Gene Regulation Resources 29 May 2013

* Registration to HSLS\_Biobase

<https://portal.biobase-international.com/cgi-bin/portal/useradditionpage.cgi>

* Access to Biobase

<https://portal.biobase-international.com/cgi-bin/portal/login.cgi>

* UCSC Genome Browser

<http://genome.ucsc.edu/cgi-bin/hgGateway>

* Database of Transcriptional Start Sites (dbTSS)

<http://dbtss.hgc.jp/>

* Search.HSLS.MolBio

<http://www.hsls.pitt.edu/guides/genetics/>

* enoLOGOS

<http://lagavulin.ccbb.pitt.edu/cgi-bin/enologos/enologos.cgi>

* WebLogos

<http://weblogo.berkeley.edu/>

* **mPromoDB**

<http://mpromdb.wistar.upenn.edu/>

* **EPD:**

 <http://epd.vital-it.ch/>

* TRED

<http://rulai.cshl.edu/cgi-bin/TRED/tred.cgi?process=searchPromForm>

* TESS (Transcription Element Search System)

<http://www.cbil.upenn.edu/cgi-bin/tess/tess>

* Consite

<http://asp.ii.uib.no:8090/cgi-bin/CONSITE/consite>

* Footer

<http://biodev.hgen.pitt.edu/footer_php/Footerv2_0.php>

* rVISTA

<http://genome.lbl.gov/vista/rvista/submit.shtml>

* Whole Genome rVISTA

<http://genome-test.lbl.gov/cgi-bin/WGRVistaInputCommon.pl>

* MEME

<http://meme.sdsc.edu/meme4_6_1/intro.html>

* Melina II

<http://melina2.hgc.jp/public/index.html>

* Mirbase

 [http://www.mirbase.org](http://www.mirbase.org/)

* Mirtarbase

 [http://mirtarbase.mbc.nctu.edu.tw](http://mirtarbase.mbc.nctu.edu.tw/)

* Targetscan

 <http://www.targetscan.org/>

* Miranda

 [http://www.microrna.org](http://www.microrna.org/)

* Pictar

 [http://pictar.mdc-berlin.de](http://pictar.mdc-berlin.de/)

 **Video Tutorials on 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)

* BioBase Explain; a brief walkthrough--start with a list of genes and identify

 --statistically overrepresented transcription factor binding sites,

 --upstream regulatory key molecules

 --common miRNA and its target genes present in that gene list

 <http://media.hsls.pitt.edu/media/molbiovideos/biobase1.swf>

 <http://media.hsls.pitt.edu/media/molbiovideos/biobase2.swf>

 <http://media.hsls.pitt.edu/media/molbiovideos/biobase3.swf>

**Sample Sequences**

Sequence: Human: EGFR

>hg18\_knownGene\_uc003tqh.1 range=chr7:55053219-55054218 5'pad=0 3'pad=0 strand=+ repeatMasking=none

