



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:26 PM UTC

PDB ID : 1AOE / pdb_00001aoe
Title : CANDIDA ALBICANS DIHYDROFOLATE REDUCTASE COMPLEXED
WITH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOS-
PHATE (NADPH) AND 1,3-DIAMINO-7-(1-ETHYEPROPYE)-7H-PYRRA
LO-[3,2-F]QUINAZOLINE (GW345)
Authors : Whitlow, M.; Howard, A.J.; Stewart, D.
Deposited on : 1997-07-02
Resolution : 1.60 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

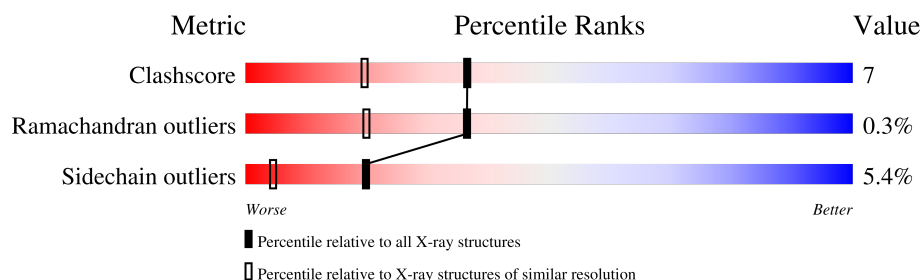
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)

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	192	 65% 28% 6%
1	B	192	 73% 19% 8%

2 Entry composition ⓘ

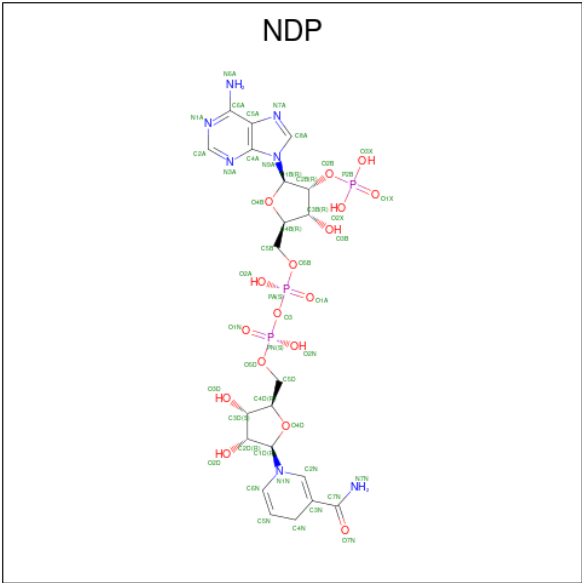
There are 4 unique types of molecules in this entry. The entry contains 3662 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DIHYDROFOLATE REDUCTASE.

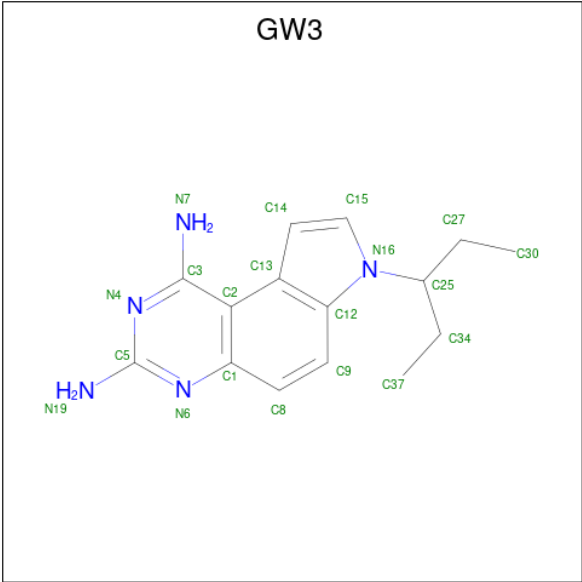
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	192	1594	1023	271	296	4	0	12	0
			Total	C	N	O	S			
1	B	192	1588	1020	264	300	4	0	10	0
			Total	C	N	O	S			

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	48	21	7	17	3	0	0
			Total	C	N	O	P		
2	B	1	48	21	7	17	3	0	0
			Total	C	N	O	P		

- Molecule 3 is 7-(1-ETHYL-PROPYL)-7H-PYRROLO-[3,2-F]QUINAZOLINE-1,3-DIAMIN E (CCD ID: GW3) (formula: C₁₅H₁₉N₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			20	15	5		
3	B	1	Total	C	N	0	0
			20	15	5		

- Molecule 4 is water.

