

S2 Table: Sequence sources

source	citation	species
Uniprot	(Consortium 2015)	<i>Bos taurus</i>
Genome		<i>Gallus gallus</i>
		<i>Homo sapiens</i>
		<i>Loxodonta africana</i>
		<i>Monodelphis domestica</i>
		<i>Mus musculus</i>
		<i>Ornithorhynchus anatinus</i>
		<i>Sarcophilus harrisii</i>
Ensembl v.84 predicted peptides	(Kersey et al. 2016)	<i>Danio rerio</i>
Genome		<i>Gadus morhua</i>
		<i>Gasterosteus aculeatus</i>
		<i>Latimeria chalumnae</i>
		<i>Lepisosteus oculatus</i>
		<i>Macropus eugenii</i>
		<i>Oreochromis niloticus</i>
		<i>Takifugu rubripes</i>
reptilian-transcriptomes.org	(Tzika et al. 2015)	<i>Alligator mississippiensis</i>
Transcriptome		<i>Chalcides ocellatus</i>
		<i>Chamaeleo chamaeleon</i>
		<i>Chrysemys picta</i>
		<i>Crocodylus porosus</i>
		<i>Eublepharis macularius</i>
		<i>Gavialis gangeticus</i>
		<i>Pantherophis guttatus</i>
		<i>Python molurus bivittatus</i>
		<i>Sphenodon punctatus</i>
		<i>Thamnophis elegans</i>
Avianbase	(Eöry et al. 2015)	<i>Aptenodytes forsteri</i>
Genome		<i>Columba livia</i>
Skatebase	(Wang et al. 2012)	<i>Callorhynchus milii</i>
Genome		<i>Leucoraja erinacea</i>
		<i>Scyliorhinus canicula</i>
SRA transcriptomes (Leinonen et al. 2011)	SRR1693777	<i>Acipenser transmontanus</i>
	SRR1604859	<i>Botryllus schlosseri</i>
	SRR652971	<i>Ginglymostoma cirratum</i>
	SRR1693776	<i>Ichthyophis bannanicus</i>
	SRR1693787	<i>Lepidosiren paradoxa</i>
	SRR1695991	<i>Lethenteron camtschaticum</i>
	SRR388685	<i>Petromyzon marinus</i>

SRR1612395
SRR2039259
SRR2028021
SRR1514129
SRR931704

Polypterus senegalus
Potamotrygon amandae
Protopterus annectens
Scyliorhinus canicula
Tachyglossus aculeatus

Published transcriptomes	(Richards et al. 2013)	<i>Carcharodon carcharias</i>
	(Matsunami et al. 2015b, 2015a)	<i>Hynobius retardatus</i>
	(Robertson and Cornman 2014, 2013)	<i>Lithobates clamitans</i>
	(Qiao et al. 2013)	<i>Odorrana margaretae</i>
	(Wang et al. 2015)	<i>Oikopleura dioica</i>
	(Genomic Resources Development Consortium et al. 2015; Nourisson et al. 2014)	<i>Rhinella marina</i>
	(Genomic Resources Development Consortium et al. 2015; Nourisson et al. 2014)	<i>Rhinella schneideri</i>
	(Deck et al. 2013)	<i>Squalus acanthias</i>
	(B. Wielstra et al. 2014; Ben Wielstra et al. 2014)	<i>Triturus cristatus</i>

