Robert AW, Schittini AV, Marchini FK, Batista M, Affonso Da Costa MB, Senegaglia AC, Brofman PRS, Abud APR, Stimamiglio MA: Tissue-derived signals for mesenchymal stem cell stimulation: Role of cardiac and umbilical cord microenvironments.

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**Supplemental Table 2.** Results of gene ontology analyses by gProfiler tool. BP, biological process; CC, cellular component; MF, molecular function; hp, human phenotype ontology; ke, KEGG pathway; mi, miRBase microRNAs; re, REACTOME pathway; co, CORUM protein complexes; tf, TRANSFAC regulatory motif.

#	p-value	1		Q (	Q&T	Q&T/Q	Q&T/T	term ID		t type
	4,17E-04	16	63	4	0,063	0,25	GO:0001580	BP	32	detection of chemical stimulus involved in sensory perception of bitter taste
	4,61E-07	367	63	13	0,206	0,035	GO:0010035	BP	26	response to inorganic substance
	1,07E-13	39	63	10	0,159	0,256	GO:0030049	BP	44	I muscle filament sliding
	2,07E-04	113	63	7	0,111	0,062	GO:0030216	BP	27	keratinocyte differentiation
	4,17E-04	16	63	4	0,063	0,25	GO:0045109	BP	31	intermediate filament organization
	1,14E-03	48	63	5	0,079	0,104	GO:0030239	BP	35	i myofibril assembly
	1,21E-02	1022	63	14	0,222	0,014	GO:0007155	BP	39	cell adhesion
	5,26E-03	29	63	4	0,063	0,138	GO:0018149	BP	64	Peptide cross-linking
	6,25E-08	62	63	8	0,127	0,129	GO:0001895	BP	45	retina homeostasis
	2,23E-02	87	63	5	0,079	0,057	GO:0002576	BP	62	platelet degranulation
	5,05E-09	320	63	14	0,222	0,044	GO:0043588	BP	54	skin development
	1,65E-04	33	63	5	0,079	0,152	GO:0045104	BP	14	I intermediate filament cytoskeleton organization
	9,39E-03	2962	63	25	0,397	0,008	GO:0065008	BP	13	regulation of biological quality
	2,05E-02	13	63	3	0,048	0,231	GO:0031581	BP	$\epsilon$	hemidesmosome assembly
	3,98E-02	16	63	3	0,048	0,188	GO:0055003	BP	36	6 cardiac myofibril assembly
	1,14E-02	35	63	4	0,063	0,114	GO:0043462	BP	8	B regulation of ATPase activity
	1,05E-02	1478	63	17	0,27	0,012	GO:0044712	BP	38	B single-organism catabolic process
_	1,35E-02	1853	63	19	0,302	0,01	GO:0022607	BP		cellular component assembly
UECM	1,14E-02	133	63	6	0,095	0,045	GO:0044420	CC		B extracellular matrix part
EE.	3,94E-20	1636	63	37	0,587	0,023	GO:0070062	CC	16	extracellular vesicular exosome
	1,06E-03	211	63	8	0,127	0,038	GO:0070161	CC	20	anchoring junction
	4,44E-08	239	63	12	0,19		GO:0045111	CC		intermediate filament cytoskeleton
	1,29E-03	2664	63	25	0,397	0,009	GO:0005829	CC	30	) cytosol
	8,89E-08	194	63	11	0,175		GO:0005882	CC		3 intermediate filament
	7,52E-06	374	63	12	0,19		GO:0003779	MF		B actin binding
	1,46E-11	621	63	20	0,317		GO:0005198	MF		' structural molecule activity
	2,46E-03	4	60	3	0,05		HP:0003704	hp		3 Scapuloperoneal weakness
	4,33E-02	23	60	4	0,067		HP:0003691	hp		Scapular winging
	4,18E-02	847	60	19	0,317		HP:0002715	hp		Abnormality of the immune system
	5,00E-02	9	60	3	0,05		HP:0006466	hp		Ankle contracture
	1,76E-03	11	60	4	0,067	0,364	HP:0001805	hp		B Thick nail
	4,21E-03	49	60	6	0,1		HP:0011006	hp		Abnormality of the musculature of the neck
	6,11E-03	5	60	3	0,05		HP:0005180	hp		Tricuspid regurgitation
	5,57E-03	111	60	8	0,133		HP:0008065	hp		P Aplasia/Hypoplasia of the skin
	1,66E-08	24	60	8	0,133		HP:0000972	hp		? Palmoplantar hyperkeratosis
	1,95E-02	19	60	4	0,067		HP:0001430	hp		5 Abnormality of the calf musculature
	3,59E-05	1146	60	26	0,433		HP:000006	hp		9 Autosomal dominant inheritance
	1,25E-16	189	60	21	0,35	0,111	HP:0000962	hp	17	7 Hyperkeratosis