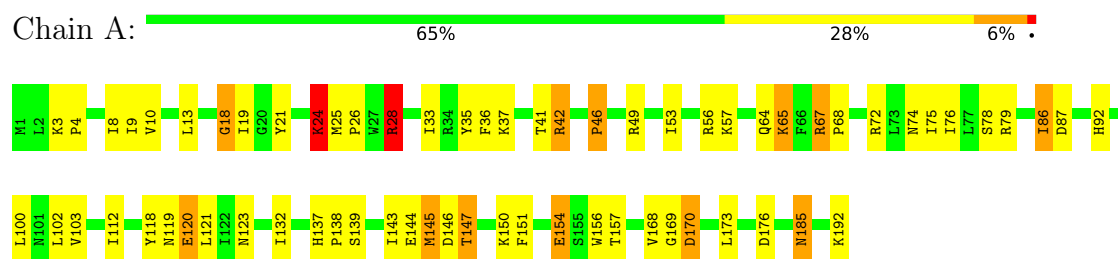
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	157	Total	O	0	7
			164	164		
4	B	176	Total	O	0	4
			180	180		

3 Residue-property plots

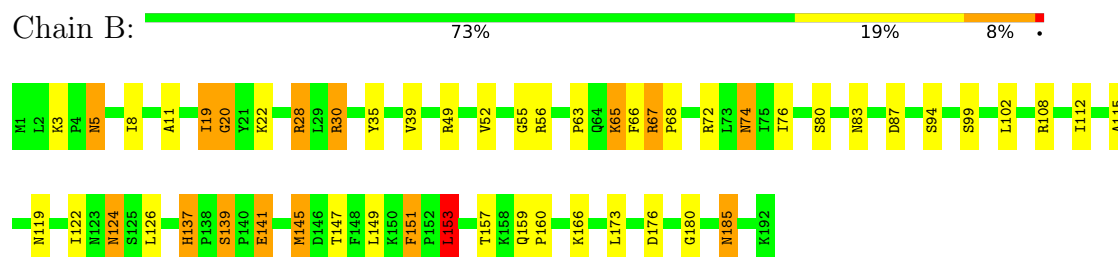
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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



• Molecule 1: DIHYDROFOLATE REDUCTASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	77.91Å 67.28Å 38.49Å 90.00° 93.07° 90.00°	Depositor
Resolution (Å)	10.00 – 1.60	Depositor
% Data completeness (in resolution range)	91.7 (10.00-1.60)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	PROFFT	Depositor
R, R_{free}	0.155 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3662	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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: NDP, GW3

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	1.44	9/1690 (0.5%)	1.83	45/2290 (2.0%)
1	B	1.47	7/1675 (0.4%)	1.82	33/2267 (1.5%)
All	All	1.46	16/3365 (0.5%)	1.82	78/4557 (1.7%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	36	PHE	N-CA	6.21	1.53	1.46
1	B	11	ALA	N-CA	5.75	1.53	1.46
1	B	145	MET	CA-CB	-5.72	1.43	1.53
1	B	180	GLY	N-CA	5.64	1.53	1.45
1	A	3	LYS	CA-CB	5.63	1.57	1.52
1	A	92	HIS	N-CA	5.62	1.52	1.46
1	A	9	ILE	N-CA	5.60	1.52	1.46
1	B	76	ILE	N-CA	5.56	1.52	1.46
1	A	156	TRP	N-CA	5.30	1.52	1.45
1	A	3	LYS	C-O	5.25	1.26	1.23
1	A	78	SER	CA-C	5.23	1.59	1.52
1	B	102	LEU	CA-CB	5.20	1.60	1.53
1	A	157	THR	CA-C	5.19	1.58	1.52
1	A	132	ILE	CA-CB	5.16	1.60	1.54
1	B	99	SER	N-CA	5.16	1.52	1.46
1	B	108	ARG	CA-C	5.14	1.58	1.52

