Supplemental Table 2: Adjusted and unadjusted GSA results for US, UK and combined GSA for all cases and HGS cases. Results are presented for the top 1000 gene sets from the combined HGS case GSA.

			GSA of North American GWAS				GSA of UK GWAS				Combined GSA			
GS ID	GS Source	GS Name	All Cases; Unadjusted	All Cases; Adjusted	HGS Cases; Unadjusted	HGS Cases; Adjusted	All Cases; Unadjusted	All Cases; Adjusted	HGS Cases; Unadjusted	HGS Cases; Adjusted	All Cases; Unadjusted	All Cases; Adjusted	HGS Cases; Unadjusted	HGS Cases; Adjusted
GO:0023034	GO:Bio L4	intracellular signaling pathway	8.6E-02	4.0E-02	1.7E-03	2.5E-02	2.9E-02	3.8E-02	3.3E-03	4.8E-01	1.7E-02	1.1E-02	7.3E-05	6.4E-02
GO:0090109	GO:Bio L4	regulation of cell-substrate junction assembly	6.3E-02	7.6E-02	3.6E-02	5.0E-02	4.8E-01	5.6E-02	1.0E-03	4.5E-01	1.3E-01	2.7E-02	4.0E-04	1.1E-01
GO:0048646	GO:Bio L4	anatomical structure formation involved in morphogenesis	1.5E-02	2.2E-02	4.0E-04	1.8E-03	1.5E-01	1.6E-02	1.2E-01	7.2E-01	1.7E-02	3.1E-03	5.3E-04	1.0E-02
GO:0031968	GO:Cell L4	organelle outer membrane	6.0E-01	6.3E-01	2.7E-01	1.7E-01	3.4E-01	4.1E-01	2.0E-04	2.5E-01	5.3E-01	6.0E-01	5.8E-04	1.7E-01
GO:0051895	GO:Bio L4	negative regulation of focal adhesion assembly	1.9E-01	2.5E-01	1.7E-02	3.3E-02	8.7E-01	9.4E-01	3.1E-03	8.6E-01	4.7E-01	5.8E-01	5.8E-04	1.3E-01
GO:0005527	GO:Mole L4	macrolide binding	1.6E-02	2.3E-02	9.0E-04	2.0E-03	6.4E-03	9.2E-02	6.4E-02	9.4E-01	1.0E-03	1.5E-02	6.2E-04	1.4E-02
GO:0016859	GO:Mole L4	cis-trans isomerase activity	6.7E-02	2.1E-01	1.5E-03	3.5E-03	2.9E-01	5.6E-01	4.7E-02	8.4E-01	9.6E-02	3.6E-01	7.5E-04	2.0E-02
GO:0042483	GO:Bio L4	negative regulation of odontogenesis	3.7E-01	2.1E-01	1.6E-01	3.0E-01	2.6E-01	9.9E-02	5.0E-04	4.3E-01	3.2E-01	1.0E-01	8.2E-04	3.9E-01
GO:0001649	GO:Bio L4	osteoblast differentiation	3.4E-02	1.6E-02	1.2E-01	9.5E-02	8.8E-02	4.6E-01	7.0E-04	5.3E-01	2.0E-02	4.2E-02	8.4E-04	2.0E-01
GO:0009798	GO:Bio L4	axis specification	7.5E-01	8.6E-01	1.8E-02	4.3E-02	8.8E-01	7.5E-01	5.8E-03	6.4E-01	9.4E-01	9.3E-01	1.0E-03	1.3E-01
GO:0001917	GO:Cell L4	photoreceptor inner segment	6.9E-01	5.3E-01	5.3E-01	2.8E-01	2.3E-01	1.7E-01	2.0E-04	1.2E-01	4.5E-01	3.0E-01	1.1E-03	1.5E-01
GO:0019867	GO:Cell L4	outer membrane	3.6E-01	6.0E-01	2.7E-01	1.8E-01	3.5E-01	1.8E-01	4.0E-04	2.0E-01	3.9E-01	3.4E-01	1.1E-03	1.6E-01
GO:0044092	GO:Bio L4	negative regulation of molecular function	5.0E-01	4.9E-02	2.6E-02	8.0E-03	3.7E-02	1.4E-01	6.2E-03	4.5E-01	9.3E-02	4.1E-02	1.6E-03	2.4E-02
GO:0060759	GO:Bio L4	regulation of response to cytokine stimulus	5.8E-01	2.4E-01	4.5E-03	3.7E-03	7.1E-01	9.7E-01	3.9E-02	7.0E-01	7.7E-01	5.7E-01	1.7E-03	1.8E-02
GO:0005070	GO:Mole L4	SH3/SH2 adaptor activity	9.3E-01	9.3E-01	1.3E-01	3.0E-01	5.5E-01	7.7E-01	1.4E-03	7.0E-01	8.6E-01	9.6E-01	1.7E-03	5.4E-01
GO:0042592	GO:Bio L4	homeostatic process	6.7E-01	1.2E-01	3.7E-01	3.1E-01	9.4E-02	4.6E-03	5.0E-04	2.2E-01	2.4E-01	4.7E-03	1.8E-03	2.5E-01
GO:0007566	GO:Bio L4	embryo implantation	1.6E-01	2.3E-01	1.6E-03	3.8E-03	7.4E-01	5.8E-01	1.2E-01	3.7E-01	3.8E-01	4.0E-01	1.9E-03	1.1E-02
GO:0001894	GO:Bio L4	tissue homeostasis	3.5E-01	8.2E-02	2.0E-01	9.2E-02	2.3E-01	4.2E-01	1.0E-03	6.1E-01	2.8E-01	1.5E-01	1.9E-03	2.2E-01
GO:0031498	GO:Bio L4	chromatin disassembly	5.0E-02	5.3E-02	6.3E-02	1.1E-01	4.7E-01	4.8E-01	3.2E-03	4.3E-01	1.1E-01	1.2E-01	1.9E-03	1.9E-01
GO:0001503	GO:Bio L4	ossification	2.2E-01	8.4E-02	1.9E-01	1.6E-01	3.9E-01	3.3E-01	1.1E-03	3.9E-01	3.0E-01	1.3E-01	2.0E-03	2.3E-01

GO:0046983	GO:Mole L4	protein dimerization activity	1.2E-01	1.9E-02	5.4E-02	9.5E-02	9.0E-01	1.0E-01	4.0E-03	3.2E-01	3.5E-01	1.4E-02	2.1E-03	1.4E-01
GO:0060348	GO:Bio L4	bone development	2.5E-01	1.1E-01	2.4E-01	2.1E-01	4.3E-01	3.8E-01	1.0E-03	4.5E-01	3.5E-01	1.8E-01	2.2E-03	3.1E-01
GO:0042481	GO:Bio L4	regulation of odontogenesis	2.5E-01	4.7E-01	4.2E-01	5.3E-01	3.2E-01	3.5E-01	6.0E-04	8.6E-01	2.9E-01	4.6E-01	2.3E-03	8.1E-01
GO:0030155	GO:Bio L4	regulation of cell adhesion	3.4E-02	3.7E-02	9.3E-03	1.3E-02	9.8E-01	8.2E-01	2.9E-02	4.6E-01	1.5E-01	1.4E-01	2.5E-03	3.7E-02
GO:0023046	GO:Bio L2	signaling process	3.0E-01	1.7E-02	1.8E-02	1.5E-02	1.6E-01	3.5E-02	1.5E-02	4.6E-01	1.9E-01	5.1E-03	2.5E-03	4.2E-02
GO:0009653	GO:Bio L4	anatomical structure morphogenesis	1.2E-01	1.0E-01	2.5E-03	1.7E-02	2.7E-01	1.5E-01	1.1E-01	7.1E-01	1.5E-01	7.8E-02	2.5E-03	6.6E-02
GO:0023060	GO:Bio L4	signal transmission	3.0E-01	1.7E-02	1.8E-02	1.5E-02	1.7E-01	3.8E-02	1.5E-02	4.6E-01	2.0E-01	5.5E-03	2.5E-03	4.2E-02
GO:0035019	GO:Bio L4	somatic stem cell maintenance	4.0E-01	7.7E-01	7.4E-01	8.3E-01	1.2E-01	1.6E-01	4.0E-04	7.1E-01	2.0E-01	3.8E-01	2.7E-03	9.0E-01
GO:0048871	GO:Bio L4	multicellular organismal homeostasis	3.7E-01	8.2E-02	1.1E-01	7.8E-02	1.1E-01	2.6E-01	2.8E-03	7.1E-01	1.7E-01	1.0E-01	2.8E-03	2.2E-01
GO:0030674	GO:Mole L4	protein binding, bridging	7.0E-01	7.3E-01	4.4E-02	1.3E-01	6.6E-01	7.5E-01	7.2E-03	9.7E-01	8.2E-01	8.8E-01	2.9E-03	3.8E-01
GO:0009887	GO:Bio L4	organ morphogenesis	1.6E-01	9.2E-02	4.2E-02	6.6E-02	2.2E-01	3.2E-02	7.8E-03	8.4E-01	1.5E-01	2.0E-02	2.9E-03	2.2E-01
GO:0023052	GO:Bio L2	signaling	2.5E-01	1.2E-02	2.1E-02	1.5E-02	1.6E-01	3.8E-02	1.5E-02	4.7E-01	1.7E-01	3.8E-03	2.9E-03	4.1E-02
GO:0015833	GO:Bio L4	peptide transport	6.4E-02	8.0E-02	2.1E-02	5.0E-02	4.7E-02	5.7E-01	1.6E-02	6.3E-01	2.0E-02	1.9E-01	3.0E-03	1.4E-01
PA2027	PharmGKB	pgkb_pwy_Glucocorticoid_and_Inflammatory_genes_Pathway_PD	2.4E-02	3.0E-02	7.0E-04	1.7E-03	1.6E-01	1.0E-01	5.0E-01	6.3E-01	2.5E-02	2.1E-02	3.1E-03	8.4E-03
GO:0032501	GO:Bio L2	multicellular organismal process	2.7E-01	2.8E-02	3.1E-02	3.4E-02	1.2E-01	9.3E-02	1.2E-02	4.1E-01	1.5E-01	1.8E-02	3.2E-03	7.3E-02
GO:0008320	GO:Mole L4	protein transmembrane transporter activity	5.9E-01	5.3E-01	2.8E-02	1.6E-01	9.7E-02	1.2E-01	1.3E-02	9.2E-01	2.2E-01	2.4E-01	3.2E-03	4.3E-01
GO:0016477	GO:Bio L4	cell migration	4.2E-03	3.3E-03	9.0E-04	2.0E-04	3.9E-01	2.2E-01	4.2E-01	2.1E-01	1.2E-02	6.0E-03	3.4E-03	4.7E-04
GO:0048519	GO:Bio L2	negative regulation of biological process	2.1E-01	2.1E-03	4.4E-02	3.7E-02	1.9E-01	4.7E-01	8.7E-03	7.0E-01	1.7E-01	7.8E-03	3.4E-03	1.2E-01
GO:0048519	GO:Bio L4	negative regulation of biological process	2.1E-01	2.1E-03	4.4E-02	3.7E-02	1.9E-01	4.7E-01	8.7E-03	7.0E-01	1.7E-01	7.8E-03	3.4E-03	1.2E-01
GO:0046907	GO:Bio L4	intracellular transport	1.6E-01	2.7E-03	3.6E-02	2.1E-02	2.9E-01	4.4E-01	1.1E-02	3.9E-01	1.8E-01	9.1E-03	3.5E-03	4.7E-02
GO:0044259	GO:Bio L4	multicellular organismal macromolecule metabolic process	2.9E-01	4.7E-02	7.5E-02	6.9E-02	9.7E-01	7.7E-01	5.3E-03	2.8E-02	6.4E-01	1.6E-01	3.5E-03	1.4E-02
GO:0007165	GO:Bio L4	signal transduction	3.6E-01	3.3E-02	2.4E-02	2.7E-02	1.1E-01	3.8E-02	1.8E-02	6.1E-01	1.6E-01	9.5E-03	3.7E-03	8.4E-02
GO:0046716	GO:Bio L4	muscle homeostasis	4.8E-01	7.9E-01	1.8E-01	8.1E-02	2.8E-01	3.5E-02	2.4E-03	4.6E-01	4.1E-01	1.3E-01	3.8E-03	1.6E-01
GO:0030877	GO:Cell L4	beta-catenin destruction complex	8.9E-01	7.0E-01	3.1E-01	3.6E-01	2.2E-01	6.0E-01	1.5E-03	1.4E-01	5.2E-01	7.8E-01	4.0E-03	2.0E-01

GO:0032502	GO:Bio L2	developmental process	3.1E-01	8.0E-02	1.4E-02	1.6E-02	3.3E-01	5.9E-02	3.6E-02	4.1E-01	3.4E-01	3.0E-02	4.4E-03	3.8E-02
GO:0060761	GO:Bio L4	negative regulation of response to cytokine stimulus	2.5E-01	8.4E-02	1.0E-03	7.0E-04	9.0E-01	8.4E-01	5.5E-01	4.4E-01	5.6E-01	2.6E-01	4.7E-03	2.8E-03
4350	KEGG	TGF-beta signaling pathway	2.3E-02	5.4E-03	4.2E-02	9.0E-02	4.7E-01	4.0E-01	1.3E-02	2.7E-01	6.1E-02	1.5E-02	4.7E-03	1.1E-01
GO:0019827	GO:Bio L4	stem cell maintenance	7.0E-01	7.7E-01	2.9E-01	4.3E-01	2.0E-01	2.7E-01	1.9E-03	7.8E-01	4.2E-01	5.3E-01	4.7E-03	7.0E-01
GO:0048278	GO:Bio L4	vesicle docking	6.3E-02	1.1E-02	1.4E-03	4.8E-03	6.6E-01	7.8E-01	4.8E-01	1.3E-01	1.7E-01	4.9E-02	5.5E-03	5.4E-03
GO:0051093	GO:Bio L4	negative regulation of developmental process	3.3E-02	7.0E-03	3.2E-02	2.1E-02	1.7E-01	3.7E-01	2.1E-02	8.8E-01	3.4E-02	1.8E-02	5.6E-03	9.2E-02
GO:0010646	GO:Bio L4	regulation of cell communication	1.5E-01	6.3E-03	3.9E-02	1.4E-02	4.3E-01	3.9E-01	1.7E-02	5.9E-01	2.4E-01	1.7E-02	5.6E-03	4.7E-02
GO:0048523	GO:Bio L4	negative regulation of cellular process	2.1E-01	8.0E-03	5.1E-02	2.8E-02	1.4E-01	4.7E-01	1.4E-02	6.8E-01	1.4E-01	2.5E-02	5.8E-03	9.5E-02
GO:0034747	GO:Cell L4	Axin-APC-beta-catenin-GSK3B complex	7.9E-01	8.4E-01	5.8E-01	8.8E-01	1.1E-01	3.6E-01	1.2E-03	6.0E-01	3.0E-01	6.6E-01	5.8E-03	8.6E-01
GO:0034329	GO:Bio L4	cell junction assembly	7.0E-01	6.7E-01	3.0E-01	5.3E-01	1.7E-01	2.9E-02	2.4E-03	7.9E-01	3.7E-01	9.7E-02	5.9E-03	7.8E-01
GO:0050794	GO:Bio L4	regulation of cellular process	2.3E-01	6.4E-03	1.1E-01	7.7E-02	1.5E-01	1.7E-01	6.5E-03	7.8E-01	1.5E-01	8.4E-03	6.0E-03	2.3E-01
GO:0045785	GO:Bio L4	positive regulation of cell adhesion	2.4E-01	6.5E-02	1.4E-02	9.4E-03	9.7E-01	4.6E-01	5.2E-02	3.6E-01	5.7E-01	1.3E-01	6.0E-03	2.3E-02
GO:0007166	GO:Bio L4	cell surface receptor linked signaling pathway	3.7E-01	1.1E-01	6.5E-02	1.7E-01	5.4E-02	7.4E-02	1.1E-02	8.1E-01	9.8E-02	4.8E-02	6.1E-03	4.1E-01
GO:0044087	GO:Bio L4	regulation of cellular component biogenesis	1.5E-01	4.0E-02	6.2E-02	7.1E-02	1.7E-01	2.5E-02	1.2E-02	9.7E-01	1.2E-01	8.0E-03	6.3E-03	2.5E-01
GO:0005742	GO:Cell L4	mitochondrial outer membrane translocase complex	6.3E-01	5.4E-01	2.3E-01	3.6E-01	2.3E-02	3.4E-02	3.3E-03	5.5E-01	7.6E-02	9.1E-02	6.3E-03	5.2E-01
GO:0005578	GO:Cell L4	proteinaceous extracellular matrix	8.4E-02	1.8E-02	1.5E-01	7.4E-02	1.3E-01	2.2E-01	5.1E-03	3.2E-01	6.1E-02	2.5E-02	6.3E-03	1.1E-01
GO:0005102	GO:Mole L4	receptor binding	8.1E-02	1.5E-01	7.0E-03	5.8E-03	5.4E-02	2.8E-02	1.1E-01	8.0E-01	2.8E-02	2.7E-02	6.5E-03	3.0E-02
GO:0050789	GO:Bio L2	regulation of biological process	2.6E-01	6.1E-03	9.5E-02	6.6E-02	1.1E-01	1.1E-01	8.4E-03	7.8E-01	1.3E-01	5.5E-03	6.5E-03	2.0E-01
GO:0030175	GO:Cell L4	filopodium	8.3E-01	9.6E-01	5.8E-01	5.7E-01	1.1E-01	1.7E-02	1.4E-03	5.8E-01	3.1E-01	8.4E-02	6.6E-03	6.9E-01
GO:0051781	GO:Bio L4	positive regulation of cell division	1.1E-01	1.8E-01	5.4E-02	6.2E-02	2.0E-01	6.7E-01	1.5E-02	3.5E-01	1.1E-01	3.8E-01	6.7E-03	1.0E-01
GO:0040011	GO:Bio L2	locomotion	5.0E-03	1.3E-02	2.5E-03	3.0E-04	3.1E-01	6.3E-02	3.3E-01	3.4E-01	1.2E-02	6.4E-03	6.7E-03	1.0E-03
3440	KEGG	Homologous recombination	2.4E-01	9.7E-02	7.6E-03	8.5E-03	1.0E-01	3.6E-01	1.1E-01	2.5E-01	1.2E-01	1.5E-01	6.8E-03	1.5E-02
GO:0033193	GO:Cell L4	Lsd1/2 complex	1.4E-01	8.5E-02	6.2E-03	2.1E-02	6.5E-01	5.4E-01	1.4E-01	5.4E-01	3.1E-01	1.9E-01	6.8E-03	6.1E-02

GO:0033205	GO:Bio L4	cytokinesis during cell cycle	2.1E-01	1.0E-01	4.3E-01	3.2E-01	4.6E-01	1.9E-01	2.1E-03	9.0E-01	3.2E-01	9.6E-02	7.2E-03	6.5E-01
GO:0065007	GO:Bio L2	biological regulation	3.0E-01	6.8E-03	1.3E-01	6.9E-02	1.4E-01	1.1E-01	6.9E-03	7.7E-01	1.8E-01	6.1E-03	7.3E-03	2.1E-01
GO:0009880	GO:Bio L4	embryonic pattern specification	2.9E-01	3.7E-01	1.6E-03	1.9E-02	7.5E-01	9.3E-01	5.8E-01	6.3E-01	5.5E-01	7.1E-01	7.4E-03	6.6E-02
GO:0045596	GO:Bio L4	negative regulation of cell differentiation	1.9E-01	4.9E-02	4.3E-02	1.7E-02	7.7E-02	2.9E-01	2.3E-02	7.9E-01	7.5E-02	7.6E-02	7.8E-03	7.2E-02
GO:0016645	GO:Mole L4	oxidoreductase activity, acting on the CH-NH group of donors	8.4E-01	1.4E-01	7.4E-03	2.1E-03	2.3E-01	6.8E-01	1.4E-01	9.4E-01	5.0E-01	3.1E-01	7.9E-03	1.4E-02
GO:0050896	GO:Bio L2	response to stimulus	4.6E-02	1.0E-02	7.8E-02	3.4E-02	2.7E-01	4.4E-02	1.3E-02	6.8E-01	6.7E-02	3.9E-03	8.0E-03	1.1E-01
GO:0051649	GO:Bio L4	establishment of localization in cell	3.0E-01	2.5E-03	1.5E-01	1.0E-01	1.1E-01	2.3E-01	6.9E-03	6.2E-01	1.5E-01	4.8E-03	8.0E-03	2.4E-01
GO:0048635	GO:Bio L4	negative regulation of muscle organ development	3.0E-01	5.3E-01	1.1E-01	3.2E-01	8.0E-01	2.3E-01	9.3E-03	8.8E-01	5.8E-01	3.8E-01	8.3E-03	6.4E-01
GO:0044243	GO:Bio L4	multicellular organismal catabolic process	2.9E-01	7.5E-02	8.1E-02	6.8E-02	9.0E-01	5.1E-01	1.3E-02	1.1E-02	6.2E-01	1.6E-01	8.3E-03	6.4E-03
GO:0016018	GO:Mole L4	cyclosporin A binding	6.1E-01	5.2E-01	8.0E-02	1.1E-01	5.0E-01	7.4E-01	1.3E-02	3.5E-01	6.6E-01	7.5E-01	8.4E-03	1.6E-01
GO:0042802	GO:Mole L4	identical protein binding	1.6E-01	3.8E-02	8.2E-02	1.8E-01	9.8E-01	1.0E-01	1.3E-02	5.9E-01	4.4E-01	2.5E-02	8.5E-03	3.5E-01
GO:0048513	GO:Bio L4	organ development	2.4E-01	7.2E-02	2.6E-02	1.7E-02	2.9E-01	9.0E-02	4.2E-02	6.4E-01	2.5E-01	3.9E-02	8.6E-03	6.0E-02
GO:0044429	GO:Cell L4	mitochondrial part	9.0E-01	6.4E-01	2.2E-01	1.5E-01	8.7E-01	8.4E-01	5.4E-03	1.6E-01	9.7E-01	8.7E-01	9.1E-03	1.1E-01
GO:0051098	GO:Bio L4	regulation of binding	1.4E-01	8.4E-02	9.4E-02	9.6E-03	8.3E-01	4.2E-01	1.3E-02	2.3E-01	3.7E-01	1.5E-01	9.1E-03	1.5E-02
GO:0050902	GO:Bio L4	leukocyte adhesive activation	4.1E-03	7.5E-03	1.5E-03	1.3E-03	9.6E-01	9.9E-01	7.9E-01	2.0E-01	2.6E-02	4.4E-02	9.2E-03	2.4E-03
GO:0006887	GO:Bio L4	exocytosis	4.3E-01	1.1E-01	3.8E-02	6.7E-02	1.7E-01	1.5E-01	3.2E-02	2.1E-01	2.7E-01	8.5E-02	9.3E-03	7.5E-02
4310	KEGG	Wnt signaling pathway	6.9E-01	3.2E-01	3.1E-01	3.7E-01	2.4E-01	6.9E-01	3.9E-03	4.4E-01	4.6E-01	5.5E-01	9.4E-03	4.6E-01
GO:0006461	GO:Bio L4	protein complex assembly	1.2E-01	9.9E-02	2.2E-01	6.0E-02	2.1E-01	2.4E-02	5.8E-03	7.7E-01	1.2E-01	1.7E-02	9.8E-03	1.9E-01
GO:0051209	GO:Bio L4	release of sequestered calcium ion into cytosol	2.6E-01	1.5E-01	1.3E-01	1.8E-01	1.0E-03	3.4E-03	1.0E-02	2.5E-01	2.4E-03	4.4E-03	1.0E-02	1.8E-01
GO:0051282	GO:Bio L4	regulation of sequestering of calcium ion	2.6E-01	1.5E-01	1.3E-01	1.8E-01	1.0E-03	3.4E-03	1.0E-02	2.5E-01	2.4E-03	4.4E-03	1.0E-02	1.8E-01
GO:0051283	GO:Bio L4	negative regulation of sequestering of calcium ion	2.6E-01	1.5E-01	1.3E-01	1.8E-01	1.0E-03	3.4E-03	1.0E-02	2.5E-01	2.4E-03	4.4E-03	1.0E-02	1.8E-01
GO:0090190	GO:Bio L4	positive regulation of branching involved in ureteric bud morphogenesis	6.9E-01	9.3E-01	4.4E-01	3.9E-01	1.6E-02	3.1E-02	3.0E-03	9.8E-02	5.9E-02	1.3E-01	1.0E-02	1.6E-01

GO:0051235	GO:Bio L4	maintenance of location	2.2E-01	1.3E-01	2.8E-01	3.2E-01	2.5E-02	2.8E-02	4.7E-03	4.3E-01	3.4E-02	2.4E-02	1.0E-02	4.1E-01
GO:0051919	GO:Bio L4	positive regulation of fibrinolysis	2.7E-01	5.6E-01	2.7E-01	2.8E-01	3.4E-01	4.0E-01	4.9E-03	5.6E-01	3.1E-01	5.6E-01	1.0E-02	4.5E-01
GO:0003006	GO:Bio L4	reproductive developmental process	4.2E-01	4.2E-01	1.7E-02	2.8E-02	7.2E-01	5.7E-01	8.1E-02	2.3E-01	6.6E-01	5.8E-01	1.0E-02	3.9E-02
GO:0044421	GO:Cell L2	extracellular region part	6.8E-02	5.0E-02	9.6E-02	4.0E-02	4.4E-01	2.2E-01	1.5E-02	5.0E-01	1.4E-01	6.1E-02	1.1E-02	9.7E-02
GO:0045275	GO:Cell L4	respiratory chain complex III	1.9E-01	3.8E-02	1.6E-02	4.9E-02	4.6E-01	5.1E-01	8.7E-02	5.2E-03	3.0E-01	9.5E-02	1.1E-02	2.4E-03
GO:0009966	GO:Bio L4	regulation of signal transduction	2.0E-01	4.1E-02	2.3E-02	4.3E-03	6.0E-01	6.0E-01	6.5E-02	5.2E-01	3.7E-01	1.2E-01	1.1E-02	1.6E-02
GO:0023051	GO:Bio L4	regulation of signaling process	2.0E-01	4.1E-02	2.3E-02	4.3E-03	6.0E-01	6.0E-01	6.5E-02	5.2E-01	3.7E-01	1.2E-01	1.1E-02	1.6E-02
GO:0000164	GO:Cell L4	protein phosphatase type 1 complex	6.8E-01	3.6E-01	4.9E-01	2.8E-01	1.7E-01	1.2E-01	3.0E-03	2.1E-01	3.6E-01	1.7E-01	1.1E-02	2.2E-01
GO:0019725	GO:Bio L4	cellular homeostasis	7.8E-01	2.2E-01	5.3E-01	5.3E-01	6.3E-02	1.0E-02	2.9E-03	2.2E-01	2.0E-01	1.6E-02	1.2E-02	3.7E-01
GO:0005488	GO:Mole L2	binding	2.8E-01	6.9E-03	7.9E-02	2.2E-02	1.7E-01	2.8E-02	2.0E-02	4.5E-01	2.0E-01	1.9E-03	1.2E-02	5.5E-02
GO:0045926	GO:Bio L4	negative regulation of growth	5.4E-01	2.7E-01	1.2E-01	3.7E-01	4.4E-01	3.6E-01	1.4E-02	5.9E-01	5.8E-01	3.3E-01	1.2E-02	5.5E-01
GO:0048731	GO:Bio L4	system development	2.9E-01	6.4E-02	3.2E-02	2.2E-02	2.0E-01	5.4E-02	5.0E-02	2.2E-01	2.3E-01	2.3E-02	1.2E-02	3.1E-02
GO:0009987	GO:Bio L2	cellular process	4.4E-01	1.5E-02	9.3E-02	3.6E-02	2.8E-01	9.7E-02	1.7E-02	4.8E-01	3.8E-01	1.1E-02	1.2E-02	8.7E-02
GO:0005662	GO:Cell L4	DNA replication factor A complex	4.4E-01	2.2E-01	9.0E-02	9.5E-02	2.7E-01	1.4E-01	1.8E-02	8.7E-01	3.8E-01	1.4E-01	1.2E-02	2.9E-01
GO:0051983	GO:Bio L4	regulation of chromosome segregation	6.9E-01	8.1E-01	5.9E-01	7.1E-01	8.3E-01	9.8E-01	2.8E-03	9.2E-01	8.9E-01	9.8E-01	1.2E-02	9.3E-01
GO:0048468	GO:Bio L4	cell development	1.6E-01	7.0E-02	9.4E-02	5.9E-02	3.2E-01	2.7E-01	1.8E-02	7.9E-01	2.0E-01	9.4E-02	1.2E-02	1.9E-01
GO:0022603	GO:Bio L4	regulation of anatomical structure morphogenesis	1.2E-01	1.8E-01	2.5E-01	1.7E-01	6.1E-01	6.6E-01	6.9E-03	6.6E-01	2.6E-01	3.8E-01	1.3E-02	3.6E-01
GO:0007267	GO:Bio L4	cell-cell signaling	9.9E-02	5.8E-03	2.8E-02	1.5E-02	2.3E-01	2.2E-01	6.2E-02	2.2E-01	1.1E-01	9.7E-03	1.3E-02	2.2E-02
GO:0010770	GO:Bio L4	positive regulation of cell morphogenesis involved in differentiation	5.1E-02	1.4E-01	2.6E-01	2.4E-01	9.2E-01	1.0E+00	7.1E-03	5.1E-01	1.9E-01	4.0E-01	1.3E-02	3.8E-01
GO:0051705	GO:Bio L4	behavioral interaction between organisms	5.7E-01	2.2E-01	3.2E-03	4.7E-03	7.2E-01	9.3E-01	5.9E-01	4.4E-01	7.8E-01	5.3E-01	1.4E-02	1.5E-02
GO:0048870	GO:Bio L4	cell motility	7.7E-03	6.3E-03	4.0E-03	1.0E-03	4.0E-01	2.7E-01	4.8E-01	2.6E-01	2.1E-02	1.3E-02	1.4E-02	2.4E-03
GO:0070997	GO:Bio L4	neuron death	4.8E-03	1.3E-02	3.9E-03	6.7E-03	2.8E-01	4.2E-01	4.9E-01	9.2E-01	1.0E-02	3.4E-02	1.4E-02	3.7E-02
GO:0031268	GO:Bio L4	pseudopodium organization	9.7E-01	8.4E-01	7.4E-01	7.7E-01	3.7E-01	5.5E-01	2.6E-03	8.7E-01	7.2E-01	8.2E-01	1.4E-02	9.4E-01

