

**Supplementary Table S5. Gene ontology (GO) enrichment analysis of the upregulated genes in TPC1 siFRMD5 (in comparison with TPC1 siNEG).**

GOID	GO Term	Ontology Source	Term PValue	Term PValue Corrected with Benjamini-Hochberg	Group PValue	Group PValue Corrected with Benjamini-Hochberg	GO Levels	GO Groups	% Associated Genes	Nr. Genes
GO:0044248	cellular catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	3,8443E-07	0,000253914	1,7671E-13	1,2547E-11	[3]	Group73	5,66	138,00
GO:1901575	organic substance catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	2,3971E-05	0,002261853	1,7671E-13	1,2547E-11	[3]	Group73	5,34	126,00
GO:0009894	regulation of catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0005648	0,010972164	1,7671E-13	1,2547E-11	[3, 4]	Group73	5,75	62,00
GO:0003723	RNA binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00021632	0,006969627	1,7671E-13	1,2547E-11	[4]	Group73	5,39	94,00
GO:0009057	macromolecule catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	5,3046E-06	0,000875914	1,7671E-13	1,2547E-11	[4]	Group73	6,02	90,00
GO:0019439	aromatic compound catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00160706	0,018786948	1,7671E-13	1,2547E-11	[4]	Group73	6,15	40,00
GO:0043603	cellular amide metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	1,4828E-05	0,001632299	1,7671E-13	1,2547E-11	[4]	Group73	6,22	73,00
GO:0044270	cellular nitrogen compound catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0018934	0,020009467	1,7671E-13	1,2547E-11	[4]	Group73	6,14	39,00
GO:0046700	heterocycle catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00169218	0,018784598	1,7671E-13	1,2547E-11	[4]	Group73	6,18	39,00
GO:1901361	organic cyclic compound catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00403709	0,02996067	1,7671E-13	1,2547E-11	[4]	Group73	5,84	40,00
GO:1901565	organonitrogen compound catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0006443	0,01165912	1,7671E-13	1,2547E-11	[4]	Group73	5,44	77,00
GO:1901566	organonitrogen compound biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	1,2533E-06	0,000331134	1,7671E-13	1,2547E-11	[4]	Group73	5,85	112,00
GO:0006518	peptide metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00024483	0,007350477	1,7671E-13	1,2547E-11	[4, 5]	Group73	6,17	54,00
GO:0030163	protein catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00303904	0,025734456	1,7671E-13	1,2547E-11	[4, 5]	Group73	5,50	55,00
GO:0031329	regulation of cellular catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00029739	0,008017297	1,7671E-13	1,2547E-11	[4, 5]	Group73	6,09	55,00
GO:0034248	regulation of cellular amide metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00235406	0,022212256	1,7671E-13	1,2547E-11	[4, 5]	Group73	6,43	32,00
GO:0034655	nucleobase-containing compound catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00214339	0,021288881	1,7671E-13	1,2547E-11	[4, 5]	Group73	6,24	36,00
GO:0044265	cellular macromolecule catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	5,3207E-06	0,000780953	1,7671E-13	1,2547E-11	[4, 5]	Group73	6,28	78,00
GO:0043604	amide biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0012976	0,016971523	1,7671E-13	1,2547E-11	[5]	Group73	5,83	51,00
GO:0010608	posttranscriptional regulation of gene expression	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00098194	0,014740233	1,7671E-13	1,2547E-11	[5, 6]	Group73	6,19	43,00

GO:0043043	peptide biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00095896	0,014730037	1,7671E-13	1,2547E-11	[5, 6]	Group73	6,15	44,00
GO:0044257	cellular protein catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00194158	0,020037686	1,7671E-13	1,2547E-11	[5, 6]	Group73	5,80	48,00
GO:0006412	translation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00240929	0,022572109	1,7671E-13	1,2547E-11	[5, 6, 7]	Group73	5,98	41,00
GO:0051603	proteolysis involved in cellular protein catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00850725	0,042730317	1,7671E-13	1,2547E-11	[5, 6, 7]	Group73	5,52	42,00
GO:0006402	mRNA catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	7,0249E-05	0,004034745	1,7671E-13	1,2547E-11	[5, 6, 7, 8]	Group73	7,99	31,00
GO:0016071	mRNA metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00452181	0,03211461	1,7671E-13	1,2547E-11	[6, 7]	Group73	5,53	49,00
GO:0016441	posttranscriptional gene silencing	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00958268	0,045209702	1,7671E-13	1,2547E-11	[6, 7]	Group73	7,88	13,00
GO:0017148	negative regulation of translation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00273635	0,024423774	1,7671E-13	1,2547E-11	[5, 6, 7, 8, 9]	Group73	9,15	13,00
GO:0061013	regulation of mRNA catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0054584	0,034833573	1,7671E-13	1,2547E-11	[5, 6, 7, 8, 9]	Group73	7,69	16,00
GO:0000956	nuclear-transcribed mRNA catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00023791	0,007308858	1,7671E-13	1,2547E-11	[6, 7, 8, 9]	Group73	9,13	20,00
GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00059753	0,011117499	1,7671E-13	1,2547E-11	[7, 8, 9, 10]	Group73	12,99	10,00
GO:0043928	exonucleolytic catabolism of deadenylated mRNA	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00128489	0,016973414	1,7671E-13	1,2547E-11	[8, 9, 10, 11]	Group73	18,18	6,00
GO:0019787	ubiquitin-like protein transferase activity	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00464497	0,032638337	1,3695E-07	4,8616E-06	[3]	Group72	6,14	32,00
GO:0044248	cellular catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	3,8443E-07	0,000253914	1,3695E-07	4,8616E-06	[3]	Group72	5,66	138,00
GO:1901575	organic substance catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	2,3971E-05	0,002261853	1,3695E-07	4,8616E-06	[3]	Group72	5,34	126,00
GO:0006914	autophagy	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00152075	0,018098343	1,3695E-07	4,8616E-06	[3, 4]	Group72	6,42	35,00
GO:0009894	regulation of catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0005648	0,010972164	1,3695E-07	4,8616E-06	[3, 4]	Group72	5,75	62,00
GO:0009057	macromolecule catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	5,3046E-06	0,000875914	1,3695E-07	4,8616E-06	[4]	Group72	6,02	90,00
GO:0009896	positive regulation of catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00740365	0,039436366	1,3695E-07	4,8616E-06	[3, 4, 5]	Group72	6,11	29,00
GO:1901565	organonitrogen compound catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0006443	0,01165912	1,3695E-07	4,8616E-06	[4]	Group72	5,44	77,00
GO:0016236	macroautophagy	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00066954	0,011952255	1,3695E-07	4,8616E-06	[4, 5]	Group72	7,77	24,00
GO:0030163	protein catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00303904	0,025734456	1,3695E-07	4,8616E-06	[4, 5]	Group72	5,50	55,00
GO:0031329	regulation of cellular catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00029739	0,008017297	1,3695E-07	4,8616E-06	[4, 5]	Group72	6,09	55,00

