**SUPPLEMENTARY MATERIAL**

**Tables**

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

|  |  |  |
| --- | --- | --- |
| **Primers** | **Sequences 5'-3'** | **Tm (°C)** |
| Oligo-dT Anchor | ACCACGCGTATCGATGTCG(T)16 | 75.2 |
| CrPrdx2fw | AGTCCGCCCCAGATTTTA | 56.8 |
| CrPrdx2rv | CCGTGCTGGTCTGTGAAC | 57.6 |
| CrPrdx3fw | TACACGGGTTTCGACGGA | 57.0 |
| CrPrdx3rv | GATCCTGGTGTCCAACTAG | 56.4 |
| CrPrdx4fw | GCTTGTTCCTTGCTCACA | 55.0 |
| CrPrdx4rv | AGACCTCACCATGCTCAT | 54.4 |
| Crβactfw | TGATGAAGATCTTGACCGAG | 54.6 |
| Crβactrv | CTTGTTTGCTGATCCACATC | 55.2 |

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

|  |  |  |
| --- | --- | --- |
| **Primers** | **Sequences 5'-3'** | **Tm (°C)** |
| CrPrdx2fw\_RT | CCGCCCCAGATTTTACGGCAA | 63.3 |
| CrPrdx2rv\_RT | GCACCTCACACCCAATATCAC | 62.5 |
| CrPrdx3fw\_RT | CGGGTTTCGACGGACACATAC | 61.5 |
| CrPrdx3rv\_RT | CTTTGAATGGTGGAGCAGGC | 60.6 |
| CrPrdx4fw\_RT | TCTGAGGGAGGTCTTGGAAA | 60.1 |
| CrPrdx4rv\_RT | AGAGCCCACGAAGAGTGTGT | 60.0 |
| Crβactfw\_RT | CCTTGGTATGGAATCTGCTG | 62.1 |
| Crβactrv\_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** |
| *Ciona robusta* | KY.Chr8.1384.v1.nonSL16 | KY.Chr10.1364.v1.ND1 | KY.Chr10.1036.v1.SL1 |
| *Ciona intestinalis* | KH.L17.4.v1.A.nonSL9 | KH.S396.2.v1.A.nonSL5 | KH.C10.328.v1.A.SL1 |
| *Botrylloides leachii* | Boleac.CG.SB\_v3.S416 | Boleac.CG.SB\_v3.S163 | Boleac.CG.SB\_v3.S416 |
| *Danio rerio* | NP\_001002468.1 | NP\_001013478.3 | NP\_001082894.1 |
| *Oryzias latipes* | XP\_011478972.1 | XP\_023819390.1 | XP\_004076406.1 |
| *Mylopharyngodon piceus* | ALD62538.1 | ALD62539.1 | ALD62540.1 |
| *Callorhinchus milii* | XP\_007905343.1 | XP\_007903837.1 | NP\_001279887.1 |
| *Xenopus laevis* | AEM44539.1 | AEM44540.1 | AEM44541.1 |
| *Rhinatrema bivittatum* | XP\_029440999.1 | XP\_029466379.1 | XP\_029459262.1 |
| *Chelonia mydas* | XP\_037743763.1 | XP\_037761793.1 | XP\_037757601.1 |
| *Python bivittatus* | XP\_007421035.1 | XP\_007429204.1 | XP\_007436716.1 |
| *Podarcis muralis* | XP\_028573219.1 | XP\_028585929.1 | XP\_028583327.1 |
| *Anas platyrhynchos* |  | XP\_027316512.2 | XP\_027304862.1 |
| *Lepidothrix coronate* |  | XP\_017664753.1 | XP\_017682647.1 |
| *Tupaia chinensis* | XP\_006161057.1 | XP\_006160463.1 | XP\_027626915.1 |
| *Myotis myotis* | XP\_036158570.1 | XP\_036191702.1 | XP\_036161216.1 |
| *Mus musculus* | NP\_035693.3 | NP\_031478.1 | NP\_001300640.1 |
| *Vicugna pacos* | XP\_006206304.1 | XP\_006200224.1 | XP\_006213064.1 |
| *Bos indicus* | XP\_019819615.1 | XP\_019808318.1 | XP\_019811886.1 |
| *Equus caballus* | XP\_023501083.1 | XP\_001493666.1 | XP\_023489068.1 |
| *Canis lupus* | XP\_038284392.1 | NP\_001243414.1 | XP\_038305572.1 |
| *Homo sapiens* | NP\_005800.3 | ABB84468.1 | NP\_006397.1 |
| *Macaca mulatta* | NP\_001248186.1 | NP\_001252755.1 | NP\_001180740.1 |
| *Clonorchis sinensis* | AEK86199.1 |  |  |
| *Schistosoma haematobium* |  | XP\_012798879.1 |  |
| *Drosophila melanogaster* |  | NP\_524387.1 |  |
