

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

A549 Cells

An immortalized cell line derived from human ADENOCARCINOMA, ALVEOLAR basal epithelial cells isolated from the lungs of a male patient in 1972. The cell line is positive for KERATIN, can synthesize LECITHIN, and contains high levels of POLYUNSATURATED FATTY ACIDS in its PLASMA MEMBRANE. It is used as a model for PULMONARY ALVEOLI function and virus infections, as a TRANSFECTION host, and for PRECLINICAL DRUG EVALUATION.

AN: almost always NIM with no subheadings; check HUMAN; do not routinely add ADENOCARCINOMA, ALVEOLAR

Tree locations:

Cell Line, Tumor A11.251.210.190.080
A11.251.860.180.080
Epithelial Cells A11.436.054

Abdominal Oblique Muscles

Muscles of the anterolateral abdominal wall consisting of the external oblique and the internal oblique muscles. The external abdominal oblique muscle fibers extend from lower thoracic ribs to the linea alba and the iliac crest. The internal abdominal oblique extend superomedially beneath the external oblique muscles.

Tree locations:

Abdominal Muscles A02.633.567.050.375

AC133 Antigen

A member of the prominin family, AC133 Antigen is a 5-transmembrane antigen occurring as several isoforms produced by alternative splicing which are processed into mature forms. In humans, it is expressed as a subset of CD34 (bright) human hematopoietic stem cells and CD34 positive leukemias. Functionally, it is associated with roles in cell differentiation, proliferation, and apoptosis. Specifically, it regulates the organization of apical plasma membrane in epithelial cells, disk morphogenesis during early retinal development, MAPK and Akt signaling pathways, and in cholesterol metabolism.

Tree locations:

Antigens, CD D23.050.301.264.035.015
D23.101.100.110.015
Glycoproteins D09.400.430.250

Acute Febrile Encephalopathy

Acute onset of fever accompanied by seizures, cerebral inflammation and a change in mental status (e.g., confusion, disorientation, and coma).

Tree locations:

Brain Diseases C10.228.140.021

Acute Retroviral Syndrome

Early stage of HIV infection. Symptoms resemble INFLUENZA or INFECTIOUS MONONUCLEOSIS.

Tree locations:

HIV Infections C02.782.815.616.400.044
C02.800.801.400.044
C20.673.480.044

ADAM10 Protein

A disintegrin and metalloproteinase domain-containing protein. It cleaves the membrane-bound precursor of TUMOR NECROSIS FACTOR-ALPHA between ALANINE 76 and VALINE 77 to its functional form, as well as several other CELL SURFACE PROTEINS to their soluble forms, including AMYLOID BETA-PROTEIN PRECURSOR and PRION PROTEIN.

Tree locations:

ADAM Proteins D08.811.277.656.675.374.102.250
D09.400.430.500.250
D12.776.395.033.250
Antigens, CD D23.050.301.264.035.048
D23.101.100.110.048

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ADAM12 Protein

A disintegrin and metalloproteinase domain-containing protein that is expressed as two alternatively-spliced forms: a long transmembrane form (ADAM12-L) and a short soluble form (ADAM12-S). It modulates the cleavage of INSULIN-LIKE GROWTH FACTOR BINDING PROTEINS and may also regulate CELL FUSION during MYOGENESIS.

Tree locations:

ADAM Proteins D08.811.277.656.675.374.102.125
D09.400.430.500.125
D12.776.395.033.125

ADAM17 Protein

A disintegrin and metalloproteinase domain-containing protein that cleaves the membrane-bound precursor of TUMOR NECROSIS FACTOR-ALPHA to its mature form. It cleaves several other CELL SURFACE PROTEINS, including INTERLEUKIN-1 RECEPTOR TYPE II; TRANSFORMING GROWTH FACTOR ALPHA; L-SELECTIN; MUCIN-1; and AMYLOID BETA-PROTEIN PRECURSOR. It can also function as an activator of the Notch signaling pathway by mediating the cleavage of NOTCH RECEPTORS.

Tree locations:

ADAM Proteins D08.811.277.656.675.374.102.375
D09.400.430.500.375
D12.776.395.033.375
Antigens, CD D23.050.301.264.035.057
D23.101.100.110.057

ADAMTS Proteins

A subfamily of ADAM proteases that are distinguished by the presence of one or more THROMBOSPONDIN type-1 repeats (TSRs). These are three-strand motifs that contain characteristic TRYPTOPHAN, ARGININE, and CYSTEINE residues respectively. In contrast to ADAM proteins, which reside on CELL MEMBRANES, ADAMTS proteases are secreted and function in the EXTRACELLULAR MATRIX.

Tree locations:

ADAM Proteins D08.811.277.656.675.374.102.500
D09.400.430.500.500
D12.776.395.033.500
Extracellular Matrix D12.776.860.300.085
Proteins

ADAMTS1 Protein

An ADAMTS protease that contains two disintegrin loops and three C-terminal thrombospondin (TS) motifs. It functions as an ANGIOGENESIS INHIBITOR as well as in normal tissue growth and fertility.

Tree locations:

ADAMTS Proteins D08.811.277.656.675.374.102.500.500
D09.400.430.500.500.500
D12.776.395.033.500.500
D12.776.860.300.085.500

ADAMTS13 Protein

An ADAMTS protease that contains eight thrombospondin (TS) motifs. It cleaves VON WILLEBRAND FACTOR to control vWF-mediated THROMBOSIS. Mutations in the ADAMTS13 gene have been identified in familial cases of PURPURA, THROMBOTIC THROMBOCYTOPENIC and defects in ADAMTS13 activity are associated with MYOCARDIAL INFARCTION; BRAIN ISCHEMIA; PRE-ECLAMPSIA; and MALARIA.

Tree locations:

ADAMTS Proteins D08.811.277.656.675.374.102.500.813
D09.400.430.500.500.813
D12.776.395.033.500.813
D12.776.860.300.085.813

ADAMTS4 Protein

An ADAMTS protease similar to ADAMTS5 PROTEIN. It contains a single C-terminal thrombospondin (TS) motif and cleaves AGGRECAN in CARTILAGE. It may also be involved in the destruction of aggrecan in ARTHRITIS.

Tree locations:

ADAMTS Proteins D08.811.277.656.675.374.102.500.844
D09.400.430.500.500.844
D12.776.395.033.500.844
D12.776.860.300.085.844

ADAMTS5 Protein

An ADAMTS protease that contains two C-terminal thrombospondin (TS) motifs. It functions primarily as an aggrecanase, cleaving AGGRECAN in CARTILAGE, and may be involved in the destruction of aggrecan in ARTHRITIS.

Tree locations:

ADAMTS Proteins D08.811.277.656.675.374.102.500.875
D09.400.430.500.500.875
D12.776.395.033.500.875
D12.776.860.300.085.875

ADAMTS7 Protein

An ADAMTS protease that contains four central and four C-terminal thrombospondin (TS) motifs. It binds to and degrades CARTILAGE OLIGOMERIC MATRIX PROTEIN.

Tree locations:

ADAMTS Proteins D08.811.277.656.675.374.102.500.937
D09.400.430.500.500.937
D12.776.395.033.500.937
D12.776.860.300.085.937

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ADAMTS9 Protein

An ADAMTS protease that contains 15 THROMBOSPONDIN (TS) motifs. It cleaves the PROTEOGLYCANS AGGREGAN and VERSICAN and also functions in protein transport from the ENDOPLASMIC RETICULUM to the GOLGI APPARATUS.

Tree locations:

ADAMTS Proteins D08.811.277.656.675.374.102.500.968
D09.400.430.500.500.968
D12.776.395.033.500.968
D12.776.860.300.085.968

Adipocytes, Beige

Brown fat-like cells that develop in the WHITE FAT from non-MYOGENIC REGULATORY FACTOR 5 expressing CELL LINEAGE.

Tree locations:

Adipocytes A11.329.114.125

Adipose Tissue, Beige

Brown fat-like adipose tissue that develops in WHITE ADIPOSE TISSUE from non-MYOGENIC REGULATORY FACTOR 5 expressing cell lineage.

Tree locations:

Adipose Tissue A10.165.114.161

Adult Germline Stem Cells

Progenitor stem cells found in the testicles.

Tree locations:

Adult Stem Cells A11.872.040.250

Aeromonas veronii

A species of Aeromonas that occurs mostly as single cells in soil and freshwater environments. It also inhabits the digestive tract of the leech HIRUDO MEDICINALIS, where it aids in the digestion of blood and prevents colonization by other bacteria. It is pathogenic in fish and potentially in humans who consume infected fish or immunocompromised patients receiving LEECH THERAPY.

AN: infection: coordinate IM with GRAM-NEGATIVE BACTERIAL INFECTIONS (IM)

Tree locations:

Aeromonas B03.440.450.019.025.845
B03.660.250.017.025.845

Alaska Natives

Persons having origins in any indigenous people of ALASKA and their descendants and who maintain tribal affiliation, or community or cultural attachment.

AN: specify ethnic group if pertinent; do not confuse with INUITS

Tree locations:

American Native Continental Ancestry M01.686.508.150.288
Group

Aldehyde Dehydrogenase, Mitochondrial

An aldehyde dehydrogenase expressed in the mitochondrial matrix that is essential for the metabolism of ETHANOL.

Tree locations:

Aldehyde Dehydrogenase D08.811.682.657.163.249.375
Mitochondrial Proteins D12.776.575.093

Alert Fatigue, Health Personnel

Mental fatigue experienced by health care providers who encounter numerous alerts and reminders from the use of CLINICAL DECISION SUPPORT SYSTEMS. As the numbers of alerts and reminders designed to provide meaningful assistance to the patient care process increases, many health personnel may ignore them.

Tree locations:

Attitude of Health Personnel F01.100.050.500
N05.300.100.169
Mental Fatigue C23.888.369.500.250
F01.145.126.937.250
Quality Assurance, Health Care N04.761.700.075
N05.700.075

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AlkB Enzymes

A family of alpha- KETOGLUTARIC ACID and Fe(II)-dependent dioxygenases that are homologous to AlkB, an enzyme that repairs alkylated nucleic acids in *E. coli*. The mammalian homologs have diverse substrate specificities and functions that include DNA REPAIR, generating unique wobble modifications in URIDINE tRNA, demethylation of nucleotides in DNA and RNA, and demethylation of LYSINE residues on certain proteins, including ACTIN and histones (HISTONE CODE).

Tree locations:

DNA Repair Enzymes D08.811.074.062
Dioxygenases D08.811.682.690.416.139

AlkB Homolog 1, Histone H2a Dioxygenase

A dioxygenase and alkylation repair homolog that functions by oxidative demethylation in RNA and DNA REPAIR of substrates which contain 3-methylcytosine. It also functions as one of the HISTONE DEMETHYLASES involved in embryonic development and maintaining the pluripotency of EMBRYONIC STEM CELLS.

Tree locations:

AlkB Enzymes D08.811.074.062.500
D08.811.682.690.416.139.500

AlkB Homolog 2, Alpha-Ketoglutarate-Dependent Dioxygenase

A dioxygenase and alkylation repair homolog that repairs alkylated DNA and RNA containing 1-methyladenine and 3-methylcytosine by oxidative demethylation. It can also repair alkylated DNA containing 1-ethenoadenine in vitro. It has highest affinity for double-stranded DNA.

Tree locations:

AlkB Enzymes D08.811.074.062.750
D08.811.682.690.416.139.750

AlkB Homolog 3, Alpha-Ketoglutarate-Dependent Dioxygenase

A dioxygenase and alkylation repair homolog that repairs alkylated DNA containing 1-methyladenine (1meA) and 3-methylcytosine (3meC) by oxidative demethylation. It has a strong preference for SINGLE-STRANDED DNA and may also act on RNA.

Tree locations:

AlkB Enzymes D08.811.074.062.875
D08.811.682.690.416.139.875

AlkB Homolog 4, Lysine Demethylase

A dioxygenase and alkylation repair homolog that mediates demethylation of ACTIN monomethylated at 'Lys-84' (K84me1). Demethylation of actin LYSINE 84 (K84me1) is required for maintaining actin and MYOSIN dynamics to support normal cleavage furrow ingression during CYTOKINESIS and CELL MIGRATION. It may also be involved in transcription regulation.

Tree locations:

AlkB Enzymes D08.811.682.690.416.139.937
Oxidoreductases, N- Demethylating D08.811.682.662.582.138

AlkB Homolog 5, RNA Demethylase

A dioxygenase and alkylation repair homolog that demethylates RNA by oxidative demethylation. It specifically demethylates N(6)-methyladenosine (m6A) RNA, the most common internal modification of MESSENGER RNA in higher eukaryotes. It can also demethylate N(6)-methyladenosine in SINGLE-STRANDED DNA.

Tree locations:

AlkB Enzymes D08.811.074.062.937
D08.811.682.690.416.139.968
Oxidoreductases, N- Demethylating D08.811.682.662.582.207

AlkB Homolog 8, tRNA Methyltransferase

A dioxygenase and alkylation repair homolog that catalyzes the methylation of 5-carboxymethyl URIDINE to 5-methylcarboxymethyl uridine at the wobble position of the ANTICODON loop in TRANSFER RNA (tRNA) via its methyltransferase domain. It has a preference for tRNA (ARGININE) and tRNA (GLUTAMATE), and does not bind tRNA (LYSINE).

Tree locations:

AlkB Enzymes D08.811.682.690.416.139.984
tRNA Methyltransferases D08.811.913.555.500.925.500

Allergists

Physicians specializing in treating individuals with hypersensitivity to ALLERGENS.

Tree locations:

Physicians M01.526.485.810.020
N02.360.810.020

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Alpha-Ketoglutarate-Dependent Dioxygenase FTO

A dioxygenase that repairs alkylated DNA and RNA by oxidative demethylation. It has highest activity towards single-stranded RNA containing 3-methyluracil, followed by SINGLE-STRANDED DNA containing 3-methylthymine and specifically demethylates N(6)-methyladenosine (m6A) RNA, the most common internal modification of MESSENGER RNA (mRNA) in higher EUKARYOTES. It contributes to the regulation of the global metabolic rate, energy HOMEOSTASIS, as well as body fat accumulation by regulating the differentiation of ADIPOCYTES into BROWN FAT CELLS or WHITE FAT CELLS.

Tree locations:

AlkB Enzymes D08.811.074.062.968
D08.811.682.690.416.139.992
Oxidoreductases, N-
Demethylating D08.811.682.662.582.242

Anesthesiologists

Physicians specializing in ANESTHESIOLOGY.

Tree locations:

Anesthetists M01.526.485.140.040
N02.360.140.040
Physicians M01.526.485.810.040
N02.360.810.040

Ankyloglossia

A severe congenital restriction of TONGUE movement, resulting from fusion or adherence of the tongue to the floor of the mouth. In partial ankyloglossia (tongue-tie) the LINGUAL FRENUM is abnormally short, or is attached too close to the tip of the tongue. OMIM: 106280

Tree locations:

Stomatognathic Diseases C07.160

Anorectal Malformations

Congenital defects in the anus and the rectum often involving the urinary and genital tracts.

Tree locations:

Digestive System Abnormalities C06.198.025
C16.131.314.047

Anterior Cruciate Ligament Injuries

Sprain or tear injuries to the ANTERIOR CRUCIATE LIGAMENT of the knee.

Tree locations:

Knee Injuries C26.558.554.213

Amaryllidaceae

A family of herbaceous plants with bulbs or rhizomes in the order Asparagales.

Tree locations:

Asparagales B01.650.940.800.575.100.099.050

Anesthetists

Persons trained and certified to administer ANESTHETICS.

Tree locations:

Health Personnel M01.526.485.140
N02.360.140

Annulus Fibrosus

Outer portion of the intervertebral disc that surrounds the NUCLEUS PULPOSUS.

Tree locations:

Intervertebral Disc A02.165.308.410.250
A02.835.232.834.432.250
A10.165.382.350.050.250

Antagomirs

Chemically-engineered oligonucleotides used to selectively inhibit expression of target genes through sequence-specific binding of corresponding microRNA (miRNA) sites.

Tree locations:

Oligonucleotides D13.695.578.424.112

Anti-Vaccination Movement

Group activities directed against VACCINATION.

Tree locations:

Human Activities I03.088

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Antigen Peptide Transporter-1

An ATP-binding cassette, sub-family B protein (P-glycoproteins) that functions in the transport of ANTIGENS from the CYTOPLASM to the ENDOPLASMIC RETICULUM for association with HISTOCOMPATIBILITY ANTIGENS CLASS I peptides. It also acts as a molecular scaffold for the final stage of MHC class I PROTEIN FOLDING.

Tree locations:

P-Glycoproteins D12.776.157.530.100.652.250
D12.776.157.530.450.074.500.500.875.250
D12.776.395.550.020.610.305
D12.776.543.550.192.610.305
D12.776.543.585.100.610.250
D12.776.543.585.450.074.500.500.875.250

Antigen Peptide Transporter-2

An ATP-binding cassette, sub-family B protein (P-glycoproteins) that functions in the transport of ANTIGENS from the CYTOPLASM to the ENDOPLASMIC RETICULUM for association with HISTOCOMPATIBILITY ANTIGENS CLASS I peptides. It functions as a heterodimer with ANTIGEN PEPTIDE TRANSPORTER-1.

Tree locations:

P-Glycoproteins D12.776.157.530.100.652.375
D12.776.157.530.450.074.500.500.875.375
D12.776.395.550.020.610.458
D12.776.543.550.192.610.458
D12.776.543.585.100.610.375
D12.776.543.585.450.074.500.500.875.375

Antigens, CD99

A cell adhesion molecule that, in humans, is encoded by a gene on the PSEUDOAUTOSOMAL REGION of SEX CHROMOSOMES. It functions in CELL ADHESION of T-LYMPHOCYTES and ROSETTE FORMATION by ERYTHROCYTES. It is also involved in the migration of LEUKOCYTES through the ENDOTHELIUM BASEMENT MEMBRANE. CD99 co-localizes with, but functions independently of PECAM-1.

Tree locations:

Antigens, CD D23.050.301.264.035.065
D23.101.100.110.065
Cell Adhesion Molecules D12.776.395.550.200.049
D12.776.543.550.200.062
D23.050.301.350.049

Apartheid

A former political system in SOUTH AFRICA which enforced segregation in all forms, including physical, political, legal and economic discrimination, against all non-white, non-European racial groups.

Tree locations:

Political Systems I01.696.050
Race Relations I01.880.735.820.500.125

APOBEC Deaminases

A family of conserved cytidine deaminases that catalyze the DEAMINATION of CYTIDINE to URIDINE. They are characterized by N and C-terminal zinc-dependent catalytic domains and have important functions in RNA EDITING; EPIGENETIC PROCESSES; and the INNATE IMMUNE RESPONSE against viruses.

Tree locations:

Cytidine Deaminase D08.811.277.151.486.250.500

APOBEC-1 Deaminase

An APOBEC deaminase catalytic subunit of the apolipoprotein B (APOB) MESSENGER RNA (mRNA) editing enzyme complex that is involved in post-transcriptional editing of a CAA codon for GLYCINE to a UAA STOP CODON in the ApoB mRNA. It also functions in CGA (ARGININE) to UGA STOP CODON editing of NEUROFIBROMIN 1 mRNA and EPIGENETIC PROCESSES.

Tree locations:

APOBEC Deaminases D08.811.277.151.486.250.500.500

APOBEC-3G Deaminase

An APOBEC deaminase that functions as an inhibitor of RETROVIRIDAE replication and inhibits the mobility of RETROTRANSPOSONS via deaminase-dependent and independent mechanisms. It is selective for SINGLE-STRANDED DNA and does not deaminate double-stranded DNA or single or DOUBLE-STRANDED RNA. It exhibits potent antiviral activity against VIF PROTEIN deficient HIV-1 through the creation of hypermutations in the VIRAL DNA. It also has anti-viral activity against SIMIAN IMMUNODEFICIENCY VIRUSES and HEPATITIS B VIRUS.

Tree locations:

APOBEC Deaminases D08.811.277.151.486.250.500.750

Apolipoprotein A-V

A minor apolipoprotein that associates with HIGH-DENSITY LIPOPROTEINS (HDL), VERY-LOW-DENSITY LIPOPROTEINS (VLDL), and CHYLOMICRONS. It regulates levels of plasma TRIGLYCERIDES by activating APOLIPOPROTEIN C-II LIPOPROTEIN LIPASE and inhibiting hepatic VLDL triglyceride hydrolysis.

Tree locations:

Apolipoproteins A D10.532.091.200.575
D12.776.070.400.200.575
D12.776.521.120.200.575

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Aponeurosis

The flattened and/or expanded “tendon-like” dense fibrous connective tissue that connects skeletal muscles to each other or to bone.

Tree locations:

Musculoskeletal System A02.083

Applied Behavior Analysis

Behavioral science applied with the aim of improving socially important issues such as behavior problems and learning. For individuals diagnosed with intellectual and developmental disabilities including AUTISM, techniques can be categorized as comprehensive or focused.

Tree locations:

Behavior Therapy F04.754.137.131

Arthroplasty, Replacement, Shoulder

Replacement of the SHOULDER JOINT.

Tree locations:

Arthroplasty, Replacement E04.555.110.110.299
E04.650.110.299
E04.680.101.110.299

Asparagaceae

A family of flowering subshrubs and shrubs in the class Magnoliopsida.

Tree locations:

Asparagales B01.650.940.800.575.100.099.060

Asparagales

An order of monocotyledons (superorder Liliales) in the class Magnoliopsida (Angiosperms).

Tree locations:

Angiosperms B01.650.940.800.575.100.099

ATP Binding Cassette Transporter, Sub-Family G

A subfamily of ATP binding cassette transporters that function primarily in the transport of lipids and STEROLS across the CELL MEMBRANE. They also export UREA and various drugs resulting in MULTIDRUG RESISTANCE. They are smaller than most other ATP binding cassette proteins, consisting of six transmembrane alpha helices and a distinct N-terminal cytoplasmic ATP-binding domain, and function as homo- or heterodimers with other ABCG transporters.

Tree locations:

ATP-Binding Cassette D12.776.157.530.100.228
Transporters D12.776.395.550.020.457
D12.776.543.550.192.457
D12.776.543.585.100.228

ATP Binding Cassette Transporter, Sub-Family G, Member 1

An ATP binding cassette transporter that functions primarily as a lipid and CHOLESTEROL exporter in MACROPHAGES. It may also function in intracellular lipid transport and homeostasis.

Tree locations:

ATP Binding Cassette D12.776.157.530.100.228.250
Transporter, Sub-Family G D12.776.395.550.020.457.250
D12.776.543.550.192.457.250
D12.776.543.585.100.228.250

ATP Binding Cassette Transporter, Sub-Family G, Member 2

An ATP binding cassette transporter, sub-family G protein that functions as a high capacity UREA exporter, transporter of STEROLS, and in the absorption and efflux of many drugs. Its efflux activity for ANTINEOPLASTIC AGENTS contributes to DRUG RESISTANCE. It functions as a homodimer and is expressed by cells in a variety of organs, as well as by NEOPLASTIC STEM CELLS.

Tree locations:

ATP Binding Cassette D12.776.157.530.100.228.500
Transporter, Sub-Family G D12.776.395.550.020.457.500
D12.776.543.550.192.457.500
D12.776.543.585.100.228.500
Antigens, CD D23.050.301.264.035.272
D23.101.100.110.272

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ATP Binding Cassette Transporter, Sub-Family G, Member 5

An ATP binding cassette transporter, sub-family G protein that functions as a heterodimer with ATP BINDING CASSETTE TRANSPORTER, SUB-FAMILY G, MEMBER 8 in the selective transport of DIETARY CHOLESTEROL and PHYTOSTEROLS into and export out of ENTEROCYTES. It also functions in selective sterol excretion by the liver into bile.

Tree locations:

ATP Binding Cassette Transporter, Sub-Family G D12.776.157.530.100.228.750
D12.776.395.550.020.457.750
D12.776.543.550.192.457.750
D12.776.543.585.100.228.750
Lipoproteins D10.532.137
D12.776.521.181

ATP Binding Cassette Transporter, Sub-Family G, Member 8

An ATP binding cassette transporter, sub-family G protein that functions as a heterodimer with ATP BINDING CASSETTE TRANSPORTER, SUB-FAMILY G, MEMBER 5 in the selective transport of DIETARY CHOLESTEROL and PHYTOSTEROLS into and export out of ENTEROCYTES. It also functions in selective sterol excretion by the liver into bile.

Tree locations:

ATP Binding Cassette Transporter, Sub-Family G D12.776.157.530.100.228.875
D12.776.395.550.020.457.875
D12.776.543.550.192.457.875
D12.776.543.585.100.228.875
Lipoproteins D10.532.160
D12.776.521.212

Attentional Bias

An increased focus or awareness of certain stimuli over others, which influence behavior.

Tree locations:

Attention F02.830.104.214.500

Audiologists

Professionals skilled at diagnostic testing of hearing, HEARING IMPAIRMENT, and CORRECTION OF HEARING IMPAIRMENT by non-medical or non-surgical means.

Tree locations:

Health Personnel M01.526.485.170
N02.360.170

Autophagosomes

Large spherical double-layered structures which function in AUTOPHAGY to engulf intracellular components such as ORGANELLES or pathogens. Their outer membrane then fuses with the LYSOSOME and the inner membrane and contents are digested by lysosomal HYDROLASES.

Tree locations:

Phagosomes A11.284.430.214.190.875.190.700.500

Autophagy-Related Protein 12

A UBIQUITIN-like modifier protein that functions in AUTOPHAGOSOME formation, CYTOPLASM to VACUOLE transport, MITOPHAGY, and nucleophagy. Conjugation with ATG5 PROTEIN or ATG10 is essential for its function. The ATG12-ATG5 conjugate acts as an E3 UBIQUITIN LIGASE-like enzyme for lipid modification of ATG8 FAMILY PROTEINS and their localization to vesicle membranes.

Tree locations:

Autophagy-Related Proteins D12.776.094.391
Ubiquitins D12.776.947.125

Autophagy-Related Protein 5

An autophagy-related protein that functions in AUTOPHAGOSOME biogenesis. It is conjugated to the ATG12 PROTEIN via a process that is similar to UBIQUITINATION and involves the ATG7 PROTEIN and ATG10 enzyme. The ATG12-ATG5 conjugate acts as an E3 UBIQUITIN LIGASE-like enzyme and is required for the localization of ATG8 PROTEINS to AUTOPHAGOSOME vesicle membranes and modification of membrane lipids.

Tree locations:

Autophagy-Related Proteins D12.776.094.250

Autophagy-Related Protein 7

An autophagy related protein that is similar to UBIQUITIN-ACTIVATING ENZYME E1. It functions in CYTOPLASM to VACUOLE transport (Cvt) and AUTOPHAGY by activating ATG12 PROTEIN for its conjugation with ATG5 PROTEIN, as well as the conjugation of ATG8 FAMILY PROTEINS with phosphatidylethanolamine for ATG8 association to Cvt vesicles and AUTOPHAGOSOME membranes. It is also required for the nitrogen starvation response in yeast, MITOPHAGY; and autophagic cell death induced by CASPASE 8 inhibition.

Tree locations:

Autophagy-Related Proteins D12.776.094.399

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Autophagy-Related Protein 8 Family

UBIQUITIN-like modifier proteins that function in CYTOPLASM to VACUOLE transport (Cvt), vesicle transport within the GOLGI APPARATUS, and AUTOPHAGOSOME biogenesis. They are also required for selective autophagic degradation of the nucleus (nucleophagy) and MITOPHAGY.

Tree locations:

Autophagy-Related Proteins D12.776.094.407
Microtubule-Associated Proteins D12.776.220.600.450.100
Ubiquitins D12.776.947.187

Autophagy-Related Protein-1 Homolog

A serine/threonine-protein kinase that functions in AUTOPHAGY in response to starvation. It acts on the PHOSPHATIDYLINOSITOL 3-KINASE complex PIK3C3 to regulate AUTOPHAGOSOME formation. It also functions as both a downstream effector and negative regulator of mammalian target of rapamycin complex 1 (mTORC1) and is activated by AMPK, which it also negatively regulates.

