

Table S1. List of putative KIAA1199 interactors identified by MS after immunoprecipitation. Molecular weight, cellular localization, functions, and number of unique peptide hits obtained on MS for each putative interactor is reported.

Protein symbol *	Mol. wt.	Localization	Pathway	IP/MS experiment number †					
				1		2		3	
				Control	IP	Control	IP	Control	IP
FAT1	506 kDa	Membrane, Cell junctions	Calcium ion binding, cell adhesion, homophilic cell adhesion, cell-cell signaling, anatomical structure morphogenesis	0	1	0	13	0	2
ITPR3	304 kDa	Intracellular Membranes, ER, nucleus, nucleoplasm,	Calcium channel activity, inositol hexakisphosphate binding, G-protein coupled receptor protein signaling pathway	0	0	0	1	0	1
SERPINE1	45 kDa	Plasma Membrane, Extracellular Matrix, Soluble fraction	Response to ROS, Chronological cell aging, platelet degranulation, blood coagulation, regulation of receptor activity	0	6	1	13	1	6
GART	108 kDa	Cytoplasm	Purine metabolism, 'de novo' IMP biosynthetic process	0	1	0	2	0	2
UBR5	308 kDa	Nucleus, intracellular, Soluble fraction	Cell proliferation, progesterone receptor signaling pathway, response to DNA damage stimulus, ubiquitin-dependent protein catabolic process, protein modification process	0	0	0	10	0	2
HSP90B1	92 kDa	ER, Microsome, Cytosol	Response to hypoxia or stress, protein folding, anti-apoptosis, protein transport	0	10	0	8	1	4

GNAI2	40 kDa	Plasma Membrane, Nucleus, cytosol	Activation of MAPKK activity, adenosine receptor signaling pathway, G-protein coupled receptor protein signaling pathway, inhibition of adenylate cyclase activity by G-protein signaling pathway	0	0	1	19	0	8
VCP	89 kDa	Proteasome complex, ER	Receptor binding, ubiquitin-dependent protein catabolic process, double strand break repair	0	7	1	11	3	5
NME2	17 kDa	Nucleus, Cytoplasm, lamellipodium	Purine metabolism, Pyrimidine metabolism, regulation of transcription, DNA-dependent; cell adhesion	0	2	1	4	0	5
GNAI3	41 kDa	Intracellular, Plasma Membrane, Cytoplasm, Golgi apparatus	G-protein activator peptide, Inhibits Gs & stimulates Gi activity, Selective, competitive P2X antagonist	0	0	0	7	0	1
ANXA6	76 kDa	Cytoplasm, Apical Plasma Membrane, Melanosome, Perinuclear region of cytoplasm	Calcium Ion Binding, Calcium dependent phospholipid binding, calcium ion transport, regulation of muscle contraction	0	11	0	2	0	0
LGALS3	26 kDa	Extracellular matrix, Nucleus, cytoplasm, Mitochondrial Inner Membrane, plasma Membrane	Skeletal system development, Cell differentiation, Extracellular Matrix Organization.	0	2	0	6	1	4

STOML2	39 kDa	Cytoplasm, Mitochondrion, Mitochondrial Inner Membrane, Cytoskeleton, Membrane	Receptor- binding	0	2	0	6	1	4
CANX	68 kDa	Cytoplasm, ER (Lumen, Membrane), RER	Calcium Ion Binding, Protein folding, ageing, post translational protein modification	1	8	1	7	1	5
MDH2	36 kDa	Nucleus, mitochondrial inner membrane, mitochondrial matrix	Protein binding, malate dehydrogenase activity, oxidoreductase activity	0	8	0	6	2	2
IPO5	124 kDa	Nucleus, Nuclear pore, nucleolus, cytoplasm	NLS-bearing substrate import into nucleus, intracellular protein transport, interspecies interaction between organisms	0	2	1	7	1	7
ITGB4	202 kDa	Plasma Membrane, Integrin Complex	Cell communication, cell adhesion, cell-matrix adhesion, integrin-mediated signaling pathway, multicellular organismal development	0	2	2	5	0	6
SLC25A3	40 kDa	Mitochondrial inner membrane, integral to plasma membrane	symporter activity, phosphate carrier activity	1	5	3	20	9	6