| *Amphioctopus fangsiao* |  |  | AGF80254.1 |
| *Sepiella maindroni* |  |  | AKN23454.1 |
| *Crassostrea gigas* | XP\_011441532.1 |  |  |
| *Aplysia californica* | XP\_005089483.1 |  |  |
| *Scylla paramamosain* |  | ASS34530.1 | ASS34531.1 |
| *Culex pipiens* | 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** | ***E*-values** |
| *Danio rerio* | 74.6 | 90.4 | 5.8e-84 |
| *Python bivittatus* | 74.6 | 88.8 | 4.7e-81 |
| *Mus musculus* | 71.1 | 92.4 | 5.7e-87 |
| *Homo sapiens* | 70.6 | 89.8 | 1.0e-87 |
| *Crassostrea gigas* | 70.6 | 88.7 | 3.3e-81 |
| *Xenopus laevis* | 67.5 | 90.4 | 9.1e-80 |
| *Botrylloides leachii* | 66.3 | 87.8 | 1.3e-72 |
| *Culex pipiens* | 65.5 | 88.7 | 7.6e-76 |
| *Clonorchis sinensis* | 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** | ***E*-values** |
| *Xenopus laevis* | 72.4 | 89.2 | 8.1e-82 |
| *Danio rerio* | 71.8 | 88.3 | 3.8e-85 |
| *Python bivittatus* | 71.3 | 88.6 | 5.6e-82 |
| *Anas platyrhynchos* | 70.4 | 89.7 | 1.5e-84 |
| *Mus musculus* | 70.0 | 88.3 | 2.0e-75 |
| *Scylla paramamosain* | 67.0 | 86.7 | 5.2e-79 |
| *Drosophila melanogaster* | 66.7 | 90.1 | 4.3e-78 |
| *Homo sapiens* | 66.7 | 87.2 | 2.0e-74 |
| *Botrylloides leachii* | 64.7 | 88.9 | 9.1e-51 |
| *Schistosoma haematobium* | 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** | ***E*-values** |
| *Botrylloides leachii* | 88.9 | 96.6 | 8.6e-100 |
| *Danio rerio* | 78.2 | 91.3 | 4.1e-102 |
| *Homo sapiens* | 77.9 | 91.5 | 3.3e-88 |
| *Xenopus laevis* | 77.2 | 91.6 | 2.3e-94 |
| *Anas platyrhynchos* | 76.7 | 90.6 | 6.4e-90 |
| *Sepiella maindroni* | 76.6 | 92.5 | 9.0e-98 |
| *Python bivittatus* | 75.5 | 91.2 | 4.1e-85 |
| *Mus musculus* | 74.6 | 90.6 | 6.6e-79 |
| *Scylla paramamosain* | 67.8 | 85.5 | 2.0e-90 |

**Figures**

   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 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 ggg 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 gtg   
  -       
 661 ttt aat 

**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.

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 ttt 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 cac ttc 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 ttg 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 ggc 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 ggt 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 

**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.

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   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   G   I   L   R   Q   I   T   M   N   D    
 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 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

**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.

*Clonorchis sinensis*  ----------------------------------------------------MALLPNQP 8

*Culex pipiens quinquefa*sciatus ------------MSFATKALLRNIPQLS-KLASSGTV----QKNLFHTARALSVAQVQKP 43

*Botrylloides leachii*  -------MKLFIICFIIVTVLANDEEQKYGGMP-GMFWPP----YQSHLLQSTKAQISKP 48

