

Supplementary material

| | 10 | 20 | 30 | 40 | 50 | 60 |
|-------------|---|---|---------------------|-----------------|----|----|
| Xenopus | MGLKLSGRYIFLVLAHVLA [.] YLLQAVKA | TGKCDAVFKGLSDCMLTLGDKV [.] ANYPQDLEEKK | | | | |
| Gallus | MGLKLNGRYISLILAVQIAHLVQAVRA | AGRCDAVFRGFSDCLLRLGDNMANYPQDLDDKR | | | | |
| Oryctolagus | MGLKLNGRYISLILAVQIAYLVQAVRA | AGKCDAVFKGFSDCLLKLGD [.] SMANYPQGLDDKT | | | | |
| Mus | MGLKLNGRYISLILAVQIAYLVQAVRA | AGKCDAVFKGFSDCLLKLGD [.] SMANYPQGLDDKT | | | | |
| Homo | MGLKLNGRYISLILAVQIAYLVQAVRA | AGKCDAVFKGFSDCLLKLGD [.] SMANYPQGLDDKT | | | | |
| | *****.***** | *:***::*:*:***:* | :*:*****::*:***:* | ***.:*****.*::* | | |
| Xenopus | NLDTICSYWDDFHVCTVTALADCQEGAA [.] DIWEKLRQSKNLNIQGSLFELCPGSA | GAPGQ | | | | |
| Gallus | NLQTICAYWDDFHACTLTALTDCQEGATDLWEKLRRESKNLDFQGSLFELCGGGS | GAAPS | | | | |
| Oryctolagus | NIKTVCTYWEDFH [.] SCTVTALTDCQEGAKDMWDKLRKESKNLN [.] IQGSLFELCG SGN | GAAGP | | | | |
| Mus | NIKTVCTYWEDFH [.] SCTVTALTDCQEGAKDMWDKLRKESKNLN [.] IQGSLFELCG SSN | GAAGS | | | | |
| Homo | NIKTVCTYWEDFH [.] SCTVTALTDCQEGAKDMWDKLRKESKNLN [.] IQGSLFELCG SSN | GAAGS | | | | |
| | *:.*:***:*** | **::***:***** | *:***::*:***::***** | ***** | .. | ** |
| Xenopus | RLLFPAFLPLL [.] MVFLSTLFIWVLQ- | 144 | | | | |
| Gallus | L-LPPALPVLLGALGAALATWGLPF | 144 | | | | |
| Oryctolagus | L-L-PALPVLLVSLWAALVTWL-PF | 142 | | | | |
| Mus | L-L-PALSVLLVSLSAALATWF-SF | 142 | | | | |
| Homo | L-L-PAFPVLLVSLSAALATWL-SF | 142 | | | | |
| | * **: | ** | : | ::* | * | |

Figure S1. Alignment of neuritin amino acid sequences of diverse species. Shown are the sequences of *Xenopus laevis* (NM_001085688), chicken (*Gallus gallus*, NM_001198731), rabbit (*Oryctolagus cuniculus*, XM_002720948), mouse (*Mus musculus*, NM_153529), and human (*Homo sapiens*, AF136631), respectively. Underlined are the sequences of the peptides NrnA (position 47 to 61) and NrnB (position 83 to 100). The markup line uses a space for a mismatch or a gap, '.' for any small positive score, ':' for a similarity which scores more than 1.0, the program used was CLUSTAL 0(1.2.4), <https://www.ebi.ac.uk/Tools/msa/clustalo/>. The sequence of the mature protein is given by the block in the middle (position 28 to 115), the amino acid residues of the suggested leader peptides (first 27 residues) as well as those that are removed once the GPI-anchor is added can be seen to the left, and to the right, respectively. Please note that with respect to the mature protein the lower three sequences (separated by the small gap from the upper two ones) differ from each other only at positions 113 and/or 114 (bold letters). This also applies to the sequences of rat, cattle, sheep, camel and donkey (not shown).