**Literature Informatics**

* Searching using MESH terms:

<http://media.hsls.pitt.edu/media/clres2705/mesh.swf>

* Pubmed Clinical Queries:

 <http://media.hsls.pitt.edu/media/clres2705/scz.swf>

* GoPubmed:

<http://media.hsls.pitt.edu/media/clres2705/gopubmed.swf>

* HugeNavigator:

<http://media.hsls.pitt.edu/media/clres2705/asthma.swf>

* Impacr Factors:

<http://media.hsls.pitt.edu/media/clres2705/impact.swf>

**Genome Biology**

* Check the status of genome sequencing for an organism: <http://media.hsls.pitt.edu/media/clres2705/rabbit.swf>
* Browse the region of human chromosome 7 part 1: <http://media.hsls.pitt.edu/media/clres2705/ucsc_genes.swf>
* Browse the region of human chromosome 7 part 2: <http://media.hsls.pitt.edu/media/clres2705/ucsc_snp.swf>
* Browse the region of human chromosome 7 part 3: <http://media.hsls.pitt.edu/media/clres2705/ucsc_promoter.swf>
* Browse the region of human chromosome 7 part 4: <http://media.hsls.pitt.edu/media/clres2705/ucsc_convert.swf>
* Place a mRNA or peptide sequence into the human genome: <http://media.hsls.pitt.edu/media/clres2705/blat.swf>
* UCSC Table Browser: [http://media.hsls.pitt.edu/media/clres2705/table browser/table browser.swf](http://media.hsls.pitt.edu/media/clres2705/table%20browser/table%20browser.swf%20)
* NCBI Mapviewer: <http://media.hsls.pitt.edu/media/clres2705/ncbimapviewer.swf>

 **Gene/Protein Information**

* Find sequence information for a gene : <http://media.hsls.pitt.edu/media/clres2705/sequence.swf>
* Find sequence information for a gene using UCSC genome browser: <http://media.hsls.pitt.edu/media/clres2705/sequence_2.swf>
* Find homologous sequence information of a gene : [http://media.hsls.pitt.edu/media/clres2705/homologene.swf](http://media.hsls.pitt.edu/media/clres2705/sequence.swf)
* Retrieve gene expression information: <http://media.hsls.pitt.edu/media/clres2705/expression.swf>
* Find protein domains, PTM, secondary str etc: <http://media.hsls.pitt.edu/media/clres2705/uniprot.swf>
* Find Hydrophobicity, mw, peptide digestion : <http://media.hsls.pitt.edu/media/clres2705/uniprot2.swf>
* Start with a protein pattern and find what proteins posses that domain: <http://media.hsls.pitt.edu/media/clres2705/scanprosite.swf>
* Search for protein domains,repeats and sites: <http://media.hsls.pitt.edu/media/clres2705/interpro.swf>
* Retrieve interacting partners of a protein: <http://media.hsls.pitt.edu/media/clres2705/ppi.swf>
* View the crystal structure of mouse p53 using Cn3D: <http://media.hsls.pitt.edu/media/clres2705/cn3d.swf>
* Start with a peptide sequence and search for protein 3D structure/model : <http://media.hsls.pitt.edu/media/clres2705/sbkb.swf>
* Find homologous sequences:

<http://media.hsls.pitt.edu/media/clres2705/blast.swf>

* Identify genetic variations present is a human gene sequence: <http://media.hsls.pitt.edu/media/clres2705/dbsnp.swf> (Part 1)

<http://media.hsls.pitt.edu/media/clres2705/OMIM.swf> (Part 2)

* Identify genetic variations associated with a human disease: <http://media.hsls.pitt.edu/media/clres2705/huge.swf> (Part 1)

<http://media.hsls.pitt.edu/media/clres2705/dbsnp2.swf> (Part 2)

* Predict the functional effect of a SNP

<http://media.hsls.pitt.edu/media/clres2705/fsnp.swf>

**Gene Regulation**

* Retrieve probe sequences published in literature for a gene: <http://media.hsls.pitt.edu/media/clres2705/probe.swf>
* Identify miRNA(s) that have been reported or predicted to interact with a gene: <http://media.hsls.pitt.edu/media/clres2705/mirna.swf>
* Identify five genes that activate EGFR etc. ( Ingenuity IPA)( Part 1): <http://media.hsls.pitt.edu/media/clres2705/ipa.swf>
* Identify five genes that inhebit EGFR etc. (Ingenuity IPA) (Part 2): [http://media.hsls.pitt.edu/media/clres2705/ipa2.swf](http://media.hsls.pitt.edu/media/clres2705/ipa.swf)
* Retrieve experimentally verified promoter sequence of a gene: <http://media.hsls.pitt.edu/media/clres2705/biobase.swf>
* Retrieve potential promoter sequence and predict transcription factors binding sites present in the promoter region:

 [http://media.hsls.pitt.edu/media/clres2705/match.swf](http://media.hsls.pitt.edu/media/clres2705/biobase.swf)

**DNA/Protein Sequence Analysis**

* Compare two peptide sequences.: <http://media.hsls.pitt.edu/media/clres2705/blast2.swf>
* Create a multiple sequence alignment plot: <http://media.hsls.pitt.edu/media/clres2705/msa.swf>
* Convert sequence formats:

<http://media.hsls.pitt.edu/media/clres2705/readseq.swf>

* Import your DNA of interest into VectorNTI <http://media.hsls.pitt.edu/media/clres2705/vnti_inportdna.swf>
* Create a multiple protein sequences alignment plot

<http://media.hsls.pitt.edu/media/clres2705/vnti_msa.swf>

* Design PCR primers using VectorNTI <http://media.hsls.pitt.edu/media/clres2705/vnti_pcr.swf>
* Clone a fragment from pBR322 into pUC19 (*in sillico* molecule construction)

<http://media.hsls.pitt.edu/media/clres2705/vnti_cloning.swf>

* VectorNTI user inter phase- a short walk-through (part 1)

[http://media.hsls.pitt.edu/media/clres2705/vnti\_walkthrough\_part1.swf](http://media.hsls.pitt.edu/media/clres2705/vnti_introduction.swf)

[http://media.hsls.pitt.edu/media/clres2705/vnti\_walkthrough\_part2.swf](http://media.hsls.pitt.edu/media/clres2705/vnti_introduction.swf)

Biological Pathway Analysis