



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 05:51 AM UTC

PDB ID : 1VRW / pdb_00001vrw
Title : Crystal structure analysis of plasmodium falciparum enoyl-acyl-carrier-protein reductase with nadh
Authors : Perozzo, R.; Kuo, M.; Sidhu, A.S.; Valiyaveetil, J.T.; Bittman, R.; Jacobs Jr., W.R.; Fidock, D.A.; Sacchettini, J.C.
Deposited on : 2005-06-30
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) : **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

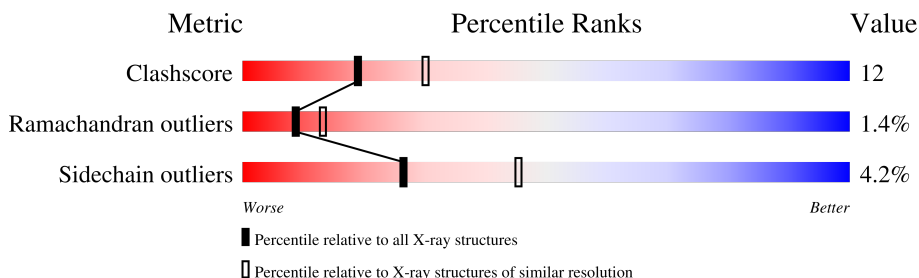
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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))
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	336	 65% 18% • 14%
1	B	336	 64% 19% • 14%

2 Entry composition [i](#)

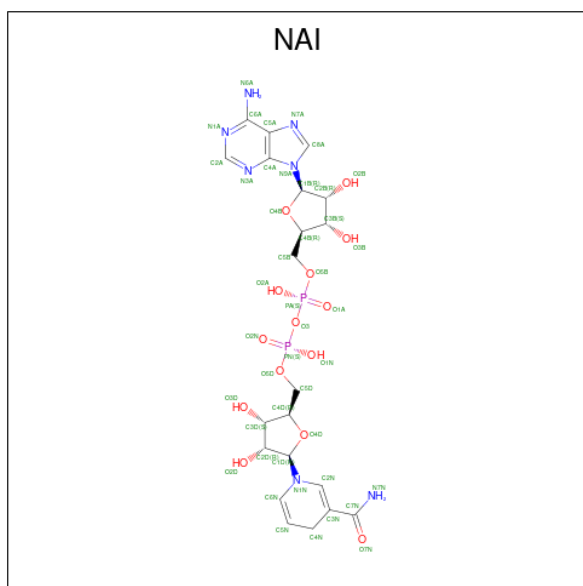
There are 2 unique types of molecules in this entry. The entry contains 4662 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ENOYL-ACYL CARRIER REDUCTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	0	0
			2287	1458	384	434	11			
1	B	289	Total	C	N	O	S	0	0	0
			2287	1458	384	434	11			

- Molecule 2 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: NAI) (formula: C₂₁H₂₉N₇O₁₄P₂).



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	133.28Å 133.28Å 83.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40	Depositor
% Data completeness (in resolution range)	(Not available) (30.00-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.176 , 0.224	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4662	wwPDB-VP
Average B, all atoms (Å ²)	31.0	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: NAI

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	0.39	0/2329	0.85	2/3141 (0.1%)
1	B	0.40	0/2329	0.86	6/3141 (0.2%)
All	All	0.40	0/4658	0.85	8/6282 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	132	PRO	N-CA-C	6.24	118.32	110.70
1	A	132	PRO	N-CA-C	6.21	118.28	110.70
1	B	273	VAL	N-CA-C	5.99	116.80	108.89
1	B	391	ILE	N-CA-C	-5.86	104.80	110.72
1	B	130	ILE	N-CA-C	5.33	115.98	108.36
1	B	126	ILE	N-CA-C	5.33	115.63	108.17
1	A	379	TYR	N-CA-C	5.32	119.92	113.38
1	B	369	ILE	N-CA-C	5.31	116.67	110.62

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	2287	0	2297	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2287	0	2297	61	0
2	A	44	0	27	0	0
2	B	44	0	27	0	0
All	All	4662	0	4648	110	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 12.

