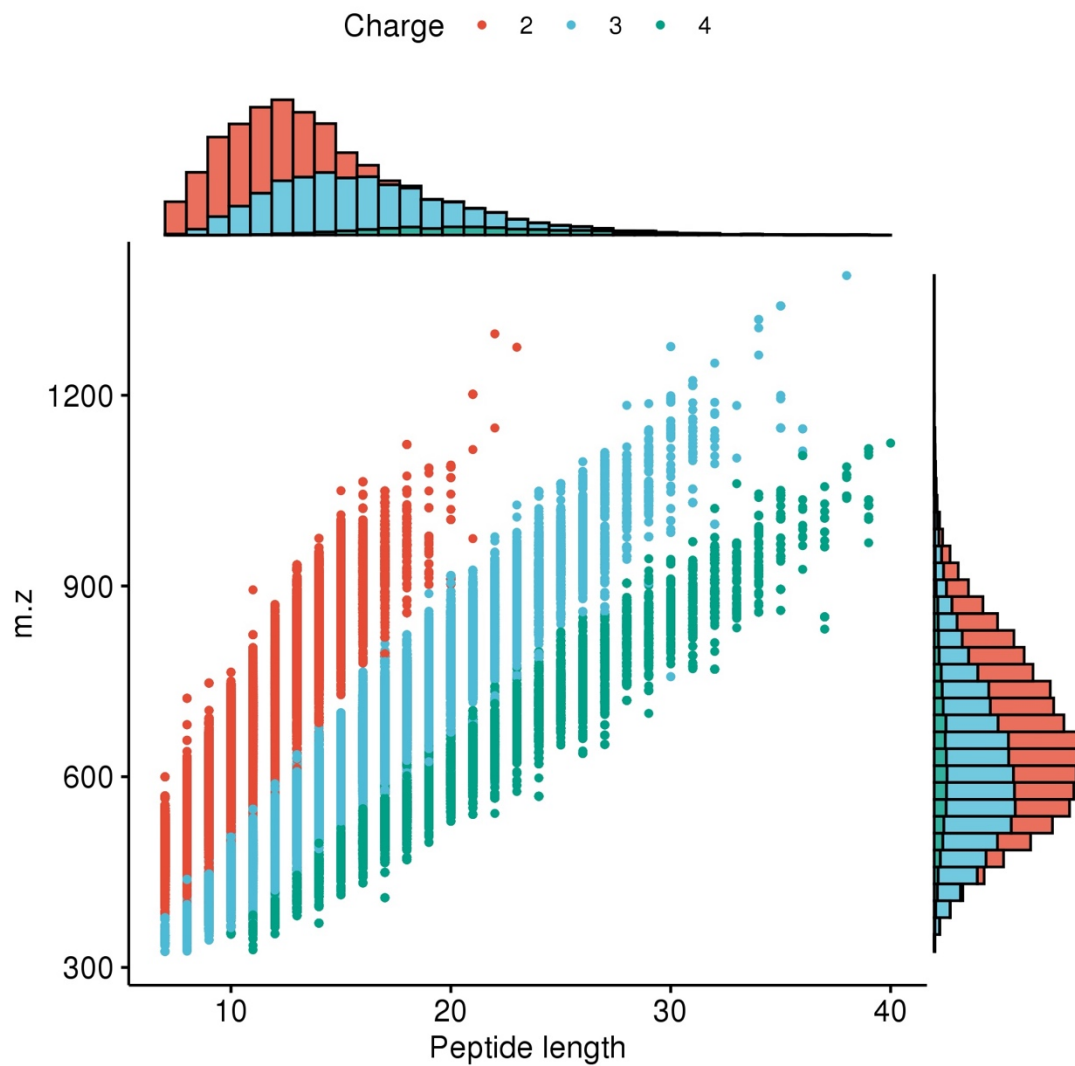
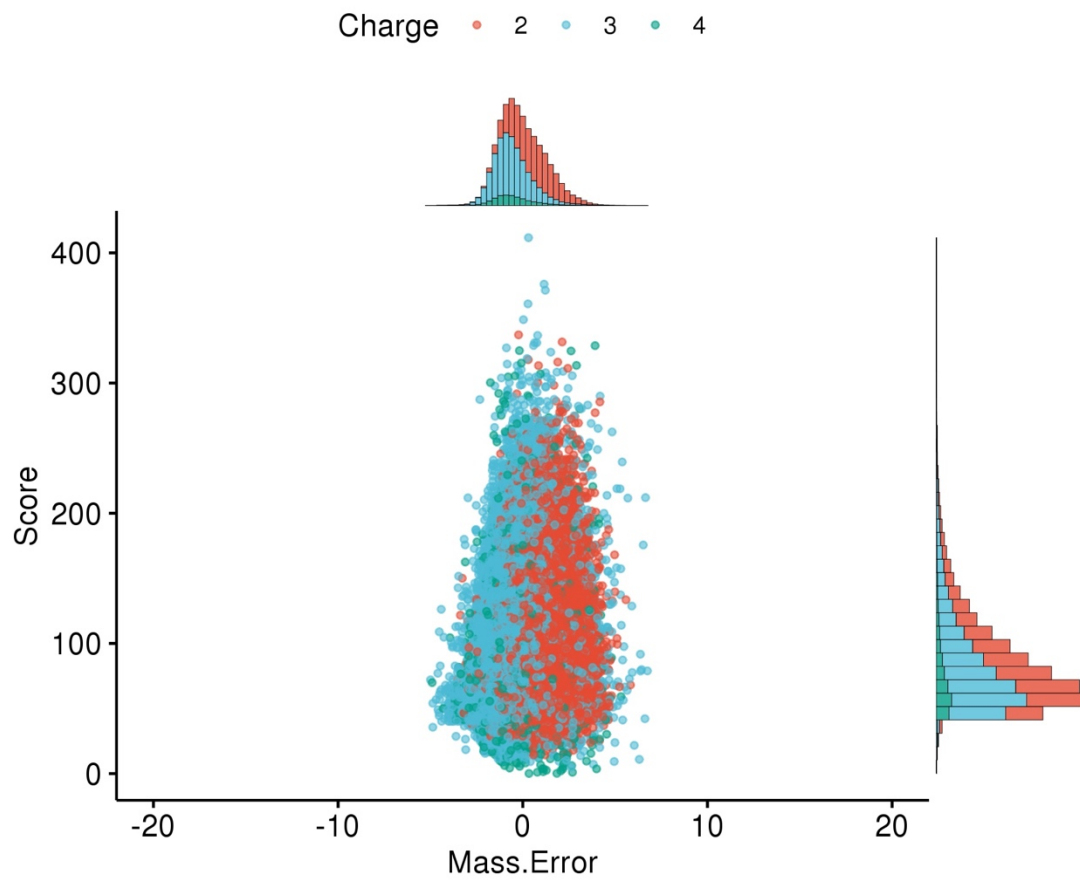


Supplementary Figure 1



Supplementary Figure 1: Distribution of the length of peptides in the identified proteins. x-axis shows AA residues number of peptides, and the y-axis shows the length of the peptide Mass-to-Charge Ratio.

