**Table 55.** Significant (FDR<0.05) GO pathways involved in longevity identified by iGSEA4GWAS software. The analysis has been performed considering all the annotated common variants in Cohort 1.

Pathway	Gene Set Name	P-value	FDR value
GO	NUCLEOBASENUCLEOSIDENUCLEOTIDE AND NUCLEIC ACID TRANSPORT	0.001	1.00E-03
GO	NEGATIVE REGULATION OF CELL CYCLE	0.001	1.00E-03
GO	POSITIVE REGULATION OF MULTICELLULAR ORGANISMAL PROCESS	0.001	1.00E-03
GO	POSITIVE REGULATION OF DEVELOPMENTAL PROCESS	0.001	1.00E-03
GO	REGULATION OF HEART CONTRACTION	0.001	1.00E-03
GO	COVALENT CHROMATIN MODIFICATION	0.001	1.00E-03
GO	GENERATION OF A SIGNAL INVOLVED IN CELL CELL SIGNALING	0.001	1.00E-03
GO	PROTEIN PROCESSING	0.001	1.00E-03
GO	NEURON DEVELOPMENT	0.001	1.00E-03
GO	CENTRAL NERVOUS SYSTEM DEVELOPMENT	0.001	1.00E-03
GO	NEGATIVE REGULATION OF BIOSYNTHETIC PROCESS	0.001	1.00E-03
GO	LIPID BINDING	0.001	1.00E-03
GO	STRUCTURAL MOLECULE ACTIVITY	0.001	1.00E-03
GO	REGULATION OF SECRETION	0.001	0.001
GO	NEURITE DEVELOPMENT	0.001	0.001
GO	STRIATED MUSCLE DEVELOPMENT	0.001	0.001
GO	LIPID TRANSPORT	0.001	0.001
GO	AXONOGENESIS	0.001	0.001
GO	CELLULAR MORPHOGENESIS DURING DIFFERENTIATION	0.001	0.001
GO	SENSORY PERCEPTION	0.001	0.001
GO	HISTONE MODIFICATION	0.001	0.001
GO	NEURON DIFFERENTIATION	0.001	0.001
GO	NEGATIVE REGULATION OF TRANSLATION	0.001	0.001
GO	REGULATION OF MULTICELLULAR ORGANISMAL PROCESS	0.001	0.001
GO	HEMATOPOIETIN INTERFERON CLASSD200 DOMAIN CYTOKINE RECEPTOR BINDING	0.001	0.001
GO	PROTEIN TYROSINE PHOSPHATASE ACTIVITY	0.001	0.001
GO	PHOSPHORIC MONOESTER HYDROLASE ACTIVITY	0.001	0.001
GO	VOLTAGE GATED CHANNEL ACTIVITY	0.001	0.001
GO	STRUCTURAL CONSTITUENT OF RIBOSOME	0.001	0.001
GO	PHOSPHORIC ESTER HYDROLASE ACTIVITY	0.001	0.001
GO	VOLTAGE GATED CATION CHANNEL ACTIVITY	0.001	0.001
GO	CALCIUM CHANNEL ACTIVITY	0.001	0.001
GO	PHOSPHOPROTEIN PHOSPHATASE ACTIVITY	0.001	0.001
GO	STRUCTURAL CONSTITUENT OF CYTOSKELETON	0.001	0.001
GO	LIPID TRANSPORTER ACTIVITY	0.001	0.001
GO	GROWTH FACTOR ACTIVITY	0.001	0.001
GO	LIPID RAFT	0.001	0.001
GO	TRANSPORT VESICLE	0.001	0.001
GO	NEGATIVE REGULATION OF CELLULAR PROTEIN METABOLIC PROCESS	0.001	0.001032258
GO	REGULATION OF PROTEIN AMINO ACID PHOSPHORYLATION	0.001	0.001033333
GO	MUSCLE DEVELOPMENT	0.001	0.001033898
GO	REGULATION OF CELLULAR PROTEIN METABOLIC PROCESS	0.001	0.001034483
GO	SUBSTRATE SPECIFIC CHANNEL ACTIVITY	0.001	0.001035088
GO	NEGATIVE REGULATION OF CELLULAR BIOSYNTHETIC PROCESS	0.001	0.001035714
GO	SKELETAL DEVELOPMENT	0.001	0.001036364
GO	SKELETAL MUSCLE DEVELOPMENT	0.001	0.001037736
GO	MONOVALENT INORGANIC CATION TRANSPORT	0.001	0.001038462
GO	POSITIVE REGULATION OF CELL PROLIFERATION	0.001	0.001039216
GO	GATED CHANNEL ACTIVITY	0.001	0.001040816
GO	ION CHANNEL ACTIVITY	0.001	0.001041667
GO	NEGATIVE REGULATION OF CELL PROLIFERATION	0.001	0.001044118
GO	PROTEIN HOMODIMERIZATION ACTIVITY	0.001	0.001044776
GO	AUXILIARY TRANSPORT PROTEIN ACTIVITY	0.001	0.001045455
GO	G PROTEIN COUPLED RECEPTOR ACTIVITY	0.001	0.001046154
GO	ESTABLISHMENT AND OR MAINTENANCE OF CHROMATIN ARCHITECTURE	0.001	0.001046875
GO	CHROMATIN BINDING	0.001	0.001047619
GO	CELL CELL ADHESION	0.001	0.001101449
GO	CATION CHANNEL ACTIVITY	0.001	0.00115493
GO	VOLTAGE GATED POTASSIUM CHANNEL ACTIVITY	0.001	0.001178082
GO	POTASSIUM CHANNEL ACTIVITY	0.001	0.001253333
GO	ONE CARBON COMPOUND METABOLIC PROCESS	0.001	0.001289474

Pathway Gene Set Name GO GENERATION OF NEURONS GO LIGAND DEPENDENT NUCLEAR RECEPTOR ACTIVITY GO REGULATION OF CELL CYCLE GO DIGESTION GO CATION TRANSPORT GO CHROMATIN MODIFICATION GO POSITIVE REGULATION OF IMMUNE SYSTEM PROCESS GO POSITIVE REGULATION OF LYMPHOCYTE ACTIVATION	0.001 0.001 0.001 0.001	FDR value 0.001333333 0.001341772 0.001378049
GO REGULATION OF CELL CYCLE GO DIGESTION GO CATION TRANSPORT GO CHROMATIN MODIFICATION GO POSITIVE REGULATION OF IMMUNE SYSTEM PROCESS	0.001 0.001	0.001378049
GO DIGESTION GO CATION TRANSPORT GO CHROMATIN MODIFICATION GO POSITIVE REGULATION OF IMMUNE SYSTEM PROCESS	0.001	+
GO CATION TRANSPORT GO CHROMATIN MODIFICATION GO POSITIVE REGULATION OF IMMUNE SYSTEM PROCESS		0.00::
GO CHROMATIN MODIFICATION GO POSITIVE REGULATION OF IMMUNE SYSTEM PROCESS	0.004	0.00139759
GO POSITIVE REGULATION OF IMMUNE SYSTEM PROCESS	0.001	0.001404762
	0.001	0.001406977
GO POSITIVE REGULATION OF LYMPHOCYTE ACTIVATION	0.001	0.001411765
	0.001	0.001426966
GO PHOSPHOLIPID BINDING	0.001	0.001433333
GO GENERATION OF PRECURSOR METABOLITES AND ENERGY	0.001	0.001436782
GO POSITIVE REGULATION OF CELLULAR COMPONENT ORGANIZATION AND BIOG	GENESIS 0.001	0.001461539
GO METHYLTRANSFERASE ACTIVITY	0.001	0.001489796
GO PROTEIN SECRETION	0.001	0.001494845
GO ACTIN CYTOSKELETON	0.001	0.001505263
GO REGULATION OF PROTEIN METABOLIC PROCESS	0.001	0.001510638
GO PROTEIN C TERMINUS BINDING	0.001	0.001646465
GO REGULATION OF PHOSPHORYLATION	0.001	0.00177
GO CELL MIGRATION	0.001	0.001841584
GO HUMORAL IMMUNE RESPONSE	0.001	0.001843137
GO REGULATION OF CELL ADHESION	0.001	0.001980769
GO NEUROGENESIS	0.001	0.002130841
GO LEUKOCYTE ACTIVATION	0.001	0.002165138
GO CELL SURFACE	0.001	0.002166667
GO ADHERENS JUNCTION	0.001	0.0022
GO STRUCTURAL CONSTITUENT OF MUSCLE	0.001	0.002232143
GO SECRETION	0.003	0.002265487
GO TRANSFERASE ACTIVITY TRANSFERRING ONE CARBON GROUPS	0.001	0.002382609
GO POTASSIUM ION TRANSPORT	0.001	0.002394737
GO SUGAR BINDING	0.002	0.002413793
GO RHODOPSIN LIKE RECEPTOR ACTIVITY GO TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE KINASE SIGNALING PATHW	0.001	0.002416667
	VAY 0.001 0.001	0.002418803 0.002420168
GO BRAIN DEVELOPMENT GO CASPASE ACTIVATION	0.001	0.002420108
GO DEVELOPMENT OF PRIMARY SEXUAL CHARACTERISTICS	0.001	0.002423729
GO NEGATIVE REGULATION OF DEVELOPMENTAL PROCESS	0.001	0.002487603
GO INTERPHASE	0.001	0.0025
GO NEGATIVE REGULATION OF PROTEIN METABOLIC PROCESS	0.003	0.002622047
GO METAL ION TRANSMEMBRANE TRANSPORTER ACTIVITY	0.001	0.002632
GO RESPONSE TO NUTRIENT LEVELS	0.001	0.002634921
GO CATION TRANSMEMBRANE TRANSPORTER ACTIVITY	0.001	0.003261539
GO LYMPHOCYTE DIFFERENTIATION	0.001	0.003389313
GO ION TRANSPORT	0.001	0.00344697
GO METAL ION TRANSPORT	0.001	0.003514925
GO REGULATION OF LYMPHOCYTE ACTIVATION	0.001	0.003595588
GO TRANSMEMBRANE RECEPTOR PROTEIN TYROSINE KINASE ACTIVITY	0.001	0.003614815
GO CELL CYCLE ARREST GO 0007050	0.001	0.00392029
GO ENZYME ACTIVATOR ACTIVITY	0.001	0.004007194
GO MOLECULAR ADAPTOR ACTIVITY	0.001	0.004205674
GO TRANSCRIPTION ACTIVATOR ACTIVITY	0.002	0.004214285
GO NEGATIVE REGULATION OF CELL DIFFERENTIATION	0.001	0.004267606
GO ANION TRANSMEMBRANE TRANSPORTER ACTIVITY	0.001	0.004293706
GO CARBOHYDRATE BINDING	0.001	0.004537931
GO CYTOPLASMIC VESICLE	0.002	0.005226028
GO PROTEIN AUTOPROCESSING	0.001	0.005238095
GO SERINE TYPE ENDOPEPTIDASE ACTIVITY	0.004	0.005858108
