

Supplementary Table S1. Node attributes from NEK7 first neighbors network. Enriched GO Biological Processes (Enriched BP) are depicted with a p-value in parentheses for each protein in the network. Only enriched terms with $p \leq 0.05$ were considered in the network analysis.

| UniProt Accession | Gene | Protein | Top Enriched BP | p-value (Top Enriched BP) | Enriched BP | Cellular Component (GO) | Node type |
|-------------------|---------|--------------------------------------------------|------------------------------|---------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|-------------|
| Q92974 | ARHGFE2 | Rho guanine nucleotide exchange factor 2 | cell division | 1,08E-21 | actin filament organization(0.0233218253872765);apoptotic process(2.55992401287653e-05);cell division(1.07942479554722e-21);cell morphogenesis(0.058401984393526);cellular hyperosmotic response(0.00317344054183859);cellular response to tumor necrosis factor(0.0263488457905523);establishment of mitotic spindle orientation(0.000138173503205002);intracellular protein transport(0.00399808016354407);mitosis(0.000102781026324568);negative regulation of apoptotic process(0.000648052387978584);negative regulation of microtubule depolymerization(2.66604448071471e-06);negative regulation of necrotic cell death(0.00238194179822328);negative regulation of neurogenesis(0.00711238456606543);neurotrophin TRK receptor signaling pathway(2.07923260218922e-06);positive regulation of NF-kappaB transcription factor activity(0.00170565228819669);regulation of cell proliferation(0.0756261506035337);regulation of Rho protein signal transduction(0.128558427410656);small GTPase mediated signal transduction(0.000947140854281652) | cytosol;golgi apparatus;cytoplasm;plasma membrane | IP-LC-MS/MS |
| Q7Z460 | CLASP1 | CLIP-associating protein 1 | cell division | 1,08E-21 | axon guidance(3.66211750441785e-08);cell division(1.07942479554722e-21);establishment of spindle orientation(0.00079522295738861);exit from mitosis(0.00238194179822328);G2/M transition of mitotic cell cycle(2.22012761453102e-07);microtubule anchoring(0.000151369603879024);microtubule bundle formation(8.00153938715998e-10);microtubule nucleation(1.85532748848651e-05);microtubule organizing center organization(9.31947268647938e-07);mitotic prometaphase(1.2831663561912e-12);negative regulation of microtubule depolymerization(2.66604448071471e-06) | cytoplasm;cytosol;golgi apparatus | IP-LC-MS/MS |
| O75122 | CLASP2 | CLIP-associating protein 2 | cell division | 1,08E-21 | axon guidance(3.66211750441785e-08);cell division(1.07942479554722e-21);establishment or maintenance of cell polarity(0.000355409196739185);microtubule anchoring(0.000151369603879024);microtubule nucleation(1.85532748848651e-05);microtubule organizing center organization(9.31947268647938e-07);mitotic prometaphase(1.2831663561912e-12);negative regulation of microtubule depolymerization(2.66604448071471e-06) | cytoplasm;cytosol;golgi apparatus;microtubule organising centre;plasma membrane | IP-LC-MS/MS |
| Q15021 | NCAPD2 | Condensin complex subunit 1 | cell division | 1,08E-21 | cell division(1.07942479554722e-21);mitotic chromosome condensation(1.00132277711672e-11) | cytoplasm;nucleus | IP-LC-MS/MS |
| P42695 | NCAPD3 | Condensin-2 complex subunit D3 | cell division | 1,08E-21 | cell division(1.07942479554722e-21);mitotic chromosome condensation(1.00132277711672e-11) | cytoplasm;nucleus | IP-LC-MS/MS |
| Q9BPX3 | NCAPG | Condensin complex subunit 3 | cell division | 1,08E-21 | cell division(1.07942479554722e-21);mitotic chromosome condensation(1.00132277711672e-11) | cytoplasm;centrosome;nucleus | IP-LC-MS/MS |
| Q8TD19 | NEK9 | Serine/threonine-protein kinase Nek9 | cell division | 1,08E-21 | cell division(1.07942479554722e-21);mitosis(0.000102781026324568) | mitochondrion;nucleus | Y2H |
| Q14980 | NUMA1 | Nuclear mitotic apparatus protein 1 | cell division | 1,08E-21 | cell division(1.07942479554722e-21);establishment of mitotic spindle orientation(0.000138173503205002);G2/M transition of mitotic cell cycle(2.22012761453102e-07);lung epithelial cell differentiation(0.0160554148239213);mitotic anaphase(0.0067198784533802);nucleus organization(0.00277784607759494) | cytoplasm;cytosol;nucleus | IP-LC-MS/MS |
| Q9P258 | RCC2 | Protein RCC2 | cell division | 1,08E-21 | cell division(1.07942479554722e-21);mitotic prometaphase(1.2831663561912e-12) | cytosol;cytoplasm;nucleus | IP-LC-MS/MS |
| Q14683 | SMC1A | Structural maintenance of chromosomes protein 1A | cell division | 1,08E-21 | cell cycle checkpoint(0.0187452092674526);cell division(1.07942479554722e-21);chromosome condensation(0.00946096245045438);DNA recombination(1.85397813404995e-05);DNA repair(1.80749553775437e-06);meiosis(0.000179532761252513);metaphase/anaphase transition of mitotic cell cycle(1.19803323460096e-07);mitotic prometaphase(1.2831663561912e-12);mitotic sister chromatid cohesion(0.00238194179822328);mitotic spindle organization(1.85532748848651e-05);mRNA splicing, via spliceosome(0.0629477854388076);negative regulation of DNA endoreplication(1.55264927967749e-06);response to radiation(0.0137380308757676);signal transduction in response to DNA damage(0.00475272381511444);stem cell maintenance(0.00051277552598452) | cytoplasm;nucleus | IP-LC-MS/MS |
