

SUPPLEMENTARY MATERIAL

Tables

Table S1. Primer sequences, and relative melting temperatures (T_m), used for reverse transcription (Oligo-dT Anchor primer) and for PCR amplification.

Primers	Sequences 5'-3'	T_m (°C)
Oligo-dT Anchor	ACCACGCGTATCGATGTCG(T) ₁₆	75.2
CrPrdx2fw	AGTCCGCCCCAGATTTTA	56.8
CrPrdx2rv	CCGTGCTGGTCTGTGAAC	57.6
CrPrdx3fw	TACACGGGTTTCGACGGA	57.0
CrPrdx3rv	GATCCTGGTGTCCAAC TAG	56.4
CrPrdx4fw	GCTTGTTCTTGCTCACA	55.0
CrPrdx4rv	AGACCTCACCATGCTCAT	54.4
Cr β actfw	TGATGAAGATCTTGACCGAG	54.6
Cr β actrv	CTTGTTTGCTGATCCACATC	55.2

Table S2. Primer sequences, and relative melting temperatures (T_m), used for qRT-PCR amplification.

Primers	Sequences 5'-3'	T_m (°C)
CrPrdx2fw_RT	CCGCCCCAGATTTTACGGCAA	63.3
CrPrdx2rv_RT	GCACCTCACACCCAATATCAC	62.5
CrPrdx3fw_RT	CGGGTTTCGACGGACACATAC	61.5
CrPrdx3rv_RT	CTTTGAATGGTGGAGCAGGC	60.6
CrPrdx4fw_RT	TCTGAGGGAGGTCTTGAAA	60.1
CrPrdx4rv_RT	AGAGCCACGAAGAGTGTGT	60.0
Cr β actfw_RT	CCTTGGTATGGAATCTGCTG	62.1
Cr β actrv_RT	GAGAGAACGGTGTTGGCGTA	65.2

Table S3. GenBank accession numbers and ANISEED transcript IDs (*Ciona robusta*, *Ciona intestinalis* and *Botrylloides leachii*) referred to amino acid sequences of Prdx2, Prdx3 and Prdx4 used for multi-alignment and phylogenetic analyses.

Species	Prdx2	Prdx3	Prdx4
<i>Ciona robusta</i>	KY.Chr8.1384.v1.nonSL16	KY.Chr10.1364.v1.ND1	KY.Chr10.1036.v1.SL1
<i>Ciona intestinalis</i>	KH.L17.4.v1.A.nonSL9	KH.S396.2.v1.A.nonSL5	KH.C10.328.v1.A.SL1
<i>Botrylloides leachii</i>	Boleac.CG.SB_v3.S416	Boleac.CG.SB_v3.S163	Boleac.CG.SB_v3.S416
<i>Danio rerio</i>	NP_001002468.1	NP_001013478.3	NP_001082894.1
<i>Oryzias latipes</i>	XP_011478972.1	XP_023819390.1	XP_004076406.1
<i>Mylopharyngodon piceus</i>	ALD62538.1	ALD62539.1	ALD62540.1
<i>Callorhinchus milii</i>	XP_007905343.1	XP_007903837.1	NP_001279887.1
<i>Xenopus laevis</i>	AEM44539.1	AEM44540.1	AEM44541.1
<i>Rhinatrema bivittatum</i>	XP_029440999.1	XP_029466379.1	XP_029459262.1
<i>Chelonia mydas</i>	XP_037743763.1	XP_037761793.1	XP_037757601.1
<i>Python bivittatus</i>	XP_007421035.1	XP_007429204.1	XP_007436716.1
<i>Podarcis muralis</i>	XP_028573219.1	XP_028585929.1	XP_028583327.1
<i>Anas platyrhynchos</i>		XP_027316512.2	XP_027304862.1
<i>Lepidothrix coronate</i>		XP_017664753.1	XP_017682647.1
<i>Tupaia chinensis</i>	XP_006161057.1	XP_006160463.1	XP_027626915.1
<i>Myotis myotis</i>	XP_036158570.1	XP_036191702.1	XP_036161216.1
<i>Mus musculus</i>	NP_035693.3	NP_031478.1	NP_001300640.1
<i>Vicugna pacos</i>	XP_006206304.1	XP_006200224.1	XP_006213064.1
<i>Bos indicus</i>	XP_019819615.1	XP_019808318.1	XP_019811886.1
<i>Equus caballus</i>	XP_023501083.1	XP_001493666.1	XP_023489068.1
<i>Canis lupus</i>	XP_038284392.1	NP_001243414.1	XP_038305572.1
<i>Homo sapiens</i>	NP_005800.3	ABB84468.1	NP_006397.1
<i>Macaca mulatta</i>	NP_001248186.1	NP_001252755.1	NP_001180740.1
<i>Clonorchis sinensis</i>	AEK86199.1		
<i>Schistosoma haematobium</i>		XP_012798879.1	
<i>Drosophila melanogaster</i>		NP_524387.1	
<i>Amphioctopus fangsiao</i>			AGF80254.1
<i>Sepiella maindroni</i>			AKN23454.1
<i>Crassostrea gigas</i>	XP_011441532.1		
<i>Aplysia californica</i>	XP_005089483.1		
<i>Scylla paramamosain</i>		ASS34530.1	ASS34531.1
<i>Culex pipiens</i>	XP_001852614.1		

Table S4. Percentages of identity, similarity and *E*-values obtained by comparing Cr-Prdx2 amino acid sequence with orthologous sequences of metazoans.

Species	% identity	% similarity	<i>E</i> -values
<i>Danio rerio</i>	74.6	90.4	5.8e-84
<i>Python bivittatus</i>	74.6	88.8	4.7e-81
<i>Mus musculus</i>	71.1	92.4	5.7e-87
<i>Homo sapiens</i>	70.6	89.8	1.0e-87
<i>Crassostrea gigas</i>	70.6	88.7	3.3e-81
<i>Xenopus laevis</i>	67.5	90.4	9.1e-80
<i>Botrylloides leachii</i>	66.3	87.8	1.3e-72
<i>Culex pipiens</i>	65.5	88.7	7.6e-76
<i>Clonorchis sinensis</i>	59.9	83.4	2.4e-67

Table S5. Percentages of identity, similarity and *E*-values obtained by comparing Cr-Prdx3 amino acid sequence with orthologous sequences of metazoans.