Tree locations:

Autophagy-Related Proteins D12.776.094.438
Intracellular Signaling Peptides and Proteins D12.644.360.081
Protein-Serine-Threonine Kinases D08.811.913.696.620.682.700.108

Autophagy-Related Proteins

Proteins and enzymes that function, often as components of MULTIPROTEIN COMPLEXES, to assemble AUTOPHAGOSOMES and carry out AUTOPHAGY.

Tree locations:

Proteins D12.776.094

Axon Fasciculation

Process of organizing neighboring AXONS into a bundle or a fascicle during neurite outgrowth mediated by CELL ADHESION MOLECULES.

Tree locations:

Neuronal Outgrowth G04.152.912.750.250
G07.345.500.325.377.687.750.500
G08.686.784.170.450.500.750.500
G11.561.620.750.250

Axon Guidance

The mechanism by which a neuronal process outgrows toward a target led by the GROWTH CONE. Local guidance cues are provided by cell surface proteins that act on the growing axon.

Tree locations:

Neuronal Outgrowth G04.152.912.750.500
G07.345.500.325.377.687.750.750
G08.686.784.170.450.500.750.750
G11.561.620.750.500

Axon Initial Segment

First segment of axon that connects distal axon segments to the neuronal CELL BODY at the axon hillock region. The axon initial segment is not protected by the MYELIN SHEATH and has properties critical for axonal growth. The axon initial segment and the axon hillock form an axonal trigger zone.

Tree locations:

Axons A08.675.542.145.250
A11.284.180.075.125
A11.671.137.170
A11.671.501.145.250

B30.2-SPRY Domain

A protein interaction domain that is characterized by a bent "beta-sandwich" consisting of two antiparallel beta-sheets. It occurs in eukaryotic proteins, including many TRIPARTITE MOTIF PROTEINS, which function in a variety of cellular processes.

Tree locations:

Protein Interaction Domains and Motifs G02.111.570.820.709.275.750.500.290

Bacillus amyloliquefaciens

A non-pathogenic species of Bacillus that occurs in soil as well as some fermented vegetables and FERMENTED DAIRY PRODUCTS. It produces BACTERIOCINS and ANTIFUNGAL AGENTS and is used in FOOD PRESERVATION as well as a PROBIOTIC.

Tree locations:

Bacillus B03.300.390.400.158.218.076
B03.353.500.100.218.076
B03.510.100.100.218.076
B03.510.415.400.158.218.076
B03.510.460.410.158.218.076

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Bacillus clausii

An alkalophilic species of Bacillus that occurs in soil. It produces ANTI-BACTERIAL AGENTS and is used as a PROBIOTIC.

Tree locations:

Bacillus B03.300.390.400.158.218.283
B03.353.500.100.218.283
B03.510.100.100.218.283
B03.510.415.400.158.218.283
B03.510.460.410.158.218.283

Bacillus coagulans

A microaerophilic, LACTIC ACID producing species of Bacillus that occurs in fermented foods. It also produces ANTI-INFECTIVE AGENTS and is used as a PROBIOTIC.

Tree locations:

Bacillus B03.300.390.400.158.218.314
B03.353.500.100.218.314
B03.510.100.100.218.314
B03.510.415.400.158.218.314
B03.510.460.410.158.218.314

Bacillus firmus

A species of Bacillus that occurs in soil and marine sediments. Many strains are alkalophilic and able to metabolize HEAVY METALS; it may therefore be a useful species for ENVIRONMENTAL BIODEGRADATION.

Tree locations:

Bacillus B03.300.390.400.158.218.345
B03.353.500.100.218.345
B03.510.100.100.218.345
B03.510.415.400.158.218.345
B03.510.460.410.158.218.345

Bacillus licheniformis

A species of Bacillus that occurs in soil and is frequently found on bird feathers. Some strains cause FOODBORNE DISEASE, whereas other strains produce ANTIFUNGAL AGENTS and ANTIBACTERIAL AGENTS and function as PROBIOTICS. This species can also produce enzymes for industrial applications.

Tree locations:

Bacillus B03.300.390.400.158.218.376
B03.353.500.100.218.376
B03.510.100.100.218.376
B03.510.415.400.158.218.376
B03.510.460.410.158.218.376

Bacillus pumilus

A species of Bacillus that occurs in soil, especially around the roots of some plants where it has anti-fungal and anti-nematode activities. It can also produce enzymes for industrial applications.

Tree locations:

Bacillus B03.300.390.400.158.218.613
B03.353.500.100.218.613
B03.510.100.100.218.613
B03.510.415.400.158.218.613
B03.510.460.410.158.218.613

Bacteria, Thermoduric

Bacteria resistant to high temperatures, as in PASTEURIZATION.

Tree locations:

Bacteria B03.135

Bacteroides thetaiotaomicron

A species of Bacteroides that is a major constituent of the human GUT MICROBIOTA. It normally produces enzymes important for the digestion of vegetable matter. However, it can also cause OPPORTUNISTIC INFECTIONS that result in intra-abdominal SEPSIS; BACTEREMIA; and PERITONITIS.

AN: infection: coordinate IM with BACTEROIDES INFECTIONS (IM)

Tree locations:

Bacteroides B03.140.094.152.700
B03.440.425.410.194.152.700

Balloon Enteroscopy

An endoscopy of the small intestines accomplished while advancing the endoscope, which is assisted by one or two balloons

Tree locations:

Endoscopy, Gastrointestinal E01.370.372.250.250.100
E01.370.388.250.250.250.070
E04.210.240.250.080
E04.502.250.250.250.080

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Bankart Lesions

An anterior capsulolabral injury associated with a tear of the anteroinferior GLENOID LABRUM.

Tree locations:

Shoulder Fractures C26.404.625.500
C26.803.250.500

Barium Enema

X-RAY examination of LOWER GASTROINTESTINAL TRACT. Imaging is done while a BARIUM COMPOUND (e.g., BARIUM SULFATE) fills the large intestine via the rectum as a CONTRAST MATERIAL.

Tree locations:

Enema E02.319.347.500
Fluoroscopy E01.370.350.700.225.313

Bathroom Equipment

Receptacles used for collection of human excrement.

Tree locations:

Equipment and Supplies E07.108

Bcl-2-Like Protein 11

A BCL-2-like protein that has a C-terminal BCL-2 homology (BH3) domain and forms heterodimers with other BCL-2 FAMILY PROTEINS. It is a strong inducer of APOPTOSIS and ANOIKIS; several isoforms are expressed (BimEL, Bim L, Bim-alpha, Bim-s; and Bim-gamma) that have different potencies for inducing apoptosis.

Tree locations:

Apoptosis Regulatory Proteins D12.644.360.075.323
D12.776.476.075.323
Membrane Proteins D12.776.543.116
Proto-Oncogene Proteins D12.776.624.664.700.025

Bdellovibrio bacteriovorus

A non-pathogenic, obligate aerobic, Gram-negative species of Bdellovibrio that occurs in water and soil, as well as the intestines of birds and mammals. It can infect and lyse pathogenic GRAM-NEGATIVE BACTERIA and can function as a PROBIOTIC and ANTI-BACTERIAL AGENT.

Tree locations:

Bdellovibrio B03.440.400.425.180.500
B03.660.125.050.500

Beclin-1

An autophagy related protein which functions as a core subunit of PHOSPHATIDYLINOSITOL 3-KINASE MULTIPROTEIN COMPLEXES. It mediates the formation of phosphatidylinositol 3-phosphate and functions in AUTOPHAGY, where it is required for maturation of the AUTOPHAGOSOME. It also functions in ENDOCYTOSIS and CYTOKINESIS as part of a separate complex. Beclin-1 associates with INTRACELLULAR MEMBRANES and interacts with the PROTO-ONCOGENE PROTEINS C-BCL-2 and BCL-X PROTEIN.

Tree locations:

Apoptosis Regulatory Proteins D12.644.360.075.335
D12.776.476.075.335
Autophagy-Related Proteins D12.776.094.500

beta-Arrestin 1

A beta-arrestin that functions in the down-regulation of signaling by G-PROTEIN-COUPLED RECEPTORS. It is also a major regulator of INSULIN signaling via the ERK 1-2 PATHWAY, and many other signaling processes, especially in NEURONS and LEUKOCYTES.

Tree locations:

beta-Arrestins D12.644.360.024.098.525.500
D12.776.157.057.005.525.500
D12.776.476.024.104.525.500
D12.776.543.090.525.500

beta-Arrestin 2

A beta-arrestin that functions similarly to BETA-ARRESTIN 1 in regulating signaling by G-PROTEIN-COUPLED RECEPTORS. It is expressed at high levels in the central nervous system where it may regulate signaling by SYNAPTIC RECEPTORS.

Tree locations:

beta-Arrestins D12.644.360.024.098.525.750
D12.776.157.057.005.525.750
D12.776.476.024.104.525.750
D12.776.543.090.525.750

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beta-Arrestins

Non-visual system arrestins that negatively regulate G-PROTEIN-COUPLED RECEPTORS (GPCRs) and may also function independently of GPCR signaling. They bind and recruit many different signaling factors, including MITOGEN-ACTIVATED PROTEIN KINASES; SRC-FAMILY-KINASES; and FILAMIN to GPCRs and may recognize different phosphorylation states of the receptors to determine the specificity of the cellular response to signaling.

Tree locations:

Arrestins D12.644.360.024.098.525
D12.776.157.057.005.525
D12.776.476.024.104.525
D12.776.543.090.525

Beta-Cryptoxanthin

A mono-hydroxylated xanthophyll that is a provitamin A precursor.

Tree locations:

Cryptoxanthins D02.455.326.271.665.202.868.374.500
D02.455.426.392.368.367.379.249.887.374.500
D02.455.849.131.868.374.500
D23.767.261.887.374.500

Bifidobacterium adolescentis

A species of Bifidobacterium that occurs in the GASTROINTESTINAL TRACT of mammals and healthy humans from birth until late adulthood. It produces ANTI-VIRAL AGENTS and ANTI-INFLAMMATORY AGENTS and is used as a PROBIOTIC.

Tree locations:

Bifidobacterium B03.510.024.100.125
B03.510.460.400.400.049.100.125

Bifidobacterium animalis

A species of Bifidobacterium that occurs in the LARGE INTESTINE of humans and other mammals and in FERMENTED DAIRY PRODUCTS. It is used as a PROBIOTIC.

Tree locations:

Bifidobacterium B03.510.024.100.250
B03.510.460.400.400.049.100.250

Bifidobacterium bifidum

A species of Bifidobacterium that occurs in the human GASTROINTESTINAL TRACT, especially in infants, and in FERMENTED DAIRY PRODUCTS. It produces BACTERIOCINS and is used as a PROBIOTIC.

Tree locations:

Bifidobacterium B03.510.024.100.313
B03.510.460.400.400.049.100.313

Bifidobacterium breve

A species of Bifidobacterium present in the human GUT MICROBIOTA. It is used as a PROBIOTIC.

Tree locations:

Bifidobacterium B03.510.024.100.375
B03.510.460.400.400.049.100.375

Bifidobacterium longum

A species of Bifidobacterium that occurs in the human GASTROINTESTINAL TRACT and VAGINA. It inhibits the growth of pathogenic bacteria, may modulate the immune response, and is used as a PROBIOTIC.

Tree locations:

Bifidobacterium B03.510.024.100.500
B03.510.460.400.400.049.100.500

Bifidobacterium longum subspecies infantis

A subspecies of Bifidobacterium longum that occurs in the GASTROINTESTINAL TRACT of human infants and is used as a PROBIOTIC. It may also be used in the treatment of IRRITABLE BOWEL SYNDROME.

Tree locations:

Bifidobacterium B03.510.024.100.500.500
longum B03.510.460.400.400.049.100.500.500

Bifidobacterium pseudocatenulatum

A species of Bifidobacterium that occurs in the GASTROINTESTINAL TRACT of mammals and healthy humans. It has anti-inflammatory activity and is used as a PROBIOTIC.

Tree locations:

Bifidobacterium B03.510.024.100.750
B03.510.460.400.400.049.100.750

Bilateral Vestibulopathy

Impairment of the vestibular function of both inner ears which can cause difficulties with balance, gait, VERTIGO, and visual blurring.

Tree locations:

Neurologic Manifestations C10.597.057
C23.888.592.057
Vestibular Diseases C09.218.568.900.442

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Biofortification

Improving the NUTRITIONAL VALUE of plant foods by augmenting the plant's environment, by using PLANT BREEDING, or by GENETIC ENGINEERING plants to increase their ability to synthesize VITAMINS or uptake essential NUTRIENTS from the soil.

Tree locations:

Crop Production J01.040.227.250

Blood Culture

Test to determine the presence of blood infection (e.g. SEPSIS; BACTEREMIA).

Tree locations:

Microbiological Techniques E01.370.225.875.185
E05.200.875.185

Body Remains

The physical entity of a deceased human or animal.

Tree locations:

Anthropology, Physical I01.076.368.792
Death C23.550.260.127
Forensic Medicine I01.198.780.937.883

Brain Contusion

A bruise of the brain from an impact of the skull.

Tree locations:

Brain Injuries, Traumatic C10.228.140.199.444.375
C10.900.300.087.235.375
C26.915.300.200.194.375
Contusions C26.974.250.500

Brain Injuries, Diffuse

Brain injuries occurring over a wide area instead of specific focal area.

Tree locations:

Brain Injuries C10.228.140.199.388
C10.900.300.087.219
C26.915.300.200.188

Brain Injuries, Traumatic

A form of acquired brain injury which occurs when a sudden trauma causes damage to the brain.

Tree locations:

Brain Injuries C10.228.140.199.444
C10.900.300.087.235
C26.915.300.200.194

Breast Cancer Lymphedema

Abnormal accumulation of lymph in the arm, shoulder and breast area associated with surgical or radiation breast cancer treatments (e.g., MASTECTOMY).

Tree locations:

Lymphedema C15.604.496.160
Postoperative Complications C23.550.767.082

Breast Carcinoma In Situ

A condition in which abnormal cells have not spread outside the duct, lobule, or nipple to other tissues of the breast. There are 3 types of breast carcinoma in situ: DUCTAL CARCINOMA IN SITU; LOBULAR CARCINOMA IN SITU; and PAGET DISEASE OF THE NIPPLE

AN: coordinate IM with BREAST NEOPLASMS (IM)

Tree locations:

Breast Neoplasms C04.588.180.130
C17.800.090.500.130
Carcinoma in Situ C04.557.470.200.240.187

Breast Density

Measurement of relative composition of different BREAST tissue types often determined from MAMMOGRAPHY; ULTRASONOGRAPHY; or MRI.

Tree locations:

Body Constitution E01.370.600.115.275
G07.100.138

BTB-POZ Domain

A homodimerization protein interaction domain occurring at the N terminus of proteins that contain multiple copies of either CYS2-HIS2 ZINC FINGERS or KELCH REPEATS. It is characterized by a tightly intertwined dimer with an extensive hydrophobic interface. A surface-exposed groove lined with conserved amino acids is formed at the dimer interface, suggesting a peptide-binding site. Many BTB proteins are transcriptional regulators that are thought to regulate CHROMATIN structure.

Tree locations:

Protein Interaction G02.111.570.820.709.275.750.500.343
Domains and Motifs

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Bunion

Abnormal swelling of the inner aspect of the first metatarsal head affecting the first METATARSOPHALANGEAL JOINT.

Tree locations:

Foot Deformities, Acquired C05.330.488.050

Buttermilk

A beverage made from cow's milk fermented by LACTIC ACID-producing bacteria, especially LACTOCOCCUS LACTIS and LACTOBACILLUS BULGARICUS.

Tree locations:

Cultured Milk Products G07.203.300.350.300.222
J02.500.350.300.222
Milk G07.203.100.700.250
G07.203.300.350.525.250
J02.200.700.250
J02.500.350.525.250

Butyrivibrio fibrisolvens

A species of Butyrivibrio that occurs primarily in the RUMEN where it has important activities in LIPID METABOLISM and the production of BUTYRATES.

Tree locations:

Butyrivibrio B03.353.625.250.500

Butyrophilins

A family of mammalian membrane glycoproteins characterized by extracellular IMMUNOGLOBULIN DOMAINS. Some members also have an intracellular B30.2-SPRY DOMAIN or SPRY DOMAIN. The butyrophilin protein (BTN) is expressed by MAMMARY GLAND EPITHELIUM during LACTATION; whereas other members are widely expressed in other tissues, including skeletal muscle, intestine, ERYTHROID CELLS (ERMAP protein); and nerve tissue (MYELIN-OLIGODENDROCYTE GLYCOPROTEIN).

Tree locations:

Membrane Glycoproteins D12.776.395.550.114
D12.776.543.550.195

C2 Domains

Protein modules that function in the targeting of proteins to CELL MEMBRANES. They consist of an eight-stranded anti-parallel beta-sandwich composed of a pair of four-stranded beta-sheets. This structural unit forms a pocket on the membrane-interacting face of the protein and co-ordinates the binding of 2 to 3 calcium ions; however, not all C2 domains bind calcium. Examples of C2 domain-containing proteins include PROTEIN KINASE C and PTEN PHOSPHOHYDROLASE.

Tree locations:

Protein Domains G02.111.570.820.709.275.750.125

Cadherin Related Proteins

Membrane proteins that contain at least two typical consecutive CADHERIN motifs but typically more than cadherin or protocadherin proteins. Their overall domain organization also differs from those of cadherins and protocadherins, and contains different and unique cytoplasmic domains.

Tree locations:

Cell Adhesion Molecules D12.776.395.550.200.188
Membrane Proteins D12.776.543.131

Calcium Release Activated Calcium Channels

Specialized calcium channels that localize to the ENDOPLASMIC RETICULUM and PLASMA MEMBRANE. They contain the pore subunit ORAI1 PROTEIN which is activated by STROMAL INTERACTION MOLECULES upon intracellular calcium depletion.

Tree locations:

Calcium Channels D12.776.157.530.400.150.740
D12.776.543.550.450.150.740
D12.776.543.585.400.150.740

Calendars (*Pub Type*)

Documents or charts that show days, weeks, and months of a year.

AN: This heading is used as a Publication Type.

Calendars as a subject are indexed under the main heading CALENDARS AS TOPIC. INDEXER: Do not use

Tree locations:

Publication Formats V02.220

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Calendars as Topic

Works about documents or charts that show days, weeks, and months of a year.

AN: do not confuse with the Publication Type CALENDARS

Tree locations:

Information Science L01.060

Call Centers

A facility set up for the purpose of handling large volumes of telephone calls. Call Centers typically utilize some form of computer automation for receiving, dispatching, screening, logging and forwarding telephone calls.

Tree locations:

Communications Media L01.178.181

Camelidae

The only extant family of the suborder Tylopoda (order Artiodactyla). Currently living members include domesticated species, DROMEDARIES (with one-hump); BACTRIAN CAMELS (with two humps); LLAMAS; ALPACAS, and wild feral camels; VICUNAS; and GUANACOS. Although they get nutrients from plants by rumination, they evolved separately from the RUMINANTS which have four-chambered stomachs. Camelidae have three-chambered stomachs.

Tree locations:

Artiodactyla B01.050.150.900.649.077.190

Cancellous Bone

A type of osseous tissue which makes up the inner part of bone. It has a spongy, honeycomb-like structure with struts or trabecula and contains the BONE MARROW. It has higher rate of BONE REMODELING turnover than CORTICAL BONE.

Tree locations:

Bone and Bones A10.165.265.414

Cancer Pain

Pain that may be caused by or related to cellular, tissue, and systemic changes that occur during NEOPLASM growth, tissue invasion, and METASTASIS.

AN: not for treatment-related pain

Tree locations:

Pain C10.597.617.185
C23.888.592.612.212

Cancer-Associated Fibroblasts

Subpopulation of heterogeneous fibroblasts within the TUMOR MICROENVIRONMENT that support NEOPLASTIC CELL TRANSFORMATION and NEOPLASTIC PROCESSES.

Tree locations:

Fibroblasts A11.329.228.105

Cannula

Short, hollow cylinders or tubes for insertion into a canal, vessel, or body cavity.

Tree locations:

Catheters E07.132.125

Carbonic Anhydrase IX

A carbonic anhydrase and transmembrane protein that consists of an N-terminal PROTEOGLYCAN-like domain, a catalytic region, a single-pass transmembrane domain, and a short intracellular tail. It functions as a dimer and is expressed primarily by cells of the GASTROINTESTINAL TRACT; BILE DUCT EPITHELIUM; and GALL BLADDER. It is expressed at high levels in many solid tumors, especially CLEAR CELL RENAL CARCINOMA, in response to CELL HYPOXIA.

Tree locations:

Antigens, Neoplasm D23.050.285.196
Carbonic Anhydrases D08.811.520.241.300.150.450
Membrane Proteins D12.776.543.178

Cardiac Rehabilitation

Restoration of functions to the maximum degree possible in a person or persons suffering from a CARDIOVASCULAR DISEASE. It also includes cardiac conditioning and SECONDARY PREVENTION in patients with elevated cardiovascular risk profile.

Tree locations:

Rehabilitation E02.760.169.063.500.185
E02.831.185
H02.403.680.600.250
N02.421.784.244

Cardiologists

Qualified medical professionals who specialize in preventing and treating disorders of the heart and CARDIOVASCULAR SYSTEM.

Tree locations:

Physicians M01.526.485.810.128
N02.360.810.128

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Cardiorespiratory Fitness

A measure of the functional capabilities of the heart, lungs and muscles, relative to the demands of specific exercise routines such as running or cycling.

Tree locations:

Athletic Performance I03.450.642.845.054.300
Health N01.400.150
Physical Fitness G11.427.685.500
I03.450.642.845.054.800.500
N01.400.545.500

Caspase Activation and Recruitment Domain

A homotypic protein interaction module of the death domain superfamily. It is composed of a bundle of six alpha-helices that is related in sequence and structure to the DEATH DOMAIN and DEATH EFFECTOR DOMAIN. The Caspase Activation and Recruitment Domain (CARD domain) typically associates with other CARD-containing proteins, forming either dimers or trimers. CARD domains may occur in isolation, or in combination with other domains in CARD signaling adaptor proteins and initiator CASPASES that function in APOPTOSIS.

Tree locations:

Death Domain Superfamily G02.111.570.820.709.275.750.500.395.250

CDX2 Transcription Factor

An antenapedia-like homeodomain transcription factor that regulates the expression of multiple genes in the INTESTINAL MUCOSA. It plays a critical role in many processes from early differentiation to maintenance of the intestinal epithelial lining of both the small and large intestine.

Tree locations:

Homeodomain Proteins D12.776.260.400.140
Nuclear Proteins D12.776.660.201
Transcription Factors D12.776.930.146

Cerebral Blood Volume

Volume of circulating blood in a region of the brain. It is a functional measure of the brain perfusion status which relates changes in this to changes in CEREBROVASCULAR CIRCULATION that are often seen in brain diseases.

Tree locations:

Blood Volume G09.188.130.185
G09.330.380.092.185

Case Managers

Professionals who are in charge of assessment, planning, facilitation, care coordination, evaluation, and advocacy for options and services to meet a patient's and family's comprehensive health needs.

Tree locations:

Administrative Personnel M01.526.070.245
Health Personnel M01.526.485.215
N02.360.215

CD48 Antigen

A 40-45 KDa GPI-linked protein in the SLAM family that consists of two IMMUNOGLOBULIN C2-SET DOMAINS. It is expressed on the surface of a variety of cells with immune functions, including THYMOCYTES; mature B-LYMPHOCYTES and T-LYMPHOCYTES; NATURAL KILLER CELLS; DENDRITIC CELLS; MAST CELLS; and EOSINOPHILS. It binds to CD2 and 2B4 (CD244) receptors to activate and modulate the immunologic response.

Tree locations:

GPI-Linked Proteins D12.776.395.550.448.180
D12.776.543.484.500.180
D12.776.543.550.418.180
Signaling Lymphocytic Activation Molecule Family D12.776.395.550.736.250
D12.776.543.550.746.250
D12.776.543.750.705.970.250
D23.050.301.264.035.915.250
D23.101.100.110.935.250

Cellulite

Skin lumpiness or skin surface dimpling often seen on the thighs, buttocks and abdomen. It is due to protrusion of SUBCUTANEOUS FAT into the DERMIS layer of skin.

Tree locations:

Skin Manifestations C23.888.885.281

Checkpoint Kinase 1

A serine/threonine-specific protein kinase which is encoded by the CHEK1 gene in humans. Checkpoint kinase 1 (also known as Chk1) coordinates DNA damage response and cell cycle checkpoint response. Under these conditions, activation of Chk1 results in the initiation of cell cycle checkpoints, cell cycle arrest, DNA repair and cell death, to prevent damaged cells from progressing through the cell cycle.

Tree locations:

Protein-Serine-Threonine Kinases D08.811.913.696.620.682.700.143

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Chitinase-3-Like Protein 1

A lectin that binds CHITIN, but lacks chitinase activity. It may be involved in tissue remodeling and cellular responses to the environment, including the response of type 2 HELPER T-CELLS to INFLAMMATION and sensitization to ALLERGENS. Mutations in the CHI3L1 gene are associated with ASTHMA.

Tree locations:

Chitinases D08.811.277.450.207.500
Lectins D12.776.503.070

Cholesterol 24-Hydroxylase

A steroid hydroxylase that functions in CHOLESTEROL homeostasis in the brain. It converts cholesterol into 24S-hydroxycholesterol, which is transported over the BLOOD-BRAIN BARRIER more rapidly than unmetabolized cholesterol.

Tree locations:

Cytochrome P450 Family D08.244.453.875.500
46 D08.811.682.690.708.170.497.500
D12.776.422.220.453.875.500
Steroid Hydroxylases D08.244.453.915.025
D08.811.682.690.708.170.915.025
D12.776.422.220.453.915.025

Chronic Traumatic Encephalopathy

Degenerative brain disease linked to repetitive brain trauma. Progressive symptoms may include MEMORY LOSS; AGGRESSION; or DEPRESSION.

Tree locations:

Brain Injuries, Traumatic C10.228.140.199.444.500
C10.900.300.087.235.500
C26.915.300.200.194.500
Brain Injury, Chronic C10.228.140.199.500.500
C10.900.300.087.250.500
C26.915.300.200.200.500
Neurodegenerative Diseases C10.574.250

Closed Fracture Reduction

A procedure in which normal alignment of a fractured bone is restored by ORTHOPEDIC MANIPULATION without incision.

Tree locations:

Fracture Fixation E04.555.300.150

Colchicaceae

A family in the order Liliales.

Tree locations:

Liliales B01.650.940.800.575.100.615.175

Chocolate

Food product prepared from fermenting, roasting, and grinding the seeds of the COCOA plant.

Tree locations:

Food G07.203.300.195
J02.500.195

Chromothripsis

Massive number of chromosomal rearrangements and shattering that occurs in cancer cells. The breakpoints are located within one chromosome or chromosome arm.

Tree locations:

Chromosome Aberrations C23.550.210.310
G05.365.590.175.310

Ciliopathies

Genetic disorders caused by defects in genes related to the primary CILIUM; BASAL BODY; or CENTROSOME. Obesity, SKELETAL DYSPLASIA and POLYDACTYLY are not examples of malformation that involve either the liver, eye or kidneys.

Tree locations:

Abnormalities, Multiple C16.131.077.245
Genetic Diseases, Inborn C16.320.184

Cognitive Remediation

Behavioral treatment that uses drill and practice, compensatory and adaptive strategies to facilitate improvement in targeted learning areas.

Tree locations:

Behavior Therapy F04.754.137.365

Collateral Ligament, Ulnar

The internal lateral ligament that travels from the medial aspect of the ELBOW uniting the distal aspect of the HUMERUS to the proximal aspect of the ULNA.

Tree locations:

Collateral Ligaments A02.513.514.162.250
A02.835.583.512.162.250

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Computed Tomography Angiography

A non-invasive method that uses a CT scanner for capturing images of blood vessels and tissues. A CONTRAST MATERIAL is injected, which helps produce detailed images that aid in diagnosing VASCULAR DISEASES.

