3000788 Intro to Comp Molec Biol

Lecture 22: Online databases and tools

November 2, 2023

Sira Sriswasdi, PhD

- Research Affairs
- Center of Excellence in Computational Molecular Biology (CMB)
- Center for Artificial Intelligence in Medicine (CU-AIM)

Some motivations

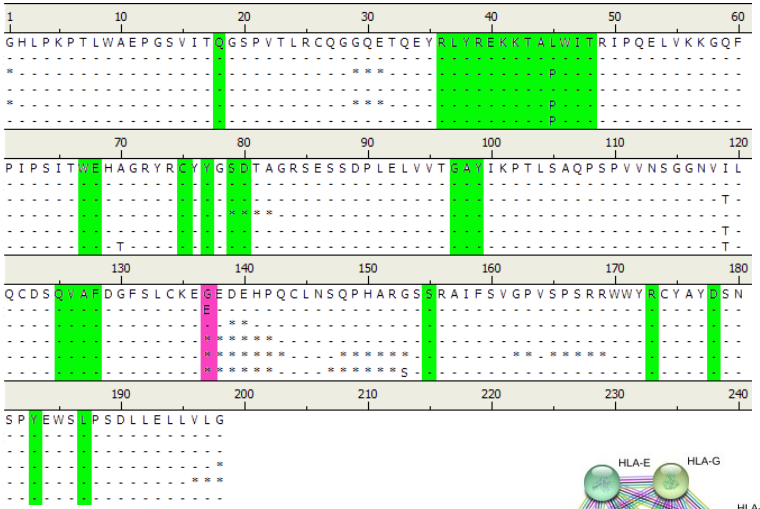
- Quick answers to quick questions
  - Impact of a newly identified mutation?
  - Where does a TF bind on genome?

- Free hypothesis generation
  - What genes are consistently up-regulated in a certain disease?

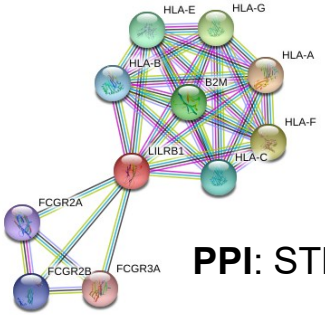
- Combine data from multiple modalities
  - Omics
  - Clinical
  - Imaging

Image from boston.lti.cs.cmu.edu

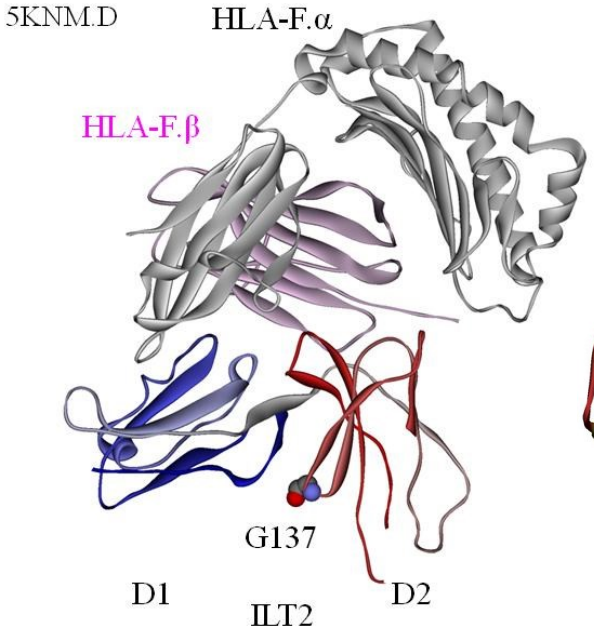
Example: G137E mutation on ILT2



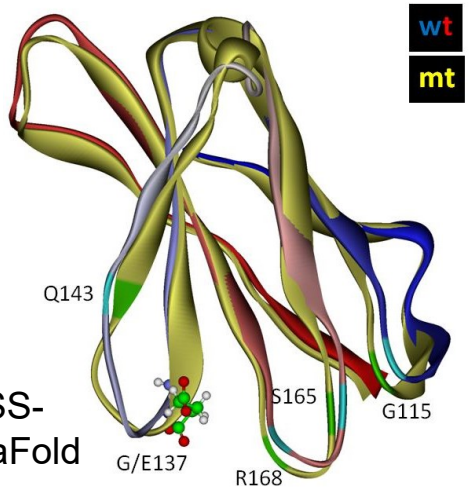
Sequence: Look up variant on ClinVar and alignment to reported sequences



PPI: STRING

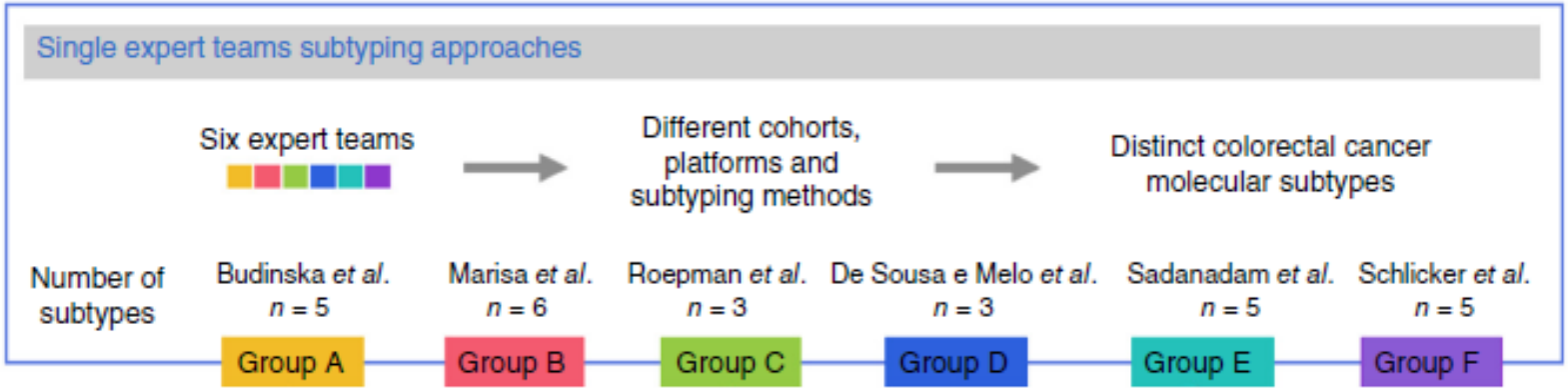


Structure: Highlight mutated residue on structure from PDB.



Modeling: SWISS-MODEL or AlphaFold

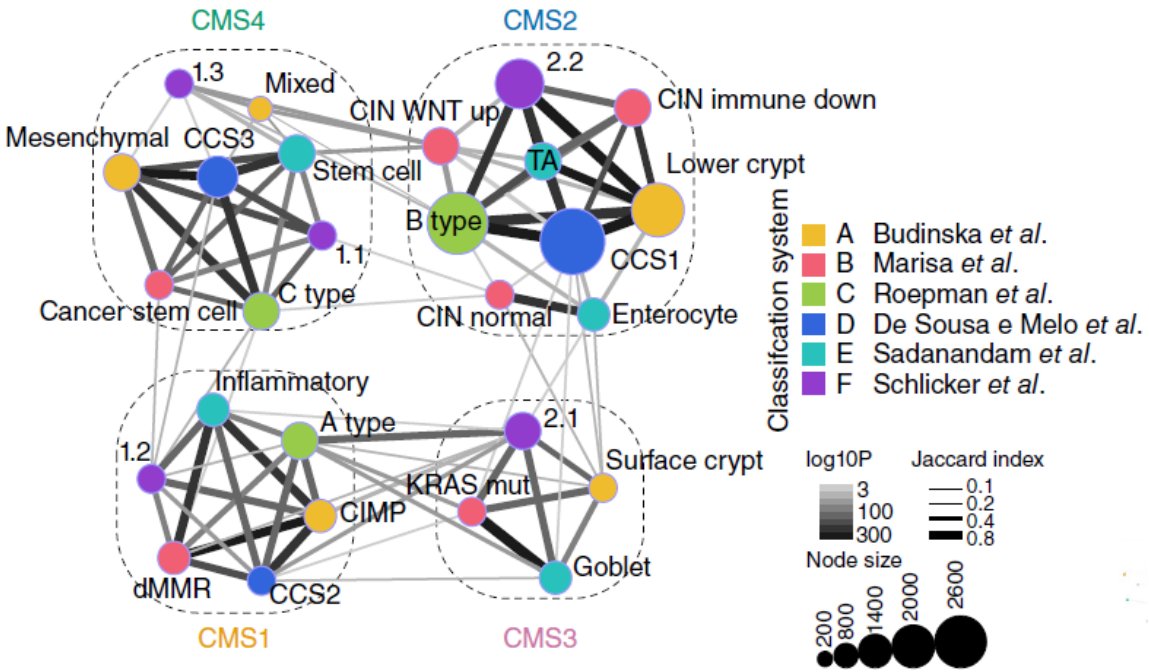
Example: Consensus cancer subtyping



Guinney *et al*. Nat Medicine 21: 1350-1356 (2015)

- Different clinicians characterize cancer patients differently
- But there should be a common molecular basis!

Example: Consensus cancer subtyping



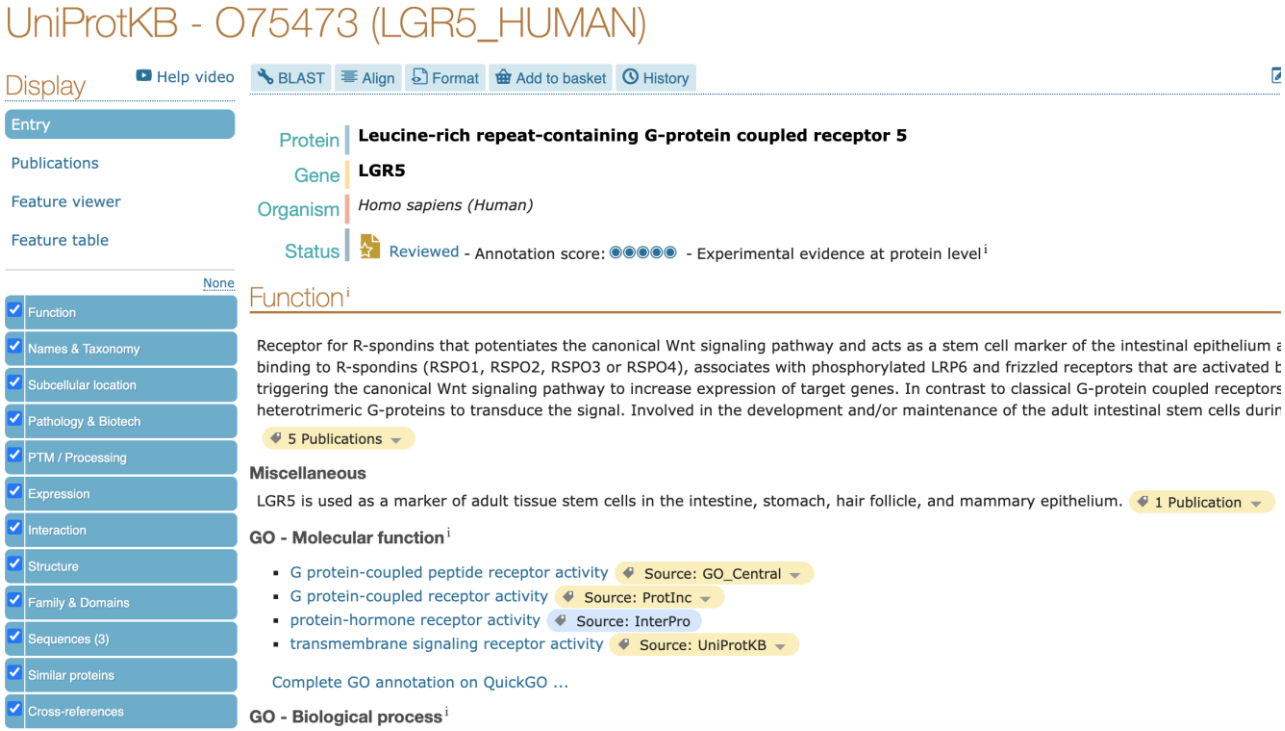
Guinney *et al*. Nat Medicine 21: 1350-1356 (2015)