GPI	63 kDa	Extracellular space, nucleus.	Angiogenesis, Carbohydrate Metabolic process, growth factor activity, isomerase activity	0	4	0	7	3	4
LRP1	505 kDa	Plasma Membrane, Nucleus, Cytoplasm, Endosome	Receptor-mediated endocytosis, Cell Proliferation, Aging, Multicellular Organismal Development, activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway	0	0	0	2	0	2
ATP6V1A	68 kDa	Mitochondrion, cytosol, microvillus, integral to plasma membrane	hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substance	0	2	0	1	0	1
P4HB	57 kDa	ER-Golgi intermediate compartment, ER lumen	Protein disulfide isomerase activity, procollagen-proline 4-dioxygenase activity	0	4	1	9	3	5
ATIC	65 kDa	Mitochondrion, Cytosol	Purine metabolism/biosynthesis	0	0	0	2	0	5
TPI	27 kDa	Soluble fraction, Nucleus, Cytosol	Glycolysis, Gluconeogenesis, Pentose-Phosphate Shunt	1	7	1	4	7	5
DNAJC7	56 kDa	Nucleus, Cytoplasm, Cytoskeleton	Chaperone cofactor-dependent protein refolding	0	0	0	3	0	2
HYOU1	111 kDa	ER, ER Lumen	Response to hypoxia/stress, ATP binding	0	2	0	1	1	3

PSMD1	106 kDa	Proteasome complex, Proteasome regulatory particle	Cell cycle check-point, G1/S transition, S-phase, M/G1 transition of mitotic cycle	0	1	0	3	1	3
ITGA6	127 kDa	Plasma membrane, cell-cell adherens junction, integrin complex,	Cell-substrate junction assembly, integrin-mediated signaling pathway, Blood coagulation, cell-adhesion, cell-matrix adhesion	0	2	0	6	2	4
HSPA4	70 kDa	Nucleus, Cytoplasm	Response to unfolded protein, response to heat, cellular chaperone-mediated protein complex assembly, protein import into mitochondrial outer membrane, mitochondrial outer membrane translocase complex assembly	0	3	1	3	2	8
AP1G1	91 kDa	Golgi membrane, cytoplasm, lysosomal membrane, trans-golgi network	Intracellular protein transport, endocytosis, viral reproduction, post-Golgi vesicle mediated transport	0	1	0	1	0	3
EPHA2	108 kDa	Plasma Membrane, Integral to plasma Membrane	Skeletal system development, Blood vessel development, vasculogenesis, protein phosphorylation, apoptosis, ephrin receptor signaling pathway	0	0	0	2	0	2
PPP6R3	98 kDa	Nucleus, Cytoplasm	Regulation of phosphoprotein phosphatase activity	0	1	5	11	2	10

TKT	68 kDa	Nucleus, Cytoplasm	Glucose, thiamin metabolic process	0	1	0	1	0	2
PSMD11	47 kDa	Proteasome complex	Protein binding	0	0	1	8	0	2
GARS	83 kDa	Soluble fraction cytoplasm, mitochondrion	Translation, tRNA aminoacylation for protein translation, glycyl-tRNA aminoacylation, cell death, gene expression	0	2	1	3	1	4
TARDBP	45 kDa	Nucleus	Transcription from RNA polymerase II promoter, mRNA processing, cell death, RNA splicing, negative regulation by host of viral transcription	0	1	1	5	1	2
GSTO1	28 kDa	Cytoplasm, cytosol	Monodehydroascorbate reductase (NADH) activity, glutathione transferase activity	0	1	0	1	0	1
BSG	42 kDa	Golgi membrane, Mitochondrion, Plasma Membrane, Sarcolemma	Pyruvate metabolic process, cell surface receptor linked signaling pathway, embryo implantation, blood coagulation, odontogenesis of dentine-containing tooth	0	2	2	6	0	1
IPO8	120 kDa	Nucleus, Cytoplasm	Intracellular protein transport, signal transduction, Ran GTPase binding	0	0	0	1	0	2
CTSD	45 kDa	Extracellular matrix, mitochondrion, lysosome,	Autophagic vacuole assembly, proteolysis, cell death	0	2	0	3	3	1
RAB5C	23 kDa	Intracellular, endosome, plasma membrane	GTP catabolic process, intracellular protein transport, nucleocytoplasmic transport, endosome organization, signal transduction	0	1	0	3	2	1
PGK1	45 kDa	Cytoplasm	Carbohydrate metabolic process, ATP binding	0	7	0	4	3	3