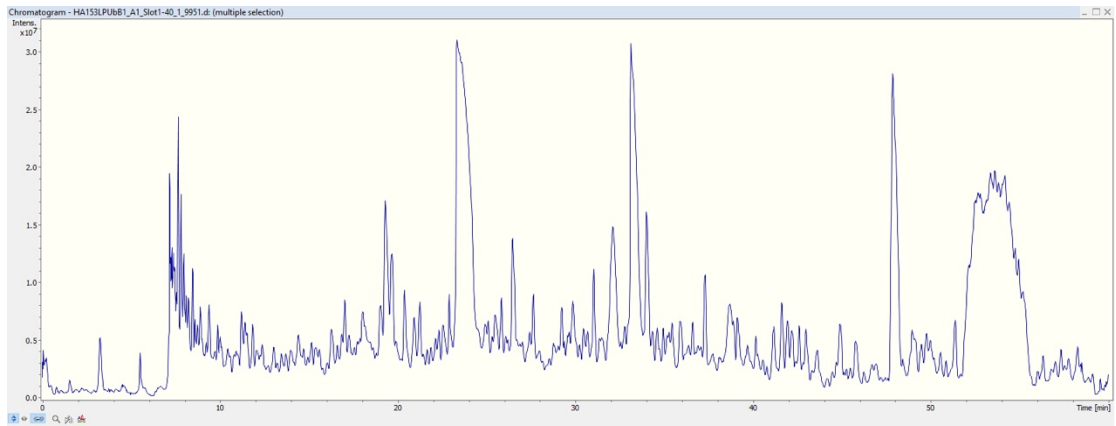
Supplementary Figure 2



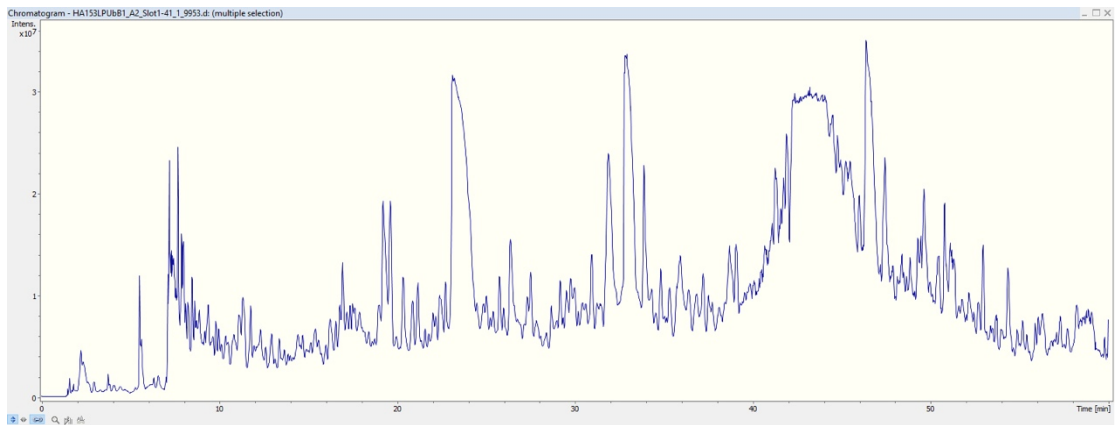
Supplementary Figure 2: Mass error in ppm for the peptides identified in LC-MS/MS. X-axis shows AA residues Mass.Error, and the y-axis shows the identified proteins score.

Supplementary Figure 3

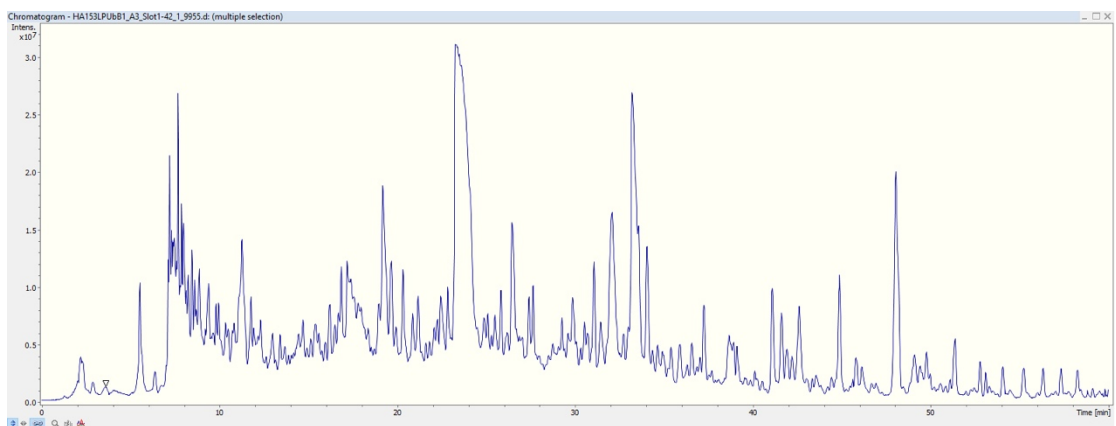
(A1)