GO:0010605	GO:Bio L4	negative regulation of macromolecule metabolic process	5.8E-01	2.3E-01	2.5E-01	1.4E-01	3.9E-01	7.1E-01	7.8E-03	8.2E-01	5.6E-01	4.6E-01	1.4E-02	3.6E-01
GO:0060896	GO:Bio L4	neural plate pattern specification	4.1E-01	5.6E-01	6.8E-03	7.4E-03	2.9E-01	6.2E-01	2.9E-01	7.8E-01	3.8E-01	7.1E-01	1.4E-02	3.6E-02
GO:0031012	GO:Cell L4	extracellular matrix	1.2E-01	3.1E-02	2.0E-01	9.3E-02	1.0E-01	2.6E-01	1.0E-02	3.0E-01	6.7E-02	4.8E-02	1.4E-02	1.3E-01
GO:0032271	GO:Bio L4	regulation of protein polymerization	1.4E-01	4.3E-02	5.4E-02	4.8E-02	2.0E-01	4.5E-02	3.7E-02	9.2E-01	1.3E-01	1.4E-02	1.4E-02	1.8E-01
GO:0009399	GO:Bio L4	nitrogen fixation	1.8E-01	3.3E-01	2.6E-03	2.9E-03	7.1E-01	3.3E-01	7.8E-01	2.1E-01	3.9E-01	3.5E-01	1.5E-02	5.2E-03
GO:0001525	GO:Bio L4	angiogenesis	1.0E-01	9.3E-02	6.2E-03	5.2E-03	5.5E-01	1.9E-01	3.3E-01	5.4E-01	2.2E-01	9.0E-02	1.5E-02	1.9E-02
GO:0043022	GO:Mole L4	ribosome binding	2.5E-01	2.2E-01	2.4E-03	2.9E-03	1.7E-01	5.0E-01	8.9E-01	3.5E-01	1.7E-01	3.5E-01	1.5E-02	8.0E-03
GO:0035239	GO:Bio L4	tube morphogenesis	4.4E-01	5.1E-01	1.4E-01	8.7E-02	8.8E-02	1.5E-03	1.6E-02	2.7E-01	1.6E-01	6.2E-03	1.5E-02	1.1E-01
GO:0044420	GO:Cell L4	extracellular matrix part	1.6E-01	7.1E-02	4.1E-01	1.5E-01	8.3E-01	4.5E-01	5.5E-03	4.5E-01	3.9E-01	1.4E-01	1.6E-02	2.5E-01
GO:0019222	GO:Bio L4	regulation of metabolic process	1.0E-01	4.4E-03	9.4E-02	4.8E-02	8.1E-02	3.4E-01	2.4E-02	7.0E-01	4.7E-02	1.1E-02	1.6E-02	1.5E-01
GO:0030234	GO:Mole L2	enzyme regulator activity	3.7E-01	2.3E-02	2.0E-01	3.0E-02	3.9E-01	1.9E-01	1.1E-02	6.6E-01	4.3E-01	2.8E-02	1.6E-02	9.6E-02
GO:0051313	GO:Bio L4	attachment of spindle microtubules to chromosome	1.0E-01	3.3E-01	9.2E-01	8.7E-01	3.2E-01	1.1E-01	2.5E-03	9.1E-01	1.5E-01	1.5E-01	1.6E-02	9.8E-01
GO:0012501	GO:Bio L4	programmed cell death	2.5E-02	4.0E-04	1.8E-02	1.6E-03	2.5E-01	3.0E-01	1.3E-01	2.7E-01	3.8E-02	1.2E-03	1.7E-02	3.8E-03
GO:0050661	GO:Mole L4	NADP or NADPH binding	1.6E-01	4.0E-02	2.5E-02	1.1E-02	9.1E-01	4.1E-01	9.6E-02	4.9E-02	4.3E-01	8.5E-02	1.7E-02	4.4E-03
GO:0042043	GO:Mole L4	neurexin binding	6.9E-02	3.3E-02	3.1E-01	3.6E-01	1.3E-01	1.8E-01	7.8E-03	7.3E-01	5.0E-02	3.6E-02	1.7E-02	6.1E-01
GO:0051094	GO:Bio L4	positive regulation of developmental process	3.6E-01	3.1E-01	4.6E-01	4.9E-01	5.1E-01	3.8E-01	5.4E-03	9.3E-01	4.9E-01	3.7E-01	1.7E-02	8.1E-01
GO:0008104	GO:Bio L4	protein localization	6.0E-01	1.1E-01	9.2E-02	2.1E-02	6.1E-02	1.3E-01	2.8E-02	7.3E-01	1.6E-01	7.7E-02	1.8E-02	7.9E-02
GO:0051239	GO:Bio L4	regulation of multicellular organismal process	1.2E-01	1.4E-02	1.4E-01	1.5E-01	1.2E-01	4.4E-01	1.8E-02	7.6E-01	7.9E-02	3.7E-02	1.8E-02	3.6E-01
GO:0000710	GO:Bio L4	meiotic mismatch repair	2.0E-04	5.0E-05	1.3E-02	2.9E-02	2.9E-01	4.1E-01	2.0E-01	7.7E-01	6.3E-04	2.4E-04	1.8E-02	1.1E-01
GO:0032272	GO:Bio L4	negative regulation of protein polymerization	4.4E-02	3.6E-02	2.1E-02	1.7E-02	4.8E-02	1.4E-02	1.2E-01	7.9E-01	1.5E-02	4.4E-03	1.8E-02	7.2E-02
GO:0016265	GO:Bio L2	death	3.1E-02	5.0E-05	1.9E-02	2.2E-03	1.9E-01	2.9E-01	1.4E-01	2.9E-01	3.6E-02	1.7E-04	1.8E-02	5.4E-03
GO:0060022	GO:Bio L4	hard palate development	2.8E-02	3.6E-02	1.5E-02	1.9E-02	8.4E-01	8.7E-01	1.8E-01	4.6E-01	1.1E-01	1.4E-01	1.9E-02	5.0E-02
GO:0030154	GO:Bio L4	cell differentiation	3.8E-01	1.3E-01	7.5E-02	4.3E-02	4.1E-01	2.7E-01	3.6E-02	9.3E-01	4.5E-01	1.6E-01	1.9E-02	1.7E-01
GO:0032231	GO:Bio L4	regulation of actin filament bundle assembly	1.6E-01	5.7E-02	2.9E-01	2.6E-01	2.8E-02	7.5E-03	9.5E-03	8.3E-01	2.9E-02	3.7E-03	1.9E-02	5.5E-01

GO:0043254	GO:Bio L4	regulation of protein complex assembly	1.7E-01	6.5E-02	5.7E-02	3.9E-02	2.2E-01	3.6E-02	4.8E-02	9.5E-01	1.6E-01	1.6E-02	1.9E-02	1.6E-01
GO:0042700	GO:Bio L4	luteinizing hormone signaling pathway	2.2E-01	5.3E-01	1.3E-01	1.1E-01	1.3E-01	1.2E-01	2.0E-02	9.7E-02	1.3E-01	2.4E-01	1.9E-02	6.0E-02
GO:0045123	GO:Bio L4	cellular extravasation	5.5E-02	4.1E-02	2.9E-03	2.3E-03	9.6E-01	9.7E-01	9.5E-01	1.6E-01	2.1E-01	1.7E-01	1.9E-02	3.3E-03
GO:0010639	GO:Bio L4	negative regulation of organelle organization	2.4E-01	1.3E-01	2.5E-01	2.1E-01	1.4E-02	2.7E-03	1.1E-02	9.7E-01	2.3E-02	3.2E-03	1.9E-02	5.3E-01
GO:0050673	GO:Bio L4	epithelial cell proliferation	3.0E-01	1.0E-01	7.6E-01	8.2E-01	3.8E-02	5.7E-02	3.7E-03	3.2E-01	6.2E-02	3.6E-02	1.9E-02	6.2E-01
GO:0080090	GO:Bio L4	regulation of primary metabolic process	6.2E-02	2.1E-03	1.3E-01	7.2E-02	7.6E-02	4.5E-01	2.3E-02	7.7E-01	3.0E-02	7.5E-03	2.0E-02	2.1E-01
GO:0044463	GO:Cell L4	cell projection part	1.0E-01	2.9E-03	4.8E-02	9.1E-03	2.6E-01	1.0E-01	6.2E-02	4.1E-01	1.2E-01	2.7E-03	2.0E-02	2.5E-02
GO:0017077	GO:Mole L4	oxidative phosphorylation uncoupler activity	2.7E-01	5.7E-01	1.5E-02	4.7E-03	6.4E-01	5.3E-01	2.0E-01	9.4E-01	4.8E-01	6.7E-01	2.0E-02	2.8E-02
GO:0000502	GO:Cell L4	proteasome complex	7.4E-01	6.6E-01	5.1E-02	5.7E-02	7.8E-01	5.7E-01	5.9E-02	9.1E-01	9.0E-01	7.4E-01	2.0E-02	2.0E-01
GO:0051238	GO:Bio L4	sequestering of metal ion	2.3E-01	1.2E-01	2.3E-01	3.0E-01	1.2E-03	6.7E-03	1.3E-02	3.5E-01	2.5E-03	6.3E-03	2.1E-02	3.4E-01
GO:0010717	GO:Bio L4	regulation of epithelial to mesenchymal transition	7.2E-02	1.8E-01	3.3E-01	3.1E-01	9.0E-01	1.0E+00	9.2E-03	5.9E-01	2.4E-01	4.9E-01	2.1E-02	4.9E-01
GO:0022414	GO:Bio L2	reproductive process	7.7E-01	6.1E-01	2.3E-02	7.6E-02	5.9E-01	2.0E-01	1.3E-01	3.4E-01	8.2E-01	3.9E-01	2.1E-02	1.2E-01
GO:0043902	GO:Bio L4	positive regulation of multi-organism process	8.4E-03	1.6E-02	5.7E-02	5.0E-02	1.7E-01	1.3E-01	5.4E-02	1.2E-01	1.1E-02	1.5E-02	2.1E-02	3.7E-02
GO:0051712	GO:Bio L4	positive regulation of killing of cells of another organism	8.4E-03	1.6E-02	5.7E-02	5.0E-02	1.7E-01	1.3E-01	5.4E-02	1.2E-01	1.1E-02	1.5E-02	2.1E-02	3.7E-02
GO:0044246	GO:Bio L4	regulation of multicellular organismal metabolic process	3.0E-01	5.7E-02	6.0E-02	1.2E-01	2.6E-01	8.2E-01	5.2E-02	3.5E-01	2.8E-01	1.9E-01	2.1E-02	1.8E-01
GO:0014870	GO:Bio L4	response to muscle inactivity	2.9E-01	1.7E-01	1.1E-02	3.6E-03	1.6E-01	6.6E-01	2.9E-01	3.6E-01	1.9E-01	3.6E-01	2.1E-02	1.0E-02
GO:0014877	GO:Bio L4	response to muscle inactivity involved in regulation of muscle adaptation	2.9E-01	1.7E-01	1.1E-02	3.6E-03	1.6E-01	6.6E-01	2.9E-01	3.6E-01	1.9E-01	3.6E-01	2.1E-02	1.0E-02
5210	KEGG	Colorectal cancer	3.8E-02	4.7E-02	2.4E-01	5.3E-01	9.3E-01	8.0E-01	1.3E-02	2.8E-01	1.5E-01	1.6E-01	2.1E-02	4.4E-01
GO:0030397	GO:Bio L4	membrane disassembly	1.4E-01	9.4E-02	4.5E-02	4.1E-02	6.0E-01	8.7E-01	7.2E-02	5.9E-01	2.9E-01	2.9E-01	2.2E-02	1.1E-01
GO:0051302	GO:Bio L4	regulation of cell division	1.8E-01	2.6E-01	9.9E-02	1.1E-01	3.0E-01	8.0E-01	3.2E-02	4.2E-01	2.1E-01	5.3E-01	2.2E-02	1.9E-01

GO:0051171	GO:Bio L4	regulation of nitrogen compound metabolic process	3.1E-02	1.7E-03	9.5E-02	4.2E-02	1.0E-01	6.5E-01	3.4E-02	8.5E-01	2.1E-02	8.7E-03	2.2E-02	1.6E-01
532	KEGG	Glycosaminoglycan biosynthesis - chondroitin sulfate	3.1E-01	1.8E-01	3.4E-03	4.7E-02	9.9E-01	9.9E-01	9.5E-01	4.5E-01	6.7E-01	4.9E-01	2.2E-02	1.0E-01
GO:0031323	GO:Bio L4	regulation of cellular metabolic process	9.6E-02	5.0E-03	1.4E-01	8.4E-02	9.5E-02	4.1E-01	2.2E-02	7.3E-01	5.2E-02	1.5E-02	2.2E-02	2.3E-01
GO:0042393	GO:Mole L4	histone binding	9.0E-01	9.6E-01	1.8E-01	2.4E-01	1.8E-01	5.4E-01	1.8E-02	4.9E-02	4.6E-01	8.6E-01	2.2E-02	6.3E-02
GO:0051640	GO:Bio L4	organelle localization	1.6E-01	4.4E-02	6.7E-01	5.7E-01	6.6E-01	3.0E-01	4.9E-03	3.5E-01	3.5E-01	6.9E-02	2.2E-02	5.3E-01
GO:0000003	GO:Bio L2	reproduction	7.8E-01	6.2E-01	2.4E-02	8.0E-02	6.0E-01	2.1E-01	1.3E-01	3.4E-01	8.2E-01	4.0E-01	2.2E-02	1.3E-01
GO:0031324	GO:Bio L4	negative regulation of cellular metabolic process	6.1E-01	1.6E-01	2.8E-01	1.6E-01	2.2E-01	6.8E-01	1.2E-02	7.5E-01	4.1E-01	3.5E-01	2.2E-02	3.7E-01
GO:0051179	GO:Bio L2	localization	3.1E-01	8.6E-03	1.8E-01	4.3E-02	1.2E-01	3.6E-02	1.9E-02	4.4E-01	1.6E-01	2.8E-03	2.2E-02	9.5E-02
GO:0031333	GO:Bio L4	negative regulation of protein complex assembly	3.9E-02	2.0E-02	2.6E-02	1.5E-02	4.6E-02	1.7E-02	1.3E-01	8.5E-01	1.3E-02	3.1E-03	2.2E-02	6.8E-02
760	KEGG	Nicotinate and nicotinamide metabolism	2.5E-02	6.7E-03	7.9E-03	2.6E-03	7.5E-01	5.1E-01	4.3E-01	9.8E-01	9.2E-02	2.3E-02	2.3E-02	1.8E-02
GO:0051894	GO:Bio L4	positive regulation of focal adhesion assembly	2.1E-02	2.1E-02	3.4E-01	1.5E-01	1.3E-01	2.5E-02	1.0E-02	7.9E-01	1.9E-02	4.6E-03	2.3E-02	3.7E-01
GO:0008233	GO:Mole L4	peptidase activity	7.8E-01	8.3E-01	3.9E-01	3.0E-01	1.9E-01	3.2E-02	8.6E-03	4.5E-01	4.3E-01	1.2E-01	2.3E-02	4.1E-01
GO:0019887	GO:Mole L4	protein kinase regulator activity	6.8E-01	4.7E-01	3.9E-01	4.6E-01	1.1E-01	5.9E-02	8.8E-03	7.3E-01	2.7E-01	1.3E-01	2.3E-02	7.0E-01
GO:0001824	GO:Bio L4	blastocyst development	4.7E-01	3.9E-01	1.5E-02	4.4E-02	1.1E-01	8.1E-02	2.3E-01	6.6E-01	2.0E-01	1.4E-01	2.3E-02	1.3E-01
GO:0022610	GO:Bio L2	biological adhesion	6.2E-01	3.1E-01	1.9E-01	1.5E-01	5.7E-01	4.9E-01	1.9E-02	3.5E-03	7.2E-01	4.3E-01	2.3E-02	4.5E-03
GO:0016667	GO:Mole L4	oxidoreductase activity, acting on sulfur group of donors	9.4E-01	7.3E-01	5.9E-01	8.5E-01	5.2E-01	1.1E-01	5.9E-03	2.6E-01	8.4E-01	2.8E-01	2.3E-02	5.6E-01
GO:0048729	GO:Bio L4	tissue morphogenesis	1.2E-01	8.9E-02	1.4E-01	1.3E-01	2.7E-01	9.1E-03	2.5E-02	9.5E-01	1.4E-01	6.6E-03	2.3E-02	3.8E-01
GO:0032605	GO:Bio L4	hepatocyte growth factor production	5.7E-01	7.9E-01	4.1E-01	5.1E-01	1.7E-01	4.9E-02	8.7E-03	2.3E-01	3.2E-01	1.7E-01	2.4E-02	3.7E-01
GO:0046789	GO:Mole L4	host cell surface receptor binding	5.7E-01	7.9E-01	4.1E-01	5.1E-01	1.7E-01	4.9E-02	8.7E-03	2.3E-01	3.2E-01	1.7E-01	2.4E-02	3.7E-01
GO:0019955	GO:Mole L4	cytokine binding	1.6E-01	3.0E-02	2.3E-02	4.9E-02	3.8E-01	6.6E-01	1.6E-01	9.2E-01	2.3E-01	9.6E-02	2.4E-02	1.8E-01
GO:0030856	GO:Bio L4	regulation of epithelial cell differentiation	3.2E-01	4.1E-01	1.9E-01	1.7E-01	5.5E-01	8.9E-01	1.9E-02	9.9E-01	4.9E-01	7.3E-01	2.4E-02	4.6E-01
GO:0032940	GO:Bio L4	secretion by cell	3.7E-01	2.1E-02	9.1E-02	1.2E-01	5.0E-02	3.1E-01	4.0E-02	7.9E-01	9.3E-02	3.9E-02	2.4E-02	3.2E-01
GO:0046903	GO:Bio L4	secretion	1.4E-01	7.6E-03	8.4E-02	1.0E-01	9.1E-02	5.3E-01	4.3E-02	8.1E-01	7.0E-02	2.6E-02	2.4E-02	2.8E-01

GO:0009892	GO:Bio L4	negative regulation of metabolic process	5.8E-01	8.0E-02	2.8E-01	1.6E-01	2.0E-01	7.4E-01	1.3E-02	7.6E-01	3.6E-01	2.3E-01	2.4E-02	3.9E-01
GO:0044253	GO:Bio L4	positive regulation of multicellular organismal metabolic process	2.8E-01	7.0E-02	8.0E-02	1.9E-01	2.0E-01	7.4E-01	4.6E-02	4.3E-01	2.1E-01	2.1E-01	2.4E-02	2.9E-01
GO:0045595	GO:Bio L4	regulation of cell differentiation	1.5E-01	3.3E-02	1.2E-01	5.5E-02	1.9E-01	6.3E-01	3.2E-02	9.4E-01	1.3E-01	1.0E-01	2.4E-02	2.1E-01
GO:0021772	GO:Bio L4	olfactory bulb development	8.1E-01	6.0E-01	3.4E-02	2.8E-02	8.7E-02	3.8E-01	1.1E-01	8.9E-01	2.6E-01	5.7E-01	2.5E-02	1.2E-01
GO:0021988	GO:Bio L4	olfactory lobe development	8.0E-01	6.4E-01	3.1E-02	2.9E-02	1.0E-01	4.2E-01	1.2E-01	8.6E-01	2.9E-01	6.2E-01	2.5E-02	1.2E-01
GO:0019899	GO:Mole L4	enzyme binding	1.6E-01	8.8E-03	1.9E-01	1.1E-01	4.8E-01	8.0E-02	2.0E-02	2.0E-01	2.7E-01	5.8E-03	2.5E-02	1.1E-01
GO:0051129	GO:Bio L4	negative regulation of cellular component organization	2.3E-01	3.9E-02	1.8E-01	1.1E-01	1.4E-02	2.6E-02	2.1E-02	8.6E-01	2.1E-02	7.9E-03	2.5E-02	3.2E-01
GO:0015232	GO:Mole L4	heme transporter activity	2.7E-01	9.1E-01	9.4E-01	9.8E-01	3.1E-01	4.5E-01	4.0E-03	3.3E-01	2.9E-01	7.8E-01	2.5E-02	6.8E-01
GO:0007162	GO:Bio L4	negative regulation of cell adhesion	4.8E-02	2.0E-01	9.4E-02	1.8E-01	7.2E-01	9.8E-01	4.0E-02	3.0E-01	1.5E-01	5.2E-01	2.5E-02	2.1E-01
GO:0051130	GO:Bio L4	positive regulation of cellular component organization	2.9E-01	1.0E-01	5.4E-01	5.0E-01	8.4E-02	1.5E-01	7.1E-03	8.3E-01	1.1E-01	7.9E-02	2.5E-02	7.8E-01
GO:0035107	GO:Bio L4	appendage morphogenesis	1.9E-01	1.9E-01	2.3E-02	6.8E-02	8.4E-03	3.2E-01	1.7E-01	9.2E-01	1.2E-02	2.3E-01	2.5E-02	2.4E-01
GO:0031966	GO:Cell L4	mitochondrial membrane	9.7E-01	6.3E-01	4.7E-01	3.0E-01	7.3E-01	8.3E-01	8.2E-03	1.1E-01	9.5E-01	8.6E-01	2.5E-02	1.4E-01
GO:0060255	GO:Bio L4	regulation of macromolecule metabolic process	1.2E-01	1.6E-02	2.2E-01	1.0E-01	9.1E-02	3.2E-01	1.8E-02	7.9E-01	5.8E-02	3.2E-02	2.6E-02	2.8E-01
GO:0030031	GO:Bio L4	cell projection assembly	9.9E-02	1.4E-01	4.5E-01	5.0E-01	1.1E-01	7.8E-01	8.7E-03	4.7E-01	6.0E-02	3.6E-01	2.6E-02	5.8E-01
GO:0071604	GO:Bio L4	transforming growth factor-beta production	3.7E-02	1.1E-01	5.0E-01	1.7E-01	1.0E+00	9.4E-01	8.0E-03	7.6E-01	1.6E-01	3.4E-01	2.6E-02	4.0E-01
GO:0044459	GO:Cell L4	plasma membrane part	3.0E-01	6.9E-03	6.7E-02	2.5E-02	7.3E-01	4.1E-01	6.0E-02	4.6E-02	5.5E-01	1.9E-02	2.6E-02	8.9E-03
GO:0007626	GO:Bio L4	locomotory behavior	2.3E-02	3.9E-02	1.1E-02	1.7E-03	1.0E-01	6.6E-02	3.7E-01	1.2E-01	1.7E-02	1.8E-02	2.6E-02	1.9E-03
GO:0060074	GO:Bio L4	synapse maturation	9.9E-01	9.9E-01	7.2E-01	6.7E-01	4.6E-01	6.6E-01	5.6E-03	2.6E-01	8.1E-01	9.3E-01	2.6E-02	4.8E-01
GO:0031090	GO:Cell L4	organelle membrane	7.4E-01	1.5E-01	4.2E-01	1.9E-01	7.4E-01	4.7E-01	9.7E-03	2.1E-01	8.7E-01	2.6E-01	2.6E-02	1.7E-01
GO:0000117	GO:Bio L4	regulation of transcription involved in G2/M-phase of mitotic cell cycle	3.6E-01	5.3E-01	1.4E-02	1.1E-02	3.1E-01	6.2E-01	2.8E-01	9.4E-01	3.5E-01	7.0E-01	2.6E-02	5.7E-02
GO:0044425	GO:Cell L4	membrane part	6.6E-01	8.6E-02	2.1E-01	5.4E-02	7.6E-01	1.7E-01	2.0E-02	1.6E-01	8.5E-01	7.5E-02	2.7E-02	4.9E-02

GO:0045822	GO:Bio L4	negative regulation of heart contraction	1.8E-01	4.1E-01	6.0E-02	7.1E-02	3.2E-02	4.0E-01	7.0E-02	5.6E-01	3.5E-02	4.6E-01	2.7E-02	1.7E-01
GO:0019098	GO:Bio L4	reproductive behavior	2.6E-01	8.0E-02	6.6E-03	6.5E-03	6.2E-01	7.1E-01	6.3E-01	1.0E+00	4.5E-01	2.2E-01	2.7E-02	3.9E-02
GO:0009792	GO:Bio L4	embryonic development ending in birth or egg hatching	5.8E-01	3.8E-01	6.3E-02	5.4E-02	3.7E-01	1.2E-01	6.6E-02	8.1E-01	5.4E-01	1.9E-01	2.7E-02	1.8E-01
GO:0050662	GO:Mole L4	coenzyme binding	2.6E-01	7.6E-02	1.3E-01	5.9E-02	9.3E-01	5.7E-01	3.3E-02	4.5E-01	5.9E-01	1.8E-01	2.7E-02	1.2E-01
GO:0005737	GO:Cell L4	cytoplasm	6.5E-01	7.0E-02	1.9E-01	8.2E-02	2.8E-01	1.9E-02	2.3E-02	3.6E-01	4.9E-01	1.0E-02	2.7E-02	1.3E-01
GO:0044093	GO:Bio L4	positive regulation of molecular function	2.3E-02	1.0E-04	6.3E-02	1.9E-02	9.2E-01	2.3E-01	6.8E-02	6.1E-01	1.0E-01	2.7E-04	2.8E-02	6.4E-02
GO:0030335	GO:Bio L4	positive regulation of cell migration	9.4E-02	1.8E-01	1.2E-01	8.1E-02	3.3E-02	1.6E-01	3.7E-02	2.7E-01	2.1E-02	1.3E-01	2.8E-02	1.1E-01
4060	KEGG	Cytokine-cytokine receptor interaction	1.5E-02	2.3E-02	1.8E-02	5.5E-02	3.2E-01	1.4E-01	2.5E-01	9.4E-01	3.0E-02	2.2E-02	2.8E-02	2.0E-01
GO:0031346	GO:Bio L4	positive regulation of cell projection organization	7.8E-01	6.4E-01	8.2E-01	9.7E-01	3.0E-01	9.2E-01	5.3E-03	1.0E+00	5.7E-01	9.0E-01	2.8E-02	1.0E+00
GO:0033554	GO:Bio L4	cellular response to stress	3.2E-02	3.1E-02	7.6E-02	7.2E-02	3.4E-01	4.4E-01	5.7E-02	6.6E-01	6.0E-02	7.3E-02	2.8E-02	1.9E-01
GO:0004096	GO:Mole L4	catalase activity	1.4E-01	6.6E-02	1.4E-02	7.2E-03	9.6E-01	9.5E-01	3.1E-01	7.7E-01	4.0E-01	2.4E-01	2.8E-02	3.4E-02
GO:0008013	GO:Mole L4	beta-catenin binding	5.5E-01	9.2E-01	5.5E-01	4.2E-01	9.7E-02	4.3E-01	8.0E-03	1.7E-01	2.1E-01	7.6E-01	2.8E-02	2.6E-01
GO:0010942	GO:Bio L4	positive regulation of cell death	4.0E-04	5.0E-05	2.6E-02	1.4E-02	6.0E-01	8.6E-01	1.7E-01	2.4E-01	2.2E-03	4.8E-04	2.8E-02	2.2E-02
GO:0030901	GO:Bio L4	midbrain development	1.8E-01	1.9E-01	7.0E-02	6.6E-02	5.5E-01	1.7E-01	6.4E-02	4.6E-01	3.2E-01	1.4E-01	2.9E-02	1.4E-01
GO:0051917	GO:Bio L4	regulation of fibrinolysis	4.5E-01	6.2E-01	3.6E-01	1.8E-01	6.6E-01	7.3E-01	1.2E-02	7.1E-01	6.6E-01	8.1E-01	2.9E-02	3.8E-01
GO:0048736	GO:Bio L4	appendage development	2.2E-01	1.6E-01	2.6E-02	7.0E-02	8.4E-03	3.4E-01	1.8E-01	9.1E-01	1.3E-02	2.1E-01	2.9E-02	2.4E-01
GO:0060341	GO:Bio L4	regulation of cellular localization	2.3E-01	7.5E-03	2.3E-01	3.1E-01	1.4E-01	3.8E-01	2.0E-02	6.7E-01	1.5E-01	2.0E-02	2.9E-02	5.3E-01
GO:0001941	GO:Bio L4	postsynaptic membrane organization	7.4E-02	4.4E-02	4.1E-02	6.7E-02	5.9E-01	6.6E-01	1.1E-01	4.2E-01	1.8E-01	1.3E-01	2.9E-02	1.3E-01
GO:0016020	GO:Cell L4	membrane	6.9E-01	4.8E-02	2.3E-01	7.0E-02	7.2E-01	1.6E-01	2.0E-02	1.7E-01	8.4E-01	4.5E-02	2.9E-02	6.3E-02
GO:0048518	GO:Bio L2	positive regulation of biological process	5.1E-02	1.3E-03	1.1E-01	1.4E-01	1.5E-01	2.2E-01	4.5E-02	5.9E-01	4.6E-02	2.6E-03	3.0E-02	2.9E-01
GO:0048518	GO:Bio L4	positive regulation of biological process	5.1E-02	1.3E-03	1.1E-01	1.4E-01	1.5E-01	2.2E-01	4.5E-02	5.9E-01	4.6E-02	2.6E-03	3.0E-02	2.9E-01
GO:0048469	GO:Bio L4	cell maturation	1.6E-01	9.0E-02	8.1E-02	4.3E-02	6.3E-01	1.8E-01	5.9E-02	3.6E-01	3.4E-01	8.3E-02	3.0E-02	7.9E-02
GO:0045637	GO:Bio L4	regulation of myeloid cell differentiation	3.4E-01	2.7E-01	3.6E-02	9.5E-02	4.7E-01	7.1E-01	1.3E-01	2.7E-01	4.5E-01	5.0E-01	3.0E-02	1.2E-01
GO:0044464	GO:Cell L2	cell part	5.1E-01	2.0E-02	2.1E-01	6.7E-02	1.4E-01	2.1E-02	2.3E-02	4.3E-01	2.5E-01	3.7E-03	3.0E-02	1.3E-01
GO:0005623	GO:Cell L2	cell	5.1E-01	2.0E-02	2.1E-01	6.7E-02	1.4E-01	2.1E-02	2.3E-02	4.4E-01	2.5E-01	3.7E-03	3.0E-02	1.3E-01

GO:0008565	GO:Mole L4	protein transporter activity	6.4E-01	3.9E-01	3.6E-02	5.7E-02	1.7E-01	3.1E-01	1.4E-01	6.0E-01	3.5E-01	3.8E-01	3.0E-02	1.5E-01
GO:0045454	GO:Bio L4	cell redox homeostasis	9.4E-01	6.6E-01	6.0E-01	8.7E-01	3.7E-01	6.8E-01	8.2E-03	3.5E-01	7.2E-01	8.1E-01	3.1E-02	6.7E-01
GO:0060089	GO:Mole L2	molecular transducer activity	5.5E-01	8.3E-02	2.1E-01	2.3E-01	1.2E-01	1.8E-01	2.4E-02	5.9E-01	2.4E-01	7.7E-02	3.1E-02	4.1E-01
GO:0043226	GO:Cell L2	organelle	4.1E-01	2.2E-02	2.2E-01	6.6E-02	9.3E-02	1.4E-02	2.2E-02	6.0E-01	1.6E-01	2.9E-03	3.1E-02	1.7E-01
GO:0034623	GO:Bio L4	cellular macromolecular complex disassembly	2.7E-01	1.6E-01	4.7E-01	3.8E-01	2.6E-01	5.1E-02	1.1E-02	9.5E-01	2.6E-01	4.7E-02	3.1E-02	7.3E-01
GO:0006810	GO:Bio L4	transport	4.1E-01	7.7E-03	3.6E-01	1.3E-01	8.9E-02	1.9E-02	1.4E-02	4.7E-01	1.6E-01	1.5E-03	3.2E-02	2.3E-01
GO:0008152	GO:Bio L2	metabolic process	3.6E-01	1.6E-02	1.1E-01	5.9E-02	2.8E-01	2.5E-01	4.7E-02	5.7E-01	3.3E-01	2.6E-02	3.2E-02	1.5E-01
4742	KEGG	Taste transduction	4.3E-01	1.9E-01	8.0E-02	8.9E-02	1.5E-01	6.5E-01	6.5E-02	3.5E-01	2.4E-01	3.8E-01	3.2E-02	1.4E-01
GO:0048522	GO:Bio L4	positive regulation of cellular process	3.6E-02	9.0E-04	1.2E-01	1.2E-01	1.8E-01	4.1E-01	4.2E-02	5.8E-01	3.9E-02	3.3E-03	3.3E-02	2.6E-01
GO:0060398	GO:Bio L4	regulation of growth hormone receptor signaling pathway	3.4E-02	1.1E-01	1.2E-02	1.1E-02	6.3E-01	6.8E-02	4.3E-01	2.9E-01	1.0E-01	4.3E-02	3.3E-02	2.1E-02
GO:0060399	GO:Bio L4	positive regulation of growth hormone receptor signaling pathway	3.4E-02	1.1E-01	1.2E-02	1.1E-02	6.3E-01	6.8E-02	4.3E-01	2.9E-01	1.0E-01	4.3E-02	3.3E-02	2.1E-02
GO:0005615	GO:Cell L4	extracellular space	1.0E-01	2.0E-01	1.0E-01	7.7E-02	3.8E-01	2.4E-01	5.1E-02	4.8E-01	1.6E-01	1.9E-01	3.3E-02	1.6E-01
GO:0010638	GO:Bio L4	positive regulation of organelle organization	4.8E-01	3.8E-01	4.1E-01	3.1E-01	7.7E-02	3.1E-01	1.3E-02	3.7E-01	1.6E-01	3.7E-01	3.3E-02	3.7E-01
GO:0043229	GO:Cell L4	intracellular organelle	4.1E-01	2.2E-02	2.3E-01	6.9E-02	9.3E-02	1.5E-02	2.3E-02	6.0E-01	1.6E-01	2.9E-03	3.3E-02	1.7E-01
GO:0050790	GO:Bio L4	regulation of catalytic activity	1.4E-01	1.3E-02	5.5E-02	5.0E-02	5.1E-01	2.1E-01	9.5E-02	7.4E-01	2.6E-01	1.9E-02	3.3E-02	1.6E-01
GO:0051234	GO:Bio L2	establishment of localization	4.0E-01	6.6E-03	4.0E-01	1.5E-01	9.7E-02	1.8E-02	1.3E-02	5.0E-01	1.6E-01	1.2E-03	3.3E-02	2.6E-01
GO:0030334	GO:Bio L4	regulation of cell migration	1.4E-02	6.2E-03	1.7E-02	1.7E-02	1.3E-02	1.9E-01	3.2E-01	4.3E-01	1.7E-03	8.9E-03	3.3E-02	4.3E-02
GO:0031018	GO:Bio L4	endocrine pancreas development	4.0E-01	4.8E-01	8.5E-02	1.2E-01	7.5E-01	7.1E-01	6.2E-02	7.2E-01	6.6E-01	7.1E-01	3.3E-02	3.0E-01
GO:0017145	GO:Bio L4	stem cell division	2.7E-01	1.1E-01	1.3E-02	3.9E-02	9.0E-01	6.6E-01	4.0E-01	9.2E-02	5.9E-01	2.6E-01	3.3E-02	2.4E-02
GO:0006766	GO:Bio L4	vitamin metabolic process	1.7E-01	5.4E-02	4.6E-01	4.0E-01	5.5E-01	8.6E-01	1.2E-02	2.4E-01	3.1E-01	1.9E-01	3.3E-02	3.2E-01
GO:0009790	GO:Bio L4	embryonic development	5.5E-01	5.2E-01	4.1E-02	6.7E-02	2.7E-01	2.0E-01	1.3E-01	8.5E-01	4.3E-01	3.4E-01	3.3E-02	2.2E-01
GO:0021537	GO:Bio L4	telencephalon development	1.2E-01	6.7E-02	3.6E-02	1.6E-02	3.7E-01	8.3E-02	1.5E-01	9.2E-01	1.8E-01	3.4E-02	3.3E-02	7.6E-02
GO:0051219	GO:Mole L4	phosphoprotein binding	8.5E-02	5.3E-02	3.5E-02	3.1E-02	7.6E-01	8.3E-01	1.5E-01	2.1E-01	2.4E-01	1.8E-01	3.3E-02	4.0E-02