Tree locations:

Multimodal Imaging E01.370.350.567.250
Tomography, X-Ray E01.370.350.350.810.335
Computed E01.370.350.600.350.700.810.335
E01.370.350.700.700.810.335
E01.370.350.700.810.810.568
E01.370.350.825.810.810.499

Cone-Rod Dystrophies

Genetically heterogeneous and sometimes syndromic (e.g., BARDET BIEDL SYNDROME; and SPINOCEREBELLAR ATAXIA TYPE 7) retinopathies with initial RETINAL CONE involvement. They are characterized by decreased VISUAL ACUITY; COLOR VISION DEFECTS; progressive loss of peripheral vision and night blindness.

AN: ROD CONE DYSTROPHIES see RETINITIS PIGMENTOSA is also available

Tree locations:

Eye Diseases, Hereditary C11.270.152
C16.320.290.152
Retinal Dystrophies C11.768.585.658.250

Connexin 26

A gap junction protein encoded by the Gap Junction Beta 2 or GJB2 gene. In the cochlea and epidermis, its hexamers form channels between cells that open to allow cell-to-cell diffusion of small molecules as well as recycling of potassium. Mutations in Connexin 26 are associated with congenital SENSORINEURAL HEARING LOSS.

Tree locations:

Connexins D12.776.543.585.250.100

Conservative Treatment

Therapeutic approaches that are limited, gradual, or well-established as opposed to radical methods.

Tree locations:

Therapeutics E02.197

Coracoid Process

A beak-like bone projection located at the lateral end of the superior anterior border of the SCAPULA.

Tree locations:

Scapula A02.835.232.087.783.356

Cortical Bone

A type of osseous tissue which makes up the outer layer of bone. It is dense, rigid, strong, and forms concentric lamellar OSTEONS.

Tree locations:

Bone and Bones A10.165.265.521

Cortical Excitability

Measurable changes in activities in the CEREBRAL CORTEX upon a stimulation. A change in cortical excitability as measured by various techniques (e.g., TRANSCRANIAL MAGNETIC STIMULATION) is associated with brain disorders.

Tree locations:

Electrophysiological Phenomena G07.265.216
Nervous System Physiological Phenomena G11.561.200

Counselors

Professionals trained in providing information, guidance, and recommendations to individual clients or families to support their decision making and development of coping skills.

Tree locations:

Occupational Groups M01.526.225

Coxa Magna

Deformity of the hip characterized by enlargement and deformation of the FEMUR HEAD and FEMUR NECK, often with associated changes in the ACETABULUM. These changes may be secondary to other diseases (e.g. LEGG-PERTHES DISEASE; ARTHRITIS; HIP DISLOCATION, CONGENITAL) or TRAUMA.

Tree locations:

Bone Diseases C05.116.296

Crush Injuries

Excessive compression of parts of the body that causes muscle swelling, fracture, and/or neurological disturbances in the affected areas. Crush injury with systemic manifestations is referred to as CRUSH SYNDROME.

AN: note entry term CRUSH FRACTURES: COMPRESSION FRACTURES is also available

Tree locations:

Wounds and Injuries C26.257

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Crystal Arthropathies

Joint disorders that are characterized by accumulation of microcrystals in and around the joint including in the SYNOVIAL FLUID. They are classified according to the chemical nature of the crystals such as CALCIUM PYROPHOSPHATE; basic CALCIUM PHOSPHATES; and monosodium urate (see URIC ACID).

Tree locations:

Joint Diseases C05.550.354

Cyclophilin C

A peptidyl-prolyl cis-trans isomerase and member of the cyclophilin family. It catalyzes the cis-trans isomerization of imide-like peptide bonds that occur between PROLINE and other amino acids to facilitate PROTEIN FOLDING.

Tree locations:

Cyclophilins D08.811.399.325.500.400.300.750

CYS2-HIS2 Zinc Fingers

A zinc finger motif of approximately 30 amino acids with the general sequence X2-Cys-X2,4-Cys-X12-His-X3,4,5-His that forms a simple beta sheet-beta sheet-alpha helix fold stabilized by zinc ions. It recognizes and binds to a variety of eukaryotic DNA sequences and is very common among sequence-specific DNA BINDING PROTEINS and TRANSCRIPTION FACTORS.

Tree locations:

Zinc Fingers G02.111.570.820.709.275.500.985.250

Cystography

Radiography of the URINARY BLADDER.

Tree locations:

Urography E01.370.350.700.830.500
E01.370.390.830.500

Cytochrome P450 Family 1

A cytochrome P450 enzyme family whose members function primarily in the metabolism of XENOBIOTICS, including drugs and POLYCYCLIC AROMATIC HYDROCARBONS.

Tree locations:

Cytochrome P-450 Enzyme D08.244.453.100
System D08.811.682.690.708.170.020
D12.776.422.220.453.100

Cytochrome P450 Family 11

A cytochrome P450 enzyme family whose members localize to the INNER MITOCHONDRIAL MEMBRANE where they function in the biosynthesis of STEROIDS.

Tree locations:

Cytochrome P-450 Enzyme D08.244.453.484
System D08.811.682.690.708.170.425
D12.776.422.220.453.484

Cytochrome P450 Family 12

A cytochrome P450 enzyme family that occurs in insects and is expressed in MITOCHONDRIA.

Tree locations:

Cytochrome P-450 Enzyme D08.244.453.485
System D08.811.682.690.708.170.438
D12.776.422.220.453.485

Cytochrome P450 Family 17

A cytochrome P450 enzyme family that functions in the biosynthesis of STEROIDS and includes STEROID 17-ALPHA-HYDROXYLASE.

Tree locations:

Cytochrome P-450 Enzyme D08.244.453.487
System D08.811.682.690.708.170.444
D12.776.422.220.453.487

Cytochrome P450 Family 19

A cytochrome P450 enzyme family that includes AROMATASE, which functions in the biosynthesis of ESTROGENS.

Tree locations:

Cytochrome P-450 Enzyme D08.244.453.489
System D08.811.682.690.708.170.447
D12.776.422.220.453.489

Cytochrome P450 Family 2

A cytochrome P450 enzyme family that includes members which function in the metabolism of STEROIDS; COUMARINS; and NICOTINE.

Tree locations:

Cytochrome P-450 Enzyme D08.244.453.491
System D08.811.682.690.708.170.450
D12.776.422.220.453.491

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Cytochrome P450 Family 21

A cytochrome P450 enzyme family that includes STEROID 21-HYDROXYLASE, which functions in the biosynthesis of STEROIDS.

Tree locations:

Cytochrome P-450 Enzyme	D08.244.453.493
System	D08.811.682.690.708.170.463 D12.776.422.220.453.493

Cytochrome P450 Family 24

A cytochrome P450 enzyme family that includes VITAMIN D3 24-HYDROXYLASE.

Tree locations:

Cytochrome P-450 Enzyme	D08.244.453.496
System	D08.811.682.690.708.170.469 D12.776.422.220.453.496

Cytochrome P450 Family 26

A cytochrome P450 enzyme family whose members function in the metabolism of RETINOIC ACID. It includes RETINOIC ACID 4-HYDROXYLASE.

Tree locations:

Cytochrome P-450 Enzyme	D08.244.453.498
System	D08.811.682.690.708.170.485 D12.776.422.220.453.498

Cytochrome P450 Family 27

A cytochrome P450 enzyme family whose members function in VITAMIN D metabolism and the biosynthesis of BILE ACIDS.

Tree locations:

Cytochrome P-450 Enzyme	D08.244.453.499
System	D08.811.682.690.708.170.493 D12.776.422.220.453.499

Cytochrome P450 Family 3

A cytochrome P450 enzyme family that includes members with critical functions in the metabolism of drugs and SEX HORMONES.

Tree locations:

Cytochrome P-450 Enzyme	D08.244.453.860
System	D08.811.682.690.708.170.495 D12.776.422.220.453.860

Cytochrome P450 Family 4

A cytochrome P450 enzyme family that includes members which function in the metabolism of FATTY ACIDS, especially ARACHIDONIC ACIDS and their derivatives.

Tree locations:

Cytochrome P-450 Enzyme	D08.244.453.870
System	D08.811.682.690.708.170.496 D12.776.422.220.453.870

Cytochrome P450 Family 46

A cytochrome P450 enzyme family that includes CHOLESTEROL 24-HYDROXYLASE, which is expressed primarily in the brain and functions in CHOLESTEROL metabolism.

Tree locations:

Cytochrome P-450 Enzyme	D08.244.453.875
System	D08.811.682.690.708.170.497 D12.776.422.220.453.875

Cytochrome P450 Family 51

A cytochrome P450 family that occurs in all EUKARYOTES. Its members function in the biosynthesis of STEROIDS and some are targets of ANTIFUNGAL AGENTS.

Tree locations:

Cytochrome P-450 Enzyme	D08.244.453.878
System	D08.811.682.690.708.170.499 D12.776.422.220.453.878

Cytochrome P450 Family 6

A cytochrome P450 enzyme family that occurs in insects. Its members function in the metabolism of XENOBIOTICS.

Tree locations:

Cytochrome P-450 Enzyme	D08.244.453.880
System	D08.811.682.690.708.170.880 D12.776.422.220.453.880

Cytochrome P450 Family 7

A cytochrome P450 enzyme family whose members function as steroid 7-alpha hydroxylases.

Tree locations:

Cytochrome P-450 Enzyme	D08.244.453.890
System	D08.811.682.690.708.170.890 D12.776.422.220.453.890

New MeSH Headings for 2017

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Cytochrome P450 Family 8

A cytochrome P450 enzyme family whose members include prostacyclin synthase and STEROID 12-ALPHA-HYDROXYLASE, which function in the biosynthesis of BILE ACIDS.

Tree locations:

Cytochrome P-450 Enzyme D08.244.453.900
System D08.811.682.690.708.170.900
D12.776.422.220.453.900

DEAD Box Protein 58

A DEAD-box RNA helicase that contains an N-terminal DEATH-LIKE DOMAIN, AAA+ ATPase domain, and C-terminal RNA HELICASE activity. It functions as an innate immune receptor through its recognition of viral nucleic acids. It also induces the expression of INTERFERON TYPE I and proinflammatory CYTOKINES. Its ligands include: 5'-triphosphorylated SINGLE-STRANDED RNA, DOUBLE-STRANDED RNA (dsRNA), and short dsRNA (less than 1 kb in length).

Tree locations:

DEAD-box RNA Helicases D08.811.913.696.445.735.720.249.750

Death Domain

A conserved protein interaction domain of the death domain superfamily that is structurally similar to the DEATH EFFECTOR DOMAIN and CASPASE RECRUITMENT DOMAIN. Death domains bind each other to form oligomers and occur on DEATH DOMAIN RECEPTORS, where they are required for APOPTOSIS signaling and non-apoptotic functions.

Tree locations:

Death Domain Superfamily G02.111.570.820.709.275.750.500.395.500

Death Domain Superfamily

A family of structurally-related protein interaction domains characterized by 6-helical closed bundle fold, with Greek key topology and an internal pseudo two-fold symmetry. Death-like domains occur in many proteins that are essential for APOPTOSIS, including CASPASE RECRUITMENT DOMAIN CONTAINING PROTEINS and DEATH DOMAIN RECEPTORS.

Tree locations:

Protein Interaction Domains and Motifs G02.111.570.820.709.275.750.500.395

Death Effector Domain

A homotypic protein interaction module of the death domain superfamily that is composed of a bundle of six alpha-helices. The death effector domain shares sequence and structural similarities with the DEATH DOMAIN and CASPASE RECRUITMENT DOMAIN. It occurs in many proteins with essential functions in APOPTOSIS.

Tree locations:

Death Domain Superfamily G02.111.570.820.709.275.750.500.395.750

Degloving Injuries

Avulsions of the superficial tissues of SKIN and SUBCUTANEOUS TISSUE from the underlying FASCIA.

Tree locations:

Soft Tissue Injuries C26.808.500

Dermatologists

Physicians who specialize in treating disorders of the skin.

Tree locations:

Physicians M01.526.485.810.215
N02.360.810.215

Desegregation

Ending segregation (separation) of different groups of people, usually based on race, in schools, housing, organizations, etc.

Tree locations:

Race Relations I01.880.735.820.500.250

Deubiquitinating Enzymes

Enzymes that remove UBIQUITIN from a protein substrate, including POLYUBIQUITIN, or from other molecules.

Tree locations:

Enzymes D08.811.037

Diastasis, Bone

Abnormal separation of bones, often from a LIGAMENT.

Tree locations:

Joint Dislocations C05.116.359.192
C26.289.192

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Diastasis, Muscle

Abnormal separation of muscles.

Tree locations:

Joint Dislocations C05.116.359.288
C26.289.288

Dibenzofurans

Compounds that include the structure of dibenzofuran.

Tree locations:

Heterocyclic Compounds, 3-Ring D03.633.300.258

Dibenzofurans, Polychlorinated

Dibenzofurans that contain chloride atoms bound to the aromatic rings of the structure.

Tree locations:

Dibenzofurans D03.633.300.258.500
Dioxins and Dioxin-like Compounds D02.309.250

Diet, Carbohydrate Loading

A diet rich in DIETARY CARBOHYDRATES.

Tree locations:

Diet G07.203.650.240.120
Diet Therapy E02.642.249.220

Dioxins and Dioxin-like Compounds

A group of toxic chemical compounds that share chemical structures and biological characteristics that are related to the potent carcinogen 2,3,7,8-tetrachlorodibenzo-p-dioxin.

AN: INDEXER: Do not use

Tree locations:

Organic Chemicals D02.309

Discoidin Domain

A protein domain originally identified in DISCOIDINS. It occurs in a variety of unrelated proteins in multicellular organisms, where it recognizes different ligands with distinct biological functions. Structurally, it consists of two antiparallel beta sheets that form a "jellyroll" configuration stabilized by two intramolecular disulfide bonds. Sequence differences within this module determine ligand specificity; in DISCOIDIN DOMAIN RECEPTORS, it binds to FIBRILLAR COLLAGENS and NON-FIBRILLAR COLLAGENS.

Tree locations:

Protein Domains G02.111.570.820.709.275.750.219

Discoidin Domain Receptor 1

A discoidin domain receptor for FIBRILLAR COLLAGEN that functions in a variety of cellular processes. For example, it regulates cell attachment to the EXTRACELLULAR MATRIX, remodeling of the extracellular matrix, CELL MIGRATION; CELL DIFFERENTIATION; CELL PROLIFERATION; and CELL SURVIVAL.

Tree locations:

Discoidin D08.811.913.696.620.682.725.400.005.500
Domain D12.776.543.750.630.005.500
Receptors D12.776.543.750.685.050.500
D12.776.543.750.705.880.300.500

Discoidin Domain Receptor 2

A discoidin domain receptor for FIBRILLAR COLLAGEN and non-fibrillar COLLAGEN TYPE X. It functions in many cellular and developmental processes that include remodeling of the EXTRACELLULAR MATRIX; CELL MIGRATION; CELL DIFFERENTIATION; and CELL PROLIFERATION; as well as OSTEOGENESIS and the maturation of CHONDROCYTES.

Tree locations:

Discoidin D08.811.913.696.620.682.725.400.005.750
Domain D12.776.543.750.630.005.750
Receptors D12.776.543.750.685.050.750
D12.776.543.750.705.880.300.750

Discoidin Domain Receptors

Receptor tyrosine kinases that bind COLLAGENS. They are characterized by the presence of extracellular DISCOIDIN DOMAINS that activate SIGNAL TRANSDUCTION PATHWAYS in response to collagen binding. They may also be cleaved by MATRIX METALLOPROTEINASES to mediate cell interactions with the EXTRACELLULAR MATRIX.

Tree locations:

Receptor Protein- D08.811.913.696.620.682.725.400.005
Tyrosine Kinases D12.776.543.750.630.005
Receptors, Collagen D12.776.543.750.685.050
Receptors, Mitogen D12.776.543.750.705.880.300

Discoidins

Lectins that were identified in DICTYOSTELIUM DISCOIDEUM. They bind to GALACTOSE and are involved in cell-substratum adhesion, maintenance of morphology during aggregation, and spore formation.

Tree locations:

Lectins D12.776.503.140
Protozoan Proteins D12.776.820.250

New MeSH Headings for 2017

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Dishevelled Proteins

A family of proteins that are key components of the WNT SIGNALING PATHWAY, where they function downstream of FRIZZLED RECEPTORS. They contain an N-terminal dishevelled-AXIN PROTEIN (DIX) domain, which mediates oligomerization; a central PDZ DOMAIN which binds to the frizzled receptor; and a C-terminal DEP domain which facilitates binding to the CELL MEMBRANE. Dishevelled proteins have important functions in CELL DIFFERENTIATION and establishing CELL POLARITY.

Tree locations:

Adaptor Proteins, Signal Transducing D12.644.360.024.288
D12.776.157.057.025
D12.776.476.024.376

DNA Ligase ATP

ATP-dependent cellular enzyme which catalyzes DNA replication, repair and recombination through formation of internucleotide ester bonds between phosphate and deoxyribose moieties. Vertebrate cells encode three well-characterized DNA ligases, DNA ligase I, III and IV, all of which are related in structure and sequence. DNA ligases either require ATP or NAD. However, archaeobacterial, viral, and some eubacterial DNA ligases are ATP-dependent.

Tree locations:

DNA Ligases D08.811.074.500.500
D08.811.464.754.600.500

Domestication

A systematic process of adapting wild species of animals and plants into new environments often in close association or proximity to humans.

Tree locations:

Agriculture J01.040.330

Double-Stranded RNA Binding Motif

An RNA-binding motif characterized by an alpha-beta-beta-beta-alpha fold that binds DOUBLE-STRANDED RNA. It occurs in many eukaryotic proteins as well as in bacterial and viral proteins.

Tree locations:

RNA-Binding Motifs G02.111.570.820.709.275.500.869.250

Dystonin

A plakin characterized by repeat sequences homologous to SPECTRIN and PLECTIN and C-terminal EF HAND MOTIFS. It functions as an integrator of INTERMEDIATE FILAMENTS, ACTIN and MICROTUBULES in cytoskeleton networks. It is required for anchoring intermediate filaments to the actin cytoskeleton in neural and muscle cells as well as anchoring KERATIN-containing intermediate filaments to HEMIDESMOSOMES in EPITHELIAL CELLS.

Tree locations:

Plakins D12.776.220.790.625

Distracted Driving

Behavior which detracts from the focus necessary to operate an automobile safely.

Tree locations:

Automobile Driving I03.125.474

DNA, Ancient

DNA isolated from fossils or other ancient specimens.

Tree locations:

DNA D13.444.308.065

Donor Conception

Assisted reproductive techniques where eggs, sperm, both eggs and sperm (double donation), or embryos from donors are used.

Tree locations:

Reproductive Techniques, Assisted E02.875.800.250
E05.820.800.250

Dynactin Complex

A multi-subunit protein of EUKARYOTIC CELLS. It functions in bidirectional intracellular transport of ORGANELLES and CYTOPLASMIC VESICLES by linking them to DYNEIN and KINESIN.

Tree locations:

Microtubule-Associated Proteins D12.776.220.600.450.150
D12.776.631.560.225
Multiprotein Complexes D05.500.142

Ecological Momentary Assessment

Repeated reports by a research participant of symptoms, affect, behavior, and cognition close in time to experience and in the participant's natural environment.

Tree locations:

Psychological Tests F04.711.336

New MeSH Headings for 2017

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Educational Personnel

Professionals responsible for teaching in an institution or place of learning such as a school, college, vocational institute, or university.

Tree locations:

Occupational Groups M01.526.702

Elbow Tendinopathy

Inflammation (tendinitis) or degeneration (tendinosis) of the tendons of the elbow.

Tree locations:

Tendinopathy C05.651.869.435
C26.874.800.500

Emergence Delirium

A form of DELIRIUM which occurs after GENERAL ANESTHESIA.

Tree locations:

Delirium C10.597.606.337.500.500
C23.888.592.604.339.500.500
F01.700.250.500.500
F03.615.350.500
Postoperative Complications C23.550.767.181

Emergency Medical Dispatch

The mobilization of EMERGENCY CARE to the locations and people that need them.

Tree locations:

Emergency Medical Services N02.421.297.043

Emergency Medical Dispatcher

Professionals responsible for relaying calls for the deployment of EMERGENCY MEDICAL SERVICES.

Tree locations:

Health Personnel M01.526.485.349

Emergency Police Dispatcher

Services for reporting EMERGENCIES to the police department.

Tree locations:

Communications Media L01.178.272
Emergency Medical Services N02.421.297.127

Emotion-Focused Therapy

Intervention that relies on free expression of emotions with coaching to enhance awareness of emotional experiences.

Tree locations:

Psychotherapy F04.754.293

Endamoeba histolytica

Anaerobic parasitic protozoan found in humans and other primates.

Tree locations:

Amoeba B01.046.500.100.700.089.500

Endocrinologists

Physicians who specialize in treating ENDOCRINE SYSTEM DISEASES.

Tree locations:

Physicians M01.526.485.810.303
N02.360.810.303

Endodontists

Dentists specializing in the treatment of injuries and diseases of the DENTAL PULP.

Tree locations:

Dentists M01.526.485.330.397
N02.360.330.397

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Endoglin

A membrane glycoprotein and ANGIOGENESIS FACTOR that is expressed by cells of the VASCULAR ENDOTHELIUM; VASCULAR SMOOTH MUSCLE; and MONOCYTES. It functions as a co-receptor for TRANSFORMING GROWTH FACTOR BETA and modulates CELL ADHESION. Mutations in the endoglin gene are associated with cases of HEREDITARY HEMORRHAGIC TELANGIECTASIA.

Tree locations:

Antigens, CD D23.050.301.264.035.294
D23.101.100.110.296
Receptors, Cell Surface D12.776.543.750.250

Endothelin-Converting Enzymes

Metalloendopeptidases which convert BIG ENDOTHELIN to ENDOTHELIN-1.

Tree locations:

Aspartic Acid Endopeptidases D08.811.277.656.074.500.270
D08.811.277.656.300.048.270
Metalloendopeptidases D08.811.277.656.300.480.229
D08.811.277.656.675.374.229

Enterococcus hirae

A species of Enterococcus that occurs in the GASTROINTESTINAL TRACT of birds and mammals, and to a lesser extent humans. Some strains cause diseases including DIARRHEA; BACTEREMIA; and ENDOCARDITIS in humans and animals.

AN: infection: coordinate IM with GRAM-POSITIVE BACTERIAL INFECTIONS (IM)

Tree locations:

Enterococcus B03.353.750.250.250.475
B03.510.550.250.250.475

Endoscopic Mucosal Resection

A method for removing lesions from gastrointestinal MUCOUS MEMBRANES. The mucosal tissue with the lesion is elevated by injecting a solution into the submucosal layer underneath it. The elevated tissue with the lesion is then cut out.

Tree locations:

Endoscopy, Gastrointestinal E01.370.372.250.250.250
E01.370.388.250.250.250.230
E04.210.240.250.230
E04.502.250.250.250.230

Enhancer of Zeste Homolog 2 Protein

A histone-lysine N-methyltransferase and catalytic subunit of Polycomb Repressive Complex 2. It methylates LYSINE 9 (H3K9me) and LYSINE 27 (H3K27me) of HISTONE H3, leading to transcriptional repression of the affected target gene. EZH2 also methylates non-histone proteins such as GATA4 TRANSCRIPTION FACTOR and the nuclear receptor RORA. It regulates CIRCADIAN CLOCKS via histone methylation at the PROMOTER REGIONS of the circadian genes and its repressive activity is also important for the identity and differentiation of EMBRYONIC STEM CELLS.

Tree locations:

Polycomb Repressive D05.500.781.750.250
Complex 2 D08.811.913.555.500.800.400.500.500
D12.776.660.235.600.200.250
D12.776.664.235.800.200.250
D12.776.930.780.890.200.250

Enthesopathy

A disorder occurring at the site of insertion of TENDONS or LIGAMENTS into bones or JOINT CAPSULES.

Tree locations:

Tendinopathy C05.651.869.653
C26.874.800.750

New MeSH Headings for 2017

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Epidemiologists

Qualified medical professionals who study the causes, incidence, and characteristic behavior of disease outbreaks or other health-related conditions and determine the interrelationships of hosts, agents, and environment related to the distribution and control of diseases.

Tree locations:

Health Personnel M01.526.485.353
N02.360.345

Epithelial Cell Adhesion Molecule

A cell adhesion molecule that is expressed on the membranes of nearly all EPITHELIAL CELLS, especially at the junctions between intestinal epithelial cells and intraepithelial LYMPHOCYTES. It also is expressed on the surface of ADENOCARCINOMA and epithelial tumor cells. It may function in the MUCOSA through homophilic interactions to provide a barrier against infection. It also regulates the proliferation and differentiation of EMBRYONIC STEM CELLS.

Tree locations:

Antigens, CD D23.050.301.264.035.300
D23.101.100.110.301
Antigens, Neoplasm D23.050.285.357
Cell Adhesion Molecules D12.776.395.550.200.263
D12.776.543.550.200.263
D23.050.301.350.263

ERG1 Potassium Channel

One of three members of the ether-a-go-go (EAG) POTASSIUM CHANNELS gene family comprising ether-a-go-go (eag), eag-like (elk) and eag-related (erg) subfamilies. Ether-a-go-go-related gene 1 (ERG1) also known as KCNH2, encodes the pore-forming subunit of a rapidly activating-delayed rectifier potassium channel that plays an essential role in the final repolarization of ventricular action potential. Loss-of-function mutations in human hERG1 is associated with life-threatening ARRHYTHMIA.

Tree locations:

Ether-A-Go-Go D12.776.157.530.400.600.900.249.500
Potassium Channels D12.776.543.550.450.750.900.249.500
D12.776.543.585.400.750.900.249.500

Eryptosis

Suicidal death of ERYTHROCYTES which results in features typical of apoptotic nucleated cells such as cell shrinkage, membrane blebbing, and scrambling of cell membrane to expose membrane PHOSPHATIDYLSERINES, which triggers engulfment and degradation by MACROPHAGES.

Tree locations:

Apoptosis G04.146.160.295

Escherichia coli O104

An enterohemorrhagic Escherichia coli of the O subfamily that can cause severe **FOODBORNE DISEASE**. The H4 serotype strain produces **SHIGA TOXINS** and has been linked to human disease outbreaks, including some cases of **HEMOLYTIC-UREMIC SYNDROME**, resulting from contamination of foods by feces containing E. coli O104.

AN: infection: coordinate IM with *ESCHERICHIA COLI INFECTIONS (IM)*

Tree locations:

Enterohemorrhagic B03.440.450.425.325.300.800.250.250
Escherichia coli B03.660.250.150.180.100.800.250.250

Esophageal Mucosa

Circular innermost layer of the ESOPHAGUS wall that mediates esophageal PERISTALSIS which pushes ingested food bolus toward the stomach.

Tree locations:

Esophagus A03.556.875.500.180
Mucous Membrane A10.615.550.146

ETS Motif

A helix-turn-helix motif characterized by three alpha-helices and four-stranded beta-sheets arranged in the order alpha1-beta1-beta2-alpha2-alpha3-beta3-beta4. The third alpha-helix contacts the major groove of DNA. The ETS motif and the flanking amino acid sequences of Ets proteins influence the binding affinity, and the alteration of a single amino acid in the Ets domain can change its DNA binding specificity.

Tree locations:

Helix-Turn-Helix G02.111.570.820.709.275.500.360.360.500
Motifs

Expropriation

Taking of goods, property, or right of use by GOVERNMENT or others.

Tree locations:

Economics I01.261.506

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Extraintestinal Pathogenic Escherichia coli

Strains of Escherichia coli that possess virulence traits which allow them to invade, colonize, and induce disease in tissues outside of the GASTROINTESTINAL TRACT. They are a cause of URINARY TRACT INFECTIONS (UROPATHOGENIC ESCHERICHIA COLI); neonatal MENINGITIS; SEPSIS; PNEUMONIA; and SURGICAL WOUND INFECTION.

AN: infection: coordinate with ESCHERICHIA COLI INFECTIONS

Tree locations:

Escherichia coli B03.440.450.425.325.300.580
B03.660.250.150.180.100.580

Extremophiles

Organisms specifically adapted to live in EXTREME ENVIRONMENTS.

Tree locations:

Organism Forms B05.256

Faecalibacterium

A genus of Gram-negative, non-spore forming, anaerobic, rod shaped bacteria in the Ruminococcaceae family, order Clostridiales that occur in the human gut.

