

Additional file 2 – Multiple alignments

Domain searches were made using the HMMER package and the local Pfam models. Interesting domains were cut out in Jalview and aligned, to the appropriate domain sequence. This was done with ClustalW and standard parameters. Sequences for the domains were procured using hmemit from the HMMER package.

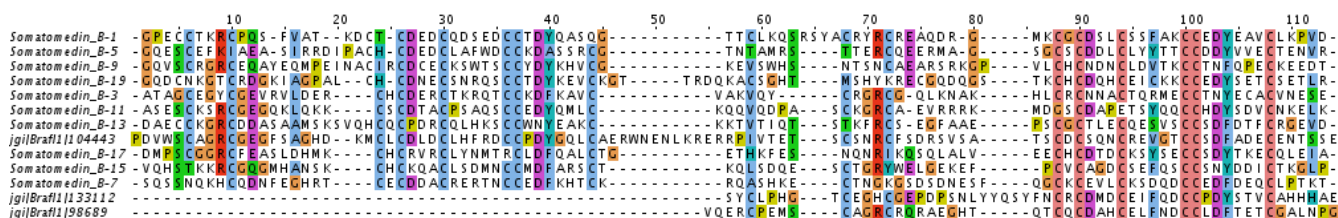


Figure 1. Somatomedin_B: Multiple alignment between three cut amphioxus transcripts and ten double Somatomedin_B domains.

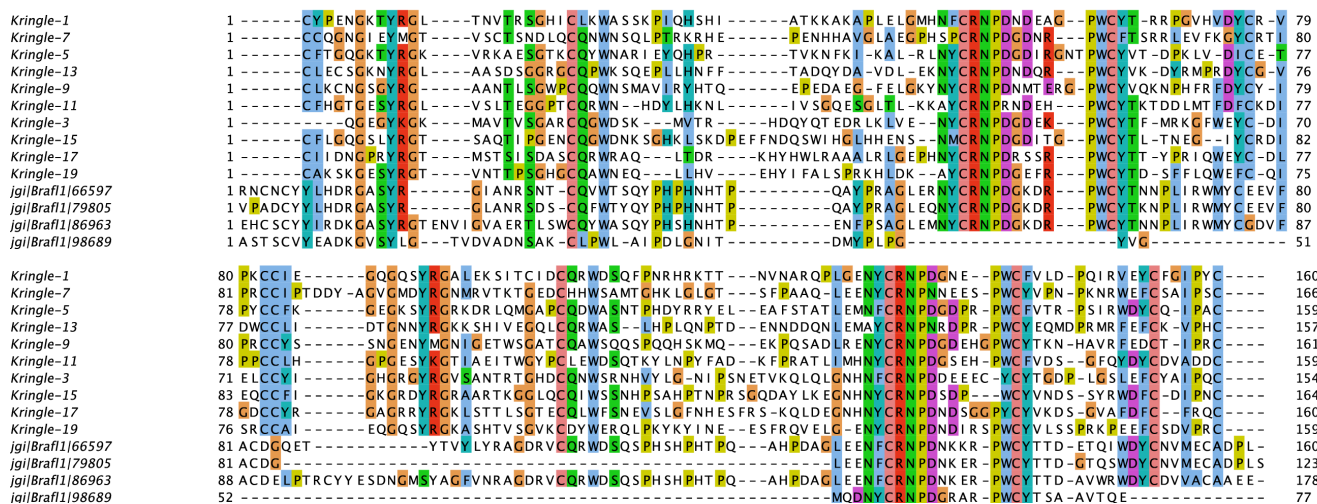


Figure 2. Kringle: Multiple alignment of four amphioxus transcripts and ten double Kringle domains. All but the last have two Kringle domains, which is the reason why the last alignment is gapped in the middle.