Species	% identity	% similarity	<i>E</i> -values
<i>Xenopus laevis</i>	72.4	89.2	8.1e-82
<i>Danio rerio</i>	71.8	88.3	3.8e-85
<i>Python bivittatus</i>	71.3	88.6	5.6e-82
<i>Anas platyrhynchos</i>	70.4	89.7	1.5e-84
<i>Mus musculus</i>	70.0	88.3	2.0e-75
<i>Scylla paramamosain</i>	67.0	86.7	5.2e-79
<i>Drosophila melanogaster</i>	66.7	90.1	4.3e-78
<i>Homo sapiens</i>	66.7	87.2	2.0e-74
<i>Botrylloides leachii</i>	64.7	88.9	9.1e-51
<i>Schistosoma haematobium</i>	64.6	85.4	3.3e-79

Table S6. Percentages of identity, similarity and *E*-values obtained by comparing Cr-Prdx4 amino acid sequence with orthologous sequences of metazoans.

Species	% identity	% similarity	<i>E</i> -values
<i>Botrylloides leachii</i>	88.9	96.6	8.6e-100
<i>Danio rerio</i>	78.2	91.3	4.1e-102
<i>Homo sapiens</i>	77.9	91.5	3.3e-88
<i>Xenopus laevis</i>	77.2	91.6	2.3e-94
<i>Anas platyrhynchos</i>	76.7	90.6	6.4e-90
<i>Sepiella maindroni</i>	76.6	92.5	9.0e-98
<i>Python bivittatus</i>	75.5	91.2	4.1e-85
<i>Mus musculus</i>	74.6	90.6	6.6e-79
<i>Scylla paramamosain</i>	67.8	85.5	2.0e-90

Figures

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1   gtt ata atc atg tcc gcc ggt aaa gct tgc att caa aag tcc gcc cca gat ttt acg gca
   M S A G K A C I Q K S A P D F T A
61  aca gca gtt gtg aac gga gat ttt cgt gat att tca cta agc gaa tat aaa gga aaa tat
   T A V V N G D F R D I S L S E Y K G K Y
121 gtt gtt ttg ttt ttt tac ccg ctc gac ttc acg ttc gtt tgc ccg acg gag atc att gcg
   V V L F F Y P L D F T F V C P T E I I A
181 ttt agt gat cgt gtg tca gag ttc cgt gat att ggg tgt gag gtg ctc gcg tgt tcc aca
   F S D R V S E F R D I G C E V L A C S T
241 gac tca cac ttc agt cat ctc gca tgg aca aac atc cca agg aag aag ggg gga atc gga
   D S H F S H L A W T N I P R K K G G I G
301 aac atg aaa atc ccg ttg att gcc gac aaa aac tgt gca ata tct aaa gac tac ggg gtt
   N M K I P L I A D K N C A I S K D Y G V
361 ttg atg gaa ggc agt gga atc gcg ttc agg gga ttg ttc atc gat acc atg gga att
   L M E G S G I A F R G L F I I D T M G I
421 ctt cgg caa ata acg att aat gat ttg cct gtc ggt cgc tca gtg gac gag acg cta cga
   L R Q I T I N D L P V G R S V D E T L R
481 ttg gtc aaa gcg ttt cag ttc aca gac cag cac ggc gag gtt tgc cct gct gtt tgg aaa
   L V K A F Q F T D Q H G E V C P A G W K
541 ccc ggc gat gat acg atc aaa cca gat gtt caa gat agc cag aaa tat ttc agt aaa caa
   P G D D T I K P D V Q D S Q K Y F S K Q
601 taa aca ccc ctg tga ata ttt cag cat cgt tta ttt aca ttt att aca aag gca gta gta
   -
661 ttt aat

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Figure S1. Cr-Prdx2 cDNA sequence and relative amino acid sequence; 5'- and 3'-UTR regions are underlined; in grey sequence obtained with the amplicon sequencing; degradation signals are boxed in bold.

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1   gtc ata cat gcg cag taa caa cac gaa acg aag aaa att cac ttt tct ata ttc taa cag
61  aat ttc ttt ctg taa tgt ttt gac ttc tgt taa tta gaa tat aca aat agt tat tac atc
121 atg ttt att aat aga ttg gta cac ggg ttt cga cgg aca cat aca ttg cag tcc agt ctt
   M F I N R L V H G F R R T H T L Q S S L
181 aac cca tgg atc tca aaa tgg aat cca aac tca gcc agt att tca aca tca tgc aga tcc
   N P W I S K W N P N S A S I S T S C R S
241 atg gtt gcc cag gta aca cag cct gct cca cca ttc aaa ggt atg tcc gtg gta gaa gga
   M V A Q V T Q P A P P F K G M S V V E G
301 aaa ttc aag gaa ata tca ctt gaa gat tac aag gga aaa tat ttg gtt ctc ttc tac
   K F K E I S L E D Y K G K Y L V L F F Y
361 cct ctt gat ttc act ttt gtt tgc ccc act gaa atc atc tca ttc agc gac aaa agt cca
   P L D F T F V C P T E I I S F S D K S P
421 gag ttt gaa aaa ctt gac aca gcg gtt gta gga gcc tca gtt gac tct ctc agc cat
   E F E K L D T A V V G A S V D S H F S H
481 ctt gcg tgg ata aat aca cct agg aaa caa ggg gga ctt gga gaa atg aaa ata ccc ctg
   L A W I N T P R K Q G G L G E M K I P L
541 ctt tcc gat ctt act aaa aat ata tca aga gat tat ggg gtg act ctg gag aat gct ggg
   L S D L T K N I S R D Y G V L L E N A G
601 att gca ttg aga ggg ttg ttc ata att gat cca tcc gcc acc ata agg cac gcg agc gtt
   I A L R G L F I I D P S G T I R H A S V
661 aat gat ttg cct gtt gga agg tct gtt gat gaa gtt ttg agg ttg gtt caa gct ttc cag
   N D L P V G R S V D E V L R L V Q A F Q
721 ttt gtt gac aaa cat ggg gag gtg tgc cct gct agt tgg aca cca gga tca aaa act atc
   F V D K H G E V C P A S W T P G S K T I
781 aaa cca agt gtg gat tct tca aag aca tat ttt gaa gag gca aat taa aac aca cat act
   K P S V D G S K T Y F E E A N -
841 gtc aac tat cat gta caa att gta ttt att ttt tgg gta caa atc gca cgc att taa tct
901 ttt ggt tgt att caa taa ata tac tgt gta ctc taa tgt aca caa ttt att tat ttg gtt
961 gta tct aat aaa tca att taa tac aac ata act att tag tat tta tta ttc ttt tta atc
1021 aca gca gcg aag acc aaa ttc att aaa aca atg aag aga agg aaa tta gca gca aaa taa
1081 cag tta tta aaa cct agt tta att gca aaa ttt tgg cga ccc aat ttc cga aac tac att
1141 tca cac aac ttt tgt aag cat gaa ata aaa tga ttt tac ttt tac aat