Tree locations:

Clostridiales B03.353.625.766
Gram-Negative Anaerobic Straight, Curved, and Helical Rods B03.440.425.410.413

Familial Multiple Lipomatosis

A rare autosomal disorder characterized by numerous encapsulated lipomas on the trunk and extremities. The lipomas are usually not painful but can cause pain when growing. In rare cases, one lipoma can become painful and progress to multiple painful lipomas; it is then referred to as Dercum's Disease Type III

Tree locations:

Genetic Diseases, Inborn C16.320.298
Lipomatosis C17.800.463.375
C18.452.584.718.625

Fasciotomy

Surgical incision on the FASCIA. It is used to decompress compartment pressure (e.g. in COMPARTMENT SYNDROMES; circumferential burns and extremity injuries) or to release contractures (e.g. in DUPUYTREN'S CONTRACTURE).

Tree locations:

Surgical Procedures, Operative E04.321

Extreme Environments

An ENVIRONMENT which falls outside the range of tolerance for the survival of organisms that are not specifically adapted to survive or thrive in it. Examples of such environments are among the hottest and coldest places on earth.

Tree locations:

Environment G16.500.275.260

Faculty, Pharmacy

Teaching and administrative staff having academic rank in a pharmacy school or department.

Tree locations:

Faculty M01.526.702.250.736

Faecalibacterium prausnitzii

A species of Faecalibacterium, previously classified in the FUSOBACTERIUM genus, that is a major constituent of the GUT MICROBIOTA in healthy humans. It has anti-inflammatory activity and reduced numbers of this species occur in patients with INFLAMMATORY BOWEL DISEASES such as CROHN DISEASE.

Tree locations:

Faecalibacterium B03.353.625.766.500
B03.440.425.410.413.500

Farms

Areas of land set aside to grow crops or raise LIVESTOCK.

Tree locations:

Manufacturing and Industrial Facilities J03.540.150

Fatty Acid-Binding Protein 7

A fatty acid-binding protein expressed by ASTROCYTES during CENTRAL NERVOUS SYSTEM development, and by MALIGNANT GLIOMA cells. It is also expressed by ASTROCYTES in response to injury or ISCHEMIA, and may function in repair of the MYELIN SHEATH.

Tree locations:

Fatty Acid-Binding Proteins D12.776.157.170.250
Nerve Tissue Proteins D12.776.631.274

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Fertilins

Sperm surface proteins involved in sperm-egg fusion. They consist of two subunits, fertilin alpha (ADAM1a) and beta (ADAM2), both of which belong to the metalloprotease-disintegrin protein family. The beta subunit does not have catalytic activity.

Tree locations:

ADAM Proteins D08.811.277.656.675.374.102.750
D09.400.430.500.750
D12.776.395.033.750

Membrane Glycoproteins D12.776.395.550.331

Fibrillin-1

A fibrillin (FBN1) that functions as a structural support protein for MICROFIBRILS. It also regulates the maturation of OSTEOBLASTS by controlling the availability and concentration of TGF-BETA and BONE MORPHOGENETIC PROTEINS. Mutations in the FBN1 gene are associated with MARFAN SYNDROME.

Tree locations:

Fibrillins D09.400.430.875.500
D12.776.395.341.500
D12.776.860.300.400.500

Fibrillin-2

A fibrillin (FBN2) that functions to regulate the assembly of ELASTIC FIBERS. Mutations in the FBN2 gene are associated with congenital contractural ARACHNODACTYLY.

Tree locations:

Fibrillins D09.400.430.875.750
D12.776.395.341.750
D12.776.860.300.400.750

Fibrillins

A family of extracellular matrix glycoproteins that is structurally similar to LATENT TGF-BETA BINDING PROTEINS, but contain additional TGF-beta binding domains, in addition to unique domains at their N and C-terminals. Fibrillins assemble into 10-12 nm MICROFIBRILS that function in a variety of cell interactions with the EXTRACELLULAR MATRIX and developmental processes such as ELASTIC TISSUE maintenance and assembly, and the targeting of growth factors to the extracellular matrix.

Tree locations:

Extracellular Matrix Proteins D12.776.860.300.400
Glycoproteins D09.400.430.875
D12.776.395.341

Fibromatosis, Plantar

A fibromatosis of the plantar fascia characterized by thickening of the fibrous bands on the plantar aponeurosis in the sole of the foot and toes.

Tree locations:

Connective Tissue Diseases C17.300.349
Contracture C05.651.197.369
Fibroma C04.557.450.565.590.340.705
Foot Diseases C05.360.375
C17.800.321.063

Fibromodulin

A small leucine-rich proteoglycan that contains 4 KERATAN SULFATE chains within the leucine repeat region. It interacts with COLLAGEN TYPE I and COLLAGEN TYPE II fibrils and may function to control the rate of EXTRACELLULAR MATRIX assembly. It also sequesters TRANSFORMING GROWTH FACTOR BETA in the extracellular matrix.

Tree locations:

Small Leucine-Rich Proteoglycans D09.698.735.700.813
D12.776.395.650.875.625
D12.776.860.300.806.813

Fibronectin Type III Domain

A highly conserved immunoglobulin-like protein domain of about 100 amino acids that forms a beta sandwich structure.

Tree locations:

Immunoglobulin Domains G02.111.570.820.709.275.750.250.500

Fiscal Policy

Use of government spending and taxation to influence the economy.

Tree locations:

Policy I01.655.125

Fitness Trackers

Devices used for measuring physical activity as an indication of HEALTH STATUS.

Tree locations:

Diagnostic Equipment E07.230.300

Forkhead Box Protein M1

A forkhead box transcription factor that is expressed primarily in adult organs which contain proliferating cells such as the thymus, testis, ovary, and small intestine. It controls the expression of CELL CYCLE genes essential for DNA REPLICATION and MITOSIS, and also functions in DNA REPAIR.

Tree locations:

Forkhead Transcription Factors D12.776.260.950.249.063
D12.776.930.977.249.063

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Forkhead Box Protein O1

A forkhead box transcription factor that is a major target of INSULIN signaling and regulator of metabolic homeostasis in response to OXIDATIVE STRESS. It binds to the insulin RESPONSE ELEMENT (IRE) and the related Daf-16 family binding element (DBE). Its activity is suppressed by insulin and it also regulates OSTEOBLAST proliferation, controls bone mass, and skeletal regulation of GLUCOSE metabolism. It promotes GLUCONEOGENESIS in HEPATOCYTES and regulates gene expression in ADIPOSE TISSUE. It is also an important CELL DEATH regulator. Chromosomal aberrations involving the FOXO1 gene occur in RHABDOMYOSARCOMA.

Tree locations:

Forkhead Transcription Factors D12.776.260.950.249.250
D12.776.930.977.249.250

Forkhead Box Protein O3

A forkhead box transcription factor and transcriptional activator which triggers type 1 programmed cell death (APOPTOSIS) in the absence of APOPTOSIS INHIBITING PROTEINS, including neuronal cell death induced by OXIDATIVE STRESS. It recognizes and binds to the DNA sequence 5'-(AG)TAAA(TC)A-3' and also functions in post-transcriptional regulation of the c-MYC PROTO-ONCOGENE.

Tree locations:

Forkhead Transcription Factors D12.776.260.950.249.125
D12.776.930.977.249.125

Fracture Dislocation

Fracture of a bone near an articulation with concomitant dislocation of that joint.

Tree locations:

Fractures, Bone C26.404.026
Joint Dislocations C05.116.359.336
C26.289.336

Fractures, Avulsion

Tearing away of the CORTICAL BONE fragment at the location of a strong ligament or tendon attachment. The bone fragment detachment site often occurs near a soft site (e.g., GROWTH PLATE) at the base where LIGAMENTS; TENDONS; or JOINT CAPSULES attach. In younger patients it is most often caused by a sudden forceful pull on a tendon in the opposite direction of the bone movement. In the elderly it is associated with osteoporotic INSUFFICIENCY FRACTURES.

Tree locations:

Fractures, Bone C26.404.038

Fused-Ring Compounds

Polycyclic compounds with adjacent rings that share the same two adjacent atoms.

Tree locations:

Polycyclic Compounds D04.210

Gardens

Places provided for the cultivation and/or display of PLANTS.

Tree locations:

Agriculture J01.040.415
Non-Medical Public and Private Facilities J03.320

Gastroenterologists

Physicians who specialize in treating diseases of the DIGESTIVE SYSTEM.

Tree locations:

Physicians M01.526.485.810.438
N02.360.810.438

Gene Editing

Genetic engineering techniques that involve DNA REPAIR mechanisms for incorporating site-specific modifications into a cell's genome.

Tree locations:

Genetic Engineering E05.393.420.270

Gentianales

An angiosperm plant order that includes the APOCYNACEAE; ASCLEPIADACEAE; GENTIANACEAE; LOGANIACEAE; and RUBIACEAE families.

Tree locations:

Angiosperms B01.650.940.800.575.100.456

Geriatricians

Physicians specializing in physiological and pathological aspects of aging and the aged, including the clinical problems of senescence and senility.

Tree locations:

Physicians M01.526.485.810.533
N02.360.810.533

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Giant Cell Tumor of Tendon Sheath

A tumor arising in the SYNOVIAL MEMBRANE; SYNOVIAL BURSA; or TENDON sheath. It is characterized by OSTEOCLAST-like GIANT CELLS; FOAM CELLS; pigmented HEMOSIDERIN-laden MACROPHAGES and inflammatory infiltrate. It is classified either as diffuse or localized tenosynovitis.

Tree locations:

Giant Cell Tumors C04.557.450.565.380.690
Synovitis C05.550.870.445
Tendinopathy C05.651.869.762

Gizzard, Non-avian

A component of the gastrointestinal tract of some reptiles (ALLIGATORS AND CROCODILES), as well as certain fish, mollusks, and insects. It functions to mechanically grind food.

Tree locations:

Animal Structures A13.433

Glycodelin

A lipocalin that is the most abundant protein synthesized and secreted by the ENDOMETRIUM from mid-LUTEAL PHASE of the MENSTRUAL CYCLE through early PREGNANCY.

Tree locations:

Glycoproteins D12.776.395.361
Lipocalins D12.776.157.469.050
Pregnancy Proteins D12.776.780.426

Government Employees

Persons employed by the GOVERNMENT.

Tree locations:

Occupational Groups M01.526.446

Giant Viruses

DNA viruses that have genomes up to several megabases in length and infect primarily single-celled EUKARYOTES.

Tree locations:

DNA Viruses B04.280.356

Global Burden of Disease

Measure of the burden of disease using the disability-adjusted-life-year (DALY). This time-based measure combines years of life lost due to premature mortality and years of life lost due to time lived in states of less than full health. The metric was developed to assess the burden of disease consistently across diseases, risk factors and regions.

Tree locations:

Health Services Research N05.425.184
Health Status Indicators N06.850.520.308.980.438.475.091

Glycogen Synthase Kinase 3 beta

A glycogen synthase kinase-3 type enzyme that functions in ENERGY METABOLISM; EMBRYONIC DEVELOPMENT; and NEUROGENESIS. It is also involved in PROTEIN BIOSYNTHESIS and regulates cell growth and proliferation as a component of the WNT SIGNALING PATHWAY and other signaling pathways. Certain polymorphisms in the GSK3B gene have been associated with PARKINSON DISEASE; ALZHEIMER DISEASE; and BIPOLAR DISORDER.

Tree locations:

Glycogen D05.500.117.875.500
Synthase Kinase D08.811.913.696.620.682.700.429.500.500
3 D08.811.913.696.620.682.700.646.625.500
D12.644.360.300.500.500
D12.776.476.081.875.500
D12.776.476.300.500.500

Gracilis Muscle

A slender and most superficial muscle in the inner THIGH which originates at the ramus of the PUBIC BONE near the PUBIC SYMPHYSIS and inserts at the proximal medial TIBIA. Its function is to abduct thigh, flex knee, and rotate leg medially. It is a common source of a MYOCUTANEOUS FLAP.

Tree locations:

Muscle, Skeletal A02.633.567.425

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Grid Cells

Neurons in the ENTORHINAL CORTEX that project to the HIPPOCAMPUS. Grid cells and PLACE CELLS play a role in cognitive representation of spatial memory and navigation.

Tree locations:

Neurons A08.675.324
A11.671.322

Gubernaculum

An embryonic structure that helps guide proper descent of gonads into their final positions. It attaches the caudal end of the fetal GONADS to the developing SCROTUM in male and the labium majorum in female. It gives rise to the caudal ligaments of the gonad: the scrotal ligament in male and the uterine round and proper ovarian ligaments in female. It includes morphofunctional equivalent structures in non-mammals.

Tree locations:

Embryonic Structures A16.551

Hamstring Muscles

A group of muscles in the posterior THIGH area that are involved in connecting the KNEE JOINT and the PELVIS.

Tree locations:

Muscle, Skeletal A02.633.567.450
A10.690.552.500.250

Hamstring Tendons

A group of tendons that attach the HAMSTRING MUSCLES proximally to the PELVIS and to the TIBIA and FIBULA at the KNEE JOINT.

Tree locations:

Tendons A02.880.307

Harassment, Non-Sexual

The act of systematic and/or continuous unwanted and irritating actions of a non-sexual nature, by a party or group against another. This behavior may include threats, BULLYING, taunts, blackmail, and demands.

AN: SEXUAL HARASSMENT is also available

Tree locations:

Social Behavior F01.145.813.213

Healthy Diet

Dietary patterns which have been found to be important in reducing disease risk.

Tree locations:

Diet G07.203.650.240.629
Healthy Lifestyle F01.829.458.205.500

Healthy Lifestyle

A pattern of behavior involving LIFE STYLE choices which ensure optimum health. Examples are eating right; maintaining physical, emotional, and spiritual wellness, and taking preemptive steps against communicable diseases.

Tree locations:

Life Style F01.829.458.205

Heart Rate Determination

Methods, techniques, and processes by which HEART RATE is measured.

Tree locations:

Heart Function Tests E01.370.370.380.425
Physical Examination E01.370.600.315

Hemochromatosis Protein

A membrane protein and MHC class I antigen. It contains an IMMUNOGLOBULIN C1-SET DOMAIN and interacts with BETA 2-MICROGLOBULIN. It may also regulate the interaction of TRANSFERRIN with the TRANSFERRIN RECEPTOR. Mutations in the HFE gene are associated with cases of FAMILIAL HEMOCHROMATOSIS.

Tree locations:

Histocompatibility Antigens Class I D12.776.395.550.489.200
D12.776.543.550.439.200
D23.050.301.500.100.363
D23.050.705.552.100.375

Hepatitis A Virus Cellular Receptor 1

An Ig domain-containing membrane receptor for HEPATITIS A VIRUS; EBOLA VIRUS; MARBURG VIRUS; and DENGUE VIRUS. It may also function to modulate ASTHMA and HYPERSENSITIVITY.

Tree locations:

Antigens, CD D23.050.301.264.035.320
D23.101.100.110.320
Membrane Glycoproteins D12.776.395.550.469
D12.776.543.550.435
Receptors, Virus D12.776.543.750.830.187

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Hepatitis A Virus Cellular Receptor 2

An Ig domain-containing membrane receptor that is expressed by TH1 CELLS. It regulates the activation of MACROPHAGES and inhibits TH1-mediated auto- and alloimmune responses to promote IMMUNE TOLERANCE.

Tree locations:

Antigens, CD D23.050.301.264.035.325
D23.101.100.110.325
Membrane Glycoproteins D12.776.395.550.479
D12.776.543.550.437
Receptors, Virus D12.776.543.750.830.219

High Fidelity Simulation Training

A controlled learning environment that closely represents reality.

Tree locations:

Simulation Training I02.903.847.250

Histidine Kinase

A member of the transferase superfamily of proteins. In the activated state, protein-histidine kinase autophosphorylates at a histidine residue, subsequently transferring high-energy phosphoryl groups to an aspartate residue of the response-regulator domain, which results in a conformational shift in the effector domain. Histidine kinases mediate signal transduction in a wide range of processes involving cellular adaptation to environmental stress.

Tree locations:

Protein Kinases D08.811.913.696.620.682.675

Homer Scaffolding Proteins

Homer proteins belong to a family of adaptor and scaffold proteins which include Homer1, Homer2 and Homer3. Homer1 and Homer2 play a role in the regulation of calcium homeostasis, whereas Homer3 functions in stimulating changes in actin dynamics in neurons and T-cells. Homer proteins are best known as scaffold proteins at the post-synaptic density where they facilitate synaptic signaling. They function as a molecular switch in metabotropic glutamate receptor (mGluR) signaling, and are associated with human Fragile X syndrome.

Tree locations:

Adaptor Proteins, Signal Transducing D12.776.476.024.381

Huntingtin Protein

A protein that is highly expressed in the nervous system as well as other tissues; its size and structure vary due to polymorphisms. Expanded CAG TRINUCLEOTIDE REPEATS have been identified in the Huntingtin (HD) Gene of patients with HUNTINGTON DISEASE and are associated with abnormal PROTEIN AGGREGATES. Huntingtin interacts with proteins involved in a variety of gene expression and cellular processes; it is also essential for embryonic development.

Tree locations:

Proteins D12.776.441

Heterocyclic Compounds, Fused-Ring

Multiple ring heterocyclic compounds containing two or more rings that share two atoms and one bond in common.

AN: general or unspecified; prefer specifics

Tree locations:

Heterocyclic Compounds D03.633

High-Intensity Interval Training

A cardiovascular exercise strategy with alternating short periods of intense anaerobic exercise with less-intense recovery periods.

Tree locations:

Exercise G11.427.410.698.277.187
I03.350.187

Homeobox Protein Nkx-2.5

A homeobox-containing transcription factor that functions in heart development. Mutations in the NKX2-5 gene are associated with ATRIAL SEPTAL DEFECTS and TETRALOGY OF FALLOT.

Tree locations:

Homeodomain Proteins D12.776.260.400.234
Transcription Factors D12.776.930.324

Host-Seeking Behavior

Searching behavior by parasitic or commensal organisms, to find animals or plants that are a source of nourishment and habitation.

Tree locations:

Appetitive Behavior F01.145.113.111.527
Biological Phenomena G16.559

Hyperekplexia

A neurological disorder characterized by an excessive startle reaction with ABNORMAL REFLEX; MYOCLONIC JERKS; and MUSCLE HYPERTONIA.

Tree locations:

Central Nervous System Diseases C10.228.590

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Hypophysitis

Inflammation of the PITUITARY GLAND.

Tree locations:

Pituitary Diseases C10.228.140.617.738.275
C19.700.419

Immunogenicity, Vaccine

The capacity of VACCINES to stimulate the ADAPTIVE IMMUNE RESPONSE to produce antibodies and antigen-specific T-CELL responses.

Tree locations:

Adaptive Immunity G12.450.050.460
Antibody Formation G12.070.500
Immune System Phenomena G12.513
Immunity, Active G12.450.050.370.500

In Vivo Dosimetry

A procedure to measure the amount of radiation absorbed by the body during RADIOTHERAPY by DOSIMETERS in the patient's skin or natural cavities.

Tree locations:

Radiation Monitoring E05.799.638.511

Independent Medical Evaluation

An assessment of HEALTH STATUS requested by third parties (e.g. insurers, adjudicating bodies, law enforcement, attorneys, etc) on a subject's functional ability. Such information may be used in optimizing treatment or making informed decisions on compensation.

Tree locations:

Health Care Evaluation Mechanisms N05.715.360.425

Informal Sector

A component of the private sector characterized by ease of entry; reliance on indigenous resources; family ownership; small scale operations; skills acquired outside of the formal sector; and unregulated markets.

Tree locations:

Private Sector I01.791.500

Hypoxidaceae

A family of perennial herbaceous plants, in the order Asparagales, with the underground storage organs, rhizomes or corms.

Tree locations:

Asparagales B01.650.940.800.575.100.099.230

Immunoglobulin Domains

Compact globular protein domains of about 80 to 110 amino acids. They are characterized by two antiparallel beta sheets stabilized by HYDROPHOBIC INTERACTIONS and disulfide bonds between opposing strands. Three major subtypes of Ig domains are recognized: variable (V), intermediate (I), and constant (C1 or C2). Members of the immunoglobulin superfamily include ANTIGEN RECEPTORS; CYTOKINE RECEPTORS; and CELL ADHESION MOLECULES which possess immunoglobulin domains.

Tree locations:

Protein Domains G02.111.570.820.709.275.750.250

Inbreeding Depression

A reduced GENETIC VARIATION and GENETIC FITNESS due to INBREEDING.

Tree locations:

Genetic Phenomena G05.410

Influenza A Virus, H5N8 Subtype

A subtype of INFLUENZA A VIRUS that is highly virulent in poultry and wild birds, but shows varying degrees of pathogenicity in mice. The H5N8 virus subtype has a polybasic amino acid motif at the HA cleavage site which explains its pathogenicity in birds, and expresses surface proteins HEMAGGLUTININ 5 and NEURAMINIDASE 8 which are typical of Highly Pathogenic Avian Influenza viruses.

AN: infection: coordinate with INFLUENZA, HUMAN in humans, or INFLUENZA IN BIRDS in birds, or ORTHOMYXOVIRIDAE INFECTIONS in other animals

Tree locations:

Influenza A virus B04.820.545.405.400.598

Infradian Rhythm

A biological rhythm with a period longer than 24 hours.

Tree locations:

Periodicity G07.180.562.595

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Inositol Polyphosphate 5-Phosphatases

Phosphoinositide phosphatases that catalyze the removal of the 5' phosphate from INOSITOL 1,4,5-TRISPHOSPHATE or myo-inositol 1,3,4,5-tetrakisphosphate, resulting in inositol 1,4-bisphosphate and phosphate. They have important functions in the metabolism of INOSITOL PHOSPHATES and inositol 1,4,5-trisphosphate signaling pathways such as CALCIUM SIGNALING.

Tree locations:

Phosphoinositide D08.811.277.352.650.624.500
Phosphatases

Interleukin-1 Receptor-Like 1 Protein

A receptor for INTERLEUKIN-33 that is related structurally to the interleukin-1 receptor. It contains three extracellular IMMUNOGLOBULIN-LIKE DOMAIN regions and associates with INTERLEUKIN-1 RECEPTOR ACCESSORY PROTEIN upon binding IL-33 to initiate signaling. It may function in the response of HELPER T CELLS to INFLAMMATION.

Tree locations:

Receptors, D12.776.543.750.705.852.420.300.375
Interleukin-1

Invasive Fungal Infections

Mycoses which manifest as infections of deep tissue or blood.

AN: *coordinate with specific fungal infection*

Tree locations:

Mycoses C01.703.492

Jagged-2 Protein

A serrate-jagged protein that functions to modulate signal transduction from NOTCH RECEPTORS in CELL DIFFERENTIATION. It may also regulate the expression of CYTOKINES.

Tree locations:

Serrate-Jagged Proteins D12.644.276.930.750
D12.776.157.125.797.750
D12.776.543.800.750
D23.529.930.750

Interferon-Induced Helicase, IFIH1

A DEAD box RNA helicase that contains two N-terminal CASPASE ACTIVATION AND RECRUITMENT DOMAINS. It functions as a sensor of viral NUCLEIC ACIDS such as DOUBLE-STRANDED RNA and activates the INNATE IMMUNE RESPONSE by inducing the expression of INTERFERON-ALPHA and INTERFERON-BETA. It may also regulate cell growth and APOPTOSIS.

Tree locations:

DEAD-box RNA D08.811.913.696.445.735.720.249.875
Helicases

Intersectoral Collaboration

Cooperative actions and ventures among health and health-related groups and organizations intended to improve health outcomes.

Tree locations:

Health Services Administration N04.226

Jagged-1 Protein

A serrate-jagged protein that functions as a ligand for NOTCH RECEPTORS. It may regulate CELL DIFFERENTIATION in HEMATOPOIESIS and PHYSIOLOGIC ANGIOGENESIS. Mutations in the Jagged-1 gene are associated with ALAGILLE SYNDROME 1.

Tree locations:

Antigens, CD D23.050.301.264.035.438
D23.101.100.110.438
Serrate-Jagged Proteins D12.644.276.930.500
D12.776.157.125.797.500
D12.776.543.800.500
D23.529.930.500

Kefir

A beverage made from milk fermented by a mixture of endogenous LACTIC ACID-producing yeast and bacteria (KEFIR GRAINS), many of which are PROBIOTICS. It should not be confused with KAFFIR LIME or KAFFIR CORN.

Tree locations:

Cultured Milk Products G07.203.300.350.300.666
J02.500.350.300.666
Milk G07.203.100.700.375
G07.203.300.350.525.375
J02.200.700.375
J02.500.350.525.375

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Kelch Repeat

An amino acid sequence of about 50 residues long that is composed of X n-long repeats which form a four-stranded anti-parallel BETA-SHEET as a structural component, or blade, of a beta-propeller.

Tree locations:

Amino Acid Motifs G02.111.570.820.709.275.500.500
Protein Interaction G02.111.570.820.709.275.750.500.448
Domains and Motifs
Repetitive G02.111.570.060.720.273
Sequences, Amino
Acid G02.111.570.820.709.275.875.273

Kelch-Like ECH-Associated Protein 1

An adaptor protein characterized by an N-terminal BTB-POZ DOMAIN and six KELCH REPEATS that functions as a substrate for the E3 UBIQUITIN LIGASE complex. It negatively-regulates NF-E2-RELATED FACTOR 2 by targeting it for ubiquitination and degradation by the PROTEASOME. It also represses genes regulated by ANTIOXIDANT RESPONSE ELEMENTS.

Tree locations:

Adaptor Proteins, Signal Transducing D12.644.360.024.306
D12.776.157.057.067
D12.776.476.024.387

Kinanthropometry

A measure of human size, shape, proportion, composition, maturation, and gross function; in relation to body movement, physical exercise, fitness, and performance.

Tree locations:

Anthropometry E01.370.600.024.450
N06.850.505.200.100.700

Koumiss

A beverage made from horse's milk that is fermented by endogenous LACTIC ACID-producing bacteria and ETHANOL-producing yeast.

Tree locations:

Cultured Milk Products G07.203.300.350.300.777
J02.500.350.300.777
Milk G07.203.100.700.438
G07.203.300.350.525.438
J02.200.700.438
J02.500.350.525.438

Ku Autoantigen

An ATP-dependent DNA HELICASE that preferentially binds SINGLE-STRANDED DNA. It is a heterodimer consisting of an 80 kDa subunit (XRCC5) and 70 kDa subunit (XRCC6) that functions with DNA LIGASE IV in the repair of DOUBLE-STRANDED DNA BREAKS and V(D)J RECOMBINATION.

Tree locations:

Antigens, Nuclear D12.776.660.625.625
D23.050.290.625
DNA Helicases D08.811.277.040.025.159.155
D08.811.399.340.155
DNA-Binding Proteins D12.776.260.525

Laboratory Critical Values

Test results which deviate substantially from normal ranges of REFERENCE VALUES or other qualitative results. They trigger CLINICAL LABORATORY SERVICES to place a special alert to ensure PATIENT SAFETY.

Tree locations:

Clinical Laboratory Techniques E01.370.225.828
E05.200.828

Lactobacillus crispatus

A species of Lactobacillus that occurs in the human GASTROINTESTINAL TRACT and the VAGINA of healthy women. It produces LACTIC ACID and HYDROGEN PEROXIDE, and is used as a PROBIOTIC. It is also used for the treatment and prevention of BACTERIAL VAGINOSIS.

Tree locations:

Lactobacillus B03.353.750.450.475.238
B03.510.460.400.410.475.475.238
B03.510.550.450.475.238

Lactobacillus gasseri

A species of Lactobacillus that occurs in the human ORAL MUCOSA; GASTROINTESTINAL TRACT; and VAGINA. It produces BACTERIOCINS, can modulate the immune response, and is used as a PROBIOTIC.

Tree locations:

Lactobacillus B03.353.750.450.475.363
B03.510.460.400.410.475.475.363
B03.510.550.450.475.363

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Lactobacillus johnsonii

A species of Lactobacillus that occurs in the human GASTROINTESTINAL TRACT and VAGINA. It produces BACTERIOCINS and HYDROGEN PEROXIDE and is used as a PROBIOTIC.