	1,58E-08	52	60	10	0,167	0.192	HP:0100578	hp	1 Lipoatrophy
	8,46E-03	199	60	10	0,167		HP:0001639	hp	25 Hypertrophic cardiomyopathy
	4,33E-02	23	60	4	0,067	,	HP:0003700	hp	59 Generalized amyotrophy
	1,03E-03	89	60	8	0,133		HP:0000975	hp	49 Hyperhidrosis
	2,52E-03	45	60	6	0,1		HP:0008404	hp	53 Nail dystrophy
	1,21E-02	6	60	3	0,05		HP:0002616	hp	22 Aortic root dilatation
	9,83E-04	61	60	7	0,117	0,115	HP:0001644	hp	42 Dilated cardiomyopathy
	1,21E-02	17	60	4	0,067	0,235	HP:0008180	hp	46 Mildly elevated creatine phosphokinase
	9,63E-05	123	60	10	0,167	0,081	HP:0003457	hp	9 EMG abnormality
	1,19E-02	88	60	7	0,117	0,08	HP:0003701	hp	51 Proximal muscle weakness
uECM	2,32E-04	102	60	9	0,15	0,088	HP:0001635	hp	47 Congestive heart failure
H	2,13E-02	133	60	8	0,133	0,06	HP:0001874	hp	34 Abnormality of neutrophils
	1,13E-03	10	60	4	0,067	0,4	HP:0003803	hp	37 Type 1 muscle fiber predominance
	8,12E-07	130	60	12	0,2	0,092	HP:0003198	hp	43 Myopathy
	5,53E-04	151	62	7	0,113	0,046	KEGG:04261	ke	10 Adrenergic signaling in cardiomyocytes
	3,81E-07	83	62	8	0,129	0,096	KEGG:05410	ke	29 Hypertrophic cardiomyopathy (HCM)
	7,30E-07	90	62	8	0,129	0,089	KEGG:05414	ke	28 Dilated cardiomyopathy
	6,20E-06	78	62	7	0,113	0,09	KEGG:04260	ke	24 Cardiac muscle contraction
	4,39E-03	208	62	7	0,113	0,034	KEGG:04510	ke	5 Focal adhesion
	5,82E-04	717	63	12	0,19	0,017	MI:hsa-miR-768-5p	mi	65 MI:hsa-miR-768-5p
	2,92E-09	33	60	9	0,15	0,273	REAC:397014	re	2 Muscle contraction
	4,10E-02	25	60	4	0,067	0,16	REAC:382054	re	3 PDGF binds to extracellular matrix proteins
	p-value		Т (	Q (	Q&T	Q&T/Q	Q&T/T	term ID	t name and depth in group
	1,23E-02	265	443	20	0,045	,	GO:0051186	BP	44 cofactor metabolic process
	3,21E-02	3	443	3	0,007		GO:0035995	BP	92 detection of muscle stretch
	1,02E-07	105	443	18	0,041		GO:0002474	BP	87 antigen processing and presentation of peptide antigen via MHC class I
	2,78E-05	72	443	13	0,029	,	GO:1902400	BP	29 intracellular signal transduction involved in G1 DNA damage checkpoint
	1,59E-02	293	443	21	0,047	,	GO:0052548	BP	58 regulation of endopeptidase activity
	2,24E-05	113	443	16	0,036		GO:0006414	BP	41 translational elongation
	8,00E-13	48	443	17	0,038		GO:0030239	BP	60 myofibril assembly
	1,48E-07	765	443	50	0,113	,	GO:0044403	BP	56 symbiosis, encompassing mutualism through parasitism
	4,13E-05	4160	443	148	0,334	,	GO:0019538	BP	86 protein metabolic process
	2,78E-07	654	443	45	0,102		GO:0016071	BP	76 mRNA metabolic process
	1,02E-04	54	443	11	0,025		GO:0046496	BP	67 nicotinamide nucleotide metabolic process
CCM	3,80E-02 7,71E-05	24	443	6	0,014	0,25	GO:0010880	BP	70 regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum
0		422	442	10	0.026	0.43		D.D.	CO pouto inflorementary response
	•	123	443	16	0,036	-	GO:0002526	BP	68 acute inflammatory response
	4,60E-03	37	443	8	0,018	0,216	GO:0030834	ВР	17 regulation of actin filament depolymerization
	4,60E-03 1,26E-24	37 39	443 443	8 23	0,018 0,052	0,216 0,59	GO:0030834 GO:0030049	BP BP	17 regulation of actin filament depolymerization 112 muscle filament sliding
	4,60E-03 1,26E-24 2,05E-04	37 39 35	443 443 443	8 23 9	0,018 0,052 0,02	0,216 0,59 0,257	GO:0030834 GO:0030049 GO:0043462	BP BP BP	17 regulation of actin filament depolymerization 112 muscle filament sliding 24 regulation of ATPase activity
	4,60E-03 1,26E-24 2,05E-04 2,78E-05	37 39 35 72	443 443 443	8 23 9 13	0,018 0,052 0,02 0,029	0,216 0,59 0,257 0,181	GO:0030834 GO:0030049 GO:0043462 GO:0051436	BP BP BP BP	17 regulation of actin filament depolymerization 112 muscle filament sliding 24 regulation of ATPase activity 104 negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
	4,60E-03 1,26E-24 2,05E-04 2,78E-05 6,86E-06	37 39 35 72 77	443 443 443 443	8 23 9 13 14	0,018 0,052 0,02 0,029 0,032	0,216 0,59 0,257 0,181 0,182	GO:0030834 GO:0030049 GO:0043462 GO:0051436 GO:0051437	BP BP BP BP	17 regulation of actin filament depolymerization 112 muscle filament sliding 24 regulation of ATPase activity 104 negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 13 positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
	4,60E-03 1,26E-24 2,05E-04 2,78E-05 6,86E-06 4,03E-06	37 39 35 72 77 62	443 443 443 443 443	8 23 9 13 14 13	0,018 0,052 0,02 0,029 0,032 0,029	0,216 0,59 0,257 0,181 0,182 0,21	GO:0030834 GO:0030049 GO:0043462 GO:0051436 GO:0051437 GO:0006521	BP BP BP BP BP	17 regulation of actin filament depolymerization 112 muscle filament sliding 24 regulation of ATPase activity 104 negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 13 positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 105 regulation of cellular amino acid metabolic process
	4,60E-03 1,26E-24 2,05E-04 2,78E-05 6,86E-06 4,03E-06 2,78E-05	37 39 35 72 77 62 72	443 443 443 443 443 443	8 23 9 13 14 13	0,018 0,052 0,02 0,029 0,032 0,029 0,029	0,216 0,59 0,257 0,181 0,182 0,21 0,181	GO:0030834 GO:0030049 GO:0043462 GO:0051436 GO:0051437 GO:0006521 GO:0006977	BP BP BP BP BP BP	17 regulation of actin filament depolymerization 112 muscle filament sliding 24 regulation of ATPase activity 104 negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 13 positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 105 regulation of cellular amino acid metabolic process 96 DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
	4,60E-03 1,26E-24 2,05E-04 2,78E-05 6,86E-06 4,03E-06 2,78E-05 1,12E-02	37 39 35 72 77 62 72 219	443 443 443 443 443 443 443	8 23 9 13 14 13 13	0,018 0,052 0,02 0,029 0,032 0,029 0,029 0,041	0,216 0,59 0,257 0,181 0,182 0,21 0,181 0,082	GO:0030834 GO:0030049 GO:0043462 GO:0051436 GO:0051437 GO:0006521 GO:0006977 GO:0006457	BP BP BP BP BP BP BP BP	17 regulation of actin filament depolymerization 112 muscle filament sliding 24 regulation of ATPase activity 104 negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 13 positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 105 regulation of cellular amino acid metabolic process 96 DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest 6 protein folding
	4,60E-03 1,26E-24 2,05E-04 2,78E-05 6,86E-06 4,03E-06 2,78E-05 1,12E-02 4,15E-05	37 39 35 72 77 62 72 219	443 443 443 443 443 443 443 443	8 23 9 13 14 13 13 18	0,018 0,052 0,02 0,029 0,032 0,029 0,029 0,041 0,032	0,216 0,59 0,257 0,181 0,182 0,21 0,181 0,082 0,159	GO:0030834 GO:0030049 GO:0043462 GO:0051436 GO:0051437 GO:0006521 GO:0006977 GO:0006457 GO:0031145	BP BP BP BP BP BP BP BP	17 regulation of actin filament depolymerization 112 muscle filament sliding 24 regulation of ATPase activity 104 negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 13 positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 105 regulation of cellular amino acid metabolic process 96 DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest 6 protein folding 111 anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
	4,60E-03 1,26E-24 2,05E-04 2,78E-05 6,86E-06 4,03E-06 2,78E-05 1,12E-02	37 39 35 72 77 62 72 219	443 443 443 443 443 443 443	8 23 9 13 14 13 13	0,018 0,052 0,02 0,029 0,032 0,029 0,029 0,041	0,216 0,59 0,257 0,181 0,182 0,21 0,181 0,082 0,159 0,087	GO:0030834 GO:0030049 GO:0043462 GO:0051436 GO:0051437 GO:0006521 GO:0006977 GO:0006457	BP BP BP BP BP BP BP BP	17 regulation of actin filament depolymerization 112 muscle filament sliding 24 regulation of ATPase activity 104 negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 13 positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle 105 regulation of cellular amino acid metabolic process 96 DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest 6 protein folding

