

Supplemental materials

Systematic analysis of protein phosphorylation networks from phosphoproteomic data

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Running title: *Computational analysis of phosphoproteomic data*

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Index

Supplemental experimental procedures	3
Preparation of benchmark sequence data	3
Preparation protein kinase (PK) data	3
Redundant clearing for experimental identified p-sites	3
Integration of protein-protein interactions (PPIs).....	4
Detection of conserved kinase-substrate relations (KSRs).....	4
The Yates' chi-squared (χ^2) test	5
Supplemental results	6
Both experimental and predicted PPIs are useful for reducing potentially false positive hits	6
Usage of the iGPS software packages.....	6
Performance of the RP-RPLC approach for the large-scale phosphorylation analysis of the human liver	7
The use of ArMone to improve coverage of the human liver phosphoproteome	8
Supplemental References	10
Supplemental Figures	12
Supplemental Fig. 1	12
Supplemental Fig. 2	13
Supplemental Fig. 3	14
Supplemental Fig. 4	15
Supplemental Fig. 5	16
Supplemental Fig. 6	17
Supplemental Tables	18
Supplemental Table S1	20
Supplemental Table S8	21
Supplemental Table S9	32
Supplemental Table S10	40
Supplemental Table S11.....	48
Supplemental Table S12	49
Supplemental Table S13	82
Supplemental Table S14	85
Supplemental Table S15	92
Supplemental Table S16	95
Supplemental Table S17	122
Supplemental Table S18	128
Supplemental Table S19	129
Supplemental Table S20	130

Note: Supplemental Table S2, S3, S4, S5, S6, and S7 are present in additionally separated files.

Supplemental experimental procedures

Preparation of benchmark sequence data

In this work, five eukaryotic organisms were considered. The benchmark sequence data were downloaded from the UniProt database (<http://www.uniprot.org>, on April 6, 2010), with 7,965, 24,204, 33,389, 59,000, and 97,433 proteins in *Saccharomyces cerevisiae*, *Caenorhabditis elegans*, *Drosophila melanogaster*, *Mus musculus* and *Homo sapiens*, respectively. We observed that the UniProt database contains a large number of identical sequences. Thus, we used CD-HIT, a program of clustering similar sequences (1), to clear redundant proteins. In the UniProt database, a protein accession number consists of six characters or numbers, and the initial character is O, P, Q, A, B, C, and D in chronological order. If two or more proteins are of 100% identity, only the sequence with the most anterior accession is reserved. Such an order was adopted throughout the study to avoid redundancy. Thus finally, there are 7,288, 23,775, 30,859, 50,623, and 81,732 proteins preserved in the five species.

Preparation protein kinase (PK) data

The full length sequences of the PKs were downloaded from the kinase.com database (<http://kinase.com/>) (2), with 131, 435, 238, 535, and 516 PKs in *S. cerevisiae*, *C. elegans*, *D. melanogaster*, *M. musculus* and *H. sapiens*, respectively. In the kinase.com database, all PKs were classified into a hierarchical structure with four levels, i.e. group, family, subfamily, and single PK (2). Based on the classification information, only those PKs for which GPS 2.0 predicted specific sites were retained. In total, there were 91, 302, 172, 415 and 407 PKs preserved in the five species (Supplemental Table S8). The sequences of these PKs were mapped to the UniProt benchmark sequences. Furthermore, we selected predictors of these PKs in GPS 2.0 (Supplemental Table S8) (3).

Redundant clearing for experimental identified p-sites

After all of the experimental p-sites were mapped to the UniProt benchmark sequences, we compared the protein sequences having heterogeneous identifiers to the UniProt benchmark sequences with the BLAST program (4). As previously described, a phosphorylation site peptide

PSP(7, 7) was defined as a p-site flanked by 7 residues upstream and 7 residues downstream (3). To eliminate redundancy and ensure matching accuracy, we adopted a previously developed method of exact string matching (ESM) (5), and used PSP(7, 7) to make a comparison with the BLAST results. Again, only the sequence with the most anterior accession in the chronological order of O>P>Q>A>B>C>D was retained.

Integration of protein-protein interactions (PPIs)

The experimental PPI data were taken from several major public databases (on April 10, 2010), including BioGRID (6), HPRD (7), DIP (8), MINT (9) and IntAct (10). All proteins were mapped to the UniProt benchmark sequences by BLAST. The non-redundant data set contains 165,012, 9,559, 32,533, 4,740 and 59,481 PPIs from *S. cerevisiae*, *C. elegans*, *D. melanogaster*, *M. musculus* and *H. sapiens*, respectively (Supplemental Table S19). Additionally, the potential PPIs in the pre-calculated STRING database (11) were also included (Supplemental Table S19).

