

GeDiPNet Cluster 176 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 00:30:18

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
T cell differentiation in thymus	GO:0033077	6	RAG1, RAG2, ADA, IL2RG, IL7R, LIG4	41	12	227.89	6.963e-14	3.922e-11
V(D)J recombination	GO:0033151	4	RAG1, RAG2, DCLRE1C, LIG4	11	12	566.27	3.208e-11	1.031e-8
DNA recombination	GO:0006310	5	RAG1, RAG2, INO80, DCLRE1C, LIG4	110	12	70.78	4.942e-9	9.235e-7
T cell differentiation	GO:0030217	4	RAG2, ADA, CHD7, IL7R	54	12	115.35	3.030e-8	4.427e-6
positive regulation of T cell differentiation in thymus	GO:0033089	3	ADA, IL2RG, IL7R	11	12	424.70	3.329e-8	4.803e-6
B cell differentiation	GO:0030183	4	RAG1, RAG2, DCLRE1C, IL2RG	80	12	77.86	1.502e-7	1.705e-5
DN2 thymocyte differentiation	GO:1904155	2	RAG2, LIG4	4	12	778.63	2.267e-6	1.591e-4
pre-B cell allelic exclusion	GO:0002331	2	RAG1, RAG2	4	12	778.63	2.267e-6	1.591e-4
chromosome organization	GO:0051276	3	INO80, DCLRE1C, LIG4	51	12	91.60	4.141e-6	2.579e-4
interleukin-7-mediated signaling pathway	GO:0038111	2	IL2RG, IL7R	8	12	389.31	1.056e-5	5.431e-4
negative regulation of thymocyte apoptotic process	GO:0070244	2	RAG1, ADA	10	12	311.45	1.696e-5	7.891e-4
double-strand break repair	GO:0006302	3	INO80, DCLRE1C, LIG4	87	12	53.70	2.080e-5	9.261e-4
negative regulation of T cell apoptotic process	GO:0070233	2	RAG1, IL7R	12	12	259.54	2.486e-5	1.058e-3
regulation of T cell differentiation	GO:0045580	2	RAG1, ADA	17	12	183.21	5.114e-5	1.831e-3
cellular homeostasis	GO:0019725	2	IL2RG, IL7R	23	12	135.41	9.493e-5	2.908e-3