*Crassostrea gigas*  MASSVNMLFFGIVCLIACTFCRAADDDKCQSFAGGSVFPQETRRTSGHAIQWSQAVISKP 60

*Ciona robusta*  -------------------------------------------------MSAGKACIQKS 11

*Xenopus laevis*  ---------------------------------------------MACPVRAVKTHIGKP 15

*Homo sapiens*  -------------------------------------------------MASGNARIGKP 11

*Mus musculus*  -------------------------------------------------MASGNAQIGKS 11

*Danio rerio*  -------------------------------------------------MSAGNAKIGQP 11

*Python bivittatus*  -------------------------------------------------MASGKAHIGKP 11

:

*Clonorchis sinensis*  APEFSGMAVVNGEFKNISLKDYRGKYVILLFYPLDFTFVCPTELIAFSDAAEEFKSKNCV 68

*Culex pipiens quinquefa*sciatus APPFSGTAVVNNDFKEIKLADFKGKYLVLFFYPLDFTFVCPTEIIAFSDRIKDFHALNAE 103

*Botrylloides leachii*  APSWEGTAIVDGEIKTIKSDDYLGKYLIFFFYPLDFTFVCPTEIIAFSDRAEEFRKIGAE 108

*Crassostrea gigas*  APDFNGTAVIKGEFKDIKLSDYKGKYLVFFFYPLDFTFVCPTEIIAFSDRVGEFKKINTE 120

*Ciona robusta*  APDFTATAVVNGDFRDISLSEYKGKYVVLFFY**P**LDF**T**FV**C**PTEIIAFSDRVSEFRDIGCE 71

*Xenopus laevis*  SPAFQATALVNGEFKEIQLSDYLGKYVVLFFYPLDFTFVCPTEIIAFSNHAEDFKKINCQ 75

*Homo sapiens*  APDFKATAVVDGAFKEVKLSDYKGKYVVLFFYPLDFTFVCPTEIIAFSNRAEDFRKLGCE 71

*Mus musculus*  APDFTATAVVDGAFKEIKLSDYRGKYVVLFFYPLDFTFVCPTEIIAFSDHAEDFRKLGCE 71

*Danio rerio*  APQFKATAVVDGQFKDIQLSDYRGKYVVLFFYPLDFTFVCPTEIIAFSERAAEFRKIGVE 71

*Python bivittatus*  VPDFHATAVVDGTIKDIKLSDYRGKYVVLFFYPLDFTFVCPTEIIAFNDRVEEFRKINCE 71

\* : . \*::.. :: :. :: \*\*\*::::\*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*\*.: :\*: .

*Clonorchis sinensis*  IIGCSTDSVYAHLQWTKMDRKVGGLGKMNIPLLSDKNMKISRAYHVLDEEEGHAFRGQFL 128

*Culex pipiens quinquefa*sciatus VVGVSVDSHFSHLAWCNTPRKSGGLGKLEYPLLADLTKKISADYGVLLEEAGISLRGLFI 163

*Botrylloides leachii*  VVACSVDSHFTHLAWTNTERKEGGLGKINIPLLSDLTHKISRDYGVLLEDLGHTLRGLFI 168

*Crassostrea gigas*  VIACSVDSQFTHLAWINTPRAKGGLGPMNIPLLSDITHEISKAYGVYLQDLGHSLRGLFI 180

*Ciona robusta*  VLACSTDSHFSHLAWTNIPRKKGGIGNMKIPLIADKNCAISKDYGVLMEGSGIAF**R**GLFI 131

*Xenopus laevis*  LIAVSVDSQFTHLAWTKVPRKEGGLGPVNIPLVSDLTHSIAKDYGVLKEEDGVAYRGLFI 135

*Homo sapiens*  VLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEDYGVLKTDEGIAYRGLFI 131

*Mus musculus*  VLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLLADVTKSLSQNYGVLKNDEGIAYRGLFI 131

*Danio rerio*  LIAASTDSHFSHLAWINTPRKQGGLGSMNIPLVADLTQSISRDYGVLKEDEGIAYRGLFV 131

*Python bivittatus*  VIAASVDSQFTHLAWINTSRKEGGLGSTNIPLVADINHNISKDYGVLKEEDGIAYRGLFI 131

::. \*.\*\* ::\*\* \* : \* \*\*:\* : \*\*::\* . :: \* \* \* : \*\* \*:

*Clonorchis sinensis*  IDPKGVLRQITVNDRPVGRSVEEAIRLLEAFHFHEQHGEVCPAKWKPK--GKTMKADPVA 186

*Culex pipiens quinquefa*sciatus IDPNGVVRQVTINDLPVGRSVDETLRLIKAFQFVEKHGEVCPANWDPKANADTIKPDPKG 223

*Botrylloides leachii*  IDPKGILRQITMNDLPVGRSVDETLRLVQAFQHTDQHGEVCPAGWQPG--SDTIIPDPEG 226

*Crassostrea gigas*  IDPKGTLRQITMNDLPVGRSVDETLRLVQAFQYTDTHGEVCPAGWKPG--SDTIIPDPKE 238

*Ciona robusta*  IDTMGILRQITINDLPVGRSVDETLRLVKAFQFTDQHGEVCPAGWKPG--DDTIKPDVQD 189

*Xenopus laevis*  IDGKGILRQITINDLPVGRSVDETLRLVQAFQYTDVHGEVCPAGWKPG--SSTIKPNVKD 193

*Homo sapiens*  IDGKGVLRQITVNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWKPG--SDTIKPNVDD 189

*Mus musculus*  IDAKGVLRQITVNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWKPG--SDTIKPNVDD 189

*Danio rerio*  IDDKGILRQITINDLPVGRSVDETLRLVQAFQHTDKYGEVCPAGWKPG--SDTIVPDVQK 189

*Python bivittatus*  IDDKGILRQITVNDLPVGRSVDETLRLVQAFQFTDQHGEVCPAGWQPG--GDTIKPTVKD 189

\*\* \* :\*\*:\*:\*\* \*\*\*\*\*\*:\*::\*\*::\*\*:. : :\*\*\*\*\*\* \*.\* .\*:

*Clonorchis sinensis*  AQEYFSSVN-- 195

*Culex pipiens quinquefa*sciatus SKEYFNKHG-- 232

*Botrylloides leachii*  KMKYFQKMREL 237

*Crassostrea gigas*  SQKYFSKQNN- 248

*Ciona robusta*  SQKYFSKQ--- 197

*Xenopus laevis*  SKEFFSKEY-- 202

*Homo sapiens*  SKEYFSKHN-- 198

*Mus musculus*  SKEYFSKHN-- 198

*Danio rerio*  SKEFFSKQ--- 197

*Python bivittatus*  SKLFFSKQQ-- 198

:\*..

**Figure S4.** Schematic Prdx2 domain organization. The AhpC-TSAdomain is highlighted in light grey, the 1-cysPrx C domain is highlighted in dark grey. For *C. robusta*, alpha helixes 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.

*Botrylloides leachii*  -----------------------------------------MATLRSCASLVTKSIAASK 19

*Drosophila melanogaster* ----MSF--------V--------AR----------SLIRNVPLMGK---AIL------- 20

*Schistosoma haematobium* ----------------------------------------------MLLQVLI------- 7

*Ciona robusta*  -----MFINRLVHGFRRTH------------------------TLQSSLNPWI------- 24

*Scylla paramamosain*  --------------------MAGL--------------LKNIAV--TATRTVL------- 17

*Danio rerio*  MAATIG---RLLGASARGAAVCGLKTLVPRNGASVI----------RAPQPLA------- 40

*Python bivittatus*  MAALTGVLRRLLKPSSGWT-----GATLWRAGAVAGRCLSGAASGRKCAADA-------- 47

*Xenopus laevis*  MAASCG---RLLASWVGRT-----GRLTGQ-LPRVAG--SSVPRNMTAVTPSI------- 42

*Anas platyrhynchos*  MAAALG---RLLRSAVPAA-----GRRLQ---------------GR-------------- 23

*Homo sapiens*  MAAAVG---RLLRASVARH-----VSAIPW-GISATAALRPAACGRTSLTNLL------- 44

*Mus musculus*  MAAAAG---RLLWSSVARH-----ASAISR-SISASTVLRPVASRRTCLTDIL------- 44

*Botrylloides leachii*  QLRLLVANHHLRPLSSSSRNHVAQVTQPAPDF---------------------------- 51