	1,05E-08	438	443	38	0,086	0,087 GO:0006091	BP	37 generation of precursor metabolites and energy
	2,58E-02	46	443	8	0,018	0,174 GO:0006958	BP	5 complement activation, classical pathway
	1,84E-11	48	443	16	0,036	0,333 GO:0031093	CC	16 platelet alpha granule lumen
	7,05E-05	211	443	21	0,047	0,1 GO:0070161	CC	31 anchoring junction
	2,28E-74	1636	443	181	0,409	0,111 GO:0065010	CC	77 extracellular membrane-bounded organelle
	2,54E-05	99	443	15	0,034	0,152 GO:0042383	CC	69 sarcolemma
	2,14E-05	47	443	11	0,025	0,234 GO:0044291	CC	53 cell-cell contact zone
	8,27E-03	134	443	14	0,032	0,104 GO:0030055	CC	79 cell-substrate junction
	4,31E-02	15	443	5	0,011	0,333 GO:0031143	CC	51 pseudopodium
	3,53E-28	621	443	74	0,167	0,119 GO:0005198	MF	90 structural molecule activity
	1,00E-10	1170	443	72	0,163	0,062 GO:0044822	MF	66 poly(A) RNA binding
	1,65E-04	25	443	8	0,018	0,32 GO:0070003	MF	30 threonine-type peptidase activity
	4,12E-05	688	443	42	0,095	0,061 GO:0005509	MF	40 calcium ion binding
	6,21E-05	15	438	8	0,018	0,533 CORUM:194	со	32 PA28gamma-20S proteasome
	3,02E-05	14	438	8	0,018	0,571 CORUM:191	со	71 20S proteasome
	2,29E-03	22		8	0,018	0,364 CORUM:181	со	109 26S proteasome
	3,39E-02	6	438	4	0,009	0,667 CORUM:2837	со	103 Profilin 1 complex
	2,38E-06	36	438	13	0,03	0,361 CORUM:193	со	11 PA700-20S-PA28 complex
	1,77E-07	16	438	10	0,023	0,625 CORUM:192	co	85 PA28-20S proteasome
	6,16E-03	133	442	19	0,043	0,143 HP:0001874	hp	63 Abnormality of neutrophils
	3,37E-02	10	442	5	0,011	0,5 HP:0100303	hp	21 Muscle fiber cytoplasmatic inclusion bodies
_	1,57E-02	250	442	27	0,061	0,108 HP:0001315	hp	55 Reduced tendon reflexes
٥	2,97E-02	99	442	15	0,034	0,152 HP:0003677	hp	84 Slow progression
0	6,06E-10	61	442 442	20	0,045	0,328 HP:0001644	hp	57 Dilated cardiomyopathy
	3,06E-04 5,02E-05	44 25	442	12 10	0,027 0,023	0,273 HP:0001437 0,4 HP:0000467	hp hp	10 Abnormality of the musculature of the lower limbs 64 Neck muscle weakness
	1,75E-11	52	442	20	0,023	0,385 HP:0100578	hp	97 Lipoatrophy
	4,23E-06	146	442	25	0,043	0,171 HP:0010876	hp	62 Abnormality of circulating protein level
	4,23E-00 4,92E-05		442	6	0,037	0,857 HP:0009025	hp	2 Increased connective tissue
	9,59E-09	121	442	26	0,059	0,215 HP:0000982	hp	14 Palmoplantar keratoderma
	3,78E-13	130	442	32	0,072	0,246 HP:0003198	hp	49 Myopathy
	4,26E-02	23	442	7	0,016	0,304 HP:0003691	hp	3 Scapular winging
	1,43E-08	123	442	26	0,059	0,211 HP:0003457	hp	47 EMG abnormality
	6,08E-04	225	442	28	0,063	0,124 HP:0011675	hp	38 Arrhythmia
	1,47E-05	78	442	15	0,034	0,192 KEGG:04260	ke	102 Cardiac muscle contraction
	1,06E-03	135	442	17	0,038	0,126 KEGG:04530	ke	74 Tight junction
	3,58E-09	106	442	22	0,05	0,208 KEGG:01200	ke	95 Carbon metabolism
	3,25E-07	69	442	16	0,036	0,232 KEGG:04610	ke	108 Complement and coagulation cascades
	3,15E-03	18	442	6	0,014	0,333 KEGG:01210	ke	35 2-Oxocarboxylic acid metabolism
	8,89E-03	30	442	7	0,016	0,233 KEGG:00020	ke	50 Citrate cycle (TCA cycle)
	1,78E-05	90	442	16	0,036	0,178 KEGG:05414	ke	52 Dilated cardiomyopathy
	3,26E-04	151	442	19	0,043	0,126 KEGG:04261	ke	54 Adrenergic signaling in cardiomyocytes
	4,75E-05	74	442	14	0,032	0,189 KEGG:01230	ke	83 Biosynthesis of amino acids
	3,88E-02	74	442	10	0,023	0,135 KEGG:05412	ke	46 Arrhythmogenic right ventricular cardiomyopathy (ARVC)
	7,92E-07	83	442	17	0,038	0,205 KEGG:05410	ke	23 Hypertrophic cardiomyopathy (HCM)
	1,35E-06	208	442	27	0,061	0,13 KEGG:04510	ke	8 Focal adhesion
	1,31E-06	48	442	13	0,029	0,271 KEGG:03050	ke	4 Proteasome

	4,73E-02	468	443	24	0,054	0,051 MI:hsa-miR-593*	mi	72 MI:hsa-miR-593*
	3,32E-02	637	443	30	0,068	0,047 MI:hsa-miR-219-1-3p	mi	27 MI:hsa-miR-219-1-3p
	1,76E-02	676	443	32	0,072	0,047 MI:mmu-miR-700	mi	65 MI:mmu-miR-700
	2,64E-02	422	443	23	0,052	0,055 MI:hsa-miR-149*	mi	12 MI:hsa-miR-149*
	7,05E-03	798	443	37	0,084	0,046 MI:hsa-miR-509-3p	mi	1 MI:hsa-miR-509-3p
	1,15E-03	48	443	13	0,029	0,271 REAC:212919	re	33 Regulation of activated PAK-2p34 by proteasome mediated degradation
	4,97E-02	15	443	6	0,014	0,4 REAC:354087	re	7 Recruitment of Grb2 to pFADK1
	3,15E-02	14	443	6	0,014	0,429 REAC:377643	re	80 Dephosphorylation of inactive c-src by PTPB1
	6,80E-03	16	443	7	0,016	0,438 REAC:372708	re	26 p130Cas linkage to MAPK signaling for integrins
	3,15E-02	14	443	6	0,014	0,429 REAC:354149	re	99 Interaction of alphallbbeta3 with Fibrinogen
	4,33E-03	4	443	4	0,009	1 REAC:140851	re	18 fibrin multimer -> fibrin multimer, crosslinked + NH4+
	3,15E-02	14	443	6	0,014	0,429 REAC:354073	re	61 Auto-phosphorylation of FADK1 at Y397
	1,15E-03	48	443	13	0,029	0,271 REAC:211715	re	20 Proteasome mediated degradation of PAK-2p34
	8,87E-04	47	443	13	0,029	0,277 REAC:68948	re	89 Ubiquitinated Orc1 is degraded by the proteasome
	3,82E-02	65	443	13	0,029	0,2 REAC:174255	re	113 Degradation multiubiquitinated Cyclin A
	2,35E-14	33	443	20	0,045	0,606 REAC:390593	re	91 ATP Hydrolysis By Myosin
٠,	3,26E-02	91	443	16	0,036	0,176 REAC:156842	re	107 Eukaryotic Translation Elongation
6	1,05E-04	60	443	16	0,036	0,267 REAC:114611	re	48 Exocytosis of Alpha granule
	3,15E-02	14	443	6	0,014	0,429 REAC:354124	re	93 Phosphorylation of pFADK1 by SRC
	1,36E-03	56	443	14	0,032	0,25 REAC:195721	re	106 Signaling by Wnt
	6,67E-04		443	14	0,032	0,264 REAC:174113	re	15 SCF-beta-TrCP mediated degradation of Emi1
	2,28E-02		443	13	0,029	0,21 REAC:188191	re	81 APC/C:Cdh1-mediated degradation of Skp2
	1,48E-03	49	443	13	0,029	0,265 REAC:353125	re	101 26S proteosome degrades ODC holoenzyme complex
	3,04E-03		443	13	0,029	0,25 REAC:180585	re	73 Vif-mediated degradation of APOBEC3G
	3,15E-02	14	443	6	0,014	0,429 REAC:377641	re	45 alphallbbeta3:c-Src clustering
	3,07E-04	50	443	14	0,032	0,28 REAC:180573	re	19 Degradation of ubiquitinated CD4
	3,15E-02	14		6	0,014	0,429 REAC:377640	re	88 Autophosphorylation of c-src
	1,15E-03	48	443	13	0,029	0,271 REAC:75825	re	100 Proteasome mediated degradation of Cyclin D1
	8,52E-04	54	443	14	0,032	0,259 REAC:187574	re	110 Degradation of ubiquitinated p27/p21 by the 26S proteasome
	2,72E-02	63	443 443	13 13	0,029 0,029	0,206 REAC:174202	re	82 Degradation of multiubiquitinated Securin
	1,15E-03 2,28E-02	48 62	443	13	0,029	0,271 REAC:68825 0,21 REAC:174084	re re	75 Ubiquitinated geminin is degraded by the proteasome 22 Autodegradation of Cdh1 by Cdh1:APC/C
	3,15E-02	14		6	0,029	0,429 REAC:354066	re	42 Translocation of FADK1 to Focal complexes
	1,15E-03	48	443	13	0,014	0,271 REAC:69613	re	94 p53-Independent G1/S DNA damage checkpoint
	3,15E-02		443	6	0,014	0,429 REAC:377644	re	98 Release of Csk from Src
	p-value					Q&T/Q Q&T/T	term ID	t type
	8,16E-05		291	17	0,058	0,081 GO:0006006	ВР	33 glucose metabolic process
	4,17E-04		291	10	0,034	0,139 GO:1902400	ВР	90 intracellular signal transduction involved in G1 DNA damage checkpoint
	6,31E-12	2475	291	90	0,309	0,036 GO:0009056	ВР	21 catabolic process
	1,65E-02	64	291	8	0,027	0,125 GO:0006096	ВР	102 glycolytic process
١.	_ 9,60E-05	62	291	10	0,034	0,161 GO:0006521	ВР	26 regulation of cellular amino acid metabolic process
- 6	4,17E-04	72	291	10	0,034	0,139 GO:0051436	BP	74 negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle
	7,56E-19	87	291	23	0,079	0,264 GO:0002576	BP	61 platelet degranulation
	4,48E-19	12323	291	263	0,904	0,021 GO:0044699	BP	92 single-organism process
	9,20E-07	29	291	9	0,031	0,31 GO:0018149	BP	103 peptide cross-linking
	3,99E-08	64	291	13	0,045	0,203 GO:0006956	BP	89 complement activation
	4,17E-04	72	291	10	0,034	0,139 GO:0006977	BP	58 DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest

