

Table S1 Top 100 proteins co-regulated with ITGA2

Uniprot_acc	Protein_names	Gene_names	Percentile_score	Co-regulation score
P17301	Integrin alpha-2	<i>ITGA2</i>	1	1
O15231-3	Zinc-finger protein 185	<i>ZNF185</i>	0.98467	0.011183
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	<i>GNB2</i>	0.98346	0.010692
P15144	Aminopeptidase N	<i>ANPEP</i>	0.980101	0.009563
Q9BUL8	Programmed cell death protein 10	<i>PDCD10</i>	0.973794	0.008049
Q12846	Syntaxin-4	<i>STX4</i>	0.96152	0.006238
P67936	Tropomyosin alpha-4 chain	<i>TPM4</i>	0.957378	0.005806
O00186	Syntaxin-binding protein 3	<i>STXBP3</i>	0.955849	0.005662
Q9UBW5	Bridging integrator 2	<i>BIN2</i>	0.952716	0.00539
P14317	Hematopoietic lineage cell-specific protein	<i>HCLS1</i>	0.9525	0.005372
P05976-2	Myosin light chain 1/3 skeletal muscle isoform	<i>MYL1</i>	0.938436	0.004429
Q15836	Vesicle-associated membrane protein 3	<i>VAMP3</i>	0.936526	0.004324
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	<i>GNB1</i>	0.936301	0.004312
P07951-2	Tropomyosin beta chain	<i>TPM2</i>	0.935799	0.004286
Q13418	Integrin-linked protein kinase	<i>ILK</i>	0.933558	0.004173
Q6IBS0	Twinfilin-2	<i>TWF2</i>	0.931218	0.00406
P60660	Myosin light polypeptide 6	<i>MYL6</i>	0.93025	0.004016
P63104	14-3-3 protein zeta/delta	<i>YWHAZ</i>	0.928382	0.003932
Q06187	Tyrosine-protein kinase BTK	<i>BTK</i>	0.924713	0.003776
P23229-3	Integrin alpha-6	<i>ITGA6</i>	0.924274	0.003759
Q9Y490	Talin-1	<i>TLN1</i>	0.921086	0.003634
Q13642-1	Four and a half LIM domains protein 1	<i>FHL1</i>	0.92058	0.003614
Q9P0K7	Ankyrin	<i>RAI14</i>	0.914414	0.003394
O14950	Myosin regulatory light chain 12B	<i>MYL12B</i>	0.914017	0.003381
Q9NYL9	Tropomodulin-3	<i>TMOD3</i>	0.908373	0.0032
Q86UX7-2	Fermitin family homolog 3	<i>FERMT3</i>	0.907957	0.003187
P28676	Grancalcin	<i>GCA</i>	0.907785	0.003182
Q8NEZ2	Vacuolar protein sorting-associated protein 37A	<i>VPS37A</i>	0.906684	0.00315
P36406-3	E3 ubiquitin-protein ligase TRIM23	<i>TRIM23</i>	0.906288	0.003138
Q15404	Ras suppressor protein 1	<i>RSU1</i>	0.904316	0.003082
O15143	Actin-related protein 2/3 complex subunit 1B	<i>ARPC1B</i>	0.902416	0.003029
Q92619	Rho GTPase-activating protein 45	<i>ARHGAP45</i>	0.89771	0.002903
Q5JSH3	WD repeat-containing protein 44	<i>WDR44</i>	0.892771	0.002781
P08648	Integrin alpha-5	<i>ITGA5</i>	0.888992	0.002694
P50225	Sulfotransferase 1A1	<i>SULT1A1</i>	0.888624	0.002685
P61026	Ras-related protein Rab-10	<i>RAB10</i>	0.887977	0.002671
Q7L591	Docking protein 3	<i>DOK3</i>	0.887934	0.00267
