

"Home Page" of NeuroMuscleDB



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"

Home Gene Information Primer Design Sequence Analysis About Database Contact

Genes with Functional Stages
Disease Associated Genes

Home Gene Information Functional stage

Species: Homo sapiens Functional stage: Proliferation Search

20 gene records browsed for species *Homo sapiens* for Proliferation functional stage

S.No.	Name/GenelD	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...

Home / Gene Information

Species

- Homo sapiens
- Bos taurus
- Homo sapiens**
- Mus musculus

Functional stage

- Proliferation
- Cytoskeletal organization
- Determination, differentiation
- Differentiation
- Differentiation control (positive and negative)
- Differentiation, migration
- Differentiation, regeneration
- Migration
- Migration, differentiation
- Migration, negative regulator of differentiation
- Negative regulator of differentiation
- Negative regulator of differentiation, migration inhibition
- Negative regulator of differentiation, proliferation control
- Negative regulator of differentiation, proliferation, determination
- Negative regulator of proliferation, negative regulator of differentiation
- Negative regulator of proliferation
- Negative regulator of proliferation
- Organization
- Organization, differentiation
- Organization, Not differentiation
- Proliferation**

S.No.	Name/GenelD	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...

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

Species

- Homo sapiens
- Bos laurus
- Homo sapiens
- Mus musculus

Functional stage

- Proliferation
- Cytoskeletal organization
- Determination, differentiation
- Differentiation
- Differentiation control (positive and negative)
- Differentiation, migration
- Differentiation, regeneration
- Migration
- Migration, differentiation
- Migration, negative regulator of differentiation
- Negative regulator of differentiation
- Negative regulator of differentiation, migration inhibition
- Negative regulator of differentiation, proliferation control
- Negative regulator of differentiation, proliferation, determination
- Negative regulator of proliferation, negative regulator of differentiation
- Negative regulator of proliferation
- Negative regulator of proliferation
- Organization
- Organization, differentiation
- Organization, Not differentiation
- Proliferation

S.No.	Name/GeneID	
	CCL2 6347	mc
	CCL3 6348	mc
	CCL4 6351	mc

Location	Gene Length	Exons	Details
Chromosome 17, NC_000017.11 (34255277..34257203)	1927 nt	3	more...
Chromosome 17, NC_000017.11 (36088256..36090160, complement)	1905 nt	3	more...
Chromosome 17, NC_000017.11 (36103827..36105621)	1795 nt	3	more...

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	1HUN
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

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

Similarity Search
Promoter Analysis
Multiple Sequence Alignment

Home / Primer Design

Home / Primer Design

Species: Gene List: Sequence Type:

Gene
Upstream

Subsequence length: From To Product range: Minimum Maximum

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

AAATGGCACCCAGCAGTTGGCGTGAGGGGCTGCTGGAGCTTGGGGGCTGGTGGCAGGAACAAGCCTTTCCGACCCCATGGAGCTGTATGAGACATCCCC
CTACTTCTACCAGGAACCCCGCTTCTATGATGGGAAAACCTACCTGCCTGTCCACCTCCAGGGCTTGAACACCAGGCTACGAGCGGACGGAGCTCACC
CTGAGCCCCGAGGCCCCAGGGCCCTTGAAGACAAGGGGCTGGGGACCCCGAGCACTGTCCAGGCCAGTGCCTGCCGTGGCCGTGTAAGGTGTGTAAGA
GGAAGTCGGTGTCCGTGGACCGGCGGGCGGCCACACTGAGGGAGAAGCGCAGGCTCAAGAAGGTGAATGAGGCCTTCGAGGCCCTGAAGAGAAGCAC
CCTGCTCAACCCCAACCAGCGGCTGCCAAGGTGGAGATCCTGCGCAGTGCCATCCAGTACATCGAGCGCCTCCAGGCCCTGCTCAGCTCCCTCAACCAG
GAGGAGCGTGACCTCCGCTACCGGGGCGGGGGGGCCCCAGCCAGGGGTAAGTGGCCATCCCATCCCCCGCCCCAAGGGGACGGGGCCAGAGGGAGGC
ACCTGGACAGCCTCAAGACCCCAAGAGGGGCTCAGAGGGTTGGTGACGTTGCCAGACAGGGTCCAGGGGCTGCAGGAGCCCTTCCCTGGTCAGAGCTGGG