- Compare clinician's decisions on a common group of patients
- Identify 4 major groups: Consensus Molecular Subtype (CMS)

Knowledgebase

Knowledgebase

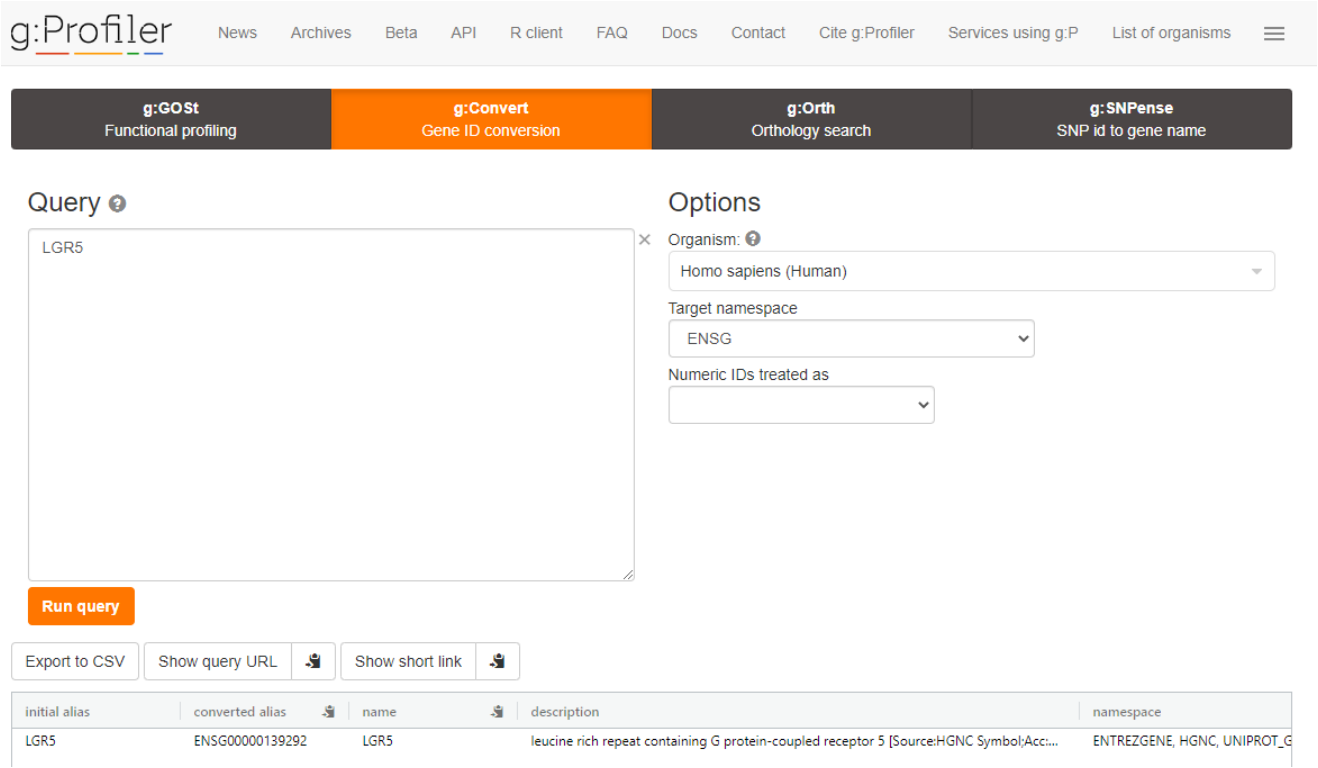
- NCBI/GenBank
- Ensembl
- Uniprot
- GeneCard
- ENCODE
- Human Protein Atlas



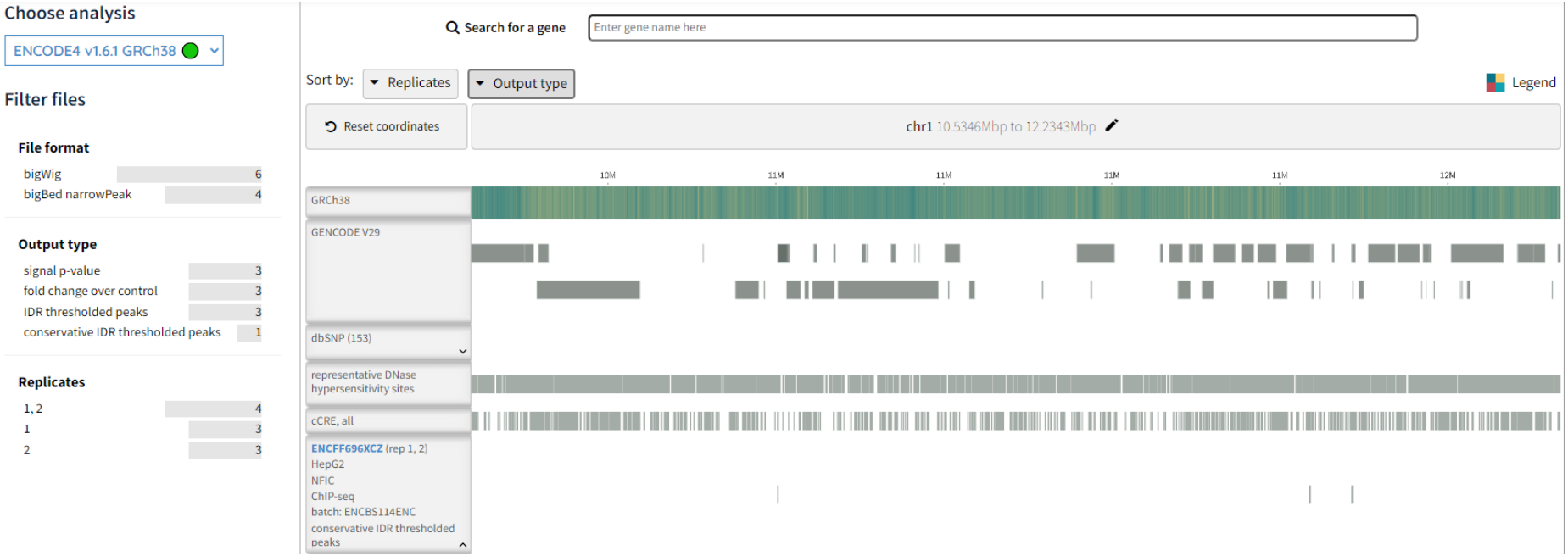
Accession IDs

ID system	Accession
Gene Symbol	LGR5
HGNC gene	4504
Entrez (NCBI)	8549
RefSeq transcript	NM_00367
Ensembl	ENSG00000139292
Uniprot protein	O75473
OMIM	606667

g:Profiler: Accession ID converter



ENCODE: Search for TF binding sites



- Processed ChIP-seq peaks for specific transcription factor

GeneCard: Gene aliases

Aliases for LGR5 Gene

Aliases for LGR5 Gene

GeneCards Symbol: *LGR5* [2]

Leucine Rich Repeat Containing G Protein-Coupled Receptor 5 [2 3 5]

GPR49 [3 4 5]

GPR67 [3 4 5]

HG38 [2 3 5]

FEX [2 3 5]

Leucine-Rich Repeat-Containing G-Protein Coupled Receptor 5 [3 4]

G-Protein Coupled Receptor HG38 [3 4]

G-Protein Coupled Receptor 49 [3 4]

G-Protein Coupled Receptor 67 [3 4]

Orphan G Protein-Coupled Receptor HG38 [3]

G Protein-Coupled Receptor 49 [2]

GRP49 [3]

External Ids for LGR5 Gene

HGNC: 4504 NCBI Entrez Gene: 8549 Ensembl: ENSG00000139292 OMIM®: 606667 UniProtKB/Swiss-Prot: O75473

Previous HGNC Symbols for LGR5 Gene

GPR67, GPR49

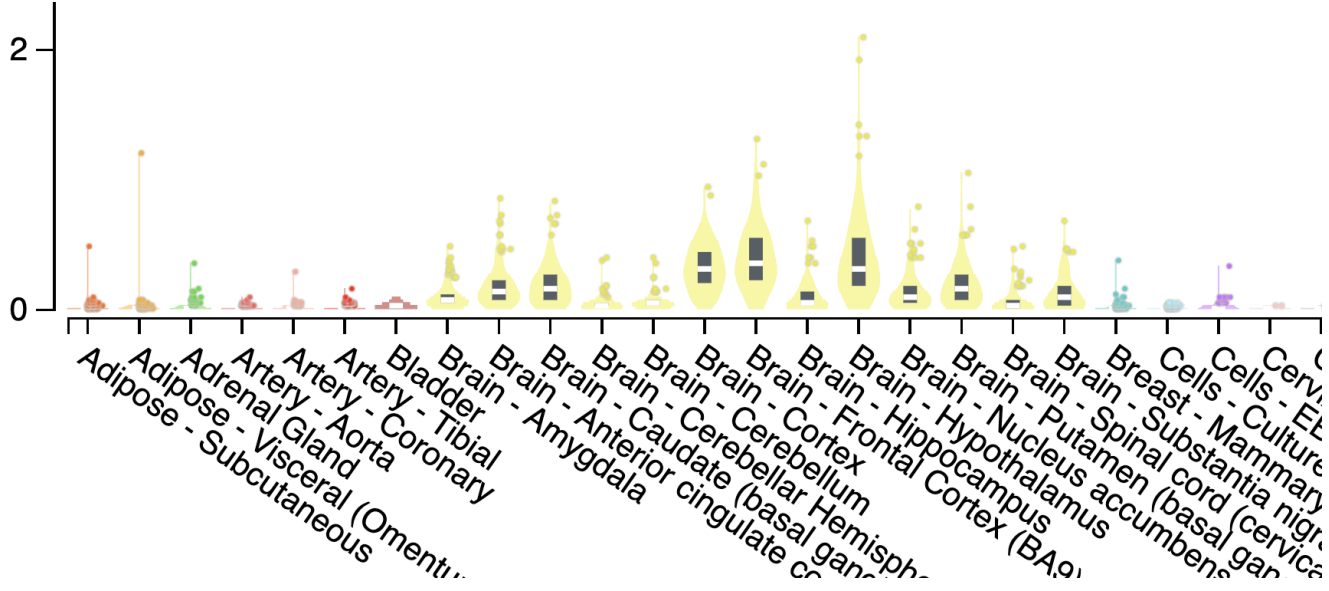
Previous GeneCards Identifiers for LGR5 Gene

