

Names	total	elements
HFD BP ND BP	417	<ul style="list-style-type: none"> cellular amino acid biosynthetic process (GO:000652) anterograde trans-synaptic signaling (GO:0098916) immune system process (GO:0002376) organelle membrane fusion (GO:0090174) protein import into nucleus (GO:0006606) regulation of an anatomical structure size (GO:0090066) nucleotide-sugar metabolic process (GO:0009225) organic acid biosynthetic process (GO:0016053) nuclear transport (GO:0051169) leukocyte mediated immunity (GO:0002443) regulation of actin polymerization or depolymerization (GO:0008064) carbohydrate derivative biosynthetic process (GO:1901137) regulation of actin filament polymerization (GO:0030853) regulation of microtubule cytoskeleton organization (GO:0070507) cellular protein metabolic process (GO:0044267) G protein-coupled receptor signaling pathway (GO:0007186) macromolecule localization (GO:0033036) pigment metabolic process (GO:0043449) nucleobase-containing compound catabolic process (GO:0034655) rRNA metabolic process (GO:016072) ubiquitin-dependent protein catabolic process (GO:0006511) macromolecule metabolic process (GO:0043170) small molecule biosynthetic process (GO:0044283) cellular protein localization (GO:0036413) nitrogen compound transport (GO:0071705) negative regulation of RNA biosynthetic process (GO:1902679) positive regulation of cellular amide metabolic process (GO:0034250) protein-containing complex assembly (GO:0050003) nucleotide-sugar biosynthetic process (GO:0009226) organic substance transport (GO:0071702) regulation of protein polymerization (GO:0032721) cellular nitrogen compound biosynthetic process (GO:0044271) purine ribonucleotide metabolic process (GO:0009150) negative regulation of transcription, DNA-templated (GO:0045892) organonitrogen compound metabolic process (GO:1901564) organ transport (GO:0006820) cellular component organization or biogenesis (GO:0071840) translation (GO:0006412) nucleobase-containing compound transport (GO:0015931) heme metabolic process (GO:0042168) carbohydrate derivative metabolic process (GO:1901135) positive regulation of immune system process (GO:0002684) protein folding (GO:0006457) maturational of SSU-rRNA (GO:0030490) ribonucleoprotein complex localization (GO:0071166) male gamete generation (GO:0048232) regulation of RNA biosynthetic process (GO:2001141) endoplasmic reticulum organization (GO:0007029) maturational of LSU-rRNA from tristructonic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000463) cellular nitrogen compound catabolic process (GO:0044270) regulation of cellular component size (GO:0032535) chemical synaptic transmission (GO:0007268) electron transport chain (GO:0022900) nucleic acid-templated transcription (GO:0097659) immune response-activating signal transduction (GO:0002757) innate immune response (GO:0045087) germ cell development (GO:0007281) cyclic-nucleotide-mediated signaling (GO:0019935) regulation of immune response (GO:0050776) proteolysis involved in cellular protein catabolic process (GO:0051603) regulation of cell activation (GO:0052865) multi-organism process (GO:0051704) intracellular protein transport (GO:0006886) cellular macromolecule catabolic process (GO:0044265) biological process (GO:0008150) response to lipopolysaccharide (GO:0032496) response to topologically incorrect protein (GO:0035966) regulation of vesicle-mediated transport (GO:0060627) cell communication (GO:0007154) regulation of supramolecular fiber organization (GO:1902903) positive regulation of cell activation (GO:0050867) cellular iron/nitrogen compound metabolic process (GO:0006725) defense response to bacterium (GO:0042742) regulation of endocytosis (GO:0030100) Unclassified (UNCLASSIFIED) cellular respiration (GO:0045333) posttranscriptional regulation of gene expression (GO:0010608) actin polymerization or depolymerization (GO:0008154) regulation of mRNA metabolic process (GO:1903311) gene expression (GO:0010467) peptide transport (GO:0015831) purine nucleotide metabolic process (GO:0006163) ribonucleoprotein complex biogenesis (GO:0022613) cell-cell signaling (GO:0007287) pyrimidine nucleobase metabolic process (GO:0006206) protein localization (GO:0008104) regulation of transcription initiation from RNA polymerase II promoter (GO:0006260) aromatic compound catabolic process (GO:0019439) ATP synthesis coupled proton transport (GO:0015986) ATP biosynthetic process (GO:0006754) purine nucleoside triphosphate metabolic process (GO:0009144) primary metabolic process (GO:0044238) protein metabolic process (GO:0019538) biosynthetic process (GO:0009058) organic substance biosynthetic process (GO:1901576) cellular component disassembly (GO:0012411) cellular nitrogen compound metabolic process (GO:0034641) modification-dependent macromolecule catabolic process (GO:0043632) ribosomal large subunit biogenesis (GO:0042273) regulation of mRNA processing (GO:0050684) RNA transport (GO:0050558) synaptic signaling (GO:0009536) response to molecule of bacterial origin (GO:0002237) positive regulation of response to stimulus (GO:0048584) proteasomal protein catabolic process (GO:0010498) positive regulation of cellular component biogenesis (GO:0044089) ribosomal small subunit biogenesis (GO:0042274) regulation of leukocyte activation (GO:0002594) positive regulation of biological process (GO:0048518) establishment of RNA localization (GO:0051236) RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (GO:0000377) humoral immune response (GO:0006959) peptide metabolic process (GO:0006518) regulation of mRNA splicing, via spliceosome (GO:0048024) positive regulation of lymphocyte activation (GO:0051251) antigen receptor-mediated signaling pathway (GO:0050851) ribonucleotide biosynthetic process (GO:0009260) protein targeting to ER (GO:0045047) pattern specification process (GO:0007389) immune response (GO:0006515) regulation of response to stimulus (GO:0048583) purine ribonucleoside triphosphate biosynthetic process (GO:0009206) response to external biotic stimulus (GO:0043207) ncRNA processing (GO:0034470) nucleoside triphosphate metabolic process (GO:0009141) retrograde vesicle-mediated transport, Golgi to endoplasmic reticulum (GO:0006890) nucleobase-containing compound metabolic process (GO:0006139) adenylate cyclase-activating G protein-coupled receptor signaling pathway (GO:0007189) ribosome biogenesis (GO:0042254) mRNA processing (GO:0006397) cofactor biosynthetic process (GO:0051188) regulation of cellular component biogenesis (GO:0044087) response to external stimulus (GO:0006005) drug metabolic process (GO:0017144) positive regulation of supramolecular fiber organization (GO:1902905) regulation of RNA polymerase II transcriptional preinitiation complex assembly (GO:0045898) RNA biosynthetic process (GO:0003274) positive regulation of actin filament polymerization (GO:0030838) cytosolic transport (GO:0016482) ncRNA metabolic process (GO:0034660) multi-organism reproductive process (GO:0044703) protein