| O95347 | SMC2 | Structural maintenance of chromosomes protein 2 | cell division | 1,08E-21 | cell division(1.07942479554722e-21);DNA recombination(1.85397813404995e-05);DNA repair(1.80749553775437e-06);kinetochore organization(8.51992342452596e-06);meiotic chromosome condensation(8.51992342452596e-06);meiotic chromosome segregation(1.02199837680929e-05);mitotic chromosome condensation(1.00132277711672e-11);sister chromatid cohesion(7.88135944206877e-08) | cytoplasm;nucleus | IP-LC-MS/MS |
| Q9UQE7 | SMC3 | Structural maintenance of chromosomes protein 3 | cell division | 1,08E-21 | cell division(1.07942479554722e-21);DNA repair(1.80749553775437e-06);meiosis(0.000179532761252513);metaphase/anaphase transition of mitotic cell cycle(1.19803323460096e-07);mitotic prometaphase(1.2831663561912e-12);mitotic spindle organization(1.85532748848651e-05);negative regulation of DNA endoreplication(1.55264927967749e-06);signal transduction(0.326898276536456);sister chromatid cohesion(7.88135944206877e-08);stem cell maintenance(0.00051277552598452) | extracellular;cytoplasm;nucleus | IP-LC-MS/MS |
| Q9NTJ3 | SMC4 | Structural maintenance of chromosomes protein 4 | cell division | 1,08E-21 | chromosome condensation(8.51992342452596e-06);meiotic chromosome segregation(1.02199837680929e-05);mitotic chromosome condensation(1.00132277711672e-11);sister chromatid cohesion(7.88135944206877e-08) | cytoplasm;nucleus | IP-LC-MS/MS |
| P53350 | PLK1 | Serine/threonine-protein kinase PLK1 | mitotic prometaphase | 1,28E-12 | activation of mitotic anaphase-promoting complex activity(0.00198572752518753);anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process(0.000642152144451947);cell proliferation(0.0149821972259697);centrosome organization(0.0198934362348523);cytokinesis(8.8559460231763e-08);G2 DNA damage checkpoint(7.14810798681335e-05);G2/M transition of mitotic cell cycle(2.22012761453102e-07);microtubule bundle formation(8.00153938715998e-10);metaphase/anaphase transition of mitotic cell cycle(1.19803323460096e-07);mitotic prometaphase(1.2831663561912e-12);mitotic prophase(0.00079522295738861);negative regulation of apoptotic process(0.000648052387978584);negative regulation of cyclin-dependent protein serine/threonine kinase activity(0.0117984957519671);negative regulation of transcription from RNA polymerase II promoter(0.0622476215191769);peptidyl-serine phosphorylation(0.000683693601291364);positive regulation of peptidyl-threonine phosphorylation(0.00593394194615603);protein destabilization(0.0114096722320805);protein localization to chromatin(0.00119236828353075);protein ubiquitination(0.143478504338707);regulation of mitotic anaphase(0.00079522295738861);regulation of protein binding(0.0137380308757676) | centrosome;cytosol;nucleus;cytoplasm | IP-LC-MS/MS |
| O95235 | KIF20A | Kinesin-like protein KIF20A | microtubule bundle formation | 8,00E-10 | cytokinesis(8.8559460231763e-08);M phase of mitotic cell cycle(0.011409762320805);microtubule bundle formation(8.00153938715998e-10);microtubule-based movement(0.116925819669428);protein transport(0.00222028449423476);vesicle-mediated transport(0.148213049014623) | golgi apparatus;cytoplasm;nucleus | IP-LC-MS/MS |
| P11137 | MAP2 | Microtubule-associated protein 2 | microtubule bundle formation | 8,00E-10 | axonogenesis(0.0625998053367013);cellular response to organic substance(0.0168254438826213);central nervous system neuron development(0.0106311072858504);dendrite morphogenesis(0.0289817832346469);microtubule bundle formation(8.00153938715998e-10);peptidyl-threonine phosphorylation(0.0164405811645699) | cytoplasm;nucleus | IP-LC-MS/MS |

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| O95782 | AP2A1 | AP-2 complex subunit alpha-1 | negative regulation of epidermal growth factor receptor signaling pathway | 1,47E-09 | antigen processing and presentation of exogenous peptide antigen via MHC class II(0.000975662001904681);axon guidance(3.66211750441785e-08);endocytosis(0.0849689645098441);epidermal growth factor receptor signaling pathway(3.98158961250694e-07);Golgi to endosome transport(0.00475272381511444);intracellular protein transport(0.00399808016354407);negative regulation of epidermal growth factor receptor signaling pathway(1.4668656642032e-09);neurotrophin TRK receptor signaling pathway(2.07923260218922e-06);regulation of defense response to virus by virus(1.93618738873914e-07);synaptic transmission(0.010157398333458);viral process(2.18153183719986e-05) | plasma membrane;golgi apparatus;cytosol | IP-LC-MS/MS |
| P63010 | AP2B1 | AP-2 complex subunit beta | negative regulation of epidermal growth factor receptor signaling pathway | 1,47E-09 | antigen processing and presentation of exogenous peptide antigen via MHC class II(0.000975662001904681);axon guidance(3.66211750441785e-08);clathrin coat assembly(0.0125752257676977);epidermal growth factor receptor signaling pathway(3.98158961250694e-07);intracellular protein transport(0.00399808016354407);negative regulation of epidermal growth factor receptor signaling pathway(1.4668656642032e-09);neurotrophin TRK receptor signaling pathway(2.07923260218922e-06);regulation of defense response to virus by virus(1.93618738873914e-07);synaptic transmission(0.010157398333458);viral process(2.18153183719986e-05) | cytosol;plasma membrane | IP-LC-MS/MS |
