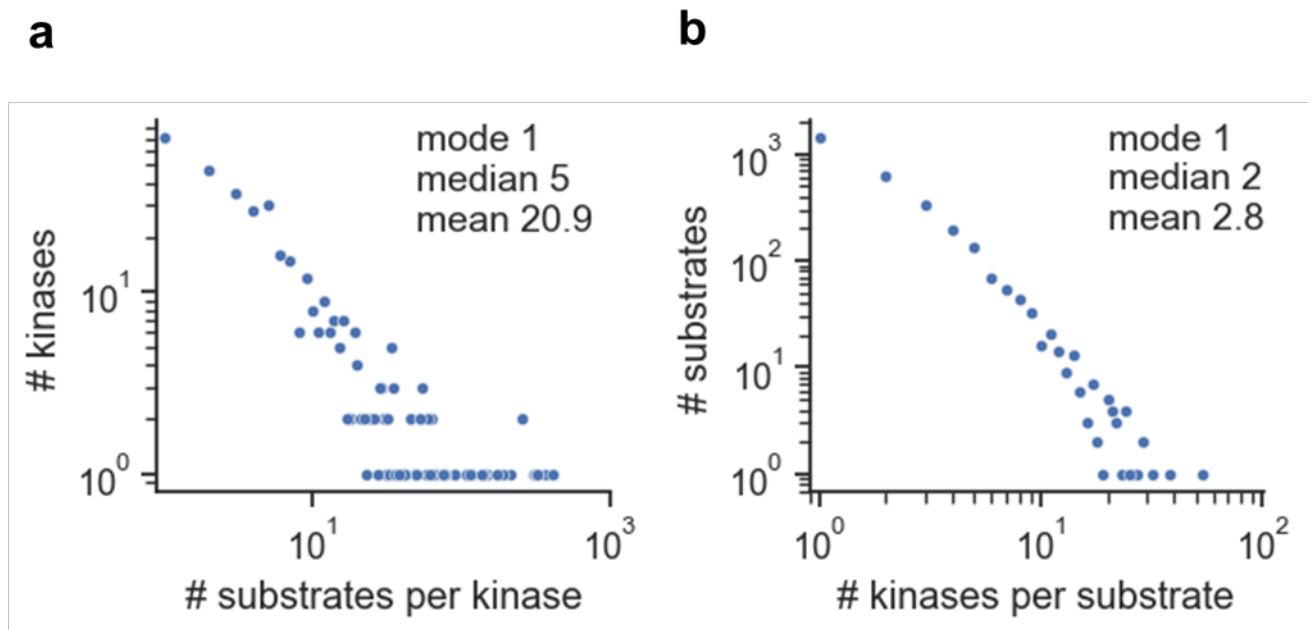


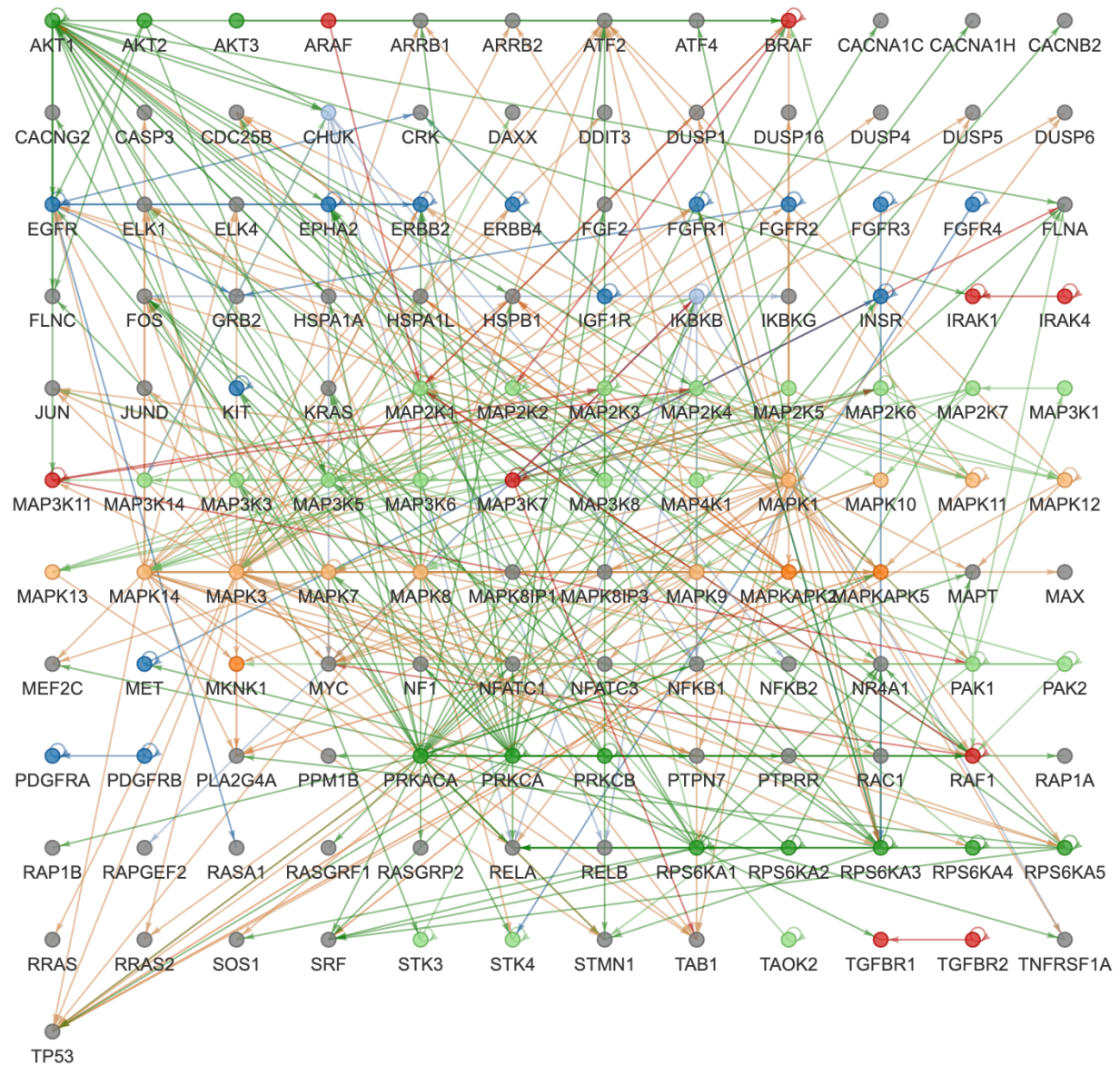
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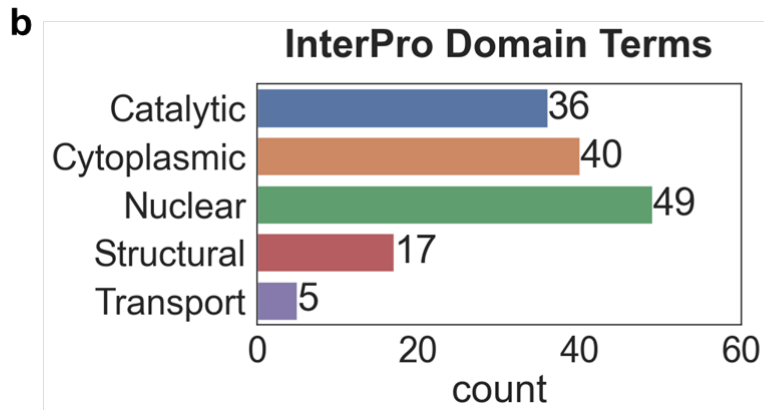
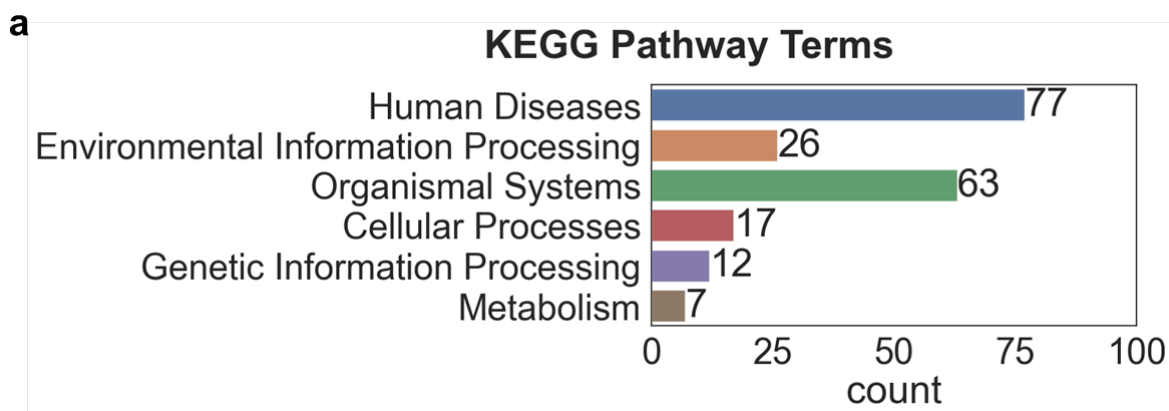
Supplementary Figure 1: Degree distributions in the KiNet dataset. (a) Substrates per kinase. (b) Kinases per substrate. Both distributions have heavy right tails, suggesting that a small number of kinases and substrates dominate the set of interactions.



