

# *What areas should NHGRI support to facilitate understanding of basic biological questions/processes using genomic assays of function?*

How I interpret the question:

- What should NHGRI be doing for me (and clinician/scientists like me)?
- What does the draft epigenome mean to the rank and file physicians trying to engage in precision medicine?
- When a patient comes into the NIH CC, how can I use Encode/Roadmap to better understand dz?
- How can I use Encode/Roadmap in animal models to better understand dz pathogenesis in humans and identify/devise new therapies?

**Ease of use of epigenomics data for  
rank and file clinician/scientists**

## Gene

Gene

jak3

[Save search](#) [Advanced](#)

## Gene sources

Genomic

## Categories

Alternatively spliced  
Annotated genes  
Protein-coding  
Pseudogene

## Sequence content

CCDS  
Ensembl  
RefSeq  
RefSeqGene

## Status

clear

✓ **Current only**

Chromosome  
locations  
more...

[Clear all](#)[Show additional filters](#)**Display Settings:**  Tabular, 20 per page, Sorted by Relevance**Send to:** 

Did you mean [jak3](#) as a gene symbol?  
Search Gene for [jak3](#) as a symbol.

**Results: 1 to 20 of 234**

&lt;&lt; First &lt; Prev Page 1 of 12 Next &gt; Last &gt;&gt;

**i** Filters activated: Current only. [Clear all](#) to show 241 items.

Name/Gene ID	Description	Location	Aliases	MIM
<input type="checkbox"/> <a href="#">JAK3</a> ID: 3718	Janus kinase 3 [ <i>Homo sapiens</i> (human)]	Chromosome 19, NC_000019.10 (17824782..17848071, complement)	JAK-3_HUMAN, JAKL, L-JAK, LJAK, JAK3	600173
<input type="checkbox"/> <a href="#">Jak3</a> ID: 16453	Janus kinase 3 [ <i>Mus musculus</i> (house mouse)]	Chromosome 8, NC_000074.6 (71676383..71690577)	fae, wil	
<input type="checkbox"/> <a href="#">Jak3</a> ID: 25326	Janus kinase 3 [ <i>Rattus norvegicus</i> (Norway rat)]	Chromosome 16, NC_005115.4 (20107468..20120678)	RATJAK3	
<input type="checkbox"/> <a href="#">jak3</a> ID: 561370	Janus kinase 3 (a protein tyrosine kinase, leukocyte) [ <i>Danio rerio</i> (zebrafish)]	Chromosome 8, NC_007119.6 (13347948..13375414)	sb:eu418	
<input type="checkbox"/> <a href="#">JAK3</a> ID: 395845	Janus kinase 3 [ <i>Gallus gallus</i> (chicken)]	NW_003769825.1 (10252..16884)	JAK	

## Filters: M

## ▼ Top

Hom  
Mus m  
Rattus  
Mesito  
Tinam  
All oth  
More...

## Find rel

Database

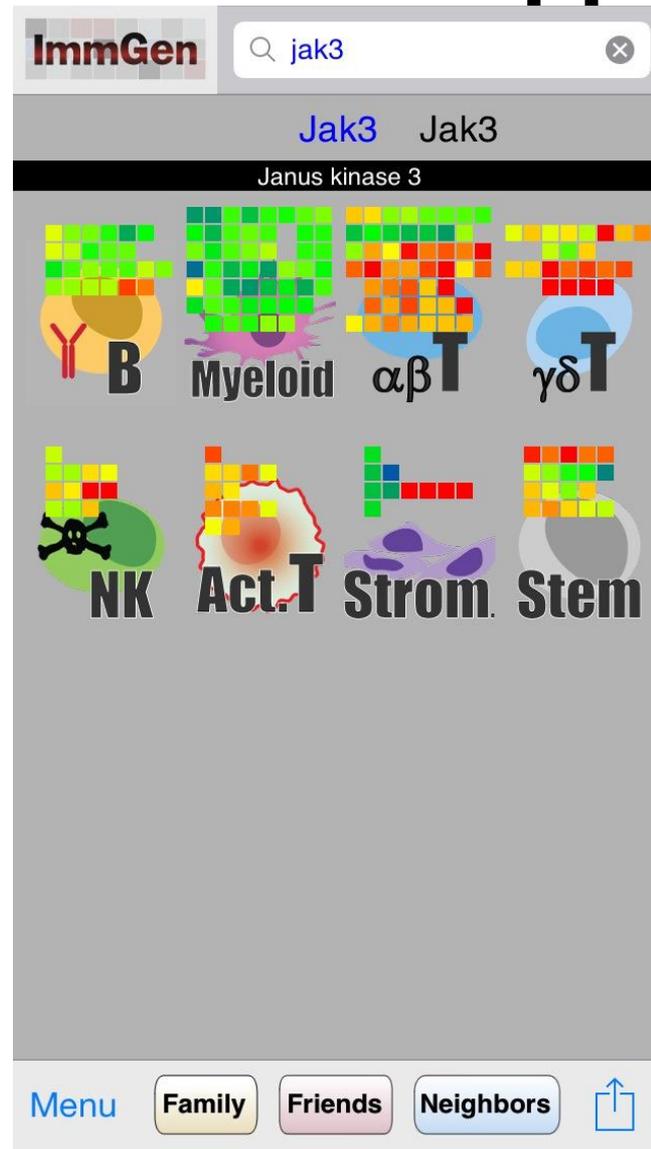
Find it

## Search

jak3[A

# Gene expression on your iPhone

## ImmGen app



Epigenomics

Epigenomics

jak3

Search

[Save search](#) [Advanced](#)

 The following term was not found in Epigenomics: jak3.