polymerization (GO:0051258) cellular catabolic process (GO:0044248) NLS-bearing protein import into nucleus (GO:0006607) cellular component assembly (GO:0022607) potassium ion transmembrane transport (GO:0071805) regulation of actin filament organization (GO:0110053) alpha-amino acid metabolic process (GO:1901605) cellular component organization (GO:0016043) macromolecule catabolic process (GO:0009057) ATP metabolic process (GO:0046034) modification-dependent protein catabolic process (GO:0019941) phagocytosis (GO:0006909) response to stimulus (GO:0050896) Ras protein signal transduction (GO:0007265) retrograde transport, endosome to Golgi (GO:0002147) endomembrane system organization (GO:0010256) response to unfolded protein (GO:0006986) detection of stimulus (GO:0051606) regulation of cellular component organization (GO:0051128) regulation of cytoskeleton organization (GO:0051493) response to organonitrogen compound (GO:0010243) ribonucleoprotein complex export from nucleus (GO:0071426) ribonucleoside triphosphate metabolic process (GO:0009199) oxidation-reduction process (GO:0055114) developmental process (GO:0032502) system process (GO:0005008) heterocycle catabolic process (GO:0046700) regulation of protein complex assembly (GO:0043254) multivesicular body sorting pathway (GO:0071985) cytoskeleton organization (GO:0007010) fatty acid catabolic process (GO:0009062) leukocyte activation (GO:0051321) transcription, DNA-templated (GO:0006351) regulation of macromolecule biosynthetic process (GO:0010556) organelle fusion (GO:0048284) organelle assembly (GO:0070925) regulation of receptor signaling pathway via STAT (GO:1904892) Golgi vesicle transport (GO:0048193) regulation of biological process (GO:0050789) purine-containing compound metabolic process (GO:0072521) COPII-coated vesicle budding (GO:0090114) ribose phosphate biosynthetic process (GO:0046390) response to toxic substance (GO:0009636) response to reactive oxygen species (GO:0003002) carboxylic acid catabolic process (GO:0046395) positive regulation of RNA polymerase II transcriptional preinitiation complex assembly (GO:0045899) actin filament organization (GO:0007015) positive regulation of protein complex assembly (GO:0031334) spermatogenesis (GO:0007283) cellular process involved in reproduction in multicellular organism (GO:0022412) generation of precursor metabolites and energy (GO:0006091) RNA catabolic process (GO:0006401) mitochondrial ATP synthesis coupled electron transport (GO:0042775) cellular metabolic process (GO:0044237) cellular macromolecule localization (GO:0070727) protein localization to nucleus (GO:0034504) protein targeting (GO:0006603) B cell activation (GO:0042113) aerobic respiration (GO:0009060) sensory perception (GO:0007600) cellular response to lipopolysaccharide (GO:0071222) adaptive immune response (GO:0001250) endoplasmic reticulum to Golgi vesicle-mediated transport (GO:0006888) organic substance metabolic process (GO:0071704) protein transport (GO:0015031) positive regulation of organelle organization (GO:0010638) regulation of transcription by RNA polymerase II (GO:0006357) cellular response to oxidative stress (GO:0034599) response to oxidative stress (GO:0006979) inflammatory response (GO:0006954) complement activation (GO:0006956) cellular response to molecule of bacterial origin (GO:0071219) small GTPase mediated signal transduction (GO:0007264) mRNA splicing, via spliceosome (GO:0003098) regulation of cellular macromolecule biosynthetic process (GO:2000112) cellular macromolecule metabolic process (GO:0044260) activation of adenylate cyclase activity (GO:0007190) cellular biosynthetic process (GO:0044249) glycolytic process (GO:0006096) purine nucleoside triphosphate biosynthetic process (GO:0009145) positive regulation of cytosolic calcium ion concentration (GO:0007204) establishment of localization in cell (GO:0051649) amide biosynthetic process (GO:0043604) purine nucleotide biosynthetic process (GO:0006164) cytoplasmic translation (GO:0002181) alternative mRNA splicing, via spliceosome (GO:0000380) cellular process (GO:0009987) oxidative phosphorylation (GO:0006119) regulation of signal transduction (GO:0009966) ribose phosphate metabolic process (GO:0019693) regulation of actin filament-based process (GO:0032970) B cell receptor signaling pathway (GO:0050853) nervous system process (GO:0050877) phosphate-containing compound metabolic process (GO:0006796) protein localization to endoplasmic reticulum (GO:0070972) nuclear export (GO:0051168) maturational of LSU-rRNA (GO:0006470) RNA splicing (GO:0008380) protein localization to organelle (GO:0033365) transport (GO:0006810) nucleoside monophosphate metabolic process (GO:0009123) immune response-activating cell surface receptor signaling pathway (GO:0002429) tetrapyrrole metabolic process (GO:0033015) purine ribonucleoside triphosphate metabolic process (GO:0009205) positive regulation of immune response (GO:0050778) translational initiation (GO:0006413) purine-containing compound biosynthetic process (GO:0072522) nucleotide phosphorylation (GO:0046939) RNA localization (GO:0006403) cellular modified amino acid metabolic process (GO:0006575) nitrogen compound metabolic process (GO:0006807) regulation of receptor signaling pathway via JAK-STAT (GO:0046425) carboxylic acid biosynthetic process (GO:0046394) cell fate commitment (GO:0045165) organic acid catabolic process (GO:0016054) cellular response to stress (GO:003354) mRNA metabolic process (GO:0016071) vesicle-mediated transport (GO:0016192) catabolic process (GO:0009056) second-messenger-mediated signaling (GO:0019932) Biological regulation (GO:0005007) response to biotic stimulus (GO:0009607) immune effector process (GO:0002252) supramolecular fiber organization (GO:0097435) organic hydroxy compound metabolic process (GO:1901615) energy coupled proton transport, down electrochemical gradient (GO:0015985) adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domain vacuolar transport (GO:0007034) signal transduction (GO:0007165) intra-Golgi vesicle-mediated transport (GO:0006891) cellular localization (GO:0051641) regulation of cellular process (GO:0050794) lymphocyte mediated immunity (GO:0002449) potassium ion transport (GO:0006813) organonitrogen compound catabolic process (GO:1901565) organic cyclic compound metabolic process (GO:1901360) anatomical structure development (GO:0048856) organonitrogen compound biosynthetic process (GO:0019156) cofactor metabolic process (GO:0051186) nucleoside triphosphate biosynthetic process (GO:0009142) cellular amino acid metabolic process (GO:0006520) cellular response to unfolded protein (GO:0034620) actin filament-based process (GO:0030029) spermatid development (GO:0007286) proton transmembrane transport (GO:1902600) carboxylic acid metabolic process (GO:0019752) DNA-adenophosphate biosynthetic process (GO:0090407) RNA-templated transcription, initiation (GO:0006352) establishment of protein localization to organelle (GO:0072594) response to inorganic substance (GO:0010035) establishment of protein localization (GO:0045184) organelle localization (GO:0051640) cellular response to stimulus (GO:0051716) purine ribonucleotide biosynthetic process (GO:0009152) RNA splicing, via transesterification reactions (GO:0003175) small molecule catabolic process (GO:0044282) positive regulation of transcription initiation from RNA polymerase II promoter (GO:0060261) transcription by RNA polymerase II (GO:0006366) immunoglobulin mediated immune response (GO:0016064) nucleoside phosphate metabolic process (GO:0006753) microtubule-based process (GO:0007017) actin cytoskeleton organization (GO:0030036) RNA processing (GO:0006364) proteolysis (GO:0006508) organelle organization (GO:0006996) metabolic process (GO:0008152) organic anion transport (GO:0015711) mitochondrion organization (GO:0007005) protein stabilization (GO:0051002) positive regulation of cytoskeleton organization (GO:0051495) chaperone-mediated protein folding (GO:0061077) response to endoplasmic reticulum stress (GO:0034976) nucleobase metabolic process (GO:0009112) membrane fusion (GO:0061025) nucleotide metabolic process (GO:0009117) heme biosynthetic process (GO:0006783) translational elongation (GO:0006414) protein export from nucleus (GO:0006611) organic acid metabolic process (GO:0006082) peptide biosynthetic process (GO:0043043) regulation of cytosolic calcium ion concentration (GO:0051480) regulation of protein stability (GO:0031647) actin filament polymerization (GO:0030041) cellular amide metabolic process (GO:0043603) regulation of cellular amide metabolic process (GO:0034248) localization (GO:0051179) regulation of transcription, DNA-templated (GO:0006355) phosphorus metabolic process (GO:0006793) ion transport (GO:0006811) RNA processing (GO:0006396) import into nucleus (GO:0051170) G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger (GO:0007187) response to other organism (GO:0051707) protein-containing complex disassembly (GO:0032984) regulation of DNA-templated transcription, initiation (GO:2000142) trans-synaptic signaling (GO:0099537) sensory perception of chemical stimulus (GO:0007006) regulation of organelle organization (GO:0033043) protein-containing complex subunit organization (GO:0043933) vesicle fusion (GO:0006906) small molecule metabolic process (GO:0044281) negative regulation of nucleic acid-templated transcription (GO:1903507) ribonucleoprotein complex subunit organization (GO:0071826) monocarboxylic acid metabolic process (GO:0032787) Golgi vesicle budding (GO:0048194) porphyrin-containing compound metabolic process (GO:0006778) cellular component biogenesis (GO:0040815) cellular response to biotic stimulus (GO:0071262) positive regulation of leukocyte activation (GO:0002696) regulation of translation (GO:0006417) multicellular organismal process (GO:0032501) regulation of actin cytoskeleton organization (GO:0002956) cell surface receptor signaling pathway (GO:0007166) immune response-regulating cell surface receptor signaling pathway (GO:0002768) nucleotide biosynthetic process (GO:0009165) endosome transport via multivesicular body sorting pathway (GO:0032509) organic substance catabolic process (GO:1901575) regulation of microtubule-based process (GO:0003286) cellular protein-containing complex assembly (GO:0034622) sulfur compound metabolic process (GO:0006790) ribonucleoprotein complex assembly (GO:0026218) protein catabolic process (GO:0030163) positive regulation of DNA-templated transcription, initiation (GO:2000144) positive regulation of cellular component organization (GO:0051130) RNA export from nucleus (GO:0006405) tricarboxylic acid cycle (GO:0006099) regulation of alternative mRNA splicing, via spliceosome (GO:0000381) energy derivation by oxidation of organic compounds (GO:0015980) ATP synthesis coupled electron transport (GO:0042773) respiratory electron transport chain (GO:0022904) proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161) ribosomal large subunit assembly (GO:0000027) ribonucleoside triphosphate biosynthetic process (GO:0009201) regulation of membrane potential (GO:0042391) nucleic acid transport (GO:0009579) metal ion transport (GO:0030001) nucleocytoplasmic transport (GO:0006913) protein import (GO:0017038) amide transport (GO:0042886) establishment of protein localization to endoplasmic reticulum (GO:0072599) regulation of lymphocyte activation (GO:0051249) regulation of nucleic acid-templated transcription (GO:1903506) cellular protein complex disassembly (GO:0034624) cell activation (GO:0001725) positive regulation of translation (GO:0045727) positive regulation of protein polymerization (GO:0032273) pre-replicative complex assembly involved in nuclear cell cycle DNA replication (GO:0006267) defense response (GO:0006952) immune response-regulating signaling pathway (GO:0002764) intracellular transport (GO:0046907) transcription initiation from RNA polymerase II promoter (GO:0006367) cellular response to topologically incorrect protein (GO:0035967) cellular protein catabolic process (GO:0044257) organic cyclic compound catabolic process (GO:1901361) response to bacterium (GO:0009617) regulation of RNA splicing (GO:0043484) activation of immune response (GO:0002253) regulation of actin filament length (GO:0030832) mRNA cis splicing, via spliceosome (GO:0045292) establishment of localization (GO:0051234) heterocycle metabolic process (GO:0046483) nucleobase-containing small molecule metabolic process (GO:0055086) regulation of immune system process (GO:0002682) reactive oxygen species metabolic process (GO:0007293) lymphocyte activation (GO:0045649) defense response to other organism (GO:0098542) nucleoside phosphate biosynthetic process (GO:1901293) organophosphate metabolic process (GO:0019637) endosomal transport (GO:0046197) Anti-CD3 complex-mediated actin nucleation (GO:0034314) antimicrobial humoral immune response mediated by antimicrobial peptide (GO:0061844) signaling (GO:0023052) ERAD pathway (GO:0036503) ribonucleotide metabolic process (GO:0009259) oxalacid metabolic process (GO:0043436) ribosome localization (GO:0003750) negative regulation of biosynthetic process (GO:0009890) mitotic cell cycle process (GO:1903047) multicellular organism development (GO:0007275) meiotic cell cycle (GO:0051321) mRNA transport (GO:0051028) regulation of cAMP-mediated signaling (GO:0043949) positive regulation of transcription, DNA-templated (GO:0045893) vesicle targeting, trans-Golgi to periciliary membrane compartment (GO:0097712) protein localization to cilium (GO:0006112) negative regulation of cellular macromolecule biosynthetic process (GO:2000113) protein transport along microtubule (GO:0098840) RNA-containing ribonucleoprotein complex export from nucleus (GO:0071428) negative regulation of cellular biosynthetic process (GO:0031327) positive regulation of RNA biosynthetic process (GO:1902680) cytokine-mediated signaling pathway (GO:0019221) negative regulation of