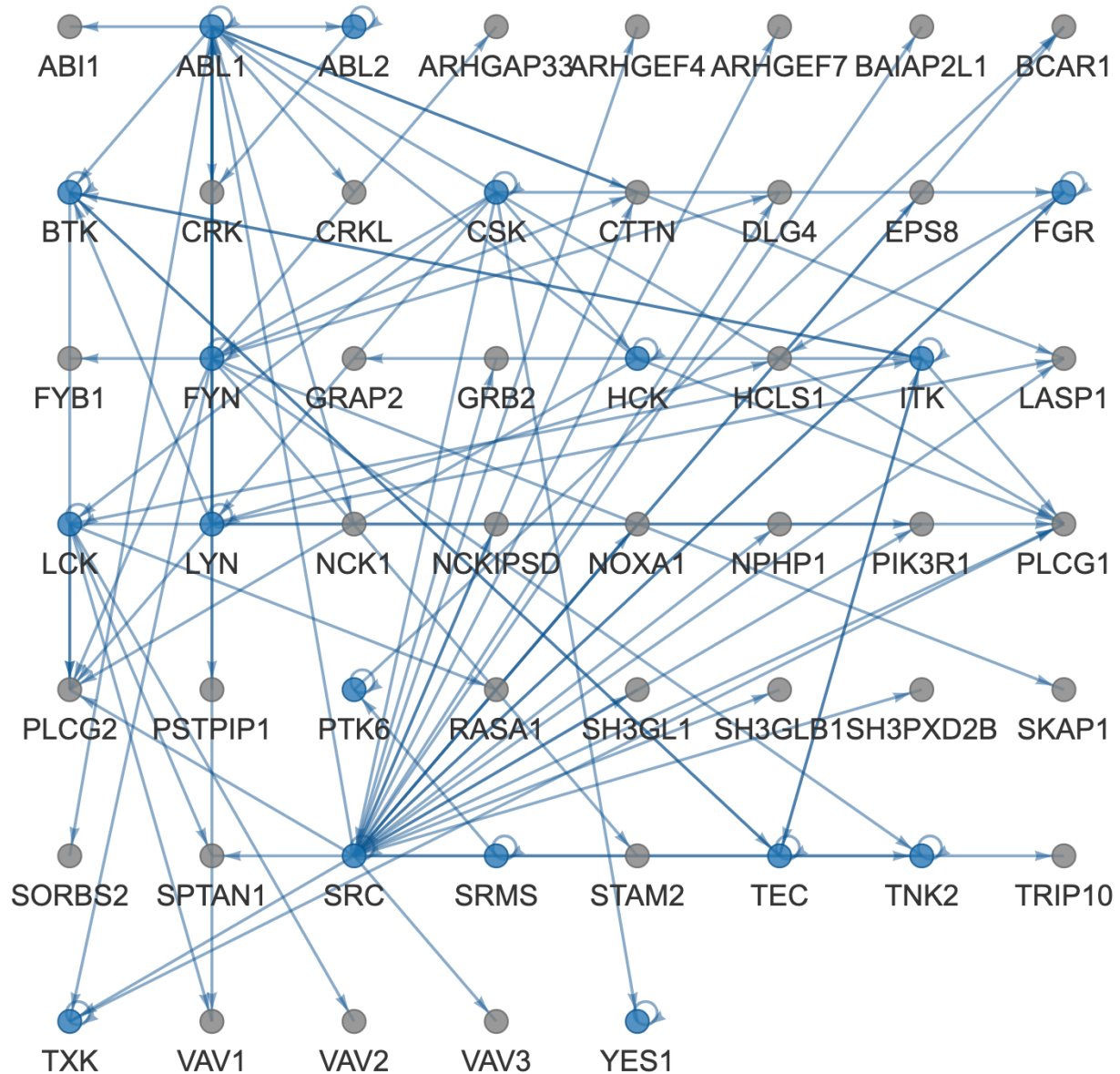
Supplementary Figure 2: Visualization of the MAPK signaling pathway. The network shown when MAPK signaling is selected in the Pathways tab and grid layout is applied.



Supplementary Figure 3: Enrichment analyses of kinase substrates in the KiNet dataset. (a) KEGG pathways. This analysis highlighted 201 enriched pathways in six KEGG categories, shown here. The full set of enriched pathways and their p-values are provided in Supplementary Table 1. **(b) InterPro domains.** This analysis highlighted 145 enriched domain terms in five functional categories, shown here. The full set of enriched domain terms and their p-values are provided in Supplementary Table 2.



Supplementary Figure 4: Visualization of proteins with SH3 domain. The network shown when SH3 domain is selected in the Domains tab and grid layout is applied. Note the prevalence of Src-type kinases, such as SRC, FYN, FGR, LCK and LYN.



Supplementary Tables

Supplementary Table 1: Data and software used in building KiNet, its underlying dataset and results presented in this paper.