GO:0044265	cellular macromolecule catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	5,3207E-06	0,000780953	1,3695E-07	4,8616E-06	[4, 5]	Group72	6,28	78,00
GO:0010506	regulation of autophagy	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01094008	0,048496123	1,3695E-07	4,8616E-06	[4, 5, 6]	Group72	6,32	23,00
GO:0031331	positive regulation of cellular catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00992724	0,046338815	1,3695E-07	4,8616E-06	[4, 5, 6]	Group72	6,22	25,00
GO:0010508	positive regulation of autophagy	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00496658	0,033645403	1,3695E-07	4,8616E-06	[4, 5, 6, 7]	Group72	8,89	12,00
GO:0044257	cellular protein catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00194158	0,020037686	1,3695E-07	4,8616E-06	[5, 6]	Group72	5,80	48,00
GO:0051603	proteolysis involved in cellular protein catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00850725	0,042730317	1,3695E-07	4,8616E-06	[5, 6, 7]	Group72	5,52	42,00
GO:0061013	regulation of mRNA catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0054584	0,034833573	1,3695E-07	4,8616E-06	[5, 6, 7, 8, 9]	Group72	7,69	16,00
GO:0048519	negative regulation of biological process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00014397	0,005943411	3,1494E-07	7,4537E-06	[1, 2, 3]	Group74	4,54	261,00
GO:0019222	regulation of metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00011434	0,005208334	3,1494E-07	7,4537E-06	[2, 3]	Group74	4,41	322,00
GO:0023051	regulation of signaling	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00546368	0,034699596	3,1494E-07	7,4537E-06	[2, 3]	Group74	4,48	172,00
GO:0048583	regulation of response to stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00220964	0,021462729	3,1494E-07	7,4537E-06	[2, 3]	Group74	4,48	203,00
GO:0006725	cellular aromatic compound metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01084506	0,048563812	3,1494E-07	7,4537E-06	[3]	Group74	4,23	258,00
GO:0006793	phosphorus metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00139501	0,01789129	3,1494E-07	7,4537E-06	[3]	Group74	4,66	164,00
GO:0009892	negative regulation of metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	4,5316E-05	0,003150687	3,1494E-07	7,4537E-06	[2, 3, 4]	Group74	4,97	169,00
GO:0010033	response to organic substance	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	7,0786E-05	0,003896196	3,1494E-07	7,4537E-06	[3]	Group74	4,91	173,00
GO:0023057	negative regulation of signaling	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00616829	0,036376402	3,1494E-07	7,4537E-06	[2, 3, 4]	Group74	5,01	76,00
GO:0034641	cellular nitrogen compound metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00062952	0,011549957	3,1494E-07	7,4537E-06	[3]	Group74	4,38	290,00
GO:0043170	macromolecule metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00100883	0,014807319	3,1494E-07	7,4537E-06	[3]	Group74	4,17	410,00
GO:0044093	positive regulation of molecular function	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	6,4609E-05	0,004064203	3,1494E-07	7,4537E-06	[3]	Group74	5,42	106,00
GO:0044249	cellular biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	9,566E-05	0,004680266	3,1494E-07	7,4537E-06	[3]	Group74	4,51	284,00
GO:0046483	heterocycle metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00909393	0,044165753	3,1494E-07	7,4537E-06	[3]	Group74	4,25	257,00
GO:0048522	positive regulation of cellular process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01040585	0,047237542	3,1494E-07	7,4537E-06	[2, 3, 4]	Group74	4,24	253,00
GO:0048523	negative regulation of cellular process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00153646	0,018122019	3,1494E-07	7,4537E-06	[2, 3, 4]	Group74	4,45	230,00

GO:0048585	negative regulation of response to stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00602008	0,035984259	3,1494E-07	7,4537E-06	[2, 3, 4]	Group74	4,91	86,00
GO:0050790	regulation of catalytic activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00041041	0,009511445	3,1494E-07	7,4537E-06	[3]	Group74	5,00	127,00
GO:0070887	cellular response to chemical stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00076148	0,012573871	3,1494E-07	7,4537E-06	[3]	Group74	4,71	167,00
GO:1901360	organic cyclic compound metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00144468	0,01783571	3,1494E-07	7,4537E-06	[3]	Group74	4,35	276,00
GO:1901564	organonitrogen compound metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	8,9487E-10	1,18213E-06	3,1494E-07	7,4537E-06	[3]	Group74	4,86	343,00
GO:1901576	organic substance biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	6,6861E-06	0,000883237	3,1494E-07	7,4537E-06	[3]	Group74	4,62	296,00
GO:0009889	regulation of biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0029225	0,025398796	3,1494E-07	7,4537E-06	[3, 4]	Group74	4,46	201,00
GO:0010646	regulation of cell communication	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00593206	0,036111753	3,1494E-07	7,4537E-06	[3, 4]	Group74	4,48	170,00
GO:0019538	protein metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	9,7509E-06	0,001170999	3,1494E-07	7,4537E-06	[3, 4]	Group74	4,64	282,00
GO:0031323	regulation of cellular metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00034921	0,008871378	3,1494E-07	7,4537E-06	[3, 4]	Group74	4,42	290,00
GO:0044260	cellular macromolecule metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0004098	0,009667003	3,1494E-07	7,4537E-06	[3, 4]	Group74	4,28	366,00
GO:0051171	regulation of nitrogen compound metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00046425	0,009734524	3,1494E-07	7,4537E-06	[3, 4]	Group74	4,43	273,00
GO:0060255	regulation of macromolecule metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00015088	0,006039631	3,1494E-07	7,4537E-06	[3, 4]	Group74	4,45	299,00
GO:0080090	regulation of primary metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00031975	0,008282149	3,1494E-07	7,4537E-06	[3, 4]	Group74	4,44	282,00
GO:0080134	regulation of response to stress	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	3,1639E-05	0,002458551	3,1494E-07	7,4537E-06	[3, 4]	Group74	5,76	89,00
GO:0006796	phosphate-containing compound metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00248995	0,023001596	3,1494E-07	7,4537E-06	[4]	Group74	4,61	161,00
GO:0007166	cell surface receptor signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01122932	0,049446441	3,1494E-07	7,4537E-06	[3, 4, 5]	Group74	4,47	150,00
GO:0009059	macromolecule biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00712991	0,038759742	3,1494E-07	7,4537E-06	[4]	Group74	4,32	226,00
GO:0009890	negative regulation of biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0074441	0,039492581	3,1494E-07	7,4537E-06	[3, 4, 5]	Group74	4,88	85,00
GO:0009966	regulation of signal transduction	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00407019	0,030037535	3,1494E-07	7,4537E-06	[3, 4, 5]	Group74	4,59	151,00
GO:0010467	gene expression	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00333153	0,026999731	3,1494E-07	7,4537E-06	[4]	Group74	4,32	259,00
GO:0010605	negative regulation of macromolecule metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00010225	0,004824166	3,1494E-07	7,4537E-06	[3, 4, 5]	Group74	4,97	155,00
GO:0010648	negative regulation of cell communication	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00588365	0,035982855	3,1494E-07	7,4537E-06	[3, 4, 5]	Group74	5,02	76,00