*Drosophila melanogaster* ---SQQKQIAARLLHQTAPLAAVRVQQPAPDFKGLAVVDNSFQEVKLEDYRGKYLVLFFY 77

*Schistosoma haematobium* ---KGALRYNRSPVSNLCRHYAAHVQRPAPDFCGTAVVDGQFKEIKLRDYAGKYLVLFFY 64

*Ciona robusta*  ----SKWNPNSASISTSCRSMVAQVTQPAPPFKGMSVVEGKFKEISLEDYKGKYLVLFFY 80

*Scylla paramamosain*  ---PRITAAAQRGLSTSVRCLAPAVTQPAPSFKAQAVVNGDFKELSLEDFRGKYLVLFFY 74

*Danio rerio*  ---C--IAAQKACFSISAARWAPAVTQAAPHFKGTAVINGEFKEISLGDFKGKYLVLFFY 95

*Python bivittatus*  -----TPLVPRFHFSTSASRFVPAVTQHAPYFKGTAVVDGDFKELSLDDFKGKYLVLFFY 102

*Xenopus laevis*  ---C---AAQKLQFSTSSGRFLPAVTQHAPQFKGTAVVNGEFKELSLEDFKGKYLVLFFY 96

*Anas platyrhynchos*  -----PQLLAHRQLSLGASRLAPAVTQHAPFFKGTAVVHGEFKELSLDDFKGKYLVLFFY 78

*Homo sapiens*  ---CSGSSQA-KLFSTSSSCHAPAVTQHAPYFKGTAVVNGEFKDLSLDDFKGKYLVLFFY 100

*Mus musculus*  ---WSASAQGKSAFSTSSSFHTPAVTQHAPYFKGTAVVNGEFKELSLDDFKGKYLVLFFY 101

. \* : \*\* \*

*Botrylloides leachii*  ---------------------------------QDSRFSHLASVNTPRSKYGFGDTRIPL 78

*Drosophila melanogaster* PLDFTFVCPTEIVAFSERIKEFHDINTEVLGVSVDSHFSHLTWCNVDRKNGGVGQLKYPL 137

*Schistosoma haematobium* PLDFTFVCPTELTAFSDRIDEFKNEGVEVVGVSTDSHFSHLAWINTPRKEGGLGCLRYPL 124

*Ciona robusta*  **P**LDF**T**FV**C**PTEIISFSDKSPEFEKLDTAVVGASVDSHFSHLAWINTPRKQGGLGEMKIPL 140

*Scylla paramamosain*  PLDFTFVCPTELIAFSDHMAAFRELNCEVVGVSTDSHFSHLAWNNMPRKQGGLGGLQYTL 134

*Danio rerio*  PLDFTFVCPTEIVAFSDKANEFHDVNCAVVGVSVDSHFTHLAWTNTPRKSGGLGKIQIPL 155

*Python bivittatus*  PLDFTFVCPTEIIAFSDKANEFHDVNCDVLAVSVDSHFCHLAWINTPRKSGGLGHMNIPL 162

*Xenopus laevis*  PLDFTFVCPTEIVAFSNKANEFHDVNCEVVAVSVDSHFCHLAWTNTPRKSGGLGQMNIPL 156

*Anas platyrhynchos*  PLDFTFVCPTEIVAFSNKANEFRDVNCEVVAVSVDSHFCHLAWINTPRKSGGLGKMNIPV 138

*Homo sapiens*  PLDFTFVCPTEIVAFSDKANEFHDVNCEVVAVSVDSHFSHLAWINTPRKNGGLGHMNIAL 160

*Mus musculus*  PLDFTFVCPTEIVAFSDKANEFHDVNCEVVAVSVDSHFSHLAWINTPRKNGGLGHMNITL 161

\*\*:\* \*\*: \* \*.. \*.\* . :

*Botrylloides leachii*  LSDFNKTISKEYGILVEQAGVALRGTYIIDTNGIVRHLSVNDFSVGRSVDEILRLVQAFQ 138

*Drosophila melanogaster* LSDLTKKISADYDVLLDKEGISLRGTFIIDPNGILRQYSINDLPVGRSVDEVLRLIKAFQ 197