All (110) 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:153:ILE:HB	1:B:157:LYS:HB2	1.60	0.80
1:A:379:TYR:OH	1:A:425:ASP:HB3	1.85	0.77
1:A:138:PHE:HE2	1:A:164:MET:HE3	1.53	0.74
1:A:138:PHE:CE2	1:A:164:MET:HE3	2.23	0.73
1:A:149:ASN:O	1:A:152:ILE:HG12	1.89	0.72
1:A:174:ALA:O	1:A:177:ILE:HG22	1.90	0.71
1:B:183:ASN:HA	1:B:188:ASN:HD21	1.55	0.71
1:A:276:GLY:HA2	1:A:325:LYS:HG2	1.71	0.71
1:B:138:PHE:HE2	1:B:164:MET:HE3	1.56	0.70
1:B:138:PHE:CE2	1:B:164:MET:HE3	2.32	0.64
1:A:252:PHE:O	1:A:256:MET:HG3	1.97	0.64
1:B:184:ASN:ND2	1:B:186:ARG:H	1.96	0.64
1:B:119:LEU:O	1:B:124:VAL:HG13	1.97	0.64
1:B:155:LYS:HD3	1:B:157:LYS:NZ	2.13	0.63
1:A:324:ASN:ND2	1:A:367:THR:HG22	2.14	0.62
1:A:184:ASN:HD22	1:A:187:TYR:HD1	1.46	0.62
1:A:379:TYR:C	1:B:301:ARG:HH21	2.08	0.62
1:B:320:ALA:HB1	1:B:369:ILE:HD13	1.82	0.61
1:A:318:ARG:HH11	1:A:318:ARG:HG2	1.65	0.61
1:B:125:LYS:N	1:B:125:LYS:HD2	2.16	0.61
1:A:407:THR:HG21	1:B:382:LEU:CD2	2.31	0.61
1:A:132:PRO:HB2	1:A:133:PRO:HD3	1.83	0.61
1:B:99:ILE:HD13	1:B:125:LYS:HB2	1.83	0.60
1:A:276:GLY:HA2	1:A:325:LYS:CG	2.31	0.60
1:A:139:MET:SD	1:A:164:MET:HE2	2.41	0.59
1:B:276:GLY:HA2	1:B:325:LYS:HD3	1.85	0.58
1:A:120:SER:HB3	1:A:153:ILE:HD11	1.86	0.58
1:B:252:PHE:O	1:B:256:MET:HG3	2.03	0.58
1:B:318:ARG:HH11	1:B:318:ARG:HG2	1.70	0.57
1:A:154:ASP:C	1:A:156:ASP:H	2.12	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:ASP:HA	1:B:151:MET:HE3	1.87	0.56
1:B:154:ASP:C	1:B:156:ASP:H	2.16	0.54
1:B:183:ASN:C	1:B:188:ASN:HD21	2.17	0.53
1:B:183:ASN:CA	1:B:188:ASN:HD21	2.19	0.53
1:A:324:ASN:HD22	1:A:367:THR:HG22	1.74	0.52
1:A:416:GLY:O	1:A:419:ILE:HG12	2.09	0.52
1:B:323:ILE:O	1:B:323:ILE:HG22	2.10	0.52
1:B:366:TYR:CD2	1:B:366:TYR:N	2.77	0.52
1:B:416:GLY:O	1:B:419:ILE:HG12	2.09	0.52
1:A:390:ASP:OD1	1:B:404:ARG:HD3	2.09	0.52
1:B:177:ILE:HD11	1:B:182:LYS:CB	2.39	0.52
1:A:99:ILE:HD13	1:A:125:LYS:HB2	1.91	0.51
1:A:379:TYR:HA	1:B:301:ARG:NH2	2.26	0.51
1:B:274:VAL:O	1:B:274:VAL:CG2	2.59	0.51
1:A:301:ARG:HH21	1:B:379:TYR:C	2.19	0.50
1:A:377:GLU:O	1:A:383:ARG:HG3	2.12	0.50
1:A:383:ARG:HE	1:B:301:ARG:HD2	1.77	0.50
1:A:167:PHE:HD1	1:A:198:VAL:HG11	1.77	0.50
1:B:274:VAL:O	1:B:274:VAL:HG23	2.12	0.50
1:B:177:ILE:HD11	1:B:182:LYS:HA	1.94	0.49
1:A:366:TYR:CD2	1:A:366:TYR:N	2.80	0.49
1:B:153:ILE:O	1:B:154:ASP:C	2.54	0.49
1:A:320:ALA:HB1	1:A:369:ILE:HD13	1.94	0.49
1:B:183:ASN:HA	1:B:188:ASN:ND2	2.24	0.49
