

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

SkateBase

RRID:SCR_005302

Type: Tool

Proper Citation

SkateBase (RRID:SCR_005302)

Resource Information

URL: <http://skatebase.org/>

Proper Citation: SkateBase (RRID:SCR_005302)

Description: Portal supporting the North East Bioinformatics Collaborative's project to sequence the genome of the Little Skate. Provided is a clearinghouse for Little Skate Genome Project and other publicly available Skate and Ray (Batoidea) genome data, and tools for data visualization and analysis. Little Skate Genome Project The little skate (*Leucoraja erinacea*) is a chondrichthyan (cartilaginous) fish native to the east coast of North America. Elasmobranchs (Skates, Rays, and Sharks) exhibit many fundamental vertebrate characteristics, including a neural crest, jaws and teeth, an adaptive immune system, and a pressurized circulatory system. These characteristics have been exploited to promote understanding about human physiology, immunology, stem cell biology, toxicology, neurobiology and regeneration. The development of standardized experimental protocols in elasmobranchs such as *L. erinacea* and the spiny dogfish shark (*Squalus acanthias*) has further positioned these organisms as important biomedical and developmental models. Despite this distinction, the only reported chondrichthyan genome is the low coverage (1.4x) draft genome of the elephant shark (*Callorhynchus milii*). To close the evolutionary gaps in available elasmobranch genome sequence data, and generate critical genomic resources for future biomedical study, the genome of *L. erinacea* is being sequenced by the North East Bioinformatics Collaborative (NEBC). As close evolutionary relatives, the little skate sequence will facilitate studies that employ dogfish shark and other elasmobranchs as model organisms. Skate tools include the SkateBLAST and the Skate Genome Browsers: Little Skate Mitochondrion, Thorny Skate Mitochondrion, and Ocellate Spot Skate Mitochondrion.

Abbreviations: SkateBase

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Keywords: little skate, leucoraja erinacea, sequence, genome, mitochondrion, thorny skate, ocellate spot skate, FASEB list

Funding: NIGMS 3P20GM103446-12S1

Resource Name: SkateBase

Resource ID: SCR_005302

Alternate IDs: nlx_144350

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260905T132533+0000

Ratings and Alerts

No rating or validation information has been found for SkateBase.

No alerts have been found for SkateBase.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 40 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

Minařík M, et al. (2024) Identification of multiple transcription factor genes potentially involved in the development of electrosensory versus mechanosensory lateral line organs. *Frontiers in cell and developmental biology*, 12, 1327924.

Sukparangsi W, et al. (2022) Evolutionary origin of vertebrate OCT4/POU5 functions in supporting pluripotency. *Nature communications*, 13(1), 5537.

Leurs N, et al. (2021) Evolution of Matrix Gla and Bone Gla Protein Genes in Jawed Vertebrates. *Frontiers in genetics*, 12, 620659.

Li L, et al. (2021) Fish lysozyme gene family evolution and divergent function in early development. *Developmental and comparative immunology*, 114, 103772.

Coppola U, et al. (2021) Origin and evolutionary landscape of Nr2f transcription factors across Metazoa. *PloS one*, 16(11), e0254282.

Sun S, et al. (2021) Evolution and Functional Characteristics of the Novel elovl8 That Play Pivotal Roles in Fatty Acid Biosynthesis. *Genes*, 12(8).

- Rasch LJ, et al. (2020) Development and regeneration of the crushing dentition in skates (Rajidae). *Developmental biology*, 466(1-2), 59.
- Fonseca E, et al. (2020) Cartilaginous fishes offer unique insights into the evolution of the nuclear receptor gene repertoire in gnathostomes. *General and comparative endocrinology*, 295, 113527.
- Völkel P, et al. (2019) Ezh1 arises from Ezh2 gene duplication but its function is not required for zebrafish development. *Scientific reports*, 9(1), 4319.
- Clusin WT, et al. (2019) Further studies of ion channels in the electroreceptor of the skate through deep sequencing, cloning and cross species comparisons. *Gene*, 718, 143989.
- Suriano CM, et al. (2018) Evidence for generative homology of cerebellum and cerebellum-like structures in an elasmobranch fish based on Pax6, Cbln1 and Grid2 expression. *The Journal of comparative neurology*, 526(14), 2187.
- Jung H, et al. (2018) The Ancient Origins of Neural Substrates for Land Walking. *Cell*, 172(4), 667.
- Letelier J, et al. (2018) A conserved Shh cis-regulatory module highlights a common developmental origin of unpaired and paired fins. *Nature genetics*, 50(4), 504.
- Cooper RL, et al. (2018) An ancient Turing-like patterning mechanism regulates skin denticle development in sharks. *Science advances*, 4(11), eaau5484.
- Parreira B, et al. (2018) Persistence of the ABCC6 genes and the emergence of the bony skeleton in vertebrates. *Scientific reports*, 8(1), 6027.
- Hultqvist G, et al. (2017) Emergence and evolution of an interaction between intrinsically disordered proteins. *eLife*, 6.
- Costa RA, et al. (2017) Evolution of the angiopoietin-like gene family in teleosts and their role in skin regeneration. *BMC evolutionary biology*, 17(1), 14.
- Fonseca E, et al. (2017) LXR α and LXR β Nuclear Receptors Evolved in the Common Ancestor of Gnathostomes. *Genome biology and evolution*, 9(1), 222.
- Biscotti M.A., et al. (2017) The small non-coding RNA processing machinery of two living fossil species, lungfish and coelacanth, gives new insights into the evolution of the Argonaute protein family. *Genome biology and evolution*, 9(3), 438.
- Vlasschaert C, et al. (2017) The evolution and functional diversification of the deubiquitinating enzyme superfamily. *Genome biology and evolution*, 9(3), 558.