GO:0043231	GO:Cell L4	intracellular membrane-bounded organelle	4.8E-01	3.7E-02	1.8E-01	3.8E-02	1.2E-01	4.1E-02	3.0E-02	5.9E-01	2.3E-01	1.1E-02	3.4E-02	1.1E-01
GO:0016679	GO:Mole L4	oxidoreductase activity, acting on diphenols and related substances as donors	8.5E-01	9.4E-02	3.6E-02	5.5E-02	3.9E-01	1.5E-01	1.5E-01	9.7E-01	7.0E-01	7.3E-02	3.4E-02	2.1E-01
GO:0046661	GO:Bio L4	male sex differentiation	1.2E-01	1.5E-01	3.1E-02	2.7E-02	7.5E-01	1.7E-01	1.8E-01	6.8E-02	3.0E-01	1.2E-01	3.4E-02	1.3E-02
GO:0002520	GO:Bio L4	immune system development	1.3E-02	7.9E-03	1.3E-02	1.4E-02	5.5E-01	3.9E-01	4.1E-01	4.5E-01	4.1E-02	2.1E-02	3.4E-02	3.8E-02
GO:0048858	GO:Bio L4	cell projection morphogenesis	2.0E-01	1.1E-01	2.9E-02	4.6E-02	7.9E-02	3.5E-01	1.9E-01	5.2E-01	8.1E-02	1.6E-01	3.4E-02	1.1E-01
GO:0033504	GO:Bio L4	floor plate development	6.1E-01	3.9E-01	3.9E-02	1.1E-01	3.1E-01	4.0E-01	1.4E-01	9.7E-01	5.0E-01	4.5E-01	3.4E-02	3.5E-01
GO:0070727	GO:Bio L4	cellular macromolecule localization	3.5E-01	7.0E-02	2.6E-01	9.8E-02	2.4E-01	4.5E-01	2.1E-02	3.8E-01	2.9E-01	1.4E-01	3.5E-02	1.6E-01
GO:0044424	GO:Cell L4	intracellular part	5.2E-01	2.9E-02	2.2E-01	8.2E-02	5.8E-02	1.1E-02	2.5E-02	5.0E-01	1.4E-01	2.9E-03	3.5E-02	1.7E-01
GO:0048634	GO:Bio L4	regulation of muscle organ development	2.7E-02	5.6E-02	4.7E-01	4.0E-01	7.2E-01	5.4E-01	1.2E-02	7.6E-01	9.5E-02	1.4E-01	3.5E-02	6.7E-01
GO:0050877	GO:Bio L4	neurological system process	2.1E-01	9.2E-02	3.0E-01	3.9E-01	3.0E-01	2.0E-01	1.9E-02	3.4E-01	2.4E-01	9.1E-02	3.5E-02	4.0E-01
GO:0070576	GO:Mole L4	vitamin D 24-hydroxylase activity	6.5E-01	3.1E-01	4.1E-01	5.7E-01	4.6E-01	2.7E-01	1.4E-02	9.9E-01	6.6E-01	2.9E-01	3.5E-02	8.9E-01
GO:0046677	GO:Bio L4	response to antibiotic	1.3E-01	1.0E-02	2.1E-02	4.4E-02	1.0E+00	1.0E+00	2.7E-01	7.9E-01	4.0E-01	5.6E-02	3.5E-02	1.5E-01
GO:0044249	GO:Bio L4	cellular biosynthetic process	1.6E-01	6.5E-03	1.1E-01	5.8E-02	2.4E-01	6.1E-01	5.5E-02	8.4E-01	1.6E-01	2.6E-02	3.5E-02	1.9E-01
GO:0017053	GO:Cell L4	transcriptional repressor complex	3.6E-01	2.6E-01	6.3E-03	1.2E-02	3.1E-01	4.7E-01	9.1E-01	8.6E-01	3.6E-01	3.8E-01	3.5E-02	5.9E-02
GO:0048514	GO:Bio L4	blood vessel morphogenesis	2.0E-01	1.8E-01	1.4E-02	9.7E-03	6.5E-01	1.9E-01	4.2E-01	6.2E-01	3.9E-01	1.5E-01	3.5E-02	3.7E-02
GO:0005622	GO:Cell L4	intracellular	5.4E-01	3.4E-02	2.3E-01	8.5E-02	5.4E-02	1.1E-02	2.6E-02	5.4E-01	1.3E-01	3.2E-03	3.5E-02	1.9E-01
GO:0044444	GO:Cell L4	cytoplasmic part	6.1E-01	6.7E-02	2.8E-01	1.1E-01	7.1E-01	1.1E-01	2.1E-02	4.2E-01	7.9E-01	4.3E-02	3.6E-02	1.8E-01
PA145011114	PharmGKB	pgkb_pwy_Warfarin_Pathway_PD	2.5E-01	2.7E-01	1.5E-02	1.8E-02	2.2E-02	2.4E-01	3.9E-01	3.1E-01	3.4E-02	2.4E-01	3.6E-02	3.4E-02
GO:0005518	GO:Mole L4	collagen binding	3.3E-01	1.8E-01	8.5E-01	5.9E-01	2.2E-01	4.4E-01	6.9E-03	1.2E-01	2.6E-01	2.8E-01	3.6E-02	2.6E-01
GO:0031975	GO:Cell L4	envelope	9.4E-01	5.5E-01	5.5E-01	3.4E-01	7.4E-01	5.7E-01	1.1E-02	1.8E-01	9.5E-01	6.8E-01	3.6E-02	2.3E-01
GO:0050793	GO:Bio L4	regulation of developmental process	7.0E-02	2.0E-02	1.0E-01	5.4E-02	4.2E-01	6.3E-01	5.6E-02	8.8E-01	1.3E-01	6.8E-02	3.6E-02	1.9E-01
GO:0015031	GO:Bio L4	protein transport	5.8E-01	8.0E-02	1.3E-01	2.7E-02	3.1E-02	9.2E-02	4.4E-02	8.3E-01	9.1E-02	4.4E-02	3.6E-02	1.1E-01
GO:0051709	GO:Bio L4	regulation of killing of cells of another organism	1.2E-02	2.5E-02	8.3E-02	7.2E-02	2.2E-01	1.8E-01	7.1E-02	1.6E-01	1.7E-02	2.8E-02	3.6E-02	6.4E-02

GO:0031967	GO:Cell L4	organelle envelope	9.3E-01	5.2E-01	5.4E-01	3.1E-01	7.1E-01	5.7E-01	1.1E-02	1.7E-01	9.3E-01	6.6E-01	3.6E-02	2.0E-01
GO:0032970	GO:Bio L4	regulation of actin filament-based process	1.9E-01	2.8E-02	8.3E-02	6.1E-02	1.9E-02	3.1E-03	7.1E-02	9.8E-01	2.4E-02	9.1E-04	3.6E-02	2.3E-01
GO:0000822	GO:Mole L4	inositol hexakisphosphate binding	7.6E-02	1.7E-01	2.5E-01	2.5E-01	7.0E-01	4.8E-01	2.4E-02	7.1E-01	2.1E-01	2.8E-01	3.6E-02	4.8E-01
GO:0070679	GO:Mole L4	inositol 1,4,5 trisphosphate binding	7.6E-02	1.7E-01	2.5E-01	2.5E-01	7.0E-01	4.8E-01	2.4E-02	7.1E-01	2.1E-01	2.8E-01	3.6E-02	4.8E-01
GO:0051270	GO:Bio L4	regulation of cellular component movement	1.7E-02	5.4E-03	1.8E-02	2.0E-02	2.8E-02	2.7E-01	3.3E-01	3.6E-01	4.1E-03	1.1E-02	3.7E-02	4.3E-02
GO:0031988	GO:Cell L4	membrane-bounded vesicle	9.6E-01	9.0E-01	3.6E-01	1.0E-01	4.2E-01	2.4E-01	1.7E-02	5.3E-01	7.7E-01	5.4E-01	3.7E-02	2.1E-01
GO:0071204	GO:Cell L4	histone pre-mRNA 3'end processing complex	5.6E-01	1.5E-01	3.2E-02	1.8E-02	4.4E-02	1.7E-01	1.9E-01	2.8E-01	1.2E-01	1.2E-01	3.7E-02	3.1E-02
GO:0000083	GO:Bio L4	regulation of transcription involved in G1/S-phase of mitotic cell cycle	2.4E-01	1.4E-01	7.7E-02	5.5E-02	3.6E-02	3.1E-01	7.9E-02	3.7E-01	5.0E-02	1.8E-01	3.7E-02	1.0E-01
GO:0051272	GO:Bio L4	positive regulation of cellular component movement	7.9E-02	1.0E-01	1.7E-01	1.1E-01	4.4E-02	2.1E-01	3.7E-02	1.7E-01	2.3E-02	1.0E-01	3.7E-02	9.3E-02
GO:0005604	GO:Cell L4	basement membrane	1.6E-01	9.7E-02	3.3E-01	1.2E-01	9.1E-01	5.1E-01	1.9E-02	3.9E-01	4.3E-01	2.0E-01	3.8E-02	1.9E-01
4012	KEGG	ErbB signaling pathway	6.1E-01	8.1E-01	7.5E-01	8.7E-01	2.5E-01	9.3E-02	8.3E-03	8.9E-02	4.4E-01	2.7E-01	3.8E-02	2.8E-01
GO:0009888	GO:Bio L4	tissue development	1.4E-01	1.1E-01	7.0E-02	8.5E-02	1.9E-01	2.0E-01	8.8E-02	9.2E-01	1.2E-01	1.0E-01	3.8E-02	2.8E-01
GO:0005834	GO:Cell L4	heterotrimeric G-protein complex	1.2E-01	1.0E-01	2.3E-02	2.6E-02	1.4E-01	4.5E-01	2.8E-01	9.7E-01	8.4E-02	1.8E-01	3.8E-02	1.2E-01
GO:0032984	GO:Bio L4	macromolecular complex disassembly	2.9E-01	1.7E-01	4.9E-01	4.0E-01	2.8E-01	5.8E-02	1.3E-02	9.4E-01	2.9E-01	5.6E-02	3.8E-02	7.5E-01
GO:0030528	GO:Mole L2	transcription regulator activity	6.2E-02	4.6E-03	1.3E-01	3.9E-02	3.7E-01	3.0E-01	4.9E-02	8.0E-01	1.1E-01	1.0E-02	3.8E-02	1.4E-01
GO:0031334	GO:Bio L4	positive regulation of protein complex assembly	7.0E-01	4.0E-01	2.9E-01	2.4E-01	5.0E-01	1.5E-01	2.2E-02	9.1E-01	7.2E-01	2.3E-01	3.9E-02	5.5E-01
GO:0048551	GO:Mole L4	metalloenzyme inhibitor activity	3.9E-02	8.8E-02	3.4E-01	1.5E-01	2.1E-01	1.7E-01	1.9E-02	7.5E-01	4.7E-02	7.8E-02	3.9E-02	3.6E-01
GO:0001967	GO:Bio L4	suckling behavior	2.6E-01	3.3E-01	1.7E-02	1.0E-01	5.7E-01	6.0E-01	3.8E-01	8.6E-02	4.4E-01	5.2E-01	3.9E-02	5.1E-02
GO:0031371	GO:Cell L4	ubiquitin conjugating enzyme complex	2.0E-01	1.8E-01	1.6E-01	1.9E-01	9.2E-01	8.0E-01	4.2E-02	6.6E-01	5.0E-01	4.2E-01	3.9E-02	3.8E-01
GO:0009890	GO:Bio L4	negative regulation of biosynthetic process	6.3E-01	3.3E-01	3.2E-01	2.0E-01	4.3E-01	9.0E-01	2.1E-02	6.5E-01	6.3E-01	6.6E-01	4.0E-02	3.9E-01
GO:0035295	GO:Bio L4	tube development	1.3E-01	2.3E-01	1.6E-01	1.1E-01	8.6E-02	3.4E-03	4.1E-02	2.8E-01	6.3E-02	6.3E-03	4.0E-02	1.3E-01

GO:0006139	GO:Bio L4	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1.4E-01	1.2E-02	1.8E-01	7.1E-02	4.0E-01	6.8E-01	3.8E-02	7.6E-01	2.2E-01	4.9E-02	4.0E-02	2.1E-01
GO:0008073	GO:Mole L4	ornithine decarboxylase inhibitor activity	2.5E-01	2.6E-01	1.4E-01	1.3E-01	1.4E-01	2.3E-01	4.9E-02	4.8E-01	1.5E-01	2.3E-01	4.0E-02	2.4E-01
GO:0032990	GO:Bio L4	cell part morphogenesis	2.3E-01	1.3E-01	3.7E-02	5.6E-02	9.5E-02	2.0E-01	1.8E-01	5.6E-01	1.0E-01	1.2E-01	4.0E-02	1.4E-01
GO:0040017	GO:Bio L4	positive regulation of locomotion	1.4E-01	2.3E-01	1.2E-01	8.3E-02	5.4E-02	2.1E-01	5.5E-02	2.9E-01	4.3E-02	2.0E-01	4.1E-02	1.2E-01
GO:0071256	GO:Cell L4	translocon complex	5.3E-01	7.3E-01	5.8E-01	6.4E-01	7.7E-02	2.5E-01	1.2E-02	7.3E-01	1.7E-01	4.9E-01	4.1E-02	8.2E-01
GO:0007617	GO:Bio L4	mating behavior	1.8E-01	5.1E-02	8.5E-03	1.4E-02	4.9E-01	9.5E-01	8.1E-01	9.9E-01	3.0E-01	2.0E-01	4.1E-02	7.5E-02
GO:0009059	GO:Bio L4	macromolecule biosynthetic process	1.3E-01	1.2E-02	1.8E-01	1.1E-01	4.8E-01	6.6E-01	3.8E-02	8.6E-01	2.4E-01	4.8E-02	4.1E-02	3.2E-01
GO:0008038	GO:Bio L4	neuron recognition	5.6E-01	6.7E-01	9.2E-02	1.2E-01	2.8E-01	1.0E-01	7.5E-02	7.9E-01	4.4E-01	2.5E-01	4.1E-02	3.1E-01
GO:0031082	GO:Cell L4	BLOC complex	1.7E-01	4.4E-02	1.9E-02	8.5E-03	2.5E-01	9.7E-01	3.6E-01	8.9E-01	1.7E-01	1.8E-01	4.1E-02	4.5E-02
GO:0002376	GO:Bio L2	immune system process	6.1E-03	2.0E-03	1.1E-02	7.3E-03	4.6E-01	2.1E-01	6.8E-01	3.0E-01	1.9E-02	3.7E-03	4.2E-02	1.6E-02
GO:0003824	GO:Mole L2	catalytic activity	1.8E-01	1.9E-02	9.8E-02	1.7E-01	7.7E-01	1.8E-01	7.3E-02	5.4E-01	4.2E-01	2.2E-02	4.2E-02	3.1E-01
GO:0007010	GO:Bio L4	cytoskeleton organization	8.9E-03	3.0E-02	6.5E-01	4.2E-01	1.9E-01	1.4E-02	1.1E-02	8.9E-01	1.3E-02	3.7E-03	4.3E-02	7.4E-01
GO:0051953	GO:Bio L4	negative regulation of amine transport	3.8E-01	3.2E-01	6.6E-02	1.4E-01	8.0E-03	4.3E-03	1.1E-01	2.1E-01	2.1E-02	1.1E-02	4.3E-02	1.4E-01
GO:0048534	GO:Bio L4	hemopoietic or lymphoid organ development	1.5E-01	6.1E-02	2.0E-02	1.7E-02	4.9E-01	3.1E-01	3.5E-01	4.2E-01	2.6E-01	9.3E-02	4.3E-02	4.2E-02
GO:0030220	GO:Bio L4	platelet formation	2.0E-03	9.0E-04	1.7E-02	2.1E-02	4.9E-01	2.6E-01	4.2E-01	3.2E-01	7.8E-03	2.2E-03	4.3E-02	4.1E-02
GO:0010564	GO:Bio L4	regulation of cell cycle process	7.4E-01	3.6E-01	8.6E-01	7.7E-01	2.5E-01	1.0E-01	8.4E-03	7.1E-01	5.0E-01	1.6E-01	4.3E-02	8.8E-01
GO:0003677	GO:Mole L4	DNA binding	4.4E-02	1.3E-02	1.6E-01	4.4E-02	5.2E-02	1.5E-01	4.4E-02	8.8E-01	1.6E-02	1.4E-02	4.3E-02	1.6E-01
GO:0008074	GO:Cell L4	guanylate cyclase complex, soluble	2.0E-01	2.9E-01	5.8E-01	5.1E-01	1.4E-01	1.2E-01	1.3E-02	5.4E-02	1.3E-01	1.5E-01	4.3E-02	1.3E-01
GO:0090183	GO:Bio L4	regulation of kidney development	7.7E-01	7.1E-01	5.8E-01	6.3E-01	4.6E-02	3.4E-02	1.2E-02	2.6E-01	1.5E-01	1.1E-01	4.3E-02	4.6E-01
GO:0090184	GO:Bio L4	positive regulation of kidney development	7.7E-01	7.1E-01	5.8E-01	6.3E-01	4.6E-02	3.4E-02	1.2E-02	2.6E-01	1.5E-01	1.1E-01	4.3E-02	4.6E-01
GO:0010467	GO:Bio L4	gene expression	3.4E-01	6.1E-02	1.9E-01	1.1E-01	3.4E-01	6.1E-01	3.9E-02	8.8E-01	3.6E-01	1.6E-01	4.3E-02	3.2E-01
GO:0032273	GO:Bio L4	positive regulation of protein polymerization	5.0E-01	2.1E-01	3.9E-01	3.5E-01	7.3E-01	5.2E-01	1.9E-02	7.4E-01	7.3E-01	3.5E-01	4.3E-02	6.1E-01
GO:0051172	GO:Bio L4	negative regulation of nitrogen compound metabolic process	1.7E-01	5.9E-02	2.4E-01	2.1E-01	4.6E-01	9.2E-01	3.0E-02	6.9E-01	2.8E-01	2.1E-01	4.3E-02	4.2E-01

GO:0045184	GO:Bio L4	establishment of protein localization	6.2E-01	9.0E-02	1.4E-01	3.1E-02	3.7E-02	1.0E-01	5.1E-02	8.4E-01	1.1E-01	5.2E-02	4.3E-02	1.2E-01
GO:0043197	GO:Cell L4	dendritic spine	3.0E-02	2.9E-03	6.0E-02	2.8E-02	6.4E-01	4.5E-01	1.2E-01	4.6E-01	9.5E-02	9.9E-03	4.3E-02	6.7E-02
GO:0070167	GO:Bio L4	regulation of biomineral formation	1.9E-01	3.3E-02	9.8E-01	9.6E-01	4.3E-01	2.5E-01	7.5E-03	5.1E-01	2.8E-01	4.7E-02	4.3E-02	8.3E-01
GO:0048640	GO:Bio L4	negative regulation of developmental growth	2.3E-01	1.4E-01	1.9E-02	3.2E-02	1.4E-01	3.3E-01	3.9E-01	7.8E-01	1.4E-01	1.9E-01	4.4E-02	1.2E-01
GO:0006884	GO:Bio L4	cell volume homeostasis	3.7E-01	5.2E-01	5.9E-01	8.0E-01	1.2E-01	4.0E-01	1.3E-02	7.0E-01	1.9E-01	5.3E-01	4.4E-02	8.8E-01
GO:0045056	GO:Bio L4	transcytosis	2.7E-01	2.3E-01	4.0E-02	7.3E-02	5.6E-01	8.5E-01	1.9E-01	5.7E-01	4.4E-01	5.2E-01	4.4E-02	1.7E-01
GO:0005886	GO:Cell L4	plasma membrane	1.6E-01	1.3E-02	1.2E-01	5.6E-02	6.2E-01	3.4E-01	6.1E-02	1.1E-01	3.3E-01	2.9E-02	4.4E-02	3.8E-02
GO:0009896	GO:Bio L4	positive regulation of catabolic process	4.4E-02	9.7E-02	2.1E-01	2.4E-01	8.9E-01	3.9E-01	3.7E-02	5.3E-01	1.7E-01	1.6E-01	4.5E-02	3.9E-01
GO:0051704	GO:Bio L2	multi-organism process	5.5E-01	3.6E-01	1.9E-02	1.1E-02	2.0E-01	7.0E-02	4.0E-01	5.8E-01	3.6E-01	1.2E-01	4.5E-02	3.8E-02
GO:0044422	GO:Cell L2	organelle part	7.3E-01	2.1E-01	4.7E-01	2.0E-01	4.2E-01	6.9E-02	1.7E-02	5.2E-01	6.7E-01	7.5E-02	4.5E-02	3.4E-01
GO:0008287	GO:Cell L4	protein serine/threonine phosphatase complex	8.2E-01	5.8E-01	9.9E-01	8.1E-01	7.1E-01	4.3E-01	7.9E-03	4.7E-01	9.0E-01	6.0E-01	4.6E-02	7.5E-01
GO:0043324	GO:Bio L4	pigment metabolic process during developmental pigmentation	4.6E-01	6.2E-01	1.6E-01	1.1E-01	5.8E-02	5.2E-01	4.8E-02	2.3E-01	1.2E-01	6.9E-01	4.6E-02	1.2E-01
GO:0043474	GO:Bio L4	pigment metabolic process during pigmentation	4.6E-01	6.2E-01	1.6E-01	1.1E-01	5.8E-02	5.2E-01	4.8E-02	2.3E-01	1.2E-01	6.9E-01	4.6E-02	1.2E-01
GO:0019538	GO:Bio L4	protein metabolic process	8.0E-01	3.2E-01	2.3E-01	2.0E-01	4.7E-01	3.2E-01	3.3E-02	5.2E-01	7.5E-01	3.3E-01	4.6E-02	3.4E-01
GO:0031641	GO:Bio L4	regulation of myelination	1.8E-02	4.6E-02	8.3E-02	1.0E-01	9.3E-01	8.8E-01	9.5E-02	7.3E-01	8.5E-02	1.7E-01	4.6E-02	2.7E-01
3010	KEGG	Ribosome	6.1E-01	7.6E-01	8.8E-01	7.5E-01	5.8E-01	7.0E-01	8.9E-03	8.4E-01	7.2E-01	8.7E-01	4.6E-02	9.2E-01
GO:0002238	GO:Bio L4	response to molecule of fungal origin	5.3E-02	9.9E-03	3.8E-01	2.4E-01	2.2E-02	6.4E-02	2.1E-02	2.9E-01	8.9E-03	5.3E-03	4.7E-02	2.5E-01
GO:0010033	GO:Bio L4	response to organic substance	1.7E-01	1.4E-02	3.4E-01	2.2E-01	3.4E-01	1.7E-01	2.4E-02	6.1E-01	2.2E-01	1.7E-02	4.7E-02	4.1E-01
GO:0046794	GO:Bio L4	virion transport	2.8E-01	2.8E-01	1.3E-02	2.1E-02	6.1E-01	1.5E-01	6.0E-01	7.2E-01	4.7E-01	1.8E-01	4.7E-02	7.8E-02
GO:0045597	GO:Bio L4	positive regulation of cell differentiation	2.5E-01	2.9E-01	2.8E-01	3.2E-01	4.6E-01	4.1E-01	2.9E-02	9.3E-01	3.7E-01	3.7E-01	4.7E-02	6.6E-01
GO:0017119	GO:Cell L4	Golgi transport complex	9.0E-01	6.0E-01	1.0E-02	1.6E-02	5.9E-02	3.6E-02	8.1E-01	6.1E-01	2.1E-01	1.0E-01	4.7E-02	5.4E-02
GO:0021794	GO:Bio L4	thalamus development	8.5E-01	8.7E-01	8.1E-01	7.6E-01	3.3E-01	6.5E-01	1.0E-02	9.4E-01	6.3E-01	8.9E-01	4.7E-02	9.5E-01
GO:0046879	GO:Bio L4	hormone secretion	5.5E-02	5.3E-03	1.6E-01	3.0E-01	8.1E-02	6.0E-01	5.2E-02	8.0E-01	2.9E-02	2.1E-02	4.7E-02	5.8E-01
GO:0001838	GO:Bio L4	embryonic epithelial tube formation	1.6E-01	8.2E-02	1.6E-01	1.3E-01	3.6E-01	3.4E-03	5.0E-02	4.4E-01	2.2E-01	2.6E-03	4.7E-02	2.2E-01

GO:0045202	GO:Cell L2	synapse	2.5E-01	2.1E-02	1.1E-01	6.6E-02	8.2E-01	6.2E-01	7.5E-02	3.7E-01	5.4E-01	6.9E-02	4.7E-02	1.2E-01
GO:0033267	GO:Cell L4	axon part	6.4E-02	3.2E-03	1.2E-01	7.8E-02	1.1E-01	1.1E-01	6.7E-02	3.0E-01	4.3E-02	3.2E-03	4.7E-02	1.1E-01
GO:0008356	GO:Bio L4	asymmetric cell division	2.1E-01	5.5E-02	1.0E-02	3.4E-02	6.3E-01	6.6E-01	8.2E-01	2.1E-01	4.0E-01	1.6E-01	4.8E-02	4.2E-02
GO:0031253	GO:Cell L4	cell projection membrane	7.6E-01	7.2E-01	4.7E-01	2.7E-01	8.0E-02	1.8E-01	1.7E-02	2.0E-01	2.3E-01	3.9E-01	4.8E-02	2.1E-01
GO:0032838	GO:Cell L4	cell projection cytoplasm	8.7E-02	4.5E-01	5.0E-02	9.5E-02	3.4E-01	5.6E-01	1.6E-01	2.3E-02	1.3E-01	6.0E-01	4.8E-02	1.6E-02
GO:0019888	GO:Mole L4	protein phosphatase regulator activity	5.5E-01	3.0E-01	9.4E-01	9.0E-01	4.3E-01	1.4E-01	8.8E-03	8.2E-03	5.8E-01	1.7E-01	4.8E-02	4.4E-02
4614	KEGG	Renin-angiotensin system	4.4E-01	2.5E-01	3.6E-02	1.8E-02	9.0E-02	9.3E-02	2.3E-01	6.0E-01	1.7E-01	1.1E-01	4.8E-02	5.8E-02
GO:0048754	GO:Bio L4	branching morphogenesis of a tube	8.9E-01	9.1E-01	4.3E-01	3.6E-01	4.1E-02	1.5E-01	1.9E-02	1.9E-01	1.6E-01	4.1E-01	4.8E-02	2.6E-01
GO:0008092	GO:Mole L4	cytoskeletal protein binding	9.3E-03	1.1E-02	2.9E-01	2.6E-01	3.1E-01	2.5E-03	2.9E-02	9.3E-01	2.0E-02	3.1E-04	4.9E-02	5.8E-01
GO:0031668	GO:Bio L4	cellular response to extracellular stimulus	2.2E-01	4.0E-02	4.7E-01	2.6E-01	8.0E-01	3.4E-01	1.8E-02	6.4E-01	4.8E-01	7.2E-02	4.9E-02	4.7E-01
GO:0071496	GO:Bio L4	cellular response to external stimulus	2.2E-01	4.0E-02	4.7E-01	2.6E-01	8.0E-01	3.4E-01	1.8E-02	6.4E-01	4.8E-01	7.2E-02	4.9E-02	4.7E-01
GO:0016614	GO:Mole L4	oxidoreductase activity, acting on CH-OH group of donors	1.5E-01	9.2E-02	8.2E-01	7.0E-01	2.4E-01	2.0E-01	1.0E-02	8.7E-01	1.5E-01	9.3E-02	4.9E-02	9.1E-01
GO:0007618	GO:Bio L4	mating	4.5E-01	1.7E-01	2.6E-02	3.4E-02	5.2E-02	1.1E-01	3.3E-01	8.5E-01	1.1E-01	9.2E-02	4.9E-02	1.3E-01
GO:0010610	GO:Bio L4	regulation of mRNA stability involved in response to stress	2.0E-01	2.0E-01	2.4E-02	1.0E-02	8.2E-01	2.5E-01	3.6E-01	9.6E-01	4.6E-01	2.0E-01	5.0E-02	5.5E-02
4510	KEGG	Focal adhesion	4.8E-01	3.5E-01	7.8E-01	7.0E-01	1.3E-01	1.6E-01	1.1E-02	3.8E-01	2.3E-01	2.2E-01	5.0E-02	6.2E-01
GO:0019904	GO:Mole L4	protein domain specific binding	8.6E-01	7.6E-01	1.1E-01	7.2E-02	7.4E-01	5.2E-02	8.2E-02	8.6E-01	9.2E-01	1.7E-01	5.1E-02	2.3E-01
GO:0043576	GO:Bio L4	regulation of respiratory gaseous exchange	4.9E-01	2.1E-01	1.6E-01	2.2E-01	2.6E-02	2.9E-01	5.7E-02	2.6E-01	6.8E-02	2.3E-01	5.1E-02	2.2E-01
GO:0016247	GO:Mole L2	channel regulator activity	1.3E-01	1.4E-02	6.4E-02	6.6E-02	6.7E-01	5.3E-01	1.4E-01	1.7E-01	3.0E-01	4.4E-02	5.1E-02	6.3E-02
5200	KEGG	Pathways in cancer	9.5E-03	3.2E-02	3.4E-02	2.6E-01	4.6E-01	5.5E-01	2.6E-01	4.1E-01	2.8E-02	9.0E-02	5.1E-02	3.5E-01
GO:0032528	GO:Bio L4	microvillus organization	2.1E-01	1.4E-01	4.6E-01	4.1E-01	5.9E-01	5.0E-01	2.0E-02	1.7E-01	3.8E-01	2.6E-01	5.1E-02	2.6E-01
GO:0016566	GO:Mole L4	specific transcriptional repressor activity	5.2E-01	3.5E-01	1.8E-02	3.5E-02	5.3E-01	4.7E-01	4.9E-01	4.9E-01	6.3E-01	4.6E-01	5.1E-02	8.5E-02
GO:0008159	GO:Mole L4	positive transcription elongation factor activity	4.8E-01	4.1E-01	2.8E-01	5.4E-01	1.0E-01	6.1E-01	3.2E-02	7.8E-01	2.0E-01	6.0E-01	5.1E-02	7.8E-01

GO:0044260	GO:Bio L4	cellular macromolecule metabolic process	3.1E-01	2.5E-02	1.6E-01	8.7E-02	4.6E-01	4.0E-01	5.9E-02	7.6E-01	4.2E-01	5.7E-02	5.2E-02	2.4E-01
GO:0050904	GO:Bio L4	diapedesis	4.3E-01	1.9E-01	9.2E-03	9.9E-03	9.5E-01	7.9E-01	9.9E-01	7.7E-01	7.7E-01	4.3E-01	5.2E-02	4.5E-02
GO:0007005	GO:Bio L4	mitochondrion organization	9.3E-01	7.9E-01	6.0E-01	8.0E-01	1.1E-01	1.6E-03	1.6E-02	2.3E-01	3.3E-01	9.7E-03	5.3E-02	4.9E-01
GO:0032991	GO:Cell L2	macromolecular complex	3.4E-01	3.2E-02	3.9E-01	1.7E-01	2.0E-01	1.5E-02	2.4E-02	2.5E-01	2.5E-01	4.2E-03	5.3E-02	1.8E-01
GO:0045216	GO:Bio L4	cell-cell junction organization	5.9E-01	4.2E-01	6.4E-01	7.3E-01	5.2E-01	4.6E-01	1.5E-02	8.8E-01	6.7E-01	5.1E-01	5.3E-02	9.3E-01
GO:0035148	GO:Bio L4	tube formation	1.7E-01	8.7E-02	1.7E-01	1.4E-01	3.8E-01	3.6E-03	5.4E-02	4.6E-01	2.4E-01	2.8E-03	5.3E-02	2.4E-01
GO:0040015	GO:Bio L4	negative regulation of multicellular organism growth	1.7E-01	2.5E-02	3.2E-02	8.9E-02	5.0E-01	4.1E-01	2.9E-01	1.4E-01	2.9E-01	5.7E-02	5.3E-02	6.7E-02
GO:0007389	GO:Bio L4	pattern specification process	6.4E-02	6.5E-02	1.1E-01	2.8E-01	4.7E-01	8.3E-01	8.8E-02	9.6E-01	1.4E-01	2.1E-01	5.3E-02	6.2E-01
GO:0042978	GO:Mole L4	ornithine decarboxylase activator activity	5.2E-01	2.1E-01	1.3E-02	1.2E-02	2.4E-01	2.7E-01	7.3E-01	2.8E-01	3.8E-01	2.2E-01	5.4E-02	2.2E-02
GO:0070937	GO:Cell L4	CRD-mediated mRNA stability complex	2.0E-02	3.7E-02	1.5E-02	6.4E-03	3.1E-01	7.4E-01	6.2E-01	8.6E-01	3.7E-02	1.3E-01	5.4E-02	3.4E-02
GO:0051241	GO:Bio L4	negative regulation of multicellular organismal process	1.4E-01	1.2E-01	1.0E-01	2.0E-01	3.4E-01	4.2E-01	9.3E-02	6.1E-01	1.9E-01	2.1E-01	5.4E-02	3.8E-01
GO:0060688	GO:Bio L4	regulation of morphogenesis of a branching structure	1.3E-01	2.9E-01	8.3E-01	7.9E-01	4.5E-02	3.2E-02	1.1E-02	2.8E-01	3.6E-02	5.2E-02	5.4E-02	5.5E-01
GO:0005576	GO:Cell L2	extracellular region	9.1E-02	2.4E-02	1.1E-01	5.7E-02	3.4E-02	3.4E-02	8.8E-02	4.5E-01	2.1E-02	6.7E-03	5.4E-02	1.2E-01
GO:0001968	GO:Mole L4	fibronectin binding	1.6E-01	3.9E-02	1.1E-02	3.7E-03	8.6E-01	9.5E-01	9.1E-01	2.0E-01	4.1E-01	1.6E-01	5.4E-02	6.1E-03
GO:0016585	GO:Cell L4	chromatin remodeling complex	3.3E-01	1.5E-01	1.8E-02	2.0E-02	7.0E-01	6.7E-01	5.3E-01	9.3E-01	5.7E-01	3.3E-01	5.4E-02	9.3E-02
GO:0010941	GO:Bio L4	regulation of cell death	9.7E-03	3.0E-04	4.4E-02	6.7E-03	3.4E-01	4.9E-01	2.2E-01	5.5E-01	2.2E-02	1.4E-03	5.5E-02	2.4E-02
GO:0014741	GO:Bio L4	negative regulation of muscle hypertrophy	1.5E-01	3.0E-01	5.4E-02	1.6E-01	1.0E+00	9.8E-01	1.8E-01	6.3E-01	4.4E-01	6.6E-01	5.5E-02	3.3E-01
GO:0031224	GO:Cell L4	intrinsic to membrane	6.0E-01	7.0E-02	2.6E-01	1.2E-01	6.7E-01	1.4E-01	3.8E-02	1.1E-01	7.7E-01	5.6E-02	5.5E-02	7.0E-02
GO:0019062	GO:Bio L4	virion attachment to host cell surface receptor	7.1E-01	7.1E-01	1.1E-02	2.9E-02	9.0E-01	4.6E-01	8.8E-01	2.8E-01	9.2E-01	6.9E-01	5.5E-02	4.7E-02
GO:0006979	GO:Bio L4	response to oxidative stress	4.7E-01	5.0E-01	6.9E-02	9.9E-02	9.6E-01	9.2E-01	1.4E-01	3.9E-01	8.1E-01	8.2E-01	5.5E-02	1.7E-01
GO:0040012	GO:Bio L4	regulation of locomotion	3.2E-02	1.4E-02	2.7E-02	2.9E-02	1.5E-02	1.4E-01	3.7E-01	5.3E-01	4.0E-03	1.4E-02	5.5E-02	7.9E-02
GO:0005839	GO:Cell L4	proteasome core complex	4.8E-01	2.7E-01	1.2E-01	1.4E-01	3.9E-01	2.8E-01	8.3E-02	8.9E-01	5.0E-01	2.7E-01	5.6E-02	3.9E-01

