



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 03:36 PM UTC

PDB ID : 1N6M / pdb_00001n6m
Title : Rotation of the stalk/neck and one head in a new crystal structure of the kinesin motor protein, Ncd
Authors : Yun, M.; Bronner, C.E.; Park, C.-G.; Cha, S.-S.; Park, H.-W.; Endow, S.A.
Deposited on : 2002-11-11
Resolution : 2.50 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)	:	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

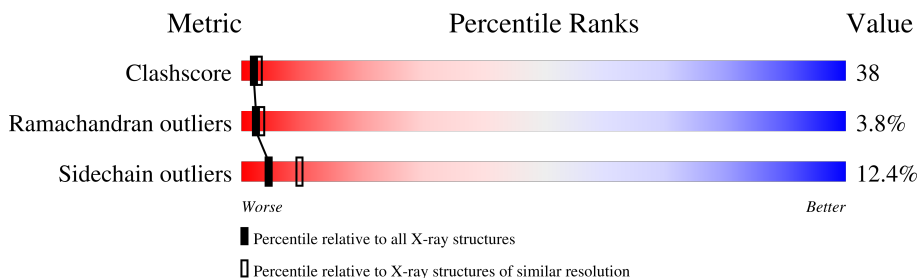
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	409	41% 38% 9% 11%
1	B	409	31% 41% 9% 18%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5886 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 Claret segregational protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	362	Total	C	N	O	S	0	0	0
			2893	1804	507	561	21			
1	B	335	Total	C	N	O	S	0	0	0
			2656	1659	464	515	18			

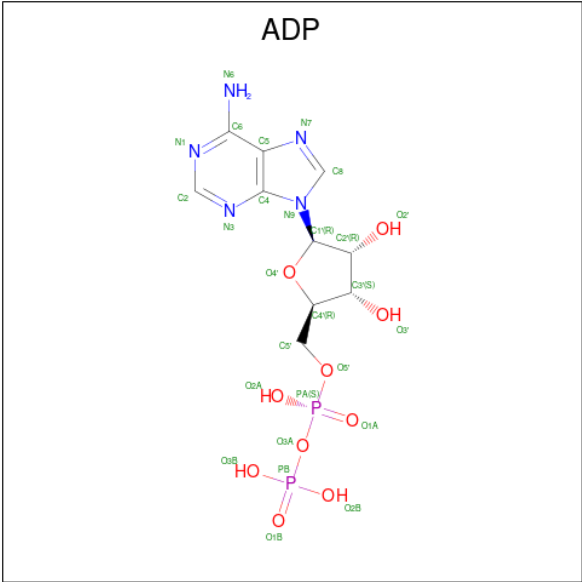
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	292	MET	-	initiating methionine	UNP P20480
A	600	LYS	ASN	engineered mutation	UNP P20480
B	292	MET	-	initiating methionine	UNP P20480
B	600	LYS	ASN	engineered mutation	UNP P20480

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 27	C 10	N 5	O 10	P 2	0	0
3	B	1	Total 27	C 10	N 5	O 10	P 2	0	0

- Molecule 4 is water.