	1,96E-03	128	291	12	0,041	0,094 GO:0055002	ВР	52 striated muscle cell development
	4,73E-07	899	291	42	0,144	0,047 GO:0007010	BP	56 cytoskeleton organization
	9,27E-09	85	291	15	0,052	0,176 GO:0072376	BP	83 protein activation cascade
	6,83E-04	188	291	15	0,052	0,08 GO:0016051	BP	75 carbohydrate biosynthetic process
	2,26E-07	46	291	11	0,038	0,239 GO:0006958	BP	69 complement activation, classical pathway
	1,04E-03	45	291	8	0,027	0,178 GO:0003229	BP	22 ventricular cardiac muscle tissue development
	2,82E-03	88	291	10	0,034	0,114 GO:0031145	ВР	96 anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process
	4,94E-02	54	291	7	0,024	0,13 GO:0046496	BP	51 nicotinamide nucleotide metabolic process
	3,23E-04	286	291	19	0,065	0,066 GO:0044262	BP	47 cellular carbohydrate metabolic process
	2,28E-06	211	291	19	0,065	0,09 GO:0070161	CC	80 anchoring junction
	1,20E-04	8	291	5	0,017	0,625 GO:0005577	CC	72 fibrinogen complex
	3,00E-72	1636	291	145	0,498	0,089 GO:0065010	CC	16 extracellular membrane-bounded organelle
	1,04E-02	43	291	7	0,024	0,163 GO:0014704	CC	84 intercalated disc
	6,32E-05	94	291	12	0,041	0,128 GO:0005581	CC	20 collagen
	4,17E-04	181	291	15	0,052	0,083 GO:0005788	CC	87 endoplasmic reticulum lumen
	1,14E-04	99	291	12	0,041	0,121 GO:0042383	CC	64 sarcolemma
	4,54E-04	134	291	13	0,045	0,097 GO:0030055	CC	60 cell-substrate junction
	2,53E-17	362	291	38	0,131	0,105 GO:0031012	CC	101 extracellular matrix
	4,69E-95	2749	291	200	0,687	0,073 GO:0044421	CC	54 extracellular region part
	4,70E-25	208	291	37	0,127	0,178 GO:0043292	CC	79 contractile fiber
	2,03E-22	82	291	25	0,086	0,305 GO:0031983	CC	42 vesicle lumen
	1,97E-04	25	291	7	0,024	0,28 GO:0070003	MF	71 threonine-type peptidase activity
Σ	1,96E-03	152		13	0,045	0,086 GO:0016853	MF	27 isomerase activity
3	1,64E-02	629	291	26	0,089	0,041 GO:0008233	MF	91 peptidase activity
	4,39E-02	11		4	0,014	0,364 GO:0016868	MF	50 intramolecular transferase activity, phosphotransferases
	3,14E-08	688	291	38	0,131	0,055 GO:0005509	MF	76 calcium ion binding
	1,56E-02	183	291	13	0,045	0,071 GO:0005539	MF	17 glycosaminoglycan binding
	1,97E-04	25	291	7	0,024	0,28 GO:0004298	MF	4 threonine-type endopeptidase activity
	1,65E-18	621		50	0,172	0,081 GO:0005198	MF	5 structural molecule activity
	1,18E-06	14		7	0,025	0,5 CORUM:191	со	32 20S proteasome
	2,17E-06	15		7 8	0,025	0,467 CORUM:194	со	2 PA28gamma-20S proteasome 100 26S proteasome
	2,07E-06 5,79E-07	22	285 285	10	0,028 0,035	0,364 CORUM:181 0,278 CORUM:193	co	24 PA700-20S-PA28 complex
	1,79E-09	16		9	0,033	0,562 CORUM:192	со	98 PA28-20S proteasome
	2,87E-03	19	286	7	0,032	0,368 HP:0001430	hp	63 Abnormality of the calf musculature
	1,83E-03	33	286	9	0,031	0,273 HP:0001724	hp	44 Aortic dilatation
	3,42E-04	123	286	18	0,063	0,146 HP:0003457	hp	93 EMG abnormality
	1,63E-08	52		16	0,056	0,308 HP:0100578	hp	97 Lipoatrophy
	2,41E-07	61	286	16	0,056	0,262 HP:0001644	hp	41 Dilated cardiomyopathy
	8,37E-03	49	286	10	0,035	0,204 HP:0011006	hp	15 Abnormality of the musculature of the neck
	1,53E-02	88	286	13	0,045	0,148 HP:0003701	hp	82 Proximal muscle weakness
	1,15E-08	189	286	29	0,101	0,153 HP:0000962	hp	28 Hyperkeratosis
	1,02E-03	146	286	19	0,066	0,13 HP:0010876	hp	23 Abnormality of circulating protein level
	1,19E-07	130	286	23	0,08	0,177 HP:0003198	hp	6 Myopathy
	1,81E-03	4	286	4	0,014	1 HP:0003704	hp	34 Scapuloperoneal weakness
	1,67E-03	78	286	10	0,035	0,128 KEGG:04260	ke	7 Cardiac muscle contraction
	1,57E-13	69	286	19	0,066	0,275 KEGG:04610	ke	31 Complement and coagulation cascades
								-

