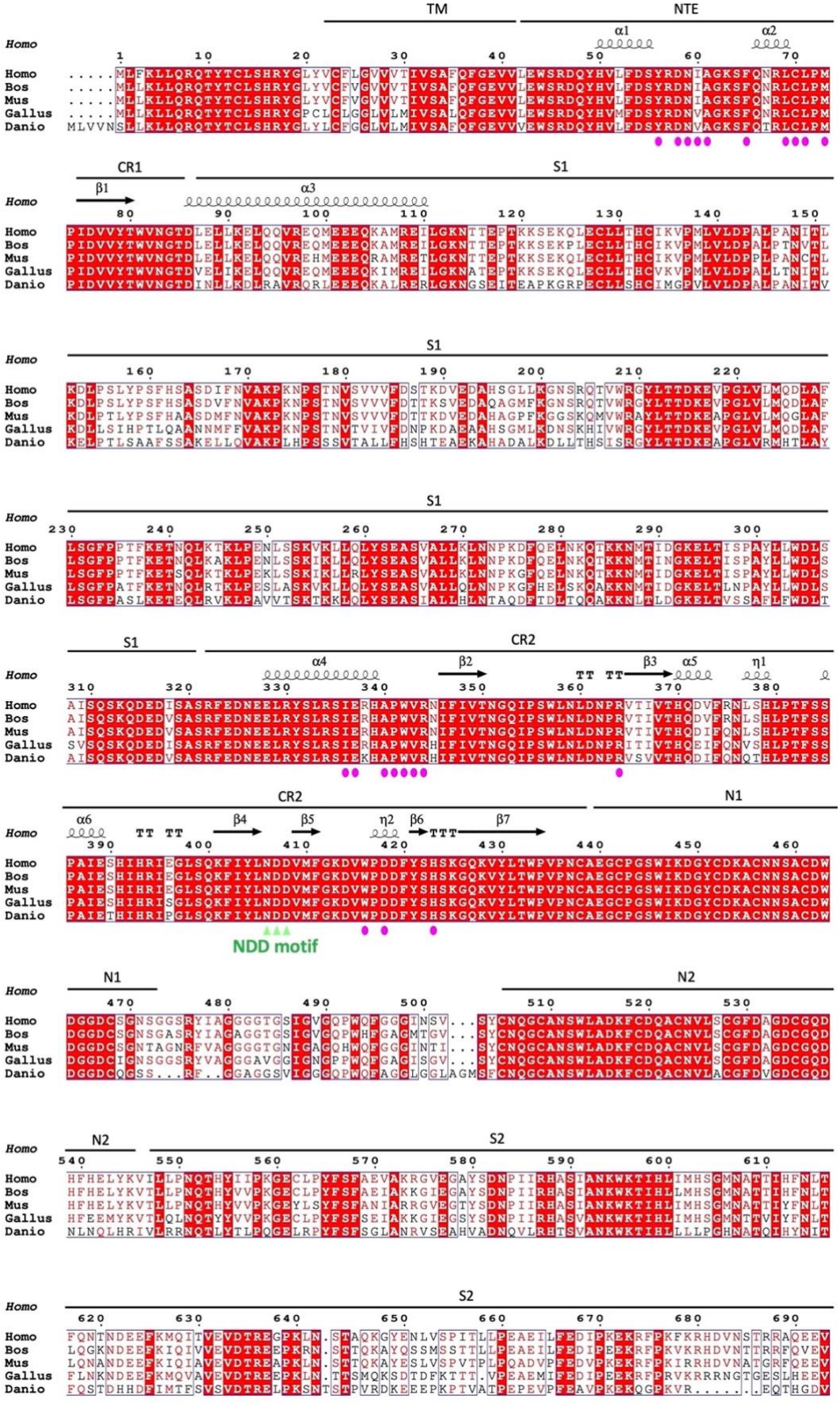
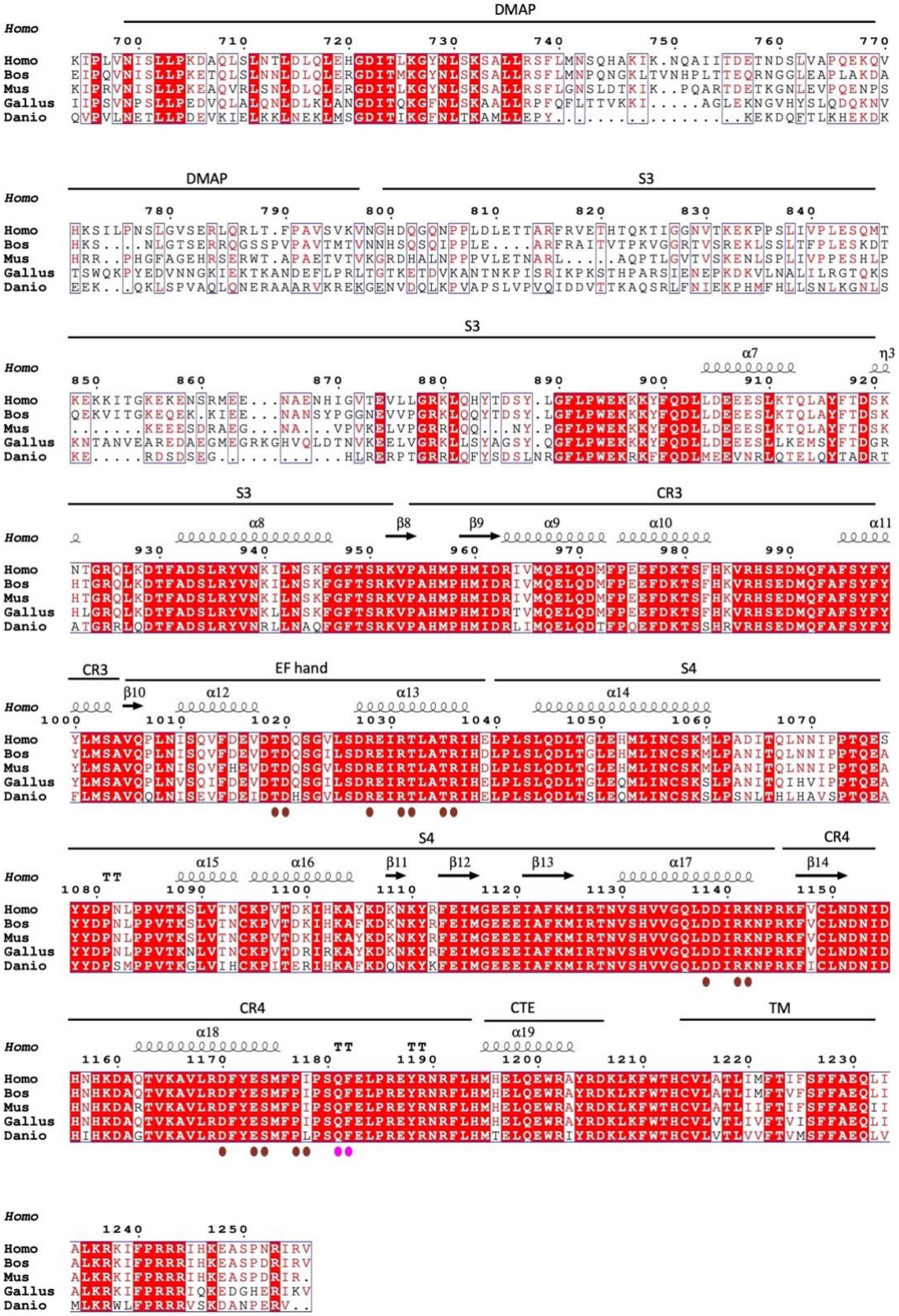
Supplementary Information