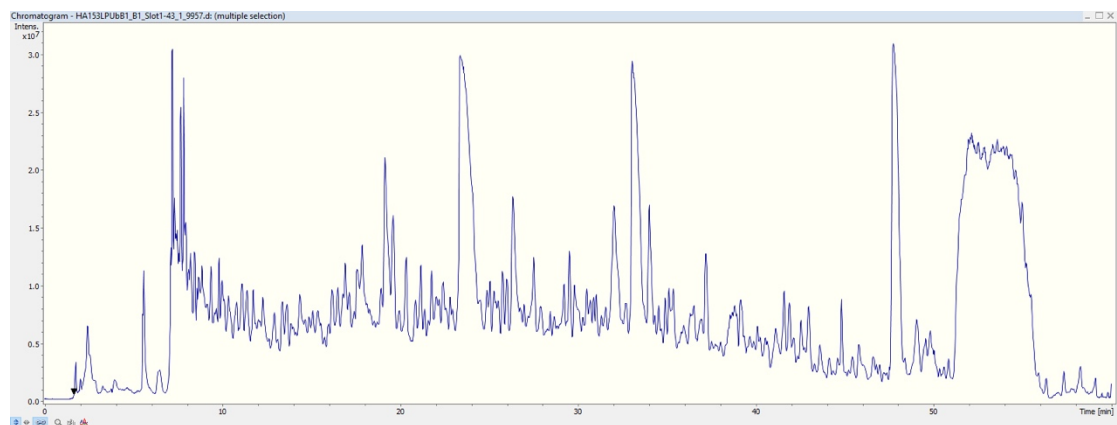
(A2)



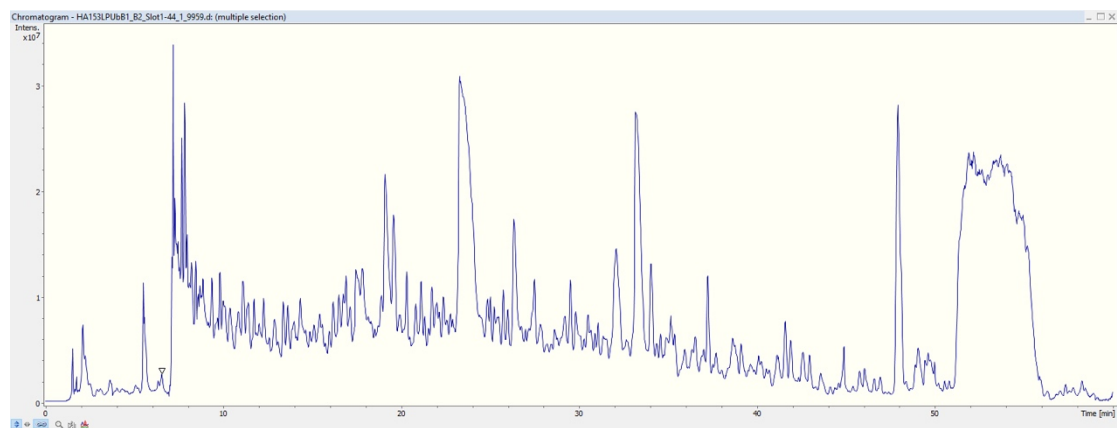
(A3)



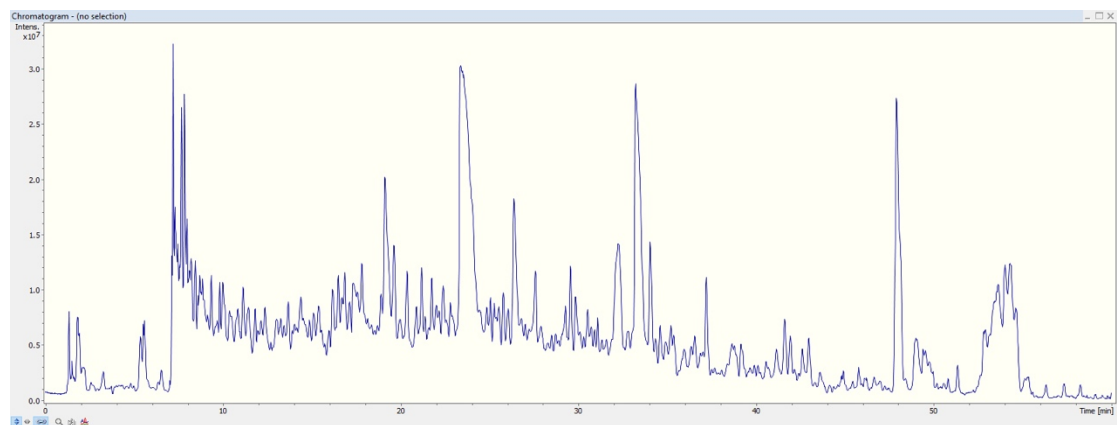
(B1)



(B2)



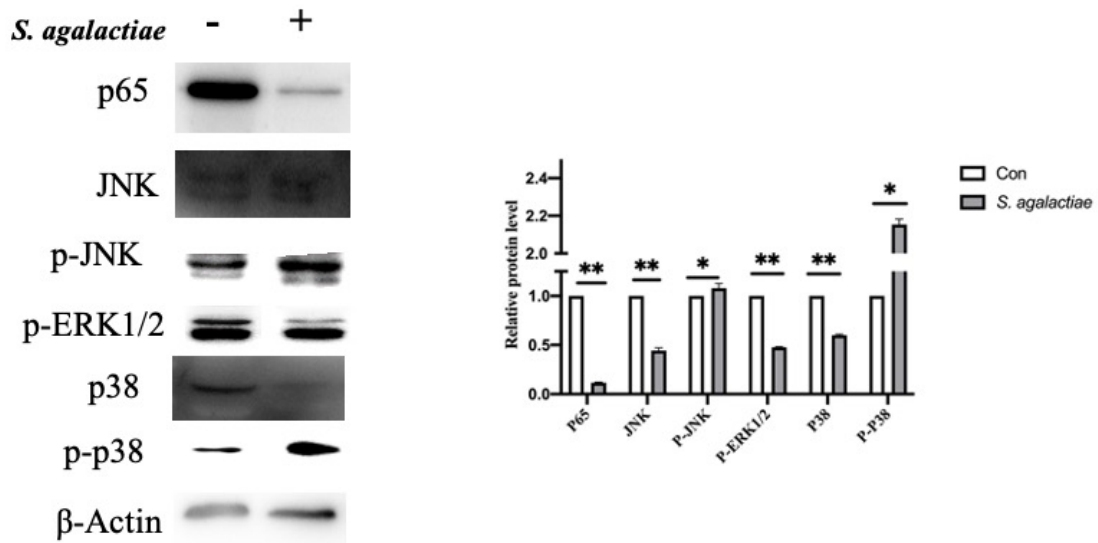
(B3)



Supplementary Figure 3: The chromatogram of LC MS/MS of independent samples of BMECs

infected with *S. agalactiae*.(Supplementary Figure 3 A- Control group(A1,A2,A3);
Supplementary Figure 3 B- *S. agalactiae* group(B1,B2,B3))

Supplementary Figure 4



Supplementary Figure 4: Quantitative analysis of protein levels of p65, JNK, p-JNK, p-ERK1/2, P38, and p-P38 expression using Western blot analysis of the BMECs infected with *S. agalactiae*. Normalized with house-keeping proteins β -Actin. $n = 3$ per group. Data are expressed as mean \pm SD. * $p < 0.05$, ** $p < 0.01$.