GC12P070121, GC12P071833, GC12P068883

Search aliases for LGR5 gene in PubMed and other databases

GTEx: Tissue-specific expression

Gene Symbol	Gencode ID	Entrez Gene ID	Location	Gene Description
LIN28B	ENSG00000187772.7	389421	chr6:104936616-105083332:+	lin-28 homolog B [Source:HGNC Symbol;Acc:HGNC:32207]



Human Protein Atlas: Protein localization

ACE2

SUMMARY | TISSUE | RNA BRAIN | RNA SINGLE CELL | RNA TISSUE CELL | PATHOLOGY | RNA IMMUNE | MS BLOOD | RNA SUBCELL | RNA CELL LINE | METABOLIC

PROTEIN SUMMARY
RNA DATA
GENE/PROTEIN
ANTIBODIES AND VALIDATION

HUMAN PROTEIN ATLAS SUMMARY[i]	
Protein[i]	Angiotensin I converting enzyme 2
Gene name[i]	ACE2
Tissue specificity[i]	Tissue enhanced (gallbladder, intestine, kidney)
Tissue expression cluster[i]	Intestine & Kidney - Transmembrane transport (mainly)
Single cell type specificity[i]	Cell type enriched (Proximal enterocytes)
Single cell type expression cluster[i]	Enterocytes - Digestion (mainly)
Immune cell specificity[i]	Not detected in immune cells
Brain specificity[i]	Not detected in human brain
Cancer prognostic summary	Prognostic marker in renal cancer (favorable) and liver cancer (favorable)
Predicted location[i]	Membrane, Secreted (different isoforms)
Extracellular location[i]	Secreted to blood

JASPAR: DNA binding motifs

Detailed information of matrix profile **MA0161.2**

Home > Matrix > MA0161.2

Profile summary

Add

Name:	NFIC
Matrix ID:	MA0161.2
Class:	SMAD/NF-1 DNA-binding domain factors
Family:	Nuclear factor 1
Collection:	CORE
Taxon:	Vertebrates
Species:	Homo sapiens
Data Type:	ChIP-seq
Validation:	12101405
Uniprot ID:	P08651
Source:	29126285
Comment:	

Sequence logo

Download SVG

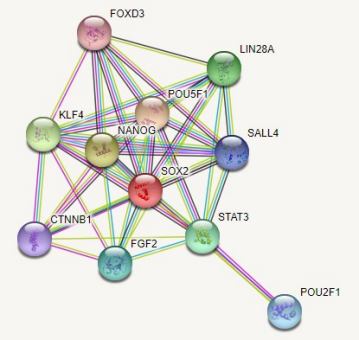
Frequency matrix

JASPAR TRANSFAC MEME RAW PFM

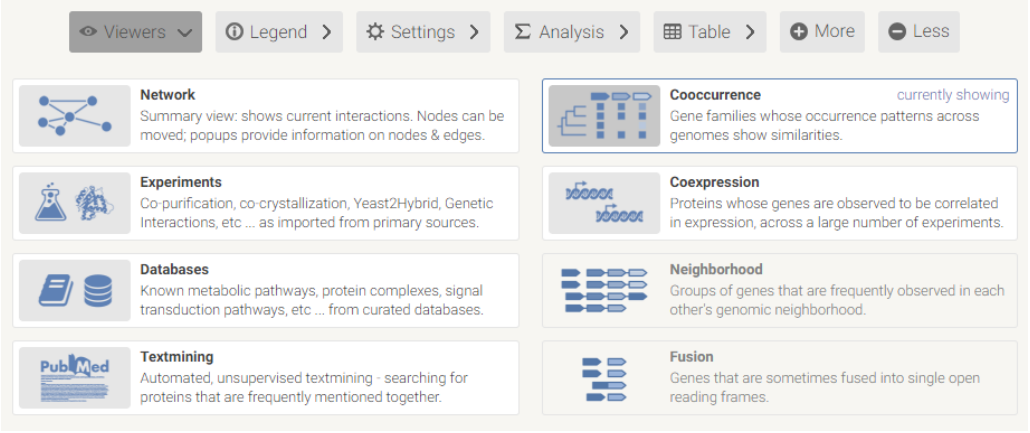
Reverse comp.

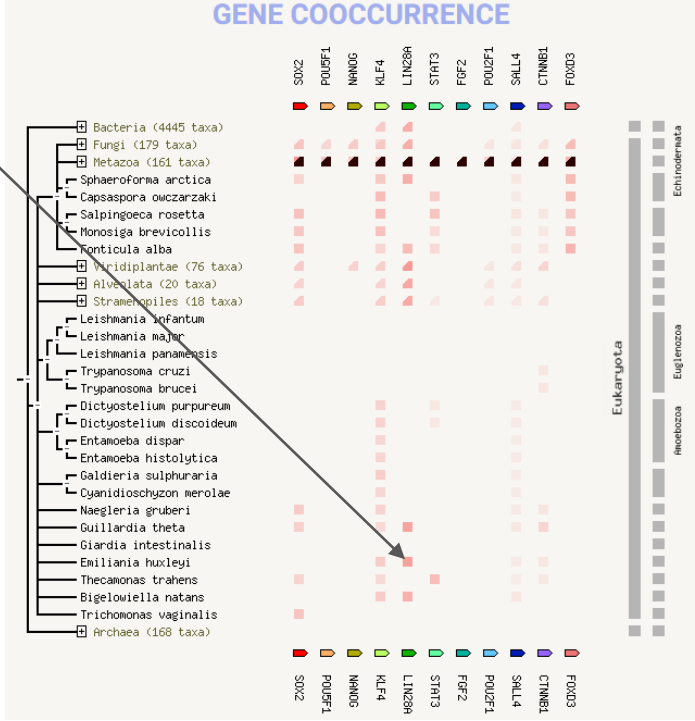
A [	2615	3896	412	154	352	310	223	264	10158	2626	334
C [	2647	2137	10542	303	333	129	121	10725	397	2951	271
G [	2478	2086	329	369	177	11087	10973	88	478	3186	276
T [	3867	3488	324	10781	10745	81	290	530	574	2844	279

STRING: Protein-protein interaction

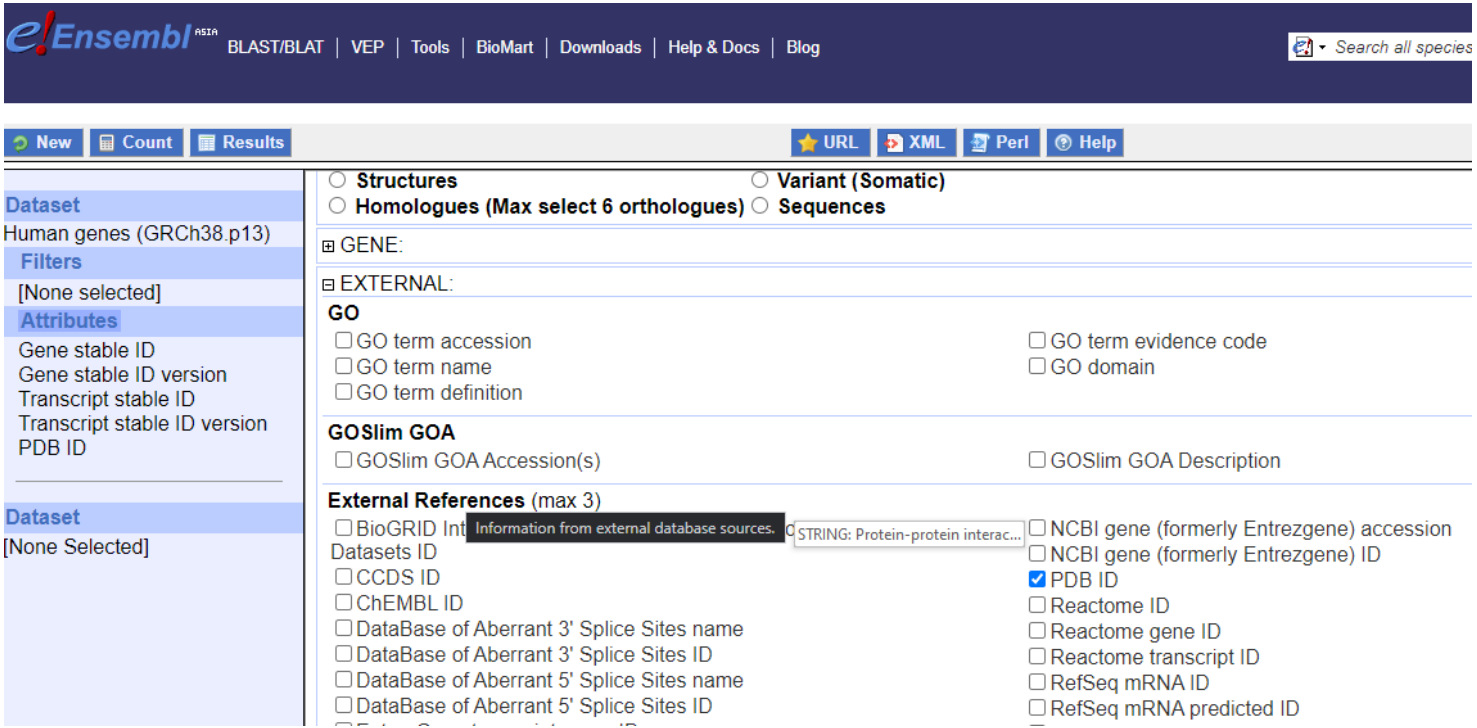



```
LIN28A      25      PEDAARAAD-EPQLLHGAGICKWFNVRMGFGFLSMTARAGVALDPPVDV
                    P  A R AD EP     +G CKWF+V+ GFGF+ +        +   D+
EOD22827    19      PNTATRVADPEPA---PSGKCKWFDVQKGFGFIDVE-------NQEQDL

LIN28A      73      FVHQSKLHMEGFRSLKEGEAVEFTFKKSAKG--LESIRVTGPGGVFCIG
                    FVHQ+ +  +GFRSL EGEA+EF   + AK   L++I VTGPGG F  G
EOD22827    58      FVHQTDIKAKGFRSLAEGEALEFKVSRDAKTNKLKAIEVTGPGGDFVEG

LIN28A      120     SERRP
                    + R P
EOD22827    107     APREP
```





