

TermID	Term	bg_pro_num	bg_term_num	fg_pro_num	fg_term_num	Ratio	pvalue	Enrichment	FDR	IDs
GO:0010951	negative regulation of endopeptidase activity	4650	36	61	10	0.27777778	1.37E-11	10.86386651	4.94E-09	F1SCE4_PIG,F1SFI6_PIG,TIM P1_PIG,A0A287B9R5_PIG,A0A287AT48_PIG,F1SCC9_PIG,A0A5G2R175_PIG,F1SMW6_PIG,PAI1_PIG,A0A287BF75_PIG
GO:0050829	defense response to Gram-negative bacterium	4650	19	61	6	0.31578947	9.43E-08	7.025606511	1.70E-05	PG2_PIG,LYSC1_PIG,LYSC3_PIG,DBMT1_PIG,A0A287B028_PIG,PAI1_PIG
GO:0050830	defense response to Gram-positive bacterium	4650	22	61	6	0.27272727	2.51E-07	6.599561976	3.03E-05	A0A5S8KUU6_PIG,PG2_PIG,LYSC1_PIG,LYSC3_PIG,DBMT1_PIG,A0A287B028_PIG
GO:0015909	long-chain fatty acid transport	4650	4	61	3	0.75	8.52E-06	5.069770055	0.000768559	APOE_PIG,F1RM45_PIG,FABP4_PIG
GO:0045087	innate immune response	4650	61	61	6	0.09836066	0.000125753	3.900481454	0.009079371	F1SJB5_PIG,A0A480MVF5_PIG,PG2_PIG,S10AC_PIG,F1S505_PIG,A0A287B028_PIG
GO:2000822	regulation of behavioral fear response	4650	2	61	2	1	0.000169305	3.771331414	0.010186489	APOE_PIG,F1RM45_PIG
GO:0071830	triglyceride-rich lipoprotein particle clearance	4650	2	61	2	1	0.000169305	3.771331414	0.008731277	APOE_PIG,F1RM45_PIG
GO:0061771	response to caloric restriction	4650	2	61	2	1	0.000169305	3.771331414	0.007639867	APOE_PIG,F1RM45_PIG
GO:1905855	positive regulation of heparan sulfate binding	4650	2	61	2	1	0.000169305	3.771331414	0.006790993	APOE_PIG,F1RM45_PIG
GO:0051651	maintenance of location in cell	4650	2	61	2	1	0.000169305	3.771331414	0.006111894	APOE_PIG,F1RM45_PIG
GO:0071831	intermediate-density lipoprotein particle clearance	4650	2	61	2	1	0.000169305	3.771331414	0.005556267	APOE_PIG,F1RM45_PIG
GO:1905890	regulation of cellular response to very-low-density lipoprotein particle stimulus	4650	2	61	2	1	0.000169305	3.771331414	0.005093245	APOE_PIG,F1RM45_PIG
GO:0090209	negative regulation of triglyceride metabolic process	4650	2	61	2	1	0.000169305	3.771331414	0.004701457	APOE_PIG,F1RM45_PIG
GO:0002548	monocyte chemotaxis	4650	2	61	2	1	0.000169305	3.771331414	0.004365638	F1SJB5_PIG,A0A5G2R7M4_PIG
GO:0010544	negative regulation of platelet activation	4650	2	61	2	1	0.000169305	3.771331414	0.004074596	APOE_PIG,F1RM45_PIG
GO:0032805	positive regulation of low-density lipoprotein particle receptor catabolic process	4650	2	61	2	1	0.000169305	3.771331414	0.003819934	APOE_PIG,F1RM45_PIG
GO:0034447	very-low-density lipoprotein particle clearance	4650	2	61	2	1	0.000169305	3.771331414	0.003595232	APOE_PIG,F1RM45_PIG
GO:1903002	positive regulation of lipid transport across blood-brain barrier	4650	2	61	2	1	0.000169305	3.771331414	0.003395496	APOE_PIG,F1RM45_PIG
GO:0007616	long-term memory	4650	2	61	2	1	0.000169305	3.771331414	0.003216786	APOE_PIG,F1RM45_PIG
GO:0097114	NMDA glutamate receptor clustering	4650	2	61	2	1	0.000169305	3.771331414	0.003055947	APOE_PIG,F1RM45_PIG
GO:1902952	positive regulation of dendritic spine maintenance	4650	2	61	2	1	0.000169305	3.771331414	0.002910426	APOE_PIG,F1RM45_PIG
GO:1905860	positive regulation of heparan sulfate proteoglycan binding	4650	2	61	2	1	0.000169305	3.771331414	0.002778133	APOE_PIG,F1RM45_PIG
GO:0010877	lipid transport involved in lipid storage	4650	2	61	2	1	0.000169305	3.771331414	0.002657345	APOE_PIG,F1RM45_PIG
GO:0097113	AMPA glutamate receptor clustering	4650	2	61	2	1	0.000169305	3.771331414	0.002546622	APOE_PIG,F1RM45_PIG
GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	4650	11	61	3	0.27272727	0.000328939	3.482884701	0.004749878	PG2_PIG,S10AC_PIG,F1S505_PIG
GO:0030855	epithelial cell differentiation	4650	27	61	4	0.14814815	0.000375429	3.425472037	0.005212689	F1S0J8_PIG,A0A5G2R7M4_PIG,A0A5G2R1T5_PIG,F6Q8K1_PIG
GO:0010469	regulation of signaling receptor activity	4650	3	61	2	0.66666667	0.000503615	3.297900981	0.006733525	A0A287B5M2_PIG,PAI1_PIG

GO:0007586	digestion	4650	3	61	2	0.66666667	0.000503615	3.297900981	0.006493042	LYSC1_PIG,LYSC3_PIG
GO:0035641	locomotory exploration behavior	4650	3	61	2	0.66666667	0.000503615	3.297900981	0.006269144	APOE_PIG,F1RM45_PIG
GO:1900221	regulation of amyloid-beta clearance	4650	3	61	2	0.66666667	0.000503615	3.297900981	0.006060172	APOE_PIG,F1RM45_PIG
GO:0002021	response to dietary excess	4650	3	61	2	0.66666667	0.000503615	3.297900981	0.005864683	APOE_PIG,F1RM45_PIG
GO:1902995	positive regulation of phospholipid efflux	4650	3	61	2	0.66666667	0.000503615	3.297900981	0.005681411	APOE_PIG,F1RM45_PIG
GO:1900223	positive regulation of amyloid-beta clearance	4650	3	61	2	0.66666667	0.000503615	3.297900981	0.005509247	APOE_PIG,F1RM45_PIG
GO:0034384	high-density lipoprotein particle clearance	4650	3	61	2	0.66666667	0.000503615	3.297900981	0.005347211	APOE_PIG,F1RM45_PIG
GO:0042982	amyloid precursor protein metabolic process	4650	3	61	2	0.66666667	0.000503615	3.297900981	0.005194433	APOE_PIG,F1RM45_PIG
GO:0051045	negative regulation of membrane protein ectodomain proteolysis	4650	3	61	2	0.66666667	0.000503615	3.297900981	0.005050144	TIMP1_PIG,A0A5G2R175_PIG
GO:0034097	response to cytokine	4650	13	61	3	0.23076923	0.000559578	3.252139216	0.005459668	A0A5S8KUU6_PIG,TIMP1_PIG,A0A5G2R175_PIG
GO:0034382	chylomicron remnant clearance	4650	4	61	2	0.5	0.000998715	3.000558448	0.009487792	APOE_PIG,F1RM45_PIG
GO:0042311	vasodilation	4650	4	61	2	0.5	0.000998715	3.000558448	0.009244515	APOE_PIG,F1RM45_PIG
GO:0042158	lipoprotein biosynthetic process	4650	4	61	2	0.5	0.000998715	3.000558448	0.009013402	APOE_PIG,F1RM45_PIG
GO:0017038	protein import	4650	4	61	2	0.5	0.000998715	3.000558448	0.008793563	APOE_PIG,F1RM45_PIG
GO:0044794	positive regulation by host of viral process	4650	4	61	2	0.5	0.000998715	3.000558448	0.008584193	APOE_PIG,F1RM45_PIG