Supplementary Table S1 Ubiquitination sites in BMECs infected with *S. agalactiae*.

Motif	Motif Score	Foreground		Background		Fold Increase
		Matches	Size	Matches	Size	
xxxxxxxxxE_K_xxxxxxxxxx	16.00	2424	18407	56854	613607	1.4
xxxxxxxxx_K_xLExxxxxxxx	32.00	319	15983	5341	556753	2.1
xxxxxxxxx_K_Exxxxxxxxxx	16.00	1686	15664	47578	551412	1.2
xxxxxxxxx_K_LxxxxxxRxx	22.81	140	13978	2614	503834	1.9
xxxxxxxxx_K_xxExxxxxxxxx	16.00	1300	13838	36160	501220	1.3
xxxxxxxxx_K_Qxxxxxxxxx	16.00	807	12538	22066	465060	1.4
xxxxxDxxxP_K_xDxxxxxxxx	41.45	35	11731	89	442994	14.9
xxRxxxxxxxx_K_xxxxxxxxxx	12.66	832	11696	24434	442905	1.3
xxxxxxxDx_K_xPxxxxxxPx	30.05	29	10864	107	418471	10.4

xxxxxxxxx_K_Lxxxxxxxx	10.91	1223	10835	39164	418364	1.2
xxxxxxxxxL_K_xxxxxxxxx	10.45	1261	9612	41636	379200	1.2
xxxxxxxxx_K_xxDxxxxxxxx	9.81	581	8351	18015	337564	1.3
xxxxxxxxx_K_Axxxxxxxx	9.32	878	7770	29474	319549	1.2
Rxxxxxxxx_K_xxxxxxxxx	8.51	484	6892	15575	290075	1.3
xxxxxxxxx_K_Dxxxxxxxx	8.61	612	6408	20701	274500	1.3
xxxxxxxxx_K_xxxxDxxxxx	8.58	383	5796	12350	253799	1.4
xxxxxxxDx_K_xxxxxxxxx	7.95	348	5413	11411	241449	1.4
xxxxxxxxx_K_Fxxxxxxxx	8.50	321	5065	10433	230038	1.4
xxxxxxxxxV_K_xxxxxxxxx	8.05	449	4744	15911	219605	1.3
xxxxxxxxx_K_Vxxxxxxxx	8.23	525	4295	19469	203694	1.3

xxxxxxxxxx_K_Ixxxxxxxxx	9.51	422	3770	15240	184225	1.4
xxxxxxxxxx_K_Yxxxxxxxxx	10.20	259	3348	8623	168985	1.5
xxxxxxxxxx_K_Hxxxxxxxxx	7.35	224	3089	8031	160362	1.4
xxxxxxxxxx_K_Txxxxxxxxx	7.44	434	2865	17928	152331	1.3
xxxxxxxxxx_K_Sxxxxxxxxx	9.47	520	2431	22254	134403	1.3
xxxxxxxxxx_K_Gxxxxxxxxx	13.14	460	1911	19467	112149	1.4
xxxxxxxxxx_K_Mxxxxxxxxx	8.48	183	1451	7529	92682	1.6
xxxxxxxxxx_K_Nxxxxxxxxx	10.50	281	1268	12928	85153	1.5
xxxxxxxxxx_K_Rxxxxxxxxx	11.52	354	987	18699	72225	1.4
xxxxxxxxxx_K_Pxxxxxxxxx	16.00	308	633	17527	53526	1.5
xxxxxxxxxx_K_Cxxxxxxxxx	16.00	136	325	6551	35999	2.3

xxxxxxxxx_K_Wxxxxxxxxx	15.28	64	189	3389	29448	2.9
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xxxxxxxxx_K_KPxxxxxxxxx	7.05	23	125	1329	26059	3.6
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Supplementary Table S2 Gene Ontology (GO) enrichment analysis of the identified ubiquitinated proteins.

