| CR2 | CR4 | HP |
|---|---|---|
| aging | aging | amino-acid betaine metabolism |
| amine transport | amine catabolism | blood circulation |
| autophagy | amino-acid betaine metabolism | carnitine metabolism |
| biological adhesion | anion transport | cellular response to nutrient levels |
| carboxylic acid transport | bone resorption | chemical homeostasis |
| catecholamine metabolism | carbohydrate transport | circulatory system process |
| cell cycle | cell maturation | cofactor metabolism |
| cell cycle process | cell redox homeostasis | forebrain cell migration |
| cell-substrate adhesion | cellular aldehyde metabolism | heart development |
| cellular aldehyde metabolism | cellular modified amino acid metabolism | heme metabolism |
| cellular biogenic amine metabolism | cellular nitrogen compound biosynthesis | negative regulation of molecular function |
| cellular di-, tri-valent inorganic cation homeostasis | cellular response to stress | neuron apoptotic process |
| cellular homeostasis | coenzyme metabolism | organic anion transport |
| cellular modified amino acid metabolism | cofactor metabolism | organic cation transport |
| cellular nitrogen compound biosynthesis | cofactor transport | oxidation-reduction process |
| cellular response to heat | cytoskeleton organization | pigment metabolism |
| cellular response to stress | developmental growth | quaternary ammonium group transport |
| chromosome segregation | drug transport | response to hypoxia |
| coenzyme metabolism | ER to Golgi vesicle-mediated transport | response to oxidative stress |
| cofactor metabolism | ER-associated protein catabolism | steroid metabolism |
| cytoskeleton organization | fluid transport | tetrapyrrole metabolism |
| developmental growth | generation of precursor metabolites and energy | transmembrane transport |
| di-, tri-valent inorganic cation homeostasis | glycerol ether metabolism | vitamin metabolism |
| DNA metabolism | grooming behavior | |
| DNA-dependent DNA replication | heterocycle catabolism | |
| ER to Golgi vesicle-mediated transport | hexose metabolism | |
| exocrine pancreas development | hexose transport | |
| extracellular matrix organization | hormone metabolism | |
| extracellular structure organization | lactation | |
| fat-soluble vitamin metabolism | lipoprotein metabolism | |
| forebrain development | monovalent inorganic cation homeostasis | |
| gland development | neurotransmitter transport | |
| hormone metabolism | nucleoside bisphosphate metabolism | |
| lipid catabolism | organic acid transport | |
| maintenance of location in cell | oxidation-reduction process | |
| mammary gland development | peptide metabolism | |
| microtubule organizing center organization | pigment biosynthesis | |
| microtubule-based process | pigment metabolism | |
| morphogenesis of an epithelium | positive regulation of coagulation | |
| multicellular organismal aging | positive regulation of proteolysis | |
| negative regulation of cell projection organization | protein autophosphorylation | |
| negative regulation of NF-kappaB transcription factor activity | protein folding | |
| neuron apoptotic process | protein oligomerization | |
| nucleoside bisphosphate metabolism | regulation of hormone levels | |
| organophosphate metabolism | regulation of receptor activity | |
| osteoblast differentiation | response to drug | |
| oxidation-reduction process | response to endogenous stimulus | |
| oxygen and reactive oxygen species metabolism | response to inorganic substance | |
| peptide metabolism | response to metal ion | |
| peptidyl-proline modification | response to organic substance | |
| pigment biosynthesis | response to peptide hormone stimulus | |
| pigment metabolism | response to protein stimulus | |

| CR2 | CR4 | HP |
|---|---|---|
| positive regulation of cellular catabolism | response to starvation | |
| protein autophosphorylation | response to unfolded protein | |
| protein folding | secondary metabolism | |
| protein oligomerization | steroid metabolism | |
| regulation of protein ubiquitination | sulfur compound metabolism | |
| regulation of receptor activity | tetrapyrrole metabolism | |
| regulation of small GTPase mediated signal transduction | tissue remodeling | |
| response to abiotic stimulus | translation | |
| response to endogenous stimulus | transmembrane transport | |
| response to hormone stimulus | vitamin biosynthesis | |
| response to inorganic substance | vitamin metabolism | |
| response to metal ion | water transport | |
| response to nutrient levels | | |
| response to protein stimulus | | |
| response to unfolded protein | | |
| response to xenobiotic stimulus | | |
| secondary metabolism | | |
| sulfur compound metabolism | | |
| tetrapyrrole metabolism | | |
| translation | | |
| transmembrane transport | | |
| urogenital system development | | |
| vesicle-mediated transport | | |
| vitamin metabolism | | |

PQR CC

| CR2 | CR4 | HP |
|---|---|---|
| adherens junction | adherens junction | cell fraction |
| apical part of cell | apical part of cell | endoplasmic reticulum |
| apical plasma membrane | apical plasma membrane | insoluble fraction |
| basolateral plasma membrane | basement membrane | integral to plasma membrane |
| brush border | basolateral plasma membrane | membrane fraction |
| cell cortex | brush border | microbody |
| cell fraction | brush border membrane | microsome |
| cell projection | cell fraction | mitochondrial matrix |
| cilium part | cell projection | mitochondrion |
| cytoplasmic vesicle | costamere | peroxisome |
| cytosol | cytoplasmic dynein complex | vesicular fraction |
| endomembrane system | cytoplasmic vesicle | |
| endoplasmic reticulum | cytosol | |
| endoplasmic reticulum part | cytosolic part | |
| extracellular matrix | endomembrane system | |
| extrinsic to membrane | endoplasmic reticulum | |
| Golgi apparatus | endoplasmic reticulum part | |
| HAUS complex | envelope | |
| insoluble fraction | extrinsic to membrane | |
| intrinsic to organelle membrane | Golgi apparatus | |
| lysosome | Golgi apparatus part | |
| membrane fraction | insoluble fraction | |
| membrane-enclosed lumen | internal side of plasma membrane | |
| microbody | lytic vacuole | |
| microsome | membrane fraction | |
| mitochondrial matrix | membrane-enclosed lumen | |