Resource	URL
<i>Kinase-substrate interaction data</i>	
PhosphoSitePlus	https://www.phosphosite.org/
iPTMNet	https://research.bioinformatics.udel.edu/iptmnet/
EPSD	https://epsd.biocuckoo.cn/
<i>Kinases and group classification</i>	
KinHub	http://www.kinhub.org/
Coral	https://phanstiel-lab.med.unc.edu/CORAL/
Dark Kinome Knowledgebase	https://darkkinome.org/
<i>Standard protein and gene names</i>	
UniProt	https://www.uniprot.org/
HGNC	https://www.genenames.org/
<i>Enrichment analyses</i>	
Enrichr	https://maayanlab.cloud/Enrichr/
GSEAPy	https://pypi.org/project/gseapy/
InterPro (domains)	https://www.ebi.ac.uk/interpro/
KEGG (pathways)	https://www.genome.jp/kegg/pathway.html
<i>Web development and visualization</i>	
tidyverse	https://cran.r-project.org/package=tidyverse
shiny	https://cran.r-project.org/package=shiny
flexdashboard	https://cran.r-project.org/package=flexdashboard
visNetwork	https://cran.r-project.org/package=visNetwork
igraph	https://cran.r-project.org/package=igraph
<i>Data extraction, analysis and visualization in Python</i>	
pandas	https://pypi.org/project/pandas/
BeautifulSoup	https://pypi.org/project/beautifulsoup4/
matplotlib_venn	https://pypi.org/project/matplotlib_venn
seaborn	https://pypi.org/project/seaborn/

Supplementary Table 2: Results of pathway enrichment analysis of kinase substrates in the KiNet dataset.

KEGG Term	KEGG Category	Adjusted p-value
Pathways in cancer	Human Diseases	1.53E-70
MAPK signaling pathway	Environmental Information Processing	6.87E-61
Hepatitis B	Human Diseases	1.39E-54
Neurotrophin signaling pathway	Organismal Systems	3.73E-53
MicroRNAs in cancer	Human Diseases	5.47E-53
Human T-cell leukemia virus 1 infection	Human Diseases	1.97E-49
Shigellosis	Human Diseases	3.75E-49
Yersinia infection	Human Diseases	3.68E-48
Viral carcinogenesis	Human Diseases	1.22E-47
Proteoglycans in cancer	Human Diseases	6.21E-44
Cell cycle	Cellular Processes	1.69E-43
T cell receptor signaling pathway	Organismal Systems	2.72E-43
Lipid and atherosclerosis	Human Diseases	7.22E-43
Cellular senescence	Cellular Processes	2.87E-42
ErbB signaling pathway	Environmental Information Processing	1.63E-41
Insulin signaling pathway	Organismal Systems	2.34E-41
Pathways of neurodegeneration	Human Diseases	2.27E-39
FoxO signaling pathway	Environmental Information Processing	2.53E-39
Epstein-Barr virus infection	Human Diseases	1.30E-38
Chronic myeloid leukemia	Human Diseases	1.72E-38
Focal adhesion	Cellular Processes	4.44E-38
PI3K-Akt signaling pathway	Environmental Information Processing	5.12E-38
Human immunodeficiency virus 1 infection	Human Diseases	1.11E-37
Kaposi sarcoma-associated herpesvirus infection	Human Diseases	3.11E-37
Salmonella infection	Human Diseases	3.68E-37
PD-L1 expression and PD-1 checkpoint pathway in cancer	Human Diseases	3.98E-36
Osteoclast differentiation	Organismal Systems	4.24E-36
Autophagy	Cellular Processes	7.90E-36
Regulation of actin cytoskeleton	Cellular Processes	1.89E-35
Measles	Human Diseases	3.70E-35
Hepatitis C	Human Diseases	5.04E-34

Apoptosis	Cellular Processes	7.65E-34
Ras signaling pathway	Environmental Information Processing	9.02E-34
Prostate cancer	Human Diseases	1.63E-33
Pancreatic cancer	Human Diseases	2.84E-33
Human cytomegalovirus infection	Human Diseases	6.36E-32
Human papillomavirus infection	Human Diseases	4.22E-31
Alzheimer disease	Human Diseases	8.93E-31
Colorectal cancer	Human Diseases	1.27E-30
cAMP signaling pathway	Environmental Information Processing	3.14E-30
Insulin resistance	Human Diseases	3.60E-30
Rap1 signaling pathway	Environmental Information Processing	4.43E-30
Fc gamma R-mediated phagocytosis	Organismal Systems	4.60E-30
Pathogenic Escherichia coli infection	Human Diseases	1.05E-29
Growth hormone synthesis, secretion and action	Organismal Systems	2.75E-29
Longevity regulating pathway	Organismal Systems	2.12E-28
Acute myeloid leukemia	Human Diseases	3.31E-28
C-type lectin receptor signaling pathway	Organismal Systems	1.07E-27
Renal cell carcinoma	Human Diseases	1.09E-27
AGE-RAGE signaling pathway in diabetic complications	Human Diseases	3.65E-27
AMPK signaling pathway	Environmental Information Processing	3.69E-27
HIF-1 signaling pathway	Environmental Information Processing	5.58E-27
Non-small cell lung cancer	Human Diseases	6.44E-27
Chemokine signaling pathway	Organismal Systems	1.02E-26
Sphingolipid signaling pathway	Environmental Information Processing	1.36E-26
Tight junction	Cellular Processes	4.33E-26
Thyroid hormone signaling pathway	Organismal Systems	5.27E-26
Transcriptional misregulation in cancer	Human Diseases	1.02E-25
Endocytosis	Cellular Processes	1.09E-25
Prolactin signaling pathway	Organismal Systems	1.32E-25
Central carbon metabolism in cancer	Human Diseases	1.32E-25
Glioma	Human Diseases	1.32E-25
mTOR signaling pathway	Environmental Information Processing	1.42E-25
Adherens junction	Cellular Processes	3.69E-25