GO:0031324	negative regulation of cellular metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00378904	0,029100727	3,1494E-07	7,4537E-06	[3, 4, 5]	Group74	4,69	131,00
GO:0034097	response to cytokine	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00028832	0,00793489	3,1494E-07	7,4537E-06	[4]	Group74	5,68	72,00
GO:0035556	intracellular signal transduction	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00738036	0,039471455	3,1494E-07	7,4537E-06	[3, 4, 5]	Group74	4,57	137,00
GO:0043085	positive regulation of catalytic activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00046043	0,009810138	3,1494E-07	7,4537E-06	[4]	Group74	5,39	85,00
GO:0043412	macromolecule modification	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00070997	0,012505024	3,1494E-07	7,4537E-06	[4]	Group74	4,56	210,00
GO:0044271	cellular nitrogen compound biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00350894	0,027756326	3,1494E-07	7,4537E-06	[4]	Group74	4,39	223,00
GO:0051172	negative regulation of nitrogen compound metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0032815	0,027092896	3,1494E-07	7,4537E-06	[3, 4, 5]	Group74	4,75	122,00
GO:0051336	regulation of hydrolase activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00553121	0,034960426	3,1494E-07	7,4537E-06	[4]	Group74	5,10	70,00
GO:0051338	regulation of transferase activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00758439	0,039916255	3,1494E-07	7,4537E-06	[4]	Group74	5,22	57,00
GO:0070848	response to growth factor	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00339685	0,02719537	3,1494E-07	7,4537E-06	[4]	Group74	5,76	44,00
GO:0071310	cellular response to organic substance	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00166787	0,018831223	3,1494E-07	7,4537E-06	[4]	Group74	4,76	138,00
GO:1901362	organic cyclic compound biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00641481	0,037495423	3,1494E-07	7,4537E-06	[4]	Group74	4,39	201,00
GO:1901566	organonitrogen compound biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	1,2533E-06	0,000331134	3,1494E-07	7,4537E-06	[4]	Group74	5,85	112,00
GO:0009968	negative regulation of signal transduction	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00563198	0,035093613	3,1494E-07	7,4537E-06	[3, 4, 5, 6]	Group74	5,11	69,00
GO:0010468	regulation of gene expression	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0051635	0,03410491	3,1494E-07	7,4537E-06	[4, 5]	Group74	4,36	221,00
GO:0034645	cellular macromolecule biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00412162	0,030248124	3,1494E-07	7,4537E-06	[4, 5]	Group74	4,38	222,00
GO:0044267	cellular protein metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	3,9564E-07	0,000174212	3,1494E-07	7,4537E-06	[4, 5]	Group74	4,86	266,00
GO:0051246	regulation of protein metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	3,0554E-06	0,000672698	3,1494E-07	7,4537E-06	[4, 5]	Group74	5,28	159,00
GO:0007167	enzyme linked receptor protein signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00289324	0,025311073	3,1494E-07	7,4537E-06	[4, 5, 6]	Group74	5,41	60,00
GO:0010558	negative regulation of macromolecule biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00486912	0,033500541	3,1494E-07	7,4537E-06	[4, 5, 6]	Group74	4,99	82,00
GO:0010629	negative regulation of gene expression	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00042099	0,009425861	3,1494E-07	7,4537E-06	[4, 5, 6]	Group74	5,08	115,00
GO:0016310	phosphorylation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00926835	0,044521775	3,1494E-07	7,4537E-06	[5]	Group74	4,62	119,00
GO:0019221	cytokine-mediated signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00074874	0,012520107	3,1494E-07	7,4537E-06	[4, 5, 6]	Group74	6,01	50,00

GO:0031098	stress-activated protein kinase signaling cascade	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00570056	0,035188999	3,1494E-07	7,4537E-06	[4, 5, 6]	Group74	6,79	22,00
GO:0032268	regulation of cellular protein metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	4,4564E-06	0,000840978	3,1494E-07	7,4537E-06	[4, 5, 6]	Group74	5,31	150,00
GO:0051247	positive regulation of protein metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00532142	0,034290701	3,1494E-07	7,4537E-06	[4, 5, 6]	Group74	4,90	90,00
GO:0051248	negative regulation of protein metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00654348	0,037582349	3,1494E-07	7,4537E-06	[4, 5, 6]	Group74	5,19	61,00
GO:0051347	positive regulation of transferase activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00168055	0,018813601	3,1494E-07	7,4537E-06	[5]	Group74	5,94	45,00
GO:0071345	cellular response to cytokine stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00042874	0,009439493	3,1494E-07	7,4537E-06	[5]	Group74	5,70	67,00
GO:0071363	cellular response to growth factor stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00730586	0,039553437	3,1494E-07	7,4537E-06	[5]	Group74	5,60	41,00
GO:1902531	regulation of intracellular signal transduction	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00851008	0,042582653	3,1494E-07	7,4537E-06	[4, 5, 6]	Group74	4,80	92,00
GO:0023014	signal transduction by protein phosphorylation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00262072	0,023875622	3,1494E-07	7,4537E-06	[3, 4, 5, 7, 8]	Group74	5,54	55,00
GO:0006464	cellular protein modification process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00040415	0,009706852	3,1494E-07	7,4537E-06	[5, 6]	Group74	4,63	203,00
GO:0032269	negative regulation of cellular protein metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00601296	0,036105122	3,1494E-07	7,4537E-06	[4, 5, 6, 7]	Group74	5,26	58,00
GO:0032270	positive regulation of cellular protein metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00477472	0,033196837	3,1494E-07	7,4537E-06	[4, 5, 6, 7]	Group74	4,96	85,00
GO:2000112	regulation of cellular macromolecule biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00792705	0,041226882	3,1494E-07	7,4537E-06	[5, 6]	Group74	4,42	181,00
GO:0031399	regulation of protein modification process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00182009	0,019547418	3,1494E-07	7,4537E-06	[5, 6, 7]	Group74	5,01	99,00
GO:2000113	negative regulation of cellular macromolecule biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00564347	0,035000116	3,1494E-07	7,4537E-06	[5, 6, 7]	Group74	5,00	78,00
GO:0006468	protein phosphorylation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0061519	0,036606602	3,1494E-07	7,4537E-06	[6, 7]	Group74	4,79	101,00
GO:0031401	positive regulation of protein modification process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00881382	0,043606952	3,1494E-07	7,4537E-06	[5, 6, 7, 8]	Group74	5,03	67,00
GO:0044249	cellular biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	9,566E-05	0,004680266	8,6913E-07	1,5427E-05	[3]	Group61	4,51	284,00
GO:1901576	organic substance biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	6,6861E-06	0,000883237	8,6913E-07	1,5427E-05	[3]	Group61	4,62	296,00
GO:0043603	cellular amide metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	1,4828E-05	0,001632299	8,6913E-07	1,5427E-05	[4]	Group61	6,22	73,00
GO:1901566	organonitrogen compound biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	1,2533E-06	0,000331134	8,6913E-07	1,5427E-05	[4]	Group61	5,85	112,00
GO:0006518	peptide metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00024483	0,007350477	8,6913E-07	1,5427E-05	[4, 5]	Group61	6,17	54,00
GO:0034248	regulation of cellular amide metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00235406	0,022212256	8,6913E-07	1,5427E-05	[4, 5]	Group61	6,43	32,00

GO:0043604	amide biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0012976	0,016971523	8,6913E-07	1,5427E-05	[5]	Group61	5,83	51,00
GO:0043043	peptide biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00095896	0,014730037	8,6913E-07	1,5427E-05	[5, 6]	Group61	6,15	44,00
GO:0006412	translation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00240929	0,022572109	8,6913E-07	1,5427E-05	[5, 6, 7]	Group61	5,98	41,00
GO:0060213	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00902835	0,044009034	1,5636E-06	2,2203E-05	[7, 8, 9, 10, 11, 12, 13]	Group69	25,00	3,00
GO:0022603	regulation of anatomical structure morphogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00042874	0,009439493	1,5636E-06	2,2203E-05	[3, 4]	Group69	5,70	67,00
GO:0003725	double-stranded RNA binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00059753	0,011117499	1,5636E-06	2,2203E-05	[5]	Group69	12,99	10,00
GO:0001738	morphogenesis of a polarized epithelium	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00641635	0,037339181	1,5636E-06	2,2203E-05	[5, 6]	Group69	8,28	13,00
GO:0010608	posttranscriptional regulation of gene expression	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00098194	0,014740233	1,5636E-06	2,2203E-05	[5, 6]	Group69	6,19	43,00
GO:2000027	regulation of animal organ morphogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01016538	0,046626646	1,5636E-06	2,2203E-05	[4, 5, 6, 7]	Group69	6,76	19,00
GO:0016441	posttranscriptional gene silencing	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00958268	0,045209702	1,5636E-06	2,2203E-05	[6, 7]	Group69	7,88	13,00
GO:0035567	non-canonical Wnt signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00230622	0,021917373	1,5636E-06	2,2203E-05	[5, 6, 7, 8]	Group69	8,97	14,00
GO:0017148	negative regulation of translation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00273635	0,024423774	1,5636E-06	2,2203E-05	[5, 6, 7, 8, 9]	Group69	9,15	13,00
GO:0007223	Wnt signaling pathway, calcium modulating pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00457277	0,032302819	1,5636E-06	2,2203E-05	[6, 7, 8, 9]	Group69	14,29	6,00
GO:0010586	miRNA metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00483356	0,033430025	1,5636E-06	2,2203E-05	[7, 8]	Group69	16,67	5,00
GO:0035280	miRNA loading onto RISC involved in gene silencing by miRNA	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00165342	0,018829085	1,5636E-06	2,2203E-05	[5, 6, 7, 8, 9, 10, 11]	Group69	42,86	3,00
GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00059753	0,011117499	1,5636E-06	2,2203E-05	[7, 8, 9, 10]	Group69	12,99	10,00
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01063148	0,047769345	1,5636E-06	2,2203E-05	[7, 8, 9, 10, 11]	Group69	13,89	5,00
GO:0006810	transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	3,0106E-05	0,002485606	1,1929E-05	0,00010587	[3]	Group70	4,64	258,00
GO:0008104	protein localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00059278	0,011186681	1,1929E-05	0,00010587	[3]	Group70	4,83	148,00
GO:0016192	vesicle-mediated transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00041163	0,009375341	1,1929E-05	0,00010587	[2, 4]	Group70	5,08	116,00
GO:0051649	establishment of localization in cell	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0002794	0,008023772	1,1929E-05	0,00010587	[3]	Group70	4,92	146,00
GO:0045184	establishment of protein localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00102526	0,014883237	1,1929E-05	0,00010587	[3, 4]	Group70	4,96	116,00

