



# Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 12:52 AM GMT

PDB ID : 1NMD  
Title : Crystal Structure of D. Discoideum Actin-Gelsolin Segment 1 Complex Crystallized In Presence Of Lithium ATP  
Authors : Vorobiev, S.M.; Welti, S.; Condeelis, J.; Almo, S.C.  
Deposited on : 2003-01-09  
Resolution : 1.90 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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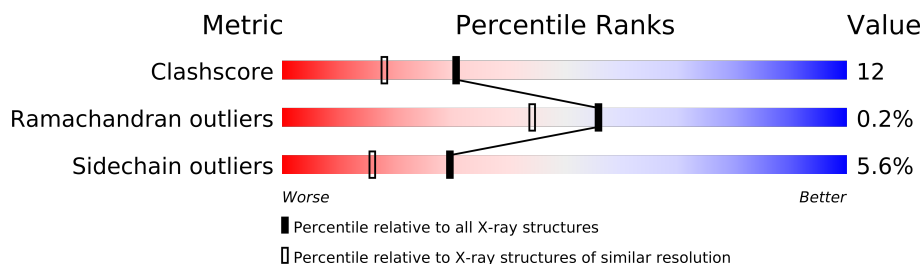
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
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 1.90 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))
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	375	
2	G	125	

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4162 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 Actin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	362	Total	C	N	O	S	0	0	0
			2789	1771	466	533	19			

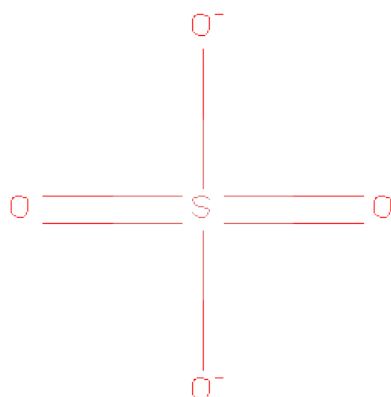
- Molecule 2 is a protein called Gelsolin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	123	Total	C	N	O	S	0	0	0
			970	627	161	181	1			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

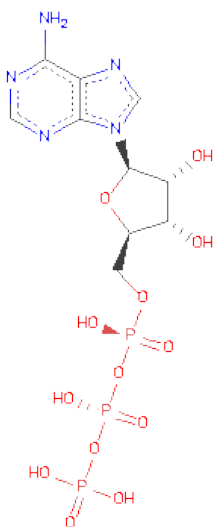
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Ca	0	0
			1	1		

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



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

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).



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

- Molecule 6 is SULFUR DIOXIDE (three-letter code: SO<sub>2</sub>) (formula: O<sub>2</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			3	2	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	251	Total	O	0	0
			251	251		
7	G	112	Total	O	0	0
			112	112		

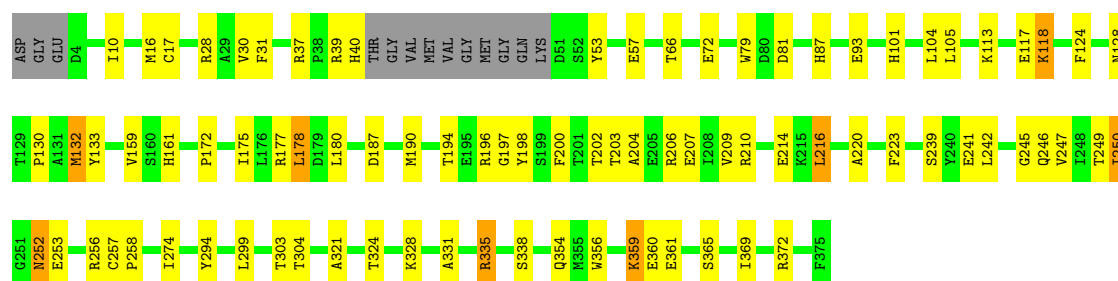
### 3 Residue-property plots

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.

Note EDS was not executed.

