



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 05:23 am GMT

PDB ID : 1GEI
Title : STRUCTURAL CHARACTERIZATION OF N-BUTYL-ISOCYANIDE
COMPLEXES OF CYTOCHROMES P450NOR AND P450CAM
Authors : Lee, D.-S.; Park, S.-Y.; Yamane, K.; Shiro, Y.
Deposited on : 2000-11-13
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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

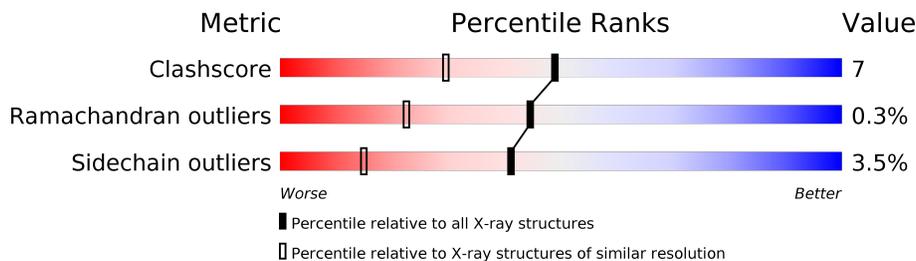
1 Overall quality at a glance

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.

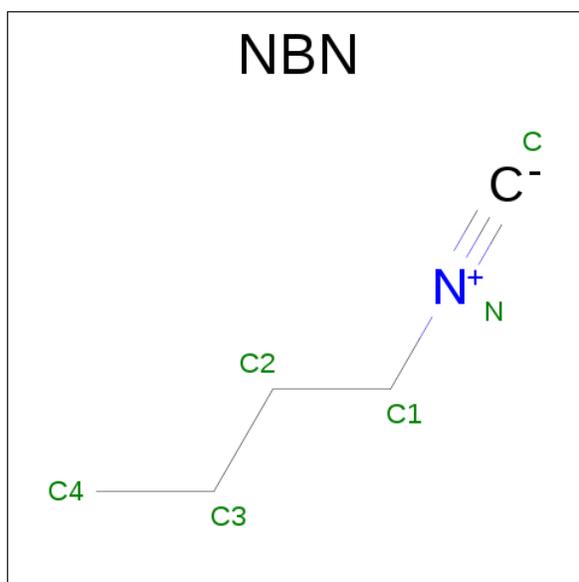


Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	2967 (1.60-1.60)
Ramachandran outliers	110173	2887 (1.60-1.60)
Sidechain outliers	110143	2886 (1.60-1.60)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	403	83% 14% ..



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	285	Total O 285 285	0	0

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.75Å 81.64Å 86.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 1.60	Depositor
% Data completeness (in resolution range)	91.2 (25.00-1.60)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.207 , 0.258	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	3433	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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: HEM, NBN

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	0.36	0/3166	0.58	1/4303 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	49	LYS	CG-CD-CE	-6.24	93.19	111.90