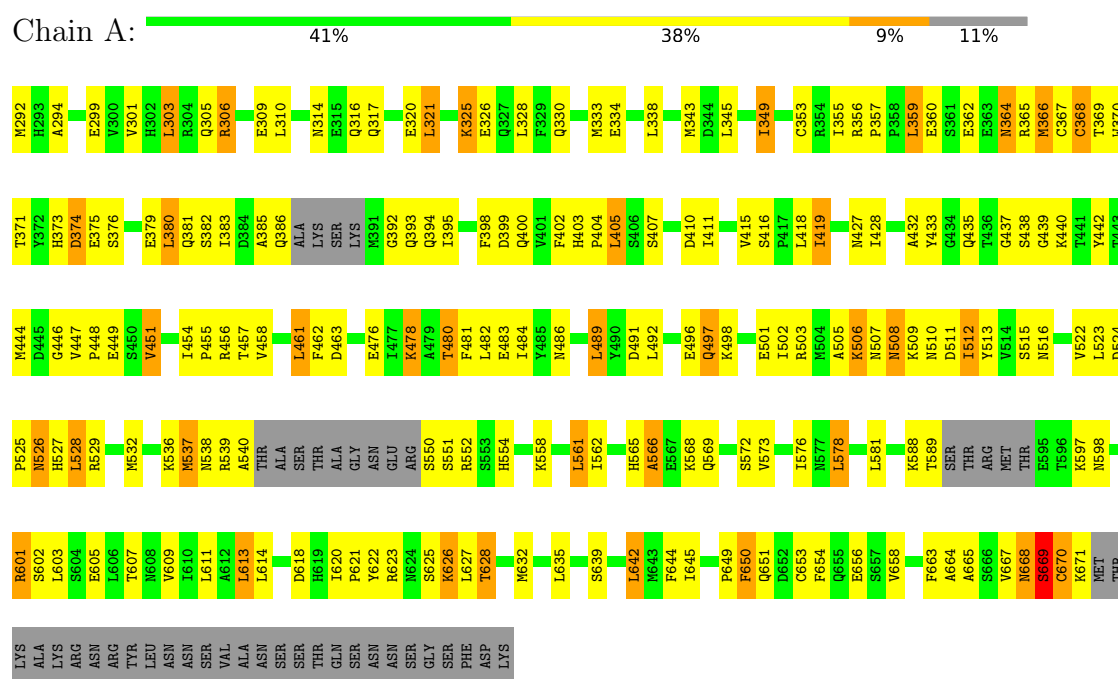
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	166	Total	O	0	0
			166	166		
4	B	115	Total	O	0	0
			115	115		

3 Residue-property plots

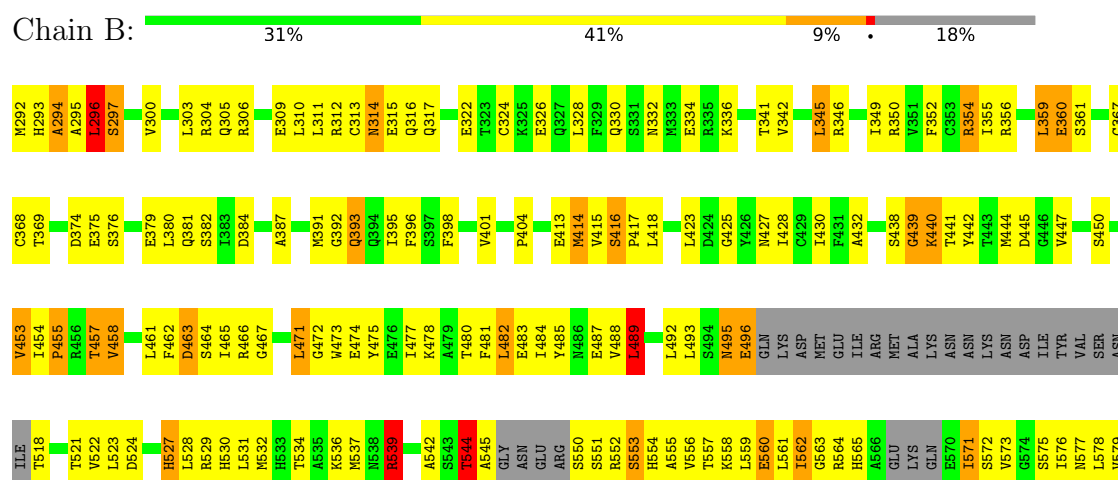
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: Claret segregational protein



• Molecule 1: Claret segregational protein



D580	L581	A582	G583	S584	E585	S586	P587	LYS	THR	SER	THR	ARG	MET	THR	GLU	THR	LYS	M598	I599	R600	R601	S602	L603	S604	E605	L606	T607	N608	V609	I610	L611	A612	L613	L614	Q615	K616	Q617	ASP	HIS	ILE	PRO	Y622	R623	N624	S625	K626	L627	T628	H629	L630	L631	M632	P633	S634	L635	G636	G637	N638	S639
K640	T641	L642	I645	F650	F654	V658	K659	S660	L661	R662	A664	A665	S666	V667	N668	SER	CYS	LYS	MET	THR	LYS	ALA	LYS	LYS	ARG	ASN	ASN	TYR	LEU	ASN	ASN	SER	VAL	ALA	ASN	SER	SER	THR	GLN	SER	ASN	ASN	SER	GLY	SER	PHE	ASP	LYS											