P50453	Serpin B9	<i>SERPINB9</i>	0.887111	0.002652
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	<i>SH3BGL3</i>	0.886785	0.002645
P33527	Multidrug resistance-associated protein 1	<i>ABCC1</i>	0.882752	0.002558
O75695	Protein XRP2	<i>RP2</i>	0.878999	0.002482
P50570-4	Dynamin-2	<i>DNM2</i>	0.878856	0.002479
Q9NX76	CKLF-like MARVEL transmembrane domain-containing protein 6	<i>CMTM6</i>	0.878175	0.002466
P68032	Actin alpha cardiac muscle 1	<i>ACTC1</i>	0.87808	0.002464
Q9Y6M5	Zinc transporter 1	<i>SLC30A1</i>	0.877413	0.002451
O95379-3	Tumor necrosis factor alpha-induced protein 8	<i>TNFAIP8</i>	0.877001	0.002444
P15498	Proto-oncogene vav	<i>VAV1</i>	0.874561	0.002397
P30740	Leukocyte elastase inhibitor	<i>SERPINB1</i>	0.870793	0.00233
P26038	Moesin	<i>MSN</i>	0.869391	0.002305
Q96P48-3	Arf-GAP with Rho-GAP domain ANK repeat and PH domain-containing protein 1	<i>ARAP1</i>	0.867956	0.00228
P19256-2	Lymphocyte function-associated antigen 3	<i>CD58</i>	0.867902	0.00228
Q96FZ7	Charged multivesicular body protein 6	<i>CHMP6</i>	0.866448	0.002255
Q16799	Reticulon-1	<i>RTN1</i>	0.864857	0.002228
P48426	Phosphatidylinositol 5-phosphate 4-kinase type-2 alpha	<i>PIP4K2A</i>	0.863475	0.002206
P06753-2	Tropomyosin alpha-3 chain	<i>TPM3</i>	0.861542	0.002174
P61225	Ras-related protein Rap-2b	<i>RAP2B</i>	0.861131	0.002168
Q15907	Ras-related protein Rab-11B	<i>RAB11B</i>	0.857073	0.002105
Q15746	Myosin light chain kinase smooth muscle	<i>MYLK</i>	0.857039	0.002105
P60953	Cell division control protein 42 homolog	<i>CDC42</i>	0.8567	0.0021
P17612	cAMP-dependent protein kinase catalytic subunit alpha	<i>PRKACA</i>	0.855523	0.002082
B011T2	Unconventional myosin-Ig	<i>MYO1G</i>	0.852461	0.002037
Q13094	Lymphocyte cytosolic protein 2	<i>LCP2</i>	0.851964	0.00203
Q9BV40	Vesicle-associated membrane protein 8	<i>VAMP8</i>	0.8516	0.002025
Q8NHU6	Tudor domain-containing protein 7	<i>TDRD7</i>	0.850397	0.002008
O75083	WD repeat-containing protein 1	<i>WDR1</i>	0.847331	0.001966
P60709	Actin cytoplasmic 1	<i>ACTB</i>	0.846471	0.001954
P61006	Ras-related protein Rab-8A	<i>RAB8A</i>	0.846377	0.001953
O95319-5	CUGBP Elav-like family member 2	<i>CELF2</i>	0.845807	0.001945
Q9H0U4	Ras-related protein Rab-1B	<i>RAB1B</i>	0.844928	0.001934
Q9NVG8	TBC1 domain family member 13	<i>TBC1D13</i>	0.84462	0.001929
Q04917	14-3-3 protein eta	<i>YWHAH</i>	0.842108	0.001897
P48059-3	LIM and senescent cell antigen-like-containing domain protein 1	<i>LIMS1</i>	0.841345	0.001887
O75558	Syntaxin-11	<i>STX11</i>	0.84096	0.001882
