

**Maximum Likelihood Trees of gene families residing on
chromosomes 1, 6, 9 and 19.**

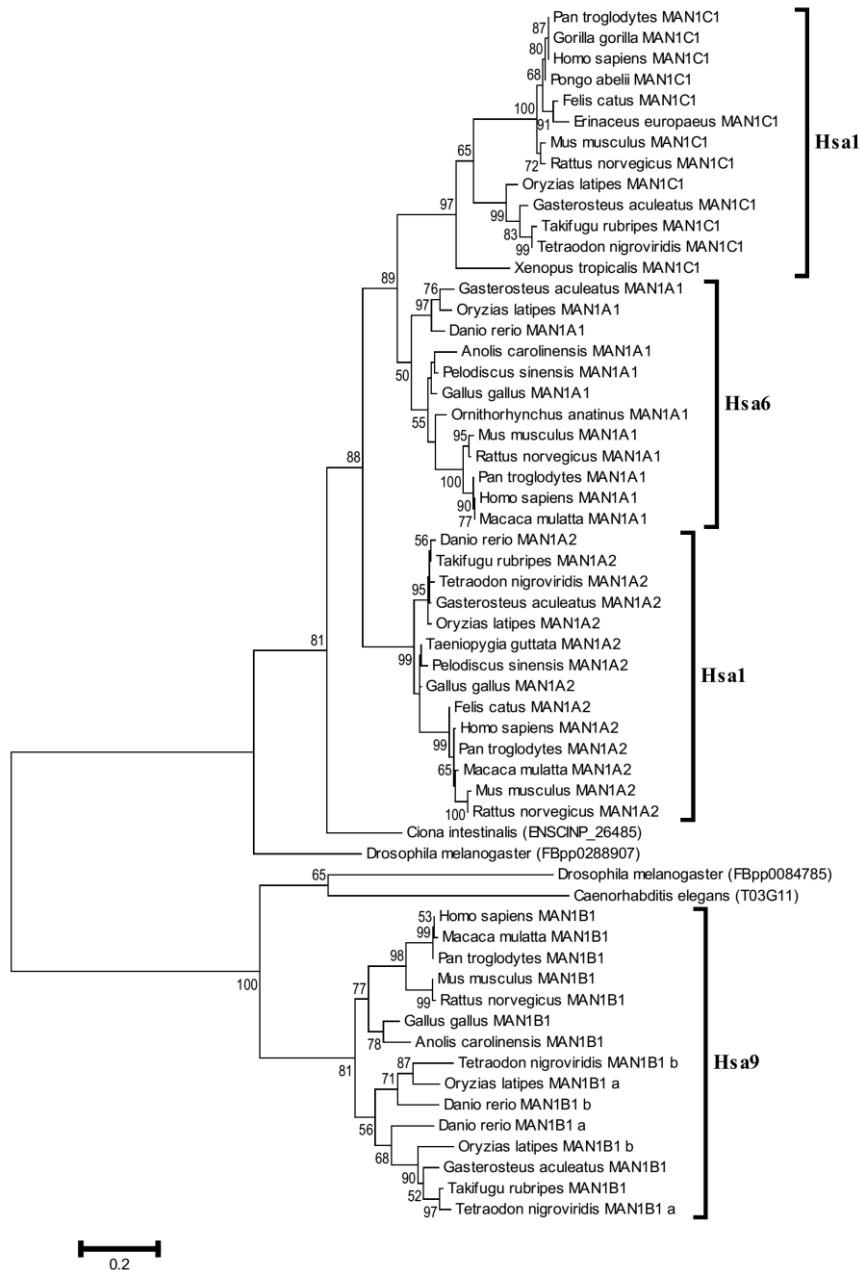
RING finger protein Family - RNF



Phylogenetic tree of RNF family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-1942.0127) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.4792)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 26 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 71 positions in the final dataset.

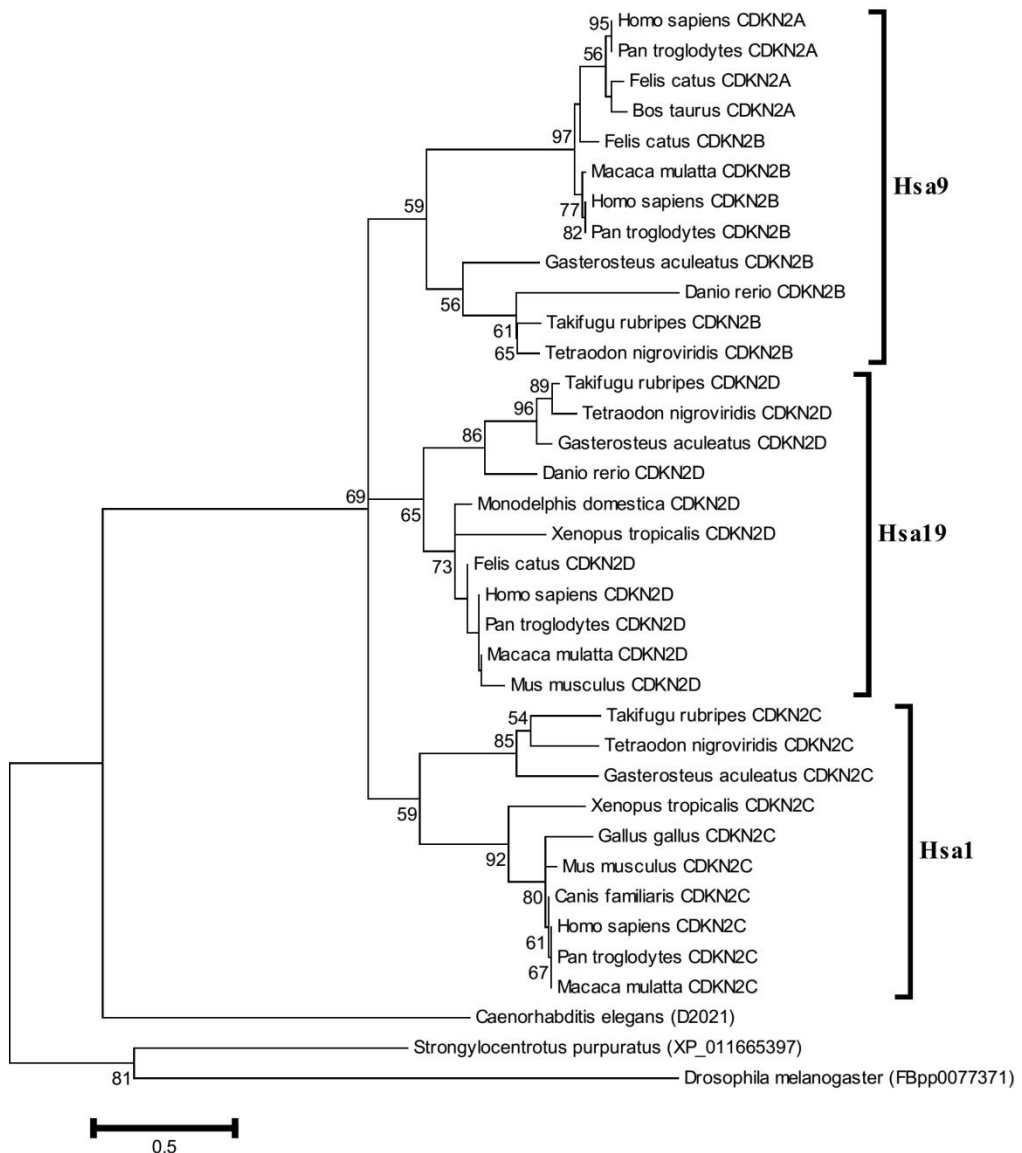
Mannosyl-oligosaccharide 1,2- α -mannosidase Family - MAN1



Phylogenetic tree of MAN1 family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-6966.9159) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.4678)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 58 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 259 positions in the final dataset.

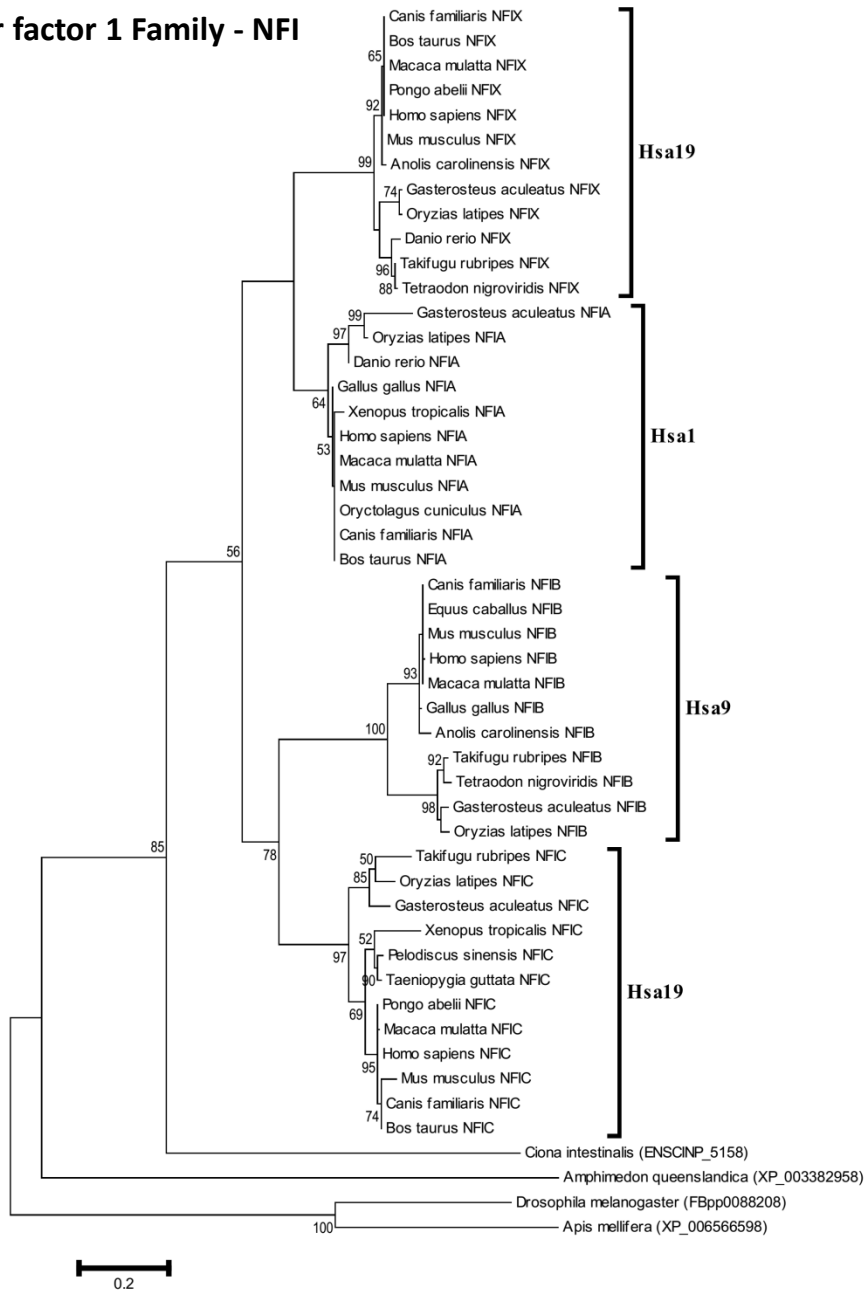
Cyclin-dependent kinase inhibitor Family - CDKN



Phylogenetic tree of CDKN family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-3189.0580) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.2871)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 36 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 97 positions in the final dataset.

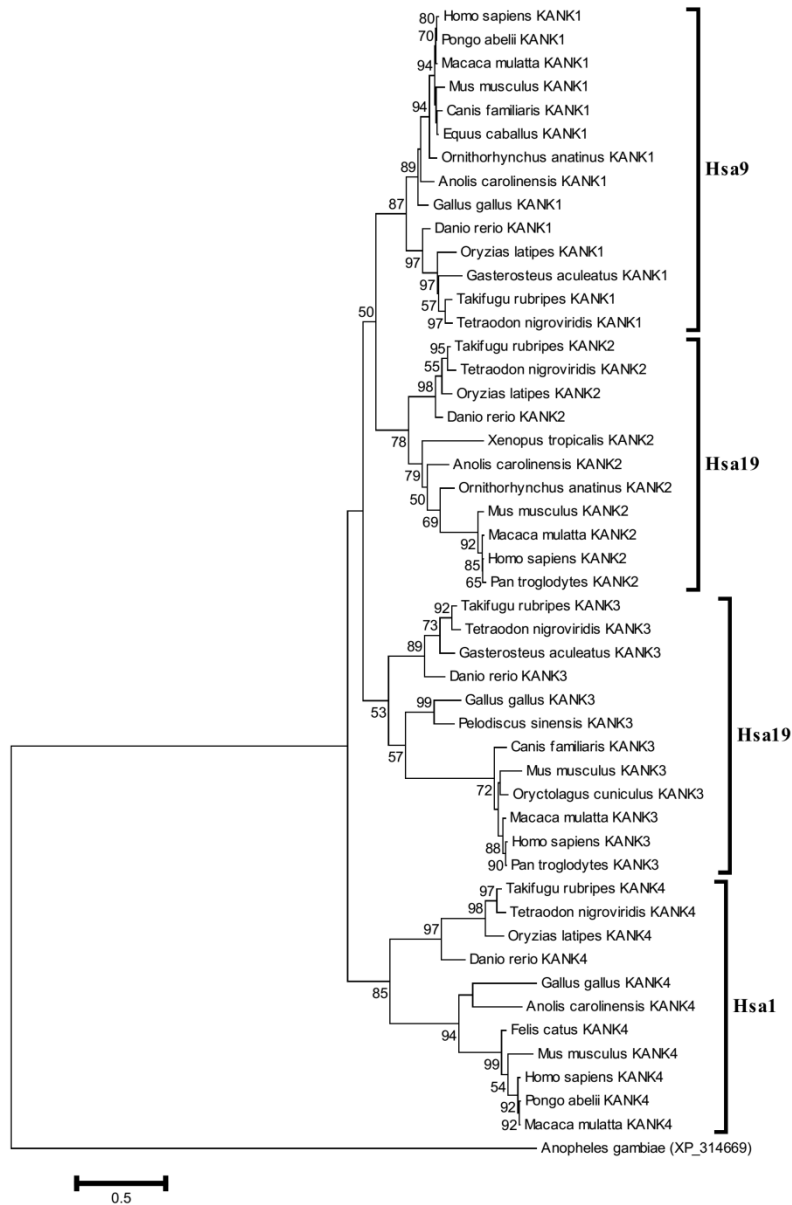
Nuclear factor 1 Family - NFI



Phylogenetic tree of NFI family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-4582.4588) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.4461)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 50 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 233 positions in the final dataset.