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	28	ARG	CD-NE-CZ	13.00	142.60	124.40
1	B	151	PHE	CA-CB-CG	10.56	124.36	113.80
1	B	56	ARG	CD-NE-CZ	10.06	138.48	124.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	137	HIS	O-C-N	8.67	127.92	121.85
1	B	49	ARG	O-C-N	7.86	132.14	123.10
1	A	112	ILE	N-CA-C	7.74	119.52	112.17
1	B	153	LEU	CB-CA-C	7.54	125.10	110.46
1	A	154	GLU	CA-CB-CG	7.33	128.77	114.10
1	A	56	ARG	CD-NE-CZ	7.11	134.35	124.40
1	B	185	ASN	O-C-N	7.06	131.46	123.27
1	A	49	ARG	NE-CZ-NH2	-6.98	112.92	119.20
1	B	67	ARG	CD-NE-CZ	6.89	134.05	124.40
1	A	146	ASP	CA-CB-CG	6.76	119.36	112.60
1	A	154	GLU	CB-CG-CD	6.69	123.97	112.60
1	B	72	ARG	O-C-N	6.61	130.94	123.27
1	B	8	ILE	O-C-N	6.52	129.84	122.93
1	B	67	ARG	CB-CA-C	6.51	118.68	108.84
1	A	144	GLU	CB-CG-CD	6.51	123.66	112.60
1	A	185	ASN	OD1-CG-ND2	6.31	128.91	122.60
1	B	141[A]	GLU	CB-CG-CD	6.29	123.29	112.60
1	B	141[B]	GLU	CB-CG-CD	6.29	123.29	112.60
1	B	74	ASN	CA-CB-CG	6.12	118.72	112.60
1	B	19	ILE	N-CA-C	6.05	119.01	113.20
1	B	30	ARG	CD-NE-CZ	5.98	132.77	124.40
1	B	119	ASN	CB-CA-C	5.92	122.03	110.67
1	A	120	GLU	CA-CB-CG	5.83	125.77	114.10
1	B	52	VAL	O-C-N	5.80	129.53	123.26
1	A	24	LYS	CG-CD-CE	5.80	124.63	111.30
1	A	123	ASN	OD1-CG-ND2	5.79	128.39	122.60
1	A	151	PHE	CA-CB-CG	5.79	119.59	113.80
1	B	49	ARG	CA-C-O	-5.78	115.26	121.45
1	B	55	GLY	N-CA-C	-5.78	104.85	112.82
1	A	67	ARG	CB-CA-C	5.76	117.55	108.84
1	A	169	GLY	CA-C-N	5.73	128.54	120.28
1	A	169	GLY	C-N-CA	5.73	128.54	120.28
1	B	108	ARG	O-C-N	5.71	130.77	123.11
1	A	139	SER	N-CA-CB	-5.70	103.38	110.79
1	A	10	VAL	O-C-N	5.65	128.55	122.67
1	B	87	ASP	CA-CB-CG	5.63	118.23	112.60
1	B	39	VAL	O-C-N	5.58	127.58	121.83
1	A	3	LYS	CB-CA-C	-5.57	107.25	111.20
1	B	3	LYS	O-C-N	5.53	126.56	121.80
1	A	3	LYS	CA-C-O	5.51	124.67	120.26
1	A	78	SER	O-C-N	5.51	129.86	123.41
1	A	8	ILE	CA-C-N	-5.50	115.34	122.99

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	8	ILE	C-N-CA	-5.50	115.34	122.99
1	B	157	THR	O-C-N	5.46	129.80	123.30
1	A	46	PRO	N-CA-C	5.45	123.70	112.47
1	A	147	THR	CA-CB-CG2	5.45	119.76	110.50
1	A	170	ASP	N-CA-C	5.44	117.97	111.71
1	A	42[A]	ARG	CA-CB-CG	5.42	124.95	114.10
1	A	42[B]	ARG	CA-CB-CG	5.42	124.95	114.10
1	A	72	ARG	O-C-N	5.41	129.89	123.24
1	B	145	MET	CA-CB-CG	5.39	124.89	114.10
1	B	22	LYS	CB-CG-CD	5.38	123.68	111.30
1	A	35	TYR	O-C-N	5.37	127.59	122.07
1	A	56	ARG	NE-CZ-NH2	5.36	124.03	119.20
1	B	35	TYR	O-C-N	5.35	127.58	122.07
1	A	185	ASN	O-C-N	5.34	129.47	123.27
1	B	145	MET	CB-CG-SD	-5.34	96.67	112.70
1	A	18	GLY	CA-C-O	-5.32	116.74	121.64
1	A	24	LYS	CA-CB-CG	5.31	124.72	114.10
1	A	86	ILE	CB-CG1-CD1	5.30	124.92	113.80
1	A	37	LYS	CG-CD-CE	5.27	123.42	111.30
1	A	118	TYR	O-C-N	5.27	127.50	122.07
1	A	132	ILE	O-C-N	5.26	129.26	123.10
1	A	121[A]	LEU	N-CA-C	5.23	118.93	112.54
1	A	121[B]	LEU	N-CA-C	5.23	118.93	112.54
1	B	112	ILE	N-CA-C	5.23	117.14	112.17
1	A	192	LYS	CA-CB-CG	5.19	124.48	114.10
1	A	157	THR	O-C-N	5.18	129.47	123.30
1	B	139	SER	O-C-N	5.13	125.12	121.12
1	A	87	ASP	CA-CB-CG	5.13	117.73	112.60
1	A	72	ARG	NE-CZ-NH1	5.12	126.62	121.50
1	B	145	MET	N-CA-C	5.08	116.97	108.99
1	B	20	GLY	O-C-N	5.07	128.48	123.76
1	A	76	ILE	O-C-N	5.04	128.70	123.26
1	B	122	ILE	O-C-N	5.03	126.95	121.87

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	1594	0	1620	26	0
1	B	1588	0	1613	21	0
2	A	48	0	26	1	0
2	B	48	0	26	0	0
3	A	20	0	19	1	0
3	B	20	0	19	1	0
4	A	164	0	0	3	0
4	B	180	0	0	2	0
All	All	3662	0	3323	48	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 7.