1:B:177:ILE:HD12	1:B:193:TYR:OH	2.13	0.49
1:A:177:ILE:HD12	1:A:193:TYR:OH	2.13	0.48
1:B:366:TYR:N	1:B:366:TYR:HD2	2.12	0.48
1:A:105:ILE:HD12	1:A:128:PHE:CD1	2.48	0.48
1:B:147:PHE:O	1:B:151:MET:HG3	2.13	0.48
1:B:155:LYS:HD3	1:B:157:LYS:HZ1	1.79	0.47
1:A:154:ASP:O	1:A:156:ASP:N	2.48	0.47
1:B:383:ARG:HG2	1:B:383:ARG:HH11	1.78	0.47
1:A:404:ARG:HD3	1:B:390:ASP:OD1	2.14	0.47
1:B:174:ALA:O	1:B:177:ILE:HG23	2.13	0.47
1:A:383:ARG:HE	1:B:301:ARG:CD	2.27	0.47
1:A:366:TYR:O	1:A:370:ASP:HB2	2.14	0.47
1:B:139:MET:SD	1:B:164:MET:HE2	2.54	0.46
1:B:377:GLU:O	1:B:383:ARG:HG3	2.16	0.46
1:B:377:GLU:OE1	1:B:385:LYS:HG2	2.16	0.46
1:A:119:LEU:HB3	1:A:124:VAL:HG22	1.98	0.46
1:A:120:SER:HB3	1:A:153:ILE:CD1	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:LEU:HD23	1:A:284:ALA:HA	1.98	0.45
1:B:137:ILE:HG23	1:B:138:PHE:N	2.30	0.45
1:A:156:ASP:OD1	1:A:156:ASP:O	2.34	0.45
1:B:170:SER:HB3	1:B:240:LYS:HE2	1.98	0.45
1:B:177:ILE:HD11	1:B:182:LYS:CA	2.46	0.45
1:A:128:PHE:HB3	1:A:130:ILE:HD11	1.99	0.45
1:A:195:ILE:O	1:A:198:VAL:HG22	2.16	0.45
1:B:153:ILE:O	1:B:155:LYS:N	2.50	0.45
1:B:158:LYS:O	1:B:159:MET:C	2.59	0.45
1:B:212:LEU:HB3	1:B:262:ILE:HG12	2.00	0.44
1:A:177:ILE:HG23	1:A:177:ILE:O	2.18	0.44
1:B:171:PHE:CE1	1:B:177:ILE:HA	2.53	0.44
1:B:131:TRP:CD1	1:B:132:PRO:HD2	2.53	0.43
1:A:203:HIS:HB2	1:A:255:ILE:HG21	2.01	0.43
1:B:103:ALA:HB1	1:B:167:PHE:CE2	2.53	0.43
1:B:154:ASP:O	1:B:156:ASP:N	2.40	0.43
1:A:263:ILE:HA	1:A:308:ASN:O	2.19	0.43
1:A:383:ARG:HG2	1:A:383:ARG:NH1	2.34	0.43
1:B:145:GLY:HA2	1:B:148:ASP:OD1	2.19	0.43
1:A:301:ARG:NH2	1:B:379:TYR:HA	2.34	0.43
1:A:318:ARG:HG2	1:A:318:ARG:NH1	2.33	0.43
1:A:154:ASP:C	1:A:156:ASP:N	2.77	0.43
1:A:226:LEU:HD23	1:A:226:LEU:HA	1.88	0.42
1:A:119:LEU:O	1:A:124:VAL:HG13	2.20	0.42
1:B:177:ILE:HD11	1:B:182:LYS:HB2	2.01	0.42
1:A:119:LEU:HB3	1:A:124:VAL:CG2	2.49	0.42
1:A:118:GLU:HG3	1:A:393:SER:N	2.34	0.41
1:A:323:ILE:O	1:A:324:ASN:C	2.62	0.41
1:A:366:TYR:N	1:A:366:TYR:HD2	2.17	0.41
1:B:131:TRP:CG	1:B:133:PRO:HD2	2.55	0.41
1:A:136:ASN:HD21	1:A:189:MET:CE	2.33	0.41
1:A:274:VAL:O	1:A:274:VAL:CG2	2.67	0.41
1:B:118:GLU:HG3	1:B:393:SER:N	2.35	0.41
1:B:366:TYR:O	1:B:367:THR:O	2.38	0.41
1:A:145:GLY:HA2	1:A:148:ASP:OD1	2.21	0.41
1:A:159:MET:HE2	1:A:161:ILE:HD11	2.02	0.41
1:B:223:GLN:HE21	1:B:324:ASN:HB3	1.86	0.41
1:B:262:ILE:O	1:B:307:ILE:HA	2.20	0.41
1:A:274:VAL:O	1:A:274:VAL:HG22	2.22	0.40