Leukocyte transendothelial migration	Organismal Systems	6.92E-25
Endometrial cancer	Human Diseases	1.93E-24
TNF signaling pathway	Environmental Information Processing	2.63E-24
Hepatocellular carcinoma	Human Diseases	3.89E-24
Axon guidance	Organismal Systems	4.47E-24
Fc epsilon RI signaling pathway	Organismal Systems	4.55E-24
Fluid shear stress and atherosclerosis	Human Diseases	5.30E-24
NOD-like receptor signaling pathway	Organismal Systems	1.38E-23
Oxytocin signaling pathway	Organismal Systems	1.50E-23
Breast cancer	Human Diseases	2.06E-23
Mitophagy	Cellular Processes	3.38E-23
Neutrophil extracellular trap formation	Organismal Systems	5.23E-23
Platelet activation	Organismal Systems	5.32E-23
cGMP-PKG signaling pathway	Environmental Information Processing	6.04E-23
B cell receptor signaling pathway	Organismal Systems	1.21E-22
Th17 cell differentiation	Organismal Systems	2.52E-22
Progesterone-mediated oocyte maturation	Organismal Systems	9.80E-22
Gastric cancer	Human Diseases	1.03E-21
Apelin signaling pathway	Environmental Information Processing	2.06E-21
Chemical carcinogenesis	Human Diseases	4.04E-21
Toxoplasmosis	Human Diseases	5.61E-21
Bacterial invasion of epithelial cells	Human Diseases	8.79E-21
Necroptosis	Cellular Processes	9.11E-21
Toll-like receptor signaling pathway	Organismal Systems	1.25E-20
Phospholipase D signaling pathway	Environmental Information Processing	5.50E-20
Spinocerebellar ataxia	Human Diseases	6.71E-20
GnRH signaling pathway	Organismal Systems	1.00E-19
Hippo signaling pathway	Environmental Information Processing	1.33E-19
NF-kappa B signaling pathway	Environmental Information Processing	1.63E-19
Long-term potentiation	Organismal Systems	1.85E-19
Signaling pathways regulating pluripotency of stem cells	Cellular Processes	2.06E-19
Amyotrophic lateral sclerosis	Human Diseases	2.67E-19
Influenza A	Human Diseases	2.74E-19
Choline metabolism in cancer	Human Diseases	3.29E-19

Small cell lung cancer	Human Diseases	6.81E-19
VEGF signaling pathway	Environmental Information Processing	7.79E-19
Parathyroid hormone synthesis, secretion and action	Organismal Systems	8.97E-19
Diabetic cardiomyopathy	Human Diseases	1.40E-18
Oocyte meiosis	Cellular Processes	1.42E-18
p53 signaling pathway	Cellular Processes	2.22E-18
Cushing syndrome	Human Diseases	2.79E-18
Alcoholism	Human Diseases	1.34E-17
Bladder cancer	Human Diseases	1.53E-17
Chagas disease	Human Diseases	3.69E-17
Non-alcoholic fatty liver disease	Human Diseases	4.86E-17
Estrogen signaling pathway	Organismal Systems	5.64E-17
Adipocytokine signaling pathway	Organismal Systems	6.68E-17
IL-17 signaling pathway	Organismal Systems	9.29E-17
Tuberculosis	Human Diseases	9.95E-17
Calcium signaling pathway	Environmental Information Processing	1.29E-16
Relaxin signaling pathway	Organismal Systems	1.74E-16
Melanoma	Human Diseases	5.32E-16
Th1 and Th2 cell differentiation	Organismal Systems	1.10E-15
Coronavirus disease	Human Diseases	1.55E-15
Adrenergic signaling in cardiomyocytes	Organismal Systems	1.70E-15
Huntington disease	Human Diseases	9.58E-15
Parkinson disease	Human Diseases	1.99E-14
Type II diabetes mellitus	Human Diseases	3.18E-14
Prion disease	Human Diseases	4.12E-14
Leishmaniasis	Human Diseases	4.34E-14
Thyroid cancer	Human Diseases	1.21E-13
RIG-I-like receptor signaling pathway	Organismal Systems	1.88E-13
Glucagon signaling pathway	Organismal Systems	1.93E-13
Pertussis	Human Diseases	2.64E-13
Inflammatory mediator regulation of TRP channels	Organismal Systems	3.86E-13
GnRH secretion	Organismal Systems	3.93E-13
Dopaminergic synapse	Organismal Systems	4.34E-13
Wnt signaling pathway	Environmental Information Processing	4.54E-13
JAK-STAT signaling pathway	Environmental Information Processing	2.21E-12
Gap junction	Cellular Processes	3.70E-12

