

Full wwPDB X-ray Structure Validation Report (i)

Jun 3, 2020 – 03:22 pm BST

PDB ID	:	2BN2
Title	:	CRYSTAL STRUCTURE OF BOVINE NEUROPHYSIN II COMPLEXED
		WITH THE VASOPRESSIN ANALOGUE PHE-TYR AMIDE
Authors	:	Rose, J.P.; Wang, B.C.
Deposited on	:	1998-12-18
$\operatorname{Resolution}$:	2.80 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

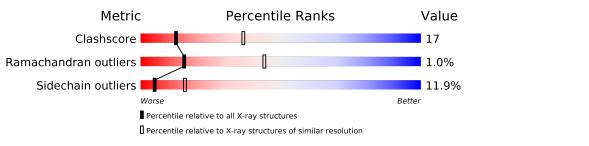
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

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 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain			
1	А	95	65%	2	1%	• 11%
1	С	95	59%	21%	•	17%
1	Е	95	55%	22%	6%	17%
1	G	95	49%	28%	5%	17%



2 Entry composition (i)

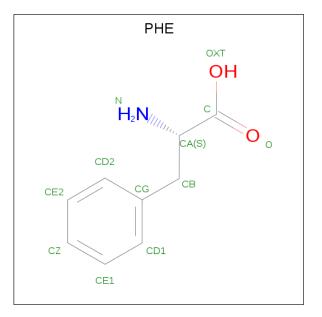
There are 3 unique types of molecules in this entry. The entry contains 2324 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Λ	85	Total	С	Ν	Ο	S	0	0	0
	A	00	595	353	105	122	15	0	0	0
1	С	79	Total	С	Ν	Ο	S	0	0	0
	U	19	547	325	99	109	14	0	0	0
1	Е	79	Total	С	Ν	Ο	S	0	0	0
		19	543	323	98	108	14	0	0	0
1	G	79	Total	С	Ν	Ο	S	0	0	0
	G	19	547	325	99	109	14	0	0	0

• Molecule 1 is a protein called NEUROPHYSIN II.

• Molecule 2 is PHENYLALANINE (three-letter code: PHE) (formula: $C_9H_{11}NO_2$).

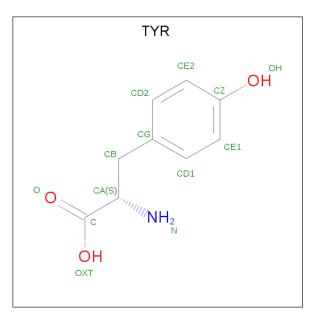


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total C N O 11 9 1 1	0	0
2	С	1	Total C N O 11 9 1 1	0	0



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	Е	1	Total C N O 11 9 1 1	0	0
2	G	1	Total C N O 11 9 1 1	0	0

 $\bullet\,$ Molecule 3 is TYROSINE (three-letter code: TYR) (formula: C_9H_{11}NO_3).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total C N O 12 9 1 2	0	0
3	С	1	Total C N O 12 9 1 2	0	0
3	Ε	1	Total C N O 12 9 1 2	0	0
3	G	1	Total C N O 12 9 1 2	0	0

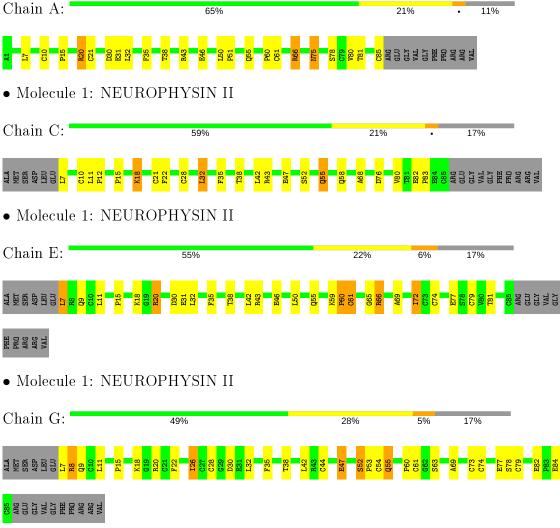


3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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 colorcoded 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: NEUROPHYSIN II





4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	121.67Å 67.96 Å 62.10 Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 - 2.80	Depositor
% Data completeness	92.0 (8.00-2.80)	Depositor
(in resolution range)	52.0 (8.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.208 , 0.262	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2324	wwPDB-VP
Average B, all atoms $(Å^2)$	23.0	wwPDB-VP



5 Model quality (i)

5.1 Standard geometry (i)

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	
	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.48	0/604	0.65	0/813
1	С	0.37	0/556	0.59	0/749
1	Е	0.47	0/552	0.67	0/744
1	G	0.39	0/556	0.60	0/749
All	All	0.43	0/2268	0.63	0/3055