GO:0046907	intracellular transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00044702	0,009680472	1,1929E-05	0,00010587	[3, 4]	Group70	5,21	100,00
GO:0060341	regulation of cellular localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00680137	0,038070355	1,1929E-05	0,00010587	[3, 4]	Group70	5,25	57,00
GO:0034613	cellular protein localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00303171	0,025837982	1,1929E-05	0,00010587	[4]	Group70	4,89	103,00
GO:0071702	organic substance transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	7,3678E-05	0,00389315	1,1929E-05	0,00010587	[4]	Group70	5,01	154,00
GO:0071705	nitrogen compound transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00040292	0,009856539	1,1929E-05	0,00010587	[4]	Group70	4,96	132,00
GO:1903827	regulation of cellular protein localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00649101	0,037443761	1,1929E-05	0,00010587	[4, 5]	Group70	5,86	35,00
GO:0042886	amide transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00150298	0,01821504	1,1929E-05	0,00010587	[5]	Group70	4,92	114,00
GO:0072657	protein localization to membrane	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00434593	0,031543817	1,1929E-05	0,00010587	[5]	Group70	5,81	40,00
GO:0015031	protein transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00092304	0,014515868	1,1929E-05	0,00010587	[4, 5, 6, 7]	Group70	5,00	112,00
GO:0006886	intracellular protein transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00553953	0,03484628	1,1929E-05	0,00010587	[4, 5, 6, 7, 8]	Group70	5,16	66,00
GO:0080135	regulation of cellular response to stress	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	3,2327E-05	0,002372467	1,1611E-05	0,00011777	[3, 4, 5]	Group46	6,72	53,00
GO:0031098	stress-activated protein kinase signaling cascade	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00570056	0,035188999	1,1611E-05	0,00011777	[4, 5, 6]	Group46	6,79	22,00
GO:0023014	signal transduction by protein phosphorylation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00262072	0,023875622	1,1611E-05	0,00011777	[3, 4, 5, 7, 8]	Group46	5,54	55,00
GO:0007275	multicellular organism development	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00186308	0,019847836	1,5386E-05	0,00012138	[2, 3]	Group71	4,38	253,00
GO:0009653	anatomical structure morphogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00022289	0,007010267	1,5386E-05	0,00012138	[2, 3]	Group71	4,96	143,00
GO:0050793	regulation of developmental process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00020963	0,006923161	1,5386E-05	0,00012138	[2, 3]	Group71	4,99	140,00
GO:0051239	regulation of multicellular organismal process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00397082	0,029974045	1,5386E-05	0,00012138	[2, 3]	Group71	4,57	156,00
GO:0000902	cell morphogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01023283	0,046773579	1,5386E-05	0,00012138	[3, 4]	Group71	5,12	58,00
GO:0022603	regulation of anatomical structure morphogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00042874	0,009439493	1,5386E-05	0,00012138	[3, 4]	Group71	5,70	67,00
GO:0035295	tube development	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00116638	0,016391337	1,5386E-05	0,00012138	[3, 4]	Group71	5,57	63,00
GO:0048731	system development	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00093547	0,014538361	1,5386E-05	0,00012138	[3, 4]	Group71	4,48	232,00
GO:2000026	regulation of multicellular organismal development	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00279194	0,024752729	1,5386E-05	0,00012138	[3, 4]	Group71	4,87	108,00
GO:0035239	tube morphogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00109299	0,015693877	1,5386E-05	0,00012138	[3, 4, 5]	Group71	5,82	53,00



GO:0048513	animal organ development	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00518778	0,033926021	1,5386E-05	0,00012138	[3, 4, 5]	Group71	4,49	173,00
GO:2000145	regulation of cell motility	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0097313	0,045585286	1,5386E-05	0,00012138	[3, 4, 5]	Group71	5,24	52,00
GO:0072359	circulatory system development	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00358849	0,027884666	1,5386E-05	0,00012138	[4, 5]	Group71	5,32	62,00
GO:0072358	cardiovascular system development	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00514764	0,03417103	1,5386E-05	0,00012138	[4, 5, 6]	Group71	5,63	44,00
GO:2000027	regulation of animal organ morphogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01016538	0,046626646	1,5386E-05	0,00012138	[4, 5, 6, 7]	Group71	6,76	19,00
GO:0001568	blood vessel development	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00870441	0,04322752	1,5386E-05	0,00012138	[3, 5, 6, 7, 8]	Group71	5,54	41,00
GO:0001525	angiogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,009983	0,046435013	1,5386E-05	0,00012138	[3, 4, 5, 6, 7, 8, 9, 10]	Group71	5,82	32,00
GO:0048514	blood vessel morphogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00502904	0,033552319	1,5386E-05	0,00012138	[4, 5, 6, 7, 8, 9]	Group71	5,84	38,00
GO:0043168	anion binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00117658	0,016023351	1,0632E-05	0,00012581	[3]	Group63	4,77	144,00
GO:0044093	positive regulation of molecular function	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	6,4609E-05	0,004064203	1,0632E-05	0,00012581	[3]	Group63	5,42	106,00
GO:0050790	regulation of catalytic activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00041041	0,009511445	1,0632E-05	0,00012581	[3]	Group63	5,00	127,00
GO:0035639	purine ribonucleoside triphosphate binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00734326	0,03943269	1,0632E-05	0,00012581	[4]	Group63	4,82	93,00
GO:0043085	positive regulation of catalytic activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00046043	0,009810138	1,0632E-05	0,00012581	[4]	Group63	5,39	85,00
GO:0051336	regulation of hydrolase activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00553121	0,034960426	1,0632E-05	0,00012581	[4]	Group63	5,10	70,00
GO:0016462	pyrophosphatase activity	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00054986	0,010841349	1,0632E-05	0,00012581	[5]	Group63	5,44	79,00
GO:0017111	nucleoside-triphosphatase activity	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00074854	0,012677147	1,0632E-05	0,00012581	[6]	Group63	5,43	76,00
GO:0016887	ATPase activity	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00383025	0,029247137	1,0632E-05	0,00012581	[7]	Group63	6,17	33,00
GO:0004386	helicase activity	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00353666	0,027644545	1,0632E-05	0,00012581	[8]	Group63	8,29	15,00
GO:0032879	regulation of localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00053678	0,010909115	1,7789E-05	0,0001263	[2, 3]	Group64	4,85	145,00
GO:0016043	cellular component organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	2,4018E-05	0,002115194	1,7789E-05	0,0001263	[3]	Group64	4,54	302,00
GO:0044085	cellular component biogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00492259	0,033519275	1,7789E-05	0,0001263	[3]	Group64	4,56	153,00
GO:0051128	regulation of cellular component organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	6,5914E-05	0,003957818	1,7789E-05	0,0001263	[3, 4]	Group64	5,17	132,00
GO:0006996	organelle organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00215967	0,021290433	1,7789E-05	0,0001263	[4]	Group64	4,53	189,00
GO:0051130	positive regulation of cellular component organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00526356	0,034084134	1,7789E-05	0,0001263	[3, 4, 5]	Group64	5,15	67,00