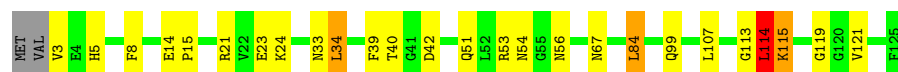
- Molecule 1: Actin

Chain A: 



- Molecule 2: Gelsolin

Chain G: 



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	178.91Å 69.05Å 56.61Å 90.00° 104.65° 90.00°	Depositor
Resolution (Å)	20.00 – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.90)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.203 , 0.250	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4162	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, SO2, 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	0.48	1/2851 (0.0%)	0.68	1/3870 (0.0%)
2	G	0.47	0/996	0.70	1/1349 (0.1%)
All	All	0.48	1/3847 (0.0%)	0.69	2/5219 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	360	GLU	CD-OE2	6.98	1.33	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	114	LEU	CA-CB-CG	7.41	132.34	115.30
1	A	335	ARG	NE-CZ-NH1	5.79	123.20	120.30

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	2789	0	2716	68	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	970	0	917	19	0
3	G	1	0	0	0	0
4	A	5	0	0	0	0
5	A	31	0	12	0	0
6	A	3	0	0	5	1
7	A	251	0	0	17	2
7	G	112	0	0	4	0
All	All	4162	0	3645	88	3

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 12.

