

#pathway ID

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GO.0030836

GO.0043206

pathway description

response to stress
response to stimulus
single-multicellular organism process
wound healing
blood coagulation
regulation of biological quality
single-organism developmental process
cell activation
single-organism transport
anatomical structure development
localization
single-organism localization
transport
platelet activation
regulation of localization
establishment of localization
cellular developmental process
movement of cell or subcellular component
cell differentiation
cell adhesion
vesicle-mediated transport
establishment of localization in cell
cell surface receptor signaling pathway
secretion by cell
regulation of cellular component movement
response to external stimulus
cellular localization
exocytosis
regulation of cell migration

immune system process
platelet degranulation
tissue development
regulation of cellular component organization
single organismal cell-cell adhesion
locomotion
protein complex subunit organization
cell development
actin filament-based process
chemotaxis
cell morphogenesis involved in differentiation
cell morphogenesis
homotypic cell-cell adhesion
platelet aggregation
actin cytoskeleton organization
neuron projection morphogenesis
neuron projection development
cell migration
organophosphate metabolic process
neuron development
cytoskeleton organization
localization of cell
regulation of anatomical structure morphogenesis
cell projection organization
cell-substrate adhesion
positive regulation of cell migration
axon guidance
axonogenesis
axon development
cell morphogenesis involved in neuron differentiation
tissue morphogenesis
extracellular matrix organization

regulation of cell morphogenesis
NAD metabolic process
integrin-mediated signaling pathway
cell-matrix adhesion
regulation of cellular component size
regulation of actin filament-based process
regulation of cytoskeleton organization
nucleotide metabolic process
canonical glycolysis
pyruvate metabolic process
regulation of actin polymerization or depolymerization
regulation of epithelial cell migration
cell junction assembly
actin filament organization
ATP metabolic process
leukocyte migration
regulation of actin cytoskeleton organization
gluconeogenesis
phagocytosis
muscle contraction
negative regulation of cellular component movement
positive regulation of epithelial cell migration
regulation of endothelial cell migration
regulation of leukocyte migration
ameboidal-type cell migration
substrate adhesion-dependent cell spreading
cell-substrate junction assembly
regulation of actin filament depolymerization
de novo protein folding
entry into host cell
positive regulation of endothelial cell migration
establishment of Golgi localization

response to gravity

thrombin receptor signaling pathway

positive regulation of actin filament depolymerization

extracellular fibril organization

| observed gene count | % total | false discovery rate |
|------------------------------------|--------------------|---------------------------------|
| 33 | 56 | 6.07E-11 |
| 31 | 53 | 0.00593 |
| 28 | 47 | 0.00214 |
| 27 | 46 | 3.00E-22 |
| 25 | 42 | 3.31E-22 |
| 25 | 42 | 2.35E-06 |
| 25 | 42 | 0.00372 |
| 24 | 41 | 1.79E-19 |
| 23 | 39 | 2.14E-05 |
| 23 | 39 | 0.00522 |
| 23 | 39 | 0.00939 |
| 22 | 37 | 0.000232 |
| 22 | 37 | 0.00121 |
| 21 | 36 | 4.58E-23 |
| 21 | 36 | 1.16E-05 |
| 21 | 36 | 0.00527 |
| 19 | 32 | 0.0162 |
| 18 | 31 | 6.15E-07 |
| 18 | 31 | 0.0265 |
| 17 | 29 | 6.56E-08 |
| 17 | 29 | 5.58E-07 |
| 17 | 29 | 0.000136 |
| 17 | 29 | 0.000938 |
| 16 | 27 | 4.76E-11 |
| 16 | 27 | 1.63E-08 |
| 16 | 27 | 0.00121 |
| 16 | 27 | 0.00392 |
| 15 | 25 | 6.80E-13 |
| 15 | 25 | 1.66E-08 |