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	285/336 (85%)	267 (94%)	15 (5%)	3 (1%)	11	18
1	B	285/336 (85%)	265 (93%)	15 (5%)	5 (2%)	6	9
All	All	570/672 (85%)	532 (93%)	30 (5%)	8 (1%)	9	13

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	324	ASN
1	B	154	ASP
1	B	367	THR
1	A	155	LYS
1	B	155	LYS
1	B	424	ASP
1	A	367	THR
1	B	323	ILE

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	250/295 (85%)	239 (96%)	11 (4%)	25	43
1	B	250/295 (85%)	240 (96%)	10 (4%)	28	47
All	All	500/590 (85%)	479 (96%)	21 (4%)	26	45

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	124	VAL
1	A	162	LEU
1	A	201	LEU
1	A	226	LEU
1	A	227	LEU
1	A	273	VAL
1	A	274	VAL
1	A	304	ASN
1	A	366	TYR
1	A	383	ARG
1	A	417	LEU
1	B	124	VAL
1	B	162	LEU
1	B	177	ILE
1	B	179	GLU
1	B	226	LEU
1	B	227	LEU
1	B	260	SER
1	B	273	VAL
1	B	366	TYR
1	B	417	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	136	ASN
1	A	183	ASN
1	A	184	ASN
1	A	188	ASN
1	A	200	ASN
1	A	203	HIS
1	A	228	ASN
1	A	254	ASN
1	A	384	GLN
1	B	184	ASN
1	B	188	ASN
1	B	192	ASN
1	B	200	ASN
1	B	223	GLN
1	B	254	ASN
1	B	259	GLN
1	B	302	ASN
1	B	384	GLN

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands 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
2	NAI	A	501	-	47,48,48	2.21	6 (12%)	64,73,73	1.96	13 (20%)
2	NAI	B	501	-	47,48,48	2.02	6 (12%)	64,73,73	1.89	12 (18%)

