

Resource Summary Report

Generated by SPARC SAWG on Aug 8, 2026

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: database, data or information resource

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: 20260807T042620+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 [SPARC SAWG](#) .

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.

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.

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.

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.