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**Links for Protein Analysis Tools**

**Search Engine:**

* Search.HSLS.MolBio: <http://www.hsls.pitt.edu/guides/genetics>
* OreFil: <http://orefil.dbcls.jp/>

**Find Genomic Context**

* UCSC BLAT: <http://genome.ucsc.edu/cgi-bin/hgBlat?hgsid=67739561>

**Find Homologous Sequences**

* NCBI BLAST: <http://blast.ncbi.nlm.nih.gov/Blast.cgi>
* EBI MPSearch: <http://www.ebi.ac.uk/MPsrch/>
* Homologene: <http://www.ncbi.nlm.nih.gov/homologene>

**Sequence Manipulation, Format Change etc.**

* Sequence Manipulation Suite : <http://bioinformatics.org/sms2/>
* Readseq : <http://thr.cit.nih.gov/molbio/readseq/>

**Multiple Sequence Alignment**

* ClustalW: <http://www.ebi.ac.uk/clustalw/index.html>
* T-coffee : <http://www.ebi.ac.uk/t-coffee/>

**Find Conserved Domains and motifs**

* NCBI CDD Search: <http://www.ncbi.nlm.nih.gov/Structure/cdd/cdd.shtml>
* EBI Interproscan : <http://www.ebi.ac.uk/InterProScan/>
* ScanProsite : <http://www.expasy.ch/tools/scanprosite/>

**Primary Structure Analysis**

* EXPASY Primary Structure: <http://ca.expasy.org/tools/#primary>
* Protscale: <http://ca.expasy.org/tools/protscale.html>
* Emboss Antigenic: <http://liv.bmc.uu.se/cgi-bin/emboss/antigenic>
* ProtPram: <http://ca.expasy.org/tools/protparam.html>

**Secondary Structure Prediction**

* Expasy Secondary Structure: <http://ca.expasy.org/tools/#secondary>
* Predict Protein: <http://cubic.bioc.columbia.edu/predictprotein/>
* NPS Secondary consensus prediction: <http://npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSA/npsa_seccons.html>

**Trans-membrane Region Prediction**

* TMHMM Server: <http://www.cbs.dtu.dk/services/TMHMM-2.0/>

**Protein-Protein Interaction Prediction**

* Scansite : <http://scansite.mit.edu/>
* Potential Interactions of Proteins: <http://bmm.cancerresearchuk.org/~pip/>

**Post Translational Modification Prediction**

* Expasy Post translational modification: <http://ca.expasy.org/tools/#ptm>
* NetPhos: <http://www.cbs.dtu.dk/services/NetPhos/>
* GPS scoring method for phosphorylation: <http://csbl.bmb.uga.edu/~ffzhou/gps_web/predict.php>
* Human Protein Reference Database: <http://www.hprd.org/>

**Protein-Protein Interaction Search**

* String: Search tool for the retrieval for interacting genes/proteins: <http://string.embl.de/>

**Structure Prediction**

* A guide to protein structure: <http://www.russell.embl-heidelberg.de/gtsp/>

**Video Tutorials:**

1. CLC Main –getting started (basic navigation steps):  <http://media.hsls.pitt.edu/media/molbiovideos/clc-navigation-ac0312.swf>
2. Browse through a DNA sequence using CLC Main Workbench(Part1): <http://media.hsls.pitt.edu/media/molbiovideos/clcmain-walkthrough-part1-ac0112.swf>
3. Browse through a DNA sequence using CLC Main Workbench(Part2): <http://media.hsls.pitt.edu/media/molbiovideos/clcmain-walkthrough-part2-ac0112.swf>
4. Import a DNA /Protein sequence into CLC Main (Part 1): <http://media.hsls.pitt.edu/media/molbiovideos/clc-import-part1-ac0112.swf>
5. Import a DNA /Protein sequence into CLC Main (Part 2): <http://media.hsls.pitt.edu/media/molbiovideos/clc-import-part2-ac0112.swf>
6. Create a restriction digestion Map: <http://media.hsls.pitt.edu/media/molbiovideos/restriction-clc-ac0212.swf>
7. Create a multiple sequence alignment plot using CLC Main (part1): <http://media.hsls.pitt.edu/media/molbiovideos/msf-clcmain-ac0212-part1.swf>
8. Create a multiple sequence alignment plot using CLC Main (part2): <http://media.hsls.pitt.edu/media/molbiovideos/msf-clcmain-ac0212-part2.swf>
9. [Design PCR primers to amplify a protein domain](http://staff.hsls.pitt.edu/intranet/dept/info-services/molbio/edit-molbio-video?v=67) (part1): <http://media.hsls.pitt.edu/media/molbiovideos/primer3-clc-ac0112.swf>
10. Design PCR primers to amplify a protein domain (part2): [http://media.hsls.pitt.edu/media/molbiovideos/molbiovideos/primer4-clc-ac0112.swf](http://media.hsls.pitt.edu/media/molbiovideos/primer3-clc-ac0112.swf)
11. Find protein domains, PTM, secondary str etc: <http://media.hsls.pitt.edu/media/clres2705/uniprot.swf>
12. Find Hydrophobicity, mw, peptide digestion: <http://media.hsls.pitt.edu/media/clres2705/uniprot2.swf>
13. Start with a protein pattern and find what proteins posses that domain: <http://media.hsls.pitt.edu/media/clres2705/scanprosite.swf>
14. Search for protein domains,repeats and sites: <http://media.hsls.pitt.edu/media/clres2705/interpro.swf>
15. Retrieve interacting partners of a protein: <http://media.hsls.pitt.edu/media/clres2705/ppi.swf>
16. View the crystal structure of mouse p53 using Cn3D: <http://media.hsls.pitt.edu/media/clres2705/cn3d.swf>
17. Start with a peptide sequence and search for protein 3D structure/model: <http://media.hsls.pitt.edu/media/clres2705/sbkb.swf>
18. Find homologous sequences: <http://media.hsls.pitt.edu/media/clres2705/blast.swf>
19. Compare two peptide sequences: <http://media.hsls.pitt.edu/media/clres2705/blast2.swf>
20. Create a multiple sequence alignment plot: <http://media.hsls.pitt.edu/media/clres2705/msa.swf>
21. Convert sequence formats: <http://media.hsls.pitt.edu/media/clres2705/readseq.swf>