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
2	NAI	A	501	-	-	4/29/72/72	0/5/5/5
2	NAI	B	501	-	-	5/29/72/72	0/5/5/5

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	NAI	PN-O3	-9.43	1.49	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	NAI	PN-O3	-7.74	1.51	1.59
2	A	501	NAI	PA-O3	-6.50	1.52	1.59
2	B	501	NAI	PA-O3	-5.81	1.53	1.59
2	B	501	NAI	C4N-C3N	-5.52	1.39	1.50
2	A	501	NAI	C4N-C3N	-5.30	1.40	1.50
2	A	501	NAI	O7N-C7N	4.32	1.34	1.24
2	B	501	NAI	O7N-C7N	4.22	1.34	1.24
2	A	501	NAI	C6N-C5N	4.00	1.45	1.33
2	B	501	NAI	C6N-C5N	3.98	1.45	1.33
2	B	501	NAI	C4A-N3A	2.45	1.39	1.34
2	A	501	NAI	C4A-N3A	2.09	1.38	1.34

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	NAI	C1B-N9A-C8A	7.32	143.34	127.09
2	B	501	NAI	C1B-N9A-C8A	7.09	142.84	127.09
2	A	501	NAI	C4A-N9A-C1B	-5.72	113.25	126.63
2	B	501	NAI	C4A-N9A-C1B	-5.65	113.42	126.63
2	A	501	NAI	O7N-C7N-N7N	-5.00	111.68	122.89
2	B	501	NAI	O7N-C7N-N7N	-4.67	112.42	122.89
2	A	501	NAI	O2A-PA-O3	-4.26	95.76	107.27
2	B	501	NAI	O2A-PA-O3	-3.96	96.57	107.27
2	A	501	NAI	C3N-C7N-N7N	3.87	124.54	117.67
2	B	501	NAI	C3N-C7N-N7N	3.59	124.05	117.67
2	B	501	NAI	O3-PA-O1A	3.48	121.17	110.70
2	A	501	NAI	C3N-C2N-N1N	3.39	128.19	123.20
2	A	501	NAI	O3-PA-O1A	3.38	120.89	110.70
2	B	501	NAI	C3N-C2N-N1N	3.23	127.95	123.20
2	A	501	NAI	O5D-PN-O2N	-2.67	98.37	108.94
2	B	501	NAI	O5D-PN-O2N	-2.66	98.40	108.94
2	B	501	NAI	O1N-PN-O3	2.53	114.12	107.27
2	A	501	NAI	O1N-PN-O3	2.45	113.89	107.27
2	A	501	NAI	C4D-O4D-C1D	-2.24	104.51	109.47
2	A	501	NAI	C4A-N9A-C8A	-2.22	103.41	105.74
2	A	501	NAI	O3-PN-O2N	-2.20	104.09	110.70
2	B	501	NAI	C4D-O4D-C1D	-2.11	104.82	109.47
2	A	501	NAI	O1N-PN-O5D	2.09	117.02	107.57
2	B	501	NAI	O1N-PN-O5D	2.04	116.81	107.57
2	B	501	NAI	O3B-C3B-C4B	-2.01	105.31	111.08

There are no chirality outliers.

All (9) torsion outliers are listed below:

