



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 08:24 AM GMT

PDB ID : 1B98
Title : NEUROTROPHIN 4 (HOMODIMER)
Authors : Robinson, R.C.; Radziejewski, C.; Stuart, D.I.; Jones, E.Y.; Choe, S.
Deposited on : 1999-02-22
Resolution : 2.75 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

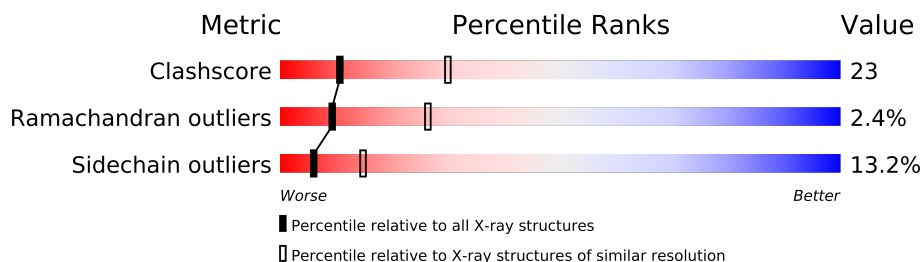
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.75 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	79885	2995 (2.80-2.72)
Ramachandran outliers	78287	2941 (2.80-2.72)
Sidechain outliers	78261	2944 (2.80-2.72)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	130	
1	M	130	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1671 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PROTEIN (NEUROTROPHIN-4).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	103	Total	C	N	O	S	0	0	0
			779	480	148	145	6			
1	M	113	Total	C	N	O	S	0	0	0
			842	517	164	155	6			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	21	Total	O	0	0
			21	21		
3	M	28	Total	O	0	0
			28	28		

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	43.80Å 50.80Å 53.00Å 90.00° 109.40° 90.00°	Depositor
Resolution (Å)	20.00 – 2.75	Depositor
% Data completeness (in resolution range)	93.0 (20.00-2.75)	Depositor
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.235 , 0.336	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1671	wwPDB-VP
Average B, all atoms (Å ²)	46.0	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: CL

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	0.78	0/790	2.23	37/1066 (3.5%)
1	M	0.81	0/856	2.57	47/1155 (4.1%)
All	All	0.79	0/1646	2.41	84/2221 (3.8%)

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	A	0	2
1	M	0	5
All	All	0	7

There are no bond length outliers.