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Figure S2. Cr-Prdx3 cDNA sequence and relative amino acid sequence; 5'- and 3'-UTR regions are underlined; in grey sequence obtained with the amplicon sequencing; polyadenylation signals are boxed in double line; degradation signals are boxed in bold.

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1  gct tct tag ttt ttg tgt ata att agg ctt ttc gtt tga tct gca ttg att tgc gca aac
61  atg gga gtc tca ttt caa ctt ttc act ctt gca tgc ttg ttc ctt gct cac agt gga ata
   M  G  V  S  F  Q  L  F  T  L  A  C  L  F  L  A  H  S  G  I
121  tgc caa gaa cgt gct gtt ttc tgg cca cca tat gaa agt cac ttg ctg caa tct acc aaa
   C  Q  E  R  A  V  F  W  P  P  Y  E  S  H  L  L  Q  S  T  K
181  gct caa atc tcg aaa cca gcg cca gac tgg gag ggt aca gcc att gtc gat ggt gaa att
   A  Q  I  S  K  P  A  P  D  W  E  G  T  A  I  V  D  G  E  I
241  aaa aca ata aag ctg gga gat tac aaa gga aaa tac ctt att ttc ttt ttt tac cct ctt
   K  T  I  K  L  G  D  Y  K  G  K  Y  L  I  F  F  F  Y  P  L
301  gat ttc act ttt gta tgt cca act gag atc att gcc ttc tca gac agg gtt gct gag ttt
   D  F  T  F  V  C  P  T  E  I  I  A  F  S  D  R  V  A  E  F
361  aag aaa att aat gct gaa gtt gtg gca gct tct gtt gat tct cac ttc acc cat ctc gca
   K  K  I  N  A  E  V  V  A  A  S  V  D  S  H  F  T  H  L  A
421  tgg tta aac acc cat cgc tct gag gga ggt ctt gga aaa ctc aac att cct ctt ctg tca
   W  L  N  T  H  R  S  E  G  L  G  K  L  N  I  P  L  L  S
481  gat ctc act cat aag ata tca agg gat tat gga gtc ctt cta gag gac ctc gga cac act
   D  L  T  H  K  I  S  R  D  Y  G  V  L  L  E  D  L  G  H  T
541  ctt cgt ggg ctc ttc atc att gat ccc aaa ggt atc ctg aga cag atc act atg aat gat
   L  R  G  L  F  I  I  D  P  K  I  I  L  R  Q  I  T  M  N  P
601  ctt cca gtt gga aga tct gta gac gag act ttg aga ttg gtc caa gca ttc caa cat act
   L  P  V  G  R  S  V  D  E  T  L  R  L  V  Q  A  F  Q  H  T
661  gat gag cat ggt gag gtc tgt cct gct ggt tgg gag cca ggt aaa gac acc att att cca
   D  E  H  G  E  V  C  P  A  G  W  E  P  G  K  D  T  I  I  P
721  gac ccc aag gat aaa ctg aag tac ttc cac aaa aca tca aaa gcc aag ggt gaa ttg taa
   D  P  K  D  K  L  K  Y  F  H  K  T  S  K  A  K  G  E  L  -
781  act gtt gaa atg tca tct gtg tct tgt ttt att ggt tgt tgt tgt ttg tag ggt gtg tgt
841  ttg ttt aag atg aag cag ctg tag ggt tat cag tgc aat ttc aag aaa gaa ata gtt taa
901  tca ctt taa tgt gtc tgt ttt caa gaa agc aat agt tta atc cct tta agt gtc tgt taa
961  aag ctg tgc gta ttt atc tta aac ttt tgt aaa att tag cag cct tta aat tga aaa aaa
1021 aaa ctg ttg tgt ttg ttg cta tta tct aat tgt gcc aaa gtt aag ttt ctg tac caa aat
1081 tat att gta att cat ttt cta aaa caa ttg tgt cat gtt ctg caa ttt aat tat tgt gtc gga
1141 ctg tcg gtt acc tgt atg tgt aat aaa gca atg ttt ttg cga ttt tgt tgg tca tgt atc
1201 gta tgt gtg gac taa aat gtg ttt atg ttt cgt ttc aac

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Figure S3. Cr-Prdx4 cDNA sequence and relative amino acid sequence; 5'- and 3'-UTR regions are underlined; in grey sequence obtained with the amplicon sequencing; polyadenylation signals are boxed in double line; degradation signals are boxed in bold.