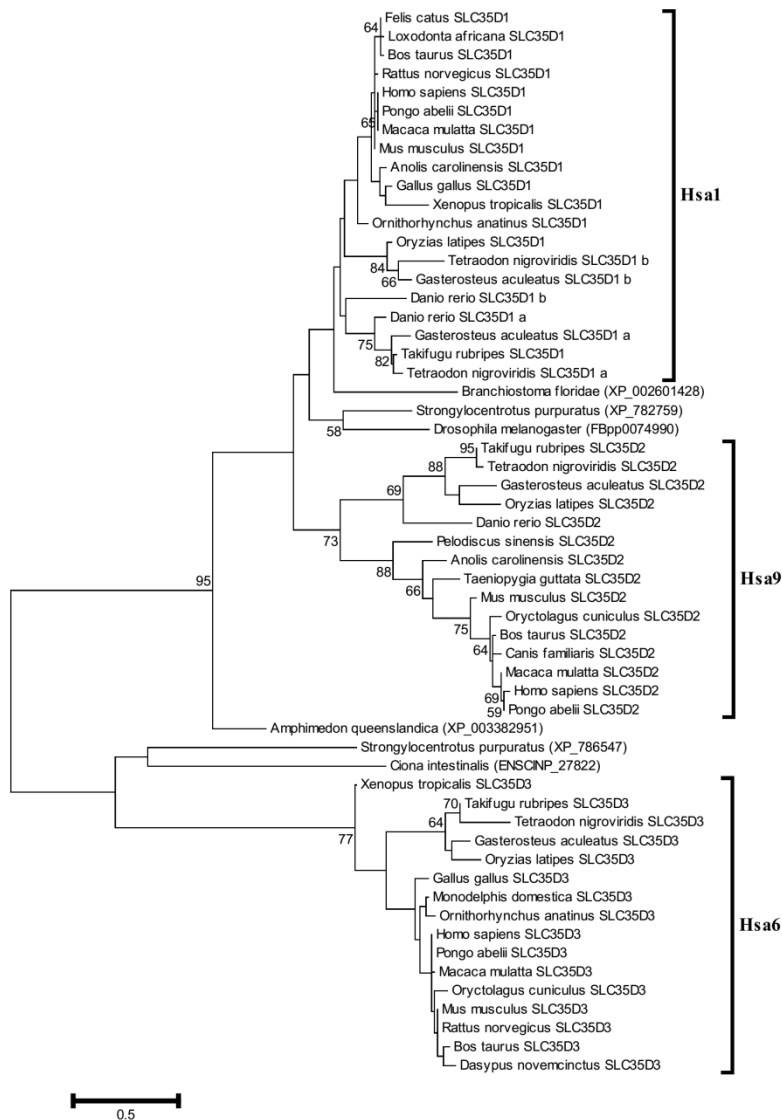
KN motif and ankyrin repeat domain Family - KANK



Phylogenetic tree of KANK family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-10533.3989) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.9893)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 49 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 282 positions in the final dataset.

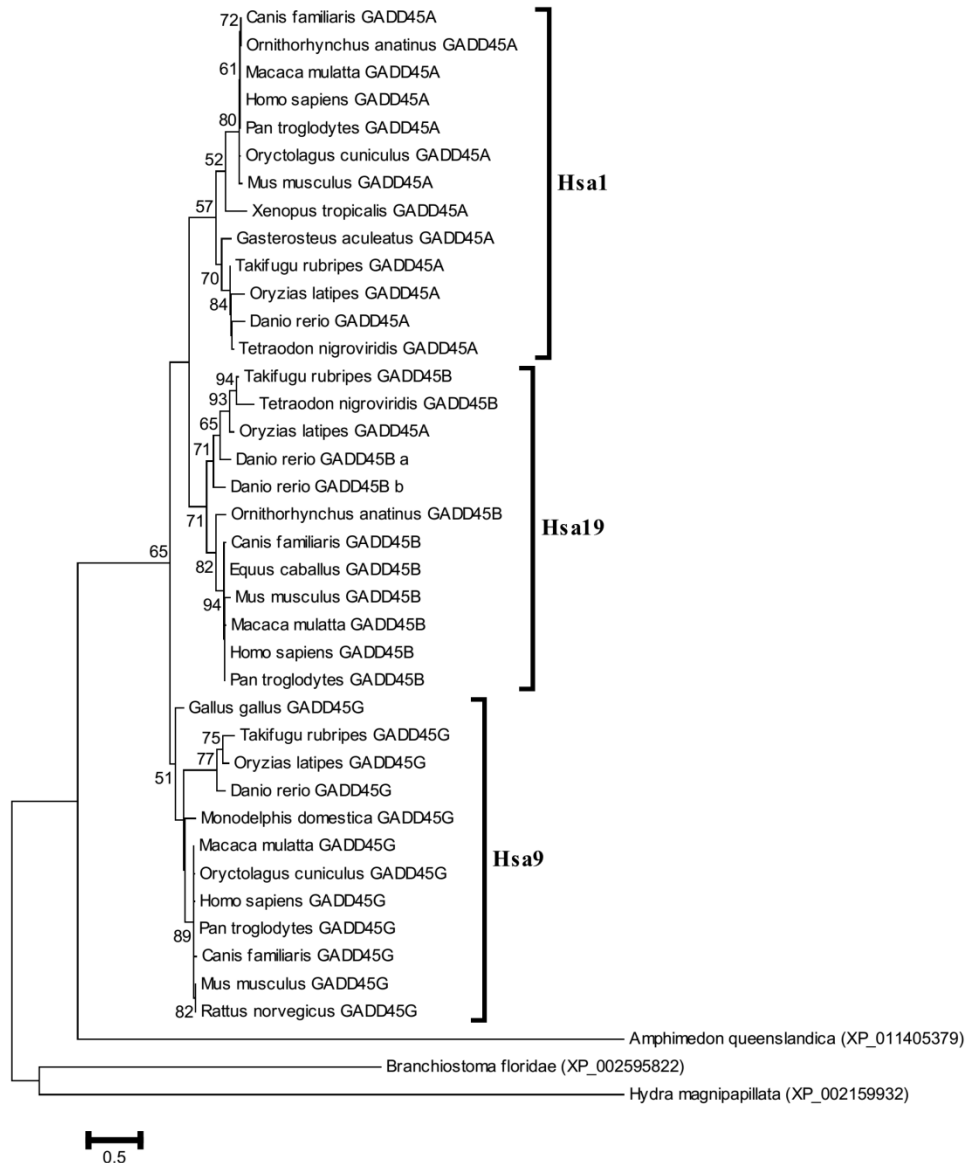
Solute carrier Family 35 – SLC35



Phylogenetic tree of SLC35 family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-3249.9514) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.5834)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 57 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 78 positions in the final dataset.

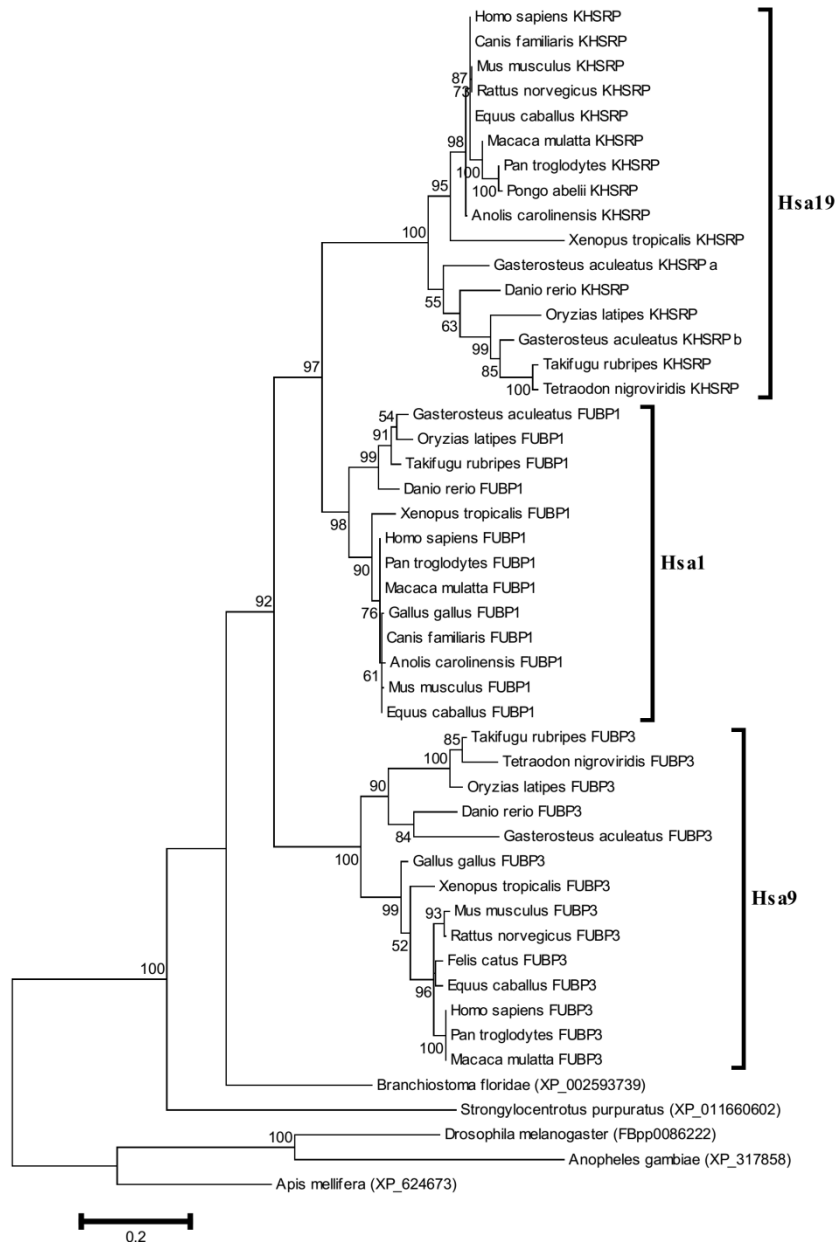
Growth arrest and DNA-damage-inducible 45 Family – GADD45



Phylogenetic tree of GADD45 family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-3394.5071) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.7142)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 40 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 128 positions in the final dataset.

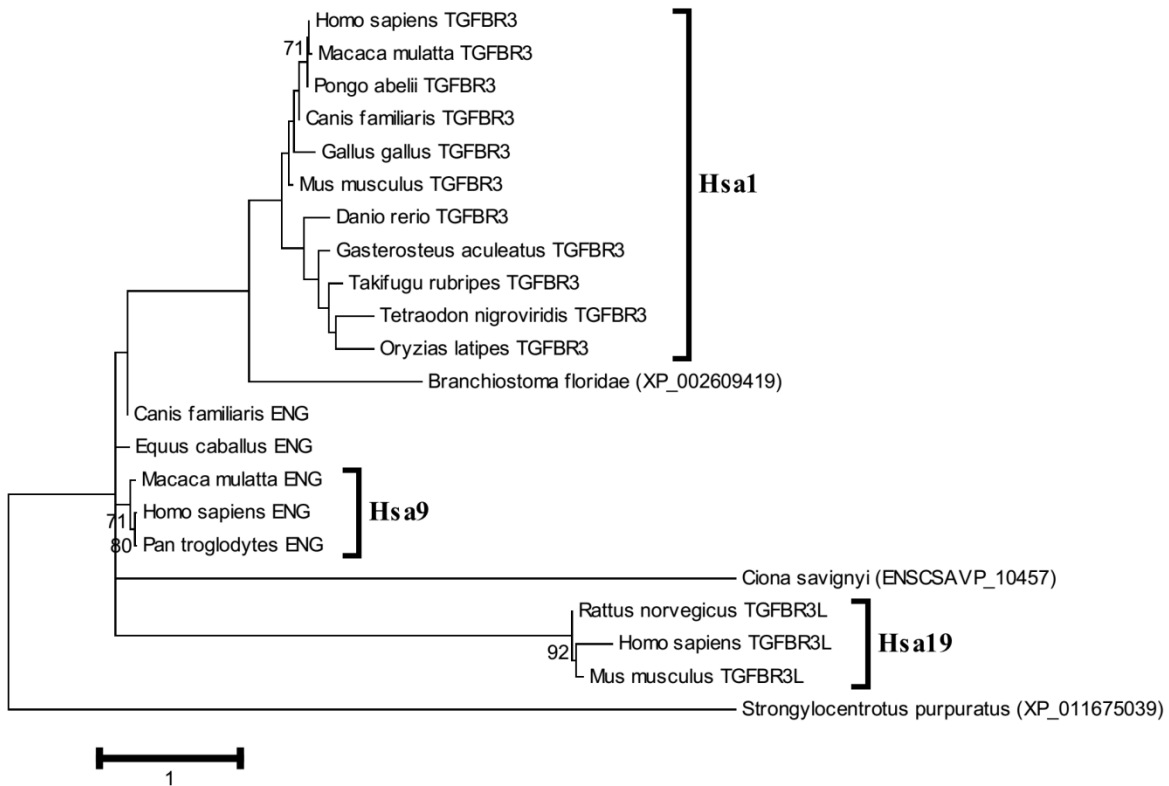
Far upstream element (FUSE) binding protein Family - FUBP



Phylogenetic tree of FUBP family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-7451.8903) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.1860)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 48 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 317 positions in the final dataset.

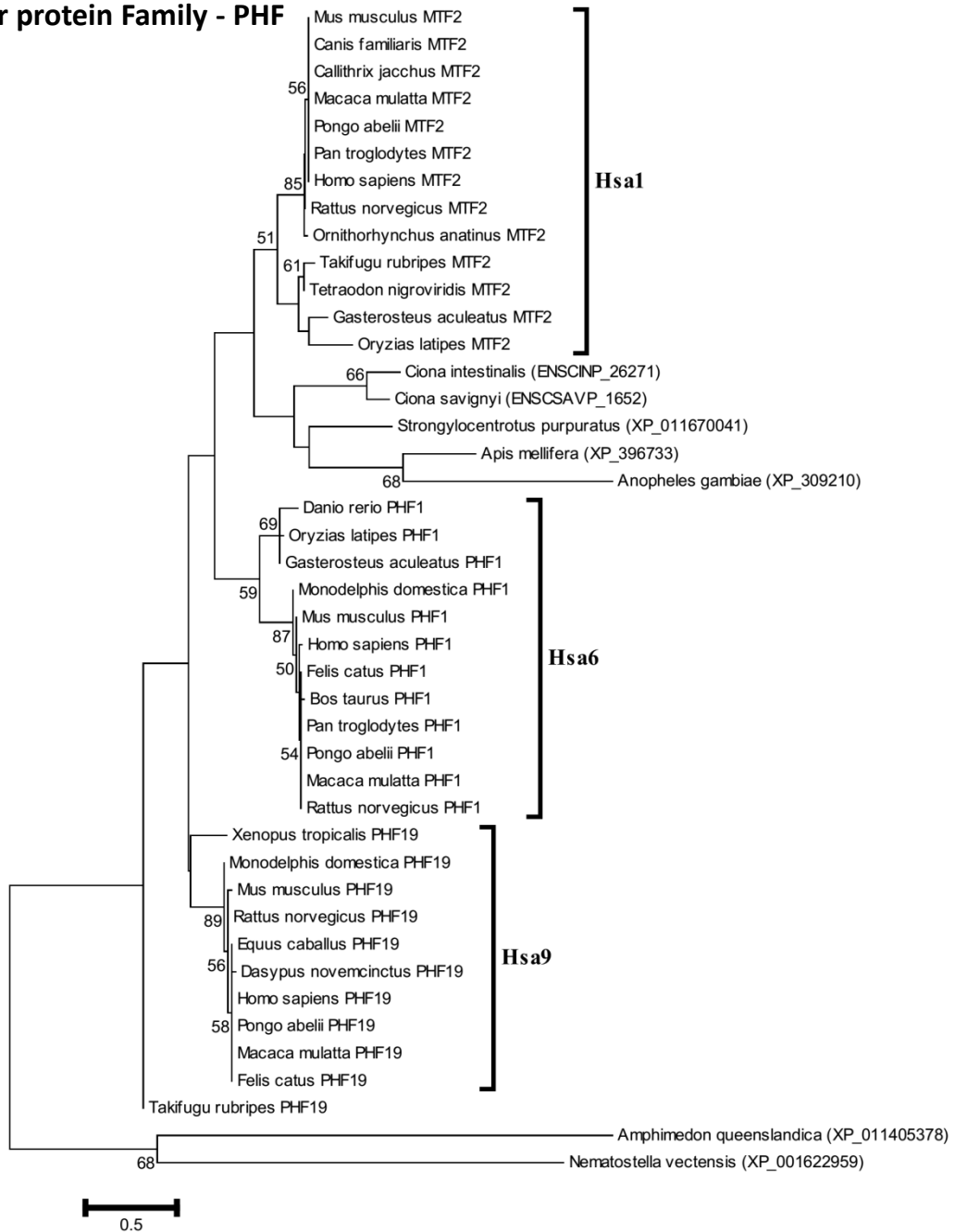
Transforming growth factor beta receptor Family - TGFBR



Phylogenetic tree of TGFBR family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-2707.3453) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 8.3530)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 22 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 104 positions in the final dataset.