All (48) 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:28:ARG:HH21	1:B:30:ARG:HG2	1.49	0.76
1:A:176:ASP:H	1:A:185:ASN:HD21	1.34	0.73
1:B:124:ASN:HD22	1:B:126:LEU:H	1.36	0.72
1:A:64:GLN:HG2	1:A:65:LYS:HE3	1.71	0.70
1:A:28:ARG:HH11	1:A:28:ARG:HB3	1.57	0.68
1:A:79[A]:ARG:NH1	4:A:492:HOH:O	2.04	0.68
1:B:137:HIS:HD2	1:B:139:SER:H	1.43	0.67
1:B:176:ASP:H	1:B:185:ASN:HD21	1.43	0.66
1:A:119:ASN:HB3	1:A:150:LYS:HE2	1.81	0.63
1:A:18:GLY:HA3	1:A:145:MET:HE3	1.80	0.63
1:B:83:ASN:ND2	1:B:94:SER:H	1.99	0.61
1:B:176:ASP:H	1:B:185:ASN:ND2	1.99	0.60
1:A:65:LYS:HD2	1:A:65:LYS:H	1.68	0.59
1:A:13:LEU:HD23	1:A:145:MET:HE1	1.84	0.59
1:A:33[A]:ILE:HD13	3:A:194:GW3:H8	1.87	0.56
1:A:176:ASP:H	1:A:185:ASN:ND2	2.03	0.56
1:B:137:HIS:CD2	1:B:139:SER:H	2.23	0.53
1:B:20:GLY:O	1:B:145:MET:HB2	2.09	0.52
1:A:21:TYR:HB3	1:A:24:LYS:HE3	1.90	0.52
1:A:65:LYS:H	1:A:65:LYS:CD	2.23	0.52
1:A:28:ARG:HB3	1:A:28:ARG:NH1	2.26	0.50
1:B:115:ALA:HB2	1:B:147:THR:HG23	1.92	0.50
1:A:42[A]:ARG:HH11	1:A:170:ASP:HB2	1.77	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:63:PRO:HB2	1:B:66:PHE:HD2	1.77	0.50
1:A:41[B]:THR:HG21	4:A:446:HOH:O	2.13	0.48
3:B:194:GW3:H303	3:B:194:GW3:C15	2.43	0.48
1:A:67:ARG:HA	1:A:68:PRO:C	2.37	0.48
1:B:5:ASN:ND2	4:B:297:HOH:O	2.46	0.48
1:B:19:ILE:HG13	1:B:147:THR:HG22	1.95	0.47
1:B:83:ASN:HD21	1:B:94:SER:H	1.62	0.47
1:B:124:ASN:ND2	1:B:126:LEU:H	2.10	0.47
1:B:67:ARG:HA	1:B:68:PRO:C	2.39	0.46
1:A:168:VAL:HG21	1:A:173:LEU:HD21	1.98	0.45
1:A:57:LYS:NZ	2:A:193:NDP:O3B	2.49	0.45
1:A:137:HIS:CD2	1:A:143:ILE:HD11	2.52	0.45
1:B:149:LEU:HD22	1:B:151:PHE:CZ	2.52	0.45
1:A:19:ILE:HG13	1:A:147:THR:HG22	2.00	0.44
1:B:159:GLN:HB3	1:B:160:PRO:HD2	1.99	0.43
1:A:53[B]:ILE:HG22	1:A:75:ILE:HD12	2.00	0.43
1:A:25:MET:HA	1:A:26:PRO:HD3	1.79	0.42
1:A:42[A]:ARG:NH1	1:A:170:ASP:H	2.18	0.42
1:A:4:PRO:CG	1:A:100:LEU:HD13	2.50	0.41
1:B:151:PHE:HB2	1:B:153:LEU:HD13	2.03	0.41
1:B:115:ALA:HB2	1:B:147:THR:CG2	2.51	0.41
1:A:150:LYS:HG3	4:A:233:HOH:O	2.21	0.40
1:B:80:SER:HB2	4:B:337:HOH:O	2.21	0.40
1:A:137:HIS:CG	1:A:138:PRO:HD2	2.56	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	202/192 (105%)	198 (98%)	3 (2%)	1 (0%)	24 10

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	200/192 (104%)	197 (98%)	3 (2%)	0	100	100
All	All	402/384 (105%)	395 (98%)	6 (2%)	1 (0%)	36	24

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	46	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	186/177 (105%)	176 (95%)	10 (5%)	20	4
1	B	185/177 (104%)	173 (94%)	12 (6%)	15	3
All	All	371/354 (105%)	349 (94%)	22 (6%)	20	4

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

Mol	Chain	Res	Type
1	A	24	LYS
1	A	28	ARG
1	A	65	LYS
1	A	74	ASN
1	A	86	ILE
1	A	102	LEU
1	A	103	VAL
1	A	120	GLU
1	A	145	MET
1	A	154	GLU
1	B	5	ASN
1	B	28	ARG
1	B	65[A]	LYS
1	B	65[B]	LYS
1	B	74	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	124	ASN
1	B	141[A]	GLU
1	B	141[B]	GLU
1	B	153	LEU
1	B	166	LYS
1	B	173[A]	LEU
1	B	173[B]	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	A	185	ASN
1	B	5	ASN
1	B	83	ASN
1	B	101	ASN
1	B	124	ASN
1	B	137	HIS
1	B	185	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](#)