| | | |
|----|----|----------|
| 15 | 25 | 0.00717 |
| 14 | 24 | 1.15E-18 |
| 14 | 24 | 0.00242 |
| 14 | 24 | 0.0464 |
| 13 | 22 | 4.35E-08 |
| 13 | 22 | 0.000902 |
| 13 | 22 | 0.00418 |
| 13 | 22 | 0.0125 |
| 12 | 20 | 2.40E-07 |
| 12 | 20 | 1.21E-05 |
| 12 | 20 | 1.88E-05 |
| 12 | 20 | 0.000542 |
| 11 | 19 | 6.09E-08 |
| 10 | 17 | 2.43E-15 |
| 10 | 17 | 1.14E-05 |
| 10 | 17 | 0.000201 |
| 10 | 17 | 0.000904 |
| 10 | 17 | 0.00215 |
| 10 | 17 | 0.00317 |
| 10 | 17 | 0.00343 |
| 10 | 17 | 0.00386 |
| 10 | 17 | 0.004 |
| 10 | 17 | 0.00559 |
| 10 | 17 | 0.0148 |
| 9 | 15 | 1.14E-07 |
| 9 | 15 | 4.80E-05 |
| 9 | 15 | 0.000136 |
| 9 | 15 | 0.000652 |
| 9 | 15 | 0.000848 |
| 9 | 15 | 0.00111 |
| 9 | 15 | 0.00194 |
| 8 | 14 | 0.000652 |

| | | |
|---|----|----------|
| 8 | 14 | 0.00323 |
| 7 | 12 | 7.77E-08 |
| 7 | 12 | 5.50E-07 |
| 7 | 12 | 6.28E-06 |
| 7 | 12 | 0.00105 |
| 7 | 12 | 0.0019 |
| 7 | 12 | 0.00618 |
| 7 | 12 | 0.0162 |
| 6 | 10 | 5.42E-08 |
| 6 | 10 | 4.63E-06 |
| 6 | 10 | 0.000214 |
| 6 | 10 | 0.000497 |
| 6 | 10 | 0.000662 |
| 6 | 10 | 0.00073 |
| 6 | 10 | 0.000776 |
| 6 | 10 | 0.004 |
| 6 | 10 | 0.00558 |
| 5 | 8 | 2.85E-05 |
| 5 | 8 | 0.00733 |
| 5 | 8 | 0.0192 |
| 5 | 8 | 0.0224 |
| 4 | 7 | 0.0109 |
| 4 | 7 | 0.0146 |
| 4 | 7 | 0.0357 |
| 4 | 7 | 0.0407 |
| 3 | 5 | 0.0124 |
| 3 | 5 | 0.0162 |
| 3 | 5 | 0.0231 |
| 3 | 5 | 0.0306 |
| 3 | 5 | 0.0313 |
| 3 | 5 | 0.0437 |
| 2 | 3 | 0.0107 |

| | | |
|---|---|--------|
| 2 | 3 | 0.0178 |
| 2 | 3 | 0.0224 |
| 2 | 3 | 0.0314 |
| 2 | 3 | 0.0314 |

matching proteins in your network (labels)