*Schistosoma haematobium* LADYQKQITRDYGVLQEELGVALRGLFIINPDGIVRQITINDLPVGRSVDEVLRLVRAFQ 184

*Ciona robusta*  LSDLTKNISRDYGVLLENAGIALR**G**LFIIDPSGTIRHASVNDLPVGRSVDEVLRLVQAFQ 200

*Scylla paramamosain*  LADLNKTISRDYGVLLEDDGVALRGLFLIDPEGVVRHMSINDLPVGRSVEETLRLLKAFQ 194

*Danio rerio*  LADLTKQVSRDYGVLLEGPGIALRGLFIIDPNGIVRHMSVNDLPVGRSVEETLRLVKAFQ 215

*Python bivittatus*  LSDLTKQISRDYGVLIEGSGLALRGLFIIDPNGIIKHLSVNDLPVGRSVEETLRLVKAFQ 222

*Xenopus laevis*  LSDLNKQISRDYGVLLETAGIALRGLFIIDPNGIIKHMSVNDLPVGRSVEETLRLVKAFQ 216

*Anas platyrhynchos*  LSDLTKQISRDYGVLLEGPGIALRGLFIIDPNGVIKHLSVNDLPVGRSVEETLRLVKAFQ 198

*Homo sapiens*  LSDLTKQISRDYGVLLEGSGLALRGLFIIDPNGVIKHLSVNDLPVGRSVEETLRLVKAFQ 220

*Mus musculus*  LSDITKQISRDYGVLLESAGIALRGLFIIDPNGVVKHLSVNDLPVGRSVEETLRLVKAFQ 221

\*:\* \* :: :\*.:\* : \*::\*\*\* ::\*: .\* ::: ::\*\*: \*\*\*\*\*:\* \*\*\*::\*\*\*

*Botrylloides leachii*  FXDEHGQLCPSSWKPGS--DSIKPTVEGSKEYFDKIE- 173

*Drosophila melanogaster* FVEQHGEVCPANWNPNSNPATIKPDVEESKKYFSKHG- 234

*Schistosoma haematobium* FTDKHGEVCPAGWQPKG--PTIKPDLKKYKEYFHKVN- 219

*Ciona robusta*  FVDKHGEVCPASWTPGS--KTIKPSVDGSKTYFEEAN- 235

*Scylla paramamosain*  FVAEHGEVCPANWQPES--PTIKPDPTGSLEYFNKVN- 229

*Danio rerio*  FVETHGEVCPASWTPKS--PTIKPTPDGSKEYFEKVN- 250

*Python bivittatus*  YVETHGEVCPANWIPDS--PTIKPSPEASKEYFAKVNK 258

*Xenopus laevis*  FVETHGEVCPAXWTPDS--PTIKPSPEGSKDYFEKVH- 251

*Anas platyrhynchos*  YVETHGEVCPANWTPDS--PTIKPSPEGSKEYFEKVHK 234

*Homo sapiens*  YVETHGEVCPANWTPDS--PTIKPSPAASKEYFQKVNQ 256

*Mus musculus*  FVETHGEVCPANWTPES--PTIKPSPTASKEYFEKVHQ 257

: \*\*::\*\*: \* \* . :\*\*\* \*\* :

**Figure S5.** Schematic Prdx3 domain organization. The AhpC-TSAdomain is highlighted in light grey, the 1-cysPrx\_C domain is highlighted in dark grey. For *C. robusta*, alpha helixes 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.

*Ciona robusta*  --------------------------MGVSFQLFTLACLFLA-----------------H 17

*Botrylloides leachii*  ------------------------------MKLFII-CFIIVTVLAN----------DEE 19

*Scylla paramamosain*  ---------------------------MSRLNLVLLACLV--------G-------LSVH 18

*Sepiella maindroni*  ----------------------------MALVGVNILCLLVLI--------------SSA 18