GO:0031410	GO:Cell L4	cytoplasmic vesicle	8.7E-01	6.5E-01	2.6E-01	5.2E-02	4.2E-01	2.2E-01	3.8E-02	5.1E-01	7.3E-01	4.3E-01	5.6E-02	1.2E-01
GO:0030036	GO:Bio L4	actin cytoskeleton organization	6.8E-03	9.3E-03	4.1E-01	2.2E-01	8.3E-02	3.7E-03	2.5E-02	7.8E-01	4.8E-03	3.9E-04	5.7E-02	4.8E-01
GO:0044446	GO:Cell L4	intracellular organelle part	7.1E-01	2.0E-01	4.7E-01	2.1E-01	3.9E-01	6.3E-02	2.1E-02	5.3E-01	6.4E-01	6.9E-02	5.7E-02	3.6E-01
5219	KEGG	Bladder cancer	1.6E-01	4.1E-01	5.3E-02	9.9E-02	9.1E-01	2.1E-01	1.9E-01	1.7E-02	4.3E-01	3.0E-01	5.7E-02	1.2E-02
GO:0070571	GO:Bio L4	negative regulation of neuron projection regeneration	4.2E-01	2.9E-01	1.3E-01	2.1E-01	8.8E-01	3.8E-01	8.1E-02	5.4E-01	7.4E-01	3.5E-01	5.8E-02	3.6E-01
GO:0000902	GO:Bio L4	cell morphogenesis	2.6E-01	2.5E-01	1.2E-01	1.1E-01	2.4E-01	3.1E-01	9.0E-02	5.9E-01	2.4E-01	2.7E-01	5.8E-02	2.4E-01
3050	KEGG	Proteasome	2.8E-01	2.8E-01	1.3E-01	4.1E-02	7.2E-01	4.7E-01	8.3E-02	9.2E-01	5.2E-01	4.0E-01	5.8E-02	1.6E-01
GO:0019838	GO:Mole L4	growth factor binding	1.8E-01	1.9E-02	1.2E-01	2.0E-01	5.7E-01	9.9E-01	8.9E-02	4.4E-01	3.4E-01	9.2E-02	5.8E-02	3.0E-01
GO:0014051	GO:Bio L4	gamma-aminobutyric acid secretion	2.9E-01	8.9E-02	1.4E-02	9.0E-03	1.4E-01	4.8E-02	7.4E-01	6.2E-01	1.7E-01	2.7E-02	5.8E-02	3.4E-02
GO:0060152	GO:Bio L4	microtubule-based peroxisome localization	2.7E-01	1.7E-01	4.4E-01	5.4E-01	2.9E-01	6.1E-01	2.4E-02	9.7E-01	2.8E-01	3.3E-01	5.9E-02	8.7E-01
GO:0008021	GO:Cell L4	synaptic vesicle	6.7E-01	2.4E-01	6.4E-02	1.7E-02	7.2E-01	4.4E-01	1.7E-01	3.6E-01	8.3E-01	3.4E-01	5.9E-02	3.7E-02
GO:0048499	GO:Bio L4	synaptic vesicle membrane organization	2.6E-01	2.0E-01	2.6E-02	1.9E-02	6.3E-01	2.6E-01	4.1E-01	5.8E-01	4.6E-01	2.1E-01	5.9E-02	6.0E-02
GO:0030882	GO:Mole L4	lipid antigen binding	3.0E-01	1.8E-01	4.6E-02	4.9E-02	2.9E-01	3.7E-01	2.3E-01	4.3E-02	3.0E-01	2.5E-01	5.9E-02	1.5E-02
GO:0060491	GO:Bio L4	regulation of cell projection assembly	8.0E-01	6.6E-01	9.3E-01	9.6E-01	3.4E-01	7.9E-01	1.2E-02	9.2E-01	6.2E-01	8.6E-01	5.9E-02	9.9E-01
GO:0009279	GO:Cell L4	cell outer membrane	9.8E-01	7.2E-01	1.4E-01	2.1E-01	2.8E-01	5.2E-02	7.8E-02	7.9E-01	6.3E-01	1.6E-01	5.9E-02	4.7E-01
GO:0031589	GO:Bio L4	cell-substrate adhesion	4.6E-01	2.2E-01	8.6E-02	6.7E-02	4.2E-01	1.3E-01	1.2E-01	1.8E-02	5.1E-01	1.3E-01	6.0E-02	9.5E-03
GO:0032879	GO:Bio L4	regulation of localization	7.6E-02	5.0E-04	1.3E-01	1.1E-01	2.0E-02	2.7E-01	8.5E-02	5.0E-01	1.1E-02	1.3E-03	6.0E-02	2.2E-01
GO:0016849	GO:Mole L4	phosphorus-oxygen lyase activity	6.6E-01	4.2E-01	1.5E-01	1.7E-01	6.2E-01	5.1E-01	7.1E-02	6.5E-01	7.7E-01	5.4E-01	6.0E-02	3.6E-01
GO:0030278	GO:Bio L4	regulation of ossification	3.7E-01	1.1E-01	9.4E-01	9.0E-01	4.9E-01	5.6E-01	1.2E-02	4.6E-01	4.9E-01	2.4E-01	6.0E-02	7.8E-01
GO:0048853	GO:Bio L4	forebrain morphogenesis	8.7E-03	3.6E-03	2.5E-02	1.2E-02	6.2E-01	6.5E-01	4.4E-01	2.0E-01	3.4E-02	1.7E-02	6.0E-02	1.7E-02
GO:0034644	GO:Bio L4	cellular response to UV	2.5E-02	3.9E-02	3.5E-02	2.7E-02	2.7E-01	1.8E-01	3.1E-01	6.7E-01	4.0E-02	4.2E-02	6.0E-02	9.0E-02
GO:0007050	GO:Bio L4	cell cycle arrest	6.8E-01	4.9E-01	4.5E-01	4.0E-01	8.2E-01	8.8E-01	2.4E-02	8.0E-02	8.8E-01	7.9E-01	6.0E-02	1.4E-01
GO:0046692	GO:Bio L4	sperm competition	4.5E-01	3.2E-01	6.0E-02	1.0E-01	8.2E-01	3.6E-01	1.8E-01	6.2E-01	7.4E-01	3.6E-01	6.0E-02	2.4E-01
5010	KEGG	Alzheimer's disease	7.7E-01	5.3E-01	1.5E-01	1.6E-01	6.8E-01	3.2E-01	7.2E-02	6.0E-02	8.6E-01	4.7E-01	6.0E-02	5.3E-02
GO:0009889	GO:Bio L4	regulation of biosynthetic process	1.0E-01	3.9E-03	2.1E-01	9.9E-02	7.4E-02	4.7E-01	5.3E-02	8.0E-01	4.4E-02	1.3E-02	6.1E-02	2.8E-01
GO:0006944	GO:Bio L4	cellular membrane fusion	6.3E-01	1.7E-01	3.2E-02	9.3E-02	7.6E-01	3.4E-01	3.4E-01	3.3E-01	8.3E-01	2.2E-01	6.1E-02	1.4E-01

GO:0019212	GO:Mole L4	phosphatase inhibitor activity	3.8E-01	3.8E-01	7.3E-01	7.0E-01	2.0E-01	5.3E-02	1.5E-02	1.9E-03	2.7E-01	9.9E-02	6.2E-02	1.0E-02
GO:0002027	GO:Bio L4	regulation of heart rate	6.3E-01	7.1E-01	5.0E-02	2.1E-01	6.8E-01	1.9E-01	2.3E-01	4.6E-01	7.9E-01	4.0E-01	6.2E-02	3.2E-01
GO:0030308	GO:Bio L4	negative regulation of cell growth	5.9E-01	4.6E-01	3.3E-01	5.4E-01	4.3E-01	3.5E-01	3.5E-02	7.9E-01	6.0E-01	4.5E-01	6.2E-02	7.9E-01
GO:0044437	GO:Cell L4	vacuolar part	1.8E-01	4.0E-02	3.3E-01	2.8E-02	5.5E-01	3.2E-01	3.4E-02	3.0E-01	3.3E-01	6.8E-02	6.2E-02	4.8E-02
GO:0010248	GO:Bio L4	establishment or maintenance of transmembrane electrochemical gradient	3.0E-01	3.4E-01	5.3E-01	4.8E-01	1.4E-01	3.5E-01	2.1E-02	7.4E-01	1.7E-01	3.7E-01	6.2E-02	7.2E-01
GO:0045165	GO:Bio L4	cell fate commitment	9.2E-01	7.8E-01	1.2E-01	1.9E-01	6.9E-02	1.9E-01	9.6E-02	3.4E-01	2.4E-01	4.3E-01	6.2E-02	2.5E-01
GO:0040007	GO:Bio L2	growth	5.9E-01	4.3E-01	3.5E-01	4.3E-01	2.2E-01	3.8E-01	3.2E-02	8.9E-01	3.9E-01	4.6E-01	6.2E-02	7.5E-01
GO:0015197	GO:Mole L4	peptide transporter activity	4.4E-01	1.9E-01	1.0E-01	9.3E-02	8.4E-02	1.5E-01	1.1E-01	5.5E-01	1.6E-01	1.3E-01	6.2E-02	2.0E-01
GO:0032059	GO:Cell L4	bleb	3.5E-01	4.0E-01	2.4E-02	5.8E-02	4.7E-01	4.5E-01	4.8E-01	7.2E-01	4.7E-01	4.9E-01	6.3E-02	1.7E-01
GO:0031643	GO:Bio L4	positive regulation of myelination	1.5E-01	3.2E-01	6.2E-01	8.4E-01	7.8E-01	5.5E-01	1.9E-02	8.0E-01	3.7E-01	4.8E-01	6.3E-02	9.4E-01
GO:0016879	GO:Mole L4	ligase activity, forming carbon-nitrogen bonds	2.9E-02	1.3E-02	3.2E-02	1.1E-01	9.0E-01	4.3E-01	3.6E-01	4.3E-01	1.2E-01	3.5E-02	6.3E-02	1.9E-01
GO:0042734	GO:Cell L4	presynaptic membrane	3.2E-01	5.4E-01	2.3E-02	7.8E-03	1.4E-01	6.7E-01	5.0E-01	5.4E-01	1.8E-01	7.3E-01	6.4E-02	2.7E-02
GO:0030011	GO:Bio L4	maintenance of cell polarity	4.1E-01	2.4E-01	1.8E-01	2.3E-01	1.3E-01	3.2E-01	6.3E-02	4.8E-01	2.1E-01	2.8E-01	6.4E-02	3.6E-01
GO:0016043	GO:Bio L2	cellular component organization	2.7E-01	4.8E-02	3.3E-01	1.3E-01	2.0E-01	1.2E-02	3.6E-02	7.8E-01	2.2E-01	4.8E-03	6.4E-02	3.4E-01
GO:0032880	GO:Bio L4	regulation of protein localization	1.3E-01	1.0E-01	4.8E-01	2.5E-01	3.8E-01	5.4E-01	2.4E-02	6.4E-01	2.0E-01	2.1E-01	6.4E-02	4.6E-01
GO:0051380	GO:Mole L4	norepinephrine binding	6.7E-02	1.3E-02	5.6E-02	1.2E-01	6.5E-01	2.1E-01	2.1E-01	1.4E-01	1.8E-01	1.9E-02	6.4E-02	8.7E-02
GO:0031646	GO:Bio L4	positive regulation of neurological system process	1.6E-02	6.2E-03	1.0E-01	1.2E-01	2.3E-01	9.4E-02	1.2E-01	6.3E-01	2.4E-02	4.9E-03	6.4E-02	2.7E-01
GO:0060044	GO:Bio L4	negative regulation of cardiac muscle cell proliferation	5.2E-03	2.7E-02	5.8E-01	4.7E-01	3.5E-02	1.3E-01	2.1E-02	3.5E-01	1.7E-03	2.3E-02	6.5E-02	4.6E-01
GO:0004016	GO:Mole L4	adenylate cyclase activity	7.6E-01	2.8E-01	7.4E-02	1.2E-01	8.5E-01	9.6E-01	1.6E-01	9.1E-01	9.3E-01	6.2E-01	6.5E-02	3.5E-01
GO:0002832	GO:Bio L4	negative regulation of response to biotic stimulus	1.6E-01	1.3E-02	1.2E-02	3.7E-02	6.8E-01	9.2E-01	9.8E-01	9.6E-01	3.5E-01	6.6E-02	6.6E-02	1.5E-01
GO:0050687	GO:Bio L4	negative regulation of defense response to virus	1.6E-01	1.3E-02	1.2E-02	3.7E-02	6.8E-01	9.2E-01	9.8E-01	9.6E-01	3.5E-01	6.6E-02	6.6E-02	1.5E-01

GO:0030048	GO:Bio L4	actin filament-based movement	9.7E-03	4.8E-03	9.3E-02	1.3E-01	4.4E-01	5.3E-01	1.3E-01	2.7E-01	2.7E-02	1.8E-02	6.6E-02	1.5E-01
PA165111376	PharmGKB	pgkb_pwy_Benzodiazepinepathway_PD	6.5E-01	6.4E-01	1.9E-01	2.2E-01	4.3E-01	5.2E-01	6.3E-02	3.9E-01	6.4E-01	6.9E-01	6.6E-02	2.9E-01
GO:0006818	GO:Bio L4	hydrogen transport	7.6E-01	6.5E-01	3.2E-01	6.9E-02	3.8E-01	4.4E-01	3.8E-02	2.3E-01	6.5E-01	6.5E-01	6.6E-02	8.1E-02
GO:0033043	GO:Bio L4	regulation of organelle organization	2.2E-01	3.9E-02	4.6E-01	3.4E-01	4.2E-03	9.0E-04	2.6E-02	7.6E-01	7.5E-03	4.0E-04	6.6E-02	6.1E-01
GO:0003704	GO:Mole L4	specific RNA polymerase II transcription factor activity	2.7E-01	2.0E-01	3.1E-01	4.1E-01	9.0E-02	1.7E-01	4.0E-02	6.3E-01	1.1E-01	1.5E-01	6.6E-02	6.1E-01
GO:0034708	GO:Cell L4	methyltransferase complex	7.3E-01	1.4E-01	2.2E-01	7.7E-02	5.1E-01	6.6E-01	5.7E-02	2.6E-01	7.3E-01	3.2E-01	6.6E-02	9.9E-02
GO:0007565	GO:Bio L4	female pregnancy	5.4E-01	7.5E-01	2.7E-02	5.5E-02	9.7E-01	4.6E-01	4.5E-01	1.6E-01	8.6E-01	7.1E-01	6.7E-02	5.1E-02
GO:0048598	GO:Bio L4	embryonic morphogenesis	2.1E-01	3.2E-01	1.1E-01	2.2E-01	6.9E-02	9.2E-02	1.1E-01	7.9E-01	7.6E-02	1.3E-01	6.7E-02	4.8E-01
GO:0045185	GO:Bio L4	maintenance of protein location	3.1E-01	3.0E-01	3.2E-01	3.4E-01	5.5E-01	1.9E-01	3.9E-02	6.2E-01	4.8E-01	2.2E-01	6.7E-02	5.4E-01
GO:0030426	GO:Cell L4	growth cone	2.0E-01	2.5E-01	1.3E-01	3.3E-02	7.1E-02	1.2E-01	9.2E-02	5.7E-01	7.6E-02	1.4E-01	6.7E-02	9.3E-02
GO:0001568	GO:Bio L4	blood vessel development	1.4E-01	1.0E-01	2.3E-02	1.7E-02	7.0E-01	2.9E-01	5.5E-01	5.9E-01	3.2E-01	1.4E-01	6.7E-02	5.5E-02
GO:0032403	GO:Mole L4	protein complex binding	6.1E-02	2.9E-03	2.9E-02	3.9E-02	2.6E-01	4.2E-01	4.4E-01	9.0E-02	8.2E-02	9.3E-03	6.8E-02	2.3E-02
GO:0030894	GO:Cell L4	replisome	6.5E-01	4.9E-01	3.1E-01	3.3E-01	6.1E-01	3.2E-01	4.1E-02	5.5E-01	7.7E-01	4.4E-01	6.8E-02	4.9E-01
GO:0061025	GO:Bio L4	membrane fusion	6.5E-01	1.8E-01	3.5E-02	1.0E-01	7.8E-01	3.5E-01	3.6E-01	3.4E-01	8.5E-01	2.4E-01	6.8E-02	1.5E-01
GO:0008154	GO:Bio L4	actin polymerization or depolymerization	1.7E-01	9.7E-02	9.6E-02	8.1E-02	9.6E-02	6.9E-03	1.3E-01	9.7E-01	8.4E-02	5.6E-03	6.9E-02	2.8E-01
GO:0009914	GO:Bio L4	hormone transport	7.5E-02	8.2E-03	1.9E-01	3.5E-01	1.0E-01	6.6E-01	6.8E-02	8.3E-01	4.5E-02	3.4E-02	7.0E-02	6.5E-01
GO:0048069	GO:Bio L4	eye pigmentation	5.1E-01	6.7E-01	2.0E-01	1.4E-01	7.7E-02	6.1E-01	6.5E-02	2.8E-01	1.7E-01	7.8E-01	7.0E-02	1.6E-01
GO:0002249	GO:Bio L4	lymphocyte anergy	5.9E-02	1.1E-01	4.5E-02	1.4E-01	9.0E-01	8.8E-01	2.9E-01	3.6E-02	2.1E-01	3.2E-01	7.0E-02	3.1E-02
GO:0019076	GO:Bio L4	release of virus from host	3.4E-01	6.7E-01	4.9E-01	3.7E-01	7.5E-01	9.6E-01	2.7E-02	5.1E-01	6.0E-01	9.3E-01	7.0E-02	5.0E-01
GO:0050858	GO:Bio L4	negative regulation of antigen receptor-mediated signaling pathway	8.5E-02	1.0E-01	2.5E-02	6.8E-02	1.1E-01	2.2E-01	5.2E-01	5.9E-02	5.4E-02	1.1E-01	7.0E-02	2.6E-02
GO:0003002	GO:Bio L4	regionalization	9.3E-02	1.1E-01	2.2E-01	5.7E-01	8.0E-01	9.4E-01	6.0E-02	9.6E-01	2.7E-01	3.5E-01	7.0E-02	8.8E-01
GO:0030021	GO:Mole L4	extracellular matrix structural constituent conferring compression resistance	5.3E-01	9.9E-01	8.2E-01	7.1E-01	2.8E-01	3.4E-01	1.6E-02	2.8E-01	4.3E-01	7.0E-01	7.0E-02	5.2E-01
GO:0009994	GO:Bio L4	oocyte differentiation	4.4E-01	9.3E-02	1.6E-01	1.2E-01	5.8E-01	3.3E-01	8.0E-02	5.0E-02	6.0E-01	1.4E-01	7.0E-02	3.7E-02
GO:0002133	GO:Cell L4	polycystin complex	7.3E-01	7.4E-01	3.3E-01	4.1E-01	3.6E-01	4.1E-02	4.0E-02	2.6E-01	6.1E-01	1.4E-01	7.0E-02	3.5E-01

GO:0022891	GO:Mole L4	substrate-specific transmembrane transporter activity	2.3E-01	1.6E-01	5.1E-01	2.8E-01	6.2E-01	6.9E-02	2.6E-02	4.4E-01	4.3E-01	6.0E-02	7.1E-02	3.9E-01
GO:0045110	GO:Bio L4	intermediate filament bundle assembly	1.6E-01	5.7E-01	5.6E-01	4.7E-01	1.8E-01	3.0E-01	2.4E-02	2.3E-01	1.3E-01	4.7E-01	7.2E-02	3.4E-01
GO:0001955	GO:Bio L4	blood vessel maturation	9.3E-01	8.4E-01	2.6E-02	2.8E-02	3.2E-01	8.5E-01	5.1E-01	2.2E-01	6.6E-01	9.5E-01	7.2E-02	3.7E-02
GO:0018993	GO:Bio L4	somatic sex determination	1.0E+00	9.8E-01	6.2E-02	8.4E-02	9.5E-01	4.9E-01	2.2E-01	4.0E-01	1.0E+00	8.3E-01	7.2E-02	1.5E-01
GO:0019835	GO:Bio L4	cytolysis	2.8E-01	1.4E-01	4.1E-01	4.4E-01	5.4E-01	7.5E-01	3.3E-02	8.1E-01	4.3E-01	3.4E-01	7.2E-02	7.3E-01
4120	KEGG	Ubiquitin mediated proteolysis	1.8E-01	1.3E-01	2.7E-02	1.4E-01	7.3E-01	6.8E-01	5.0E-01	3.9E-01	3.9E-01	3.0E-01	7.2E-02	2.1E-01
GO:0030900	GO:Bio L4	forebrain development	1.8E-01	4.3E-02	1.3E-01	4.9E-02	1.3E-01	4.3E-01	1.1E-01	9.4E-01	1.1E-01	9.3E-02	7.2E-02	1.9E-01
GO:0005774	GO:Cell L4	vacuolar membrane	1.9E-01	5.2E-02	2.7E-01	2.1E-02	5.0E-01	2.6E-01	5.0E-02	3.4E-01	3.2E-01	7.3E-02	7.2E-02	4.2E-02
GO:0007281	GO:Bio L4	germ cell development	7.3E-01	2.0E-01	6.2E-02	9.5E-02	9.8E-01	5.7E-01	2.2E-01	3.6E-01	9.5E-01	3.6E-01	7.3E-02	1.5E-01
GO:0016504	GO:Mole L4	peptidase activator activity	1.2E-01	3.0E-02	3.1E-02	3.7E-02	1.9E-01	4.0E-01	4.4E-01	6.9E-01	1.0E-01	6.6E-02	7.3E-02	1.2E-01
GO:0006935	GO:Bio L4	chemotaxis	3.0E-02	7.1E-02	5.8E-02	1.1E-02	1.3E-01	6.3E-02	2.4E-01	2.1E-01	2.6E-02	2.9E-02	7.3E-02	1.6E-02
GO:0042330	GO:Bio L4	taxis	3.0E-02	7.1E-02	5.8E-02	1.1E-02	1.3E-01	6.3E-02	2.4E-01	2.1E-01	2.6E-02	2.9E-02	7.3E-02	1.6E-02
GO:0046782	GO:Bio L4	regulation of viral transcription	1.4E-01	1.7E-01	3.1E-01	6.1E-01	4.1E-01	1.7E-01	4.6E-02	1.0E-01	2.3E-01	1.3E-01	7.3E-02	2.4E-01
GO:0002024	GO:Bio L4	diet induced thermogenesis	6.6E-02	1.3E-02	4.6E-02	1.1E-01	4.2E-02	3.0E-01	3.0E-01	2.1E-01	1.9E-02	2.6E-02	7.4E-02	1.1E-01
GO:0021846	GO:Bio L4	cell proliferation in forebrain	9.0E-01	3.8E-01	7.0E-02	2.7E-02	7.8E-01	7.8E-01	2.0E-01	5.0E-01	9.5E-01	6.5E-01	7.4E-02	7.2E-02
4260	KEGG	Cardiac muscle contraction	1.8E-01	1.5E-01	2.3E-02	1.6E-02	6.1E-01	2.2E-01	6.0E-01	1.2E-01	3.5E-01	1.5E-01	7.4E-02	1.4E-02
GO:0048859	GO:Bio L4	formation of anatomical boundary	6.5E-01	7.2E-01	4.9E-02	9.4E-02	4.3E-01	5.4E-01	2.9E-01	9.6E-01	6.3E-01	7.6E-01	7.4E-02	3.1E-01
GO:0003001	GO:Bio L4	generation of a signal involved in cell-cell signaling	1.7E-01	1.2E-02	1.5E-01	2.4E-01	3.6E-02	1.8E-01	9.2E-02	8.6E-01	3.7E-02	1.6E-02	7.4E-02	5.3E-01
GO:0030427	GO:Cell L4	site of polarized growth	2.1E-01	2.4E-01	1.4E-01	3.5E-02	6.7E-02	1.3E-01	9.8E-02	5.9E-01	7.5E-02	1.4E-01	7.4E-02	1.0E-01
GO:0003103	GO:Bio L4	positive regulation of diuresis	1.9E-01	2.9E-01	9.5E-02	2.6E-02	8.1E-01	6.9E-01	1.5E-01	9.1E-01	4.4E-01	5.2E-01	7.5E-02	1.1E-01
GO:0017147	GO:Mole L4	Wnt-protein binding	2.2E-01	4.2E-02	2.9E-02	4.9E-02	2.8E-01	1.7E-01	4.9E-01	1.9E-01	2.3E-01	4.3E-02	7.5E-02	5.2E-02
GO:0032886	GO:Bio L4	regulation of microtubule-based process	4.1E-01	2.6E-01	5.6E-01	5.1E-01	4.6E-01	3.9E-01	2.6E-02	7.8E-01	5.0E-01	3.3E-01	7.5E-02	7.6E-01
GO:0032797	GO:Cell L4	SMN complex	6.9E-02	2.5E-01	5.7E-02	1.0E-02	1.1E-01	1.3E-01	2.6E-01	4.8E-01	4.6E-02	1.4E-01	7.6E-02	3.1E-02
GO:0031344	GO:Bio L4	regulation of cell projection organization	3.2E-01	8.4E-02	5.6E-01	5.3E-01	1.6E-01	8.8E-01	2.6E-02	9.8E-01	2.1E-01	2.7E-01	7.6E-02	8.6E-01
GO:0051775	GO:Bio L4	response to redox state	9.9E-02	8.6E-02	2.1E-01	1.6E-01	2.8E-01	4.3E-01	7.0E-02	7.3E-01	1.3E-01	1.6E-01	7.6E-02	3.7E-01

GO:0032989	GO:Bio L4	cellular component morphogenesis	2.5E-01	2.8E-01	1.3E-01	1.4E-01	2.4E-01	1.9E-01	1.2E-01	6.2E-01	2.3E-01	2.1E-01	7.6E-02	2.9E-01
GO:0031095	GO:Cell L4	platelet dense tubular network membrane	3.1E-01	5.6E-01	7.0E-01	6.1E-01	8.6E-01	8.7E-01	2.1E-02	2.7E-01	6.2E-01	8.3E-01	7.7E-02	4.7E-01
GO:0030529	GO:Cell L4	ribonucleoprotein complex	6.1E-01	3.8E-01	1.1E-01	2.0E-01	5.3E-01	6.0E-01	1.3E-01	3.1E-01	6.9E-01	5.7E-01	7.7E-02	2.4E-01
GO:0019226	GO:Bio L4	transmission of nerve impulse	1.9E-01	6.3E-03	5.9E-02	3.0E-02	5.9E-01	3.3E-01	2.5E-01	1.4E-01	3.5E-01	1.5E-02	7.7E-02	2.7E-02
4810	KEGG	Regulation of actin cytoskeleton	6.1E-01	3.5E-01	3.3E-01	3.7E-01	7.0E-02	1.6E-01	4.5E-02	2.9E-01	1.8E-01	2.2E-01	7.7E-02	3.5E-01
GO:0005215	GO:Mole L2	transporter activity	3.2E-01	5.4E-02	4.1E-01	1.0E-01	5.7E-01	9.6E-02	3.6E-02	2.9E-01	5.0E-01	3.2E-02	7.7E-02	1.3E-01
GO:0007308	GO:Bio L4	oocyte construction	9.5E-01	9.9E-01	5.4E-01	5.5E-01	5.7E-01	6.9E-01	2.7E-02	3.9E-02	8.7E-01	9.4E-01	7.7E-02	1.0E-01
GO:0007309	GO:Bio L4	oocyte axis specification	9.5E-01	9.9E-01	5.4E-01	5.5E-01	5.7E-01	6.9E-01	2.7E-02	3.9E-02	8.7E-01	9.4E-01	7.7E-02	1.0E-01
GO:0006949	GO:Bio L4	syncytium formation	2.3E-01	2.7E-01	1.0E-01	2.2E-01	8.5E-02	4.1E-01	1.5E-01	2.2E-01	9.8E-02	3.6E-01	7.8E-02	1.9E-01
5110	KEGG	Vibrio cholerae infection	6.7E-01	7.9E-01	3.1E-01	4.7E-01	5.0E-01	4.8E-01	4.8E-02	6.8E-01	7.0E-01	7.4E-01	7.8E-02	6.8E-01
GO:0070633	GO:Bio L4	transepithelial transport	3.2E-01	2.8E-01	1.7E-01	1.8E-01	6.2E-01	8.4E-01	8.9E-02	8.5E-01	5.2E-01	5.8E-01	7.8E-02	4.4E-01
GO:0065003	GO:Bio L4	macromolecular complex assembly	5.0E-01	3.2E-01	4.4E-01	1.1E-01	1.2E-02	3.4E-03	3.4E-02	6.8E-01	3.7E-02	8.5E-03	7.8E-02	2.6E-01
GO:0046849	GO:Bio L4	bone remodeling	1.0E-01	1.9E-02	2.5E-01	2.7E-01	1.6E-01	5.0E-01	6.1E-02	6.2E-01	8.3E-02	5.4E-02	7.9E-02	4.6E-01
GO:0009787	GO:Bio L4	regulation of abscisic acid mediated signaling pathway	4.2E-02	2.2E-01	4.9E-02	2.5E-01	6.5E-01	6.7E-01	3.1E-01	2.4E-01	1.3E-01	4.2E-01	7.9E-02	2.3E-01
GO:0009789	GO:Bio L4	positive regulation of abscisic acid mediated signaling pathway	4.2E-02	2.2E-01	4.9E-02	2.5E-01	6.5E-01	6.7E-01	3.1E-01	2.4E-01	1.3E-01	4.2E-01	7.9E-02	2.3E-01
GO:0044057	GO:Bio L4	regulation of system process	2.2E-01	2.0E-02	1.9E-01	2.5E-01	1.4E-01	2.4E-01	8.2E-02	7.3E-01	1.4E-01	3.0E-02	7.9E-02	5.0E-01
GO:0000149	GO:Mole L4	SNARE binding	7.6E-01	4.2E-01	2.5E-02	9.7E-03	7.2E-01	7.5E-01	6.2E-01	3.7E-01	8.8E-01	6.8E-01	7.9E-02	2.4E-02
GO:0010648	GO:Bio L4	negative regulation of cell communication	3.2E-01	7.9E-02	2.6E-01	2.0E-01	1.1E-01	1.4E-01	6.0E-02	7.3E-01	1.5E-01	6.0E-02	8.0E-02	4.3E-01
GO:0023057	GO:Bio L4	negative regulation of signaling process	4.1E-01	7.8E-02	3.8E-01	2.6E-01	2.0E-01	2.1E-01	4.2E-02	6.8E-01	2.9E-01	8.3E-02	8.1E-02	4.8E-01
GO:0030008	GO:Cell L4	TRAPP complex	8.9E-01	8.2E-01	5.4E-01	7.5E-01	5.9E-01	1.3E-01	2.9E-02	5.6E-02	8.6E-01	3.5E-01	8.1E-02	1.7E-01
GO:0015002	GO:Mole L4	heme-copper terminal oxidase activity	7.0E-01	5.2E-01	1.1E-01	8.8E-02	4.8E-01	5.3E-01	1.4E-01	6.2E-01	7.0E-01	6.3E-01	8.1E-02	2.1E-01
GO:0016675	GO:Mole L4	oxidoreductase activity, acting on heme group of donors	7.0E-01	5.2E-01	1.1E-01	8.8E-02	4.8E-01	5.3E-01	1.4E-01	6.2E-01	7.0E-01	6.3E-01	8.1E-02	2.1E-01
GO:0016998	GO:Bio L4	cell wall macromolecule catabolic process	4.1E-01	7.0E-01	1.2E-01	3.2E-01	1.1E-01	7.1E-01	1.3E-01	8.9E-01	1.8E-01	8.5E-01	8.1E-02	6.4E-01