Works Cited

- Consortium, T.U. 2015. UniProt: a hub for protein information. *Nucleic Acids Res.* **43**: D204–D212.
- Deck, C.A., McKay, S.J., Fiedler, T.J., LeMoine, C.M.R., Kajimura, M., Nawata, C.M., Wood, C.M., and Walsh, P.J. 2013. Transcriptome responses in the rectal gland of fed and fasted spiny dogfish shark (*Squalus acanthias*) determined by suppression subtractive hybridization. *Comp. Biochem. Physiol. Part D Genomics Proteomics* **8**: 334–343.
- Eöry, L. et al. 2015. Avianbase: a community resource for bird genomics. *Genome Biol.* **16**: 21.
- Genomic Resources Development Consortium et al. 2015. Genomic Resources Notes Accepted 1 August 2014–30 September 2014. *Mol. Ecol. Resour.* **15**: 228–229.
- Kersey, P.J. et al. 2016. Ensembl Genomes 2016: more genomes, more complexity. *Nucleic Acids Res.* **44**: D574–D580.
- Leinonen, R., Sugawara, H., and Shumway, M. 2011. The Sequence Read Archive. *Nucleic Acids Res.* **39**: D19–D21.
- Matsunami, M., Kitano, J., Kishida, O., Michimae, H., Miura, T., and Nishimura, K. 2015a. Data from: Transcriptome analysis of predator- and prey-induced phenotypic plasticity in the Hokkaido salamander (*Hynobius retardatus*). (Accessed July 28, 2016).
- Matsunami, M., Kitano, J., Kishida, O., Michimae, H., Miura, T., and Nishimura, K. 2015b. Transcriptome analysis of predator- and prey-induced phenotypic plasticity in the Hokkaido salamander (*Hynobius retardatus*). *Mol. Ecol.* **24**: 3064–3076.
- Nourisson, C., Carneiro, M., Vallinoto, M., and Sequeira, F. 2014. Data from: “De novo transcriptome assembly and polymorphism detection in ecological important widely distributed Neotropical toads from the *Rhinella marina* species complex (Anura: Bufonidae)” in Genomic Resources Notes Accepted 1 August 2014–30 September 2014. (Accessed July 28, 2016).
- Qiao, L., Yang, W., Fu, J., and Song, Z. 2013. Transcriptome Profile of the Green Odorous Frog (*Odorrana margaretae*). *PLoS ONE* **8**: e75211.
- Richards, V.P., Suzuki, H., Stanhope, M.J., and Shivji, M.S. 2013. Characterization of the heart transcriptome of the white shark (*Carcharodon carcharias*). *BMC Genomics* **14**: 697.
- Robertson, L.S., and Cornman, R.S. 2013. Data from: Transcriptome resources for the frogs *Lithobates clamitans* and *Pseudacris regilla*, emphasizing antimicrobial peptides and conserved loci for phylogenetics. (Accessed July 28, 2016).
- Robertson, L.S., and Cornman, R.S. 2014. Transcriptome resources for the frogs *Lithobates clamitans* and *Pseudacris regilla*, emphasizing antimicrobial peptides and conserved loci for phylogenetics. *Mol. Ecol. Resour.* **14**: 178–183.
- Tzika, A.C., Ullate-Agote, A., Grbic, D., and Milinkovitch, M.C. 2015. Reptilian Transcriptomes v2.0:

An Extensive Resource for Sauropsida Genomics and Transcriptomics. *Genome Biol. Evol.* **7**: 1827–1841.

- Wang, K., Omotezako, T., Kishi, K., Nishida, H., and Onuma, T.A. 2015. Maternal and zygotic transcriptomes in the appendicularian, *Oikopleura dioica*: novel protein-encoding genes, intra-species sequence variations, and trans-spliced RNA leader. *Dev. Genes Evol.* **225**: 149–159.
- Wang, Q. et al. 2012. Community annotation and bioinformatics workforce development in concert—Little Skate Genome Annotation Workshops and Jamborees. *Database J. Biol. Databases Curation* **2012**. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3308154/> (Accessed July 28, 2016).
- Wielstra, B., Duijm, E., Lagler, P., Lammers, Y., Meilink, W.R.M., Ziermann, J.M., and Arntzen, J.W. 2014. Data from: Parallel tagged amplicon sequencing of transcriptome-based genetic markers for *Triturus newts* with the Ion Torrent next-generation sequencing platform. (Accessed July 28, 2016).
- Wielstra, B., Duijm, E., Lagler, P., Lammers, Y., Meilink, W.R.M., Ziermann, J.M., and Arntzen, J.W. 2014. Parallel tagged amplicon sequencing of transcriptome-based genetic markers for *Triturus newts* with the Ion Torrent next-generation sequencing platform. *Mol. Ecol. Resour.* **14**: 1080–1089.