

Cluster 0 – Aerobic Energy Metabolism and Respiratory Chain

Biological Process

GO:0022900 – Electron transport chain

Electron flow through respiratory complexes.

GO:0022904 – Respiratory electron transport chain

Mitochondrial electron transfer supporting respiration.

GO:0006119 – Oxidative phosphorylation

ATP generation coupled to electron transport.

GO:0042775 – ATP synthesis coupled electron transport

Proton gradient-dependent ATP production.

GO:0009060 – Aerobic respiration

Oxygen-dependent cellular energy production.

Molecular Function

GO:0009055 – Electron transfer activity

Redox reactions transferring electrons.

GO:0004129 – Cytochrome-c oxidase activity

Terminal electron transfer to oxygen.

GO:0015078 – Proton transmembrane transporter activity

Proton pumping across the membrane.

GO:0008324 – Cation transmembrane transporter activity

Cation flux across membranes.

Cellular Component

GO:0005743 – Mitochondrial inner membrane

Site of oxidative phosphorylation complexes.

GO:0005751 – Mitochondrial respiratory chain complex I

NADH dehydrogenase complex.

GO:0031966 – Mitochondrial membrane
General mitochondrial membrane localization.

Cluster 1 – Mitochondrial Respiration Focused on NADH-Dependent Complex I

Biological Process

GO:0006120 – Mitochondrial electron transport (NADH to ubiquinone)
Electron flow within complex I.

GO:0015986 – ATP synthesis coupled proton transport
ATP production using proton gradients.

GO:0006754 – ATP generation from ADP
ATP formation driven by oxidative pathways.

GO:0042775 – ATP synthesis coupled electron transport
ATP coupling to electron movement.

Molecular Function

GO:0008137 – NADH dehydrogenase activity
Oxidation of NADH in complex I.

GO:0009055 – Electron transfer activity
Electron flow in redox reactions.

GO:0015078 – Proton transporter activity
Proton translocation across membranes.

Cellular Component

GO:0005747 – Mitochondrial respiratory chain complex I
Primary NADH-oxidizing complex.

GO:0005743 – Mitochondrial inner membrane
Location of complex I.

Cluster 2 – Skin Differentiation and Epithelial Cytoskeleton

Biological Process

GO:0045109 – Regulation of receptor signaling via JAK-STAT

Control of cytokine-responsive pathways in the epidermis.

GO:0045104 – Positive regulation of stem cell proliferation

Expansion of epidermal progenitors.

GO:0031424 – Keratinocyte differentiation

Maturation of skin epithelial cells.

GO:0030216 – Keratinocyte proliferation

Growth of epidermal layers.

GO:0043588 – Skin development

Formation of epidermal tissue.

Molecular Function

GO:0030280 – Structural constituent of epidermis

Proteins giving mechanical strength to epidermis.

GO:0005198 – Structural molecule activity

General architectural functions in cells.

GO:0005200 – Structural constituent of cytoskeleton

Cytoskeletal support elements.

Cellular Component

GO:0005882 – Intermediate filament

Keratin filament structures.

GO:0045111 – Intercellular junction

Cell-cell adhesion sites.

GO:0045095 – Cell junction

General junctional complexes.

GO:0001533 – Cornified envelope

Outer epidermal structural layer.

Cluster 3 – Protein Translation and Ribosome Biogenesis

Biological Process

GO:0006412 – Translation

Protein synthesis from mRNA.

GO:0002181 – Cytoplasmic translation

Translation in the cytosol.

GO:0042254 – Ribosome biogenesis

Assembly of ribosomal subunits.

GO:0010467 – Gene expression regulation

General control of gene activity.

GO:0042274 – Ribosomal large subunit biogenesis

Formation of 60S subunit components.

Molecular Function

GO:0003735 – Structural constituent of ribosome

Core ribosomal proteins.

GO:0005198 – Structural molecule activity

Structural macromolecules.

GO:0003723 – RNA binding

Interaction with RNA molecules.

