

Results

[Go To Start Page](#)

Input Parameters [\[Show Detail\]](#)

Training Results [\[Expand All\]](#) [\[Download All\]](#) [\[Sparse Matrix\]](#) Display pValues and Scores as Scientific (4 significant digits) ▼ Table

row limit 50 ▼

1: GO: Molecular Function [\[Display Chart\]](#) 198 input genes in category / 607 annotations before applied cutoff / 19963 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0030280	structural constituent of skin epidermis		3.984E-13	2.418E-10	1.690E-9	2.418E-10	11	44
2	GO:0004252	serine-type endopeptidase activity		9.965E-9	3.024E-6	2.113E-5	6.049E-6	17	303
3	GO:0005198	structural molecule activity		1.770E-8	3.543E-6	2.476E-5	1.074E-5	29	892
4	GO:0008236	serine-type peptidase activity		2.335E-8	3.543E-6	2.476E-5	1.417E-5	17	321
5	GO:0017171	serine hydrolase activity		2.928E-8	3.554E-6	2.483E-5	1.777E-5	17	326

[Show 36 more annotations](#)

2: GO: Biological Process [\[Display Chart\]](#) 198 input genes in category / 4266 annotations before applied cutoff / 20720 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0008544	epidermis development		1.057E-28	4.508E-25	4.028E-24	4.508E-25	43	500
2	GO:0030216	keratinocyte differentiation		2.750E-26	5.865E-23	5.241E-22	1.173E-22	29	195
3	GO:0031424	keratinization		2.582E-25	3.171E-22	2.833E-21	1.101E-21	22	89
4	GO:0009913	epidermal cell differentiation		2.973E-25	3.171E-22	2.833E-21	1.268E-21	34	331
5	GO:0030855	epithelial cell differentiation		3.329E-24	2.840E-21	2.538E-20	1.420E-20	53	1051

[Show 45 more annotations](#)

3: GO: Cellular Component [\[Display Chart\]](#) 199 input genes in category / 416 annotations before applied cutoff / 20932 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	GO:0001533	cornified envelope		5.214E-43	2.169E-40	1.433E-39	2.169E-40	30	69
2	GO:0070161	anchoring junction		1.555E-9	3.234E-7	2.138E-6	6.469E-7	39	1419
3	GO:0097209	epidermal lamellar body		8.003E-9	9.490E-7	6.272E-6	3.329E-6	4	4
4	GO:0005911	cell-cell junction		1.104E-8	9.490E-7	6.272E-6	4.594E-6	23	590
5	GO:0005614	interstitial matrix		1.156E-8	9.490E-7	6.272E-6	4.808E-6	6	18

[Show 39 more annotations](#)

4: Human Phenotype [\[Display Chart\]](#) 82 input genes in category / 2832 annotations before applied cutoff / 5060 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	HP:0001035	Abnormality of keratinization		4.288E-15	1.214E-11	1.035E-10	1.214E-11	26	250
2	HP:0000962	Hyperkeratosis		1.673E-13	2.369E-10	2.020E-9	4.738E-10	24	241
3	HP:0100872	Abnormality of the plantar skin of foot		7.815E-13	7.377E-10	6.290E-9	2.213E-9	21	188
4	HP:0000982	Palmoplantar keratoderma		1.046E-12	7.403E-10	6.312E-9	2.961E-9	19	149
5	HP:0000972	Palmoplantar hyperkeratosis		2.730E-12	1.218E-9	1.038E-8	7.732E-9	19	157

[Show 45 more annotations](#)**5: Mouse Phenotype** [\[Display Chart\]](#) 149 input genes in category / 3181 annotations before applied cutoff / 12941 genes in category

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	MP:0001240	abnormal epidermis stratum corneum morphology	1.976E-11	3.625E-8	3.133E-7	6.284E-8	15	129
2	MP:0001216	abnormal epidermal layer morphology	2.279E-11	3.625E-8	3.133E-7	7.251E-8	20	264
3	MP:0005501	abnormal skin physiology	3.429E-11	3.634E-8	3.141E-7	1.091E-7	20	270
4	MP:0005023	abnormal wound healing	4.570E-11	3.634E-8	3.141E-7	1.454E-7	17	187
5	MP:0002796	impaired skin barrier function	1.947E-9	1.239E-6	1.071E-5	6.194E-6	10	62

[Show 45 more annotations](#)**6: Domain** [\[Display Chart\]](#) 198 input genes in category / 1121 annotations before applied cutoff / 18678 genes in category

ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	PF01023	S 100	5.599E-12	3.055E-9	2.322E-8	6.276E-9	9	27
2	IPR013787	S100 Ca-bd sub	8.176E-12	3.055E-9	2.322E-8	9.165E-9	9	28
3	SM01394	S 100	8.176E-12	3.055E-9	2.322E-8	9.165E-9	9	28
4	PS00303	S100 CABP	2.586E-10	7.246E-8	5.507E-7	2.898E-7	8	27
5	IPR001751	S100/CaBP-9k CS	3.587E-10	8.042E-8	6.112E-7	4.021E-7	8	28

[Show 45 more annotations](#)**7: Pathway** [\[Display Chart\]](#) 165 input genes in category / 1589 annotations before applied cutoff / 13609 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1457791	Formation of the cornified envelope	BioSystems: REACTOME	1.926E-22	1.547E-19	1.229E-18	3.060E-19	20	71
2	1457790	Keratinization	BioSystems: REACTOME	1.947E-22	1.547E-19	1.229E-18	3.093E-19	29	214
3	M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	MSigDB C2 BIOCARTEA (v7.5.1)	5.794E-14	3.069E-11	2.439E-10	9.207E-11	44	1026
4	M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	MSigDB C2 BIOCARTEA (v7.5.1)	8.120E-11	3.118E-8	2.478E-7	1.290E-7	33	751
5	1270302	Developmental Biology	BioSystems: REACTOME	9.811E-11	3.118E-8	2.478E-7	1.559E-7	40	1078

[Show 21 more annotations](#)**8: Pubmed** [\[Display Chart\]](#) 201 input genes in category / 55075 annotations before applied cutoff / 44761 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	32989256	Suppression of DDX39B sensitizes ovarian cancer cells to DNA-damaging chemotherapeutic agents via destabilizing BRCA1 mRNA.	Pubmed	2.840E-32	1.564E-27	1.798E-26	1.564E-27	23	107
2	26644517	A keratin scaffold regulates epidermal barrier formation, mitochondrial lipid composition, and activity.	Pubmed	3.811E-26	1.050E-21	1.206E-20	2.099E-21	17	62
3	34905516	Translational implications of Th17-skewed inflammation due to genetic deficiency of a cadherin stress sensor.	Pubmed	2.280E-23	4.186E-19	4.811E-18	1.256E-18	13	30
4	19199708	Proteomic analysis of human parotid gland exosomes by multidimensional protein identification technology (MudPIT).	Pubmed	9.568E-21	1.317E-16	1.514E-15	5.270E-16	25	417
5	23376485	Proteomic analysis of podocyte exosome-enriched fraction from normal human urine.	Pubmed	3.688E-19	4.062E-15	4.669E-14	2.031E-14	42	1744

[Show 45 more annotations](#)**9: Interaction** [\[Display Chart\]](#) 196 input genes in category / 8688 annotations before applied cutoff / 19896 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	int:CCR1	CCR1 interactions		3.343E-43	2.904E-39	2.802E-38	2.904E-39	50	360
2	int:SSUH2	SSUH2 interactions		1.186E-39	5.152E-36	4.970E-35	1.030E-35	39	199
3	int:C18orf21	C18orf21 interactions		2.362E-38	6.840E-35	6.598E-34	2.052E-34	35	151
4	int:OR2A4	OR2A4 interactions		1.885E-37	4.093E-34	3.949E-33	1.637E-33	34	145
5	int:PPP2R2B	PPP2R2B interactions		1.123E-36	1.951E-33	1.882E-32	9.757E-33	39	235

Show 45 more annotations

10: Cytoband [Display Chart] 201 input genes in category / 153 annotations before applied cutoff / 33040 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	1q21-q22	1q21-q22		4.356E-9	3.717E-7	2.086E-6	6.665E-7	6	23
2	1q21	1q21		4.859E-9	3.717E-7	2.086E-6	7.435E-7	9	91
3	18q12.1	18q12.1		1.789E-5	9.126E-4	5.120E-3	2.738E-3	4	26
4	18q21.3	18q21.3		3.531E-5	1.080E-3	6.062E-3	5.402E-3	3	11
5	2q14	2q14		3.531E-5	1.080E-3	6.062E-3	5.402E-3	3	11