Detection of conserved kinase-substrate relations (KSRs)

The InParanoid program in PERL script was downloaded (<http://inparanoid.sbc.su.se/>, ver. 1.35, released on June 1st, 2004) (12). Using the default parameters, we calculated orthologs pairwise from benchmark protein sequences. Furthermore, a well-established algorithm was adopted to identify clusters of orthologous groups of proteins (COGs) for the five eukaryotic proteomes (13, 14). Although the two approaches are accurate and efficient, there were still several false positive hits which occurred. For example, although the ortholog of yeast CDC28 in human is CDC2/CDK1, the InParanoid mis-predicted yeast CDC28 and human CDK3 as an orthologous pair. Such obvious errors were manually corrected.

With the predicted and corrected COGs, we computed the KSR which both the PK and substrate are conserved across species for eukaryotic phosphoproteomes. For mammalian liver phosphoproteomes, we further calculated the site-specific kinase-substrate relation (ssKSR) which the PK, the substrate, and p-sites are conserved.

The Yates' chi-squared (χ^2) test

Because not all p-sites identified in human liver were covered by the whole human phosphoproteome collected from the public databases and scientific literature, the Yates's corrected version of Pearson's chi-squared test was adopted for statistical comparison (From Wikipedia) (15).

Given the prediction results for a PK X , the entries in the 2×2 table were defined as below:

a = number of predicted ssKSRs for X in the liver PPN;

b = number of predicted ssKSRs for X in the whole PPN;

c = number of predicted ssKSRs not for X in the liver PPN;

d = number of predicted ssKSRs not for X in the whole PPN;

$N_l = a + c$, totally predicted ssKSRs in the liver PPN (12,874 for *H. sapiens* and 4,502 for *M. musculus*);

$N_w = b + d$, totally predicted ssKSRs in the whole PPN (113,923 for *H. sapiens* and 45,032 for *M. musculus*, see Table 3);

$N_y = a + b$; $N_n = c + d$; $N = N_l + N_w = N_y + N_n$.

	Liver	Whole	
Number of predicted ssKSRs for X	a	b	N_y
Number of predicted ssKSRs not for X	c	d	N_n
	N_l	N_w	N

The enrichment ratio of predicted ssKSRs for X in the liver PPN against the whole PPN was calculated as below:

$$E - ratio = \frac{a / N_l}{b / N_w}$$

E-ratio>1 means predicted ssKSRs for X to be over-represented in the liver PPN, whereas E-ratio<1 means predicted ssKSRs for X to be under-represented. The χ^2 was calculated as below:

$$\chi_{Yates}^2 = \frac{N(\max(0, |ad - bc| - N/2))^2}{N_l N_w N_y N_n}$$

Then the p -value (<0.01) was calculated by the function of CHIDIST(χ^2 , degrees_freedom) in Excel. The degrees_freedom is equal to 1 for the 2×2 table.

Supplemental results

Both experimental and predicted PPIs are useful for reducing potentially false positive hits

It was estimated that ~50% of the yeast PPIs identified from high-throughput experiments might be false positive hits (16). Interestingly, approximately 50% of the experimentally identified PPIs is covered by the STRING integrated and predicted PPI database (Supplemental Fig. 1). Thus, we strongly suspected the usefulness of experimental PPIs, if all of the *bona fide* experimental PPIs were possibly fully covered by STRING. We then carefully exploited the usefulness of the experimental PPI information. From the testing data set, the iGPS successfully predicted 3,158 experimentally identified ssKSRs for 2,210 p-sites (Supplemental Table S20). From these results, there are 441 (~14%) ssKSRs supported by solely experimental PPIs, while 768 (24%) ssKSRs are supported by both the experimental and predicted PPIs (Supplemental Table S20). In this regard, excluding the experimentally supported PPIs would reduce the prediction performance for PK annotation. For the large-scale prediction for 145,646 p-sites in eukaryotic phosphoproteomes, there are 12,177 (~6.5%) ssKSRs supported by only experimental PPIs (Supplemental Table S20). In particular, there are 6,280 (~30%) ssKSRs in yeast supported by only experimental PPIs (Supplemental Table S20). In this regard, both the experimental and predicted PPIs were adopted in the iGPS.

Usage of the iGPS software packages

The online service is not provided because it's too time-consuming to visualize the program in a web browser. The local packages of iGPS 1.0 are freely available for academic research at: <http://igps.biocuckoo.org>. The iGPS 1.0 can be used to predict ssKSRs from phosphoproteomic data for five eukaryotic species, while *H. sapiens* was selected as the default organism (Supplemental Fig. 2A). Also, the experimental and STRING PPI filter together with the low threshold were chosen as the default parameters (Supplemental Fig. 2A). For prediction, the data can be inputted in three formats, such as PhosPep, ELM, and FASTA. First experimentalists can directly input phospho-peptides (The PhosPep format) such as "GLVAAYSGDpSDNEEELVER" and

“APGAIGPYpSQAVLVDR” (A “p” denotes the next residue to be a p-site) from the phosphoproteomic analysis. For convenience, one or multiple phospho-peptides can be inputted, while iGPS will first map these peptides to the benchmark sequences and then perform the prediction. Second, Diella *et al.* defined a tab-delimited format (The ELM format) for the storage of the phosphoproteomic data (17, 18). The iGPS supports this format as input, while only first four columns (acc, sequence, position and code) will be used for further prediction. Furthermore, one or multiple protein sequences in FASTA format can be directly inputted. However, this format is not recommended because *ab initio* prediction of ssKSRs merely from protein sequences will generate too much false positive hits. The users should parse the results by themselves and make sure the positions of real p-sites according to the phosphoproteomic data.