<i>Clonorchis sinensis</i>	-----MALLPNQP	8
<i>Culex pipiens quinquefasciatus</i>	-----MSFATKALLRNIPQLS-KLASSGTV---QKNLFHTARALSVAQVQKP	43
<i>Botrylloides leachii</i>	-----MKLFIIICFIIVTVLANDEEQKYGGMP-GMFWPP---YQSHLLQSTKAQISKP	48
<i>Crassostrea gigas</i>	MASSVNMLFFGVICLIACFTCRAADDDKCQS FAGGSVFVPQETRRTSGHAIQWSQAVISKP	60
<i>Ciona robusta</i>	-----MSAGKACIQKS	11
<i>Xenopus laevis</i>	-----MACPVRAVKTHIGKP	15
<i>Homo sapiens</i>	-----MASGNARIQKP	11
<i>Mus musculus</i>	-----MASGNAQIGKS	11
<i>Danio rerio</i>	-----MSAGNAKIQGP	11
<i>Python bivittatus</i>	-----MASGKAHIGKP	11
	:	
<i>Clonorchis sinensis</i>	APEFSGMAVVNGEFKNISLKDYRGKYVILFLFYPLDFTFVCPTELIAFSDAAEEFKSKNCV	68
<i>Culex pipiens quinquefasciatus</i>	APPFSGTAVVNDKEIKLADFPGKYLVLEFFYPPLDFTFVCPTETI IAFSDRIKDFHALNAE	103
<i>Botrylloides leachii</i>	APSWEGETAIVDGEIKTIKSDDYLGKYLIFFFYPPLDFTFVCPTETI IAFSDRAEEFRKIGAE	108
<i>Crassostrea gigas</i>	APDFNGTAVIKGEFKDIKLSDYKGKYLVEFFYPPLDFTFVCPTETI IAFSDRVGEFKINTE	120
<i>Ciona robusta</i>	APDETATAVVNGLFRDISLSEYKGYVVLFFYPPLDFTFVCPTETI IAFSDRVSEFRDIGCE	71
<i>Xenopus laevis</i>	SPAFAQTALVNGEFGKQLSLDTLGKYVVLFFYPPLDFTFVCPTETI IAFSNHAEDFKKINCQ	75
<i>Homo sapiens</i>	APDFKATAVVDGAFKEVKLSLDYKGKYVVLFFYPPLDFTFVCPTETI IAFSNRAEDFRKLGC	71
<i>Mus musculus</i>	APDETATAVVDGAFKEIKLSLDYRGKYVVLFFYPPLDFTFVCPTETI IAFSDHAEDFRKLGC	71
<i>Danio rerio</i>	APQFKATAVVDGQFKDIQLSDYRGKYVVLFFYPPLDFTFVCPTETI IAFSERAAEFKINAVE	71
<i>Python bivittatus</i>	VPDFHATAVVDGTIKDKLSLDYRGKYVVLFFYPPLDFTFVCPTETI IAFNDRVEEFRKINCE	71
	* : . * : : . : : . : : * : : : * : : : : : : : : : : : :	
<i>Clonorchis sinensis</i>	IIGCSTDSVYAHLQWTMDRKGVGGLGKMNIPLLSDKNMKISRAYHVLDEEGHAFRGQFL	128
<i>Culex pipiens quinquefasciatus</i>	VVGVSVDSSHESHLAWCNTPRKSGGLGKLEYPLLADLTKKISADYGVLLEEAGISLRGLFI	163
<i>Botrylloides leachii</i>	VVACSVDSHFTHLAWNTTERKEGGLGKINIPLLSDLTHKISRDAYGVLLDELGHTRLGLFI	168
<i>Crassostrea gigas</i>	VVIACVSQFTHLAWINTPRAKGGLGPMNIPLLSDTITHEISKAYGVYLQDLGHSRLGLFI	180
<i>Ciona robusta</i>	VLA CS FDS HFSHLAWTN PRKKG GIGNMKI PLI AD KNC A ISKD Y GVLM EGS GIA FR GLFI	131
<i>Xenopus laevis</i>	LIAVSVDSQFTHLAWTKVPRKEGGLGPVNIPLVSDLTHSIADYGV LK EEDG VAY RGLFI	135
<i>Homo sapiens</i>	VLGVSVD SQF THLAWINTPRKEGGLGPLNI PLLADVTRRLSEDYGV LKT DEGI AY RGLFI	131
<i>Mus musculus</i>	VLGVSVD SQF THLAWINTPRKEGGLGPLNI PLLADVTKSLSQNYGV LKN DEGI AY RGLFI	131
<i>Danio rerio</i>	LIAASTDSHESHLAWINTPRKQGGLGSMNIPLVADLTQ SISRDAYGV LK EDEGI AY RGLFV	131
<i>Python bivittatus</i>	VIAASVDSQFTHLAWINTSRKEGGLGSTNIPLVADINHNSKDYGV LK EEDG VAIY RGLFI	131
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<i>Clonorchis sinensis</i>	IDPKGVLRQITVNDRPVGRSVEEAIRLLEAFHFHEQHGEVCPAKWKPK--GKTMKADPVA	186
<i>Culex pipiens quinquefasciatus</i>	IDPNGVVRQVTINDLPVGRSVDETLRLIKAFAQFVEKHGEVCPANWDPKANADTIKDPKG	223
<i>Botrylloides leachii</i>	IDPKGILRQITIMNDLPVGRSVDETLRLVQAFOQHTDQHGEVCPAGWQPG--SDTIIPDPEG	226
<i>Crassostrea gigas</i>	IDPKGTILROITIMNDLPVGRSVDETLRLVQAFOYTDTGHEVCPAGWKPG--SDTIIPDPEG	238
<i>Ciona robusta</i>	IDTGKILRQITINDLPVGRSVDETLRLVKAFOQTDGHEVCPAGWKPG--DDTIKPDVQD	189