Cellular Component

GO:0005840 – Ribosome

Cytosolic 80S ribosomes.

GO:1990904 – Ribonucleoprotein complex

RNA-protein assemblies.

GO:0022626 – Cytosolic large ribosomal subunit
60S subunit localization.

GO:0015935 – Small ribosomal subunit
40S subunit localization.

Cluster 4 – Ciliary Motility and Microtubule-Based Movement

Biological Process

GO:0007018 – Microtubule-based movement
Transport and motility driven by microtubules.

GO:0003341 – Cilium movement
Beating of motile cilia.

GO:0060271 – Cilium assembly
Formation of ciliary structures.

GO:0007017 – Microtubule-based process
General microtubule-dependent activities.

GO:0060294 – Cilium organization
Structural arrangement of cilia.

Molecular Function

GO:0045505 – Dynein complex binding
Interaction with dynein motor proteins.

GO:0008569 – Motor activity
ATP-dependent mechanical force generation.

GO:0003777 – Microtubule motor activity
Movement along microtubules.

GO:0051959 – Dynein intermediate chain binding
Binding to dynein subunits.

Cellular Component

GO:0030286 – Dynein complex

Motor complexes for ciliary motion.

GO:0005875 – Microtubule-associated complex

Structures interacting with microtubules.

GO:0005930 – Axoneme

Core structure of cilia.

GO:0031514 – Motile cilium

Cilia capable of movement.

Cluster 5 – Transcriptional Regulation and Nuclear DNA-Binding Factors

Biological Process

GO:0006357 – Regulation of transcription by RNA Pol II

Control of Pol II-dependent gene expression.

GO:0045893 – Positive regulation of transcription

Activation of transcription.

GO:0045892 – Negative regulation of transcription

Repression of transcription.

GO:0045944 – Positive regulation of DNA-templated transcription

Enhancement of gene expression.

GO:0000122 – Negative regulation of RNA Pol II transcription

Downregulation of transcription.

Molecular Function

GO:0140110 – Transcription regulator activity

Modulation of transcription.

GO:0000981 – DNA-binding transcription factor activity

Sequence-specific DNA binding.

GO:1990837 – Sequence-specific DNA binding

Recognition of defined DNA motifs.

GO:0000977 – Promoter binding

Interaction with promoter regions.

GO:0000987 – Core promoter binding

Binding to basal promoter elements.

Cellular Component**GO:0000785 – Chromatin**

DNA-protein complexes in the nucleus.

GO:0005694 – Chromosome

Chromosomal structures.

GO:0005667 – Transcription regulator complex

Nuclear regulatory assemblies.

GO:0016604 – Nuclear body

Subnuclear compartments.

Cluster 6 – Ion Transport and Channel Activity

Biological Process**GO:0030001 – Metal ion transport**

Movement of metal ions across membranes.

GO:0098655 – Cation transmembrane transport

Translocation of cations across membranes.

GO:0006812 – Cation transport

General cation movement.

GO:0034220 – Ion transmembrane transport

Ion flux driven across a membrane barrier.

GO:0006811 – Ion transport

Overall movement of ions within or between cells.

Molecular Function**GO:0005261 – Cation channel activity**

Selective passage of cations through channels.

GO:0046873 – Metal ion transmembrane transporter activity

Transport of metal ions through membranes.

GO:0005216 – Ion channel activity

Permitting ion flow across membranes.

GO:0015267 – Channel activity

General gated channel function.

Cellular Component**GO:0034703 – Cation channel complex**

Protein complexes enabling cation flow.

GO:0034702 – Ion channel complex

Assemblies forming ion channels.

GO:1902495 – Transmembrane transporter complex

Transporter complexes embedded in membranes.

GO:0098797 – Plasma membrane region

Localized sites on the plasma membrane.

GO:0098796 – Membrane protein complex

Protein assemblies within membranes.

Cluster 7 – Extracellular Matrix and Collagen Organization

Biological Process**GO:0030198 – Extracellular matrix organization**

Formation and arrangement of ECM structures.