Finally, before clicking on the “Submit” button for prediction, at least one PK predictor in the left column should be chosen (Supplemental Fig. 2A). When the prediction process is finalized, the protein phosphorylation network (PPN) can be visualized by clicking on the “Network” button (Supplemental Fig. 2B). If users have multiple files containing too many data for input, the “Batch Predictor” button in the Tools menu can be clicked. The Batch Predictor will process all of the files which have been added to the list, and then the prediction result is exported to the Result Export fold (Supplemental Fig. 2C).

From public databases and the scientific literature, we collected 145,646 experimentally identified phosphorylation sites (p-sites) in 28,457 substrates, with 14,534, 5,555, 15,622, 49,119 and 60,816 p-sites in *S. cerevisiae*, *C. elegans*, *D. melanogaster*, *M. musculus* and *H. sapiens*, respectively (Supplemental Table S1). With the PPI information, we predicted 186,922 (total PPIs) and 34,873 (experimental PPIs) ssKSRs (Table 3 & Supplemental Table S11). With these prediction results, we constructed the EPNdb (The database of eukaryotic phosphorylation network) 1.0. The users can search this database for pre-calculated ssKSRs (Supplemental Fig. 2D). More details on the usage of iGPS are available in the manual.

Performance of the RP-RPLC approach for the large-scale phosphorylation analysis of the human liver

The good orthogonality of this new RP-RPLC approach used for the phosphorylation analysis

has been demonstrated in our previous study (19). It was further validated in this study as the phosphopeptides in each pooled fraction collected from the first dimension appeared to be almost randomly distributed across the entire separation window in the second dimension. To evaluate the fractionation efficiency, the overlapped identifications among three consecutive pooled fractions from three different regions of the first dimensional separation were investigated. An average of 28% overlap between adjacent fractions was achieved, even with a collection window of only 1 min (Supplemental Fig. 3). The high resolution of the RPLC mode and the good orthogonality of this 2D system were demonstrated clearly. Thus, it is not surprising that a comprehensive phosphoproteome analysis can be achieved by this powerful multidimensional separation. It was found that multiply phosphorylated peptides with the highly hydrophilic nature tended to elute in the early regions in the first dimensional RPLC separation at high pH (Supplemental Fig. 4). As previously described (19), the interference from co-eluted phosphopeptides with same characteristics, such as multiply phosphorylated peptides clustered in the early fractions, may hamper their effective identifications. However, pooling two fractions with an equal time interval from the first dimensional separation could effectively reduced this effect. Therefore, the coverage of global phosphorylation analysis was improved by this powerful multidimensional separation with high orthogonality.

The use of ArMone to improve coverage of the human liver phosphoproteome

Since different phosphopeptides have their unique mass spectra characteristics, it is necessary to set different filtering strategies for the identification of phosphopeptide with different types. ArMone software suite exploits this filtering strategy and has been demonstrated to be an effective platform. According to the different characteristics of mass spectra, identified phosphopeptides were classified into four groups, and the distribution of identified phosphopeptides from these groups was shown in Supplemental Fig. 5 (Identification results were listed in Supplemental Table S4, S5, S6 and S7, respectively). As previously reported (20), over 75% of the identified phosphopeptides can be found in the MS2/MS3 class, which indicates that most of the phosphopeptides prefer to lose the phosphate as the major pathway in CID (collision-induced dissociation). At the same time, over 30% increase in phosphopeptide identifications can still be observed by incorporating the other three new identification results from ArMone. It is obviously that

the classification filtering strategy can effectively improve the phosphoproteome coverage.

On the other hand, the distribution of multiply phosphorylated peptides in different classes further demonstrates the necessity of classification filtering strategy. Over 50% in the NeutralMS3 identification results contained more than one p-site, whereas majority in the NoNeutral class were singly phosphorylated peptides (Supplemental Fig. 6). That means, multiply phosphorylated peptides are more likely to lose the phosphate and generate low quality MS2 spectra, thus, are identified mainly in the NeutralMS3 class. Whereas the singly phosphorylated peptides, who have better MS2 fragmentations, accounted for a large part of the NoNeutral class. Besides phosphopeptides with different number of p-sites, the phosphopeptides with different types of phosphorylated residues also have different characteristics in their mass spectra. As mentioned in our previous study (21), only the results with well matched MS2/MS3 pairs can be retained in the MS2/MS3 strategy. However, as is well known, phosphotyrosine peptides rarely generate neutral loss peak in MS2 spectra, and so they do not have MS3 spectra. Therefore, it is difficult to identify pY based on the MS2 and MS3 pairs. By combining identification results from NoNeutral and NeutralMS2 groups, more comprehensive identifications of phosphoserine (pS), phosphothreonine (pT) and phosphotyrosine (pY) were observed in our results (Fig. 6B), which was similar to the results reported by Olsen *et al.* (22), while the percentage of pY sites was doubled compared with that in MS2/MS3 strategy (21, 23, 24). Clearly, this classification filtering strategy can overcome the possible bias for the conventional approach using only one filtering criteria, and thus improve the phosphoproteome coverage effectively.