	0.455.06	02	200	12	0.045	0.457 KECC:05.440	1	11 11
	8,45E-06	83	286	13	0,045	0,157 KEGG:05410	ke	11 Hypertrophic cardiomyopathy (HCM)
	6,66E-03	74	286	9	0,031	0,122 KEGG:01230	ke	77 Biosynthesis of amino acids
	1,65E-05	48	286	10	0,035	0,208 KEGG:03050	ke	81 Proteasome
	1,71E-02	66	286	8	0,028	0,121 KEGG:00010	ke	86 Glycolysis / Gluconeogenesis
	1,50E-05	87	286	13	0,045	0,149 KEGG:04512	ke	62 ECM-receptor interaction
	1,54E-04	106	286	13	0,045	0,123 KEGG:01200	ke	88 Carbon metabolism
	6,66E-03	74	286	9	0,031	0,122 KEGG:05412	ke	59 Arrhythmogenic right ventricular cardiomyopathy (ARVC)
	5,31E-05	54	286	10	0,035	0,185 KEGG:05150	ke	49 Staphylococcus aureus infection
	2,26E-05	90	286	13	0,045	0,144 KEGG:05414	ke	13 Dilated cardiomyopathy
	6,22E-03	109	286	11	0,038	0,101 KEGG:05146	ke	85 Amoebiasis
	1,81E-08	208	286	24	0,084	0,115 KEGG:04510	ke	94 Focal adhesion
	4,23E-03	28	286	6	0,021	0,214 KEGG:00030	ke	43 Pentose phosphate pathway
	4,32E-02	745	291	25	0,086	0,034 MI:hsa-miR-886-5p	mi	40 MI:hsa-miR-886-5p
	2,36E-02	717	291	25	0,086	0,035 MI:hsa-miR-768-5p	mi	8 MI:hsa-miR-768-5p
	2,00E-02	798	291	27	0,093	0,034 MI:hsa-miR-509-3p	mi	38 MI:hsa-miR-509-3p
	4,03E-03	48	286	10	0,035	0,208 REAC:68825	re	18 Ubiquitinated geminin is degraded by the proteasome
	2,17E-03	128	286	17	0,059	0,133 REAC:109581	re	55 Apoptosis
_	3,71E-03	58	286	11	0,038	0,19 REAC:70693	re	95 Ornithine metabolism
MCM MCM	2,34E-02	3	286	3	0,01	1 REAC:140842	re	57 n fibrin monomers -> fibrin multimer
3	3,87E-04	16	286	7	0,024	0,438 REAC:372708	re	10 p130Cas linkage to MAPK signaling for integrins
	8,55E-03	52	286	10	0,035	0,192 REAC:180585	re	35 Vif-mediated degradation of APOBEC3G
	4,18E-02	62	286	10	0,035	0,161 REAC:174084	re	48 Autodegradation of Cdh1 by Cdh1:APC/C
	2,18E-04	97	286	16	0,056	0,165 REAC:71387	re	65 Metabolism of carbohydrates
	2,81E-08	33	286	13	0,045	0,394 REAC:397014	re	29 Muscle contraction
	1,02E-02	53	286	10	0,035	0,189 REAC:174113	re	12 SCF-beta-TrCP mediated degradation of Emi1
	3,30E-03	47	286	10	0,035	0,213 REAC:68948	re	73 Ubiquitinated Orc1 is degraded by the proteasome
	4,03E-03	48	286	10	0,035	0,208 REAC:212919	re	45 Regulation of activated PAK-2p34 by proteasome mediated degradation
	1,21E-02	54	286	10	0,035	0,185 REAC:187574	re	67 Degradation of ubiquitinated p27/p21 by the 26S proteasome
	5,93E-03	50	286	10	0,035	0,2 REAC:180573	re	70 Degradation of ubiquitinated CD4
	4,03E-03	48	286	10	0,035	0,208 REAC:75825	re	1 Proteasome mediated degradation of Cyclin D1
	1,69E-02	56	286	10	0,035	0,179 REAC:195721	re	30 Signaling by Wnt
	4,81E-02	63	286	10	0,035	0,159 REAC:174202	re	25 Degradation of multiubiquitinated Securin
	4,18E-02	62	286	10	0,035	0,161 REAC:188191	re	14 APC/C:Cdh1-mediated degradation of Skp2
	4,03E-03	48	286	10	0,035	0,208 REAC:69613	re	46 p53-Independent G1/S DNA damage checkpoint
	7,87E-11	60	286	19	0,066	0,317 REAC:114611	re	3 Exocytosis of Alpha granule
	8,84E-04	4	286	4	0,014	1 REAC:140851	re	37 fibrin multimer -> fibrin multimer, crosslinked + NH4+
	3,92E-03	344	291	19	0,065	0,055 TF:M00806_1	tf	36 Factor: NF-1; motif: NTGGNNNNNNGCCAANN; match class: 1
	p-value		Т	Q (	Q&Ť	Q&T/Q Q&T/T	term ID	t group
	2,30E-10	39	51	8	0,157	0,205 GO:0030049	BP	16 muscle filament sliding
	7,73E-03	2962	51	22	0,431	0,007 GO:0065008	BP	44 regulation of biological quality
	5,54E-03	35	51	4	0,078	0,114 GO:0043462	BP	27 regulation of ATPase activity
_	1,06E-02	41	51	4	0,078	0,098 GO:0055010	BP	28 ventricular cardiac muscle tissue morphogenesis
CECM	1,43E-02	168	51	6	0,118	0,036 GO:0060047	BP	20 heart contraction
2	2,39E-02	16	51	3	0,059	0,188 GO:0001580	BP	10 detection of chemical stimulus involved in sensory perception of bitter taste
	2,00E-02	48	51	4	0,078	0,083 GO:0030239	BP	22 myofibril assembly
	7,68E-03	337	51	8	0,157	0,024 GO:0007517	BP	13 muscle organ development
	7,41E-07	62	51	7	0,137	0,113 GO:0001895	BP	41 retina homeostasis
	.,			•	0,207	-,-10 00.0001000	٥.	

	3,22E-02 2,30E-10 2,95E-03 1,24E-13 1,09E-04 1,24E-03 7,35E-09 1,06E-02 4,46E-03 6,31E-07 2,78E-02	54 39 128 1636 367 2664 191 41 688 374	51 51 51 51 51 51 51 51	4 8 6 28 10 22 11 4 11	0,078 0,157 0,118 0,549 0,196 0,431 0,216 0,078	0,074 G0:0046496 0,205 G0:0033275 0,047 G0:0055002 0,017 G0:0070062 0,027 G0:0015629 0,008 G0:0005829 0,058 G0:0044449	BP BP CC CC CC	12 nicotinamide nucleotide metabolic process 15 actin-myosin filament sliding 5 striated muscle cell development 2 extracellular vesicular exosome 1 actin cytoskeleton 24 cytosol
	2,95E-03 1,24E-13 1,09E-04 1,24E-03 7,35E-09 1,06E-02 4,46E-03 6,31E-07	128 1636 367 2664 191 41 688	51 51 51 51 51 51	6 28 10 22 11 4	0,118 0,549 0,196 0,431 0,216	0,047 GO:0055002 0,017 GO:0070062 0,027 GO:0015629 0,008 GO:0005829	BP CC CC CC	5 striated muscle cell development 2 extracellular vesicular exosome 1 actin cytoskeleton
	1,24E-13 1,09E-04 1,24E-03 7,35E-09 1,06E-02 4,46E-03 6,31E-07	1636 367 2664 191 41 688	51 51 51 51 51 51	28 10 22 11 4	0,549 0,196 0,431 0,216	0,017 GO:0070062 0,027 GO:0015629 0,008 GO:0005829	CC CC	extracellular vesicular exosome     actin cytoskeleton
	1,09E-04 1,24E-03 7,35E-09 1,06E-02 4,46E-03 6,31E-07	367 2664 191 41 688	51 51 51 51 51	10 22 11 4	0,196 0,431 0,216	0,027 GO:0015629 0,008 GO:0005829	CC CC	1 actin cytoskeleton
	1,24E-03 7,35E-09 1,06E-02 4,46E-03 6,31E-07	2664 191 41 688	51 51 51 51	22 11 4	0,431 0,216	0,008 GO:0005829	CC	•
	7,35E-09 1,06E-02 4,46E-03 6,31E-07	191 41 688	51 51 51	11 4	0,216	•		24 Cyt0301
	1,06E-02 4,46E-03 6,31E-07	41 688	51 51	4	,	0,030 00.0044443		39 contractile fiber part
	4,46E-03 6,31E-07	688	51		0,070	0,098 GO:0008307	MF	18 structural constituent of muscle
	6,31E-07				0,216	0,016 GO:0005509	MF	4 calcium ion binding
	•		51	12	0,235	0,032 GO:0003779	MF	37 actin binding
		12	47	2	0,043	0,167 CORUM:725	co	36 P2X7 receptor signalling complex
	1,24E-02	123	47	7	0,149	0,057 HP:0003457	hp	21 EMG abnormality
	8,38E-07	52	47	8	0,17	0,154 HP:0100578	hp	7 Lipoatrophy
	1,51E-02	23	47	4	0,085	0,174 HP:0003691	hp	17 Scapular winging
	6,72E-03	19	47	4	0,085	0,211 HP:0001430	hp	30 Abnormality of the calf musculature
_	3,28E-02	199	47	8	0,17	0,04 HP:0001639	hp	31 Hypertrophic cardiomyopathy
CECM	4,87E-02	2	47	2	0,043	1 HP:0001704	hp	11 Tricuspid valve prolapse
2	2,24E-02	189	47	8	0,17	0,042 HP:0000962	hp	46 Hyperkeratosis
	2,47E-03	61	47	6	0,128	0,098 HP:0001644	hp	29 Dilated cardiomyopathy
	4,16E-03	17	47	4	0,085	0,235 HP:0008180	hp	6 Mildly elevated creatine phosphokinase
	8,11E-05	130	47	9	0,191	0,069 HP:0003198	hp	34 Myopathy
	5,00E-02	102	47	6	0,128	0,059 HP:0001635	hp	43 Congestive heart failure
	1,26E-04	208	51	8	0,157	0,038 KEGG:04510	ke	33 Focal adhesion
	7,30E-05	83	51	6	0,118	0,072 KEGG:05410	ke	32 Hypertrophic cardiomyopathy (HCM)
	1,58E-02	74	51	4	0,078	0,054 KEGG:05412	ke	26 Arrhythmogenic right ventricular cardiomyopathy (ARVC)
	1,24E-03	135	51	6	0,118	0,044 KEGG:04530	ke	35 Tight junction
	1,11E-03	78	51	5	0,098	0,064 KEGG:04260	ke	42 Cardiac muscle contraction
	1,18E-04	90	51	6	0,118	0,067 KEGG:05414	ke	23 Dilated cardiomyopathy
	2,56E-02	151	51	5	0,098	0,033 KEGG:04261	ke	38 Adrenergic signaling in cardiomyocytes
	4,43E-02	626	50	8	0,16	0,013 MI:mmu-miR-695	mi	25 MI:mmu-miR-695
	5,00E-02	3	51	2	0,039	0,667 REAC:349794	re	14 Exocytosis of Alpha Actinins
	9,73E-09	33	51	8	0,157	0,242 REAC:390593	re	19 ATP Hydrolysis By Myosin
	6,75E-03	19	49	3	0,061	0,158 TF:M00403_2	tf	8 Factor: aMEF-2; motif: CKGDYTAAAAATAACYMM; match class: 2