Tree locations:

Lactobacillus B03.353.750.450.475.453
B03.510.460.400.410.475.475.453
B03.510.550.450.475.453

Lactobacillus paracasei

A species of Lactobacillus that occurs in the GUT MICROBIOTA of healthy humans as well as FERMENTED DAIRY PRODUCTS and fermented vegetables. It is used as a PROBIOTIC.

Tree locations:

Lactobacillus B03.353.750.450.475.559
B03.510.460.400.410.475.475.559
B03.510.550.450.475.559

Lactobacillus pentosus

A species of Lactobacillus that occurs in fermented foods where its ability to produce LACTIC ACID; ANTI-INFECTIVE AGENTS; and BACTERIOCINS make it useful as a FOOD PRESERVATION agent. It is also used as a PROBIOTIC.

Tree locations:

Lactobacillus B03.353.750.450.475.586
B03.510.460.400.410.475.475.586
B03.510.550.450.475.586

Lactobacillus sakei

A species of Lactobacillus that occurs in fermented meat and fish. It produces the BACTERIOCIN Sakacin P and is used for FOOD PRESERVATION and as a PROBIOTIC.

Tree locations:

Lactobacillus B03.353.750.450.475.775
B03.510.460.400.410.475.475.775
B03.510.550.450.475.775

Lactobacillus salivarius

A species of Lactobacillus that occurs in the human GASTROINTESTINAL TRACT and ORAL MUCOSA. It produces BACTERIOCINS and is used as a PROBIOTIC.

Tree locations:

Lactobacillus B03.353.750.450.475.850
B03.510.460.400.410.475.475.850
B03.510.550.450.475.850

Latent Autoimmune Diabetes in Adults

Autoimmune diabetes in adults with slowly progressive PANCREATIC BETA CELL failure and the presence of circulating autoantibodies to PANCREATIC ISLETS cell antigens.

Tree locations:

Autoimmune Diseases C20.111.576
Diabetes Mellitus C18.452.394.750.714
C19.246.656

Leucine-Rich Repeat Serine-Threonine Protein Kinase-2

A serine/threonine protein kinase with GTPase activity that contains 12 LEUCINE-rich repeats in its central region and 7 WD repeats C-terminal to its kinase and GTPase domains. It localizes to TRANSPORT VESICLES; the OUTER MITOCHONDRIAL MEMBRANE; and the GOLGI APPARATUS. It functions in PROTEIN TRANSPORT; regulates neuron morphology in the central nervous system, and also functions in the trafficking of SYNAPTIC VESICLES. Mutations in the LRRK2 gene have been identified in autosomal dominant cases of PARKINSON DISEASE (PARK8).

Tree locations:

Parkinson Disease D12.776.637.750
Associated Proteins
Protein-Serine-Threonine Kinases D08.811.913.696.620.682.700.534

Leuconostoc mesenteroides

A species of Leuconostoc that occurs on fruits and vegetables and in their fermented products, as well as FERMENTED DAIRY PRODUCTS. It produces LACTIC ACID and BACTERIOCINS and is used as a PROBIOTIC; however, it has also caused infections in immunocompromised patients.

Tree locations:

Leuconostoc B03.353.750.475.450.500
B03.510.550.475.450.500

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Life History Traits

Morphological or behavioral traits influenced by various living conditions that a population encounters especially as it pertains to REPRODUCTION and survival of the population (see POPULATION DYNAMICS) such as age at first reproductive event, number and size of offspring, and lifespan.

Tree locations:

Biological Evolution G05.045.513
Biological Phenomena G16.575

Lipid Droplet Associated Proteins

Proteins, such as PERILIPINS, that localize to LIPID DROPLETS either transiently or constitutively.

Tree locations:

Carrier Proteins D12.776.157.464

Liver X Receptors

Nuclear receptors that bind OXYSTEROLS and function as heterodimers with RETINOID X RECEPTORS. They have important functions in regulating cholesterol homeostasis, ENERGY METABOLISM; INFLAMMATION; and the immune response.

Tree locations:

DNA-Binding Proteins D12.776.260.531
Receptors, Cytoplasmic and Nuclear D12.776.826.194

Lumican

A small leucine-rich proteoglycan that contains 10 tandem leucine repeats and four N-linked sites within the leucine repeat region that may be substituted with KERATAN SULFATE. These properties and its horseshoe shape allow it to mediate interactions among COLLAGEN molecules within fibrils. It is expressed in most mesenchymal tissues as well as the CORNEA, where it functions to maintain transparency.

Tree locations:

Small Leucine-Rich Proteoglycans D09.698.735.700.875
D12.776.395.650.875.750
D12.776.860.300.806.875

Lysine Acetyltransferases

Acetyltransferases that can transfer an acyl group to specific LYSINE residues within HISTONES (HISTONE ACETYLTRANSFERASES) and/or non-histone proteins.

Tree locations:

Acetyltransferases D08.811.913.050.134.415

Liliales

An order of monocots that grow from bulbs or corms, as herbs or vines.

Tree locations:

Angiosperms B01.650.940.800.575.100.615

Lipocalin-2

A lipocalin of approximately 200 amino acids that functions as an iron transporter and is expressed by cells of BONE MARROW and many other cells with secretory functions. It is involved in APOPTOSIS and may function to limit pathogenic bacterial growth as part of the INNATE IMMUNE RESPONSE.

Tree locations:

Acute-Phase Proteins D12.776.124.050.475
Lipocalins D12.776.157.469.325
Proto-Oncogene Proteins D12.776.624.664.700.123

Loteae

A tribe of the PEA FAMILY. The genus Lotus, a member of this tribe and formerly known as Tetragonolobus, is unrelated to other plants with the common name of lotus (NELUMBO and NYMPHAEA).

AN: note entry terms LOTUS JAPONICUS and LOTUS CORNICULATUS: lotus seeds and lotus nuts are from a different plant genus, NELUMBO, especially NELUMBO NUCIFERA

Tree locations:

Fabaceae B01.650.940.800.575.100.401.544

Lymphadenopathy

Disease of LYMPH NODES which are abnormal in size, number or consistency.

Tree locations:

Lymphatic Diseases C15.604.338

Manufacturing and Industrial Facilities

Places provided for the processing, fabrication, assembly, and production of a line of products, services, commodities, or merchandise.

Tree locations:

Non-Medical Public and Private Facilities J03.540

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Margins of Excision

The edges of tissue removed in a surgery for assessment of the effectiveness of a surgical procedure in achieving the local control of a neoplasm and the adequacy of tumor removal. When the margin is negative or not involved by tumor (e.g., CANCER) it suggests all of the tumor has been removed by the surgery.

Tree locations:

Morphological and Microscopic Findings C23.149.625
Tissues A10.830

Maternal Inheritance

Transmission of genetic characters, qualities, and traits, solely from maternal extra-nuclear elements such as MITOCHONDRIAL DNA or MATERNAL MESSENGER RNA.

Tree locations:

Extrachromosomal Inheritance G05.420.275.750

Maximal Respiratory Pressures

A respiratory function test that includes the maximal inspiratory pressure and maximal expiratory pressure. It is determined by SPIROMETRY that measures the patient's RESIDUAL VOLUME and TOTAL LUNG CAPACITY and assesses the strength of RESPIRATORY MUSCLES.

Tree locations:

Respiratory Function Tests E01.370.386.700.550

Medicare Access and CHIP Reauthorization Act of 2015

An Act that amends Title XVIII of the Social Security Act to repeal the Medicare sustainable growth rate, that strengthens Medicare access by improving physician payments, and that reauthorizes the Children's Health Insurance Program (CHIP).

AN: CATALOGER: Use NAF entry

Tree locations:

Medicare N03.219.521.346.506.564.663.250
N03.219.521.576.343.840.254
N03.706.615.696.500

Melanthiaceae

A family in the order Liliales, of bulbous or rhizomatous woodland and alpine perennial herbs.

Tree locations:

Liliales B01.650.940.800.575.100.615.625

Mastic Resin

Dried tree sap from the MASTIC TREE that is used in TRADITIONAL MEDICINE and chewed as gum.

Tree locations:

Resins, Plant D20.215.721.500.626

Mating Factor

A protein also known as pheromone mating factor that occurs on the surfaces of organisms such as yeast and fungi.

Tree locations:

Peptides D12.644.368
Pheromones D23.641.200

Medically Unexplained Symptoms

Persistent health symptoms which remain unexplained after a complete medical evaluation. A cluster of symptoms that consistently appear together but without a known cause are referred to as a MEDICALLY UNEXPLAINED SYNDROME (MUS).

Tree locations:

Signs and Symptoms C23.888.541

Megasphaera elsdenii

A species of Megasphaera that occurs primarily in the RUMEN and is able to metabolize LACTIC ACID.

Tree locations:

Megasphaera B03.440.425.400.500.500

Meniscus

Crescent-shaped cartilaginous tissue interposed between two articulating bones.

Tree locations:

Fibrocartilage A02.165.308.538
A10.165.382.350.163

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Mental Navigation Tests

Measures of spatial cognition and memory.

Tree locations:

Neuropsychological Tests F04.711.513.502

Mentoring

The art and practice of training, guiding, COUNSELING, and providing support to a less experienced, trained, or knowledgeable person.

Tree locations:

Education I02.588
Education, Professional I02.358.859

Metadata

Structured data elements used to describe other data.

Tree locations:

Information Science L01.654

Metatarsal Valgus

A foot anomaly in which the forefoot is angled outward relative to the hindfoot.

Tree locations:

Foot Deformities C05.330.663

Metatarsus Varus

A foot anomaly in which the forefoot (METATARSUS) is angled inward relative to the heel.

Tree locations:

Foot Deformities C05.330.711

Methyl CpG Binding Domain

A protein domain of about 70 amino acids in length that folds into a sandwich structure consisting of a beta sheet, alpha helix, and C-terminal hairpin loop which forms a hydrophobic methylated-DNA binding patch. It binds to methylated CPG ISLANDS in eukaryotes and occurs with other DNA and CHROMATIN binding domains such as AT-HOOK MOTIFS in eukaryotic DNA BINDING PROTEINS.

Tree locations:

Protein Domains G02.111.570.820.709.275.750.438

Methyl-Accepting Chemotaxis Proteins

Transmembrane sensor receptor proteins that are central components of the chemotactic systems of a number of motile bacterial species which include ESCHERICHIA COLI and SALMONELLA TYPHIMURIUM. Methyl-accepting chemotaxis proteins derive their name from a sensory adaptation process which involves methylation at several glutamyl residues in their cytoplasmic domain. Methyl-accepting chemotaxis proteins trigger chemotactic responses across spatial chemical gradients, causing organisms to move either toward favorable stimuli or away from toxic ones.

Tree locations:

Bacterial Proteins D12.776.097.533
Intracellular Signaling Peptides and Proteins D12.644.360.420
Proteins D12.776.476.420
Receptors, Cell Surface D12.776.543.750.054

Microaneurysm

Aneurysm of the MICROVASCULATURE. Charcot-Bouchard aneurysms are aneurysms of the brain vasculature which is a common cause of CEREBRAL HEMORRHAGE. Retinal microaneurysm is an early diagnostic sign of DIABETIC RETINOPATHY.

AN: coordinate with specific site

Tree locations:

Aneurysm C14.907.055.817

Microtrauma, Physical

Small injuries caused by external force applied to the body including bones, muscles, nerves and tendons.

Tree locations:

Wounds and Injuries C26.599

Minimal Clinically Important Difference

A statistically significant minimum set of clinical outcomes that demonstrates a clinical benefit of an intervention or treatment.

Tree locations:

Patient Outcome Assessment N04.761.559.590.399.750
N05.715.360.575.575.399.750

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Mismatch Repair Endonuclease PMS2

A MutL protein and component of the DNA MISMATCH REPAIR system. Its ENDONUCLEASE activity introduces SINGLE-STRAND DNA BREAKS which create entry points for EXO1 exonuclease to remove the strand containing the mismatch. It may also function in DNA DAMAGE signaling.

Tree locations:

Endodeoxyribonucleases D08.811.277.352.335.350.600
MutL Proteins D08.811.074.766.250
D08.811.277.040.025.215.250
D12.776.260.540.250

Mitochondrial Uncoupling Proteins

Mitochondrial anion carrier proteins that function as dimers and form proton channels in the INNER MITOCHONDRIAL MEMBRANE which creates proton leaks and uncouples OXIDATIVE PHOSPHORYLATION from ATP synthesis, resulting in the generation of heat instead of ATP.

Tree locations:

Mitochondrial Membrane D12.776.543.585.475.688
Transport Proteins D12.776.575.750.688
Solute Carrier Proteins D12.776.157.530.937.598
D12.776.543.585.937.696

Moral Status

A philosophical description of intrinsic self-worth and dignity which bestows basic rights of life, liberty, and freedom from harm.

Tree locations:

Ethics K01.752.566.479.417
Morals F01.829.500.720

Morgue

Location where dead bodies are kept until they are buried or cremated.

Tree locations:

Health Facilities N02.278.590
Hospital Departments N02.278.216.500.968.467
N04.452.442.422.467

Morton Neuroma

A nerve inflammation in the foot caused by chronic compression of the plantar nerve between the METATARSAL BONES.

AN: non-neoplastic

Tree locations:

Metatarsalgia C05.360.500.500
C05.550.610.500
C10.597.617.560.500
C23.888.592.612.540.500
Neuralgia C10.597.617.682.275
C10.668.829.600.375
C23.888.592.612.664.275

Mosquito Vectors

Mosquitoes (members of the family CULICIDAE) that transmit pathogens or their intermediate forms from one host to another.

Tree locations:

Insect Vectors N06.850.310.350.100.500.500

Mucosal-Associated Invariant T Cells

A subset of T-lymphocytes that are present in large numbers at MUCOUS MEMBRANES and respond to INFECTIONS. They express a conserved invariant T-CELL RECEPTOR ALPHA-CHAIN that enables them to respond to infections by sensing RIBOFLAVIN metabolites of pathogens.

Tree locations:

T-Lymphocyte A11.118.637.555.567.569.500.100
Subsets A15.145.229.637.555.567.569.500.100
A15.382.490.555.567.569.500.100

Multiple Chronic Conditions

Two or more concurrent chronic physical, mental, or behavioral health problems in an individual.

Tree locations:

Chronic Disease C23.550.291.500.500

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MutL Protein Homolog 1

Eukaryotic homolog of the bacterial MutL DNA MISMATCH REPAIR protein. It heterodimerizes with MISMATCH REPAIR ENDONUCLEASE PMS2 to form MutL alpha, which is recruited to DNA mismatch sites by the MUTS DNA MISMATCH-BINDING PROTEIN. Mutations in the human MLH1 gene are associated with COLORECTAL NEOPLASMS, HEREDITARY NONPOLYPOSIS.

Tree locations:

MutL Proteins D08.811.074.766.500
D08.811.277.040.025.215.500
D12.776.260.540.500

MutL Proteins

DNA repair proteins that include the bacterial MutL protein and its eukaryotic homologs. They consist of a conserved N-terminal region with weak ATPase activity, an endonuclease motif, and a C-terminal domain that forms MutL homodimers or heterodimers between MLH1 and the PMS1, MISMATCH REPAIR ENDONUCLEASE PMS2; or MLH3 proteins. These complexes function in DNA repair pathways, primarily DNA MISMATCH REPAIR, where MutL/MLH1 and the MUTS DNA MISMATCH-BINDING PROTEIN are targeted to damaged DNA.

Tree locations:

Adenosine Triphosphatases D08.811.277.040.025.215
DNA Repair Enzymes D08.811.074.766
DNA-Binding Proteins D12.776.260.540

Mycobiome

The full spectrum of FUNGI that exist within a particular biological niche such as an organism, soil, a body of water, etc.

Tree locations:

Microbiota G06.591.875
G16.500.275.157.049.100.500.875
N06.230.124.049.100.500.750

Myeloid-Derived Suppressor Cells

A heterogeneous, immature population of myeloid cells that can suppress the activity of T-CELLS and NATURAL KILLER CELLS in the INNATE IMMUNE RESPONSE and ADAPTIVE IMMUNE RESPONSE. They play important roles in ONCOGENESIS; INFLAMMATION; and INFECTION.

Tree locations:

Myeloid Cells A11.627.817

Myocardial Contusions

Bruise to the heart muscle due to blunt thoracic trauma.

Tree locations:

Contusions C26.974.250.875
Heart Injuries C26.891.375.750

N-Myc Proto-Oncogene Protein

A basic helix-loop-helix leucine zipper (bHLHZ) transcription factor and proto-oncogene protein that functions in cell growth and proliferation. In mammals, it is highly expressed in the brain during embryogenesis and is essential for brain development; it is not expressed in adult tissues. Amplification or overexpression of N-Myc occurs in at least 20% of tumors and is associated with a poor prognosis in cases of NEUROBLASTOMA; ALVEOLAR RHABDOMYOSARCOMA; SMALL CELL LUNG CARCINOMA; and neuroendocrine prostate cancer.

Tree locations:

Basic Helix-Loop-Helix Leucine Zipper Transcription Factors D12.776.260.103.500.625
D12.776.260.108.092.625
D12.776.930.125.500.563
D12.776.930.127.092.625
Proto-Oncogene Proteins D12.776.624.664.700.158

Nanog Homeobox Protein

A homeodomain protein and transcription regulator that functions in BLASTOCYST INNER CELL MASS and EMBRYONIC STEM CELL proliferation and CELL SELF RENEWAL. It confers pluripotency on embryonic stem cells and prevents their differentiation towards extraembryonic ENDODERM and trophoblast (TROPHOBLAST) CELL LINEAGES.

Tree locations:

Homeodomain Proteins D12.776.260.400.530
Transcription Factors D12.776.930.542

National Center for Advancing Translational Sciences (U.S.)

A unit of the National Institutes of Health that seeks to catalyze the generation of innovative methods and technologies that will enhance the development, testing, and implementation of diagnostics and therapeutics across a wide range of human diseases and conditions. The Center was established in 2011.

AN: add UNITED STATES; research support by this agency is checked as RESEARCH SUPPORT, N.I.H., EXTRAMURAL or RESEARCH SUPPORT, N.I.H., INTRAMURAL; CATALOGER: Use NAF entry

Tree locations:

National Institutes of Health (U.S.) I01.409.418.750.600.650.496.175
Health (U.S.) N03.540.348.500.500.600.480.175

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National Center for Complementary and Integrative Health (U.S.)

The mission of NCCIH is to define, through rigorous scientific investigation, the usefulness and safety of complementary and integrative health interventions and their roles in improving health and health care. The Center was established in 1999 and was known as NCCAM National Center of Complementary and Alternative Medicine until 2015.

AN: add UNITED STATES; research support by this agency is checked as RESEARCH SUPPORT, N.I.H., EXTRAMURAL or RESEARCH SUPPORT, N.I.H., INTRAMURAL; CATALOGER: Use NAF entry

Tree locations:

National Institutes of Health (U.S.) I01.409.418.750.600.650.496.188
N03.540.348.500.500.600.480.188

Neonatal Sepsis

Blood infection that occurs in an infant younger than 90 days old. Early-onset sepsis is seen in the first week of life and most often appears within 24 hours of birth. Late-onset occurs after 1 week and before 3 months of age.

Tree locations:

Infant, Newborn, Diseases C16.614.627
Sepsis C01.539.757.580
C23.550.470.790.500.470

Neonatologists

Physicians who specialize in providing medical care to newborn infants.

Tree locations:

Pediatricians M01.526.485.810.758.500
N02.360.810.758.500

Nephrologists

Qualified medical professionals who specialize in treating KIDNEY DISEASES.

Tree locations:

Physicians M01.526.485.810.628
N02.360.810.628

Network Meta-Analysis

Meta-analysis of randomized trials in which estimates of comparative treatment effects are visualized and interpreted from a network of interventions that may or may not have been evaluated directly against each other. Common considerations in network meta-analysis include conceptual and statistical heterogeneity and incoherence.

Tree locations:

Meta-Analysis as Topic E05.318.780.500.500
E05.581.500.501.500
N05.715.360.780.515.500
N06.850.520.445.500.500

Neurologists

Qualified medical professionals who specialize in treating NERVOUS SYSTEM DISEASES.

Tree locations:

Physicians M01.526.485.810.652
N02.360.810.652

Neuronal Outgrowth

Formation of neuronal processes (AXONS; NEURITES) toward a target cell.

Tree locations:

Neurogenesis G04.152.912.750
G07.345.500.325.377.687.750
G08.686.784.170.450.500.750
G11.561.620.750

NF-KappaB Inhibitor alpha

An I-kappa B protein that inhibits the activity of dimeric NF-KAPPA B P50-REL complexes, sequesters transcription factor NF-kappaB as an inactive complex in the cytoplasm; and prevents NF-kappaB nuclear translocation and DNA binding.

Tree locations:

I-kappa B Proteins D12.644.360.378.500
D12.776.260.420.500
D12.776.476.381.500
D12.776.930.326.500

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NIMA-Interacting Peptidylprolyl Isomerase

A highly-conserved peptidyl-prolyl cis/trans isomerase (PPIase) that binds to and isomerizes specific phosphorylated SERINE- or THREONINE-PROLINE (pSer/Thr-Pro) motifs and causes conformational changes in certain proteins associated with the CELL CYCLE. It displays a preference for an acidic residue N-terminal to the isomerized proline bond and regulates MITOSIS, possibly by attenuating the mitosis-promoting activity of NIMA-RELATED KINASE 1.

Tree locations:

Peptidylprolyl Isomerase D08.811.399.325.500.700

NIMA-Related Kinases

A highly-conserved family of protein serine-threonine kinases that regulate the CELL CYCLE; MITOSIS; and the response to DNA DAMAGE. They are also involved in the assembly and function of microtubule-based structures such as CILIA and CENTRIOLES.

Tree locations:

Cell Cycle Proteins D12.776.167.457
Protein-Serine-Threonine Kinases D08.811.913.696.620.682.700.581

Nitrogen-Fixing Bacteria

Bacteria that are capable of NITROGEN FIXATION.

Tree locations:

Bacteria B03.585

NLR Proteins

Intracellular signaling proteins that are defined by the presence of a NUCLEOTIDE-binding region and LEUCINE-rich repeats. Their general structure consists of any of a variety of effector domains at their N-termini such as a caspase recruitment domain (CARD), a central nucleotide-binding domain, and a variable number of C-terminal leucine-rich repeats. They are important for pathogen recognition in the INNATE IMMUNE RESPONSE of animals and plants. Members of the NLR protein family include the NOD SIGNALING ADAPTOR PROTEINS.

Tree locations:

Intracellular Signaling Peptides and Proteins D12.644.360.539

NIMA-Related Kinase 1

A NIMA-related kinase that functions in CELL CYCLE regulation, the control of CILIA assembly, and CENTROSOME duplication. It is activated at G2 PHASE CELL CYCLE CHECKPOINTS in response to DNA DAMAGE.

Tree locations:

NIMA-Related Kinases D08.811.913.696.620.682.700.581.500
D12.776.167.457.500

Nipple Discharge

Fluid that seeps out of one or both nipples of the breast.

Tree locations:

Body Fluids A12.207.824

NLR Family, Pyrin Domain-Containing 3 Protein

An NLR protein that contains an N-terminal PYRIN DOMAIN and ATP-binding site and 9 C-terminal LEUCINE-rich repeats; it is expressed primarily by MACROPHAGES. It is a core component of the INFLAMMASOME and directs its assembly in response to pathogen infection and damage-associated stimuli. Mutations in the NLRP3 gene are associated with FAMILIAL COLD AUTOINFLAMMATORY SYNDROME.

Tree locations:

NLR Proteins D12.644.360.539.250

Nogo Proteins

Myelin proteins that are expressed as three isoforms: Nogo-A, Nogo-B, and Nogo-C. These share a C-terminal reticulon homology domain (RHD), consisting of two hydrophobic membrane domains flanking a 66 amino acid (Nogo-66) hydrophilic region. A long transmembrane region allows conformations that either span the entire membrane or fold into a hairpin conformation. Nogo inhibits NEURITE outgrowth and modulates wiring and the restriction of SYNAPTIC PLASTICITY in the adult central nervous system. It also regulates neurite fasciculation, branching, and extension in the developing nervous system.

Tree locations:

Myelin Proteins D12.776.543.620.738
D12.776.631.580.738

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Nogo Receptor 1

A high affinity receptor for myelin-associated inhibitors (MAIs) that include NOGO-A PROTEIN; OLIGODENDROCYTE MYELIN GLYCOPROTEIN; and MYELIN-ASSOCIATED GLYCOPROTEIN. It is expressed primarily by neurons in the brain and OLFACTORY BULBS. During embryonic development, it is expressed in the PERIPHERAL NERVOUS SYSTEM. It localizes to GROWTH CONES and may inhibit neurite outgrowth following SPINAL INJURY.

Tree locations:

Nogo Receptors D12.776.395.550.448.738.500
D12.776.543.484.500.738.500
D12.776.543.550.418.738.500
D12.776.543.750.600.500
D12.776.631.651.500

Nogo Receptor 2

A Nogo receptor that binds to MYELIN-ASSOCIATED GLYCOPROTEIN. It localizes to the GROWTH CONES of neurons in the THALAMUS; CORTEX: AMYGDALA; OLFACTORY BULBS; and HYPOTHALAMUS.

Tree locations:

Nogo Receptors D12.776.395.550.448.738.250
D12.776.543.484.500.738.250
D12.776.543.550.418.738.250
D12.776.543.750.600.250
D12.776.631.651.250

Nogo Receptors

GPI-linked proteins consisting of eight elongated leucine-rich repeats at their N-termini that are connected to the GPI by a "stalk" region rich in prolines, serines and threonines. They bind to NOGO PROTEIN; however, some Nogo receptors also bind MYELIN ASSOCIATED GLYCOPROTEIN and other cell surface glycoproteins. Interactions between nogo receptors and their ligands modulate nerve growth and NEURONAL PLASTICITY.

Tree locations:

GPI-Linked Proteins D12.776.395.550.448.738
D12.776.543.484.500.738
D12.776.543.550.418.738
Nerve Tissue Proteins D12.776.631.651
Receptors, Cell Surface D12.776.543.750.600

Non-Medical Public and Private Facilities

Spaces and needed equipment provided for a specific, non-medical function or service used by the public or specific group of persons.

**AN: used for searching; INDEXER: Do not use;
CATALOGER: Do not use**

Tree locations:

No Data Available

Non-Neuronal Cholinergic System

The system of ACETYLCHOLINE-synthesizing enzymes, transporters, receptors and degrading enzymes that characterize non-neuronal cholinergic cells such as airway and skin EPITHELIAL CELLS.

Tree locations:

Metabolic Networks and Pathways G03.493.628
Signal Transduction G02.111.820.690
G04.835.690

Non-ST Elevated Myocardial Infarction

A myocardial infarction that does not produce elevations in the ST segments of the ELECTROCARDIOGRAM. ST segment elevation of the ECG is often used in determining the treatment protocol (see also ST Elevation Myocardial Infarction).

Tree locations:

Myocardial Infarction C14.280.647.500.469
C14.907.585.500.656

Nuclear Pharmacy

An application of PHARMACY involving the preparation and dispensing of radioactive materials for use in medications.

Tree locations:

Pharmacy H02.646.250

Nucleons

Subatomic particles that are either protons or neutrons.

Tree locations:

Elementary Particles G01.249.660

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Nucleus Pulposus

Fibrocartilage inner core of the intervertebral disc. Prolapsed or bulged nucleus pulposus leads to INTERVERTEBRAL DISC DISPLACEMENT while proliferation of cells in the nucleus pulposus is associated with INTERVERTEBRAL DISC DEGENERATION.

Tree locations:

Intervertebral Disc A02.165.308.410.500
A02.835.232.834.432.500
A10.165.382.350.050.500

Nurse Specialists

Nursing professionals whose practice is limited to A particular area or discipline of medicine.

Tree locations:

Nurses M01.526.485.650.648
N02.360.650.648

Nurses, Neonatal

Qualified nursing professionals specializing in care of newborn infants.