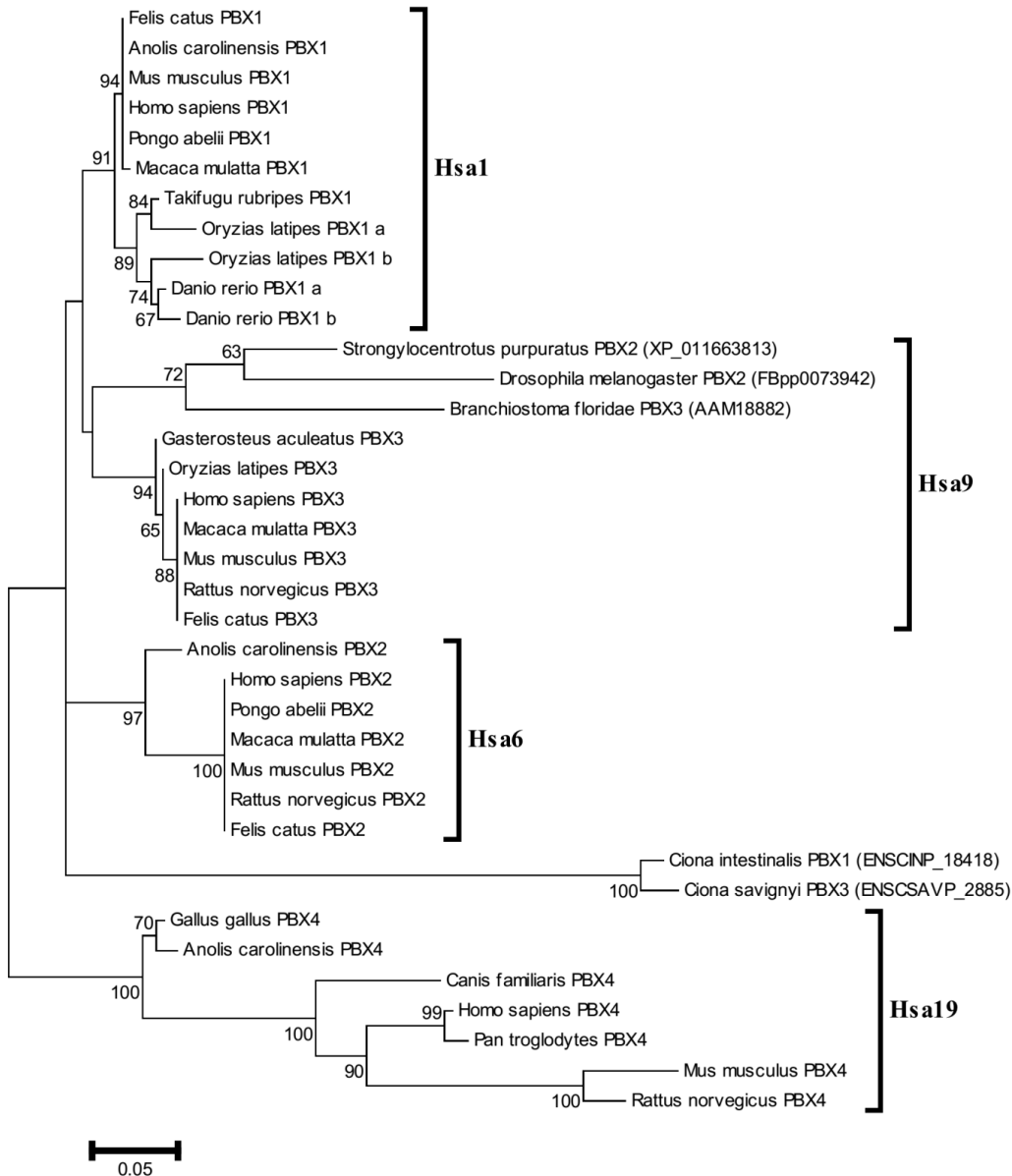
PHD finger protein Family - PHF



Phylogenetic tree of PHF family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-1456.5399) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 6.7924)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 43 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 49 positions in the final dataset.

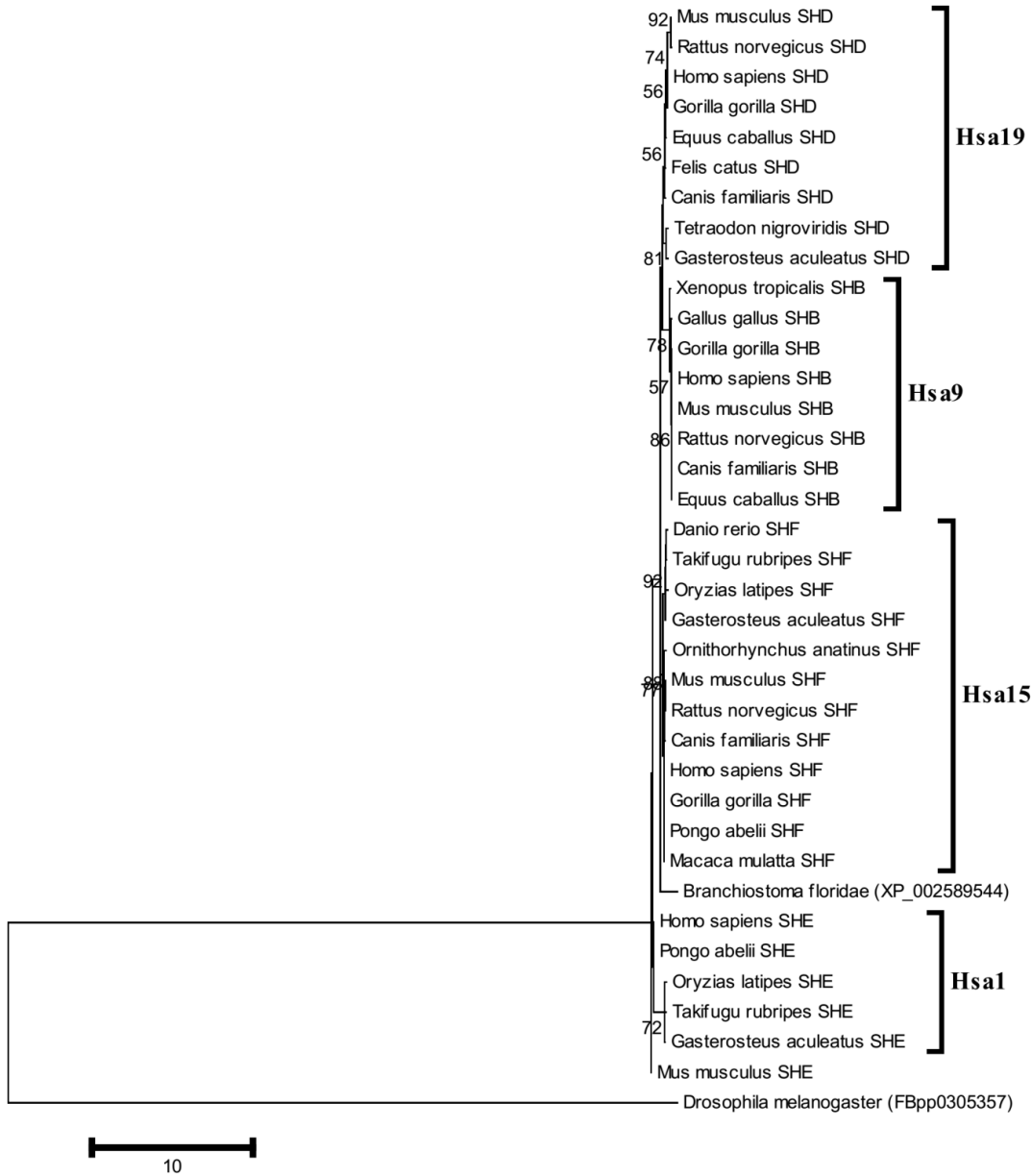
pre-B-cell leukemia homeobox - PBX



Phylogenetic tree of PBX family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-2584.1004) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.6633)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 37 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 236 positions in the final dataset.

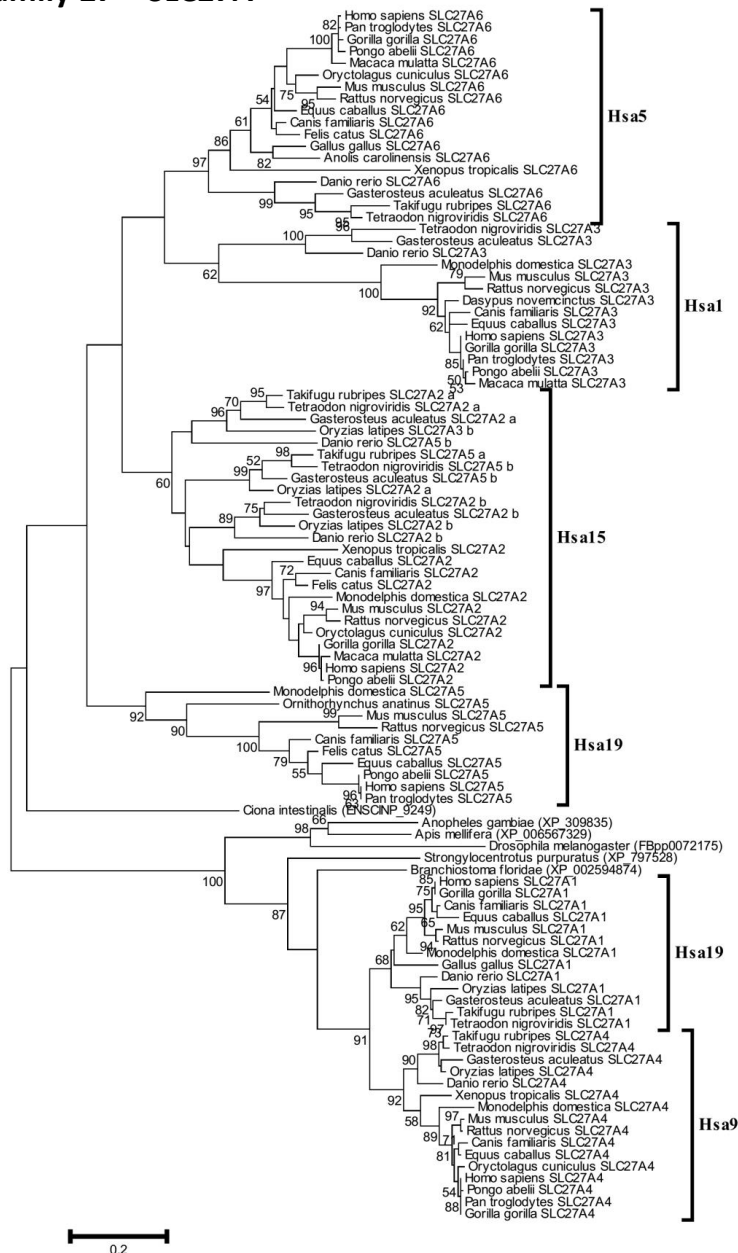
Src homology 2 domain containing adaptor protein - SH



Phylogenetic tree of SH family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-1152.2466) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.9993)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 37 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 49 positions in the final dataset.

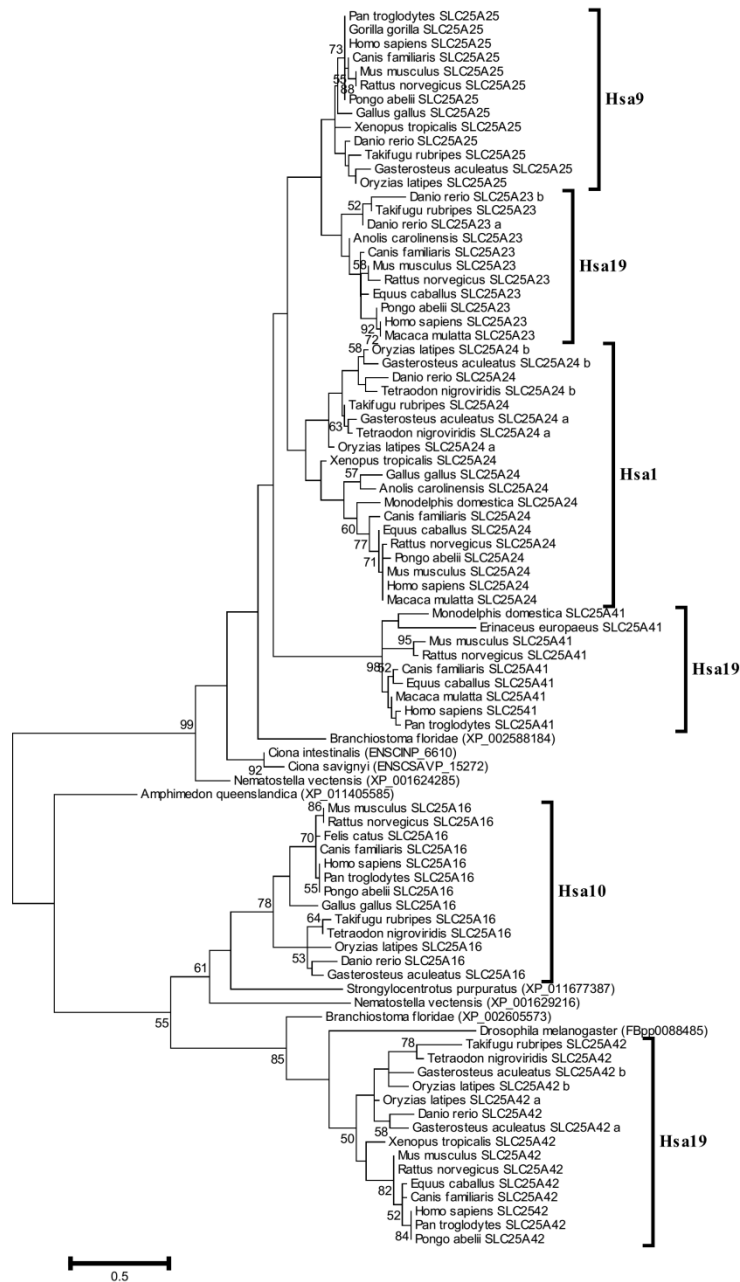
Solute carrier family 27 – SLC27A



Phylogenetic tree of SLC27A family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-11142.7088) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.3149)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 102 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 192 positions in the final dataset.

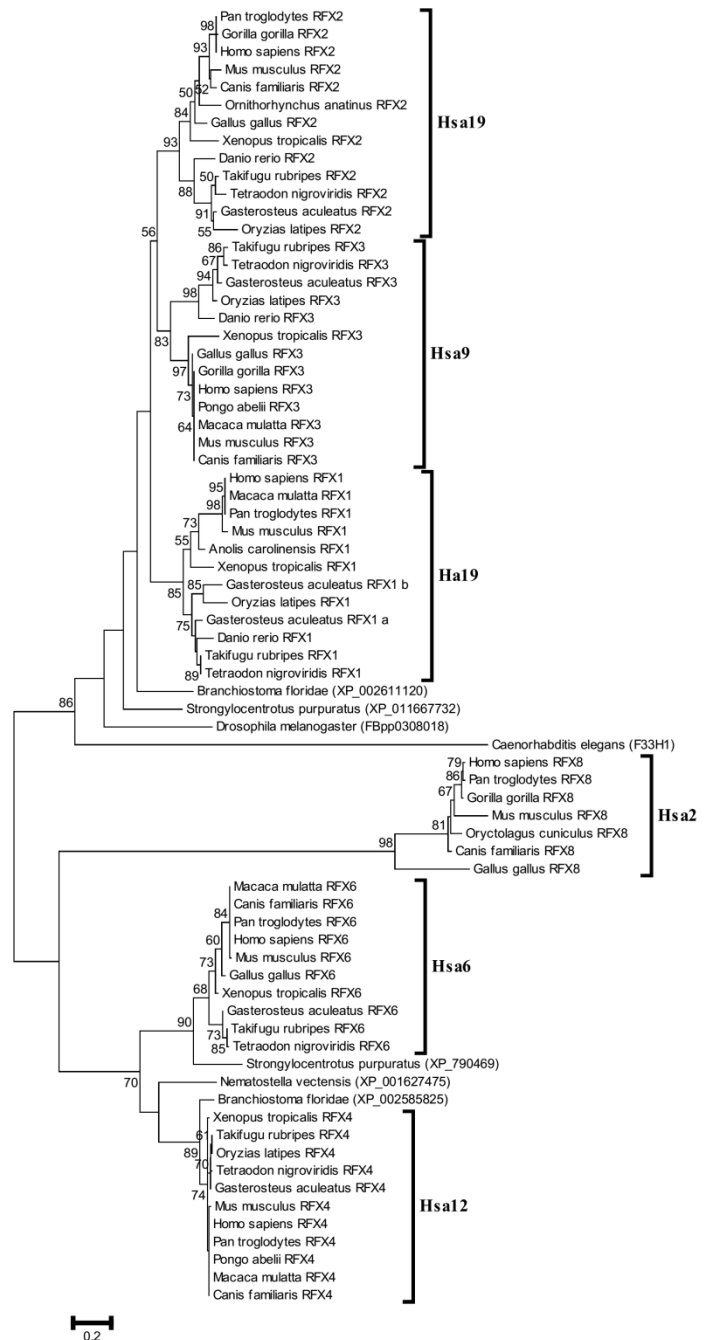
Solute carrier family 25 – SLC25A



Phylogenetic tree of SLC25A family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-2862.7998) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.0999)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 89 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 67 positions in the final dataset.

