

# Results

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### 1: GO: Molecular Function [\[Display Chart\]](#) 205 input genes in category / 739 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:0050839	cell adhesion molecule binding		2.624E-7	1.939E-4	1.393E-3	1.939E-4	22	600
2	GO:0045296	cadherin binding		2.601E-6	9.609E-4	6.903E-3	1.922E-3	15	341
3	GO:0051015	actin filament binding		7.434E-6	1.831E-3	1.315E-2	5.493E-3	12	240
4	GO:0005298	proline:sodium symporter activity		1.051E-5	1.942E-3	1.395E-2	7.768E-3	3	5
5	GO:0003779	actin binding		1.581E-5	2.337E-3	1.679E-2	1.169E-2	17	497

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### 2: GO: Biological Process [\[Display Chart\]](#) 204 input genes in category / 4990 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:0060429	epithelium development		1.139E-19	5.684E-16	5.168E-15	5.684E-16	66	1979
2	GO:0030855	epithelial cell differentiation		3.487E-17	8.700E-14	7.910E-13	1.740E-13	45	1051
3	GO:0048729	tissue morphogenesis		1.382E-14	2.299E-11	2.090E-10	6.896E-11	43	1132
4	GO:0002065	columnar/cuboidal epithelial cell differentiation		6.263E-14	7.813E-11	7.104E-10	3.125E-10	19	193
5	GO:0048565	digestive tract development		1.569E-13	1.565E-10	1.423E-9	7.827E-10	21	261

[Show 45 more annotations](#)

### 3: GO: Cellular Component [\[Display Chart\]](#) 204 input genes in category / 424 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:0005902	microvillus		2.867E-12	1.216E-9	8.058E-9	1.216E-9	15	131
2	GO:0045177	apical part of cell		6.451E-11	9.691E-9	6.423E-8	2.735E-8	26	569
3	GO:0005903	brush border		6.857E-11	9.691E-9	6.423E-8	2.907E-8	15	163
4	GO:0098590	plasma membrane region		1.091E-10	1.157E-8	7.668E-8	4.628E-8	43	1498
5	GO:0016324	apical plasma membrane		1.064E-9	9.023E-8	5.980E-7	4.511E-7	22	464

[Show 44 more annotations](#)

### 4: Human Phenotype [\[Display Chart\]](#) 84 input genes in category / 3303 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:0002581	Pancreatic insufficiency		3.406E-7	3.750E-4	3.255E-3	1.125E-3	9	58
2	HP:0012092	Abnormality of exocrine pancreas physiology		3.406E-7	3.750E-4	3.255E-3	1.125E-3	9	58
3	HP:0001738	Exocrine pancreatic insufficiency		3.406E-7	3.750E-4	3.255E-3	1.125E-3	9	58
4	HP:0002594	Pancreatic hypoplasia		2.975E-5	2.457E-2	2.133E-1	9.828E-2	5	23
5	HP:0004924	Abnormal oral glucose tolerance		4.510E-5	2.979E-2	2.586E-1	1.490E-1	4	13

[Show 11 more annotations](#)

**5: Mouse Phenotype** [\[Display Chart\]](#) 164 input genes in category / 3720 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:0005381	digestive/alimentary phenotype	2.917E-15	1.085E-11	9.548E-11	1.085E-11	55	1391
2	MP:0000462	abnormal digestive system morphology	8.676E-12	1.495E-8	1.316E-7	3.228E-8	43	1090
3	MP:0000477	abnormal intestine morphology	1.206E-11	1.495E-8	1.316E-7	4.485E-8	28	482
4	MP:0001663	abnormal digestive system physiology	5.391E-11	5.013E-8	4.411E-7	2.005E-7	30	589
5	MP:0010155	abnormal intestine physiology	2.136E-9	1.589E-6	1.398E-5	7.945E-6	19	277

[Show 45 more annotations](#)**6: Domain** [\[Display Chart\]](#) 204 input genes in category / 1243 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	PF01390	SEA	<a href="#">Pfam</a>	3.350E-6	1.758E-3	1.354E-2	4.164E-3	5	22
2	PS50024	SEA	<a href="#">PROSITE</a>	4.243E-6	1.758E-3	1.354E-2	5.274E-3	5	23
3	IPR000082	SEA dom	<a href="#">InterPro</a>	4.243E-6	1.758E-3	1.354E-2	5.274E-3	5	23
4	SM00200	SEA	<a href="#">SMART</a>	1.269E-5	3.945E-3	3.039E-2	1.578E-2	4	14
5	IPR023415	LDLR class-A CS	<a href="#">InterPro</a>	7.135E-5	1.356E-2	1.045E-1	8.869E-2	5	40