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](#)

4 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	NDP	A	193	-	51,52,52	1.74	7 (13%)	71,80,80	1.34	8 (11%)
2	NDP	B	193	-	51,52,52	1.62	9 (17%)	71,80,80	1.24	9 (12%)
3	GW3	A	194	-	22,22,22	3.18	8 (36%)	28,32,32	3.02	11 (39%)
3	GW3	B	194	-	22,22,22	3.23	5 (22%)	28,32,32	2.43	11 (39%)

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	NDP	A	193	-	-	1/34/77/77	0/5/5/5
2	NDP	B	193	-	-	1/34/77/77	0/5/5/5
3	GW3	A	194	-	-	0/8/8/8	0/3/3/3
3	GW3	B	194	-	-	2/8/8/8	0/3/3/3

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	194	GW3	C15-N16	-11.12	1.26	1.39
3	A	194	GW3	C15-N16	-10.76	1.26	1.39
3	A	194	GW3	C12-N16	-6.99	1.25	1.39
3	B	194	GW3	C1-N6	6.45	1.47	1.37
2	B	193	NDP	P2B-O2B	6.31	1.70	1.59
3	B	194	GW3	C12-N16	-6.20	1.27	1.39
2	A	193	NDP	P2B-O2B	6.13	1.70	1.59
2	A	193	NDP	PA-O3	-5.52	1.53	1.59
3	A	194	GW3	C1-N6	4.16	1.44	1.37
2	A	193	NDP	C7N-C3N	4.02	1.57	1.48
2	B	193	NDP	C7N-C3N	3.52	1.56	1.48
2	A	193	NDP	C4N-C3N	-3.46	1.43	1.50
2	B	193	NDP	C4N-C3N	-3.43	1.43	1.50
2	B	193	NDP	P2B-O2X	-2.89	1.44	1.54
3	A	194	GW3	C3-N4	-2.80	1.28	1.33
3	A	194	GW3	C25-N16	2.78	1.51	1.46
2	B	193	NDP	C4N-C5N	-2.70	1.42	1.49

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	193	NDP	C6N-N1N	2.64	1.43	1.37
2	A	193	NDP	P2B-O3X	-2.62	1.45	1.54
3	B	194	GW3	C3-N4	-2.56	1.29	1.33
2	B	193	NDP	C3B-C2B	2.48	1.58	1.53
3	A	194	GW3	C2-C1	-2.42	1.38	1.42
2	A	193	NDP	C2A-N1A	2.42	1.38	1.33
2	A	193	NDP	C3B-C2B	2.40	1.58	1.53
3	A	194	GW3	C13-C2	-2.28	1.40	1.44
2	B	193	NDP	PN-O2N	-2.13	1.45	1.55
3	A	194	GW3	C13-C12	2.06	1.43	1.41
2	B	193	NDP	PA-O2A	-2.05	1.45	1.55
3	B	194	GW3	C8-C9	2.03	1.41	1.36

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	194	GW3	C9-C12-C13	-7.89	115.96	122.35
3	A	194	GW3	C12-C13-C14	-7.09	101.25	106.93
3	A	194	GW3	N6-C5-N4	-6.27	119.24	127.21
3	B	194	GW3	C12-N16-C15	5.54	112.10	107.77
3	B	194	GW3	C12-C13-C14	-5.50	102.52	106.93
3	A	194	GW3	N19-C5-N4	4.57	124.07	117.22
3	B	194	GW3	N6-C5-N4	-4.54	121.44	127.21
2	A	193	NDP	C3N-C2N-N1N	-4.44	116.69	123.20
3	A	194	GW3	C12-N16-C15	3.99	110.89	107.77
2	A	193	NDP	O2B-P2B-O1X	-3.68	96.20	109.33
3	B	194	GW3	C3-C2-C1	3.63	117.45	114.90
3	B	194	GW3	C9-C12-C13	-3.55	119.47	122.35
3	A	194	GW3	C13-C12-N16	3.48	111.14	107.99
2	A	193	NDP	C1D-N1N-C2N	-3.43	115.49	121.14
2	B	193	NDP	C6N-N1N-C2N	3.28	122.83	119.32
3	A	194	GW3	C13-C14-C15	-3.24	104.30	107.04
2	B	193	NDP	O2N-PN-O3	3.20	115.93	107.27
3	A	194	GW3	C25-N16-C15	-3.07	120.73	125.07
3	B	194	GW3	C9-C8-C1	-3.06	117.14	120.80
2	B	193	NDP	O2B-P2B-O1X	-3.01	98.59	109.33
3	B	194	GW3	C13-C14-C15	-3.01	104.49	107.04
2	A	193	NDP	C6N-N1N-C2N	2.96	122.49	119.32
3	B	194	GW3	C13-C12-N16	2.78	110.50	107.99
3	A	194	GW3	C5-N4-C3	2.73	124.50	116.72
2	A	193	NDP	P2B-O2B-C2B	-2.68	116.27	123.43
3	B	194	GW3	C8-C1-C2	2.65	124.17	119.31