*Mus musculus*  MEARSK------------LLDGTTASRRWTRKLVLLLPPLLLFLLRTESL--QGLESDER 46

*Python bivittatus*  MEVGRQARGPPSESQAAARMSGRCGRLKPVSEPLAVYSMVLLMLAATMSEEAGTAEAAQS 60

*Danio rerio*  MD--VSRC-----------V------KTPREWLGVLWA-LLLL-SESVVC-------DGA 32

*Homo sapiens*  --MEALPL-----------LAAT-TPDHGRHRRLLLLP-LLLFLLPAGAVQG--WETEER 43

*Xenopus laevis*  MALQLRRY-----------L---------RGSPAVTLC-LLLLSAAAVTCEEEQSQARPG 39

*Anas platyrhynchos*  MEAGRRGL-----------RAGT-RTGTGTGGSALLVA-V-LAVLAVCGAAAEAEDPRAA 46

.

*Ciona robusta*  SGICQ------ERAV------FWPPYESHLLQSTKAQISKPAPDWEGTAIVDGEIKTIKL 65

*Botrylloides leachii*  QKYGG------MPGM------FWPPYQSHLLQSTKAQISKPAPSWEGTAIVDGEIKTIKS 67

*Scylla paramamosain*  GSLAEEQCHTFAGGAVYPNTEGR--ASGHTLQWTSAMISKPAPTWEGTAVVDGQLQELKL 76

*Sepiella maindroni*  VCIADEKCYSFAGGQVYPQEDRK--MSGHTIQWSKAIISKPAPDWNGTAVINGKFEEIGL 76

*Mus musculus*  FRTRENECHFYAGGQVYPGEASRVSVADHSLHLSKAKISKPAPYWEGTAVINGEFKELKL 106

*Python bivittatus*  YGYGDEKCHYYAGGEVYPGEASRVPVKDHSLHLSKAKISKTAPDWEGTAVINGEFKELKL 120

*Danio rerio*  NGKREQECYNYAGGHVYPGEAFRVPVSDHSLHLSKAKISKPAPHWEGTAVINGEFKELKL 92

*Homo sapiens*  PRTREEECHFYAGGQVYPGEASRVSVADHSLHLSKAKISKPAPYWEGTAVIDGEFKELKL 103

*Xenopus laevis*  RTAPDGECHFYAGGQVYPGEASRVPVSDHSLHLSKAKISKPAPYWEGTAVINGEFKELKL 99

*Anas platyrhynchos*  RQRGDEQCHYYAGGQVYPGEAARLPVTDHSLHLSQAKISKPAPYWEGTAVINGEFKELKL 106

. .\* :: :.\* \*\*\* \*\* \*:\*\*\*:::\*::: :

*Ciona robusta*  GDYKGKYLIFFFY**P**LDF**T**FV**C**PTEIIAFSDRVAEFKKINAEVVAASVDSHFTHLAWLNTH 125

*Botrylloides leachii*  DDYLGKYLIFFFYPLDFTFVCPTEIIAFSDRAEEFRKIGAEVVACSVDSHFTHLAWTNTE 127

*Scylla paramamosain*  TDYRGKYLVFFFYPLDFTFVCPTEILAFNDRVEEFRALNAEVVACSIDSHFTHLAWTSTP 136

*Sepiella maindroni*  RSYKGKYLVFFFYPLDFTFVCPTEIIAFSDRIEEFKDLNTKVVACSVDSQFTHLAWLNTP 136

*Mus musculus*  TDYRGKYLVFFFYPLDFTFVCPTEIIAFGDRIEEFKSINTEVVACSVDSQFTHLAWINTP 166

*Python bivittatus*  TDYEGKYVVFFFYPLDFTFVCPTEIIAFSDRIEEFRAIDAEVVACSVDSQFTHLAWINTP 180

*Danio rerio*  SDYKGKYLVFFFYPLDFTFVCPTEIIAFSDRVHEFQAINAEVVACSVDSQFTHLAWINTP 152

*Homo sapiens*  TDYRGKYLVFFFYPLDFTFVCPTEIIAFGDRLEEFRSINTEVVACSVDSQFTHLAWINTP 163

*Xenopus laevis*  TDYKGKYLVFFFYPLDFTFVCPTEIIAFGDRIEEFRSINTEVVACSVDSQFTHLAWINTP 159

*Anas platyrhynchos*  TDYEGKYLVFFFYPLDFTFVCPTEIIAFSDRIEEFRAINTEVVACSVDSKFTHLAWINTP 166

