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1: GO: Molecular Function [Display Chart] 193 input genes in category / 599 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		1.053E-11	6.307E-9	4.398E-8	6.307E-9	10	44
2	GO:0004252	serine-type endopeptidase activity		6.777E-9	2.030E-6	1.415E-5	4.060E-6	17	303
3	GO:0004175	endopeptidase activity		1.216E-8	2.388E-6	1.665E-5	7.283E-6	25	685
4	GO:0008236	serine-type peptidase activity		1.595E-8	2.388E-6	1.665E-5	9.553E-6	17	321
5	GO:0017171	serine hydrolase activity		2.002E-8	2.398E-6	1.672E-5	1.199E-5	17	326

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2: GO: Biological Process [Display Chart] 192 input genes in category / 4055 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		6.204E-24	2.516E-20	2.235E-19	2.516E-20	38	500
2	GO:0030216	keratinocyte differentiation		1.799E-21	3.648E-18	3.241E-17	7.295E-18	25	195
3	GO:0031424	keratinization		6.119E-21	8.271E-18	7.349E-17	2.481E-17	19	89
4	GO:0030855	epithelial cell differentiation		7.460E-20	7.562E-17	6.719E-16	3.025E-16	47	1051
5	GO:0009913	epidermal cell differentiation		5.328E-19	4.321E-16	3.839E-15	2.161E-15	28	331

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3: GO: Cellular Component [Display Chart] 193 input genes in category / 431 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		1.988E-28	8.568E-26	5.693E-25	8.568E-26	22	69
2	GO:0005911	cell-cell junction		5.939E-7	1.280E-4	8.504E-4	2.560E-4	20	590
3	GO:0070161	anchoring junction		2.251E-6	2.538E-4	1.687E-3	9.701E-4	32	1419
4	GO:0016328	lateral plasma membrane		2.356E-6	2.538E-4	1.687E-3	1.015E-3	8	93
5	GO:0097209	epidermal lamellar body		3.066E-6	2.643E-4	1.756E-3	1.322E-3	3	4

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4: Human Phenotype [Display Chart] 86 input genes in category / 3025 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		5.207E-10	1.575E-6	1.353E-5	1.575E-6	21	250
2	HP:0007446	Palmoplantar blistering		8.729E-9	9.752E-6	8.379E-5	2.640E-5	6	11
3	HP:0000962	Hyperkeratosis		1.171E-8	9.752E-6	8.379E-5	3.543E-5	19	241
4	HP:0011368	Epidermal thickening		1.323E-8	9.752E-6	8.379E-5	4.001E-5	23	358
5	HP:0011124	Abnormal epidermal morphology		1.705E-8	9.752E-6	8.379E-5	5.159E-5	11	70

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5: Mouse Phenotype [Display Chart] 149 input genes in category / 3089 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:0005501	abnormal skin physiology		2.658E-10	8.212E-7	7.073E-6	8.212E-7	19	270
2	MP:0000428	abnormal craniofacial morphology		1.317E-8	1.356E-5	1.168E-4	4.067E-5	38	1242
3	MP:0005382	craniofacial phenotype		1.317E-8	1.356E-5	1.168E-4	4.067E-5	38	1242
4	MP:0000432	abnormal head morphology		1.973E-8	1.524E-5	1.312E-4	6.095E-5	33	990
5	MP:0002796	impaired skin barrier function		3.367E-8	2.080E-5	1.792E-4	1.040E-4	9	62

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6: Domain [Display Chart] 194 input genes in category / 1110 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	Pfam	4.658E-12	2.517E-9	1.910E-8	5.170E-9	9	27
2	IPR013787	S100 Ca-bd sub	InterPro	6.803E-12	2.517E-9	1.910E-8	7.551E-9	9	28
3	SM01394	S 100	SMART	6.803E-12	2.517E-9	1.910E-8	7.551E-9	9	28
4	PS00303	S100 CABP	PROSITE	2.198E-10	6.098E-8	4.628E-7	2.439E-7	8	27
5	IPR001751	S100/CaBP-9k CS	InterPro	3.049E-10	6.769E-8	5.138E-7	3.385E-7	8	28

