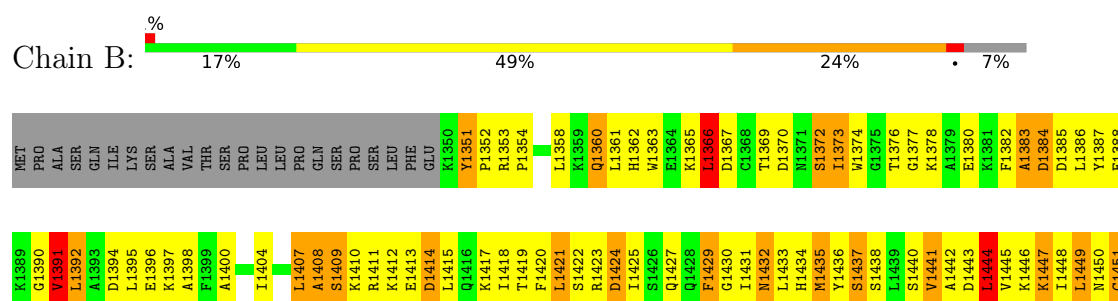
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Actin, alpha skeletal muscle



• Molecule 2: BNI1 protein



Lys	L1698	D1636	L1573	Q1512	D1452
Ile	E1699	V1637	A1574	I1513	R1453
Val	D1700	V1638	V1575	Y1514	D1454
Glj	E1701	K1639	G1576	L1515	F1455
Glj	V1702	V1640	N1577	Q1516	L1456
Glj	K1703	S1641		L1517	Q1457
Glj	L1704	I1642	N1580	M1518	T1458
Lys	T1705	E1643	D1581	V1519	P1459
	I1706	Q1644		M1520	S1460
	M1707	L1645		L1521	V1461
	E1708	V1646	K1584	E1522	V1462
	F1709	N1647	Q1585	S1523	E1463
	E1710	D1648	A1586	Y1524	F1464
	S1711	C1649	Q1587	M1525	L1465
	L1712		G1588	G1526	S1466
	M1713	F1652	F1589	S1527	K1467
	H1714	S1653	K1590	S1528	S1468
	T1715	Q1654	L1591	M1529	E1469
		S1655	S1592	R1530	I1470
	E1718	I1656	T1593	A1531	I1471
	D1719	V1657	L1594	L1532	E1472
	S1720	M1658	Q1595	T1533	V1473
	G1721	V1659	R1596	V1534	S1474
	D1722	E1660	L1597	V1535	V1475
	K1723	R1661	I1600	T1536	N1476
	F1724	S1662	K1601	S1537	L1477
	A1725	V1663	D1602	Y1538	A1478
	K1726	E1664	T1603	E1539	R1479
	I1727	I1665	T1604	R1540	N1480
	S1728	G1666	N1605	E1541	Y1481
	F1729	N1667	S1606	A1482	A1481
	F1730	L1668	M1607	Y1542	P1483
	K1731	S1669	T1608	M1543	Y1484
	L1732	D1670	F1609	E1544	S1485
	F1733	S1671	L1610	L1545	T1486
		S1672	N1611		D1487
	F1736	K1673	Y1612	K1548	W1488
	I1737	F1674	V1613	L1549	E1489
	R1738	R1675	E1614	K1550	G1490
	E1739	P1676	K1615	K1551	V1491
	Y1740	L1677	I1616	V1552	
	K1741	D1678	V1617	D1553	R1492
	K1742	K1679	R1618	K1554	N1493
	A1743	V1680	L1619	L1494	E1495
	Q1744	L1681	M1620	V1556	L1496
	A1745	I1682	Y1621	S1557	D1496
	Q1746	K1683	P1622	A1558	A1497
	N1747	T1684	S1623	L1559	K1498
	L1748	L1685	F1624	Q1560	P1499
		P1686	N1625	E1561	P1500
	E1751	V1687	D1626	S1562	E1501
	E1752	L1688	F1627	D1563	K1502
		P1689	L1628	M1564	D1503
	R1755	E1690	S1629	L1565	P1504
	L1756	A1691	E1630	R1566	N1505
	Y1757	R1692	L1631	M1567	D1506
	I1758	K1693	E1632	V1568	L1507
	K1759	K1694		F1569	Q1508
	H1760		P1633	M1570	R1509
	Lys	L1697	V1634	V1571	A1510
			L1635	I1572	D1511

