

Table 1

Protein	Gene ID	Pure (of 9)	Crosslinked (of 6)
Heat shock 70 kDa protein 1	HSP71	8	6
Actin, cytoplasmic 1	ACTB	7	6
Heat shock protein HSP 90-beta	HS90B	7	6
Kinesin-like protein KIF11	KIF11	7	2
Cytoskeleton-associated protein 4	CKAP4	5	5
Tubulin beta-2C chain	TBB2C	5	5
Tubulin alpha-1B chain	TBA1B	5	3
Tubulin beta chain	TBB5	4	6
Vesicle-associated membrane protein-associated protein A	VAPA	3	3
Cytoplasmic dynein 1 heavy chain 1	DYHC1	2	4
Clathrin heavy chain 1	CLH1	2	3
Filamin-A	FLNA	2	3
Membrane-associated progesterone receptor component 1	PGRC1	2	3
Myb-binding protein 1A	MBB1A	2	2
Protein transport protein Sec61 subunit beta	SC61B	2	2

Protein	Gene ID	Pure (of 9)	Crosslinked (of 6)
Heat shock cognate 71 kDa protein	HSP7C	1	6
Heat shock protein HSP 90-alpha	HS90A	1	6
Lamina-associated polypeptide 2, isoforms beta/gamma	LAP2B	1	4
Heat shock protein 75 kDa, mitochondrial	TRAP1	1	3
Membrane-associated progesterone receptor component 2	PGRC2	1	3
Ezrin	EZRI		6
Annexin A2	ANXA2		4
Neural cell adhesion molecule 1	NCAM1		4
Vesicular integral-membrane protein VIP36	LMAN2		4
Annexin A5	ANXA5		3
Annexin A6	ANXA6		3
Dynamin-like 120 kDa protein, mitochondrial	OPA1		3
Integrin beta-1	ITB1		3
Lysosome membrane protein 2	SCR2		3
Lysosome-associated membrane glycoprotein	LAMP1		3
Microtubule-associated protein 4	MAP4		3
Myristoylated alanine-rich C-kinase substrate	MARCS		3
Tubulin alpha-1A chain	TBA1A		3
Cell adhesion molecule 1	CADM1		3
Erlin-2	ERLN2		3
Dynein light chain 1, cytoplasmic	DYL1		2
Flotillin-2	FLOT2		2
Lysosome-associated membrane glycoprotein	LAMP2		2
MAGUK p55 subfamily member 6	MPP6		2
Myosin light polypeptide 6	MYL6		2
Protein transport protein Sec23A	SC23A		2
Vesicle transport through interaction with t-SNAREs homolog 1A	VTI1A		2
Vesicle-associated membrane protein-associated protein B/C	VAPB		2
Vesicle-trafficking protein SEC22b	SC22B		2

Table 1. P2X1 interacting cytoskeletal proteins. Using HisFLAG tagged human P2X1 as bait a number of interacting proteins were pulled down associated with P2X1 attached to anti-FLAG agarose beads. After washing the beads proteins were eluted with FLAG peptide and run on SDS PAGE. Protein bands were excised and identified on either 4000 Q-Trap system or Thermo Orbitrap (PNAAC, University of Leicester, UK). A hit protein was identified by a minimum of 3 peptides of $\geq 95\%$ peptide identification probability and 99.9% protein identification probability using the Scaffold2 program (Proteome Software Inc., USA). Proteins labelled 'pure' were identified in runs without DSP crosslinker present and 'crosslinked' in runs where DSP was present.