GO:0097435	supramolecular fiber organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00397494	0,029834643	1,7789E-05	0,0001263	[4]	Group64	5,74	43,00
GO:0033043	regulation of organelle organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00330584	0,026956866	1,7789E-05	0,0001263	[4, 5]	Group64	5,19	72,00
GO:0007010	cytoskeleton organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00829588	0,042149432	1,7789E-05	0,0001263	[5]	Group64	4,98	73,00
GO:0051017	actin filament bundle assembly	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00958268	0,045209702	1,7789E-05	0,0001263	[5, 6, 7, 9]	Group64	7,88	13,00
GO:0043548	phosphatidylinositol 3-kinase binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0015113	0,018149337	2,3242E-05	0,00015002	[3]	Group52	17,65	6,00
GO:0005520	insulin-like growth factor binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00642184	0,037207231	2,3242E-05	0,00015002	[4]	Group52	15,63	5,00
GO:0043559	insulin binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00097195	0,01475805	2,3242E-05	0,00015002	[3, 4, 5]	Group52	50,00	3,00
GO:0043243	positive regulation of protein-containing complex disassembly	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00312759	0,026149014	2,3242E-05	0,00015002	[4, 5, 6, 7]	Group52	15,38	6,00
GO:0010828	positive regulation of glucose transmembrane transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00885185	0,043469477	2,3242E-05	0,00015002	[4, 5, 6, 7, 8, 9, 10, 11]	Group52	12,50	6,00
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0013313	0,017241579	2,3242E-05	0,00015002	[5, 6, 7, 8, 9, 10]	Group52	11,00	11,00
GO:0043903	regulation of interspecies interactions between organisms	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01024824	0,046682496	5,4863E-05	0,00029964	[2, 3]	Group53	7,02	17,00
GO:0051702	interaction with symbiont	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00616433	0,036516078	5,4863E-05	0,00029964	[2, 3]	Group53	9,52	10,00
GO:0016032	viral process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00016263	0,006138108	5,4863E-05	0,00029964	[3]	Group53	6,11	59,00
GO:0051817	modulation of process of other organism involved in symbiotic interaction	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00797737	0,041325882	5,4863E-05	0,00029964	[3]	Group53	9,17	10,00
GO:0019058	viral life cycle	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00316945	0,026332362	5,4863E-05	0,00029964	[4]	Group53	6,92	24,00
GO:1903902	positive regulation of viral life cycle	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00387927	0,029451212	5,4863E-05	0,00029964	[3, 4, 5, 6]	Group53	11,76	8,00
GO:0050839	cell adhesion molecule binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	5,1606E-05	0,003408561	5,1606E-05	0,00030533	[3]	Group37	7,30	40,00
GO:0045296	cadherin binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00038678	0,009640416	5,1606E-05	0,00030533	[4]	Group37	7,67	27,00
GO:0016765	transferase activity, transferring alkyl or aryl (other than methyl) groups	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00999203	0,046313923	6,8927E-05	0,00034956	[3]	Group47	10,94	7,00
GO:0004659	prenyltransferase activity	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00593399	0,035957828	6,8927E-05	0,00034956	[4]	Group47	20,00	4,00
GO:0045338	farnesyl diphosphate metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00049996	0,010319564	6,8927E-05	0,00034956	[5, 6, 7]	Group47	60,00	3,00
GO:0006695	cholesterol biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,000154	0,005983353	6,8927E-05	0,00034956	[6, 7]	Group47	14,10	11,00
GO:0006790	sulfur compound metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0080568	0,041574333	0,00011946	0,00056543	[3]	Group58	6,33	25,00

GO:0046148	pigment biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00353662	0,027808812	0,00011946	0,00056543	[3]	Group58	11,94	8,00
GO:0051186	cofactor metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	9,0345E-05	0,004590212	0,00011946	0,00056543	[3]	Group58	7,41	36,00
GO:0006732	coenzyme metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00677903	0,038269661	0,00011946	0,00056543	[4]	Group58	7,04	19,00
GO:0051188	cofactor biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00397827	0,029690914	0,00011946	0,00056543	[4]	Group58	7,56	18,00
GO:0051597	response to methylmercury	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00375033	0,028971875	0,00011946	0,00056543	[4]	Group58	33,33	3,00
GO:0010288	response to lead ion	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00300434	0,025939472	0,00011946	0,00056543	[5]	Group58	18,52	5,00
GO:0006783	heme biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00026534	0,007789075	0,00011946	0,00056543	[4, 6, 7]	Group58	24,00	6,00
GO:0032879	regulation of localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00053678	0,010909115	0,00013732	0,0005735	[2, 3]	Group56	4,85	145,00
GO:0040012	regulation of locomotion	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00599816	0,036180668	0,00013732	0,0005735	[2, 3]	Group56	5,32	55,00
GO:0051128	regulation of cellular component organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	6,5914E-05	0,003957818	0,00013732	0,0005735	[3, 4]	Group56	5,17	132,00
GO:0060341	regulation of cellular localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00680137	0,038070355	0,00013732	0,0005735	[3, 4]	Group56	5,25	57,00
GO:0035239	tube morphogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00109299	0,015693877	0,00013732	0,0005735	[3, 4, 5]	Group56	5,82	53,00
GO:2000145	regulation of cell motility	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0097313	0,045585286	0,00013732	0,0005735	[3, 4, 5]	Group56	5,24	52,00
GO:0072359	circulatory system development	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00358849	0,027884666	0,00013732	0,0005735	[4, 5]	Group56	5,32	62,00
GO:0042802	identical protein binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00013338	0,005872969	0,00013338	0,00059185	[3]	Group36	5,35	104,00
GO:0042803	protein homodimerization activity	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00098608	0,014636023	0,00013338	0,00059185	[4]	Group36	6,15	44,00
GO:0070291	N-acyl ethanolamine metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00020575	0,00715261	0,00020575	0,00081158	[5, 6, 7, 8]	Group24	75,00	3,00
GO:0002262	myeloid cell homeostasis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01053875	0,047677021	0,00022285	0,00083274	[2, 5]	Group51	7,78	13,00
GO:0048872	homeostasis of number of cells	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00142667	0,017948925	0,00022285	0,00083274	[4]	Group51	7,61	22,00
GO:0030099	myeloid cell differentiation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00282726	0,0248987	0,00022285	0,00083274	[4, 5, 6, 7, 8]	Group51	6,55	29,00
GO:0030316	osteoclast differentiation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00616433	0,036516078	0,00022285	0,00083274	[6, 7, 8, 9, 10]	Group51	9,52	10,00
GO:0000278	mitotic cell cycle	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00954564	0,045358974	0,00027925	0,00099132	[3]	Group67	5,16	57,00
GO:1903047	mitotic cell cycle process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00144421	0,017998116	0,00027925	0,00099132	[3, 4]	Group67	5,77	52,00
GO:0006974	cellular response to DNA damage stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00117532	0,016172897	0,00027925	0,00099132	[4]	Group67	5,80	53,00