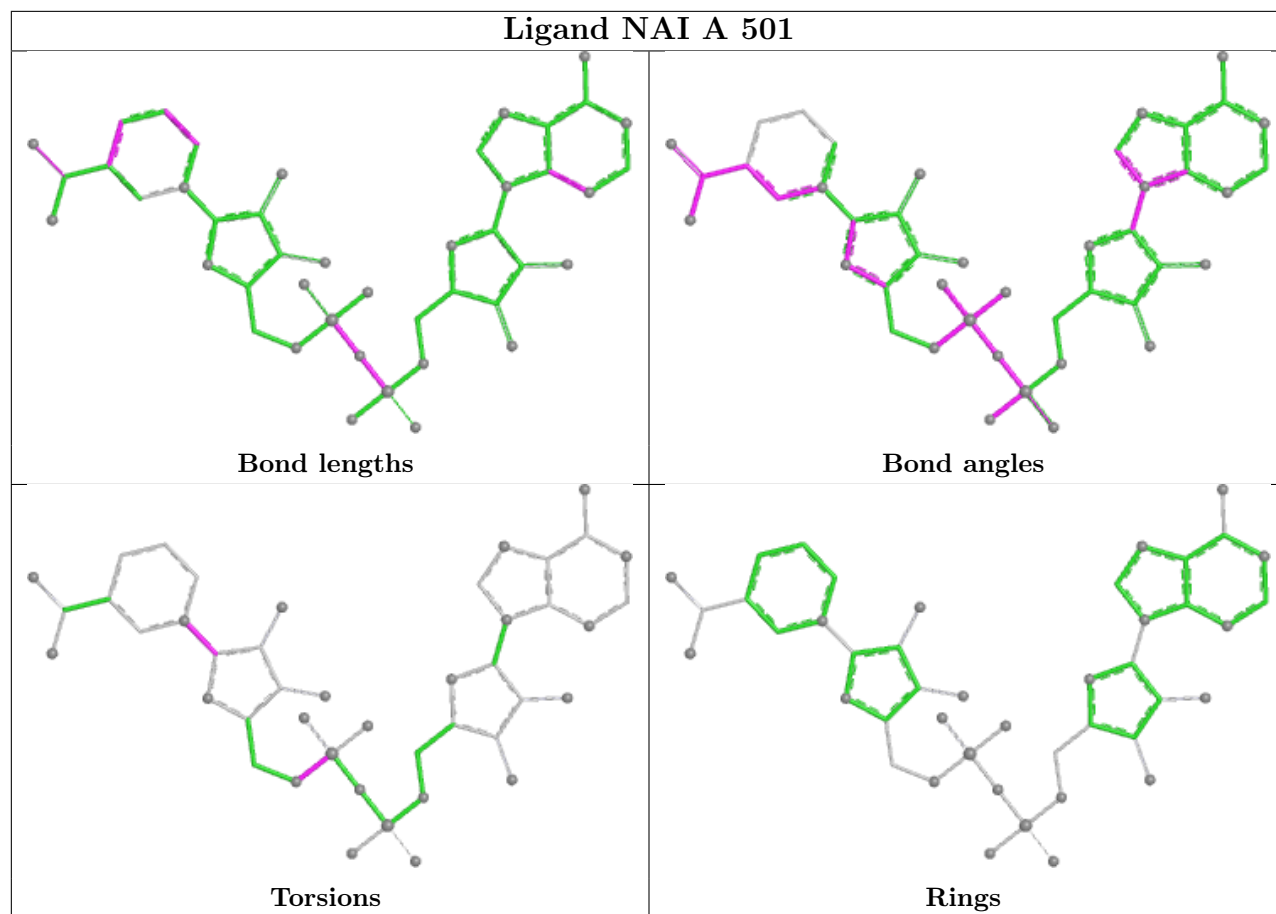
Mol	Chain	Res	Type	Atoms
2	A	501	NAI	C5D-O5D-PN-O3
2	A	501	NAI	C5D-O5D-PN-O1N
2	B	501	NAI	C5D-O5D-PN-O3
2	B	501	NAI	C5D-O5D-PN-O1N
2	A	501	NAI	C5D-O5D-PN-O2N
2	B	501	NAI	C5D-O5D-PN-O2N
2	A	501	NAI	O4D-C1D-N1N-C6N
2	B	501	NAI	O4D-C1D-N1N-C6N
2	B	501	NAI	C2D-C1D-N1N-C6N