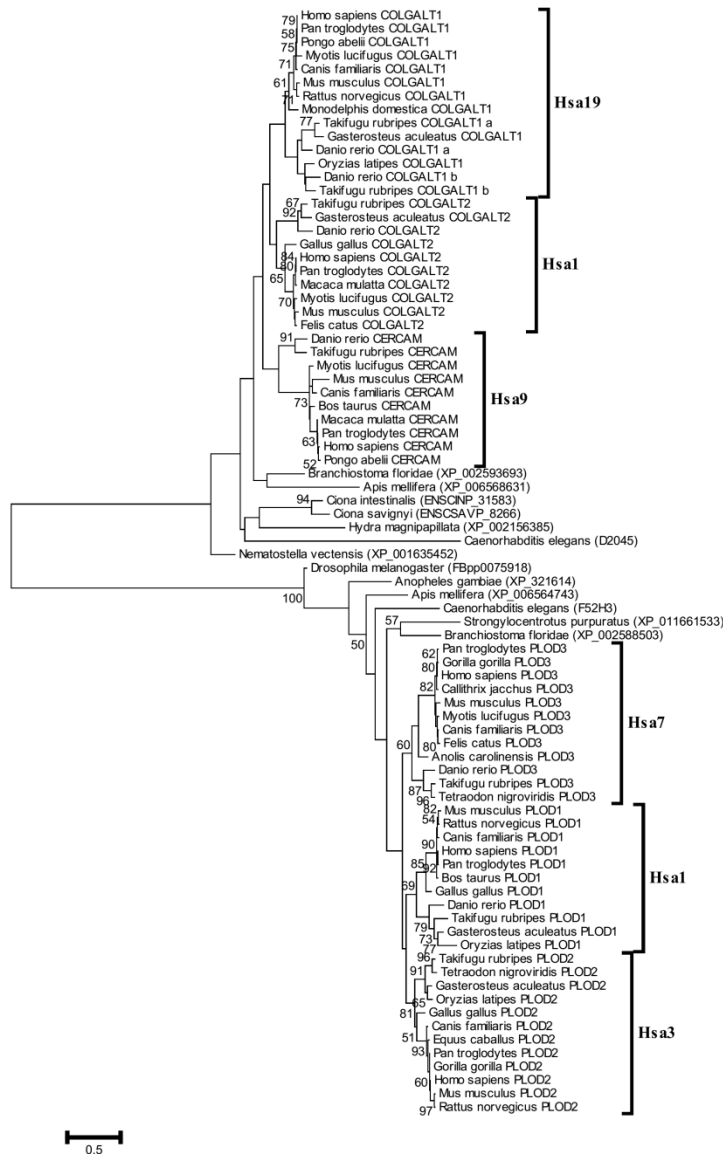
Regulatory factor X protein - RFX



Phylogenetic tree of RFX family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-4912.8183) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.7491)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 73 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 121 positions in the final dataset.

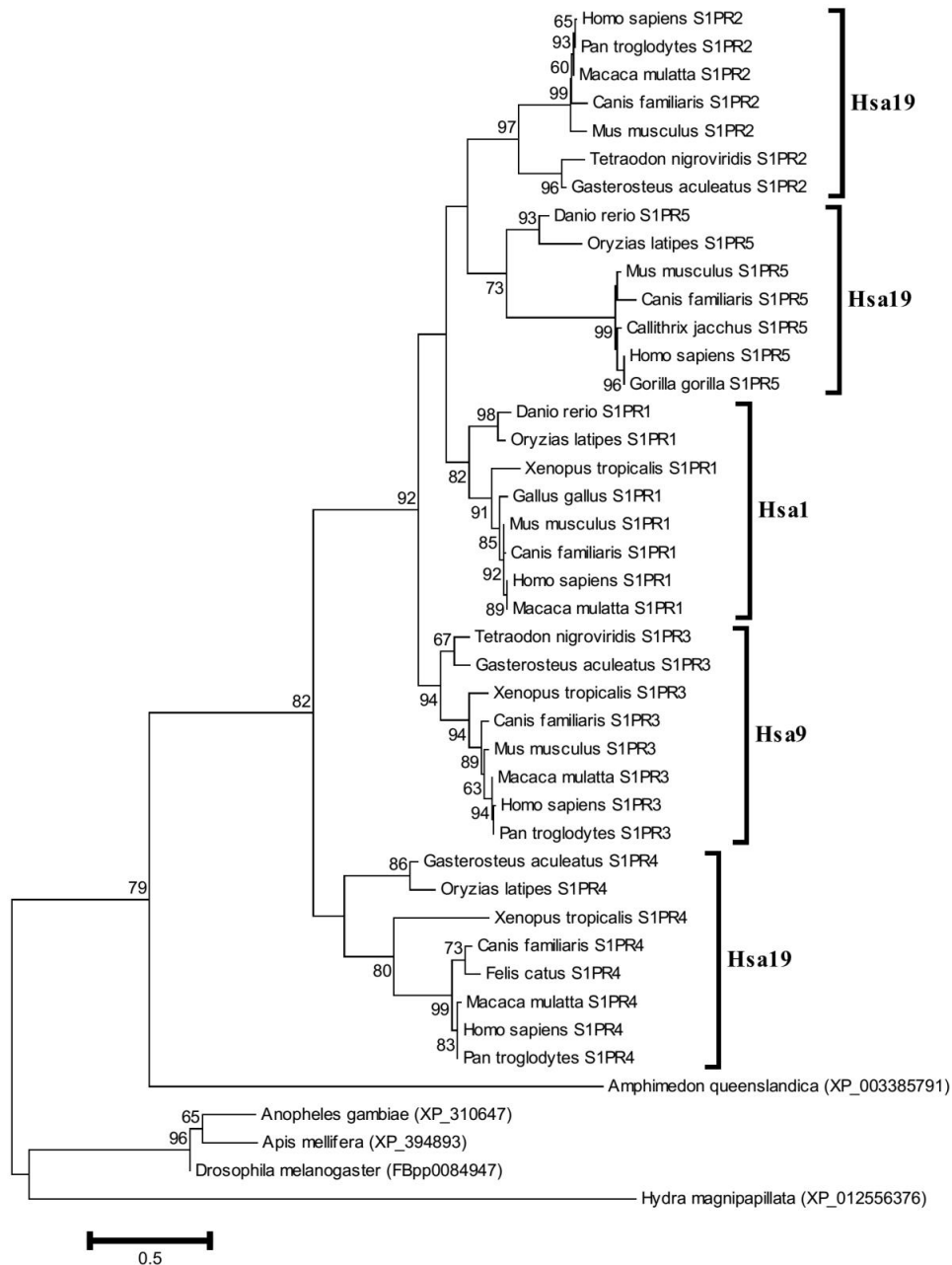
Hydroxylysine galactosyltransferase - COLGALT



Phylogenetic tree of COLGALT family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-11134.0663) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 4.7319)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 82 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 187 positions in the final dataset.

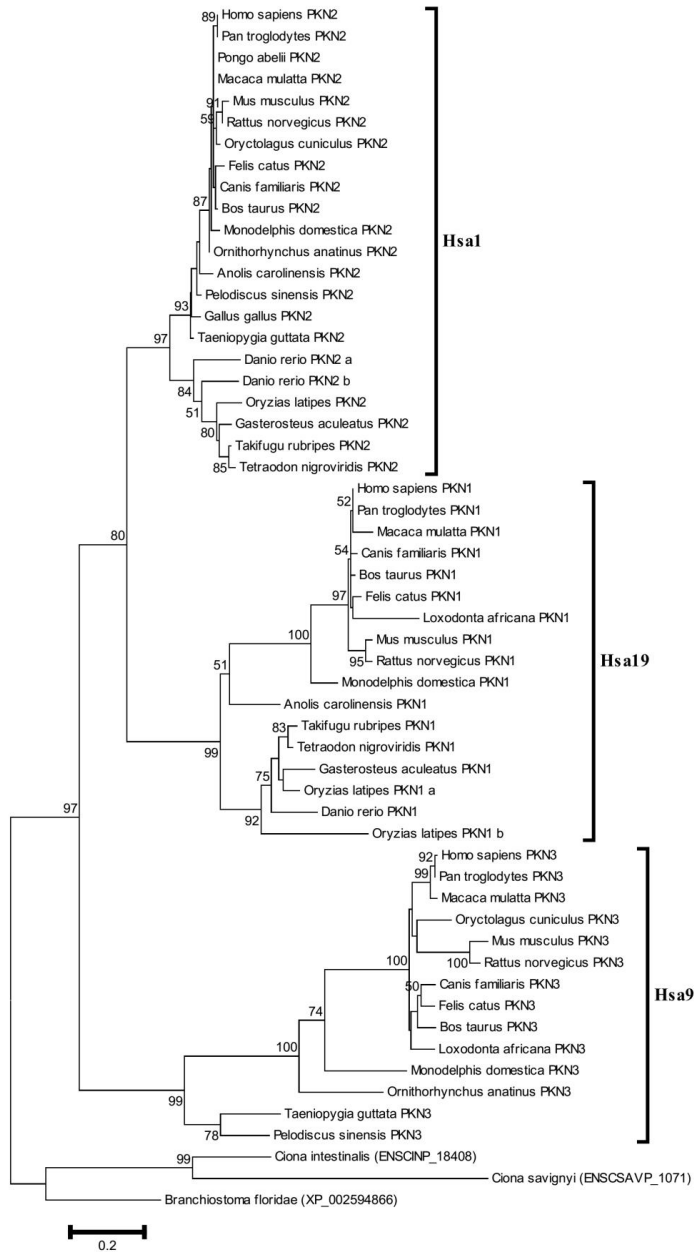
Sphingosine-1-phosphate receptor – S1PR



Phylogenetic tree of S1PR family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-4897.5756) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.4390)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 43 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 157 positions in the final dataset.

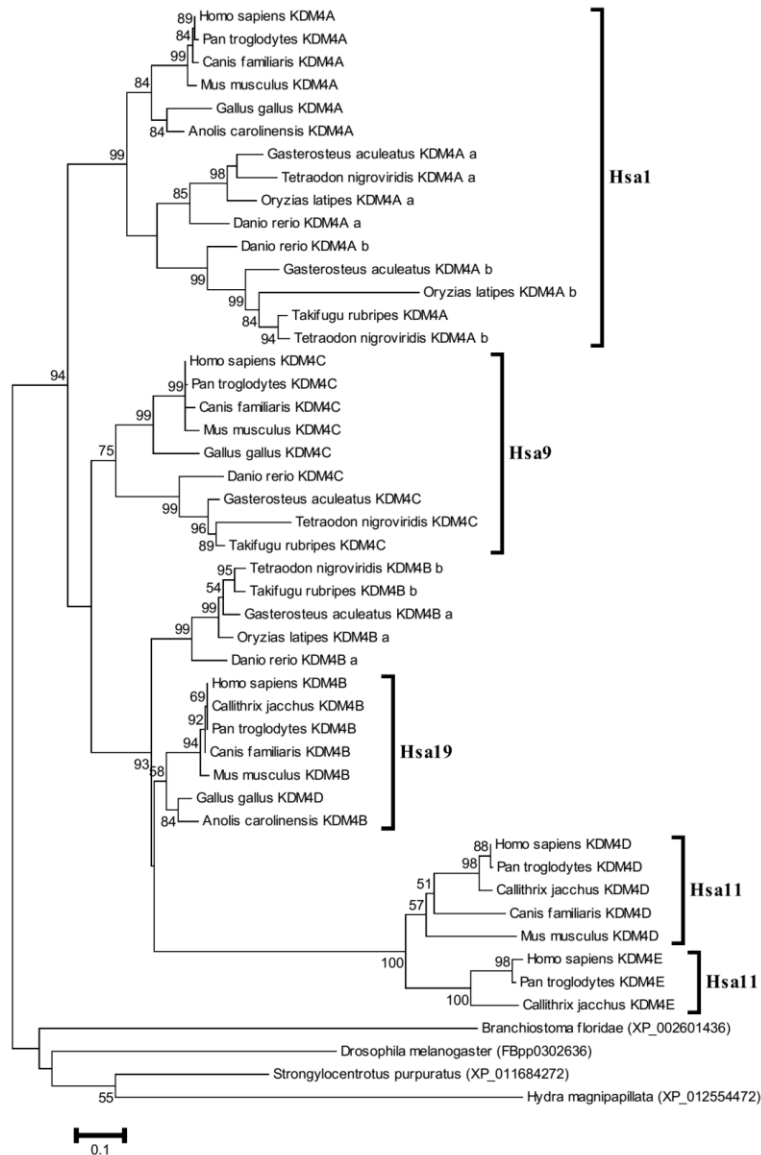
Protein-kinase C-related kinase - PKN



Phylogenetic tree of PKN family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-5657.8652) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.9335)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 56 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 209 positions in the final dataset.

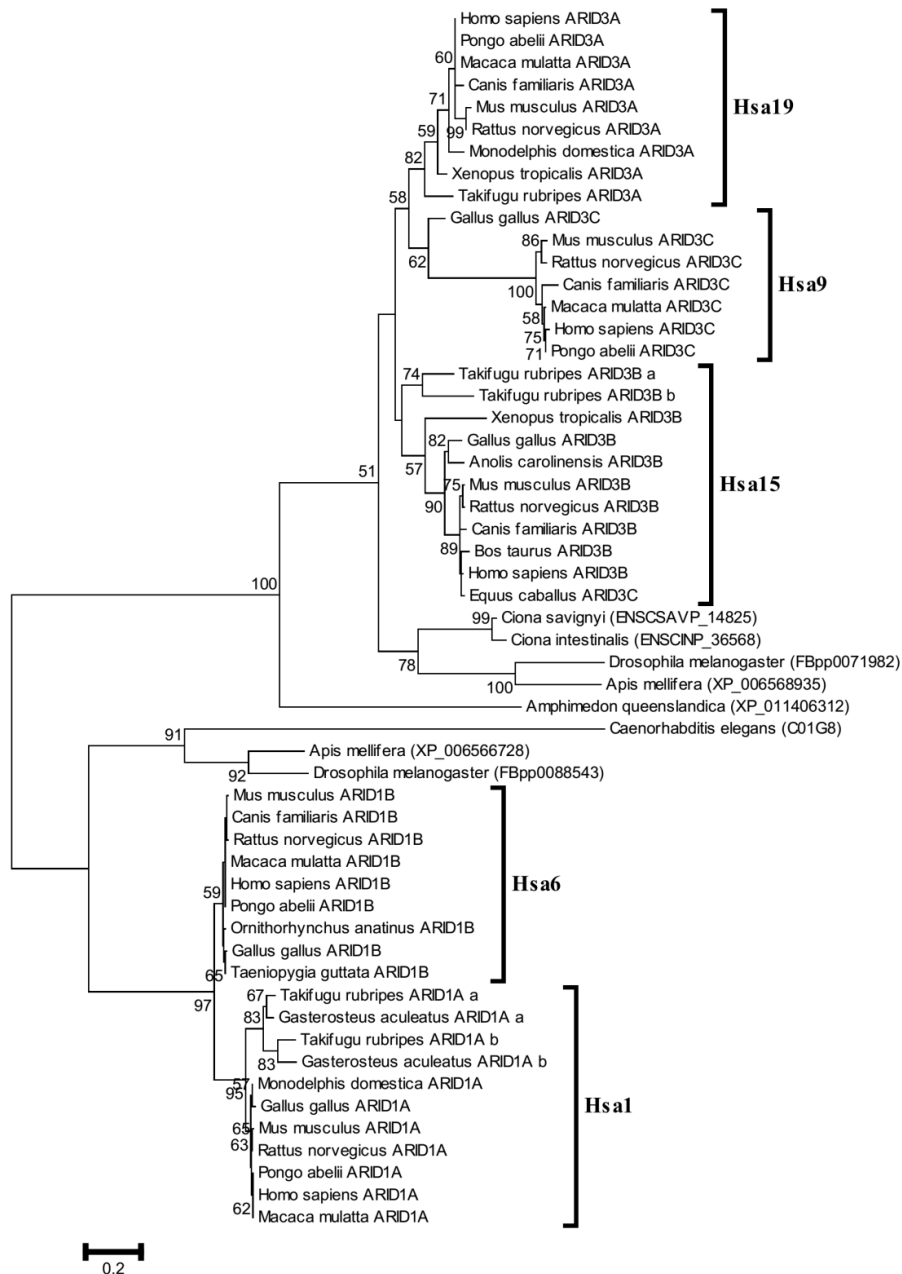
Lysine-specific demethylase - KDM



Phylogenetic tree of KDM family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-8340.4583) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.8890)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 48 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 317 positions in the final dataset.