Q92835-2	Phosphatidylinositol 345-trisphosphate 5-phosphatase 1	<i>INPP5D</i>	0.840558	0.001877
P08567	Pleckstrin	<i>PLEK</i>	0.840122	0.001871
O14639-6	Actin-binding LIM protein 1	<i>ABLIM1</i>	0.836541	0.001827
P40261	Nicotinamide N-methyltransferase	<i>NNMT</i>	0.836091	0.001822
Q6NZI2	Caveolae-associated protein 1	<i>CAVIN1</i>	0.834615	0.001804
P28062	Proteasome subunit beta type-8	<i>PSMB8</i>	0.83354	0.001791
A6NKT7	RanBP2-like and GRIP domain-containing protein 3	<i>RGPD3</i>	0.832624	0.00178
P62330	ADP-ribosylation factor 6	<i>ARF6</i>	0.832254	0.001776
Q9Y6E0-2	Serine/threonine-protein kinase 24	<i>STK24</i>	0.831789	0.00177
Q9Y3A3	MOB-like protein phocein	<i>MOB4</i>	0.828771	0.001736
P18564	Integrin beta-6	<i>ITGB6</i>	0.82654	0.001711
P52566	Rho GDP-dissociation inhibitor 2	<i>ARHGDIB</i>	0.825465	0.001699
P47755	F-actin-capping protein subunit alpha-2	<i>CAPZA2</i>	0.823673	0.00168
O15511	Actin-related protein 2/3 complex subunit 5	<i>ARPC5</i>	0.819507	0.001636
Q14192	Four and a half LIM domains protein 2	<i>FHL2</i>	0.819384	0.001635
Q96F07-2	Cytoplasmic FMR1-interacting protein 2	<i>CYFIP2</i>	0.818828	0.001629
P61160	Actin-related protein 2	<i>ACTR2</i>	0.811383	0.001555
P59998	Actin-related protein 2/3 complex subunit 4	<i>ARPC4</i>	0.811067	0.001552
Q8WUW1	Protein BRICK1	<i>BRK1</i>	0.810229	0.001544
O00299	Chloride intracellular channel protein 1	<i>CLIC1</i>	0.810174	0.001544
O14975	Very long-chain acyl-CoA synthetase	<i>SLC27A2</i>	0.809606	0.001538
Q01518-2	Adenylyl cyclase-associated protein 1	<i>CAP1</i>	0.809392	0.001536
P05067	Amyloid beta A4 protein	<i>APP</i>	0.808967	0.001532
P05556	Integrin beta-1	<i>ITGB1</i>	0.808645	0.001529
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2	<i>GNAI2</i>	0.806934	0.001513
P09493-3	Tropomyosin alpha-1 chain	<i>TPM1</i>	0.806452	0.001509
P06756-3	Integrin alpha-V	<i>ITGAV</i>	0.804506	0.001491
Q15382	GTP-binding protein Rheb	<i>RHEB</i>	0.803824	0.001485

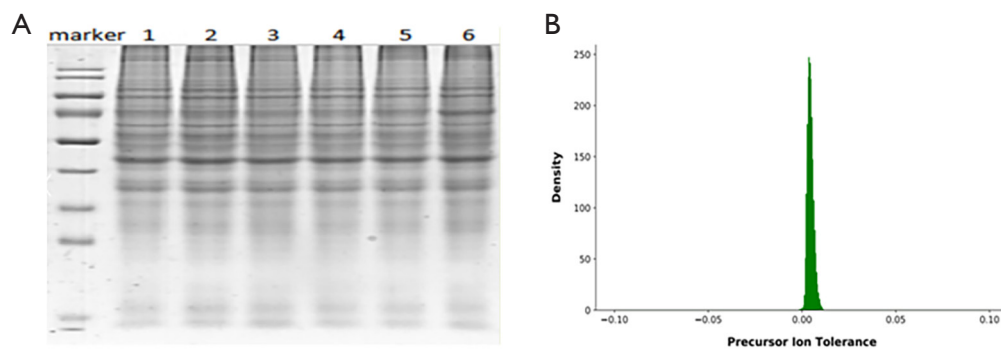


Figure S1 Assessment of the sample quality and the system reliability for (phospho)-proteomic analysis. (A) The sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) gel with 6 samples presented matching degree of the protein concentration and molecular weight gradient and indicated an excellent sample quality. (B) According to the mass tolerance distribution of the precursor ion, the peak shape is concentrated close to 0 and indicated the mass spectrometer error mass deviation is small.