All (84) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	114	ARG	CD-NE-CZ	37.25	175.75	123.60
1	A	98	ARG	CD-NE-CZ	15.65	145.51	123.60
1	M	103	ASP	C-N-CA	15.52	160.51	121.70
1	A	60	ARG	NE-CZ-NH2	-15.29	112.65	120.30
1	M	28	ARG	NE-CZ-NH2	14.12	127.36	120.30
1	M	36	ARG	CD-NE-CZ	12.98	141.77	123.60
1	M	114	ARG	NE-CZ-NH2	-12.71	113.94	120.30
1	A	83	ARG	CD-NE-CZ	12.71	141.39	123.60
1	M	98	ARG	NE-CZ-NH1	12.61	126.60	120.30
1	A	79	ARG	NE-CZ-NH1	12.13	126.37	120.30
1	M	103	ASP	O-C-N	-12.02	103.47	122.70
1	A	60	ARG	CD-NE-CZ	11.97	140.35	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	98	ARG	CD-NE-CZ	11.25	139.35	123.60
1	A	79	ARG	CD-NE-CZ	10.45	138.24	123.60
1	M	103	ASP	CA-C-O	10.40	141.93	120.10
1	M	26	ASP	CB-CG-OD1	10.32	127.59	118.30
1	A	28	ARG	NE-CZ-NH2	-9.97	115.32	120.30
1	M	37	GLU	OE1-CD-OE2	9.72	134.97	123.30
1	M	32	ASP	CB-CG-OD1	9.72	127.05	118.30
1	A	55	TYR	CA-CB-CG	9.29	131.06	113.40
1	M	83	ARG	NE-CZ-NH1	9.26	124.93	120.30
1	M	103	ASP	CA-CB-CG	-9.13	93.32	113.40
1	A	125	SER	N-CA-CB	-8.91	97.13	110.50
1	M	103	ASP	N-CA-C	8.77	134.68	111.00
1	M	98	ARG	NH1-CZ-NH2	-8.43	110.13	119.40
1	A	83	ARG	NE-CZ-NH1	8.31	124.45	120.30
1	M	27	ARG	NE-CZ-NH2	8.28	124.44	120.30
1	A	55	TYR	CB-CG-CD1	7.89	125.73	121.00
1	M	36	ARG	CG-CD-NE	7.88	128.35	111.80
1	A	28	ARG	NE-CZ-NH1	7.68	124.14	120.30
1	A	125	SER	N-CA-C	7.64	131.64	111.00
1	A	60	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	A	79	ARG	NE-CZ-NH2	-7.62	116.49	120.30
1	M	79	ARG	NE-CZ-NH1	-7.46	116.57	120.30
1	M	33	LEU	CB-CG-CD1	7.26	123.34	111.00
1	M	114	ARG	NE-CZ-NH1	7.05	123.82	120.30
1	A	26	ASP	CB-CG-OD2	-6.88	112.10	118.30
1	A	84	ARG	CD-NE-CZ	6.85	133.19	123.60
1	M	79	ARG	CG-CD-NE	6.71	125.89	111.80
1	M	125	SER	C-N-CA	6.60	138.20	121.70
1	A	125	SER	CB-CA-C	-6.57	97.62	110.10
1	A	52	LEU	C-N-CA	6.55	138.08	121.70
1	A	67	GLU	N-CA-CB	6.53	122.36	110.60
1	A	16	VAL	N-CA-CB	-6.52	97.16	111.50
1	M	32	ASP	CB-CG-OD2	-6.51	112.44	118.30
1	M	37	GLU	O-C-N	-6.51	112.29	122.70
1	A	55	TYR	CB-CG-CD2	-6.50	117.10	121.00
1	M	36	ARG	NE-CZ-NH1	6.45	123.53	120.30
1	M	91	LYS	CB-CA-C	-6.40	97.60	110.40
1	A	111	ARG	NE-CZ-NH1	-6.29	117.16	120.30
1	A	16	VAL	CG1-CB-CG2	6.25	120.90	110.90
1	A	80	GLY	CA-C-O	-6.19	109.46	120.60
1	M	105	GLN	N-CA-CB	6.16	121.68	110.60
1	A	100	LEU	N-CA-CB	6.13	122.66	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	79	ARG	NE-CZ-NH2	6.06	123.33	120.30
1	A	114	ARG	NE-CZ-NH1	-6.01	117.30	120.30
1	M	70	GLY	N-CA-C	5.98	128.04	113.10
1	M	82	ASP	CB-CG-OD2	-5.93	112.96	118.30
1	A	95	SER	N-CA-CB	5.87	119.31	110.50
1	M	34	ARG	CG-CD-NE	5.83	124.05	111.80
1	M	98	ARG	NE-CZ-NH2	5.79	123.19	120.30
1	M	106	GLY	C-N-CA	5.67	135.88	121.70
1	A	32	ASP	CB-CG-OD1	5.65	123.38	118.30
1	A	74	GLY	CA-C-O	-5.63	110.47	120.60
1	M	37	GLU	CB-CA-C	5.52	121.44	110.40
1	M	104	ALA	CA-C-N	5.49	129.28	117.20
1	A	122	THR	N-CA-CB	5.41	120.58	110.30
1	A	73	ALA	C-N-CA	5.39	133.62	122.30
1	M	64	ASP	CB-CG-OD1	5.38	123.14	118.30
1	M	28	ARG	NH1-CZ-NH2	-5.37	113.50	119.40
1	M	28	ARG	CD-NE-CZ	5.34	131.08	123.60
1	M	83	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	74	GLY	CA-C-N	5.25	126.70	116.20
1	M	64	ASP	CA-CB-CG	5.23	124.90	113.40
1	M	81	VAL	N-CA-CB	5.19	122.92	111.50
1	A	62	LYS	CA-CB-CG	5.18	124.81	113.40
1	M	55	TYR	O-C-N	-5.17	114.42	122.70
1	M	104	ALA	CA-C-O	-5.14	109.31	120.10
1	A	80	GLY	CA-C-N	5.14	128.50	117.20
1	A	34	ARG	NE-CZ-NH1	-5.12	117.74	120.30
1	M	92	ALA	N-CA-CB	5.11	117.26	110.10
1	M	37	GLU	N-CA-CB	-5.03	101.54	110.60
1	M	34	ARG	CA-C-N	5.03	126.26	116.20
1	A	75	GLY	C-N-CA	5.02	132.83	122.30