GO REGULATION OF BODY FLUID LEVELS	0.002	0.006120805
GO POSITIVE REGULATION OF RESPONSE TO STIMULUS	0.001	0.006178808
GO VESICLE	0.002	0.006193333
GO REGULATION OF CELL DIFFERENTIATION	0.001	0.006611842
GO ELECTRON TRANSPORT GO 0006118	0.003	0.007051948
GO PROTEIN BINDING BRIDGING	0.003	0.007052288
	0.002	0.007296775
GO LYMPHOCYTE ACTIVATION		
GO LYMPHOCYTE ACTIVATION GO NEGATIVE REGULATION OF PROGRAMMED CELL DEATH	0.002	0.007358974
GO LYMPHOCYTE ACTIVATION	0.002 0.003 0.003	0.007358974 0.007745223 0.008189874

	Pathwav	Gene Set Name	P-value	FDR value
DOCUMENT PROSINE KINASE ACTIVITY				
GO         NUCLEAR EXPORT         0.002         0.0093807385           O         PROTEIN DOMAIN SEPCIFIC BINDING         0.001         0.007980575           SO         PROTEIN DIMERIZATION ACTIVITY         0.002         0.0098           SO         APOPTOTIC PROGRAM         0.004         0.0033         0.10033425           SO         CYTOPLASMIC MEMBRANE BOUND VESICLE         0.003         0.10137425           SO         POSTIVE REGULATION OF UNLECOMASMINICEOSIDENUCLEOTIDE AND NUCLEIC ACID ME TABOLIC PROCESS         0.001         0.011177625           SO         NEGATIVE REGULATION OF SAPOPTOSIS         0.002         0.011177615         0.002         0.011177615           SO         NEGATIVE REGULATION OF SAPOPTOSIS         0.002         0.0117761525         0.003         0.012717525           SO         REGULATION OF PROTEIN MCCESS         0.003         0.012717525         0.003         0.012717525           CAMP MEDIATED SIGNALING         0.005         0.0013         0.012717525         0.003         0.012717525           CO         CAMP MEDIATED SIGNALING         0.005         0.012475268         0.003         0.012354444           SO         CAMP MEDIATED SIGNALING         0.005         0.012475273         0.005         0.012475273           CO <td></td> <td></td> <td></td> <td></td>				
GO         NUCLEAR EXPORT         0.002         0.0099807985           O         PROTEIN DIMERSATION ACTIVITY         0.002         0.0098           GO         PROTEIN DIMERSATION ACTIVITY         0.002         0.0098           GO         APPORTOTE PROGRAM         0.004         0.0043         0.0043         0.0043         0.0043         0.0043         0.0043         0.0074         0.004         0.0043         0.0074         0.004         0.0043         0.0074         0.004         0.00172         0.002         0.0033         0.00784         0.002         0.011767862         0.003         0.011767862         0.003         0.011767862         0.003         0.011767862         0.003         0.011767862         0.003         0.011767862         0.003         0.01271279         0.003         0.01271279         0.003         0.01271279         0.003         0.01271279         0.003         0.01271279         0.003         0.01271279         0.003         0.01271279         0.003         0.01271279         0.003         0.01271279         0.003         0.01271279         0.003         0.01271279         0.003         0.01271279         0.004         0.01271279         0.004         0.01271279         0.004         0.01271279         0.004         0.01271279		TRANSLATION	0.007	
PROTEIN DIMERZATION ACTIVITY			0.002	
APOPTOTIC PROCRAM		PROTEIN DOMAIN SPECIFIC BINDING	0.001	0.009789157
CYTOPLASMIC MIMBRANE BOUND VISICIE		PROTEIN DIMERIZATION ACTIVITY		
POSITIVE REGULATION OF INUCLEDASSENUCLEGOSIDNOLECTIDE AND NUCLEIC ACID METABOLIC PROCESS   0.002	GO	APOPTOTIC PROGRAM	0.004	0.010473054
GO         POSITIVE REGULATION OF CELL DIFFERENTIATION         0.001         0.011787155           GO         NEGALIZATION OF PROTEIN MODIFICATION PROCESS         0.002         0.01730715           GO         REGULATION OF PROTEIN MODIFICATION PROCESS         0.003         0.01201299           GO         EXOCYTOSIS         0.003         0.01232472           GO         CAMP MERIATED SIGNALING         0.003         0.0132472           GO         CAMP MERIATED SIGNALING         0.003         0.0132472           GO         CRORAN MORPHOGENES         0.003         0.0132472           GO         CRORAN MORPHOGENES         0.003         0.0132472           GO         PROTEIN AMINO ACID DEPHOSPHORYLATION         0.002         0.0140287           GO         PROTEIN COMPLEX ASSEMBLY         0.001         0.01424752           GO         PROTEIN COMPLEX ASSEMBLY         0.001         0.01424772           GO         SH3 SH2 ADAPTOR ACTIVITY         0.006         0.0152139           GO         PROTEIN AMINO ACID AUTOPHOSPHORYLATION         0.006         0.01521368           GO         PROTEIN AMINO ACID AUTOPHOSPHORYLATION         0.002         0.0153298936           GO         PROTEIN AMINO ACID AUTOPHOSPHORYLATION         0.002         0.015329	GO	CYTOPLASMIC MEMBRANE BOUND VESICLE	0.003	0.01083432
GO         NEGATIVE REGULATION OF APOPTOSIS         0.002         0.011770112           G         SEGULATION OF PROTEIN MODIFICATION PROCESS         0.003         0.011793122           GO         SECULATION OF IMMUNE SYSTEM PROCESS         0.003         0.012911290           GO         EXOCYTOSIS         0.003         0.01291479           GO         CAMP MEDIATED SIGNALING         0.006         0.013544444           GO         ORGAN MORPHOGENESIS         0.003         0.01356923           GO         CYTOSKELETAL ROTEIN BINDING         0.004         0.014926066           GO         PROTEIN COMPLEX ASSEMBLY         0.001         0.014926066           GO         PROTEIN COMPLEX ASSEMBLY         0.005         0.0149216066           GO         RESPONSE TO EXTRACELLULAR STIMULUS         0.005         0.0149216066           GO         RESPONSE TO EXTRACELLULAR STIMULUS         0.005         0.014921308           GO         PROTEIN AMINO ACID ALIDOPHOSPHORYLATION         0.002         0.015393130           GO         PROTEIN AMINO ACID ALIDOPHOSPHORYLATION         0.002         0.015393180           GO         MARCHANAL RECEPTOR PROTEIN KINASE ACTIVITY         0.004         0.015502646           GO         MICHANIA RECEPTOR PROTEIN KINASE ACTIVITY	GO	POSITIVE REGULATION OF NUCLEOBASENUCLEOSIDENUCLEOTIDE AND NUCLEIC ACID METABOLIC PROCESS	0.002	0.011117647
REGULATION OF PROTEIN MODIFICATION PROCESS   0.002   0.117978322	GO	POSITIVE REGULATION OF CELL DIFFERENTIATION	0.001	0.011768786