4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.60Å 66.60Å 94.80Å 90.00° 98.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.260 , 0.302	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5886	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

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, ADP

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	0.55	0/2939	0.98	9/3962 (0.2%)
1	B	0.55	0/2697	1.08	18/3637 (0.5%)
All	All	0.55	0/5636	1.03	27/7599 (0.4%)

There are no bond length outliers.

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	495	ASN	N-CA-C	11.77	127.14	113.02
1	A	451	VAL	N-CA-C	9.91	121.41	110.21
1	B	624	ASN	N-CA-C	-8.36	103.21	113.50
1	A	669	SER	N-CA-C	-7.86	102.79	112.38
1	B	297	SER	N-CA-C	-7.72	103.84	113.18

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	2893	0	2860	178	0
1	B	2656	0	2621	249	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	27	0	12	6	0
3	B	27	0	12	6	0
4	A	166	0	0	4	0
4	B	115	0	0	1	0
All	All	5886	0	5505	421	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 38.

The worst 5 of 421 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:B:622:TYR:CD2	1:B:632:MET:HB2	1.97	0.99
1:A:359:LEU:HD13	1:A:359:LEU:H	1.22	0.98
1:A:497:GLN:HE21	1:A:498:LYS:N	1.63	0.95
1:A:382:SER:HB2	1:A:651:GLN:HE22	1.37	0.88
1:B:562:ILE:HG22	1:B:573:VAL:HG22	1.55	0.86

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	354/409 (87%)	309 (87%)	33 (9%)	12 (3%)	3	4
1	B	323/409 (79%)	263 (81%)	46 (14%)	14 (4%)	2	2
All	All	677/818 (83%)	572 (84%)	79 (12%)	26 (4%)	2	3

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	506	LYS
1	B	392	GLY
1	B	458	VAL
1	B	632	MET
1	B	633	PRO

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	330/370 (89%)	288 (87%)	42 (13%)	4	9
1	B	301/370 (81%)	265 (88%)	36 (12%)	5	10
All	All	631/740 (85%)	553 (88%)	78 (12%)	4	9

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	482	LEU
1	B	631	LEU
1	B	496	GLU
1	B	560	GLU
1	B	641	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 35 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	527	HIS
1	B	530	HIS
1	B	624	ASN
1	A	527	HIS
1	A	516	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 4 ligands modelled in this entry, 2 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	ADP	A	998	2	28,29,29	1.69	4 (14%)	43,45,45	2.00	7 (16%)
3	ADP	B	999	2	28,29,29	1.59	5 (17%)	43,45,45	2.08	9 (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
3	ADP	A	998	2	-	5/16/32/32	0/3/3/3
3	ADP	B	999	2	-	3/16/32/32	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)
3	A	998	ADP	C5-N7	-4.37	1.31	1.39
3	A	998	ADP	PA-O3A	-3.57	1.55	1.59
3	B	999	ADP	C5-N7	-3.48	1.32	1.39
3	B	999	ADP	PA-O3A	-3.32	1.55	1.59
3	A	998	ADP	C1'-N9	2.65	1.53	1.46

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	999	ADP	N3-C2-N1	-6.60	118.59	128.58
3	A	998	ADP	N3-C2-N1	-6.31	119.03	128.58
3	A	998	ADP	C5-C4-N3	-5.90	118.59	126.72
3	B	999	ADP	C5-C4-N3	-5.55	119.08	126.72
3	B	999	ADP	C2-N3-C4	4.66	123.21	111.83