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	232.00Å 56.23Å 100.94Å 90.00° 107.70° 90.00°	Depositor
Resolution (Å)	30.00 – 3.05 30.00 – 3.05	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-3.05) 99.1 (30.00-3.05)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 3.05Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.289 , 0.313 0.283 , 0.310	Depositor DCC
R_{free} test set	1145 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	89.0	Xtriage
Anisotropy	0.721	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 71.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6162	wwPDB-VP
Average B, all atoms (Å ²)	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HIC, CA, 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	0.70	1/2842 (0.0%)	1.54	71/3852 (1.8%)
2	B	0.56	1/3395 (0.0%)	1.23	46/4577 (1.0%)
All	All	0.62	2/6237 (0.0%)	1.38	117/8429 (1.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	355	MET	SD-CE	6.29	1.95	1.79
2	B	1675	HIS	CB-CG	5.22	1.57	1.50

The worst 5 of 117 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	210	ARG	N-CA-C	-20.25	89.28	111.36
1	A	163	VAL	N-CA-C	13.09	121.11	108.15
2	B	1659	VAL	N-CA-C	-10.55	97.84	112.50
1	A	306	TYR	N-CA-C	-10.53	94.43	110.32
1	A	154	ASP	N-CA-C	-10.37	95.14	110.48

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	127	PHE	Mainchain

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	2795	0	2766	593	0
2	B	3335	0	3349	457	0
3	A	1	0	0	0	0
4	A	31	0	12	13	0
All	All	6162	0	6127	1027	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 84.

The worst 5 of 1027 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:350:SER:OG	2:B:1411:ARG:HB3	1.39	1.21
1:A:350:SER:HB2	2:B:1411:ARG:HD3	1.27	1.15
1:A:259:GLU:HG3	1:A:263:GLN:HG3	1.29	1.11
2:B:1456:LEU:HD21	2:B:1532:LEU:HD23	1.25	1.10
1:A:196:ARG:HH22	1:A:251:GLY:HA3	1.15	1.09

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	352/375 (94%)	205 (58%)	91 (26%)	56 (16%)	0	0
2	B	409/443 (92%)	232 (57%)	118 (29%)	59 (14%)	0	0
All	All	761/818 (93%)	437 (57%)	209 (28%)	115 (15%)	0	0

5 of 115 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	23	GLY
1	A	61	LYS
1	A	90	PHE
1	A	98	PRO
1	A	99	GLU

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	302/317 (95%)	235 (78%)	67 (22%)	1	3
2	B	374/404 (93%)	308 (82%)	66 (18%)	2	7
All	All	676/721 (94%)	543 (80%)	133 (20%)	1	5

5 of 133 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	1656	ILE
2	B	1680	VAL
2	B	1739	GLU
1	A	280	ASN
1	A	274	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1476	ASN

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Mol	Chain	Res	Type
2	B	1744	GLN
2	B	1508	GLN
2	B	1644	GLN
2	B	1493	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	HIC	A	73	1	10,11,12	0.51	0	9,14,16	4.53	5 (55%)

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
1	HIC	A	73	1	-	2/5/6/8	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	73	HIC	NE2-CE1-ND1	-9.55	109.01	112.66
1	A	73	HIC	CZ-NE2-CD2	6.72	134.86	126.03
1	A	73	HIC	CZ-NE2-CE1	-4.79	115.40	126.71
1	A	73	HIC	CD2-NE2-CE1	4.18	108.36	106.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	73	HIC	CE1-ND1-CG	2.18	109.29	105.80

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	73	HIC	CA-CB-CG-CD2
1	A	73	HIC	CA-CB-CG-ND1

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	73	HIC	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	2000	3	32,33,33	1.99	7 (21%)	48,52,52	1.75	10 (20%)

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	2000	3	-	1/22/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2000	ATP	C2-N1	7.50	1.47	1.33
4	A	2000	ATP	C5-C6	3.80	1.51	1.41
4	A	2000	ATP	C5-N7	-3.67	1.32	1.39
4	A	2000	ATP	PB-O3A	2.51	1.62	1.59
4	A	2000	ATP	PB-O3B	2.46	1.62	1.59