.\* \*\*\*::\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*:\*\*.\*\* \*\*: :.::\*\*\*.\*:\*\*:\*\*\*\*\*\* .\*

*Ciona robusta*  RSEGGLGKLNIPLLSDLTHKISRDYGVLLEDLGHTL**R**GLFIIDPKGILRQITMNDLPVGR 185

*Botrylloides leachii*  RKEGGLGKINIPLLSDLTHKISRDYGVLLEDLGHTLRGLFIIDPKGILRQITMNDLPVGR 187

*Scylla paramamosain*  RKDGGLGKLKIPLLSDITHKISKDYGVYLEDQGIALRGLFIIDNKGVLRQITMNDLPVGR 196

*Sepiella maindroni*  RNKGGLGHLKIPLLSDITHEISKAYGVYLQNLGHSLRGLFIIDTKGILRQITMNDLPVGR 196

*Mus musculus*  RRQGGLGPIRIPLLSDLNHQISKDYGVYLEDSGHTLRGLFIIDDKGVLRQITLNDLPVGR 226

*Python bivittatus*  RKQGGLGPVKIPLLSDLTHQISKDYGVYLEDQGHALRGLFIIDDKKILRQITMNDLPVGR 240

*Danio rerio*  RKQGGLGPMKIPLLSDLTHQISKDYGVFLEDQGHTLRGLFIIDGKGVLRQITMNDLPVGR 212

*Homo sapiens*  RRQGGLGPIRIPLLSDLTHQISKDYGVYLEDSGHTLRGLFIIDDKGILRQITLNDLPVGR 223

*Xenopus laevis*  RKQGGLGPMKIPLLSDLTHQISKDYGVYLEDQGHTLRGLFIIDDKGVLRQITMNDLPVGR 219

*Anas platyrhynchos*  RKQGGLGPMKIPLLSDLTHQISKDYGVYLEDQGHTLRGLFIIDDKRILRQITMNDLPVGR 226

\* .\*\*\*\* :.\*\*\*\*\*\*:.\*:\*\*: \*\*\* \*:: \* :\*\*\*\*\*\*\*\* \* :\*\*\*\*\*:\*\*\*\*\*\*\*

*Ciona robusta*  SVDETLRLVQAFQHTDEHGEVCPA-GWEPGKDTIIPDPKDKLKYFHKTSKAKGEL 239

*Botrylloides leachii*  SVDETLRLVQAFQHTDQHGEVCPA-GWQPGSDTIIPDPEGKMKYFQKMREL---- 237

*Scylla paramamosain*  SVDETLRLVQAFQFTDEHGEVCPA-GWKPGDDTIIPNPQEKLKYFKKANQ----- 245

*Sepiella maindroni*  SVDETLRLVQAFQYTDSHGEVCPA-GWKPGADTIIPDPKDKLKYFEKANS----- 245

*Mus musculus*  SVDETLRLVQAFQYTDKHGEDNPRSSWKTEVFRQAKLKSTSVMMFGPSQ------ 275

*Python bivittatus*  SVDETLRLVQAFQYTDKHGEVCPA-GWKPGSETIIPDPAGKLKYFGKVN------ 288

*Danio rerio*  SVDETLRLVQAFQYTDKHGEVCPA-GWKPGSDTIIPDPAGKLKYFDKLN------ 260

*Homo sapiens*  SVDETLRLVQAFQYTDKHGEVCPA-GWKPGSETIIPDPAGKLKYFDKLN------ 271

*Xenopus laevis*  SVDETLRLVQAFQYTDKHGEVCPA-GWKPGSETIIPDPAGKLKYFDKQH------ 267

*Anas platyrhynchos*  SVDETLRLVQAFQYTDKHGEVCPA-GWKPGSETIIPDPAGKLKYFDKLN------ 274

\*\*\*\*\*\*\*\*\*\*\*\*\*.\*\*.\*\*\* \* .\*: .: \*

**Figure S6.** Schematic Prdx4 domain organization. The AhpC-TSAdomain is highlighted in light grey, the 1-cysPrx\_C domain is highlighted in dark grey. For *C. robusta*, alpha helixes 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.