Primers information

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

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

"Similarity Search" Tool

The screenshot shows a web-based 'Similarity Search' tool interface. At the top, there are three red callout boxes: 'User have options to select any of the BLAST program of his choice (Blastp, Blastn and Blastx).', 'Query type may be Gene/RefSeq mRNA/Upstream/ Protein', and 'Dataset may either be Nucleotide or Protein'. Below these is a navigation bar with 'Home / Sequence Analysis / Smilarity Search'. The main form has three dropdown menus: 'Blast Program' (set to Blastn), 'Query Type' (set to Gene), and 'Data Set' (set to Nucleotide). Below these are parameter fields: 'Word size' (25), 'Maximum number of alignments' (100), 'Minimum percent identity' (65), and 'Output' (Alignment). A large text area is labeled 'Paste sequence in FASTA format'. A red callout box on the right points to this area with the text 'User have to paste his query sequence here as an input'. At the bottom left are 'Alignment' and 'Reset' buttons.

User have options to select any of the BLAST program of his choice (Blastp, Blastn and Blastx).

Query type may be Gene/RefSeq mRNA/Upstream/ Protein

Dataset may either be Nucleotide or Protein

Select percentage identity i.e. if one selects 65, all the output results will be sharing at least 65% sequence identity with your input query

User have to paste his query sequence here as an input

Home / Sequence Analysis / Smilarity Search

Blast Program: Blastn

Query Type: Gene

Data Set: Nucleotide

Parameter

Word size: 25

Maximum number of alignments: 100

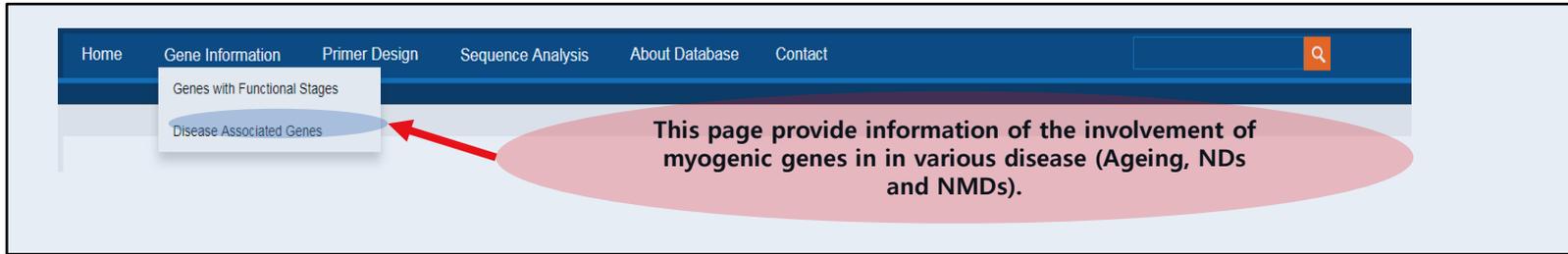
Minimum percent identity: 65

Output: Alignment