<i>Xenopus laevis</i>	IDDGKILRQITINDLPVGRSVDETLRLVQAFOYTDVHGEVCPAGWKPG--SSTIKPNVKD	193
<i>Homo sapiens</i>	IDGKGVLRQITVNDLPVGRSVDEALRLVQAFOYTDEHGEVCPAGWKPG--SDTIKPNVDD	189
<i>Mus musculus</i>	IDAKGVLRQITVNDLPVGRSVDEALRLVQAFOYTDEHGEVCPAGWKPG--SDTIKPNVDD	189
<i>Danio rerio</i>	IDDKGILRQITINDLPVGRSVDETLRLVQAFOQHTDKYGEVCPAGWKPG--SDTIKPDVQK	189
<i>Python bivittatus</i>	IDDKGILRQITVNDLPVGRSVDETLRLVQAFOQHTDQHGEVCPAGWQPG--GDTIKPTVKD	189
	** * : * : * : * : * : * : * : * : * : * : * : * : * : *	
<i>Clonorchis sinensis</i>	AQEYFSSVN--	195
<i>Culex pipiens quinquefasciatus</i>	SKEYFNKHG--	232
<i>Botrylloides leachii</i>	KMKYFQKMREL	237
<i>Crassostrea gigas</i>	SQKYFSKQNN-	248
<i>Ciona robusta</i>	SQKYFSKQ---	197
<i>Xenopus laevis</i>	SKEFFSKEY--	202
<i>Homo sapiens</i>	SKEYFSKHN--	198
<i>Mus musculus</i>	SKEYFSKHN--	198
<i>Danio rerio</i>	SKEFFSKQ---	197
<i>Python bivittatus</i>	SKLFFSKQ--	198
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<i>Botrylloides leachii</i>	-----MATLRSCASLVTKSIAASK	19
<i>Drosophila melanogaster</i>	---MSF-----V-----AR-----SLIRNVPLMGK---AIL-----	20
<i>Schistosoma haematobium</i>	-----MLLQVLI-----	7
<i>Ciona robusta</i>	-----MFINRLVHGFRTH-----TLQSSSLNPWI-----	24
<i>Scylla paramamosain</i>	-----LKNIAV--TATRTVL-----	17
<i>Danio rerio</i>	MAATIG---RLLGASARGAAVCGCLKTLVPRNGASVI-----RAPQPLA-----	40
<i>Python bivittatus</i>	MAALTGVLRRLLKPSSGWT-----GATLWRAGAVAGRCLSGAASGRKCAADA-----	47
<i>Xenopus laevis</i>	MAASCG---RLLASWVGRT-----GRLTGQ-LPRVAG---SSVPRNMTAVTPSI-----	42
<i>Anas platyrhynchos</i>	MAAALG---RLLRSAPVAA-----GRRLQ-----GR-----	23
<i>Homo sapiens</i>	MAAAVG---RLLRASVARH-----VSAIPW-GISATAALRPACGRSTSLTNLL-----	44
<i>Mus musculus</i>	MAAAAG---RLLWSSVARH-----ASAIRS-SISASTVLRPVASRRTCLTDIL-----	44
<i>Botrylloides leachii</i>	QLRLLVANHHRLPLSSSSRNHVAQVTQPAPDF-----	51
<i>Drosophila melanogaster</i>	---SQQKQIAARLLHQTAPLAAVRVQQPAPDFKGLAVVDNSFQEVKLEDYRGKYLVLFFY	77
<i>Schistosoma haematobium</i>	---KGALRYNRSFVSNLCRHYAAHVQRPAPDFCGTAVVDGQFKEIKLRDYAGKYLVLFFY	64
<i>Ciona robusta</i>	---SKWNPNSASISTSCRMVAQVTQPAPDFKGMSSVVEGKFKEISLEDYKSKYLVLFFY	80
<i>Scylla paramamosain</i>	---PRITAAQRLGSTSVRCLAPAVTQPAPSFKAQAVVNGDFKELSLEDYRGKYLVLFFY	74
<i>Danio rerio</i>	---C---IAAQKACFSISAARWAPVTAAPHFKGTAVINGEFKEISLGDFKGYLVLFY	95
<i>Python bivittatus</i>	---TLPVRFHFSTASRFPVPAVTQHAPYFKGTAVVDGDFKELSDDDFKGYLVLFY	102
<i>Xenopus laevis</i>	---C---AAQKLQFSTSSGRFLPAVTQHAPQFKGTAVVNGEFKELSLEDYKGYLVLFY	96
<i>Anas platyrhynchos</i>	---PQLLAHRQLSLGASRLAPVTAHAPFFKGTAVVHGEFKEISLDDFKGYLVLFY	78
<i>Homo sapiens</i>	---CSGSSQA-KLFSTSSSCHAPAVTQHAPYFKGTAVVNGEFKDLSDDFKGYLVLFY	100
<i>Mus musculus</i>	---WSASAQGSASFSTSSSFHTPAVTQHAPYFKGTAVVNGEFKELSDDFKGYLVLFY	101
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<i>Botrylloides leachii</i>	-----QDSRFSHLASVNTPRSKYFGFDTRIPL	78
<i>Drosophila melanogaster</i>	PLDFTFVCPTETVAFSERIKEFHDIINTEVLGVSVDSHFSLHTWCNVDKNGGVQLKYPL	137
<i>Schistosoma haematobium</i>	PLDFTFVCPTETLAFSDRIDEFKNEGVVGVSTDSHFSLHAWINTPRKEGGLGCLRYPL	124
<i>Ciona robusta</i>	PLDFTFVCPTETISFSDKSPFEFKLDTAVVGASVLSHFSLHAWINTPRKQGGGLGEMKIP	140