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	CYS	Mainchain
1	A	21	SER	Mainchain
1	M	103	ASP	Mainchain
1	M	104	ALA	Mainchain
1	M	37	GLU	Mainchain
1	M	55	TYR	Mainchain
1	M	99	ALA	Mainchain

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	779	0	740	41	0
1	M	842	0	812	44	0
2	A	1	0	0	0	0
3	A	21	0	0	1	0
3	M	28	0	0	6	0
All	All	1671	0	1552	71	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 23.

All (71) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:41:LEU:HD22	1:A:100:LEU:HD23	1.41	1.02
1:A:14:LEU:HD22	1:M:123:LEU:HB2	1.55	0.88
1:A:13:GLU:OE1	1:M:122:THR:HG21	1.90	0.71
1:A:124:LEU:HA	1:M:13:GLU:HG3	1.74	0.67
1:A:91:LYS:HB2	3:A:211:HOH:O	1.94	0.66
1:M:33:LEU:HD22	1:M:96:TYR:CD1	2.31	0.65
1:A:84:ARG:HD3	1:M:84:ARG:HH12	1.62	0.65
1:M:103:ASP:HA	3:M:154:HOH:O	2.01	0.61
1:A:110:TRP:HE1	1:M:48:GLY:CA	2.12	0.61
1:A:87:VAL:CG1	1:A:124:LEU:HD12	2.31	0.61
1:M:34:ARG:HG3	1:M:34:ARG:HH11	1.69	0.58
1:A:126:ARG:O	1:A:127:THR:C	2.41	0.57
1:M:58:GLU:OE1	1:M:60:ARG:NH2	2.38	0.56
1:A:86:TRP:HE3	1:A:125:SER:HG	1.54	0.55
1:M:44:VAL:HG11	1:M:47:ALA:HB3	1.88	0.55
1:A:98:ARG:NH1	1:M:53:ARG:O	2.40	0.54
1:M:16:VAL:HA	1:M:79:ARG:HB3	1.88	0.54
1:M:104:ALA:N	3:M:154:HOH:O	2.40	0.54
1:M:32:ASP:OD2	1:M:34:ARG:HD3	2.09	0.53
1:M:81:VAL:O	1:M:83:ARG:HD3	2.08	0.53
1:M:89:GLU:OE1	1:M:124:LEU:HD11	2.08	0.53
1:M:32:ASP:OD1	1:M:34:ARG:HG2	2.08	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:122:THR:HG21	1:M:13:GLU:HG2	1.92	0.52
1:A:58:GLU:OE1	1:A:60:ARG:NH2	2.43	0.52
1:A:97:VAL:HG11	1:A:115:ILE:HD11	1.92	0.52
1:A:28:ARG:HH11	1:A:28:ARG:HG3	1.75	0.52
1:A:16:VAL:HG22	1:A:79:ARG:O	2.10	0.51
1:A:87:VAL:HG12	1:A:125:SER:HB3	1.93	0.51
1:A:87:VAL:HB	1:A:125:SER:CB	2.40	0.51
1:A:61:CYS:HB3	1:A:74:GLY:HA2	1.93	0.50
1:A:14:LEU:HD22	1:M:123:LEU:CB	2.36	0.49
1:A:59:THR:HB	1:A:117:THR:C	2.31	0.49
1:A:110:TRP:HE1	1:M:48:GLY:HA3	1.78	0.49
1:M:16:VAL:HG22	1:M:79:ARG:O	2.13	0.48
1:A:61:CYS:CB	1:A:74:GLY:HA2	2.44	0.48
1:A:101:THR:O	1:A:108:VAL:HA	2.13	0.48
1:A:41:LEU:HD22	1:A:100:LEU:CD2	2.29	0.48
1:M:79:ARG:HD2	1:M:79:ARG:HH11	1.53	0.47
1:M:95:SER:OG	1:M:117:THR:HG21	2.14	0.47
1:M:62:LYS:HE2	3:M:147:HOH:O	2.14	0.47
1:M:47:ALA:HB2	1:M:110:TRP:HZ2	1.79	0.47