Show 2 more annotations

11: Transcription Factor Binding Site [Display Chart] 188 input genes in category / 729 annotations before applied cutoff / 26918 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	TATAAA V\$TATA 01	TATAAA V\$TATA 01	TFBS	8.561E-11	6.241E-8	4.474E-7	6.241E-8	30	1070
2	TGANTCA V\$AP1 C	TGANTCA V\$AP1 C	TFBS	2.943E-10	1.073E-7	7.690E-7	2.145E-7	27	918
3	M30042	KMT2D TARGET GENES	MSigDB	3.763E-6	9.145E-4	6.557E-3	2.744E-3	19	801
4	GGGTGGRR V\$PAX4 03	GGGTGGRR V\$PAX4 03	TFBS	1.994E-5	3.635E-3	2.606E-2	1.454E-2	21	1068

12: Gene Family [Display Chart] 147 input genes in category / 100 annotations before applied cutoff / 18084 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	459	S100 calcium binding proteins EF-hand domain containing	genenames.org	2.928E-12	2.928E-10	1.519E-9	2.928E-10	8	21
2	1353	Small proline rich proteins	genenames.org	1.163E-10	5.817E-9	3.017E-8	1.163E-8	6	11
3	616	Kallikreins	genenames.org	1.950E-9	6.500E-8	3.372E-7	1.950E-7	6	16
4	1188	Desmosomal cadherins	genenames.org	1.439E-7	3.598E-6	1.867E-5	1.439E-5	4	7
5	739	Serpin peptidase inhibitors	genenames.org	4.918E-7	9.837E-6	5.103E-5	4.918E-5	6	37

Show 13 more annotations

13: Coexpression [Display Chart] 201 input genes in category / 8310 annotations before applied cutoff / 26258 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M40004	BUSSLINGER ESOPHAGEAL LATE SUPRABASAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	3.748E-71	3.114E-67	2.990E-66	3.114E-67	50	140
2	M10702	JAEGER METASTASIS DN	MSigDB C2: CGP Curated Gene Sets (v7.5.1)	3.407E-59	1.415E-55	1.359E-54	2.831E-55	52	259
3	M40122	DESCARTES MAIN FETAL SQUAMOUS EPITHELIAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	2.011E-57	5.569E-54	5.348E-53	1.671E-53	42	130
4	M4306	ONDER CDH1 TARGETS 2 DN	MSigDB C2: CGP Curated Gene Sets (v7.5.1)	4.499E-56	9.347E-53	8.975E-52	3.739E-52	60	472
5	M40299	DESCARTES FETAL STOMACH SQUAMOUS EPITHELIAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	6.941E-55	1.154E-51	1.108E-50	5.768E-51	34	67

Show 45 more annotations

14: Coexpression Atlas [\[Display Chart\]](#) 201 input genes in category / 3143 annotations before applied cutoff / 21235 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	esophagus	esophagus	Human Protein Atlas	2.293E-116	7.208E-113	6.221E-112	7.208E-113	86	247
2	PCBC ctl BronchioEpithel 500	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 500	PCBC	6.589E-100	1.036E-96	8.937E-96	2.071E-96	94	496
3	PCBC ctl BronchioEpithel 1000	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 1000	PCBC	3.719E-91	3.896E-88	3.363E-87	1.169E-87	109	990
4	PCBC ctl BronchioEpithel 100	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 100	PCBC	6.736E-81	5.292E-78	4.568E-77	2.117E-77	52	98
5	BM Top 100 - esophagus	BM Top 100 - esophagus	Body Map	7.976E-74	5.014E-71	4.327E-70	2.507E-70	47	86

[Show 45 more annotations](#)**15: ToppCell Atlas** [\[Display Chart\]](#) 201 input genes in category / 21856 annotations before applied cutoff / 45195 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	eb18aa179db1818f408c38e442ecfed8582d7dbc	TCGA-Head and Esophagus World / Sample Type by Project: Shred V9	TCGA OncoMap	4.890E-144	1.069E-139	1.130E-138	1.069E-139	79	172
2	3188c7bd225cbcf46a21e2fb784336cdd9665995	TCGA-Skin-Primary Tumor-Melanoma-Skin Cutaneous Melanoma TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	3.570E-137	1.950E-133	2.062E-132	7.802E-133	78	190
3	e2b26a03c6ab24d9b0f4150c47597be37767d86e	TCGA-Skin-Primary Tumor TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	3.570E-137	1.950E-133	2.062E-132	7.802E-133	78	190
4	01fb45add4661bc86cd0a34fac35177907152dbb	TCGA-Skin-Primary Tumor-Melanoma TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	3.570E-137	1.950E-133	2.062E-132	7.802E-133	78	190
5	03de28e1c963e99623e8b0e33bf2e8ef67dc3baa	Smart-seq2-tissue-resident (Smart-seq2)-myeloid-myeloid monocytic tissue-resident (Smart-seq2) / Per Platform+tissue group, by lineage subgroup, cell group, cell type	Immune and Hematologic Cells from 24 tissues of the Tabula Sapiens: a multiple organ single cell transcriptomic atlas of humans.	1.773E-119	7.749E-116	8.190E-115	3.875E-115	71	196

