Symbol	Molecular Function	Biological Process	Cellular Component	Category
CTSE	GO:0004190;aspartic-type endopeptidase activity|GO:0008233; peptidase activity	GO:0007586;digestion|GO:0006508;proteolysis|GO:0019886;antigen processing and presentation of exogenous peptide antigen via MHC class II	GO:0005768;endosome	Antigen_Processing_and_Presentation_geneOntology
PSMD2	GO:0005515;protein binding|GO:0030234; enzyme regulator activity	GO:0042176;regulation of protein catabolic process|GO:0031145;anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process|GO:0051437;positive regulation of ubiquitin-protein ligase activity during mitotic cell cycle|GO:0051436;negative regulation of ubiquitin-protein ligase activity during mitotic cell cycle	GO:0005838;proteasome regulatory particle|GO:0000502;proteasome complex|GO:0005829;cytosol	Antigen_Processing_and_Presentation_geneOntology
CXCL2	GO:0008009;chemokine activity	GO:0006935;chemotaxis|GO:0006954;inflammatory response|GO:0006955;immune response	GO:0005625;soluble fraction|GO:0005576;extracellular region|GO:0005615;extracellular space	Chemokine_geneOntology
CYR61	GO:0005520;insulin-like growth factor binding|GO:0008201; heparin binding	GO:0001569;patterning of blood vessels|GO:0006935;chemotaxis|GO:0008283;cell proliferation|GO:0007155;cell adhesion|GO:0001558;regulation of cell growth|GO:0009653;anatomical structure morphogenesis	GO:0005576;extracellular region	Chemokine_geneOntology
CMTM1	GO:0005125;cytokine	GO:0006935;chemotaxis	GO:0016021;integral to	Cytokines_geneOntology

	activity		membrane|GO:0005615;extracellular space|GO:0016020;membrane	
CXCL2	GO:0008009;chemokine activity	GO:0006935;chemotaxis|GO:0006954;inflammatory response|GO:0006955;immune response	GO:0005625;soluble fraction|GO:0005576;extracellular region|GO:0005615;extracellular space	Cytokines_geneOntology
CYR61	GO:0005520;insulin-like growth factor binding|GO:0008201;heparin binding	GO:0001569;patterning of blood vessels|GO:0006935;chemotaxis|GO:0008283;cell proliferation|GO:0007155;cell adhesion|GO:0001558;regulation of cell growth|GO:0009653;anatomical structure morphogenesis	GO:0005576;extracellular region	Cytokines_geneOntology
VEGFC	GO:0008083;growth factor activity|GO:0043185;vascular endothelial growth factor receptor 3 binding	GO:0030154;cell differentiation|GO:0016331;morphogenesis of embryonic epithelium|GO:0002052;positive regulation of neuroblast proliferation|GO:0048010;vascular endothelial growth factor receptor signaling pathway|GO:0001525;angiogenesis|GO:0006929;substrate-bound cell migration|GO:0007275;multicellular organismal development|GO:0009887;organ morphogenesis|GO:0007165;signal	GO:0016020;membrane|GO:0005615;extracellular space|GO:0031093;platelet alpha granule lumen|GO:0005576;extracellular region	Cytokines_geneOntology

		transduction		
SDC1	GO:0008092;cytoskeletal protein binding|GO:0008022;protein C-terminus binding		GO:0016020;membrane|GO:0005887;integral to plasma membrane	Cytokines_Receptors_geneOntology
TNFRSF6B	GO:0005515;protein binding|GO:0004872;receptor activity	GO:0006915;apoptosis|GO:0006916;anti-apoptosis	GO:0005576;extracellular region|GO:0005625;soluble fraction	Cytokines_Receptors_geneOntology
GRB2	GO:0005070;SH3/SH2 adaptor activity|GO:0043560;insulin receptor substrate binding|GO:0005154;epidermal growth factor receptor binding	GO:0007265;Ras protein signal transduction|GO:0008286;insulin receptor signaling pathway|GO:0044419;interspecies interaction between organisms|GO:0007173;epidermal growth factor receptor signaling pathway|GO:0007267;cell-cell signaling	GO:0005829;cytosol|GO:0005794;Golgi apparatus	NaturalKiller_Cell_Cytotoxicity_geneOntology
GRB2	GO:0005070;SH3/SH2 adaptor activity|GO:0043560;insulin receptor substrate binding|GO:0005154;epidermal growth	GO:0007265;Ras protein signal transduction|GO:0008286;insulin receptor signaling pathway|GO:0044419;interspecies interaction between organisms|GO:0007173;epidermal growth factor receptor signaling	GO:0005829;cytosol|GO:0005794;Golgi apparatus	TCRsignalingPathway_geneOntology

	factor receptor binding	pathway|GO:0007267;cell-cell signaling		
CBL	GO:0005509;calcium ion binding|GO:0003700;transcription factor activity|GO:0004871;signal transducer activity|GO:0008270;zinc ion binding|GO:0004842;ubiquitin-protein ligase activity|GO:0005515;protein binding|GO:0016874;ligase activity|GO:0017124;SH3 domain binding	GO:0007166;cell surface receptor linked signal transduction|GO:0048260;positive regulation of receptor-mediated endocytosis|GO:0016567;protein ubiquitination|GO:0007173;epidermal growth factor receptor signaling pathway|GO:0019941;modification-dependent protein catabolic process	GO:0005886;plasma membrane|GO:0005737;cytoplasm|GO:0005634;nucleus|GO:0005829;cytosol	TCRsignalingPathway_geneOntology
TNFRSF6B	GO:0005515;protein binding|GO:0004872;receptor activity	GO:0006915;apoptosis|GO:0006916;anti-apoptosis	GO:0005576;extracellular region|GO:0005625;soluble fraction	TNF_Family_Member_Receptors_geneOntology