

# Results

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### 1: GO: Molecular Function [\[Display Chart\]](#) 166 input genes in category / 629 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:0008092	cytoskeletal protein binding		1.725E-7	1.085E-4	7.621E-4	1.085E-4	28	1123
2	GO:0005198	structural molecule activity		4.990E-6	1.280E-3	8.985E-3	3.139E-3	22	892
3	GO:0008201	heparin binding		6.103E-6	1.280E-3	8.985E-3	3.839E-3	10	197
4	GO:0003779	actin binding		1.809E-5	2.609E-3	1.832E-2	1.138E-2	15	497
5	GO:1901681	sulfur compound binding		2.074E-5	2.609E-3	1.832E-2	1.305E-2	12	329

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### 2: GO: Biological Process [\[Display Chart\]](#) 167 input genes in category / 4287 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:0009887	animal organ morphogenesis		2.110E-10	7.371E-7	6.590E-6	9.046E-7	41	1729
2	GO:0097435	supramolecular fiber organization		3.439E-10	7.371E-7	6.590E-6	1.474E-6	30	992
3	GO:0035295	tube development		2.565E-9	3.666E-6	3.277E-5	1.100E-5	41	1880
4	GO:0060429	epithelium development		3.487E-9	3.737E-6	3.341E-5	1.495E-5	42	1979
5	GO:0001763	morphogenesis of a branching structure		7.249E-9	6.215E-6	5.557E-5	3.107E-5	15	276

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### 3: GO: Cellular Component [\[Display Chart\]](#) 167 input genes in category / 443 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:0098858	actin-based cell projection		7.977E-8	1.891E-5	1.262E-4	3.534E-5	14	287
2	GO:0005902	microvillus		1.003E-7	1.891E-5	1.262E-4	4.444E-5	10	131
3	GO:0032432	actin filament bundle		1.281E-7	1.891E-5	1.262E-4	5.674E-5	9	102
4	GO:0098590	plasma membrane region		2.652E-7	2.937E-5	1.959E-4	1.175E-4	32	1498
5	GO:0009986	cell surface		6.914E-7	4.048E-5	2.701E-4	3.063E-4	27	1178

[Show 40 more annotations](#)

### 4: Human Phenotype [\[Display Chart\]](#) 66 input genes in category / 2477 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:0100811	Aplasia/Hypoplasia of the colon		3.920E-8	4.855E-5	4.074E-4	9.710E-5	5	9
2	HP:0004388	Microcolon		3.920E-8	4.855E-5	4.074E-4	9.710E-5	5	9
3	HP:0010956	Fetal megacystis		1.308E-7	1.080E-4	9.063E-4	3.240E-4	4	5
4	HP:0005245	Intestinal hypoplasia		1.776E-6	8.807E-4	7.391E-3	4.399E-3	5	17
5	HP:0000021	Megacystis		1.778E-6	8.807E-4	7.391E-3	4.403E-3	4	8

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### 5: Mouse Phenotype [\[Display Chart\]](#) 135 input genes in category / 3005 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:0005620	abnormal muscle contractility		8.402E-8	2.525E-4	2.168E-3	2.525E-4	18	381
2	MP:0001544	abnormal cardiovascular system physiology		1.029E-6	1.546E-3	1.328E-2	3.093E-3	41	1841
3	MP:0002106	abnormal muscle physiology		1.865E-5	1.868E-2	1.604E-1	5.604E-2	24	903
4	MP:0005023	abnormal wound healing		2.578E-5	1.937E-2	1.663E-1	7.747E-2	10	187
5	MP:0000230	abnormal systemic arterial blood pressure		4.207E-5	2.528E-2	2.171E-1	1.264E-1	11	240

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**6: Domain [Display Chart]** 166 input genes in category / 1200 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	SM00643	C345C	SMART	1.308E-5	8.406E-3	6.446E-2	1.570E-2	4	17
2	PF01759	NTR	Pfam	2.102E-5	8.406E-3	6.446E-2	2.522E-2	4	19
3	IPR018933	Netrin module non-TIMP	InterPro	2.102E-5	8.406E-3	6.446E-2	2.522E-2	4	19
4	PS50189	NTR	PROSITE	4.670E-5	9.841E-3	7.546E-2	5.604E-2	4	23
5	IPR001134	Netrin domain	InterPro	4.670E-5	9.841E-3	7.546E-2	5.604E-2	4	23