 No items found.

[Genome view for human JAK3](#)

See genome view for: [mouse Jak3](#)

See Also: [jak3](#) in the Gene database.

### Search details

(jak3[All Fields])

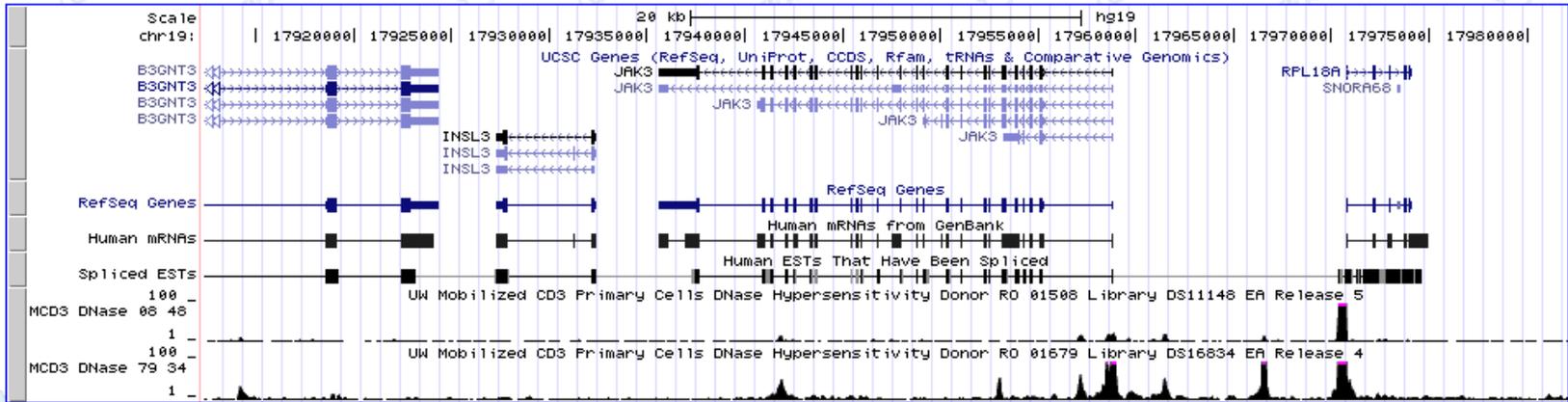
Search

See m

# UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr19:17,912,348-17,982,088    size 69,741 bp.



Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position.

move start < 2.0 > move end < 2.0 >

Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes.

**Mapping and Sequencing Tracks**

[Base Position](#)    
[Chromosome Band](#)    
[GC Percent](#)    
[Short Match](#)    
[Restr Enzymes](#)    
[Wiki Track](#)

# Ease of use of epigenomics data for rank and file clinician/scientists

- Integration and visualization of gene expression, epigenomics, 3D chromatin changes (ideally on cell phone app)
- Optimal integration of cross-species epigenomes
- Most effective use will require more user-friendly, highly intuitive modes of accessing datasets
- Facilitate use of epigenomic therapies?
  - Empiric vs targeted use
  - Restoration of “epigenetic homeostasis” – e.g. lupus
- Whose problem? Maybe not NHGRI?
- NCBI/NLM? Dz-specific Institutes? All/joint effort?

*What technological breakthroughs would really change how biological questions can be addressed?*

- Identification of rare variants/mutations of regulatory elements
- Mendelian disorders of the regulome
- How will I be able to figure out when a patient has a pathological regulome mutation?
- Actionable?
- High-throughput assays for regulomopathies?

# How many types of cells?

- 400 different types of cells in the body

# How many types of cells?

- It depends....
- activation vs. differentiation
- Diverse modes of activation, receptors, signals
- Cell-cycle, metabolism, senescence
- Integration of new datasets with “Encode/Roadmap” data?

# How do I get my data into “Encode”.

## Quality control vs. crowd sourcing

- Long tailed data - diverse and heterogeneous small data sets produced by individual scientists
- Represent the vast majority of scientific data

# How do I get my data into “Encode”?

## (Should I be able?)

- Level of coordination?
- Assurance that all appropriate data are included: source/preparation of cells, purity, cell stimulation, etc
- Better “history” of acquired cells (dz history, allergies, infectious disease, geography, smoking, etc)
- Quality control of archived regulomes?
- Lost opportunities vs Garbage in/Garbage out
- Ease of analysis/comparisons
- Development of tools/visualization for meta-analysis

# ***What technological breakthroughs would really change how biological questions can be addressed?***

- Epigenomics of single cells
- Dynamic views of the epigenome
  - signal transduction meets chromatin biology
  - What changes quickly, what doesn't
  - Rapid analysis/measurement in realtime
  - Longitudinal studies? Autoantibodies precede dz by many years
  - Aging/twin (again – example of lupus – 25% concordance)
- Better use of natural variation of *Mus musculus* Primates?
  - ENU mutagenesis
- Humanized mice to understand segments human regulomes
  - E.g. polymorphic regions associated with disease (e.g. *IL10*)
  - Moving from association to causality
- Other model organisms, optimal use of evolutionary lessons