Supplemental References

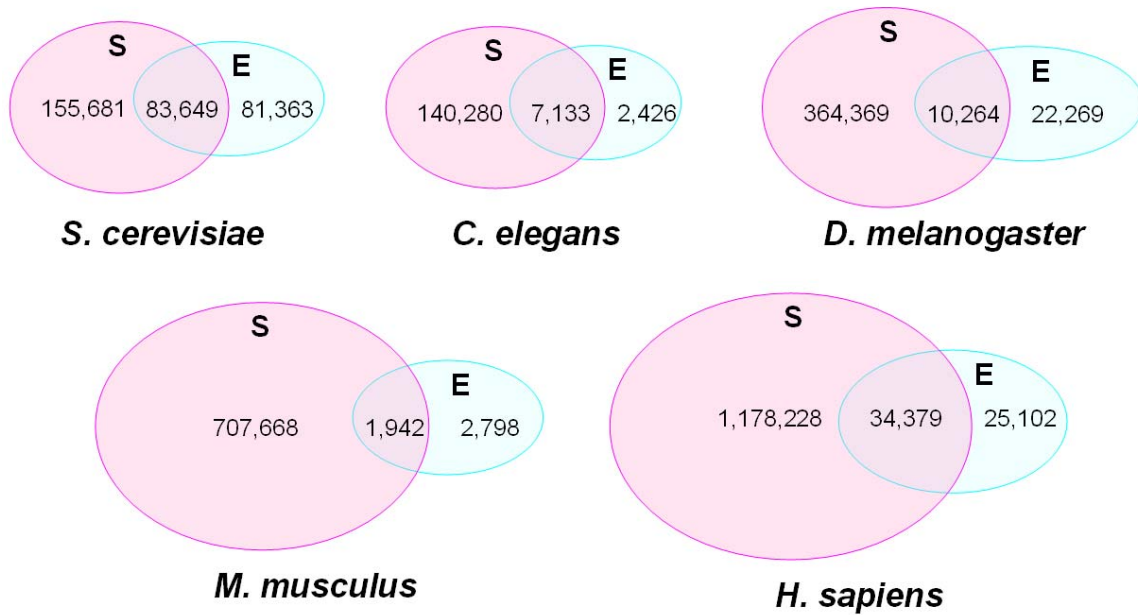
1. Li, W., and Godzik, A. (2006) Cd-hit: a fast program for clustering and comparing large sets of protein or nucleotide sequences. *Bioinformatics* **22**, 1658-1659.
2. Manning, G., Whyte, D. B., Martinez, R., Hunter, T., and Sudarsanam, S. (2002) The protein kinase complement of the human genome. *Science* **298**, 1912-1934.
3. Xue, Y., Ren, J., Gao, X., Jin, C., Wen, L., and Yao, X. (2008) GPS 2.0, a tool to predict kinase-specific phosphorylation sites in hierarchy. *Mol. Cell. Proteomics* **7**, 1598-1608.
4. Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J., Zhang, Z., Miller, W., and Lipman, D. J. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Res.* **25**, 3389-3402.
5. Tan, C. S., Bodenmiller, B., Pasculescu, A., Jovanovic, M., Hengartner, M. O., Jorgensen, C., Bader, G. D., Aebersold, R., Pawson, T., and Linding, R. (2009) Comparative analysis reveals conserved protein phosphorylation networks implicated in multiple diseases. *Sci. Signal.* **2**, ra39.
6. Stark, C., Breitkreutz, B. J., Reguly, T., Boucher, L., Breitkreutz, A., and Tyers, M. (2006) BioGRID: a general repository for interaction datasets. *Nucleic Acids Res.* **34**, D535-539.
7. Keshava Prasad, T. S., Goel, R., Kandasamy, K., Keerthikumar, S., Kumar, S., Mathivanan, S., Telikicherla, D., Raju, R., Shafreen, B., Venugopal, A., Balakrishnan, L., Marimuthu, A., Banerjee, S., Somanathan, D. S., Sebastian, A., Rani, S., Ray, S., Harrys Kishore, C. J., Kanth, S., Ahmed, M., Kashyap, M. K., Mohmood, R., Ramachandra, Y. L., Krishna, V., Rahiman, B. A., Mohan, S., Ranganathan, P., Ramabadran, S., Chaerkady, R., and Pandey, A. (2009) Human Protein Reference Database--2009 update. *Nucleic Acids Res.* **37**, D767-772.
8. Salwinski, L., Miller, C. S., Smith, A. J., Pettit, F. K., Bowie, J. U., and Eisenberg, D. (2004) The Database of Interacting Proteins: 2004 update. *Nucleic Acids Res.* **32**, D449-451.
9. Chatr-aryamontri, A., Ceol, A., Palazzi, L. M., Nardelli, G., Schneider, M. V., Castagnoli, L., and Cesareni, G. (2007) MINT: the Molecular INteraction database. *Nucleic Acids Res.* **35**, D572-574.
10. Aranda, B., Achuthan, P., Alam-Faruque, Y., Armean, I., Bridge, A., Derow, C., Feuermann, M., Ghanbarian, A. T., Kerrien, S., Khadake, J., Kerssemakers, J., Leroy, C., Menden, M., Michaut, M., Montecchi-Palazzi, L., Neuhauser, S. N., Orchard, S., Perreau, V., Roechert, B., van Eijk, K., and Hermjakob, H. (2010) The IntAct molecular interaction database in 2010. *Nucleic Acids Res.* **38**, D525-531.
11. Jensen, L. J., Kuhn, M., Stark, M., Chaffron, S., Creevey, C., Muller, J., Doerks, T., Julien, P., Roth, A., Simonovic, M., Bork, P., and von Mering, C. (2009) STRING 8--a global view on proteins and their functional interactions in 630 organisms. *Nucleic Acids Res.* **37**, D412-416.
12. Remm, M., Storm, C. E., and Sonnhammer, E. L. (2001) Automatic clustering of orthologs and in-paralogs from pairwise species comparisons. *J. Mol. Biol.* **314**, 1041-1052.
13. Tatusov, R. L., Koonin, E. V., and Lipman, D. J. (1997) A genomic perspective on protein families. *Science* **278**, 631-637.
14. Tatusov, R. L., Fedorova, N. D., Jackson, J. D., Jacobs, A. R., Kiryutin, B., Koonin, E. V., Krylov, D. M., Mazumder, R., Mekhedov, S. L., Nikolskaya, A. N., Rao, B. S., Smirnov, S., Sverdlov, A. V., Vasudevan, S., Wolf, Y. I., Yin, J. J., and Natale, D. A. (2003) The COG database: an

