"**Home Page**" of NeuroMuscleDB

Home | Gene Information | Primer Design | Sequence Analysis | About Database | Contact

Genes with Functional Stages

Disease Associated Genes

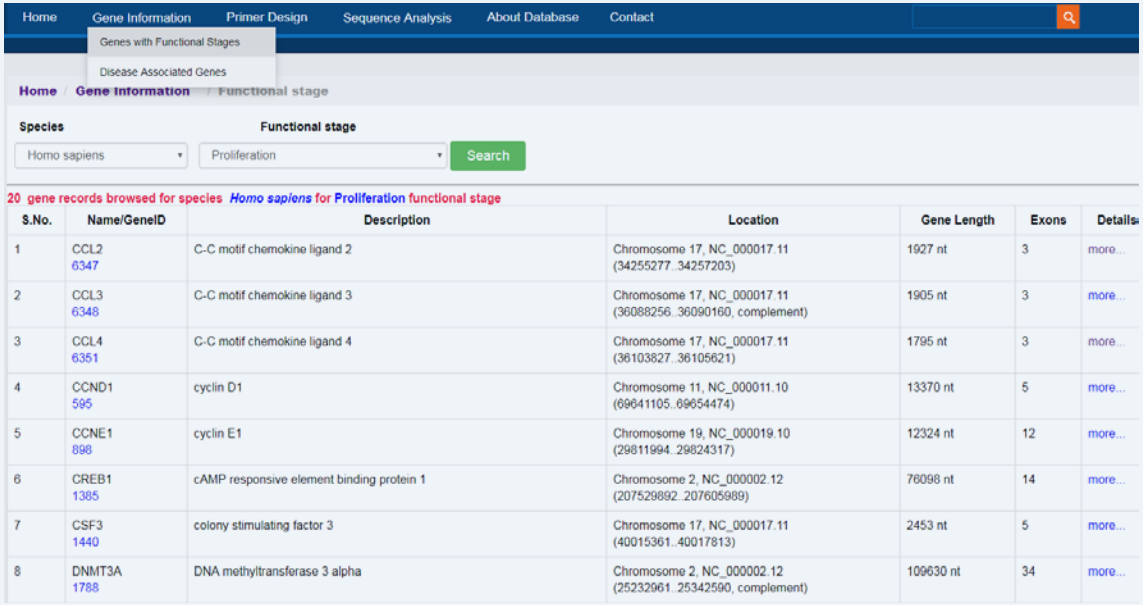
This page provide information of the genes involved in different stages of muscle formation.