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	194	GW3	C14-C15-N16	2.62	112.34	110.31
2	A	193	NDP	O4D-C1D-C2D	-2.53	101.20	106.62
3	B	194	GW3	C2-C1-N6	-2.51	117.56	122.45
2	B	193	NDP	P2B-O2B-C2B	-2.49	116.78	123.43
2	B	193	NDP	O7N-C7N-C3N	-2.47	116.24	120.90
2	A	193	NDP	O2N-PN-O3	2.41	113.80	107.27
2	A	193	NDP	N6A-C6A-N1A	2.26	123.40	118.38
2	B	193	NDP	C3N-C2N-N1N	-2.22	119.94	123.20
2	B	193	NDP	O2X-P2B-O1X	2.14	119.19	110.83
2	B	193	NDP	C2B-C3B-C4B	-2.13	97.41	101.99
3	B	194	GW3	C5-N4-C3	2.03	122.52	116.72
2	B	193	NDP	C1D-N1N-C2N	-2.02	117.82	121.14
3	A	194	GW3	C9-C8-C1	-2.01	118.39	120.80

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	193	NDP	O4D-C1D-N1N-C2N
2	B	193	NDP	O4D-C1D-N1N-C2N
3	B	194	GW3	N16-C25-C27-C30
3	B	194	GW3	C34-C25-C27-C30

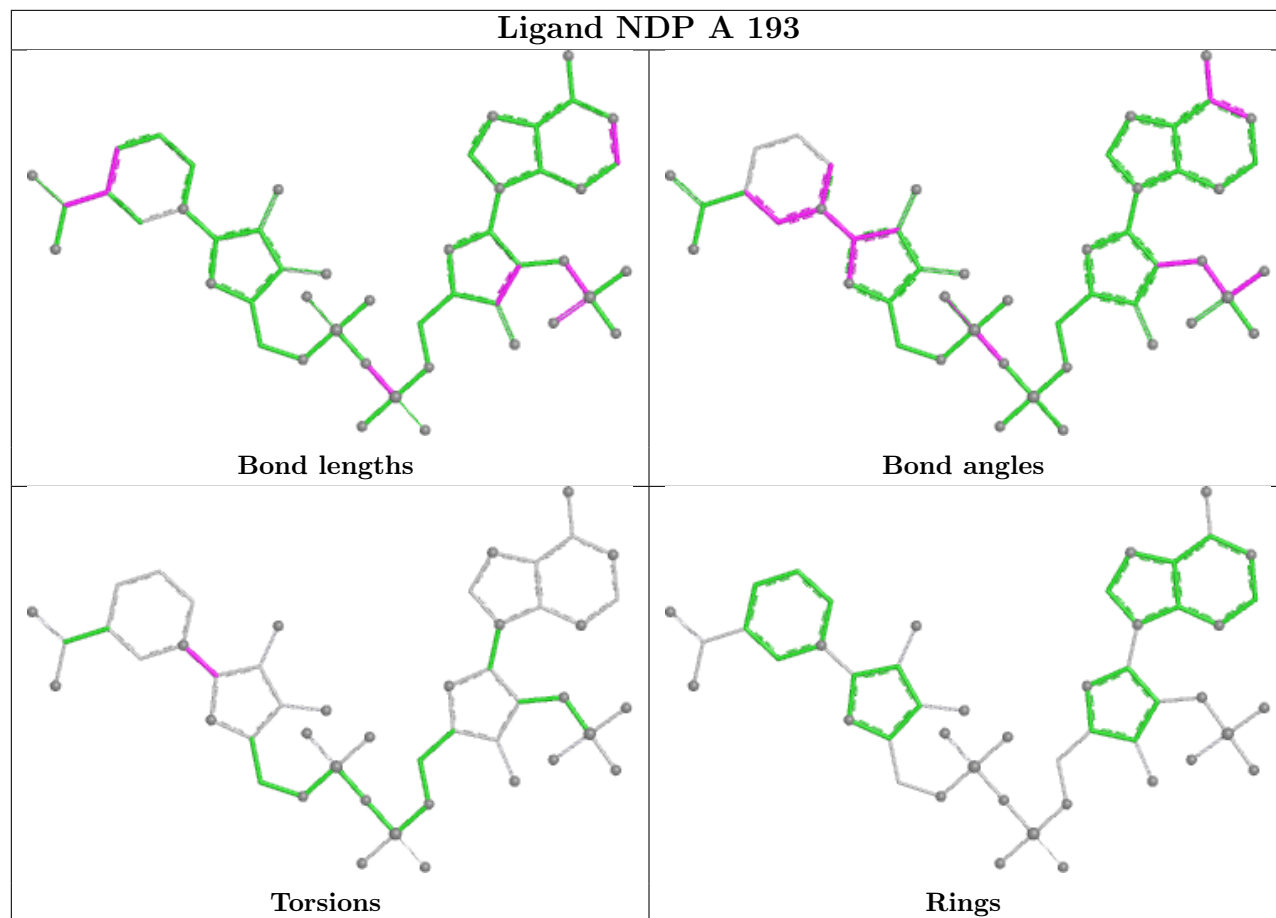
There are no ring outliers.