[Show 45 more annotations](#)**16: Computational** [\[Display Chart\]](#) 133 input genes in category / 367 annotations before applied cutoff / 10012 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	M2266 GNF2 SPRR1B	Neighborhood of SPRR1B	MSigDb: C4 - CGN: Cancer Gene Neighborhood (v7.2)	6.368E-30	2.337E-27	1.515E-26	2.337E-27	18	24
2	M4992 MODULE 297	Genes in the cancer module 297.	MSigDb: C4 - CM: Cancer Modules (v7.2)	9.243E-27	1.131E-24	7.331E-24	3.392E-24	24	80
3	M9185 MODULE 357	Intermediate filaments and keratins.	MSigDb: C4 - CM: Cancer Modules (v7.2)	9.243E-27	1.131E-24	7.331E-24	3.392E-24	24	80
4	M18170	Intermediate filaments.	MSigDb: C4 - CM: Cancer Modules	2.462E-	2.258E-	1.464E-	9.034E-22	22	75

	MODULE 154		(v7.2)	24	22	21			
5	M9365 GNF2 SERPINB5	Neighborhood of SERPINB5	MSigDb: C4 - CGN: Cancer Gene Neighborhood (v7.2)	6.982E- 18	5.124E- 16	3.323E- 15	2.562E-15	13	28

Show 23 more annotations

17: MicroRNA [Display Chart] 201 input genes in category / 8029 annotations before applied cutoff / 59110 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	hsa-miR-1197:mirSVR lowEffect	hsa-miR-1197:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	1.271E-16	1.020E-12	9.763E-12	1.020E-12	35	1829
2	hsa-miR-4289:mirSVR lowEffect	hsa-miR-4289:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	1.423E-12	5.712E-9	5.465E-8	1.142E-8	29	1715
3	hsa-miR-124-3p:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	5.921E-12	1.585E-8	1.516E-7	4.754E-8	26	1446
4	hsa-miR-325-3p:TargetScan	hsa-miR-325-3p	TargetScan	8.967E-12	1.775E-8	1.698E-7	7.200E-8	28	1722
5	hsa-miR-4270:mirSVR highEffect	hsa-miR-4270:mirSVR nonconserved highEffect-0.5	MicroRNA.org	1.105E-11	1.775E-8	1.698E-7	8.873E-8	20	827

Show 45 more annotations

18: Drug [Display Chart] 201 input genes in category / 21379 annotations before applied cutoff / 22767 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	ctd:D004054	Diethylstilbestrol	CTD	7.494E-20	1.602E-15	1.690E-14	1.602E-15	51	1304
2	ctd:D012906	Smoke	CTD	1.238E-17	1.324E-13	1.396E-12	2.647E-13	41	937
3	CID000128831	CK17	Stitch	6.101E-17	4.348E-13	4.586E-12	1.304E-12	14	57
4	CID000005538	9cRA	Stitch	5.378E-16	2.875E-12	3.032E-11	1.150E-11	53	1735
5	ctd:C002202	4-oxoretinoic acid	CTD	1.007E-13	4.307E-10	4.543E-9	2.154E-9	15	115

Show 45 more annotations

19: Disease [Display Chart] 191 input genes in category / 6491 annotations before applied cutoff / 19383 genes in category

	ID	Name	Source	pValue	FDR B&H	FDR B&Y	Bonferroni	Genes from Input	Genes in Annotation
1	C0037274	Dermatologic disorders	DisGeNET BeFree	9.961E-22	6.465E-18	6.049E-17	6.465E-18	38	544
2	C0033860	Psoriasis	DisGeNET BeFree	1.838E-16	5.965E-13	5.581E-12	1.193E-12	45	1105
3	C0870082	Hyperkeratosis	DisGeNET BeFree	1.654E-15	3.579E-12	3.348E-11	1.074E-11	16	97
4	C0037277	Skin Diseases, Genetic	DisGeNET BeFree	7.141E-15	1.159E-11	1.084E-10	4.635E-11	13	56
5	C1168401	Squamous cell carcinoma of the head and neck	DisGeNET BeFree	1.381E-14	1.793E-11	1.677E-10	8.965E-11	50	1519

Show 45 more annotations