| P60953 | CDC42 | Cell division control protein 42 homolog | negative regulation of epidermal growth factor receptor signaling pathway | 1,47E-09 | actin cytoskeleton organization(0.113880769962122);actin filament branching(0.0015892030798619);actin filament bundle assembly(0.0360549205440896);adherens junction organization(0.000186941490812127);axon guidance(3.66211750441785e-08);blood coagulation(0.000380021218663613);canonical Wnt receptor signaling pathway(0.0477277613096136);cardiac conduction system development(0.00396370073863742);cellular protein localization(0.0342039283272441);epidermal growth factor receptor signaling pathway(3.98158961250694e-07);epithelial cell-cell adhesion(0.00514677187861983);epithelial-mesenchymal cell signaling(0.00475272381511444);establishment of Golgi localization(0.0027784607759494);establishment or maintenance of apical/basal cell polarity(0.00396370073863742);establishment or maintenance of cell polarity(0.000355409196739185);filopodium assembly(0.0244592068650961);Golgi organization(0.0214201776692546);hair follicle morphogenesis(0.0202755742288883);hair follicle placode formation(0.00907030082044425);heart contraction(0.00828805647114202);keratinization(0.0210389447716819);keratinocyte development(0.00317344054183859);macrophage differentiation(0.00750458282164871);multicellular organism growth(0.0541632394554003);muscle cell differentiation(0.0202755742288883);negative regulation of epidermal growth factor receptor signaling pathway(1.4668656642032e-09);negative regulation of gene expression(0.0422933273540914);negative regulation of protein complex assembly(0.00396370073863742);neuron fate determination(0.0027784607759494);nuclear migration(0.00671987845333802);organelle transport along microtubule(0.00317344054183859);positive regulation of DNA replication(0.0237012527950014);positive regulation of gene expression(0.00295023504379598);positive regulation of hair follicle cell proliferation(0.00198572752518753);positive regulation of intracellular protein transport(0.0027784607759494);positive regulation of JNK cascade(0.000550113489024593);positive regulation of metalloenzyme activity(0.00396370073863742);positive regulation of muscle cell differentiation(0.00985131728675537);positive regulation of neuron apoptotic process(0.0408330827936499);positive regulation of peptidyl-serine phosphorylation(0.0263488457905523);positive regulation of phosphatidylinositol 3-kinase activity(0.0141250226389181);positive regulation of pseudopodium assembly(0.00396370073863742);positive regulation of synapse structural plasticity(0.00356872536940053);regulation of attachment of spindle microtubules to kinetochore(0.00750458282164871);regulation of filopodium assembly(0.0027784607759494);regulation of mitosis(5.40396186519786e-05);regulation of protein catabolic process(0.0218011092166748);regulation of protein heterodimerization activity(0.00514677187861983);regulation of protein kinase activity(0.00985131728675537);regulation of protein stability(0.0148980923117477);regulation of small GTPase mediated signal transduction(0.110809982525537);small GTPase mediated signal transduction(0.000947140854281652);sprouting angiogenesis(0.014511709725624);submandibular salivary gland formation(0.00317344054183859);T cell costimulation(0.0371619790485928) | cytosol;golgi apparatus;microtubule organising centre;plasma membrane;cytoplasm | IP-LC-MS/MS |
| P62979 | RPS27A | Ubiquitin-40S ribosomal protein S27a | negative regulation of epidermal growth factor receptor signaling pathway | 1,47E-09 | activation of MAPK activity(0.0629477854388076);anaphase-promoting complex-dependent proteasomal ubiquitin-dependent protein catabolic process(0.000642152144451947);antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent(0.0011491052785394);apoptotic process(2.55992401287653e-05);cellular membrane organization(0.0312269670665579);cytokine-mediated signaling pathway(0.0813241556455092);DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest(0.0349452104460717);DNA repair(1.80749553775437e-06);egress of virus within host cell(0.00435836682781625);endosomal transport(0.027102606500391);epidermal growth factor receptor signaling pathway(3.98158961250694e-07);fibroblast growth factor receptor signaling pathway(0.0488068215511484);G1 phase of mitotic cell cycle(0.000119490098783552);G1/S transition of mitotic cell cycle(0.00226378704275956);I-kappaB kinase/NF-kappaB cascade(0.0191282539288057);innate immune response(0.185361105329795);JNK cascade(0.0304797616903373);M/G1 transition of mitotic cell cycle(0.0304797616903373);MyD88-dependent toll-like receptor signaling pathway(0.0677899665355223);negative regulation of epidermal growth factor receptor signaling pathway(1.4668656642032e-09);negative regulation of transcription from RNA polymerase II promoter(0.0622476215191769);negative regulation of transforming growth factor