GO:0045541	negative regulation of cholesterol biosynthetic process	4650	4	61	2	0.5	0.000998715	3.000558448	0.00838456	APOE_PIG,F1RM45_PIG
GO:0051000	positive regulation of nitric-oxide synthase activity	4650	4	61	2	0.5	0.000998715	3.000558448	0.008194002	APOE_PIG,F1RM45_PIG
GO:0019835	cytolysis	4650	4	61	2	0.5	0.000998715	3.000558448	0.008011913	LYSC1_PIG,LYSC3_PIG
GO:1905907	negative regulation of amyloid fibril formation	4650	4	61	2	0.5	0.000998715	3.000558448	0.007837741	APOE_PIG,F1RM45_PIG
GO:0009612	response to mechanical stimulus	4650	4	61	2	0.5	0.000998715	3.000558448	0.007670981	F1RK90_PIG,F1RP76_PIG
GO:0050709	negative regulation of protein secretion	4650	5	61	2	0.4	0.001650465	2.782393793	0.012412869	APOE_PIG,F1RM45_PIG
GO:0048844	artery morphogenesis	4650	5	61	2	0.4	0.001650465	2.782393793	0.012159545	APOE_PIG,F1RM45_PIG
GO:0008152	metabolic process	4650	5	61	2	0.4	0.001650465	2.782393793	0.011916354	LYSC1_PIG,LYSC3_PIG
GO:0043254	regulation of protein-containing complex assembly	4650	5	61	2	0.4	0.001650465	2.782393793	0.0116827	APOE_PIG,F1RM45_PIG
GO:0034372	very-low-density lipoprotein particle remodeling	4650	5	61	2	0.4	0.001650465	2.782393793	0.011458033	APOE_PIG,F1RM45_PIG
GO:0006707	cholesterol catabolic process	4650	5	61	2	0.4	0.001650465	2.782393793	0.011241844	APOE_PIG,F1RM45_PIG
GO:0043537	negative regulation of blood vessel endothelial cell migration	4650	5	61	2	0.4	0.001650465	2.782393793	0.011033661	APOE_PIG,F1RM45_PIG
GO:0051044	positive regulation of membrane protein ectodomain proteolysis	4650	5	61	2	0.4	0.001650465	2.782393793	0.010833049	APOE_PIG,F1RM45_PIG
GO:0045088	regulation of innate immune	4650	5	61	2	0.4	0.001650465	2.782393793	0.010639602	APOE_PIG,F1RM45_PIG
GO:0019934	cGMP-mediated signaling	4650	5	61	2	0.4	0.001650465	2.782393793	0.010452942	APOE_PIG,F1RM45_PIG
GO:0042159	lipoprotein catabolic process	4650	5	61	2	0.4	0.001650465	2.782393793	0.010272719	APOE_PIG,F1RM45_PIG
GO:0007263	nitric oxide mediated signal transduction	4650	5	61	2	0.4	0.001650465	2.782393793	0.010098605	APOE_PIG,F1RM45_PIG
GO:0034374	low-density lipoprotein particle remodeling	4650	5	61	2	0.4	0.001650465	2.782393793	0.009930295	APOE_PIG,F1RM45_PIG

GO:0060999	positive regulation of dendritic spine development	4650	5	61	2	0.4	0.001650465	2.782393793	0.009767503	APOE_PIG,F1RM45_PIG
GO:0019068	virion assembly	4650	5	61	2	0.4	0.001650465	2.782393793	0.009609963	APOE_PIG,F1RM45_PIG
GO:0032489	regulation of Cdc42 protein signal transduction	4650	6	61	2	0.33333333	0.002454804	2.609983251	0.014066414	APOE_PIG,F1RM45_PIG
GO:0034380	high-density lipoprotein particle assembly	4650	6	61	2	0.33333333	0.002454804	2.609983251	0.013846626	APOE_PIG,F1RM45_PIG
GO:1900272	negative regulation of long-term synaptic potentiation	4650	6	61	2	0.33333333	0.002454804	2.609983251	0.013633601	APOE_PIG,F1RM45_PIG
GO:0043691	reverse cholesterol transport	4650	6	61	2	0.33333333	0.002454804	2.609983251	0.013427032	APOE_PIG,F1RM45_PIG
GO:0055089	fatty acid homeostasis	4650	6	61	2	0.33333333	0.002454804	2.609983251	0.013226628	APOE_PIG,F1RM45_PIG
GO:0010033	response to organic substance	4650	6	61	2	0.33333333	0.002454804	2.609983251	0.013032119	TIMP1_PIG,A0A5G2R175_PIG
GO:0034375	high-density lipoprotein particle remodeling	4650	6	61	2	0.33333333	0.002454804	2.609983251	0.012843248	APOE_PIG,F1RM45_PIG
GO:0010873	positive regulation of cholesterol esterification	4650	7	61	2	0.28571429	0.003407748	2.467532546	0.017574243	APOE_PIG,F1RM45_PIG
GO:0010467	gene expression	4650	7	61	2	0.28571429	0.003407748	2.467532546	0.017326718	APOE_PIG,F1RM45_PIG
GO:0033700	phospholipid efflux	4650	7	61	2	0.28571429	0.003407748	2.467532546	0.017086069	APOE_PIG,F1RM45_PIG
GO:0070328	triglyceride homeostasis	4650	7	61	2	0.28571429	0.003407748	2.467532546	0.016852013	APOE_PIG,F1RM45_PIG
GO:0019731	antibacterial humoral response	4650	7	61	2	0.28571429	0.003407748	2.467532546	0.016624283	A0A480MV5_PIG,F1S505_PIG
GO:0050728	negative regulation of inflammatory response	4650	24	61	3	0.125	0.003573508	2.446905206	0.017200487	APOE_PIG,F1RM45_PIG,A0A5S8KUU6_PIG
GO:0006874	cellular calcium ion homeostasis	4650	25	61	3	0.12	0.004023173	2.395431345	0.019110069	APOE_PIG,F1RM45_PIG,A0A5S6HMA0_PIG
GO:0006952	defense response	4650	8	61	2	0.25	0.004505389	2.346267743	0.021122666	A0A287AFU9_PIG,Q0Z8R0_PIG
GO:0006953	acute-phase response	4650	8	61	2	0.25	0.004505389	2.346267743	0.020851863	HPT_PIG,A0A287B028_PIG
GO:0045807	positive regulation of endocytosis	4650	8	61	2	0.25	0.004505389	2.346267743	0.020587915	APOE_PIG,F1RM45_PIG
GO:0046889	positive regulation of lipid biosynthetic	4650	8	61	2	0.25	0.004505389	2.346267743	0.020330566	APOE_PIG,F1RM45_PIG
GO:0002250	adaptive immune response	4650	9	61	2	0.22222222	0.005743891	2.240793801	0.025599317	F1SJB5_PIG,CATL1_PIG
GO:1902430	negative regulation of amyloid-beta formation	4650	9	61	2	0.22222222	0.005743891	2.240793801	0.02528713	APOE_PIG,F1RM45_PIG
GO:0032757	positive regulation of interleukin-8 production	4650	9	61	2	0.22222222	0.005743891	2.240793801	0.024982466	A0A287B028_PIG,PAI1_PIG
GO:0061136	regulation of proteasomal protein catabolic process	4650	9	61	2	0.22222222	0.005743891	2.240793801	0.024685056	APOE_PIG,F1RM45_PIG
GO:0042632	cholesterol homeostasis	4650	29	61	3	0.10344828	0.006158231	2.210544054	0.026154368	APOE_PIG,F1RM45_PIG,FABP4_PIG
GO:0009725	response to hormone	4650	10	61	2	0.2	0.007119494	2.1475509	0.029885316	TIMP1_PIG,A0A5G2R175_PIG
GO:0010875	positive regulation of cholesterol efflux	4650	10	61	2	0.2	0.007119494	2.1475509	0.029541807	APOE_PIG,F1RM45_PIG
GO:0033344	cholesterol efflux	4650	10	61	2	0.2	0.007119494	2.1475509	0.029206104	APOE_PIG,F1RM45_PIG