GO         ERQUILATION OF IMMUNIE SYSTEM PROCESS         0.003         0.10211299           GO         EXCYTOSIS         0.003         0.1322472           GO         CAMP MEDIATED SIGNALING         0.006         0.01324072           GO         ORGAN MORPHOGENESIS         0.003         0.013565636           GO         PROTEIR AMINO ACID DEPHOSPHORYLATION         0.002         0.014070923           GO         CYTOSRELETAL ROTEIN BINDING         0.004         0.014070923           GO         PROTEIN COMPLEX ASSEMBLY         0.001         0.014320086           GO         PROTEIN COMPLEX ASSEMBLY         0.005         0.014320086           GO         RESPONSE TO EXTRACELLULAR STIMULUS         0.005         0.01432139           GO         RESPONSE TO EXTRACELLULAR STIMULUS         0.005         0.01532139           GO         RESPONSE TO EXTRACELLULAR STIMULUS         0.004         0.01532036           GO         RISHAR ASSEMBLY         0.004         0.01533038           GO         PROTEIN AMINO ACID AUTOPHOSPHORYLATION         0.002         0.01631188           GO         MARISMAN BRANCH BRUND VESICLE         0.003         0.01613178           GO         MARISMAN BRANCH BRUND VESICLE         0.004         0.015380208 <tr< td=""><td>GO</td><td>NEGATIVE REGULATION OF APOPTOSIS</td><td>0.002</td><td>0.011770115</td></tr<>	GO	NEGATIVE REGULATION OF APOPTOSIS	0.002	0.011770115
EXOCYTOSIS	GO	REGULATION OF PROTEIN MODIFICATION PROCESS	0.002	0.011795322
GO CAMP MEDIATED SIGNALING ORGAN MORPHOGENESIS OD 035354444 ORGAN MORPHOGENESIS OD 035355565 OPROTEIN AMINO ACID DEPHOSPHORYLATION OD 0312555565 OPROTEIN COMPLEX ASSEMBLY OD 0312555656 ORGAN MORPHOGENESIS OD 0312555565 ORGAN MESPONSE TO EXTRACELLULAR STIMULUS OD 03126356566 ORGAN MEMBRANE RECEPTIOR PROTEIN KINASE ACTIVITY OD 0315021399 ORGAN MEMBRANE RECEPTIOR PROTEIN KINASE ACTIVITY OD 0315021399 ORGAN MEMBRANE RECEPTIOR PROTEIN KINASE ACTIVITY ORGAN MEMBRANE BOUND VESICLE ORGAN MEMBRANE RECEPTIOR PROTEIN KINASE ACTIVITY ORGAN MEMBRANE BOUND VESICLE ORGAN MEMBRANE BOUND VES	GO	REGULATION OF IMMUNE SYSTEM PROCESS	0.003	0.012011299
ORGAN MORPHOGENESIS	GO	EXOCYTOSIS	0.003	0.01322472
GO	GO	CAMP MEDIATED SIGNALING	0.006	0.013544444
GO         CYTOSKELFIA PROTEIN BINDING         0.004         0.014819676           GO         PROTEIN COMPLEX ASSEMBLY         0.005         0.014326068           GO         RESPONSE TO EXTRACELLULAR STIMULUS         0.005         0.014424732           GO         SH3 SH2 ADAPTOR ACTIVITY         0.006         0.015021399           GO         TRANSMEMBRANE RECEPTOR PROTEIN KINASE ACTIVITY         0.004         0.01539266           GO         PROTEIN AMINO ACID AUTOPHOSPHORYLATION         0.002         0.015192666           GO         INTERPHASE OF MITOTIC CELL CYCLE         0.003         0.016139208           GO         MAGNESIUM JON BINDING         0.005         0.01539208           GO         PROTEIN OLIGOMERIZATION         0.005         0.01539208           GO         MEMBRANE BOUND VESICLE         0.004         0.016466321           GO         INDUCTION OF APOPTOSIS BY INTRACELLULAR SIGNALS         0.006         0.016728033           GO         CHROMATIN         0.005         0.016866667           GO         I KAPPAB KINASE NE KAPPAB CASCADE         0.004         0.017806122           GO         SERINE HYPORLASE ACTIVITY         0.01         0.01790863           GO         TCELL ACTIVATION         0.02         0.01883704	GO	ORGAN MORPHOGENESIS	0.003	0.013585636
GO PROTEIN COMPLEX ASSEMBLY O. 0.0143276036 OR RESPONSE TO EXTRACELLULAR STIMULUS O. 0.0143276036 OR RESPONSE TO EXTRACELLULAR STIMULUS O. 0.0143276036 OR PROTEIN MINO ACID MOTOPHOSPHORYLATION O. 0.00502139 O. 0.015398936 OR PROTEIN AMINO ACID MOTOPHOSPHORYLATION O. 0.002 O. 0.015398936 OR PROTEIN AMINO ACID MOTOPHOSPHORYLATION O. 0.003 O. 0.01631358 OR PROTEIN OLIGOMERIZATION O. 0.005 O. 0.01631358 OR PROTEIN OLIGOMERIZATION O. 0.005 O. 0.01631358 OR PROTEIN OLIGOMERIZATION O. 0.005 O. 0.016380208 OR MEMBRANE BOUND VESICLE OR 0.006 OR MOTOPOSS BY INTRACELLULAR SIGNALS OR 0.006 OR 0.016726803 OR 0.007 OR 0.0	GO	PROTEIN AMINO ACID DEPHOSPHORYLATION	0.002	0.014076923
GO RESPONSE TO EXTRACELLULAR SIMULUS ON RESPONSE TO EXTRACELLULAR SIMULUS ON SH3 SH2 ADAPTOR ACTIVITY ON 0.005 0.01502138 ON TRANSMEMBRANE RECEPTOR PROTEIN KINASE ACTIVITY ON 0.004 0.015502188 ON PROTEIN AMINIO ACID AUTOPHIOSPHORYLATION ON 0.005 0.015502188 ON MAGNESIUMI ION BINDING ON 0.005 0.016193718 ON 0.006 0.00750218368 ON MAGNESIUMI ION BINDING ON 0.005 0.016193718 ON 0.0075 0.016726032 ON 0.0075 0.016726032 ON 0.0075 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0175 0.0	GO	CYTOSKELETAL PROTEIN BINDING	0.004	0.014081967
SH3 SH2 ADAPTOR ACTIVITY	GO	PROTEIN COMPLEX ASSEMBLY	0.001	0.014326086
TRANSMEMBRANE RECEPTOR PROTEIN KINASE ACTIVITY	GO	RESPONSE TO EXTRACELLULAR STIMULUS	0.005	0.014424732
GO         PROTEIN AMINO ACID AUTOPHOSPHORYLATION         0.002         0.015502666           GO         INTERPHASE OF MITOTIC CELL CYCLE         0.003         0.01631358           GO         MAGNESIUM ION BINDING         0.005         0.016193718           GO         PROTEIN OLIGOMERIZATION         0.005         0.016180208           GO         MEMBRANE BOUND VESICLE         0.004         0.016465212           GO         INDUCTION OF APOPTOSIS BY INTRACELLULAR SIGNALS         0.006         0.016726803           GO         CHROMATIN         0.005         0.0168666627           GO         I KAPPAB KINASE NF KAPPAB CASCADE         0.004         0.01790612           GO         SERINE HYDROLASE ACTIVITY         0.01         0.01790633           GO         CYTOKINE METABOLIC PROCESS         0.005         0.01885094           GO         TCELL ACTIVATION         0.005         0.018876904           GO         ELECTRON CARRIER ACTIVITY         0.005         0.018760001           GO         GYPASE ACTIVATOR ACTIVITY         0.005         0.01930197           GO         GEPASE ACTIVATOR ACTIVITY         0.005         0.01920197           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.006         0.01920197 <t< td=""><td>GO</td><td>SH3 SH2 ADAPTOR ACTIVITY</td><td>0.006</td><td>0.01502139</td></t<>	GO	SH3 SH2 ADAPTOR ACTIVITY	0.006	0.01502139
GO         INTERPHASE DE MITOTIC CELL CYCLE         0.003         0.016131358           GO         MAGNESIUM ION BINDING         0.005         0.0161893718           GO         PROTEIN OLIGOMERIZATION         0.005         0.016380208           GO         MEMBRANE BOUND VESICE         0.004         0.016450321           GO         INDUCTION OF APOPOSIS BY INTRACELULAR SIGNALS         0.006         0.016727803           GO         CHROMATIN         0.005         0.01686667           GO         SERINE HYDROLASE ACTIVITY         0.01         0.01790863           GO         SERINE HYDROLASE ACTIVITY         0.01         0.01790863           GO         CYTOKINE METABOLIC PROCESS         0.005         0.01885094           GO         ELECTRON CARRIER ACTIVITY         0.002         0.01887094           GO         ELECTRON CARRIER ACTIVITY         0.002         0.01887094           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.005         0.01940197           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.005         0.019441176           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.007         0.020731708           GO         RESPONSE TO WOUNDING         0.004         0.019441176           GO	GO	TRANSMEMBRANE RECEPTOR PROTEIN KINASE ACTIVITY	0.004	0.015398936
