

GeDiPNet Cluster 567 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build_cluster_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:02:53

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Renal cell carcinoma	KEGG	3	BRAF, PTPN11, SOS2	70	8	64.34	1.040e-5	3.009e-4
Chronic myeloid leukemia	KEGG	3	BRAF, PTPN11, SOS2	77	8	58.49	1.387e-5	3.820e-4
Spry regulation of FGF signaling	Reactome	2	BRAF, PTPN11	16	8	187.66	4.638e-5	1.028e-3
Neurotrophin signaling pathway	KEGG	3	BRAF, PTPN11, SOS2	120	8	37.53	5.252e-5	1.132e-3
Natural killer cell mediated cytotoxicity	KEGG	3	BRAF, PTPN11, SOS2	133	8	33.86	7.140e-5	1.450e-3
Hepatocellular carcinoma	KEGG	3	BRAF, SOS2, SMARCB1	170	8	26.49	1.481e-4	2.592e-3
Proteoglycans in cancer	KEGG	3	BRAF, PTPN11, SOS2	204	8	22.08	2.540e-4	3.959e-3
Chemical carcinogenesis - reactive oxygen species	KEGG	3	BRAF, PTPN11, SOS2	227	8	19.84	3.479e-4	5.046e-3
Endometrial cancer	KEGG	2	BRAF, SOS2	59	8	50.89	6.518e-4	8.196e-3
Acute myeloid leukemia	KEGG	2	BRAF, SOS2	68	8	44.15	8.652e-4	1.015e-2
Non-small cell lung cancer	KEGG	2	BRAF, SOS2	73	8	41.13	9.965e-4	1.132e-2
Glioma	KEGG	2	BRAF, SOS2	76	8	39.51	1.080e-3	1.201e-2
EGFR tyrosine kinase inhibitor resistance	KEGG	2	BRAF, SOS2	80	8	37.53	1.195e-3	1.298e-2
ErbB signaling pathway	KEGG	2	BRAF, SOS2	86	8	34.91	1.380e-3	1.446e-2
Colorectal cancer	KEGG	2	BRAF, SOS2	87	8	34.51	1.412e-3	1.472e-2