Figure S1. Sequence analysis of the SUMOylation site conservation around lysine 83 of stanniocalcin-1 proteins from 24 different species. *Homo sapiens* (human) sequence was used as an input in the PSI-BLAST data base. After 5 subsequent submissions, excluding hypothetical, synthetic and some predicted sequences, these 24 sequences were used for an alignment using the COBALT platform (NCBI). COBALT program constructed a phylogenetic tree using the Fast Minimum Distance method, with a 0.85 maximum sequence difference and the Kimura (protein) distance. The 24 sequences were analyzed at the position 83, looking for the conservation of the SUMOylation site in the species. We identified that the site first appears in tetrapodes. We correlated here the fact that before tetrapodes (where there are no SUMOylation site at position 83), with the fact that the stanniocalcin-1 function was limited for calcium homeostasis in bony fish but in tetrapoda several new functions have been described.

ANALYSED SEG SPECIES PO	QUENCE /	AT 3
Haliotis diversicolor     Branchiostoma floridae     Ciona intestinalis     Oncorhynchus keta     Oncorhynchus mykiss     Catostomus commersonii     Danio rerio     Platichthys flesus     Platichthys olivaceus	D <u>T</u> FN NNSF S <u>N</u> FN A <u>T</u> FN A <u>T</u> FN A <u>V</u> FN A <u>T</u> FN A <u>T</u> FN A <u>T</u> FN	GASTROPODA CEPHALOCHORDATA TUNICATE BONY FISHES
<ul> <li>Psetta maxima</li> <li>Takifugu rubripes</li> <li>Tetraodon nigroviridis</li> <li>Micropterus dolomieu</li> </ul>	ATEN ATEN ATEN ATEN	
<ul> <li>Xenopus laevis</li> <li>Monodelphis domestica</li> <li>Ornithorhynchus anatinus</li> <li>Gallus gallus</li> <li>Equus caballus</li> <li>Sus scrofa</li> <li>Bos taurus</li> <li>Mus musculus</li> <li>Rattus norvegicus</li> <li>Homo sapiens (input)</li> <li>Macaca mulatia</li> </ul>	AKFD AKFD AKFD AKFD AKFD AKFD AKFD AKFD	<del>-</del> TETRAPODA