GO:0030199 – Collagen fibril organization

Assembly of collagen fibers.

GO:0038063 – Extracellular structure organization

Organization of extracellular components.

Molecular Function

GO:0030020 – Extracellular matrix structural constituent
ECM elements providing structural integrity.

GO:0005201 – ECM constituent (collagen)
Collagen proteins forming structural frameworks.

GO:0005198 – Structural molecule activity
Supporting architectural roles.

Cellular Component

GO:0005581 – Collagen-containing extracellular matrix
ECM enriched in collagen.

GO:0005788 – Endoplasmic reticulum lumen
Compartment for collagen synthesis and folding.

GO:0062023 – Collagen-containing ECM region
Defined ECM subregion rich in collagen.

GO:0031012 – Extracellular matrix
General ECM localization.

Cluster 8 – RNA Processing, Splicing, and RNP Complexes

Biological Process

GO:0006396 – RNA processing
Post-transcriptional RNA modification.

GO:0006397 – mRNA processing
Maturation of mRNA molecules.

GO:0008380 – RNA splicing
Removal of introns from RNA.

GO:0016070 – RNA metabolic process
General RNA turnover and modification.

GO:0000398 – pre-mRNA splicing
Splicing of precursor mRNA.

Molecular Function

GO:0003723 – RNA binding

Recognition of RNA molecules.

GO:0003729 – mRNA binding

Interaction with mRNA.

GO:0003730 – mRNA 3'-UTR binding

Binding to the 3' untranslated region.

GO:0004540 – Ribonuclease activity

Cleavage of RNA molecules.

Cellular Component

GO:1990904 – Ribonucleoprotein complex

RNA-protein functional assemblies.

GO:0035770 – RNP granule

Granules containing RNA-protein complexes.

GO:0005681 – Spliceosomal complex

Assemblies performing RNA splicing.

GO:0036464 – Cytoplasmic RNP granule

Cytoplasmic storage/processing granules.

GO:0071013 – Catalytic step 2 spliceosome

Spliceosome in the catalytic phase of splicing.

Cluster 9 – DNA Repair and Genome Stability

Biological Process

GO:0006259 – DNA metabolic process

General DNA maintenance and metabolism.

GO:0006281 – DNA repair

Restoration of damaged DNA.

GO:0006974 – Cellular response to DNA damage stimulus

Recognition and response to DNA lesions.

GO:0006310 – DNA recombination

Exchange and rearrangement of DNA segments.

GO:0006302 – Double-strand break repair

Correction of DSB lesions.

Molecular Function

GO:0003677 – DNA binding

Interaction with DNA.

GO:0008094 – DNA-dependent ATPase activity

ATP-driven DNA remodeling.

GO:0003697 – Single-stranded DNA binding

Binding to ssDNA during repair.

GO:0003684 – Damaged DNA binding

Recognition of altered DNA.

Cellular Component

GO:0005694 – Chromosome

Chromosomal DNA.

GO:0000781 – Telomeric region of chromosome

Terminal chromosomal domains.

GO:0000228 – Nuclear chromosome

Chromosomes within the nucleus.

Cluster 10 – Ubiquitination and Protein Quality Control

Biological Process

GO:0006511 – Ubiquitin-dependent protein catabolic process

Protein degradation via ubiquitination.

GO:0016567 – Protein ubiquitination

Attachment of ubiquitin to proteins.

GO:0032446 – Protein modification by small protein conjugation

Conjugation of ubiquitin-like proteins.

GO:0051603 – Proteolysis in protein quality control

Targeted degradation of misfolded proteins.

Molecular Function**GO:0004842 – Ubiquitin-protein ligase activity**

Catalysis of ubiquitin transfer to substrates.

GO:0016746 – Transferase activity

Catalysis of group-transfer reactions.

GO:0061630 – Ubiquitin ligase binding

Interaction with E3 ligases.

Cellular Component**GO:0000151 – Ubiquitin ligase complex**

Complexes mediating ubiquitination.

GO:0140535 – Proteasomal ubiquitin-independent degradation complex

Proteasome-associated degradation.