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Q&T/T	t name and depth in group
GO:0001580	P01037,P01833,P12273,P25311
GO:0010035	P08779,P13645,P02533,P02768,Q6FH91,P05109,Q06830,P05089,Q05639,P04040,Q8WZ42,P02452,C9JEU5
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GO:0045109	P35527,P02533,Q04695,P15924
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30.0030233	1 20000) 40=1110) 40112 1=11 00002
GO:0007155	Q6ZN40,P05109,Q9HB00,P01040,Q02413,P25311,P15924,Q15582,P35609,P02452,D9ZGF2,P12110,B4DIT7,C9J7N5
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HP:0006466	P21333,D9ZGF2,P12110
HP:0001805	P08779,P13647,P02533,Q15149

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 HP:0001635
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KEGG:04261 P13533,Q6FH91,Q6ZN40,P12829,P12883,Q6IB42,P68032

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GO:0002474 9,Q86SZ7,H7BZJ3

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GO:0006414

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GO:0031093 GO:0070161	P02768,O43707,P00488,B4DPH4,E9KL23,P01023,Q5H9A7,P02671,D3DP13,P04275,E9KL26,P08697,P10909,H9KV75,P35609,C9JEU5 Q13813,P13533,Q9HB00,Q53SB5,P12883,Q02413,P15924,O75369,G3XAM7,Q14126,Q15124,Q702N8,Q5SZF2,H0YJ34,Q9NVD7,Q9 Y490,Q9Y4G6,H9KV75,Q7Z3H5,P35609,Q15149
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GO:0005198	Q15323,P08779,P13647,Q8N1N4,P35527,P13645,P02533,G3XAP6,P02545,Q13813,Q03252,Q6ZN40,Q53SB5,Q6IB42,P35908,P3555 5,P15924,F8VR50,O15230,A2TDC0,O94875,E9PR44,P02549,Q5TZZ9,Q7Z612,I6L965,P07942,C9J9K3,P11532,P13535,H3BNG3,E9PBF 6,A6NLG9,F2Z2S8,P25398,P30050,G3XAM7,D3DSM4,Q7Z554,Q5T7N0,A2TDB8,P51884,P52179,P53621,P54296,G3V1Y7,I3L3P7,M0 QX76,Q96IR1,P62906,P68133,P68366,Q00610,B2ZZ89,F8VR69,Q05707,Q09666,O43209,Q15124,Q16363,D6RAF1,Q5VST9,D6RGG3, A8KA83,Q9Y490,Q9Y4G6,Q9Y6C2,E7EVA0,K7EQW8,Q5TCU3,P35609,Q8WZ42,P02452,Q15149
GO:0044822 GO:0070003	K7EJ44,P13639,Q76LA1,Q6IAT1,O43707,Q0QF37,E9PKE3,Q06830,P15924,P81605,Q5STU3,B4E0R6,H3BV41,O75369,B4DJV2,O9487 5,I6L965,E5RGW4,Q6FH10,C9J9K3,P09382,Q53T09,P13667,H3BNG3,Q86TY5,F2Z2S8,F8W0K0,P25398,K7ENG2,A6NLN1,D6RHJ3,P30 050,D9IAI1,G3XAM7,P46109,Q5T7N0,P49327,E7EU85,P61981,I3L3P7,M0QX76,J3QLI9,B7Z7P8,Q96IR1,P62906,D0PNI1,Q00610,B2Z Z89,F8VR69,Q05707,I3L3Q7,Q08257,Q09666,B4DY09,B1ANR0,D6RF44,Q14204,E7EQG2,C9IZL7,Q15717,Q6IBS0,H0YC73,Q702N8,Q 99714,D6R9P3,Q9NQC3,B0QY90,E7EVA0,H7BZJ3,K9JA46,P21333,Q15149 014818,P25786,H0YMZ1,P28070,Q6IAT9,P28074,P49721,G3V3U4

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CORUM:194	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P28074,P49721,G3V3U4
CORUM:191	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P28074,P49721,G3V3U4
CORUM:181	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P28074,P49721,G3V3U4
CORUM:2837	K7EJ44,E9PKE3,Q00610,O43209
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REAC:174255	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P28074,K7ENY6,P49721,H3BQV2,G3V3U4,Q06323,C9J0E9,Q86SZ7 P13533,Q6FH91,Q6ZN40,P12829,Q53SB5,Q6IB42,A2TDC0,P06753,P11532,P13535,G3V3L5,K7EN02,P28289,Q7Z554,P68133,K7EQ
REAC:390593	W8,Q5TCU3,P35609,Q8WZ42,P68032
REAC:156842	P13639,Q7Z612,C9J9K3,H3BNG3,F2Z2S8,F8WF65,P25398,Q53YD7,E9PN91,P30050,Q5T7N0,I3L3P7,M0QX76,Q96IR1,P62906,F8VR6
NEAC.130042	
REAC:114611	P02768,O43707,P00488,B4DPH4,E9KL23,P01023,Q5H9A7,P02671,D3DP13,P04275,E9KL26,P08697,P10909,H9KV75,P35609,C9JEU5
REAC:354124	F5H823,P02671,D3DP13,P04275,Q9Y490,C9JEU5
REAC:195721	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P28074,K7ENY6,P49721,H3BQV2,G3V3U4,E7ERH2,Q06323,C9J0E9,Q86SZ7
REAC:174113	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P28074,K7ENY6,P49721,H3BQV2,G3V3U4,E7ERH2,Q06323,C9J0E9,Q86SZ7
REAC:188191	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P28074,K7ENY6,P49721,H3BQV2,G3V3U4,Q06323,C9J0E9,Q86SZ7
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REAC:377641	F5H823,P02671,D3DP13,P04275,Q9Y490,C9JEU5
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REAC:377640	F5H823,P02671,D3DP13,P04275,Q9Y490,C9JEU5
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REAC:377644 Q&T/T	F5H823,P02671,D3DP13,P04275,Q9Y490,C9JEU5 t name and depth in group
QQ1/1	P17174,Q0QF37,M0R261,E9PR44,P06744,Q6FHV6,P11216,P15259,P17858,Q6FHU2,P35573,P36871,F2Z393,Q8N5Y3,Q04446,Q151
GO:0006006	24,B4E022
GO:1902400	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7

