



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 01:28 PM UTC

PDB ID : 1CDK / pdb\_00001cdk  
Title : CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT (E.C.2.7.1.37) (PROTEIN KINASE A) COMPLEXED WITH PROTEIN KINASE INHIBITOR PEPTIDE FRAGMENT 5-24 (PKI(5-24) ISOELECTRIC VARIANT CA) AND MN<sup>2+</sup> ADENYLYL IMIDODIPHOSPHATE (MNAMP-PNP) AT PH 5.6 AND 7C AND 4C  
Authors : Bossemeyer, D.; Engh, R.A.; Kinzel, V.; Ponstingl, H.; Huber, R.  
Deposited on : 1994-07-04  
Resolution : 2.00 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](mailto: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>.

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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)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

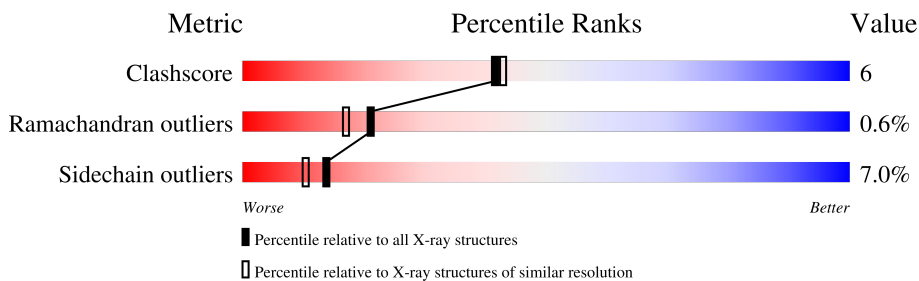
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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  $\geq 3$ , 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  $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	350	
1	B	350	
2	I	20	
2	J	20	

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6361 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 CAMP-DEPENDENT PROTEIN KINASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	343	Total	C	N	O	P	S	107	0	0
			2828	1832	475	512	1	8			
1	B	343	Total	C	N	O	P	S	100	0	0
			2829	1833	475	512	1	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	LYS	MET	conflict	UNP P00517
A	69	PHE	TYR	conflict	UNP P00517
A	108	TYR	PHE	conflict	UNP P00517
A	286	ASP	ASN	conflict	UNP P00517
B	63	LYS	MET	conflict	UNP P00517
B	69	PHE	TYR	conflict	UNP P00517
B	108	TYR	PHE	conflict	UNP P00517
B	286	ASP	ASN	conflict	UNP P00517

- Molecule 2 is a protein called PROTEIN KINASE INHIBITOR.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	I	20	Total	C	N	O	7	0	0
			157	94	32	31			
2	J	20	Total	C	N	O	8	0	0
			157	94	32	31			

- Molecule 3 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mn	0	0
			2	2		
3	B	2	Total	Mn	0	0
			2	2		



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C 6 6	0	0
5	B	1	Total C 6 6	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	129	Total O 129 129	0	0
6	I	20	Total O 20 20	0	0
6	B	140	Total O 140 140	0	0
6	J	23	Total O 23 23	0	0

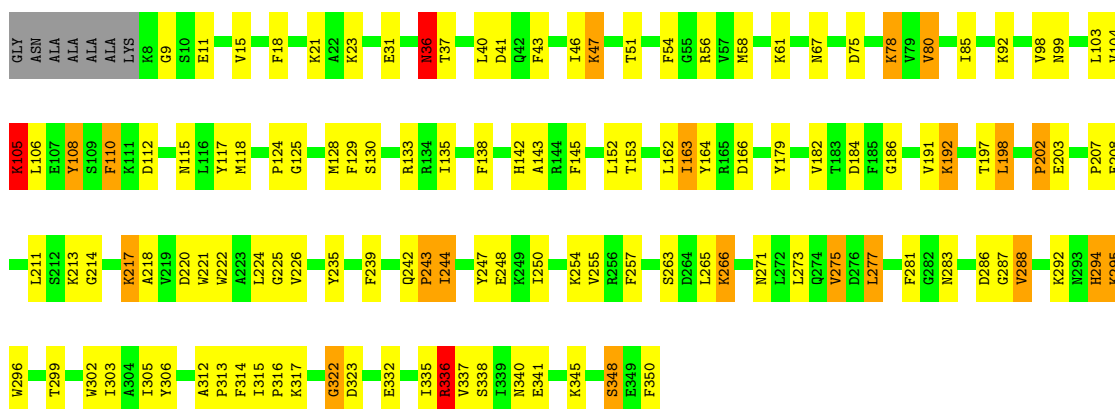
### 3 Residue-property plots [i](#)

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. 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. 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.