Paste sequence in FASTA format

Alignment Reset

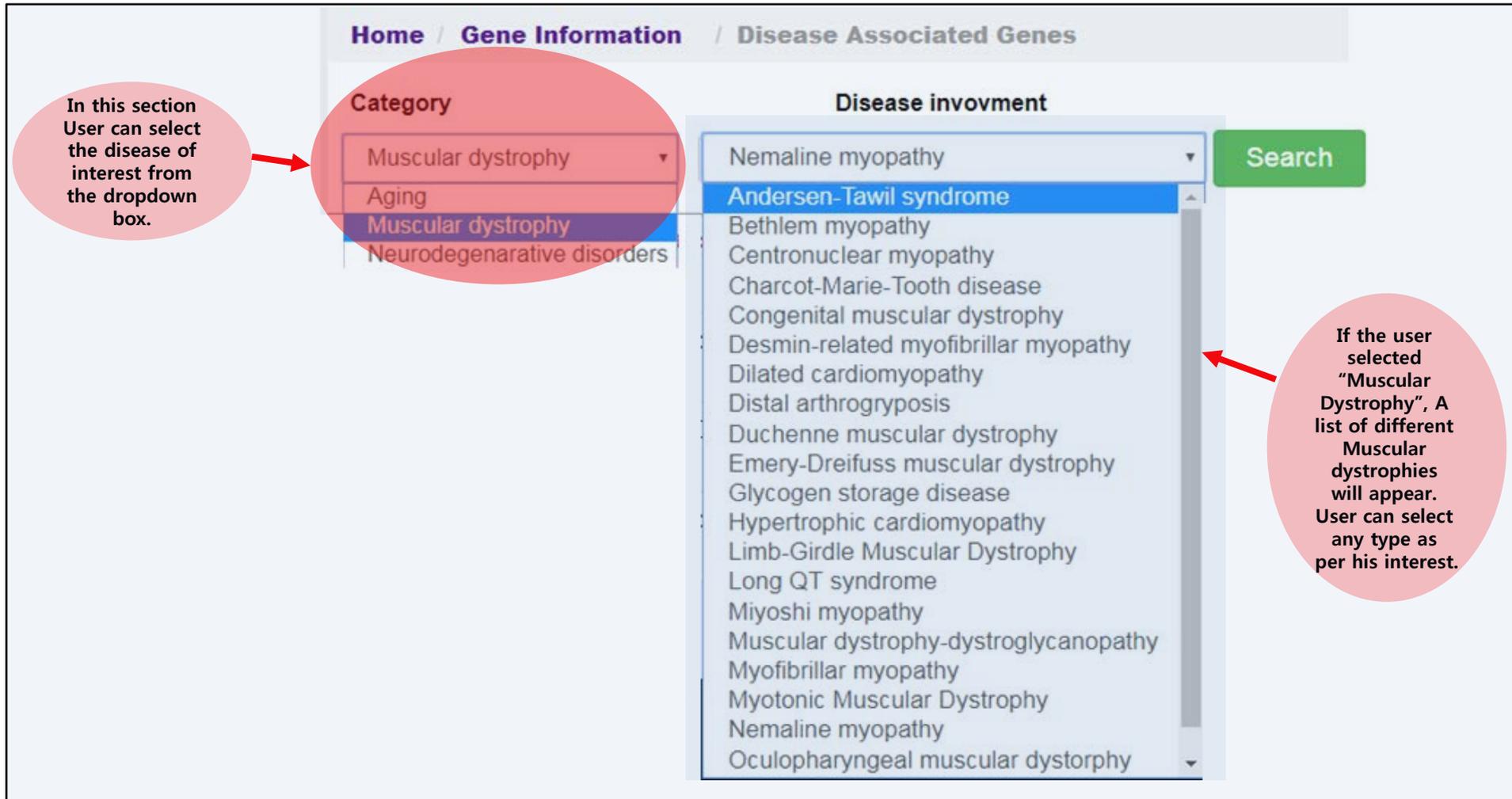
Accessing "Disease Associated Genes" Page



Home Gene Information Primer Design Sequence Analysis About Database Contact

Genes with Functional Stages
Disease Associated Genes

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



Home / Gene Information / Disease Associated Genes

Category

- Muscular dystrophy
- Aging
- Muscular dystrophy
- Neurodegenerative disorders

Disease invovment

- Nemaline myopathy
- Andersen-Tawil syndrome
- Bethlem myopathy
- Centronuclear myopathy
- Charcot-Marie-Tooth disease
- Congenital muscular dystrophy
- Desmin-related myofibrillar myopathy
- Dilated cardiomyopathy
- Distal arthrogyposis
- Duchenne muscular dystrophy
- Emery-Dreifuss muscular dystrophy
- Glycogen storage disease
- Hypertrophic cardiomyopathy
- Limb-Girdle Muscular Dystrophy
- Long QT syndrome
- Miyoshi myopathy
- Muscular dystrophy-dystroglycanopathy
- Myofibrillar myopathy
- Myotonic Muscular Dystrophy
- Nemaline myopathy
- Oculopharyngeal muscular dystorphy

Search

In this section User can select the disease of interest from the dropdown box.

If the user selected "Muscular Dystrophy", A list of different Muscular dystrophies will appear. User can select any type as per his interest.

Category		Disease involvement						
Muscular dystrophy		Limb-Girdle Muscular Dystrophy		Search				
5 gene records browsed for species <i>Homo sapiens</i> 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)	86916 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..71689763)	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 myopathies 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 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