GO:0040030	GO:Bio L4	regulation of molecular function, epigenetic	1.2E-01	2.2E-01	4.5E-01	4.3E-01	2.0E-01	5.3E-01	3.5E-02	7.5E-01	1.1E-01	3.7E-01	8.1E-02	6.9E-01
GO:0070887	GO:Bio L4	cellular response to chemical stimulus	4.4E-01	1.0E-01	2.9E-01	1.4E-01	6.9E-02	2.9E-02	5.5E-02	7.1E-01	1.3E-01	2.0E-02	8.1E-02	3.2E-01
GO:0050809	GO:Mole L4	diazepam binding	1.9E-01	2.9E-01	9.3E-02	1.3E-01	3.1E-01	4.4E-01	1.7E-01	1.9E-01	2.3E-01	3.9E-01	8.1E-02	1.1E-01
GO:0046136	GO:Bio L4	positive regulation of vitamin metabolic process	5.2E-03	1.4E-02	3.8E-02	3.4E-02	9.3E-01	5.9E-01	4.2E-01	1.1E-01	3.1E-02	4.8E-02	8.2E-02	2.5E-02
GO:0032891	GO:Bio L4	negative regulation of organic acid transport	9.0E-02	4.5E-02	1.0E-01	8.4E-02	4.7E-02	4.9E-02	1.6E-01	3.6E-01	2.7E-02	1.6E-02	8.2E-02	1.4E-01
GO:0010494	GO:Cell L4	stress granule	6.4E-01	5.1E-01	2.1E-02	2.4E-02	1.8E-01	4.2E-01	7.7E-01	5.1E-01	3.6E-01	5.5E-01	8.2E-02	6.6E-02
GO:0044283	GO:Bio L4	small molecule biosynthetic process	4.8E-02	2.9E-03	6.7E-02	5.6E-02	6.6E-02	4.6E-01	2.4E-01	2.4E-01	2.1E-02	1.0E-02	8.3E-02	7.1E-02
GO:0048382	GO:Bio L4	mesendoderm development	7.1E-01	7.4E-01	3.8E-02	1.1E-01	3.1E-01	2.4E-01	4.3E-01	9.2E-01	5.5E-01	4.8E-01	8.3E-02	3.3E-01
GO:0034622	GO:Bio L4	cellular macromolecular complex assembly	4.9E-01	3.6E-01	2.2E-01	1.3E-01	1.5E-02	1.7E-02	7.3E-02	9.2E-01	4.3E-02	3.7E-02	8.4E-02	3.7E-01
GO:0001763	GO:Bio L4	morphogenesis of a branching structure	8.8E-01	9.4E-01	4.8E-01	3.7E-01	3.8E-02	1.9E-01	3.4E-02	2.6E-01	1.5E-01	4.8E-01	8.4E-02	3.2E-01
GO:0070169	GO:Bio L4	positive regulation of biomineral formation	9.7E-02	1.5E-02	8.7E-01	7.8E-01	5.3E-01	4.6E-01	1.9E-02	5.2E-01	2.0E-01	4.0E-02	8.4E-02	7.7E-01
GO:0000307	GO:Cell L4	cyclin-dependent protein kinase holoenzyme complex	8.0E-01	4.4E-01	2.2E-02	4.6E-02	2.1E-01	6.0E-01	7.7E-01	3.5E-01	4.7E-01	6.1E-01	8.5E-02	8.3E-02
GO:0000835	GO:Cell L4	ER ubiquitin ligase complex	2.9E-01	8.3E-01	7.1E-01	8.1E-01	1.0E-01	7.1E-02	2.4E-02	1.1E-01	1.3E-01	2.3E-01	8.5E-02	3.0E-01
GO:0040008	GO:Bio L4	regulation of growth	2.7E-01	3.6E-01	5.1E-01	7.8E-01	3.5E-01	2.8E-01	3.3E-02	7.1E-01	3.2E-01	3.3E-01	8.6E-02	8.8E-01
4630	KEGG	Jak-STAT signaling pathway	7.1E-02	1.9E-01	3.1E-02	5.7E-02	7.4E-01	9.1E-01	5.5E-01	5.9E-02	2.1E-01	4.7E-01	8.6E-02	2.2E-02
GO:0051222	GO:Bio L4	positive regulation of protein transport	3.7E-02	3.9E-02	3.1E-01	1.4E-01	1.3E-01	4.3E-01	5.5E-02	8.1E-01	3.0E-02	8.6E-02	8.7E-02	3.6E-01
GO:0000768	GO:Bio L4	syncytium formation by plasma membrane fusion	2.1E-01	2.4E-01	9.3E-02	2.0E-01	7.7E-02	4.3E-01	1.9E-01	2.0E-01	8.3E-02	3.4E-01	8.7E-02	1.7E-01
GO:0010948	GO:Bio L4	negative regulation of cell cycle process	8.0E-01	8.2E-01	6.1E-01	4.9E-01	1.9E-01	2.0E-01	2.9E-02	6.2E-01	4.4E-01	4.6E-01	8.8E-02	6.7E-01
GO:0005057	GO:Mole L4	receptor signaling protein activity	1.3E-01	1.6E-01	1.5E-01	3.9E-01	7.0E-01	7.7E-02	1.2E-01	4.6E-01	3.0E-01	6.6E-02	8.8E-02	4.9E-01
GO:0003705	GO:Mole L4	RNA polymerase II transcription factor activity, enhancer binding	3.0E-01	6.2E-01	4.7E-02	6.8E-02	9.0E-01	6.1E-01	3.7E-01	7.3E-01	6.2E-01	7.5E-01	8.8E-02	2.0E-01
GO:0005903	GO:Cell L4	brush border	1.9E-01	9.5E-02	1.6E-01	7.8E-02	4.9E-01	6.7E-01	1.1E-01	1.8E-01	3.1E-01	2.4E-01	8.8E-02	7.3E-02

GO:0050906	GO:Bio L4	detection of stimulus involved in sensory perception	5.2E-01	4.6E-01	5.5E-01	7.4E-01	9.6E-01	9.6E-01	3.2E-02	4.8E-01	8.5E-01	8.0E-01	8.8E-02	7.2E-01
GO:0033588	GO:Cell L4	Elongator holoenzyme complex	7.5E-01	6.6E-01	3.6E-01	3.2E-01	8.6E-01	6.7E-01	4.9E-02	2.9E-02	9.3E-01	8.0E-01	8.8E-02	5.2E-02
GO:0044433	GO:Cell L4	cytoplasmic vesicle part	8.2E-01	9.6E-01	5.5E-01	4.6E-01	3.3E-01	3.9E-01	3.2E-02	3.6E-01	6.3E-01	7.4E-01	8.8E-02	4.7E-01
GO:0031974	GO:Cell L2	membrane-enclosed lumen	3.1E-01	2.1E-01	1.2E-01	2.7E-02	8.2E-01	7.9E-01	1.5E-01	6.2E-01	6.0E-01	4.7E-01	8.8E-02	8.5E-02
GO:0000139	GO:Cell L4	Golgi membrane	4.0E-01	6.5E-02	2.4E-01	3.7E-01	6.4E-01	6.0E-01	7.4E-02	2.5E-01	6.1E-01	1.6E-01	8.9E-02	3.1E-01
GO:0060323	GO:Bio L4	head morphogenesis	1.9E-01	4.0E-01	9.5E-02	9.9E-02	8.4E-01	8.5E-01	1.8E-01	5.1E-01	4.6E-01	7.1E-01	8.9E-02	2.0E-01
GO:0050434	GO:Bio L4	positive regulation of viral transcription	7.8E-02	8.8E-02	8.5E-01	7.5E-01	4.0E-01	9.2E-02	2.1E-02	6.6E-02	1.4E-01	4.7E-02	8.9E-02	2.0E-01
GO:0005198	GO:Mole L2	structural molecule activity	2.8E-01	2.6E-01	4.9E-01	2.9E-01	6.7E-01	7.3E-01	3.6E-02	9.0E-01	5.1E-01	5.1E-01	8.9E-02	6.1E-01
GO:0009368	GO:Cell L4	endopeptidase Clp complex	2.9E-01	2.1E-01	3.9E-01	4.6E-01	8.7E-02	4.8E-02	4.6E-02	5.3E-01	1.2E-01	5.6E-02	9.0E-02	5.9E-01
GO:0031175	GO:Bio L4	neuron projection development	3.5E-01	1.2E-01	1.0E-01	8.3E-02	2.0E-01	4.1E-01	1.8E-01	5.7E-01	2.6E-01	2.0E-01	9.0E-02	1.9E-01
GO:0043233	GO:Cell L4	organelle lumen	3.2E-01	2.7E-01	1.2E-01	3.5E-02	8.1E-01	7.6E-01	1.5E-01	5.9E-01	6.0E-01	5.3E-01	9.0E-02	1.0E-01
100	KEGG	Steroid biosynthesis	6.6E-01	7.8E-01	6.2E-01	6.5E-01	7.1E-01	3.8E-01	2.9E-02	6.2E-01	8.2E-01	6.5E-01	9.0E-02	7.7E-01
GO:0043242	GO:Bio L4	negative regulation of protein complex disassembly	1.9E-01	6.7E-02	5.7E-01	3.7E-01	9.9E-02	9.2E-03	3.2E-02	6.9E-01	9.4E-02	5.1E-03	9.0E-02	6.0E-01
GO:0016860	GO:Mole L4	intramolecular oxidoreductase activity	7.2E-01	5.2E-01	3.1E-01	2.1E-01	6.3E-01	8.4E-01	5.8E-02	2.1E-01	8.1E-01	8.0E-01	9.1E-02	1.8E-01
4146	KEGG	Peroxisome	7.1E-01	4.0E-01	4.1E-01	2.2E-01	1.2E-01	1.6E-02	4.5E-02	2.4E-01	2.9E-01	3.9E-02	9.2E-02	2.1E-01
5213	KEGG	Endometrial cancer	4.0E-01	6.6E-01	8.5E-01	8.8E-01	4.3E-01	3.9E-01	2.2E-02	4.2E-02	4.7E-01	6.1E-01	9.3E-02	1.6E-01
GO:0007290	GO:Bio L4	spermatid nucleus elongation	1.1E-01	8.6E-02	6.5E-01	6.5E-01	3.0E-01	2.2E-01	2.9E-02	1.8E-01	1.5E-01	9.3E-02	9.3E-02	3.7E-01
GO:0070424	GO:Bio L4	regulation of nucleotide-binding oligomerization domain containing signaling pathway	2.6E-01	2.2E-01	5.4E-02	7.7E-02	6.8E-02	1.8E-01	3.5E-01	1.0E-01	8.8E-02	1.6E-01	9.3E-02	4.6E-02
GO:0070426	GO:Bio L4	positive regulation of nucleotide-binding oligomerization domain containing signaling pathway	2.6E-01	2.2E-01	5.4E-02	7.7E-02	6.8E-02	1.8E-01	3.5E-01	1.0E-01	8.8E-02	1.6E-01	9.3E-02	4.6E-02
4062	KEGG	Chemokine signaling pathway	3.4E-02	5.5E-02	4.2E-01	3.0E-01	2.1E-01	6.8E-02	4.4E-02	5.0E-01	4.2E-02	2.5E-02	9.3E-02	4.4E-01
GO:0043236	GO:Mole L4	laminin binding	5.2E-01	6.1E-01	3.5E-01	1.4E-01	6.9E-01	7.1E-01	5.4E-02	3.7E-01	7.2E-01	8.0E-01	9.3E-02	2.0E-01
GO:0043366	GO:Bio L4	beta selection	5.6E-01	3.8E-01	3.9E-01	3.5E-01	5.6E-01	2.4E-01	4.8E-02	9.3E-01	6.8E-01	3.1E-01	9.4E-02	6.9E-01

GO:0030027	GO:Cell L4	lamellipodium	6.2E-01	5.8E-01	7.0E-01	3.8E-01	5.3E-01	7.9E-02	2.7E-02	7.7E-01	6.9E-01	1.9E-01	9.4E-02	6.5E-01
GO:0043901	GO:Bio L4	negative regulation of multi-organism process	2.4E-01	2.1E-02	1.9E-02	3.8E-02	8.1E-01	9.8E-01	1.0E+00	9.6E-01	5.1E-01	1.0E-01	9.4E-02	1.6E-01
GO:0010469	GO:Bio L4	regulation of receptor activity	4.4E-01	4.5E-01	2.4E-01	5.9E-01	3.3E-01	1.1E-01	8.1E-02	7.1E-01	4.2E-01	1.9E-01	9.4E-02	7.9E-01
GO:0044455	GO:Cell L4	mitochondrial membrane part	9.2E-01	6.7E-01	6.3E-01	6.4E-01	6.7E-01	4.2E-01	3.0E-02	1.8E-01	9.1E-01	6.4E-01	9.4E-02	3.6E-01
GO:0043560	GO:Mole L4	insulin receptor substrate binding	1.3E-01	1.6E-01	8.4E-02	3.9E-02	4.7E-01	7.7E-01	2.3E-01	6.9E-01	2.3E-01	3.8E-01	9.4E-02	1.2E-01
GO:0019080	GO:Bio L4	viral genome expression	1.7E-01	2.0E-01	3.5E-01	6.7E-01	4.6E-01	2.0E-01	5.5E-02	1.2E-01	2.8E-01	1.7E-01	9.5E-02	2.9E-01
5120	KEGG	Epithelial cell signaling in Helicobacter pylori infection	8.3E-01	9.7E-01	9.8E-01	8.4E-01	3.6E-01	3.3E-01	2.0E-02	6.6E-01	6.6E-01	6.9E-01	9.5E-02	8.8E-01
GO:0072093	GO:Bio L4	metanephric renal vesicle formation	7.2E-01	3.5E-01	5.8E-02	5.5E-02	7.4E-02	6.1E-02	3.3E-01	5.1E-01	2.1E-01	1.0E-01	9.5E-02	1.3E-01
GO:0000086	GO:Bio L4	G2/M transition of mitotic cell cycle	8.4E-02	3.4E-01	4.6E-02	6.6E-02	4.0E-01	5.9E-01	4.2E-01	1.7E-01	1.5E-01	5.2E-01	9.5E-02	6.2E-02
GO:0071554	GO:Bio L2	cell wall organization or biogenesis	4.4E-01	7.3E-01	1.3E-01	3.5E-01	1.2E-01	7.4E-01	1.5E-01	8.3E-01	2.1E-01	8.8E-01	9.5E-02	6.4E-01
GO:0044036	GO:Bio L4	cell wall macromolecule metabolic process	4.4E-01	7.3E-01	1.3E-01	3.5E-01	1.2E-01	7.4E-01	1.5E-01	8.3E-01	2.1E-01	8.8E-01	9.5E-02	6.4E-01
GO:0021915	GO:Bio L4	neural tube development	1.2E-01	6.5E-02	1.4E-01	7.2E-02	2.8E-01	7.4E-03	1.3E-01	4.9E-01	1.5E-01	4.2E-03	9.5E-02	1.5E-01
GO:0043169	GO:Mole L4	cation binding	3.4E-01	2.1E-02	3.8E-01	1.2E-01	2.1E-01	2.2E-01	5.1E-02	2.5E-01	2.6E-01	2.9E-02	9.5E-02	1.3E-01
GO:0014850	GO:Bio L4	response to muscle activity	1.1E-01	2.1E-01	2.4E-02	8.9E-02	8.8E-01	8.8E-01	8.3E-01	5.4E-01	3.3E-01	5.0E-01	9.6E-02	1.9E-01
GO:0060325	GO:Bio L4	face morphogenesis	1.5E-01	3.3E-01	7.2E-02	7.4E-02	7.7E-01	7.7E-01	2.7E-01	4.3E-01	3.6E-01	6.0E-01	9.6E-02	1.4E-01
GO:0034621	GO:Bio L4	cellular macromolecular complex subunit organization	5.9E-01	4.5E-01	3.0E-01	2.0E-01	1.1E-02	6.9E-03	6.4E-02	9.7E-01	4.0E-02	2.1E-02	9.6E-02	5.1E-01
GO:0048840	GO:Bio L4	otolith development	6.7E-02	1.8E-01	1.5E-01	2.3E-01	3.7E-01	4.8E-01	1.3E-01	1.1E-01	1.2E-01	3.0E-01	9.7E-02	1.1E-01
GO:0044252	GO:Bio L4	negative regulation of multicellular organismal metabolic process	2.4E-01	1.1E-01	1.1E-01	8.8E-02	4.3E-01	5.1E-01	1.9E-01	1.5E-01	3.4E-01	2.2E-01	9.7E-02	7.1E-02
GO:0031965	GO:Cell L4	nuclear membrane	1.3E-01	1.8E-01	1.9E-01	1.9E-01	5.8E-01	5.0E-01	1.0E-01	3.0E-01	2.8E-01	3.1E-01	9.7E-02	2.2E-01
5217	KEGG	Basal cell carcinoma	3.9E-01	2.4E-01	1.7E-01	1.6E-01	7.2E-02	3.3E-01	1.2E-01	9.3E-01	1.3E-01	2.8E-01	9.7E-02	4.3E-01
GO:0042995	GO:Cell L4	cell projection	1.3E-01	3.7E-03	1.8E-01	2.1E-02	6.2E-01	3.8E-01	1.1E-01	6.3E-01	2.8E-01	1.1E-02	9.8E-02	7.1E-02

GO:0021869	GO:Bio L4	forebrain ventricular zone progenitor cell division	7.0E-01	1.6E-01	1.0E-01	3.5E-02	3.0E-01	3.1E-01	2.0E-01	7.4E-01	5.4E-01	1.9E-01	9.8E-02	1.2E-01
GO:0005849	GO:Cell L4	mRNA cleavage factor complex	5.4E-01	8.7E-01	3.5E-01	2.3E-01	8.9E-01	9.5E-01	5.8E-02	5.4E-02	8.4E-01	9.8E-01	9.8E-02	6.6E-02
680	KEGG	Methane metabolism	6.8E-01	4.4E-01	1.4E-01	7.8E-02	1.3E-01	2.1E-01	1.5E-01	9.5E-01	3.0E-01	3.1E-01	9.8E-02	2.7E-01
GO:0042596	GO:Bio L4	fear response	4.5E-02	8.2E-02	3.0E-02	8.9E-02	1.3E-01	3.3E-01	6.7E-01	8.7E-01	3.6E-02	1.3E-01	9.9E-02	2.8E-01
GO:0009057	GO:Bio L4	macromolecule catabolic process	3.2E-01	2.0E-01	4.3E-01	2.0E-01	2.5E-01	1.1E-01	4.8E-02	3.5E-01	2.8E-01	1.1E-01	9.9E-02	2.6E-01
GO:0052173	GO:Bio L4	response to defenses of other organism during symbiotic interaction	5.0E-02	1.7E-02	4.1E-01	3.2E-01	2.9E-01	4.7E-01	5.0E-02	1.3E-01	7.7E-02	4.7E-02	9.9E-02	1.8E-01
GO:0075136	GO:Bio L4	response to host	5.0E-02	1.7E-02	4.1E-01	3.2E-01	2.9E-01	4.7E-01	5.0E-02	1.3E-01	7.7E-02	4.7E-02	9.9E-02	1.8E-01
GO:0001550	GO:Bio L4	ovarian cumulus expansion	9.7E-01	9.0E-01	7.2E-01	3.1E-01	1.4E-01	1.2E-01	2.8E-02	3.5E-01	4.0E-01	3.6E-01	9.9E-02	3.5E-01
GO:0022605	GO:Bio L4	oogenesis stage	9.7E-01	9.0E-01	7.2E-01	3.1E-01	1.4E-01	1.2E-01	2.8E-02	3.5E-01	4.0E-01	3.6E-01	9.9E-02	3.5E-01
GO:0009893	GO:Bio L4	positive regulation of metabolic process	2.3E-01	1.4E-01	2.6E-01	2.8E-01	3.2E-01	3.0E-01	7.7E-02	5.2E-01	2.7E-01	1.7E-01	1.0E-01	4.2E-01
GO:0033605	GO:Bio L4	positive regulation of catecholamine secretion	2.9E-01	1.9E-01	1.8E-01	2.7E-01	6.2E-01	9.8E-01	1.2E-01	9.8E-01	4.9E-01	5.1E-01	1.0E-01	6.1E-01
GO:0010604	GO:Bio L4	positive regulation of macromolecule metabolic process	2.1E-01	1.4E-01	3.0E-01	2.8E-01	3.3E-01	2.5E-01	6.9E-02	6.9E-01	2.5E-01	1.5E-01	1.0E-01	5.1E-01
GO:0021985	GO:Bio L4	neurohypophysis development	7.1E-01	1.5E-01	1.0E-01	3.4E-02	2.0E-01	6.2E-01	2.0E-01	7.4E-01	4.2E-01	3.2E-01	1.0E-01	1.2E-01
GO:0000900	GO:Mole L4	translation repressor activity, nucleic acid binding	4.6E-01	4.9E-01	5.6E-02	8.2E-02	1.8E-01	6.6E-01	3.7E-01	4.1E-01	2.9E-01	6.8E-01	1.0E-01	1.5E-01
GO:0050808	GO:Bio L4	synapse organization	1.4E-01	1.4E-01	1.1E-01	1.1E-01	7.0E-01	5.8E-01	1.8E-01	3.2E-01	3.2E-01	2.8E-01	1.0E-01	1.5E-01
GO:0044085	GO:Bio L2	cellular component biogenesis	5.4E-01	2.1E-01	2.6E-01	1.0E-01	1.4E-02	1.6E-02	7.8E-02	7.0E-01	4.4E-02	2.3E-02	1.0E-01	2.6E-01
GO:0048610	GO:Bio L4	reproductive cellular process	7.7E-01	3.6E-01	1.0E-01	1.0E-01	9.9E-01	4.5E-01	2.1E-01	1.2E-01	9.7E-01	4.6E-01	1.0E-01	6.8E-02
GO:0003700	GO:Mole L4	transcription factor activity	4.4E-03	3.0E-04	1.2E-01	7.1E-02	5.0E-01	2.2E-01	1.7E-01	9.1E-01	1.6E-02	7.1E-04	1.0E-01	2.4E-01
GO:0043012	GO:Bio L4	regulation of fusion of sperm to egg plasma membrane	5.8E-01	6.2E-01	9.9E-01	9.9E-01	3.4E-01	3.4E-01	2.1E-02	6.8E-01	5.1E-01	5.4E-01	1.0E-01	9.4E-01
GO:0007031	GO:Bio L4	peroxisome organization	8.9E-01	7.6E-01	6.6E-01	5.1E-01	5.4E-02	5.9E-03	3.2E-02	3.6E-01	1.9E-01	2.9E-02	1.0E-01	4.9E-01
GO:0004872	GO:Mole L4	receptor activity	6.7E-01	1.2E-01	4.1E-01	3.7E-01	8.8E-02	2.4E-01	5.1E-02	6.7E-01	2.3E-01	1.3E-01	1.0E-01	5.9E-01

GO:0045182	GO:Mole L2	translation regulator activity	6.0E-01	1.3E-01	4.2E-02	4.5E-02	6.1E-01	5.3E-01	5.0E-01	6.7E-01	7.3E-01	2.5E-01	1.0E-01	1.4E-01
GO:0043412	GO:Bio L4	macromolecule modification	5.3E-01	7.3E-02	2.2E-01	2.7E-01	8.8E-01	6.2E-01	9.6E-02	3.6E-01	8.2E-01	1.9E-01	1.0E-01	3.2E-01
GO:0043005	GO:Cell L4	neuron projection	4.6E-02	2.0E-04	1.3E-01	2.2E-02	4.1E-01	4.4E-01	1.6E-01	4.1E-01	9.4E-02	9.0E-04	1.0E-01	5.2E-02
GO:0003299	GO:Bio L4	muscle hypertrophy in response to stress	6.2E-01	4.3E-01	3.3E-02	1.0E-02	4.4E-01	9.6E-01	6.4E-01	7.4E-01	6.3E-01	7.8E-01	1.0E-01	4.4E-02
GO:0022404	GO:Bio L4	molting cycle process	1.6E-01	2.4E-01	4.9E-01	5.9E-01	8.8E-01	9.2E-01	4.3E-02	7.7E-01	4.2E-01	5.6E-01	1.0E-01	8.1E-01
GO:0044248	GO:Bio L4	cellular catabolic process	3.0E-01	1.8E-01	3.0E-01	1.0E-01	4.5E-01	7.0E-02	7.2E-02	2.7E-01	4.1E-01	6.9E-02	1.0E-01	1.3E-01
GO:0046670	GO:Bio L4	positive regulation of retinal cell programmed cell death	1.2E-01	3.1E-01	2.3E-01	4.4E-01	5.4E-01	7.1E-01	9.4E-02	3.1E-01	2.3E-01	5.6E-01	1.0E-01	4.1E-01
GO:0042611	GO:Cell L4	MHC protein complex	8.3E-03	5.7E-03	2.2E-02	1.8E-02	3.8E-01	3.9E-01	9.7E-01	1.3E-01	2.2E-02	1.6E-02	1.0E-01	1.7E-02
GO:0044431	GO:Cell L4	Golgi apparatus part	5.6E-01	1.3E-01	2.6E-01	3.1E-01	5.0E-01	6.3E-01	8.3E-02	2.4E-01	6.4E-01	2.8E-01	1.0E-01	2.7E-01
GO:0002046	GO:Mole L4	opsin binding	5.3E-02	1.9E-02	1.7E-01	1.2E-01	5.7E-01	7.3E-01	1.3E-01	9.0E-01	1.4E-01	7.4E-02	1.0E-01	3.5E-01
4514	KEGG	Cell adhesion molecules (CAMs)	5.0E-01	2.1E-01	2.9E-01	2.6E-01	3.3E-01	7.9E-01	7.4E-02	2.6E-01	4.6E-01	4.7E-01	1.0E-01	2.5E-01
GO:0070684	GO:Bio L4	seminal clot liquefaction	7.3E-01	4.6E-01	4.0E-01	3.0E-01	4.5E-01	7.2E-01	5.5E-02	3.0E-01	6.9E-01	7.0E-01	1.0E-01	3.0E-01
GO:0032844	GO:Bio L4	regulation of homeostatic process	9.0E-02	4.0E-02	2.0E-01	3.2E-01	3.5E-02	1.1E-01	1.1E-01	2.0E-01	2.1E-02	2.8E-02	1.1E-01	2.4E-01
GO:0032388	GO:Bio L4	positive regulation of intracellular transport	5.2E-02	5.7E-02	2.9E-01	1.3E-01	1.3E-01	3.3E-01	7.5E-02	5.8E-01	4.1E-02	9.4E-02	1.1E-01	2.7E-01
GO:0045768	GO:Bio L4	positive regulation of anti-apoptosis	6.3E-01	1.0E-01	1.8E-01	2.1E-01	4.6E-01	9.5E-01	1.2E-01	5.9E-01	6.5E-01	3.2E-01	1.1E-01	3.8E-01
GO:0002251	GO:Bio L4	organ or tissue specific immune response	2.8E-01	1.9E-01	1.5E-01	1.3E-01	5.3E-01	6.2E-01	1.5E-01	7.1E-01	4.3E-01	3.7E-01	1.1E-01	3.1E-01
GO:0016918	GO:Mole L4	retinal binding	3.4E-01	2.1E-01	7.3E-01	6.6E-01	2.8E-01	4.7E-01	3.1E-02	9.9E-01	3.2E-01	3.3E-01	1.1E-01	9.3E-01
GO:0090048	GO:Bio L4	negative regulation of transcription regulator activity	8.4E-01	6.0E-01	1.7E-01	5.3E-02	9.5E-01	9.7E-01	1.3E-01	4.0E-02	9.8E-01	9.0E-01	1.1E-01	1.5E-02
GO:0031557	GO:Bio L4	induction of programmed cell death in response to chemical stimulus	3.9E-02	2.9E-01	3.0E-02	6.3E-02	2.3E-01	3.1E-01	7.5E-01	7.2E-01	5.1E-02	3.0E-01	1.1E-01	1.8E-01
GO:0014047	GO:Bio L4	glutamate secretion	5.5E-01	7.8E-02	3.3E-02	2.4E-02	2.9E-03	1.3E-02	6.9E-01	9.7E-01	1.2E-02	7.9E-03	1.1E-01	1.1E-01
GO:0090047	GO:Bio L4	positive regulation of transcription regulator activity	3.9E-01	1.8E-01	3.0E-02	3.1E-03	3.7E-01	4.0E-02	7.6E-01	1.5E-01	4.2E-01	4.3E-02	1.1E-01	4.0E-03
GO:0009615	GO:Bio L4	response to virus	2.9E-01	1.5E-01	8.8E-02	5.5E-02	4.5E-01	6.4E-01	2.6E-01	8.5E-01	3.9E-01	3.2E-01	1.1E-01	1.9E-01
GO:0031252	GO:Cell L4	cell leading edge	7.1E-01	8.1E-01	7.1E-01	4.8E-01	3.6E-01	2.4E-01	3.2E-02	2.2E-01	6.0E-01	5.1E-01	1.1E-01	3.5E-01

GO:0043218	GO:Cell L4	compact myelin	9.1E-01	2.9E-01	6.6E-01	1.9E-01	1.7E-01	3.6E-02	3.5E-02	8.9E-01	4.4E-01	5.8E-02	1.1E-01	4.7E-01
GO:0042175	GO:Cell L4	nuclear envelope-endoplasmic reticulum network	1.3E-01	1.1E-01	2.1E-01	2.0E-01	1.8E-01	1.6E-01	1.1E-01	5.9E-01	1.1E-01	9.1E-02	1.1E-01	3.7E-01
GO:0001880	GO:Bio L4	Mullerian duct regression	2.3E-01	1.8E-01	7.4E-02	1.4E-01	4.4E-01	1.3E-01	3.1E-01	7.2E-01	3.3E-01	1.1E-01	1.1E-01	3.2E-01
GO:0019841	GO:Mole L4	retinol binding	8.1E-01	8.0E-01	8.1E-01	5.8E-01	2.7E-01	5.0E-01	2.9E-02	8.4E-01	5.5E-01	7.6E-01	1.1E-01	8.4E-01
PA165110621	PharmGKB	pgkb_pwy_Renin_Angiotensin_Aldosterone_System_acting_Drug_Pathways	5.9E-01	4.9E-01	6.5E-02	4.1E-02	9.8E-01	7.7E-01	3.5E-01	5.8E-02	8.9E-01	7.4E-01	1.1E-01	1.7E-02
PA165110622	PharmGKB	pgkb_pwy_Renin_Angiotensin_Aldosterone_System_acting_Drug_Pathways	5.9E-01	4.9E-01	6.5E-02	4.1E-02	9.8E-01	7.7E-01	3.5E-01	5.8E-02	8.9E-01	7.4E-01	1.1E-01	1.7E-02
PA2023	PharmGKB	pgkb_pwy_ACE_inhibitor_Pathway	5.9E-01	4.9E-01	6.5E-02	4.1E-02	9.8E-01	7.7E-01	3.5E-01	5.8E-02	8.9E-01	7.4E-01	1.1E-01	1.7E-02
GO:0004791	GO:Mole L4	thioredoxin-disulfide reductase activity	8.5E-01	1.6E-01	5.2E-01	6.2E-01	4.2E-01	2.1E-01	4.5E-02	8.3E-02	7.2E-01	1.5E-01	1.1E-01	2.0E-01
GO:0032507	GO:Bio L4	maintenance of protein location in cell	5.8E-01	4.2E-01	9.7E-01	9.1E-01	5.2E-01	2.3E-01	2.4E-02	5.2E-01	6.6E-01	3.2E-01	1.1E-01	8.2E-01
GO:0007018	GO:Bio L4	microtubule-based movement	1.4E-01	1.3E-01	6.2E-02	7.9E-02	5.3E-01	6.8E-01	3.8E-01	9.8E-01	2.7E-01	3.0E-01	1.1E-01	2.8E-01
GO:0005789	GO:Cell L4	endoplasmic reticulum membrane	2.0E-01	1.4E-01	2.3E-01	2.3E-01	1.6E-01	1.5E-01	1.0E-01	6.9E-01	1.4E-01	1.0E-01	1.1E-01	4.5E-01
GO:0007091	GO:Bio L4	mitotic metaphase/anaphase transition	8.3E-01	3.2E-01	9.4E-01	9.2E-01	5.5E-01	8.9E-02	2.5E-02	9.1E-01	8.1E-01	1.3E-01	1.1E-01	9.8E-01
GO:0060760	GO:Bio L4	positive regulation of response to cytokine stimulus	6.3E-01	5.9E-01	9.6E-01	9.4E-01	5.6E-01	9.0E-01	2.4E-02	5.6E-01	7.2E-01	8.7E-01	1.1E-01	8.6E-01
GO:0070168	GO:Bio L4	negative regulation of biomineral formation	8.5E-01	7.3E-01	8.9E-01	9.9E-01	2.3E-01	6.5E-01	2.6E-02	8.2E-01	5.2E-01	8.3E-01	1.1E-01	9.8E-01
GO:0001556	GO:Bio L4	oocyte maturation	2.7E-01	7.0E-02	1.1E-01	5.2E-02	4.9E-01	4.0E-01	2.1E-01	5.5E-02	4.0E-01	1.3E-01	1.1E-01	2.0E-02
1040	KEGG	Biosynthesis of unsaturated fatty acids	5.1E-01	5.1E-01	5.4E-01	5.3E-01	2.7E-01	5.9E-02	4.4E-02	1.4E-01	4.2E-01	1.3E-01	1.1E-01	2.7E-01
GO:0051828	GO:Bio L4	entry into other organism during symbiotic interaction	6.0E-01	7.1E-01	2.4E-02	6.7E-02	9.9E-01	7.5E-01	9.9E-01	5.4E-01	9.1E-01	8.7E-01	1.1E-01	1.6E-01
GO:0052126	GO:Bio L4	movement in host environment	6.0E-01	7.1E-01	2.4E-02	6.7E-02	9.9E-01	7.5E-01	9.9E-01	5.4E-01	9.1E-01	8.7E-01	1.1E-01	1.6E-01
GO:0052192	GO:Bio L4	movement in environment of other organism during symbiotic interaction	6.0E-01	7.1E-01	2.4E-02	6.7E-02	9.9E-01	7.5E-01	9.9E-01	5.4E-01	9.1E-01	8.7E-01	1.1E-01	1.6E-01