beta receptor signaling pathway(0.0408330827936499);negative regulation of type I interferon production(0.0129631326162411);negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle(0.0244592068650961);neurotrophin TRK receptor signaling pathway(2.07923260218922e-06);Notch receptor processing(0.00985131728675537);Notch signaling pathway(0.0660669339128394);nuclear-transcribed mRNA catabolic process, nonsense-mediated decay(1.52489109676196e-05);nucleotide-binding oligomerization domain containing signaling pathway(0.00946096245045438);positive regulation of I-kappaB kinase/NF-kappaB cascade(0.000104124416778128);positive regulation of NF-kappaB transcription factor activity(0.00170565228819669);positive regulation of transcription from RNA polymerase II promoter(0.0927501700886529);positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle(0.027102606500391);protein polyubiquitination(0.0455618279243012);regulation of apoptotic process(0.114796980424188);regulation of transcription from RNA polymerase II promoter in response to hypoxia(0.00867933221970861);S phase of mitotic cell cycle(0.00113115411855978);SRP-dependent cotranslational protein targeting to membrane(2.22649669967908e-05);T cell receptor signaling pathway(0.0548725510465976);Toll signaling pathway(0.0371619790485928);toll-like receptor 1 signaling pathway(0.0308535128892836);toll-like receptor 2 signaling pathway(0.0304797616903373);toll-like receptor 3 signaling pathway(0.0301057132976248);toll-like receptor 4 signaling pathway(0.0378985472205216);transcription initiation from RNA polymerase II promoter(0.00378158476124163);transforming growth factor beta receptor signaling pathway(0.0839781930192875);translational elongation(1.01608240187251e-05);translational initiation(1.13865950608156e-05);translational termination(5.1891407422798e-06);TRIF-dependent toll-like receptor signaling pathway(0.0259715168833515);viral transcription(5.12859789334388e-06) | cytosol;endosome;nucleus;plasma membrane | IP-LC-MS/MS and Y2H |
| P63261 | ACTG1 | Actin, cytoplasmic 2 | axon guidance | 3,66E-08 | adherens junction organization(0.000186941490812127);axon guidance(3.66211750441785e-08);blood coagulation(0.000380021218663613);cell junction assembly(0.0172100031534075);cellular component movement(0.0397348296846733);sarcomere organization(0.0248377338747033) | cytoplasm;cytosol | Y2H |
| Q9HC98 | NEK6 | Serine/threonine-protein kinase Nek6 | cytokinesis | 8,86E-08 | apoptotic process(2.55992401287653e-05);chromosome segregation(0.0278551722240494);cytokinesis(8.8559460231763e-08);G2 DNA damage checkpoint(7.14810798681335e-05);mitosis(0.000102781026324568);peptidyl-serine phosphorylation(0.000683693601291364);positive regulation of I-kappaB kinase/NF-kappaB cascade(0.000104124416778128);protein autophosphorylation(0.00553059148756651);regulation of cellular senescence(0.00198572752518753);regulation of mitotic metaphase/anaphase transition(0.0027784607759494);spindle assembly(0.000278090461892406) | cytoplasm;microtubule organising centre;nucleus | INTERACTOR FROM DATABASE |
| Q8TDX7 | NEK7 | Serine/threonine-protein kinase Nek7 | cytokinesis | 8,86E-08 | cytokinesis(8.8559460231763e-08);regulation of mitotic cell cycle(0.0110205428022322);spindle assembly(0.000278090461892406) | cytoplasm;microtubule organising centre;nucleus | BAIT |
| Q9NYV4 | CDK12 | Cyclin-dependent kinase 12 | phosphorylation of RNA polymerase II C-terminal domain | 1,55E-07 | cell cycle(0.00072258391376332);mRNA processing(0.0846389790890049);phosphorylation of RNA polymerase II C-terminal domain(1.55443845820606e-07);protein autophosphorylation(0.00553059148756651);regulation of MAP kinase activity(0.00198572752518753);RNA splicing(0.052384942992678) | nucleus | IP-LC-MS/MS |

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|--------|---------|-----------------------------------------------------------------------------------|---------------------------------------------------------------------------|-------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------|---------------------|
| Q14004 | CDK13 | Cyclin-dependent kinase 13 | phosphorylation of RNA polymerase II C-terminal domain | 1,55E-07 | alternative mRNA splicing, via spliceosome(0.00514677187861983);cell cycle(0.00072258391376332);hemopoiesis(0.0415637892109395);phosphorylation of RNA polymerase II C-terminal domain(1.55443845820606e-07);positive regulation of cell proliferation(0.0244588556691904);regulation of mitosis(5.40396186519786e-05);modulation by virus of host morphology or physiology(0.129144645146173) | nucleus | IP-LC-MS/MS |
| P61769 | B2M | Beta-2-microglobulin | regulation of defense response to virus by virus | 1,94E-07 | antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent(0.0011491052785394);antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent(0.0221817395881307);antigen processing and presentation of exogenous protein antigen via MHC class Ib, TAP-dependent(0.001985727521518753);interferon-gamma-mediated signaling pathway(0.0484474237223889);positive regulation of T cell mediated cytotoxicity(0.00985131728675537);protein refolding(0.00554051119633074);regulation of defense response to virus by virus(1.93618738873914e-07);regulation of immune response(0.0462849647567519);response to cadmium ion(0.0218011092166748);response to drug(0.229842437886628);response to molecule of bacterial origin(0.0117984957519671);T cell differentiation in thymus(0.035315408718385);viral process(2.18153183719986e-05) | endosome;endoplasmic reticulum;plasma membrane;extracellular;golgi apparatus | Y2H |