GO:0055072	iron ion homeostasis	4650	11	61	2	0.18181818	0.008628506	2.064064411	0.03499877	A0A5S8KUU6_PIG,A0A5G2QW05_PIG
GO:0001937	negative regulation of endothelial cell proliferation	4650	12	61	2	0.16666667	0.010267308	1.988543418	0.041183312	APOE_PIG,F1RM45_PIG
GO:0006641	triglyceride metabolic process	4650	12	61	2	0.16666667	0.010267308	1.988543418	0.040730749	APOE_PIG,F1RM45_PIG
GO:0010977	negative regulation of neuron projection development	4650	13	61	2	0.15384615	0.01203235	1.91964956	0.047213893	APOE_PIG,F1RM45_PIG
GO:0002248	connective tissue replacement involved in inflammatory response wound healing	4650	1	61	1	1	0.01311828	1.882123118	0.050921494	TIMP1_PIG
GO:0046883	regulation of hormone secretion	4650	1	61	1	1	0.01311828	1.882123118	0.050379776	F1SJB5_PIG

GO:1903278	positive regulation of sodium ion export across plasma membrane	4650	1	61	1	1	0.01311828	1.882123118	0.049849462	A0A5S6HMA0_PIG
GO:1905049	negative regulation of metalloproteinase activity	4650	1	61	1	1	0.01311828	1.882123118	0.049330197	TIMP1_PIG
GO:2001044	regulation of integrin-mediated signaling pathway	4650	1	61	1	1	0.01311828	1.882123118	0.048821638	TIMP1_PIG
GO:0072719	cellular response to cisplatin	4650	1	61	1	1	0.01311828	1.882123118	0.048323458	A0A287ACN2_PIG
GO:0010711	negative regulation of collagen catabolic process	4650	1	61	1	1	0.01311828	1.882123118	0.047835343	Q0Z8R0_PIG
GO:0071621	granulocyte chemotaxis	4650	1	61	1	1	0.01311828	1.882123118	0.047356989	F1SJB5_PIG
GO:0097187	dentinogenesis	4650	1	61	1	1	0.01311828	1.882123118	0.046888108	PAI1_PIG
GO:0061044	negative regulation of vascular wound healing	4650	1	61	1	1	0.01311828	1.882123118	0.046428421	PAI1_PIG
GO:0070232	regulation of T cell apoptotic process	4650	1	61	1	1	0.01311828	1.882123118	0.045977659	A0A5G2R7M4_PIG
GO:0030850	prostate gland development	4650	1	61	1	1	0.01311828	1.882123118	0.045535567	F1SJB5_PIG
GO:0002685	regulation of leukocyte migration	4650	1	61	1	1	0.01311828	1.882123118	0.045101895	F1SJB5_PIG
GO:0014839	myoblast migration involved in skeletal muscle regeneration	4650	1	61	1	1	0.01311828	1.882123118	0.044676405	F1SJB5_PIG
GO:0032652	regulation of interleukin-1 production	4650	1	61	1	1	0.01311828	1.882123118	0.044258868	F1SJB5_PIG
GO:0032691	negative regulation of interleukin-1 beta production	4650	1	61	1	1	0.01311828	1.882123118	0.043849064	A0A5S8KUU6_PIG
GO:0034633	retinol transport	4650	1	61	1	1	0.01311828	1.882123118	0.043446779	A0A287A3Z4_PIG
GO:0098737	protein insertion into plasma membrane	4650	1	61	1	1	0.01311828	1.882123118	0.043051808	F1SU64_PIG
GO:0035491	positive regulation of leukotriene production involved in inflammatory response	4650	1	61	1	1	0.01311828	1.882123118	0.042663954	PAI1_PIG
GO:0060265	positive regulation of respiratory burst involved in inflammatory response	4650	1	61	1	1	0.01311828	1.882123118	0.042283026	A0A287B028_PIG
GO:0032929	negative regulation of superoxide anion generation	4650	1	61	1	1	0.01311828	1.882123118	0.04190884	A0A5S8KUU6_PIG
GO:0002526	acute inflammatory response	4650	1	61	1	1	0.01311828	1.882123118	0.041541219	HPT_PIG
GO:0032490	detection of molecule of bacterial origin	4650	1	61	1	1	0.01311828	1.882123118	0.041179991	A0A287B028_PIG
GO:1902305	regulation of sodium ion transmembrane transport	4650	1	61	1	1	0.01311828	1.882123118	0.040824991	F1S505_PIG
GO:0008016	regulation of heart contraction	4650	1	61	1	1	0.01311828	1.882123118	0.040476059	K7GQ50_PIG
GO:0060311	negative regulation of elastin catabolic process	4650	1	61	1	1	0.01311828	1.882123118	0.040133042	Q0Z8R0_PIG
GO:1901331	positive regulation of odontoblast differentiation	4650	1	61	1	1	0.01311828	1.882123118	0.039795789	PAI1_PIG
GO:0045919	positive regulation of cytolysis	4650	1	61	1	1	0.01311828	1.882123118	0.039464158	A0A287B028_PIG
GO:0045627	positive regulation of T-helper 1 cell differentiation	4650	1	61	1	1	0.01311828	1.882123118	0.039138008	F1SJB5_PIG
GO:0070171	negative regulation of tooth mineralization	4650	1	61	1	1	0.01311828	1.882123118	0.038817204	F1SUE4_PIG
GO:0050828	regulation of liquid surface tension	4650	1	61	1	1	0.01311828	1.882123118	0.038501617	F1S505_PIG

GO:0071478	cellular response to radiation	4650	1	61	1	1	0.01311828	1.882123118	0.03819112	A0A287ACN2_PIG
GO:2001023	regulation of response to drug	4650	1	61	1	1	0.01311828	1.882123118	0.037885591	A0A287ACN2_PIG
GO:0014912	negative regulation of smooth muscle cell migration	4650	1	61	1	1	0.01311828	1.882123118	0.037584912	PAI1_PIG
GO:0045629	negative regulation of T-helper 2 cell differentiation	4650	1	61	1	1	0.01311828	1.882123118	0.037288968	F1SJB5_PIG
GO:0015920	lipopolysaccharide transport	4650	1	61	1	1	0.01311828	1.882123118	0.036997648	A0A287B028_PIG
GO:1903896	positive regulation of IRE1-mediated unfolded protein response	4650	1	61	1	1	0.01311828	1.882123118	0.036710844	A0A287AM82_PIG
GO:0060480	lung goblet cell differentiation	4650	1	61	1	1	0.01311828	1.882123118	0.036428453	A0A287AM82_PIG
GO:0035821	modulation of process of other organism	4650	1	61	1	1	0.01311828	1.882123118	0.036150373	A0A480MVF5_PIG
GO:0042129	regulation of T cell proliferation	4650	1	61	1	1	0.01311828	1.882123118	0.035876507	A0A5G2R7M4_PIG
GO:0070346	positive regulation of fat cell proliferation	4650	1	61	1	1	0.01311828	1.882123118	0.035606759	FABP4_PIG
GO:0002395	immune response in nasopharyngeal-associated lymphoid tissue	4650	1	61	1	1	0.01311828	1.882123118	0.035341037	F1S505_PIG
GO:0048245	eosinophil chemotaxis	4650	1	61	1	1	0.01311828	1.882123118	0.035079251	A0A5G2R7M4_PIG
GO:0071677	positive regulation of mononuclear cell migration	4650	1	61	1	1	0.01311828	1.882123118	0.034821316	A0A5G2R7M4_PIG