3 monomers are involved in 3 short contacts:

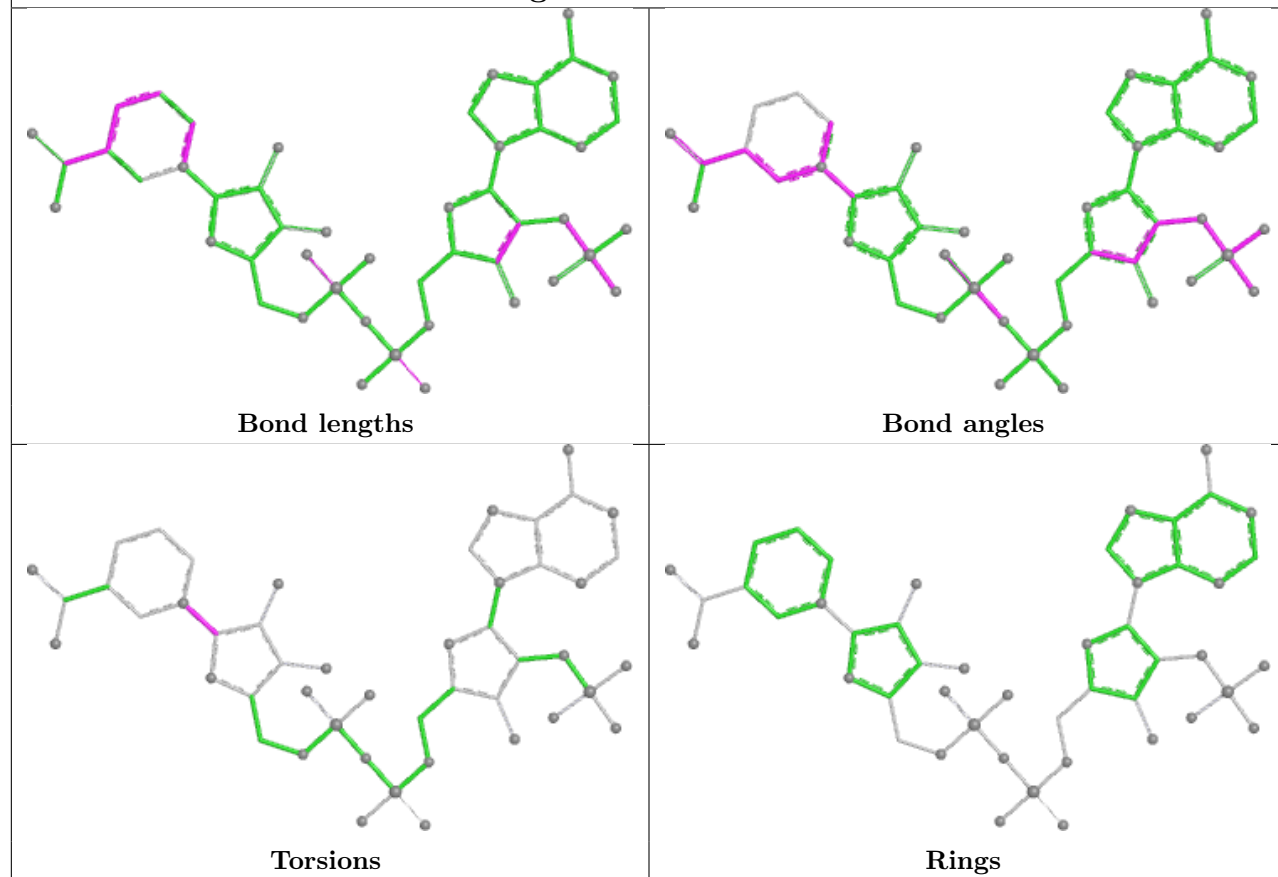
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	193	NDP	1	0
3	A	194	GW3	1	0
3	B	194	GW3	1	0