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7: Pathway [Display Chart] 158 input genes in category / 1378 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	1457790	Keratinization	BioSystems: REACTOME	4.217E-16	5.811E-13	4.536E-12	5.811E-13	23	214
2	1457791	Formation of the cornified envelope	BioSystems: REACTOME	2.500E-15	1.723E-12	1.345E-11	3.446E-12	15	71
3	M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	MSigDB C2 BIOCARTA (v7.5.1)	1.055E-14	4.845E-12	3.782E-11	1.454E-11	44	1026
4	M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affilaited proteins, ECM regulators and secreted factors	MSigDB C2 BIOCARTA (v7.5.1)	3.386E-14	1.166E-11	9.105E-11	4.666E-11	37	751
5	1457778	Metal sequestration by antimicrobial proteins	BioSystems: REACTOME	1.177E-9	3.244E-7	2.532E-6	1.622E-6	5	6

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8: Pubmed [Display Chart] 195 input genes in category / 57411 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	3.839E-27	2.204E-22	2.542E-21	2.204E-22	20	107
2	23376485	Proteomic analysis of podocyte exosome-enriched fraction from normal human urine.	Pubmed	2.132E-21	6.121E-17	7.061E-16	1.224E-16	44	1744
3	19199708	Proteomic analysis of human parotid gland exosomes by multidimensional protein identification technology (MudPIT).	Pubmed	4.489E-21	8.590E-17	9.909E-16	2.577E-16	25	417
4	31220272	Altered keratinocyte differentiation is an early driver of keratin mutation-based palmoplantar keratoderma.	Pubmed	8.033E-21	1.153E-16	1.330E-15	4.612E-16	14	60
5	26644517	A keratin scaffold regulates epidermal barrier formation, mitochondrial lipid composition, and activity.	Pubmed	9.353E-19	1.074E-14	1.239E-13	5.370E-14	13	62

Show 45 more annotations

9: Interaction [Display Chart] 190 input genes in category / 8009 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		1.221E-38	9.780E-35	9.355E-34	9.780E-35	46	360
2	int:OR2A4	OR2A4 interactions		8.402E-35	3.365E-31	3.218E-30	6.729E-31	32	145
3	int:PPP2R2B	PPP2R2B interactions		1.924E-34	5.136E-31	4.913E-30	1.541E-30	37	235
4	int:SSUH2	SSUH2 interactions		1.639E-31	3.281E-28	3.138E-27	1.312E-27	33	199
5	int:C18orf21	C18orf21 interactions		3.555E-31	5.694E-28	5.447E-27	2.847E-27	30	151

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10: Cytoband [Display Chart] 193 input genes in category / 146 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	1q21		3.406E-9	2.493E-7	1.387E-6	4.973E-7	9	91
2	1q21-q22	1q21-q22		3.415E-9	2.493E-7	1.387E-6	4.986E-7	6	23
3	18q21.3	18q21.3		3.607E-7	1.755E-5	9.767E-5	5.266E-5	4	11
4	12q13.13	12q13.13		4.649E-5	1.697E-3	9.442E-3	6.787E-3	5	67
5	7q21.12	7q21.12		9.288E-4	2.712E-2	1.509E-1	1.356E-1	2	8

11: Transcription Factor Binding Site [Display Chart] 176 input genes in category / 788 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	1.565E-11	1.233E-8	8.939E-8	1.233E-8	30	1070
2	GGGAGGRR V$MAZ Q6	GGGAGGRR V$MAZ Q6	TFBS	1.005E-6	3.959E-4	2.869E-3	7.918E-4	31	1836
3	TGANTCA V$AP1 C	TGANTCA V$AP1 C	TFBS	2.663E-6	6.994E-4	5.069E-3	2.098E-3	20	918
4	TGCCAAR V$NF1 Q6	TGCCAAR V$NF1 Q6	TFBS	2.589E-5	5.100E-3	3.696E-2	2.040E-2	14	572
5	V$HNF4 Q6	V$HNF4 Q6	TFBS	6.656E-5	8.816E-3	6.389E-2	5.245E-2	8	206