| P51948 | MNAT1 | CDK-activating kinase assembly factor MAT1 | G2/M transition of mitotic cell cycle | 2,22E-07 | 7-methylguanosine mRNA capping(0.0125752257676977);adult heart development(0.0133507342602218);apoptotic process(2.55992401287653e-05);cell proliferation(0.0149821972259697);G1 phase of mitotic cell cycle(0.000119490098783552);G1/S transition of mitotic cell cycle(0.00226378704275956);G2/M transition of mitotic cell cycle(2.22012761453102e-07);multicellular organismal metabolic process(0.00238194179822328);negative regulation of apoptotic process(0.000648052387978584);nucleotide-excision repair, DNA damage removal(0.00828805647114202);positive regulation of smooth muscle cell proliferation(0.0316001243941674);positive regulation of transcription from RNA polymerase II promoter(0.0927501700886529);positive regulation of viral transcription(0.0172100031534075);protein complex assembly(0.0566408305012186);protein phosphorylation(0.0718967487859126);regulation of cyclin-dependent protein serine/threonine kinase activity(0.0488068215511484);response to calcium ion(0.0382663905687807);S phase of mitotic cell cycle(0.00113115411855978);termination of RNA polymerase I transcription(0.00828805647114202);transcription elongation from RNA polymerase I promoter(0.00750458282164871);transcription elongation from RNA polymerase II promoter(0.028605443441922);transcription initiation from RNA polymerase I promoter(0.00985131728675537);transcription initiation from RNA polymerase II promoter(0.00378158476124163);transcription-coupled nucleotide-excision repair(0.0191282539288057);ventricular system development(0.00514677187861983);viral process(2.18153183719986e-05) | cytoplasm | Y2H |
| Q92878 | RAD50 | DNA repair protein RAD50 | positive regulation of kinase activity | 1,55E-06 | DNA duplex unwinding(0.0198934362348523);double-strand break repair via homologous recombination(0.0297313675389651);nucleic acid phosphodiester bond hydrolysis(0.056287745319328);positive regulation of kinase activity(1.55264927967749e-06);positive regulation of protein autophosphorylation(0.00514677187861983);reciprocal meiotic recombination(0.014511709725624);regulation of mitotic recombination(0.00079522295738861);telomere maintenance via telomerase(0.00435836682781625) | nucleus | IP-LC-MS/MS |
| Q969S3 | ZNF622 | Zinc finger protein 622 | positive regulation of kinase activity | 1,55E-06 | intrinsic apoptotic signaling pathway in response to oxidative stress(0.00750458282164871);positive regulation of apoptotic process(0.000452048250651337);positive regulation of JNK cascade(0.000550113489024593);positive regulation of kinase activity(1.55264927967749e-06) | golgi apparatus;nucleus | IP-LC-MS/MS |
| P62701 | RPS4X | 40S ribosomal protein S4, X isoform | viral transcription | 5,13E-06 | multicellular organismal development(0.221601652248025);nuclear-transcribed mRNA catabolic process, nonsense-mediated decay(1.52489109676196e-05);positive regulation of cell proliferation(0.0244588556691904);positive regulation of translation(0.0221817395881307);SRP-dependent cotranslational protein targeting to membrane(2.22649669967908e-05);translational elongation(1.01608240187251e-05);translational initiation(1.13865950608156e-05);translational termination(5.31891407422798e-06);viral transcription(5.12859789334388e-06) | cytosol | IP-LC-MS/MS and Y2H |
| P62753 | RPS6 | 40S ribosomal protein S6 | viral transcription | 5,13E-06 | glucose homeostasis(0.0530971252543661);insulin receptor signaling pathway(0.0773102795637299);nuclear-transcribed mRNA catabolic process, nonsense-mediated decay(1.52489109676196e-05);positive regulation of apoptotic process(0.000452048250651337);ribosomal small subunit assembly(0.00356872536940053);ribosomal small subunit biogenesis(0.00277784607759494);rRNA processing(0.0480877370312025);SRP-dependent cotranslational protein targeting to membrane(2.22649669967908e-05);TOR signaling cascade(0.00554051119633074);translational elongation(1.01608240187251e-05);translational initiation(1.13865950608156e-05);translational termination(5.31891407422798e-06);viral transcription(5.12859789334388e-06) | cytosol;nucleus | IP-LC-MS/MS and Y2H |
| P28331 | NDUFS1 | NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial | apoptotic process | 2,56E-05 | apoptotic process(2.55992401287653e-05);ATP metabolic process(0.014511709725624);mitochondrial electron transport, NADH to ubiquinone(0.215211662167688);reactive oxygen species metabolic process(0.0137380308757676);regulation of mitochondrial membrane potential(0.0133507342602218) | mitochondrion | Y2H |