updated version includes eukaryotes. *BMC Bioinformatics* **4**, 41.

15. Liu, Z., Cao, J., Ma, Q., Gao, X., Ren, J., and Xue, Y. (2011) GPS-YNO2: computational prediction of tyrosine nitration sites in proteins. *Mol. Biosyst.* **7**, 1197-1204.
16. von Mering, C., Krause, R., Snel, B., Cornell, M., Oliver, S. G., Fields, S., and Bork, P. (2002) Comparative assessment of large-scale data sets of protein-protein interactions. *Nature* **417**, 399-403.
17. Diella, F., Cameron, S., Gemund, C., Linding, R., Via, A., Kuster, B., Sicheritz-Ponten, T., Blom, N., and Gibson, T. J. (2004) Phospho.ELM: a database of experimentally verified phosphorylation sites in eukaryotic proteins. *BMC Bioinformatics* **5**, 79.
18. Diella, F., Gould, C. M., Chica, C., Via, A., and Gibson, T. J. (2008) Phospho.ELM: a database of phosphorylation sites--update 2008. *Nucleic Acids Res.* **36**, D240-244.
19. Song, C., Ye, M., Han, G., Jiang, X., Wang, F., Yu, Z., Chen, R., and Zou, H. (2010) Reversed-phase-reversed-phase liquid chromatography approach with high orthogonality for multidimensional separation of phosphopeptides. *Anal. Chem.* **82**, 53-56.
20. Jiang, X., Ye, M., Han, G., Dong, X., and Zou, H. (2010) Classification filtering strategy to improve the coverage and sensitivity of phosphoproteome analysis. *Anal. Chem.* **82**, 6168-6175.
21. Jiang, X., Han, G., Feng, S., Jiang, X., Ye, M., Yao, X., and Zou, H. (2008) Automatic validation of phosphopeptide identifications by the MS2/MS3 target-decoy search strategy. *J. Proteome Res.* **7**, 1640-1649.
22. Olsen, J. V., Blagoev, B., Gnäd, F., Macek, B., Kumar, C., Mortensen, P., and Mann, M. (2006) Global, in vivo, and site-specific phosphorylation dynamics in signaling networks. *Cell* **127**, 635-648.
23. Han, G., Ye, M., Zhou, H., Jiang, X., Feng, S., Jiang, X., Tian, R., Wan, D., Zou, H., and Gu, J. (2008) Large-scale phosphoproteome analysis of human liver tissue by enrichment and fractionation of phosphopeptides with strong anion exchange chromatography. *Proteomics* **8**, 1346-1361.
24. Han, G., Ye, M., Liu, H., Song, C., Sun, D., Wu, Y., Jiang, X., Chen, R., Wang, C., Wang, L., and Zou, H. (2010) Phosphoproteome analysis of human liver tissue by long-gradient nanoflow LC coupled with multiple stage MS analysis. *Electrophoresis* **31**, 1080-1089.
25. Linding, R., Jensen, L. J., Ostheimer, G. J., van Vugt, M. A., Jorgensen, C., Miron, I. M., Diella, F., Colwill, K., Taylor, L., Elder, K., Metalnikov, P., Nguyen, V., Pasculescu, A., Jin, J., Park, J. G., Samson, L. D., Woodgett, J. R., Russell, R. B., Bork, P., Yaffe, M. B., and Pawson, T. (2007) Systematic discovery of in vivo phosphorylation networks. *Cell* **129**, 1415-1426.
26. Linding, R., Jensen, L. J., Pasculescu, A., Olhovsky, M., Colwill, K., Bork, P., Yaffe, M. B., and Pawson, T. (2008) NetworkKIN: a resource for exploring cellular phosphorylation networks. *Nucleic Acids Res.* **36**, D695-699.