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12: Gene Family [Display Chart] 157 input genes in category / 111 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	4.987E-12	5.535E-10	2.929E-9	5.535E-10	8	21
2	1353	Small proline rich proteins	genenames.org	1.734E-10	9.624E-9	5.092E-8	1.925E-8	6	11
3	616	Kallikreins	genenames.org	1.871E-7	6.922E-6	3.663E-5	2.077E-5	5	16
4	609	Keratins, type II	genenames.org	3.201E-6	8.883E-5	4.700E-4	3.553E-4	5	27
5	863	EF-hand domain containing	genenames.org	2.197E-5	4.877E-4	2.580E-3	2.438E-3	10	219

Show 21 more annotations

13: Coexpression [Display Chart] 195 input genes in category / 7976 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)	5.721E-78	4.563E-74	4.363E-73	4.563E-74	53	140
2	M40122	DESCARTES MAIN FETAL SQUAMOUS EPITHELIAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	3.922E-56	1.564E-52	1.495E-51	3.128E-52	41	130
3	M40237	DESCARTES FETAL LUNG SQUAMOUS EPITHELIAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	4.131E-55	1.098E-51	1.050E-50	3.295E-51	46	207
4	M4306	ONDER CDH1 TARGETS 2 DN	MSigDB C2: CGP Curated Gene Sets (v7.5.1)	4.037E-43	8.051E-40	7.698E-39	3.220E-39	50	472
5	M10702	JAEGER METASTASIS DN	MSigDB C2: CGP Curated Gene Sets (v7.5.1)	1.476E-42	2.354E-39	2.251E-38	1.177E-38	41	259

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14: Coexpression Atlas [Display Chart] 195 input genes in category / 3064 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	3.228E-100	9.891E-97	8.511E-96	9.891E-97	77	247
2	PCBC ctl BronchioEpithel 500	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 500	PCBC	5.999E-76	9.191E-73	7.908E-72	1.838E-72	78	496

3	PCBC ctl BronchioEpithel 1000	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 1000	PCBC	1.411E-73	1.441E-70	1.240E-69	4.323E-70	95	990
4	BM Top 100 - esophagus	BM Top 100 - esophagus	Body Map	8.743E-66	6.697E-63	5.763E-62	2.679E-62	43	86
5	PCBC ctl BronchioEpithel 100	Progenitor-Cell-Biology-Consortium reference BronchioEpithel top-relative-expression-ranked 100	PCBC	1.375E-54	8.427E-52	7.251E-51	4.214E-51	39	98

Show 45 more annotations

15: ToppCell Atlas [Display Chart] 195 input genes in category / 21730 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	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.	5.026E-116	8.381E-112	8.853E-111	1.092E-111	69	196
2	e621d4f9d4ba5e3ef17d2b477e5e14ea0251147e	Smart-seq2-tissue-resident (Smart-seq2)-myeloid-myeloid monocytic-leukocyte|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.	7.713E-116	8.381E-112	8.853E-111	1.676E-111	69	197
3	3188c7bd225cbcf46a21e2fb784336cdd9665995	TCGA-Skin-Primary Tumor-Melanoma-Skin Cutaneous Melanoma|TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	7.244E-115	3.148E-111	3.326E-110	1.574E-110	68	190
4	e2b26a03c6ab24d9b0f4150c47597be37767d86e	TCGA-Skin-Primary Tumor|TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	7.244E-115	3.148E-111	3.326E-110	1.574E-110	68	190
5	01fb45add4661bc86cd0a34fac35177907152dbb	TCGA-Skin-Primary Tumor-Melanoma|TCGA-Skin / Sample Type by Project: Shred V9	TCGA OncoMap	7.244E-115	3.148E-111	3.326E-110	1.574E-110	68	190

