

Resource Summary Report

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StellaBase: Nematostella vectensis genomics database

RRID:SCR_005153

Type: Tool

Proper Citation

StellaBase: Nematostella vectensis genomics database (RRID:SCR_005153)

Resource Information

URL: <http://stellabase.org>

Proper Citation: StellaBase: Nematostella vectensis genomics database (RRID:SCR_005153)

Description: StellaBase is a genomics database of Nematostella vectensis. It allows users to query the assembled Nematostella genome, a confirmed gene library, and a predicted genome using both keyword and homology based search functions. Data provided by these searches will elucidate gene family evolution in early animals. Unique research tools, including a Nematostella genetic stock library, a primer library, a literature repository and a gene expression library will provide support to the burgeoning Nematostella research community. Supported by: National Science Foundation (Grant No. 0212773 to JRF)

Synonyms: StellaBase

Resource Type: data or information resource, database

Keywords: gene family evolution, nematostella vectensis, nematostella vectensis genome

Resource Name: StellaBase: Nematostella vectensis genomics database

Resource ID: SCR_005153

Alternate IDs: nif-0000-03497

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260804T043236+0000

Ratings and Alerts

No rating or validation information has been found for StellaBase: Nematostella vectensis genomics database.

No alerts have been found for StellaBase: Nematostella vectensis genomics database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Salinas-Saavedra M, et al. (2018) Germ layer-specific regulation of cell polarity and adhesion gives insight into the evolution of mesoderm. *eLife*, 7.

Logashina YA, et al. (2017) New Disulfide-Stabilized Fold Provides Sea Anemone Peptide to Exhibit Both Antimicrobial and TRPA1 Potentiating Properties. *Toxins*, 9(5).

Zhang L, et al. (2011) Gene discovery, comparative analysis and expression profile reveal the complexity of the *Crassostrea gigas* apoptosis system. *Developmental and comparative immunology*, 35(5), 603.

Mazza ME, et al. (2010) A conserved cluster of three PRD-class homeobox genes (homeobrain, rx and orthopedia) in the Cnidaria and Protostomia. *EvoDevo*, 1(1), 3.

Baldwin WS, et al. (2009) The cytochrome P450 (CYP) gene superfamily in *Daphnia pulex*. *BMC genomics*, 10, 169.

Oulhen N, et al. (2009) A variant mimicking hyperphosphorylated 4E-BP inhibits protein synthesis in a sea urchin cell-free, cap-dependent translation system. *PloS one*, 4(3), e5070.

Materna SC, et al. (2006) The C2H2 zinc finger genes of *Strongylocentrotus purpuratus* and their expression in embryonic development. *Developmental biology*, 300(1), 108.

Robertson AJ, et al. (2006) The genomic underpinnings of apoptosis in *Strongylocentrotus purpuratus*. *Developmental biology*, 300(1), 321.

Byrum CA, et al. (2006) Protein tyrosine and serine-threonine phosphatases in the sea urchin, *Strongylocentrotus purpuratus*: identification and potential functions. *Developmental biology*, 300(1), 194.

Ryan JF, et al. (2006) The cnidarian-bilaterian ancestor possessed at least 56 homeoboxes: evidence from the starlet sea anemone, *Nematostella vectensis*. *Genome biology*, 7(7), R64.

Morales J, et al. (2006) Translational control genes in the sea urchin genome. *Developmental biology*, 300(1), 293.

Walton KD, et al. (2006) Genomics and expression profiles of the Hedgehog and Notch signaling pathways in sea urchin development. *Developmental biology*, 300(1), 153.

Croce JC, et al. (2006) A genome-wide survey of the evolutionarily conserved Wnt pathways in the sea urchin *Strongylocentrotus purpuratus*. *Developmental biology*, 300(1), 121.