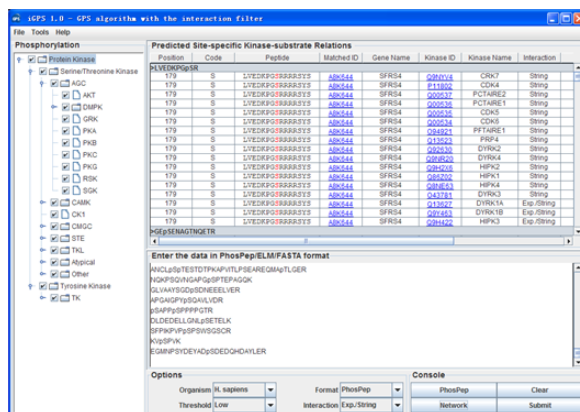
Supplemental Figures

Supplemental Fig. 1 – The overlapping rate of the experimental and computational PPIs. Approximately 50% of the experimentally identified PPIs are covered by the pre-predicted PPIs.

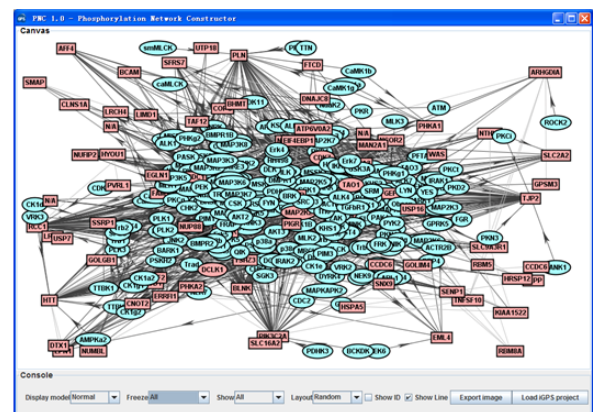


Supplemental Fig. 2 – The utility of the iGPS software. (A) The data can be inputted in three formats, such as PhosPep, ELM, or FASTA. At least one PK predictor should be chosen before the prediction. (B) The PNC (Phosphorylation network constructor) 1.0 was developed for the visualization of predicted KSRs. (C) The batch prediction. The procedure is to click on the “Batch Predictor” button and then click on the “Add File” button to add one or more files, then to click on the “>>” button to specify the export fold. (D) The EPNdb 1.0 contains pre-predicted ssKSRs in five eukaryotic organisms for searching.

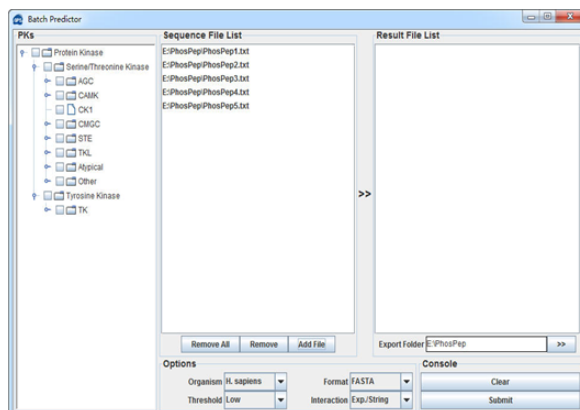
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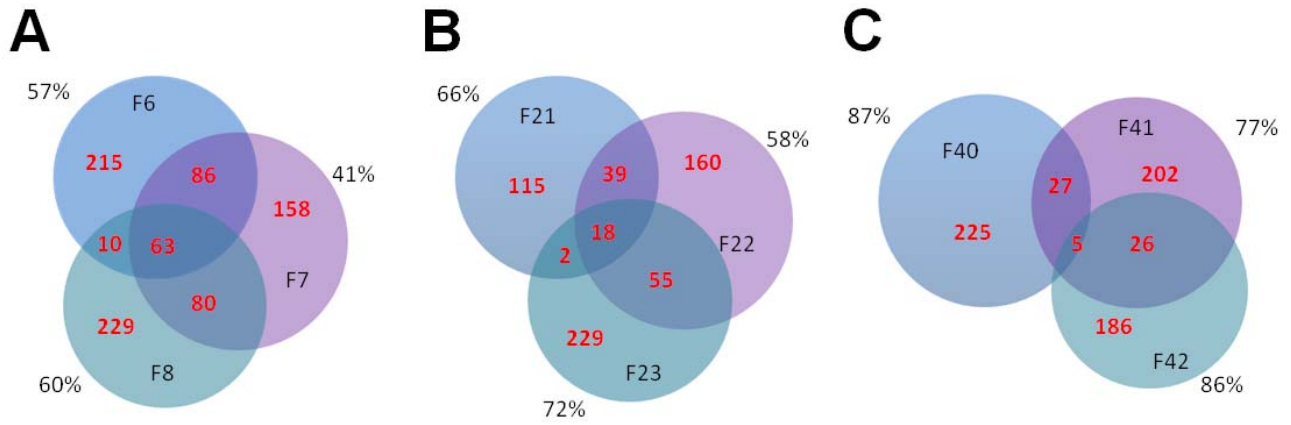
C