1:M:105:GLN:HB3	3:M:151:HOH:O	2.13	0.47
1:A:67:GLU:HG2	1:A:67:GLU:O	2.14	0.47
1:A:86:TRP:CE3	1:A:123:LEU:HB3	2.50	0.46
1:A:16:VAL:CG1	1:A:121:CYS:HB2	2.46	0.46
1:A:16:VAL:HG13	1:A:78:CYS:HB3	1.98	0.45
1:A:87:VAL:HG13	1:A:124:LEU:HD12	1.98	0.45
1:M:33:LEU:HD23	1:M:112:TRP:HB3	1.98	0.45
1:M:62:LYS:HE3	3:M:152:HOH:O	2.17	0.45
1:M:38:VAL:HG11	1:M:111:ARG:HE	1.82	0.44
1:A:17:CYS:HB3	1:A:119:CYS:SG	2.57	0.44
1:A:14:LEU:HD23	1:A:15:ALA:N	2.33	0.44
1:A:84:ARG:NH1	1:M:84:ARG:HH11	2.15	0.43
1:M:44:VAL:HB	1:M:52:LEU:HD23	2.00	0.43
1:A:28:ARG:NH1	1:A:28:ARG:HG3	2.34	0.43
1:M:25:THR:HG22	1:M:55:TYR:HB3	2.00	0.43
1:A:76:GLY:O	1:A:89:GLU:HA	2.19	0.43
1:M:32:ASP:OD1	1:M:34:ARG:HD3	2.18	0.42
1:M:102:ALA:O	1:M:103:ASP:HB2	2.20	0.42
1:M:32:ASP:CG	1:M:34:ARG:HD3	2.41	0.41
1:A:28:ARG:H	1:A:28:ARG:HG3	1.57	0.41
1:M:39:GLU:O	1:M:101:THR:HB	2.19	0.41
1:A:80:GLY:HA2	1:M:86:TRP:NE1	2.36	0.41
1:M:78:CYS:CB	1:M:121:CYS:SG	3.09	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:84:ARG:NH1	1:M:84:ARG:NH1	2.68	0.41
1:M:107:ARG:HB2	3:M:154:HOH:O	2.20	0.41
1:A:14:LEU:CD2	1:M:123:LEU:HD12	2.51	0.41
1:M:78:CYS:SG	1:M:121:CYS:CB	3.08	0.40
1:M:34:ARG:HG3	1:M:34:ARG:NH1	2.36	0.40
1:A:81:VAL:HB	1:M:80:GLY:O	2.20	0.40
1:A:31:VAL:HA	1:A:36:ARG:O	2.20	0.40

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	97/130 (75%)	90 (93%)	5 (5%)	2 (2%)	11	30
1	M	109/130 (84%)	100 (92%)	6 (6%)	3 (3%)	8	21
All	All	206/260 (79%)	190 (92%)	11 (5%)	5 (2%)	9	26

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	74	GLY
1	M	104	ALA
1	M	69	GLY
1	M	70	GLY
1	A	126	ARG

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	77/96 (80%)	68 (88%)	9 (12%)	8	21
1	M	82/96 (85%)	70 (85%)	12 (15%)	5	11
All	All	159/192 (83%)	138 (87%)	21 (13%)	6	15

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

Mol	Chain	Res	Type
1	A	26	ASP
1	A	28	ARG
1	A	37	GLU
1	A	44	VAL
1	A	81	VAL
1	A	83	ARG
1	A	93	LYS
1	A	95	SER
1	A	124	LEU
1	M	13	GLU
1	M	16	VAL
1	M	20	VAL
1	M	33	LEU
1	M	34	ARG
1	M	36	ARG
1	M	50	SER
1	M	52	LEU
1	M	60	ARG
1	M	83	ARG
1	M	103	ASP
1	M	107	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	M	94	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.