GO:0032720	negative regulation of tumor necrosis factor production	4650	14	61	2	0.14285714	0.013920149	1.856356126	0.0366801	A0A5S8KUU6_PIG,A0A287B028_PIG
GO:0043407	negative regulation of MAP kinase activity	4650	17	61	2	0.11764706	0.020286267	1.692797865	0.053067698	APOE_PIG,F1RM45_PIG
GO:0032496	response to lipopolysaccharide	4650	19	61	2	0.10526316	0.025083258	1.600616063	0.065144288	A0A5S8KUU6_PIG,A0A480MVF5_PIG
GO:2000483	negative regulation of interleukin-8 secretion	4650	2	61	1	0.5	0.026067255	1.583904706	0.067216278	F1SJB5_PIG
GO:0086009	membrane repolarization	4650	2	61	1	0.5	0.026067255	1.583904706	0.066739567	A0A5S6HMA0_PIG
GO:0070459	prolactin secretion	4650	2	61	1	0.5	0.026067255	1.583904706	0.06626957	F1SJB5_PIG
GO:0007187	G protein-coupled receptor signaling pathway	4650	2	61	1	0.5	0.026067255	1.583904706	0.065806146	F1SJB5_PIG
GO:0001300	chronological cell aging	4650	2	61	1	0.5	0.026067255	1.583904706	0.065349159	PAI1_PIG
GO:0050896	response to stimulus	4650	2	61	1	0.5	0.026067255	1.583904706	0.064898475	OBP_PIG
GO:0031394	positive regulation of prostaglandin biosynthetic process	4650	2	61	1	0.5	0.026067255	1.583904706	0.064453965	F1SJB5_PIG
GO:1901018	positive regulation of potassium ion transmembrane transporter activity	4650	2	61	1	0.5	0.026067255	1.583904706	0.064015503	A0A5S6HMA0_PIG
GO:0002377	immunoglobulin production	4650	2	61	1	0.5	0.026067255	1.583904706	0.063582966	A0A075B7I9_PIG
GO:0032695	negative regulation of interleukin-12 production	4650	2	61	1	0.5	0.026067255	1.583904706	0.063156234	A0A5S8KUU6_PIG
GO:0046632	alpha-beta T cell differentiation	4650	2	61	1	0.5	0.026067255	1.583904706	0.062735193	F1SJB5_PIG
GO:0071918	urea transmembrane transport	4650	2	61	1	0.5	0.026067255	1.583904706	0.062319728	F1RPU5_PIG
GO:0010165	response to X-ray	4650	2	61	1	0.5	0.026067255	1.583904706	0.06190973	F1SJB5_PIG
GO:0048246	macrophage chemotaxis	4650	2	61	1	0.5	0.026067255	1.583904706	0.061505091	A0A5G2R7M4_PIG
GO:1900138	negative regulation of phospholipase A2 activity	4650	2	61	1	0.5	0.026067255	1.583904706	0.061105707	F1SJB5_PIG
GO:0090399	replicative senescence	4650	2	61	1	0.5	0.026067255	1.583904706	0.060711477	PAI1_PIG

GO:1900229	negative regulation of single-species biofilm formation in or on host organism	4650	2	61	1	0.5	0.026067255	1.583904706	0.060322301	F1S505_PIG
GO:0043086	negative regulation of catalytic activity	4650	2	61	1	0.5	0.026067255	1.583904706	0.059938082	TIMP1_PIG
GO:0070365	hepatocyte differentiation	4650	2	61	1	0.5	0.026067255	1.583904706	0.059558727	F1SJB5_PIG
GO:0030277	maintenance of gastrointestinal epithelium	4650	2	61	1	0.5	0.026067255	1.583904706	0.059184144	A0A287A3Z4_PIG
GO:0031018	endocrine pancreas development	4650	2	61	1	0.5	0.026067255	1.583904706	0.058814243	F1SJB5_PIG
GO:0070254	mucus secretion	4650	2	61	1	0.5	0.026067255	1.583904706	0.058448937	A0A287AM82_PIG
GO:1902041	regulation of extrinsic apoptotic signaling pathway via death domain receptors	4650	2	61	1	0.5	0.026067255	1.583904706	0.058088141	A0A5G2R7M4_PIG
GO:0009792	embryo development ending in birth or egg hatching	4650	2	61	1	0.5	0.026067255	1.583904706	0.057731772	F1RP76_PIG
GO:0050891	multicellular organismal water homeostasis	4650	2	61	1	0.5	0.026067255	1.583904706	0.057379749	F1S505_PIG
GO:0002232	leukocyte chemotaxis involved in inflammatory response	4650	2	61	1	0.5	0.026067255	1.583904706	0.057031993	A0A287B028_PIG
GO:0044849	estrous cycle	4650	2	61	1	0.5	0.026067255	1.583904706	0.056688427	F1SJB5_PIG
GO:2000098	negative regulation of smooth muscle cell-matrix adhesion	4650	2	61	1	0.5	0.026067255	1.583904706	0.056348976	PAI1_PIG
GO:0048639	positive regulation of developmental growth	4650	2	61	1	0.5	0.026067255	1.583904706	0.056013565	A0A287AM82_PIG
GO:0033031	positive regulation of neutrophil apoptotic process	4650	2	61	1	0.5	0.026067255	1.583904706	0.055682124	F1SJB5_PIG
GO:0031247	actin rod assembly	4650	2	61	1	0.5	0.026067255	1.583904706	0.055354582	A0A287AFA5_PIG
GO:0045920	negative regulation of exocytosis	4650	2	61	1	0.5	0.026067255	1.583904706	0.055030871	F1SJB5_PIG
GO:1903899	positive regulation of PERK-mediated unfolded protein response	4650	2	61	1	0.5	0.026067255	1.583904706	0.054710924	A0A287AM82_PIG
GO:1903288	positive regulation of potassium ion import across plasma membrane	4650	2	61	1	0.5	0.026067255	1.583904706	0.054394676	A0A5S6HMA0_PIG
GO:1903281	positive regulation of calcium	4650	2	61	1	0.5	0.026067255	1.583904706	0.054082063	A0A5S6HMA0_PIG
GO:0030216	keratinocyte differentiation	4650	20	61	2	0.1	0.027638151	1.558491013	0.057013557	F1SJB5_PIG,F1RP76_PIG
GO:0043524	negative regulation of neuron apoptotic process	4650	20	61	2	0.1	0.027638151	1.558491013	0.056689617	APOE_PIG,F1RM45_PIG
GO:0009617	response to bacterium	4650	23	61	2	0.08695652	0.035892171	1.445000269	0.073203807	FABP4_PIG,F6Q8K1_PIG
GO:1903078	positive regulation of protein localization to plasma membrane	4650	23	61	2	0.08695652	0.035892171	1.445000269	0.07279255	A0A5G2R7M4_PIG,A0A287AM82_PIG
GO:0007186	G protein-coupled receptor signaling pathway	4650	24	61	2	0.08333333	0.038830232	1.41083002	0.078311249	APOE_PIG,F1RM45_PIG
GO:0090280	positive regulation of calcium ion import	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.077913977	A0A5G2R7M4_PIG
GO:0071385	cellular response to glucocorticoid stimulus	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.077483513	F1SJB5_PIG
GO:0090435	protein localization to nuclear envelope	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.077057779	A0A287AGQ8_PIG
GO:0010248	establishment or maintenance of transmembrane electrochemical gradient	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.076636698	A0A5S6HMA0_PIG