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

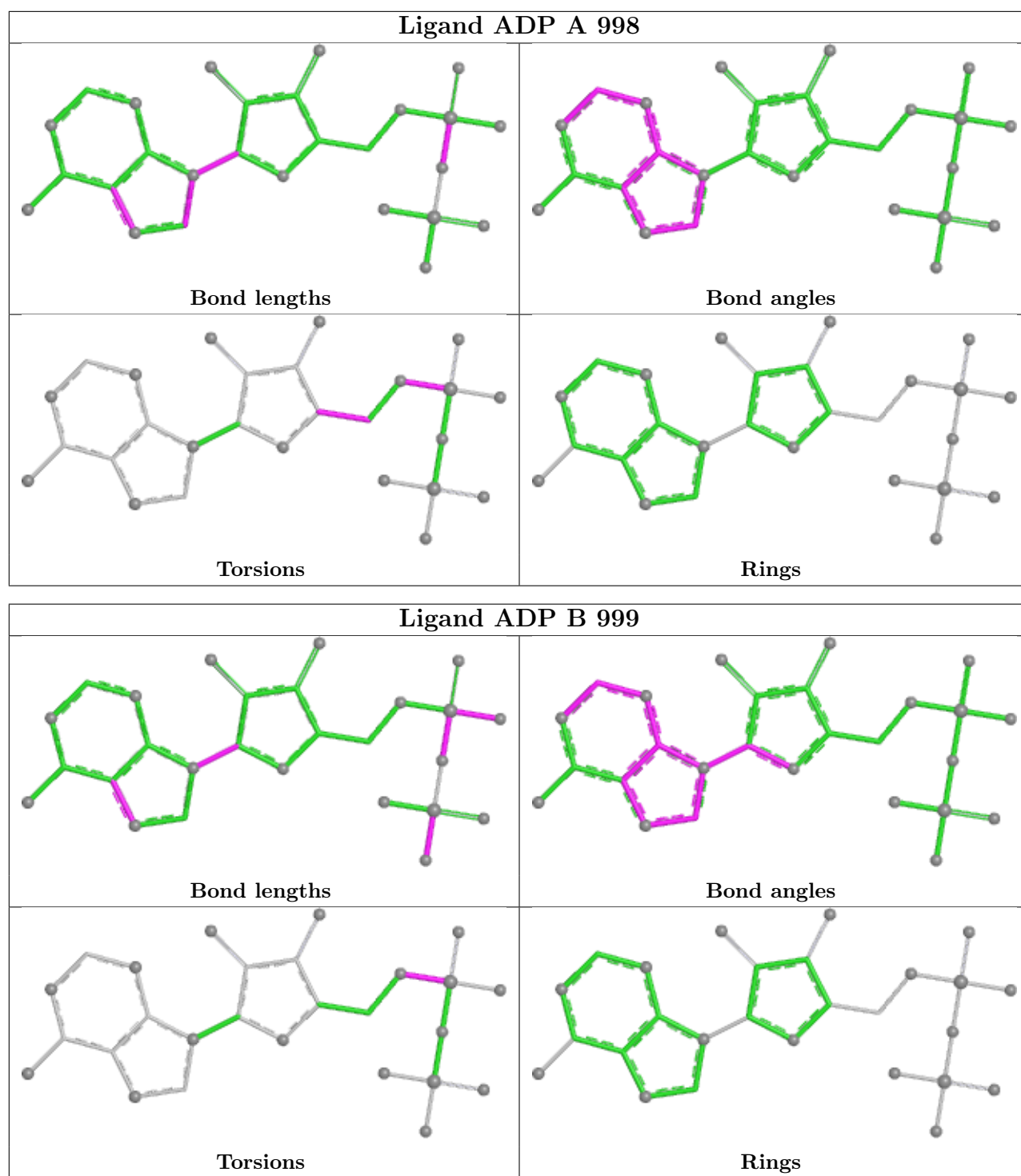
Mol	Chain	Res	Type	Atoms
3	A	998	ADP	C5'-O5'-PA-O1A
3	A	998	ADP	C5'-O5'-PA-O2A
3	A	998	ADP	C5'-O5'-PA-O3A
3	A	998	ADP	O4'-C4'-C5'-O5'
3	B	999	ADP	C5'-O5'-PA-O1A

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	998	ADP	6	0
3	B	999	ADP	6	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 ⓘ

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 [i](#)

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.