GO Level 1	GO Terms Description	Terms Level	GO Terms ID	Mapping	Background	All Mapping	All Background	Fold Enrichment	Fisher's exact test p value	-log10(p value)	Related proteins
Cellular Component	cell junction	3	GO:0030054	121	251	1090	3460	1.53	-08	7.93	Q58DS5 A0A3Q1LGC4 A0A3Q1LGY1 A0A3Q1LHZ6 A0A3Q1LHZ6 A0A3Q1LI53 EIBFE8 A6QLR4 A0A3Q1LS30 A0A3Q1LS30 A0A3Q1LS30 A0A3Q1M1P3 A0A3Q1LNQ9 A0A3Q1LPW3 A0A3Q1LQ16 O18738 A0A3Q1MIJ3 A0A3Q1MIJ3 A0A3Q1LSD2 F1MBJ1 Q08DA1 F1N0Y1 F1N0Y1 A0A3Q1LV65 A0A3Q1LV65 U3Q4C5 A0A3Q1LWU2 A0A3Q1MJ12 A0A3Q1N7L7 A0A3Q1LZJ0 A0A3Q1M024 A0A3Q1M0Y7 F1N169 A0A3Q1M0Y7 A0A3Q1M0Y7 A0A3Q1M1M7 A0A3Q1M1M7 A4IF71 A4IF71 A0A3Q1M4X1 Q5E9C0 F1MDH3 F1MDH3 A0A3Q1N5M2 F1MM04 A0A3Q1MSS9 A0A3Q1M8K4 E1BFQ6 A0A3Q1M910 F1MD37 A0A3Q1MBS5 A0A3Q1MBS5 A5D7D1 A0A3Q1MLZ6 F1MM14 F1MM14 F1MM14 A0A3Q1MT26 A0A3Q1MF81 A0A3Q1MSP7 A5D7D1 A5D7D1 A0A3Q1M1B0 A0A3Q1MIC7 A0A3Q1MKM2 A0A3Q1MKM2 A0A3Q1MLQ5 A0A3Q1MN97 A0A3Q1MN97 A0A3Q1MPD9 A0A3Q1MPQ1 A0A3Q1MQD5 A0A3Q1MYG1 Q6R8F2 A0A3Q1MT17 A0A3Q1MT17 A0A3Q1MU33 A0A3Q1N173 A2VDK6 F1MWG7 Q0VCX4 Q0VCX4 A0A3Q1NFL2 A0A3Q1NFL2 Q0P5F3 P53712 P53712 A1L5A7 A2VE52 A2VE67 A2VE81 A5PJY9 A6QP29 A7Z069 E1B899 E1BA03 E1BCP6 E1BDU8 E1BDU8 E1BFQ6 E1BKS1 E1BKT9 E1BLF1 E1BMX5 F1MD34 Q3T0L5 F1MF78 F1ML18 F1MM34 F1MM34 F1MMT3 F1MQ37 F1MQ37 F1MQ37 F1MTP5 F1MUF6 F1MVT1 F1MWK8 F1MYN2 F1MYN2 F1MZJ7 F1N169 F1N169 F1N2D3 F1N2D3 F1N2K8 F1N2K8 F1N365 F1N365 F1N3G9 F6QH17 G3MWR4 G3MYQ6 G5E5R6 G5E5V6 G5E5X0 P60712 P18246 P79132 Q08DQ6 Q1JQB5 Q1RMR3 Q2TA49 Q2YDE9 Q32LP2 Q32LP2 Q3B7M5 Q3MHP3 Q3MHW6 Q3SWY2 Q3SYU6 Q3SZE3 Q58CU2 Q5E9H3 Q5KR49 Q5KR49 Q58CQ2 Q58CQ2 F6R8L1 A0A3Q1LL62 A0A3Q1LXL0 A0A3Q1LPQ6 A0A452DI45 A0A452DI45 A0A3Q1LRD1 Q27971 Q3ZCF0 F6R8E7 F6R8E7 A0A3Q1LTW9 G3MZH3 A0A3Q1MAH8 E1BE25 E1BE25 U3Q4C5 A0A3Q1LWU2 A0A3Q1LX60 A0A3Q1LXL0 A0A3Q1LXR9 A0A452DIM2 A0A3Q1N7L7 A0A3Q1M0Y7 F1N169 A0A3Q1M0Y7 A0A3Q1M0Y7 E1BDP6 E1BDP6 A0A3Q1M3I7 A0A3Q1M3N4 A0A3Q1M4X1 A0A3Q1N5M2 A0A3Q1MBS5 A0A3Q1MBS5 A5D7D1 A0A3Q1MVC7 A0A3Q1MLZ6 A0A3Q1ME09 F1MM14 F1MM14 F1MM14 A0A3Q1MFL7 A0A3Q1MFL7 A5D7D1 A5D7D1 A0A3Q1MH34 A0A3Q1MH34 A0A3Q1M1B0 A0A3Q1MLQ5 A0A3Q1MN97 A0A3Q1MN97 A0A3Q1MRI6 A0A3Q1MRI6 A0A3Q1MRI6 Q6R8F2 A0A3Q1NL10 A0A3Q1MXU7 A0A3Q1N6D1 A0A3Q1N6D1 A0A3SSZP82 P60661 A0A498UZ20 A0A498UZ20 A0JN82 A1L5A7 A6QLB7 A7MB57 E1B801 E1BDU8 E1BDU8 E1BKM4 F1MH50 F1MH50 F1MJ56 F1MJ56 F1MPZ9 F1MPZ9 F1MQ37 F1MQ37 F1MSI1 F1MTP5 F1N169 F1N169 F6PXE3 F6QQ60 Q3SYX9 G5E5V6 P60712 P02510 P31976 P31976 P31976 P68103 Q08DQ6 Q0P5A1 Q0VC68 Q0VC68 Q17QZ9 Q1JQB5 Q1RMR3 Q28141 Q28141 Q2NKY7 Q2TA49 Q32LP2 Q32LP2 Q3B7M5 Q3MHR7 Q3MHR7 Q3SX47 Q3SX47 Q3SYU6 Q3SZK8 Q3T0F7 Q3ZBF7 Q3ZBV8 Q5KR47 Q5KR49
											anchoring junction