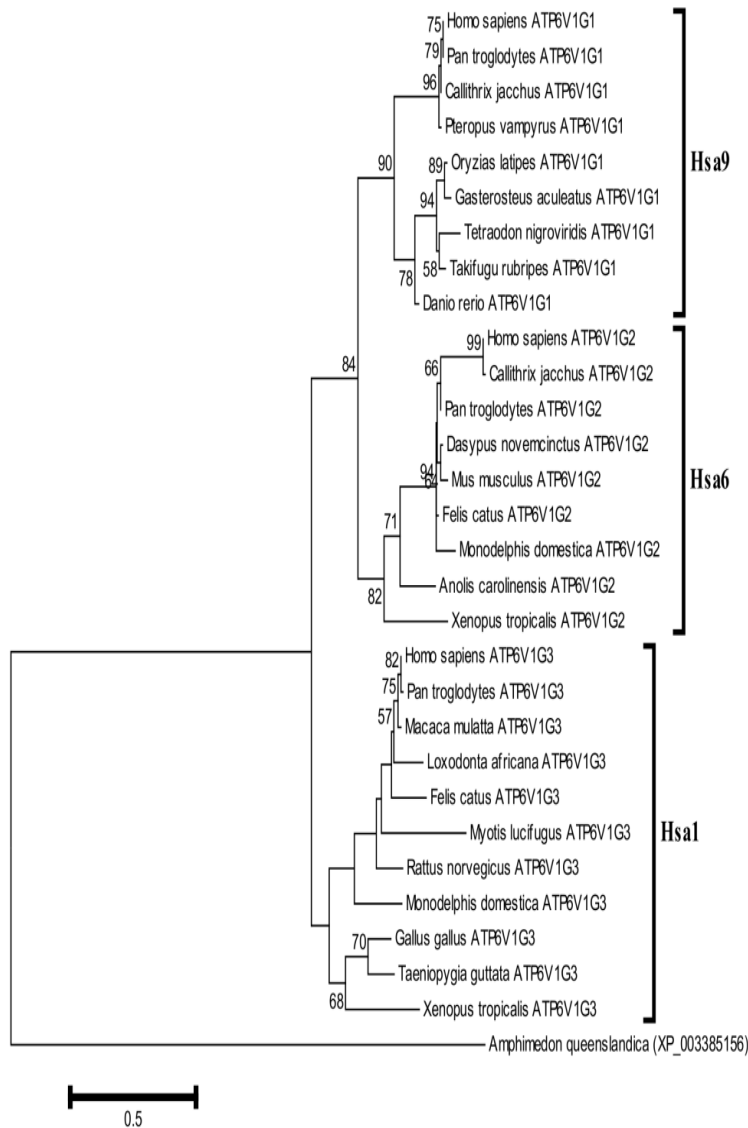
AT-rich interactive domain-containing protein - ARID



Phylogenetic tree of ARID family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-5682.5244) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches ; only the values $\geq 50\%$ are shown here. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.5825)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 55 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 185 positions in the final dataset.

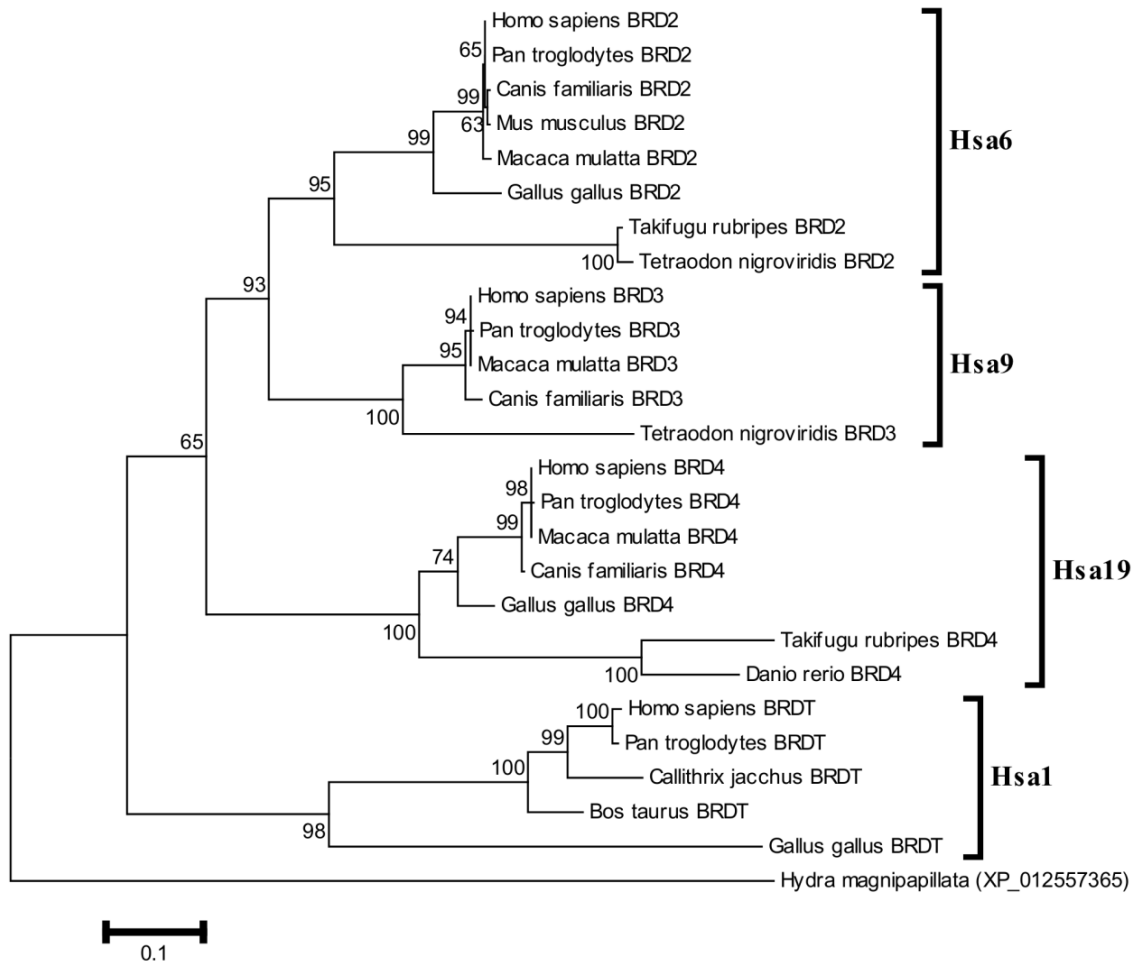
ATPase, H⁺ transporting subunits – ATP6V1G



Phylogenetic tree of ATP6V1G family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-2672.6131) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.5685)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 30 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 116 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

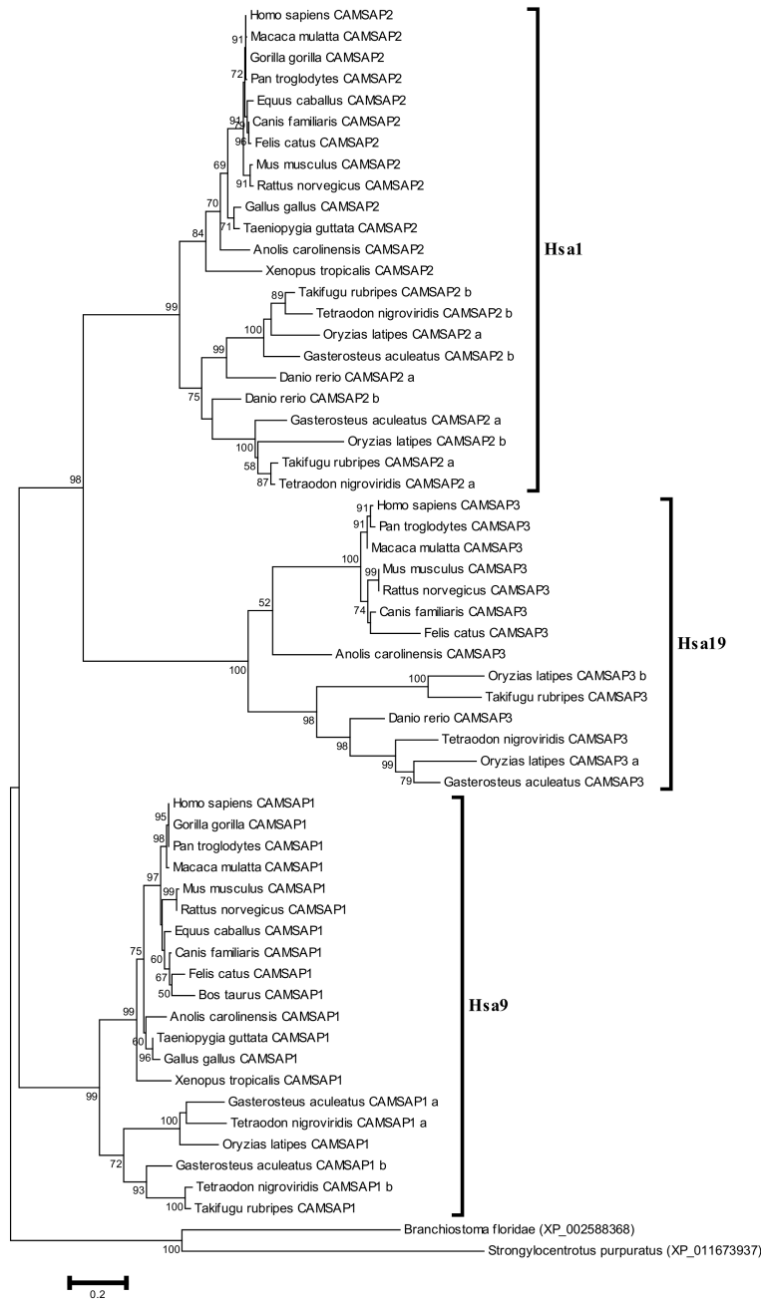
Bromodomain containing family - BRD



Phylogenetic tree of BRD family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-6858.4268) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.2440)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 26 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 425 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

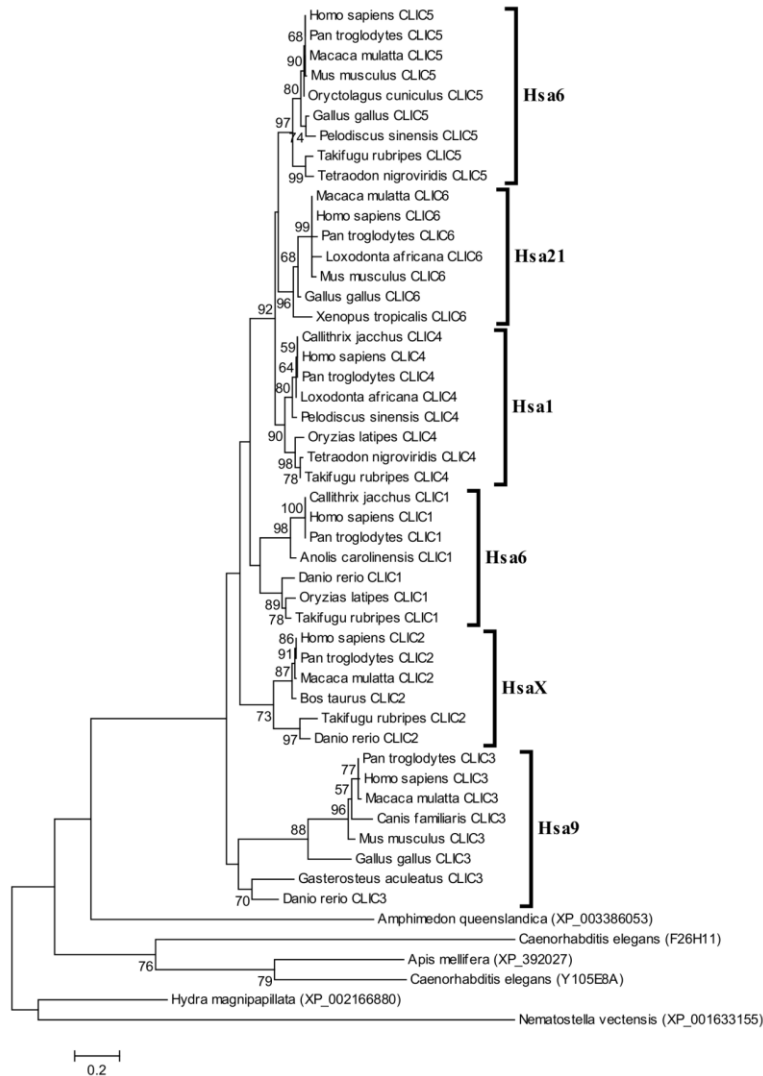
Calmodulin regulated spectrin associated protein family - CAMSAP



Phylogenetic tree of CAMSAP family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-11584.3600) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.8492)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 59 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 293 positions in the final dataset. Evolutionary analyses were conducted in MEGA5 .