<i>Scylla paramamosain</i>	PLDFTFVCPTETIAFSDHMAAFRELNCEVVGVSVDSHFSLHAWNNMPRKQGGGLGQYTL	134
<i>Danio rerio</i>	PLDFTFVCPTETVAFSDKANEFHVNCAVVGVSVDSHFTHLAWTNTPRKSGGLGKIQIPL	155
<i>Python bivittatus</i>	PLDFTFVCPTETIAFSDKANEFHVNCDVLAVSVDSHFCHLAWINTPRKSGGLGHMNIPL	162
<i>Xenopus laevis</i>	PLDFTFVCPTETVAFSNKANEFHVNCEVAVSVDSHFCHLAWTNTPRKSGGLGQMNIP	156
<i>Anas platyrhynchos</i>	PLDFTFVCPTETVAFSNKANEFRDNCVAVSVDSHFCHLAWINTPRKSGGLGKMNIPL	138
<i>Homo sapiens</i>	PLDFTFVCPTETVAFSDKANEFHVNCEVAVSVDSHFSLHAWINTPRKNGGLGHMNIPL	160
<i>Mus musculus</i>	PLDFTFVCPTETVAFSDKANEFHVNCEVAVSVDSHFSLHAWINTPRKNGGLGHMNIPL	161
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<i>Botrylloides leachii</i>	LSDFNKTIKEYGILVEQAGVALRGTYIIDTNGIVRHLVNDVSVGRSDEILRLVQAFQ	138
<i>Drosophila melanogaster</i>	LSDLTKKISADYDVLLDKEGISLRGTFIIDPNGILRQYSINDLPVGRSDEVLRLIKAFQ	197
<i>Schistosoma haematobium</i>	LADYQKQITRDYGVLEQELGVALRGLFIINPDGIVRQITINDLPVGRSDEVLRLVRAQFQ	184
<i>Ciona robusta</i>	LSDITKQISRDYGVLLLENAGIALRGLFIIPSGTIRHASVNDLPVGRSDEVLRLVQAFQ	200
<i>Scylla paramamosain</i>	LADLNKTIISRDYGVLLLEDDGVALRGLFLIDPEGVVRHMSINDLPVGRSVEETLRLVKAQFQ	194
<i>Danio rerio</i>	LADLTQVSRDYGVLLGEGGIALRGLFIIDPNGIVRHMSSVNDLPVGRSVEETLRLVKAQFQ	215
<i>Python bivittatus</i>	LSDLTKQISRDYGVLLIEGSGIALRGLFIIDPNGIKHLSVNDLPVGRSVEETLRLVKAQFQ	222
<i>Xenopus laevis</i>	LSDLNKQISRDYGVLLTAGIALRGLFIIDPNGIKHMSVNDLPVGRSVEETLRLVKAQFQ	216
<i>Anas platyrhynchos</i>	LSDLTKQISRDYGVLLGEGGIALRGLFIIDPNGVIKHLVNDLPVGRSVEETLRLVKAQFQ	198
<i>Homo sapiens</i>	LSDLTKQISRDYGVLLGEGGIALRGLFIIDPNGVIKHLVNDLPVGRSVEETLRLVKAQFQ	220
<i>Mus musculus</i>	LSDITKQISRDYGVLLSAGIALRGLFIIDPNGVVKHLVNDLPVGRSVEETLRLVKAQFQ	221
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<i>Botrylloides leachii</i>	FXDEHGQCLPSSWKPGRS--DSIKPTVEGSKEYFDKIE-	173
<i>Drosophila melanogaster</i>	FVEQHGEVCPANWNPNSNPATIKPDVEESKKYFSKHG-	234
<i>Schistosoma haematobium</i>	FTDKHGEVCPAGWQPKG--PTIKPDLKKYKEYFHKVN-	219
<i>Ciona robusta</i>	FVDRKHGEVCPASWTPGS--KTIKPSVDGSKTYFEEAN-	235
<i>Scylla paramamosain</i>	FVAEHGEVCPANWQPS--PTIKPDPTGSLEYFNKVN-	229
<i>Danio rerio</i>	FVETHGEVCPASWTPKS--PTIKPTPDGSKEYFEKVN-	250
<i>Python bivittatus</i>	YVETHGEVCPANWIPDS--PTIKPSPEASKEYFAKVNK	258
<i>Xenopus laevis</i>	FVETHGEVCPAXWTPDS--PTIKPSPEGSKEYFEKVH-	251
<i>Anas platyrhynchos</i>	YVETHGEVCPANWTPDS--PTIKPSPEGSKEYFEKVHK	234
<i>Homo sapiens</i>	YVETHGEVCPANWTPDS--PTIKPSPAASKEYFQKVNQ	256
<i>Mus musculus</i>	FVETHGEVCPANWTPES--PTIKPSPTASKEYFEKVHQ	257
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Figure S5. Schematic Prdx3 domain organization. The AhpC-TSA domain is highlighted in light grey, the 1-cysPrx_C domain is highlighted in dark grey. For *C. robusta*, alpha helices and beta sheets are boxed with dotted and continues lines respectively; amino acids of the catalytic center are indicated in bold and underlined. *= identical amino acids (completely preserved), := very similar amino acids (semi-conservative substitution), .= similar amino acids (conservative substitution); numerals refer to character counts.

