Projecting PamChip® data on Proteome maps:
Inferring Group differences at several levels

Peptides on PamChip (PTK 86402 and STK 87102) can be phosphorylated by a number of kinases.

Statistically Significant Peptides List from PamChip Data

From T-tests and ANOV-Dunnett tests, of comparative phosphorylation profiles, a list of the Log2 Fold Change (LFC; also called Log2 Ratios or Delta) are generated and exported to excel.

Statistically Significant Peptides List for Proteome map

Using the desired p-value threshold, you can select the UNIQUE UniPROT IDs using excel. For example, select all UniPROT IDs that have significant differences <p value 0.05. Copy these IDs, together with the LFC value to a new column. Negative values are not accepted and must be converted to absolute values. There should be no header row, and 2 columns, one with the UniPROT ID, and 1 with LFC. The file should be saved as tab delimited text.

Mapping your PamChip data on a Proteome map

URL for Tool, free for Research Use: https://bionic-vis.biologie.uni-greifswald.de. Select species Homo Sapiens;, add a comment; upload the Tab txt file from previous step or copy-paste it, Click Submit; After the maps are generated you can click the icon and download a file showing the different levels of the proteome data. PamChip data representation is shown on Page 2.

Proteomaps show the quantitative composition of proteomes. Each protein is represented by a polygon: areas reflect protein abundance, and functionally related proteins are arranged in common and similarly colored regions. For further reading please see www.proteomaps.net

version 1.0	2.0		user maps	+

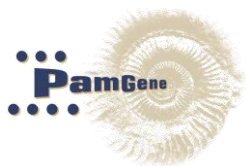|		
organism?	Homo sapiens (Human)	select
comment?		
tsv file?		browse
or data? Insert an example? **Please consider!**		

PamAcademy

Proteome Map of PamChip® Data:
Inferring Group differences at several levels

Peptides on PamChip (PTK 86402 and STK 87102) can be phosphorylated by a number of kinases. A representation of major pathways and the PamChip substrates are illustrated on the Proteome map. The map represents the UniPROT Ids as provided in the Array Layout files of combined PTK and STK PamChips.

Panel 1
- Environmental Information Processing
- Genetic Information Processing
- Human Diseases
- Organismal Systems
- Metabolism
- Cellular Processes

Panel 2
- Signaling Molecules and Interaction
- Translation
- DNA Maintenance
- Folding, Sorting and Degradation
- Signal Transduction
- Transcription
- Cellular Community
- Cell Growth and Death
- Cardiovascular Diseases
- Development
- Immune System
- Endocrine System
- Nervous System
- Central Carbon Metabolism
- Circulatory System
- Biosynthesis
- Other Enzymes
- Cytoskeleton
- Vesicular transport

Panel 3
- Ion channels
- Cell adhesion molecules (CAMs)
- Enzyme-linked receptors
- Rap1 signaling pathway
- NF-kappa B signaling pathway
- JAK-STAT signaling pathway
- DNA replication control
- Ribosome
- Spliceosome
- Chromosome related
- CD Molecules
- PI3K-Akt signaling pathway
- Peptidases
- MAPK signaling pathway
- Transcription factors
- Basal transcription factors
- Calcium signaling pathway
- cAMP signaling pathway
- Ras signaling pathway
- ErbB signaling pathway
- Nuclear membrane
- Focal adhesion
- Tight junction
- Cytokinesis
- Axon guidance
- Fc gamma R-mediated phagocytosis
- Chemokine signaling pathway
- Amino acid metabolism
- Protein kinases
- Carbohydrate metabolism
- Glycolysis
- Other enzymes
- Adherens junction
- Cytoskeleton proteins
- Apoptosis
- Cell cycle
- Regulation of actin cytoskeleton
- Phagosome
- Exosome

Panel 4
CD70, KCNB1, MEF2L1, EPHA1, DDR1, EPHB1, CTNNB1, ATM, CSNK2A1, CDK1, CHRND, PECAM1, EPHA4, STAT6, VASP, SYK, PPP2CB, TOP2A, DBK2, PDCD1, RET, NTRK3, MAPK7, RASA1, MYC, EIF4E, KIF11, GABRB2, KCNA6, MST1R, EPOR, NTRK1, PRKACG, RAPGEF3, RP56, KIF2C, NEK2, KCNA1, KCNA3, CD28, TYRO3, EPHA7, TEK2, CKB, RAF1, BRCA1, CENPA, AURKB, LCK, GPR6, KCNA2, MUSK, NTRK2, NFKB1, ATF2, MAP2K1, C1R, CHRM4, BT1A, RAP1B, EGFR, MAPK14, PRKCB, RAB1A, CDK7, CD3E, FYN, CDK2, MAPK10, MAPK12, MAP2, REL, PRRX2, CD247, CREB1, PDGFRB, MAPK3, MAPT, NR4A1, AR, ERF, VTN, JAK1, MAPK1, AKT1, IKBKB, PGR, ESR1, ELK1, ADRB2, BAD, GAB2, CACNA1C, CRK, RPS6KA1, CFTR, RBL2, CHRM5, CD27, TEK, EPHA2, ERBB3, ERBB4, SHC1, STAT4, RB1, PTK2B, ZAP70, PTPN11, PTK2, CAMK2G, GAB1, CDKN1B, TES, TP53, FOXO3, RYR1, CHRM1, LAT, CBL, PIK3R1, STAT5A, MYBL2, LMNA, PHKA1, ARAF, MTOR, ERBB2, VCL, FPB11, DYRK1A, NOS3, GRIN1, INSR, FLT4, KDR, SRC, PDE5A, PTPN6, PRKAR2A, CDC25A, FGFR1, MET, FLT1, TH, PDPK1, YES1, PRKAR2B, CDK4, DSP, PRPH, FGFR2, CSF1R, SOCS3A, PYGL, PLCG2, PTPN17, FER, PTK6, LMNB1, CDC25C, MARCKS, EPHA4, FGFR3, GYS2, FRK, TNNT1, MXRA, PFKL, PFKFB3, CFL1, NCF1, PXN, STAT1, LIPE, FABP3, SLC9A1, POU2AF, PDHA2, ENO2, FES, TEC, RDX, KRT8, FGA, JAK2, STAT3, SCN2A, ENO2, PLCG1, KRT6B

Size refers to "weight". In this example, Panel 4 "weight" refers to the number of peptides (phosphosites) on the PamChip for the UniPROT accession number

PamGene

https://bionic-vis.biologie.uni-greifswald.de