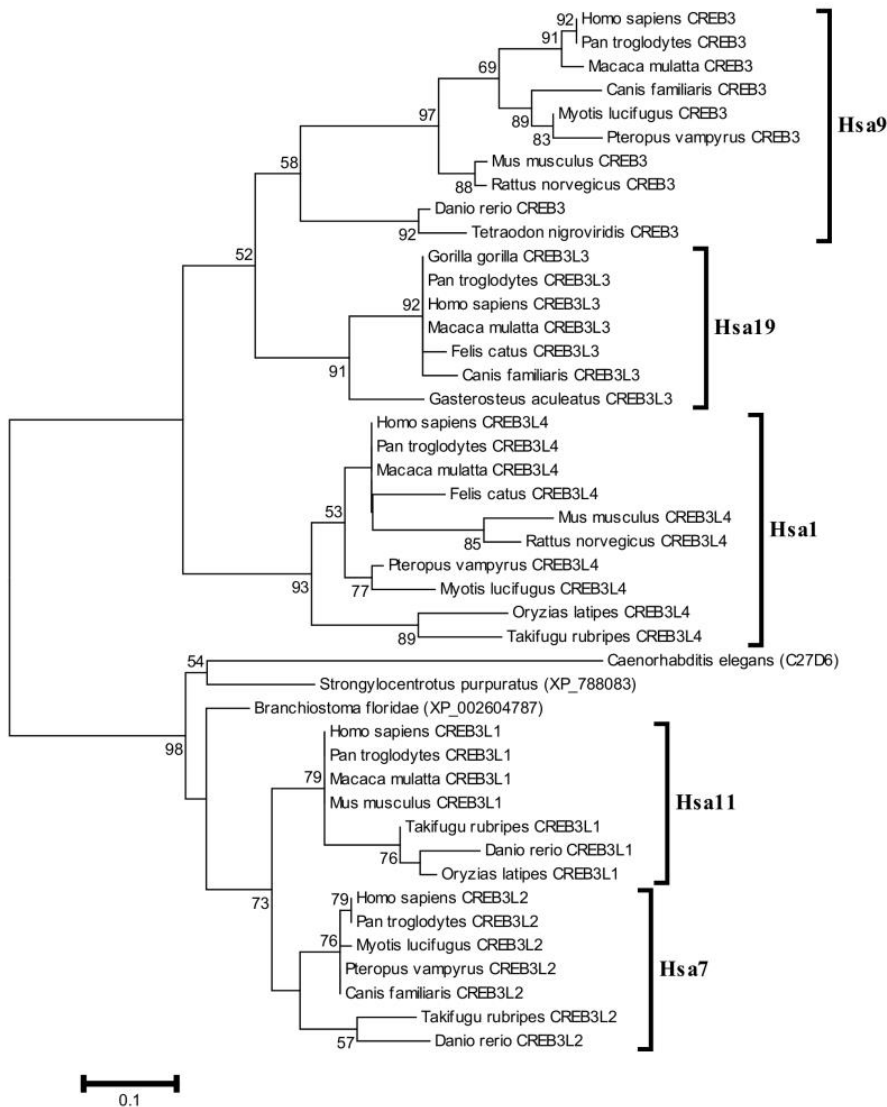
Chloride intracellular channel family - CLIC



Phylogenetic tree of CLIC family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-5664.1715) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.9886)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 51 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 173 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

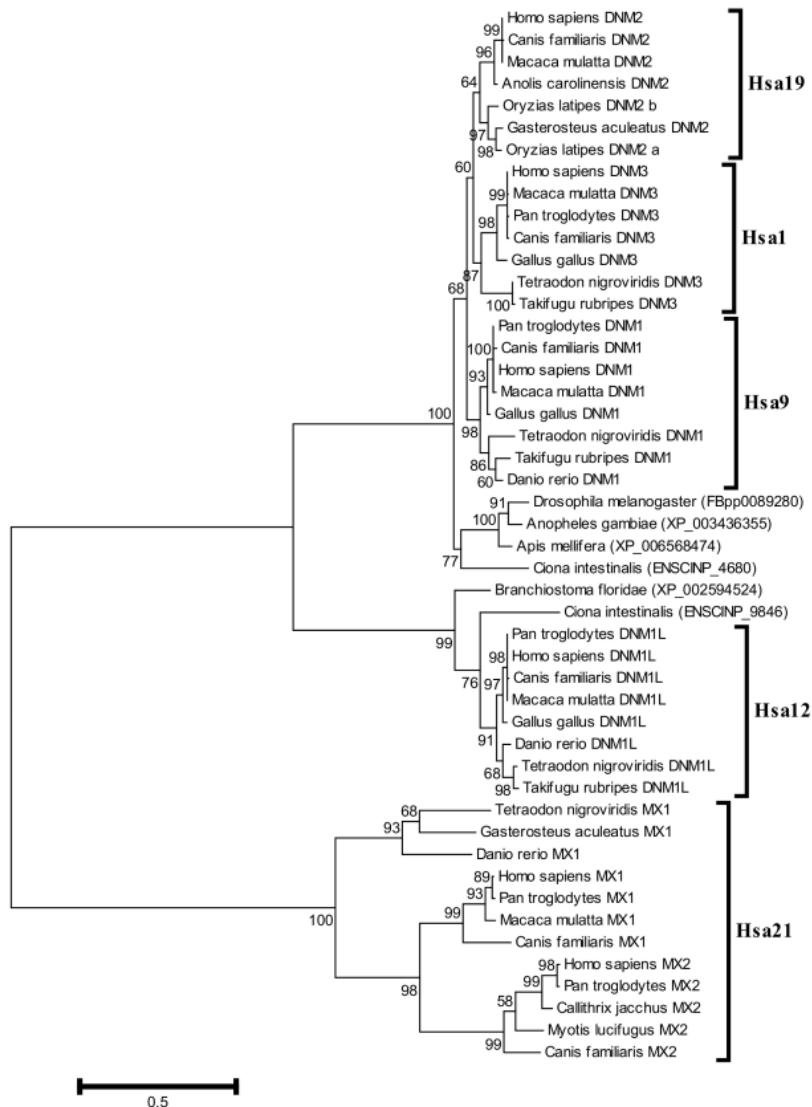
cAMP responsive element binding protein family - CREB



Phylogenetic tree of CREB family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-1425.2775) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.8537)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 44 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 74 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

Dynamin family - DNM



Phylogenetic tree of DNM family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-12391.2592) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.2824)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 48 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 464 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

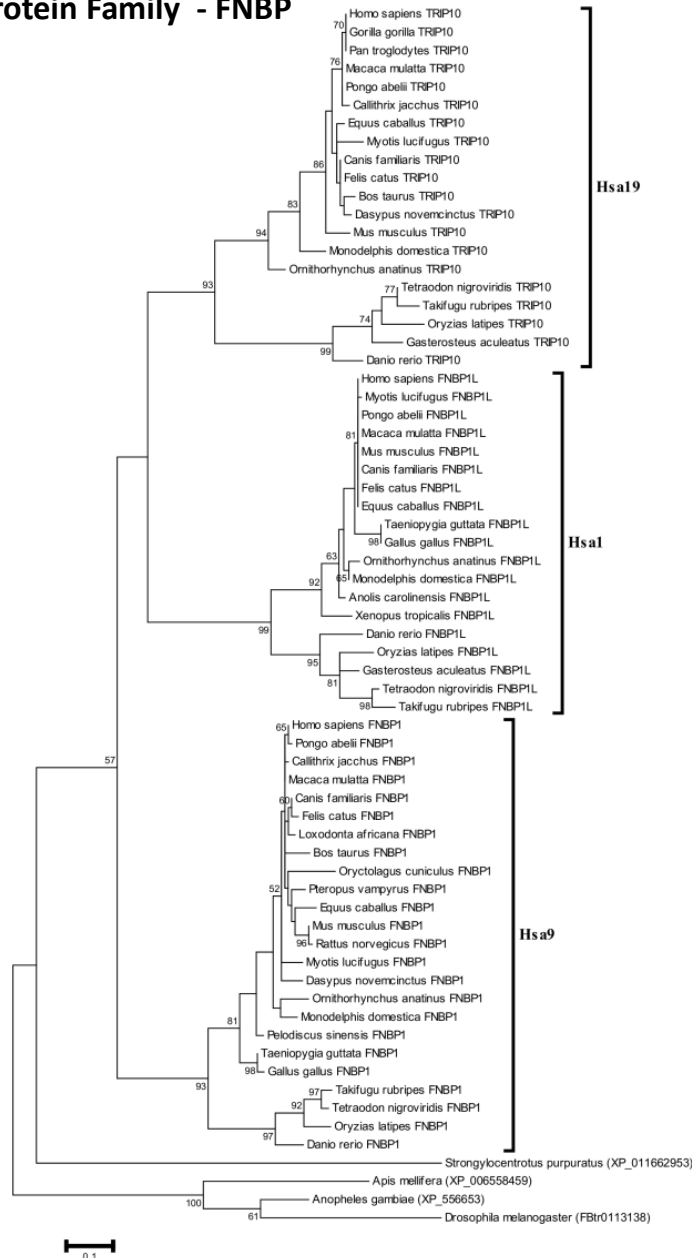
Family with sequence similarity 129 - FAM129



Phylogenetic tree of FAM129 family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-9732.4364) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 5.4001)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 36 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 269 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

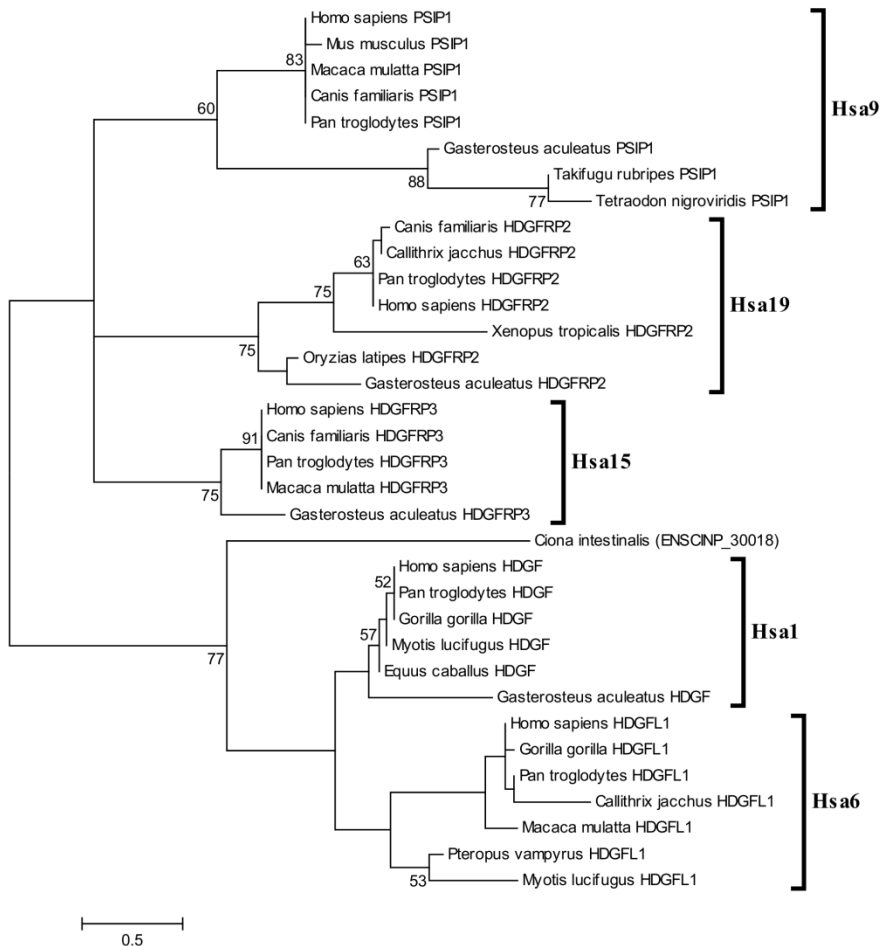
Formin binding protein Family - FNBP



Phylogenetic tree of FNBP family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-3784.2092) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.9652)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 67 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 127 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

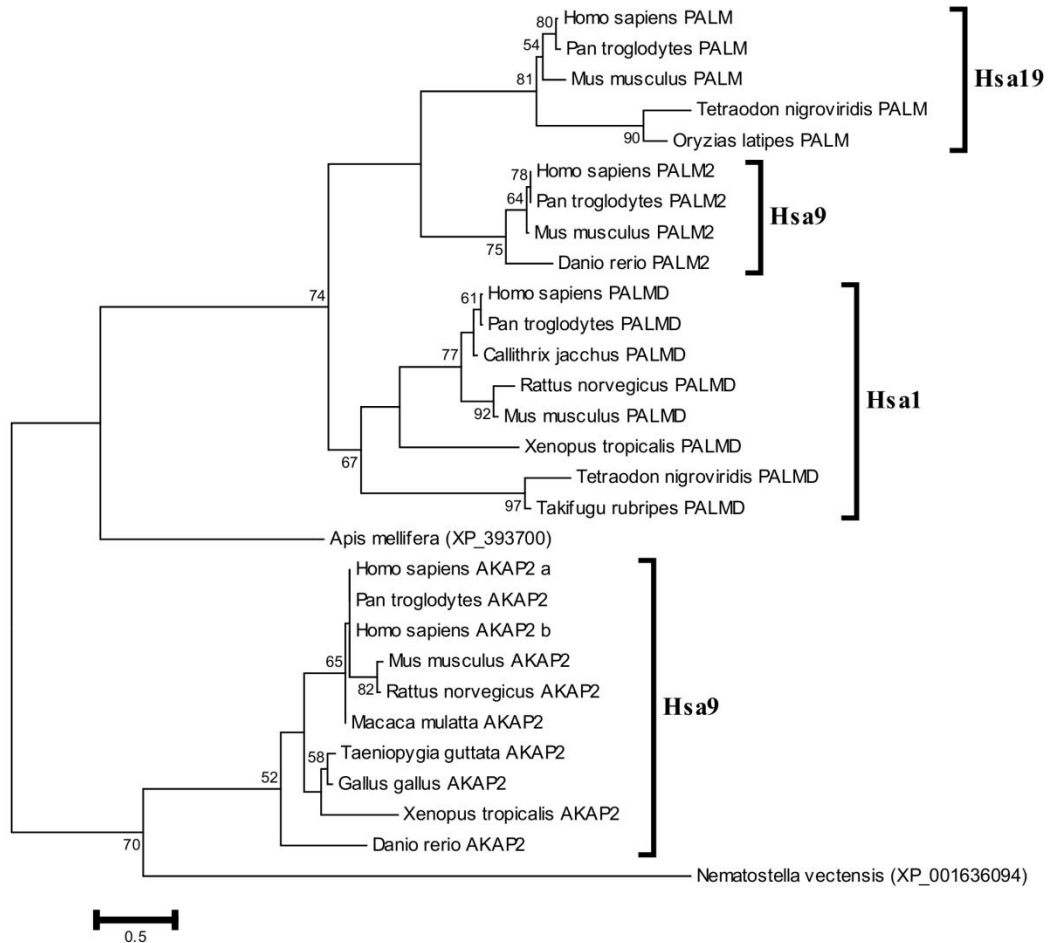
Hepatoma derived growth factor family - HDGF



Phylogenetic tree of HDGF family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-949.1877) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 12.2433)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 34 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 26 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

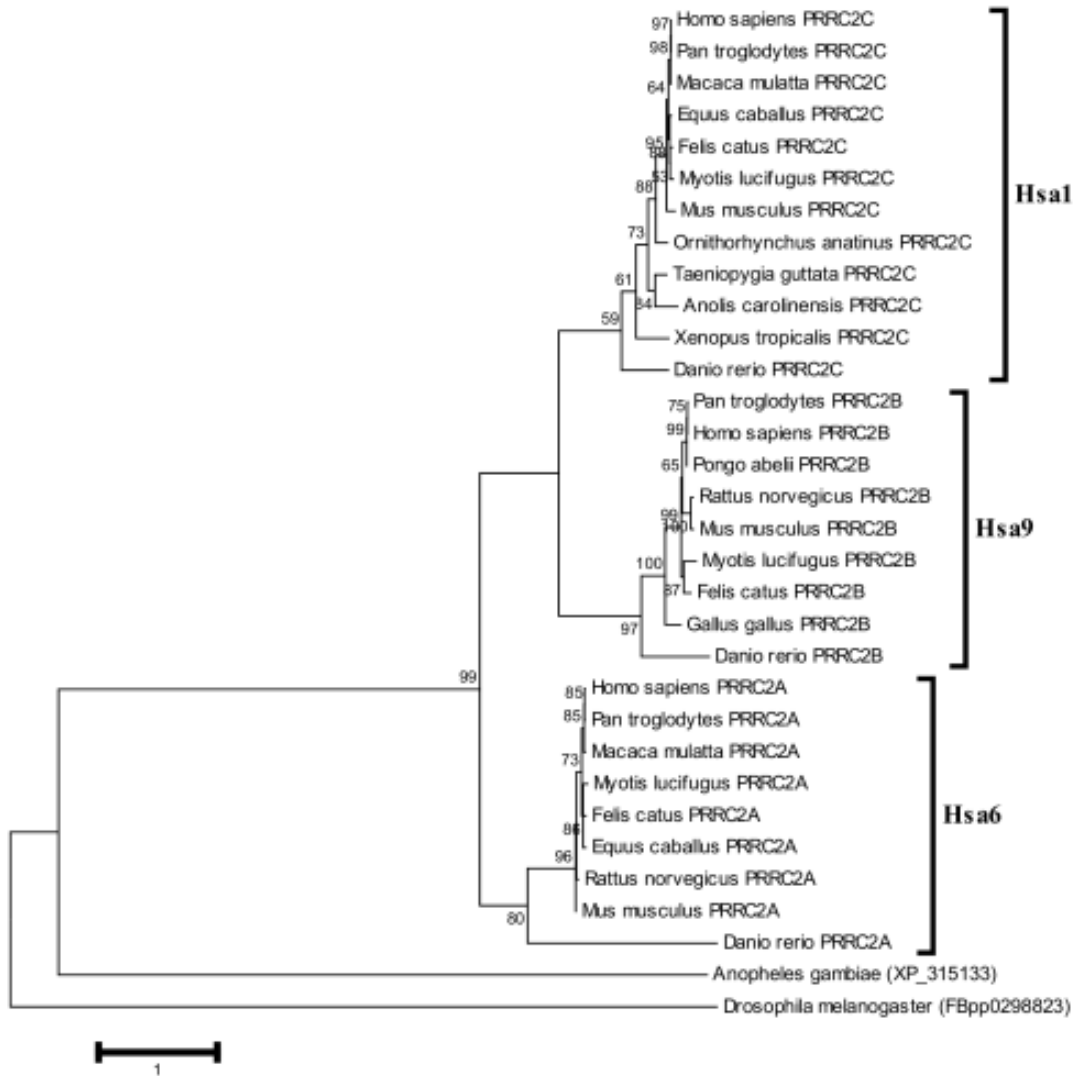
Palmdelphin - PALM



Phylogenetic tree of PALM family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-4267.0816) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 18.9161)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 29 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 113 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