TIMM50	40 kDa	Nucleus, mitochondrion, mitochondrial inner membrane, mitochondrial inner membrane presequence translocase complex , membrane	Release of cytochrome c from mitochondria, protein dephosphorylation, mitochondrial membrane organization, protein transport, transmembrane transport	1	5	8	9	1	5
EZR	69 kDa	Ruffle, uropod, nucleolus, cytoplasm, cytosol	Cytoskeletal anchoring at plasma membrane, leukocyte cell-cell adhesion, axon guidance, regulation of cell shape, membrane to membrane docking	1	8	0	6	5	3
RBP1	16 kDa	Cytoplasm	Vitamin A metabolic process, transport, regulation of granulocyte differentiation, response to vitamin A, retinol metabolic process	1	6	0	3	0	0
CCT2	57 kDa	Nucleus but NOT nucleolus, cytoplasm	Protein folding, cellular protein metabolic process, 'de novo' posttranslational protein folding	0	4	0	7	7	4
MSN	68 kDa	Nucleus, nucleolus, cytoplasm	Structural constituent of cytoskeleton, actin binding	0	8	0	2	0	0
GPC1	62 kDa	Extracellular matrix, plasma membrane	Axon guidance	0	0	0	4	0	1
CCT8	60 kDa	Cytoplasm, microtubule org. center	ATP binding, ATPase activity, unfolded protein binding	0	5	2	9	9	10

RARS	75 kDa	Nucleus but NOT nucleolus, cytoplasm, mitochondrion	Arginine-tRNA ligase activity, nucleotide binding, protein binding	0	4	5	6	0	6
SNAP23	23 kDa	Nucleus but NOT nucleolus, microsomes, Golgi apparatus, plasma membrane enriched fraction	Protein binding	0	0	0	8	0	1
SMC4	147 kDa	Nucleus but NOT nucleolus, condensin complex	Nucleotide binding, nucleoside-triphosphatase activity, protein binding, protein heterodimerization activity	0	3	1	5	5	4
CD109	162 kDa	Plasma membrane, anchored to membrane, extracellular region	Serine-type endopeptidase inhibitor activity	0	0	0	7	0	1
PDIA6	48 kDa	ER-Golgi intermediate compartment, plasma membrane, melanosome	Protein disulfide isomerase activity, protein binding	0	5	2	8	5	4

TAGLN2	22 kDa	Plasma membrane, nuclear membrane	Protein binding	0	2	0	4	7	4
Septin9	65 kDa	Cytoplasm, cytoskeleton	GTP catabolic process, protein heterooligomerization, cell cycle, cell division	0	4	1	0	0	2
PSMA3	28 kDa	Nucleus, cytoplasm, proteasome core complex	Threonine-type endopeptidase activity	0	3	0	1	0	0
ANXA5	36 kDa	Cytoplasm, plasma membrane	Phospholipase inhibitor activity, calcium-dependent phospholipid binding	0	1	0	2	2	0
GNB2	37 kDa	Plasma membrane, perinuclear region of cytoplasm	G-protein-coupled receptor binding, GTPase activity	0	0	0	5	0	1
KHSRP	73 kDa	Nucleus, cytoplasm	DNA binding, RNA binding, protein binding	1	5	0	1	0	0
MFGE8	43 kDa	Extracellular space, external side of plasma membrane	Phosphatidylserine binding, integrin binding, calcium ion binding, phosphatidylethanolamine binding	0	0	0	6	0	1
SMARCC2	133 kDa	nucleoplasm, chromatin	DNA binding, protein binding, transcription co-activator activity	0	2	0	1	3	4
CS	52 kDa	Mitochondrial matrix	Citrate (Si)-synthase activity	0	2	0	2	4	9
SET	33 kDa	Nucleoplasm, cytoplasm, ER	Histone binding, transcription repressor activity, protein phosphatase type 2A regulator activity	0	3	0	2	0	0