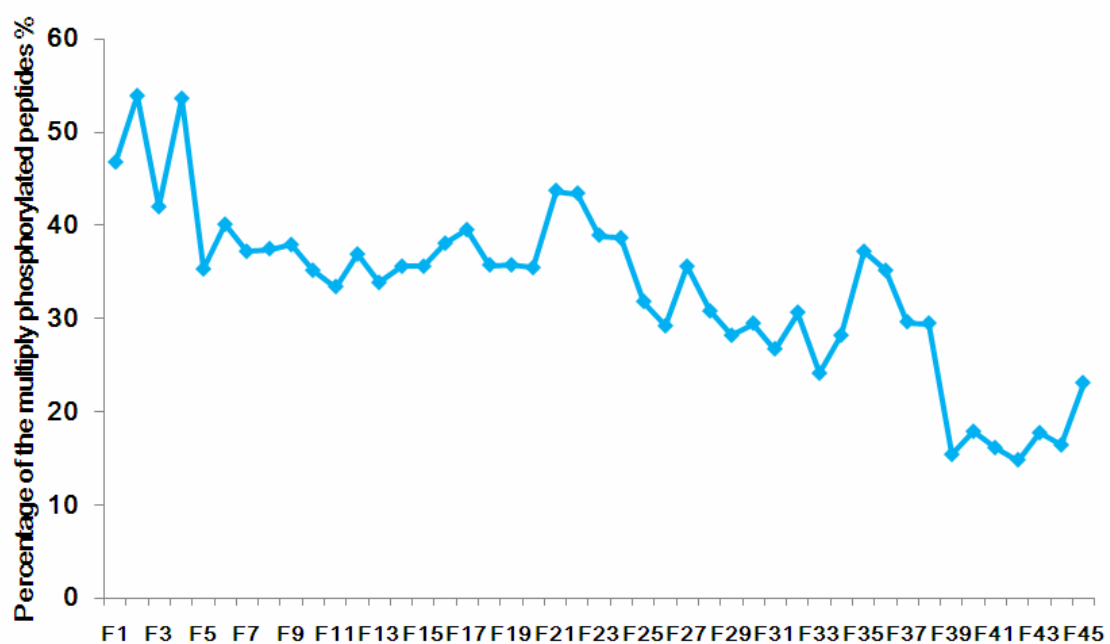
D

ID	Position	Code	Peptide	M. ID	M. Position	Gene Name	Kinase Name	Kinase ID	Interaction	Predictor	Score	Cutoff
GRUGP2	272	S	TATGKVFVGLPSPV	GRUGP2	272	LMND1	HPK3	GRUGP2	Exp.Ring	CMCCOVRK	5.8	1.17
GRUGP4	277	S	VYFPGVPLPGLGSA	GRUGP4	277	LMND1	HPK3	GRUGP4	Exp.Ring	CMCCOVRK	1.6	1.17
GRUGP4	384	S	LATGKVFVGLPSPV	GRUGP4	384	LMND1	HPK3	GRUGP4	Exp.Ring	CMCCOVRK	1.3	1.17
GRUGP4	284	S	VYFPGVPLPGLGSA	GRUGP4	284	LMND1	HPK3	GRUGP4	Exp.Ring	CMCCOVRK	2.6	1.17
GRUGP4	295	S	PVQPRVFPVAFAL	GRUGP4	295	LMND1	HPK3	GRUGP4	Exp.Ring	CMCCOVRK	1.7	1.17
GRUGP4	424	S	VLLQVFPVPLPGLGSA	GRUGP4	424	LMND1	HPK3	GRUGP4	Exp.Ring	CMCCOVRK	3.0	1.17
GRUGP4	272	S	TATGKVFVGLPSPV	GRUGP4	272	LMND1	FER	GRUGP4	Exp.Ring	TAF1er	3.25	3.01
GRUGP4	527	S	PCEVFPVPLPGLGSA	GRUGP4	527	LMND1	FER	GRUGP4	Exp.Ring	TAF1er	3.25	3.01
PS3667	508	T	PQKXKATVYQSPV	PS3667	508	LMNK1	PAK5	PS3667	Exp.Ring	STE/STE20	6.333	1.22
PS3667	274	S	QETTFVPLPGLGSA	PS3667	274	LMNK1	PAK5	PS3667	Exp.Ring	STE/STE20	1.233	1.22
PS3667	295	S	PQKXKATVYQSPV	PS3667	295	LMNK1	PAK5	PS3667	Exp.Ring	STE/STE20	1.8	1.22
PS3667	508	T	PQKXKATVYQSPV	PS3667	508	LMNK1	PAK5	PS3667	Exp.Ring	STE/STE20	6.333	1.22
PS3667	274	S	QETTFVPLPGLGSA	PS3667	274	LMNK1	PAK5	PS3667	Exp.Ring	STE/STE20	1.233	1.22
PS3667	295	S	PQKXKATVYQSPV	PS3667	295	LMNK1	PAK5	PS3667	Exp.Ring	STE/STE20	1.8	1.22
PS3667	508	T	PQKXKATVYQSPV	PS3667	508	LMNK1	BRCKA	PS3667	Exp.Ring	ACC/CMAPK	6.121	1.24
PS3667	310	S	PQKXKATVYQSPV	PS3667	310	LMNK1	BRCKA	PS3667	Exp.Ring	ACC/CMAPK	2.218	0.83
PS3667	210	S	QVQVQVQVQVQVQV	PS3667	210	LMNK1	p38a	PS3667	Exp.Ring	CMCC/CMAPK	1.381	0.83
PS3667	302	S	RKCTIDRFGVGLGSA	PS3667	302	LMNK1	p38a	PS3667	Exp.Ring	CMCC/CMAPK	1.882	0.83
PS3667	229	T	RILRIRVFPVPLPGLGSA	PS3667	229	LMNK1	p38a	PS3667	Exp.Ring	CMCC/CMAPK	1.004	0.83
PS3667	113	S	QVQVQVQVQVQVQV	PS3667	113	LMNK1	p38a	PS3667	Exp.Ring	CMCC/CMAPK	0.874	0.83
PS3667	508	T	PQKXKATVYQSPV	PS3667	508	LMNK1	PKH2	PS3667	Exp.Ring	ACC	2.126	1.59
PS3667	298	S	PLPFLVPLPGLGSA	PS3667	298	LMNK1	PKH2	PS3667	Exp.Ring	ACC	2.147	1.59