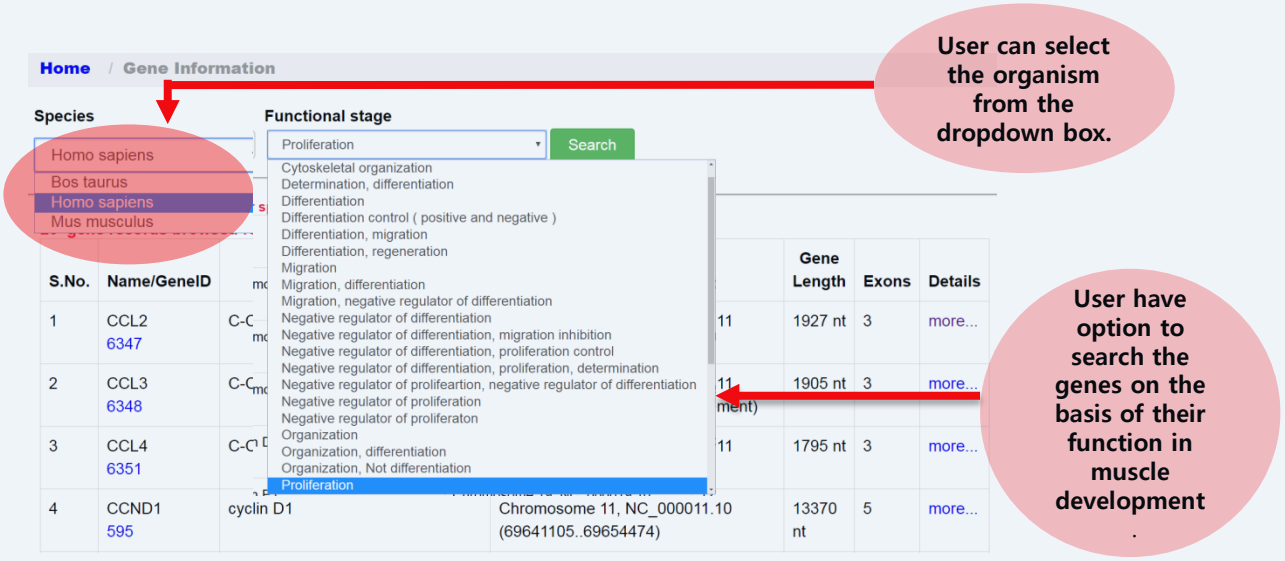
ABOUT DATABASE

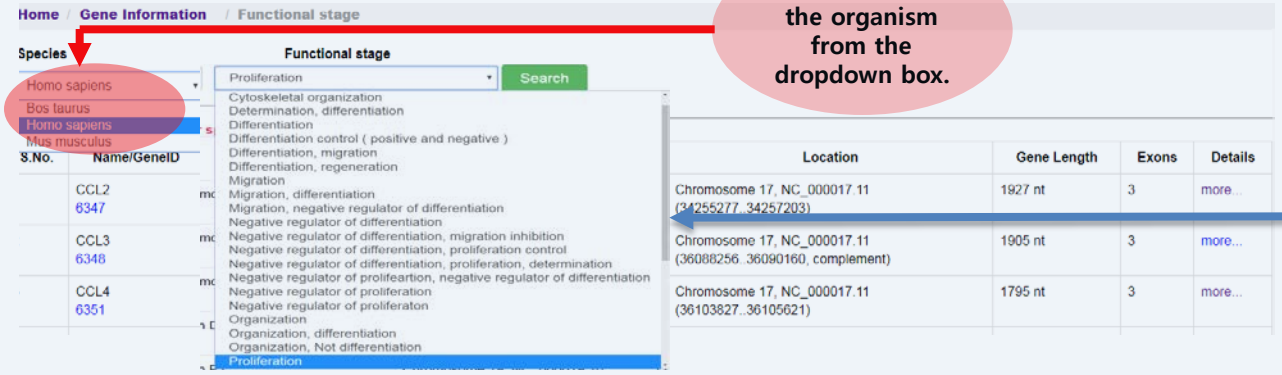
Neuro-Muscle Database (NeuroMuscleDB) is an authoritative collection of genes related to muscle development from Homo sapiens, Mus musculus and Bos taurus. NeuroMuscleDB is the first comprehensive database developed to catalog and categorizes available information of muscle related genes to facilitate easy retrieval of information according to their involvement at different stages of muscle development. The database carries a short description of genes (location, start and end position of genomic accession, etc.), GeneID, number of exons, PDB ID, protein accession number along with their Uniprot ID in addition to information of Refseq information, GO terms of individual genes and their Pubmed links. NeuroMuscleDB is equipped with flexible search features including user-friendly browser and hyper-text link-outs to nucleotide and protein sequence databases and tools for primers designing, multiple sequence alignment, transcriptional factor identification, and promoter analysis. NeuroMuscleDB covering maximum information on one platform will provide useful information for experimental and computational analyses of myogenesis related genes. The user friendly mode of the database carry information for all sequences submitted in the primary database and focus on the gene sequence, three dimensional structure and other features relevant to the process of myogenesis. We believe that NeuroMuscleDB will be useful for researchers to get the desired information and performing different analysis for genes related to myogenesis.

This page provide information of the involvement of myogenic genes in various disease (Ageing, NDs and NMDs).

Accessing "**Gene with Functional Stages**"







User can select the organism from the dropdown box.

User have option to search the genes on the basis of their function in muscle development.