GO:0048546	digestive tract morphogenesis	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.076220194	A0A287AM82_PIG
GO:0033629	negative regulation of cell adhesion mediated by integrin	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.075808193	PAI1_PIG
GO:0006814	sodium ion transport	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.075400623	A0A5S6HMA0_PIG
GO:0010716	negative regulation of extracellular matrix disassembly	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.074997411	Q0Z8R0_PIG
GO:0002281	macrophage activation involved in immune response	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.074598488	A0A287B028_PIG
GO:0032722	positive regulation of chemokine production	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.074203787	A0A287B028_PIG
GO:0042063	gliogenesis	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.073813241	F1SJB5_PIG
GO:0097435	supramolecular fiber organization	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.073426784	Q0Z8R0_PIG
GO:0002175	protein localization to paranode region of axon	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.073044353	F1SU64_PIG
GO:0015840	urea transport	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.072665885	F1RPU5_PIG
GO:0034144	negative regulation of toll-like receptor 4 signaling pathway	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.072291318	A7J149_PIG
GO:0097350	neutrophil clearance	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.071920594	F1SJB5_PIG
GO:0090023	positive regulation of neutrophil chemotaxis	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.071553652	A0A287B028_PIG
GO:0010882	regulation of cardiac muscle contraction by calcium ion signaling	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.071190435	A0A5S6HMA0_PIG
GO:0034145	positive regulation of toll-like receptor 4 signaling pathway	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.070830888	A0A287B028_PIG
GO:0051666	actin cortical patch localization	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.070474954	A0A5G2QKX8_PIG
GO:0060313	negative regulation of blood vessel remodeling	4650	3	61	1	0.33333333	0.038849074	1.410619326	0.070122579	Q0Z8R0_PIG
GO:0006898	receptor-mediated endocytosis	4650	26	61	2	0.07692308	0.044969526	1.347081691	0.080766164	APOE_PIG,F1RM45_PIG
GO:0006955	immune response	4650	26	61	2	0.07692308	0.044969526	1.347081691	0.080366331	A0A480MVF5_PIG,A0A075B7I9_PIG
GO:0090090	negative regulation of canonical Wnt signaling pathway	4650	27	61	2	0.07407407	0.04816532	1.317265554	0.085653598	APOE_PIG,F1RM45_PIG
GO:0090201	negative regulation of release of cytochrome c from mitochondria	4650	8	16	2	0.25	0.000307129	3.512679763	0.02610593	LMNA_PIG,F1SFG7_PIG
GO:0006334	nucleosome assembly	4650	20	16	2	0.1	0.002034471	2.691548587	0.086464999	H4_PIG,A0A287BQW3_PIG
GO:0098925	retrograde trans-synaptic signaling by nitric oxide	4650	1	16	1	1	0.00344086	2.46333297	0.097491039	A0A5G2QIK9_PIG
GO:0007614	short-term memory	4650	1	16	1	1	0.00344086	2.46333297	0.07311828	A0A287ALW7_PIG
GO:1901987	regulation of cell cycle phase transition	4650	1	16	1	1	0.00344086	2.46333297	0.058494624	A0A287A8H0_PIG
GO:0034653	retinoic acid catabolic process	4650	1	16	1	1	0.00344086	2.46333297	0.04874552	B3F0B7_PIG
GO:0097749	membrane tubulation	4650	2	16	1	0.5	0.006870618	2.163004166	0.083428939	F1SFG7_PIG
GO:0090343	positive regulation of cell aging	4650	2	16	1	0.5	0.006870618	2.163004166	0.073000321	LMNA_PIG
GO:0010571	positive regulation of nuclear cell cycle DNA replication	4650	2	16	1	0.5	0.006870618	2.163004166	0.064889175	A0A287A8H0_PIG
GO:0033306	phytol metabolic process	4650	2	16	1	0.5	0.006870618	2.163004166	0.058400257	I3L8Q5_PIG
GO:0010750	positive regulation of nitric oxide mediated signal transduction	4650	2	16	1	0.5	0.006870618	2.163004166	0.053091143	A0A5G2QIK9_PIG

GO:0000002	mitochondrial genome maintenance	4650	2	16	1	0.5	0.006870618	2.163004166	0.048666881	F1SFG7_PIG
GO:1900114	positive regulation of histone H3-K9 trimethylation	4650	2	16	1	0.5	0.006870618	2.163004166	0.044923275	LMNA_PIG
GO:0035583	sequestering of TGFbeta in extracellular matrix	4650	2	16	1	0.5	0.006870618	2.163004166	0.041714469	A0A286ZWQ1_PIG
GO:1901388	regulation of transforming growth factor beta activation	4650	2	16	1	0.5	0.006870618	2.163004166	0.038933505	A0A286ZWQ1_PIG
GO:2000463	positive regulation of excitatory postsynaptic potential	4650	2	16	1	0.5	0.006870618	2.163004166	0.036500161	A0A287ALW7_PIG
GO:0006564	L-serine biosynthetic process	4650	2	16	1	0.5	0.006870618	2.163004166	0.034353092	SERA_PIG
GO:0072201	negative regulation of mesenchymal cell proliferation	4650	3	16	1	0.33333333	0.010289308	1.987613821	0.0485884	LMNA_PIG
GO:1903243	negative regulation of cardiac muscle hypertrophy in response to stress	4650	3	16	1	0.33333333	0.010289308	1.987613821	0.046031116	LMNA_PIG
GO:2000647	negative regulation of stem cell proliferation	4650	4	16	1	0.25	0.013696963	1.86337572	0.058212092	A0A5G2QCT3_PIG
GO:0055015	ventricular cardiac muscle cell development	4650	4	16	1	0.25	0.013696963	1.86337572	0.055440088	LMNA_PIG
GO:0060087	relaxation of vascular smooth muscle	4650	4	16	1	0.25	0.013696963	1.86337572	0.052920084	A0A5G2QIK9_PIG
GO:0030951	establishment or maintenance of microtubule cytoskeleton polarity	4650	4	16	1	0.25	0.013696963	1.86337572	0.050619211	LMNA_PIG
GO:0007007	inner mitochondrial membrane	4650	4	16	1	0.25	0.013696963	1.86337572	0.048510077	F1SFG7_PIG
GO:1900180	regulation of protein localization to nucleus	4650	4	16	1	0.25	0.013696963	1.86337572	0.046569674	LMNA_PIG
GO:0071310	cellular response to organic substance	4650	4	16	1	0.25	0.013696963	1.86337572	0.044778533	A0A287ALW7_PIG