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	Ε	0	2
1	G	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Ε	60	PRO	Peptide
1	Е	72	ILE	Mainchain
1	G	60	PRO	Peptide

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	595	0	544	16	0
1	С	547	0	497	19	0
1	Ε	543	0	491	18	0
1	G	547	0	497	26	0
2	А	11	0	8	0	0
2	С	11	0	8	1	0
2	Ε	11	0	8	0	0
2	G	11	0	8	3	0
3	А	12	0	9	1	0
3	С	12	0	9	1	0
3	Е	12	0	9	0	0
3	G	12	0	9	1	0
All	All	2324	0	2097	74	0

the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

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 17.

All (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:60:PRO:HG3	1:A:66:ARG:HH11	1.30	0.96
1:A:60:PRO:HG3	1:A:66:ARG:NH1	1.90	0.85
1:E:72:ILE:HG22	1:E:74:CYS:SG	2.20	0.82
1:G:26:ILE:CD1	1:G:28:CYS:SG	2.69	0.80
1:E:15:PRO:HD2	1:E:32:LEU:HD21	1.65	0.79
1:G:7:LEU:HD13	1:G:53:PRO:HB2	1.65	0.79
1:E:30:ASP:HA	1:E:69:ALA:HA	1.66	0.76
1:C:18:LYS:HG3	1:C:32:LEU:HD21	1.68	0.75
1:A:46:GLU:HG2	1:E:50:LEU:HD22	1.68	0.74
1:C:15:PRO:O	1:C:18:LYS:HG2	1.87	0.73
1:E:35:PHE:HB3	1:E:38:THR:OG1	1.89	0.72
1:G:11:LEU:HG	1:G:47:GLU:HG2	1.73	0.70
1:E:7:LEU:HD23	1:E:55:GLN:HB2	1.72	0.70
1:G:26:ILE:HD11	1:G:28:CYS:SG	2.35	0.67
1:G:15:PRO:O	1:G:18:LYS:HG2	1.98	0.64
1:A:7:LEU:HD23	1:A:55:GLN:HB3	1.82	0.61
1:G:35:PHE:HB3	1:G:38:THR:OG1	2.02	0.60
1:A:35:PHE:HB3	1:A:38:THR:OG1	2.03	0.59
1:E:61:CYS:HB3	1:E:65:GLY:O	2.02	0.58
1:E:38:THR:HG22	1:G:32:LEU:O	2.03	0.58



Continued from pre		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:E:72:ILE:CG2	1:E:74:CYS:SG	2.91	0.57	
1:G:26:ILE:HD12	1:G:28:CYS:SG	2.46	0.56	
1:G:9:GLN:HA	1:G:55:GLN:O	2.04	0.56	
1:C:10:CYS:HB2	1:C:21:CYS:O	2.06	0.56	
1:A:80:VAL:HG12	1:A:81:THR:O	2.06	0.55	
1:A:78:SER:HB2	1:C:80:VAL:HG22	1.88	0.54	
1:G:22:PHE:HB2	1:G:26:ILE:HG13	1.89	0.53	
1:A:75:ASN:HD22	1:A:75:ASN:H	1.55	0.53	
1:A:75:ASN:ND2	1:A:75:ASN:H	2.07	0.52	
1:C:35:PHE:HB3	1:C:38:THR:OG1	2.09	0.52	
1:A:75:ASN:HD22	1:A:75:ASN:N	2.07	0.52	
1:E:9:GLN:NE2	1:E:20:ARG:HD2	2.24	0.52	
1:C:47:GLU:HB3	3:C:99:TYR:CE1	2.44	0.52	
1:E:7:LEU:HD22	1:E:7:LEU:N	2.25	0.51	
1:A:78:SER:CB	1:C:80:VAL:HG22	2.40	0.51	
1:C:22:PHE:O	1:C:76:ASP:HA	2.11	0.50	
1:E:61:CYS:HB3	1:E:65:GLY:C	2.33	0.49	
1:G:53:PRO:HB3	2:G:98:PHE:CZ	2.48	0.49	
1:E:59:LYS:O	1:E:66:ARG:HA	2.13	0.49	
1:C:28:CYS:SG	1:C:68:ALA:HB1	2.54	0.48	
1:G:8:ARG:O	1:G:55:GLN:N	2.46	0.48	
1:G:52:SER:O	2:G:98:PHE:N	2.46	0.47	
1:G:26:ILE:HD13	1:G:79:CYS:SG	2.54	0.47	
1:C:28:CYS:CB	1:C:68:ALA:HB1	2.45	0.47	
1:G:18:LYS:HE3	1:G:32:LEU:HD21	1.97	0.47	
1:E:43:ARG:HG3	1:E:43:ARG:NH1	2.30	0.46	
1:A:21:CYS:HB3	3:A:99:TYR:OH	2.15	0.46	
1:G:47:GLU:OE2	1:G:54:CYS:SG	2.73	0.46	
1:C:32:LEU:H	1:C:32:LEU:HD22	1.81	0.46	
1:G:8:ARG:O	1:G:54:CYS:HA	2.16	0.46	
1:C:7:LEU:HD23	1:C:55:GLN:HB2	1.97	0.45	
1:A:10:CYS:O	1:A:20:ARG:NH1	2.48	0.45	
1:A:50:LEU:HA	1:A:51:PRO:HD3	1.77	0.45	
1:C:82:GLU:HA	1:C:83:PRO:HD3	1.83	0.44	
1:C:22:PHE:CZ	1:C:68:ALA:HA	2.53	0.44	
1:G:22:PHE:HB2	1:G:26:ILE:CG1	2.47	0.43	
1:E:59:LYS:HA	1:E:60:PRO:HD2	1.85	0.43	
1:E:72:ILE:HG23	1:E:79:CYS:HB3	2.01	0.43	
1:G:82:GLU:OE2	1:G:84:GLU:HB3	2.18	0.43	
1:A:61:CYS:SG	1:A:85:CYS:SG	3.17	0.43	
1:C:18:LYS:NZ	1:C:18:LYS:HB3	2.34	0.43	