S.No.	Name/GeneID	Description	Location	Gene Length	Exons	Details
1	CCL2 6347	C-C motif chemokine ligand 2	Chromosome 17, NC_000017.11 (34255277..34257203)	1927 nt	3	more...
2	CCL3 6348	C-C motif chemokine ligand 3	Chromosome 17, NC_000017.11 (36088256..36090160, complement)	1905 nt	3	more...
3	CCL4 6351	C-C motif chemokine ligand 4	Chromosome 17, NC_000017.11 (36103827..36105621)	1795 nt	3	more...
4	CCND1 595	cyclin D1	Chromosome 11, NC_000011.10 (69641105..69654474)	13370 nt	5	more...
5	CCNE1 898	cyclin E1	Chromosome 19, NC_000019.10 (29811994..29824317)	12324 nt	12	more...
6	CREB1 1385	cAMP responsive element binding protein 1	Chromosome 2, NC_000002.12 (207529892..207605989)	76098 nt	14	more...
7	CSF3 1440	colony stimulating factor 3	Chromosome 17, NC_000017.11 (40015361..40017813)	2453 nt	5	more...
8	DNMT3A 1788	DNA methyltransferase 3 alpha	Chromosome 2, NC_000002.12 (25232961..25342590, complement)	109630 nt	34	more...
9	FHL3 2275	four and a half LIM domains 3	Chromosome 1, NC_000001.11 (37996765..38005515, complement)	8751 nt	6	more...
10	FN1 2335	fibronectin 1	Chromosome 2, NC_000002.12 (215360440..215436167, complement)	75728 nt	47	more...
11	IGF1R 3480	insulin like growth factor 1 receptor	Chromosome 15, NC_000015.10 (98648539..98964530)	315992 nt	25	more...
12	JUN 3725	Jun proto-oncogene, AP-1 transcription factor subunit	Chromosome 1, NC_000001.11 (58780791..58784113, complement)	3323 nt	1	more...
13	KCNQ5 56479	potassium voltage-gated channel subfamily Q member 5	Chromosome 6, NC_000006.12 (72621843..73198851)	577009 nt	16	more...

This page displays gene summary of all the genes involved in the above selected function.

User can click “more” to display additional information about the selected gene.

This section gives information about the status of the selected gene. The record which has been curated by NCBI staff is termed as "REVIEWED" while The record which has been predicted by automated computational analysis are termed as "MODEL"

Additional information for the selected gene.

Refseq information: 6

SNo.	Status	RNA nucleotide accession	Protein accession	Genomic nucleotide accession	Start position on genomic DNA	End position on genomic DNA	Orientation	Assembly	Symbol	UniProtkb ID	PDB ID
1	REVIEWED	-	-	NG_033066.2	5001	6795	+	-	CCL4	P13236	1HUM
2	REVIEWED	NM_002984.3	NP_002975.1	NC_000017.11	36103826	36105620	+	Reference GRCh3	CCL4	P13236	1HUN
3	REVIEWED	NM_002984.3	NP_002975.1	NC_018928.2	34495397	34497191	+	Alternate CHM1_	CCL4	P13236	1HUN
4	REVIEWED	NM_002984.3	NP_002975.1	NG_033066.2	5001	6795	+	-	CCL4	P13236	1HUN
5	REVIEWED	NM_002984.3	NP_002975.1	NT_187614.1	338747	340541	+	Reference GRCh3	CCL4	P13236	1HUN
6	REVIEWED	NM_002984.3	NP_002975.1	NT_187661.1	57923	59717	+	Reference GRCh3	CCL4	P13236	1HUN