| CR2 | CR4 | HP |
|---|---|---|
| mitochondrion | microbody | |
| nuclear outer membrane-endoplasmic reticulum membrane network | microsome | |
| oligosaccharyltransferase complex | mitochondrial matrix | |
| organelle membrane | mitochondrion | |
| peroxisome | nuclear outer membrane-endoplasmic reticulum membrane network | |
| proteinaceous extracellular matrix | oligosaccharyltransferase complex | |
| small ribosomal subunit | organelle membrane | |
| soluble fraction | perinuclear region of cytoplasm | |
| vacuole | peroxisome | |
| vesicle | proton-transporting V-type ATPase complex | |
| vesicular fraction | ribonucleoprotein complex | |
| | site of polarized growth | |
| | small ribosomal subunit | |
| | soluble fraction | |
| | spindle pole | |
| | vacuole | |
| | vesicle | |
| | vesicular fraction | |

PQR MF

| CR2 | CR4 | HP |
|---|---|---|
| acyl-CoA dehydrogenase activity | acetylgalactosaminyltransferase activity | 5-aminolevulinate synthase activity |
| amine transmembrane transporter activity | acyl-CoA dehydrogenase activity | cation binding |
| anion transmembrane transporter activity | anion binding | coenzyme binding |
| ATPase activity | ATPase activity | cofactor binding |
| butyrate-CoA ligase activity | beta-glucuronidase activity | electron carrier activity |
| calcium ion binding | butyrate-CoA ligase activity | exopeptidase activity |
| carbohydrate binding | carboxy-lyase activity | heme binding |
| carbon-nitrogen ligase activity, with glutamine as amido-N-donor | carboxylesterase activity | ion binding |
| carboxy-lyase activity | carboxylic acid binding | iron ion binding |
| cation binding | chloride ion binding | organic anion transmembrane transporter activity |
| chloride ion binding | cofactor binding | organic cation transmembrane transporter activity |
| coenzyme binding | drug transmembrane transporter activity | peptidase activity |
| cofactor binding | electron carrier activity | tetrapyrrole binding |
| damaged DNA binding | enzyme activator activity | transition metal ion binding |
| diphosphotransferase activity | enzyme binding | |
| drug transmembrane transporter activity | exopeptidase activity | |
| electron carrier activity | fibroblast growth factor binding | |
| enzyme activator activity | glutathione transferase activity | |
| enzyme binding | heme binding | |
| exopeptidase activity | hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear amides | |
| extracellular matrix binding | identical protein binding | |
| ferric-chelate reductase activity | intramolecular oxidoreductase activity | |
| glutathione transferase activity | ion binding | |
| heat shock protein binding | iron ion binding | |
| heme binding | kinase binding | |
| identical protein binding | lipoprotein particle receptor binding | |
| intramolecular oxidoreductase activity, interconverting keto- and enol-groups | low-density lipoprotein particle receptor binding | |
| ion binding | magnesium ion binding | |
| iron ion binding | manganese ion binding | |
| kinase binding | molybdenum ion binding | |
| lipase activity | neurotransmitter transporter activity | |
| magnesium ion binding | O-acyltransferase activity | |

| CR2 | CR4 | HP |
|---|---|---|
| manganese ion binding | oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, | |
| neurotransmitter transporter activity | oxidoreductase activity, oxidizing metal ions | |
| NF-kappaB binding | palmitoyl-CoA hydrolase activity | |
| O-acyltransferase activity | PDZ domain binding | |
| oxidoreductase activity, acting on CH or CH2 groups | protein dimerization activity | |
| oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, | protein domain specific binding | |
| oxidoreductase activity, oxidizing metal ions | protein homodimerization activity | |
| platelet-derived growth factor binding | pyridoxal phosphate binding | |
| polypeptide N-acetylgalactosaminyltransferase activity | pyruvate dehydrogenase (acetyl-transferring) kinase activity | |
| protein dimerization activity | selenium binding | |
| protein domain specific binding | steroid dehydrogenase activity | |
| protein homodimerization activity | steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | |
| pyruvate dehydrogenase (acetyl-transferring) kinase activity | structural constituent of ribosome | |
| SH3 domain binding | structural molecule activity | |
| steroid dehydrogenase activity | sugar transmembrane transporter activity | |
| steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | symporter activity | |
| structural constituent of ribosome | tetrapyrrole binding | |
| structural molecule activity | transaminase activity | |
| syntaxin binding | transferase activity, transferring alkyl or aryl (other than methyl) groups | |
| tetrapyrrole binding | transferase activity, transferring nitrogenous groups | |
| transaminase activity | translation factor activity, nucleic acid binding | |
| transferase activity, transferring alkyl or aryl (other than methyl) groups | unfolded protein binding | |
| transferase activity, transferring nitrogenous groups | vitamin B6 binding | |
| translation factor activity, nucleic acid binding | vitamin binding | |
| unfolded protein binding | voltage-gated chloride channel activity | |
| vitamin B6 binding | | |
| vitamin binding | | |