GO:0007050	cell cycle arrest	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00658446	0,037654012	0,00027925	0,00099132	[3, 4, 5, 6]	Group67	7,20	18,00
GO:0044772	mitotic cell cycle phase transition	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00557376	0,034895413	0,00027925	0,00099132	[4, 5]	Group67	5,92	35,00
GO:0090068	positive regulation of cell cycle process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01055324	0,047579613	0,00027925	0,00099132	[3, 4, 5, 6]	Group67	6,62	20,00
GO:0042770	signal transduction in response to DNA damage	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00328226	0,026930861	0,00027925	0,00099132	[4, 5, 6]	Group67	8,97	13,00
GO:0072331	signal transduction by p53 class mediator	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00770793	0,040245749	0,00027925	0,00099132	[4, 5, 6]	Group67	6,83	20,00
GO:1901990	regulation of mitotic cell cycle phase transition	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00690286	0,038153462	0,00027925	0,00099132	[5, 6, 7]	Group67	6,26	27,00
GO:2000045	regulation of G1/S transition of mitotic cell cycle	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00711597	0,038843803	0,00027925	0,00099132	[6, 7, 8]	Group67	8,18	13,00
GO:0031571	mitotic G1 DNA damage checkpoint	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01084532	0,048400886	0,00027925	0,00099132	[5, 6, 7, 8, 9, 10, 11]	Group67	10,77	7,00
GO:0032879	regulation of localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00053678	0,010909115	0,00036152	0,00122229	[2, 3]	Group66	4,85	145,00
GO:0060341	regulation of cellular localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00680137	0,038070355	0,00036152	0,00122229	[3, 4]	Group66	5,25	57,00
GO:0034613	cellular protein localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00303171	0,025837982	0,00036152	0,00122229	[4]	Group66	4,89	103,00
GO:0032386	regulation of intracellular transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0044923	0,032077484	0,00036152	0,00122229	[4, 5]	Group66	6,47	27,00
GO:1903827	regulation of cellular protein localization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00649101	0,037443761	0,00036152	0,00122229	[4, 5]	Group66	5,86	35,00
GO:0072657	protein localization to membrane	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00434593	0,031543817	0,00036152	0,00122229	[5]	Group66	5,81	40,00
GO:1904375	regulation of protein localization to cell periphery	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00302544	0,025951985	0,00036152	0,00122229	[5, 6]	Group66	9,45	12,00
GO:1905475	regulation of protein localization to membrane	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00090187	0,014528869	0,00036152	0,00122229	[5, 6]	Group66	8,65	18,00
GO:1905477	positive regulation of protein localization to membrane	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00174604	0,018905882	0,00036152	0,00122229	[4, 5, 6, 7]	Group66	9,63	13,00
GO:0072659	protein localization to plasma membrane	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00169805	0,018692721	0,00036152	0,00122229	[6]	Group66	7,51	22,00
GO:1903078	positive regulation of protein localization to plasma membrane	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00194354	0,01990249	0,00036152	0,00122229	[5, 6, 7, 8]	Group66	13,11	8,00
GO:0048583	regulation of response to stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00220964	0,021462729	0,00040729	0,00131445	[2, 3]	Group62	4,48	203,00
GO:0033554	cellular response to stress	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	6,7283E-07	0,000222203	0,00040729	0,00131445	[3]	Group62	5,74	126,00
GO:0048585	negative regulation of response to stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00602008	0,035984259	0,00040729	0,00131445	[2, 3, 4]	Group62	4,91	86,00
GO:0080134	regulation of response to stress	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	3,1639E-05	0,002458551	0,00040729	0,00131445	[3, 4]	Group62	5,76	89,00

GO:0006974	cellular response to DNA damage stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00117532	0,016172897	0,00040729	0,00131445	[4]	Group62	5,80	53,00
GO:0080135	regulation of cellular response to stress	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	3,2327E-05	0,002372467	0,00040729	0,00131445	[3, 4, 5]	Group62	6,72	53,00
GO:0031098	stress-activated protein kinase signaling cascade	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00570056	0,035188999	0,00040729	0,00131445	[4, 5, 6]	Group62	6,79	22,00
GO:0072331	signal transduction by p53 class mediator	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00770793	0,040245749	0,00040729	0,00131445	[4, 5, 6]	Group62	6,83	20,00
GO:2001020	regulation of response to DNA damage stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00415625	0,030333709	0,00040729	0,00131445	[4, 5, 6]	Group62	7,53	18,00
GO:0006282	regulation of DNA repair	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00496658	0,033645403	0,00040729	0,00131445	[5, 6, 7, 8]	Group62	8,89	12,00
GO:0019221	cytokine-mediated signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00074874	0,012520107	0,00074874	0,00204464	[4, 5, 6]	Group43	6,01	50,00
GO:0001959	regulation of cytokine-mediated signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00229538	0,021972449	0,00074874	0,00204464	[4, 5, 6, 7]	Group43	8,67	15,00
GO:0001961	positive regulation of cytokine-mediated signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00435788	0,031457711	0,00074874	0,00204464	[4, 5, 6, 7, 8]	Group43	12,73	7,00
GO:0046661	male sex differentiation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00074433	0,012769634	0,00074433	0,0021139	[3, 4, 5]	Group12	9,36	16,00
GO:0055102	lipase inhibitor activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00071719	0,012465877	0,00071719	0,00212168	[6]	Group20	25,00	5,00
GO:0090559	regulation of membrane permeability	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00669038	0,037931312	0,00069836	0,00215581	[3]	Group54	10,00	9,00
GO:0006839	mitochondrial transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00472711	0,033039756	0,00069836	0,00215581	[4]	Group54	7,14	20,00
GO:0010917	negative regulation of mitochondrial membrane potential	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00077017	0,01256045	0,00069836	0,00215581	[5]	Group54	33,33	4,00
GO:0008637	apoptotic mitochondrial changes	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00440738	0,031642117	0,00069836	0,00215581	[5, 6]	Group54	9,02	12,00
GO:1902108	regulation of mitochondrial membrane permeability involved in apoptotic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00264759	0,023955263	0,00069836	0,00215581	[5, 6, 7, 8]	Group54	12,50	8,00
GO:0097345	mitochondrial outer membrane permeabilization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00532364	0,034138508	0,00069836	0,00215581	[4, 5, 6, 7, 8, 9, 10, 11]	Group54	12,28	7,00
GO:0070087	chromo shadow domain binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00097195	0,01475805	0,00097195	0,00255588	[4]	Group23	50,00	3,00
GO:1903371	regulation of endoplasmic reticulum tubular network organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00097195	0,01475805	0,00097195	0,00255588	[5, 6, 7]	Group29	50,00	3,00
GO:0010256	endomembrane system organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00111057	0,015774863	0,00111057	0,00281609	[4]	Group41	6,74	32,00
GO:0007030	Golgi organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00192354	0,020166637	0,00111057	0,00281609	[5]	Group41	9,15	14,00
GO:0033197	response to vitamin E	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00146665	0,017939325	0,00146665	0,00325413	[4, 5, 7]	Group04	28,57	4,00
GO:0051058	negative regulation of small GTPase mediated signal transduction	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00918873	0,044300407	0,00146115	0,00334649	[5, 6, 7, 8]	Group38	11,11	7,00