GO:0001918	GO:Mole L4	farnesylated protein binding	7.0E-01	3.9E-01	3.2E-01	7.2E-02	2.4E-02	1.6E-02	7.5E-02	5.7E-02	8.5E-02	3.9E-02	1.1E-01	2.7E-02
GO:0007412	GO:Bio L4	axon target recognition	4.3E-01	7.7E-01	1.3E-01	1.2E-01	6.7E-02	7.3E-02	1.8E-01	1.8E-01	1.3E-01	2.2E-01	1.1E-01	1.0E-01
GO:0033596	GO:Cell L4	TSC1-TSC2 complex	1.9E-01	2.0E-01	5.3E-01	3.5E-01	1.8E-01	1.5E-02	4.5E-02	1.7E-01	1.6E-01	2.1E-02	1.1E-01	2.3E-01
GO:0014874	GO:Bio L4	response to stimulus involved in regulation of muscle adaptation	5.4E-01	2.8E-01	3.7E-02	1.1E-02	2.5E-01	8.1E-01	6.4E-01	7.5E-01	4.1E-01	5.7E-01	1.1E-01	4.9E-02
GO:0003723	GO:Mole L4	RNA binding	9.6E-01	8.0E-01	8.4E-01	6.9E-01	4.8E-01	1.9E-01	2.9E-02	6.2E-01	8.2E-01	4.4E-01	1.1E-01	7.9E-01
GO:0042633	GO:Bio L4	hair cycle	1.7E-01	2.6E-01	5.1E-01	6.1E-01	9.0E-01	9.3E-01	4.7E-02	7.8E-01	4.4E-01	5.8E-01	1.1E-01	8.3E-01
GO:0048306	GO:Mole L4	calcium-dependent protein binding	3.0E-01	6.1E-01	5.7E-01	4.3E-01	6.8E-01	9.8E-01	4.2E-02	8.7E-01	5.3E-01	9.0E-01	1.1E-01	7.4E-01
2010	KEGG	ABC transporters	1.0E-01	2.9E-03	8.5E-02	5.8E-02	8.1E-01	8.3E-01	2.8E-01	8.7E-01	2.9E-01	1.7E-02	1.1E-01	2.0E-01
PA162356267	PharmGKB	pgkb_pwy_EGFR_Inhibitors_Pathway_PD	4.2E-01	7.8E-01	9.0E-01	7.5E-01	6.0E-01	3.1E-01	2.7E-02	1.7E-01	6.0E-01	5.9E-01	1.1E-01	4.0E-01
GO:0070013	GO:Cell L4	intracellular organelle lumen	4.1E-01	2.6E-01	1.5E-01	3.9E-02	8.6E-01	7.6E-01	1.7E-01	5.5E-01	7.2E-01	5.1E-01	1.1E-01	1.0E-01
GO:0030897	GO:Cell L4	HOPS complex	7.2E-03	4.3E-03	4.1E-02	2.6E-02	9.5E-01	7.3E-01	5.9E-01	7.5E-01	4.1E-02	2.1E-02	1.1E-01	9.5E-02
GO:0008180	GO:Cell L4	signalosome	5.4E-01	4.9E-01	1.2E-01	2.2E-01	9.2E-01	9.0E-01	2.0E-01	8.2E-01	8.4E-01	8.0E-01	1.2E-01	4.9E-01
GO:0044430	GO:Cell L4	cytoskeletal part	3.3E-01	1.1E-01	8.8E-01	8.9E-01	1.2E-01	1.5E-02	2.8E-02	7.2E-01	1.7E-01	1.2E-02	1.2E-01	9.3E-01
GO:0042138	GO:Bio L4	meiotic DNA double-strand break formation	6.9E-01	8.3E-01	3.4E-01	3.2E-01	9.6E-01	6.0E-01	7.2E-02	1.0E+00	9.3E-01	8.5E-01	1.2E-01	6.8E-01
GO:0090079	GO:Mole L4	translation regulator activity, nucleic acid binding	3.8E-01	6.2E-02	4.6E-02	4.8E-02	4.2E-01	6.8E-01	5.3E-01	7.1E-01	4.5E-01	1.8E-01	1.2E-01	1.5E-01
GO:0007548	GO:Bio L4	sex differentiation	1.5E-01	3.6E-01	1.3E-01	9.4E-02	5.0E-01	2.4E-01	1.9E-01	1.9E-01	2.7E-01	3.0E-01	1.2E-01	9.1E-02
GO:0005840	GO:Cell L4	ribosome	2.6E-01	3.5E-01	2.5E-01	4.9E-01	4.5E-01	7.5E-01	1.0E-01	8.9E-01	3.7E-01	6.1E-01	1.2E-01	8.0E-01
GO:0006903	GO:Bio L4	vesicle targeting	7.6E-01	5.1E-01	7.2E-01	7.4E-01	5.4E-01	4.3E-01	3.5E-02	2.3E-01	7.8E-01	5.5E-01	1.2E-01	4.7E-01
GO:0051536	GO:Mole L4	iron-sulfur cluster binding	2.4E-01	1.2E-01	1.1E-01	2.5E-01	8.5E-01	5.7E-01	2.3E-01	6.0E-01	5.3E-01	2.5E-01	1.2E-01	4.4E-01
GO:0016080	GO:Bio L4	synaptic vesicle targeting	1.4E-01	8.3E-02	7.8E-01	6.0E-01	1.6E-01	1.4E-01	3.2E-02	3.0E-01	1.1E-01	6.3E-02	1.2E-01	4.9E-01
190	KEGG	Oxidative phosphorylation	9.0E-01	6.9E-01	3.1E-01	2.5E-01	4.5E-01	1.4E-01	8.1E-02	1.4E-01	7.7E-01	3.2E-01	1.2E-01	1.5E-01
GO:0046649	GO:Bio L4	lymphocyte activation	1.1E-01	6.0E-02	1.6E-01	2.3E-01	6.4E-01	5.0E-01	1.5E-01	3.9E-01	2.5E-01	1.3E-01	1.2E-01	3.1E-01
GO:0001957	GO:Bio L4	intramembranous ossification	2.1E-01	5.4E-01	4.6E-02	5.6E-02	3.3E-01	5.8E-02	5.5E-01	1.5E-01	2.5E-01	1.4E-01	1.2E-01	4.9E-02
GO:0051128	GO:Bio L4	regulation of cellular component organization	1.4E-01	3.5E-03	4.4E-01	2.1E-01	3.7E-02	4.8E-02	5.6E-02	8.1E-01	3.3E-02	1.6E-03	1.2E-01	4.7E-01
PA2035	PharmGKB	pgkb_pwy_Cyclophosphamide_Pathway	6.0E-02	3.9E-02	4.0E-02	1.1E-01	5.9E-01	5.3E-01	6.3E-01	6.1E-01	1.5E-01	1.0E-01	1.2E-01	2.4E-01
GO:0000910	GO:Bio L4	cytokinesis	4.1E-01	2.3E-01	4.5E-01	2.7E-01	9.8E-01	6.8E-01	5.7E-02	8.5E-01	7.7E-01	4.5E-01	1.2E-01	5.6E-01
GO:0001653	GO:Mole L4	peptide receptor activity	6.0E-01	3.4E-01	3.4E-01	4.0E-01	4.0E-01	7.3E-01	7.5E-02	8.5E-01	5.8E-01	5.9E-01	1.2E-01	7.1E-01

GO:0031312	GO:Cell L4	extrinsic to organelle membrane	7.8E-01	7.2E-01	1.4E-01	1.3E-01	8.2E-01	8.3E-01	1.8E-01	1.0E-01	9.2E-01	9.0E-01	1.2E-01	7.2E-02
GO:0010891	GO:Bio L4	negative regulation of sequestering of triglyceride	9.9E-01	6.8E-01	9.4E-01	8.3E-01	3.3E-01	2.5E-01	2.7E-02	4.9E-01	6.9E-01	4.7E-01	1.2E-01	7.7E-01
GO:0021604	GO:Bio L4	cranial nerve structural organization	2.7E-02	2.6E-01	2.1E-01	5.4E-01	6.4E-01	6.5E-01	1.2E-01	4.5E-01	8.8E-02	4.7E-01	1.2E-01	5.9E-01
GO:0007440	GO:Bio L4	foregut morphogenesis	8.3E-01	4.4E-01	8.9E-01	9.6E-01	7.7E-01	5.4E-01	2.9E-02	9.1E-01	9.2E-01	5.8E-01	1.2E-01	9.9E-01
GO:0016188	GO:Bio L4	synaptic vesicle maturation	5.7E-01	6.2E-01	1.0E-01	8.8E-02	7.6E-01	7.2E-01	2.5E-01	5.0E-01	8.0E-01	8.1E-01	1.2E-01	1.8E-01
GO:0017171	GO:Mole L4	serine hydrolase activity	6.4E-01	9.3E-01	6.6E-01	5.9E-01	1.4E-01	2.9E-02	3.9E-02	2.9E-01	3.0E-01	1.2E-01	1.2E-01	4.8E-01
GO:0019042	GO:Bio L4	latent virus infection	2.0E-02	7.0E-02	1.0E-01	1.3E-01	1.3E-01	7.0E-01	2.5E-01	3.7E-01	1.8E-02	2.0E-01	1.2E-01	1.9E-01
GO:0019046	GO:Bio L4	reactivation of latent virus	2.0E-02	7.0E-02	1.0E-01	1.3E-01	1.3E-01	7.0E-01	2.5E-01	3.7E-01	1.8E-02	2.0E-01	1.2E-01	1.9E-01
GO:0048609	GO:Bio L4	reproductive process in a multicellular organism	9.6E-01	5.3E-01	1.2E-01	2.1E-01	8.9E-01	4.0E-01	2.2E-01	6.4E-01	9.9E-01	5.4E-01	1.2E-01	4.0E-01
GO:0051650	GO:Bio L4	establishment of vesicle localization	6.2E-01	2.5E-01	8.8E-01	8.9E-01	5.8E-01	2.5E-01	3.0E-02	1.1E-01	7.2E-01	2.3E-01	1.2E-01	3.3E-01
GO:0033279	GO:Cell L4	ribosomal subunit	4.7E-01	7.7E-01	5.0E-01	7.4E-01	7.0E-01	8.2E-01	5.3E-02	8.7E-01	6.9E-01	9.2E-01	1.2E-01	9.3E-01
GO:0007599	GO:Bio L4	hemostasis	5.2E-01	2.1E-01	5.4E-02	3.2E-02	1.9E-01	5.1E-01	5.0E-01	8.5E-01	3.3E-01	3.5E-01	1.2E-01	1.3E-01
GO:0030336	GO:Bio L4	negative regulation of cell migration	1.4E-02	4.0E-03	3.0E-02	3.6E-02	3.5E-02	5.1E-01	9.0E-01	5.9E-01	4.2E-03	1.5E-02	1.2E-01	1.0E-01
GO:0019048	GO:Bio L4	virus-host interaction	1.1E-01	1.1E-01	1.5E-01	1.2E-01	5.5E-02	1.9E-01	1.8E-01	2.3E-01	3.8E-02	1.0E-01	1.2E-01	1.3E-01
GO:0010458	GO:Bio L4	exit from mitosis	4.3E-01	3.3E-01	8.0E-01	8.7E-01	1.8E-01	6.5E-02	3.4E-02	2.0E-01	2.8E-01	1.0E-01	1.3E-01	4.8E-01
GO:0008610	GO:Bio L4	lipid biosynthetic process	4.1E-01	3.4E-01	4.3E-01	7.3E-01	3.2E-01	5.6E-01	6.4E-02	3.8E-01	4.0E-01	5.1E-01	1.3E-01	6.3E-01
GO:0051961	GO:Bio L4	negative regulation of nervous system development	4.7E-01	4.5E-01	7.2E-01	8.4E-01	4.2E-01	8.9E-01	3.8E-02	6.5E-01	5.2E-01	7.7E-01	1.3E-01	8.8E-01
GO:0051964	GO:Bio L4	negative regulation of synaptogenesis	4.7E-01	4.5E-01	7.2E-01	8.4E-01	4.2E-01	8.9E-01	3.8E-02	6.5E-01	5.2E-01	7.7E-01	1.3E-01	8.8E-01
GO:0045787	GO:Bio L4	positive regulation of cell cycle	4.2E-01	5.5E-01	5.1E-01	5.7E-01	3.3E-01	7.0E-01	5.4E-02	7.8E-01	4.1E-01	7.5E-01	1.3E-01	8.1E-01
GO:0045277	GO:Cell L4	respiratory chain complex IV	6.8E-01	1.3E-01	3.0E-02	1.3E-02	7.6E-01	8.9E-01	9.4E-01	6.3E-01	8.6E-01	3.7E-01	1.3E-01	4.6E-02
GO:0001554	GO:Bio L4	luteolysis	2.4E-01	4.4E-01	4.3E-01	6.3E-01	6.8E-01	8.2E-01	6.4E-02	2.2E-01	4.6E-01	7.3E-01	1.3E-01	4.1E-01

GO:0016820	GO:Mole L4	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances	3.0E-01	2.3E-02	3.6E-01	1.4E-01	6.7E-01	8.2E-01	7.7E-02	8.7E-01	5.2E-01	9.4E-02	1.3E-01	3.8E-01
GO:0005929	GO:Cell L4	cilium	9.5E-02	2.8E-02	8.7E-02	9.7E-02	4.7E-01	1.3E-01	3.2E-01	6.7E-01	1.8E-01	2.4E-02	1.3E-01	2.4E-01
GO:0009725	GO:Bio L4	response to hormone stimulus	3.6E-01	1.9E-02	5.1E-01	3.1E-01	4.1E-01	2.4E-01	5.5E-02	8.1E-01	4.3E-01	3.0E-02	1.3E-01	6.0E-01
GO:0001300	GO:Bio L4	chronological cell aging	1.3E-01	2.0E-01	4.8E-02	2.8E-02	9.1E-01	4.3E-01	5.8E-01	3.0E-01	3.7E-01	3.0E-01	1.3E-01	4.9E-02
GO:0031650	GO:Bio L4	regulation of heat generation	5.5E-01	5.4E-01	1.9E-01	3.2E-01	5.9E-01	6.7E-01	1.5E-01	1.0E-01	6.9E-01	7.3E-01	1.3E-01	1.4E-01
GO:0031652	GO:Bio L4	positive regulation of heat generation	5.5E-01	5.4E-01	1.9E-01	3.2E-01	5.9E-01	6.7E-01	1.5E-01	1.0E-01	6.9E-01	7.3E-01	1.3E-01	1.4E-01
GO:0004342	GO:Mole L4	glucosamine-6-phosphate deaminase activity	7.1E-01	7.6E-01	6.4E-01	5.9E-01	1.1E-01	1.7E-01	4.4E-02	2.7E-02	2.8E-01	3.9E-01	1.3E-01	8.1E-02
GO:0042180	GO:Bio L4	cellular ketone metabolic process	1.6E-01	1.7E-02	3.5E-01	3.1E-01	1.1E-02	3.4E-02	7.9E-02	3.7E-01	1.3E-02	5.0E-03	1.3E-01	3.6E-01
GO:0042321	GO:Bio L4	negative regulation of circadian sleep/wake cycle, sleep	8.9E-02	4.8E-02	8.5E-02	6.8E-02	1.5E-01	8.9E-02	3.3E-01	4.2E-01	7.2E-02	2.7E-02	1.3E-01	1.3E-01
GO:0042754	GO:Bio L4	negative regulation of circadian rhythm	8.9E-02	4.8E-02	8.5E-02	6.8E-02	1.5E-01	8.9E-02	3.3E-01	4.2E-01	7.2E-02	2.7E-02	1.3E-01	1.3E-01
4144	KEGG	Endocytosis	1.6E-01	9.1E-02	7.1E-02	4.0E-02	4.9E-01	7.0E-01	3.9E-01	6.6E-01	2.8E-01	2.4E-01	1.3E-01	1.2E-01
GO:0043244	GO:Bio L4	regulation of protein complex disassembly	3.2E-01	1.3E-01	4.6E-01	2.7E-01	1.8E-01	2.1E-02	6.1E-02	8.3E-01	2.2E-01	1.8E-02	1.3E-01	5.6E-01
GO:0042886	GO:Bio L4	amide transport	7.9E-01	8.0E-01	3.6E-01	4.0E-01	6.5E-01	4.7E-01	7.9E-02	1.5E-02	8.5E-01	7.5E-01	1.3E-01	3.6E-02
GO:0016012	GO:Cell L4	sarcoglycan complex	2.2E-01	2.7E-01	1.9E-01	1.7E-01	4.1E-01	5.4E-01	1.5E-01	6.7E-02	3.0E-01	4.3E-01	1.3E-01	6.1E-02
GO:0060326	GO:Bio L4	cell chemotaxis	3.3E-02	5.5E-02	4.3E-02	2.2E-02	4.3E-02	1.6E-01	6.6E-01	2.3E-01	1.1E-02	5.0E-02	1.3E-01	3.3E-02
534	KEGG	Glycosaminoglycan biosynthesis - heparan sulfate	5.7E-01	3.4E-01	3.0E-02	9.4E-02	6.4E-01	9.6E-01	9.5E-01	2.3E-01	7.3E-01	6.9E-01	1.3E-01	1.1E-01
GO:0051439	GO:Bio L4	regulation of ubiquitin-protein ligase activity during mitotic cell cycle	5.8E-01	2.2E-01	3.1E-01	3.0E-01	8.6E-01	6.5E-01	9.1E-02	8.6E-01	8.4E-01	4.2E-01	1.3E-01	6.0E-01
4660	KEGG	T cell receptor signaling pathway	2.6E-01	4.1E-01	8.0E-01	6.0E-01	4.5E-01	4.1E-01	3.6E-02	1.2E-01	3.7E-01	4.6E-01	1.3E-01	2.6E-01
GO:0016229	GO:Mole L4	steroid dehydrogenase activity	8.0E-01	9.8E-01	8.1E-01	6.9E-01	3.9E-01	7.0E-01	3.6E-02	6.3E-01	6.8E-01	9.4E-01	1.3E-01	7.9E-01
GO:0051651	GO:Bio L4	maintenance of location in cell	5.8E-01	5.3E-01	9.7E-01	9.3E-01	5.7E-01	2.9E-01	3.0E-02	3.3E-01	7.0E-01	4.5E-01	1.3E-01	6.7E-01

GO:0003016	GO:Bio L4	respiratory system process	5.9E-01	2.8E-01	3.2E-01	2.4E-01	3.9E-02	3.9E-01	9.1E-02	3.4E-01	1.1E-01	3.5E-01	1.3E-01	2.8E-01
GO:0050854	GO:Bio L4	regulation of antigen receptor-mediated signaling pathway	2.4E-01	2.2E-01	5.3E-02	1.2E-01	2.8E-01	8.5E-02	5.5E-01	4.6E-02	2.5E-01	9.3E-02	1.3E-01	3.3E-02
GO:0001520	GO:Cell L4	outer dense fiber	6.8E-01	4.6E-02	1.6E-01	7.0E-02	5.3E-01	7.3E-01	1.8E-01	1.9E-01	7.3E-01	1.5E-01	1.3E-01	7.0E-02
430	KEGG	Taurine and hypotaurine metabolism	3.2E-01	2.1E-01	4.0E-02	2.1E-02	3.7E-01	4.0E-01	7.4E-01	8.5E-02	3.7E-01	2.9E-01	1.3E-01	1.3E-02
GO:0008368	GO:Mole L4	Gram-negative bacterial binding	8.9E-01	7.0E-01	3.3E-01	4.6E-01	9.7E-01	9.9E-01	8.8E-02	6.5E-01	9.9E-01	9.5E-01	1.3E-01	6.6E-01
GO:0016741	GO:Mole L4	transferase activity, transferring one-carbon groups	1.6E-01	1.9E-01	4.4E-02	1.8E-02	6.7E-01	4.4E-01	6.7E-01	7.0E-01	3.5E-01	3.0E-01	1.3E-01	6.6E-02
GO:0006644	GO:Bio L4	phospholipid metabolic process	7.9E-01	5.9E-01	3.2E-01	5.5E-01	8.9E-02	3.3E-01	9.1E-02	4.8E-01	2.6E-01	5.1E-01	1.3E-01	6.2E-01
4666	KEGG	Fc gamma R-mediated phagocytosis	9.8E-01	9.0E-01	3.2E-01	2.8E-01	2.7E-01	6.8E-02	9.1E-02	2.6E-01	6.2E-01	2.3E-01	1.3E-01	2.6E-01
GO:0006793	GO:Bio L4	phosphorus metabolic process	3.8E-01	1.5E-01	5.2E-01	6.1E-01	6.1E-01	3.4E-01	5.6E-02	5.7E-02	5.7E-01	2.1E-01	1.3E-01	1.5E-01
GO:0060021	GO:Bio L4	palate development	2.2E-01	4.0E-01	4.2E-01	4.7E-01	9.7E-01	6.8E-01	7.0E-02	2.1E-01	5.4E-01	6.3E-01	1.3E-01	3.3E-01
GO:0005344	GO:Mole L4	oxygen transporter activity	7.4E-02	8.8E-02	1.8E-01	1.1E-01	2.9E-01	7.0E-01	1.6E-01	4.5E-01	1.0E-01	2.3E-01	1.3E-01	2.0E-01
GO:0016565	GO:Mole L4	general transcriptional repressor activity	6.8E-01	5.6E-01	3.5E-01	3.2E-01	8.2E-01	6.7E-01	8.6E-02	9.7E-01	8.8E-01	7.5E-01	1.3E-01	6.7E-01
GO:0008656	GO:Mole L4	caspase activator activity	2.9E-01	6.9E-02	6.8E-02	4.0E-02	1.3E-01	3.8E-01	4.4E-01	5.3E-01	1.6E-01	1.2E-01	1.3E-01	1.0E-01
GO:0008285	GO:Bio L4	negative regulation of cell proliferation	1.7E-01	1.1E-02	2.0E-01	2.6E-01	6.1E-01	7.4E-01	1.5E-01	6.4E-02	3.4E-01	4.6E-02	1.4E-01	8.6E-02
GO:0019211	GO:Mole L4	phosphatase activator activity	8.4E-01	8.5E-01	6.2E-01	7.7E-01	6.8E-01	1.3E-01	4.9E-02	6.1E-02	8.9E-01	3.6E-01	1.4E-01	1.9E-01
GO:0045196	GO:Bio L4	establishment or maintenance of neuroblast polarity	5.3E-02	1.2E-01	4.6E-02	4.2E-02	8.0E-01	8.7E-01	6.6E-01	4.4E-01	1.8E-01	3.4E-01	1.4E-01	9.3E-02
PA165111375	PharmGKB	pgkb_pwy_Benzodiazepine_pathway_PK	5.9E-01	4.5E-01	1.6E-01	1.8E-01	8.1E-01	7.2E-01	2.0E-01	2.2E-01	8.3E-01	6.9E-01	1.4E-01	1.7E-01
GO:0005732	GO:Cell L4	small nucleolar ribonucleoprotein complex	1.9E-01	2.3E-01	3.8E-02	1.2E-01	7.6E-01	7.8E-01	8.0E-01	5.2E-01	4.2E-01	4.9E-01	1.4E-01	2.3E-01
GO:0048308	GO:Bio L4	organelle inheritance	8.5E-01	6.9E-01	8.5E-01	7.5E-01	9.6E-01	6.3E-01	3.6E-02	5.4E-02	9.8E-01	7.9E-01	1.4E-01	1.7E-01
GO:0050819	GO:Bio L4	negative regulation of coagulation	6.9E-01	4.5E-01	4.3E-01	3.3E-01	1.7E-01	3.3E-01	7.2E-02	5.5E-01	3.6E-01	4.4E-01	1.4E-01	4.9E-01
GO:0006082	GO:Bio L4	organic acid metabolic process	2.9E-01	3.8E-02	3.8E-01	3.2E-01	1.7E-02	2.8E-02	8.3E-02	3.7E-01	3.1E-02	8.5E-03	1.4E-01	3.7E-01

GO:0001704	GO:Bio L4	formation of primary germ layer	4.5E-01	3.7E-01	1.6E-01	2.0E-01	4.1E-01	3.9E-02	1.9E-01	9.8E-01	5.0E-01	7.6E-02	1.4E-01	5.1E-01
GO:0045767	GO:Bio L4	regulation of anti-apoptosis	5.3E-01	1.2E-01	2.0E-01	1.8E-01	1.4E-01	8.3E-01	1.5E-01	6.9E-01	2.7E-01	3.4E-01	1.4E-01	3.9E-01
GO:0070572	GO:Bio L4	positive regulation of neuron projection regeneration	5.1E-01	6.7E-01	5.4E-01	6.8E-01	1.4E-01	2.8E-01	5.8E-02	3.2E-01	2.6E-01	5.0E-01	1.4E-01	5.5E-01
GO:0019898	GO:Cell L4	extrinsic to membrane	4.5E-01	4.7E-01	2.3E-01	7.2E-02	4.0E-01	3.3E-01	1.4E-01	7.6E-01	4.9E-01	4.4E-01	1.4E-01	2.2E-01
GO:0031240	GO:Cell L4	external side of cell outer membrane	9.7E-01	9.9E-01	8.1E-01	7.4E-01	1.4E-01	2.4E-02	3.9E-02	8.9E-01	4.2E-01	1.1E-01	1.4E-01	9.3E-01
GO:0007163	GO:Bio L4	establishment or maintenance of cell polarity	3.1E-01	4.5E-01	6.4E-01	6.1E-01	5.9E-01	4.7E-01	4.9E-02	8.7E-01	4.9E-01	5.4E-01	1.4E-01	8.7E-01
GO:0050900	GO:Bio L4	leukocyte migration	1.2E-01	1.5E-01	4.2E-02	2.7E-02	2.8E-02	2.6E-01	7.5E-01	3.0E-01	2.3E-02	1.7E-01	1.4E-01	4.7E-02
GO:0051124	GO:Bio L4	synaptic growth at neuromuscular junction	1.3E-02	3.5E-02	3.5E-02	1.3E-01	9.4E-01	8.6E-01	8.9E-01	1.9E-01	6.7E-02	1.3E-01	1.4E-01	1.2E-01
GO:0043209	GO:Cell L4	myelin sheath	6.6E-01	3.5E-01	3.8E-01	6.1E-02	2.3E-01	4.6E-02	8.2E-02	1.0E+00	4.4E-01	8.3E-02	1.4E-01	2.3E-01
480	KEGG	Glutathione metabolism	1.9E-01	5.7E-01	4.3E-01	6.6E-01	5.3E-01	2.2E-01	7.4E-02	2.6E-01	3.3E-01	3.9E-01	1.4E-01	4.7E-01
GO:0034986	GO:Mole L4	iron chaperone activity	8.0E-01	8.6E-01	5.3E-01	4.3E-01	5.4E-01	7.4E-01	6.0E-02	2.2E-02	7.9E-01	9.2E-01	1.4E-01	5.4E-02
GO:0023036	GO:Bio L4	initiation of signal transduction	4.8E-01	6.1E-01	4.6E-01	4.2E-01	2.5E-01	6.8E-01	6.9E-02	8.4E-01	3.8E-01	7.8E-01	1.4E-01	7.2E-01
GO:0023038	GO:Bio L4	signal initiation by diffusible mediator	4.8E-01	6.1E-01	4.6E-01	4.2E-01	2.5E-01	6.8E-01	6.9E-02	8.4E-01	3.8E-01	7.8E-01	1.4E-01	7.2E-01
GO:0007289	GO:Bio L4	spermatid nucleus differentiation	2.6E-01	2.3E-01	3.6E-01	4.6E-01	5.8E-01	4.8E-01	8.9E-02	4.3E-01	4.3E-01	3.5E-01	1.4E-01	5.1E-01
260	KEGG	Glycine, serine and threonine metabolism	7.6E-01	5.1E-01	6.8E-02	1.3E-02	2.5E-01	3.2E-01	4.8E-01	6.5E-01	5.1E-01	4.6E-01	1.4E-01	4.8E-02
GO:0012506	GO:Cell L4	vesicle membrane	9.9E-01	9.7E-01	7.3E-01	5.9E-01	5.8E-01	4.1E-01	4.4E-02	2.5E-01	8.9E-01	7.6E-01	1.4E-01	4.3E-01
GO:0060324	GO:Bio L4	face development	1.9E-01	3.9E-01	9.5E-02	9.9E-02	8.2E-01	8.5E-01	3.4E-01	5.2E-01	4.4E-01	6.9E-01	1.4E-01	2.0E-01
GO:0016817	GO:Mole L4	hydrolase activity, acting on acid anhydrides	5.5E-02	2.7E-02	3.3E-01	1.4E-01	8.2E-01	5.4E-01	9.8E-02	7.6E-01	1.9E-01	7.7E-02	1.4E-01	3.5E-01
GO:0048199	GO:Bio L4	vesicle targeting, to, from or within Golgi	9.6E-01	9.5E-01	6.7E-01	6.1E-01	4.4E-01	4.5E-01	4.8E-02	9.3E-01	7.9E-01	7.9E-01	1.4E-01	8.9E-01
GO:0031645	GO:Bio L4	negative regulation of neurological system process	2.5E-02	1.2E-01	5.0E-02	9.0E-02	8.1E-02	1.7E-01	6.5E-01	6.5E-01	1.4E-02	9.9E-02	1.4E-01	2.3E-01
5211	KEGG	Renal cell carcinoma	9.0E-02	5.3E-01	4.6E-01	7.8E-01	3.5E-01	4.2E-01	7.0E-02	6.0E-02	1.4E-01	5.5E-01	1.4E-01	1.9E-01
GO:0005542	GO:Mole L4	folic acid binding	5.9E-01	9.3E-01	5.2E-02	2.2E-02	7.9E-01	4.8E-01	6.2E-01	3.7E-02	8.2E-01	8.0E-01	1.4E-01	6.7E-03
GO:0034641	GO:Bio L4	cellular nitrogen compound metabolic process	3.9E-01	3.1E-01	1.1E-01	8.4E-02	1.1E-01	4.0E-01	3.0E-01	1.3E-01	1.8E-01	3.9E-01	1.4E-01	5.9E-02