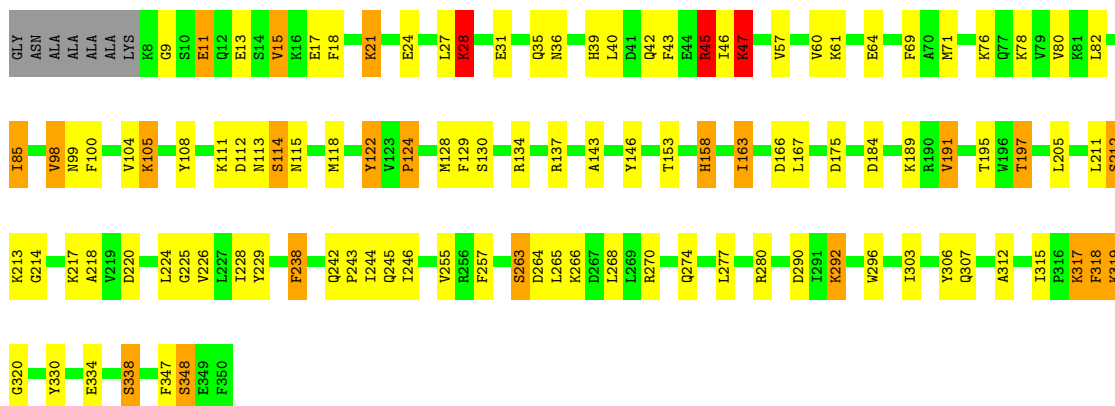
- Molecule 1: CAMP-DEPENDENT PROTEIN KINASE

Chain A:  62% 30% 6% ..



- Molecule 1: CAMP-DEPENDENT PROTEIN KINASE

Chain B:  67% 24% 6% ..



- Molecule 2: PROTEIN KINASE INHIBITOR

Chain I:  60% 35% 5%



- Molecule 2: PROTEIN KINASE INHIBITOR

Chain J: 80% 15% 5%

A horizontal bar chart showing the validation progress for Chain J. The bar is color-coded: green for 80%, yellow for 15%, and orange for 5%.



## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.61Å 80.60Å 110.10Å 90.00° 88.59° 90.00°	Depositor
Resolution (Å)	5.00 – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) (5.00-2.00)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.197 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	6361	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	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: TPO, ANP, MN, MYR

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	1.35	9/2888 (0.3%)	1.86	62/3888 (1.6%)
1	B	1.33	5/2890 (0.2%)	1.83	49/3892 (1.3%)
2	I	1.39	0/159	1.55	0/212
2	J	1.43	1/159 (0.6%)	1.70	0/212
All	All	1.34	15/6096 (0.2%)	1.83	111/8204 (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	1	25
1	B	0	28
2	I	0	5
2	J	0	2
All	All	1	60

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	323	ASP	N-CA	-16.14	1.26	1.46
1	A	128	MET	SD-CE	-9.13	1.56	1.79
1	B	163	ILE	CA-C	7.42	1.61	1.52
1	B	128	MET	SD-CE	-6.58	1.63	1.79
1	B	57	VAL	CA-CB	-6.42	1.46	1.54

The worst 5 of 111 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	322	GLY	O-C-N	19.16	141.19	122.41
1	A	323	ASP	N-CA-CB	14.69	133.56	110.21
1	B	9	GLY	N-CA-C	13.05	130.86	113.37
1	B	318	PHE	N-CA-C	10.86	124.86	108.46
1	B	319	LYS	CA-C-N	10.74	138.73	121.87

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	192	LYS	CA

5 of 60 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	108	TYR	Sidechain
1	A	164	TYR	Sidechain
1	A	166	ASP	Mainchain
1	A	23	LYS	Mainchain
1	A	51	THR	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	2828	0	2805	44	0
1	B	2829	0	2810	30	0
2	I	157	0	149	4	0
2	J	157	0	149	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	31	0	13	0	0
4	B	31	0	13	0	0
5	A	6	0	11	0	0
5	B	6	0	11	1	0
6	A	129	0	0	3	0
6	B	140	0	0	4	0
6	I	20	0	0	0	0
6	J	23	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6361	0	5961	74	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 6.

