

Supplementary Material

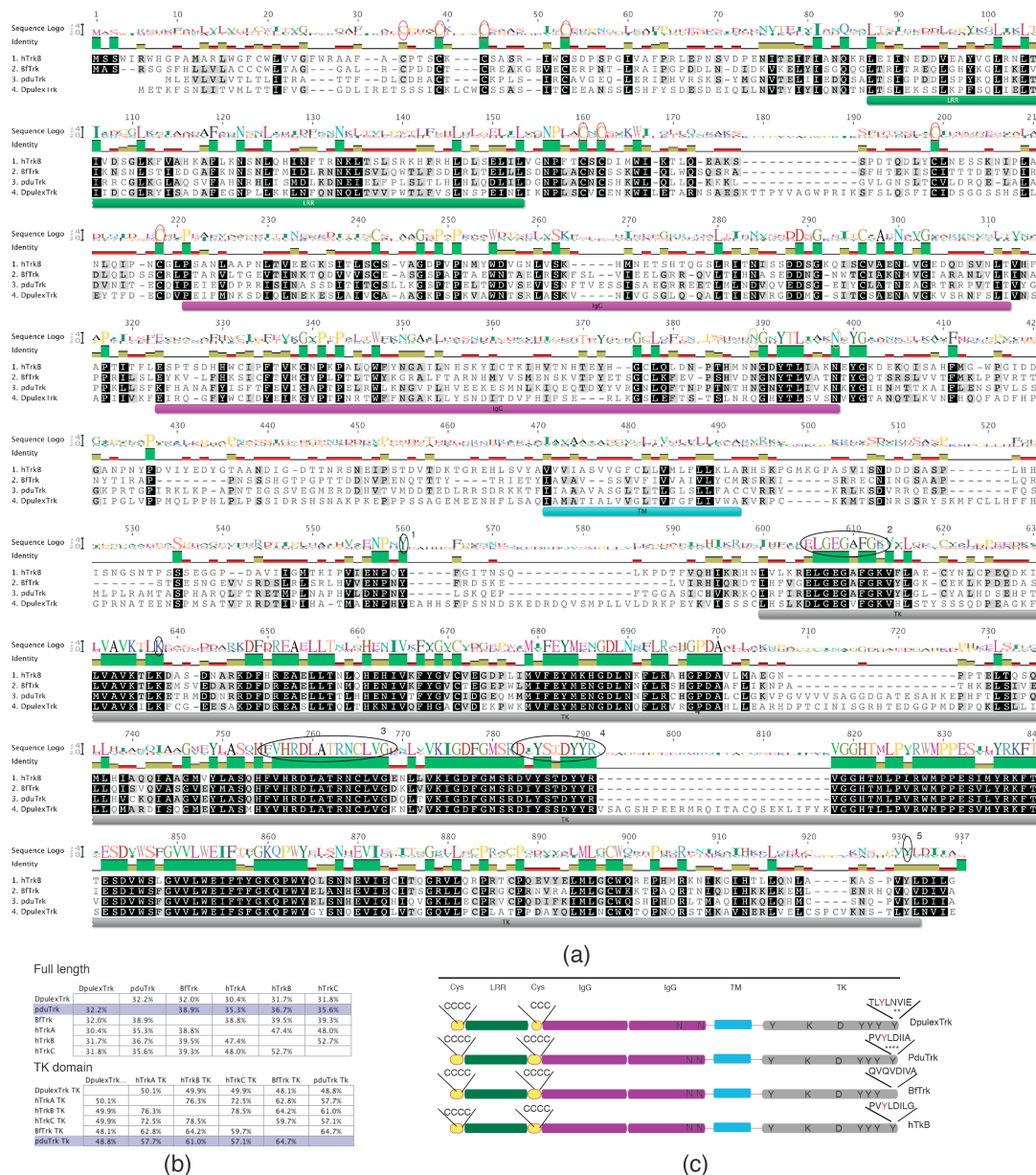
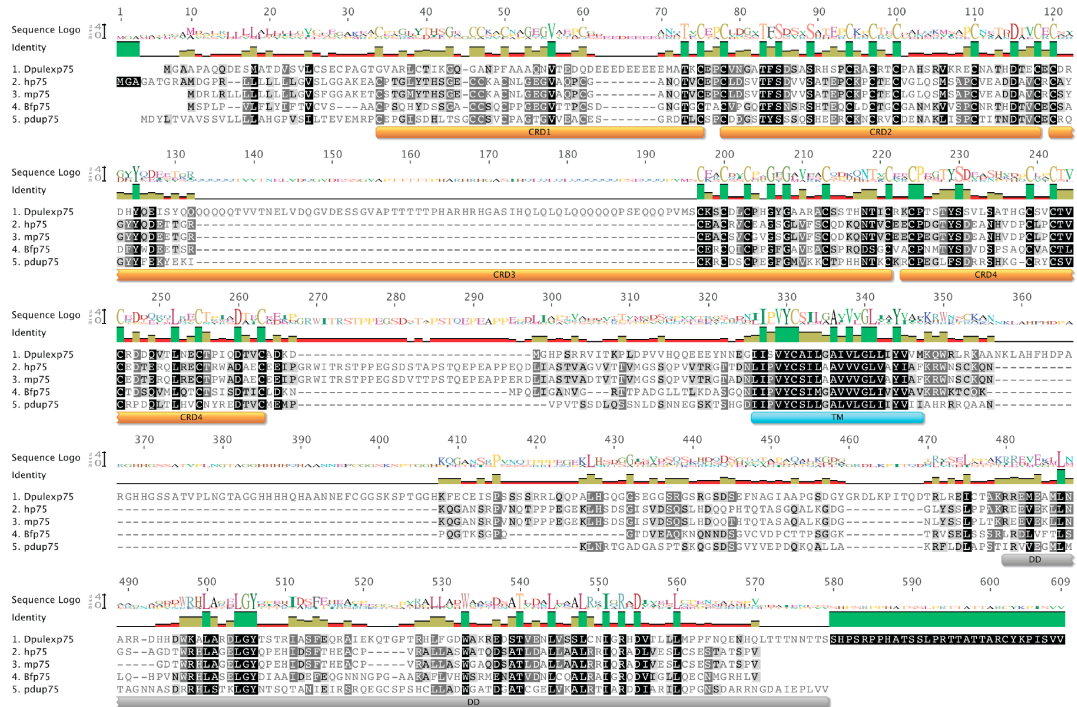