[Show 41 more annotations](#)**7: Pathway [Display Chart]** 132 input genes in category / 1268 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	M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	MSigDB C2 BIOCARTA (v7.5.1)	5.215E-10	6.613E-7	5.107E-6	6.613E-7	33	1026
2	1269870	Smooth Muscle Contraction	BioSystems: REACTOME	1.140E-6	7.225E-4	5.580E-3	1.445E-3	6	36
3	96530	Vascular smooth muscle contraction	BioSystems: KEGG	2.610E-6	1.103E-3	8.520E-3	3.310E-3	9	121
4	M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	MSigDB C2 BIOCARTA (v7.5.1)	1.066E-5	3.316E-3	2.561E-2	1.351E-2	21	751
5	M5884	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans	MSigDB C2 BIOCARTA (v7.5.1)	1.477E-5	3.316E-3	2.561E-2	1.872E-2	12	275

[Show 10 more annotations](#)**8: Pubmed [Display Chart]** 169 input genes in category / 39280 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	26930384	Transcriptome of the inner circular smooth muscle of the developing mouse intestine: Evidence for regulation of visceral smooth muscle genes by the hedgehog target gene, cJun.	Pubmed	8.714E-18	3.423E-13	3.819E-12	3.423E-13	15	140
2	23376485	Proteomic analysis of podocyte exosome-enriched fraction from normal human urine.	Pubmed	1.106E-13	2.172E-9	2.423E-8	4.345E-9	32	1744
3	23533145	In-depth proteomic analyses of exosomes isolated from expressed prostatic secretions in urine.	Pubmed	4.155E-13	5.440E-9	6.069E-8	1.632E-8	25	1070
4	14627618	Smooth muscle contraction and relaxation.	Pubmed	1.880E-10	1.775E-6	1.980E-5	7.385E-6	6	22
5	24006456	Extracellular matrix secretion by cardiac fibroblasts: role of microRNA-29b and microRNA-30c.	Pubmed	2.260E-10	1.775E-6	1.980E-5	8.877E-6	12	248

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No results to display

**10: Cytoband [Display Chart]** 168 input genes in category / 152 annotations before applied cutoff / 33040 genes in category

No results to display

**11: Transcription Factor Binding Site [Display Chart]** 163 input genes in category / 783 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	WWTAAGGC UNKNOWN	WWTAAGGC UNKNOWN	TFBS	4.461E-8	3.493E-5	2.529E-4	3.493E-5	9	118
2	TATAAA V\$TATA 01	TATAAA V\$TATA 01	TFBS	5.625E-7	1.345E-4	9.739E-4	4.404E-4	22	1070
3	CAGGTG V\$E12 Q6	CAGGTG V\$E12 Q6	TFBS	6.444E-7	1.345E-4	9.739E-4	5.046E-4	31	1950
4	V\$SRF Q6	V\$SRF Q6	TFBS	6.871E-7	1.345E-4	9.739E-4	5.380E-4	10	211
5	TGGAAA V\$NFAT Q4 01	TGGAAA V\$NFAT Q4 01	TFBS	1.102E-6	1.725E-4	1.249E-3	8.627E-4	26	1491

[Show 32 more annotations](#)**12: Gene Family [Display Chart]** 115 input genes in category / 103 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
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1	733	Secreted frizzled-related proteins	<a href="#">genenames.org</a>	2.482E-6	2.557E-4	1.334E-3	2.557E-4	3	5
2	542	Endogenous ligands	<a href="#">genenames.org</a>	1.371E-4	6.492E-3	3.387E-2	1.412E-2	8	237
3	483	Chemokine ligands Endogenous ligands	<a href="#">genenames.org</a>	1.891E-4	6.492E-3	3.387E-2	1.948E-2	4	45
4	396	A-kinase anchoring proteins FERM domain containing	<a href="#">genenames.org</a>	8.114E-4	2.089E-2	1.090E-1	8.357E-2	3	29
5	585	Small heat shock proteins	<a href="#">genenames.org</a>	2.124E-3	4.357E-2	2.273E-1	2.188E-1	2	11