<i>Ciona robusta</i>	-----MGVSFQLFTLACLFLA-----H	17
<i>Botrylloides leachii</i>	-----MKLFII-CFIIVTVLAN-----DEE	19
<i>Scylla paramamosain</i>	-----MSRLNLVLLACLVL-----G-----LSVH	18
<i>Sepiella maindroni</i>	-----MALVGVNLLCLLVLI-----SSA	18
<i>Mus musculus</i>	MEARSK-----LLDGTASRRWTRKLVLLPPLLFLLRTESE--QGLESDE	46
<i>Python bivittatus</i>	MEVGRQARGPPSESQAARMSGRGRLKPVSEPLAVYSMVLLMLAATMSEEAGTAEAAQS	60
<i>Danio rerio</i>	MD--VSRC-----V-----KTPREWLGVLWA-LLLL-SESVVC-----DGA	32
<i>Homo sapiens</i>	--MEALPL-----LAAT-TPDHGRHRRLLLP-LLLFLLPAGAVQG--WETEER	43
<i>Xenopus laevis</i>	MALQLRRY-----L-----RGSFAVTLCL-LLLLSAAAVTCEEEQSQARPG	39
<i>Anas platyrhynchos</i>	MEAGRRL-----RAGT-RTGTGTGGSALLVA-V-LAVLAVCGAAAEADPRAA	46
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<i>Ciona robusta</i>	SGICQ-----ERAV-----FWPPYSHLLQSTKAQISKAPAPWEGTAIVDGEIKTIKL	65
<i>Botrylloides leachii</i>	QKYGG-----MPGM-----FWPPYQSHLLQSTKAQISKAPAPWEGTAIVDGEIKTIKS	67
<i>Scylla paramamosain</i>	GSLAEEQCHTFAGGAVYPNTEGR--ASGHTLQWTSAMISKAPAPWEGTAVVDGQLQELKL	76
<i>Sepiella maindroni</i>	VCIADKCYSFAGGQVYPQEDRK--MSGHTIQWSKAIISKAPADWNGTAVINGKFEEIGL	76
<i>Mus musculus</i>	FRTRENECHFYGAGGQVYPGEASRVSVADHSLHLSKAKISKAPAPWEGTAVINGEFKELKL	106
<i>Python bivittatus</i>	YGYGDEKCHYYAGGEVYPGEASRVSVADHSLHLSKAKISKAPADWEGTAVINGEFKELKL	120
<i>Danio rerio</i>	NGKREQECYNYAGGHVYPGEAFRVPSVDSHLSHLSKAKISKAPAPWEGTAVINGEFKELKL	92
<i>Homo sapiens</i>	PRTREEECHFYGAGGQVYPGEASRVSVADHSLHLSKAKISKAPAPWEGTAVIDGFEKELKL	103
<i>Xenopus laevis</i>	RTAPDGECHFYGAGGQVYPGEASRVPSVDSHLSHLSKAKISKAPAPWEGTAVINGEFKELKL	99
<i>Anas platyrhynchos</i>	RQRGDEQCHYYAGGQVYPGEAARLPVTDHSLHLSQAKISKAPAPWEGTAVINGEFKELKL	106
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<i>Ciona robusta</i>	GDYKGYLVFFFYPLDFTFVCPTETIAFSDRVAEFRKINAENVVAASVDSHFTHLAWINTP	125
<i>Botrylloides leachii</i>	DDYLGKYLIFFFYPLDFTFVCPTETIAFSDRAEEFRKIGAEVVACSVDSHFTHLAWINTP	127
<i>Scylla paramamosain</i>	TDYRGKYLIVFFFYPLDFTFVCPTETIAFNDRVEEFRALNAEVVACSIDSHFTHLAWINTP	136
<i>Sepiella maindroni</i>	RSYKGYLVFFFYPLDFTFVCPTETIAFSDRIEEFKDLNPKVVACSVDSQFTHLAWINTP	136
<i>Mus musculus</i>	TDYRGKYLIVFFFYPLDFTFVCPTETIAFGDRIEEFKSINTEVVACSVDSQFTHLAWINTP	166
<i>Python bivittatus</i>	TDYEGKYLVFFFYPLDFTFVCPTETIAFSDRIEEFRAIDAEVVACSVDSQFTHLAWINTP	180
<i>Danio rerio</i>	SDYKGYLVFFFYPLDFTFVCPTETIAFSDRVHEFQAINAEVVACSVDSQFTHLAWINTP	152
<i>Homo sapiens</i>	TDYRGKYLIVFFFYPLDFTFVCPTETIAFGDRLEEFKRSINTEVVACSVDSQFTHLAWINTP	163
<i>Xenopus laevis</i>	TDYKGYLVFFFYPLDFTFVCPTETIAFGDRIEEFRSINTEVVACSVDSQFTHLAWINTP	159
<i>Anas platyrhynchos</i>	TDYEGKYLVFFFYPLDFTFVCPTETIAFSDRIEEFRAINTEVVACSVDSKFTHLAWINTP	166
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<i>Ciona robusta</i>	RSEGGGLKLNPLLSDLTHQISRDYGVLLDLGHTLRGLFIIDKILRQITMNDLPVGR	185
<i>Botrylloides leachii</i>	RKEGGGLKINIPLLSDLTHKISRDIYGVLLDLGHTLRGLFIIDPKGILRQITMNDLPVGR	187
<i>Scylla paramamosain</i>	RKDGGGLKGLKIPLSDITHKISKDYGVYLEDQGIALRGLFIIDNKGVLRLQITMNDLPVGR	196
<i>Sepiella maindroni</i>	RNKGGLGHLKIPLSDITHKISKAYGVYLNQNLGHSRLGLFIIDTKGILRQITMNDLPVGR	196
<i>Mus musculus</i>	RRQGGLGPIRIPLLSDLNHQISKDYGVYLEDGHTLRGLFIIDDKGVLRLQITMNDLPVGR	226
<i>Python bivittatus</i>	RKQGGLGPVKIPLSDLTHQISKDYGVYLEDQGHALRGLFIIDDKILRLQITMNDLPVGR	240
<i>Danio rerio</i>	RKQGGLGPMKIPLSDLTHQISKDYGVYLEDQGHTLRGLFIIDKGVLRLQITMNDLPVGR	212
<i>Homo sapiens</i>	RRQGGLGPIRIPLLSDLTHQISKDYGVYLEDGHTLRGLFIIDDKGILRQITMNDLPVGR	223
<i>Xenopus laevis</i>	RKQGGLGPMKIPLSDLTHQISKDYGVYLEDQGHTLRGLFIIDDKGVLRLQITMNDLPVGR	219
<i>Anas platyrhynchos</i>	RKQGGLGPMKIPLSDLTHQISKDYGVYLEDQGHTLRGLFIIDDKRILRLQITMNDLPVGR	226
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<i>Ciona robusta</i>	SVDETLLRLVQAFQHTDEHGEVCPA-GWEPGKDTIIPDPKDKLKYFHKTSKAKGEL	239
<i>Botrylloides leachii</i>	SVDETLLRLVQAFQHTDEHGEVCPA-GWQPGSDTIIPDPEGKMKYFQKMREL----	237
<i>Scylla paramamosain</i>	SVDETLLRLVQAFQHTDEHGEVCPA-GWKPGDDTIIPNPQEKLYFKKANQ----	245
<i>Sepiella maindroni</i>	SVDETLLRLVQAFQYTDHGEVCPA-GWKPGADTIIPDPKDKLKYFEKANS----	245
<i>Mus musculus</i>	SVDETLLRLVQAFQYTDKHGEDNPRSSWKTEVFRQAKLKSTSVMMFGPSQ----	275
<i>Python bivittatus</i>	SVDETLLRLVQAFQYTDKHGEVCPA-GWKPGSETIIPDPAGKLYFGKVN-----	288
<i>Danio rerio</i>	SVDETLLRLVQAFQYTDKHGEVCPA-GWKPGSDTIIPDPAGKLYFDKLN-----	260
<i>Homo sapiens</i>	SVDETLLRLVQAFQYTDKHGEVCPA-GWKPGSETIIPDPAGKLYFDKLN-----	271
<i>Xenopus laevis</i>	SVDETLLRLVQAFQYTDKHGEVCPA-GWKPGSETIIPDPAGKLYFDKQH-----	267
<i>Anas platyrhynchos</i>	SVDETLLRLVQAFQYTDKHGEVCPA-GWKPGSETIIPDPAGKLYFDKLN-----	274
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Figure S6. Schematic Prdx4 domain organization. The AhpC-TSA domain is highlighted in light grey, the 1-cysPrx_C domain is highlighted in dark grey. For *C. robusta*, alpha helices and beta sheets are boxed with dotted and continues lines respectively; amino acids of the catalytic center are indicated in bold and underlined. *= identical amino acids (completely preserved), := very similar amino acids (semi-conservative substitution), .= similar amino acids (conservative substitution); numerals refer to character counts.