Figure S1. Analysis of the full-length amino acid sequence of *Platynereis* Trk (*PduTrk*) and conserved domains. (a) Multiple amino acid sequence alignment for the full length *Platynereis* Trk. Predicted domains are indicated below the sequences. LRR, green: Leucine reach repeats domains, IgG, purple: immunoglobulin domain, TM, light blue: transmembrane domain, TK, gray: intracellular tyrosine kinase domain. Conserved amino acids and signatures are highlighted. Different conserved signatures of the Tk domain are numbered in the alignment, as in fig.1a. (b) Identity matrix showing the amino acids identity (%) for the full length (upper panel) and for the intracellular (lower panel) amino acid sequence of *Platynereis* Trk relative to the ortholog receptors of the species used in the alignment: Pdu (*Platynereis dumerilii*), Bf (*Brachistoma floridae*), Dpulex (*Daphnia pulex*), h (*Homo sapiens*). (c) Schematics of the domains found in *Platynereis*, in comparison with *Daphnia* Trk, human hTrkB, and BfTrk.

TrkB, amphioxus Trk. Conversely to amphioxus, *Platynereis* PLCy docking site (PVYLDIIA) is highly conserved. The important tyrosine of this signature is highlighted in red. Asterisks indicate the amino acid conservation around the Y.



(a)

	Dpulexp75	hp75	mp75	8fp75	pdup75
Dpulexp75		17.6%	17.5%	21.4%	20.1%
hp75			92.1%	31.2%	23.9%
mp75				31.3%	25.4%
8fp75					29.3%
pdup75					

(b)



(c)

Figure S2. Analysis of the full-length amino acid sequence of *Platynereis* p75 (*Pdup75*) and conserved domains (a) Multiple amino acids sequence alignment for the full length of *Platynereis* p75. Predicted domains: CRD1-4 (cystein rich domain), orange. TM, light blue: transmembrane domain; the intracellular domain (grey) bearing the dead domain (DD). (b) Identity matrix showing the amino acids identity (%) for the full length amino acid sequence of *Platynereis* p75 relative to the ortholog receptors of the species used in the alignment: Pdu (*Platynereis dumerilii*), Bf (*Brachiostoma floridae*), Dpulex (*Daphnia pulex*), h (*Homo sapiens*), m (*Mus musculus*). (c) Schematics of the domains found in *Platynereis* as compared to *Daphnia*, human Trk. Note that a 3rd CRD is absent in *Daphnia* sequence.