

Supplementary table S3. Analysis of selected teneurins

Species (common name)	Protein Name	RefSeq/ID	Total aa	ICD aa	NLS (score)*	Furin cleavage (score)**
<i>H. sapiens</i> (human)	Teneurin-1	NP_055068	2725	317	2 (4.8, 6.0)	aa2618 (0.78)
	Teneurin-2	Q9NT68	2774	374	0	aa528 (0.65), aa2663 (0.57)
	Teneurin-3	NP_001073946	2699	308	1 (2.9)	aa473 (0.81), aa2592 (0.67)
	Teneurin-4	NP_001092286	2769	340	1 (4.2)	aa2662 (0.73)
<i>M. musculus</i> (mouse)	Teneurin-1	NP_035985	2731	317	2 (5.0, 5.0)	aa2624 (0.78)
	Teneurin-2	NP_035986	2764	374	0	aa528 (0.65), aa 2654 (0.57)
	Teneurin-3	NP_035987	2715	308	1 (2.9)	aa473 (0.81), aa2608 (0.67)
	Teneurin-4	NP_035988	2796	365	0	aa2689 (0.73)
<i>G.gallus</i> (chicken)	Teneurin-1	NP_990193	2705	298	2 (4.8, 9.0)	aa2598 (0.79)
	Teneurin-2	NP_989428	2802	402	1 (2.7)	aa556 (0.65), aa2692 (0.62)
	Teneurin-3	HE578904	2712	308	1 (3.0)	aa470 (0.76), aa2605 (0.67)
	Teneurin-4	XM_425655	2852	376	1 (3.7)	aa2698 (0.69)
<i>D. rerio</i> (zebrafish)	Teneurin-1	XP_691552	2721	297	0	0
	Teneurin-2A	XP_697293†	2710	324	0	aa484 (0.71), aa1588 (0.60), aa2606 (0.79)
	Teneurin-2B	XP_691651	2688	307	0	aa461 (0.70), aa2578 (0.77)
	Teneurin-3	Q9W7R4‡	2760	371	1 (2.8)	aa533 (0.83), aa2653 (0.70)
	Teneurin-4	NP_571044	2824	411	1 (3.2)	aa2717 (0.62)
<i>C. intestinalis</i> (sea squirt)	Teneurin	XR_052936	3111	649	2 (2.6, 3.5)	aa737(0.83), aa1530 (0.67), aa2913 (0.73)
<i>B. floridae</i> (amphioxus)	Teneurin	XP_002206906	2566	317	0	aa475 (0.58), aa832 (0.80), aa2565 (0.60)
<i>S. purpuratus</i> (purple sea urchin)	Teneurin	XP_001180001	2834	484	0	aa640 (0.89), aa677 (0.88), aa1968 (0.58)
<i>C. elegans</i> (roundworm)	Ten-1L	NP_001022723	2684	216	2 (3.8, 2.5)	aa361 (0.81)
<i>D. melanogaster</i> (fruit fly)	Ten-m/Odz	NP_524215	2997	226	1 (2.8)	aa2975 (0.59)
	Ten-a	Q9VYN8	3004	165	2 (4.3, 3.7)	aa431 (0.66), aa503 (0.68), aa2986 (0.87)
<i>S. mansoni</i> (fluke)	Teneurin	XP_002576635	2950	137	0	aa276 (0.74), aa1625 (0.57)
<i>M. brevicollis</i> (choanoflagellate)	Teneurin	XP_001749414	2699	159	1 (3.1)	0

\*Nuclear localization signal, as predicted by NLS Mapper (cutoff score = 2.5)

\*\*Furin-specific cleavage predicted by ProP 1.0 (cutoff score = 0.55)

†plus EST CR929815 plus novel predicted ORF (see Supplemental Table III)

‡plus EST BC122397