All (88) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:299:LEU:HB2	7:A:606:HOH:O	1.53	1.07
1:A:220:ALA:HB3	7:A:608:HOH:O	1.61	0.98
1:A:331:ALA:HA	7:A:606:HOH:O	1.66	0.94
6:A:403:SO2:S	7:A:500:HOH:O	2.35	0.84
1:A:40:HIS:HB2	7:A:601:HOH:O	1.78	0.83
1:A:274:ILE:HG22	7:A:573:HOH:O	1.79	0.81
1:A:190:MET:SD	1:A:206:ARG:HG3	2.24	0.78
1:A:39:ARG:HA	1:A:66:THR:HG23	1.67	0.77
1:A:324:THR:HG22	7:A:620:HOH:O	1.85	0.77
1:A:161:HIS:HD2	7:A:607:HOH:O	1.69	0.75
1:A:17:CYS:HB2	7:A:447:HOH:O	1.87	0.73
1:A:187:ASP:OD2	1:A:206:ARG:NH1	2.21	0.73
1:A:324:THR:HG23	7:A:449:HOH:O	1.88	0.72
1:A:216:LEU:HD23	1:A:250:ILE:HG13	1.71	0.72
2:G:40:THR:HB	2:G:99:GLN:HE22	1.60	0.66
2:G:3:VAL:HG23	2:G:3:VAL:O	1.94	0.66
1:A:16:MET:CE	1:A:30:VAL:HG12	2.27	0.64
1:A:79:TRP:CD2	1:A:118:LYS:HG2	2.34	0.63
2:G:67:ASN:H	2:G:99:GLN:NE2	1.97	0.62
1:A:194:THR:HA	1:A:198:TYR:O	1.99	0.62
1:A:304:THR:O	1:A:335:ARG:NH1	2.33	0.62
1:A:354:GLN:CB	7:G:497:HOH:O	2.50	0.60
2:G:15:PRO:HG3	2:G:51:GLN:HB2	1.85	0.59
1:A:361:GLU:HB3	1:A:369:ILE:HD13	1.84	0.58
2:G:53:ARG:HD3	7:G:498:HOH:O	2.03	0.58
2:G:21:ARG:HD2	2:G:42:ASP:OD1	2.05	0.57
1:A:161:HIS:CD2	7:A:607:HOH:O	2.50	0.57
1:A:39:ARG:CB	7:A:605:HOH:O	2.52	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:53:TYR:CD1	1:A:57:GLU:HG2	2.40	0.56
1:A:132:MET:HG2	1:A:133:TYR:N	2.20	0.56
1:A:172:PRO:HA	1:A:175:ILE:HD12	1.88	0.55
1:A:202:THR:HB	6:A:403:SO2:O2	2.06	0.55
1:A:252:ASN:HD22	1:A:253:GLU:N	2.05	0.55
1:A:361:GLU:HB3	1:A:369:ILE:CD1	2.37	0.54
1:A:207:GLU:HG2	1:A:210:ARG:NH2	2.21	0.54
1:A:72:GLU:HA	1:A:72:GLU:OE1	2.07	0.53
1:A:335:ARG:HD3	7:A:606:HOH:O	2.08	0.53
1:A:16:MET:HE2	1:A:30:VAL:HG12	1.91	0.53
2:G:113:GLY:HA2	7:G:443:HOH:O	2.09	0.53
1:A:124:PHE:HD1	1:A:359:LYS:HE2	1.74	0.52
1:A:223:PHE:CZ	1:A:256:ARG:HG2	2.44	0.52
1:A:190:MET:HG2	1:A:209:VAL:HG21	1.91	0.52
1:A:324:THR:CG2	7:A:449:HOH:O	2.54	0.52
1:A:223:PHE:HZ	1:A:256:ARG:HG2	1.76	0.51
1:A:87:HIS:HD2	7:A:650:HOH:O	1.93	0.51
1:A:252:ASN:C	1:A:252:ASN:HD22	2.14	0.50
1:A:372:ARG:HD3	7:A:450:HOH:O	2.11	0.49
1:A:196:ARG:HH21	1:A:249:THR:HG22	1.77	0.49
2:G:33:ASN:ND2	2:G:34:LEU:HD13	2.27	0.49
1:A:204:ALA:HB2	6:A:403:SO2:O1	2.12	0.49
1:A:37:ARG:NH2	1:A:81:ASP:OD2	2.43	0.48
2:G:8:PHE:CE1	2:G:84:LEU:HD13	2.49	0.48
1:A:203:THR:N	6:A:403:SO2:O2	2.47	0.48
2:G:33:ASN:HD22	2:G:34:LEU:HD13	1.78	0.48
1:A:194:THR:O	1:A:197:GLY:N	2.35	0.48
1:A:79:TRP:CE2	1:A:118:LYS:HG2	2.48	0.48
1:A:303:THR:O	1:A:303:THR:HG22	2.14	0.48
1:A:203:THR:HB	6:A:403:SO2:S	2.54	0.47
1:A:190:MET:HG3	1:A:209:VAL:HG11	1.97	0.47
1:A:241:GLU:HG3	1:A:247:VAL:HG22	1.97	0.47
2:G:107:LEU:HD23	2:G:114:LEU:HD13	1.95	0.47
1:A:53:TYR:HD1	1:A:57:GLU:HG2	1.79	0.46
1:A:113:LYS:O	1:A:117:GLU:HG3	2.16	0.46
1:A:10:ILE:HB	1:A:105:LEU:HD23	1.98	0.45
1:A:31:PHE:CE2	1:A:93:GLU:HG3	2.52	0.45
1:A:294:TYR:CE1	1:A:321:ALA:HB2	2.52	0.45
1:A:210:ARG:O	1:A:214:GLU:HG3	2.17	0.44
1:A:223:PHE:HA	7:A:608:HOH:O	2.18	0.44
1:A:335:ARG:HA	1:A:338:SER:OG	2.18	0.44
1:A:241:GLU:HG3	1:A:247:VAL:CG2	2.47	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:G:23:GLU:HG2	2:G:121:VAL:HG11	2.00	0.43
1:A:242:LEU:HD12	1:A:246:GLN:HB3	2.00	0.43
2:G:3:VAL:CG2	2:G:3:VAL:O	2.66	0.43
2:G:114:LEU:C	2:G:114:LEU:HD23	2.39	0.43
1:A:104:LEU:C	1:A:104:LEU:HD23	2.39	0.43
2:G:3:VAL:HG22	7:G:408:HOH:O	2.18	0.43
2:G:53:ARG:HA	2:G:53:ARG:HD3	1.79	0.43
1:A:257:CYS:HB3	1:A:258:PRO:HD3	2.00	0.42
1:A:252:ASN:C	1:A:252:ASN:ND2	2.73	0.42
1:A:124:PHE:O	1:A:128:ASN:HA	2.20	0.42
1:A:304:THR:OG1	1:A:335:ARG:HD2	2.19	0.41
1:A:198:TYR:HB3	1:A:200:PHE:CE1	2.55	0.41
1:A:178:LEU:HD13	1:A:180:LEU:HB3	2.03	0.41
2:G:39:PHE:HB3	2:G:119:GLY:O	2.21	0.41
1:A:101:HIS:O	1:A:130:PRO:HD2	2.20	0.41
2:G:5:HIS:HB3	2:G:8:PHE:CD1	2.56	0.41
2:G:113:GLY:O	2:G:115:LYS:HD3	2.20	0.40
1:A:196:ARG:HD2	1:A:253:GLU:OE2	2.22	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:A:403:SO2:S	6:A:403:SO2:S[2_555]	1.47	0.73
7:A:504:HOH:O	7:A:504:HOH:O[2_555]	1.76	0.44
7:A:500:HOH:O	7:A:500:HOH:O[2_555]	2.05	0.15