GO         MAGNESIUM ION BINDING         0.005         0.016193718           GO         PROTEIN OLIGOMERIZATION         0.005         0.016380208           GO         MEMBRANE BOUND VESICLE         0.004         0.016466321           GO         INDUCTION OF APOPTOSIS BY INTRACELLULAR SIGNALS         0.006         0.016726803           GO         CHEROMATIN         0.005         0.016366667           GO         SERINE HYDROLASE ACTIVITY         0.01         0.017906612           GO         SERINE HYDROLASE ACTIVITY         0.01         0.01790663           GO         CYTOKINE METABOLIC PROCESS         0.005         0.018530302           GO         T.CELL ACTIVATION         0.002         0.018570001           GO         POSITIVE REGULATION OF PHOSPHORYLATION         0.002         0.018750001           GO         SERINE TYPE PETIDASE ACTIVITY         0.005         0.0192097           GO         SERINE TYPE PETIDASE ACTIVITY         0.006         0.01920197           GO         RESPONSE TO WOUNDING         0.004         0.01941176           GO         HEMESTIAL TO PROCESS         0.004         0.02731708           GO         HOMEOSTATIC PROCESS         0.004         0.02731708           GO         HORMON	GO	PROTEIN AMINO ACID AUTOPHOSPHORYLATION	0.002	0.015502646
GO         PROTEIN OLIGOMERIZATION         0.005         0.016380208           GO         MEMBRANE BOUND VESICLE         0.004         0.016466321           GO         INDUCTION OF APOPTOSIS BY INTRACELLULAR SIGNALS         0.006         0.005         0.016586667           GO         CHROMATIN         0.005         0.01866667           GO         SERINE HYDROLASE ACTIVITY         0.01         0.01780612           GO         SERINE HYDROLASE ACTIVITY         0.005         0.01853030           GO         TCTCKINE METABOLIC PROCESS         0.005         0.01853030           GO         TCELL ACTIVATION         0.002         0.01850300           GO         POSITIVE REGULATION OF PHOSPHORYLATION         0.003         0.0195097           GO         FELL ACTIVATION         0.003         0.0195097           GO         POSITIVE REGULATION OF PHOSPHORYLATION         0.003         0.0195097           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.003         0.01920197           GO         RESPONSE TO WOUNDING         0.004         0.0192197           GO         RESPONSE TO WOUNDING         0.004         0.02737184           GO         REGULATION OF T CELL ACTIVATION         0.006         0.021735651	GO	INTERPHASE OF MITOTIC CELL CYCLE	0.003	0.01613158
GO         MEMBRANE BOUND VESICE         0.004         0.016466321           GO         INDUCTION OF APOPTOSIS BY INTRACELLULAR SIGNALS         0.006         0.01672803           GO         CHROMATIN         0.005         0.016866667           GO         I KAPPAB KINASE NE KAPPAB CASCADE         0.004         0.017306122           GO         SERINE HYDROLASE ACTIVITY         0.01         0.01790633           GO         CYTOKINE METABOLIC PROCESS         0.005         0.018303032           GO         T CELL ACTIVATION         0.002         0.01858794           GO         ELECTRON CARRIER ACTIVITY         0.002         0.01858796           GO         POSITIVE REGULATION OF PHOSPHORYLATION         0.003         0.0199059703           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.005         0.01920197           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.006         0.01920197           GO         HORSOSTATIC PROCESS         0.004         0.019441176           GO         HORSOSTATIC PROCESS         0.004         0.019441176           GO         HORMONE ACTIVITY         0.007         0.02071844           GO         HORMONE ACTIVITY         0.007         0.0217364           GO         HORMON				
GO         INDUCTION OF APOPTOSIS BY INTRACELLULAR SIGNALS         0.006         0.16726803           GO         CHROMATIN         0.003         0.0036         0.0036         0.00366667           GO         I KAPPAB KINASE NF KAPPAB CASCADE         0.004         0.017806122           GO         SERINE HYDROLASE ACTIVITY         0.01         0.01790863           GO         CYTOKINE METABOLIC PROCESS         0.005         0.018530302           GO         T CELL ACTIVATION         0.005         0.018576003           GO         POSITIVE REGULATION OF PHOSPHORYLATION         0.002         0.018760001           GO         POSITIVE REGULATION OF PHOSPHORYLATION         0.003         0.01920197           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.003         0.01920197           GO         RESPONSE TO WOUNDING         0.004         0.019441176           GO         HOMEOSTATIC PROCESS         0.004         0.01942175           GO         HOMEOSTATIC PROCESS         0.004         0.022731708           GO         HORMONE ACTIVITY         0.007         0.02273166           GO         HORMONE ACTIVITY         0.007         0.022175362           GO         HORMONE ACTIVITY         0.007         0.022175362				
GO         CHROMATIN         0.005         0.016866667           GO         I KAPPAB KINASE NF KAPPAB CASCADE         0.004         0.07806126           GO         SERINE HYDROLASE ACTIVITY         0.01         0.01790823           GO         CYTOKINE METABOLIC PROCESS         0.005         0.018530302           GO         T CELL ACTIVATION         0.005         0.01838794           GO         ELECTRON CARRIER ACTIVITY         0.002         0.018760001           GO         POSITIVE REGULATION OF PHOSPHORYLATION         0.003         0.019059703           GO         GTPASE ACTIVATOR ACTIVITY         0.003         0.01920197           GO         SERINE TYPE PERTIDASE ACTIVITY         0.008         0.01920197           GO         RESPONSE TO WOUNDING         0.004         0.019411176           GO         HOMEDSTATIC PROCESS         0.004         0.020731708           GO         CYTOKINE ACTIVITY         0.007         0.027317362           GO         HEMOSTASIS         0.009         0.0221275362           GO         HORMONE ACTIVITY         0.007         0.02235849           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.008         0.0221935261           GO         HEMOSTASIS <td< td=""><td></td><td></td><td></td><td></td></td<>				
GO   1 KAPPAB KINASE NF KAPPAB CASCADE   0.004   0.017806122				