GO:0031461 – Ubiquitin-dependent protein catabolic complex

Complexes for ubiquitin-mediated degradation.

Cluster 11 – Solute and Anion Transport (Apical Membrane)

Biological Process**GO:0015711 – Organic anion transport**

Movement of organic anions.

GO:0055085 – Transmembrane transport

Substance movement across membranes.

GO:0006811 – Ion transport

Ion displacement within or across membranes.

GO:0034220 – Ion transmembrane transport

Ion flow across membranes.

GO:0015698 – Inorganic anion transport

Transport of inorganic anions.

Molecular Function**GO:0015293 – Symporter activity**

Coupled transport of solutes.

GO:0046943 – Carboxylic acid transporter activity

Transport of carboxylate-containing molecules.

GO:0022857 – Transmembrane transporter activity

Movement of solutes through membranes.

GO:0015370 – Solute:sodium symporter activity

Co-transport of solutes with sodium.

Cellular Component**GO:0016324 – Apical plasma membrane**

Upper surface of polarized epithelial cells.

GO:0045177 – Apical part of cell

Apical cellular domain.

GO:0098590 – Membrane region

Specific membrane subregions.

Cluster 12 – Weak Signal Transduction and Low-Specificity Receptors

Cellular Component**GO:0043235 – Cytoplasmic vesicle**

Intracellular vesicles.

GO:0043005 – Neuron projection

Neuronal extensions.

GO:0098590 – Membrane region

General membrane domains.

GO:0030054 – Cell junction

Cell-cell contact points.

GO:0001750 – Photoreceptor outer segment

Photoreceptor membrane compartment.

Molecular Function**GO:0004888 – Transmembrane signaling receptor activity**

Signal reception across membranes.

GO:0038023 – Signaling receptor activity

General ligand-binding receptor function.

GO:0004714 – Receptor tyrosine kinase activity

Catalysis by RTKs.

GO:0004713 – Transmembrane receptor protein kinase activity

Kinase activity of transmembrane receptors.

GO:0004672 – Protein kinase activity

Phosphorylation of protein substrates.

Biological Process**GO:0007169 – Receptor tyrosine kinase signaling pathway**

Signaling via RTKs.

GO:0007166 – Cell surface receptor signaling

Transduction of signals across cell membranes.

GO:0043085 – Positive regulation of catalytic activity

Enhancement of enzymatic functions.

Cluster 13 – Antigen Processing and Presentation (MHC Class I & II)

Cellular Component

GO:0098553 – Cytoplasmic side of membrane

Cytosolic-facing membrane surfaces.

GO:0098576 – Endocytic vesicle membrane

Membranes of endocytic vesicles.

GO:0030134 – COPII-coated ER-to-Golgi vesicle

Transport vesicles from ER to Golgi.

GO:0012507 – ER to Golgi membrane

Membrane regions mediating ER-Golgi transport.

Molecular Function

GO:0042605 – Peptidase inhibitor activity

Inhibition of proteolytic enzymes.

GO:0003823 – Antigen binding

Recognition of antigenic peptides.

GO:0042277 – Peptide binding

Interaction with peptides.

Biological Process

GO:0048002 – Antigen processing and presentation

Preparation and display of antigens.

GO:0019882 – MHC class I antigen processing

Presentation of endogenous antigens.

GO:0019883 – MHC class II antigen processing

Presentation of exogenous antigens.

GO:0002474 – Antigen presentation via MHC class I

Presentation of peptide antigens to T cells.

Cluster 14 – Cytokine Signaling and Immune Response

Cellular Component

GO:0098552 – Side of membrane

Lateral membrane surfaces.

GO:0009897 – External side of plasma membrane

Extracellular-facing membrane.

GO:0043235 – Cytoplasmic vesicle

Intracellular vesicles.

GO:0009986 – Cell surface

Cell membrane exterior.

Molecular Function

GO:0004896 – Cytokine receptor activity

Binding and response to cytokines.