This document contains**:**


TM
NTE
α1
α2
Homo
CR1
S1
β1
α3
S1
S1
S1
CR2
α4
β2
β3
α5
η1
CR2
N1
α6
β4
β5
η2
β6
β7
NDD motif
N1
N2
N2
S2
S2
Homo
Bos
Mus
Gallus
Danio



Supplementary Figure 1. Sequence alignment of five vertebrate PTase proteins. The positions of the N-, C-terminal transmembrane helix, N-terminal extension (NTE), CR1-4, S1-4, N1, N2, DMAP, and EF hand are marked by dark bars above the sequence. The α-helices and β-strands resolved in the current core are shown above the sequence by coils and arrow lines. The residues involved in NTE region dimer interface and EF hand-CR4 dimer interface are shown as pink and brown cycles below the sequence. The conserved NDD motif is marked by green triangle below its sequence. Homo: *Homo sapiens*; Bos: *Bos taurus*; Mus: *Mus musculus*; Gallus: *Gallus gallus*; Danio: *Danio rerio*.

Supplementary Table 1. Primers used in this study

Fig 2c.	**& Supp 6b**	
C70S	for	GGAAAGTCCTTTCAGAATCGGCTTAGTCTGCCCATGCCGATTGAC
Fig 2g.		
D1018V	For	CTCAAGTCTTTGATGAAGTTGTTACAGATCAATCTGGTGTC
L1025S	For	GATACAGATCAATCTGGTGTCTCGTCTGACAGAGAAATCCG
L1033P	For	GACAGAGAAATCCGAACACCGGCTACCAGAATTCACGAAC
Fig 3e.		
Del S3	For	GAGACCACAGCAAGATTTAGAGTGGAAGATACATTTGCAGATTCCCTC
Del 902-924	For	CCATGGGAGAAAAAAAAGTATTTCCAAAGGCAACTAAAAGATACATTTGCAGATTCC
Supp 6 e,f		
D58A	For	GTTTTGTTTGATTCCTATAGAGCCAATATTGCTGGAAAGTCC
R364A	For	GGCTGAACCTTGACAATCCTGCAGTGACAATAGTAACACACC
R68A	For	GGAAAGTCCTTTCAGAATGCGCTTTGTCTGCCCATGCCG
D418A	For	GGATGTCTGGCCAGATGCTTTTTACAGTCACTCC
D418A + R68A		Used R68A ; Template Used D418A; primers
Supp 7c.		
R1028A	For	GGTGTCTTGTCTGACGCAGAAATCCGAACACTGG
R1031A	For	GTCTGACAGAGAAATCGCAACACTGGCTACCAGAATTC
R1028A+R1031A	For	CAATCTGGTGTCTTGTCTGACGCGGAAATCGCCACACTGGCTACCAGAATTCA
Supp 8b.		
N406A	For	CAGAAGTTTATTTACCTAGCTGATGATGTCATGTTTGG
D408A	For	GTTTATTTACCTAAATGATGCTGTCATGTTTGGGAAGG