

• Analysis performed: 200805\_065012  
• Analyzed sequences (hits resulting from 714 blast searches, 51 animal groups x 14 query sequences):68459 (out of which unique: 8056, programmatically recognized as VEGF/PDGF family members: 90.0%).  
• The tree background color indicates the presence of the proteins with the corresponding color according to our hypotheses.  
• The red-to-white background of the table indicates a heuristic reliability of the results, where a brighter color indicates a higher reliability. This is calculated using the number of fully sequenced genomes, the number of species in the phylum and the number of protein sequences available for that phylum.  
• The numbers in the table denote the number of: orthologs found (black), P = paralogs found, ? = homologs found, whose relationship could not be programmatically determined, Σ = total homologs found.