The worst 5 of 74 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:336:ARG:HH11	1:A:336:ARG:HB2	1.49	0.77
1:A:75:ASP:HB3	1:A:78:LYS:HG2	1.71	0.72
1:B:80:VAL:HG22	1:B:85:ILE:HD11	1.74	0.70
1:A:211:LEU:HB2	1:A:213:LYS:HE2	1.78	0.65
1:A:340:ASN:HD21	1:B:137:ARG:HH22	1.46	0.64

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	340/350 (97%)	324 (95%)	13 (4%)	3 (1%)	14	9
1	B	340/350 (97%)	320 (94%)	19 (6%)	1 (0%)	36	35
2	I	18/20 (90%)	16 (89%)	2 (11%)	0	100	100
2	J	18/20 (90%)	16 (89%)	2 (11%)	0	100	100
All	All	716/740 (97%)	676 (94%)	36 (5%)	4 (1%)	21	17

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	ASN

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Mol	Chain	Res	Type
1	A	46	ILE
1	B	320	GLY
1	A	9	GLY

### 5.3.2 Protein sidechains [i](#)

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	301/304 (99%)	278 (92%)	23 (8%)	12	9
1	B	302/304 (99%)	281 (93%)	21 (7%)	14	10
2	I	15/15 (100%)	15 (100%)	0	100	100
2	J	15/15 (100%)	15 (100%)	0	100	100
All	All	633/638 (99%)	589 (93%)	44 (7%)	14	10

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	45	ARG
1	B	263	SER
1	B	47	LYS
1	B	105	LYS
1	B	277	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	283	ASN
2	J	16	ASN
1	B	35	GLN
1	B	39	HIS
1	B	67	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues are 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	TPO	A	197	1	8,10,11	1.39	1 (12%)	10,14,16	2.02	4 (40%)
1	TPO	B	197	1	8,10,11	2.59	2 (25%)	10,14,16	2.30	5 (50%)

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	TPO	A	197	1	-	1/9/11/13	-
1	TPO	B	197	1	-	2/9/11/13	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	197	TPO	P-OG1	-6.80	1.47	1.59
1	A	197	TPO	P-O1P	2.37	1.57	1.50
1	B	197	TPO	P-O3P	-2.09	1.47	1.54

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	197	TPO	O3P-P-OG1	-3.77	91.16	105.85
1	B	197	TPO	P-OG1-CB	3.41	132.59	123.33
1	A	197	TPO	O3P-P-O2P	3.22	119.89	107.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	197	TPO	O3P-P-O2P	3.08	119.36	107.80
1	A	197	TPO	O-C-CA	-3.08	116.86	124.77

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	197	TPO	O-C-CA-CB
1	B	197	TPO	O-C-CA-CB
1	B	197	TPO	CB-OG1-P-O3P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	197	TPO	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	MYR	B	403	-	5,5,15	0.53	0	4,4,15	0.58	0
5	MYR	A	403	-	5,5,15	0.53	0	4,4,15	0.48	0
4	ANP	A	400	3	33,33,33	1.57	4 (12%)	45,52,52	1.22	4 (8%)
4	ANP	B	400	3	33,33,33	1.48	5 (15%)	45,52,52	1.29	2 (4%)

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	MYR	B	403	-	-	1/3/3/13	-
5	MYR	A	403	-	-	0/3/3/13	-
4	ANP	A	400	3	-	1/18/38/38	0/3/3/3
4	ANP	B	400	3	-	2/18/38/38	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	400	ANP	PG-O1G	5.43	1.54	1.46
4	B	400	ANP	PG-O1G	4.45	1.52	1.46
4	A	400	ANP	PG-O3G	-4.09	1.45	1.56
4	B	400	ANP	PG-O3G	-3.69	1.47	1.56
4	B	400	ANP	PB-O2B	-3.46	1.47	1.56

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	400	ANP	O1G-PG-N3B	-4.93	104.52	111.77
4	A	400	ANP	O2B-PB-O1B	4.82	120.20	109.87
4	B	400	ANP	O2B-PB-O1B	4.81	120.19	109.87
4	A	400	ANP	O1G-PG-N3B	-3.69	106.33	111.77
4	A	400	ANP	O1B-PB-N3B	-3.07	107.25	111.77

There are no chirality outliers.