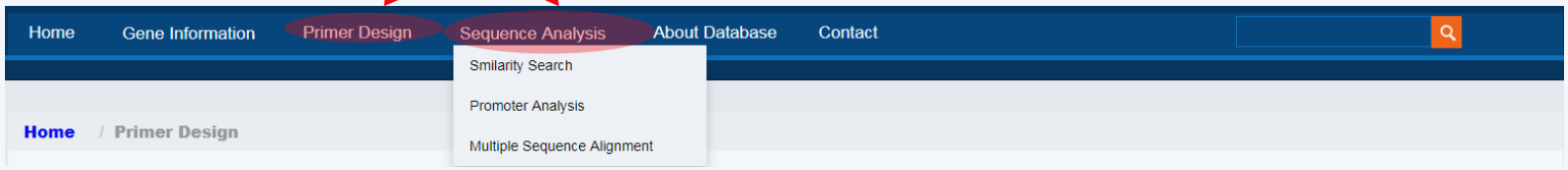
Download information

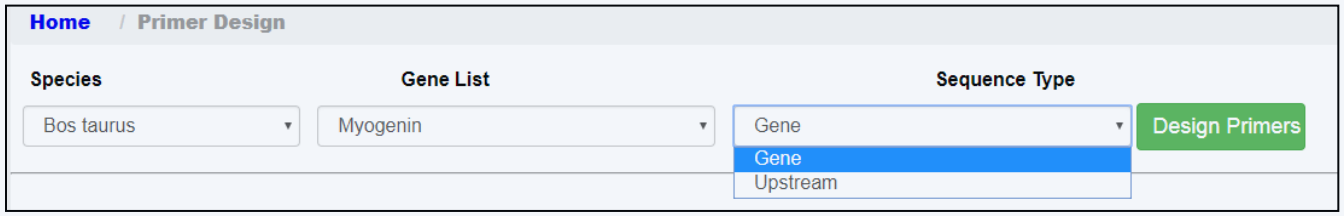
Download sequences

In this page other related information to the selected gene (PubMed links, GO Terms) is also provided. The page is also featured with options to "**Download information**" and "**Download Sequence**" of the selected gene

Different analysis tool provided within the database for analysis of gene and mRNA

"Sequence Analysis" tools





Subsequence length From 1 To 700

Product range Minimum 500 Maximum 600

Redesign Downstream

Designed primers for the Gene of gene MYOG (myogenin) of species *Homo sapiens*

Selected sub sequence

Target gene sequence length: 2910	Selected subsequence from: 1 to:700	Selected subsequence size:700

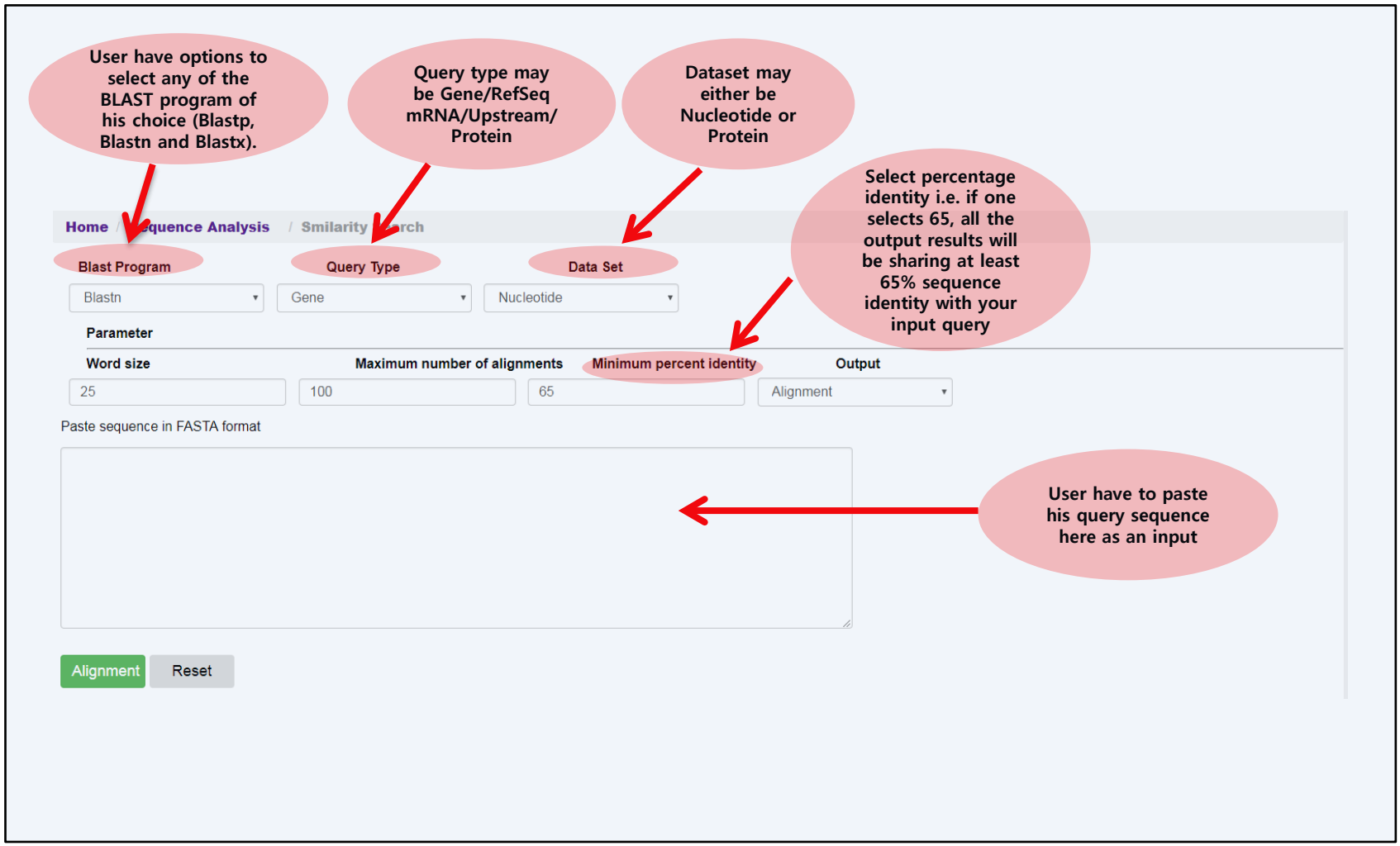
AAATGGCACCCAGCAGTTGGCGTGAGGGGCTGCTGGAGCTTGGGGGCTGGTGGCAGGAACAAGCCTTTTCCGACCCCATGGAGCTGTATGAGACATCCCC
CTACTTCTACCAGGAACCCCGCTTCTATGATGGGGAAAACTACCTGCCTGTCCACCTCCAGGGCTTCGAACCACCAGGCTACGAGCGGACGGAGCTCACC
CTGAGCCCCGAGGCCCCAGGGCCCCTTGAGGACAAGGGGCTGGGGACCCCCGAGCACTGTCCAGGCCAGTGCCTGCCGTGGGCGTGTAAGGTGTGTAAGA
GGAAGTCGGTGTCCGTGGACCGGCGGCGGGCGGCCACACTGAGGGAGAAGCGCAGGCTCAAGAAGGTGAATGAGGCCTTCGAGGCCCTGAAGAGAAGCAC
CCTGCTCAACCCCAACCAGCGGCTGCCCAAGGTGGAGATCCTGCGCAGTGCCATCCAGTACATCGAGCGCCTCCAGGCCCTGCTCAGCTCCCTCAACCAG
GAGGAGCGTGACCTCCGCTACCGGGGCGGGGGCGGGCCCCAGCCAGGGGTAAGTGGCCATCCCATCCCCCTGCCCCAAGGGGACGGGGCCAGAGGGAGGC
ACCTGGACAGCCTCAAGACCCCAAGAGGGGCTCAGAGGGTTGGTGCAGGTGCCAGACAGGGTCGAGGGGCTGCAGGAGCCCTTCCCTGGTCAGAGCTGGG