macromolecule biosynthetic process (GO:0010558) negative regulation of nitrogen compound metabolic process (GO:0051172) protein localization zone assembly (GO:1903349) regulation (GO:0000003) reproductive process (GO:0022414) coenzyme metabolic process (GO:0006732) coenzyme biosynthetic process (GO:0009180) regulation of RNA metabolic process (GO:0051252) intracellular transport (GO:0006793) response to lipid (GO:0033993) meiotic cell cycle process (GO:1903046) negative regulation of nucleobase-containing compound metabolic process (GO:0045934) negative regulation of transcription by RNA polymerase II (GO:0000122) axone assembly (GO:0035082) regulation of cAMP-mediated signaling (GO:0043949) establishment of protein localization to vacuole (GO:0072666) negative regulation of RNA metabolic process (GO:0051253) mitotic nuclear division (GO:0140014) microtubule cytoskeleton organization involved in mitosis (GO:1902850) meiotic nuclear division (GO:0140013) positive regulation of cellular process (GO:0048522) cortical cytoskeleton organization (GO:0030865) positive regulation of nucleic acid-templated transcription (GO:1903508) establishment or maintenance of cell polarity (GO:0007163) mRNA export from nucleus (GO:0006406) ribosomal subunit export from nucleus (GO:0000054) maturational of LSU-rRNA from tristructonic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000462) cellular response to lipid (GO:0071396) cilium assembly (GO:0060271) cAMP-mediated signaling (GO:0019933) crystallite formation (GO:0042407) mitotic cell cycle (GO:0000278) receptor signaling pathway via JAK-STAT1 (GO:0007259) cell chemotaxis (GO:0005326) receptor signaling pathway via STAT (GO:0097696) inositol phosphate-mediated signaling (GO:0048016) Golgi organization (GO:0007030) cellium organization (GO:0047827) regulation of mRNA metabolic process (GO:0031326) protein modification by small protein conjugation or removal (GO:0070647) late endosome to vacuole transport (GO:0045324) intracellular transport involved in cilium assembly (GO:0035735) positive regulation of transcription by RNA polymerase II (GO:0045944) regulation of nucleobase-containing compound metabolic process (GO:0019219) negative regulation of cellular metabolic process (GO:0031324) positive regulation of RNA metabolic process (GO:0051254) regulation of biosynthetic process (GO:0009889) mRNA-containing ribonucleoprotein complex export from nucleus (GO:0071427) microtubule-based protein transport (GO:0091118) positive regulation of lipase activity (GO:0000193) embryo development (GO:0009790) microtubule bundle formation (GO:0001578) positive regulation of nucleobase-containing compound metabolic process (GO:0045935) regulation of cell communication (GO:0010646) regulation of RNA stability (GO:0043487) regulation of translational initiation (GO:0006446) regionalization (GO:0003002) RNA metabolic process (GO:0016070) animal organ development (GO:0048513) RNA 3'-end processing (GO:0031123) RNA 3'-end processing (GO:0031124) regulation of signaling (GO:0023051) Golgi to plasma membrane transport (GO:0006893) mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122) mRNA 3'-end processing (GO:0031124) post-Golgi vesicle-mediated transport (GO:0006892) pyrimidine nucleotide metabolic process (GO:0006749) regulation of mRNA stability (GO:0043488) positive regulation of cell population proliferation (GO:0008284) ubiquitin-dependent ERAD pathway (GO:0030433) response to nitrogen compound (GO:1901698) IMP metabolic process (GO:0046404) nucleobase-containing small molecule biosynthetic process (GO:0034404) RNA phosphodiester bond hydrolysis, endonucleolytic (GO:0090502) spliceosomal snRNP assembly (GO:0000387) pyrimidine nucleotide metabolic process (GO:0006226) microtubule cytoskeleton organization (GO:0000202) regulation of transcription factor activity (GO:0071417) double-strand break repair via break-induced replication (GO:0000727) import into cell (GO:0098571) nucleic acid metabolic process (GO:0090304) mRNA catabolic process (GO:0006402)
HFD BP	30	<ul style="list-style-type: none"> regulation of cell communication (GO:0010646) regulation of RNA stability (GO:0043487) regulation of translational initiation (GO:0006446) regionalization (GO:0003002) RNA metabolic process (GO:0016070) animal organ development (GO:0048513) RNA 3'-end processing (GO:0031123) RNA 3'-end processing (GO:0031124) regulation of signaling (GO:0023051) Golgi to plasma membrane transport (GO:0006893) mitochondrial electron transport, ubiquinol to cytochrome c (GO:0006122) mRNA 3'-end processing (GO:0031124) post-Golgi vesicle-mediated transport (GO:0006892) pyrimidine nucleotide metabolic process (GO:0006749) regulation of mRNA stability (GO:0043488) positive regulation of cell population proliferation (GO:0008284) ubiquitin-dependent ERAD pathway (GO:0030433) response to nitrogen compound (GO:1901698) IMP metabolic process (GO:0046404) nucleobase-containing small molecule biosynthetic process (GO:0034404) RNA phosphodiester bond hydrolysis, endonucleolytic (GO:0090502) spliceosomal snRNP assembly (GO:0000387) pyrimidine nucleotide metabolic process (GO:0006226) microtubule cytoskeleton organization (GO:0000202) regulation of transcription factor activity (GO:0071417) double-strand break repair via break-induced replication (GO:0000727) import into cell (GO:0098571) nucleic acid metabolic process (GO:0090304) mRNA catabolic process (GO:0006402)

Names	total	elements		
HFD MF ND MF	128	RNA binding (GO:0003723)		
		secondary active transmembrane transporter activity (GO:0015291)		
		voltage-gated cation channel activity (GO:0022843)		
		receptor ligand activity (GO:0048018)		
		transition metal ion binding (GO:0046914)		
		polyubiquitin modification-dependent protein binding (GO:0031593)		
		ATPase activity (GO:0016887)		
		translation initiation factor activity (GO:0003743)		
		signaling receptor binding (GO:0005102)		
		translation initiation factor binding (GO:0031369)		
		carbon-oxygen lyase activity (GO:0016835)		
		heat shock protein binding (GO:0031072)		
		ATP binding (GO:0005524)		
		lyase activity (GO:0016829)		
		ion channel activity (GO:0005216)		
		sequence-specific double-stranded DNA binding (GO:1990837)		
		single-stranded RNA binding (GO:0003727)		
		molecular_function (GO:0003674)		
		regulatory region nucleic acid binding (GO:0001067)		
		ion gated channel activity (GO:0022839)		
		actin binding (GO:0003779)		
		small molecule binding (GO:0036094)		
		catalytic activity, acting on a protein (GO:0140096)		
		metal ion binding (GO:0046872)		
		carbohydrate derivative binding (GO:0097367)		
		ribosome binding (GO:0043022)		
		drug binding (GO:0008144)		
		ATPase activity, coupled (GO:0042623)		
		nucleoside-triphosphatase regulator activity (GO:0060589)		
		signal sequence binding (GO:0005048)		
		ligase activity, forming carbon-sulfur bonds (GO:0016877)		
		DNA-binding transcription factor activity, RNA polymerase II-specific (GO:0000981)		