GO:0046578	regulation of Ras protein signal transduction	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00624691	0,036676299	0,00146115	0,00334649	[6, 7, 8]	Group38	7,58	16,00
GO:0043559	insulin binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00097195	0,01475805	0,00143933	0,00340641	[3, 4, 5]	Group45	50,00	3,00
GO:0008643	carbohydrate transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0030825	0,025936192	0,00143933	0,00340641	[5]	Group45	8,70	14,00
GO:0010828	positive regulation of glucose transmembrane transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00885185	0,043469477	0,00143933	0,00340641	[4, 5, 6, 7, 8, 9, 10, 11]	Group45	12,50	6,00
GO:0007569	cell aging	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00140467	0,017842019	0,00140467	0,00343902	[3]	Group44	10,34	12,00
GO:0090398	cellular senescence	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00119379	0,016091736	0,00140467	0,00343902	[4]	Group44	12,86	9,00
GO:2000772	regulation of cellular senescence	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00020483	0,007313081	0,00140467	0,00343902	[4, 5, 6]	Group44	18,18	8,00
GO:0048545	response to steroid hormone	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00164864	0,018937808	0,00164864	0,00344274	[4, 5]	Group15	6,79	29,00
GO:0043169	cation binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00162443	0,018823465	0,00162443	0,00349499	[3]	Group42	4,51	203,00
GO:0046872	metal ion binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00120791	0,016117612	0,00162443	0,00349499	[4]	Group42	4,55	200,00
GO:0046914	transition metal ion binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00058682	0,011234617	0,00162443	0,00349499	[5]	Group42	5,68	65,00
GO:0070482	response to oxygen levels	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0021618	0,021153586	0,0021618	0,00414831	[3]	Group49	6,75	28,00
GO:0001666	response to hypoxia	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00817135	0,042001352	0,0021618	0,00414831	[3, 5]	Group49	6,40	24,00
GO:0036293	response to decreased oxygen levels	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00334785	0,026966546	0,0021618	0,00414831	[4]	Group49	6,70	26,00
GO:0071453	cellular response to oxygen levels	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00912035	0,044131801	0,0021618	0,00414831	[4]	Group49	7,11	17,00
GO:0010039	response to iron ion	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00205382	0,020553729	0,00205382	0,00416631	[5]	Group33	16,67	6,00
GO:0060213	positive regulation of nuclear-transcribed mRNA poly(A) tail shortening	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00902835	0,044009034	0,00214339	0,00422725	[7, 8, 9, 10, 11, 12, 13]	Group59	25,00	3,00
GO:0034655	nucleobase-containing compound catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00214339	0,021288881	0,00214339	0,00422725	[4, 5]	Group59	6,24	36,00
GO:0006402	mRNA catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	7,0249E-05	0,004034745	0,00214339	0,00422725	[5, 6, 7, 8]	Group59	7,99	31,00
GO:0061013	regulation of mRNA catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0054584	0,034833573	0,00214339	0,00422725	[5, 6, 7, 8, 9]	Group59	7,69	16,00
GO:0000956	nuclear-transcribed mRNA catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00023791	0,007308858	0,00214339	0,00422725	[6, 7, 8, 9]	Group59	9,13	20,00
GO:0110156	methylguanosine-cap decapping	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00194092	0,020188617	0,00214339	0,00422725	[7, 8]	Group59	26,67	4,00

GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00059753	0,011117499	0,00214339	0,00422725	[7, 8, 9, 10]	Group59	12,99	10,00
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01063148	0,047769345	0,00214339	0,00422725	[7, 8, 9, 10, 11]	Group59	13,89	5,00
GO:0043928	exonucleolytic catabolism of deadenylated mRNA	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00128489	0,016973414	0,00214339	0,00422725	[8, 9, 10, 11]	Group59	18,18	6,00
GO:0050680	negative regulation of epithelial cell proliferation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00226702	0,021859324	0,00226702	0,00423574	[4, 5, 6]	Group16	9,35	13,00
GO:0034248	regulation of cellular amide metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00235406	0,022212256	0,00251239	0,00445949	[4, 5]	Group60	6,43	32,00
GO:0010608	posttranscriptional regulation of gene expression	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00098194	0,014740233	0,00251239	0,00445949	[5, 6]	Group60	6,19	43,00
GO:0043043	peptide biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00095896	0,014730037	0,00251239	0,00445949	[5, 6]	Group60	6,15	44,00
GO:0006412	translation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00240929	0,022572109	0,00251239	0,00445949	[5, 6, 7]	Group60	5,98	41,00
GO:0006402	mRNA catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	7,0249E-05	0,004034745	0,00251239	0,00445949	[5, 6, 7, 8]	Group60	7,99	31,00
GO:0016441	posttranscriptional gene silencing	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00958268	0,045209702	0,00251239	0,00445949	[6, 7]	Group60	7,88	13,00
GO:0017148	negative regulation of translation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00273635	0,024423774	0,00251239	0,00445949	[5, 6, 7, 8, 9]	Group60	9,15	13,00
GO:0061013	regulation of mRNA catabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0054584	0,034833573	0,00251239	0,00445949	[5, 6, 7, 8, 9]	Group60	7,69	16,00
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01063148	0,047769345	0,00251239	0,00445949	[7, 8, 9, 10, 11]	Group60	13,89	5,00
GO:0061024	membrane organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0024574	0,022860711	0,0024574	0,00447372	[4]	Group22	5,56	55,00
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00502893	0,03372189	0,00263126	0,00455657	[4]	Group35	9,80	10,00
GO:0002478	antigen processing and presentation of exogenous peptide antigen	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00171105	0,018680111	0,00263126	0,00455657	[4]	Group35	8,65	16,00
GO:0060323	head morphogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00273174	0,024548518	0,00273174	0,00461795	[3, 4, 5]	Group21	15,79	6,00
GO:0006629	lipid metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00937805	0,044885512	0,00287133	0,00474103	[3]	Group65	4,93	75,00
GO:1901615	organic hydroxy compound metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00013405	0,005712426	0,00287133	0,00474103	[3]	Group65	6,86	42,00
GO:0006066	alcohol metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	1,998E-05	0,002030259	0,00287133	0,00474103	[3, 4]	Group65	8,17	34,00
GO:0008202	steroid metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00518595	0,034082759	0,00287133	0,00474103	[4]	Group65	6,65	24,00
GO:1901617	organic hydroxy compound biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00201228	0,020291785	0,00287133	0,00474103	[4]	Group65	7,41	22,00
GO:0016125	sterol metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00019292	0,007079005	0,00287133	0,00474103	[4, 5]	Group65	9,84	18,00

GO:0046165	alcohol biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00090762	0,014445367	0,00287133	0,00474103	[4, 5]	Group65	8,90	17,00
GO:1902652	secondary alcohol metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00020651	0,006994962	0,00287133	0,00474103	[4, 5]	Group65	9,78	18,00
GO:0045338	farnesyl diphosphate metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00049996	0,010319564	0,00287133	0,00474103	[5, 6, 7]	Group65	60,00	3,00
GO:0006695	cholesterol biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,000154	0,005983353	0,00287133	0,00474103	[6, 7]	Group65	14,10	11,00
GO:0019842	vitamin binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01053875	0,047677021	0,00353469	0,0057037	[3]	Group50	7,78	13,00
GO:0048029	monosaccharide binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00578091	0,035518978	0,00353469	0,0057037	[3]	Group50	10,23	9,00
GO:0050662	coenzyme binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0067867	0,038149916	0,00353469	0,0057037	[3]	Group50	6,69	22,00
GO:0031418	L-ascorbic acid binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00844242	0,04256656	0,00353469	0,0057037	[4, 5]	Group50	18,18	4,00
GO:0031122	cytoplasmic microtubule organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00387927	0,029451212	0,00387927	0,00612062	[4, 5, 7]	Group02	11,76	8,00
GO:0097001	ceramide binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00489063	0,033474229	0,00527774	0,00797275	[3, 4]	Group48	21,05	4,00
GO:0005319	lipid transporter activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00748774	0,039565202	0,00527774	0,00797275	[5, 6]	Group48	8,13	13,00
GO:0035621	ER to Golgi ceramide transport	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00049996	0,010319564	0,00527774	0,00797275	[5, 6, 7]	Group48	60,00	3,00
GO:0046624	sphingolipid transporter activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00194092	0,020188617	0,00527774	0,00797275	[6, 7]	Group48	26,67	4,00
GO:0034770	histone H4-K20 methylation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00520889	0,033896301	0,00520889	0,00803982	[7, 8, 9, 10, 11]	Group05	30,00	3,00
GO:1905288	vascular associated smooth muscle cell apoptotic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00520889	0,033896301	0,00520889	0,00803982	[7]	Group40	30,00	3,00
GO:1905461	positive regulation of vascular associated smooth muscle cell apoptotic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00257175	0,023592267	0,00520889	0,00803982	[8, 9, 10]	Group40	37,50	3,00
GO:0044262	cellular carbohydrate metabolic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00702309	0,038495868	0,00702309	0,00940829	[3, 4]	Group10	6,67	22,00
GO:0045995	regulation of embryonic development	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00699011	0,038474753	0,00699011	0,00954419	[4, 5]	Group11	8,51	12,00
GO:0000287	magnesium ion binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00687178	0,038141254	0,00687178	0,00956659	[5]	Group00	7,33	17,00
GO:0006972	hyperosmotic response	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00733915	0,039571501	0,00733915	0,00964962	[4]	Group31	15,15	5,00
GO:0070555	response to interleukin-1	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00682191	0,03802425	0,00682191	0,00968712	[5]	Group25	7,51	16,00
GO:0120193	tight junction organization	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00669038	0,037931312	0,00669038	0,00969423	[6]	Group27	10,00	9,00
GO:0040014	regulation of multicellular organism growth	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00762354	0,039963081	0,00762354	0,0098413	[3, 4, 5]	Group07	10,53	8,00