All (4) torsion outliers are listed below:

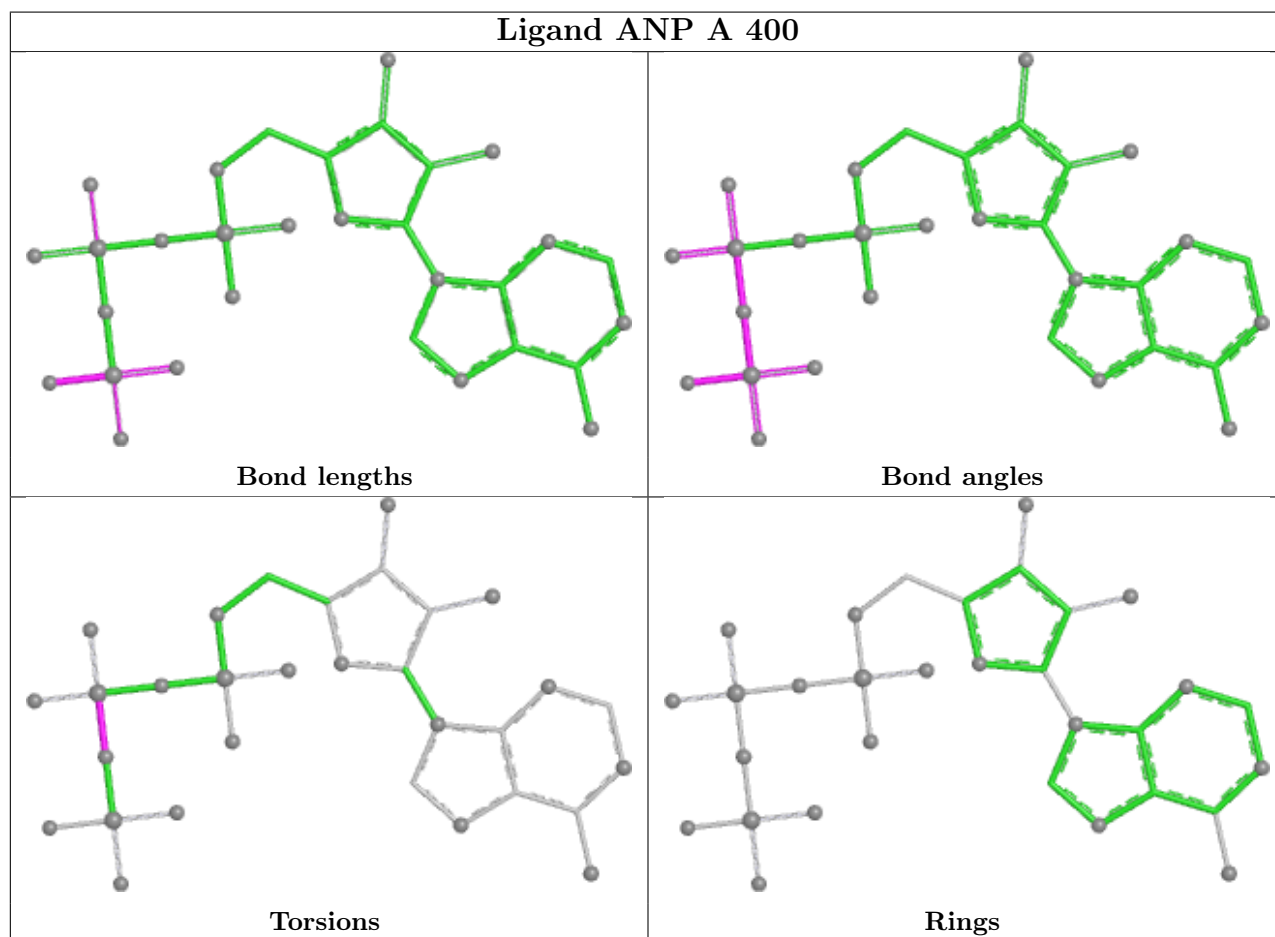
Mol	Chain	Res	Type	Atoms
4	A	400	ANP	PG-N3B-PB-O1B
4	B	400	ANP	PG-N3B-PB-O1B
5	B	403	MYR	C9-C10-C11-C12
4	B	400	ANP	PG-N3B-PB-O3A