Biomart: Gene/Protein data mapping download



Biomart: Gene/Protein data mapping download

New | Count | Results | URL | XML | Perl | Help

Dataset 11465 / 69292 Genes
Human genes (GRCh38.p13)

Filters

Chromosome/scaffold: 1 , 4 , 5

Attributes

Gene stable ID
Gene stable ID version
Transcript stable ID
Transcript stable ID version
PDB ID

Dataset

[None Selected]

Please restrict your query using criteria below
(If filter values are truncated in any lists, hover over the list item to see the full text)

REGION:

☑ Chromosome/scaffold

1
2
3
4
5
6
7
8
9
10
11
12
13

Biomart: Gene/Protein data mapping download

Dataset 11465 / 69292 Genes
Human genes (GRCh38.p13)

Filters

Chromosome/scaffold: 1 , 4 , 5

Attributes

Gene stable ID
Gene stable ID version
Transcript stable ID
Transcript stable ID version
PDB ID

Dataset

[None Selected]

Export all results to File TSV ☐ Unique results only Go

Email notification to

View 10 rows as HTML ☐ Unique results only

Gene stable ID	Gene stable ID version	Transcript stable ID	Transcript stable ID version	PDB ID
ENSG00000160072	ENSG00000160072.20	ENST00000673477	ENST00000673477.1	
ENSG00000160072	ENSG00000160072.20	ENST00000308647	ENST00000308647.8	
ENSG00000142611	ENSG00000142611.17	ENST00000511072	ENST00000511072.5	
ENSG00000142611	ENSG00000142611.17	ENST00000378391	ENST00000378391.6	2N1I
ENSG00000142611	ENSG00000142611.17	ENST00000378391	ENST00000378391.6	6BW4
ENSG00000142611	ENSG00000142611.17	ENST00000514189	ENST00000514189.5	
ENSG00000142611	ENSG00000142611.17	ENST00000270722	ENST00000270722.10	2N1I
ENSG00000142611	ENSG00000142611.17	ENST00000270722	ENST00000270722.10	6BW4
ENSG00000142611	ENSG00000142611.17	ENST00000463591	ENST00000463591.1	
ENSG00000142611	ENSG00000142611.17	ENST00000509860	ENST00000509860.1	

Data repository

Data repository

454 sequencing of Human HapMap individual NA18505 genomic paired-end library (SRR000001)

Metadata | Analysis | Reads | Data access

Run	Spots	Bases	Size	GC content	Published	Access Type
SRR000001	471.0k	129.5Mbp	312.5M	41.3%	2008-04-04	public

Quality graph (bigger)

This run has 4 reads per spot:

L=4, 100%	˜L=187, σ=95.9, 100%	L=44, 50%	˜L=123, σ=65.5, 50%

Legend

Experiment	Library Name	Platform	Strategy	Source	Selection	Layout	Action
SRX000007	SID2748	LS454	WGS	GENOMIC	RANDOM	PAIRED	BLAST

Biosample	Sample Description	Organism	Links
SAMN00001583 (SRS000100)	Human HapMap individual Coriell catalog ID NA18505	Homo sapiens	• dbSNP Batch ID 1061891 • Individual record in dbSNP

Bioproject	SRA Study	Title
PRJNA33627	SRP000001	Paired-end mapping reveals extensive structural variation in the human genome

Show abstract

ProteomeXchange ProteomeCentral

<<< Full experiment listing

PXD027487

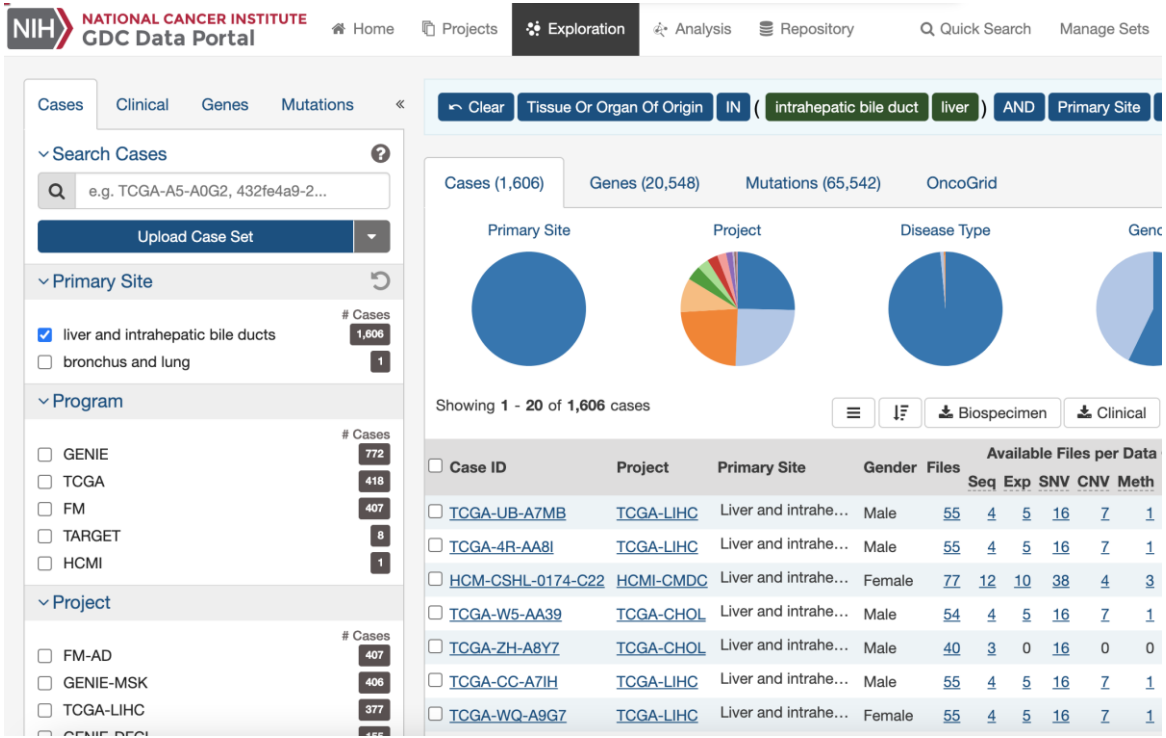
PXD027487 is an **original dataset** announced via ProteomeXchange.

Dataset Summary

Title	Interactome of GIGYF2 and EIF4E2 with and without SMG1i treatement
Description	Translation of messenger RNAs (mRNAs) with premature translation termination codons produces truncated proteins with potentially deleterious effects. This is prevented by nonsense-mediated mRNA decay (NMD) of these mRNAs. NMD is triggered by ribosomes terminating upstream of a splice site marked by an exon-junction complex (EJC), but also acts on many mRNAs lacking a splice junction after their termination codon. We developed a genome-wide CRISPR flow cytometry screen to identify regulators of mRNAs with premature termination codons in K562 cells. This screen recovered essentially all core NMD factors and suggested a role for EJC factors in degradation of PTCs without downstream splicing. Among the strongest hits were the translational repressors GIGYF2 and EIF4E2. GIGYF2 and EIF4E2 mediate translational repression but not mRNA decay of a subset of NMD targets and interact with NMD factors genetically and physically. Our results suggest a model wherein recognition of a stop codon as premature can lead to its translational repression through GIGYF2 and EIF4E2.
HostingRepository	PRIDE
AnnounceDate	2021-10-12
AnnouncementXML	Submission_2021-10-12_00:39:40.790.xml
DigitalObjectIdentifier	
ReviewLevel	Peer-reviewed dataset
DatasetOrigin	Original dataset

- Reanalysis with a common pipeline

Genomic Data Commons



- Cancer multi-omics
  - Exome
  - RNA-seq
  - Methylation
- Clinical and demographic data
- Some with histopathological images and radiographic images

PDB: 3D structures

RCSB PDB | Deposit | Search | Visualize | Analyze | Download | Learn | More | Documentation | Careers | MyPDB

Refinements

SCIENTIFIC NAME OF SOURCE ORGANISM
- Homo sapiens (13)
- Xenopus tropicalis (11)
- Mus musculus (10)
- Danio rerio (2)
- unidentified (1)

TAXONOMY
- Eukaryota (32)
- unclassified sequences (1)

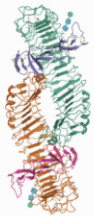
EXPERIMENTAL METHOD
- X-RAY DIFFRACTION (32)
- SOLUTION NMR (1)

POLYMER ENTITY TYPE
- Protein (33)

REFINEMENT RESOLUTION (Å)
- 1.5 - 2.0 (2)
- 2.0 - 2.5 (11)
- 2.5 - 3.0 (9)
- 3.0 - 3.5 (8)
- 4.0 - 4.5 (1)
- > 4.5 (1)

Summary | Gallery | Compact | -- Tabular Report -- | ↓ Score | Download Files | All | Selected

Displaying 1 to 25 of 33 **Structures** | Page 1 of 2 | ← Previous | Next → | Display 25 per page



3D View

4BSU

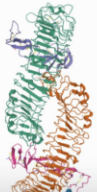
Download File | View File

Structure of the ectodomain of LGR5 in complex with R-spondin-1 (Fu1Fu2) in C2 crystal form

Peng, W.C., de Lau, W., Forneris, F., Granneman, J.C.M., Huch, M., Clevers, H., Gros, P.

(2013) Cell Rep **3**: 1885

Released	2013-06-26
Method	X-RAY DIFFRACTION 3.2 Å
Organisms	Homo sapiens
Macromolecule	LEUCINE-RICH REPEAT-CONTAINING G-PROTEIN COUPLED RECEPTOR 5 (protein)
	R-SPONDIN-1 (protein)
Unique Ligands	NAG
Unique branched monosaccharides	BMA, NAG



4BST

Download File | View File

Structure of the ectodomain of LGR5 in complex with R-spondin-1 (Fu1Fu2) in P6122 crystal form

Peng, W.C., de Lau, W., Forneris, F., Granneman, J.C.M., Huch, M., Clevers, H., Gros, P.