[Show 45 more annotations](#)**7: Pathway** [\[Display Chart\]](#) 166 input genes in category / 1395 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	1383050	Defective C1GALT1C1 causes Tn polyagglutination syndrome (TNPS)	BioSystems: REACTOME	4.948E-8	2.301E-5	1.799E-4	6.902E-5	6	18
2	1383051	Defective GALNT3 causes familial hyperphosphatemic tumoral calcinosis (HFTC)	BioSystems: REACTOME	4.948E-8	2.301E-5	1.799E-4	6.902E-5	6	18
3	1383052	Defective GALNT12 causes colorectal cancer 1 (CRCS1)	BioSystems: REACTOME	4.948E-8	2.301E-5	1.799E-4	6.902E-5	6	18
4	M18312	Maturity onset diabetes of the young	MSigDB C2 BIOCARTA (v7.5.1)	4.397E-7	1.316E-4	1.029E-3	6.135E-4	6	25
5	1268737	Termination of O-glycan biosynthesis	BioSystems: REACTOME	5.659E-7	1.316E-4	1.029E-3	7.895E-4	6	26

[Show 26 more annotations](#)**8: Pubmed** [\[Display Chart\]](#) 208 input genes in category / 51059 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	23376485	Proteomic analysis of podocyte exosome-enriched fraction from normal human urine.	<a href="#">Pubmed</a>	3.182E-20	1.065E-15	1.217E-14	1.625E-15	44	1744
2	24952961	A high-resolution spatiotemporal atlas of gene expression of the developing mouse brain.	<a href="#">Pubmed</a>	4.173E-20	1.065E-15	1.217E-14	2.131E-15	46	1937
3	19056867	Large-scale proteomics and phosphoproteomics of urinary exosomes.	<a href="#">Pubmed</a>	2.195E-19	3.735E-15	4.265E-14	1.121E-14	34	1016
4	23533145	In-depth proteomic analyses of exosomes isolated from expressed prostatic secretions in urine.	<a href="#">Pubmed</a>	1.840E-13	2.348E-9	2.681E-8	9.393E-9	28	1070
5	31776260	WNT/RYK signaling restricts goblet cell differentiation during lung development and repair.	<a href="#">Pubmed</a>	3.314E-13	3.384E-9	3.864E-8	1.692E-8	9	42

[Show 45 more annotations](#)**9: Interaction** [\[Display Chart\]](#) 204 input genes in category / 8565 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:CEACAM1	CEACAM1 interactions	1.476E-6	9.997E-3	9.630E-2	1.264E-2	5	20
2	int:EBF2	EBF2 interactions	2.334E-6	9.997E-3	9.630E-2	1.999E-2	7	59
3	int:GNG8	GNG8 interactions	5.754E-6	1.643E-2	1.582E-1	4.928E-2	9	125
4	int:APC	APC interactions	1.961E-5	3.510E-2	3.381E-1	1.679E-1	14	356
5	int:RANBP9	RANBP9 interactions	2.049E-5	3.510E-2	3.381E-1	1.755E-1	12	266

**10: Cytoband [Display Chart]** 206 input genes in category / 166 annotations before applied cutoff / 33040 genes in category

No results to display

**11: Transcription Factor Binding Site [Display Chart]** 201 input genes in category / 885 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	M29941	DLX2 TARGET GENES	MSigDB	5.605E-9	4.960E-6	3.653E-5	4.960E-6	15	290
2	M29981	GREB1 TARGET GENES	MSigDB	5.511E-8	2.438E-5	1.796E-4	4.877E-5	25	954
3	TATAAA V\$TATA 01	TATAAA V\$TATA 01	TFBS	4.749E-7	1.401E-4	1.032E-3	4.203E-4	25	1070
4	TTGTTT V\$FOXO4 01	TTGTTT V\$FOXO4 01	TFBS	1.030E-6	1.985E-4	1.462E-3	9.120E-4	31	1599
5	CAGGTG V\$E12 Q6	CAGGTG V\$E12 Q6	TFBS	1.122E-6	1.985E-4	1.462E-3	9.926E-4	35	1950