| P69905 | HBA1 | Hemoglobin subunit alpha | positive regulation of cell death | 6,25E-05 | bicarbonate transport(0.000296553918214628);hydrogen peroxide catabolic process(7.14810798681335e-05);oxygen transport(0.00435836682781625);positive regulation of cell death(6.24593832389618e-05);protein heterooligomerization(0.00145447178972716);small molecule metabolic process(8.53030688034272e-05) | cytosol | Y2H |
| P68871 | HBB | Hemoglobin subunit beta | positive regulation of cell death | 6,25E-05 | bicarbonate transport(0.000296553918214628);blood coagulation(0.000380021218663613);hydrogen peroxide catabolic process(7.14810798681335e-05);nitric oxide transport(0.00079522295738861);positive regulation of cell death(6.24593832389618e-05);positive regulation of nitric oxide biosynthetic process(0.0214201776692546);protein heterooligomerization(0.00145447178972716);regulation of blood pressure(0.0386339403190874);regulation of blood vessel size(0.00985131728675537);renal absorption(0.00119236828353075);small molecule metabolic process(8.53030688034272e-05) | cytosol | Y2H |
| P13196 | ALAS1 | 5-aminolevulinatase, nonspecific, mitochondrial | small molecule metabolic process | 8,53E-05 | cellular lipid metabolic process(0.0274790386490435);heme biosynthetic process(0.0175942591521723);protoporphyrinogen IX biosynthetic process(0.00396370073863742);small molecule metabolic process(8.53030688034272e-05) | mitochondrion;nucleus | Y2H |
| Q9UDW1 | UQCRI10 | Cytochrome b-c1 complex subunit 9 Coiled-coil and C2 domain-containing protein 1A | small molecule metabolic process | 8,53E-05 | mitochondrial electron transport, ubiquinol to cytochrome c(0.00554051119633074);small molecule metabolic process(8.53030688034272e-05) | mitochondrion cytoplasm;microtubule organising centre;nucleus | Y2H |
| Q6P1N0 | CC2D1A | | positive regulation of I-kappaB kinase/NF-kappaB kinase/NF-kappaB cascade | 0,000104124 | positive regulation of I-kappaB kinase/NF-kappaB cascade(0.00010412416778128) | | Y2H |

| | | | | | | | | |
|--------|----------|--------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|-------------|-------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------|------------------------|
| Q6FHJ7 | SFRP4 | Secreted frizzled-related protein 4 A1Pase family AAA domain-containing protein 3A | negative regulation of sodium-dependent phosphate transport negative regulation of apoptotic process | 0,000397767 | 0,000648052 | brain development(0.110501482347968);cell differentiation(0.174175540579659);decidualization(0.0102413655062746);embryo development(0.0776462790738453);epithelium development(0.00238194179822328);gonad development(0.0110205428022322);mammary gland involution(0.00356872536940053);menstrual cycle phase(0.0015892030798619);negative regulation of canonical Wnt receptor signaling pathway(0.0520284308747686);negative regulation of cell proliferation(0.208638489973648);negative regulation of JNK cascade(0.0125752257676977);negative regulation of sequence-specific DNA binding transcription factor activity(0.0289817832346469);negative regulation of sodium-dependent phosphate transport(0.000397766922540126);phosphate ion homeostasis(0.00435836682781625);positive regulation of apoptotic process(0.000452048250651337);positive regulation of canonical Wnt receptor signaling pathway(0.0304797616903373);positive regulation of epidermal cell differentiation(0.000397766922540126);positive regulation of gene expression(0.00295023504379598);positive regulation of receptor internalization(0.00671987845333802);response to hormone stimulus(0.0259715168833515);vasculature development(0.00828805647114202);Wnt receptor signaling pathway(0.109264889579327) | cytoplasm;extracellular;nucl eus | Y2H |
| Q9NV17 | ATAD3A | | | 0,000648052 | | cell growth(0.0441120704062429);negative regulation of apoptotic process(0.000648052387978584) | mitochondrion | IP-LC-MS/MS |
| P41220 | RGS2 | Regulator of G-protein signaling 2 Pleckstrin homology domain-containing family A member 8 | cell cycle ER to Golgi ceramide transport | 0,000722584 | | brown fat cell differentiation(0.0267258756052151);cell cycle(0.00072258391376332);negative regulation of cardiac muscle hypertrophy(0.00238194179822328);negative regulation of G-protein coupled receptor protein signaling pathway(0.00671987845333802);negative regulation of MAP kinase activity(0.0198934362348523);negative regulation of phospholipase activity(0.0015892030798619);positive regulation of cardiac muscle contraction(0.00317344054183859);regulation of adrenergic receptor signaling pathway(0.00079522295738861);regulation of translation(0.0259715168833515);relaxation of cardiac muscle(0.00514677187861983);relaxation of vascular smooth muscle(0.00435836682781625);spermatogenesis(0.171372063324065);termination of G-protein coupled receptor signaling pathway(0.0566408305012186) | cytosol;plasma membrane;mitochondrion;nu cleus | Y2H |
| Q96JA3 | PLEKHA8 | | small GTPase mediated signal transduction | 0,000795223 | | ER to Golgi ceramide transport(0.00079522295738861);glycolipid transport(0.00514677187861983);protein transport(0.00222028449423476) | golgi apparatus | Y2H |
| Q8N110 | DOCK4 | Dedicator of cytokinesis protein 4 | signal transduction | 0,000947141 | | cell chemotaxis(0.00985131728675537);small GTPase mediated signal transduction(0.000947140854281652) | cytosol | IP-LC-MS/MS |