Tree locations:

Nurses, Pediatric M01.526.485.650.648.940.500
N02.360.650.648.940.500

Nurses, Pediatric

Qualified nursing professionals specializing in the care of children from birth to adolescence.

Tree locations:

Nurse Specialists M01.526.485.650.648.940
N02.360.650.648.940

Occupational Therapists

Professionals trained to help individuals develop or regain skills needed to achieve independence in their lives.

Tree locations:

Health Personnel M01.526.485.710
N02.360.710

Ocimum sanctum

A plant species of the genus OCIMUM, family LAMIACEAE that has been used in TRADITIONAL MEDICINE.

Tree locations:

Ocimum B01.650.940.800.575.100.583.520.647.750

Oncologists

Physicians specializing in MEDICAL ONCOLOGY or its sub-specialties of RADIATION ONCOLOGY or SURGICAL ONCOLOGY.

Tree locations:

Physicians M01.526.485.810.699
N02.360.810.699

Oogonial Stem Cells

Primordial germ cells found in embryonic OOGONIA and postnatal OVARIES.

Tree locations:

Stem Cells A11.872.677

Open Fracture Reduction

Restoration of normal alignment of a fractured bone via an OPERATIVE SURGICAL PROCEDURE.

Tree locations:

Fracture Fixation E04.555.300.690

Ophthalmologists

Qualified medical professionals specializing in medical and surgical treatment of defects and diseases of the eye.

Tree locations:

Physicians M01.526.485.810.705
N02.360.810.705

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Optometrists

Qualified professionals trained in primary eye and vision care, including measurement of visual abilities, diagnosing disorders of the visual system and provision of treatment such as prescriptions for correction of visual defects with lenses or glasses and vision therapy.

Tree locations:

Health Personnel M01.526.485.725
N02.360.725

ORAI1 Protein

The pore-forming subunit of calcium release activated calcium channels. It is activated by STROMAL INTERACTION MOLECULE 1 upon intracellular calcium depletion.

Tree locations:

Calcium Release D12.776.157.530.400.150.740.500
Activated Calcium D12.776.543.550.450.150.740.500
Channels D12.776.543.585.400.150.740.500

ORAI2 Protein

A calcium release-activated calcium-like (CRAC-like) channel subunit which functions with STROMAL INTERACTION MOLECULE 1 to regulate cell calcium influx and increase (Ca²⁺)-selective current.

Tree locations:

Calcium Release D12.776.157.530.400.150.740.750
Activated Calcium D12.776.543.550.450.150.740.750
Channels D12.776.543.585.400.150.740.750

Orientation, Spatial

Change in position or alignment in response to an external stimulus.

Tree locations:

Orientation F01.058.577.500
F02.830.606.793
Spatial Behavior F01.145.875.439

Orthodontic Friction

Physical resistance to motion between dental surfaces.

Tree locations:

Biomechanical Phenomena G01.154.090.625

Orthopedic Surgeons

Physicians specializing in medical, surgical, and physical methods used to treat and correct deformities, diseases, and injuries to the skeletal system, its articulations, and associated structures.

Tree locations:

Surgeons M01.526.485.810.910.875
N02.360.810.910.875

Otolaryngologists

Physicians specializing in the treatment of disorders of the ear, nose, and throat.

Tree locations:

Physicians M01.526.485.810.734
N02.360.810.734

Oxygen Radical Absorbance Capacity

A measure of the ability of a substance, such as a food, to quench oxygen free radicals in vitro.

Tree locations:

Investigative Techniques E05.657

Oxysterols

Oxygenated derivatives of cholesterol or its sterol precursors. They are generated from sterol metabolism and the interaction of cholesterol with REACTIVE OXYGEN SPECIES.

Tree locations:

Cholesterol D04.210.500.247.222.284.800
D04.210.500.247.808.197.800
D10.570.938.208.825

Paenibacillus larvae

A species of Paenibacillus that causes American Foulbrood, a fatal disease of honeybees (APIS) and honeybee colonies.

Tree locations:

Paenibacillus B03.300.390.400.645.500
B03.353.500.645.500
B03.510.100.645.500
B03.510.415.400.645.500
B03.510.460.410.645.500

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Paenibacillus polymyxa

A species of Paenibacillus formerly classified as Bacillus polymyxa that occurs in marine sediments and soil, especially around plant roots and RHIZOMES where it performs NITROGEN FIXATION. It has activity against several species of pathogenic bacteria and produces POLYMYXINS.

Tree locations:

Nitrogen-Fixing Bacteria B03.585.860
Paenibacillus B03.300.390.400.645.750
B03.353.500.645.750
B03.510.100.645.750
B03.510.415.400.645.750
B03.510.460.410.645.750

Parenchymal Tissue

The tissue that constitutes the essential or functional part of an organ (e.g., parenchyma of lung, parenchyma of liver, or parenchyma of kidney).

AN: human and animal; PALISADE PARENCHYMA CELLS see MESOPHYLL CELLS is available for plants

Tree locations:

Tissues A10.806

Parkinson Disease Associated Proteins

Proteins associated with sporadic or familial cases of PARKINSON DISEASE.

Tree locations:

Proteins D12.776.637

Patched Receptors

A family of 12-pass transmembrane proteins originally identified in Drosophila that are receptors for HEDGEHOG PROTEINS. They have important roles in regulating CELL PROLIFERATION; CELL DIFFERENTIATION; and BODY PATTERNING and may also function as TUMOR SUPPRESSOR PROTEINS.

Tree locations:

Receptors, Cell Surface D12.776.543.750.058
Tumor Suppressor Proteins D12.776.624.776.633

Patched-1 Receptor

A patched receptor for several HEDGEHOG PROTEINS that associates with the SMOOTHENED RECEPTOR to modulate hedgehog signaling. It is also a TUMOR SUPPRESSOR PROTEIN; mutations in the patched-1 gene are associated with BASAL CELL NEVUS SYNDROME; SQUAMOUS CELL CARCINOMA of the ESOPHAGUS; trichoepitheliomas, and CARCINOMA, TRANSITIONAL CELL of the URINARY BLADDER.

Tree locations:

Patched Receptors D12.776.543.750.058.500
D12.776.624.776.633.500

Patched-2 Receptor

A patched receptor that may function redundantly with the PATCHED-1 RECEPTOR to modulate hedgehog signaling. It may also play a role in epidermal development and as a TUMOR SUPPRESSOR PROTEIN. Mutations in the patched-2 gene are associated with BASAL CELL NEVUS SYNDROME; CARCINOMA, BASAL CELL; and MEDULLOBLASTOMA.

Tree locations:

Patched Receptors D12.776.543.750.058.750
D12.776.624.776.633.750

Paternal Inheritance

A form of inheritance where the traits of the offspring are paternal in origin due to the expression of extra-nuclear genetic material such as MITOCHONDRIAL DNA or Y chromosome genes. CENTRIOLES are also paternally inherited.

Tree locations:

Inheritance Patterns G05.420.623

Pathologists

Physicians who assess changes in cellular or tissue structure and function to diagnose disease processes.

Tree locations:

Physicians M01.526.485.810.746
N02.360.810.746

Patient Comfort

Patient care intended to prevent or relieve suffering in conditions that ensure optimal quality living.

Tree locations:

Patient Care N02.421.585.683

Patient Portals

A secure online website that provides patients convenient 24-hour access to personal health information via an Internet connection.

Tree locations:

Electronic Health Records E05.318.308.940.968.249.500.500
Health Records, Personal E05.318.308.940.968.249.750

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Patient Reported Outcome Measures

Assessment of the quality and effectiveness of health care as measured and directly reported by the patient.

Tree locations:

Health Care Surveys E05.318.308.980.344.500
N03.349.380.210.750
N05.425.210.500
N05.715.360.300.800.344.500
N06.850.520.308.980.344.500

Patient Outcome Assessment N04.761.559.590.399.875
N05.715.360.575.575.399.875

PAX3 Transcription Factor

A paired box transcription factor that functions in CELL PROLIFERATION; CELL MIGRATION; and APOPTOSIS. It also is involved in MYOGENESIS and neural development. Mutations in the PAX3 gene are associated with WAARDENBURG SYNDROME TYPE 1.

Tree locations:

Paired Box Transcription Factors D12.776.260.645.782
D12.776.930.700.782

PAX6 Transcription Factor

A paired box transcription factor that has important functions in the development of the eye, nose, central nervous system and pancreas. Mutations in the PAX6 gene are associated with ocular disorders such as ANIRIDIA.

Tree locations:

Paired Box Transcription Factors D12.776.260.645.813
D12.776.930.700.813

PAX8 Transcription Factor

A paired box transcription factor that functions in the development of THYROCYTES and the control of thyroid-specific gene expression. Mutations in the PAX8 gene are associated with THYROID DYSGENESIS and THYROID NEOPLASMS.

Tree locations:

Paired Box Transcription Factors D12.776.260.645.906
D12.776.930.700.906

Pediatric Emergency Medicine

Branch of EMERGENCY MEDICINE dealing with the emergency care of children.

Tree locations:

Emergency Medicine H02.403.250.500
Pediatrics H02.403.670.450

Pediatricians

Qualified medical professionals specializing in maintaining health and providing medical care to children from birth through adolescence.

Tree locations:

Physicians M01.526.485.810.758
N02.360.810.758

Pediocins

Bacteriocins produced by species of PEDIOCOCCUS. They range from 3.5-4.6 kDa in mass, contain a conserved YGNGVXCXK motif and beta sheet at their N-terminals, and a more diverse hydrophobic or amphiphilic C-terminal alpha helical domain. They function as antimicrobial peptides against several pathogenic species of GRAM POSITIVE BACTERIA, including LISTERIA MONOCYTOGENES and are useful as FOOD PRESERVATIVES.

Tree locations:

Bacteriocins D12.776.097.151.743
D12.776.543.695.110.850

Pediococcus acidilactici

A species of *Pediococcus* that occurs in fermented foods where its ability to produce LACTIC ACID and PEDIOCINS makes it useful in FOOD PRESERVATION. It is also used as a PROBIOTIC.

Tree locations:

Pediococcus B03.353.750.450.737.500
B03.510.550.450.737.500

Pediococcus pentosaceus

A species of *Pediococcus* that occurs in fermented foods where its ability to produce LACTIC ACID and PEDIOCINS make it useful as a FOOD PRESERVATION agent. It is also used as a PROBIOTIC.

Tree locations:

Pediococcus B03.353.750.450.737.750
B03.510.550.450.737.750

Peptidyl-Prolyl Cis-Trans Isomerase NIMA-Interacting 4

A NIMA-interacting peptidylprolyl isomerase. It binds to double-stranded DNA and functions in the biogenesis of RIBOSOMES.

Tree locations:

DNA-Binding Proteins D12.776.260.650
Peptidylprolyl Isomerase D08.811.399.325.500.850

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Perfectionism

A personality trait characterized by a person's striving for flawlessness and setting excessively high performance standards, accompanied by overly critical self-evaluations and concerns regarding others' evaluations.

Tree locations:

Personality F01.752.823

Perilipin-1

A lipid droplet protein that is expressed primarily by ADIPOCYTES of WHITE ADIPOSE TISSUE and BROWN ADIPOSE TISSUE. It co-localizes with MACROPHAGES and FOAM CELLS of atherosclerotic lesions and stabilizes LIPID DROPLETS by inhibiting HORMONE SENSITIVE LIPASE. It may also protect TRIGLYCERIDES against hydrolysis within the PLASMA MEMBRANE and modulate CHOLESTEROL ESTER HYDROLASE activity.

Tree locations:

Perilipins D12.776.157.464.500.500

Perilipin-2

A perilipin that is expressed by many different cell types. It binds FATTY ACIDS and CHOLESTEROL, stabilizes TRIGLYCERIDES, and localizes to both the surface and hydrophobic core of LIPID DROPLETS, as well as the ENDOPLASMIC RECTICULUM and PLASMA MEMBRANE in MACROPHAGES. It also plays a central role in the biogenesis of lipid droplets and FOAM CELLS and is highly expressed by macrophages at atherosclerotic lesions in human arteries along with the INFLAMMATION markers TNF-ALPHA; MCP-1 RECEPTOR; and IL-6.

Tree locations:

Perilipins D12.776.157.464.500.750

Perilipin-3

A perilipin that localizes to LIPID DROPLETS; CYTOPLASM; ENDOSOMES; and PLASMA MEMBRANE, especially in MACROPHAGES. It functions as a transporter of free fatty acids to lipid droplets to promote their biogenesis and growth. It is also required for the transport of the MANNOSE-6-PHOSPHATE RECEPTOR from endosomes to the TRANS-GOLGI NETWORK. Its structure consists of four helix bundles that interact with the hydrophobic lipid droplet surface.

Tree locations:

Perilipins D12.776.157.464.500.875

Perilipin-4

A perilipin protein characterized by an extensive 11-mer repeat region, which forms five adjacent alpha-helices. It is expressed primarily in WHITE ADIPOSE TISSUE and differentiating ADIPOCYTES, as well as skeletal muscle and heart. It is soluble in the cytoplasm but re-localizes to the surface of LIPID DROPLETS under high lipid conditions.

Tree locations:

Perilipins D12.776.157.464.500.906

Perilipin-5

A perilipin that functions in LIPOGENESIS; LIPOLYSIS; and fatty acid oxidation in BROWN ADIPOSE TISSUE; heart, liver, and skeletal muscle. It recruits MITOCHONDRIA to the surface of LIPID DROPLETS where it functions in both the storage of fatty acids as TRIGLYCERIDES, and their release for mitochondrial fatty acid oxidation in response to metabolic needs.

Tree locations:

Perilipins D12.776.157.464.500.937

Perilipins

A family of vertebrate and insect lipid droplet associated proteins. They consist of a conserved N-terminal PAT domain (an alpha-helical region of about 110 amino acids), an 11-mer repeat region, and lipid-binding hydrophobic regions or 4-helix bundles near their C-termini. Perilipins transiently or constitutively localize to LIPID DROPLETS in ADIPOCYTES and FOAM CELLS, especially in regions adjacent to the PLASMA MEMBRANE and ENDOPLASMIC RECTICULUM. They are critical for lipid droplet synthesis and homeostasis as well as the regulation of lipid metabolism. Genetic variations in perilipins are associated with ATHEROSCLEROSIS; OBESITY; and DIABETES MELLITUS.

Tree locations:

Lipid Droplet Associated Proteins D12.776.157.464.500

Peripheral Blood Stem Cells

Hematopoietic stem cells found in peripheral blood circulation.

Tree locations:

Hematopoietic Stem Cells A11.872.378.795

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Perirhinal Cortex

An area in the temporal lobe that is important for memory encoding and retrieval. It is bordered caudally by the parahippocampal cortex (see HIPPOCAMPUS) and ventrally and medially by the ENTORHINAL CORTEX.

Tree locations:

Temporal Lobe A08.186.211.730.885.287.500.863.574

Peroxisome Proliferator-Activated Receptor Gamma Coactivator 1-alpha

A transcriptional co-activator for NUCLEAR RECEPTORS. It is characterized by an N-terminal LxxLL sequence, a region that interacts with PPAR GAMMA, and a C-terminal RNA RECOGNITION MOTIF. It increases expression of MITOCHONDRIAL UNCOUPLING PROTEIN to regulate genes involved in metabolic reprogramming in response to dietary restriction and the integration of CIRCADIAN RHYTHMS with ENERGY METABOLISM.

Tree locations:

Nuclear Receptor Coactivators D12.644.360.024.314.650
D12.776.157.057.080.650
D12.776.476.024.394.650
D12.776.660.675.650
D12.776.930.617.650
RNA Recognition Motif Proteins D12.776.157.725.813.875
D12.776.664.962.813.875

Phage Therapy

Therapeutic use of BACTERIOPHAGES to treat diseases.

Tree locations:

Biological Therapy E02.095.841

Pharmaceutical Research

RESEARCH activity focused on pharmaceutical products and services.

AN: pharmaceutical research as a field or the progress or status of pharmaceutical research; do not add routinely for specific pharmaceutical research studies; do not confuse with PHARMACY RESEARCH

Tree locations:

Biomedical Research H01.770.644.145.442

Pharmacogenomic Testing

The detection of genetic variability (e.g., PHARMACOGENOMIC VARIANTS) relevant to PHARMACOGENETICS and PRECISION MEDICINE. The purpose of such genetic testing is to help determine the most effective treatment options and their optimum dosages with least potential risks for DRUG-RELATED SIDE EFFECTS AND ADVERSE REACTIONS.

Tree locations:

Genetic Testing E01.370.225.562.500
E05.200.562.500
E05.393.435.500
N02.421.308.430.500
N02.421.726.233.221.500

Pharmacogenomic Variants

Naturally occurring genetic variations associated with drug response (e.g., dosage, extent and rate of metabolic processes). While these variants are not markers for GENETIC PREDISPOSITION TO DISEASE they influence PHARMACOKINETICS and pharmacodynamics and often occur on genes encoding drug metabolism enzymes and transporters (e.g., ANGIOTENSIN CONVERTING ENZYME; CYTOCHROME P-450 CYP2D6).

Tree locations:

Polymorphism, Genetic G05.365.795.446

Pharmacy Research

RESEARCH activity focused on PHARMACY.

AN: pharmacy research as a field or the progress or status of pharmacy research; do not add routinely for specific pharmacy research studies; do not confuse with PHARMACEUTICAL RESEARCH

Tree locations:

Biomedical Research H01.770.644.145.452
Pharmacy H02.646.375

Phobia, Social

Anxiety disorder characterized by the persistent and irrational fear, anxiety, or avoidance of social or performance situations.

Tree locations:

Phobic Disorders F03.080.725.500

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Phosphatidylinositol-3,4,5-Trisphosphate 5-Phosphatases

Phosphoinositide phosphatases that catalyze the dephosphorylation (hydrolysis) of phosphatidylinositol-3,4,5-trisphosphate (PtdIns(3,4,5)P(3)) to produce PtdIns(3,4)P(2), which negatively regulates the PI3K (3-PHOSPHOINOSITIDE-DEPENDENT PROTEIN KINASES) pathways. They contain an SH2 DOMAIN and STERILE ALPHA MOTIF and have important functions in regulating the immune response and other cellular processes in vertebrates.

Tree locations:

Phosphoinositide D08.811.277.352.650.624.750
Phosphatases

Phototaxis

A behavioral change that results in an organism moving or orienting toward or away from the light source.

Tree locations:

Taxis Response F01.145.113.780.875
F01.145.875.439.500.875
G07.568.500.590.875
G11.427.410.568.850.875

Pilots

Persons skilled and/or qualified to operate an aircraft or ship.

Tree locations:

Occupational Groups M01.526.727

Placenta Growth Factor

An angiogenic protein belonging to the Vascular Endothelial Growth Factor family of growth factors originally isolated and cloned from human placental cDNA library. There are four isoforms of PLGF 1-4 which result from alternative splicing. Placenta Growth Factor is secreted as a glycosylated homodimer which acts as a mitogen for endothelial cells, and its expression is markedly upregulated during hypoxia and in tissue inflammation and cancer.

Tree locations:

Pregnancy Proteins D12.776.780.551
Vascular Endothelial Growth Factors D12.644.276.100.800.100

Pneumonia, Necrotizing

Severe complication of pneumonia characterized by liquefaction of lung tissue.

Tree locations:

Pneumonia C08.381.677.608
C08.730.610.608

Phosphoinositide Phosphatases

Phosphatases that catalyze the hydrolysis of phosphate groups on PHOSPHATIDYLINOSITOLS.

Tree locations:

Phosphoric Monoester Hydrolases D08.811.277.352.650.624

Physiatrists

Physicians specializing in treating physical disorders and injuries affecting the brain, spinal cord, nerves, bones, joints, ligaments, muscles, and tendons.

Tree locations:

Physicians M01.526.485.810.764
N02.360.810.764

Place Cells

Pyramidal neurons in the HIPPOCAMPUS that play a role in cognitive representation of a specific location within a space.

Tree locations:

Pyramidal Cells A08.675.790.500
A11.671.790.500

Pleckstrin Homology Domains

Protein domains of approximately 120 amino acids that form two perpendicular anti-parallel beta sheets connected by a loop of variable length and a C-terminal amphipathic helix. PH domains occur in many INTRACELLULAR SIGNALING PROTEINS and CYTOSKELETAL PROTEINS where they bind PHOSPHATIDYLINOSITOLS within the CELL MEMBRANE and INTRACELLULAR MEMBRANES, as well as proteins that include the Betagamma-subunits of HETEROTRIMERIC GTP-BINDING PROTEINS, and PROTEIN KINASE C. These interactions allow the targeting of proteins to different cellular compartments and SIGNAL TRANSDUCTION PATHWAYS.

Tree locations:

Protein Domains G02.111.570.820.709.275.750.469

Pogostemon

Genus in the Lamiaceae family. VOLATILE OILS from several species of Pogostemon are used in PERFUME; INSECT REPELLENTS; and ALTERNATIVE THERAPIES.

Tree locations:

Lamiaceae B01.650.940.800.575.100.583.520.754

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Poly (ADP-Ribose) Polymerase-1

A poly(ADP-ribose) polymerase that contains two ZINC FINGERS in its N-terminal DNA-binding region. It modifies NUCLEAR PROTEINS involved in chromatin architecture and BASE EXCISION REPAIR with POLY ADENOSINE DIPHOSPHATE RIBOSE.

Tree locations:

Poly(ADP-ribose) D08.811.913.400.725.115.690.420
Polymerases

Polyelectrolytes

Naturally-occurring or artificially made water-soluble POLYMERS whose repeating units are ionizable. Polyelectrolytes demonstrate attributes that are typical of salts, such as electrical conductivity, and typical of polymers, such as viscosity.

Tree locations:

Electrolytes D01.248.249
Polymers D05.750.230

Postcards as Topic

Works about cards on which a message may be written or printed for mailing without an envelope. Art & Architectural Thesaurus Online

www.getty.edu/research/conducting_research/vocabularies/aat/
accessed 12/18/2008

AN: do not confuse with Publication Type POSTCARDS

Tree locations:

Correspondence as Topic L01.143.506.423.906.377.500
Information Science L01.731

Prion Proteins

Membrane glycosylphosphatidylinositol-anchored glycoproteins that may aggregate into rod-like structures. The prion protein (PRNP) gene is characterized by five TANDEM REPEAT SEQUENCES that encode a highly unstable protein region of five octapeptide repeats. Mutations in the repeat region and elsewhere in this gene are associated with CREUTZFELDT-JAKOB DISEASE; FATAL FAMILIAL INSOMNIA; GERSTMANN-STRAUSSLER DISEASE; Huntington disease-like 1, and KURU.

Tree locations:

Antigens, CD D23.050.301.264.035.534
D23.101.100.110.534
GPI-Linked Proteins D12.776.395.550.448.600
D12.776.543.484.500.625
D12.776.543.550.418.600
Prions D12.776.785.340

Polychlorinated Dibenzodioxins

Dibenzodioxin derivatives that contain multiple chloride atoms bound to the benzene ring structures.

Tree locations:

Dioxins D02.309.500.450
Heterocyclic Compounds, 3-Ring D03.633.300.786

Positron Emission Tomography Computed Tomography

An imaging technique that combines a POSITRON-EMISSION TOMOGRAPHY (PET) scanner and a CT X RAY scanner. This establishes a precise anatomic localization in the same session.

Tree locations:

Multimodal Imaging E01.370.350.567.500
Positron-Emission E01.370.350.350.800.700.500
Tomography E01.370.350.600.350.800.399.500
E01.370.350.710.800.399.500
E01.370.350.825.800.399.500
E01.370.384.730.800.399.500
Tomography, X-Ray E01.370.350.350.810.645
Computed E01.370.350.600.350.700.810.490
E01.370.350.700.700.810.645
E01.370.350.700.810.810.723
E01.370.350.825.810.810.700

Posterior Cruciate Ligament Reconstruction

Rebuilding of the POSTERIOR CRUCIATE LIGAMENT to restore functional stability of the knee.

Tree locations:

Arthroplasty E04.555.110.557
E04.680.101.557
Orthopedic Procedures E02.718.688

Private Facilities

Places designed, built, or installed to provide for a specific, non-medical function or service used by a specific, restricted group of persons.

AN: do not add as a coordinate with a specific facility unless the private aspect is emphasized

Tree locations:

Non-Medical Public and Private Facilities J03.700

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Professional Practice Gaps

Difference between observed and ideal DELIVERY OF HEALTH CARE and healthcare outcomes that reflect the current state of knowledge.

Tree locations:

Delivery of Health Care N04.590.374.650
N05.300.643

Promyelocytic Leukemia Protein

A tripartite motif protein that contains three ZINC FINGERS, including a RING FINGER DOMAIN, at its N-terminal. Several nuclear and one cytoplasmic isoforms result from alternative splicing of the PML gene; most nuclear isoforms localize to subnuclear structures (PML nuclear bodies) that are disrupted in ACUTE PROMYELOCYTIC LEUKEMIA cells.

Tree locations:

Nuclear Proteins D12.776.660.745
Transcription Factors D12.776.930.713
Tripartite Motif Proteins D12.776.934.500
Tumor Suppressor Proteins D12.776.624.776.654

Prophylactic Mastectomy

Surgical removal of one or both breasts to prevent or reduce the risk of developing breast cancer in persons who may be predisposed.

Tree locations:

Mastectomy E04.466.911
Prophylactic Surgical Procedures E04.625.500

Propionibacterium freudenreichii

A species of Propionibacterium that occurs in raw milk and cheese. It produces ANTI-INFECTIVE AGENTS and ANTI-INFLAMMATORY AGENTS and is used as a PROBIOTIC.

Tree locations:

Propionibacterium B03.510.024.049.600.600.800
B03.510.460.400.400.600.600.800

Propofol Infusion Syndrome

Rare and often fatal drug complication which affects patients undergoing long-term treatment with high doses of PROPOFOL. It is characterized by METABOLIC ACIDOSIS; HYPERLIPIDEMIA; RHABDOMYOLYSIS; cardiovascular CIRCULATORY COLLAPSE; CARDIAC FAILURE; and KIDNEY FAILURE.

Tree locations:

Drug-Related Side Effects and Adverse Reactions C25.100.844

Proprotein Convertase 9

A proprotein convertase that is essential for CHOLESTEROL homeostasis. It binds to and is required for the lysosomal degradation of the LDL RECEPTOR (LDLR); the VLDL receptor, and the APOLIPOPROTEIN E RECEPTOR. It also regulates neuronal APOPTOSIS.

Tree locations:

Proprotein Convertases D08.811.277.656.837.688
Serine Endopeptidases D08.811.277.656.300.760.718
D08.811.277.656.959.350.718

Prostaglandin-E Synthases

Oxidoreductases that catalyze the GLUTATHIONE-dependent oxidation of PROSTAGLANDIN H2 to PROSTAGLANDIN E2.

Tree locations:

Intramolecular Oxidoreductases D08.811.399.475.600

Protein Conformation, alpha-Helical

A secondary structure of proteins that is a right-handed helix or coil, where each amino (N-H) group of the peptide backbone contributes a hydrogen bond to the carbonyl(C=O) group of the amino acid four residues N-terminal to it (n-4). It is the most common type of secondary structure.

AN: *IM general only; coordinate NIM with specific protein*

Tree locations:

Protein Structure, Secondary G02.111.570.820.709.600.020

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Protein Conformation, beta-Strand

A secondary structure of proteins where the amino (N-H) groups of a polypeptide backbone, three to ten amino acids in length, establish hydrogen bonds with the carbonyl (C=O) groups in the backbone of adjacent strands. These may form a beta-sheet, where the side chains of the adjacent strands point in the same direction.

AN: *IM general only; coordinate NIM with specific protein*

Tree locations:

Protein Structure, Secondary G02.111.570.820.709.600.750

Protein Deglycase DJ-1

A protein deglycase that repairs methylglyoxal- and glyoxal-glycated amino acids and proteins, releasing repaired proteins and lactate or glycolate. It deglycates CYSTEINE, ARGININE and LYSINE residues to reactivate proteins by reversing glycation and prevent the formation of ADVANCED GLYCATION END PRODUCTS. It protects cells against OXIDATIVE STRESS and CELL DEATH by functioning as an oxidative stress sensor and redox-sensitive MOLECULAR CHAPERONE and PROTEASE. Mutations in the PARK7 gene are associated with autosomal-recessive, early-onset PARKINSON DISEASE.