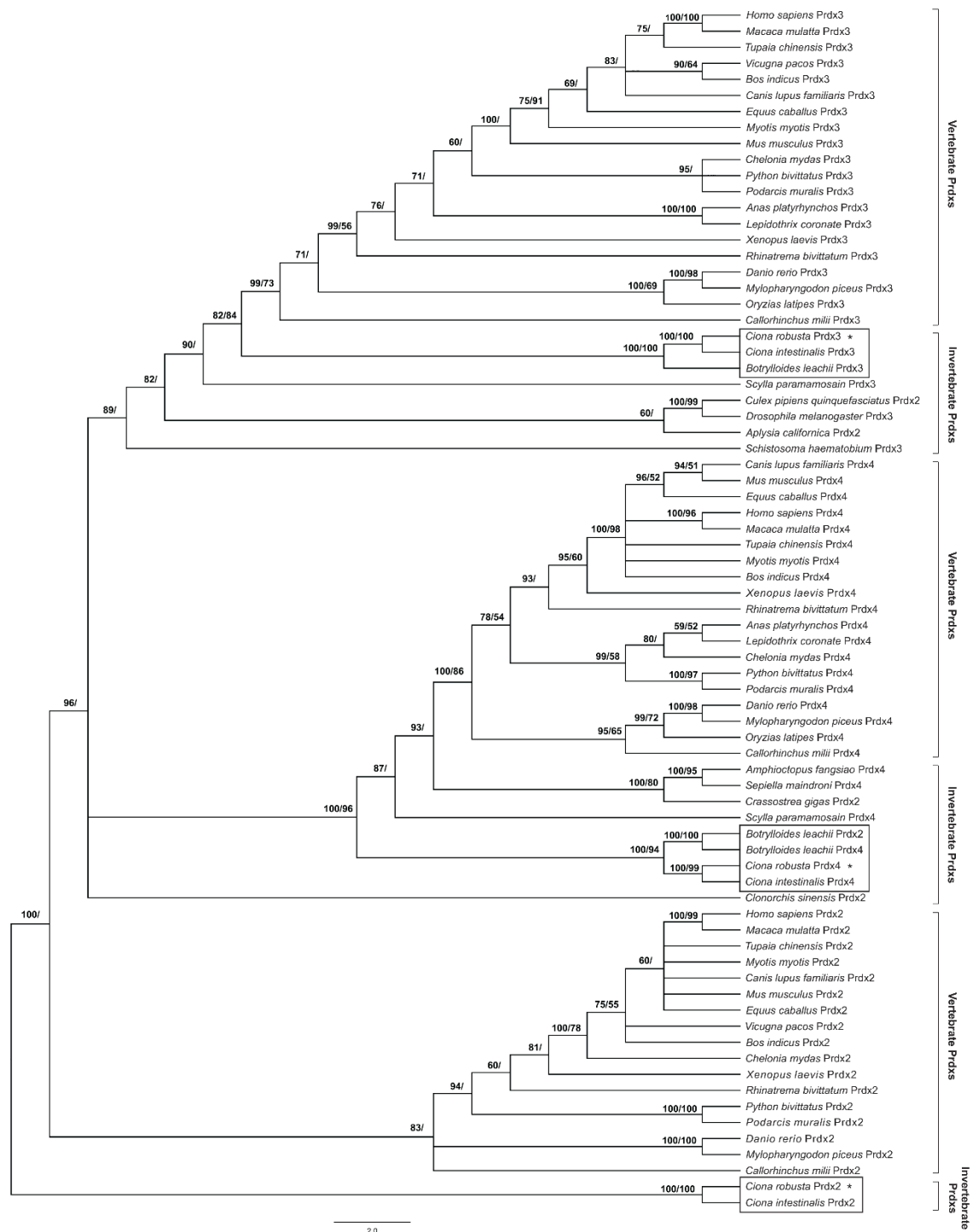


Figure S7. Phylogenetic relationships among Prdx isoforms of various organisms reconstructed on the amino acid sequences and using both Bayesian interference (BI) and Maximum likelihood (ML) methods. Bayesian posterior probability (first number) and bootstrap values higher (and equal to) than 50% are indicated on each node, respectively. The scale for branch length (2.0 substitution/site) is shown below the tree.