GO:0071346	cellular response to interferon-gamma	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00668725	0,038076986	0,00668725	0,00989156	[5, 6, 7, 8]	Group39	7,73	15,00
GO:0060333	interferon-gamma-mediated signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00350715	0,027909299	0,00668725	0,00989156	[5, 6, 7, 8, 9]	Group39	10,31	10,00
GO:0001832	blastocyst growth	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00844242	0,04256656	0,00844242	0,0099902	[3, 4, 8, 9]	Group01	18,18	4,00
GO:0046686	response to cadmium ion	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00823525	0,04200295	0,00823525	0,01008108	[5]	Group13	10,39	8,00
GO:0051438	regulation of ubiquitin-protein transferase activity	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00843374	0,042685699	0,00843374	0,01014907	[5, 8, 9, 10, 11]	Group18	11,29	7,00
GO:0042592	homeostatic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00822063	0,042090878	0,00822063	0,01023973	[3]	Group08	4,75	100,00
GO:0048013	ephrin receptor signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00883455	0,043546427	0,00883455	0,01028284	[6, 7, 8]	Group14	9,57	9,00
GO:0032966	negative regulation of collagen biosynthetic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00902835	0,044009034	0,00902835	0,01033891	[4, 5, 6]	Group03	25,00	3,00
GO:0035457	cellular response to interferon-alpha	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00902835	0,044009034	0,00902835	0,01033891	[6]	Group06	25,00	3,00
GO:0006465	signal peptide processing	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00902835	0,044009034	0,00902835	0,01033891	[5, 6, 7]	Group28	25,00	3,00
GO:0006334	nucleosome assembly	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0096128	0,045190427	0,0096128	0,01034104	[6, 7, 8, 9]	Group17	8,16	12,00
GO:0007166	cell surface receptor signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01122932	0,049446441	0,00816427	0,01035112	[3, 4, 5]	Group55	4,47	150,00
GO:0034097	response to cytokine	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00028832	0,00793489	0,00816427	0,01035112	[4]	Group55	5,68	72,00
GO:0071310	cellular response to organic substance	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00166787	0,018831223	0,00816427	0,01035112	[4]	Group55	4,76	138,00
GO:0019221	cytokine-mediated signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00074874	0,012520107	0,00816427	0,01035112	[4, 5, 6]	Group55	6,01	50,00
GO:0071345	cellular response to cytokine stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00042874	0,009439493	0,00816427	0,01035112	[5]	Group55	5,70	67,00
GO:0001959	regulation of cytokine-mediated signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00229538	0,021972449	0,00816427	0,01035112	[4, 5, 6, 7]	Group55	8,67	15,00
GO:0014015	positive regulation of gliogenesis	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00956808	0,045302629	0,00956808	0,01045129	[5, 6, 7, 8, 9, 10]	Group34	10,13	8,00
GO:0007166	cell surface receptor signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01122932	0,049446441	0,00952971	0,01057202	[3, 4, 5]	Group68	4,47	150,00
GO:0070848	response to growth factor	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00339685	0,02719537	0,00952971	0,01057202	[4]	Group68	5,76	44,00
GO:0071310	cellular response to organic substance	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00166787	0,018831223	0,00952971	0,01057202	[4]	Group68	4,76	138,00
GO:0071559	response to transforming growth factor beta	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0002821	0,007928841	0,00952971	0,01057202	[3, 5]	Group68	8,59	22,00
GO:0090287	regulation of cellular response to growth factor stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00116796	0,016240735	0,00952971	0,01057202	[3, 4, 6]	Group68	7,59	23,00

GO:0007167	enzyme linked receptor protein signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00289324	0,025311073	0,00952971	0,01057202	[4, 5, 6]	Group68	5,41	60,00
GO:0071363	cellular response to growth factor stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00730586	0,039553437	0,00952971	0,01057202	[5]	Group68	5,60	41,00
GO:0090288	negative regulation of cellular response to growth factor stimulus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01005185	0,0464283	0,00952971	0,01057202	[3, 4, 5, 6, 7]	Group68	7,83	13,00
GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00339685	0,02719537	0,00952971	0,01057202	[5, 6, 7]	Group68	5,76	44,00
GO:0007179	transforming growth factor beta receptor signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00053682	0,010744583	0,00952971	0,01057202	[5, 6, 7, 8]	Group68	9,05	18,00
GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00893731	0,043726634	0,00952971	0,01057202	[4, 5, 6, 7, 8, 9]	Group68	8,59	11,00
GO:0017015	regulation of transforming growth factor beta receptor signaling pathway	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00030373	0,008024428	0,00952971	0,01057202	[5, 6, 7, 8, 9]	Group68	11,02	14,00
GO:0051607	defense response to virus	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01005658	0,046288278	0,01005658	0,01065697	[3, 4, 5, 6]	Group19	6,90	18,00
GO:0007160	cell-matrix adhesion	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00948471	0,045232154	0,00948471	0,01068912	[4]	Group32	7,08	17,00
GO:0043090	amino acid import	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01063148	0,047769345	0,01063148	0,01110052	[6, 8, 9]	Group09	13,89	5,00
GO:0006446	regulation of translational initiation	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01105509	0,048842039	0,01105509	0,01121302	[4, 6, 7, 8, 9]	Group26	9,88	8,00
GO:0043548	phosphatidylinositol 3-kinase binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0015113	0,018149337	0,01122656	0,01122656	[3]	Group57	17,65	6,00
GO:0036312	phosphatidylinositol 3-kinase regulatory subunit binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00520889	0,033896301	0,01122656	0,01122656	[4]	Group57	30,00	3,00
GO:0043559	insulin binding	GO_MolecularFunction-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00097195	0,01475805	0,01122656	0,01122656	[3, 4, 5]	Group57	50,00	3,00
GO:0048015	phosphatidylinositol-mediated signaling	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00497913	0,033558346	0,01122656	0,01122656	[5, 6, 7]	Group57	7,77	16,00
GO:0014065	phosphatidylinositol 3-kinase signaling	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00869579	0,043347713	0,01122656	0,01122656	[6, 7, 8]	Group57	7,98	13,00
GO:0014066	regulation of phosphatidylinositol 3-kinase signaling	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,00199253	0,020247202	0,01122656	0,01122656	[5, 6, 7, 8, 9]	Group57	9,49	13,00
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,0013313	0,017241579	0,01122656	0,01122656	[5, 6, 7, 8, 9, 10]	Group57	11,00	11,00
GO:0006915	apoptotic process	GO_BiologicalProcess-EBI-UniProt-GOA-ACAP-ARAP_08.05.2020_00h00	0,01091582	0,048551518	0,01091582	0,01123222	[4]	Group30	4,72	97,00