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	3099	0	3115	43	0
2	A	43	0	30	1	0
3	A	6	0	9	0	0
4	A	285	0	0	10	0
All	All	3433	0	3154	43	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 (43) 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:268:ASN:OD1	1:A:270:SER:HB2	1.86	0.76
1:A:66:ARG:HD3	4:A:766:HOH:O	1.97	0.63
1:A:162:ASN:HB3	4:A:684:HOH:O	1.98	0.63
1:A:127:GLN:O	1:A:131:LYS:HB2	1.99	0.62
1:A:78:GLN:O	1:A:81:LYS:HG2	2.00	0.62
1:A:35:LYS:HE2	1:A:39:GLY:HA2	1.81	0.62
1:A:174:ARG:NH2	4:A:740:HOH:O	2.20	0.60
1:A:12:ARG:HB3	1:A:17:GLU:O	2.02	0.60
1:A:174:ARG:HD2	1:A:191:LEU:HD12	1.83	0.59
1:A:260:ASP:HB3	4:A:728:HOH:O	2.03	0.58
1:A:274:GLN:HG2	4:A:598:HOH:O	2.03	0.57
1:A:322:GLU:H	1:A:322:GLU:CD	2.08	0.57
1:A:35:LYS:CE	1:A:39:GLY:HA2	2.36	0.55
1:A:141:VAL:HA	1:A:145:ALA:HB3	1.89	0.55
1:A:8:PHE:CG	1:A:9:PRO:HA	2.44	0.52
1:A:325:PHE:O	1:A:328:PRO:HD3	2.11	0.51
1:A:377:LYS:HD3	1:A:402:ILE:HD11	1.93	0.51
1:A:271:LEU:HD22	1:A:274:GLN:NE2	2.26	0.50
1:A:127:GLN:HG3	4:A:686:HOH:O	2.11	0.50
1:A:102:GLU:N	1:A:103:PRO:CD	2.75	0.49
1:A:271:LEU:HB3	1:A:333:MET:HE1	1.95	0.48
1:A:203:LEU:HD23	1:A:215:CYS:HB3	1.96	0.47
1:A:171:ASN:ND2	4:A:740:HOH:O	2.46	0.47
1:A:217:GLU:O	1:A:221:PRO:HG2	2.17	0.45
1:A:379:ALA:HB2	1:A:402:ILE:HG12	1.97	0.45
1:A:339:PRO:HD2	1:A:340:GLN:OE1	2.16	0.45
1:A:70:PRO:HG2	1:A:291:LYS:HB3	1.99	0.44
1:A:84:PRO:HB3	4:A:761:HOH:O	2.16	0.44
1:A:261:GLN:HG2	4:A:728:HOH:O	2.18	0.44
1:A:262:LEU:HG	1:A:266:LYS:HE3	1.99	0.44
1:A:272:ALA:HB3	1:A:273:PRO:HD3	2.00	0.43
1:A:271:LEU:CB	1:A:333:MET:HE1	2.48	0.43
1:A:377:LYS:CD	1:A:402:ILE:HD11	2.48	0.43
1:A:102:GLU:N	1:A:103:PRO:HD2	2.33	0.43
1:A:174:ARG:HD2	1:A:191:LEU:CD1	2.49	0.42
1:A:8:PHE:CD1	1:A:9:PRO:HA	2.55	0.42
1:A:24:LYS:HE3	4:A:737:HOH:O	2.20	0.42
1:A:236:LEU:O	2:A:501:HEM:HAC	2.20	0.41
1:A:351:ARG:O	1:A:352:CYS:C	2.59	0.41
1:A:275:PHE:HB2	1:A:333:MET:HE3	2.03	0.41
1:A:258:HIS:CB	1:A:261:GLN:HG3	2.50	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:257:GLN:HB2	1:A:257:GLN:HE21	1.62	0.40
1:A:198:LEU:HD13	1:A:211:ILE:HD13	2.04	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	397/403 (98%)	386 (97%)	10 (2%)	1 (0%)	44 22

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	132	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	340/342 (99%)	328 (96%)	12 (4%)	41 15

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	102	GLU
1	A	124	LEU
1	A	131	LYS
1	A	167	LEU
1	A	182	ARG
1	A	189	GLN
1	A	237	LEU
1	A	250	LEU
1	A	257	GLN
1	A	270	SER
1	A	380	VAL

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	114	GLN
1	A	118	GLN
1	A	169	GLN
1	A	170	GLN
1	A	171	ASN
1	A	201	GLN
1	A	231	GLN
1	A	257	GLN
1	A	371	GLN

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 carbohydrates 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	HEM	A	501	1,3	28,50,50	1.79	7 (25%)	17,82,82	1.23	2 (11%)
3	NBN	A	502	2	4,5,5	2.26	1 (25%)	3,4,4	0.36	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
2	HEM	A	501	1,3	-	0/6/54/54	0/0/8/8
3	NBN	A	502	2	-	0/2/3/3	0/0/0/0

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	C3B-CAB	-3.40	1.41	1.47
2	A	501	HEM	C3C-CAC	-3.36	1.41	1.47
2	A	501	HEM	C4D-ND	2.07	1.39	1.36
2	A	501	HEM	C1C-NC	2.50	1.39	1.36
2	A	501	HEM	C4A-NA	2.62	1.41	1.36
2	A	501	HEM	C4C-NC	3.18	1.40	1.36
2	A	501	HEM	C1B-NB	4.40	1.42	1.36
3	A	502	NBN	C1-N	4.48	1.56	1.45

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	HEM	C4A-C3A-C2A	-2.86	105.00	107.00
2	A	501	HEM	CBA-CAA-C2A	-2.04	108.58	112.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	1	0

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.