Primers information

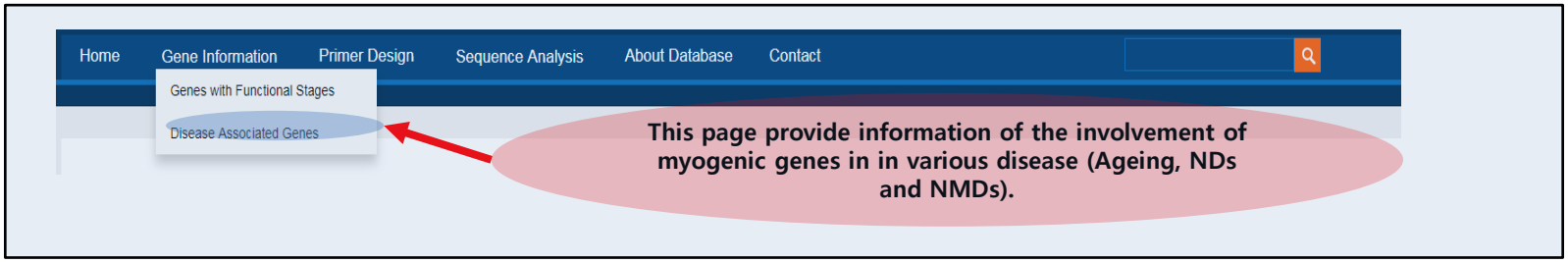
S.No.	Primers	Sequences	Start	Length	Tm	GC %	Hairpin_TH	End stability	Product size
1	Forward primer Reverse primer	CCAGGAACCCCGCTTCTATG CTCTTGGGGTCTTGAGGCTG	109 626	20 20	60.179 60.036	60.000 60.000	37.58 0.00	2.2300 4.8500	518 bp
2	Forward primer Reverse primer	GCAGGAACAAGCCTTTTCCG GGATGGGATGGCCACTTACC	52 566	20 20	60.039 60.179	55.000 60.000	45.27 35.15	4.3000 2.8500	515 bp
3	Forward primer Reverse primer	TACCAGGAACCCCGCTTCTA CTCTTGGGGTCTTGAGGCTG	107 626	20 20	59.958 60.036	55.000 60.000	37.58 0.00	2.1000 4.8500	520 bp
4	Forward primer Reverse primer	GCAGGAACAAGCCTTTTCCG CTCTTGGGGTCTTGAGGCTG	52 626	20 20	60.039 60.036	55.000 60.000	45.27 0.00	4.3000 4.8500	575 bp
5	Forward primer Reverse primer	GCAGGAACAAGCCTTTTCCG GATGGGATGGCCACTTACCC	52 565	20 20	60.039 60.179	55.000 60.000	45.27 40.79	4.3000 3.6900	514 bp