GO   SERINE HYDROLASE ACTIVITY   0.01   0.01790863   CYTOKINE METABOLIC PROCESS   0.005   0.018530302   0.005   0.018530302   0.005   0.018530302   0.005   0.01858794   0.005   0.0188794   0.005   0.0188794   0.005   0.0188794   0.005   0.0188794   0.005   0.0188794   0.006   0.0188794   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.007   0.0				
GO         CYTOKINE METABOLIC PROCESS         0.005         0.018530302           GO         TCELL ACTIVATION         0.005         0.018580794           GO         ELECTRON CARRIER ACTIVITY         0.002         0.018760001           GO         POSITIVE REGULATION OF PHOSPHORYLATION         0.003         0.019059703           GO         GERISE TYPE PEPTIDASE ACTIVITY         0.005         0.01920197           GO         RESPONSE TO WOUNDING         0.004         0.019441176           GO         HOMEOSTATIC PROCESS         0.004         0.02731708           GO         CYTOKINE ACTIVITY         0.007         0.02771844           GO         CYTOKINE ACTIVITY         0.007         0.02771844           GO         REGULATION OF T CELL ACTIVATION         0.006         0.021275362           GO         HORMONE ACTIVITY         0.007         0.021933691           GO         HEMOSTASIS         0.009         0.02210562           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.0233849           GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.022497652           GO         DEPHOSPHORYLATION         0.03         0.022585849           GO         TRANSCRIPT				
GO         T CELL ACTIVATION         0.005         0.01858794           GO         ELECTRON CARRIER ACTIVITY         0.002         0.018760001           GO         POSTIVE REGULATION OF PHOSPHORYLATION         0.003         0.019059703           GO         GTPASE ACTIVATOR ACTIVITY         0.005         0.01920197           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.008         0.01920197           GO         RESPONSE TO WOUNDING         0.004         0.020731708           GO         HOMEOSTATIC PROCESS         0.004         0.020731708           GO         CYTOKINE ACTIVITY         0.007         0.020731844           GO         HORMONE ACTIVITY         0.007         0.021932691           GO         HEMOSTASIS         0.009         0.021275362           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.02235849           GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.002           GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.02247652           GO         DEPHOSPHORYLATION         0.003         0.022878503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO				
GO   ELECTRON CARRIER ACTIVITY   0.002   0.018760001				
GO         POSITIVE REGULATION OF PHOSPHORYLATION         0.003         0.019059703           GO         GTPASE ACTIVATOR ACTIVITY         0.005         0.01920197           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.008         0.01920197           GO         RESPONSE TO WOUNDING         0.004         0.020731708           GO         HOMEOSTATIC PROCESS         0.004         0.020731708           GO         CYTOKINE ACTIVITY         0.007         0.020731708           GO         HORMONE ACTIVITY         0.007         0.021275362           GO         HORMONE ACTIVITY         0.007         0.021275362           GO         HEMOSTASIS         0.009         0.022105262           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.02235849           GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.022436019           GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.022497652           GO         DEPHOSPHORYLATION         0.003         0.022878503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.025192661				
GO         GTPASE ACTIVATOR ACTIVITY         0.005         0.1920197           GO         SERINE TYPE PEPTIDASE ACTIVITY         0.008         0.1920297           GO         RESPONSE TO WOUNDING         0.004         0.019441176           GO         HOMEOSTATIC PROCESS         0.004         0.0207731784           GO         CYTOKINE ACTIVITY         0.007         0.020771844           GO         REGULATION OF T CELL ACTIVATION         0.006         0.021275362           GO         HOMMONE ACTIVITY         0.007         0.021933691           GO         HEMOSTASIS         0.009         0.022105262           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.02235849           GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.022436019           GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.022437652           GO         DEPHOSPHORYLATION         0.003         0.022878503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO         CELL ACTIVATION         0.007         0.022995347           GO         CELL ACTIVATION         0.005         0.025192661           GO <td< td=""><td></td><td></td><td></td><td></td></td<>				
GO         SERINE TYPE PEPTIDASE ACTIVITY         0.008         0.01920297           GO         RESPONSE TO WOUNDING         0.004         0.019441176           GO         HOMEOSTATIC PROCESS         0.004         0.020731708           GO         CYTOKINE ACTIVITY         0.007         0.020771844           GO         REGULATION OF T CELL ACTIVATION         0.006         0.021275362           GO         HORMONE ACTIVITY         0.007         0.0221932691           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.02235849           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.02235849           GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.022497652           GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.022497652           GO         DEPHOSPHORYLATION         0.003         0.022497653           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.024709677           GO         CELL ACTIVATION         0.005         0.025192561           GO         SPHINGOLIPID METABOLIC PROCESS         0.005         0.025681818				
GO         RESPONSE TO WOUNDING         0.004         0.019441176           GO         HOMEOSTATIC PROCESS         0.004         0.020731708           GO         CYTOKINE ACTIVITY         0.007         0.020771844           GO         REGULATION OF T CELL ACTIVATION         0.006         0.021275362           GO         HORMONE ACTIVITY         0.007         0.021932691           GO         HEMOSTASIS         0.009         0.022105262           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.02238849           GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.00238849           GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.022497652           GO         DEPHOSPHORYLATION         0.003         0.022878503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.0229978503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.0229978503           GO         TERMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.024709677           GO         CELL ACTIVATION         0.005         0.02599524           GO         MICROTUBULE BINDING         0.005         0.02580543				
