



Homologous Gene Sets from NCBI

A new way for finding homologous gene sets provided by NCBI RefSeq through database search <https://www.ncbi.nlm.nih.gov/>
National Center for Biotechnology Information • National Library of Medicine • National Institutes of Health • Department of Health and Human Services

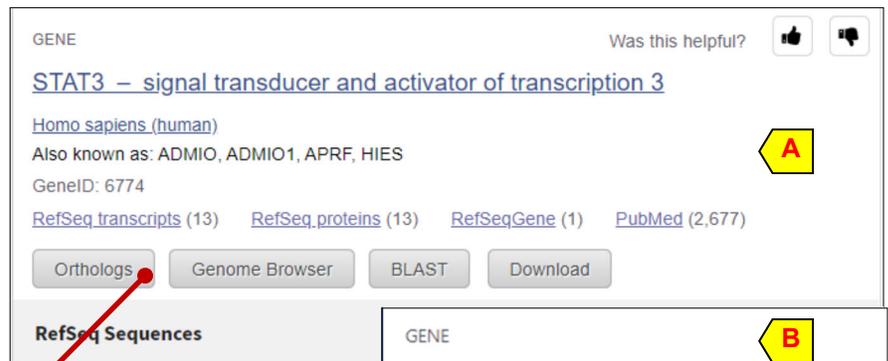
Scope

NCBI has a new way for users to find evolutionarily related genes within and across organisms represented in the NCBI RefSeq dataset. The goal of this new service is to facilitate comparative genomic research from the increasing number of annotated eukaryotic reference genomes.

Access and Results Presentation

These gene sets are searchable within NCBI's sequence databases including Nucleotide, Protein, Gene, Assembly, Genome or the "All Databases" search page. You can find a gene set by entering a gene symbol combined with a taxonomic group (e.g. mammals STAT3) or by selecting the 'orthologs' option from the suggest menu (e.g. STAT3 orthologs) in the search box. The responsive design adopts the results presentation based on your input.

- Simple gene symbol query produces a box (A) above the regular search results containing a link to the main STAT3 gene record and other links to its related datasets. A set of action buttons below launch additional services.
- A gene symbol combined with "orthologs" or "homologs" term narrows the search scope and present a focused presentation (B).



STAT3 – signal transducer and activator of transcription 3

The protein encoded by this gene is a member of the STAT protein family. In response to cytokines and growth factor family members are phosphorylated by the receptor associated kinases, and then form homo- or heterodimers that translocate to the cell nucleus where they act as transcription activators. This protein is activated through phosphorylation in response to various cytokines and growth factors including IFNs, EGF, IL5, IL6, HGF, LIF and BMP2. This protein mediates the expression of a variety of genes in response to cell stimuli, and thus plays a key role in many cellular processes such as cell growth and apoptosis. The small GTPase Rac1 has been shown to bind and regulate the activity of this protein. PIAS3 protein is a specific inhibitor of this protein. Mutations in this gene are associated with infantile-onset multisystem autoimmune disease and hyper-immunoglobulin E syndrome. Alternative splicing results in multiple transcript variants encoding distinct isoforms. [provided by RefSeq, Sep 2015]

Genes similar to STAT3

NCBI Orthologs

How was this calculated?

0 items

Genes Literature

SEARCH THE TAXONOMY TREE 282 genes for: jawed vertebrates (*Gnathostomata*)

Enter taxonomic name Add to cart Protein alignment Download

jawed vertebrates
 birds
 alligators and others
 turtles
 lizards

0 selected.

Species	Gene	Architecture	aa
<input type="checkbox"/> Homo sapiens human	STAT3 signal		770

Similar genes

How was this calculated?

0 items

Genes

SEARCH THE TAXONOMY TREE 1,296 genes for: Bilateria

Enter taxonomic name Add to cart Protein alignment Download

Bilateria

Clicking the Orthologs button or the "... orthologs from vertebrates" link launches the "NCBI Orthologs" display (C) and presents you with a set of vertebrate orthologous genes calculated by NCBI based on a combination of protein sequence similarity, local synteny information, and manual assertion.

The second in B, links to a set of genes that share protein domain architecture with the orthologous gene set, an expanded set than orthologs (D).

Interactive Gene List with Easy Access to Additional Functions

The NCBI Orthologs and Similar Genes pages display genes in rows that can be expanded to reveal more detailed information or activate additional functions:

- **A:** Toggle the table with arrow to see RefSeq transcripts and proteins for a gene
- **B:** See links to the NCBI genome browser and InterPro protein families
- **C:** Click the architecture cartoon to get details of the domain matches
- **D:** Filter the list based on categories defined in a taxonomy tree
- **E:** Check and “Add to cart” to select a subset
- **F:** Use “Protein alignment” to align selected proteins
- **G:** Hit “Download” to save selected genes to file

Genes similar to STAT3 <https://www.ncbi.nlm.nih.gov/gene/6774/ortholog/similargenes/?scope=33213>

NCBI Orthologs

How was this calculated?

1 item **Genes** Literature

SEARCH THE TAXONOMY TREE

Enter taxonomic name

23 genes for: even-toed ungulates (*Artiodactyla*)

Add to cart **Protein alignment** **Download**

File types: Tabular data (CSV)

one sequence per gene
 all sequences per gene

Download

1 selected.

Species	Gene	Architecture
<input type="checkbox"/> <i>Sus scrofa</i> pig	STAT3 signal transducer and activator of transcription 3	
<input checked="" type="checkbox"/> <i>Bos taurus</i> cattle	STAT3 signal transducer and activator of transcription 3	770

RefSeq transcripts (5) **RefSeq proteins (5)** **Architecture** **aa**

RefSeq transcripts (5)	RefSeq proteins (5)	Architecture	aa
NM_001012671.2	NP_001012689.2		770
XM_010816228.3	XP_010814530.1		769
XM_024979865.1	XP_024835633.1		770
XM_024979866.1	XP_024835634.1		722
XM_024979867.1	XP_024835635.1		721

Genome Browser InterPro

XP_024835635.1 721 aa

- 2 - 120 aa **smart00964** STAT_int: STAT protein, protein interaction domain
- 139 - 318 aa **cd16853** STAT3_CCD: Coiled-coil domain of Signal Transducer and Activator of Transcription 3 (STAT3)
- 321 - 484 aa **cd16847** STAT3_DBD: DNA-binding domain of Signal Transducer and Activator of Transcription 3 (STAT3)
- 554 - 714 aa **cd10374** SH2_STAT3: Src homology 2 (SH2) domain found in signal transducer and activator of transcription (STAT) 3 proteins

NCBI SPARCLE

Download data

File types: Tabular data (CSV)

one sequence per gene
 all sequences per gene

Download

Additional Information

Further information on how these sets are calculated

Orthologs: <https://www.ncbi.nlm.nih.gov/kis/info/how-are-orthologs-calculated/>

Similar genes: <https://www.ncbi.nlm.nih.gov/kis/info/how-are-similar-genes-calculated/>

Write to us to share your thoughts and suggestions: info@ncbi.nlm.nih.gov