ACTN1,ALDOA,CDC42,CFL1,CNN2,CORO1A,CSRP1,F11,FERMT3,GAP
ACTN1,ALDOA,BIN2,CORO1C,CSRP1,F11,FERMT3,FKBP1A,GAPDH,G
ACTC1,ACTN1,ALDOA,CNN2,CORO1A,CORO1C,CSRP1,F11,FERMT3,F
ACTN1,ALDOA,CDC42,CFL1,CNN2,CSRP1,F11,FERMT3,GP1BA,HBD,H
ACTN1,ALDOA,CDC42,CFL1,CSRP1,F11,FERMT3,GP1BA,HBD,HSPB1,I
ACTN1,ALDOA,CORO1A,CSRP1,F11,FERMT3,GAPDH,GP1BA,HBD,HS
ACTC1,ACTN1,CNN2,CORO1C,FERMT3,FKBP1A,GP1BA,HSPA8,ITGA2
ACTN1,ALDOA,CFL1,CORO1A,CSRP1,FERMT3,FKBP1A,GP1BA,HSPB1
ACTN1,ALDOA,BIN2,CDC42,CFL1,CORO1C,FKBP1A,HBD,HSPA8,ITGA
ACTC1,ACTN1,CNN2,CORO1C,FERMT3,FKBP1A,GP1BA,HSPA8,ITGA2
ACTN1,ALDOA,BIN2,CDC42,CORO1C,FKBP1A,HBD,ILK,ITGA2B,ITGB3
ACTN1,ALDOA,BIN2,CDC42,CFL1,CORO1C,FKBP1A,HBD,HSPA8,ITGA
ACTN1,ALDOA,BIN2,CDC42,CFL1,CORO1C,FKBP1A,HBD,ITGA2B,ITGE
ACTN1,ALDOA,CFL1,CSRP1,FERMT3,GP1BA,HSPB1,ILK,ITGB3,MMRN
ACTN1,CNN2,CORO1A,CORO1C,FKBP1A,HSPB1,ILK,ITGA2B,ITGB1,IT
ACTN1,ALDOA,BIN2,CDC42,CFL1,CORO1C,FKBP1A,HBD,ITGA2B,ITGE
ACTN1,CORO1C,FERMT3,GP1BA,HSPA8,ITGA2B,ITGB1,ITGB3,MSN,M
ACTC1,BIN2,CDC42,CORO1C,HSPA8,HSPB1,ILK,ITGA2B,ITGB3,MSN,M
ACTN1,CORO1C,FERMT3,HSPA8,ITGA2B,ITGB1,ITGB3,MSN,MYL12A
ACTN1,CORO1A,CSRP1,FERMT3,FKBP1A,GP1BA,HSPB1,ILK,ITGB1,IT
ACTN1,ALDOA,BIN2,CDC42,CFL1,CORO1C,ITGA2B,ITGB3,MMRN1,PI
ACTN1,ALDOA,CDC42,CFL1,HSPA8,ITGA2B,ITGB3,MMRN1,MYL12A,
CFL1,CORO1A,FERMT3,FKBP1A,GP1BA,HSPB1,ILK,ITGA2B,ITGB1,ITG
ACTN1,ALDOA,CFL1,CORO1A,HSPA8,ITGA2B,ITGB3,MMRN1,PF4,PF
ACTN1,CNN2,CORO1A,CORO1C,HSPB1,ILK,ITGA2B,ITGB3,MSN,PF4,I
BIN2,CDC42,CFL1,CNN2,HSPA8,HSPB1,ITGA2B,ITGB1,ITGB3,MYL12/
ACTN1,ALDOA,CDC42,CFL1,HSPA8,ITGA2B,ITGB3,MMRN1,MYL12A,
ACTN1,ALDOA,CFL1,CORO1A,ITGA2B,ITGB3,MMRN1,PF4,PFN1,PLEK
CNN2,CORO1A,CORO1C,HSPB1,ILK,ITGA2B,ITGB3,MSN,PF4,PF4V1,P

ACTN1,CFL1,CNN2,FKBP1A,GAPDH,ITGB1,ITGB3,MSN,PF4,PF4V1,PII
ACTN1,ALDOA,CFL1,ITGA2B,ITGB3,MMRN1,PF4,PFN1,PLEK,PPIA,SP
ACTC1,CFL1,CORO1C,FKBP1A,ILK,ITGB3,MSN,PFN1,PGK1,PKM,RAP1
ALDOA,CNN2,HSPA8,ILK,ITGB1,MSN,MYL12A,PFN1,PLEK,RAP1B,SH3
CSRP1,FERMT3,FKBP1A,HSPB1,ILK,ITGA2B,ITGB1,ITGB3,MSN,MYL12
BIN2,CORO1C,HSPA8,ILK,ITGA2B,ITGB3,MSN,MYL12A,PF4,PF4V1,PF
ALDOA,BIN2,CFL1,CORO1A,FERMT3,FKBP1A,HSPA8,ILK,TMSB4X,TRI
ACTN1,CORO1C,FERMT3,HSPA8,ITGA2B,ITGB3,MSN,MYL12A,PIP4K
ACTC1,ALDOA,CNN2,CORO1C,ITGB1,PFN1,PLEK,TLN1,TMSB4X,TPM
BIN2,CDC42,CFL1,HSPA8,ITGA2B,ITGB1,ITGB3,MYL12A,PF4,PF4V1,T
ACTN1,CDC42,CFL1,FERMT3,HSPA8,ILK,ITGA2B,ITGB3,MYL12A,TLN
ACTN1,CDC42,CFL1,FERMT3,GP1BA,HSPA8,ITGA2B,ITGB3,MYL12A,
CSRP1,FERMT3,FKBP1A,HSPB1,ILK,ITGA2B,ITGB3,MYL12A,PLEK,TLN
CSRP1,FERMT3,HSPB1,ILK,ITGA2B,ITGB3,MYL12A,PLEK,TLN1,VCL
ALDOA,CNN2,CORO1C,ITGB1,PFN1,PLEK,TLN1,TMSB4X,VASP,ZYX
CDC42,CFL1,HSPA8,ILK,ITGA2B,ITGB3,MYL12A,TLN1,VASP,VCL
CDC42,CFL1,HSPA8,ILK,ITGA2B,ITGB3,MYL12A,TLN1,VASP,VCL
BIN2,CFL1,CORO1A,CORO1C,ILK,ITGB3,MSN,PF4,PF4V1,PPIA
ALDOA,ENO2,GAPDH,HSPA8,LDHB,PGK1,PIP4K2A,PLEK,PRDX6,TPI1
CDC42,CFL1,HSPA8,ILK,ITGA2B,ITGB3,MYL12A,TLN1,VASP,VCL
ALDOA,CORO1C,GAPDH,ITGB1,PFN1,PLEK,TMSB4X,TUBB1,VASP,ZY
BIN2,CFL1,CORO1A,CORO1C,ILK,ITGB3,MSN,PF4,PF4V1,PPIA
ALDOA,CDC42,CFL1,CORO1A,CORO1C,HSPB1,ILK,MYL12A,PF4,SPAR
CFL1,CORO1A,HSPA8,ILK,ITGA2B,ITGB3,MYL12A,PLEK,TLN1,VASP
ACTN1,CORO1A,FERMT3,ILK,ITGA2B,ITGB1,ITGB3,VCL,ZYX
CORO1A,HSPB1,ILK,ITGA2B,ITGB3,PF4,PF4V1,PFN1,SPARC
CDC42,CFL1,HSPA8,ITGA2B,ITGB1,ITGB3,MYL12A,TLN1,VASP
CDC42,CFL1,HSPA8,ITGA2B,ITGB3,MYL12A,TLN1,VASP,VCL
CDC42,CFL1,HSPA8,ITGA2B,ITGB3,MYL12A,TLN1,VASP,VCL
CDC42,CFL1,HSPA8,ITGA2B,ITGB3,MYL12A,TLN1,VASP,VCL
ACTC1,CFL1,FKBP1A,ILK,ITGB1,ITGB3,PFN1,VASP,VCL
ACTN1,FKBP1A,ILK,ITGA2B,ITGB1,ITGB3,LTBP1,SPARC