Tree locations:

Hydrolases D08.811.277.785
Parkinson Disease Associated Proteins D12.776.637.875

Protein Domains

Discrete protein structural units that may fold independently of the rest of the protein and have their own functions.

Tree locations:

Protein Structural Elements G02.111.570.820.709.275.750
Protein Structure, Tertiary G02.111.570.820.709.610.500

Protein Phosphatase 2C

One of four major classes of mammalian serine/threonine specific protein phosphatases. Protein phosphatase 2C is a monomeric enzyme about 42 kDa in size. It shows broad substrate specificity dependent on divalent cations (mainly manganese and magnesium). Three isozymes are known in mammals: PP2C -alpha, -beta and -gamma. In yeast, there are four PP2C homologues: phosphatase PTC1 that have weak tyrosine phosphatase activity, phosphatase PTC2, phosphatase PTC3, and PTC4. Isozymes of PP2C also occur in Arabidopsis thaliana where the kinase-associated protein phosphatase (KAPP) containing a C-terminal PP2C domain, dephosphorylates Ser/Thr receptor-like kinase RLK5.

Tree locations:

Phosphoprotein D08.811.277.352.650.625.716
Phosphatases

Protein Structural Elements

Distinguishing three-dimensional structures characteristically formed by homologous protein sequences.

Tree locations:

Protein Conformation G02.111.570.820.709.275

Proteogenomics

The systematic study of annotated genomic information to global protein expression in order to determine the relationship between genomic sequences and both expressed proteins and predicted protein sequences.

Tree locations:

Proteomics H01.158.201.843.500
H01.158.273.180.350.700.500
H01.158.273.343.350.700.500
H01.181.122.738.500

Provitamins

Precursor forms of vitamins.

Tree locations:

Vitamins D27.505.696.377.605.600.354
G07.203.300.631.600.500
J02.500.631.600.500

Psacalium

A genus of the Asteraceae family. Several of its species are used in TRADITIONAL MEDICINE.

Tree locations:

Asteraceae B01.650.940.800.575.100.100.605

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Pseudoautosomal Regions

Homologous chromosomal regions at either end of the X CHROMOSOME or Y CHROMOSOME. These two regions pair regularly at male MEIOSIS and undergo RECOMBINATION. Pseudoautosomal region 1 (PAR1) is located at the tip of the short 'p' arms (Xp22 and Yp11) and Pseudoautosomal region 2 (PAR2) is located at the tip of the long 'q' arms (Xq28 and Yq12).

Tree locations:

Genetic Loci G05.360.340.024.380.906
Sex Chromosomes A11.284.187.865.400
G05.360.162.865.400

Psychosocial Support Systems

Organized efforts to address ongoing psychological and social problems of individuals, their partners, families and caregivers.

Tree locations:

Social Support I01.880.853.500.600.500

Public Health Systems Research

A field of study that examines the organization, financing, and delivery of public health services within communities, and the impact of these services on public health.

Tree locations:

Health Care Quality, Access, and Evaluation N05.632
Research H01.770.644.608

Punctal Plugs

Small devices that are inserted into the tear ducts (NASOLACRIMAL DUCTS). They are used to block the drainage of TEARS for the treatment of DRY EYE SYNDROMES.

Tree locations:

Prostheses and Implants E07.695.698

Pseudomonas chlororaphis

A non-pathogenic species of Pseudomonas that occurs in soil, especially in the RHIZOSPHERE surrounding plant roots, as well as on the leaves of plants. It has anti-fungal and anti-nematode activities and is used in agriculture as a biocontrol agent.

Tree locations:

Pseudomonas B03.440.400.425.625.223
B03.660.250.580.590.140

PTB-Associated Splicing Factor

An RNA splicing factor that also binds DNA. It is essential for pre-mRNA splicing in the formation of early SPLICEOSOMES and catalytic step II. It binds specifically to polypyrimidine tracts in INTRONS and is involved in the regulation of ALTERNATIVE SPLICING by SIGNAL TRANSDUCTION PATHWAYS.

Tree locations:

DNA-Binding Proteins D12.776.260.693
RNA Splicing Factors D12.776.157.725.829.282
D12.776.664.962.829.282

Pulmonologists

Physicians who specialize in treating disorders of the RESPIRATORY SYSTEM, especially diagnosing and treating diseases and defects of the lungs and bronchial tree.

Tree locations:

Physicians M01.526.485.810.865
N02.360.810.865

Pyrin

A tripartite motif protein that consists of an N-terminal pyrin domain, a central coiled-coil region and B-box type ZINC FINGER, and C-terminal regions that mediate homotrimerization and interactions with other proteins (the B30.2/SPRY DOMAIN). It is expressed primarily by mature GRANULOCYTES and associates with the cytoskeleton in the perinuclear area as well as AUTOPHAGOSOMES, where it co-ordinates the assembly of AUTOPHAGY-RELATED PROTEINS and degradation of INFLAMMASOME components. It functions in INNATE IMMUNITY and INFLAMMATION; mutations in the Pyrin protein (MEFV) gene are associated with FAMILIAL MEDITERRANEAN FEVER.

Tree locations:

Cytoskeletal Proteins D12.776.220.909
Tripartite Motif Proteins D12.776.934.750

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Pyrin Domain

A protein interaction domain of the death domain superfamily. It is characterized by a 6-helix bundle similar to those that occur in DEATH DOMAIN RECEPTORS. Pyrin domains are present in a variety of proteins, especially those that function in INFLAMMASOMES; AUTOPHAGY; and APOPTOSIS. They form homodimers or heterodimers with death domain proteins to facilitate the assembly of signaling complexes.

Tree locations:

Death Domain G02.111.570.820.709.275.750.500.395.875
Superfamily

Radiation Oncologists

Physicians specializing in the treatment of cancer by RADIOTHERAPY.

Tree locations:

Oncologists M01.526.485.810.699.500
N02.360.810.699.500
Radiologists M01.526.485.810.877.500
N02.360.810.877.500

Radiologists

Physicians specializing in the use of x-ray and other forms of radiant energy to diagnosis and treatment of disease.

Tree locations:

Physicians M01.526.485.810.877
N02.360.810.877

Regulatory Factor X Transcription Factors

A family of eukaryotic transcription factors that recognize and bind to a highly-conserved cis-regulatory sequence (X-box) within the promoter region of MHC CLASS II GENES. They contain a conserved winged-helix DNA binding domain and function as homo or heterodimers.

Tree locations:

Winged-Helix Transcription Factors D12.776.260.950.624
D12.776.930.977.624

Retinoic Acid 4-Hydroxylase

A cytochrome P450 enzyme that resides in the ENDOPLASMIC RETICULUM. It catalyzes the conversion of trans-RETINOIC ACID to 4-hydroxyretinoic acid.

Tree locations:

Cytochrome P450 Family D08.244.453.498.500
26 D08.811.682.690.708.170.485.500
D12.776.422.220.453.498.500

Radiation Dosimeters

Devices that measure exposure to IONIZING RADIATION.

Tree locations:

Radiation Equipment and Supplies E07.710.725

Radiologic and Imaging Nursing

A nursing specialty that deals specifically with the care of patients undergoing diagnostic, neurological, cardiovascular, interventional, ultrasonography, computerized tomography, nuclear medicine, magnetic resonance, radiation oncology or other related procedures .

Tree locations:

Specialties, Nursing H02.478.676.772

Receptor, Notch3

A notch receptor characterized by a large extracellular domain containing 34 EPIDERMAL GROWTH FACTOR-like repeats. It functions to regulate CELL DIFFERENTIATION; APOPTOSIS; and CELL PROLIFERATION. Mutations in the EGF repeats of Notch-3 are associated with CADASIL.

Tree locations:

Receptors, Notch D12.776.543.750.725.875
D12.776.930.770.875

Regulatory Factor X1

A regulatory factor X transcription factor that is required for the expression of MHC CLASS II GENES. It also binds to inverted repeats of HEPATITIS B VIRUS DNA and is required for viral gene expression. RFX1 functions as a monomer or heterodimer with other RFX transcription factors.

Tree locations:

Regulatory Factor X Transcription Factors D12.776.260.950.624.500
D12.776.930.977.624.500

Retinoic Acid Receptor alpha

A nuclear receptor protein which in humans is encoded by the RARA gene. It belongs to a family of transcription regulators of ligand-responsive regulatory proteins which include steroid hormone receptors. In addition to a C-terminal ligand-binding domain, these nuclear receptors contain a highly-conserved N-terminal zinc-finger domain that mediates binding ligand-responsive elements.

Tree locations:

Receptors, Retinoic Acid D12.776.826.701.250
D12.776.930.775.250

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Rheumatologists

Physicians who specialize in treating RHEUMATIC DISEASES.

Tree locations:

Physicians M01.526.485.810.888
N02.360.810.888

Rib Cage

The bony thoracic enclosure consisting of the vertebral column; the RIBS; the STERNUM; and the COSTAL CARTILAGE.

Tree locations:

Bone and Bones A02.835.232.570

RNA Recognition Motif

An approximately 80 amino acid RNA binding motif that consists of four anti-parallel surface beta sheets and two alpha helices arranged in a beta-alpha-beta-beta-alpha-beta configuration. One of the surface beta sheets interacts with two or three specific RNA bases. Interactions between additional sequences and the RNA, as well as within the RNA recognition motif increase the affinity and specificity of the protein-RNA interaction.

Tree locations:

RNA-Binding Motifs G02.111.570.820.709.275.500.869.500

RNA Splicing Factors

RNA-binding proteins that facilitate or inhibit RNA SPLICING.

Tree locations:

RNA-Binding Proteins D12.776.157.725.829
D12.776.664.962.829

RNA-Binding Motifs

Amino acid motifs that bind RNA.

Tree locations:

Amino Acid Motifs G02.111.570.820.709.275.500.869

Rotator Cuff Injuries

Injuries to the ROTATOR CUFF of the shoulder joint.

Tree locations:

Rupture C26.761.340
Shoulder Injuries C26.803.063
Tendon Injuries C26.874.400

Rotator Cuff Tear Arthropathy

Rapidly destructive shoulder joint and bone disease found mainly in elderly, and predominantly in women. It is characterized by SHOULDER PAIN; JOINT INSTABILITY; and the presence of crystalline CALCIUM PHOSPHATES in the SYNOVIAL FLUID. It is associated with ROTATOR CUFF INJURIES.

Tree locations:

Chondrocalcinosis C05.550.114.264.500
Crystal Arthropathies C05.550.354.250

S100 Calcium-Binding Protein A4

An S100 protein characterized by four helix bundles that form N- and C-terminal EF HAND MOTIFS. It functions as a homodimer and interacts with both intracellular and extracellular signaling proteins. Aberrant S100A4 activity is associated with NEOPLASM METASTASIS; FIBROSIS; and RHEUMATOID ARTHRITIS.

Tree locations:

S100 Proteins D12.776.157.125.750.813

Saccharomyces boulardii

A species of Saccharomyces that is used as a PROBIOTIC, such as in the treatment of DIARRHEA and PSEUDOMEMBRANOUS ENTEROCOLITIS associated with CLOSTRIDIUM INFECTIONS.

Tree locations:

Saccharomyces B01.300.107.795.785.400
B01.300.930.705.328

Salter-Harris Fractures

Fractures involving a GROWTH PLATE.

Tree locations:

Fracture Dislocation C05.116.359.336.875
C26.289.336.875
C26.404.026.500

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

School Teachers

Members of staff responsible for TEACHING students in a school from pre-kindergarten through twelfth grade.

Tree locations:

Educational Personnel M01.526.702.500

SEC Translocation Channels

Multiprotein complexes found in bacteria, archaea, and eukaryotes that form protein transport channels of the SEC pathway.

Tree locations:

Membrane Transport Proteins D12.776.157.530.875
D12.776.543.585.875
Protein Translocation Systems D05.500.890.625

Sentinel Lymph Node

First lymph node to receive drainage from the primary tumor. SENTINEL LYMPH NODE BIOPSY is performed to determine early METASTASIS status because cancer cells may appear first in the sentinel node.

Tree locations:

Lymph Nodes A10.549.400.750
A15.382.520.604.412.750

Sentinel Species

Organisms used to determine measurable environmental risks or hazards to human health and or well-being, thereby serving as advance or early warning signs of impending danger to humans. Examples of sentinel species are monkeys, guinea pigs, and the fabled canary in the coal mine.

Tree locations:

Organism Forms B05.698

Sequestosome-1 Protein

A multidomain protein that is highly conserved among multicellular organisms. It contains a ZZ-type ZINC FINGER domain, C-terminal UBIQUITIN - associated (UBA) domain, and interacts with many other signaling proteins and enzymes including, atypical PROTEIN KINASE C; TNF RECEPTOR-ASSOCIATED FACTOR 6; subunits of the mTORC1 complex, and CASPASE-8. It functions in AUTOPHAGY as a receptor for the degradation of ubiquitinated substrates, and to co-ordinate signaling in response to OXIDATIVE STRESS.

Tree locations:

Adaptor Proteins, Signal Transducing D12.644.360.024.329
D12.776.157.057.160
D12.776.476.024.422
Autophagy-Related Proteins D12.776.094.750

Serrate-Jagged Proteins

Cell surface proteins that consist of multiple extracellular EPIDERMAL GROWTH FACTOR - like repeat sequences (EGF repeats), including calcium-binding EGF repeats. They function as transmembrane ligands for NOTCH RECEPTORS to control CELL DIFFERENTIATION during development.

Tree locations:

Calcium-Binding Proteins D12.776.157.125.797
Intercellular Signaling Peptides and D12.644.276.930
Proteins D23.529.930
Membrane Proteins D12.776.543.800

Sexual Minorities

Individuals including lesbian, gay, bisexual, transgender, queer, intersex, gender non-conforming people, and other populations whose sexual orientation or GENDER IDENTITY and reproductive development is considered outside cultural, societal, or physiological norms.

Tree locations:

Persons M01.777

Shoulder Injuries

Injuries involving the SHOULDERS.

Tree locations:

Wounds and Injuries C26.803

Shoulder Prosthesis

Replacement for a SHOULDER JOINT.

Tree locations:

Joint Prosthesis E07.695.400.852

Signaling Lymphocytic Activation Molecule Associated Protein

A signal transducing adaptor protein that contains a single SH2 DOMAIN and is essential for the regulation of SLAM FAMILY RECEPTORS in the immune response. Mutations in the SLAM-associated protein gene have been identified in cases of X-LINKED LYMPHOPROLIFERATIVE DISEASE.

Tree locations:

Adaptor Proteins, Signal Transducing D12.644.360.024.332
D12.776.157.057.166
D12.776.476.024.426

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Signaling Lymphocytic Activation Molecule Family

Type-I membrane glycoproteins that are expressed primarily on the surface of CD4 or CD8-positive T-CELLS; NATURAL KILLER CELLS; and some populations of B CELLS. They are characterized by an N-terminal, extracellular IMMUNOGLOBULIN-LIKE DOMAIN and a membrane-proximal IMMUNOGLOBULIN C2-SET DOMAIN. SLAMF receptors typically signal through homophilic interactions and are important for mediating the immune response and immune cell differentiation.

Tree locations:

Antigens, CD	D23.050.301.264.035.915
	D23.101.100.110.935
Membrane Glycoproteins	D12.776.395.550.736
	D12.776.543.550.746
Receptors, Immunologic	D12.776.543.750.705.970

Signaling Lymphocytic Activation Molecule Family Member 1

A 70-kDa SLAM family receptor that consists of an extracellular IMMUNOGLOBULIN-LIKE DOMAIN and an IMMUNOGLOBULIN C2-SET DOMAIN. It is expressed primarily by THYMOCYTES and activated T-LYMPHOCYTES, as well as by MACROPHAGES and DENDRITIC CELLS. It binds SLAMF1 receptors on other cells to mediate T-cell maturation and proliferation. It is also a receptor for the MEASLES VIRUS.

Tree locations:

Signaling Lymphocytic	D12.776.395.550.736.500
Activation Molecule Family	D12.776.543.550.746.500
	D12.776.543.750.705.970.500
	D23.050.301.264.035.915.500
	D23.101.100.110.935.500

Simplified Acute Physiology Score

A severity of disease classification system designed to measure the severity of disease for patients aged 15 and over admitted to intensive care units.

Tree locations:

Severity of	E05.318.308.980.438.475.456.500.750
Illness Index	L01.280.960.500.475.456.500.750
	N05.715.360.300.800.438.375.364.500.750
	N06.850.520.308.980.438.475.364.500.750

Single Molecule Imaging

High resolution imaging techniques that allow visualization of individual molecules of proteins, lipids, or nucleic acids within cells or tissues.

Tree locations:

Microscopy	E01.370.350.515.899
	E05.595.899
Molecular Imaging	E01.370.350.557.750
	E05.601.555.500

Single Photon Emission Computed Tomography Computed Tomography

An imaging technique using a device which combines TOMOGRAPHY, EMISSION-COMPUTED, SINGLE-PHOTON and TOMOGRAPHY, X-RAY COMPUTED in the same session.

Tree locations:

Multimodal Imaging	E01.370.350.567.750
Tomography, Emission-	E01.370.350.350.800.800.750
Computed, Single-Photon	E01.370.350.600.350.800.800.500
	E01.370.350.710.800.800.750
	E01.370.350.825.800.800.750
	E01.370.384.730.800.800.750
Tomography, X-Ray	E01.370.350.350.810.723
Computed	E01.370.350.600.350.700.810.645
	E01.370.350.700.700.810.723
	E01.370.350.700.810.810.762
	E01.370.350.825.810.810.750

Single-Balloon Enteroscopy

A balloon-assisted enteroscopy utilizing a flexible endoscope with one overtube balloon control unit.

Tree locations:

Balloon Enteroscopy	E01.370.372.250.250.100.750
	E01.370.388.250.250.070.750
	E04.210.240.250.080.750
	E04.502.250.250.250.080.500

Sleep Hygiene

Habits and practices conducive to getting the right amount and quality of sleep, and include responding to environmental factors that may influence one's sleep.

Tree locations:

Health Behavior	F01.145.488.725
Sleep	F02.830.855.734

Slit Lamp Microscopy

A procedure that uses a SLIT LAMP to examine structures in the front of the EYE, such as the CONJUNCTIVA; CORNEA; IRIS; and AQUEOUS HUMOR.

Tree locations:

Diagnostic Techniques, Ophthalmological	E01.370.380.727
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New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Small Fiber Neuropathy

Disorder of the peripheral nerves that primarily impair small nerve fibers. The affected small nerve fibers include myelinated A-delta fibers (see A FIBERS) and unmyelinated C FIBERS. Because these small fibers innervate skin and help control autonomic function, their neuropathy presents with neuropathic pain, reduced thermal and pain sensitivity, and autonomic dysfunction (e.g. abnormal sweating or facial flushing). Small fiber neuropathy can be idiopathic or associated with underlying diseases (e.g., AMYLOIDOSIS; DIABETES MELLITUS; SARCOIDOSIS; or VASCULITIS).

Tree locations:

Peripheral Nervous System Diseases C10.668.829.860

Small Leucine-Rich Proteoglycans

A proteoglycan family (SLRPs) that is defined by a central domain which consists of a variable number of repeats of the motif LXXLxLXXNxL, where L may be LEUCINE; ISOLEUCINE; VALINE; or other hydrophobic amino acids. The N-terminal contains four conserved CYSTEINE residues and may be modified depending on function. SLRPs provide structural support to the EXTRACELLULAR MATRIX and are critical for regulating its assembly and dynamics at CELL-MATRIX JUNCTIONS.

Tree locations:

Extracellular Matrix Proteins D12.776.860.300.806
Proteoglycans D09.698.735.700
D12.776.395.650.875

SMARCB1 Protein

A component of the SWI-SNF CHROMATIN REMODELING complex that functions as a PROTEIN PHOSPHATASE 1 regulator and to stabilize CHROMATIN at PROMOTER REGIONS. It is important for regulating CELL PROLIFERATION and CELL DIFFERENTIATION. Mutations in the SMARCB1 gene are associated with malignant RHABDOID TUMORS.

Tree locations:

Chromosomal Proteins, Non-Histone D12.776.660.235.650
D12.776.664.235.900
DNA-Binding Proteins D12.776.260.716
Transcription Factors D12.776.930.809

Smoothed Receptor

A frizzled-like, G-protein-coupled receptor that associates with PATCHED RECEPTORS to transduce signals from HEDGEHOG PROTEINS and initiate hedgehog signaling to ZINC FINGER PROTEIN GLI1. It may normally inhibit signaling in the absence of SONIC HEDGEHOG PROTEIN binding to PATCHED RECEPTOR-1.

Tree locations:

Frizzled Receptors D12.776.543.750.695.017.500
D12.776.543.750.850.500.500

Snail Family Transcription Factors

A transcription factor family characterized by the presence of several C-terminal CYS2-HIS2 ZINC FINGERS. They function in many developmental processes including the induction of the EPITHELIAL-MESENCHYMAL TRANSITION; maintenance of embryonic MESODERM; growth arrest, CELL SURVIVAL; and CELL MIGRATION.

Tree locations:

Transcription Factors D12.776.930.815

Social Segregation

Barriers based on group membership.

Tree locations:

Social Problems I01.880.735.820

Soluble Guanylyl Cyclase

A mammalian enzyme composed of a heterodimer of alpha and beta subunits. Each subunit consists of four domains; N-terminal HNOX domain, PAS-like domain, a coiled-coil domain, and a C-terminal catalytic domain. All four domains are homologous proteins with a similar conformation of functional domains. Soluble guanylate cyclase catalyzes the formation of cyclic GMP from GTP, and is a key enzyme of the nitric oxide signaling pathway involved in the regulation of a variety of biological and physiological processes in mammals.

Tree locations:

Guanylate Cyclase D08.811.520.650.600.750
D12.644.360.350.500
D12.776.476.350.500

Solute Carrier Proteins

A large diverse group of membrane transport proteins whose families are generally classified according to function. Most SLCs localize to the CELL MEMBRANE; however, some families such as SLC25, localize to MITOCHONDRIAL MEMBRANES or other ORGANELLES.

Tree locations:

Membrane Transport Proteins D12.776.157.530.937
D12.776.543.585.937

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Splicing Factor U2AF

An RNA splicing factor that performs a critical function in both constitutive and enhancer-dependent RNA SPLICING. It recruits RIBONUCLEOPROTEIN, U2 SMALL NUCLEAR to the splice site and mediates interactions between it, the RNA molecule, and other splicing factors for accurate 3'-splice site selection.

Tree locations:

RNA Splicing Factors D12.776.157.725.829.750
D12.776.664.962.829.750

Sports and Recreational Facilities

Places designed, built, or installed for LEISURE ACTIVITIES outside of the home.

Tree locations:

Non-Medical Public and Private Facilities J03.925

Src Homology 2 Domain-Containing, Transforming Protein 2

An SHC-signaling adaptor protein that links GROWTH FACTOR RECEPTORS to SIGNAL TRANSDUCTION PATHWAYS in neurons.

Tree locations:

Shc Signaling Adaptor Proteins D12.644.360.024.330.750
D12.776.157.057.162.750
D12.776.476.024.424.750

ST Elevation Myocardial Infarction

A clinical syndrome defined by MYOCARDIAL ISCHEMIA symptoms; persistent elevation in the ST segments of the ELECTROCARDIOGRAM; and release of BIOMARKERS of myocardial NECROSIS (e.g., elevated TROPONIN levels). ST segment elevation in the ECG is often used in determining the treatment protocol (see also NON-ST ELEVATION MYOCARDIAL INFARCTION).

Tree locations:

Myocardial Infarction C14.280.647.500.875
C14.907.585.500.875

Spontaneous Perforation

A pathological hole in an organ, blood vessel or other soft part of the body, occurring in the absence of external force.

AN: includes spontaneous perforation unexplained or as a result of disease; coordinate with organ/diseases term

Tree locations:

Pathological Conditions, Anatomical C23.300.940

Src Homology 2 Domain-Containing, Transforming Protein 1

An SHC-signaling adaptor protein that transduces PHOSPHOTYROSINE-dependent signals downstream of RECEPTOR PROTEIN-TYROSINE KINASES and non-receptor tyrosine kinases. It is required for TGF-BETA-induced CELL MIGRATION; NEOLPASM INVASION; and METASTASIS of BREAST NEOPLASMS; its SH2 DOMAIN is essential for tumor survival. It also functions in signaling downstream of ANGIOPOIETIN RECEPTOR TIE-2, regulating the migration of ENDOTHELIAL CELLS; and PHYSIOLOGIC NEOVASCULARIZATION.

Tree locations:

Shc Signaling Adaptor Proteins D12.644.360.024.330.500
D12.776.157.057.162.500
D12.776.476.024.424.500

Src Homology 2 Domain-Containing, Transforming Protein 3

An SHC-signaling adaptor protein that links GROWTH FACTOR RECEPTORS to SIGNAL TRANSDUCTION PATHWAYS in neurons, including NEUROTROPHINS signaling in the CENTRAL NERVOUS SYSTEM.

Tree locations:

Shc Signaling Adaptor Proteins D12.644.360.024.330.875
D12.776.157.057.162.875
D12.776.476.024.424.875

Staghorn Calculi

Renal calculi with a characteristic shape like antlers of a deer, formed as it extends into multiple calices of the RENAL PELVIS. A large number of staghorn calculi as well as other URINARY CALCULI are composed of STRUVITE.

Tree locations:

Kidney Calculi C12.777.419.600.500.500
C12.777.967.249.500.500
C12.777.967.500.503.500
C13.351.968.419.600.500.500
C13.351.968.967.249.500.500
C13.351.968.967.500.503.500
C23.300.175.850.550.500

New MeSH Headings for 2017

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Stair Climbing

Ascending or descending stairs.

Tree locations:

Walking G11.427.410.568.900.875
G11.427.410.698.277.937.500
I03.350.937.500

Standing Orders

Medical procedures and prescriptions regarding treatment of a patient that can be exercised by other health care personnel when predetermined conditions have been met.

Tree locations:

Clinical Protocols E02.183.875
N05.715.360.775.225.750

Stenosis, Pulmonary Vein

Narrowing of the PULMONARY VEIN.

Tree locations:

Vascular Diseases C14.907.798

Strategic Planning

A rigorous and systematic process which entails defining plans, decisions, and sequence of steps to be taken in the future.

Tree locations:

Planning Techniques N04.452.718.500

Streptococcus gallolyticus subspecies gallolyticus

A subspecies of Streptococcus gallolyticus. It and other subspecies have been reported to cause infections resulting in BACTEREMIA; ENDOCARDITIS; and neonatal MENINGITIS.

AN: infection: coordinate IM with STREPTOCOCCAL INFECTIONS (IM)

Tree locations:

Streptococcus gallolyticus B03.353.750.737.872.243.500
B03.510.400.800.872.243.500
B03.510.550.737.872.243.500

Standardized Nursing Terminology

Standardized terms used in the nursing field (e.g., NURSING INFORMATICS).

Tree locations:

Terminology as Topic L01.143.506.598.400.889
Vocabulary, Controlled L01.453.245.945.600

Stenosis, Pulmonary Artery

Narrowing of the PULMONARY ARTERIES.

Tree locations:

Arterial Occlusive Diseases C14.907.137.825

Sterile Alpha Motif

A putative protein interaction module, approximately 70 amino acids long, that forms a small five-helix bundle with two large interfaces which may homo- and hetero-oligomerize, or bind non-sterile-alpha motif targets. The sterile alpha motif is present in a wide variety of eukaryotic proteins that function in diverse biological processes.

Tree locations:

Amino Acid Motifs G02.111.570.820.709.275.500.898
Protein Interaction G02.111.570.820.709.275.750.500.813
Domains and Motifs

Streptococcus gallolyticus

A species of Streptococcus that occurs in the GASTROINTESTINAL TRACT of birds, mammals and healthy humans.

Tree locations:

Streptococcus B03.353.750.737.872.243
B03.510.400.800.872.243
B03.510.550.737.872.243

Streptococcus iniae

A species of Streptococcus that is pathogenic in fish and may also cause disease in humans who routinely handle infected fish. Those who are of Asian descent, elderly, or have chronic diseases such as DIABETES MELLITUS; RHEUMATIC HEART DISEASE; or LIVER CIRRHOSIS are more susceptible to Streptococcus iniae infections.