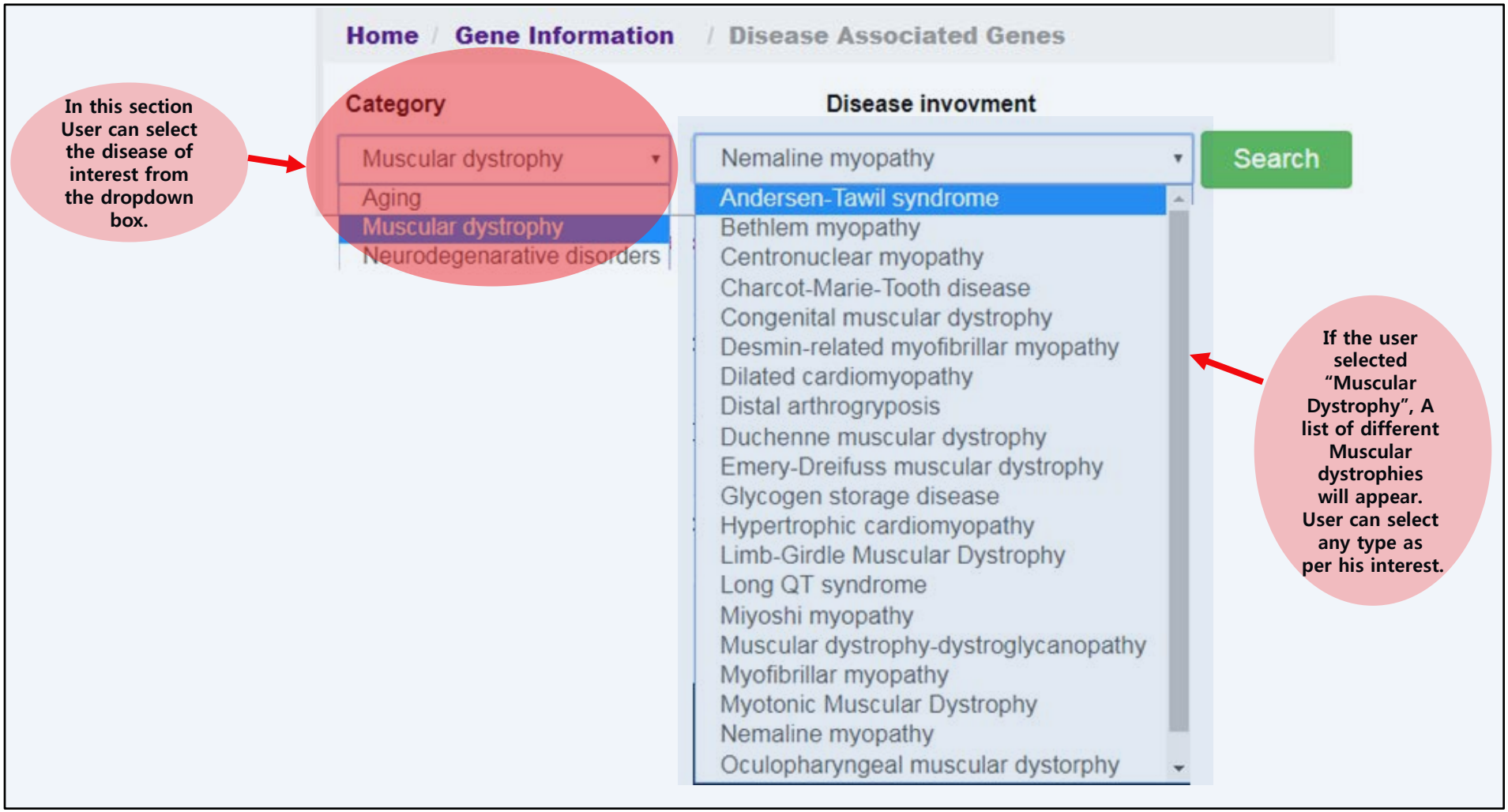
Here we are demonstrating the use of "Primer design" tool for designing primer for Myogenin