GO:0140375 – Transmembrane signaling receptor activity

Signal initiation across membranes.

GO:0019955 – Cytokine binding

Recognition of cytokine ligands.

GO:0004888 – Receptor activity

General ligand-dependent receptor activity.

Biological Process

GO:0019221 – Cytokine-mediated signaling pathway

Signal transduction activated by cytokines.

GO:0071345 – Cellular response to cytokine stimulus

Changes induced by cytokines.

GO:0034097 – Response to cytokine

General cytokine response.

Cluster 15 – Glycoprotein and Proteoglycan Biosynthesis (Golgi)

Biological Process

GO:0009100 – Glycoprotein metabolic process

Formation and modification of glycoproteins.

GO:0009101 – Glycoprotein biosynthetic process

Synthesis of glycoproteins.

GO:0006493 – Protein O-linked glycosylation

Addition of glycan chains to proteins.

GO:0030166 – Proteoglycan biosynthetic process

Synthesis of proteoglycans.

GO:0006029 – Proteoglycan metabolic process

Modification of proteoglycans.

Molecular Function

GO:0016757 – Transferase activity (glycosyl groups)

Transfer of sugar moieties to substrates.

GO:0008194 – UDP-glycosyltransferase activity

Glycan transfer from UDP-sugars.

GO:0016758 – Glycosyltransferase activity

Catalysis of glycan attachment.

GO:0016740 – Transferase activity

General group-transfer reactions.

GO:0008146 – Sulfotransferase activity

Addition of sulfate groups.

Cellular Component

GO:0000139 – Golgi membrane

Golgi-associated membranes.

GO:0005794 – Golgi apparatus

Golgi stacks.

GO:0005795 – Golgi stack

Layers of Golgi cisternae.

GO:0031985 – Golgi-associated vesicle

Vesicles derived from the Golgi.

GO:0032580 – Golgi cisterna

Single Golgi compartment.

Cluster 16 – Complex Carbohydrate and Glycolipid Metabolism (Lysosomal)

Biological Process

GO:0005975 – Carbohydrate metabolic process

Processing of carbohydrates.

GO:1901136 – Carbohydrate derivative metabolic process

Metabolism of modified sugars.

GO:0046466 – Membrane lipid biosynthetic process

Synthesis of membrane lipids.

GO:0019377 – Galactose-containing compound metabolism

Metabolism of galactose derivatives.

GO:0006687 – Glycosphingolipid metabolic process

Modification of glycosphingolipids.

Molecular Function

GO:0004553 – Hydrolase activity (O-glycosyl compounds)

Hydrolysis of sugar-containing molecules.

GO:0016798 – Hydrolase acting on glycosyl bonds

Cleavage of glycosidic bonds.

GO:0016787 – Hydrolase activity

General hydrolytic cleavage.

GO:0016788 – Hydrolase acting on ester bonds

Ester bond hydrolysis.

Cellular Component

GO:0005775 – Vacuolar/lysosomal lumen

Site of lysosomal degradation.

GO:0043202 – Lysosomal lumen

Interior of the lysosome.

GO:0005764 – Lysosome

Lysosomal organelle.

GO:0042582 – Lysosomal vesicles

Vesicles associated with lysosomal function.

GO:0035578 – Azurophil granule lumen

Granule lumen with degradative enzymes.

Cluster 17 – Actin Cytoskeleton and Cellular Motility

Biological Process

GO:0030036 – Actin cytoskeleton organization

Arrangement of actin structures.

GO:0007010 – Cytoskeleton organization

General cytoskeletal arrangement.

GO:0097435 – Supramolecular fiber organization

Assembly of large cytoskeletal fibers.

GO:0030239 – Myofibril assembly

Formation of myofibrillar structures.

GO:0031032 – Actomyosin structure organization

Arrangement of actin-myosin assemblies.

Molecular Function

GO:0003779 – Actin binding

Interaction with actin filaments.

GO:0051015 – Actin filament binding

Binding to F-actin.

GO:0008092 – Cytoskeletal protein binding

Interaction with cytoskeletal proteins.