AN: infection: coordinate IM with STREPTOCOCCAL INFECTIONS (IM)

Tree locations:

Streptococcus B03.353.750.737.872.405
B03.510.400.800.872.405
B03.510.550.737.872.405

New MeSH Headings for 2017

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Streptococcus salivarius

A species of Streptococcus that occurs in the human oral cavity and upper respiratory tract. It is a constituent of DENTAL PLAQUE and some strains may be pathogenic if they enter the bloodstream. However, other strains such as Streptococcus salivarius K12 produce BACTERIOCINS and are used as PROBIOTICS.

Tree locations:

Streptococcus B03.353.750.737.872.663
B03.510.400.800.872.663
B03.510.550.737.872.663

Stroke Rehabilitation

Restoration of functions to the maximum degree possible in a person or persons suffering from a stroke.

Tree locations:

Neurological Rehabilitation E02.760.169.063.500.477.500
E02.831.477.500
H02.403.680.600.750.500
N02.421.784.511.500

Stromal Interaction Molecule 1

A stromal interaction molecule that functions in the regulation of calcium influx following depletion of intracellular calcium in the ENDOPLASMIC RETICULUM. It translocates to the plasma membrane upon calcium depletion where it activates the CALCIUM RELEASE ACTIVATED CALCIUM CHANNEL ORAI1.

Tree locations:

Stromal Interaction Molecules D12.776.157.125.806.500
D12.776.543.875.500

Stromal Interaction Molecule 2

A stromal interaction molecule that functions as a highly sensitive calcium sensor in the ENDOPLASMIC RETICULUM and CYTOSOL. It can regulate CALCIUM RELEASE ACTIVATED CALCIUM CHANNELS in response to minor variations in intracellular calcium.

Tree locations:

Stromal Interaction Molecules D12.776.157.125.806.750
D12.776.543.875.750

Stromal Interaction Molecules

Membrane-associated calcium-binding proteins that are characterized by N-terminal EF HAND MOTIFS and a STERILE ALPHA MOTIF. They function as sensors of ENDOPLASMIC RETICULUM calcium levels and translocate from the ER to the plasma membrane to activate CALCIUM CHANNELS in response to intracellular calcium depletion.

Tree locations:

Calcium-Binding Proteins D12.776.157.125.806
Membrane Proteins D12.776.543.875

Struvite

The mineral magnesium ammonium phosphate with the formula NH_4MgPO_4 . It is associated with urea-splitting organisms in a high magnesium, high phosphate, alkaline environment. Accumulation of crystallized struvite is found in the urinary tract as struvite CALCULI and as scale on sewage system equipment and wastewater pipes.

Tree locations:

Magnesium Compounds D01.524.775
Phosphates D01.029.260.700.675.374.887
D01.695.625.675.650.887

Student Run Clinic

Healthcare setting managed by medical personnel in training.

Tree locations:

Health Facilities N02.278.912

Study Guide (Pub Type)

Tool used to help facilitate learning and comprehension of a topic or to help prepare for an examination.

AN: This heading is used as a Publication Type. Study guides as a subject are indexed under the main heading STUDY GUIDE AS TOPIC. INDEXER: Do not use

Tree locations:

Publication Formats V02.928

Study Guide as Topic

Works about use of aids to help facilitate learning and comprehension of a topic or to help prepare for an examination.

AN: do not confuse with Publication Type STUDY GUIDE

Tree locations:

Teaching I02.903.923

Superconductivity

The ability of an element or metallic alloy to allow the passage of ELECTRONS without ELECTRICAL RESISTANCE and expel MAGNETIC FIELDS below a certain threshold temperature called superconducting transition temperature.

Tree locations:

Electromagnetic Phenomena G01.358.500.875

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Superoxide Dismutase-1

A superoxide dismutase (SOD1) that requires copper and zinc ions for its activity to destroy SUPEROXIDE FREE RADICALS within the CYTOPLASM. Mutations in the SOD1 gene are associated with AMYOTROPHIC LATERAL SCLEROSIS-1.

Tree locations:

Superoxide Dismutase D08.811.682.881.500

Suppressor of Cytokine Signaling 1 Protein

A suppressor of cytokine signaling protein that consists of an N-terminal kinase-inhibitory region, a central SH2 DOMAIN, a characteristic C-terminal SOCS box (a 40-amino acid motif, which functions to recruit E3 UBIQUITIN-PROTEIN LIGASE COMPLEXES). SOCS1 functions as a negative regulator of CYTOKINES that signal through the JANUS KINASES-STAT 3 TRANSCRIPTION FACTOR (JAK/STAT3) pathway by inhibiting the activity of JANUS KINASES.

Tree locations:

Suppressor of Cytokine Signaling D12.644.360.024.374.500
Proteins D12.776.157.057.249.500
D12.776.476.024.437.500

Suppressor of Cytokine Signaling 3 Protein

A suppressor of cytokine signaling protein that consists of an N-terminal kinase-inhibitory region, a central SH2 DOMAIN, a characteristic C-terminal SOCS box (a 40-amino acid motif, which functions to recruit E3 UBIQUITIN-PROTEIN LIGASE COMPLEXES). SOCS3 inhibits cytokine signaling by binding to RECEPTOR PROTEIN-TYROSINE KINASES as well as CYTOKINE RECEPTOR GP130; ERYTHROPOIETIN RECEPTORS; INSULIN RECEPTOR; and the LEPTIN RECEPTOR. Its functions include suppression of ERYTHROPOIESIS in the fetal liver.

Tree locations:

Suppressor of Cytokine Signaling D12.644.360.024.374.750
Proteins D12.776.157.057.249.750
D12.776.476.024.437.750

Surgical Oncology

A surgical specialty concerned with management of cancer.

Tree locations:

Medical Oncology H02.403.429.515.750
Specialties, Surgical H02.403.810.796

Surgical Wound

An incision made during a surgical procedure.

Tree locations:

Wounds and Injuries C26.859

Sustained Virologic Response

The continuous, long-term suppression of VIRAL LOAD, generally to undetectable levels, as the result of treatment with ANTIVIRAL AGENTS.

Tree locations:

Treatment Outcome E01.789.800.570
N04.761.559.590.800.665
N05.715.360.575.575.800.665

Sutureless Surgical Procedures

Surgical techniques in which SUTURES are not applied to surgical wounds.

Tree locations:

Wound Closure Techniques E04.987.887

Syk Kinase

An SH2 domain-containing non-receptor tyrosine kinase that regulates signal transduction downstream of a variety of receptors including B-CELL ANTIGEN RECEPTORS. It functions in both INNATE IMMUNITY and ADAPTIVE IMMUNITY and also mediates signaling in CELL ADHESION; OSTEOGENESIS; PLATELET ACTIVATION; and vascular development.

Tree locations:

Intracellular Signaling D12.644.360.900
Peptides and Proteins D12.776.476.913
Protein-Tyrosine Kinases D08.811.913.696.620.682.725.650

New MeSH Headings for 2017

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Synoviocytes

Cells on the luminal surface of the SYNOVIAL MEMBRANE. Type A synoviocytes are MACROPHAGES responsible for waste removal from the joint cavity. Fibroblast-like type B synoviocytes are involved in production of joint matrix constituents (e.g., HYALURONAN; COLLAGEN; and FIBRONECTIN).

Tree locations:

Connective Tissue Cells A11.329.835

Talipes

Deformity in which the foot is misaligned with respect to the TALUS in the ANKLE JOINT. While mostly congenital, as in CLUBFOOT, acquired deformities are included. Acquired talipedes are often associated with other foot deformities such as SYNDACTYLY and POLYDACTYLY.

Tree locations:

Foot Deformities, Acquired C05.330.488.655
Foot Deformities, Congenital C05.330.495.681
C05.660.585.512.380.813
C16.131.621.585.512.500.681

Tannerella forsythia

A periodontal pathogen which is a gram-negative member of BACTEROIDETES. It is implicated in PERIODONTITIS.

AN: infection: coordinate IM with GRAM-NEGATIVE BACTERIAL INFECTIONS (IM)

Tree locations:

Bacteroidetes B03.140.900

Tarsal Coalition

Congenital, complete or partial fusion of the TARSAL BONES of the foot. PES PLANUS is usually a feature.

Tree locations:

Foot Deformities, Congenital C05.330.495.787
C05.660.585.512.380.875
C16.131.621.585.512.500.787
Synostosis C05.116.099.370.894.909
C05.660.906.909
C16.131.621.906.909

Synthetic Lethal Mutations

Mutations in genes which lead to cell or organism death when occurring in combination with mutations in one or more other genes.

Tree locations:

Mutation G05.365.590.917

Talipes Cavus

A foot deformity in which the arch of the foot is high and often the heel adducted.

Tree locations:

Talipes C05.330.488.655.500
C05.330.495.681.500
C05.660.585.512.380.813.500
C16.131.621.585.512.500.681.500

Tardive Dyskinesia

Drug-related movement disorder characterized by uncontrollable movements in certain muscles. It is associated with a long-term exposure to certain neuroleptic medications (e.g., METOCLOPRAMIDE).

Tree locations:

Dyskinesia, Drug-Induced C10.228.662.262.500.500
C10.597.350.275.500
C23.888.592.350.275.500

Tartrate-Resistant Acid Phosphatase

One of several acid phosphatases in humans, other mammals, plants, and a few prokaryotes. The protein fold of tartrate-resistant acid phosphatase (TRAP) resembles that of the catalytic domain of plant purple acid phosphatase and other serine/threonine-protein phosphatases that also contain a metallophosphoesterase domain. One gene produces the various forms which include purple acid phosphatases from spleen and other tissues. Tartrate-resistant acid phosphatase is a biomarker for pathological states in which it is over-expressed. Such conditions include GAUCHER DISEASE; HODGKIN DISEASE; BONE RESORPTION; and NEOPLASM METASTASIS.

Tree locations:

Acid Phosphatase D08.811.277.352.650.025.500
Phosphoprotein D08.811.277.352.650.625.862
Phosphatases

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Taxis Response

A behavior in free-moving organism that results in motion or orientation toward or away from an external stimulus.

Tree locations:

Behavior, Animal F01.145.113.780
Locomotion G07.568.500.590
G11.427.410.568.850
Orientation, Spatial F01.145.875.439.500

Teacher Training

A curriculum-centered process of equipping individuals with professional knowledge and skills required to become effective teachers.

Tree locations:

Education, Professional I02.358.984

Tenocytes

Elongated FIBROBLASTS and fibrocytes that lie between the collagen fibers and form the TENDON proper.

Tree locations:

Connective Tissue Cells A11.329.840

Tensins

A family of multidomain microfilament proteins that bind ACTIN FILAMENTS and INTEGRINS at FOCAL ADHESIONS. They generally consist of an N-terminal domain with homology to PHOSPHOTYROSINE PHOSPHATASE, a C2 DOMAIN; unique central regions rich in PROLINE; ALANINE; GLYCINE; and SERINE; an SH2 DOMAIN; and a C-terminal phosphotyrosine-binding region. They are involved in CELL MIGRATION; CELL ADHESION; SIGNAL TRANSDUCTION; and reorganization of the CYTOSKELETON.

Tree locations:

Microfilament Proteins D05.750.078.730.719
D12.776.220.525.719

Teratozoospermia

Conditions in which sperm show abnormal morphology.

Tree locations:

Infertility, Male C12.294.365.700.877

Tertiary Lymphoid Structures

Aggregates of immune cells formed near the sites of chronically inflamed, infected, or tumorous tissues.

Tree locations:

Lymphoid Tissue A10.549.725
A15.382.520.604.725
Pathological Conditions, Anatomical C23.300.955

Thermotolerance

The ability of an organism to reduce susceptibility to heat shock, and adapt to HOT TEMPERATURE.

Tree locations:

Acclimatization G07.025.133.500
G16.012.500.133.500

Thyroid Epithelial Cells

Epithelial cells of the THYROID GLAND that produce and secrete THYROXINE and TRIIODOTHYRONINE.

Tree locations:

Epithelial Cells A11.436.911

Tibial Meniscus Injuries

Injuries to the TIBIAL MENISCUS of the leg.

Tree locations:

Leg Injuries C26.558.781

Traditional Pulse Diagnosis

Technique used in AYURVEDIC MEDICINE, and EAST ASIAN TRADITIONAL MEDICINE, in which reading PULSE is used in the diagnosis of diseases.

Tree locations:

Diagnostic Techniques and Procedures E01.370.503

New MeSH Headings for 2017

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Transcription Activator-Like Effector Nucleases

Artificial nucleases that cleave DNA at a defined distance from specific DNA sequences recognized by TRANSCRIPTION ACTIVATOR-LIKE EFFECTORS. They are composed of an endodeoxyribonuclease fused to DNA-binding domains of the transcription activator-like effectors.

Tree locations:

Endodeoxyribonucleases D08.811.277.352.335.350.850

Transcription Activator-Like Effectors

Virulence factors of pathogenic plant bacteria, such as XANTHOMONAS species, that bind to specific sequences in the PROMOTER REGIONS of host DNA to induce transcription of specific host genes. Variations in the DNA binding domain of TALE family members account for the variations in DNA specificity. The TALE DNA-binding domains are used in various GENETIC TECHNIQUES by fusing them with various DNA modifying enzymes to detect and manipulate sequence-specific targeted DNA sites.

Tree locations:

Bacterial Proteins D12.776.097.890
Trans-Activators D12.776.260.755.700
D12.776.930.900.550
Virulence Factors D23.946.896.490

Transcription Factor HES-1

A basic-helix-loop-helix transcription factor that functions as a transcriptional repressor for genes transcribed by bHLH proteins. For example, it may negatively regulate MYOGENESIS by inhibiting MyoD1 and ASH1 proteins. It is also required for the stability of FANCONI ANEMIA COMPLEMENTATION GROUP PROTEINS and their localization to the cell nucleus in response to DNA DAMAGE.

Tree locations:

Basic Helix-Loop-Helix Transcription Factors D12.776.260.103.844
D12.776.930.125.844

Transcriptional Regulator ERG

A trans-activator and member of the erythroblast transformation-specific family of transcription factors that contain a characteristic ETS MOTIF. It is required for PLATELET CELL ADHESION to the subendothelium and associates with CHIMERIC ONCOGENE PROTEINS in PROSTATE CANCER; EWING'S SARCOMA; and ACUTE MYELOID LEUKEMIA.

Tree locations:

Trans-Activators D12.776.260.755.100
D12.776.930.900.625

Transportation Facilities

Places such as AIRPORTS, bus stations, and train stations that are used for managing arriving and departing transport vehicles, and included facilities for handling passengers.

Tree locations:

Non-Medical Public and Private Facilities J03.970

Trefoil Factor-1

A 60 amino acid (6.5 kDa) trefoil factor that contains a single trefoil domain. It is expressed primarily by surface EPITHELIAL CELLS of the GASTRIC MUCOSA, where it associates with MUCIN 5AC.

Tree locations:

Trefoil Factors D12.644.937.500

Trefoil Factor-2

A 106 amino acid (12 kDa) trefoil factor that contains two trefoil domains and associates with MUCIN-6. It is expressed in the GASTROINTESTINAL TRACT by cells of BRUNNER GLANDS; PYLORIC GLANDS and mucous neck cells. It inhibits GASTROINTESTINAL MOTILITY and GASTRIC ACID secretion and may help maintain the structural integrity of gastric mucus.

Tree locations:

Trefoil Factors D12.644.937.750

Trefoil Factor-3

A 59 amino acid (6.6 kDa) trefoil factor that contains a single trefoil domain. It is expressed in all tissues with MUCOUS MEMBRANES, including GOBLET CELLS of the SMALL INTESTINE and LARGE INTESTINE. It associates with MUCIN-2 in the small intestine and may regulate epithelial CELL MIGRATION and WOUND HEALING.

Tree locations:

Trefoil Factors D12.644.937.875

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Trefoil Factors

A family of small peptides expressed primarily by MUCOUS MEMBRANE EPITHELIAL CELLS in vertebrates. Their structure is highly conserved and is defined by a three-leaved (trefoil) domain of 42 or 43 amino acids; it includes six cysteines that create the trefoil structure through disulfide bridges. Trefoil peptides may form dimers with each other, or associate with MUCINS and other factors. They are important for maintaining epithelial integrity and for protection from noxious agents.

Tree locations:

Peptides D12.644.937

Tripartite Motif Proteins

A protein family defined by the presence of three ZINC FINGER domains, one of which is a RING FINGER DOMAIN, a coiled-coil region, and a highly variable C-terminal region. They function in many cellular processes including APOPTOSIS and CELL CYCLE regulation.

Tree locations:

Proteins D12.776.934

Tumor Hypoxia

Hypoxic conditions in tumor cells due to the tumor outgrowing its blood supply. It is associated with increased METASTASIS and resistance to RADIOTHERAPY and DRUG THERAPY.

Tree locations:

Cell Hypoxia G03.197.300.500
G04.270.300.500

Tumor Protein p73

A homolog of p53 TUMOR SUPPRESSOR PROTEIN that encodes full-length trans-activating and N-terminally-truncated (DeltaN) isoforms. Detection of splice variants and isoforms in the nervous system (human TELENCEPHALON, CHOROID PLEXUS; CEREBROSPINAL FLUID), embryonic tissue, human BREAST CANCER; OVARIAN CANCER, suggest roles in cellular differentiation.

Tree locations:

DNA-Binding Proteins D12.776.260.885
Nuclear Proteins D12.776.660.912
Transcription Factors D12.776.930.969
Tumor Suppressor Proteins D12.776.624.776.820

Trichodesmium

A nitrogen-fixing genus of filamentous cyanobacteria that occurs in tropical and subtropical oceans.

Tree locations:

Cyanobacteria B03.280.875
B03.440.475.100.875
Nitrogen-Fixing Bacteria B03.585.950

Tudor Domain

A conserved, approximately 50 amino acid, protein sequence that adopts a characteristic strongly bent, five stranded anti-parallel beta-sheet barrel-like fold. The Tudor domain recognizes dimethylated ARGININE through its negatively-charged surface and occurs in many proteins that co-localize with RNA; RIBONUCLEOPROTEINS or SINGLE-STRANDED DNA complexes in the CELL NUCLEUS; MITOCHONDRIA; or KINETOCHORES.

Tree locations:

Protein Interaction G02.111.570.820.709.275.750.500.844
Domains and Motifs

Tumor Necrosis Factor alpha-Induced Protein 3

A UBIQUITIN editing enzyme that functions as both a ubiquitin ligase and deubiquitinase. It contains several ZINC FINGERS and functions in the immune response and INFLAMMATION by modulating signals from TNF-ALPHA; IL1-BETA; or pathogens via TOLL-LIKE RECEPTORS to terminate NF-KAPPA B activity.

Tree locations:

Intracellular Signaling D12.644.360.950
Peptides and Proteins D12.776.476.938
Ubiquitin-Protein Ligases D08.811.464.938.750.813
Ubiquitin-Specific Proteases D08.811.037.750.500
D08.811.277.656.300.887.750

Tumor Suppressor p53-Binding Protein 1

A nuclear and cytoplasmic protein that associates with KINETOCHORES and contains a C-terminal TUDOR DOMAIN. It plays a critical role in the cellular response to DNA DAMAGE and localizes to DOUBLE-STRAND DNA BREAKS. It may also function in M PHASE CELL CYCLE CHECKPOINTS and as an enhancer of TUMOR SUPPRESSOR PROTEIN P53-mediated transcriptional activation.

Tree locations:

Chromosomal Proteins, Non-Histone D12.776.660.235.850
D12.776.664.235.950
DNA-Binding Proteins D12.776.260.805

New MeSH Headings for 2017

Listed in alphabetical order with Heading, Scope Note, Annotation (AN), and Tree Locations

Twist Transcription Factors

A highly-conserved family of basic helix-loop-helix (bHLH) transcription factors. They function as dimers with other bHLH proteins and bind E-BOX ELEMENTS to control gene expression during EMBRYOGENESIS and the EPITHELIAL-MESENCHYMAL TRANSITION.

Tree locations:

Basic Helix-Loop-Helix Transcription Factors D12.776.260.103.906
D12.776.930.125.906

Twist-Related Protein 2

A twist family transcription factor that is expressed in MESODERM as well as the DERMIS during mammalian EMBRYOGENESIS. It is structurally and functionally similar to TWIST-RELATED PROTEIN 1; it also regulates OSTEOGENESIS and the expression of CYTOKINES in response to INFLAMMATION.

Tree locations:

Twist Transcription Factors D12.776.260.103.906.500
D12.776.930.125.906.500

Ulnar Collateral Ligament Reconstruction

Surgical reconstruction of injured or insufficient ULNAR COLLATERAL LIGAMENT in the ELBOW JOINT.

Tree locations:

Orthopedic Procedures E02.718.750
E04.555.860
Reconstructive Surgical Procedures E04.680.900

Ultradian Rhythm

A biological rhythm with a period shorter than 24 hours.

Tree locations:

Periodicity G07.180.562.797

Uncoupling Protein 1

A mitochondrial uncoupling protein that is expressed in BROWN ADIPOSE TISSUE. It is critical for NONSHIVERING THERMOGENESIS to prevent heat loss in NEONATES.

Tree locations:

Mitochondrial Uncoupling Proteins D12.776.157.530.937.598.500
D12.776.543.585.475.688.500
D12.776.543.585.937.696.500
D12.776.575.750.688.500

Uncoupling Protein 2

A mitochondrial uncoupling protein that is expressed in many tissues and exhibits the greatest expression in SKELETAL MUSCLE. It regulates mitochondrial ATP production and the generation of REACTIVE OXYGEN SPECIES.

Tree locations:

Mitochondrial Uncoupling Proteins D12.776.157.530.937.598.750
D12.776.543.585.475.688.750
D12.776.543.585.937.696.750
D12.776.575.750.688.750

Uncoupling Protein 3

A mitochondrial uncoupling protein that is expressed in heart and skeletal muscle tissues. It functions to regulate tissue respiration, energy balance, and THERMOGENESIS. Mutations in the UCP3 gene are associated with OBESITY.

Tree locations:

Mitochondrial Uncoupling Proteins D12.776.157.530.937.598.875
D12.776.543.585.475.688.875
D12.776.543.585.937.696.875
D12.776.575.750.688.875

Urologists

Physicians specializing in the diagnosis, and treatment of diseases of the urinary tract in both sexes, and the genital tract in the male.

Tree locations:

Physicians M01.526.485.810.955
N02.360.810.955

Vaccination Refusal

Refusal to receive VACCINATION.

Tree locations:

Treatment Refusal F01.145.488.800.500
I01.880.604.473.650.968.500
N03.706.437.650.875.500
N05.300.150.600.800.500

Value-Based Insurance

Approach to improve the quality of care by selectively encouraging or discouraging the use of specific health care services, based on their potential benefit to patients' health, relative to their cost. One element is lowering beneficiary cost sharing or out-of-pocket spending to increase medication adherence.

Tree locations:

Insurance, Health N03.219.521.576.343.972
Quality Improvement N04.761.744.750

New MeSH Headings for 2017

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Vaping

The act of inhaling and exhaling vapors produced from ELECTRONIC CIGARETTES.

Tree locations:

Behavior F01.145.979
Tobacco Use Cessation F01.145.488.750.850

Virophages

Circular, double-stranded DNA viruses that invade giant DNA viruses (GIANT VIRUSES) which infect eukaryotes.

Tree locations:

DNA Viruses B04.280.950

Walking Speed

The rate at which steps are made while walking.

Tree locations:

Gait E01.370.600.250.500
G11.427.410.568.900.750.500

Werner Syndrome Helicase

A DNA-dependent helicase and 3'-5' exonuclease. It has 3'->5' exonuclease activity towards double-stranded DNA with a 5'-overhang and binds preferentially to DNA substrates containing alternate secondary structures, such as replication forks and HOLLIDAY JUNCTIONS. Mutations in the WRN gene are associated with WERNER SYNDROME.

Tree locations:

Exodeoxyribonucleases D08.811.277.352.335.375.875
D08.811.277.352.365.290.500
RecQ Helicases D08.811.277.040.025.159.249.500
D08.811.399.340.249.500

Wolfiporia

A genus of wood-decaying, edible fungi in the Polyporaceae family. Its type species is Wolfiporia extensa.

Tree locations:

Polyporaceae B01.300.179.120.760.845

Vigna

Plant genus in the pea family (Fabaceae).

Tree locations:

Fabaceae B01.650.940.800.575.100.401.976

Walk Test

A measure of endurance tests that show how far and fast an individual can walk without stopping within a certain period of time.

Tree locations:

Exercise Test E01.370.370.380.250.500

WD40 Repeats

Protein interaction motifs of approximately 40 amino acids that usually terminate in TRYPTOPHAN and ASPARTIC ACID. They form characteristic beta-propeller structures and occur in many eukaryotic proteins that function in a variety of cellular processes. Proteins that contain WD40 repeats often function as assembly platforms for MULTIPROTEIN COMPLEXES.

Tree locations:

Amino Acid Motifs G02.111.570.820.709.275.500.927
Protein Interaction Domains and Motifs G02.111.570.820.709.275.750.500.875
Repetitive Sequences, Amino Acid G02.111.570.060.720.515
G02.111.570.820.709.275.875.515

Wnt-5a Protein

A Wnt protein and ligand for FRIZZLED RECEPTORS that may function as an inhibitor or activator of the WNT SIGNALING PATHWAY. For example, it activates signaling in the presence of Frizzled-4 but is inhibitory when coupled with ROR2 TYROSINE KINASE. It is required for axis formation during EMBRYOGENESIS and inhibits the proliferation, migration, and invasiveness of cancer cells.

Tree locations:

Proto-Oncogene Proteins D12.776.624.664.700.962
Wnt Proteins D12.776.467.984.050
D23.529.984.050

Work-Life Balance

The optimal arrangement of an individual's on-the-job and private time to facilitate health and personal satisfaction without negatively impacting productivity and professional success.

Tree locations:

Social Sciences I01.940
Work I03.946.950

New MeSH Headings for 2017

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X-Box Binding Protein 1

A basic leucine zipper transcription factor that regulates expression of MHC CLASS II GENES through its binding to a conserved X-box DNA sequence in the promoter region. It regulates the expression of genes involved in the UNFOLDED PROTEIN RESPONSE.

Tree locations:

Basic-Leucine Zipper Transcription Factors D12.776.260.108.937
D12.776.930.127.937

Zinc Finger E-box-Binding Homeobox 1

A transcription factor characterized by N-terminal and C-terminal CYS2-HIS2 ZINC FINGERS separated by a homeobox. It represses the expression of E-CADHERIN to induce the EPITHELIAL-MESENCHYMAL TRANSITION. It also represses PROTO-ONCOGENE PROTEINS C-BCL-6; regulates the cell type-specific expression of SODIUM-POTASSIUM-EXCHANGING ATPASE; and promotes neuronal differentiation.

Tree locations:

Homeodomain Proteins D12.776.260.400.906
Repressor Proteins D12.776.260.703.800
D12.776.930.780.945

Zona Pellucida Glycoproteins

Membrane glycoproteins that constitute the ZONA PELLUCIDA in mammals and function in the recognition and binding of SPERMATOOZOA.

Tree locations:

Egg Proteins D12.776.290.906
Membrane Glycoproteins D12.776.395.550.995
D12.776.543.550.995
Receptors, Cell Surface D12.776.543.750.981

Xanthorrhoeaceae

A family of flowering plants in the order Asparagales.

Tree locations:

Asparagales B01.650.940.800.575.100.099.970

Zinc Finger Protein GLI1

A transcriptional activator and oncogene protein that contains two CYS2-HIS2 ZINC FINGERS. Two isoforms are expressed; both regulate the expression of specific genes during development of craniofacial features, digits, the CENTRAL NERVOUS SYSTEM; and the GASTROINTESTINAL TRACT. They also regulate SONIC HEDGEHOG PROTEIN signaling and cell proliferation.

Tree locations:

Proto-Oncogene Proteins D12.776.624.664.700.989
Trans-Activators D12.776.260.755.850
D12.776.930.900.700