

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
GO:0045177	apical part of cell	29/425	384/19717	5.5693E-09	1.55763E-06	1.4692E-06	KCNK1/ERBB3/MUC1/EPCAM/C	29
GO:0005911	cell-cell junction	30/425	416/19717	8.7507E-09	1.55763E-06	1.4692E-06	CGN/CLDN7/PCDH1/PKP3/EPCA	30
GO:0016324	apical plasma membrane	25/425	318/19717	2.9297E-08	3.47663E-06	3.27926E-06	KCNK1/ERBB3/MUC1/EPCAM/C	25
GO:0005903	brush border	13/425	99/19717	2.0816E-07	1.85266E-05	1.74749E-05	MYH14/PLS1/KCNK1/CDHR5/U	13
GO:0031253	cell projection membrane	21/425	326/19717	9.0348E-06	0.00064328	0.00060676	RAB25/PLEK2/KCNK1/EP8L3/P	21
GO:0031225	anchored component of mem	14/425	170/19717	1.987E-05	0.001016295	0.000958599	PRSS8/CEACAM6/PRSS22/EFNA	14
GO:0070160	tight junction	12/425	128/19717	2.1466E-05	0.001016295	0.000958599	CGN/CLDN7/EPCAM/MARVELD:	12
GO:0098862	cluster of actin-based cell proj	13/425	150/19717	2.2838E-05	0.001016295	0.000958599	MYH14/PLS1/KCNK1/CDHR5/U	13
GO:0043296	apical junction complex	12/425	143/19717	6.4321E-05	0.002522181	0.002378994	CGN/CLDN7/EPCAM/MARVELD:	12
GO:0005923	bicellular tight junction	11/425	123/19717	7.2634E-05	0.002522181	0.002378994	CGN/CLDN7/EPCAM/MARVELD:	11
GO:0016323	basolateral plasma membrane	15/425	217/19717	7.7933E-05	0.002522181	0.002378994	CLDN7/ERBB3/EPCAM/CLDN4/\	15
GO:0031526	brush border membrane	7/425	53/19717	0.00013482	0.003999705	0.003772637	KCNK1/CDHR5/AMN/SLC7A11/i	7
GO:0030057	desmosome	5/425	25/19717	0.00016911	0.00463091	0.004368008	PKP3/PERP/EVPL/PPL/DSG3	5
GO:0001726	ruffle	12/425	172/19717	0.00036614	0.0093104	0.008781838	PTK6/S100A6/EP8L3/PLA2G4F,	12
GO:0005902	microvillus	8/425	83/19717	0.0004195	0.009956049	0.009390833	S100P/CDHR5/PLEKHG6/USH1C	8
GO:0031528	microvillus membrane	4/425	23/19717	0.00136166	0.030296908	0.028576918	S100P/CDHR5/CA9/CDHR2	4
GO:0089717	spanning component of memt	3/425	12/19717	0.00189265	0.039634301	0.037384216	CDHR5/CDHR2/NPC1L1	3
GO:0001533	cornified envelope	6/425	65/19717	0.00273611	0.054114149	0.051042027	PKP3/EVPL/PPL/DSG3/PI3/SC	6
GO:0032587	ruffle membrane	7/425	94/19717	0.00421643	0.079002584	0.074517517	EP8L3/PLA2G4F/EPHA2/EP8L	7
GO:0042599	lamellar body	3/425	17/19717	0.00540042	0.095398707	0.089982813	SPINK5/KLK7/ABCA12	3
GO:0098858	actin-based cell projection	11/425	208/19717	0.00562745	0.095398707	0.089982813	S100P/CDHR5/PLEKHG6/USH1C	11
GO:0035577	azurophil granule membrane	5/425	58/19717	0.00816397	0.13210795	0.124608031	CEACAM6/ABCA13/MGST1/CD	5
GO:0005922	connexin complex	3/425	21/19717	0.00991124	0.147016686	0.138670381	GJB4/GJB5/GJC2	3
GO:0098533	ATPase dependent transmeml	3/425	21/19717	0.00991124	0.147016686	0.138670381	ATP1B1/ABCG8/ATP1A4	3
GO:0031258	lamellipodium membrane	3/425	22/19717	0.01129551	0.159225464	0.150186053	PLEK2/EPHA2/DOCK8	3
GO:0031256	leading edge membrane	9/425	170/19717	0.01162883	0.159225464	0.150186053	PLEK2/EP8L3/PLA2G4F/EPHA2	9