Ubiquitin mediated proteolysis	Genetic Information Processing	3.86E-12
Long-term depression	Organismal Systems	5.55E-12
Cholinergic synapse	Organismal Systems	1.42E-11
Natural killer cell mediated cytotoxicity	Organismal Systems	1.81E-11
Amphetamine addiction	Human Diseases	3.98E-11
Aldosterone synthesis and secretion	Organismal Systems	2.44E-10
Homologous recombination	Genetic Information Processing	2.67E-09
Non-homologous end-joining	Genetic Information Processing	2.95E-09
Vascular smooth muscle contraction	Organismal Systems	6.88E-09
Cocaine addiction	Human Diseases	7.13E-09
Epithelial cell signaling in Helicobacter pylori infection	Human Diseases	8.19E-09
Circadian entrainment	Organismal Systems	1.34E-07
RNA transport	Genetic Information Processing	1.44E-07
Aldosterone-regulated sodium reabsorption	Organismal Systems	2.66E-07
Melanogenesis	Organismal Systems	4.29E-07
Regulation of lipolysis in adipocytes	Organismal Systems	6.28E-07
Fanconi anemia pathway	Genetic Information Processing	1.24E-06
Legionellosis	Human Diseases	1.38E-06
Serotonergic synapse	Organismal Systems	2.47E-06
Primary immunodeficiency	Human Diseases	2.63E-06
Notch signaling pathway	Environmental Information Processing	2.88E-06
Circadian rhythm	Organismal Systems	7.54E-06
Thermogenesis	Organismal Systems	1.19E-05
Endocrine and other factor-regulated calcium reabsorption	Organismal Systems	2.07E-05
Protein processing in endoplasmic reticulum	Genetic Information Processing	2.19E-05
Phosphatidylinositol signaling system	Environmental Information Processing	3.55E-05
Hypertrophic cardiomyopathy	Human Diseases	5.45E-05
Insulin secretion	Organismal Systems	5.98E-05
Arrhythmogenic right ventricular cardiomyopathy	Human Diseases	1.63E-04

Cell adhesion molecules	Environmental Information Processing	1.84E-04
Base excision repair	Genetic Information Processing	2.45E-04
Gastric acid secretion	Organismal Systems	3.56E-04
Dilated cardiomyopathy	Human Diseases	4.06E-04
Hedgehog signaling pathway	Environmental Information Processing	4.39E-04
Inositol phosphate metabolism	Metabolism	4.89E-04
Renin secretion	Organismal Systems	5.43E-04
Retrograde endocannabinoid signaling	Organismal Systems	5.96E-04
Cortisol synthesis and secretion	Organismal Systems	5.96E-04
TGF-beta signaling pathway	Environmental Information Processing	6.58E-04
Vasopressin-regulated water reabsorption	Organismal Systems	6.68E-04
Glutamatergic synapse	Organismal Systems	7.52E-04
Glycolysis / Gluconeogenesis	Metabolism	9.21E-04
Ferroptosis	Cellular Processes	9.21E-04
Morphine addiction	Human Diseases	1.07E-03
Viral myocarditis	Human Diseases	1.13E-03
Salivary secretion	Organismal Systems	1.51E-03
Spliceosome	Genetic Information Processing	1.59E-03
Cytosolic DNA-sensing pathway	Organismal Systems	2.18E-03
Phagosome	Cellular Processes	2.23E-03
DNA replication	Genetic Information Processing	2.36E-03
Amoebiasis	Human Diseases	2.47E-03
Basal cell carcinoma	Human Diseases	2.64E-03
Purine metabolism	Metabolism	2.76E-03
mRNA surveillance pathway	Genetic Information Processing	3.30E-03
Systemic lupus erythematosus	Human Diseases	3.57E-03
Inflammatory bowel disease	Human Diseases	3.86E-03
Carbohydrate digestion and absorption	Organismal Systems	4.17E-03
Pyruvate metabolism	Metabolism	4.17E-03
Maturity onset diabetes of the young	Human Diseases	4.63E-03
Mismatch repair	Genetic Information Processing	6.48E-03
Nucleotide excision repair	Genetic Information Processing	9.07E-03
Bile secretion	Organismal Systems	9.17E-03

Pancreatic secretion	Organismal Systems	1.15E-02
Pentose phosphate pathway	Metabolism	1.44E-02
Citrate cycle (TCA cycle)	Metabolism	1.44E-02
Thyroid hormone synthesis	Organismal Systems	1.95E-02
Hematopoietic cell lineage	Organismal Systems	4.65E-02
Folate biosynthesis	Metabolism	4.76E-02

Supplementary Table 3: Results of domain enrichment analysis of kinase substrates in the KiNet dataset.