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GO:0009056	D6RGG3,C9JTK6,Q9UBG0,E9PPU6,Q86SZ7,P68032,K9JA46,B4E022,P21333,P02452,D9ZGF2,P12110
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	6,I6L965,B4DQI1,P06727,P06744,P06753,B4E1L6,Q6FH10,E9PS78,P07942,P07954,P08697,C9J6H2,Q6FHV6,P09238,F5H7T4,D6R974
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	707,Q06323,Q07092,Q07954,Q07960,B4DVE1,E7EVH9,D3DQB3,Q9BZQ0,Q13011,H7C5L0,A8K8J9,Q5JXH9,Q14126,E7EQG2,Q15084
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GO:0006956	P01023,P01031,P01859,P01861,E9KL26,Q6LAM0,B4DQI1,B4E1L6,F5H7T4,P0C0L4,P0C0L5,P10909,A8K008
GO:0006977	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
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GO:0007010	5,D6RAF1,Q6IBS0,Q71U36,Q9NVD7,B4E3S0,Q9Y490,H9KV75,Q8WZ42,P68032,P21333
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GO:0016051	P17174,Q0QF37,P06744,Q6FHV6,P15259,Q6FHU2,E5RG13,P35573,P36871,F2Z393,Q8N5Y3,Q00610,Q04446,B7Z3K3,B4E022
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GO:0003229	P13533,Q6FH91,Q6ZN40,P12883,Q6IB42,P15924,K7EN02,Q05707
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	P17174,Q5U077,Q0QF37,B4DJV2,P06744,Q6FHV6,P11216,P15259,P17858,Q6FHU2,B4DG62,E5RG13,P35573,P36871,Q8N5Y3,Q8N
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nCM			
-			GO:0

GO:0043292

GO:0070161 GO:0005577	Q13813,P13533,Q9HB00,Q53SB5,P12883,Q02413,P15924,O75369,P31151,G3XAM7,Q14126,Q15124,H0YJ34,Q9NVD7,F5GX07,Q9Y 490,H9KV75,P35609,Q15149 P02671,D3DP13,P02751,P08697,C9JEU5
GO:0065010 GO:0014704	Q86YZ3,P08779,P13647,Q8N1N4,P35527,P13645,P02533,P02768,Q04695,P05787,Q86Y46,P07384,P13639,Q13813,D9YZU5,S4R37 1,Q6IAT1,P17174,P02790,O43707,Q5T0749,Q0QF37,P05109,K7ESE8,C3PTT6,Q96K68,P12273,E9PKE3,P35908,Q06830,P253 11,P15924,P81605,O14818,Q15582,Q5SRT3,Q96AR9,O15230,D6RD66,O75369,B4DJV2,M0R261,P00738,B4DPH4,E9KL23,P01023,P 01031,E9PR44,J9ZVQ3,P02671,P02751,P02760,P02765,P02787,P02792,Q5TZZ9,P04275,E9KL26,Q6LAM0,P05543,I6L965,P06744,P0 6753,E9PS78,P07942,P07954,Q6FHV6,P10909,P14543,Q5CAQ5,P17858,Q6FHU2,Q6AWD1,A6NLG9,Q1RMG2,P25786,H0YMZ1,P27 348,P28070,Q6IAT9,A8HT81,Q5T0D2,D9IAI1,B4E3A8,P31947,B0YJ88,P36871,P36955,F2Z393,D3DSM4,I3L297,P47756,P49721,P501 35,J3KTF8,Q8N9C4,G3V3U4,P61981,E9PLD0,D0PNI1,Q00610,B2ZZ89,Q04446,Q06323,Q07960,B4DVE1,Q13011,A8K8J9,Q14126,Q1 5084,Q53SS8,Q15404,B5MBZ8,Q16363,Q16531,Q16555,C8CHS3,Q562R1,Q6EMK4,Q6IBS0,Q6UWP8,Q71U36,Q8IUX7,B4DV28,D6R GG3,C9JTK6,E9PPU6,Q865Z7,Q9UM54,Q9Y490,Q9Y5Z4,E9PPL6,H9KV75,K7ERG3,Q8WZ42,P68032,K9JA46,B4E022,P21333,D9ZGF2,P12110,B4DIT7,C9JEU5,Q15149 Q13813,Q53SB5,P15924,G3XAM7,P47756,Q15124,H9KV75
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GO:0070003	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4
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GO:0008233	,P25786,H0YMZ1,P28070,Q6IAT9,B4DND4,P49721,G3V3U4,Q53XL8,Q8IUX7,B4DV28
GO:0016868	P15259,Q6FHU2,P36871,Q15124
	Q86YZ3,G3XAP6,P07384,Q13813,O43707,Q6FH91,P12829,P05109,Q9HB00,Q02413,Q6IB42,P35555,O14958,E9PEH6,Q5SR54,Q5TZ
	Z9,E9PHK0,B4E1L6,P09238,F5H7T4,P11532,P13797,P14543,Q5CAQ5,P31151,P35442,H3BUU9,P55290,Q07954,D3DQB3,Q9BZQ0,Q
GO:0005509	14126,Q16853,Q9HCU0,H9KV75,K7ERG3,P35609,Q8WZ42
GO:0005539	G3XAP6,J9ZVQ3,P02751,E9PHK0,P05546,Q6FH10,P13727,A6NLG9,E7EPZ9,P35442,Q9BZQ0,Q7Z7G0,Q96PD5
GO:0004298	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4
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	SM4,P51884,P52179,C9JQZ8,P54296,Q00610,B2ZZ89,Q05707,Q15124,Q16363,D6RAF1,Q71U36,D6RGG3,Q9Y490,K7ERG3,P35609,
GO:0005198	Q8WZ42,P02452,Q15149
CORUM:191	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4
CORUM:194	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4
CORUM:181	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8
CORUM:193	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
CORUM:192	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q06323,Q86SZ7
HP:0001430	P02545,Q14315,P13533,Q53SB5,P12883,P11532,Q8WZ42
HP:0001724	P02545,P35555,O75369,P02461,E7EPZ9,D2JYH4,Q15746,P21333,P02452
TIF.0001724	P02545,P13533,Q6FH91,Q6ZN40,Q53SB5,P12883,E9PR44,P06753,P11532,K7EN02,Q04446,Q14126,Q16363,P35609,Q8WZ42,P680
HP:0003457	32,D9ZGF2,P12110
111.0003437	P02545,P13533,Q6FH91,Q6ZN40,Q53SB5,P12883,P35555,E9PR44,P11532,K7EN02,Q14126,Q16363,P35609,Q8WZ42,P68032,P213
HP:0100578	33
111.0100370	P02545,P13533,Q6FH91,Q6ZN40,Q53SB5,P12883,E9PR44,P06753,P11532,K7EN02,P36871,Q5JXH9,Q14126,Q16363,P35609,Q8WZ
HP:0001644	42
HP:0011006	P02545,P13533,Q53SB5,P12883,E9PEH6,E9PR44,P06753,Q8WZ42,D9ZGF2,P12110
HP:0003701	P02545,Q14315,P13533,Q53SB5,P12883,E9PR44,P06753,P11532,Q5JXH9,Q8WZ42,D9ZGF2,P12110,Q15149
	P08779,P13647,P35527,P13645,P02533,Q04695,P02545,P13533,Q6FH91,Q6ZN40,P01040,Q53SB5,P12883,Q02413,P35908,P15924
HP:0000962	,E9PR44,P11532,K7EN02,Q05707,Q14126,Q16363,C8CHS3,P35609,Q8WZ42,P68032,D9ZGF2,P12110,Q15149
	P02545,Q14315,O43707,P13533,P12883,O95831,E9PR44,P02787,P05543,P11532,P15259,P35573,P36871,J3KTF8,Q5JXH9,Q8WZ42
HP:0010876	,D9ZGF2,P12110,Q15149
	P02545,Q14315,P13533,Q6FH91,Q6ZN40,Q53SB5,P12883,Q6IB42,E9PR44,P06753,P11532,P15259,K7EN02,P35573,Q5JXH9,Q1412
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HP:0003704	P13533,Q53SB5,P12883,Q5JXH9
KEGG:04260	P13533,Q6FH91,Q6ZN40,P12829,P12883,Q6IB42,P06753,K7EN02,K7ERG3,P68032