(2013) Cell Rep **3**: 1885

Released	2013-06-19
Method	X-RAY DIFFRACTION 4.3 Å

AlphaFold: Predicted 3D structures

3D viewer

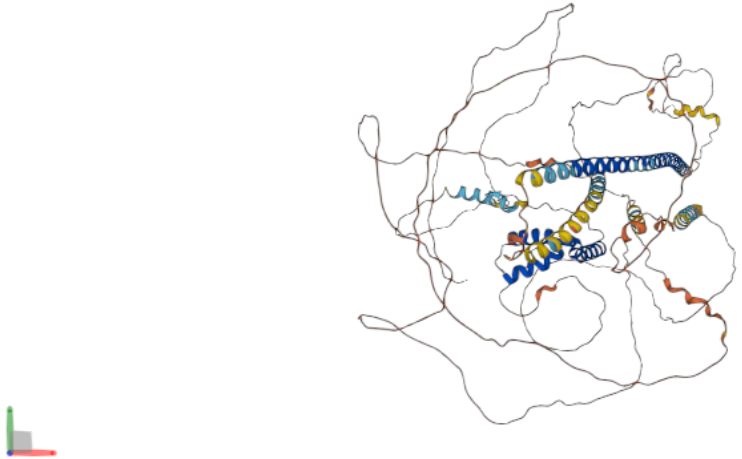
Model Confidence:

- Very high (pLDDT > 90)
- Confident (90 > pLDDT > 70)
- Low (70 > pLDDT > 50)
- Very low (pLDDT < 50)

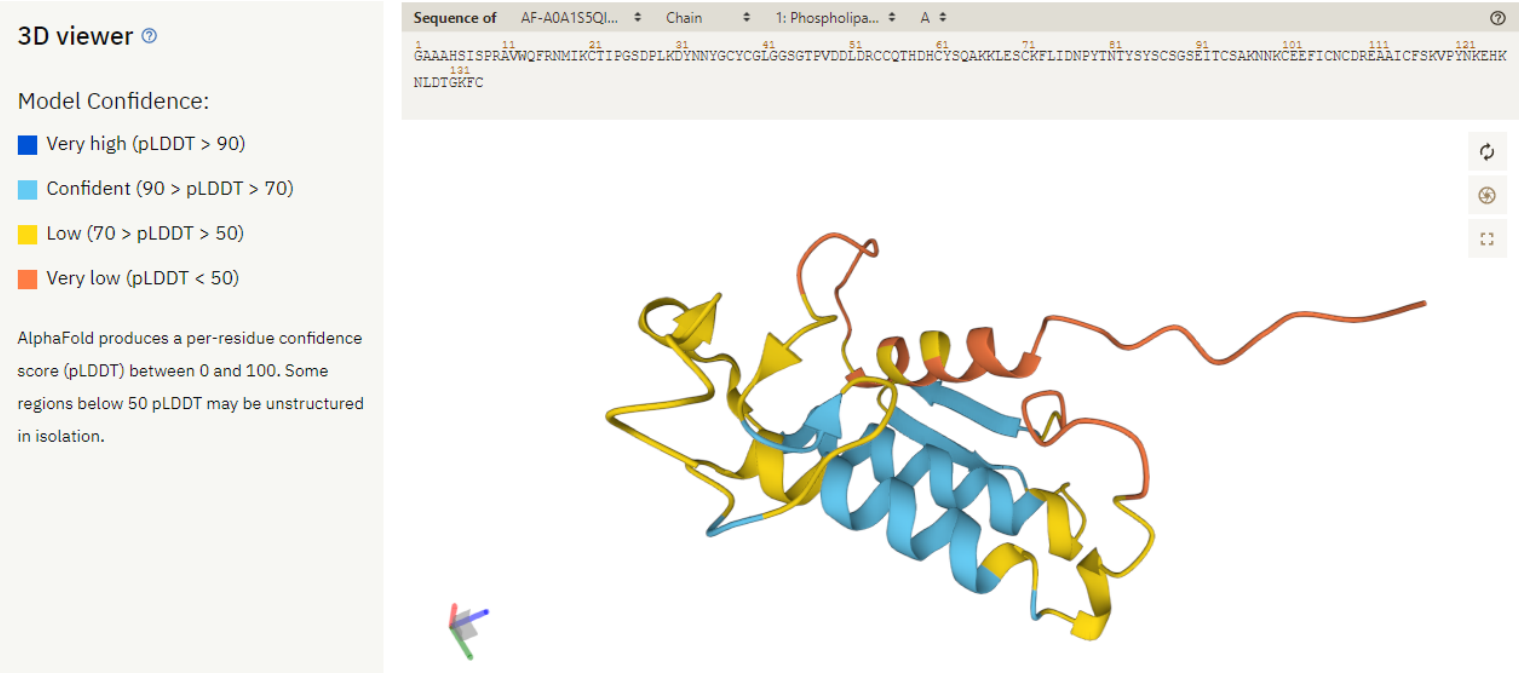
AlphaFold produces a per-residue confidence score (pLDDT) between 0 and 100. Some regions below 50 pLDDT may be unstructured in isolation.

Sequence of AF-A0A0G2JT... Chain 1: Transcriptio... A

```
1         11        21        31        41        51        61        71        81        91       101       111       121
MSSKQATSPFACTVDGEETMTQDLTSREKEEGSDQHPASHLPLHPIMHNKPHSEELPTLVSTIQQDADWDSVLSSQQRMESENNKLCSLYSFRNTSTSPHKPDEGSREREIMNSVTFGTPERRK
      131       141       151       161       171       181       191       201       211       221       231       241
GSLADVVDTLKQKKLEEMTRTEQEDSSCMEKLLSKDWKEKMERLNTSELLGEIKGTPESLAEKERQLSTMITQLISLREQLLAAHDEQKKLAASQIEKQRQQMDLARQQQEQIARQQQQLLQQQ
  251       261       271       281       291       301       311       321       331       341       351       361       371
HKINLLQQQIQVQGHMPPLMIPIFPHDQRTLAAAAAAQQGFLFPPGITYKPGDNYPVQFIPSTMAAAAASGLSPLQLQKGHVSHPQINPRLKGISDRLGRNLDPYEHGGGHSYNHKQIEQLYAA
```



AlphaFold: Predicted 3D structures



Gene Expression Omnibus / ArrayExpress

Study type — see all

TOP 10

- chip-chip by tiling array 706
- chip-seq 1,467
- comparative genomic hybridization by array 883
- genotyping by array 254
- methylation profiling by array 617
- other 222
- rna-seq of coding rna 1,437
- rna-seq of non coding rna 241
- transcription profiling by array 9,339
- unknown experiment type 218

You query contains a term which has too many synonyms and more specific phrases in EFO. The results shown below do not include those expanded terms.

Search results for breast cancer metastasis

1 – 20 of 1,417+ results

Sort by: Relevance

E-MTAB-4801 • 9 January 2019 • 3 links • 3 files

Variation in RNA expression in a panel of 30 breast cancer cell lines

... type comparison design EFO_0001745 cell line cell line BT20 BT474 BT549 ... 27 other values Homo sapiens female mammary gland invasive ductal carcinoma breast ductal adenocarcinoma metaplastic breast carcinoma squamous cell breast carcinoma, acantholytic variant breast adenocarcinoma breast...

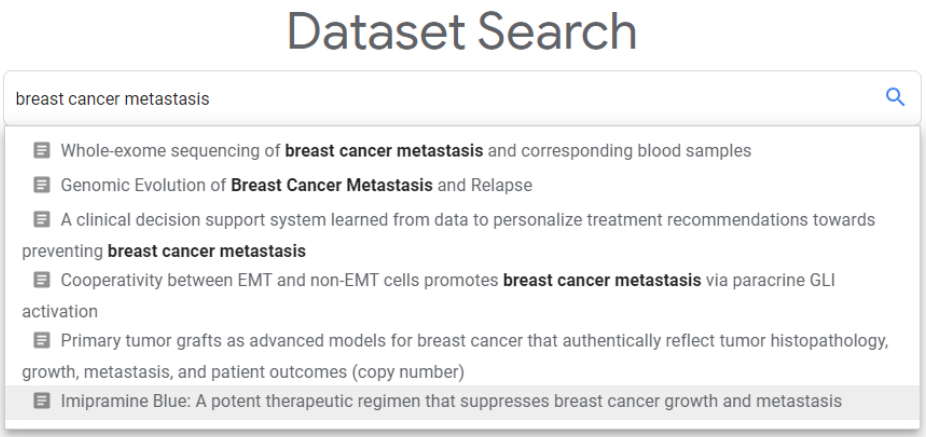
E-MTAB-8807 • 4 April 2020 • 1 link • 2 files

Estrogen receptor beta inhibits cholesterol biosynthesis through overexpression of mir-181a-5p in Triple Negative Breast Cancer

... carcinoma squamous cell breast carcinoma, acantholytic variant not specified invasive breast ductal carcinoma invasive lobular carcinoma adenocarcinoma atypical carcinoma carcinoma ER beta negative ER beta positive HCC1806 null null null epithelial cell squamous cell breast carcinoma, acantholytic...

- Search for omics datasets

Google Dataset / FigShare



- Google Dataset compiles links from major public data repositories
- Figshare is a free repository that scientists often use for non-omics data

MSigDB: Curated gene sets

Human MSigDB Collections

UC San Diego BROAD INSTITUTE

The 33196 gene sets in the Human Molecular Signatures Database (MSigDB) are divided into 9 major collections, and several sub-collections. See the table below for a brief description of each, and the Human MSigDB Collections: Details and Acknowledgments page for more detailed descriptions. See also the MSigDB Release Notes.

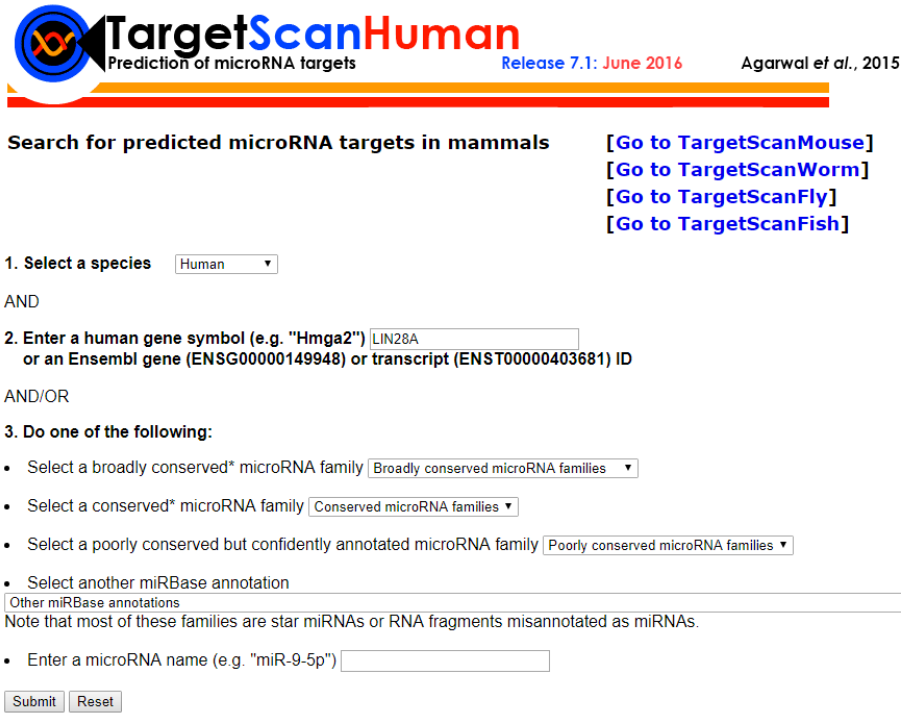
Click on the "browse gene sets" links in the table below to view the gene sets in a collection. Or download the gene sets in a collection by clicking on the links below the "Download Files" headings. For a description of the GMT file format see the Data Formats in the Documentation section. The gene sets can be downloaded as NCBI (Entrez) Gene Identifiers or HUGO (HGNC) Gene Symbols. There are also JSON bundles containing the HUGO (HGNC) Gene Symbols along with some useful metadata. An XML file containing all the Human MSigDB gene sets is available as well.