## 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	358/375 (96%)	346 (97%)	11 (3%)	1 (0%)	50	37
2	G	121/125 (97%)	118 (98%)	3 (2%)	0	100	100
All	All	479/500 (96%)	464 (97%)	14 (3%)	1 (0%)	56	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	245	GLY

### 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	296/315 (94%)	282 (95%)	14 (5%)	36	22
2	G	98/103 (95%)	90 (92%)	8 (8%)	17	6
All	All	394/418 (94%)	372 (94%)	22 (6%)	30	16

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ARG
1	A	118	LYS
1	A	132	MET
1	A	159	VAL
1	A	177	ARG
1	A	178	LEU
1	A	216	LEU
1	A	239	SER
1	A	250	ILE
1	A	252	ASN
1	A	328	LYS
1	A	356	TRP
1	A	359	LYS
1	A	365	SER
2	G	14	GLU
2	G	24	LYS
2	G	34	LEU
2	G	54	ASN
2	G	56	ASN
2	G	84	LEU
2	G	114	LEU
2	G	115	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	HIS
1	A	92	ASN
1	A	252	ASN
1	A	280	ASN
1	A	314	ASN
2	G	56	ASN
2	G	58	GLN
2	G	83	GLN
2	G	99	GLN

### 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, 1 is monoatomic - leaving 3 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	$\# Z  > 2$
5	ATP	A	401	-	33,33,33	1.13	3 (9%)	52,52,52	1.65	8 (15%)
6	SO2	A	403	-	2,2,2	1.50	0	1,1,1	0.83	0
4	SO4	A	404	-	4,4,4	2.42	3 (75%)	6,6,6	0.61	0

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
5	ATP	A	401	-	-	0/22/38/38	0/1/3/3
6	SO2	A	403	-	-	0/0/0/0	0/0/0/0
4	SO4	A	404	-	-	0/0/0/0	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	401	ATP	C2-N1	3.51	1.40	1.33
4	A	404	SO4	O3-S	3.32	1.58	1.47
4	A	404	SO4	O4-S	2.48	1.55	1.47
4	A	404	SO4	O2-S	2.42	1.54	1.47
5	A	401	ATP	PB-O3B	-2.23	1.55	1.59
5	A	401	ATP	PB-O2B	-2.11	1.45	1.55

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	401	ATP	O4'-C1'-N9	6.97	114.92	108.44
5	A	401	ATP	O3A-PB-O3B	-3.61	94.33	101.66
5	A	401	ATP	O2G-PG-O1G	3.06	120.43	110.44
5	A	401	ATP	N3-C2-N1	-2.93	126.26	128.71
5	A	401	ATP	N6-C6-N1	-2.41	114.62	119.36
5	A	401	ATP	C1'-N9-C4	-2.23	122.78	126.64
5	A	401	ATP	O2B-PB-O3B	2.18	115.47	105.14
5	A	401	ATP	C5-C6-N6	2.02	125.28	120.72

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 ⓘ

EDS was not executed - this section will therefore be empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.