		catalytic activity, acting on RNA (GO:0140098)		
		G protein-coupled receptor activity (GO:0004930)		
		hydro-lyase activity (GO:0016836)		
		hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides (GO:0016818)		
		DNA binding (GO:0003677)		
		protein phosphatase binding (GO:0019903)		
		peptidase activity, acting on L-amino acid peptides (GO:0070011)		
		pyrophosphatase activity (GO:0016462)		
		peptide receptor activity (GO:0001653)		
		transmembrane transporter activity (GO:0022857)		
		isomerase activity (GO:0016853)		
		RNA polymerase II proximal promoter sequence-specific DNA binding (GO:0000978)		
		enzyme regulator activity (GO:0030234)		
		hydrolase activity, acting on acid anhydrides (GO:0016817)		
		voltage-gated potassium channel activity (GO:0005249)		
		G protein-coupled peptide receptor activity (GO:0008528)		
		ligase activity (GO:0016874)		
		ion binding (GO:0043167)		
		GTPase regulator activity (GO:0030695)		
		cytokine activity (GO:0005125)		
		metal ion transmembrane transporter activity (GO:0046873)		
		potassium ion transmembrane transporter activity (GO:0015079)		
		inorganic molecular entity transmembrane transporter activity (GO:0015318)		
		phosphatase binding (GO:0019902)		
		nucleoside-triphosphatase activity (GO:0017111)		
		ribonucleotide binding (GO:0032553)		
		organic anion transmembrane transporter activity (GO:0008514)		
		ubiquitin binding (GO:0043130)		
		hydrolase activity (GO:0016787)		
		GTPase activity (GO:0003924)		
		heterocyclic compound binding (GO:1901363)		
		double-stranded DNA binding (GO:0003690)		
		signaling receptor activator activity (GO:0030546)		
		purine nucleotide binding (GO:0017076)		
		transcription regulator activity (GO:0140110)		
		DNA-binding transcription factor activity (GO:0003700)		
		potassium channel activity (GO:0005267)		
		mRNA binding (GO:0003729)		
		methylated histone binding (GO:0035064)		
		oxidoreductase activity (GO:0016491)		
		ion transmembrane transporter activity (GO:0015075)		
		transmembrane signaling receptor activity (GO:0004888)		
		Unclassified (UNCLASSIFIED)		
		structural constituent of nuclear pore (GO:0017056)		
		catalytic activity (GO:0003824)		
		ribonucleoprotein complex binding (GO:0043021)		
		single-stranded DNA binding (GO:0003697)		
		transcription regulatory region sequence-specific DNA binding (GO:0000976)		
		neurotransmitter receptor activity (GO:0030594)		
		rRNA binding (GO:0019843)		
		gated channel activity (GO:0022836)		
		cytoskeletal protein binding (GO:0008092)		
		cation channel activity (GO:0005261)		
		channel activity (GO:0015267)		
		signaling receptor activity (GO:0038023)		
		cofactor binding (GO:0048037)		
		structural constituent of ribosome (GO:0003735)		
		molecular transducer activity (GO:0060089)		
		neurotransmitter binding (GO:0042165)		
		passive transmembrane transporter activity (GO:0022803)		
		electron transfer activity (GO:0009055)		
		protein-containing complex binding (GO:0044877)		
		sequence-specific DNA binding (GO:0043565)		
		receptor regulator activity (GO:0030545)		
		RNA polymerase II regulatory region DNA binding (GO:0001012)		
		unfolded protein binding (GO:0051082)		
		RNA polymerase II regulatory region sequence-specific DNA binding (GO:0000977)		
		cytokine binding (GO:0019955)		
		cation transmembrane transporter activity (GO:0008324)		
		GTP binding (GO:0005525)		
		nucleoside phosphate binding (GO:1901265)		
		oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616)		
		inorganic cation transmembrane transporter activity (GO:0022890)		
		transporter activity (GO:0005215)		
		hormone activity (GO:0005179)		
		actin filament binding (GO:0051015)		
		enzyme binding (GO:0019899)		
		anion binding (GO:0043168)		
		ubiquitin-like modifier activating enzyme activity (GO:0008641)		
		peptidase activity (GO:0008233)		
		purine ribonucleotide binding (GO:0032555)		
		nucleotide binding (GO:0000166)		
		structural molecule activity (GO:0005198)		
		chaperone binding (GO:0051087)		
		binding (GO:0005488)		
		transcription regulatory region DNA binding (GO:0044212)		
		DNA-binding transcription activator activity, RNA polymerase II-specific (GO:0001228)		
		purine ribonucleoside triphosphate binding (GO:0035639)		
		nucleic acid binding (GO:0003676)		
		protein binding (GO:0005515)		
		mRNA 3'-UTR binding (GO:0003730)		
		organic cyclic compound binding (GO:0097159)		
		DNA-binding transcription activator activity (GO:0001216)		
		translation regulator activity (GO:0045182)		
		cytokine receptor binding (GO:0005126)		
ND MF	13	RNA polymerase activity (GO:0097747)		
		voltage-gated ion channel activity (GO:0005244)		
		sterol binding (GO:0032934)		
		voltage-gated channel activity (GO:0022832)		
		carbohydrate binding (GO:0030246)		
		monooxygenase activity (GO:0004497)		
		NADH dehydrogenase activity (GO:0003954)		
		steroid hydroxylase activity (GO:0008395)		
		G protein-coupled receptor binding (GO:0001664)		
		carbohydrate kinase activity (GO:0019200)		
		5'-3' RNA polymerase activity (GO:0034062)		
		transferase activity (GO:0016740)		
		DNA-directed 5'-3' RNA polymerase activity (GO:0003899)		
HFD MF	4	proton transmembrane transporter activity (GO:0015078)		
		anion transmembrane transporter activity (GO:0008509)		
		DNA-dependent ATPase activity (GO:0008094)		
		snRNA binding (GO:0017069)		

Names	total	elements		
HFD BP ND BP	234	<p>complement activation (GO:0006956)</p> <p>immune system process (GO:0002376)</p> <p>mRNA splicing, via spliceosome (GO:0000398)</p> <p>regulation of anatomical structure size (GO:0090066)</p> <p>regulation of cellular macromolecule biosynthetic process (GO:2000112)</p> <p>cellular macromolecule metabolic process (GO:0044260)</p> <p>organic cyclic compound biosynthetic process (GO:1901362)</p> <p>locomotion (GO:0040011)</p> <p>angiogenesis (GO:0001525)</p> <p>leukocyte mediated immunity (GO:0002443)</p> <p>regulation of actin polymerization or depolymerization (GO:0008064)</p> <p>regulation of actin filament polymerization (GO:0030833)</p> <p>regulation of peptidase activity (GO:0052547)</p> <p>cell motility (GO:0048870)</p> <p>cellular protein metabolic process (GO:0044267)</p> <p>glycolytic process (GO:0006096)</p> <p>G protein-coupled receptor signaling pathway (GO:0007186)</p> <p>anatomical structure morphogenesis (GO:0009653)</p> <p>amide biosynthetic process (GO:0043604)</p> <p>extracellular matrix organization (GO:0030198)</p> <p>ubiquitin-dependent protein catabolic process (GO:0006511)</p> <p>growth (GO:0040007)</p> <p>cytoplasmic translation (GO:0002181)</p> <p>neuron projection development (GO:0031175)</p> <p>cellular process (GO:0009987)</p> <p>aromatic compound biosynthetic process (GO:0019438)</p> <p>regulation of actin filament-based process (GO:0032970)</p> <p>negative regulation of protein metabolic process (GO:0051248)</p> <p>macromolecule metabolic process (GO:0043170)</p> <p>small molecule biosynthetic process (GO:0044283)</p> <p>B cell receptor signaling pathway (GO:0050853)</p> <p>extracellular