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**12: Gene Family [Display Chart]** 154 input genes in category / 117 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	648 Mucins	genenames.org	1.689E-8	1.976E-6	1.056E-5	1.976E-6	6	21
2	488 Claudins	genenames.org	3.948E-5	2.309E-3	1.234E-2	4.619E-3	4	23
3	524 HNF class homeoboxes	genenames.org	2.150E-4	8.383E-3	4.480E-2	2.515E-2	2	3
4	672 Parkinson disease associated genes	genenames.org	3.126E-4	9.145E-3	4.887E-2	3.658E-2	3	16
5	590 CD molecules V-set domain containing Sialic acid binding Ig like lectins	genenames.org	4.979E-4	1.165E-2	6.226E-2	5.826E-2	7	163

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**13: Coexpression [Display Chart]** 207 input genes in category / 8538 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	M40301 DESCARTES FETAL STOMACH MUC13 DMBT1 POSITIVE CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	3.655E-31	3.120E-27	3.005E-26	3.120E-27	25	97
2	M40212 DESCARTES FETAL INTESTINE INTESTINAL EPITHELIAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	1.489E-30	6.356E-27	6.120E-26	1.271E-26	34	276
3	M19062 DODD NASOPHARYNGEAL CARCINOMA UP	MSigDB C2: CGP Curated Gene Sets (v7.5.1)	1.576E-28	4.485E-25	4.319E-24	1.346E-24	68	1818
4	M40175 DESCARTES FETAL EYE CORNEAL AND CONJUNCTIVAL EPITHELIAL CELLS	MSigDB C8: Cell Type Signatures (v7.5.1)	2.220E-28	4.739E-25	4.564E-24	1.896E-24	31	243
5	M246 ANDERSEN CHOLANGIOCARCINOMA CLASS2	MSigDB C2: CGP Curated Gene Sets (v7.5.1)	4.223E-27	7.212E-24	6.945E-23	3.606E-23	27	175

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**14: Coexpression Atlas [Display Chart]** 206 input genes in category / 3455 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	duodenum	duodenum	Human Protein Atlas	7.962E-42	2.751E-38	2.400E-37	2.751E-38	47	321
2	small intestine	small intestine	Human Protein Atlas	2.294E-39	3.963E-36	3.458E-35	7.927E-36	46	339
3	rectum	rectum	Human Protein Atlas	2.695E-32	3.104E-29	2.708E-28	9.311E-29	32	168
4	Arv SC-hpx blastocyst 1000 K2	AravindRamakr StemCell-hypoxiaGrown fromBlastocyst-derived-humanEmbryonicStemCells top-relative-expression-ranked 1000 k-means-cluster#2	PCBC	9.725E-31	8.400E-28	7.329E-27	3.360E-27	36	266
5	colon	colon	Human Protein Atlas	3.508E-30	2.424E-27	2.115E-26	1.212E-26	30	159

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**15: ToppCell Atlas** [\[Display Chart\]](#) 207 input genes in category / 21909 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	e55b4acecf4e363b5afa287c747c2e58c4597f3a	TCGA-Head and Esophagus-Primary Tumor-Esophageal Carcinoma-Adenocarcinoma-3 TCGA-Head and Esophagus / Sample Type by Project: Shred V9	TCGA OncoMap	5.014E-81	1.099E-76	1.161E-75	1.099E-76	50	146
2	92a8931a51db619fb5f0638d319c02e7838f6559	TCGA-Head and Esophagus-Primary Tumor-Esophageal Carcinoma-Adenocarcinoma TCGA-Head and Esophagus / Sample Type by Project: Shred V9	TCGA OncoMap	2.429E-78	2.661E-74	2.813E-73	5.322E-74	49	149
3	e8b25d52f921cc2877088c37a508828886f1e2ed	LargeIntestine GW trimst-2-Epithelial-mature enterocytic-Colonocyte LargeIntestine GW trimst-2 / Per Region, Age group, Lineage, cell class, cell type	Cells of the human intestinal tract mapped across space and time	1.983E-63	1.086E-59	1.148E-58	4.345E-59	45	199
4	c04a5f96d66eb6cf48dd62bd011a833a22d90ffe	LargeIntestine GW trimst-2-Epithelial LargeIntestine GW trimst-2 / Per Region, Age group, Lineage, cell class, cell type	Cells of the human intestinal tract mapped across space and time	1.983E-63	1.086E-59	1.148E-58	4.345E-59	45	199
5	75a82bbabd97b168dbf1c3f43a9bdad48ce18c78	TCGA-Cervix-Primary Tumor-Endocervical Adenocarcinoma-Mucinous Adenocarcinoma-7 TCGA-Cervix / Sample Type by Project: Shred V9	TCGA OncoMap	2.319E-62	1.016E-58	1.074E-57	5.081E-58	42	159