GO:0044877 – Macromolecular complex binding

Association with large complexes.

GO:0000146 – Motor activity regulation

Regulation of actin-associated motor activity.

Cellular Component**GO:0015629 – Actin cytoskeleton**

Actin filament networks.

GO:0030017 – Sarcomere

Contractile units of muscle.

GO:0043292 – Contractile fiber

Force-generating cytoskeletal fibers.

GO:0099512 – Supramolecular actin structures

High-order actin structures.

GO:0005856 – Cytoskeleton

General cytoskeletal framework.

Cluster 18 – Amino Acid and Organic Acid Metabolism (Mitochondrial)

Biological Process**GO:0019752 – Carboxylic acid metabolic process**

Metabolism of carboxylate-containing compounds.

GO:0044281 – Small molecule metabolic process

General molecule catabolism and synthesis.

GO:0006520 – Cellular amino acid metabolic process

Metabolism of amino acids.

GO:0046395 – Carboxylic acid catabolic process

Breakdown of carboxylic acids.

GO:0032787 – Monocarboxylic acid metabolic process

Processing of monocarboxylates.

Molecular Function

GO:0016491 – Oxidoreductase activity

Redox catalysis.

GO:0000166 – Nucleotide binding

Binding to nucleotides.

GO:0016874 – Ligase activity

Formation of chemical bonds.

GO:0042802 – Identical protein binding

Self-association of proteins.

GO:0016740 – Transferase activity

Chemical group transfer.

Cellular Component

GO:0005759 – Mitochondrial matrix

Internal mitochondrial compartment.

GO:0005739 – Mitochondrion

Mitochondrial organelle.

GO:0005777 – Peroxisome

Peroxisomal localization.

GO:0070062 – Extracellular exosome

Extracellular vesicles.

GO:1902494 – Mitochondrial protein complex

Multi-protein mitochondrial complexes.

Cluster 19 – Lipid Biosynthesis and ER-Associated Enzymatic Pathways

Biological Process

GO:0008610 – Lipid biosynthetic process

Synthesis of lipids.

GO:0006629 – Lipid metabolic process

General lipid metabolism.

GO:0046486 – Glycerophospholipid metabolic process

Metabolism of membrane phospholipids.

GO:0008654 – Phospholipid biosynthetic process

Phospholipid synthesis.

GO:0006644 – Phospholipid metabolic process

Processing of phospholipids.

Molecular Function

GO:0016491 – Oxidoreductase activity

Redox catalysis.

GO:0016705 – Oxidoreductase (paired donors)

Oxygen incorporation reactions.

GO:0004497 – Monooxygenase activity

Oxygen atom insertion.

GO:0016740 – Transferase activity

Group-transfer catalysis.

GO:0005506 – Iron ion binding

Binding to iron ions, often in P450 enzymes.

Cellular Component

GO:0005789 – ER membrane

Endoplasmic reticulum membranes.

GO:0005783 – ER

Endoplasmic reticulum.

GO:0005811 – Lipid particle

Neutral lipid storage organelles.

GO:0005739 – Mitochondrion

Mitochondrial localization (lower).

GO:0000506 – ER-associated complex

Complexes involved in ER functions.

Cluster 20 – Extracellular Matrix, Cell Adhesion, Tissue Remodeling

Biological Process

GO:0030198 – ECM organization

Assembly of ECM components.

GO:0007155 – Cell adhesion

Attachment of cells to neighbors or ECM.

GO:0006508 – Proteolysis

Protein cleavage events.

GO:0030155 – Regulation of cell differentiation

Control of differentiation.

GO:0009887 – Animal organ development

Formation of tissues and organs.

Molecular Function

GO:0005201 – ECM structural constituent

Structural ECM molecules.

GO:0005198 – Structural molecule activity

General structural roles.

GO:0005539 – Glycosaminoglycan binding

Interaction with GAG chains.

GO:0005102 – Signaling receptor binding

Binding to receptors.

GO:0004222 – Metalloendopeptidase activity

Matrix metalloproteinase function.