HOMEOSTATIC PROCESS   0.004   0.02731708				
GO         CYTOKINE ACTIVITY         0.007         0.020771844           GO         REGULATION OF T CELL ACTIVATION         0.006         0.021275362           GO         HORMONE ACTIVITY         0.007         0.021932691           GO         HEMOSTASIS         0.009         0.022105262           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.0223849           GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.022436019           GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.022497652           GO         DEPHOSPHORYLATION         0.003         0.022878503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022497652           GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.025995347           GO         CELL ACTIVATION         0.005         0.025618182           GO         SPHINGOLIPID METABOLIC PROCESS         0.003         0.025618182           GO         MICROTUBULE BINDING         0.005         0.02580543           GO         CYTOKINE PRODUCTION         0.006         0.02780543           GO         ANTI APOPTOSIS         0.006         0.02780504           GO				
GO         REGULATION OF T CELL ACTIVATION         0.006         0.021275362           GO         HORMONE ACTIVITY         0.007         0.021932691           GO         HEMOSTASIS         0.009         0.022105262           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.02235849           GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.022436019           GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.022497652           GO         DEPHOSPHORYLATION         0.003         0.022497652           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.024709677           GO         CELL ACTIVATION         0.005         0.025192661           GO         SPHINGOLIPID METABOLIC PROCESS         0.003         0.025618182           GO         MICROTUBULE BINDING         0.005         0.025618436           GO         CYTOKINE PRODUCTION         0.006         0.02580543           GO         CYTOKINE PRODUCTION         0.006         0.027125001           GO         CHROMOSOME SEGREGATION         0.006         0.027125001				
GO				
GO         HEMOSTASIS         0.009         0.022105262           GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.02235849           GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.022436019           GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.022497652           GO         DEPHOSPHORYLATION         0.003         0.022878503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.024709677           GO         CELL ACTIVATION         0.005         0.025192661           GO         SPHINGOLIPID METABOLIC PROCESS         0.003         0.025618182           GO         MICROTUBULE BINDING         0.005         0.025809498           GO         TISSUE DEVELOPMENT         0.006         0.02580543           GO         CYTOKINE PRODUCTION         0.004         0.026536034           GO         INFLAMMATORY RESPONSE         0.006         0.027125001           GO         CHROMOSOME SEGREGATION         0.006         0.027125001           GO         CHROMOSOME SEGREGATION FACTOR ACTIVITY         0.004         0.030563878 <t< td=""><td></td><td></td><td></td><td></td></t<>				
GO         POSITIVE REGULATION OF TRANSCRIPTION         0.005         0.02235849           GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.022436019           GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.022497652           GO         DEPHOSPHORYLATION         0.003         0.0222878503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.024709677           GO         CELL ACTIVATION         0.005         0.024709677           GO         SPHINGOLIPID METABOLIC PROCESS         0.003         0.0256818182           GO         MICROTUBULE BINDING         0.005         0.025689498           GO         TISSUE DEVELOPMENT         0.006         0.02580543           GO         CYTOKINE PRODUCTION         0.004         0.026580543           GO         INFLAMMATORY RESPONSE         0.008         0.0269964           GO         INFLAMMATORY RESPONSE         0.006         0.027125001           GO         CHROMOSOME SEGREGATION         0.009         0.029568888           GO         RIGULATION OF MAP KINASE ACTIVITY         0.004         0.030563878				
GO         TRANSLATION FACTOR ACTIVITY NUCLEIC ACID BINDING         0.012         0.022436019           GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.022497652           GO         DEPHOSPHORYLATION         0.003         0.022878503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.024709677           GO         CELL ACTIVATION         0.005         0.025192667           GO         SPHINGOLIPID METABOLIC PROCESS         0.003         0.025681882           GO         MICROTUBULE BINDING         0.005         0.025689498           GO         TISSUE DEVELOPMENT         0.006         0.02580543           GO         CYTOKINE PRODUCTION         0.004         0.026536034           GO         ANTI APOPTOSIS         0.008         0.02695964           GO         INFLAMMATORY RESPONSE         0.006         0.027125001           GO         CHROMOSOME SEGREGATION         0.009         0.029568888           GO         RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY         0.004         0.030563878           GO         BONE REMODELING         0.001         0.031513043				
GO         REGULATION OF CYTOKINE BIOSYNTHETIC PROCESS         0.007         0.022497652           GO         DEPHOSPHORYLATION         0.003         0.022878503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.024709677           GO         CELL ACTIVATION         0.005         0.025192661           GO         SPHINGOLIPID METABOLIC PROCESS         0.003         0.025618182           GO         MICROTUBULE BINDING         0.005         0.025689498           GO         TISSUE DEVELOPMENT         0.006         0.02580543           GO         CYTOKINE PRODUCTION         0.004         0.026536034           GO         ANTI APOPTOSIS         0.008         0.02695964           GO         INFLAMMATORY RESPONSE         0.006         0.027125001           GO         CHROMOSOME SEGREGATION         0.009         0.029568888           GO         RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY         0.004         0.030563878           GO         BONE REMODELING         0.01         0.031513043           GO         POSITIVE REGULATION OF CATALYTIC ACTIVITY         0.008         0.032506492           G				1