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### 13: Coexpression [Display Chart] 168 input genes in category / 7839 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	M14791	SABATES COLORECTAL ADENOMA DN	<a href="#">MSigDB C2: CGP Curated Gene Sets (v7.5.1)</a>	1.576E-24	1.236E-20	1.179E-19	1.236E-20	28	299
2	15785748-Table3	Human Uterine Santin05 178genes	<a href="#">GeneSigDB</a>	1.003E-23	3.931E-20	3.752E-19	7.863E-20	22	151
3	M40209	DESCARTES FETAL INTESTINE SMOOTH MUSCLE CELLS	<a href="#">MSigDB C8: Cell Type Signatures (v7.5.1)</a>	5.429E-18	1.419E-14	1.354E-13	4.256E-14	13	50
4	M17572	SMID BREAST CANCER LUMINAL B DN	<a href="#">MSigDB C2: CGP Curated Gene Sets (v7.5.1)</a>	1.069E-16	2.094E-13	1.999E-12	8.377E-13	28	587
5	20421987-TableS1	Human Lung Hou10 1067genes	<a href="#">GeneSigDB</a>	1.955E-14	3.065E-11	2.925E-10	1.532E-10	28	722

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### 14: Coexpression Atlas [Display Chart] 168 input genes in category / 3420 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	gudmap developingLowerUrinaryTract adult bladder 1000	DevelopingLowerUrinaryTract adult bladder 1000	<a href="#">Gudmap Mouse MOE430.2</a>	1.676E-24	5.732E-21	4.995E-20	5.732E-21	42	734
2	gudmap developingLowerUrinaryTract P1 bladder B 1000 k1	DevelopingLowerUrinaryTract P1 bladder B 1000 k1	<a href="#">Gudmap Mouse MOE430.2</a>	2.268E-23	3.878E-20	3.380E-19	7.757E-20	25	192
3	gudmap developingLowerUrinaryTract P2 bladder detrusor (LCM) 500	DevelopingLowerUrinaryTract P2 bladder detrusor (LCM) 500	<a href="#">Gudmap Mouse MOE430.2</a>	2.494E-22	2.844E-19	2.478E-18	8.531E-19	31	388
4	gudmap developingLowerUrinaryTract adult bladder 500 k4	DevelopingLowerUrinaryTract adult bladder 500 k4	<a href="#">Gudmap Mouse MOE430.2</a>	3.839E-22	3.282E-19	2.860E-18	1.313E-18	20	107
5	gudmap developingLowerUrinaryTract P1 bladder 1000 B	DevelopingLowerUrinaryTract P1 bladder 1000 B	<a href="#">Gudmap Mouse MOE430.2</a>	1.070E-21	7.318E-19	6.377E-18	3.659E-18	40	774

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### 15: ToppCell Atlas [Display Chart] 168 input genes in category / 20501 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	60c93ff2591f3896a34e58762be960b27ff4f83c	SmallIntestine GW trimst-2-Mesenchymal-myocytic-SMC (PART1/CAPN3+) SmallIntestine GW trimst-2 / Per Region, Age group, Lineage, cell class, cell type	Cells of the human intestinal tract mapped across space and time	9.059E-40	1.857E-35	1.951E-34	1.857E-35	30	195
2	8debc80e0b8de623ad10fefe410a569a157a9faa	SmallIntestine GW trimst-1.5-Mesenchymal-myocytic SmallIntestine GW trimst-1.5 / Per Region, Age group, Lineage, cell class, cell type	Cells of the human intestinal tract mapped across space and time	7.234E-38	7.415E-34	7.790E-33	1.483E-33	29	197
3	87d0e3b08154e5f704287a337ea7ae1ac40b4ac3	SmallIntestine GW trimst-1-Mesenchymal-mvocytic-SMC	Cells of the	3.981E-36	2.720E-32	2.858E-31	8.161E-32	28	197