ALDOA,CDC42,CFL1,CORO1A,CORO1C,ILK,MYL12A,SPARC
ALDOA,ENO2,GAPDH,LDHB,PGK1,PKM,TPI1
FERMT3,ILK,ITGA2B,ITGB1,ITGB3,PLEK,ZYX
ACTN1,ILK,ITGA2B,ITGB1,ITGB3,VCL,ZYX
CFL1,CORO1A,ILK,PFN1,PLEK,SH3BGRL3,VASP
CFL1,CNN2,ILK,PFN1,PLEK,SH3BGRL3,VASP
CDC42,CFL1,ILK,PFN1,PLEK,SH3BGRL3,VASP
ALDOA,ENO2,GAPDH,HSPA8,LDHB,PGK1,TPI1
ALDOA,ENO2,GAPDH,PGK1,PKM,TPI1
ALDOA,ENO2,GAPDH,LDHB,PGK1,TPI1
CFL1,CORO1A,PFN1,PLEK,SH3BGRL3,VASP
CORO1C,HSPB1,ITGB3,PFN1,SH3BGRL3,SPARC
ACTN1,ILK,ITGB1,ITGB3,VASP,VCL
ALDOA,CFL1,CORO1A,TMSB4X,VASP,ZYX
ALDOA,ENO2,GAPDH,HSPA8,PGK1,TPI1
CORO1A,ITGB1,ITGB3,MSN,PF4,PPIA
CFL1,ILK,PFN1,PLEK,SH3BGRL3,VASP
ALDOA,ENO2,GAPDH,PGK1,TPI1
BIN2,CDC42,CFL1,CORO1A,CORO1C
ALDOA,MYL12A,TLN1,TPM4,VCL
ACTN1,CNN2,CORO1C,ILK,VCL
HSPB1,ITGB3,PFN1,SPARC
HSPB1,ITGB3,SH3BGRL3,SPARC
ITGA2B,MSN,PF4,PF4V1
CFL1,CORO1C,ILK,ITGB1
FERMT3,ILK,ITGB3
ACTN1,ITGB3,TLN1
CFL1,PLEK,SH3BGRL3
FKBP1A,HSPA8,TUBB1
ITGB1,ITGB3,PPIA
HSPB1,ITGB3,SPARC
CDC42,YWHAZ