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16: Computational [Display Chart] 133 input genes in category / 353 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)	2.340E-32	8.261E-30	5.324E-29	8.261E-30	19	24
2	M4992 MODULE 297	Genes in the cancer module 297.	MSigDb: C4 - CM: Cancer Modules (v7.2)	9.084E-18	1.069E-15	6.889E-15	3.207E-15	18	80
3	M9185 MODULE 357	Intermediate filaments and keratins.	MSigDb: C4 - CM: Cancer Modules (v7.2)	9.084E-18	1.069E-15	6.889E-15	3.207E-15	18	80
4	M18170 MODULE 154	Intermediate filaments.	MSigDb: C4 - CM: Cancer Modules (v7.2)	1.653E-15	1.458E-13	9.399E-13	5.834E-13	16	75
5	M18849 MODULE 153	Genes in the cancer module 153.	MSigDb: C4 - CM: Cancer Modules (v7.2)	3.301E-13	2.331E-11	1.502E-10	1.165E-10	11	34

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17: MicroRNA [Display Chart] 195 input genes in category / 7706 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-653:mirSVR lowEffct	hsa-miR-653:mirSVR conserved lowEffect-0.1-0.5	MicroRNA.org	1.557E-13	1.200E-9	1.143E-8	1.200E-9	31	1868
2	hsa-miR-1197:mirSVR lowEffct	hsa-miR-1197:mirSVR nonconserved lowEffect-0.1-0.5	MicroRNA.org	3.115E-12	1.200E-8	1.144E-7	2.401E-8	29	1829
3	hsa-miR-26b-5p:Functional MTI (Weak)	Functional MTI (Weak)	miRTarbase	2.992E-11	7.685E-8	7.321E-7	2.305E-7	28	1873
4	hsa-miR-2053:mirSVR highEffct	hsa-miR-2053:mirSVR nonconserved highEffect-0.5	MicroRNA.org	6.301E-11	1.214E-7	1.157E-6	4.856E-7	28	1935
5	hsa-miR-30e:mirSVR highEffct	hsa-miR-30e:mirSVR conserved highEffect-0.5	MicroRNA.org	1.087E-10	1.327E-7	1.264E-6	8.375E-7	28	1982

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18: Drug [Display Chart] 195 input genes in category / 22457 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:D052638	Particulate Matter	CTD	3.723E-17	8.360E-13	8.859E-12	8.360E-13	54	1747
2	ctd:D004054	Diethylstilbestrol	CTD	1.050E-16	1.172E-12	1.242E-11	2.357E-12	46	1304
3	ctd:D012906	Smoke	CTD	1.566E-16	1.172E-12	1.242E-11	3.517E-12	39	937
4	CID000005538	9cRA	Stitch	6.081E-16	3.414E-12	3.617E-11	1.366E-11	52	1735
5	ctd:D009151	Mustard Gas	CTD	7.362E-13	3.307E-9	3.504E-8	1.653E-8	41	1340

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19: Disease [Display Chart] 183 input genes in category / 6359 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	C0033860	Psoriasis	DisGeNET BeFree	1.541E-19	9.798E-16	9.146E-15	9.798E-16	48	1105
2	C0011615	Dermatitis, Atopic	DisGeNET BeFree	1.288E-17	4.095E-14	3.823E-13	8.190E-14	36	666
3	C0013595	Eczema	DisGeNET BeFree	2.497E-17	5.294E-14	4.942E-13	1.588E-13	36	680
4	C0037274	Dermatologic disorders	DisGeNET BeFree	5.316E-15	8.452E-12	7.890E-11	3.381E-11	30	544
5	C0878500	Intraepithelial Neoplasia	DisGeNET BeFree	2.574E-11	3.274E-8	3.056E-7	1.637E-7	16	186

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