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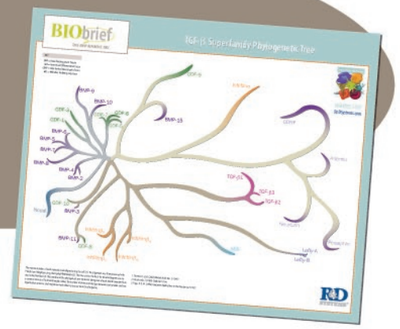
is pleased to introduce the BIObrief,
a take-away reference
tool for cell biology researchers.



Branches of the TGF-β superfamily phylogenetic tree represent the divergence of each family member from a hypothetical common ancestor. The branch length reflects the number of amino acid changes between each protein and the common ancestor.

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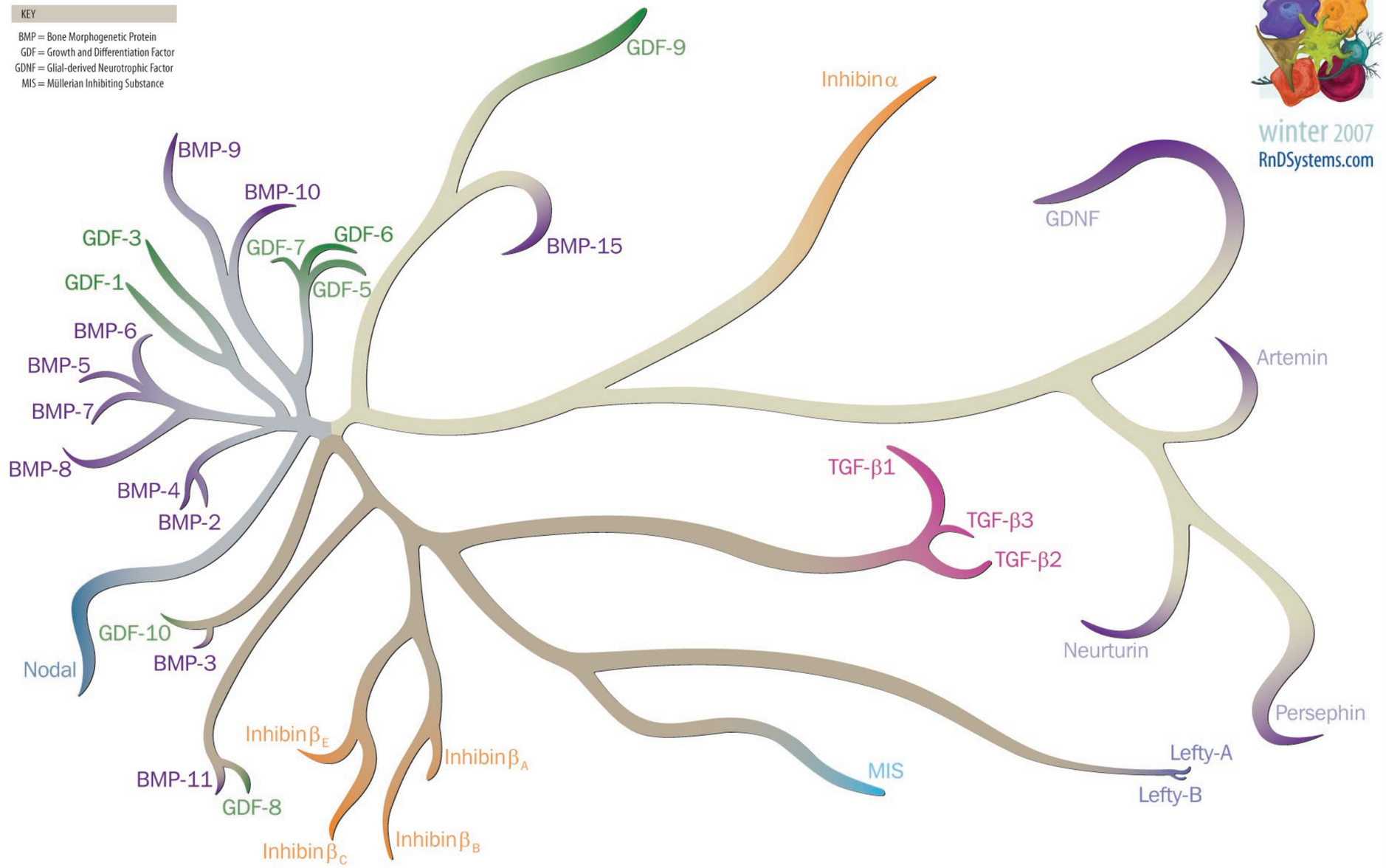
TGF-β Superfamily Phylogenetic Tree

KEY

BMP = Bone Morphogenetic Protein
GDF = Growth and Differentiation Factor
GDNF = Glial-derived Neurotrophic Factor
MIS = Müllerian Inhibiting Substance



Tools for Cell Biology Research
winter 2007
RnDSystems.com

The mature domains of each molecule were aligned using ClustalX [1]. The alignment was then processed with Protdist and Neighbor using the Dayhoff PAM Matrix [2]. The tree used as the basis for the dendrogram was created using TreeView [3]. The branches of the phylogenetic tree represent divergence of each branch member from a common ancestor. The branch lengths reflect the number of amino acid changes between each protein and that hypothetical ancestor, and imply how much time has passed since the divergence.

1. Chenna, R. *et al.* (2003) Nucleic Acids Res. **31**:3497.
2. Felsenstein, J. (1989) Cladistics **5**:164.
3. Page, R. D. M. (1996) Computer Applications in the Biosciences **12**:357.

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NOTE: Activins are homodimers or heterodimers of the various inhibin β subunit isoforms, while inhibins are heterodimers of a unique α subunit and one of the various β subunits. The activin/inhibin nomenclature reflects the subunit composition of the proteins: Activin A (β_A- β_A), Activin B (β_B- β_B), Activin AB (β_A- β_B), Inhibin A (α - β_A) and Inhibin B (α - β_B).

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