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2000	ATP	N3-C2-N1	-4.84	121.26	128.58
4	A	2000	ATP	N9-C8-N7	-4.20	107.97	113.94
4	A	2000	ATP	C2-N3-C4	4.12	121.89	111.83
4	A	2000	ATP	C5-C4-N3	-3.99	121.22	126.72
4	A	2000	ATP	C5-N7-C8	3.68	109.23	103.45

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	2000	ATP	PG-O3B-PB-O2B

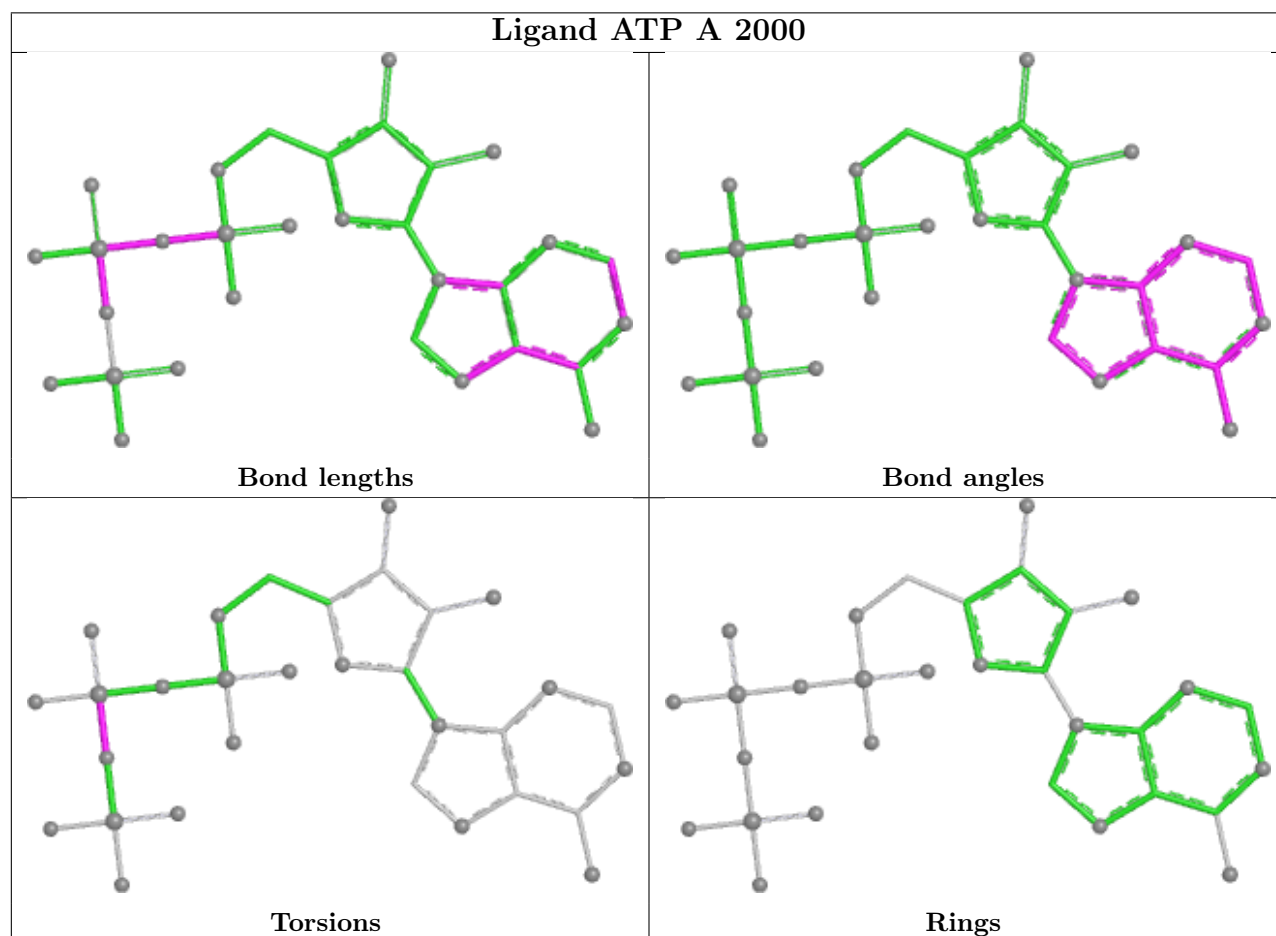
There are no ring outliers.