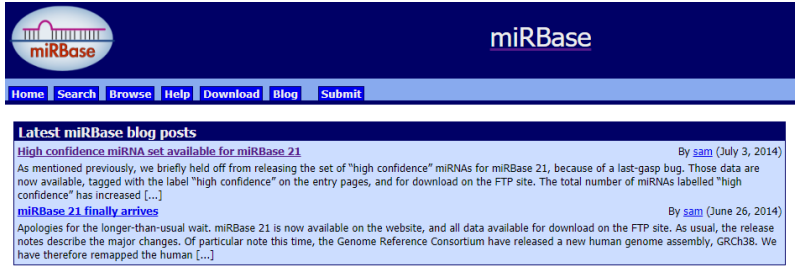
H: hallmark gene sets (browse 50 gene sets)	Hallmark gene sets summarize and represent specific well-defined biological states or processes and display coherent expression. These gene sets were generated by a computational methodology based on identifying overlaps between gene sets in other MSigDB collections and retaining genes that display coordinate expression. details	Download GMT Files Gene Symbols NCBI (Entrez) Gene IDs JSON bundle
C1: positional gene sets (browse 299 gene sets)	Gene sets corresponding to human chromosome cytogenetic bands. details	Download GMT Files Gene Symbols NCBI (Entrez) Gene IDs JSON bundle
C2: curated gene sets (browse 6449 gene sets)	Gene sets in this collection are curated from various sources, including online pathway databases and the biomedical literature. Many sets are also contributed by individual domain experts. The gene set page for each gene set lists its source. The C2 collection is divided into the following two sub-collections: Chemical and genetic perturbations (CGP) and Canonical pathways (CP). details	Download GMT Files Gene Symbols NCBI (Entrez) Gene IDs JSON bundle

- Function-based / Disease-based / Publication-based / Genomic location-based
- For gene panel, enrichment test, etc.

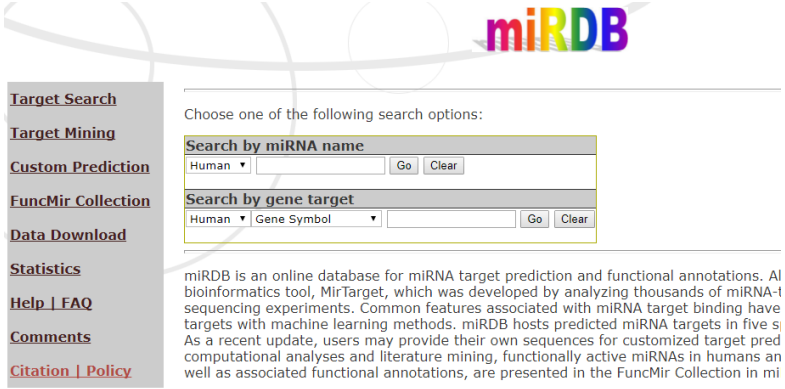
Analysis tools

miRNA target

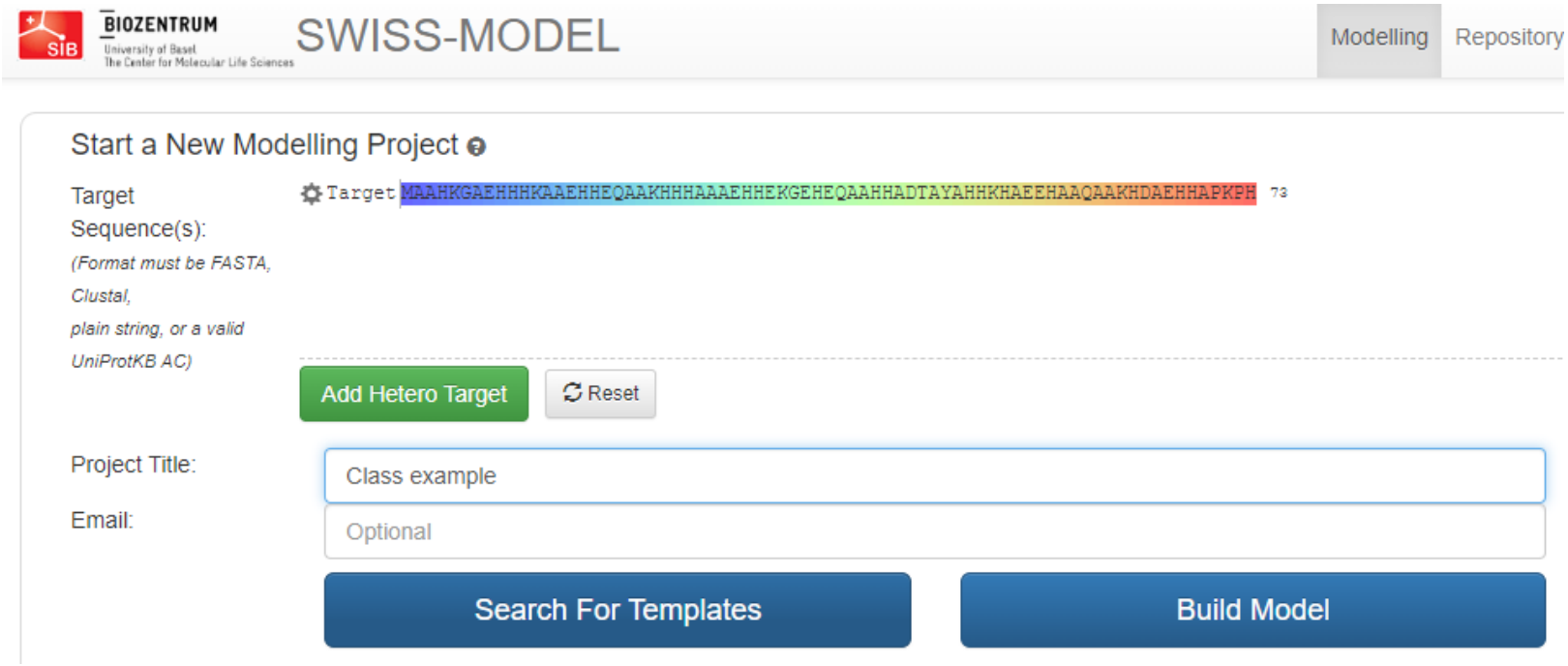




miRBase: the microRNA database



SWISS-MODEL: Homology modeling



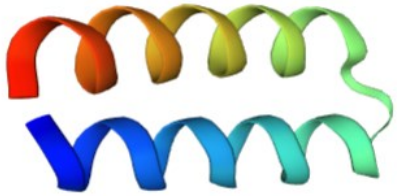
Template search

Template Results

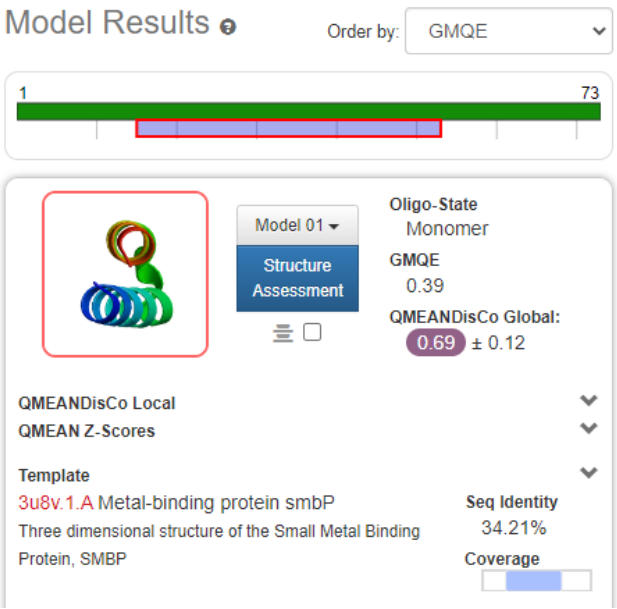
Templates | More

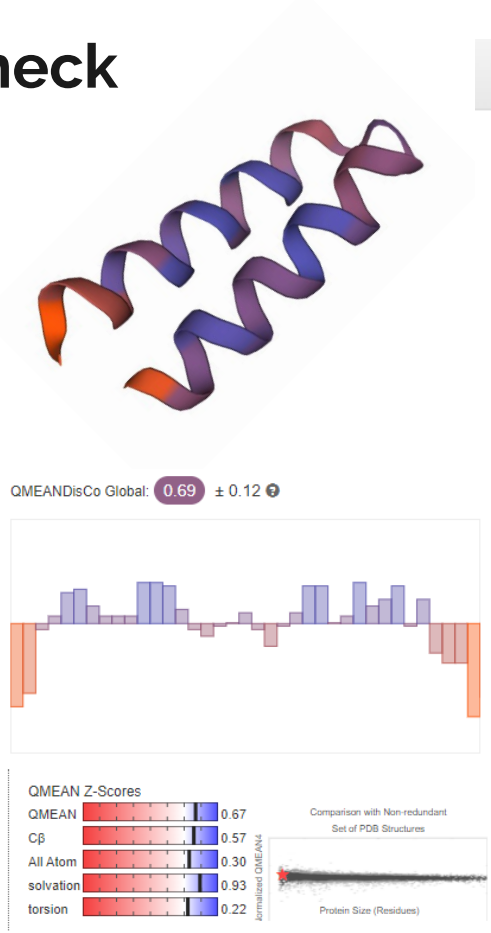
Sort	Coverage	GMQE	QSQE	Identity	Method	Oligo State	Ligands
☑	3u8v.1.A Metal-binding protein smbP *Three dimensional structure of the Small Metal Binding Protein, SMBP*						
⌄		0.39	-	34.21	X-ray, 1.9Å	monomer ✓	1 x NI

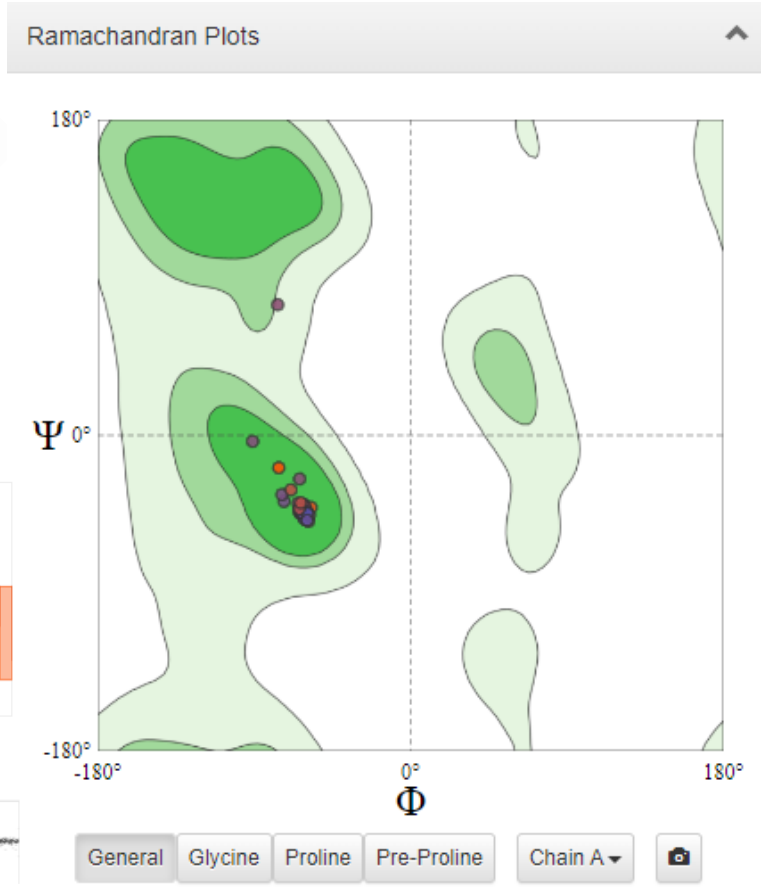
- Identify known 3D structures with similar amino acid sequences