GO         DEPHOSPHORYLATION         0.003         0.022878503           GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.024709677           GO         CELL ACTIVATION         0.005         0.025192661           GO         SPHINGOLIPID METABOLIC PROCESS         0.003         0.025618182           GO         MICROTUBULE BINDING         0.005         0.025689498           GO         TISSUE DEVELOPMENT         0.006         0.02580543           GO         CYTOKINE PRODUCTION         0.004         0.026536034           GO         ANTI APOPTOSIS         0.008         0.0265964           GO         INFLAMMATORY RESPONSE         0.006         0.027125001           GO         CHROMOSOME SEGREGATION         0.009         0.029568888           GO         RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY         0.004         0.030563878           GO         REGULATION OF MAP KINASE ACTIVITY         0.005         0.030881578           GO         BONE REMODELING         0.01         0.031513043           GO         POSITIVE REGULATION OF CATALYTIC ACTIVITY         0.008         0.032506492           GO				
GO         TRANSCRIPTION COFACTOR ACTIVITY         0.007         0.022995347           GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.024709677           GO         CELL ACTIVATION         0.005         0.025192661           GO         SPHINGOLIPID METABOLIC PROCESS         0.003         0.025618182           GO         MICROTUBULE BINDING         0.005         0.02580543           GO         CYTOKINE PRODUCTION         0.006         0.02580543           GO         ANTI APOPTOSIS         0.008         0.02695964           GO         INFLAMMATORY RESPONSE         0.006         0.027125001           GO         CHROMOSOME SEGREGATION         0.009         0.029568888           GO         RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY         0.004         0.030563878           GO         REGULATION OF MAP KINASE ACTIVITY         0.005         0.030881578           GO         BONE REMODELING         0.01         0.031513043           GO         SYNAPSE         0.011         0.032512933           GO         POSITIVE REGULATION OF TRANSFERASE ACTIVITY         0.012         0.033068378           GO         POSITIVE REGULATION OF CASPASE ACTIVITY         0.012         0.033068378 <td< td=""><td></td><td></td><td></td><td></td></td<>				
GO         CHROMOSOME ORGANIZATION AND BIOGENESIS         0.005         0.024709677           GO         CELL ACTIVATION         0.005         0.025192661           GO         SPHINGOLIPID METABOLIC PROCESS         0.003         0.025618182           GO         MICROTUBULE BINDING         0.005         0.025689498           GO         TISSUE DEVELOPMENT         0.006         0.02580543           GO         CYTOKINE PRODUCTION         0.004         0.026536034           GO         ANTI APOPTOSIS         0.008         0.02695964           GO         INFLAMMATORY RESPONSE         0.006         0.027125001           GO         CHROMOSOME SEGREGATION         0.009         0.02956888           GO         RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY         0.004         0.030563878           GO         REGULATION OF MAP KINASE ACTIVITY         0.005         0.030881578           GO         BONE REMODELING         0.01         0.031513043           GO         POSITIVE REGULATION OF CATALYTIC ACTIVITY         0.008         0.032506492           GO         POSITIVE REGULATION OF CASPASE ACTIVITY         0.012         0.033068378           GO         POSITIVE REGULATION OF CASPASE ACTIVITY         0.013         0.033948936 <td></td> <td></td> <td></td> <td></td>				
GO       CELL ACTIVATION       0.005       0.025192661         GO       SPHINGOLIPID METABOLIC PROCESS       0.003       0.025618182         GO       MICROTUBULE BINDING       0.005       0.025689498         GO       TISSUE DEVELOPMENT       0.006       0.02580543         GO       CYTOKINE PRODUCTION       0.004       0.026536034         GO       ANTI APOPTOSIS       0.008       0.02695964         GO       INFLAMMATORY RESPONSE       0.006       0.027125001         GO       CHROMOSOME SEGREGATION       0.009       0.029568888         GO       RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY       0.004       0.030563878         GO       REGULATION OF MAP KINASE ACTIVITY       0.005       0.030881578         GO       BONE REMODELING       0.01       0.031513043         GO       POSITIVE REGULATION OF CATALYTIC ACTIVITY       0.008       0.032506492         GO       SYNAPSE       0.011       0.032512933         GO       POSITIVE REGULATION OF TRANSFERASE ACTIVITY       0.012       0.033068378         GO       POSITIVE REGULATION OF CASPASE ACTIVITY       0.013       0.033948936				
GO       SPHINGOLIPID METABOLIC PROCESS       0.003       0.025618182         GO       MICROTUBULE BINDING       0.005       0.025689498         GO       TISSUE DEVELOPMENT       0.006       0.02580543         GO       CYTOKINE PRODUCTION       0.004       0.026536034         GO       ANTI APOPTOSIS       0.008       0.02695964         GO       INFLAMMATORY RESPONSE       0.006       0.027125001         GO       CHROMOSOME SEGREGATION       0.009       0.029568888         GO       RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY       0.004       0.030563878         GO       REGULATION OF MAP KINASE ACTIVITY       0.005       0.030881578         GO       BONE REMODELING       0.01       0.031513043         GO       POSITIVE REGULATION OF CATALYTIC ACTIVITY       0.008       0.032506492         GO       SYNAPSE       0.011       0.032512933         GO       POSITIVE REGULATION OF TRANSFERASE ACTIVITY       0.012       0.033068378         GO       POSITIVE REGULATION OF CASPASE ACTIVITY       0.013       0.033948936				
GO       MICROTUBULE BINDING       0.005       0.025689498         GO       TISSUE DEVELOPMENT       0.006       0.02580543         GO       CYTOKINE PRODUCTION       0.004       0.026536034         GO       ANTI APOPTOSIS       0.008       0.02695964         GO       INFLAMMATORY RESPONSE       0.006       0.027125001         GO       CHROMOSOME SEGREGATION       0.009       0.029568888         GO       RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY       0.004       0.030563878         GO       REGULATION OF MAP KINASE ACTIVITY       0.005       0.030881578         GO       BONE REMODELING       0.01       0.031513043         GO       POSITIVE REGULATION OF CATALYTIC ACTIVITY       0.008       0.032506492         GO       SYNAPSE       0.011       0.032512933         GO       POSITIVE REGULATION OF TRANSFERASE ACTIVITY       0.012       0.033068378         GO       POSITIVE REGULATION OF CASPASE ACTIVITY       0.013       0.033948936				