structure organization (GO:0043062)</p> <p>cell migration (GO:0016477)</p> <p>nervous system process (GO:0050877)</p> <p>negative regulation of RNA biosynthetic process (GO:1902679)</p> <p>protein-containing complex assembly (GO:0065003)</p> <p>axo-dendritic transport (GO:0008088)</p> <p>tube morphogenesis (GO:0035239)</p> <p>cellular lipid metabolic process (GO:0044255)</p> <p>cell projection morphogenesis (GO:0048858)</p> <p>RNA splicing (GO:0008380)</p> <p>regulation of protein polymerization (GO:0032271)</p> <p>regulation of biological quality (GO:0065008)</p> <p>multicellular organism development (GO:0007275)</p> <p>negative regulation of transcription, DNA-templated (GO:0045892)</p> <p>muscle structure development (GO:0061061)</p> <p>organonitrogen compound metabolic process (GO:1901564)</p> <p>immune response-activating cell surface receptor signaling pathway (GO:0002429)</p> <p>positive regulation of immune response (GO:0050778)</p> <p>translation (GO:0006412)</p> <p>cellular component organization or biogenesis (GO:0071840)</p> <p>translational initiation (GO:0006413)</p> <p>tube development (GO:0035295)</p> <p>protein folding (GO:0006457)</p> <p>nucleotide phosphorylation (GO:0046939)</p> <p>nitrogen compound metabolic process (GO:0006807)</p> <p>IMP metabolic process (GO:0046040)</p> <p>regulation of RNA biosynthetic process (GO:2001141)</p> <p>regulation of cellular component size (GO:0032535)</p> <p>neurogenesis (GO:0022008)</p> <p>nucleic acid-templated transcription (GO:0097659)</p> <p>catabolic process (GO:0009056)</p> <p>immune response-activating signal transduction (GO:0002757)</p> <p>negative regulation of actin filament polymerization (GO:0030837)</p> <p>axon development (GO:0061564)</p> <p>supramolecular fiber organization (GO:0097435)</p> <p>proteolysis involved in cellular protein catabolic process (GO:0051603)</p> <p>regulation of immune response (GO:0050776)</p> <p>multi-organism process (GO:0051704)</p> <p>adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domain (GO:0002429)</p> <p>cellular macromolecule catabolic process (GO:0044265)</p> <p>biological process (GO:0008150)</p> <p>anatomical structure formation involved in morphogenesis (GO:0048646)</p> <p>developmental growth (GO:0048589)</p> <p>cell development (GO:0048468)</p> <p>signal transduction (GO:0007165)</p> <p>cell communication (GO:0007154)</p> <p>negative regulation of endopeptidase activity (GO:0010951)</p> <p>regulation of supramolecular fiber organization (GO:1902903)</p> <p>lymphocyte mediated immunity (GO:0002449)</p> <p>cell differentiation (GO:0030154)</p> <p>Unclassified (UNCLASSIFIED)</p> <p>organonitrogen compound catabolic process (GO:1901565)</p> <p>posttranscriptional regulation of gene expression (GO:0010608)</p> <p>actin polymerization or depolymerization (GO:0008154)</p> <p>anatomical structure development (GO:0048856)</p> <p>organonitrogen compound biosynthetic process (GO:1901566)</p> <p>proteasome assembly (GO:0043248)</p> <p>purine nucleotide metabolic process (GO:0006163)</p> <p>ribonucleoprotein complex biogenesis (GO:0022613)</p> <p>regulation of cellular protein metabolic process (GO:0032268)</p> <p>positive chemotaxis (GO:0050918)</p> <p>sprouting angiogenesis (GO:0002040)</p> <p>generation of neurons (GO:0048699)</p> <p>actin filament-based process (GO:0030029)</p> <p>system development (GO:0048731)</p> <p>primary metabolic process (GO:0044238)</p> <p>protein metabolic process (GO:0019538)</p> <p>actin filament depolymerization (GO:0030042)</p> <p>ribosomal large subunit biogenesis (GO:0004273)</p> <p>modification-dependent macromolecule catabolic process (GO:0043632)</p> <p>response to inorganic substance (GO:0010035)</p> <p>cellular response to stimulus (GO:0051716)</p> <p>movement of cell or subcellular component (GO:0006928)</p> <p>RNA splicing, via transesterification reactions (GO:0000375)</p> <p>transcription by RNA polymerase II (GO:0006366)</p> <p>immunoglobulin mediated immune response (GO:0016064)</p> <p>proteasomal protein catabolic process (GO:0010498)</p> <p>ribosomal small subunit biogenesis (GO:0042274)</p> <p>positive regulation of cellular component biogenesis (GO:1902905)</p> <p>microtubule-based process (GO:0007017)</p> <p>RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (GO:0000377)</p> <p>actin cytoskeleton organization (GO:0030036)</p> <p>vasculature development (GO:0001944)</p> <p>humoral immune response (GO:0006959)</p> <p>proteolysis (GO:0006508)</p> <p>organelle organization (GO:0006996)</p> <p>peptide metabolic process (GO:0006518)</p> <p>metabolic process (GO:0008152)</p> <p>regulation of mRNA splicing, via spliceosome (GO:0048024)</p> <p>protein stabilization (GO:0050821)</p> <p>positive regulation of cytoskeleton organization (GO:0051495)</p> <p>chaperone-mediated protein folding (GO:0061077)</p> <p>nucleobase metabolic process (GO:0009112)</p> <p>cell morphogenesis involved in neuron differentiation (GO:0048667)</p> <p>animal organ morphogenesis (GO:0009887)</p> <p>antigen receptor-mediated signaling pathway (GO:0050851)</p> <p>cell part morphogenesis (GO:0032990)</p> <p>regulation of protein metabolic process (GO:0051246)</p> <p>protein depolymerization (GO:0051261)</p> <p>immune response (GO:0006955)</p> <p>translational elongation (GO:0006414)</p> <p>neuron development (GO:0048666)</p> <p>peptide biosynthetic process (GO:0043043)</p> <p>regulation of protein stability (GO:0031647)</p> <p>regulation of transcription, DNA-templated (GO:0006355)</p> <p>cellular amide metabolic process (GO:0043603)</p> <p>actin filament polymerization (GO:0030041)</p> <p>ion transport (GO:0006811)</p> <p>localization of cell (GO:0051674)</p> <p>cell morphogenesis involved in differentiation (GO:0000904)</p> <p>protein-containing complex disassembly (GO:0032984)</p> <p>dendrite development (GO:0016358)</p> <p>ribosome biogenesis (GO:0042254)</p> <p>negative regulation of proteolysis (GO:0045861)</p> <p>regulation of cellular component biogenesis (GO:0044087)</p> <p>sensory perception of chemical stimulus (GO:0007606)</p> <p>regulation of organelle organization (GO:0033043)</p> <p>protein-containing complex subunit organization (GO:0043933)</p> <p>positive regulation of supramolecular fiber organization (GO:1902905)</p> <p>negative regulation of nucleic acid-templated transcription (GO:1903507)</p> <p>small molecule metabolic process (GO:0044281)</p> <p>ribonucleoprotein complex subunit organization (GO:0071826)</p> <p>RNA biosynthetic process (GO:0032774)</p> <p>positive regulation of actin filament polymerization (GO:0030838)</p> <p>tissue development (GO:0009888)</p> <p>cellular component biogenesis (GO:0044085)</p> <p>protein polymerization (GO:0051258)</p> <p>cellular catabolic process (GO:0044248)</p> <p>regulation of translation (GO:0006417)</p> <p>circulatory system development (GO:0072359)</p> <p>cellular component assembly (GO:0022607)</p> <p>blood vessel development (GO:0001568)</p> <p>regulation of actin