		(PART1/CAPN3+) SmallIntestine GW trimst-1 / Per Region, Age group, Lineage, cell class, cell type	human intestinal tract mapped across space and time						
4	0d0682c2951a085b1b5a7615c29990fc7a4f41a	LargeIntestine GW trimst-2-Mesenchymal-myocytic-SMC (PART1/CAPN3+) LargeIntestine GW trimst-2 / Per Region, Age group, Lineage, cell class, cell type	Cells of the human intestinal tract mapped across space and time	1.807E-34	9.263E-31	9.731E-30	3.705E-30	27	196
5	40fca58a612a53f980d099afb3d54cf9fdd15f8	SmallIntestine GW trimst-1.5-Mesenchymal-myocytic-SMC (PART1/CAPN3+) SmallIntestine GW trimst-1.5 / Per Region, Age group, Lineage, cell class, cell type	Cells of the human intestinal tract mapped across space and time	6.864E-33	2.814E-29	2.957E-28	1.407E-28	26	194

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#### 16: Computational [Display Chart] 105 input genes in category / 334 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)	4.192E-12	1.400E-9	8.947E-9	1.400E-9	24	413
2 M4051 MODULE 1	Ovary genes.	MSigDb: C4 - CM: Cancer Modules (v7.2)	1.093E-9	1.826E-7	1.167E-6	3.652E-7	20	368
3 M9982 MODULE 2	DRG (dorsal root ganglia) genes.	MSigDb: C4 - CM: Cancer Modules (v7.2)	2.291E-9	2.551E-7	1.630E-6	7.653E-7	20	384
4 M7383 MODULE 5	Lung genes.	MSigDb: C4 - CM: Cancer Modules (v7.2)	1.849E-8	1.249E-6	7.982E-6	6.177E-6	20	434
5 M14358 MODULE 88	Heart, liver, kidney and pancreas metabolic and xenobiotic response genes.	MSigDb: C4 - CM: Cancer Modules (v7.2)	1.870E-8	1.249E-6	7.982E-6	6.246E-6	28	834

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#### 17: MicroRNA [Display Chart] 169 input genes in category / 8045 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-6867-5p		MirDB	6.042E-15	3.420E-11	3.273E-10	4.861E-11	26	1281
2 hsa-miR-206:mirSVR highEffect	hsa-miR-206:mirSVR conserved highEffect-0.5	MicroRNA.org	8.698E-15	3.420E-11	3.273E-10	6.998E-11	25	1184
3 hsa-miR-155:mirSVR highEffect	hsa-miR-155:mirSVR conserved highEffect-0.5	MicroRNA.org	1.275E-14	3.420E-11	3.273E-10	1.026E-10	27	1446
4 hsa-miR-1468-3p		MirDB	1.804E-14	3.628E-11	3.472E-10	1.451E-10	26	1343
5 hsa-miR-651-3p		MirDB	2.574E-14	4.142E-11	3.964E-10	2.071E-10	29	1753

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#### 18: Drug [Display Chart] 168 input genes in category / 22590 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:D004237	Diuron	CTD	9.878E-15	2.231E-10	2.366E-9	2.231E-10	46	1735
2 ctd:C022884	undecane	CTD	2.332E-11	2.634E-7	2.793E-6	5.268E-7	15	199
3 ctd:D015735	Mifepristone	CTD	8.855E-10	6.668E-6	7.070E-5	2.000E-5	21	553
4 ctd:D011092	Polyethylene Glycols	CTD	1.842E-9	1.040E-5	1.103E-4	4.161E-5	14	230
5 ctd:C510784	ormosil	CTD	5.166E-9	2.334E-5	2.474E-4	1.167E-4	11	135

Show 45 more annotations

#### 19: Disease [Display Chart] 165 input genes in category / 5592 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 C0009319	Colitis	DisGeNET	7.057E-	3.946E-	3.633E-	3.946E-6	32	1094

			BeFree	10	6	5			
2	C1608393	Megacystis microcolon intestinal hypoperistalsis syndrome	<a href="#">DisGeNET BeFree</a>	2.308E-9	6.452E-6	5.940E-5	1.290E-5	5	8
3	C1608393	Megacystis microcolon intestinal hypoperistalsis syndrome	<a href="#">DisGeNET Curated</a>	5.107E-9	8.553E-6	7.875E-5	2.856E-5	4	4
4	C0009404	Colorectal Neoplasms	<a href="#">DisGeNET BeFree</a>	6.118E-9	8.553E-6	7.875E-5	3.421E-5	22	589
5	C0007222	Cardiovascular Diseases	<a href="#">DisGeNET BeFree</a>	2.429E-8	2.494E-5	2.296E-4	1.358E-4	36	1551

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