											F1MQJ7 F1MUF6 F1N2D3 F1N2D3 F1N2K8 F1N2K8 F1N365 F1N365 F6QH17 G5E5X0 P60712 P18246 P79132 Q08DQ6 Q1JQB5 Q2TA49 Q2YDE9 Q32LP2 Q32LP2 Q3B7M5 Q3SWY2 Q3SZE3 Q58CU2 Q5E9H3
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											Q5E9C0 F1MDH3 F1MDH3 A0A3Q1N5M2 A0A3Q1MSS9 A0A3Q1M8K4 E1BFQ6 F1MD37 A0A3Q1MBS5 A0A3Q1MBS5 A0A3Q1MT26 A0A3Q1MN97 A0A3Q1MN97
											A0A3Q1MPQ1 A0A3Q1MQD5 Q6R8F2 A0A3Q1N173 Q0VCX4 Q0VCX4 A0A3Q1NFL2 A0A3Q1NFL2 Q0P5F3 P53712 P53712 A1L5A7 A2VE52 A5PJY9 E1BCP6
adherens		GO:000						1.713E			E1BDU8 E1BDU8 E1BFQ6 E1BKS1 E1BKT9 E1BMX5 F1MD34 F1MF78 F1MM34 F1MM34 F1MQ37 F1MQ37 F1MQJ7 F1MUF6 F1N2D3 F1N2D3 F1N365 F1N365
junction	6	5912	65	125	1090	3460	1.65	-06	5.77		F6QH17 G5E5X0 P60712 P18246 P79132 Q08DQ6 Q1JQB5 Q2TA49 Q2YDE9 Q32LP2 Q32LP2 Q3B7M5 Q3SWY2 Q3SZE3 Q58CU2 Q5E9H3
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											A0A3Q1M4X1 A0A3Q1N5M2 F1MM04 A0A3Q1M8K4 E1BFQ6 A0A3Q1M910 A0A3Q1MBS5 A0A3Q1MBS5 A5D7D1 A0A3Q1MLZ6 F1MM14 F1MM14 F1MM14
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cell-cell		GO:000						5.005E			F1MTP5 F1MUF6 F1MVT1 F1MWK8 F1MYN2 F1MYN2 F1MZJ7 F1N169 F1N169 F1N2D3 F1N2D3 F1N2K8 F1N2K8 F1N3G9 G3MWR4 G5E5R6 G5E5V6 G5E5X0
junction	5	5911	78	161	1090	3460	1.54	-06	5.3		P18246 Q08DQ6 Q32LP2 Q32LP2 Q3SWY2 Q3SYU6
											A0A3Q1NB49 A0A3Q1MPC4 A6QLR4 A0A3Q1LK55 A0A3Q1LQ16 O18738 Q27971 Q3SWZ3 A0A3Q1NDF8 A0A3Q1LUG0 Q08DA1 A0A3Q1M0G1 A0A3Q1M0G1
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											Q6R8F2 A0A3Q1MVY3 A0A3Q1N402 A0A3Q1NFL2 A0A3Q1NFL2 A0A3S5ZPB2 P53712 P53712 P19120 A7MBH9 A8E4P3 E1BCP6 E1BE98 E1BIG2 E1BKS1 E1BNE7
											F1MCQ7 F1MCQ7 F1MJ56 F1MJ56 F1MM34 F1MM34 F1N261 F1N3G9 F6PXE3 F6QH17 F6RFP6 G3MWR4 G3N3P0 P60712 P04272 P04272 P04896 P18246 P19120
membrane		GO:009						5.513E			P19120 P19120 P31976 P31976 P31976 P31976 P79132 Q1JPD9 Q27965 Q27965 Q27965 Q3SZK6 Q3SZK8 Q3T0D8 Q3ZBG9 Q3ZBG9 Q3ZCA7 Q3ZCA7 Q66WT7
region	5	8589	60	116	1090	3460	1.64	-06	5.26		Q6EWQ7
cortical											Q27971 U3Q4C5 A0A3Q1LWU2 A0A3Q1LXR9 F1N169 A0A3Q1M3I7 A0A3Q1MBS5 A0A3Q1MBS5 A5D7D1 A0A3Q1MFL7 A0A3Q1MFL7 A5D7D1 A5D7D1
cytoskeleton		GO:003						7.13E-			A0A3Q1MLQ5 A0A3Q1MN97 A0A3Q1MN97 A0A3Q1MXU7 A6QLB7 F1MH50 F1MH50 F1MQ37 F1MQ37 F1MTP5 F1N169 F1N169 F1N715 F1N715 F6QQ60 P60712
n	7	0863	25	37	1090	3460	2.14	06	5.15		P31976 P31976 P31976 P31976 P68103 Q1RMR3 Q2NKY7 Q32LP2 Q32LP2 Q3B7M5
											A0A3Q1NB49 A0A3Q1MPC4 A6QLR4 A0A3Q1LK55 A0A3Q1LQ16 O18738 Q27971 Q3SWZ3 A0A3Q1NDF8 A0A3Q1LUG0 Q08DA1 A0A3Q1M0G1 A0A3Q1M0G1
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membrane		GO:004						1.029E			F1MCQ7 F1MJ56 F1MJ56 F1MM34 F1MM34 F1N261 F1N3G9 F6PXE3 F6QH17 F6RFP6 G3MWR4 P60712 P04272 P04272 P04896 P18246 P19120 P19120 P31976
raft	7	5121	57	111	1090	3460	1.63	-05	4.99		P31976 P31976 P31976 P79132 Q1JPD9 Q27965 Q27965 Q27965 Q3SZK6 Q3SZK8 Q3T0D8 Q3ZBG9 Q3ZBG9 Q3ZCA7 Q3ZCA7 Q66WT7
structural											Q5KR49 Q5KR49 Q58CQ2 Q58CQ2 Q0VCH1 Q2T9U2 A0A3Q1LHZ6 A0A3Q1LHZ6 F6RQ55 Q5E958 A0A3Q1LPQ6 O18738 F1MX14 P39872 A0A3Q1LSD2
molecule		GO:000						7.128E			A0A3Q1LV17 A0A3Q1MGK4 U3Q4C5 A0A3Q1LWU2 A0A3Q1LXR9 A0A3Q1N7L7 A0A3Q1M1M7 A0A3Q1M1M7 A4IF71 A4IF71 E1BDP6 E1BDP6 F1MDH3 F1MDH3
activity	2	5198	98	181	972	2989	1.66	-10	9.15		A0A3Q1N5M2 A0A3Q1M5X1 Q32PD5 Q5E973 F1MM14 F1MM14 F1MM14 Q3ZC98 A0A3Q1MR16 A0A3Q1MR16 A0A3Q1MR16 A0A3Q1N1L10 A0A3Q1MXU7 Q56JX3