cytoskeleton organization (GO:0032956)</p> <p>negative regulation of hydrolase activity (GO:0051346)</p> <p>immune response-regulating cell surface receptor signaling pathway (GO:0002768)</p> <p>regulation of actin filament organization (GO:0110053)</p> <p>cellular component organization (GO:0016043)</p> <p>macromolecule catabolic process (GO:0009057)</p> <p>modification-dependent protein catabolic process (GO:0019941)</p> <p>organic substance catabolic process (GO:1901575)</p> <p>nucleobase-containing compound biosynthetic process (GO:0034654)</p> <p>response to stimulus (GO:0050896)</p> <p>cellular protein-containing complex assembly (GO:0034622)</p> <p>neuron differentiation (GO:0030182)</p> <p>ribonucleoprotein complex assembly (GO:0022618)</p> <p>protein catabolic process (GO:0030163)</p> <p>regulation of cellular component organization (GO:0051128)</p> <p>regulation of cytoskeleton organization (GO:0051493)</p> <p>positive regulation of cellular component organization (GO:0051130)</p> <p>response to hypoxia (GO:0001666)</p> <p>cell morphogenesis (GO:0000902)</p> <p>oxidation-reduction process (GO:0055114)</p> <p>developmental process (GO:0032502)</p> <p>regulation of protein complex assembly (GO:0043254)</p> <p>cytoskeleton organization (GO:0007010)</p> <p>heterocycle biosynthetic process (GO:0018130)</p> <p>transcription, DNA-templated (GO:0006351)</p> <p>proteasome-mediated ubiquitin-dependent protein catabolic process (GO:0043161)</p> <p>organelle assembly (GO:0070925)</p> <p>ribosomal large subunit assembly (GO:0000027)</p> <p>purine-containing compound metabolic process (GO:0072521)</p> <p>regulation of lymphocyte activation (GO:0051249)</p> <p>negative regulation of cellular protein metabolic process (GO:0032269)</p> <p>regulation of nucleic acid-templated transcription (GO:1903506)</p> <p>negative regulation of peptidase activity (GO:0010466)</p> <p>response to toxic substance (GO:0009636)</p> <p>cellular protein complex disassembly (GO:0043624)</p> <p>positive regulation of protein polymerization (GO:0032273)</p> <p>cellular component morphogenesis (GO:0032989)</p> <p>response to reactive oxygen species (GO:0000302)</p> <p>negative regulation of cellular component organization (GO:0051129)</p> <p>actin filament organization (GO:0007015)</p> <p>collagen fibril organization (GO:0030199)</p> <p>regulation of synapse organization (GO:0050807)</p> <p>immune response-regulating signaling pathway (GO:0002764)</p> <p>positive regulation of protein complex assembly (GO:0031334)</p> <p>cellular protein catabolic process (GO:0044257)</p> <p>regulation of endopeptidase activity (GO:0052548)</p> <p>generation of precursor metabolites and energy (GO:0006091)</p> <p>response to bacterium (GO:0009617)</p> <p>cellular metabolic process (GO:0044237)</p> <p>regulation of RNA splicing (GO:0043484)</p> <p>activation of immune response (GO:0002253)</p> <p>regulation of actin filament length (GO:0030832)</p> <p>blood vessel morphogenesis (GO:0048514)</p> <p>nucleobase-containing small molecule metabolic process (GO:0055086)</p> <p>B cell activation (GO:0042113)</p> <p>sensory perception (GO:0007600)</p> <p>adaptive immune response (GO:0002250)</p> <p>lymphocyte activation (GO:0046649)</p> <p>reactive oxygen species metabolic process (GO:0072593)</p> <p>organic substance metabolic process (GO:0071704)</p> <p>axonogenesis (GO:0007409)</p> <p>Arp2/3 complex-mediated actin nucleation (GO:0034314)</p> <p>cardiovascular system development (GO:0072358)</p> <p>neuron projection morphogenesis (GO:0048812)</p> <p>positive regulation of organelle organization (GO:0010638)</p> <p>signaling (GO:0023052)</p> <p>regulation of transcription by RNA polymerase II (GO:0006357)</p> <p>cellular response to oxidative stress (GO:0034599)</p> <p>plasma membrane bounded cell projection morphogenesis (GO:0120039)</p> <p>response to oxidative stress (GO:0006979)</p>		
ND BP	50	<p>positive regulation of locomotion (GO:0040017)</p> <p>negative regulation of catalytic activity (GO:0043086)</p> <p>regulation of anatomical structure morphogenesis (GO:0022603)</p> <p>positive regulation of cellular component movement (GO:0051272)</p> <p>organelle transport along microtubule (GO:0072384)</p> <p>biological regulation (GO:0065007)</p> <p>positive regulation of transcription, DNA-templated (GO:0045893)</p> <p>positive regulation of nucleic acid-templated transcription (GO:1903508)</p> <p>nucleus localization (GO:0051647)</p> <p>RNA metabolic process (GO:0016070)</p> <p>myeloid leukocyte migration (GO:0097529)</p> <p>nuclear migration (GO:0007097)</p> <p>leukocyte chemotaxis (GO:0030595)</p> <p>carboxylic acid metabolic process (GO:0019752)</p> <p>cellular component disassembly (GO:0022411)</p> <p>muscle contraction (GO:0006936)</p> <p>regulation of microtubule polymerization or depolymerization (GO:0031110)</p> <p>nucleoside phosphate metabolic process (GO:0006753)</p> <p>enzyme linked receptor protein signaling pathway (GO:0007167)</p> <p>positive regulation of RNA biosynthetic process (GO:1902680)</p> <p>response to endoplasmic reticulum stress (GO:0034976)</p> <p>neuron projection guidance (GO:0097485)</p> <p>nucleotide metabolic process (GO:0009117)</p> <p>microtubule cytoskeleton organization (GO:0000226)</p> <p>organic acid metabolic process (GO:0006082)</p> <p>leukocyte migration (GO:0050900)</p> <p>cellular developmental process (GO:0048869)</p> <p>axon guidance (GO:0007411)</p> <p>chemotaxis (GO:0006935)</p> <p>positive regulation of macromolecule biosynthetic process (GO:0010557)</p> <p>regulation of cellular biosynthetic process (GO:0031326)</p> <p>cell projection organization (GO:0030030)</p> <p>nucleic acid metabolic process (GO:0090304)</p> <p>positive regulation of cell motility (GO:2000147)</p> <p>regulation of macromolecule biosynthetic process (GO:0010556)</p> <p>regulation of biological process (GO:0050789)</p> <p>regulation of gene expression (GO:0010468)</p> <p>positive regulation of transcription by RNA polymerase II (GO:0045944)</p> <p>regulation of nucleobase-containing compound metabolic process (GO:0019219)</p> <p>nervous system development (GO:0007399)</p> <p>regulation of RNA metabolic process (GO:0051252)</p> <p>positive regulation of RNA metabolic process (GO:0051254)</p> <p>regulation of biosynthetic process (GO:0009889)</p> <p>negative regulation of nucleobase-containing compound metabolic process (GO:0045934)</p> <p>regulation of cell motility (GO:2000145)</p> <p>taxis (GO:0042330)</p> <p>positive regulation of cell migration (GO:0030335)</p> <p>ribonucleotide metabolic process (GO:0009259)</p> <p>oxoacid metabolic process (GO:0043436)</p> <p>positive regulation of nucleobase-containing compound metabolic process (GO:0045935)</p>		