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:43:ARG:NH1	1:E:46:GLU:OE1	2.51	0.43
1:E:81:THR:HB	1:G:77:GLU:HG2	2.01	0.43
1:G:53:PRO:HB3	2:G:98:PHE:CE2	2.54	0.43
1:C:47:GLU:O	2:C:98:PHE:HA	2.18	0.42
1:G:74:CYS:HA	1:G:78:SER:O	2.19	0.42
1:G:44:CYS:HB3	3:G:99:TYR:OH	2.19	0.42
1:G:73:CYS:O	1:G:79:CYS:HA	2.19	0.42
1:C:47:GLU:HG3	1:C:47:GLU:O	2.19	0.42
1:A:75:ASN:ND2	1:A:75:ASN:N	2.67	0.41
1:G:30:ASP:HA	1:G:69:ALA:HA	2.01	0.41
1:C:12:PRO:O	1:C:43:ARG:HD2	2.20	0.41
1:G:26:ILE:HG13	1:G:26:ILE:O	2.21	0.41
1:C:15:PRO:HD2	1:C:32:LEU:HG	2.04	0.40

Continued from previous page...

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	А	83/95~(87%)	78~(94%)	4 (5%)	1 (1%)	13 39
1	С	77/95~(81%)	64 (83%)	13~(17%)	0	100 100
1	Е	77/95~(81%)	69 (90%)	7(9%)	1 (1%)	12 36
1	G	77/95~(81%)	71~(92%)	5~(6%)	1 (1%)	12 36
All	All	314/380~(83%)	282 (90%)	29 (9%)	3 (1%)	15 44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	61	CYS
1	Е	61	CYS



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Mol	Chain	Res	Type
1	А	15	PRO

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	Perce	entiles
1	А	66/74~(89%)	59~(89%)	7 (11%)	6	20
1	С	60/74~(81%)	53~(88%)	7(12%)	5	16
1	Ε	59/74~(80%)	51~(86%)	8 (14%)	3	11
1	G	60/74~(81%)	52~(87%)	8 (13%)	4	12
All	All	245/296~(83%)	215~(88%)	30~(12%)	5	15

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	20	ARG
1	А	30	ASP
1	A A	31	GLU
1	А	32	LEU
1	А	43	ARG
1	А	66	ARG
1	A A	75	ASN
1	C C C C C C C	11	LEU
1	С	18	LYS
1	С	32	LEU
1	С	42	LEU
1	С	52	SER
1		55	GLN
1	С	58	GLN
1	Е	7	LEU
1	Е	11	LEU
1	Е	18	LYS
1	Е	20	ARG
1	Е	31	GLU
1	Е	42	LEU



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\mathbf{Mol}	Chain	\mathbf{Res}	Type			
1	Ε	66	ARG			
1	Е	77	GLU			
1	G	8	ARG			
1	G	20	ARG			
1	G	26	ILE			
1	G	42	LEU			
1	G	47	GLU			
1	G	52	SER			
1	G	55	GLN			
1	G	63	SER			

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Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	\mathbf{Res}	Type
1	А	75	ASN
1	С	48	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

8 ligands are modelled in this entry.There are no bond length outliers.There are no bond angle outliers.There are no chirality outliers.There are no torsion outliers.There are no ring outliers.



No monomer is involved in short contacts.

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 (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.