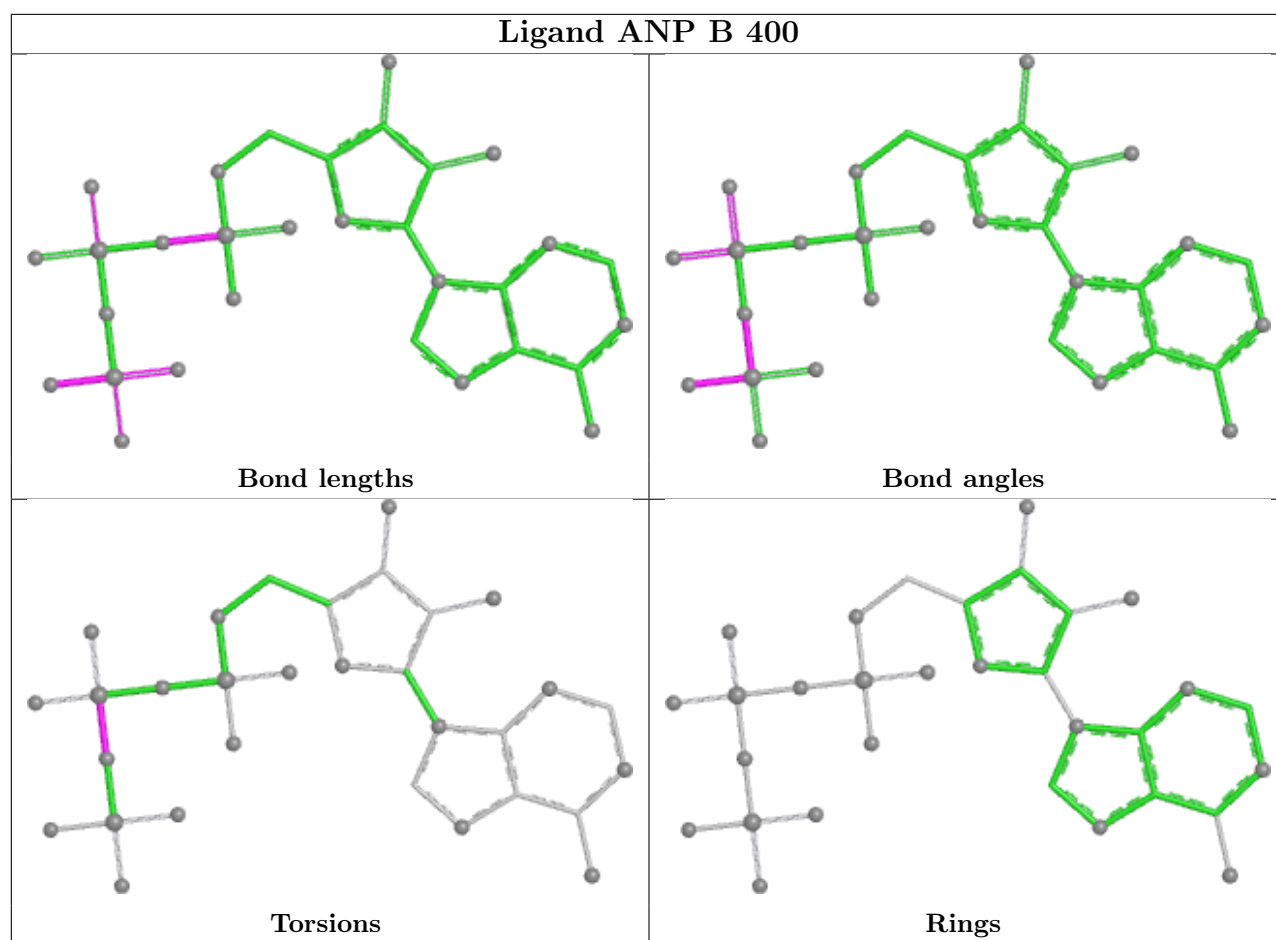
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	403	MYR	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.