Model quality check







- Overview

AI-assisted protein folding (ColabFold)

3. Enter the amino acid sequence(s) to fold

Enter the amino acid sequence(s) to fold:

- If you enter only a single sequence, the monomer model will be used.
- If you enter multiple sequences, the multimer model will be used.

sequence_1: " MAAHKGAEHHHKAAEHHEQAAKHHHAAAEHHEKGEHEQA

sequence_2: " Insert text here

https://github.com/sokrypton/ColabFold

5. Run AlphaFold and download prediction

Once this cell has been executed, a zip-archive w

In case you are having issues with the relaxation
violations.

run_relax: ☑

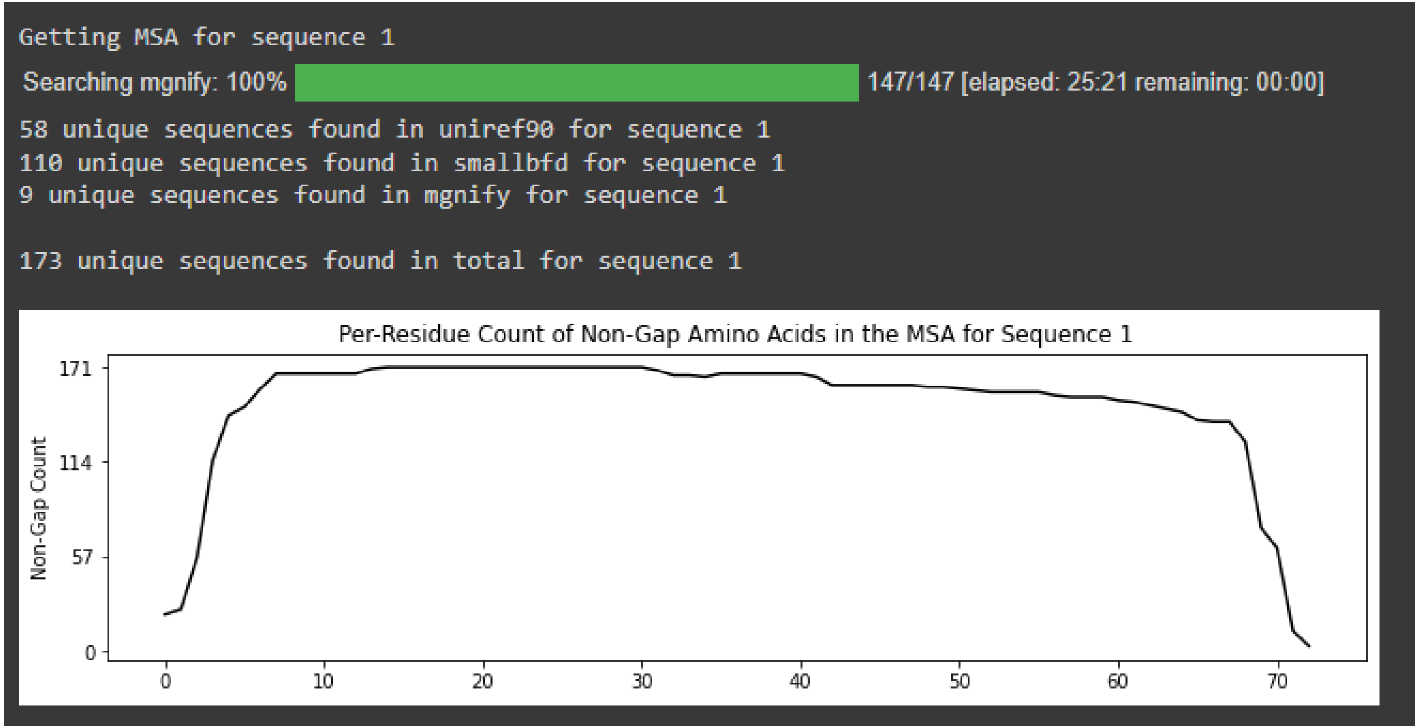
Relaxation is faster with a GPU, but we have fou
reverting to using without GPU.

relax_use_gpu: ☐

Show code

- Accessible, simplified Python interface

ColabFold on-screen outputs



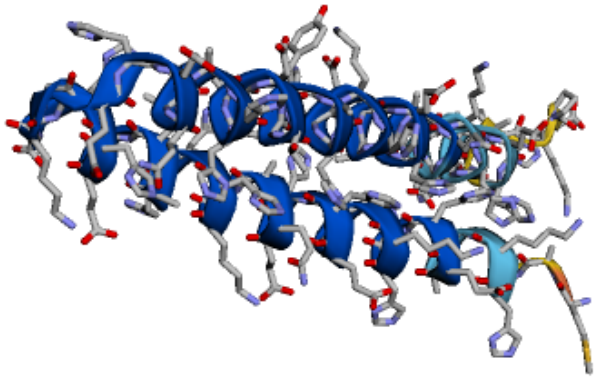
```
Getting MSA for sequence 1
Searching mgnify: 100%                    147/147 [elapsed: 25:21 remaining: 00:00]
58 unique sequences found in uniref90 for sequence 1
110 unique sequences found in smallbfd for sequence 1
9 unique sequences found in mgnify for sequence 1

173 unique sequences found in total for sequence 1
```

AlphaFold output in PDB format

selected_prediction.pdb - Notepad

File Edit Format View Help

```
ATOM      1  N   MET A   1      21.997  -7.681 -15.856  1.00 47.20           N
ATOM      2  H   MET A   1      22.579  -7.136 -15.236  1.00 47.20           H
ATOM      3  H2  MET A   1      22.491  -8.529 -16.097  1.00 47.20           H
ATOM      4  H3  MET A   1      21.827  -7.147 -16.697  1.00 47.20           H
ATOM      5  CA  MET A   1      20.726  -8.011 -15.175  1.00 47.20           C
ATOM      6  HA  MET A   1      20.096  -8.607 -15.835  1.00 47.20           H
ATOM      7  C   MET A   1      19.955  -6.731 -14.844  1.00 47.20           C
ATOM      8  CB  MET A   1      20.994  -8.837 -13.903  1.00 47.20           C
ATOM      9  HB2 MET A   1      21.674  -8.300 -13.243  1.00 47.20           H
ATOM     10  HB3 MET A   1      20.050  -8.988 -13.379  1.00 47.20           H
ATOM     11  O   MET A   1      19.729  -6.438 -13.681  1.00 47.20           O
ATOM     12  CG  MET A   1      21.574 -10.218 -14.209  1.00 47.20           C
ATOM     13  HG2 MET A   1      20.933 -10.709 -14.941  1.00 47.20           H
ATOM     14  HG3 MET A   1      22.577 -10.123 -14.623  1.00 47.20           H
ATOM     15  SD  MET A   1      21.645 -11.258 -12.738  1.00 47.20           S
ATOM     16  CE  MET A   1      21.921 -12.878 -13.501  1.00 47.20           C
ATOM     17  HE1 MET A   1      22.851 -12.867 -14.069  1.00 47.20           H
ATOM     18  HE2 MET A   1      21.089 -13.121 -14.162  1.00 47.20           H
ATOM     19  HE3 MET A   1      21.987 -13.637 -12.721  1.00 47.20           H
ATOM     20  N   ALA A   2      19.598  -5.931 -15.854  1.00 54.34           N
ATOM     21  H   ALA A   2      19.735  -6.197 -16.818  1.00 54.34           H
ATOM     22  CA  ALA A   2      18.910  -4.655 -15.629  1.00 54.34           C
ATOM     23  HA  ALA A   2      19.241  -4.225 -14.683  1.00 54.34           H
ATOM     24  C   ALA A   2      17.385  -4.836 -15.515  1.00 54.34           C
ATOM     25  CB  ALA A   2      19.332  -3.685 -16.734  1.00 54.34           C
ATOM     26  HB1 ALA A   2      18.880  -2.710 -16.551  1.00 54.34           H
ATOM     27  HB2 ALA A   2      18.993  -4.039 -17.707  1.00 54.34           H
ATOM     28  HB3 ALA A   2      20.415  -3.561 -16.744  1.00 54.34           H
ATOM     29  O   ALA A   2      16.797  -4.300 -14.587  1.00 54.34           O
ATOM     30  N   ALA A   3      16.797  -5.715 -16.340  1.00 57.44           N
ATOM     31  H   ALA A   3      17.335  -6.061 -17.121  1.00 57.44           H
ATOM     32  CA  ALA A   3      15.353  -5.979 -16.393  1.00 57.44           C
ATOM     33  HA  ALA A   3      14.852  -5.081 -16.755  1.00 57.44           H
ATOM     34  C   ALA A   3      14.700  -6.342 -15.044  1.00 57.44           C
```



Model Confidence

- Very low (pLDDT < 50)
- Low (70 > pLDDT > 50)
- Confident (90 > pLDDT > 70)
- Very high (pLDDT > 90)

GenePattern / Galaxy

Features

Powerful genomics tools in a user-friendly interface

GenePattern provides hundreds of analytical tools for the analysis of gene expression (RNA-seq and microarray), sequence variation and copy number, proteomic, flow cytometry, and network analysis. These tools are all available through a Web interface with no programming experience required.

GenePattern Notebook

The GenePattern Notebook environment extends the Jupyter Notebook system, allowing researchers to create documents that interleave formatted text, graphics and other multimedia, executable code, and GenePattern analyses, creating a single "research narrative" that puts scientific discussion and analyses in the same place.