GO:0032835	GO:Bio L4	glomerulus development	5.5E-02	1.0E-01	4.7E-01	5.3E-01	1.6E-01	1.9E-02	6.8E-02	7.0E-01	5.0E-02	1.4E-02	1.4E-01	7.4E-01
GO:0017076	GO:Mole L4	purine nucleotide binding	5.6E-02	6.1E-03	2.2E-01	3.7E-01	9.7E-01	5.3E-01	1.5E-01	3.5E-01	2.1E-01	2.2E-02	1.4E-01	3.9E-01
GO:0051379	GO:Mole L4	epinephrine binding	8.9E-01	1.0E+00	3.7E-02	9.2E-02	4.2E-01	1.1E-01	8.8E-01	4.0E-01	7.4E-01	3.5E-01	1.4E-01	1.6E-01
4640	KEGG	Hematopoietic cell lineage	3.1E-01	1.6E-01	7.0E-02	3.6E-02	9.7E-01	5.2E-01	4.6E-01	3.2E-01	6.6E-01	2.9E-01	1.4E-01	6.4E-02
GO:0009266	GO:Bio L4	response to temperature stimulus	2.7E-01	1.5E-01	2.9E-01	3.2E-01	8.3E-01	8.5E-01	1.1E-01	5.5E-01	5.6E-01	3.9E-01	1.4E-01	4.8E-01
GO:0060560	GO:Bio L4	developmental growth involved in morphogenesis	4.8E-01	4.0E-01	8.0E-02	7.7E-02	8.1E-02	5.4E-02	4.1E-01	6.1E-01	1.7E-01	1.1E-01	1.4E-01	1.9E-01
GO:0016192	GO:Bio L4	vesicle-mediated transport	7.9E-01	8.0E-02	1.8E-01	5.0E-02	3.5E-01	3.3E-01	1.8E-01	8.6E-01	6.3E-01	1.2E-01	1.4E-01	1.8E-01
GO:0044282	GO:Bio L4	small molecule catabolic process	5.9E-01	5.3E-01	2.8E-01	2.8E-01	3.3E-01	1.0E-01	1.2E-01	2.7E-01	5.1E-01	2.1E-01	1.4E-01	2.7E-01
GO:0010035	GO:Bio L4	response to inorganic substance	9.0E-01	5.9E-01	2.9E-01	2.2E-01	4.5E-01	6.5E-01	1.1E-01	4.4E-01	7.7E-01	7.6E-01	1.4E-01	3.3E-01
GO:0040013	GO:Bio L4	negative regulation of locomotion	1.9E-02	5.4E-03	3.6E-02	4.4E-02	3.5E-02	3.9E-01	9.2E-01	6.2E-01	5.5E-03	1.5E-02	1.5E-01	1.2E-01
GO:0001547	GO:Bio L4	antral ovarian follicle growth	3.0E-01	3.6E-01	5.4E-01	4.3E-01	2.8E-01	2.6E-01	6.1E-02	3.1E-02	2.9E-01	3.1E-01	1.5E-01	7.2E-02
GO:0001708	GO:Bio L4	cell fate specification	6.0E-01	4.1E-01	9.5E-02	1.1E-01	3.7E-01	5.8E-01	3.5E-01	7.5E-01	5.5E-01	5.8E-01	1.5E-01	2.9E-01
410	KEGG	beta-Alanine metabolism	6.8E-01	4.3E-01	2.9E-01	1.3E-01	1.8E-01	3.8E-01	1.1E-01	1.6E-01	3.8E-01	4.6E-01	1.5E-01	9.9E-02
GO:0008559	GO:Mole L4	xenobiotic-transporting ATPase activity	2.9E-01	6.2E-01	2.8E-01	1.3E-01	7.2E-01	3.6E-01	1.2E-01	2.7E-01	5.4E-01	5.6E-01	1.5E-01	1.6E-01
GO:0031642	GO:Bio L4	negative regulation of myelination	9.0E-03	2.4E-02	4.2E-02	5.3E-02	9.8E-01	7.2E-01	7.9E-01	5.4E-01	5.0E-02	8.6E-02	1.5E-01	1.3E-01
GO:0021516	GO:Bio L4	dorsal spinal cord development	3.1E-01	6.3E-01	8.9E-02	6.8E-02	7.9E-01	9.6E-01	3.7E-01	5.7E-01	5.9E-01	9.1E-01	1.5E-01	1.6E-01
GO:0070444	GO:Bio L4	oligodendrocyte progenitor proliferation	5.0E-01	9.1E-01	2.0E-01	1.4E-01	4.4E-01	9.4E-01	1.7E-01	8.8E-01	5.5E-01	9.9E-01	1.5E-01	3.7E-01
GO:0002039	GO:Mole L4	p53 binding	3.5E-01	4.6E-01	3.1E-01	2.7E-01	2.9E-01	4.2E-01	1.1E-01	5.5E-01	3.3E-01	5.1E-01	1.5E-01	4.3E-01
GO:0031937	GO:Bio L4	positive regulation of chromatin silencing	7.2E-01	2.9E-01	9.8E-02	1.2E-01	7.4E-01	6.5E-01	3.5E-01	6.5E-01	8.7E-01	5.0E-01	1.5E-01	2.7E-01
GO:0032144	GO:Cell L4	4-aminobutyrate transaminase complex	1.8E-01	8.8E-02	6.0E-02	5.1E-02	1.4E-01	2.8E-02	5.7E-01	2.5E-01	1.2E-01	1.7E-02	1.5E-01	6.9E-02
GO:0005095	GO:Mole L4	GTPase inhibitor activity	1.4E-01	8.5E-02	1.9E-01	7.7E-02	4.8E-01	1.4E-01	1.8E-01	9.7E-01	2.5E-01	6.5E-02	1.5E-01	2.7E-01
GO:0003717	GO:Mole L4	RNA polymerase II transcription termination factor activity	9.6E-01	8.3E-01	1.5E-01	1.6E-01	1.6E-01	7.2E-01	2.4E-01	8.8E-01	4.4E-01	9.0E-01	1.5E-01	4.1E-01

GO:0055021	GO:Bio L4	regulation of cardiac muscle tissue growth	2.3E-02	8.8E-02	6.2E-01	7.7E-01	1.0E-01	3.2E-01	5.5E-02	2.6E-01	1.7E-02	1.3E-01	1.5E-01	5.2E-01
GO:0060343	GO:Bio L4	trabecula formation	8.1E-01	7.8E-01	6.6E-02	7.2E-02	8.8E-01	8.6E-01	5.2E-01	3.5E-01	9.6E-01	9.4E-01	1.5E-01	1.2E-01
GO:0050878	GO:Bio L4	regulation of body fluid levels	3.2E-01	1.7E-01	7.2E-02	2.8E-02	7.3E-02	5.7E-01	4.8E-01	9.4E-01	1.1E-01	3.2E-01	1.5E-01	1.2E-01
GO:0030730	GO:Bio L4	sequestering of triglyceride	2.5E-01	1.2E-01	3.8E-01	2.8E-01	6.8E-01	5.4E-01	9.1E-02	4.5E-01	4.7E-01	2.4E-01	1.5E-01	3.9E-01
GO:0002517	GO:Bio L4	T cell tolerance induction	1.2E-01	2.0E-01	7.8E-02	1.6E-01	8.7E-01	9.4E-01	4.5E-01	3.8E-02	3.3E-01	5.0E-01	1.5E-01	3.7E-02
GO:0030881	GO:Mole L4	beta-2-microglobulin binding	5.1E-01	3.3E-01	9.9E-02	1.0E-01	4.5E-01	1.5E-01	3.5E-01	8.4E-02	5.7E-01	2.0E-01	1.5E-01	5.0E-02
GO:0001817	GO:Bio L4	regulation of cytokine production	5.2E-01	5.4E-01	5.5E-01	1.9E-01	4.1E-01	4.0E-01	6.3E-02	2.7E-01	5.4E-01	5.4E-01	1.5E-01	2.1E-01
GO:0010522	GO:Bio L4	regulation of calcium ion transport into cytosol	2.9E-01	1.5E-01	1.2E-01	2.0E-01	9.6E-02	2.5E-01	2.8E-01	1.7E-01	1.3E-01	1.6E-01	1.5E-01	1.5E-01
4950	KEGG	Maturity onset diabetes of the young	4.4E-01	5.5E-01	2.2E-01	2.4E-01	9.4E-01	5.6E-01	1.6E-01	2.2E-01	7.8E-01	6.7E-01	1.5E-01	2.1E-01
PA2026	PharmGKB	pgkb_pwy_Glucocorticoid_and_Inflammatory_genes_Pathway_HPA_axis	7.5E-01	9.6E-01	6.5E-02	2.0E-01	7.9E-01	4.8E-01	5.4E-01	4.4E-01	9.0E-01	8.2E-01	1.5E-01	3.0E-01
GO:0022604	GO:Bio L4	regulation of cell morphogenesis	5.2E-01	3.1E-01	4.1E-01	2.1E-01	4.1E-01	7.9E-01	8.6E-02	7.1E-01	5.5E-01	5.9E-01	1.5E-01	4.3E-01
GO:0008280	GO:Cell L4	cohesin core heterodimer	4.6E-01	5.1E-01	1.2E-01	1.4E-01	9.4E-01	7.7E-01	2.9E-01	4.5E-01	7.9E-01	7.6E-01	1.5E-01	2.4E-01
GO:0043473	GO:Bio L2	pigmentation	1.9E-02	1.3E-03	1.0E-01	4.0E-02	5.6E-01	3.8E-01	3.5E-01	5.9E-01	6.0E-02	4.3E-03	1.5E-01	1.1E-01
GO:0048630	GO:Bio L4	skeletal muscle tissue growth	6.5E-02	2.2E-02	9.3E-02	2.3E-01	5.0E-01	9.6E-01	3.8E-01	4.0E-01	1.5E-01	1.0E-01	1.5E-01	3.1E-01
GO:0040001	GO:Bio L4	establishment of mitotic spindle localization	6.2E-02	1.4E-01	1.9E-01	1.8E-01	7.0E-01	6.9E-01	1.8E-01	6.9E-01	1.8E-01	3.3E-01	1.5E-01	3.9E-01
GO:0016441	GO:Bio L4	posttranscriptional gene silencing	2.7E-01	4.3E-01	3.5E-01	3.2E-01	7.2E-01	4.6E-01	1.0E-01	9.0E-01	5.1E-01	5.2E-01	1.5E-01	6.4E-01
GO:0005504	GO:Mole L4	fatty acid binding	6.4E-01	9.4E-01	7.8E-01	7.4E-01	2.7E-01	1.3E-01	4.5E-02	3.6E-01	4.7E-01	3.7E-01	1.5E-01	6.2E-01
GO:0001846	GO:Mole L4	opsonin binding	6.8E-01	2.9E-01	4.0E-01	2.4E-01	1.1E-01	2.7E-01	9.0E-02	3.0E-01	2.7E-01	2.8E-01	1.5E-01	2.6E-01
GO:0010171	GO:Bio L4	body morphogenesis	2.7E-01	5.1E-01	1.4E-01	1.5E-01	8.2E-01	8.3E-01	2.6E-01	4.5E-01	5.6E-01	7.9E-01	1.5E-01	2.4E-01
GO:0002475	GO:Bio L4	antigen processing and presentation via MHC class Ib	5.2E-01	3.4E-01	8.7E-02	1.1E-01	5.0E-01	5.1E-01	4.1E-01	8.8E-02	6.1E-01	4.7E-01	1.5E-01	5.4E-02
GO:0016469	GO:Cell L4	proton-transporting two-sector ATPase complex	9.2E-01	7.2E-01	8.4E-01	5.3E-01	2.0E-01	3.0E-01	4.3E-02	2.8E-01	4.9E-01	5.4E-01	1.6E-01	4.3E-01

GO:0030695	GO:Mole L4	GTPase regulator activity	3.5E-01	6.8E-02	2.9E-01	3.3E-02	9.3E-01	6.6E-01	1.2E-01	7.4E-01	7.0E-01	1.9E-01	1.6E-01	1.2E-01
GO:0060322	GO:Bio L4	head development	2.0E-01	4.9E-01	1.4E-01	1.5E-01	6.3E-01	9.2E-01	2.6E-01	6.3E-01	3.9E-01	8.1E-01	1.6E-01	3.1E-01
GO:0051017	GO:Bio L4	actin filament bundle assembly	4.8E-01	2.6E-01	6.8E-01	6.0E-01	9.2E-02	2.1E-02	5.3E-02	9.8E-01	1.8E-01	3.4E-02	1.6E-01	9.0E-01
460	KEGG	Cyanoamino acid metabolism	2.8E-01	5.7E-01	1.4E-01	2.2E-01	5.2E-02	9.3E-02	2.5E-01	6.7E-01	7.5E-02	2.1E-01	1.6E-01	4.3E-01
GO:0042089	GO:Bio L4	cytokine biosynthetic process	8.2E-01	5.3E-01	2.9E-01	6.2E-02	2.2E-01	9.4E-02	1.2E-01	2.3E-01	4.9E-01	2.0E-01	1.6E-01	7.5E-02
GO:0005968	GO:Cell L4	Rab-protein geranylgeranyltransferase complex	4.3E-01	1.1E-01	1.2E-01	1.1E-01	2.9E-01	8.3E-01	3.0E-01	4.1E-01	3.8E-01	3.0E-01	1.6E-01	1.9E-01
GO:0080135	GO:Bio L4	regulation of cellular response to stress	4.6E-02	3.6E-01	2.5E-01	2.5E-01	2.2E-01	1.8E-01	1.4E-01	1.9E-01	5.5E-02	2.4E-01	1.6E-01	2.0E-01
GO:0042127	GO:Bio L4	regulation of cell proliferation	2.7E-01	2.2E-02	5.0E-01	4.8E-01	1.9E-01	4.8E-01	7.2E-02	2.2E-01	2.0E-01	5.8E-02	1.6E-01	3.4E-01
GO:0080134	GO:Bio L4	regulation of response to stress	1.4E-01	9.8E-02	2.6E-01	1.9E-01	8.0E-02	1.3E-01	1.4E-01	3.3E-01	6.2E-02	6.9E-02	1.6E-01	2.4E-01
GO:0005577	GO:Cell L4	fibrinogen complex	1.1E-01	2.9E-01	5.3E-02	2.3E-02	1.5E-01	2.7E-01	6.9E-01	6.2E-01	8.3E-02	2.8E-01	1.6E-01	7.4E-02
GO:0046813	GO:Bio L4	virion attachment, binding of host cell surface receptor	7.6E-01	9.6E-01	5.4E-02	1.1E-01	7.1E-01	9.3E-01	6.8E-01	1.4E-01	8.8E-01	9.9E-01	1.6E-01	8.2E-02
GO:0035172	GO:Bio L4	hemocyte proliferation	3.9E-02	2.4E-02	4.5E-02	2.8E-02	8.6E-01	9.4E-01	8.3E-01	6.4E-01	1.5E-01	1.1E-01	1.6E-01	9.0E-02
GO:0033593	GO:Cell L4	BRCA2-MAGE-D1 complex	3.9E-02	2.4E-02	4.5E-02	2.8E-02	8.6E-01	9.4E-01	8.3E-01	6.4E-01	1.5E-01	1.1E-01	1.6E-01	9.0E-02
GO:0002061	GO:Mole L4	pyrimidine binding	4.8E-01	5.5E-01	6.7E-01	5.6E-01	2.2E-01	1.6E-01	5.6E-02	9.0E-01	3.4E-01	3.0E-01	1.6E-01	8.5E-01
GO:0007030	GO:Bio L4	Golgi organization	1.5E-02	2.2E-02	2.2E-01	2.5E-01	9.5E-01	4.9E-01	1.7E-01	7.1E-01	7.6E-02	5.8E-02	1.6E-01	4.8E-01
GO:0032206	GO:Bio L4	positive regulation of telomere maintenance	5.4E-01	3.0E-01	5.4E-01	4.3E-01	2.8E-01	8.5E-01	6.8E-02	4.3E-02	4.3E-01	6.1E-01	1.6E-01	9.1E-02
3430	KEGG	Mismatch repair	1.7E-03	1.7E-03	1.8E-01	3.1E-01	6.8E-01	4.6E-01	2.0E-01	8.2E-01	9.0E-03	6.4E-03	1.6E-01	6.0E-01
4610	KEGG	Complement and coagulation cascades	5.6E-01	4.7E-01	8.3E-02	6.3E-02	8.9E-02	5.7E-01	4.5E-01	9.5E-01	2.0E-01	6.2E-01	1.6E-01	2.3E-01
GO:0051276	GO:Bio L4	chromosome organization	6.6E-01	6.7E-01	7.3E-01	6.2E-01	1.3E-01	8.1E-02	5.1E-02	7.4E-01	3.0E-01	2.1E-01	1.6E-01	8.2E-01
GO:0010521	GO:Mole L4	telomerase inhibitor activity	2.1E-01	1.2E-01	3.7E-01	2.7E-01	1.8E-02	4.3E-02	1.0E-01	7.4E-01	2.4E-02	3.3E-02	1.6E-01	5.2E-01
GO:0045786	GO:Bio L4	negative regulation of cell cycle	8.1E-01	9.0E-01	8.8E-01	7.8E-01	4.4E-01	5.0E-01	4.3E-02	3.1E-01	7.2E-01	8.1E-01	1.6E-01	5.8E-01
GO:0017025	GO:Mole L4	TATA-binding protein binding	9.5E-01	7.6E-01	1.2E-01	7.3E-02	4.6E-01	6.4E-01	3.3E-01	6.5E-01	8.0E-01	8.3E-01	1.6E-01	1.9E-01
GO:0005581	GO:Cell L4	collagen	3.3E-02	6.8E-02	2.2E-01	1.5E-01	8.6E-01	9.8E-01	1.7E-01	4.0E-01	1.3E-01	2.5E-01	1.6E-01	2.3E-01
GO:0051656	GO:Bio L4	establishment of organelle localization	4.4E-01	1.8E-01	9.5E-01	8.7E-01	4.9E-01	2.4E-01	4.0E-02	4.5E-01	5.5E-01	1.8E-01	1.6E-01	7.6E-01

GO:0010647	GO:Bio L4	positive regulation of cell communication	9.0E-02	1.7E-02	2.2E-01	8.1E-02	7.3E-02	1.3E-01	1.8E-01	1.6E-01	3.9E-02	1.5E-02	1.6E-01	6.8E-02
GO:0033292	GO:Bio L4	T-tubule organization	9.4E-01	8.5E-01	8.8E-01	9.0E-01	8.2E-01	9.1E-01	4.3E-02	6.6E-01	9.7E-01	9.7E-01	1.6E-01	9.0E-01
4650	KEGG	Natural killer cell mediated cytotoxicity	3.6E-02	1.0E-01	2.0E-01	4.1E-01	6.7E-01	2.5E-01	1.9E-01	7.3E-02	1.1E-01	1.2E-01	1.6E-01	1.4E-01
GO:0031984	GO:Cell L4	organelle subcompartment	4.1E-01	1.4E-01	7.1E-02	1.5E-01	5.0E-01	1.7E-01	5.4E-01	9.6E-01	5.3E-01	1.1E-01	1.6E-01	4.2E-01
GO:0035176	GO:Bio L4	social behavior	9.0E-01	8.2E-01	1.2E-01	7.8E-02	6.4E-01	7.6E-01	3.2E-01	6.4E-01	8.9E-01	9.2E-01	1.6E-01	2.0E-01
GO:0051271	GO:Bio L4	negative regulation of cellular component movement	2.4E-02	7.5E-03	4.2E-02	5.1E-02	4.0E-02	5.1E-01	9.0E-01	5.7E-01	7.5E-03	2.5E-02	1.6E-01	1.3E-01
GO:0019213	GO:Mole L4	deacetylase activity	4.9E-01	5.6E-01	1.1E-01	4.7E-02	5.6E-01	5.4E-01	3.5E-01	8.8E-01	6.3E-01	6.7E-01	1.6E-01	1.7E-01
GO:0022038	GO:Bio L4	corpus callosum development	2.1E-01	1.4E-01	3.9E-02	5.1E-02	7.5E-01	8.7E-01	9.9E-01	1.7E-01	4.4E-01	3.9E-01	1.6E-01	5.1E-02
GO:0010883	GO:Bio L4	regulation of lipid storage	1.6E-01	2.1E-01	4.9E-01	3.1E-01	3.0E-01	5.2E-01	7.9E-02	8.4E-01	1.9E-01	3.6E-01	1.6E-01	6.1E-01
GO:0033293	GO:Mole L4	monocarboxylic acid binding	7.5E-01	8.4E-01	9.1E-01	8.9E-01	3.3E-01	2.4E-01	4.3E-02	3.6E-01	5.9E-01	5.3E-01	1.6E-01	6.9E-01
GO:0042720	GO:Cell L4	mitochondrial inner membrane peptidase complex	6.7E-01	5.8E-01	4.8E-01	5.7E-01	3.5E-01	3.0E-01	8.0E-02	5.6E-01	5.7E-01	4.8E-01	1.6E-01	6.8E-01
GO:0016011	GO:Cell L4	dystroglycan complex	2.6E-01	3.1E-01	2.1E-01	1.9E-01	4.5E-01	3.1E-01	1.8E-01	7.8E-02	3.7E-01	3.2E-01	1.6E-01	7.8E-02
3060	KEGG	Protein export	5.9E-01	6.5E-01	1.1E-01	4.2E-01	4.4E-01	9.1E-01	3.6E-01	8.7E-01	6.1E-01	9.1E-01	1.6E-01	7.3E-01
GO:0051589	GO:Bio L4	negative regulation of neurotransmitter transport	2.1E-01	2.4E-01	6.1E-02	7.6E-02	1.2E-02	8.3E-03	6.4E-01	4.6E-01	1.7E-02	1.4E-02	1.7E-01	1.5E-01
GO:0007506	GO:Bio L4	gonadal mesoderm development	6.4E-01	3.9E-01	1.7E-01	2.4E-01	7.5E-01	9.5E-01	2.4E-01	2.1E-01	8.3E-01	7.4E-01	1.7E-01	2.0E-01
GO:0001659	GO:Bio L4	temperature homeostasis	2.1E-01	4.8E-02	9.3E-02	2.0E-01	9.0E-02	4.0E-01	4.2E-01	4.1E-01	9.3E-02	9.5E-02	1.7E-01	2.9E-01
GO:0001833	GO:Bio L4	inner cell mass cell proliferation	1.9E-01	9.4E-02	2.1E-01	1.6E-01	9.5E-01	9.9E-01	1.8E-01	9.2E-01	4.9E-01	3.1E-01	1.7E-01	4.2E-01
GO:0031256	GO:Cell L4	leading edge membrane	7.7E-01	7.9E-01	2.6E-01	3.4E-01	2.5E-02	5.5E-02	1.5E-01	5.4E-01	9.6E-02	1.8E-01	1.7E-01	4.9E-01
GO:0008431	GO:Mole L4	vitamin E binding	2.6E-01	3.7E-01	1.5E-01	1.9E-01	5.8E-01	7.4E-01	2.6E-01	5.0E-01	4.4E-01	6.2E-01	1.7E-01	3.1E-01
GO:0046668	GO:Bio L4	regulation of retinal cell programmed cell death	3.0E-01	6.4E-01	3.2E-01	3.6E-01	1.0E-01	1.5E-01	1.2E-01	2.3E-01	1.4E-01	3.2E-01	1.7E-01	2.9E-01
GO:0016044	GO:Bio L4	cellular membrane organization	6.0E-01	1.3E-01	1.9E-01	9.2E-02	5.7E-01	4.3E-01	2.1E-01	8.6E-01	7.1E-01	2.2E-01	1.7E-01	2.8E-01
3450	KEGG	Non-homologous end-joining	8.8E-01	7.5E-01	5.5E-01	6.9E-01	8.6E-01	3.8E-01	7.2E-02	7.7E-01	9.7E-01	6.4E-01	1.7E-01	8.6E-01
330	KEGG	Arginine and proline metabolism	5.5E-01	2.5E-01	7.1E-01	7.3E-01	1.2E-01	2.5E-01	5.5E-02	4.2E-01	2.5E-01	2.3E-01	1.7E-01	6.7E-01

GO:0034383	GO:Bio L4	low-density lipoprotein particle clearance	8.9E-01	7.7E-01	6.9E-01	8.3E-01	2.4E-01	1.4E-01	5.7E-02	2.1E-01	5.4E-01	3.4E-01	1.7E-01	4.8E-01
GO:0007416	GO:Bio L4	synapse assembly	2.2E-01	1.8E-01	1.6E-01	2.1E-01	8.5E-01	9.1E-01	2.5E-01	2.3E-01	5.0E-01	4.5E-01	1.7E-01	1.9E-01
GO:0051090	GO:Bio L4	regulation of transcription factor activity	4.4E-01	2.6E-01	9.0E-02	1.3E-02	7.2E-01	2.0E-01	4.5E-01	8.4E-02	6.8E-01	2.1E-01	1.7E-01	8.5E-03
GO:0090046	GO:Bio L4	regulation of transcription regulator activity	4.4E-01	2.6E-01	9.0E-02	1.3E-02	7.2E-01	2.0E-01	4.5E-01	8.4E-02	6.8E-01	2.1E-01	1.7E-01	8.5E-03
GO:0000155	GO:Mole L4	two-component sensor activity	3.4E-01	5.3E-01	6.2E-01	6.1E-01	5.0E-01	4.5E-01	6.5E-02	5.7E-01	4.7E-01	5.8E-01	1.7E-01	7.2E-01
GO:0016358	GO:Bio L4	dendrite development	3.4E-01	1.2E-01	1.3E-01	2.2E-01	1.3E-01	2.0E-01	3.0E-01	4.4E-01	1.8E-01	1.2E-01	1.7E-01	3.2E-01
GO:0000095	GO:Mole L4	S-adenosylmethionine transmembrane transporter activity	8.1E-01	7.6E-01	5.3E-01	5.4E-01	6.5E-01	6.7E-01	7.6E-02	8.2E-02	8.7E-01	8.5E-01	1.7E-01	1.8E-01
232	KEGG	Caffeine metabolism	4.3E-01	2.3E-01	5.1E-01	2.4E-01	2.3E-01	5.5E-01	7.9E-02	1.6E-01	3.2E-01	3.9E-01	1.7E-01	1.6E-01
GO:0070064	GO:Mole L4	proline-rich region binding	9.0E-01	5.5E-01	5.0E-01	5.0E-01	4.1E-01	5.5E-01	8.0E-02	8.2E-01	7.3E-01	6.6E-01	1.7E-01	7.7E-01
GO:0012505	GO:Cell L4	endomembrane system	6.6E-01	2.9E-01	5.4E-01	4.8E-01	5.5E-01	2.9E-01	7.5E-02	4.4E-01	7.3E-01	2.9E-01	1.7E-01	5.4E-01
GO:0051049	GO:Bio L4	regulation of transport	1.8E-01	3.0E-04	3.2E-01	2.6E-01	2.3E-01	3.8E-01	1.3E-01	5.3E-01	1.7E-01	1.1E-03	1.7E-01	4.1E-01
GO:0021544	GO:Bio L4	subpallium development	3.0E-01	9.0E-02	1.1E-01	8.2E-02	4.7E-01	7.2E-01	3.6E-01	8.9E-01	4.1E-01	2.4E-01	1.7E-01	2.6E-01
GO:0060041	GO:Bio L4	retina development in camera-type eye	9.0E-01	4.6E-01	6.4E-01	8.6E-01	1.1E-01	1.5E-01	6.3E-02	9.9E-01	3.3E-01	2.6E-01	1.7E-01	9.9E-01
340	KEGG	Histidine metabolism	2.6E-01	2.1E-01	7.5E-02	2.9E-01	4.1E-01	3.5E-01	5.4E-01	4.8E-01	3.4E-01	2.7E-01	1.7E-01	4.1E-01
GO:0016010	GO:Cell L4	dystrophin-associated glycoprotein complex	6.4E-01	7.2E-01	1.5E-01	9.7E-02	6.1E-01	5.8E-01	2.7E-01	1.5E-01	7.6E-01	7.8E-01	1.7E-01	7.7E-02
520	KEGG	Amino sugar and nucleotide sugar metabolism	3.3E-01	4.9E-01	3.3E-01	2.6E-01	1.5E-01	1.7E-01	1.2E-01	1.6E-01	2.0E-01	2.9E-01	1.7E-01	1.7E-01
GO:0000278	GO:Bio L4	mitotic cell cycle	2.6E-01	1.9E-01	6.6E-01	5.9E-01	6.9E-01	2.6E-01	6.3E-02	8.8E-01	4.9E-01	1.9E-01	1.7E-01	8.6E-01
GO:0004383	GO:Mole L4	guanylate cyclase activity	3.8E-01	6.2E-01	7.1E-01	6.4E-01	2.6E-01	1.7E-01	5.8E-02	2.5E-01	3.3E-01	3.4E-01	1.7E-01	4.6E-01
GO:0021758	GO:Bio L4	putamen development	1.7E-01	4.0E-02	7.7E-01	7.1E-01	7.9E-01	9.8E-01	5.4E-02	7.5E-01	4.1E-01	1.7E-01	1.7E-01	8.7E-01
512	KEGG	O-Glycan biosynthesis	4.8E-01	3.4E-01	5.5E-01	6.2E-01	7.1E-01	5.6E-01	7.6E-02	6.3E-01	7.1E-01	5.0E-01	1.7E-01	7.6E-01
GO:0019067	GO:Bio L4	viral assembly, maturation, egress, and release	5.9E-01	9.0E-01	6.5E-01	4.0E-01	9.4E-01	7.3E-01	6.4E-02	7.2E-01	8.8E-01	9.3E-01	1.7E-01	6.5E-01
970	KEGG	Aminoacyl-tRNA biosynthesis	5.6E-01	7.4E-01	8.0E-01	7.6E-01	6.7E-01	2.8E-01	5.3E-02	6.5E-01	7.4E-01	5.3E-01	1.7E-01	8.4E-01
GO:0051240	GO:Bio L4	positive regulation of multicellular organismal process	1.2E-01	3.5E-02	2.7E-01	1.2E-01	2.4E-01	3.9E-02	1.5E-01	3.7E-01	1.4E-01	1.0E-02	1.7E-01	1.8E-01

PA2032	PharmGKB	pgkb_pwy_VEGF_Pathway	4.7E-01	8.3E-01	5.8E-01	5.9E-01	2.4E-01	7.7E-01	7.2E-02	1.5E-01	3.6E-01	9.2E-01	1.7E-01	3.1E-01
GO:0008542	GO:Bio L4	visual learning	6.6E-03	8.1E-03	6.0E-02	7.0E-02	6.8E-01	9.4E-01	7.1E-01	2.9E-01	2.9E-02	4.5E-02	1.8E-01	1.0E-01
GO:0060023	GO:Bio L4	soft palate development	8.2E-02	1.6E-01	7.4E-02	9.0E-02	2.9E-01	6.3E-01	5.7E-01	8.9E-01	1.1E-01	3.3E-01	1.8E-01	2.8E-01
GO:0016458	GO:Bio L4	gene silencing	6.3E-01	6.5E-01	4.2E-01	4.5E-01	7.5E-01	8.7E-01	1.0E-01	9.2E-01	8.2E-01	8.8E-01	1.8E-01	7.8E-01
GO:0048524	GO:Bio L4	positive regulation of viral reproduction	2.5E-01	2.9E-01	4.6E-01	6.7E-01	7.4E-02	1.5E-01	9.2E-02	1.9E-01	9.1E-02	1.8E-01	1.8E-01	3.8E-01
GO:0045161	GO:Bio L4	neuronal ion channel clustering	9.3E-01	4.1E-01	3.2E-01	1.7E-01	7.4E-01	4.6E-01	1.3E-01	3.8E-01	9.5E-01	5.0E-01	1.8E-01	2.5E-01
GO:0045739	GO:Bio L4	positive regulation of DNA repair	4.4E-01	4.5E-01	1.2E-01	1.5E-01	2.5E-02	1.0E-01	3.5E-01	1.4E-01	6.0E-02	1.9E-01	1.8E-01	1.0E-01
GO:0032806	GO:Cell L4	carboxy-terminal domain protein kinase complex	2.8E-01	1.7E-01	3.8E-01	3.8E-01	9.8E-01	6.1E-01	1.1E-01	2.0E-01	6.3E-01	3.5E-01	1.8E-01	2.7E-01
PA2033	PharmGKB	pgkb_pwy_Antiarrhythmic_Drug_Pathways	1.5E-01	1.0E-01	6.8E-02	1.4E-01	7.7E-01	9.8E-01	6.3E-01	5.3E-01	3.6E-01	3.2E-01	1.8E-01	2.6E-01
GO:0060548	GO:Bio L4	negative regulation of cell death	3.3E-01	2.0E-01	2.0E-01	6.3E-02	1.5E-01	1.8E-01	2.1E-01	6.8E-01	2.0E-01	1.5E-01	1.8E-01	1.8E-01
GO:0002578	GO:Bio L4	negative regulation of antigen processing and presentation	3.6E-01	9.9E-02	7.1E-02	1.8E-02	5.2E-01	9.3E-01	6.1E-01	3.7E-01	5.0E-01	3.1E-01	1.8E-01	4.0E-02
GO:0071674	GO:Bio L4	mononuclear cell migration	3.6E-01	9.9E-02	7.1E-02	1.8E-02	5.2E-01	9.3E-01	6.1E-01	3.7E-01	5.0E-01	3.1E-01	1.8E-01	4.0E-02
GO:0060420	GO:Bio L4	regulation of heart growth	2.9E-02	1.0E-01	6.7E-01	8.1E-01	1.2E-01	3.6E-01	6.5E-02	3.0E-01	2.2E-02	1.6E-01	1.8E-01	5.8E-01
GO:0030119	GO:Cell L4	AP-type membrane coat adaptor complex	9.3E-01	9.6E-01	1.6E-01	1.9E-01	1.7E-01	8.9E-01	2.8E-01	7.1E-01	4.5E-01	9.9E-01	1.8E-01	4.0E-01
GO:0009988	GO:Bio L4	cell-cell recognition	4.2E-01	5.6E-01	1.4E-01	1.8E-01	5.3E-01	7.6E-01	3.1E-01	6.4E-01	5.6E-01	7.9E-01	1.8E-01	3.7E-01
GO:0046332	GO:Mole L4	SMAD binding	3.0E-01	4.4E-01	4.7E-01	7.2E-01	4.6E-01	5.1E-01	9.3E-02	4.5E-01	4.1E-01	5.6E-01	1.8E-01	6.9E-01
GO:0008494	GO:Mole L4	translation activator activity	2.4E-01	2.8E-02	9.8E-02	7.3E-02	8.3E-01	4.7E-01	4.5E-01	7.5E-01	5.2E-01	7.0E-02	1.8E-01	2.1E-01
51	KEGG	Fructose and mannose metabolism	2.3E-01	2.6E-01	9.8E-01	9.0E-01	2.6E-01	6.3E-01	4.5E-02	1.9E-01	2.3E-01	4.6E-01	1.8E-01	4.7E-01
GO:0043368	GO:Bio L4	positive T cell selection	6.2E-01	5.5E-01	3.7E-01	8.1E-01	5.0E-01	2.0E-01	1.2E-01	9.9E-01	6.7E-01	3.5E-01	1.8E-01	9.8E-01
GO:0015669	GO:Bio L4	gas transport	5.3E-02	1.0E-01	2.7E-01	1.6E-01	4.2E-01	7.9E-01	1.6E-01	6.2E-01	1.1E-01	2.8E-01	1.8E-01	3.3E-01
GO:0003963	GO:Mole L4	RNA-3'-phosphate cyclase activity	7.7E-01	7.9E-01	5.2E-02	8.6E-02	3.3E-01	3.6E-01	8.6E-01	2.7E-02	6.0E-01	6.4E-01	1.8E-01	1.7E-02
GO:0010193	GO:Bio L4	response to ozone	1.7E-01	1.2E-01	8.6E-02	7.6E-02	6.1E-01	4.0E-01	5.2E-01	5.4E-01	3.4E-01	1.9E-01	1.8E-01	1.7E-01
GO:0031047	GO:Bio L4	gene silencing by RNA	4.3E-01	4.0E-01	3.0E-01	2.6E-01	5.6E-01	6.0E-01	1.5E-01	9.6E-01	5.8E-01	5.8E-01	1.8E-01	5.9E-01
3040	KEGG	Spliceosome	7.9E-01	4.4E-01	8.8E-01	7.0E-01	5.5E-01	2.1E-01	5.1E-02	6.8E-01	8.0E-01	3.1E-01	1.8E-01	8.3E-01
GO:0034728	GO:Bio L4	nucleosome organization	8.8E-01	7.4E-01	5.0E-01	1.8E-01	7.0E-03	7.5E-03	9.1E-02	7.4E-01	3.8E-02	3.4E-02	1.9E-01	4.0E-01
GO:0031983	GO:Cell L4	vesicle lumen	6.2E-02	5.8E-01	2.2E-01	3.0E-01	7.0E-02	4.0E-01	2.1E-01	7.6E-01	2.8E-02	5.7E-01	1.9E-01	5.7E-01