GO:0010628	positive regulation of gene expression	4650	57	16	2	0.03508772	0.015868719	1.799458136	0.049957078	LMNA_PIG,A0A287ALW7_PIG
GO:0031936	negative regulation of chromatin silencing	4650	5	16	1	0.2	0.017093616	1.767166066	0.051891333	A0A287BQW3_PIG
GO:0006352	DNA-templated transcription	4650	5	16	1	0.2	0.017093616	1.767166066	0.050101977	H4_PIG
GO:0030261	chromosome condensation	4650	5	16	1	0.2	0.017093616	1.767166066	0.048431911	A0A287BQW3_PIG
GO:0045910	negative regulation of DNA recombination	4650	5	16	1	0.2	0.017093616	1.767166066	0.046869591	A0A287BQW3_PIG
GO:0051965	positive regulation of synapse assembly	4650	5	16	1	0.2	0.017093616	1.767166066	0.045404917	A0A287ALW7_PIG
GO:0044030	regulation of DNA methylation	4650	5	16	1	0.2	0.017093616	1.767166066	0.04402901	A0A287BQW3_PIG
GO:0051259	protein complex oligomerization	4650	5	16	1	0.2	0.017093616	1.767166066	0.042734039	F1SFG7_PIG
GO:0072378	blood coagulation	4650	5	16	1	0.2	0.017093616	1.767166066	0.041513067	A0A5G2QCT3_PIG
GO:0035904	aorta development	4650	6	16	1	0.16666667	0.0204793	1.6886849	0.048353902	A0A286ZWQ1_PIG
GO:0006520	cellular amino acid metabolic process	4650	6	16	1	0.16666667	0.0204793	1.6886849	0.04704704	SERA_PIG
GO:0061003	positive regulation of dendritic spine morphogenesis	4650	6	16	1	0.16666667	0.0204793	1.6886849	0.04580896	A0A287ALW7_PIG
GO:0098532	histone H3-K27 trimethylation	4650	6	16	1	0.16666667	0.0204793	1.6886849	0.044634371	A0A287BQW3_PIG
GO:0010971	positive regulation of G2/M transition of mitotic cell cycle	4650	6	16	1	0.16666667	0.0204793	1.6886849	0.043518512	A0A287A8H0_PIG
GO:0060976	coronary vasculature development	4650	6	16	1	0.16666667	0.0204793	1.6886849	0.042457085	A0A286ZWQ1_PIG



GO:0046849	bone remodeling	4650	6	16	1	0.16666667	0.0204793	1.6886849	0.041446202	SPP24_PIG
GO:0008053	mitochondrial fusion	4650	7	16	1	0.14285714	0.023854048	1.622437912	0.047153351	F1SFG7_PIG
GO:0048285	organelle fission	4650	7	16	1	0.14285714	0.023854048	1.622437912	0.046081684	F1SFG7_PIG
GO:0003429	growth plate cartilage chondrocyte morphogenesis	4650	7	16	1	0.14285714	0.023854048	1.622437912	0.045057646	A0A287BLM4_PIG
GO:0006998	nuclear envelope organization	4650	7	16	1	0.14285714	0.023854048	1.622437912	0.044078132	LMNA_PIG
GO:2000146	negative regulation of cell motility	4650	7	16	1	0.14285714	0.023854048	1.622437912	0.043140299	A0A5G2QCT3_PIG
GO:0016584	nucleosome positioning	4650	8	16	1	0.125	0.027217894	1.565145488	0.048198353	A0A287BQW3_PIG
GO:0090398	cellular senescence	4650	8	16	1	0.125	0.027217894	1.565145488	0.047214713	F1SFG7_PIG
GO:2000737	negative regulation of stem cell differentiation	4650	8	16	1	0.125	0.027217894	1.565145488	0.046270419	A0A287BQW3_PIG
GO:2000679	positive regulation of transcription regulatory region DNA binding	4650	8	16	1	0.125	0.027217894	1.565145488	0.045363156	A0A287BQW3_PIG
GO:1902236	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	4650	9	16	1	0.11111111	0.030570869	1.51469221	0.049971613	F1SFG7_PIG
GO:0046039	GTP metabolic process	4650	9	16	1	0.11111111	0.030570869	1.51469221	0.049028753	F1SFG7_PIG
GO:0048193	Golgi vesicle transport	4650	9	16	1	0.11111111	0.030570869	1.51469221	0.048120813	A0A287ALW7_PIG
GO:0006355	regulation of transcription	4650	85	16	2	0.02352941	0.033566014	1.474100222	0.05187475	A0A287BQW3_PIG,A0A287ALW7_PIG
GO:1900025	negative regulation of substrate adhesion-dependent cell spreading	4650	10	16	1	0.1	0.033913008	1.469633686	0.051475102	A0A5G2QCT3_PIG
GO:0003281	ventricular septum development	4650	10	16	1	0.1	0.033913008	1.469633686	0.05057203	A0A286ZWQ1_PIG
GO:0034504	protein localization to nucleus	4650	11	16	1	0.09090909	0.037244343	1.428939687	0.054582226	LMNA_PIG
GO:0080182	histone H3-K4 trimethylation	4650	11	16	1	0.09090909	0.037244343	1.428939687	0.053657104	A0A287BQW3_PIG
GO:0061025	membrane fusion	4650	12	16	1	0.08333333	0.040564905	1.391849533	0.057466949	F1SFG7_PIG
GO:0008217	regulation of blood pressure	4650	12	16	1	0.08333333	0.040564905	1.391849533	0.056524868	A0A5G2QIK9_PIG
GO:0006342	chromatin silencing	4650	12	16	1	0.08333333	0.040564905	1.391849533	0.055613177	A0A287BQW3_PIG
GO:0000266	mitochondrial fission	4650	13	16	1	0.07692308	0.043874729	1.357785554	0.059196063	F1SFG7_PIG
GO:0007601	visual perception	4650	14	16	1	0.07142857	0.047173846	1.326298719	0.062652764	F1SFG7_PIG
GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	4650	14	16	1	0.07142857	0.047173846	1.326298719	0.061688875	LMNA_PIG
GO:0005615	extracellular space	4866	280	65	29	0.10357143	1.04E-19	18.98371833	7.99E-18	F1SJB5_PIG,F1SCE4_PIG,HP T_PIG,APOE_PIG,F1RM45_PIG,A0A5G2QW05_PIG,A0A480MVF5_PIG,PG2_PIG,A0A5G2R7M4_PIG,Q0Z8R0_PIG,DM BT1_PIG,A0A287A3Z4_PIG,TIMP1_PIG,A0A287B5M2_PIG,A0A287B9R5_PIG,A0A287AT48_PIG,A7J149_PIG,F1SCC9_PIG,I3LQ76_PIG,A0A5G2R175_PIG,F1SUE4_PIG,F1S505_PIG,F1SMW6_PIG,A0A287B028_PIG,CATL1_PIG,PAI1_PIG,A0A287BF75_PIG,A0A075B7I9_PIG,A0A287AM82_PIG
GO:0005576	extracellular region	4866	125	65	12	0.096	6.17E-08	7.20957262	2.38E-06	HPT_PIG,A0A5S8KUU6_PIG,F1SFI6_PIG,A0A480MVF5_PIG,A0A287AFU9_PIG,OBP_PIG,LYSC1_PIG,LYSC3_PIG,TIMP1_PIG,S10AC_PIG,A0A5G2R175_PIG,F1S505_PIG
GO:0045095	keratin filament	4866	13	65	5	0.38461538	4.31E-07	6.365140407	1.11E-05	A0A287A8E9_PIG,A0A287AG48_PIG,F1S0J8_PIG,A0A287BH52_PIG,A0A286ZL11_PIG
GO:0031012	extracellular matrix	4866	44	65	6	0.13636364	2.13E-05	4.671117576	0.0004105	APOE_PIG,F1RM45_PIG,DM BT1_PIG,TIMP1_PIG,A0A5G2R175_PIG,F1SUE4_PIG

GO:0120001	apical plasma membrane urothelial plaque	4866	3	65	2	0.66666667	0.000522629	3.281806724	0.008048482	A0A5G2R1T5_PIG,F6Q8K1_PIG