InterPro Term	Category	Adjusted p-value
Protein kinase domain	Catalytic	2.53E-130
Serine-threonine/tyrosine-protein kinase, catalytic domain	Catalytic	3.14E-38
Tyrosine-protein kinase, catalytic domain	Catalytic	1.08E-36
SH2 domain	Cytoplasmic	1.96E-30
AGC-kinase, C-terminal	Catalytic	4.83E-22
Protein kinase, C-terminal	Catalytic	3.32E-21
SH3 domain	Cytoplasmic	2.88E-20
Pleckstrin homology domain	Cytoplasmic	5.30E-17
Nuclear hormone receptor, ligand-binding domain	Nuclear	5.77E-12
Zinc finger, nuclear hormone receptor-type	Nuclear	9.81E-12
Diacylglycerol/phorbol-ester binding	Cytoplasmic	7.69E-11
Protein kinase C-like, phorbol ester/diacylglycerol-binding domain	Cytoplasmic	4.55E-10
Calponin homology domain	Structural	1.13E-08
BRCT domain	Cytoplasmic	3.33E-08
Basic-leucine zipper domain	Nuclear	7.17E-08
Ion transport domain	Transport	3.31E-07
Ubiquitin-associated domain	Cytoplasmic	1.23E-06
Ets domain	Nuclear	1.53E-06
PB1 domain	Cytoplasmic	7.65E-06
Rel homology dimerisation domain	Nuclear	1.15E-05
Rel homology domain (RHD), DNA-binding domain	Nuclear	1.15E-05
RNA recognition motif domain	Nuclear	1.46E-05
Zinc finger, PHD-type	Nuclear	1.91E-05
Myc-type, basic helix-loop-helix (bHLH) domain	Nuclear	3.04E-05
Histone deacetylase domain	Nuclear	4.49E-05
STAT transcription factor, protein interaction	Nuclear	4.49E-05
STAT transcription factor, DNA-binding	Nuclear	4.49E-05
STAT transcription factor, all-alpha domain	Nuclear	4.49E-05
Zinc finger, PHD-finger	Nuclear	5.60E-05
Cyclin-like	Cytoplasmic	1.11E-04
CRIB domain	Cytoplasmic	2.29E-04
p21 activated kinase binding domain	Cytoplasmic	2.63E-04
SLC12A transporter, C-terminal	Transport	2.65E-04
Dbl homology (DH) domain	Catalytic	3.11E-04
Tyrosine specific protein phosphatases domain	Catalytic	3.52E-04

RGS domain	Cytoplasmic	4.59E-04
WW domain	Cytoplasmic	5.90E-04
SAP domain	Nuclear	6.52E-04
Peptidase C14, p20 domain	Catalytic	6.90E-04
IPT domain	Nuclear	6.90E-04
PAS fold	Nuclear	6.99E-04
Protein-tyrosine phosphatase, catalytic	Catalytic	6.99E-04
Forkhead-associated (FHA) domain	Catalytic	7.72E-04
Amino acid permease/ SLC12A domain	Transport	7.77E-04
Furin-like cysteine-rich domain	Cytoplasmic	1.07E-03
14-3-3 domain	Cytoplasmic	1.07E-03
Receptor L-domain	Cytoplasmic	1.07E-03
Integrin beta subunit, tail	Structural	1.07E-03
Transcription factor, MADS-box	Nuclear	1.11E-03
NFkappaB IPT domain	Nuclear	1.11E-03
Kinase associated domain 1 (KA1)	Catalytic	1.11E-03
PAS domain	Cytoplasmic	1.28E-03
Actin-depolymerising factor homology domain	Structural	1.87E-03
Phosphatidylinositol 3-/4-kinase, catalytic domain	Catalytic	1.94E-03
Bromodomain	Nuclear	1.98E-03
PTB/PI domain	Cytoplasmic	1.98E-03
Peptidase C14A, caspase catalytic domain	Catalytic	2.08E-03
DEP domain	Cytoplasmic	2.51E-03
PTP type protein phosphatase	Catalytic	2.59E-03
Cold-shock protein, DNA-binding	Nuclear	2.76E-03
Cold shock domain	Nuclear	2.76E-03
MAD homology, MH1	Nuclear	2.76E-03
Integrin beta subunit, VWA domain	Structural	2.76E-03
SMAD domain, Dwarfing-type	Nuclear	2.76E-03
Integrin beta N-terminal	Structural	2.76E-03
Cyclin, N-terminal	Cytoplasmic	3.02E-03
PDZ domain	Cytoplasmic	3.20E-03
Cyclin, C-terminal domain	Cytoplasmic	3.20E-03
HD/PDEase domain	Catalytic	3.37E-03
Pointed domain	Nuclear	3.39E-03
Transient receptor ion channel domain	Transport	3.99E-03
MCM N-terminal domain	Nuclear	3.99E-03
3'5'-cyclic nucleotide phosphodiesterase, catalytic domain	Catalytic	3.99E-03
Calmodulin-regulated spectrin-associated protein, CH domain	Structural	3.99E-03