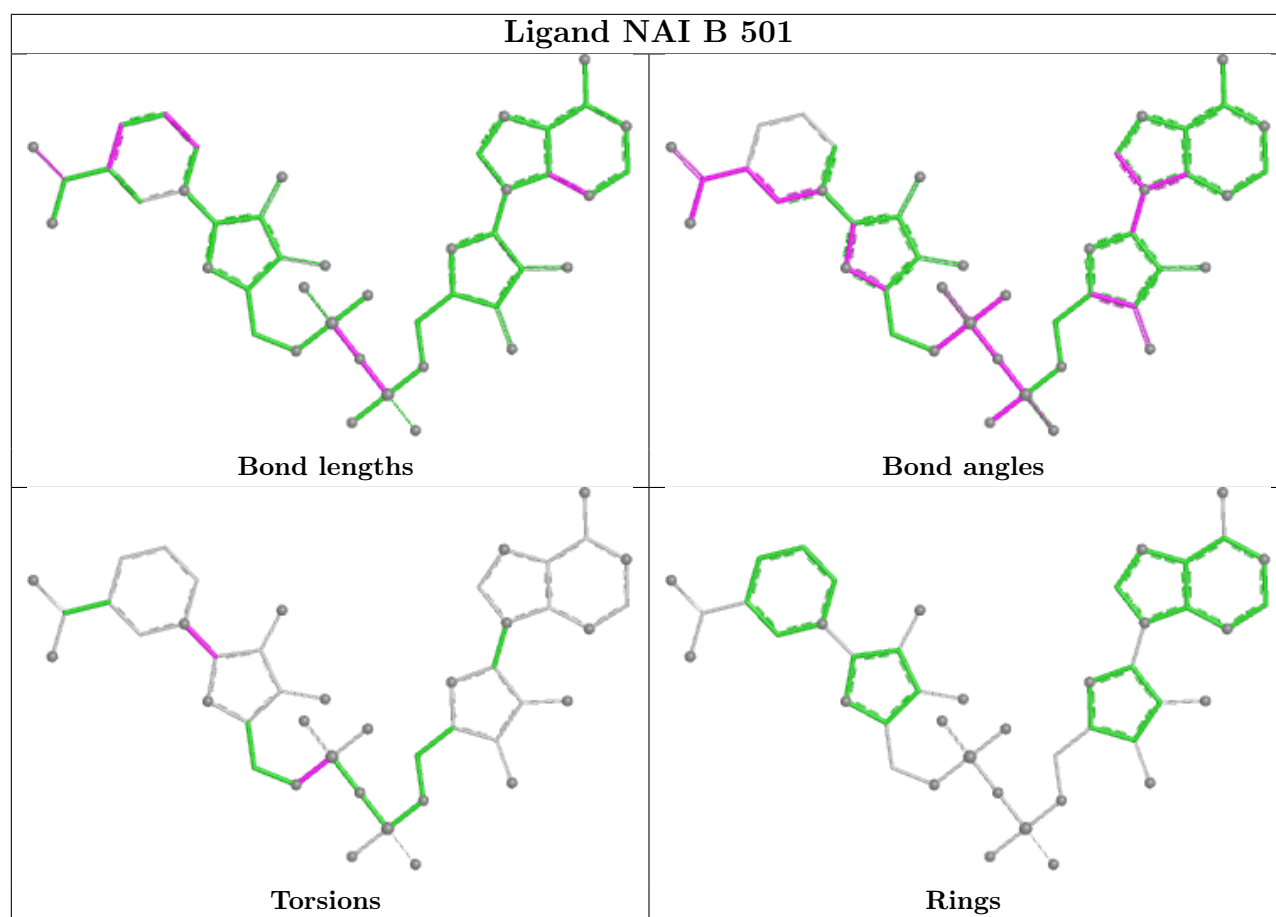
There are no ring outliers.

No monomer is involved in short contacts.

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.

Ligand NAI A 501





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.