Molecular

Function											A0A3SSZP82 O18789 P60661 A0A452DIF2 P81947 Q9XS13 Q3T087 Q3T087 A0A452DJE9 A0A452DJF6 A0JN82 P79103 A6QLG5 F1MYG5 A7YY47 E1B7R4 E1B7R4 E1BKT9 Q76182 F1MHU9 F1ML72 F1MWF0 F1MYG5 FIN2K8 F1N2K8 Q28021 F1N316 F1N316 F1N715 F1N715 F6QQ60 Q3SYX9 G8JKV5 P60712 P02510 P31976 P31976 P31976 P46193 P46193 P46193 P48616 P49951 P49951 P61356 P61356 P79132 Q0P5A1 Q0VC68 Q0VC68 Q2HJ49 Q2NKY7 Q32PB8 Q32PB8 Q32PB9 Q32P19 Q3MHR7 Q3MHR7 Q3SYR7 Q3SZ90 Q3SZK8 Q3T003 Q3T057 Q3T0D5 Q3T0F4 Q3T0V4 Q3T0W9 Q3T0W9 Q3T0X6 Q3T169 Q3ZBH8 Q56JV9 Q56JX5 Q56JX8 Q58CU2 Q58DW0 Q58DW3 Q5E964 Q5EAD6 Q5EAD6 Q5KR47 Q5KR49 Q66WT7 Q86211 Q86211
structural constituent of cytoskeleton	GO:000	3	5200	28	42	972	2989	2.05	-06	5.19	Q5KR49 Q5KR49 Q58CQ2 Q58CQ2 Q2T9U2 F6RQ55 A0A3Q1LPQ6 A0A3Q1LSD2 A0A3Q1LV17 A0A3Q1MGK4 U3Q4C5 A0A3Q1LWU2 A0A3Q1LXR9 E1BDP6 E1BDP6 F1MDH3 F1MDH3 F1MM14 F1MM14 F1MM14 A0A3Q1MRI6 A0A3Q1MRI6 A0A3Q1MRI6 A0A3Q1INL10 A0A3Q1MXU7 P81947 A0JN82 E1BKT9 F1MWF0 F1N2K8 F1N2K8 Q3SYX9 P60712 P48616 Q2HJ49 Q3MHR7 Q3MHR7 Q58CU2 Q5KR49
actin binding structural constituent of ribosome	GO:000	5	3779	63	126	972	2989	1.54	-05	4.43	Q5KR49 Q5KR49 Q58CQ2 Q58CQ2 Q0VCHI A0A3Q1LTP6 A0A3Q1LPQ6 O18738 F1MRT9 F1MRT9 A0A452DI45 A0A452DI45 G3MXG3 F6R8E7 F6R8E7 A0A3Q1LTW9 G3MZH3 A0A3Q1MAH8 E1BE25 E1BE25 U3Q4C5 A0A3Q1LWU2 A0A3Q1LX60 A0A3Q1LX60 A0A3Q1N7L7 F1N169 A0A3Q1M3G5 A0A3Q1M317 A0A3Q1M3N4 A0A3Q1N5M2 F1N7F3 F1N7F3 A0A3Q1MBS5 A0A3Q1MBS5 A5D7D1 A0A3Q1ME09 A0A3Q1MFL7 Q5E9F7 A0A3Q1MFL7 A0A3Q1MFP7 A5D7D1 A5D7D1 A0A3Q1MN97 A0A3Q1MN97 P53712 P53712 A0A498UZ20 A0A498UZ20 A2VDN7 A2VDN7 A2VDN7 A6QLB7 A7Z057 E1BDU8 E1BDU8 E1BN47 E1BN47 F1MF78 F1MH50 F1MH50 F1MJ56 F1MJ56 F1MM34 F1MM34 F1MMQ6 F1MQ37 F1MQ37 F1MTP5 F1MWF0 F1MYN2 F1MYN2 F1N169 F1N169 F1N2A1 F1N2A1 F1N365 F1N365 F6QQ60 Q3SYX9 P04272 P04272 P31976 P31976 P31976 P31976 P31976 Q28046 Q28046 Q2HJ49 Q2HJ57 Q32LP2 Q32LP2 Q3B7M5 Q3MHR7 Q3MHR7 Q3SX08 Q3SYU6 Q5KR47 Q5KR49 Q95L54
protein phosphatase binding chemokine receptor binding G protein-coupled receptor binding	GO:001	6	9903	31	57	972	2989	1.67	349	3.08	Q5E958 P39872 Q32PD5 Q5E973 Q56JX3 O18789 Q9XS13 Q3T087 Q3T087 A0A452DJF6 P79103 A6QLG5 Q76182 F1ML72 G8JKV5 P61356 P61356 Q32PB8 Q32PB8 Q32PB9 Q3SYR7 Q3SZ90 Q3T003 Q3T057 Q3T0D5 Q3T0F4 Q3T0V4 Q3T0W9 Q3T0W9 Q3T0X6 Q3T169 Q3ZBH8 Q56JV9 Q56JX5 Q56JX8 Q58DW0 Q58DW0 Q58DW3 Q5EAD6 Q5EAD6 Q86211 Q86211
	GO:004	6	2379	7	8	972	2989	2.69	734	2.66	A0A3Q1MPC4 A0A3Q1LNA6 A0A3Q1LNA6 A0A3Q1LTS1 F6R8E7 F6R8E7 A0A3Q1LTT9 A0A3Q1M1M7 A0A3Q1M1M7 A0A3Q1MVS3 A0A3Q1MVS3 A0A3Q1M317 F1N7F3 F1MCQ7 F1N7F3 A0A3Q1M8T4 A0A3Q1N1C0 A0A3Q1MT26 A0A3Q1MFW6 A0A3Q1MIB0 Q3T0E7 A0A3Q1MQD5 Q6R8F2 A7Z051 Q0VCX4 Q0VCX4 A0A3Q1NFL2 A0A3Q1NFL2 F1MYG5 A7Z064 F1MCQ7 F1MCQ7 F1MNN6 P00442 F1MX38 F1MX38 F1MYG5 F1N0D6 G3X757 G3X757 P48616 Q1RMH8 Q76915 Q76915
	GO:000	5	1664	32	62	972	2989	1.59	628	2.65	A0A3Q1LR68 Q3ZC98 F1MHM5 F1MHM5 F1MQ21 F1MX38 F1MX38 F1N0D6 Q3MHP3 Q0VCHI A0A3Q1LR68 F1N169 A0A3Q1M278 A0A3Q1M317 A0A3Q1MSP7 Q3ZC98 A0A3Q1MQC6 P19120 A7MBH9 E1BA29 E1BCP6 E1BKM4 F1MHM5 F1MHM5 F1MQ21 F1MQ37 F1MQ37 F1MX38 F1MX38 F1N0D6 F1N169 F1N169 F6QH17 G5E6P3 P04896 P19120 P19120 P19120 P38409 P49884 P79132 Q1JPD9 Q27965 Q27965 Q27965 Q2HJG5 Q3MHP3 Q3SZK8 Q3ZBM5 Q3ZCA7 Q3ZCA7 Q66WT7