| Q13637 | RAB32 | Ras-related protein Rab-32 | signal transduction | 0,000947141 | | phagosome maturation(0.014511709725624);protein transport(0.00222028449423476);small GTPase mediated signal transduction(0.000947140854281652) | mitochondrion | IP-LC-MS/MS |
| Q9UBX3 | SLC25A10 | Mitochondrial dicarboxylate carrier | sulfide oxidation, using sulfide:quinone oxidoreductase | 0,001985728 | | cellular nitrogen compound metabolic process(0.0316001243941674);gluconeogenesis(0.0323455491879884);mitochondrial transport(0.0125752257676977);sulfide oxidation, using sulfide:quinone oxidoreductase(0.00198572752518753);sulfur amino acid catabolic process(0.00317344054183859) | mitochondrion;nucleus | IP-LC-MS/MS |
| Q14444 | CAPRN1 | Caprin-1 | positive regulation of dendritic spine morphogenesis | 0,005146772 | | negative regulation of translation(0.0168254438826213);positive regulation of dendrite morphogenesis(0.0117984957519671);positive regulation of dendritic spine morphogenesis(0.00514677187861983) | cytoplasm;cytosol;plasma membrane | IP-LC-MS/MS |
| O95831 | AIFM1 | Apoptosis-inducing factor 1, mitochondrial | mitochondrial respiratory chain complex I assembly | 0,006327064 | | activation of cysteine-type endopeptidase activity involved in apoptotic process(0.0342039283272441);apoptotic DNA fragmentation(0.0141250226389181);cell redox homeostasis(0.0882539107748017);intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress(0.0164405811645699);mitochondrial respiratory chain complex I assembly(0.00632706430591511);neuron apoptotic process(0.0338328441383591);neuron differentiation(0.0327178169977812) | cytosol;mitochondrion;nucl eus;cytoplasm | IP-LC-MS/MS |
| P68104 | EEF1A1 | Elongation factor 1-alpha 1 | GTP catabolic process | 0,006613914 | | GTP catabolic process(0.00661391418924925);regulation of transcription, DNA-dependent(0.370743827761495);transcription, DNA-dependent(0.371144387841689) | cytosol;cytoplasm;nucleus | IP-LC-MS/MS and Y2H |
| P49411 | TUFM | Elongation factor Tu, mitochondrial | GTP catabolic process | 0,006613914 | | GTP catabolic process(0.00661391418924925) | mitochondrion | IP-LC-MS/MS and Y2H |
| Q9UMS0 | NFU1 | NFU1 iron-sulfur cluster scaffold homolog, mitochondrial | iron-sulfur cluster assembly | 0,009460962 | | iron-sulfur cluster assembly(0.00946096245045438) | mitochondrion;cytosol;mitochon drion;nucleus | Y2H |
| Q9BVA1 | TUBB2B | Tubulin beta-2B chain | posttranslational protein folding | 0,015284171 | | _de novo_ posttranslational protein folding(0.0152841705730629);microtubule-based process(0.0625998053367013);neuron migration(0.0921602276650665);protein polymerization(0.0701904671294709) | cytoplasm;plasma membrane | Y2H |
| Q96P70 | IPO9 | Importin-9 | protein import into nucleus | 0,032717817 | | protein import into nucleus(0.0327178169977812) | cytoplasm;nucleus | IP-LC-MS/MS |
| Q7Z6G8 | ANKS1B | Ankyrin repeat and sterle alpha motif domain-containing protein 1B | NOT DEFINED | | | NOT DEFINED | cytoplasm;plasma membrane | Y2H |
| Q5SW79 | CEP170 | Centrosomal protein of 170 kDa | NOT DEFINED | | | NOT DEFINED | centrosome;cytoplasm | IP-LC-MS/MS |
| O94868 | FCHSD2 | FCH and double SH3 domains protein 2 | NOT DEFINED | | | NOT DEFINED | NOT DEFINED | Y2H |
| Q3KQU3 | MAP7D1 | MAP7 domain-containing protein 1 | NOT DEFINED | | | NOT DEFINED | cytoplasm | IP-LC-MS/MS and Y2H |
| Q9HD45 | TM9SF3 | Transmembrane 9 superfamily member 3 | NOT DEFINED | | | NOT DEFINED | NOT DEFINED | Y2H |
| Q5T4D3 | TMTC4 | Transmembrane and TIRK repeat-containing protein 4 | NOT DEFINED | | | NOT DEFINED | NOT DEFINED | Y2H |

IP-MS/MS: Immunoprecipitation/Mass spectrometry; YTH: Yeast two hybrid

Supplementary Table S2. *In silico* analysis of protein interaction with NEK7 retrieved by the Yeast Two-Hybrid System Screens. The sequences of NEK7 interacting proteins retrieved from Y2H were analyzed for the domain composition and presence of disordered amino acid residues.

| Gene | Coded protein residues (retrieved/complete sequence) | Composition domains (Pfam, PROSITE or InterPro) ¹ | Regions of disorder (PONDR VL-XT) ² | |
|---------|------------------------------------------------------------|----------------------------------------------------------------------------------------------|------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|
| | | | Percentage of disordered resi dues | Segment disordered ³ |
| B2M | 1-119/119 | IG MHC; C1 set | 19.33 | [1]-[3]; [24]-[30]; [57]-[68]; [119]-[119] |
| NEK9 | 764-976/979 | FAMILY NOT NAMED | 62.91 | [1]-[43]; [50]-[77]; [92]-[131]; [182]-[202]; [212]-[213] |
| RGS2 | 1-211/211 | Regulator of G-protein signaling; RGS superfamily | 22.75 | [1]-[5]; [17]-[39]; [55]-[65]; [125]-[129]; [206]-[207]; [210]-[211] |
| MNAT1 | 1-309/309 | Ubiquitin-interacting motif (UIM) repeat profile; CDK-activating kinase assembly factor MAT1 | 45.31 | [63]-[85]; [94]-[100]; [104]-[105]; [133]-[133]; [137]-[173]; [181]-[200]; [205]-[212]; [259]-[273]; [275]-[285] |
| SFRP4 | 1-346/346 | Fz domain; UNC-6/NTR/C345C module | 31.50 | [53]-[57]; [101]-[106]; [151]-[153]; [167]-[185]; 235-[239]; [276]-[346] |