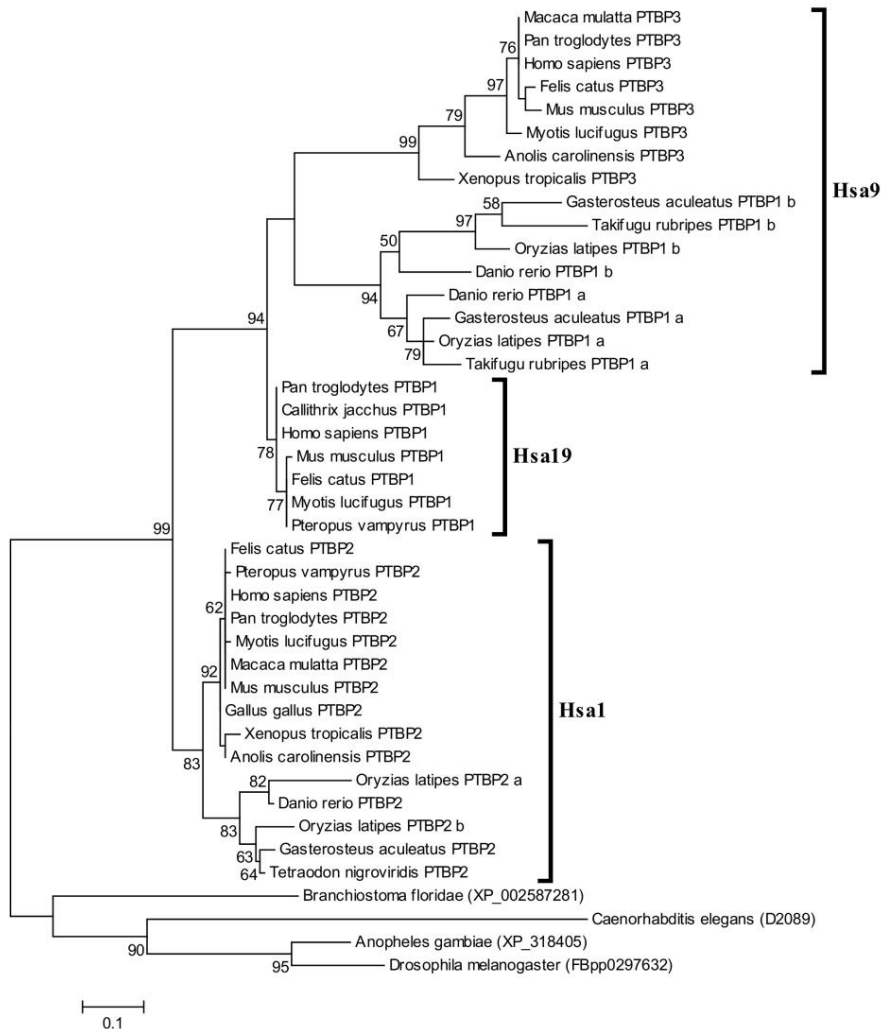
Proline rich coiled coil - PRRC2



Phylogenetic tree of PRRC2 family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-32888.1436) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 5.6992)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 32 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 1179 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

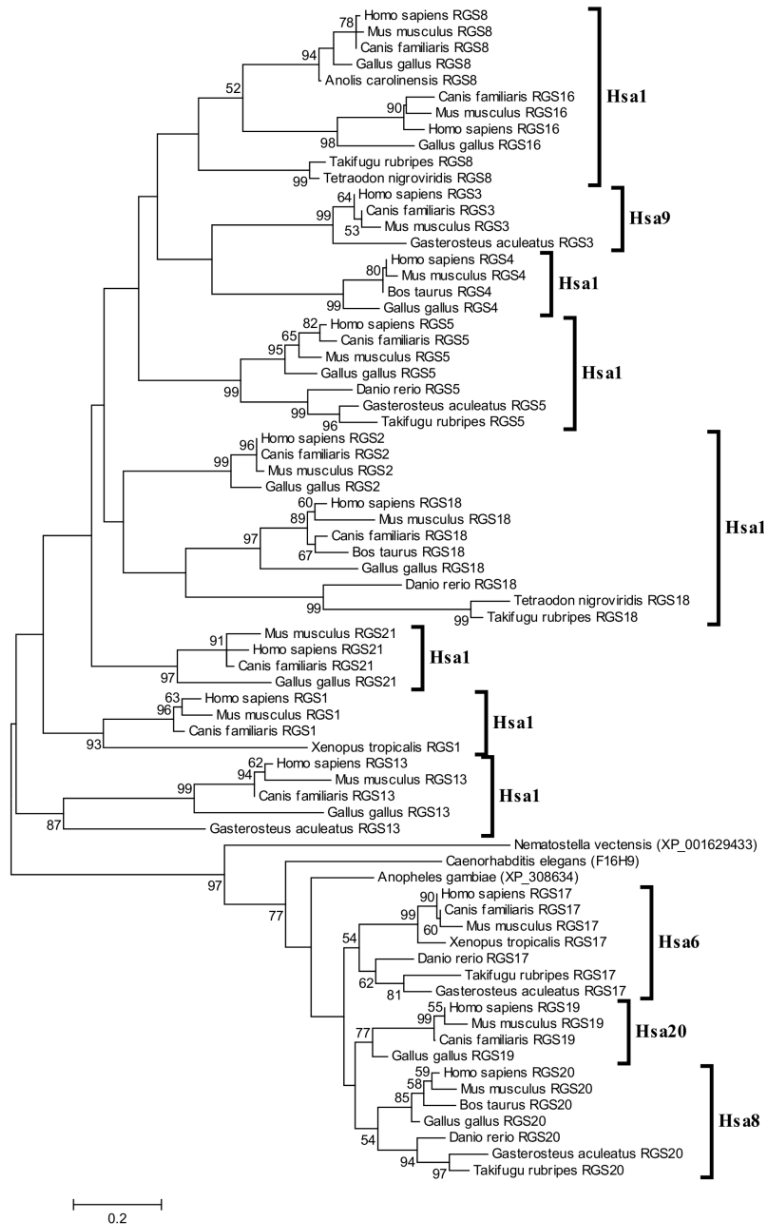
Polypyrimidine tract binding protein family - PTBP



Phylogenetic tree of PTBP family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-2418.1650) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 0.7390)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 42 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 146 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

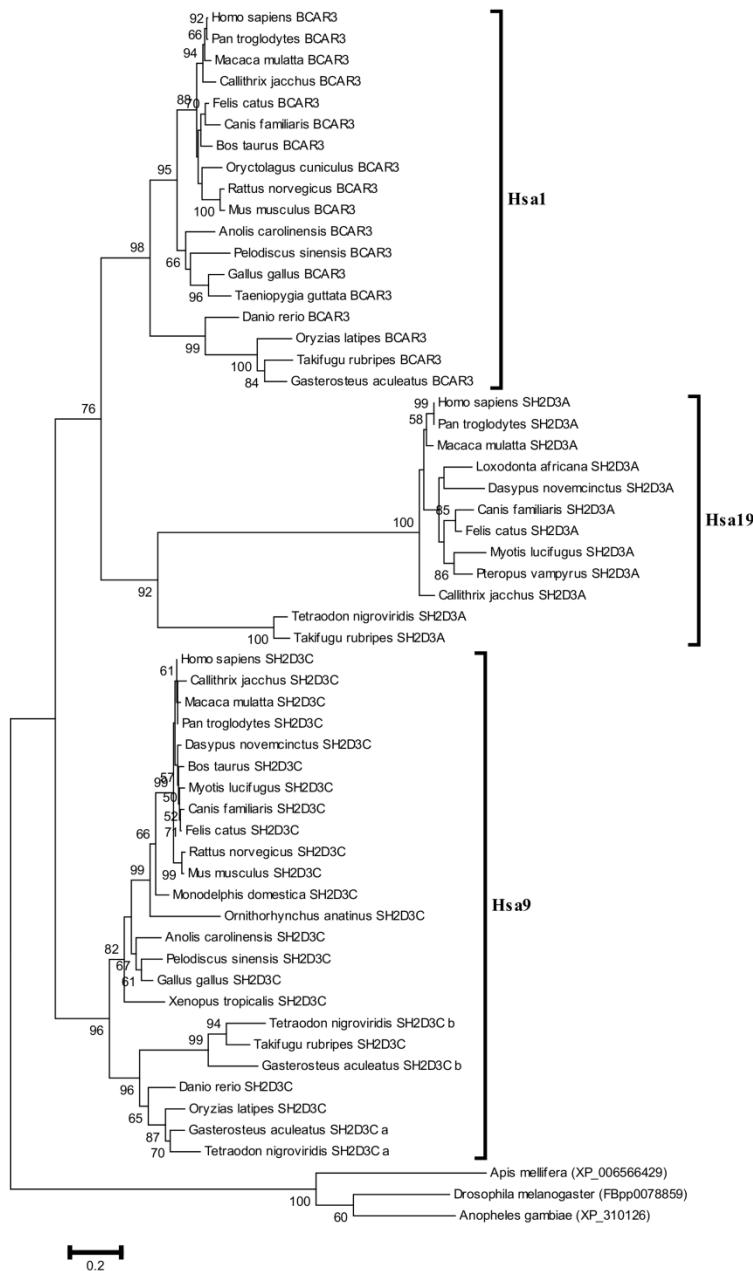
Regulator of G-protein signaling family - RGS



Phylogenetic tree of RGS family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-6337.8390) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.4563)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 72 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 122 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

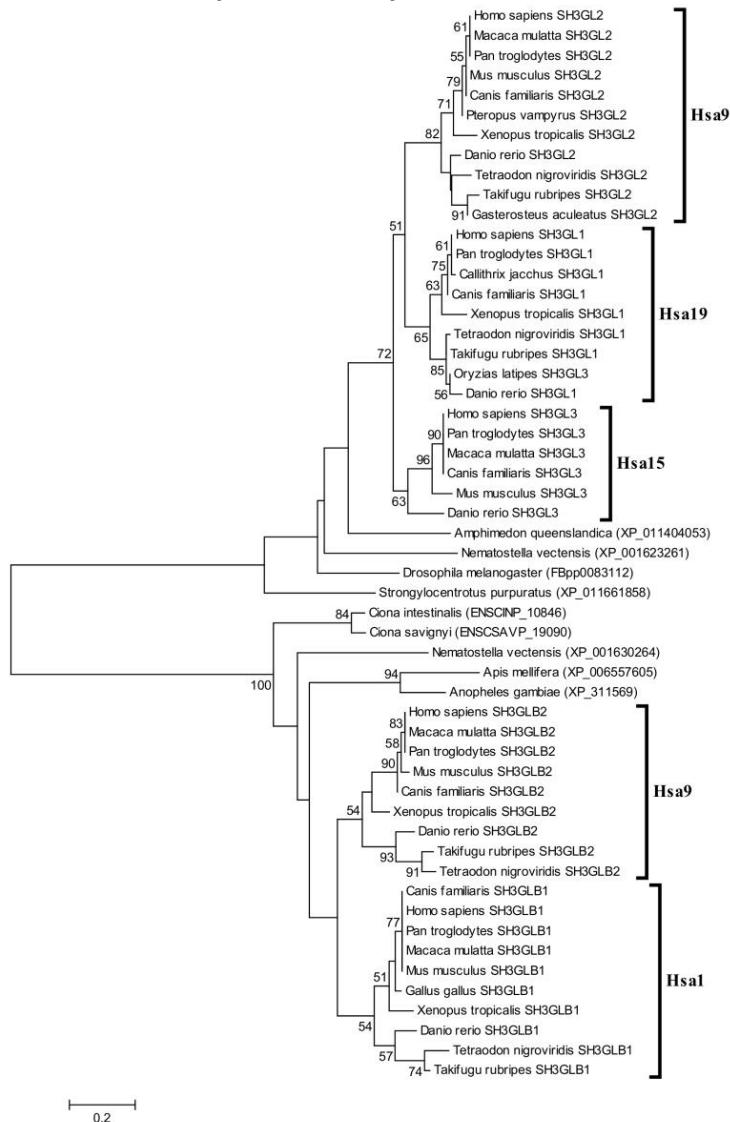
SH2 domain containing protein - SH2D



Phylogenetic tree of SH2D family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-12409.4224) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.8070)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 57 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 318 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

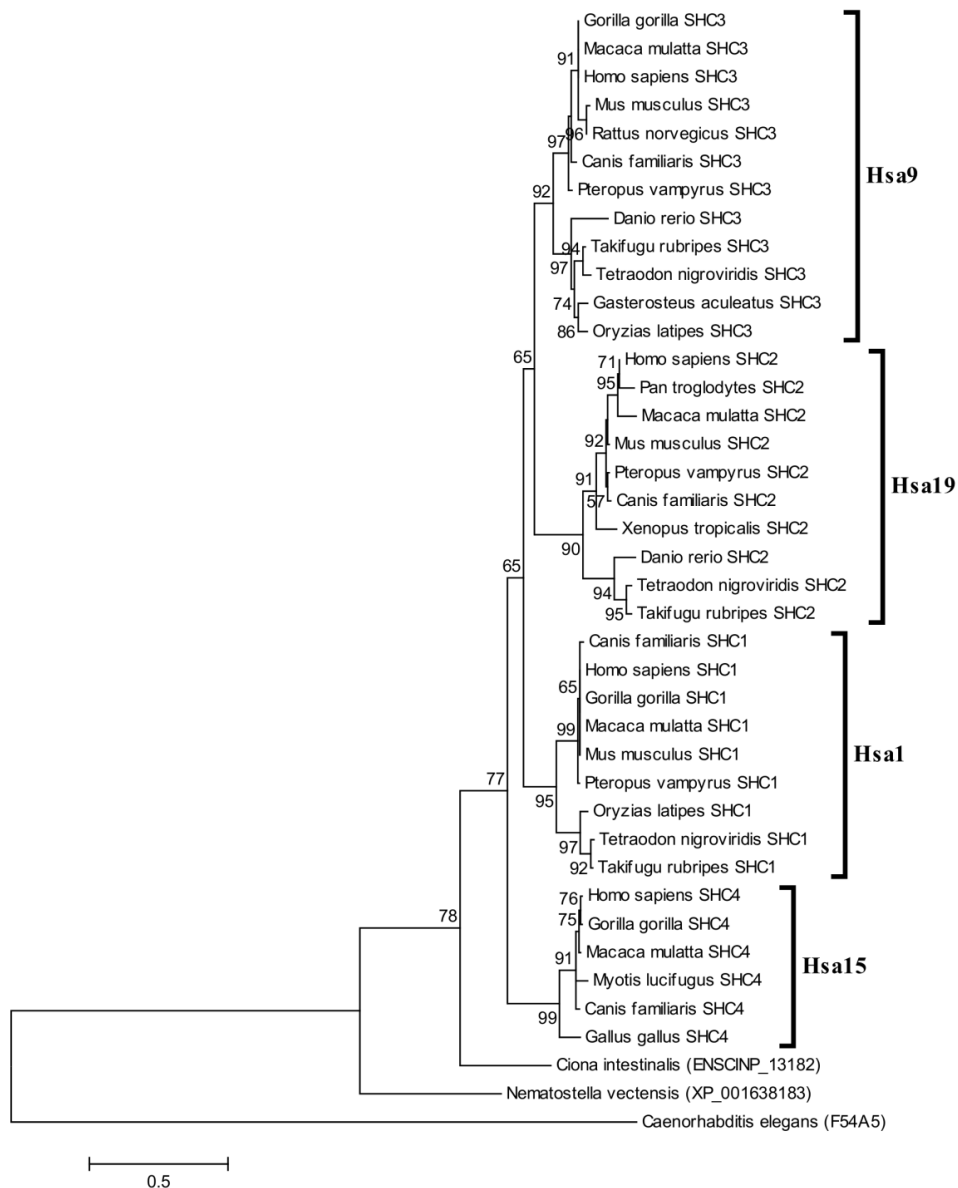
SH3 domain GRB2 like endophilin family - SH3GL