PKM,SPARC
GP1BA,PLEK
CFL1,PLEK
FKBP1A,ILK

DH,GP1BA,HBD,HSPA8,HSPB1,ILK,ITGB1,ITGB3,MMRN1,MYL12A,PF4,PF4V1,PFN1,PKM,PLEK,PPIA,RAP1B,SPARC,TLN1,TMSB4X,VCL,ZYX

P1BA,HBD,HSPA8,HSPB1,ITGB3,LTBP1,MMRN1,MYL12A,PF4,PF4V1,PFN1,PKM,PLEK,PPIA,RAP1B,SPARC,TLN1,TMSB4X,VCL,ZYX

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ILK,ITGB1,ITGB3,MMRN1,MYL12A,PF4,PFN1,PLEK,PPIA,RAP1B,SPARC,TLN1,TMSB4X,VCL,ZYX

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TLN1,MYL12A,PF4,PFN1,PLEK,PPIA,RAP1B,SPARC,TLN1,TMSB4X,VCL,ZYX

ITGB3,MSN,PF4,PF4V1,PFN1,PPIA,RAP1B,SH3BGRL3,SPARC,TMSB4X,VCL,ZYX

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MYL12A,PGK1,PIP4K2A,PLEK,RAP1B,TAGLN2,TLN1,TMSB4X,VCL,ZYX

MYL12A,PF4,PF4V1,PPIA,TLN1,TPM4,VASP,VCL,ZYX

,PGK1,PIP4K2A,PLEK,RAP1B,TAGLN2,TLN1,TMSB4X,VASP,VCL,ZYX

ITGB3,MMRN1,MSN,MYL12A,PLEK,TLN1,VCL,ZYX

PF4,PFN1,PLEK,PPIA,SPARC,TLN1,TMSB4X,VCL,ZYX

PF4,PFN1,PLEK,PPIA,SPARC,TLN1,TMSB4X,VCL,ZYX

ITGB3,LTBP1,MYL12A,PF4,PF4V1,PLEK,VASP,ZYX

N1,PLEK,PPIA,SPARC,TLN1,TMSB4X,VCL,ZYX

PF4V1,PFN1,SH3BGRL3,SPARC,TMSB4X,VCL,ZYX

A,PF4,PF4V1,PKM,SPARC,TLN1,VASP,ZYX

PF4,PFN1,PLEK,PPIA,SPARC,TLN1,VCL,ZYX

C,PPIA,SPARC,TLN1,TMSB4X,VCL,ZYX

PFN1,SH3BGRL3,SPARC,TMSB4X,VCL,ZYX

P4K2A,PLEK,PPIA,TRIM4,VASP
ARC,TLN1,TMSB4X,VCL
.B,TAGLN2,VASP,VCL
3BGRL3,SPARC,VASP,YWHAZ
2A,PLEK,TLN1,VCL
PIA,TLN1,VASP
M4,TUBB1,VASP,ZYX
2A,RAP1B,TLN1,VASP,VCL
4,VASP,ZYX
LN1,VASP
L,VASP,VCL
TLN1,VASP,VCL
1,VCL

K

C

A,PF4,PF4V1,PFN1,PKM,PLEK,PPIA,PRDX6,RAP1B,SPARC,TLN1,TRIM4,V1,PFN1,PKM,PLEK,PPIA,PRDX6,TLN1,TMSB4X,TRIM4,VASP,VCL
A,PF4,PIP4K2A,PKM,PLEK,PPIA,RAP1B,TLN1,TMSB4X,TPI1,YWHAZ
PIA,RAP1B,SPARC,TLN1,TMSB4X,VCL,YWHAZ
PARC,TLN1,TMSB4X,VCL,YWHAZ
RAP1B,SPARC,TLN1,VASP,VCL,YWHAZ
RAP1B,SPARC,TAGLN2,TLN1,TMSB4X,TPI1,VCL
SPARC,TLN1,TMSB4X,VCL,YWHAZ
LN1,TMSB4X,VCL,YWHAZ
RAP1B,SPARC,TAGLN2,TLN1,VCL
A,SPARC,TLN1,VCL
LN1,VCL,YWHAZ
ISB4X,VCL,YWHAZ
L,YWHAZ
4X,VCL,YWHAZ
ISB4X,VCL
,VCL

MSB4X,TRIM4,VCL,YWHAZ

-,YWHAZ,ZYX

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