1 monomer is involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2000	ATP	13	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 [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	356/375 (94%)	-0.20	3 (0%)	82 63	41, 99, 154, 190	0
2	B	411/443 (92%)	-0.41	3 (0%)	84 66	57, 108, 159, 207	2 (0%)
All	All	767/818 (93%)	-0.31	6 (0%)	82 63	41, 103, 157, 207	2 (0%)

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1589	PHE	2.6
1	A	262	PHE	2.4
1	A	193	LEU	2.4
2	B	1657	VAL	2.3
1	A	8	LEU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	HIC	A	73	11/12	0.93	0.07	57,67,67,67	0

6.3 Carbohydrates [i](#)

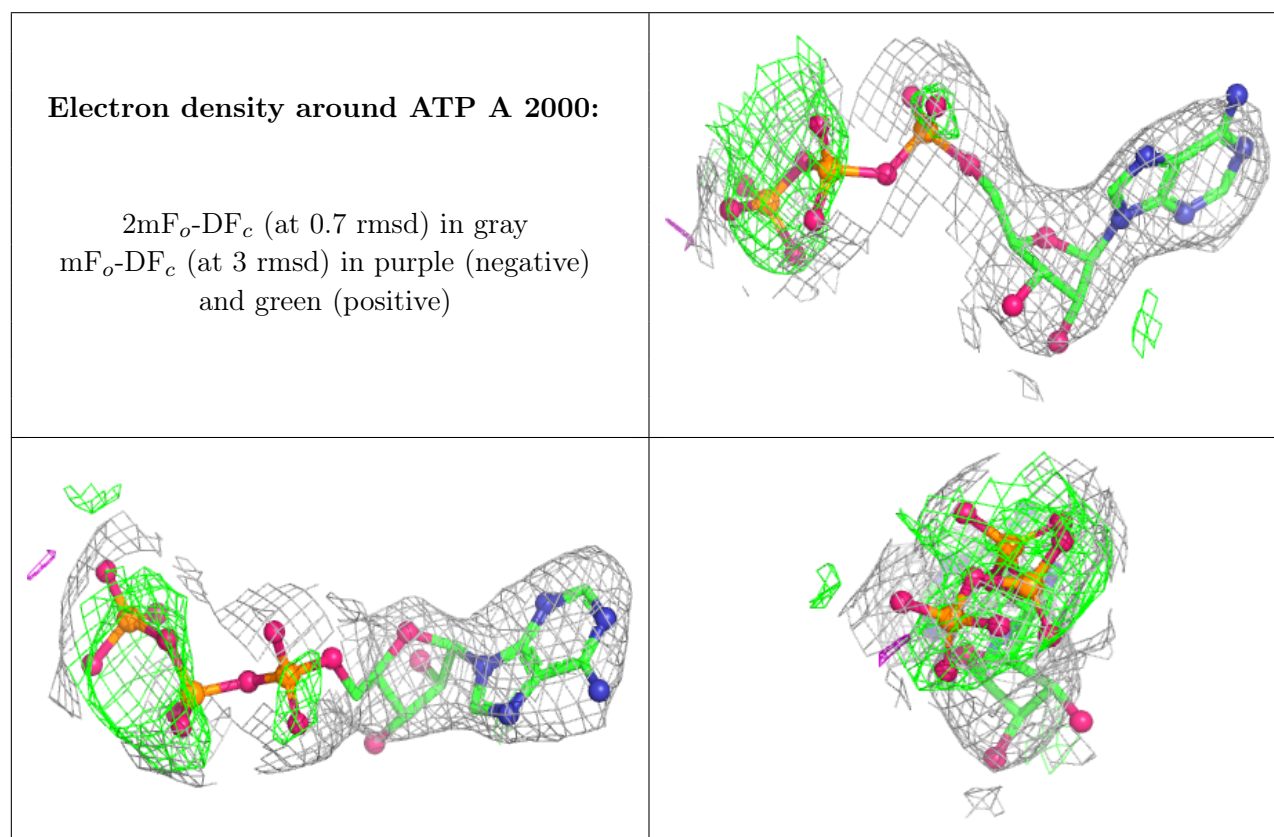
There are no oligosaccharides in this entry.

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
3	CA	A	382	1/1	0.86	0.33	97,97,97,97	0
4	ATP	A	2000	31/31	0.93	0.11	97,97,97,97	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.