GO       CYTOKINE PRODUCTION       0.004       0.026536034         GO       ANTI APOPTOSIS       0.008       0.02695964         GO       INFLAMMATORY RESPONSE       0.006       0.027125001         GO       CHROMOSOME SEGREGATION       0.009       0.029568888         GO       RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY       0.004       0.030563878         GO       REGULATION OF MAP KINASE ACTIVITY       0.005       0.030881578         GO       BONE REMODELING       0.01       0.031513043         GO       POSITIVE REGULATION OF CATALYTIC ACTIVITY       0.008       0.032506492         GO       SYNAPSE       0.011       0.032512933         GO       POSITIVE REGULATION OF TRANSFERASE ACTIVITY       0.012       0.033068378         GO       POSITIVE REGULATION OF CASPASE ACTIVITY       0.013       0.033948936	GO	MICROTUBULE BINDING	0.005	1
GO       ANTI APOPTOSIS       0.008       0.02695964         GO       INFLAMMATORY RESPONSE       0.006       0.027125001         GO       CHROMOSOME SEGREGATION       0.009       0.029568888         GO       RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY       0.004       0.030563878         GO       REGULATION OF MAP KINASE ACTIVITY       0.005       0.03881578         GO       BONE REMODELING       0.01       0.031513043         GO       POSITIVE REGULATION OF CATALYTIC ACTIVITY       0.008       0.032506492         GO       SYNAPSE       0.011       0.032512933         GO       POSITIVE REGULATION OF TRANSFERASE ACTIVITY       0.012       0.033068378         GO       POSITIVE REGULATION OF CASPASE ACTIVITY       0.013       0.033948936	GO	TISSUE DEVELOPMENT	0.006	0.02580543
GO         INFLAMMATORY RESPONSE         0.006         0.027125001           GO         CHROMOSOME SEGREGATION         0.009         0.029568888           GO         RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY         0.004         0.030563878           GO         REGULATION OF MAP KINASE ACTIVITY         0.005         0.030881578           GO         BONE REMODELING         0.01         0.031513043           GO         POSITIVE REGULATION OF CATALYTIC ACTIVITY         0.008         0.032506492           GO         SYNAPSE         0.011         0.032512933           GO         POSITIVE REGULATION OF TRANSFERASE ACTIVITY         0.012         0.033068378           GO         POSITIVE REGULATION OF CASPASE ACTIVITY         0.013         0.033948936	GO	CYTOKINE PRODUCTION	0.004	0.026536034
GO         CHROMOSOME SEGREGATION         0.009         0.029568888           GO         RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY         0.004         0.030563878           GO         REGULATION OF MAP KINASE ACTIVITY         0.005         0.030881578           GO         BONE REMODELING         0.01         0.031513043           GO         POSITIVE REGULATION OF CATALYTIC ACTIVITY         0.008         0.032506492           GO         SYNAPSE         0.011         0.032512933           GO         POSITIVE REGULATION OF TRANSFERASE ACTIVITY         0.012         0.033068378           GO         POSITIVE REGULATION OF CASPASE ACTIVITY         0.013         0.033948936	GO	ANTI APOPTOSIS	0.008	0.02695964
GO         RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY         0.004         0.030563878           GO         REGULATION OF MAP KINASE ACTIVITY         0.005         0.030881578           GO         BONE REMODELING         0.01         0.031513043           GO         POSITIVE REGULATION OF CATALYTIC ACTIVITY         0.008         0.032506492           GO         SYNAPSE         0.011         0.032512933           GO         POSITIVE REGULATION OF TRANSFERASE ACTIVITY         0.012         0.033068378           GO         POSITIVE REGULATION OF CASPASE ACTIVITY         0.013         0.033948936	GO	INFLAMMATORY RESPONSE	0.006	0.027125001
GO         REGULATION OF MAP KINASE ACTIVITY         0.005         0.030881578           GO         BONE REMODELING         0.01         0.031513043           GO         POSITIVE REGULATION OF CATALYTIC ACTIVITY         0.008         0.032506492           GO         SYNAPSE         0.011         0.032512933           GO         POSITIVE REGULATION OF TRANSFERASE ACTIVITY         0.012         0.033068378           GO         POSITIVE REGULATION OF CASPASE ACTIVITY         0.013         0.033948936	GO	CHROMOSOME SEGREGATION	0.009	0.029568888
GO         BONE REMODELING         0.01         0.031513043           GO         POSITIVE REGULATION OF CATALYTIC ACTIVITY         0.008         0.032506492           GO         SYNAPSE         0.011         0.032512933           GO         POSITIVE REGULATION OF TRANSFERASE ACTIVITY         0.012         0.033068378           GO         POSITIVE REGULATION OF CASPASE ACTIVITY         0.013         0.033948936	GO	RNA POLYMERASE II TRANSCRIPTION FACTOR ACTIVITY	0.004	0.030563878
GO         POSITIVE REGULATION OF CATALYTIC ACTIVITY         0.008         0.032506492           GO         SYNAPSE         0.011         0.032512933           GO         POSITIVE REGULATION OF TRANSFERASE ACTIVITY         0.012         0.033068378           GO         POSITIVE REGULATION OF CASPASE ACTIVITY         0.013         0.033948936	GO	REGULATION OF MAP KINASE ACTIVITY	0.005	0.030881578
GO         SYNAPSE         0.011         0.032512933           GO         POSITIVE REGULATION OF TRANSFERASE ACTIVITY         0.012         0.033068378           GO         POSITIVE REGULATION OF CASPASE ACTIVITY         0.013         0.033948936	GO	BONE REMODELING	0.01	0.031513043
GO POSITIVE REGULATION OF TRANSFERASE ACTIVITY 0.012 0.033068378 GO POSITIVE REGULATION OF CASPASE ACTIVITY 0.013 0.033948936	GO	POSITIVE REGULATION OF CATALYTIC ACTIVITY	0.008	0.032506492
GO POSITIVE REGULATION OF CASPASE ACTIVITY 0.013 0.033948936	GO	SYNAPSE	0.011	0.032512933
	GO	POSITIVE REGULATION OF TRANSFERASE ACTIVITY	0.012	0.033068378
GO LYTIC VACUOLE 0.006 0.035405062	GO	POSITIVE REGULATION OF CASPASE ACTIVITY	0.013	0.033948936
	GO	LYTIC VACUOLE	0.006	0.035405062

Pathway	Gene Set Name	P-value	FDR value
GO	LYSOSOME	0.006	0.035405062
GO	GLYCOPROTEIN METABOLIC PROCESS	0.01	0.038836133
GO	RECEPTOR MEDIATED ENDOCYTOSIS	0.01	0.039230127
GO	NEGATIVE REGULATION OF GROWTH	0.012	0.04075
GO	G PROTEIN SIGNALING COUPLED TO CAMP NUCLEOTIDE SECOND MESSENGER	0.016	0.040800832
GO	NEGATIVE REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER	0.009	0.042355374
GO	ENDOPEPTIDASE ACTIVITY	0.018	0.044094652
GO	BASEMENT MEMBRANE	0.005	0.04452049
GO	EMBRYONIC DEVELOPMENT	0.012	0.044865303
GO	TUBULIN BINDING	0.019	0.045465585
GO	POSITIVE REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE II PROMOTER	0.012	0.046798386
GO	WOUND HEALING	0.016	0.04945783