GO:0034363	intermediate-density lipoprotein particle	4866	4	65	2	0.5	0.00103624	2.984539551	0.013298416	APOE_PIG,F1RM45_PIG
GO:0043083	synaptic cleft	4866	4	65	2	0.5	0.00103624	2.984539551	0.011398643	APOE_PIG,F1RM45_PIG
GO:0034362	low-density lipoprotein particle	4866	5	65	2	0.4	0.001712182	2.766450076	0.016479752	APOE_PIG,F1RM45_PIG
GO:0005882	intermediate filament	4866	20	65	3	0.15	0.002205124	2.656566996	0.01886606	A0A287A8E9_PIG,F1S0J8_PIG,A0A5G2QXD3_PIG
GO:0034364	high-density lipoprotein particle	4866	7	65	2	0.28571429	0.003533958	2.451738649	0.027211475	APOE_PIG,F1RM45_PIG
GO:0042627	chylomicron	4866	9	65	2	0.22222222	0.005954578	2.225149002	0.041682047	APOE_PIG,F1RM45_PIG
GO:0034361	very-low-density lipoprotein particle	4866	12	65	2	0.16666667	0.010638468	1.973120903	0.068263504	APOE_PIG,F1RM45_PIG
GO:0031232	extrinsic component of external side of plasma membrane	4866	1	65	1	1	0.013357994	1.874258748	0.079120427	F1SJB5_PIG
GO:0120003	hinge region between urothelial plaques of apical plasma membrane	4866	1	65	1	1	0.013357994	1.874258748	0.073468968	F1SU64_PIG
GO:0016323	basolateral plasma membrane	4866	41	65	3	0.07317073	0.01689894	1.772140535	0.086747892	F1SJB5_PIG,A0A5S6HMA0_PIG,A0A287ALK8_PIG
GO:0031090	organelle membrane	4866	2	65	1	0.5	0.026540262	1.576094802	0.127725009	A0A5S6HMA0_PIG
GO:0030658	transport vesicle membrane	4866	2	65	1	0.5	0.026540262	1.576094802	0.120211773	DMBT1_PIG
GO:0016328	lateral plasma membrane	4866	20	65	2	0.1	0.028598734	1.543653188	0.12233903	F1SJB5_PIG,A0A5S6HMA0_PIG
GO:0042383	sarcolemma	4866	22	65	2	0.09090909	0.034182715	1.466193449	0.138529949	A0A287A8E9_PIG,F1SJB5_PIG
GO:0070695	FHF complex	4866	3	65	1	0.33333333	0.039549078	1.402863637	0.15226395	A0A287BM99_PIG
GO:0005890	sodium	4866	3	65	1	0.33333333	0.039549078	1.402863637	0.145013286	A0A5S6HMA0_PIG
GO:0062023	collagen-containing extracellular	4866	44	16	3	0.06818182	0.000355921	3.448646677	0.016372355	A0A287BLM4_PIG,A0A286Z WQ1_PIG,A0A5G2QCT3_PIG
GO:0000786	nucleosome	4866	15	16	2	0.13333333	0.001038263	2.983692699	0.023880045	H4_PIG,A0A287BQW3_PIG
GO:0031431	Dbf4-dependent protein kinase complex	4866	1	16	1	1	0.003288122	2.483052122	0.050417865	A0A287A8H0_PIG
GO:0008074	guanylate cyclase complex	4866	1	16	1	1	0.003288122	2.483052122	0.037813399	A0A5G2QIK9_PIG
GO:0030061	mitochondrial crista	4866	2	16	1	0.5	0.006566105	2.182692162	0.060408168	F1SFG7_PIG
GO:0042025	host cell nucleus	4866	48	16	2	0.04166667	0.010470605	1.980028212	0.08027464	H4_PIG,A0A287BQW3_PIG
GO:0005638	lamin filament	4866	4	16	1	0.25	0.013091775	1.883001476	0.086031662	LMNA_PIG
GO:0071953	elastic fiber	4866	4	16	1	0.25	0.013091775	1.883001476	0.075277705	A0A5G2QCT3_PIG
GO:0001527	microfibril	4866	6	16	1	0.16666667	0.019577241	1.708248513	0.100061454	A0A286Z WQ1_PIG
GO:0016604	nuclear body	4866	76	16	2	0.02631579	0.025077284	1.600719498	0.115355507	LMNA_PIG,A0A287BQW3_PIG
GO:0098982	GABA-ergic synapse	4866	8	16	1	0.125	0.026022735	1.584647056	0.108822348	A0A5G2QIK9_PIG
GO:0016235	aggresome	4866	12	16	1	0.08333333	0.038794727	1.4112273	0.14871312	A0A287A8H0_PIG
GO:0005719	nuclear euchromatin	4866	13	16	1	0.07692308	0.0419631	1.377132432	0.148484817	A0A287BQW3_PIG
GO:0005720	nuclear heterochromatin	4866	13	16	1	0.07692308	0.0419631	1.377132432	0.137878758	A0A287BQW3_PIG
GO:0030126	COPI vesicle coat	4866	13	16	1	0.07692308	0.0419631	1.377132432	0.128686841	A0A481CG38_PIG
GO:0000139	Golgi membrane	4866	104	16	2	0.01923077	0.044680327	1.349883662	0.128455939	A0A481CG38_PIG,A0A287AL W7_PIG
GO:0004867	serine-type endopeptidase inhibitor activity	4452	49	62	9	0.18367347	1.44E-08	7.84166315	1.57E-06	F1SCE4_PIG,A0A480MVF5_PIG,A0A287B9R5_PIG,A0A287 AT48_PIG,F1SCC9_PIG,I3LQ 76_PIG,F1SMW6_PIG,PAI1_PIG,A0A287BF75_PIG
GO:0008191	metalloendopeptidase inhibitor	4452	6	62	3	0.5	4.99E-05	4.301486986	0.002722134	F1SFI6_PIG,TIMP1_PIG,A0A5 G2R175_PIG
GO:0016209	antioxidant activity	4452	7	62	3	0.42857143	8.65E-05	4.062783633	0.003144283	HPT_PIG,APOE_PIG,F1RM45_PIG
GO:0046911	metal chelating activity	4452	2	62	2	1	0.000190857	3.719291225	0.005200861	APOE_PIG,F1RM45_PIG
GO:0036094	small molecule binding	4452	9	62	3	0.33333333	0.000203594	3.691235274	0.004438347	A0A5S6HQ91_PIG,OBP_PIG, F1SG31_PIG
GO:0050750	low-density lipoprotein particle receptor binding	4452	12	62	3	0.25	0.000517524	3.2860698	0.00940168	A0A287AFA5_PIG,APOE_PIG, F1RM45_PIG
GO:0071813	lipoprotein particle binding	4452	3	62	2	0.66666667	0.000567425	3.246091392	0.008835621	APOE_PIG,F1RM45_PIG
GO:0003796	lysozyme activity	4452	3	62	2	0.66666667	0.000567425	3.246091392	0.007731168	LYSC1_PIG,LYSC3_PIG

GO:0070326	very-low-density lipoprotein particle receptor binding	4452	3	62	2	0.66666667	0.000567425	3.246091392	0.006872149	APOE_PIG,FIRM45_PIG
GO:0002020	protease binding	4452	32	62	4	0.125	0.000915901	3.038151344	0.009983324	Q0Z8R0_PIG,TIMP1_PIG,A0A5G2R175_PIG,PAI1_PIG
GO:0001540	amyloid-beta binding	4452	16	62	3	0.1875	0.001265968	2.897577354	0.01254459	APOE_PIG,FIRM45_PIG,Q0Z8R0_PIG
GO:0060228	phosphatidylcholine-sterol O-acyltransferase activator activity	4452	5	62	2	0.4	0.001857616	2.731044063	0.016873345	APOE_PIG,FIRM45_PIG
GO:0043395	heparan sulfate proteoglycan binding	4452	5	62	2	0.4	0.001857616	2.731044063	0.015575395	APOE_PIG,FIRM45_PIG
GO:0008289	lipid binding	4452	41	62	4	0.09756098	0.002349	2.629117073	0.018288639	APOE_PIG,FIRM45_PIG,A7J149_PIG,FIS505_PIG
GO:0120020	cholesterol transfer activity	4452	10	62	2	0.2	0.00799203	2.097342905	0.058075417	APOE_PIG,FIRM45_PIG
GO:0048156	tau protein binding	4452	12	62	2	0.16666667	0.011513599	1.938788914	0.078436391	APOE_PIG,FIRM45_PIG
GO:0001671	ATPase activator activity	4452	12	62	2	0.16666667	0.011513599	1.938788914	0.073822485	A0A5S6HMA0_PIG,A0A287A GQ8_PIG