Phylogenetic tree of SH3GL family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-2509.1403) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.7074)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 54 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 85 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

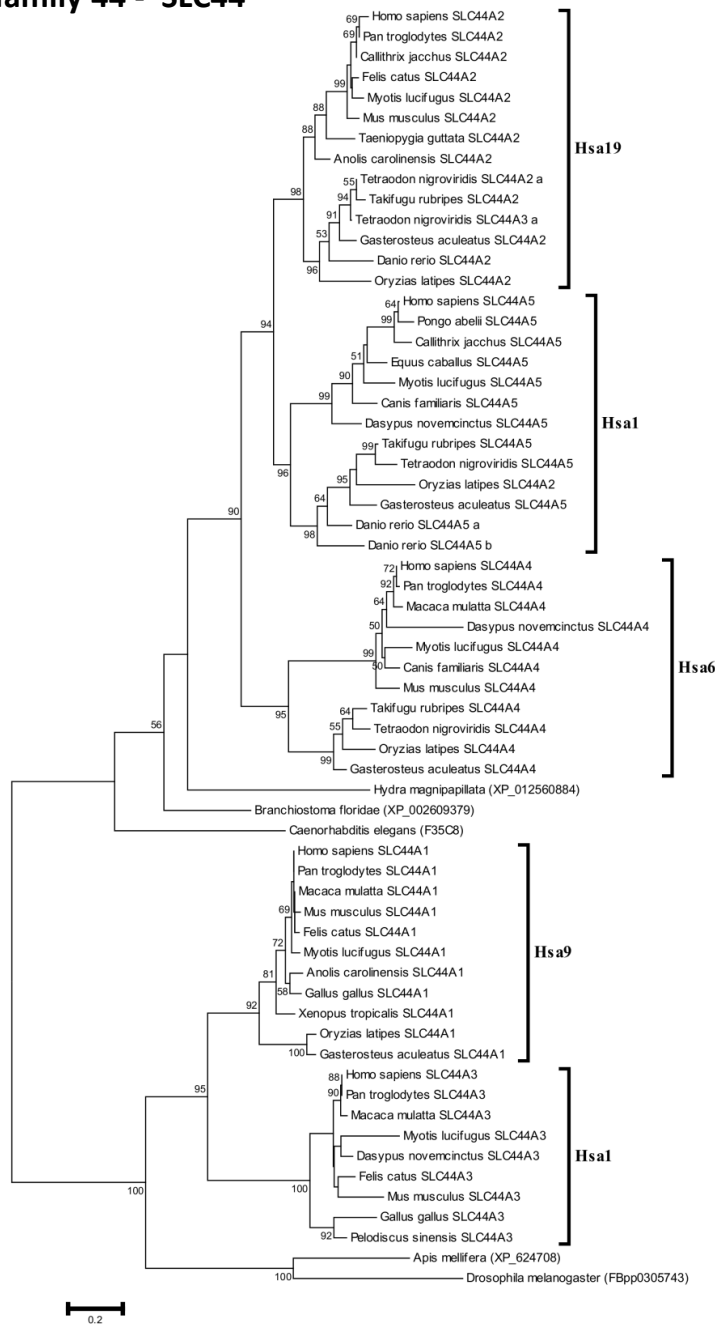
Src homology 2 domain containing) transforming protein family - SHC



Phylogenetic tree of SHC family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-3633.1865) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.4057)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 40 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 192 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

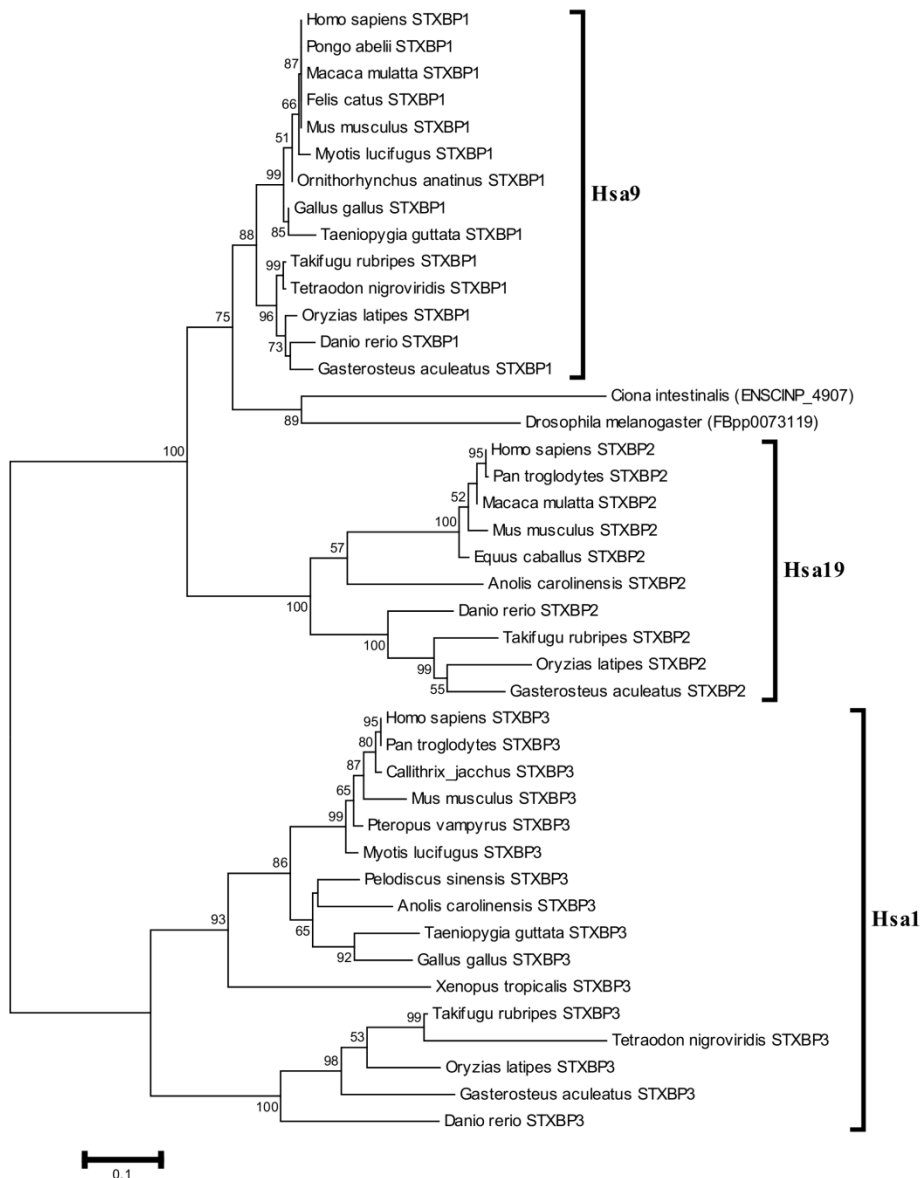
Solute carrier family 44 - SLC44



Phylogenetic tree of SLC44 family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-13297.8183) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 2.4506)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 63 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 295 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

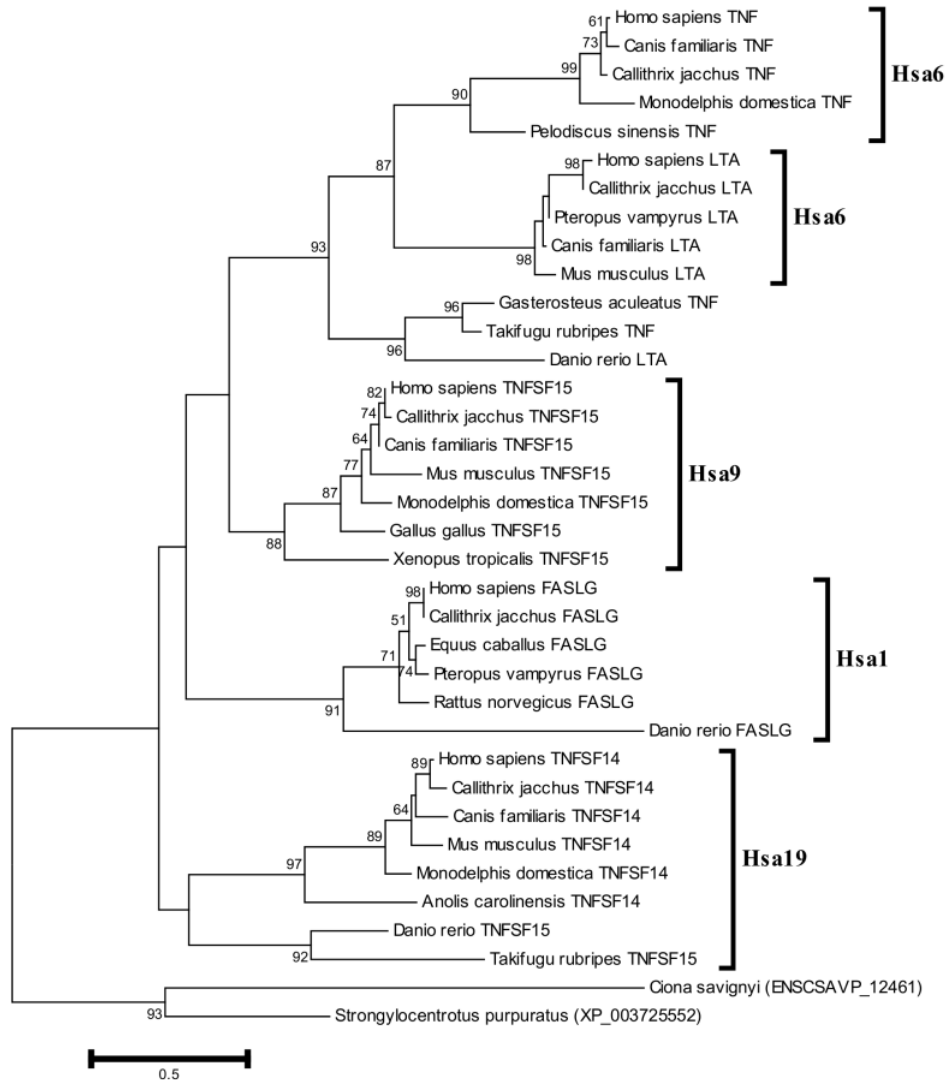
Syntaxin binding protein - STXBP



Phylogenetic tree of STXBP family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-7862.1213) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.4258)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 42 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 340 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

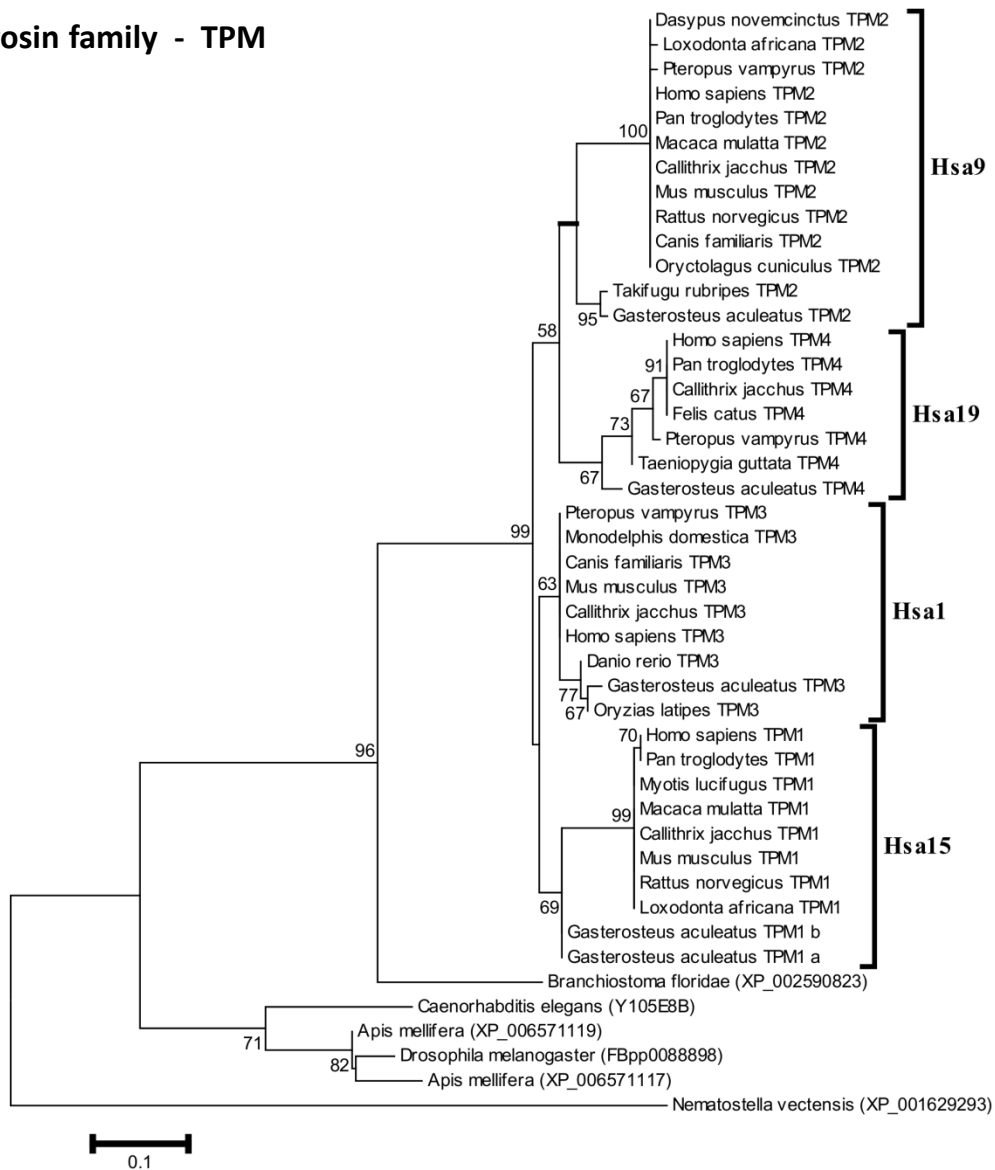
Fas ligand (TNF superfamily) - TNF



Phylogenetic tree of TNF family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-4025.3960) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 3.7589)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 36 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 103 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.

Tropomyosin family - TPM



Phylogenetic tree of TPM family.

The evolutionary history was inferred by using the Maximum Likelihood method based on the Whelan And Goldman model. The tree with the highest log likelihood (-1593.5868) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically as follows. When the number of common sites was < 100 or less than one fourth of the total number of sites, the maximum parsimony method was used; otherwise BIONJ method with MCL distance matrix was used. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+G, parameter = 1.1986)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 45 amino acid sequences. All positions containing gaps and missing data were eliminated. There were a total of 143 positions in the final dataset. Evolutionary analyses were conducted in MEGA5.