| UQCR10 | 1-63/63 | UCR UQCRX QCR9 | 11.11 | [1]-[6]; [63]-[63] |
| NDUFS1 | 451-727/727 | Molybdopterin; DUF1982 | 19.10 | [2]-[13]; [21]-[27]; [37]-[40]; [121]-[122]; [139]-[151]; [179]-[182]; [256]-[263]; [267]-[267] |
| ALAS1 | 94-640/640 | AA TRANSFER CLASS 2; Aminotran 1 2; Preseq ALAS | 23.40 | [1]-[12]; [31]-[66]; [88]-[93]; [119]-[127]; [243]-[250]; [279]-[279]; [283]-[284]; [336]-[336]; [394]-[418]; [445]-[451]; [464]-[483]; [545]-[545] |
| NFU1 | 22-208/254 | Nfu N | 13.10 | [127]-[145] |
| TUBBB2B | 247-430/445 | Tubulin C-terminal domain | 15.76 | [1]-[3]; [33]-[39]; [76]-[83]; [160]-[170] |
| HBA1 | 1-142/142 | Globin | 7.04 | [1]-[10] |
| HBB | 1-147/147 | Globin | 5.44 | [2]-[9] |
| EEF1A1 | 340-432/462 | GTP EFTU D3 | 39.02 | [35]-[54]; [96]-[123] |
| TUFM | 13-455/455 | GTP-binding elongation factor family, EF-Tu/EF-1A subfamily | 36.12 | [1]-[4]; [88]-[101]; [153]-[157]; [179]-[200]; [208]-[226]; [247]-[254]; [258]-[280]; [299]-[336]; [384]-[399]; [428]-[431]; [436]-[442] |
| PLEKHA8 | 103-418/459 | Glycolipid transfer protein | 45.25 | [1]-[12]; [36]-[48]; [75]-[80]; [82]-[100]; [109]-[130]; [151]-[198]; [218]-[230]; [286]-[295] |
| ACTG1 | 187-375/375 | Actin | 25.93 | [16]-[22]; [42]-[63]; [116]-[131]; [178]-[181] |
| RPS6 | 1-228/249 | Ribosomal protein S6e | 64.47 | [18]-[33]; [78]-[100]; [121]-[228] |
| CC2D1A | 501-940/951 | C2 domain | 38.64 | [1]-[3]; [5]-[47]; [68]-[81]; [221]-[229]; [259]-[275]; [287]-[299]; [305]-[305]; [313]-[343]; [360]-[382]; [401]-[401]; [426]-[440] |
| RPS4X | 5-263/263 | S4 domain; KOW motif; Ribosomal family S4e | 15.83 | [1]-[2]; [5]-[6]; [8]-[9]; [63]-[67]; [230]-[259] |
| RPS27A | 1-156/156 | Ubiquitin; Ribosomal S27; UBIQUITIN 1 | 51.92 | [17]-[43]; [69]-[120]; [155]-[156] |
| ANKS1B | 6-426/426 | Sterile alpha motif; Phosphotyrosine interaction domain | 29.58 | [1]-[3]; [162]-[204]; [237]-[254]; [290]-[297]; [369]-[409] |
| FCHSD2 | 627-740/740 | FAMILY NOT NAMED | 94.74 | [1]-[108] |
| MAP7D1 | 715-841/841 | E-MAP-115 (FAMILY NOT NAMED) | 85.83 | [1]-[75]; [81]-[107]; [119]-[125] |
| TMTC4 | 467-741/741 | TPR 1; TPR 2 | 21.45 | [1]-[4]; [59]-[77]; [102]-[109]; [169]-[184]; [256]-[267] |
| TM9SF3 | 398-589/589 | EMP70 | 0.00 | No found |

¹Domain composition of the recovered sequences obtained by Pfam, PROSITE or InterPro databases (other domains may be present). ²Using a scanning of 28 amino acid residues as a parameter analysis. If a residue value exceeds a threshold of 0.5 the residue is considered disordered. ³Disordered segments represented in amino acid residues.

Supplementary Table S3. Proposed cellular localization and colocalization of NEK7 with its interacting partners throughout the cell cycle. Endogenous proteins were accessed by immunofluorescence and their localization in the main structures through the cell cycle is described in the table.

| | Protein/Cellular component | | | | | | | | | | | |
|---------------------|-----------------------------------------|----------------------------------------------------------------------|----------------------------------------------|----------------|------------|-----------------------------|----------------|-------------------------------------------|-------------------------------------------|----------------------------------------|-----------------------------|------------|
| | NEK7 | RGS2 | RPS6 | CC2D1A | PLEKHA8 | ANKS1B | ACTG1 | TUBB | NEK9 | MNAT1 | TMTC4 | |
| Interphase | cytoplasm, DNA | cytoplasm, centrosome, presumed microtubule-organising center (MTOC) | cytoplasm, DNA | cytoplasm, DNA | cytoplasm | cytoplasm, DNA | cytoplasm, DNA | cytoplasm, centrosome | cytoplasm, DNA | cytoplasm, DNA | cytoplasm, DNA | |
| Prophase | cytoplasm, DNA | DNA | cytoplasm, DNA | cytoplasm | cytoplasm | unobserved | cytoplasm, DNA | mitotic spindle, spindle pole, centrosome | cytoplasm, centrosome | cytoplasm, centrosome | DNA | |
| Prometaphase | cytoplasm, centrosome | cytoplasm, mitotic spindle, spindle pole, centrosome | cytoplasm, DNA | cytoplasm | cytoplasm | DNA | cytoplasm, DNA | DNA | cytoplasm, centrosome | cytoplasm, spindle pole, centrosome | unobserved | |
| Mitosis | Metaphase | cytoplasm, mitotic spindle, spindle pole | mitotic spindle, spindle pole | DNA | unobserved | cytoplasm | unobserved | unobserved | mitotic spindle, spindle pole, centrosome | cytoplasm, spindle pole, centrosome | unobserved | unobserved |
| | Anaphase | cytoplasm, spindle midzone | mitotic spindle, spindle midzone, centrosome | unobserved | unobserved | cytoplasm | unobserved | unobserved | mitotic spindle, spindle pole, | cytoplasm, spindle midzone, centrosome | cytoplasm | unobserved |
| | Telophase | cytoplasm, DNA | unobserved | DNA | unobserved | cytoplasm/ contractile ring | unobserved | unobserved | cytoplasm/ contractile ring | cytoplasm, centrosome | cytoplasm, contractile ring | unobserved |
| Cytokinesis | cytoplasm, cytoplasmic bridge, midbody? | cytoplasm, centrosome, cytoplasmic bridge, midbody? | unobserved | unobserved | cytoplasm | unobserved | unobserved | cytoplasm, cytoplasmic bridge, midbody? | cytoplasm, cytoplasmic bridge | absent | unobserved | |