[Show 45 more annotations](#)**16: Computational** [\[Display Chart\]](#) 147 input genes in category / 385 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	M15336 MODULE 6	Trachea genes.	MSigDb: C4 - CM: Cancer Modules (v7.2)	1.261E-12	4.853E-10	3.170E-9	4.853E-10	29	413
2	M16667 MODULE 342	Genes in the cancer module 342.	MSigDb: C4 - CM: Cancer Modules (v7.2)	2.546E-10	4.901E-8	3.201E-7	9.803E-8	19	213
3	M14358 MODULE 88	Heart, liver, kidney and pancreas metabolic and xenobiotic response genes.	MSigDb: C4 - CM: Cancer Modules (v7.2)	5.798E-10	7.441E-8	4.860E-7	2.232E-7	37	834
4	M17558 MODULE 55	Genes in the cancer module 55.	MSigDb: C4 - CM: Cancer Modules (v7.2)	7.488E-9	7.207E-7	4.707E-6	2.883E-6	35	831
5	M14121 MODULE 165	Genes in the cancer module 165.	MSigDb: C4 - CM: Cancer Modules (v7.2)	2.542E-5	1.957E-3	1.278E-2	9.785E-3	8	82

[Show 4 more annotations](#)**17: MicroRNA** [\[Display Chart\]](#) 208 input genes in category / 8319 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-524-5p		MirDB	5.279E-15	4.392E-11	4.217E-10	4.392E-11	34	1878
2	hsa-miR-520d-5p		MirDB	2.754E-14	1.145E-10	1.100E-9	2.291E-10	33	1868
3	hsa-miR-1303:mirSVR	hsa-miR-1303:mirSVR nonconserved	MicroRNA.org	1.212E-	3.360E-	3.227E-	1.008E-9	32	1848

	lowEffect	lowEffect-0.1-0.5		13	10	9			
4	hsa-miR-663b:mirSVR lowEffect	hsa-miR-663b:mirSVR nonconserved lowEffect-0.1-0.5	<a href="#">MicroRNA.org</a>	1.571E-12	2.924E-9	2.808E-8	1.307E-8	25	1205
5	hsa-miR-152:mirSVR lowEffect	hsa-miR-152:mirSVR conserved lowEffect-0.1-0.5	<a href="#">MicroRNA.org</a>	1.758E-12	2.924E-9	2.808E-8	1.462E-8	30	1791

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**18: Drug** [\[Display Chart\]](#) 207 input genes in category / 23818 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:C088658	zoledronic acid	<a href="#">CTD</a>	5.059E-15	1.205E-10	1.284E-9	1.205E-10	48	1471
2	ctd:D004054	Diethylstilbestrol	<a href="#">CTD</a>	2.393E-12	2.850E-8	3.037E-7	5.700E-8	41	1304
3	ctd:D019324	beta-Naphthoflavone	<a href="#">CTD</a>	4.671E-12	3.033E-8	3.232E-7	1.113E-7	32	829
4	ctd:D012906	Smoke	<a href="#">CTD</a>	5.094E-12	3.033E-8	3.232E-7	1.213E-7	34	937
5	ctd:C016517	indole-3-carbinol	<a href="#">CTD</a>	1.779E-10	7.233E-7	7.707E-6	4.236E-6	35	1128

Show 45 more annotations

**19: Disease** [\[Display Chart\]](#) 198 input genes in category / 5990 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	C0334037	Intestinal metaplasia	<a href="#">DisGeNET</a> <a href="#">BeFree</a>	3.127E-18	1.138E-14	1.055E-13	1.873E-14	26	266
2	C1335302	Pancreatic Ductal Adenocarcinoma	<a href="#">DisGeNET</a> <a href="#">BeFree</a>	3.800E-18	1.138E-14	1.055E-13	2.276E-14	45	959
3	C1832661	ANOPHTHALMIA AND PULMONARY HYPOPLASIA	<a href="#">DisGeNET</a> <a href="#">BeFree</a>	7.449E-16	1.487E-12	1.379E-11	4.462E-12	51	1409
4	C0009324	Ulcerative Colitis	<a href="#">DisGeNET</a> <a href="#">BeFree</a>	1.548E-15	2.319E-12	2.151E-11	9.275E-12	48	1277
5	C0004763	Barrett Esophagus	<a href="#">DisGeNET</a> <a href="#">BeFree</a>	2.365E-15	2.747E-12	2.548E-11	1.417E-11	29	450

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