HPRT1	25 kDa	Cytoplasm, cytosol	Hypoxanthine phosphoribosyltransferase activity	0	2	0	2	2	1
EIF3E	52 kDa	Nucleoplasm, cytoplasm	Contributes to translation initiation factor activity	0	0	0	4	0	2
CBR1	30 kDa	Cytoplasm	Prostaglandin-E2 9-reductase activity, 15-hydroxyprostaglandin dehydrogenase (NADP+) activity	0	1	0	2	0	0
PSMB2	23 kDa	Nucleus, cytoplasm, proteasome core complex	Threonine-type endopeptidase activity	0	0	0	2	0	1
TNPO1	102 kDa	Nucleus, cytoplasm	Protein transporter activity	0	0	0	2	0	1
UBE3C	124 kDa	Nucleus, proteasome complex	Ubiquitin-protein ligase activity	0	0	0	5	0	1
UGGT1	177 kDa	ER-Golgi intermediate compartment	UDP-glucose:glycoprotein glucosyltransferase activity	0	1	0	4	0	0
TLN1	270 kDa	Cytoplasm, cytosol, centrosome	Actin binding, insulin receptor binding, structural constituent of cytoskeleton	0	1	0	1	0	0
QARS	88 kDa	Cytoplasm, cytosol, mitochondrial matrix	Glutamine-tRNA ligase activity	0	0	0	4	1	4
ALDOA	39 kDa	Actin cytoskeleton, platelet alpha granule lumen	Fructose-bisphosphate aldolase activity, actin binding, tubulin binding	0	1	0	6	4	6
GANAB	107 kDa	ER lumen, golgi app., melanosome	Glucan-1,3-alpha-glucosidase activity	0	2	0	9	1	1

GMPS	77 kDa	Cytoplasm, cytosol	GMP synthase (glutamine-hydrolyzing) activity, ATP binding	0	3	0	1	1	2
PRPF6	107 kDa	Nucleoplasm, spliceosomal complex	Assembly of spliceosomal tri-snRNP, spliceosome assembly, nuclear mRNA splicing, via spliceosome	0	0	1	8	0	1
ACADVL	70 kDa	Mitochondrial inner membrane, mitochondrial matrix, mitochondrial nucleoid	Long-chain-acyl-CoA dehydrogenase activity	0	1	2	6	1	8
UQCRC2	48 kDa	Mitochondrial respiratory chain complex III	Metalloendopeptidase activity	0	1	2	4	1	4
OPA1	112 kDa	Mitochondrion	Nucleotide binding, magnesium ion binding, GTPase activity	0	0	2	8	0	2
SRRT	101 kDa	Nucleus, nucleoplasm, cytoplasm	Nucleic acid binding, protein binding	0	0	1	5	0	3
FASN	273 kDa	Cytoplasm, mitochondrion, Golgi apparatus, plasma membrane, cytosol	Fatty acid synthase activity	0	0	1	7	0	4
CAPNS1	28 kDa	Cytoplasm, plasma membrane	Calcium-dependent cysteine-type endopeptidase activity, protein heterodimerization activity	0	2	1	4	1	1

DDX39B	49 kDa	Nucleus, spliceosomal complex	ATP-dependent RNA helicase activity	0	2	0	3	1	1
POLR2B	134 kDa	Nucleus, nucleoplasm, DNA-directed RNA polymerase II, core complex	DNA-directed RNA polymerase activity, contributes to protein kinase activity	0	0	0	5	1	4
CTTND1	108 kDa	Nucleus, Cytoplasm, Adherens junction	Morphogenesis of a branching structure, Cell adhesion, signal transduction, multicellular organismal development	0	0	0	1	0	1
PA2G4	44 kDa	Nucleus but not nucleoplasm, ribonucleoprotein complex	Ubiquitin protein ligase binding, sequence-specific DNA binding transcription factor activity, RNA binding	0	3	0	3	4	1
IARS	145 kDa	Nucleus but not nucleolous, cytoplasm	Isoleucine-tRNA ligase activity, ATP binding	0	4	1	5	4	4
ACOT9	50 kDa	Mitochondrion	Acetyl-CoA hydrolase activity	0	0	0	1	0	1

* All peptides met the following criteria in at least 2 out of 3 experiments: a) presence in the KIAA1199 immunoprecipitates (i.e., IP) and absent in control; or b) present at least four-times more frequently in the KIAA1199 immunoprecipitates than in controls.

† Number of unique peptide hits obtained on MS.