TCTGGCTGTAACATGGACCTAGAGGACATTTTTACTGCAGGAGAAGGAAC

AGTGGGGATGGGGTGGACTTGCCAAAGGAATATAGCTCAAGTTCCTGCAG

CCCAAAAAAGCTCAGTTTCTTTTGGCCAAAGCTTCCGCGAGTTTCCCTGG

CATTTCTCCTGCGGGAGCTACAGGGGCAGTGGGACACTTAGCCTCTCTAA

AAGCACCTCCACGGCTGTTTGTGTCAAGCCTTTATTCCAAGAGCTTCACT

TTTGCGAAGTAATGTGCTTCACACATTGGCTTCAAAGTACCCATGGCTGG

TTGCAATAAACATTAAGGAGGCCTGTCTCTGCACCCGGAGTTGGGTGCCC

TCATTTCAGATGATTTCGAGGGTGCTTGACAAGATCTGAAGGACCCTCGG

ACTTTAGAGCACCACCTCGGACGCCTGGCACCCCTGCCGCGCGGGCACGG

CGACCTCCTCAGCTGCCAGGCCAGCCTCTGATCCCCGAGAGGGTCCCGTA

GTGCTGCAGGGGAGGTGGGGACCCGAATAAAGGAGCAGTTTCCCCGTCGG

TGCCATTATCCGACGCTGGCTCTAAGGCTCGGCCAGTCTGTCTAAAGCTG

GTACAAGTTTGCTTTGTAAAACAAAAGAAGGGAAAGGGGGAAGGGGACCC

TGGCACAGATTTGGCTCGACCTGGACATAGGCTGGGCCTGCAAGTCCGCG

GGGACCGGGTCCAGAGGGGCAGTGCTGGGAACGCCCCTCTCGGAAATTAA

CTCCTCAGGGCACCCGCTCCCCTCCCATGCGCCGCCCCACTCCCGCCGGA

GACTAGGTCCCGCGGGGGCCACCGCTGTCCACCGCCTCCGGCGGCCGCTG

GCCTTGGGTCCCCGCTGCTGGTTCTCCTCCCTCCTCCTCGCATTCTCCTC

CTCCTCTGCTCCTCCCGATCCCTCCTCCGCCGCCTGGTCCCTCCTCCTCC

CGCCCTGCCTCCCCGCGCCTCGGCCCGCGCGAGCTAGACGTCCGGGCAGC

Sequence Mouse: EGFR

>mm9\_knownGene\_uc007ibo.1 range=chr11:16651206-16652205 5'pad=0 3'pad=0 strand=+ repeatMasking=none

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CATTCCTCTGATAGCTAAGAAGTAGGGACATTGGTTGGTCTTTGCTGAAG

GAATTTAGTTGTGGGTCCTGAAGTTCAGGGACACATTTCTACTGGTCAAA

TTCTAAGTGAACTTACTTGGCAATTTGCCTCCTGATGTGCGGCAGGGCTA

GCTGAGGTCACTAGAGGATGCTAACTGCTCTAAAGATTTGTTCACTGCTG

TTATGTCAAGTCTCTGCTTTTGTGGAGGAATTTGCCTCATGTGTACGTTG

CTTTGCTTTTCAAGCACTCCAGACTGGCTCCAGGTGTAGAAAATGCCATG

TTCTTCAACATGCATGCTTTCATCCAGCAAATATACTGAGGCCCTTCTAA

GTGTCAGGAGTTGGCTGCCCTTCTTTCAGAAGACATGGAGGGTTCTTGAT

GGGATCTGAAGGACCCTTGGACTTCTTAGTGCCACTTCAGACTTGAGGCA

CCCGCCTCTGCCTGTGCTGTTGGAAACTGCTGCCAAGTCAGCCTGACCCT

TCTGAGATCCTGGAGAAGTTATGGAGAATACGTGAACAGCGTCCCCACCT

GTGTTATTCTCCAACCTGTGCTCTGTGGTTGGACAGTTTGTAACCGAGGT

GGTCCAGAGTTGTTTGGTTAATTGAAAGAAAGGAAGGAAGAAGGTGGGAG

ACAGAGGGAAGGAAGGAGGGGACCCTGGCATAGATTGGCTGGACTTCCTA

GGTCCTGAAATGCAGCGGAGCGGAGTCCCCTCAGAAATTAACTCCAAAGG

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CTAGTGGTGGCCAAGGCCATCCACCACCACCTTCCGGTCACTGCCTGCTT

TCGATCCTCGCGGAGAGCGCTTCCTCTCTCCTGACATTCTCCTCCTCTTC

GCTCCTCTGGATCCCTCCTCCTTCTTTAGTCCCTCCTCCTCCCGCCCAGC

>SEQ1; M: CTCAATCGTAGA at 52

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>SEQ2; M: CTCAATCGTAGA at 172

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>SEQ3; M: CTCAATCGTAGA at 112

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>SEQ4; M: CTCAATCGTAGA at 173

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>SEQ5; M: CTCAATCGTAGA at 185

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>SEQ6; M: CTCAATCGTAGA at 105

tagggaaaccctttaactccgctactgacgttaaggtttggtgccccaagcttacccagggaccctacgagacggttataacctccgtattagcgtcagccggtCTCAATCGTAGAtcagaggcgagaaacatgacaaactaaatctatgtacgctggggatgaatgattgaccttgtgctcgatatagaatatgcgact

>SEQ7; M: CTCAATCGTAGA at 177

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>SEQ8; M: CTCAATCGTAGA at 172

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>SEQ9; M: CTCAATCGTAGA at 93

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>SEQ10; M: CTCAATCGTAGA at 3

ttCTCAATCGTAGAgtatgcttagaggttaggttcatttgctccgggatatagtcccttcttactaggtggtatcgcccaagtctaagcctccaggtcgcatggagagagatccggaggaggatccagcatgcgctcttcccaagcgatccgagggccgtcagctctcaagtcttagtggagttcacatggctggatgac

Sequences for WebLogo

TGCTTACTAAT

TGCTTACTAAT

TGCTGACTAAT

TGCTGACTAAT

TGCTTACAAAT

TGCTGACAAAT

TGCTGACAAAT

AGCTTACTAAT

AGCTTACTAAT

GGCTGACTAAT

AGCTGACTAAT

TGATTACTAAT

TGATTACTAAT

AGCTGACAAAT

TGGTTACAAAT

TCCTTACTAAT

GTCTTACTAAT

GGCTTACAAAC

GGCTTACAAAC

TTATTACTAAT

TGCTTATAAAT

CGCTGACTAAT