HFD BP	40	<p>protein import into nucleus (GO:0006606)</p> <p>transmembrane transport (GO:0055085)</p> <p>alternative mRNA splicing, via spliceosome (GO:0000380)</p> <p>intracellular signal transduction (GO:0035556)</p> <p>maturation of SSU-rRNA (GO:0030490)</p> <p>cation transport (GO:0006812)</p> <p>mRNA metabolic process (GO:0016071)</p> <p>response to biotic stimulus (GO:0009607)</p> <p>innate immune response (GO:0045087)</p> <p>immune effector process (GO:0002252)</p> <p>intra-Golgi vesicle-mediated transport (GO:0006891)</p> <p>defense response to bacterium (GO:0042742)</p> <p>ion transmembrane transport (GO:0034220)</p> <p>regulation of mRNA metabolic process (GO:1903311)</p> <p>regulation of transcription initiation from RNA polymerase II promoter (GO:0060260)</p> <p>peptidyl-lysine modification (GO:0018205)</p> <p>cellular nitrogen compound metabolic process (GO:0034641)</p> <p>regulation of mRNA processing (GO:0050684)</p> <p>regulation of proteolysis (GO:0030162)</p> <p>positive regulation of transcription initiation from RNA polymerase II promoter (GO:0060261)</p> <p>bone morphogenesis (GO:0060349)</p> <p>positive regulation of lymphocyte activation (GO:0051251)</p> <p>regulation of cellular amide metabolic process (GO:0034248)</p> <p>response to external biotic stimulus (GO:0043207)</p> <p>RNA processing (GO:0006396)</p> <p>import into nucleus (GO:0051170)</p> <p>response to other organism (GO:0051707)</p> <p>regulation of DNA-templated transcription, initiation (GO:2000142)</p> <p>mRNA processing (GO:0006397)</p> <p>regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0090092)</p> <p>regulation of RNA polymerase II transcriptional preinitiation complex assembly (GO:0045898)</p> <p>negative regulation of organelle organization (GO:0010639)</p> <p>positive regulation of DNA-templated transcription, initiation (GO:2000144)</p> <p>regulation of alternative mRNA splicing, via spliceosome (GO:0000381)</p> <p>defense response (GO:0006952)</p> <p>positive regulation of RNA polymerase II transcriptional preinitiation complex assembly (GO:0045899)</p> <p>transcription initiation from RNA polymerase II promoter (GO:0006367)</p> <p>regulation of immune system process (GO:0002682)</p> <p>defense response to other organism (GO:0098542)</p> <p>RNA polymerase II preinitiation complex assembly (GO:0051123)</p>		

Names	total	elements		
HFD BP ND BP	85	RNA binding (GO:0003723)		
		ribonucleotide binding (GO:0032553)		
		hydrolase activity (GO:0016787)		
		extracellular matrix structural constituent (GO:0005201)		
		heterocyclic compound binding (GO:1901363)		
		double-stranded DNA binding (GO:0003690)		
		cell adhesion molecule binding (GO:0050839)		
		purine nucleotide binding (GO:0017076)		
		translation initiation factor activity (GO:0003743)		
		transcription regulator activity (GO:0140110)		
		DNA-binding transcription factor activity (GO:0003700)		
		mRNA binding (GO:0003729)		
		extracellular matrix binding (GO:0050840)		
		oxidoreductase activity (GO:0016491)		
		ion transmembrane transporter activity (GO:0015075)		
		transmembrane signaling receptor activity (GO:0004888)		
		integrin binding (GO:0005178)		
		Unclassified (UNCLASSIFIED)		
		catalytic activity (GO:0003824)		
		ribonucleoprotein complex binding (GO:0043021)		
		oxidoreductase activity, acting on peroxide as acceptor (GO:0016684)		
		molecular_function (GO:0003674)		
		heparin binding (GO:0008201)		
		serine hydrolase activity (GO:0017171)		
		regulatory region nucleic acid binding (GO:0001067)		
		rRNA binding (GO:0019843)		
		endopeptidase activity (GO:0004175)		
		cytoskeletal protein binding (GO:0008092)		
		cation channel activity (GO:0005261)		
		actin binding (GO:0003779)		
		small molecule binding (GO:0036094)		
		signaling receptor activity (GO:0038023)		
		catalytic activity, acting on a protein (GO:0140096)		
		metal ion binding (GO:0046872)		
		carbohydrate derivative binding (GO:0097367)		
		ribosome binding (GO:0043022)		
		drug binding (GO:0008144)		
		molecular transducer activity (GO:0060089)		
		structural constituent of ribosome (GO:0003735)		
		protein-containing complex binding (GO:0044877)		
		DNA-binding transcription factor activity, RNA polymerase II-specific (GO:0000981)		
		G protein-coupled receptor activity (GO:0004930)		
		sequence-specific DNA binding (GO:0043565)		
		RNA polymerase II regulatory region DNA binding (GO:0001012)		
		enzyme inhibitor activity (GO:0004857)		
		RNA polymerase II regulatory region sequence-specific DNA binding (GO:0000977)		
		unfolded protein binding (GO:0051082)		
		cation transmembrane transporter activity (GO:0008324)		
		protease binding (GO:0002020)		
		metalloendopeptidase activity (GO:0004222)		
		oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor (GO:0016616)		
		nucleoside phosphate binding (GO:1901265)		
		inorganic cation transmembrane transporter activity (GO:0022890)		
		peptidase inhibitor activity (GO:0030414)		
		transporter activity (GO:0005215)		
		endopeptidase inhibitor activity (GO:0004866)		
		actin filament binding (GO:0051015)		
		anion binding (GO:0043168)		
		DNA binding (GO:0003677)		
		peptidase regulator activity (GO:0061134)		
		serine-type endopeptidase activity (GO:0004252)		
		peptidase activity (GO:0008233)		
		peptidase activity, acting on L-amino acid peptides (GO:0070011)		
		glycosaminoglycan binding (GO:0005539)		
		purine ribonucleotide binding (GO:0032555)		
		transmembrane transporter activity (GO:0022857)		
		isomerase activity (GO:0016853)		
		enzyme regulator activity (GO:0030234)		
		nucleotide binding (GO:0000166)		
		structural molecule activity (GO:0005198)		
		hydrolase activity, acting on acid phosphorus-nitrogen bonds (GO:0016825)		
		binding (GO:0005488)		
		ligase activity (GO:0016874)		
		transcription regulatory region DNA binding (GO:0044212)		
		purine ribonucleoside triphosphate binding (GO:0035639)		
		protein binding (GO:0005515)		
		nucleic acid binding (GO:0003676)		
		ion binding (GO:0043167)		
		protein serine/threonine kinase activity (GO:0004674)		
		organic cyclic compound binding (GO:0097159)		
		metal ion transmembrane transporter activity (GO:0046873)		
		inorganic molecular entity transmembrane transporter activity (GO:0015318)		
		translation regulator activity (GO:0045182)		
		metallopeptidase activity (GO:0008237)		
ND BP	6	growth factor binding (GO:0019838)		
		sequence-specific double-stranded DNA binding (GO:1990837)		
		disulfide oxidoreductase activity (GO:0015036)		
		transcription regulatory region sequence-specific DNA binding (GO:0000976)		
		molecular function regulator (GO:0098772)		
		collagen binding (GO:0005518)		
HFD BP	11	transferase activity, transferring phosphorus-containing groups (GO:0016772)		
		active transmembrane transporter activity (GO:0022804)		
		heat shock protein binding (GO:0031072)		
		translation initiation factor binding (GO:0031369)		
		ATP binding (GO:0005524)		
		protein kinase activity (GO:0004672)		
		phosphotransferase activity, alcohol group as acceptor (GO:0016773)		
		2-oxoglutarate-dependent dioxygenase activity (GO:0016706)		
		kinase activity (GO:0016301)		
		monovalent inorganic cation transmembrane transporter activity (GO:0015077)		
		transferase activity (GO:0016740)		