GO:0004866	endopeptidase inhibitor activity	4452	12	62	2	0.16666667	0.011513599	1.938788914	0.069721236	F1SFI6_PIG,A0A480MV5_PIG
GO:0001530	lipopolysaccharide binding	4452	13	62	2	0.15384615	0.013485868	1.870121108	0.077366293	PG2_PIG,A0A287B028_PIG
GO:0004869	cysteine-type endopeptidase inhibitor activity	4452	13	62	2	0.15384615	0.013485868	1.870121108	0.073497978	F1SFI6_PIG,Q0Z8R0_PIG
GO:0030197	extracellular matrix constituent	4452	1	62	1	1	0.013926325	1.856163466	0.07228426	A0A287B5M2_PIG
GO:0019841	retinol binding	4452	1	62	1	1	0.013926325	1.856163466	0.068998611	A0A287A3Z4_PIG
GO:0004021	L-alanine	4452	1	62	1	1	0.013926325	1.856163466	0.065998672	F1RP04_PIG
GO:0019911	structural constituent of myelin sheath	4452	1	62	1	1	0.013926325	1.856163466	0.063248727	F1SU64_PIG
GO:0019863	IgE binding	4452	1	62	1	1	0.013926325	1.856163466	0.060718778	A0A5G2R7M4_PIG
GO:0036041	long-chain fatty acid binding	4452	1	62	1	1	0.013926325	1.856163466	0.05838344	FABP4_PIG
GO:0051427	hormone receptor binding	4452	1	62	1	1	0.013926325	1.856163466	0.056221091	FABP4_PIG
GO:0016918	retinal binding	4452	1	62	1	1	0.013926325	1.856163466	0.054213195	A0A287A3Z4_PIG
GO:0005509	calcium ion binding	4452	196	62	7	0.03571429	0.018181789	1.740363379	0.068338449	F1SJB5_PIG,I3L7Z6_PIG,A0A287ALK8_PIG,S10AC_PIG,K7GQ50_PIG,F1RYW2_PIG,F1SUE4_PIG
GO:0034632	retinol transmembrane transporter activity	4452	2	62	1	0.5	0.027661793	1.55811967	0.100504515	A0A287A3Z4_PIG
GO:0005372	water transmembrane transporter activity	4452	2	62	1	0.5	0.027661793	1.55811967	0.097262434	F1RPU5_PIG
GO:0004322	ferroxidase activity	4452	2	62	1	0.5	0.027661793	1.55811967	0.094222983	A0A5G2QW05_PIG
GO:0097655	serpin family protein binding	4452	2	62	1	0.5	0.027661793	1.55811967	0.091367741	CATL1_PIG
GO:0070891	lipoteichoic acid binding	4452	2	62	1	0.5	0.027661793	1.55811967	0.088680455	A0A287B028_PIG
GO:0004859	phospholipase inhibitor activity	4452	2	62	1	0.5	0.027661793	1.55811967	0.086146727	F1SJB5_PIG
GO:0015204	urea transmembrane transporter activity	4452	2	62	1	0.5	0.027661793	1.55811967	0.083753763	F1RPU5_PIG
GO:0015265	urea channel activity	4452	2	62	1	0.5	0.027661793	1.55811967	0.081490148	F1RPU5_PIG
GO:0071723	lipopeptide binding	4452	2	62	1	0.5	0.027661793	1.55811967	0.07934567	A0A287B028_PIG
GO:0005501	retinoid binding	4452	2	62	1	0.5	0.027661793	1.55811967	0.077311166	A0A287A3Z4_PIG
GO:0030492	hemoglobin binding	4452	2	62	1	0.5	0.027661793	1.55811967	0.075378386	HPT_PIG
GO:0008483	transaminase activity	4452	2	62	1	0.5	0.027661793	1.55811967	0.073539889	F1RP04_PIG
GO:0035375	zymogen binding	4452	2	62	1	0.5	0.027661793	1.55811967	0.071788939	DMBT1_PIG
GO:0005198	structural molecule activity	4452	50	62	3	0.06	0.03170887	1.49881924	0.080378297	F1RK90_PIG,F1S0J8_PIG,A0A5G2QXD3_PIG
GO:0097110	scaffold protein binding	4452	23	62	2	0.08695652	0.040021515	1.397706477	0.099144207	A0A287A8E9_PIG,A0A287BH52_PIG
GO:0048306	calcium-dependent protein binding	4452	23	62	2	0.08695652	0.040021515	1.397706477	0.096941003	F1SJB5_PIG,I3L7Z6_PIG
GO:0050786	RAGE receptor binding	4452	3	62	1	0.33333333	0.041208977	1.385008164	0.097647359	S10AC_PIG
GO:0005391	sodium	4452	3	62	1	0.33333333	0.041208977	1.385008164	0.095569756	A0A5S6HMA0_PIG
GO:0030414	peptidase inhibitor activity	4452	3	62	1	0.33333333	0.041208977	1.385008164	0.093578719	A0A480MV5_PIG
GO:0008199	ferric iron binding	4452	3	62	1	0.33333333	0.041208977	1.385008164	0.091668949	A0A5S8KUU6_PIG
GO:0005176	ErbB-2 class receptor binding	4452	3	62	1	0.33333333	0.041208977	1.385008164	0.08983557	A0A287B5M2_PIG

GO:0019834	phospholipase A2 inhibitor activity	4452	3	62	1	0.33333333	0.041208977	1.385008164	0.088074089	F1SJB5_PIG
GO:0004617	phosphoglycerate dehydrogenase activity	4452	1	13	1	1	0.002920036	2.534611803	0.113881402	SERA_PIG
GO:0001972	retinoic acid binding	4452	1	13	1	1	0.002920036	2.534611803	0.056940701	B3F0B7_PIG
GO:0050436	microfibril binding	4452	2	13	1	0.5	0.005832199	2.234167637	0.075818592	A0A286ZWQ1_PIG
GO:0030060	L-malate dehydrogenase activity	4452	3	13	1	0.33333333	0.00873651	2.058662031	0.085180971	SERA_PIG
GO:0003680	AT DNA binding	4452	4	13	1	0.25	0.011632987	1.934308771	0.090737296	A0A287BQW3_PIG
GO:1901612	cardiolipin binding	4452	4	13	1	0.25	0.011632987	1.934308771	0.075614413	F1SFG7_PIG
GO:0019166	trans-2-enoyl-CoA reductase (NADPH) activity	4452	4	13	1	0.25	0.011632987	1.934308771	0.064812354	I3L8Q5_PIG
GO:0004383	guanylate cyclase activity	4452	4	13	1	0.25	0.011632987	1.934308771	0.05671081	A0A5G2QIK9_PIG
GO:0070051	fibrinogen binding	4452	4	13	1	0.25	0.011632987	1.934308771	0.050409609	A0A5G2QCT3_PIG
GO:0050431	transforming growth factor beta binding	4452	6	13	1	0.16666667	0.017402517	1.759387936	0.067869816	A0A286ZWQ1_PIG
GO:0070300	phosphatidic acid binding	4452	7	13	1	0.14285714	0.020275609	1.693026093	0.07188625	F1SFG7_PIG
GO:0046982	protein heterodimerization activity	4452	82	13	2	0.02439024	0.022917882	1.639825528	0.074483115	H4_PIG,A0A287BQW3_PIG
GO:0016504	peptidase activator activity	4452	8	13	1	0.125	0.023140945	1.635618917	0.069422834	A0A5G2QCT3_PIG
GO:0005540	hyaluronic acid binding	4452	8	13	1	0.125	0.023140945	1.635618917	0.06446406	FIREZ1_PIG
GO:0031492	nucleosomal DNA binding	4452	9	13	1	0.11111111	0.025998543	1.585050988	0.067596212	A0A287BQW3_PIG
GO:0043539	protein serine/threonine kinase activator activity	4452	11	13	1	0.09090909	0.031690605	1.499069467	0.07724585	A0A287A8H0_PIG
GO:0001968	fibronectin binding	4452	11	13	1	0.09090909	0.031690605	1.499069467	0.072701977	A0A5G2QCT3_PIG
GO:0003690	double-stranded DNA binding	4452	14	13	1	0.07142857	0.040171147	1.396085769	0.087037485	A0A287BQW3_PIG