Integrin beta subunit, cytoplasmic domain	Structural	3.99E-03
Zinc finger, GATA-type	Nuclear	5.82E-03
Ras GTPase-activating domain	Cytoplasmic	5.82E-03
Phosphatidylinositol-4-phosphate 5-kinase, core	Cytoplasmic	5.95E-03
Myb domain	Nuclear	5.95E-03
MATH/TRAF domain	Catalytic	6.05E-03
Ran binding domain	Cytoplasmic	6.05E-03
Peptidase C14, caspase non-catalytic subunit p10	Catalytic	6.05E-03
Rho GTPase-activating protein domain	Cytoplasmic	8.45E-03
Potassium channel, inwardly rectifying, transmembrane domain	Transport	9.28E-03
CARD domain	Cytoplasmic	9.29E-03
Syndecan/Neurexin domain	Structural	1.01E-02
W2 domain	Nuclear	1.01E-02
DIX domain	Cytoplasmic	1.01E-02
Raf-like Ras-binding	Cytoplasmic	1.01E-02
Sirtuin family, catalytic core domain	Catalytic	1.01E-02
CAP Gly-rich domain	Structural	1.12E-02
Phosphoinositide 3-kinase, accessory (PIK) domain	Catalytic	1.12E-02
K Homology domain	Nuclear	1.15E-02
Rhodanese-like domain	Catalytic	1.15E-02
Helicase, C-terminal	Nuclear	1.18E-02
HECT domain	Catalytic	1.18E-02
Kinesin motor domain	Structural	1.26E-02
Ankyrin repeat-containing domain	Cytoplasmic	1.36E-02
Band 4.1 domain	Cytoplasmic	1.42E-02
K Homology domain, type 1	Nuclear	1.44E-02
Tubulin/FtsZ, 2-layer sandwich domain	Structural	1.45E-02
WH2 domain	Structural	1.45E-02
APBB1IP, PH domain	Cytoplasmic	1.47E-02
MYST, zinc finger domain	Nuclear	1.47E-02
PIK-related kinase, FAT	Catalytic	1.47E-02
Chromo/chromo shadow domain	Nuclear	1.47E-02
Zinc finger, RanBP2-type	Nuclear	1.47E-02
PWI domain	Nuclear	1.47E-02
Ephrin receptor, transmembrane domain	Catalytic	1.47E-02
Histone acetyltransferase domain, MYST-type	Catalytic	1.47E-02
Ephrin receptor ligand binding domain	Cytoplasmic	1.47E-02
Helicase superfamily 1/2, ATP-binding domain	Nuclear	1.47E-02

Integrin beta, epidermal growth factor-like domain 1	Structural	1.47E-02
Rho GTPase-binding/formin homology 3 (GBD/FH3) domain	Structural	1.71E-02
Bromo adjacent homology (BAH) domain	Nuclear	1.71E-02
Phosphatidylinositol 3-kinase, C2 domain	Catalytic	1.82E-02
MCM OB domain	Nuclear	1.82E-02
Ras-like guanine nucleotide exchange factor, N-terminal	Cytoplasmic	1.85E-02
Ubiquitin specific protease domain	Catalytic	2.01E-02
Sterile alpha motif domain	Nuclear	2.36E-02
Tubulin/FtsZ, GTPase domain	Structural	2.57E-02
MAD homology 1, Dwarfing-type	Nuclear	2.80E-02
IRS-type PTB domain	Cytoplasmic	2.80E-02
Small GTP-binding protein domain	Cytoplasmic	2.95E-02
Peptidase C19, ubiquitin carboxyl-terminal hydrolase	Catalytic	3.09E-02
Tetratricopeptide repeat-containing domain	Cytoplasmic	3.12E-02
Cold-shock (CSD) domain	Nuclear	3.12E-02
Rab-binding domain FIP-RBD	Catalytic	3.12E-02
FATC domain	Catalytic	3.12E-02
MCM domain	Nuclear	3.12E-02
PIK-related kinase	Catalytic	3.12E-02
CP2 transcription factor	Nuclear	3.12E-02
E2F transcription factor, CC-MB domain	Nuclear	3.12E-02
Histidine kinase/HSP90-like ATPase	Catalytic	3.12E-02
Serine/threonine-protein kinase OSR1/WNK, CCT domain	Catalytic	3.12E-02
Helicase/UvrB, N-terminal	Nuclear	3.12E-02
Growth factor receptor domain 4	Cytoplasmic	3.12E-02
Glutamine amidotransferase	Catalytic	3.12E-02
Formin, GTPase-binding domain	Structural	3.12E-02
Formin, FH3 domain	Structural	3.12E-02
Initiation factor eIF-4 gamma, MA3	Nuclear	3.12E-02
Dual specificity protein phosphatase domain	Catalytic	3.50E-02
Zinc finger, LIM-type	Nuclear	3.68E-02
PAS fold-3	Cytoplasmic	3.86E-02
Basic leucine zipper domain, Maf-type	Nuclear	3.86E-02
FERM domain	Cytoplasmic	4.52E-02
Dual specificity phosphatase, catalytic domain	Catalytic	4.82E-02