GO:0034643	GO:Bio L4	mitochondrion localization, microtubule-mediated	8.3E-01	6.6E-01	5.6E-01	6.0E-01	3.9E-02	9.5E-02	8.1E-02	9.2E-01	1.4E-01	2.4E-01	1.9E-01	8.8E-01
GO:0051654	GO:Bio L4	establishment of mitochondrion localization	8.3E-01	6.6E-01	5.6E-01	6.0E-01	3.9E-02	9.5E-02	8.1E-02	9.2E-01	1.4E-01	2.4E-01	1.9E-01	8.8E-01
GO:0044306	GO:Cell L4	neuron projection terminus	3.3E-02	2.2E-03	5.5E-02	1.2E-01	1.2E-01	1.4E-01	8.3E-01	6.8E-01	2.6E-02	2.8E-03	1.9E-01	2.8E-01
GO:0019773	GO:Cell L4	proteasome core complex, alpha-subunit complex	3.3E-01	2.1E-01	6.9E-02	1.6E-01	5.9E-01	2.0E-01	6.6E-01	5.7E-01	5.1E-01	1.8E-01	1.9E-01	3.1E-01
GO:0048167	GO:Bio L4	regulation of synaptic plasticity	1.6E-01	3.0E-01	1.6E-01	1.7E-01	3.3E-02	5.8E-03	2.9E-01	5.2E-01	3.3E-02	1.3E-02	1.9E-01	3.0E-01
GO:0035240	GO:Mole L4	dopamine binding	9.1E-02	9.7E-03	6.8E-02	1.0E-01	2.8E-01	5.0E-01	6.8E-01	5.7E-01	1.2E-01	3.0E-02	1.9E-01	2.3E-01
GO:0009820	GO:Bio L4	alkaloid metabolic process	1.1E-01	7.6E-02	1.1E-01	8.7E-02	2.1E-01	7.2E-01	4.3E-01	3.3E-01	1.1E-01	2.1E-01	1.9E-01	1.3E-01
GO:0032612	GO:Bio L4	interleukin-1 production	3.3E-02	9.6E-02	1.4E-01	5.3E-02	2.0E-01	3.8E-01	3.3E-01	5.5E-01	4.0E-02	1.6E-01	1.9E-01	1.3E-01
GO:0070435	GO:Cell L4	Shc-EGFR complex	4.2E-01	2.0E-01	7.5E-01	4.1E-01	3.3E-01	2.0E-01	6.2E-02	1.1E-01	4.2E-01	1.7E-01	1.9E-01	1.9E-01
GO:0042168	GO:Bio L4	heme metabolic process	2.1E-01	6.0E-01	1.6E-01	2.5E-01	7.9E-01	5.6E-01	2.9E-01	2.5E-01	4.7E-01	7.0E-01	1.9E-01	2.4E-01
4540	KEGG	Gap junction	2.0E-01	2.2E-01	5.1E-01	2.7E-01	4.6E-01	9.4E-01	9.1E-02	3.5E-01	3.1E-01	5.4E-01	1.9E-01	3.2E-01
GO:0045321	GO:Bio L4	leukocyte activation	1.4E-01	6.5E-02	1.6E-01	2.1E-01	7.2E-01	5.4E-01	2.9E-01	4.9E-01	3.3E-01	1.5E-01	1.9E-01	3.4E-01
GO:0051726	GO:Bio L4	regulation of cell cycle	6.1E-01	3.5E-01	8.6E-01	8.0E-01	7.1E-01	5.3E-01	5.4E-02	9.2E-01	7.9E-01	5.0E-01	1.9E-01	9.6E-01
GO:0009374	GO:Mole L4	biotin binding	7.0E-01	5.1E-01	8.3E-01	8.1E-01	1.5E-01	3.6E-01	5.6E-02	8.3E-01	3.5E-01	5.0E-01	1.9E-01	9.4E-01
GO:0043533	GO:Mole L4	inositol 1,3,4,5 tetrakisphosphate binding	1.0E-01	3.7E-01	5.7E-01	5.5E-01	9.3E-01	8.5E-01	8.2E-02	6.3E-01	3.2E-01	6.8E-01	1.9E-01	7.1E-01
GO:0051875	GO:Bio L4	pigment granule localization	1.5E-02	3.1E-03	2.1E-01	2.6E-01	5.2E-01	1.6E-01	2.2E-01	1.3E-01	4.5E-02	4.3E-03	1.9E-01	1.5E-01
GO:0060033	GO:Bio L4	anatomical structure regression	3.3E-01	2.6E-01	1.1E-01	2.0E-01	5.6E-01	1.9E-01	4.2E-01	8.4E-01	5.0E-01	2.0E-01	1.9E-01	4.6E-01
GO:0030656	GO:Bio L4	regulation of vitamin metabolic process	1.2E-02	2.3E-02	7.8E-02	7.0E-02	2.5E-01	5.5E-01	6.0E-01	2.2E-01	2.0E-02	6.8E-02	1.9E-01	8.1E-02
GO:0019012	GO:Cell L2	virion	2.3E-01	2.5E-01	6.4E-01	5.4E-01	3.6E-01	4.5E-02	7.4E-02	3.7E-01	2.9E-01	6.2E-02	1.9E-01	5.2E-01
GO:0044423	GO:Cell L2	virion part	2.3E-01	2.5E-01	6.4E-01	5.4E-01	3.6E-01	4.5E-02	7.4E-02	3.7E-01	2.9E-01	6.2E-02	1.9E-01	5.2E-01
GO:0019028	GO:Cell L4	viral capsid	2.3E-01	2.5E-01	6.4E-01	5.4E-01	3.6E-01	4.5E-02	7.4E-02	3.7E-01	2.9E-01	6.2E-02	1.9E-01	5.2E-01
GO:0006910	GO:Bio L4	phagocytosis, recognition	6.4E-01	5.4E-01	9.9E-01	9.3E-01	2.6E-02	1.1E-01	4.8E-02	5.3E-01	8.5E-02	2.3E-01	1.9E-01	8.4E-01
GO:0030595	GO:Bio L4	leukocyte chemotaxis	4.5E-02	8.2E-02	7.1E-02	3.0E-02	3.2E-02	1.3E-01	6.6E-01	2.4E-01	1.1E-02	6.0E-02	1.9E-01	4.2E-02
GO:0003013	GO:Bio L4	circulatory system process	2.5E-01	5.4E-02	1.6E-01	2.9E-01	9.4E-02	5.7E-01	2.9E-01	1.4E-01	1.1E-01	1.4E-01	1.9E-01	1.7E-01
GO:0016885	GO:Mole L4	ligase activity, forming carbon-carbon bonds	5.2E-01	5.2E-01	8.6E-01	6.6E-01	1.9E-01	4.2E-01	5.5E-02	4.6E-01	3.3E-01	5.5E-01	1.9E-01	6.7E-01

GO:0048070	GO:Bio L4	regulation of pigmentation during development	1.4E-02	7.9E-03	1.2E-01	1.2E-01	4.2E-01	1.8E-01	4.1E-01	8.2E-01	3.6E-02	1.1E-02	1.9E-01	3.3E-01
GO:0030677	GO:Cell L4	ribonuclease P complex	4.4E-01	7.3E-02	4.9E-02	8.5E-02	6.2E-01	9.3E-01	9.7E-01	1.2E-01	6.2E-01	2.5E-01	1.9E-01	5.9E-02
GO:0048532	GO:Bio L4	anatomical structure arrangement	1.6E-02	3.1E-01	3.1E-01	6.7E-01	7.2E-01	7.4E-01	1.5E-01	5.7E-01	6.2E-02	5.7E-01	1.9E-01	7.5E-01
GO:0043900	GO:Bio L4	regulation of multi-organism process	7.1E-02	1.5E-02	1.6E-01	1.6E-01	2.7E-01	8.1E-01	3.0E-01	6.6E-01	9.5E-02	6.7E-02	1.9E-01	3.5E-01
GO:0051798	GO:Bio L4	positive regulation of hair follicle development	4.7E-01	2.1E-01	7.0E-01	4.3E-01	1.6E-01	2.9E-01	6.8E-02	2.4E-01	2.7E-01	2.3E-01	1.9E-01	3.3E-01
GO:0016886	GO:Mole L4	ligase activity, forming phosphoric ester bonds	8.2E-01	7.6E-01	1.5E-01	2.3E-01	6.3E-01	6.6E-01	3.1E-01	7.9E-02	8.6E-01	8.5E-01	1.9E-01	9.2E-02
GO:0060600	GO:Bio L4	dichotomous subdivision of an epithelial terminal unit	4.1E-01	6.5E-01	2.4E-01	2.7E-01	5.7E-01	9.7E-01	2.0E-01	1.9E-01	5.8E-01	9.2E-01	1.9E-01	2.0E-01
GO:0000170	GO:Mole L4	sphingosine hydroxylase activity	3.0E-01	2.1E-01	8.1E-02	1.1E-01	6.1E-01	4.0E-01	5.9E-01	4.6E-01	4.9E-01	3.0E-01	1.9E-01	2.0E-01
GO:0010573	GO:Bio L4	vascular endothelial growth factor production	2.7E-02	8.5E-02	2.2E-01	1.1E-01	6.7E-01	6.6E-01	2.2E-01	1.2E-01	9.0E-02	2.2E-01	1.9E-01	7.1E-02
GO:0008148	GO:Mole L4	negative transcription elongation factor activity	1.8E-01	1.6E-01	9.7E-02	2.5E-01	5.9E-01	7.5E-01	5.0E-01	6.7E-01	3.5E-01	3.7E-01	1.9E-01	4.7E-01
GO:0031490	GO:Mole L4	chromatin DNA binding	2.7E-01	1.6E-01	1.8E-01	3.0E-01	7.1E-01	2.3E-01	2.7E-01	3.7E-01	5.1E-01	1.6E-01	1.9E-01	3.6E-01
GO:0060206	GO:Bio L4	estrous cycle phase	5.2E-01	6.5E-01	3.3E-01	3.8E-01	8.9E-01	9.4E-01	1.4E-01	8.4E-01	8.2E-01	9.1E-01	1.9E-01	6.8E-01
GO:0032300	GO:Cell L4	mismatch repair complex	2.0E-04	5.0E-04	1.4E-01	2.7E-01	6.5E-01	8.6E-01	3.5E-01	7.1E-01	1.3E-03	3.8E-03	2.0E-01	5.1E-01
GO:0002262	GO:Bio L4	myeloid cell homeostasis	1.9E-02	1.1E-02	9.0E-02	6.0E-02	8.1E-01	7.4E-01	5.4E-01	9.1E-01	8.0E-02	4.8E-02	2.0E-01	2.1E-01
GO:0032579	GO:Cell L4	apical lamina of hyaline layer	8.3E-02	1.3E-01	2.5E-01	1.1E-01	8.6E-01	9.3E-01	2.0E-01	5.9E-01	2.6E-01	3.7E-01	2.0E-01	2.4E-01
GO:0008643	GO:Bio L4	carbohydrate transport	2.4E-01	3.7E-02	7.9E-01	6.1E-01	4.7E-02	4.0E-02	6.2E-02	6.3E-02	6.0E-02	1.1E-02	2.0E-01	1.6E-01
GO:0009791	GO:Bio L4	post-embryonic development	3.5E-01	2.5E-01	4.4E-01	4.8E-01	4.7E-01	8.8E-01	1.1E-01	8.2E-01	4.6E-01	5.6E-01	2.0E-01	7.6E-01
GO:0060136	GO:Bio L4	embryonic process involved in female pregnancy	5.5E-01	3.6E-01	7.0E-02	1.6E-01	6.4E-01	5.3E-01	7.0E-01	8.1E-01	7.2E-01	5.0E-01	2.0E-01	3.9E-01
GO:0051707	GO:Bio L4	response to other organism	2.6E-01	1.1E-01	1.6E-01	4.9E-02	2.0E-01	2.4E-01	3.0E-01	6.0E-01	2.0E-01	1.3E-01	2.0E-01	1.3E-01
GO:0060011	GO:Bio L4	Sertoli cell proliferation	1.8E-01	3.8E-01	1.9E-01	1.5E-01	5.1E-01	2.2E-01	2.5E-01	4.6E-03	3.1E-01	2.9E-01	2.0E-01	5.7E-03
GO:0005930	GO:Cell L4	axoneme	2.5E-01	2.4E-01	2.2E-01	1.6E-01	5.4E-01	1.2E-01	2.2E-01	5.6E-01	4.0E-01	1.4E-01	2.0E-01	3.0E-01

GO:0045912	GO:Bio L4	negative regulation of carbohydrate metabolic process	7.9E-01	6.1E-01	1.2E-01	4.0E-02	8.5E-01	8.4E-01	4.1E-01	9.5E-01	9.4E-01	8.6E-01	2.0E-01	1.6E-01
GO:0005068	GO:Mole L4	transmembrane receptor protein tyrosine kinase adaptor protein activity	7.9E-01	4.9E-01	6.0E-01	6.9E-01	5.6E-01	2.0E-01	8.3E-02	4.2E-01	8.0E-01	3.2E-01	2.0E-01	6.5E-01
GO:0001562	GO:Bio L4	response to protozoan	3.4E-01	3.4E-01	7.5E-01	6.6E-01	7.6E-02	1.6E-01	6.6E-02	2.4E-01	1.2E-01	2.2E-01	2.0E-01	4.5E-01
GO:0048002	GO:Bio L4	antigen processing and presentation of peptide antigen	1.3E-03	1.6E-03	5.7E-02	4.3E-02	8.6E-02	4.3E-02	8.7E-01	9.8E-01	1.1E-03	7.2E-04	2.0E-01	1.8E-01
GO:0048500	GO:Cell L4	signal recognition particle	2.0E-01	3.6E-01	6.4E-01	6.3E-01	8.8E-01	7.4E-01	7.9E-02	6.6E-01	4.8E-01	6.2E-01	2.0E-01	7.8E-01
GO:0035095	GO:Bio L4	behavioral response to nicotine	8.6E-01	4.3E-01	3.0E-01	4.0E-01	9.3E-01	8.2E-01	1.7E-01	7.0E-01	9.8E-01	7.2E-01	2.0E-01	6.3E-01
GO:0001709	GO:Bio L4	cell fate determination	6.1E-01	3.3E-01	6.7E-02	1.1E-01	6.9E-01	2.0E-01	7.6E-01	8.9E-01	7.8E-01	2.5E-01	2.0E-01	3.3E-01
GO:0001948	GO:Mole L4	glycoprotein binding	7.5E-01	5.0E-01	3.7E-01	3.2E-01	1.8E-01	1.8E-01	1.4E-01	1.4E-01	4.1E-01	3.1E-01	2.0E-01	1.8E-01
GO:0001675	GO:Bio L4	acrosome assembly	2.2E-01	1.1E-01	1.5E-01	1.4E-01	5.4E-01	8.6E-01	3.3E-01	2.0E-01	3.7E-01	3.2E-01	2.0E-01	1.3E-01
5320	KEGG	Autoimmune thyroid disease	5.3E-02	8.5E-02	1.5E-01	2.2E-01	2.1E-01	7.2E-01	3.4E-01	9.6E-01	6.1E-02	2.3E-01	2.0E-01	5.3E-01
GO:0019059	GO:Bio L4	initiation of viral infection	7.8E-01	5.6E-01	7.3E-02	1.3E-01	9.9E-01	9.5E-01	7.0E-01	7.4E-01	9.7E-01	8.7E-01	2.0E-01	3.3E-01
5220	KEGG	Chronic myeloid leukemia	2.8E-01	4.3E-01	6.7E-01	8.6E-01	9.8E-01	6.3E-01	7.6E-02	1.2E-01	6.4E-01	6.2E-01	2.0E-01	3.3E-01
GO:0010884	GO:Bio L4	positive regulation of lipid storage	2.4E-01	1.2E-01	2.9E-01	2.1E-01	2.8E-01	3.9E-01	1.8E-01	5.2E-01	2.4E-01	1.9E-01	2.0E-01	3.5E-01
GO:0032972	GO:Bio L4	regulation of muscle filament sliding speed	2.4E-01	2.6E-01	1.5E-01	1.6E-01	4.1E-01	7.7E-01	3.5E-01	9.0E-01	3.3E-01	5.2E-01	2.0E-01	4.2E-01
GO:0070469	GO:Cell L4	respiratory chain	6.5E-01	4.0E-01	4.3E-01	4.0E-01	8.4E-01	2.1E-01	1.2E-01	1.3E-01	8.8E-01	2.9E-01	2.0E-01	2.0E-01
GO:0022804	GO:Mole L4	active transmembrane transporter activity	1.7E-01	6.7E-02	5.1E-01	2.3E-01	8.4E-01	3.5E-01	1.0E-01	5.5E-01	4.3E-01	1.1E-01	2.0E-01	3.9E-01
GO:0043027	GO:Mole L4	caspase inhibitor activity	2.0E-02	9.5E-03	1.1E-01	2.0E-01	1.9E-01	1.3E-01	4.5E-01	9.9E-01	2.4E-02	9.6E-03	2.0E-01	5.2E-01
GO:0010888	GO:Bio L4	negative regulation of lipid storage	1.5E-01	4.1E-01	5.8E-01	4.2E-01	3.0E-01	4.9E-01	8.8E-02	9.0E-01	1.9E-01	5.3E-01	2.0E-01	7.5E-01
GO:0009629	GO:Bio L4	response to gravity	1.6E-01	4.1E-01	8.4E-02	2.2E-01	9.5E-01	9.0E-01	6.2E-01	4.9E-01	4.3E-01	7.4E-01	2.0E-01	3.5E-01
GO:0021670	GO:Bio L4	lateral ventricle development	4.4E-01	6.2E-01	6.0E-02	1.2E-01	6.3E-01	5.0E-01	8.5E-01	7.1E-01	6.3E-01	6.7E-01	2.0E-01	2.9E-01
GO:0035287	GO:Bio L4	head segmentation	4.4E-01	6.2E-01	6.0E-02	1.2E-01	6.3E-01	5.0E-01	8.5E-01	7.1E-01	6.3E-01	6.7E-01	2.0E-01	2.9E-01
GO:0048857	GO:Bio L4	neural nucleus development	5.5E-02	2.2E-01	4.5E-01	8.0E-01	8.8E-01	6.5E-01	1.2E-01	7.5E-01	1.9E-01	4.2E-01	2.1E-01	9.1E-01
GO:0001819	GO:Bio L4	positive regulation of cytokine production	5.3E-02	1.9E-01	1.9E-01	4.3E-02	2.7E-01	2.6E-01	2.8E-01	2.0E-01	7.5E-02	2.0E-01	2.1E-01	5.0E-02

GO:0010890	GO:Bio L4	positive regulation of sequestering of triglyceride	5.6E-02	2.2E-02	9.0E-02	6.4E-02	6.4E-01	4.5E-01	5.8E-01	4.1E-01	1.5E-01	5.5E-02	2.1E-01	1.2E-01
GO:0002209	GO:Bio L4	behavioral defense response	2.9E-02	5.0E-02	9.4E-02	1.6E-01	2.1E-01	6.4E-01	5.5E-01	7.7E-01	3.6E-02	1.4E-01	2.1E-01	3.9E-01
GO:0043511	GO:Cell L4	inhibin complex	2.7E-01	2.1E-01	1.8E-01	1.6E-01	8.7E-01	8.6E-01	2.8E-01	8.0E-01	5.7E-01	4.8E-01	2.1E-01	3.9E-01
GO:0043512	GO:Cell L4	inhibin A complex	2.7E-01	2.1E-01	1.8E-01	1.6E-01	8.7E-01	8.6E-01	2.8E-01	8.0E-01	5.7E-01	4.8E-01	2.1E-01	3.9E-01
GO:0005932	GO:Cell L4	microtubule basal body	2.8E-01	2.6E-01	1.8E-01	1.8E-01	6.0E-01	3.6E-01	2.9E-01	9.5E-01	4.7E-01	3.2E-01	2.1E-01	4.8E-01
GO:0016840	GO:Mole L4	carbon-nitrogen lyase activity	1.7E-01	1.5E-01	8.6E-02	3.0E-01	2.1E-01	2.6E-01	6.1E-01	4.9E-01	1.6E-01	1.7E-01	2.1E-01	4.3E-01
4320	KEGG	Dorso-ventral axis formation	4.0E-01	1.6E-01	7.4E-01	6.8E-01	3.1E-01	7.1E-01	7.0E-02	2.1E-02	3.8E-01	3.5E-01	2.1E-01	7.6E-02
GO:0044438	GO:Cell L4	microbody part	9.8E-01	9.5E-01	5.5E-01	4.7E-01	6.2E-01	3.2E-01	9.5E-02	1.3E-01	9.1E-01	6.6E-01	2.1E-01	2.3E-01
GO:0033116	GO:Cell L4	ER-Golgi intermediate compartment membrane	8.0E-01	8.6E-01	2.0E-01	2.1E-01	9.9E-02	3.0E-02	2.6E-01	6.8E-01	2.8E-01	1.2E-01	2.1E-01	4.1E-01
GO:0060135	GO:Bio L4	maternal process involved in female pregnancy	3.6E-01	9.2E-01	7.0E-02	6.8E-02	4.9E-01	8.4E-02	7.5E-01	6.7E-02	4.8E-01	2.8E-01	2.1E-01	2.9E-02
GO:0006998	GO:Bio L4	nuclear envelope organization	1.9E-01	1.8E-01	1.9E-01	1.3E-01	8.2E-01	7.5E-01	2.7E-01	1.9E-01	4.5E-01	4.1E-01	2.1E-01	1.2E-01
GO:0008217	GO:Bio L4	regulation of blood pressure	1.4E-01	1.4E-02	7.1E-02	1.5E-01	4.5E-01	3.5E-01	7.4E-01	1.1E-01	2.4E-01	3.0E-02	2.1E-01	8.9E-02
GO:0051960	GO:Bio L4	regulation of nervous system development	2.5E-02	1.0E-02	6.8E-01	5.2E-01	2.5E-02	3.7E-01	7.7E-02	8.6E-01	5.3E-03	2.5E-02	2.1E-01	8.0E-01
PA153627758	PharmGKB	pgkb_pwy_Anti_diabetic_drug_pathway_Potassium_channel_inhibitors_PD	5.8E-02	9.5E-02	2.4E-01	2.5E-01	7.7E-01	2.2E-01	2.2E-01	3.6E-01	1.9E-01	1.0E-01	2.1E-01	3.0E-01
GO:0000159	GO:Cell L4	protein phosphatase type 2A complex	7.2E-01	3.9E-01	9.6E-01	8.5E-01	7.7E-01	4.7E-01	5.5E-02	4.8E-01	8.8E-01	4.9E-01	2.1E-01	7.7E-01
GO:0006519	GO:Bio L4	cellular amino acid and derivative metabolic process	8.3E-01	4.4E-01	3.1E-01	2.2E-01	9.7E-02	3.1E-01	1.7E-01	2.2E-01	2.8E-01	4.1E-01	2.1E-01	2.0E-01
GO:0070201	GO:Bio L4	regulation of establishment of protein localization	9.4E-02	5.3E-02	3.4E-01	1.7E-01	2.6E-01	3.9E-01	1.6E-01	7.7E-01	1.2E-01	9.9E-02	2.1E-01	3.9E-01
GO:0008267	GO:Mole L4	poly-glutamine tract binding	8.0E-01	4.8E-01	7.8E-01	7.1E-01	4.7E-01	2.7E-01	6.8E-02	8.8E-01	7.4E-01	4.0E-01	2.1E-01	9.2E-01
GO:0010149	GO:Bio L4	senescence	4.1E-02	8.1E-02	2.7E-01	2.4E-01	3.4E-01	7.6E-02	2.0E-01	1.2E-01	7.3E-02	3.7E-02	2.1E-01	1.3E-01
GO:0016725	GO:Mole L4	oxidoreductase activity, acting on CH or CH2 groups	9.7E-01	1.0E+00	3.9E-01	6.0E-01	2.5E-01	4.0E-01	1.3E-01	9.3E-01	5.9E-01	7.7E-01	2.1E-01	8.9E-01

GO:0014042	GO:Bio L4	positive regulation of neuron maturation	1.1E-01	1.5E-01	5.1E-01	3.4E-01	4.7E-01	2.2E-01	1.0E-01	5.4E-01	2.0E-01	1.5E-01	2.1E-01	4.9E-01
GO:0019740	GO:Bio L4	nitrogen utilization	1.1E-01	1.5E-01	5.1E-01	3.4E-01	4.7E-01	2.2E-01	1.0E-01	5.4E-01	2.0E-01	1.5E-01	2.1E-01	4.9E-01
GO:0032848	GO:Bio L4	negative regulation of cellular pH reduction	1.1E-01	1.5E-01	5.1E-01	3.4E-01	4.7E-01	2.2E-01	1.0E-01	5.4E-01	2.0E-01	1.5E-01	2.1E-01	4.9E-01
GO:0006880	GO:Bio L4	intracellular sequestering of iron ion	6.6E-01	6.9E-01	6.6E-01	5.8E-01	3.4E-01	2.6E-01	8.2E-02	6.2E-01	5.6E-01	4.9E-01	2.1E-01	7.2E-01
GO:0004325	GO:Mole L4	ferrochelatase activity	6.6E-01	8.0E-01	2.4E-01	1.8E-01	4.6E-01	2.9E-01	2.2E-01	6.1E-01	6.7E-01	5.6E-01	2.1E-01	3.5E-01
GO:0016507	GO:Cell L4	fatty acid beta-oxidation multienzyme complex	1.7E-01	4.0E-01	8.5E-01	8.0E-01	6.3E-01	5.0E-01	6.3E-02	4.0E-01	3.5E-01	5.2E-01	2.1E-01	6.9E-01
GO:0032204	GO:Bio L4	regulation of telomere maintenance	7.4E-01	6.1E-01	4.9E-01	7.4E-01	9.0E-02	2.6E-01	1.1E-01	1.5E-01	2.5E-01	4.5E-01	2.1E-01	3.6E-01
GO:0005521	GO:Mole L4	lamin binding	7.0E-03	1.8E-02	1.1E-01	8.3E-02	7.9E-01	7.2E-01	5.1E-01	2.2E-01	3.4E-02	6.9E-02	2.1E-01	9.1E-02
GO:0016875	GO:Mole L4	ligase activity, forming carbon-oxygen bonds	7.4E-01	8.4E-01	7.9E-01	7.5E-01	4.3E-01	6.6E-01	6.9E-02	6.7E-01	6.9E-01	8.8E-01	2.1E-01	8.5E-01
GO:0010886	GO:Bio L4	positive regulation of cholesterol storage	6.5E-01	8.9E-01	5.9E-01	4.5E-01	1.5E-01	2.4E-01	9.2E-02	3.7E-01	3.2E-01	5.5E-01	2.1E-01	4.7E-01
GO:0009991	GO:Bio L4	response to extracellular stimulus	4.9E-01	1.1E-01	5.0E-01	3.1E-01	8.4E-01	3.9E-01	1.1E-01	8.9E-01	7.8E-01	1.8E-01	2.1E-01	6.3E-01
GO:0010623	GO:Bio L4	developmental programmed cell death	5.2E-01	8.2E-01	5.3E-01	5.4E-01	2.2E-01	2.8E-01	1.0E-01	4.1E-01	3.6E-01	5.7E-01	2.1E-01	5.5E-01
GO:0009308	GO:Bio L4	amine metabolic process	6.6E-01	2.9E-01	1.5E-01	1.3E-01	1.6E-01	5.8E-01	3.6E-01	1.9E-01	3.4E-01	4.7E-01	2.1E-01	1.2E-01
GO:0030238	GO:Bio L4	male sex determination	5.9E-01	7.3E-01	8.1E-02	1.4E-01	9.0E-01	9.1E-01	6.7E-01	5.5E-01	8.7E-01	9.4E-01	2.1E-01	2.7E-01
3320	KEGG	PPAR signaling pathway	4.6E-01	1.0E-01	8.7E-01	9.2E-01	1.5E-02	8.2E-03	6.3E-02	1.6E-01	4.0E-02	6.7E-03	2.1E-01	4.3E-01
GO:0042605	GO:Mole L4	peptide antigen binding	5.0E-01	4.9E-01	1.3E-01	1.2E-01	3.5E-01	6.0E-02	4.1E-01	6.6E-01	4.7E-01	1.3E-01	2.1E-01	2.9E-01
4670	KEGG	Leukocyte transendothelial migration	4.0E-01	4.3E-01	3.7E-01	2.3E-01	1.1E-01	4.8E-02	1.5E-01	1.1E-01	1.8E-01	1.0E-01	2.1E-01	1.2E-01
GO:0009268	GO:Bio L4	response to pH	1.1E-01	1.6E-01	9.3E-02	8.9E-02	8.3E-01	7.2E-01	5.9E-01	6.2E-02	3.0E-01	3.6E-01	2.1E-01	3.4E-02
4940	KEGG	Type I diabetes mellitus	1.8E-02	1.6E-02	1.0E-01	4.0E-02	2.4E-01	7.0E-01	5.5E-01	4.3E-01	2.7E-02	6.0E-02	2.1E-01	8.7E-02
GO:0045823	GO:Bio L4	positive regulation of heart contraction	3.5E-01	9.6E-02	6.9E-02	1.8E-01	7.2E-01	8.0E-01	8.0E-01	3.3E-01	5.9E-01	2.7E-01	2.1E-01	2.3E-01
GO:0043383	GO:Bio L4	negative T cell selection	5.2E-01	4.1E-01	3.8E-01	8.0E-01	9.6E-01	7.1E-01	1.4E-01	4.1E-01	8.5E-01	6.4E-01	2.1E-01	6.9E-01
GO:0016051	GO:Bio L4	carbohydrate biosynthetic process	3.2E-01	2.1E-01	6.8E-02	2.5E-01	5.2E-01	2.4E-01	8.1E-01	1.6E-01	4.6E-01	2.0E-01	2.2E-01	1.7E-01

GO:0044255	GO:Bio L4	cellular lipid metabolic process	3.9E-01	2.0E-01	5.8E-01	7.7E-01	6.2E-02	1.0E-01	9.5E-02	5.7E-01	1.1E-01	9.8E-02	2.2E-01	8.0E-01
GO:0007411	GO:Bio L4	axon guidance	4.7E-01	2.8E-01	1.8E-01	4.6E-01	3.6E-01	5.0E-02	3.1E-01	6.4E-01	4.7E-01	7.4E-02	2.2E-01	6.5E-01
GO:0005602	GO:Cell L4	complement component C1 complex	6.5E-01	3.4E-01	1.6E-01	2.0E-01	8.0E-02	3.9E-01	3.5E-01	2.7E-01	2.1E-01	4.0E-01	2.2E-01	2.1E-01
GO:0008250	GO:Cell L4	oligosaccharyltransferase complex	8.6E-01	8.4E-01	2.6E-01	3.9E-01	8.6E-01	7.4E-01	2.1E-01	6.2E-01	9.6E-01	9.2E-01	2.2E-01	5.8E-01
565	KEGG	Ether lipid metabolism	3.1E-01	3.2E-01	2.2E-01	5.0E-01	7.6E-02	4.6E-01	2.5E-01	7.0E-03	1.1E-01	4.3E-01	2.2E-01	2.3E-02
GO:0070761	GO:Cell L4	pre-snoRNP complex	5.8E-01	1.7E-01	2.6E-01	3.2E-01	5.7E-01	8.8E-01	2.2E-01	1.2E-01	7.0E-01	4.4E-01	2.2E-01	1.7E-01
GO:0010853	GO:Mole L4	cyclase activator activity	5.8E-02	3.4E-01	1.2E-01	6.9E-02	4.5E-01	5.2E-01	4.7E-01	6.6E-01	1.2E-01	4.8E-01	2.2E-01	1.9E-01
GO:0030250	GO:Mole L4	guanylate cyclase activator activity	5.8E-02	3.4E-01	1.2E-01	6.9E-02	4.5E-01	5.2E-01	4.7E-01	6.6E-01	1.2E-01	4.8E-01	2.2E-01	1.9E-01
GO:0022900	GO:Bio L4	electron transport chain	5.1E-01	3.1E-01	5.0E-01	5.7E-01	1.7E-01	7.3E-02	1.1E-01	4.6E-02	3.0E-01	1.1E-01	2.2E-01	1.2E-01