"**Similarity Search**" Tool



Accessing "**Disease Associated Genes**" Page





Category: Muscular dystrophy | Disease invovment: Limb-Girdle Muscular Dystrophy | Search

5 gene records browsed for species *Homo sapiens* for Limb-Girdle Muscular Dystrophy

S.No.	Name/GeneID	Functional stage	Description	Location	Gene Length	Exons	Details
1	DAG1 1605	cell adhesion	dystroglycan 1	Chromosome 3, NC_000003.12 (49468703..49535618)	66916 nt	9	more...
2	DES 1674	Proliferation and differentiation	desmin	Chromosome 2, NC_000002.12 (219418377..219426739)	8363 nt	9	more...
3	DYSF 8291	Differentiation	dysferlin	Chromosome 2, NC_000002.12 (71453155..71686763)	233609 nt	58	more...
4	MYLK 4638	Differentiation, migration	myosin light chain kinase	Chromosome 3, NC_000003.12 (123612296..123884302, complement)	272007 nt	36	more...
5	SGCA 6442	Differentiation	sarcoglycan alpha	Chromosome 17, NC_000017.11 (50165517..50175932)	10416 nt	10	more...

This section provide link to the literature citing the role of the selected gene in particular Muscular dystrophy

Desmin gene (Gene Id: 1674 Symbol: DES) in *Homo sapiens*
Functional stage: Proliferation and differentiation

Involved disease information

Category	Linked disease	Linked articles	Other references
Muscular dystrophy	Desmin-related myofibrillar myopathy	20718792	NA
Muscular dystrophy	Dilated cardiomyopathy	17325244	https://www.ncbi.nlm.nih.gov/books/NBK1309/
Muscular dystrophy	Limb-Girdle Muscular Dystrophy		https://www.ncbi.nlm.nih.gov/books/NBK1408/

Desmin-related myofibrillar myopathy: Desmin-related myopathies are a heterogeneous group of disorders characterized predominantly by skeletal myopathy and cardiac conduction disturbances in combination with accumulation of desmin deposits in skeletal and cardiac muscle. Desmin is the major intermediate filament in skeletal, cardiac, and in some smooth muscle cells and it is important in the maintenance of cytoskeletal integrity by linking Z bands to the plasma membrane. In desmin-related myopathies, desmin accumulates in disorganized masses that lack normal filament formation. The two genes that have been identified as associated with desminopathy are desmin and alpha-B crystalline. The desmin gene mutations that have been identified in desmin-related myopathy have generally been autosomal dominant inheritance, although there is one report of recessive inheritance involving compound heterozygosity.
http://www.sciencedirect.com/topics/neuroscience/desmin-related-myofibrillar-myopathy

Dilated cardiomyopathy: Dilated cardiomyopathy (DCM) is a condition in which the heart's ability to pump blood is decreased because the heart's main pumping chamber, the left ventricle, is enlarged and weakened. In some cases, it prevents the heart from relaxing and filling with blood as it should. Dilated cardiomyopathy (DCM) is the most common type, occurring mostly in adults 20 to 60. It affects the heart's ventricles and atria, the lower and upper chambers of the heart, respectively.
http://www.heart.org/HEARTORG/Conditions/More/Cardiomyopathy/Dilated-Cardiomyopathy_UCM_444187_Article.jsp#.WgQPMo-CyUk

Limb-Girdle Muscular Dystrophy: Limb-girdle muscular dystrophy is a term for a group of diseases that cause weakness and wasting of the muscles in the shoulders and hips. The muscles most affected are those closest to the body (proximal muscles), specifically the muscles of the shoulders, upper arms, pelvic area, and thighs.
https://ghr.nlm.nih.gov/condition/limb-girdle-muscular-dystrophy

This section provides a short description of the disease

Here we are demonstrating the use of "Disease Associated Genes" function