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

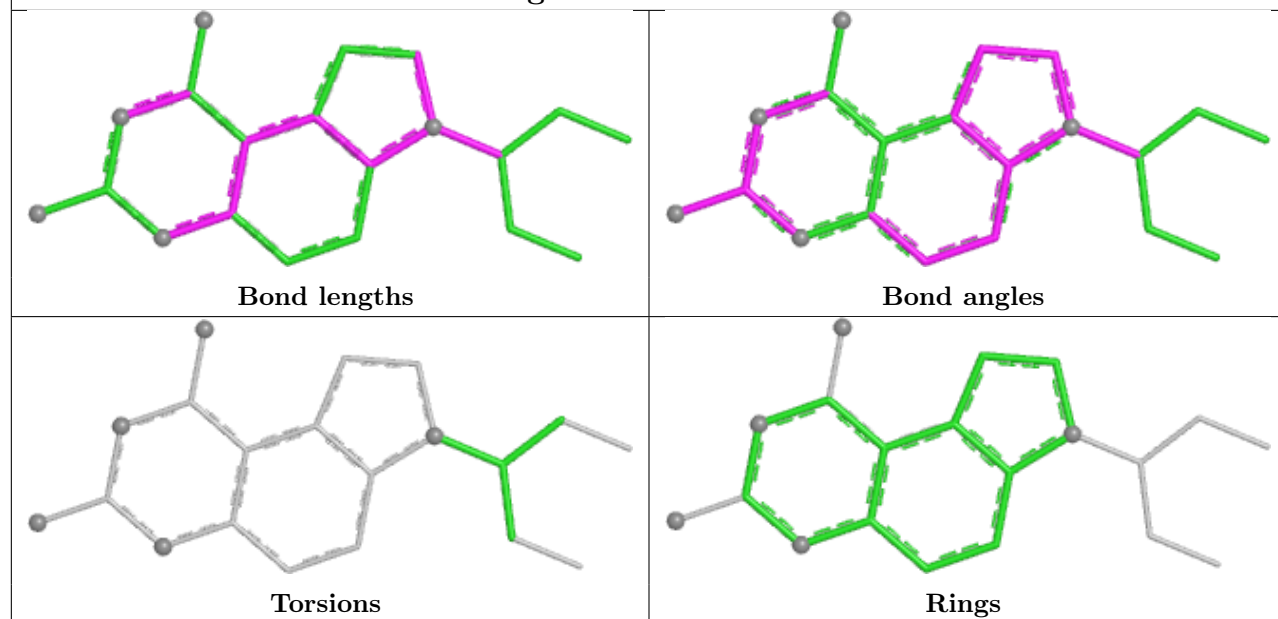
equivalents in the CSD to analyse the geometry.

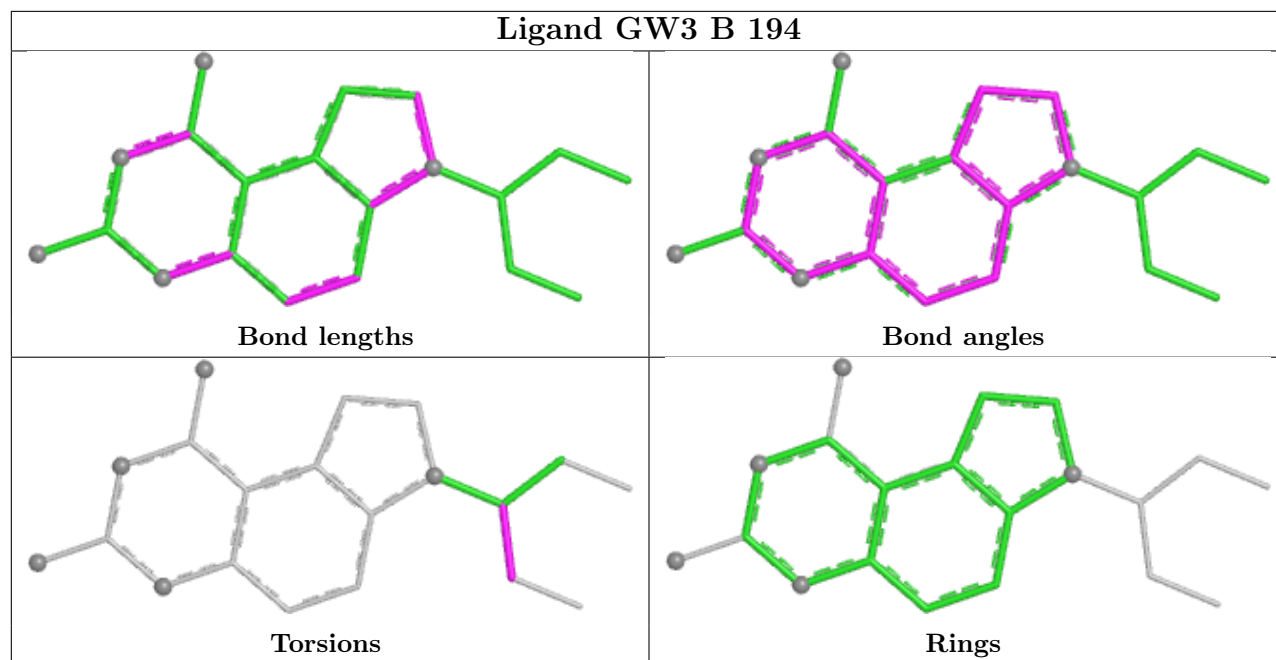


Ligand NDP B 193



Ligand GW3 A 194





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.