Blog > GP updates

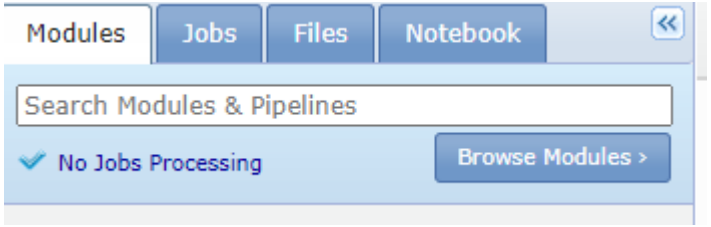
- GenePattern Coverage and Support December 23, 2021 - January 2, 2022
- End of Support for GParc
- End of support for modules using the deprecated GenePattern patch mechanism.
- End of support for Cufflinks suite of modules
- End of support for MAGeCK

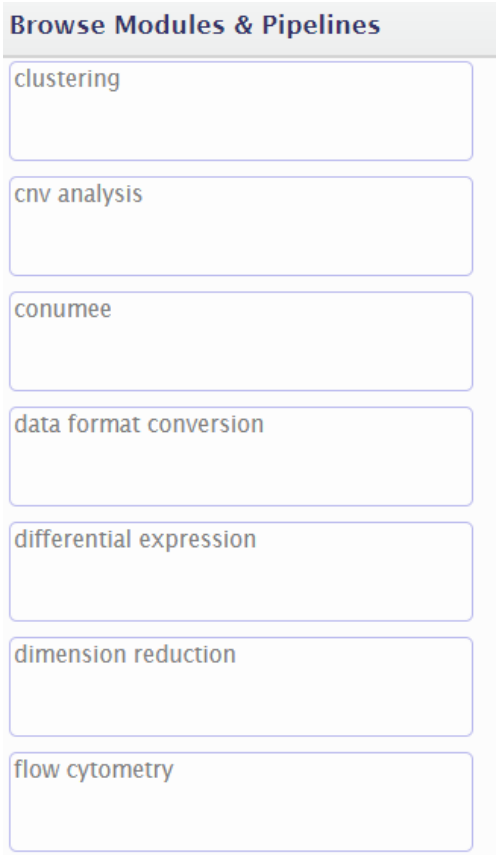
view more >

Papers > Related Publications

- Comparability and reproducibility of biomedical data
- ToppCluster: a multiple gene list feature analyzer for

Content

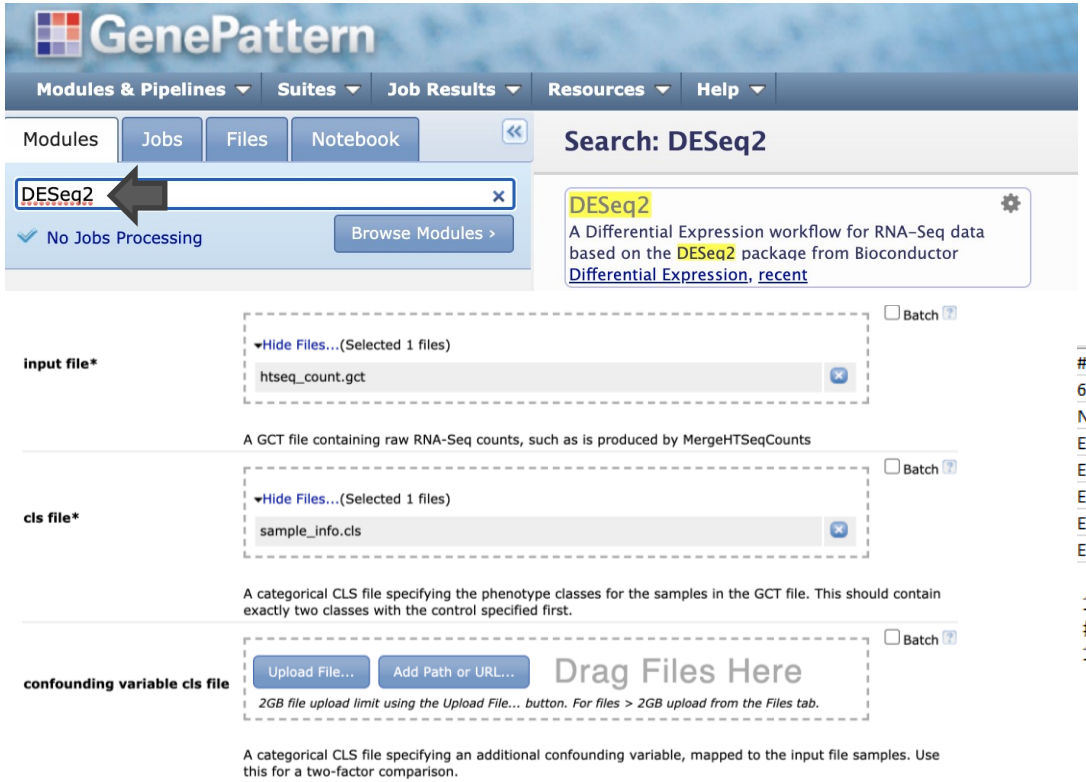




- Modules = standard bioinformatics tools

- Notebook = Python environment (similar to Google Colab) with specific bioinformatics library

DESeq2 on GenePattern



- Input expression data (RNA-seq read count) and sample label
- .gct and .cls are text files

#1.2					
60488	12				
Name	Description	sample1	sample2	sample3	sample4
ENSG00000242268.2	ENSG00000242268.2	2	10	0	2
ENSG00000270112.3	ENSG00000270112.3	8	6	0	0
ENSG00000167578.15	ENSG00000167578.15	102	633	468	1200
ENSG00000273842.1	ENSG00000273842.1	0	0	0	0
ENSG00000078237.5	ENSG00000078237.5	370	364	1220	692

```
12 2 1
# alive dead
1 1 0 0 1 0 0 0 1 0 1 1
```

DESeq2 output

471244. DESeq2

Source: GenePattern production (new)
submitted: Oct 25 01:06:41 AM, *completed:* Oct 25 01:10:38 AM, *size:* 30 MB
Show details

Comments (0)

Tags (0)

input.file: expression.gct

cls.file: label.cls

class_example.Positive.vs.Negative.DESeq2_results_report.txt (670.0 KB) (Last modified: 2022-10-25 01:10:26.0)

class_example.Positive.vs.Negative.QC.DispEsts.png (78.0 KB) (Last modified: 2022-10-25 01:10:26.0)

class_example.Positive.vs.Negative.QC.MAplot.png (9.0 KB) (Last modified: 2022-10-25 01:10:26.0)

class_example.Positive.vs.Negative.mean_values_by_class.txt (230.0 KB) (Last modified: 2022-10-25 01:10:26.0)

class_example.Positive.vs.Negative.normalized_counts.gct (14.5 MB) (Last modified: 2022-10-25 01:10:26.0)

class_example.Positive.vs.Negative.normalized_counts.txt (14.5 MB) (Last modified: 2022-10-25 01:10:26.0)

class_example.Positive.vs.Negative....0_downregulated_genes_report.txt (3.0 KB) (Last modified: 2022-10-25 01:10:26.0)

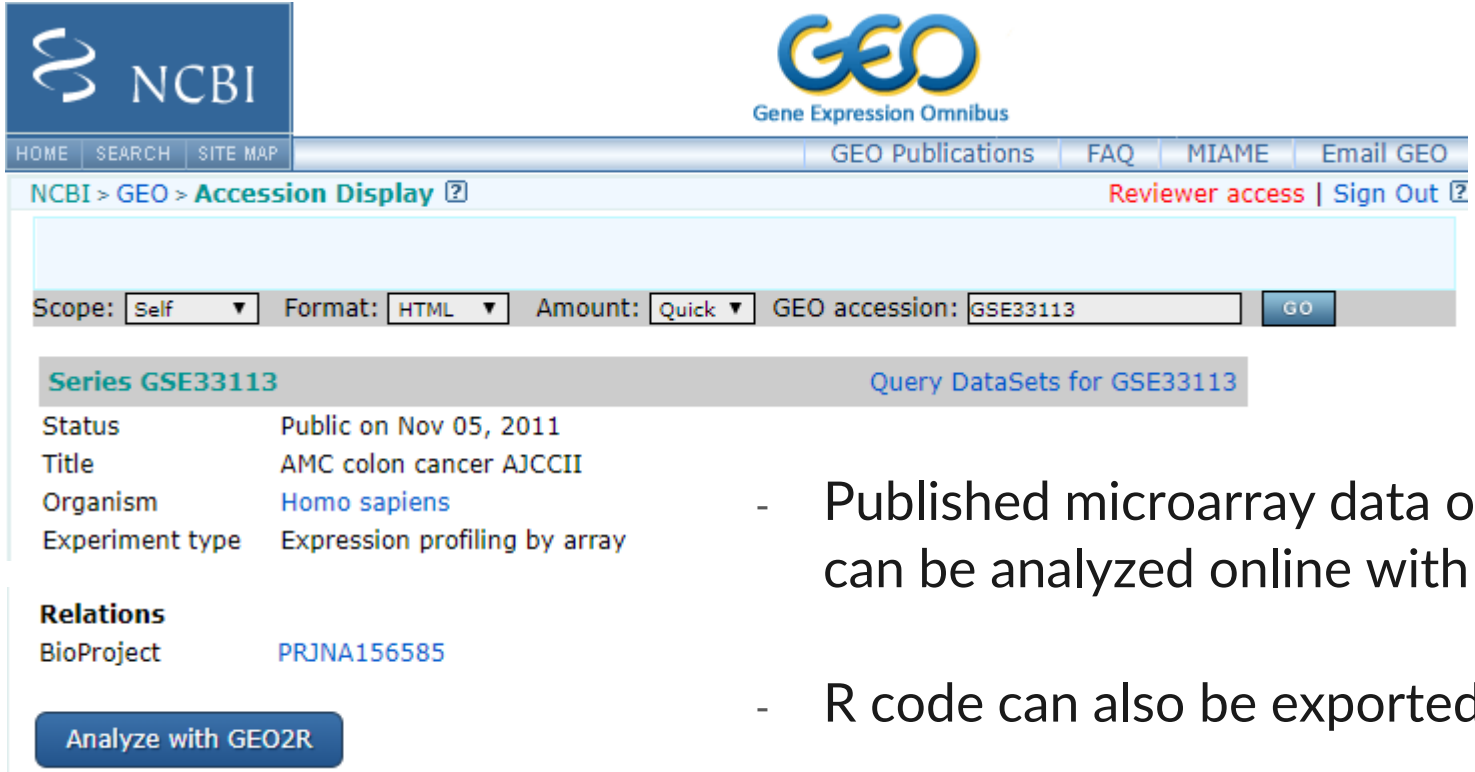
class_example.Positive.vs.Negative.top20_upregulated_genes_report.txt (3.0 KB) (Last modified: 2022-10-25 01:10:26.0)

stderr.txt (1.0 KB) (Last modified: Tue Oct 25 01:10:37 UTC 2022)

stdout.txt (4.0 KB) (Last modified: Tue Oct 25 01:10:37 UTC 2022)

gp_execution_log.txt (1.0 KB) (Last modified: Tue Oct 25 01:10:38 UTC 2022)

GEO2R: Differential expression



- Published microarray data on GEO can be analyzed online with GEO2R
- R code can also be exported

Demo time!

- ColabFold interface
- STRING
- GEO2R
- Biomart

Any question?

- See you on Nov 6
- Look out for instruction on how to set up Python on the course website