	P00488,B4DPH4,Q96EF3,E9KL23,P01023,P01031,P02671,D3DP13,P04275,E9KL26,Q6LAM0,P05546,B4DQl1,B4E1L6,P08697,F5H7T4
KEGG:04610	,POCOL4,POCOL5,C9JEU5
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KEGG:03050	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
KEGG:00010	Q5U077,P06744,Q6FHV6,P15259,P17858,Q6FHU2,B4DG62,P36871
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KEGG:05414	P02545,P13533,Q6FH91,Q6ZN40,Q53SB5,P12883,Q6IB42,P06753,P11532,K7EN02,K7ERG3,Q8WZ42,P68032
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KEGG:04510	7,Q9Y490,H9KV75,J3QSU6,P35609,P21333,P02452,D9ZGF2,P12110
KEGG:00030	M0R261,P06744,P17858,P36871,F2Z393,B4E022
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MI:hsa-miR-886-5p	Q13011,H7C5L0,Q14126,E9PPU6,Q9Y490,Q8WZ42,P21333,Q5U0D2,P12110
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MI:hsa-miR-768-5p	2,B4DN87,D2JYH4,B4DVE1,Q15404,H9KV75,Q8WZ42,P68032,P21333,C9JEU5
	Q15323,S4R371,P05089,O14818,O15230,P00738,P01031,Q5H9A7,P02671,E9KL26,P05543,P05546,F5H7T4,P10909,K7EN02,G3XAM
MI:hsa-miR-509-3p	7,P36871,I3L297,C9IY88,Q15746,Q16531,Q8IUX7,E5RK99,E7ESF6,Q8WZ42,P68032,D9ZGF2
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REAC:109581	7,Q15149
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REAC:140842	P02671,D3DP13,C9JEU5
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REAC:174084	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
REAC:71387	P17174,Q5U077,Q0QF37,M0R261,P06744,Q6FHV6,P15259,P17858,Q6FHU2,B4DG62,P35573,P36871,F2Z393,Q8N5Y3,Q04446,B4E
NEAC./130/	022
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REAC:174113	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
REAC:68948	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
REAC:212919	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
REAC:187574	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
REAC:180573	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
REAC:75825	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7

	REAC:195721	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
	REAC:174202	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
	REAC:188191	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
	REAC:69613	O14818,P25786,H0YMZ1,P28070,Q6IAT9,P49721,G3V3U4,Q53XL8,Q06323,Q86SZ7
		P02768,O43707,P00488,B4DPH4,E9KL23,P01023,Q5H9A7,P02671,D3DP13,P02751,P04275,E9KL26,B4E1L6,P08697,P10909,P35442,
	REAC:114611	H9KV75,P35609,C9JEU5
	REAC:140851	P00488,P02671,D3DP13,C9JEU5
		P05787,D9YZU5,P04040,Q5STU3,Q5H9A7,Q6LAM0,Q6FHV6,P09238,P13797,P14543,P23141,B4DHX4,Q02952,Q05682,B4DVE1,H7C
	TF:M00806_1	5L0,K7EM02,B3KV49,Q15149
	Q&T/T	
	GO:0030049	MYH3,MYH6,Q6FH91,Q6ZN40,MYL4,Q53SB5,Q6IB42,ACTN2
		B7ZBT8,H0YIS1,H9ZYJ2,D9YZU5,S4R371,ACTN4,MYH6,Q6FH91,Q6ZN40,MYL4,PIGR,DSG1,C3PTT6,Q96K68,PIP,E9PKE3,PRDX1,FBN1,
	GO:0065008	F8VV32,DCD,ACTN2,FLNA
	GO:0043462	MYH6,Q6FH91,Q6ZN40,MYL4
Σ	GO:0055010	MYH6,Q6FH91,Q6ZN40,Q6IB42
CECM	GO:0060047	MYH6,Q6FH91,Q6ZN40,MYL4,Q53SB5,Q6IB42
Ŭ	GO:0001580	RTP3,PIGR,PIP
	GO:0030239	MYH3,MYH6,Q6ZN40,Q6IB42
	GO:0007517	MYH3,LMNA,MYH6,Q6FH91,Q6ZN40,Q6IB42,D9ZGF2,Q5U0D2
	GO:0001895	B7ZBT8,PIGR,C3PTT6,Q96K68,PIP,PRDX1,F8VV32
	GO:0046496	J3KS22,Q5U077,Q0QF37,B4E022
	GO:0033275	MYH3,MYH6,Q6FH91,Q6ZN40,MYL4,Q53SB5,Q6IB42,ACTN2
	GO:0055002	MYH3,LMNA,FLNC,MYH6,Q6ZN40,Q6IB42
	<b>33</b> 13333332	
		K7ERE3,PPM1L,MYH3,H9ZYJ2,D9YZU5,S4R371,Q76LA1,Q6IAT1,J3KS22,ACTN4,Q5U077,KPRP,Q0QF37,K7ESE8,PIGR,C3PTT6,Q96K68
	GO:0070062	,PIP,E9PKE3,PRDX1,TGM3,F8VV32,DCD,E7DVW5,K9JA46,B4E022,FLNA,D9ZGF2
	GO:0015629	MYH3,D6RA88,ACTN4,MYH6,Q6FH91,Q6ZN40,MYL4,Q6IB42,ACTN2,FLNA
	00100125025	MYH3,H9ZYJ2,LMNA,FLNC,D9YZU5,S4R371,Q6IAT1,Q5U077,MYH6,Q6FH91,Q6ZN40,MYL4,K7ESE8,Q53SB5,DSG1,Q6IB42,E9PKE3,P
	GO:0005829	RDX1,ACTN2,K9JA46,B4E022,FLNA
	G0:0044449	MYH3,D6RA88,FLNC,ACTN4,MYH6,Q6FH91,Q6ZN40,MYL4,Q53SB5,Q6IB42,ACTN2
	GO:0008307	D6RA88,Q6ZN40,Q6IB42,ACTN2
	GO:0005509	B7ZBT8,D6RA88,ACTN4,Q6FH91,MYL4,Q9HB00,DSG1,Q6IB42,TGM3,FBN1,ACTN2
	GO:0003779	MYH3,FLNC,ACTN4,MYH6,Q6FH91,Q6ZN40,MYL4,Q6IB42,PIP,ACTN2,FLNA,Q5U0D2
	CORUM:725	ACTN4,E9PKE3
	HP:0003457	LMNA,MYH6,Q6FH91,Q6ZN40,Q53SB5,ACTN2,D9ZGF2
	HP:0100578	LMNA,MYH6,Q6FH91,Q6ZN40,Q53SB5,FBN1,ACTN2,FLNA
	HP:0003691	LMNA,MYH6,Q53SB5,FLNA
5		LMNA,FLNC,MYH6,Q53SB5
CECM	HP:0001639	LMNA,D9YZU5,MYH6,Q6FH91,Q6ZN40,Q53SB5,Q6IB42,ACTN2
0	HP:0001704	FBN1,FLNA
	HP:0000962	LMNA,MYH6,Q6FH91,Q6ZN40,Q53SB5,DSG1,ACTN2,D9ZGF2
	HP:0001644	
		LMNA,MYH6,Q6FH91,Q6ZN40,Q53SB5,ACTN2
	HP:0008180	LMNA,FLNC,MYH6,D9ZGF2
	HP:0003198	LMNA,FLNC,MYH6,Q6FH91,Q6ZN40,Q53SB5,Q6IB42,ACTN2,D9ZGF2
	HP:0001635	LMNA,MYH6,Q6ZN40,Q53SB5,FBN1,FLNA
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KEGG:05412 LMNA,ACTN4,Q53SB5,ACTN2

 KEGG:04530
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 KEGG:04260
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 KEGG:05414
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KEGG:04261 MYH6,Q6FH91,Q6ZN40,MYL4,Q6IB42

MI:mmu-miR-695 PPM1L,H9ZYJ2,D9YZU5,B3KVA7,J3KS22,Q6FH91,J3KRG2,D9ZGF2

REAC:349794 ACTN4,ACTN2

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