Cellular Component

GO:0031012 – Extracellular matrix

ECM localization.

GO:0062023 – Collagen-containing ECM

Collagen-rich ECM regions.

GO:0005604 – Basement membrane

Specialized ECM layer.

GO:0070062 – Extracellular exosome

Extracellular vesicles.

GO:0001527 – Microfibril

Fibrillar ECM components.

Cluster 21 – Immune Response and Inflammatory Signaling

Biological Process

GO:0006955 – Immune response

Activation of immune mechanisms.

GO:0002376 – Immune system process

General immune functions.

GO:0050778 – Positive regulation of immune response

Enhancement of immune activity.

GO:0002250 – Adaptive immune response

Antigen-dependent immunity.

GO:0002682 – Regulation of immune system process

Control of immune activities.

Molecular Function

GO:0038023 – Signaling receptor activity

Reception of external signals.

GO:0004888 – Transmembrane signaling receptor

Receptors transmitting signals across membranes.

GO:0005102 – Signaling receptor binding

Ligand binding to receptors.

GO:0140375 – Cytokine receptor activity

Cytokine signal recognition.

GO:0005126 – Cytokine binding

Interaction with cytokines.

Cellular Component**GO:0009897 – External side of plasma membrane**

Outer membrane surface.

GO:0098552 – Cytoplasmic side of membrane

Inner membrane surface.

GO:0009986 – Cell surface

Cell membrane exterior.

GO:0072562 – Blood microparticle

Extracellular vesicles from blood cells.

GO:0070062 – Extracellular exosome

Secreted vesicles.

Cluster 22 – Microtubule Cytoskeleton and Cell Division

Biological Process**GO:0007017 – Microtubule-based process**

Processes dependent on microtubules.

GO:0000226 – Microtubule cytoskeleton organization

Formation and arrangement of microtubules.

GO:0007018 – Microtubule-based movement

Transport along microtubules.

GO:0007010 – Cytoskeleton organization

General organization of cytoskeleton.

GO:0000278 – Mitotic cell cycle

Progression through mitosis.

Molecular Function

GO terms: motor activity, microtubule binding

Functions typical of kinesins and dyneins.

Cellular Component

Microtubule cytoskeleton, centrosome, centriole

Localizations characteristic of dividing cells.

Cluster 23 – Vesicle Trafficking and Endomembrane Transport

Biological Process

GO:0016192 – Vesicle-mediated transport

Transport via vesicular carriers.

GO:0016050 – Endomembrane system

Processes within membrane-bound compartments.

GO:0051649 – Establishment of localization in cell

Positioning of molecules in cells.

GO:0046907 – Intracellular transport

Movement of substances inside cells.

GO:0015031 – Protein transport

Protein trafficking.

Molecular Function

GO:0000149 – SNARE binding

Binding to SNARE fusion machinery.

Transport and protein-binding activities

Functions required for vesicle trafficking.

Cellular Component

Endosomes, transport vesicles, Golgi-associated membranes

Key organelles of vesicular transport.

Cluster 24 – Small GTPase Signaling and Intracellular Signal Regulation

Biological Process

GO:0007264 – Small GTPase-mediated signal transduction

Signaling via Ras, Rho, Rab GTPases.

GO:0051056 – Regulation of small GTPase pathways

Control of GTPase activity.

GO:0016192 – Vesicle-mediated transport

Transport involving GTPase regulators.

GO:1902531 – Regulation of intracellular signal transduction

Modulation of signaling within cells.

GO:0035556 – Intracellular signal transduction

General intracellular signaling.

Molecular Function

GO:0030695 – GTPase regulator activity

Regulation of GTPase switching.

GO:0005096 – GTPase activator activity

Activation of GTP hydrolysis.

GO:0030234 – Enzyme regulator activity

Control of enzyme function.

GO:0008047 – Enzyme activator

Enhancement of catalytic activity.

Cellular Component

Cytosol and endomembrane regions

Diffuse intracellular localization of GTPase regulators.