

Table S1 Fibrin orthologs investigated in this study. Protein sequences were obtained through translation of open reading frames from NCBI database blastN* search or from alignment of nucleotide sequences received from trace archive database. Identities were determined through amino acid sequence alignment (MegAlign, Lasergene 7).

Classes and species	Length (Amino acids)	Identity to human (%)
Chondrichthyes		
<i>Callorhynchus milii</i>	N-terminal sequence data incompletely	--
Osteichthyes		
<i>Takifugu rubripes</i>	205	63.9
<i>Tetraodon nigroviridis</i>	205	62.9
<i>Gasterosteus aculeatus</i>	207	62.1
<i>Danio rerio</i> *	210	62.9
NM_001017873		
Amphibia		
<i>Xenopus tropicalis</i> *	203	67.6
XM_002938894		
Reptilia		
<i>Anolis carolinensis</i>	230	67.9
Aves		
<i>Gallus gallus</i> *	206	71.4
XM_424544		
<i>Taeniopygia guttata</i> *	207	69.4
XM_002195064		
Mammalia		
<i>Ornithorhynchus anatinus</i> *	212	82.1
XM_001511157		
<i>Monodelphis domestica</i> *	211	88.7
XM_001380133		
<i>Macropus eugenii</i>	211	88.2
<i>Erinaceus europaeus</i>	212	92.8
<i>Myotis lucifugus</i>	211	93.4
<i>Pteropus vampyrus</i>	211	95.8
<i>Dasypus novemcinctus</i>	211	94.8
<i>Dipodomys ordii</i>	211	92.9
<i>Spermophilus tridecemlineatus</i>	211	92.0
<i>Cavia porcellus</i>	211	86.3
<i>Mus musculus</i> *	217	92.9
AB236893		
<i>Oryctolagus cuniculus</i> *	211	95.8
XM_002709021		
<i>Sorex araneus</i>	211	93.9
<i>Rattus norvegicus</i> *	217	92.0
NM_001025042		
<i>Tupaia belangeri</i>	211	95.3
<i>Ochotona princeps</i>	211	96.2
<i>Loxodonta africana</i>	211	96.2

<i>Bos taurus</i> *	211	96.2
NM_001015541		
<i>Equua caballus</i> *	211	96.7
NM_001099443		
<i>Sus scrofa</i>	211	96.7
<i>Tursiops truncatus</i>	211	94.8
<i>Felix catus</i>	211	96.7
<i>Canis familiaris</i>	211	95.8
<i>Otolemur garnettii</i>	212	97.2
<i>Tarsius syrichta</i>	212	93.4
<i>Macaca mulatta</i> *	211	98.6
XM_001090650		
<i>Papio hamadryas</i>	211	98.6
<i>Callithrix jacchus</i> *	211	97.2
XM_002755124		
<i>Pongo pygmaeus abelii</i>	211	98.6
<i>Pan troglodytes</i> *	211	100.0
XM_508336		
<i>Homo sapiens</i> *	211	100.0
NM_203371		

Additional information

To evaluate the evolutionary trait and origin of fibin, public data base were mined and fibin sequences from 40 species were retrieved from various vertebrate species including mammals, marsupials, monotremes, birds, reptiles, amphibians, teleost fishes and chondrichthyes (see above). This indicates that fibin exists in the vertebrate genome since more than 450 million years. In ray-finned fishes, e.g., *Danio rerio* and *Tetraodon nigroviridis*, we identified a fibin paralog which probably arose by whole genome duplication. Fibin paralogs were not found in tetrapods. Fibin-like sequences were not found in lamprey (primitive chordate), sea urchin and the known genomes of *Caenorhabditis elegans*, *Drosophila melanogaster*, and *Anopheles gambiae*.

Structural comparison of the retrieved orthologs revealed that fibin is highly conserved during vertebrate evolution (62 % amino acid identity between fish and mammals). The amino acid length varies between 203 (clawed frog) and 230 (anole). Most of the mammalian fibin orthologs comprised 211 amino acids. No significant homology to any other proteins or protein domains was found with common bioinformatic tools. Alignment of orthologs revealed several conserved regions, e.g. an amino acids block (position 20-58) in close proximity to the N terminus. Secondary structure and posttranslational modification prediction tools indicated no transmembrane domains, coiled coil regions, O-glycosylation, prenylation, amidation, myristoylation and GPI anchoring sites but predicted a conserved N-terminal signal sequence of 18 amino acids and one N-glycosylation site (Asn³⁰).