	cadherin		GO:004						0.0028		
	binding protein	5	5296	8	10	972	2989	2.46	075	2.55	A0A3Q1LMZ4 A0A3Q1LMZ4 A0A3Q1M1M7 A0A3Q1M1M7 F1MM14 F1MM14 F1MM14 A0A3Q1MQD5 Q0VCX4 Q0VCX4 A6QP29 Q3T0L5 F1MM34 F1MM34
	localization										
	related to										A0A3Q1LJR3 Q5E958 A0A3Q1LPK3 Q2NKU2 P62992 P62992 A0A3Q1ME09 Q3T087 Q3T087 A0A452DJF6 P79103 A6QLG5 E1BB38 Q76182 F1ML72 G8JKV5 P62992
	endoplasmic reticulum	7	0972	30	54	1077	3408	1.76	998	3.52	Q862II
	cellular response to interleukin-6	7	1354	10	12	1077	3408	2.64	257	3.49	A0A3Q1LGS4 A0A3Q1M2S8 A0A3Q1NFY8 E1BCP6 E1BD36 F1MX38 F1MX38 F1N0D6 F1N4V2 F1N4V2 Q5EA56 Q76915 Q76915
	cellular response to interleukin-6	6	0741	10	12	1077	3408	2.64	257	3.49	A0A3Q1LGS4 A0A3Q1M2S8 A0A3Q1NFY8 E1BCP6 E1BD36 F1MX38 F1MX38 F1N0D6 F1N4V2 F1N4V2 Q5EA56 Q76915 Q76915
	embryo implantation	6	7566	11	14	1077	3408	2.49	001	3.4	A0A3Q1LQ16 A0A3Q1M0G1 A0A3Q1M0G1 A0A3Q1MPD9 Q6R8F2 E1BIE5 E1BJG5 P00442 Q9TRY0 Q9TRY0 F6RFP6 Q0VCK9 Q2HJ20
Biological Process	regulation of protein localization										
	related to		GO:190						0.0004		F1MMQ6 F1MQ96 F1MQJ7 P60712 P31976 P31976 P31976 P31976 P49951 P49951 P62261 P62261 P63103 Q17QH5 Q3SYS6 Q3SYS6 Q3T0Y8 Q3ZBL4 Q3ZBT5 Q3ZBT5
	membrane cellular response to steroid hormone stimulus	7	5475	37	72	1077	3408	1.63	642	3.33	Q3ZC13 Q3ZC13 Q3ZC13
	response to sterol	6	6314	6	6	1077	3408	3.16	866	3.01	F6RJG0 A0A3Q1LQ16 A0A3Q1M0G1 A0A3Q1M0G1 A0A3Q1MCE5 Q08DE0 Q1LZF6 Q1LZF6
	response to cholesterol	7	0723	6	6	1077	3408	3.16	866	3.01	F6RJG0 A0A3Q1LQ16 A0A3Q1M0G1 A0A3Q1M0G1 A0A3Q1MCE5 Q08DE0 Q1LZF6 Q1LZF6

cell-cell										Q58DS5 A0A3Q1LHZ6 A0A3Q1LHZ6 A0A3Q1LV65 A0A3Q1LV65 A0A3Q1M1M7 A0A3Q1M1M7 A4IF71 A4IF71 A0A3Q1M4X1 F1MDH3 F1MDH3 A0A3Q1N5M2
junction	GO:000						0.0010			A5D7D1 A0A3Q1MT26 A5D7D1 A5D7D1 A0A3Q1MN97 A0A3Q1MN97 Q6R8F2 A0A3Q1MT17 A0A3Q1MT17 A0A3Q1N173 Q0VCX4 Q0VCX4 P53712 P53712 A2VE67
assembly	7	7043	27	50	1077	3408	1.71	784	2.97	A2VE81 E1BKM4 E1BLF1 F1MM34 F1MM34 F1MQ96 F1MTP5 F1MYP2 F1MYP2 F1N2D3 F1N2D3 G5ESR6 P18246
regulation										
of										
bicellular										
tight										
junction	GO:200						0.0022			
assembly	7	0810	8	10	1077	3408	2.53	87	2.64	F1MJ09 A0A3Q1M3N4 A0A3Q1MJ08 A0A3Q1N173 A2VE81 F1N2D3 F1N2D3 Q28021 P18246
regulation										
of defense										
response to	GO:005						0.0026			A0A3Q1LKE6 A0A3Q1LR68 A0A3Q1LW13 A0A3Q1LW13 A0A3Q1M5W7 Q3SYT9 A0A3Q1M6N0 A0A3Q1M8R6 A0A3Q1M8R6 Q58DK4 A0A3Q1N3E8 A0A3Q1N402
virus	7	0688	13	20	1077	3408	2.06	081	2.58	E1BCF8 F1M156 Q28141 Q28141
digestive										
system										
developme	GO:005						0.0031			A0A3Q1NB49 A0A3Q1MPC4 A0A3Q1LQ16 F1N4L1 A0A3Q1M0G1 A0A3Q1M0G1 F1N7F3 F1N7F3 A0A3Q1M8K4 E1BFQ6 A0A3Q1MJR9 A0A3Q1MPD9 Q6R8F2
nt	6	5123	16	27	1077	3408	1.88	187	2.51	E1B7Q4 Q08DE0 E1BFQ6 F1MPZ9 F1MPZ9 F1MUZ3 Q58CU2
anterograd										
e trans-										A0A3Q1LKG0 Q3SWZ3 F6R8E7 F6R8E7 G3MZH3 F1N0Y1 F1N0Y1 E1BC18 A0A3Q1LWU2 A6H7H8 F1MP30 Q0IIF7 Q0IIF7 A0A3Q1NMQ3 A0A3Q1MSS9
synaptic	GO:009						0.0037			A0A3Q1M8M2 Q3ZC83 A0A3Q1MPD9 E1BC18 Q0P5F3 A0A452DIF2 A0A498UZ20 A0A498UZ20 A5D7P3 A5D7P3 A6H799 A6H799 A6H799 F1MHC2 F1N140 F1N140
signaling	7	8916	31	63	1077	3408	1.56	314	2.43	F1N4V1 F6QH17 P06623 P46411 Q0VC68 Q0VC68 Q29455 Q3ZBT5 Q3ZBT5 Q66WT7 Q769I5 Q769I5
modulation										
by host of										
viral	GO:004						0.0050			
process	6	4788	6	7	1077	3408	2.71	427	2.3	A0A3Q1LTS1 P19120 O97594 A8E4P3 P04272 P04272 P19120 P19120 P19120 Q66WT7
