

Table S3. Physical characteristics of all available full-length DIA1 proteins and their similarity to orthologues from key species.

Species ^a	Length (amino acids)	pI ^b	Molecular mass ^c (kDa)	BLASTP ^d similarity to ^e :						
				<i>H. sapiens</i>	<i>G. gallus</i>	<i>D. rerio</i> (a)	<i>C. intestinalis</i>	<i>S. purpuratus</i>	<i>D. melanogaster</i>	<i>N. vectensis</i>
METAZOA^f										
Cnidaria										
<i>Nematostella vectensis</i>	402	5.6	44.7	8e-46	4e-44	6e-49	1e-15	6e-47	7e-08	-
Echinodermata										
<i>Strongylocentrotus purpuratus</i>	431	7.9	49.7	6e-80	3e-81	5e-84	3e-17	-	2e-08	2e-42
Arthropoda										
Hexapoda										
<i>Aedes aegypti</i>	395	6.0	45.7	6e-16	6e-15	2e-14	1e-04	5e-16	6e-14	5e-15
<i>Anopheles gambiae</i>	412	5.4	47.3	2e-06	3e-08	9e-09	0.10	5e-12	4e-10	0.018
<i>Culex pipiens</i>	400	5.1	45.2	2e-13	4e-13	8e-16	5e-04	1e-15	2e-13	2e-18
<i>Drosophila ananassae</i>	347	5.0	40.0	4e-04	3e-04	1e-06	>10	2e-06	1e-134	6e-09
<i>Drosophila erecta</i>	346	5.5	40.0	6e-07	2e-07	3e-08	>10	5e-09	2e-171	5e-10
<i>Drosophila melanogaster</i>	348	5.3	40.0	1e-06	7e-07	2e-08	>10	2e-08	-	5e-08
<i>Drosophila persimilis</i>	351	5.5	40.0	7e-09	2e-08	9e-10	>10	6e-08	3e-135	2e-06
<i>Drosophila pseudoobscura</i>	351	5.4	40.0	1e-07	2e-08	1e-09	>10	6e-08	8e-135	2e-06
<i>Drosophila sechellia</i>	350	5.7	40.3	5e-07	2e-07	7e-09	5.0	1e-08	0.0	5e-07
<i>Drosophila willistoni</i>	345	5.2	40.2	3e-10	3e-07	3e-07	4.6	4e-09	2e-92	1e-09
<i>Drosophila yakuba</i>	345	5.8	40.0	9e-09	3e-09	9e-11	>10	4e-07	3e-175	4e-10
<i>Nasonia vitripennis</i>	404	5.1	46.2	3e-53	7e-53	2e-54	1e-11	9e-47	2e-08	4e-36
Chordata										
Urochordata										
<i>Ciona intestinalis</i>	477	9.3	54.5	2e-29	1e-31	3e-34	-	3e-17	>10	4e-14
Cephalochordata										
<i>Branchiostoma floridae</i>	398	5.2	46.1	3e-101	5e-98	9e-104	2e-31	5e-81	7e-12	6e-43
Vertebrata										
Neopterygii										
<i>Danio rerio</i> (a)	432	8.6	50.0	0.0	0.0	-	6e-32	8e-82	2e-07	1e-46
<i>Danio rerio</i> (b)	429	8.7	49.4	0.0	0.0	0.0	6e-31	4e-80	2e-06	3e-44
<i>Gasterosteus aculeatus</i>	434	8.9	50.0	0.0	0.0	0.0	6e-33	5e-81	3e-06	2e-44
<i>Oryzias latipes</i>	434	8.8	50.1	0.0	0.0	0.0	2e-32	3e-83	3e-06	2e-44
<i>Takifugu rubripes</i>	435	8.8	50.1	0.0	0.0	0.0	3e-34	8e-84	1e-07	6e-47
<i>Tetraodon nigroviridis</i>	425	8.7	49.2	0.0	0.0	0.0	6e-32	6e-82	1e-05	9e-45
Tetrapoda										
Aves										
<i>Gallus gallus</i>	429	8.6	49.0	0.0	-	0.0	3e-29	4e-79	7e-06	9e-42
Amphibia										
<i>Xenopus tropicalis</i>	429	8.7	49.3	0.0	0.0	0.0	7e-32	3e-80	1e-06	7e-45
Mammalia										
<i>Bos taurus</i>	430	8.8	49.5	0.0	0.0	0.0	1e-29	6e-80	2e-06	3e-41
<i>Canis familiaris</i>	430	8.8	49.5	0.0	0.0	0.0	1e-29	6e-80	2e-06	3e-41
<i>Homo sapiens</i>	430	8.8	49.4	-	0.0	0.0	1e-29	7e-80	2e-06	3e-41
<i>Macaca mulatta</i>	430	8.8	49.5	-	0.0	0.0	1e-29	7e-80	2e-06	3e-41

<i>Monodelphis domestica</i>	430	8.8	49.3	0.0	0.0	0.0	9e-30	6e-80	8e-07	2e-42
<i>Mus musculus</i>	430	8.9	49.5	0.0	0.0	0.0	2e-30	5e-79	9e-06	8e-41
<i>Pan troglodytes</i>	430	8.8	49.5	0.0	0.0	0.0	1e-29	6e-80	2e-06	3e-41
<i>Pongo pygmaeus</i>	430	8.8	49.5	0.0	0.0	0.0	1e-29	7e-80	2e-06	3e-41
<i>Pteropus vampyrus</i>	430	8.9	49.5	0.0	0.0	0.0	4e-29	7e-80	2e-05	8e-41
<i>Rattus norvegicus</i>	430	8.9	49.5	0.0	0.0	0.0	2e-30	5e-79	9e-06	8e-41
<i>Tursiops truncatus</i>	430	8.8	49.5	0.0	0.0	0.0	1e-29	7e-80	2e-06	3e-41

^aSee Table S1 for accession numbers of full length DIA1 proteins.

^bIsoelectric point calculated using the assumption that all residues have pKa values equivalent to that of isolated residues, and so may not accurately represent the value for the folded protein.

^cIsotopically averaged molecular weight prediction in kiloDaltons.

^dThe BLASTP E-value (Expect value) measures the statistical significance threshold for protein sequence matches. The smaller the number, the better the match. Computer shorthand nomenclature is used to present E-values when values are small. For example, 5e-01 = 0.5 and 5e-04 = 0.0005. Values lower than 1e-250 are indicated as zero. When E-values were greater than 10, details are not provided. A dash is used when protein alignments have 100% identity.

^eProteins were compared to DIA1 from *Homo sapiens*, *Ciona intestinalis*, *Strongylocentrotus purpuratus*, or *Drosophila melanogaster*, or *Nematostella vectensis* by protein BLAST. The DIA1 proteins used for comparison were chosen as representatives from class Mammalia, class Aves, and class Neopterygii within the subphylum Vertebrata, subphylum Urochordata, phylum Echinodermata, phylum Arthropoda, and phylum Cnidaria, respectively.

^fDIA1 homologues were not found in the phylum Porifera or Nematoda. Partial homologues, including those found in the phylum Mollusca and Annelida (Table S2), are not shown.