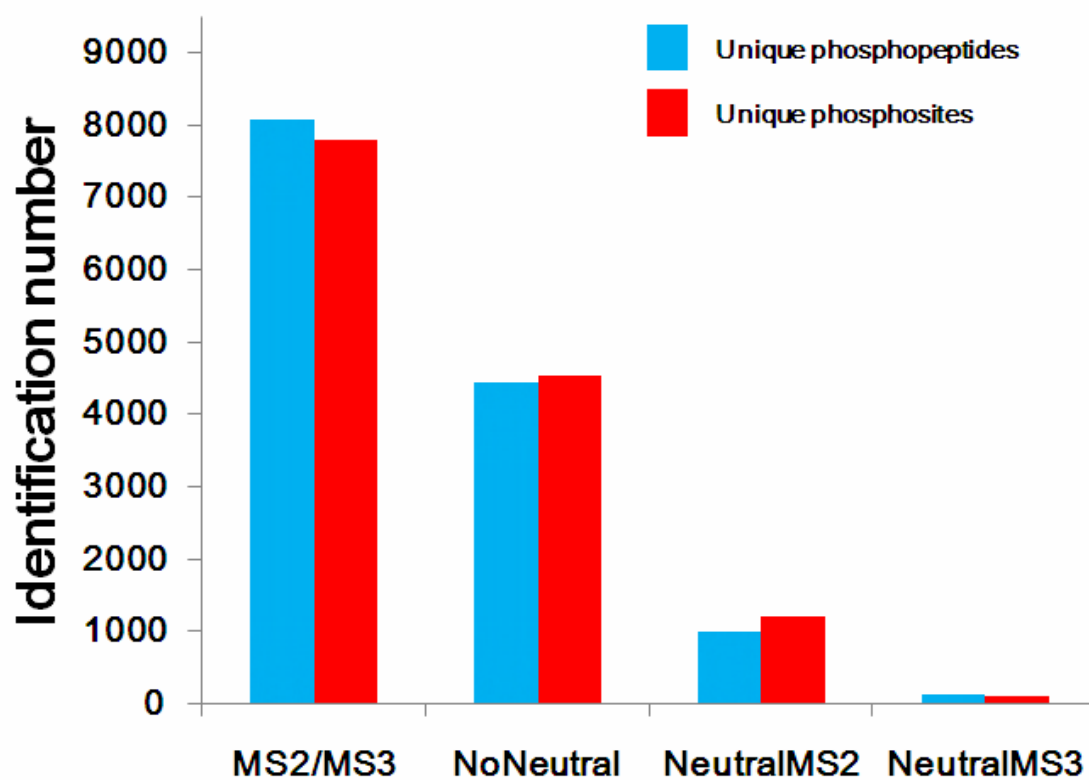
Supplemental Fig. 3 – Overlaps between the adjacent fractions from (A) the early, (B) the intermediate and (C) the later eluted regions found in the first dimensional separation. Percentages represent the proportion of phosphopeptides in each fraction that were not identified in other fractions. F is the abbreviation of fraction.



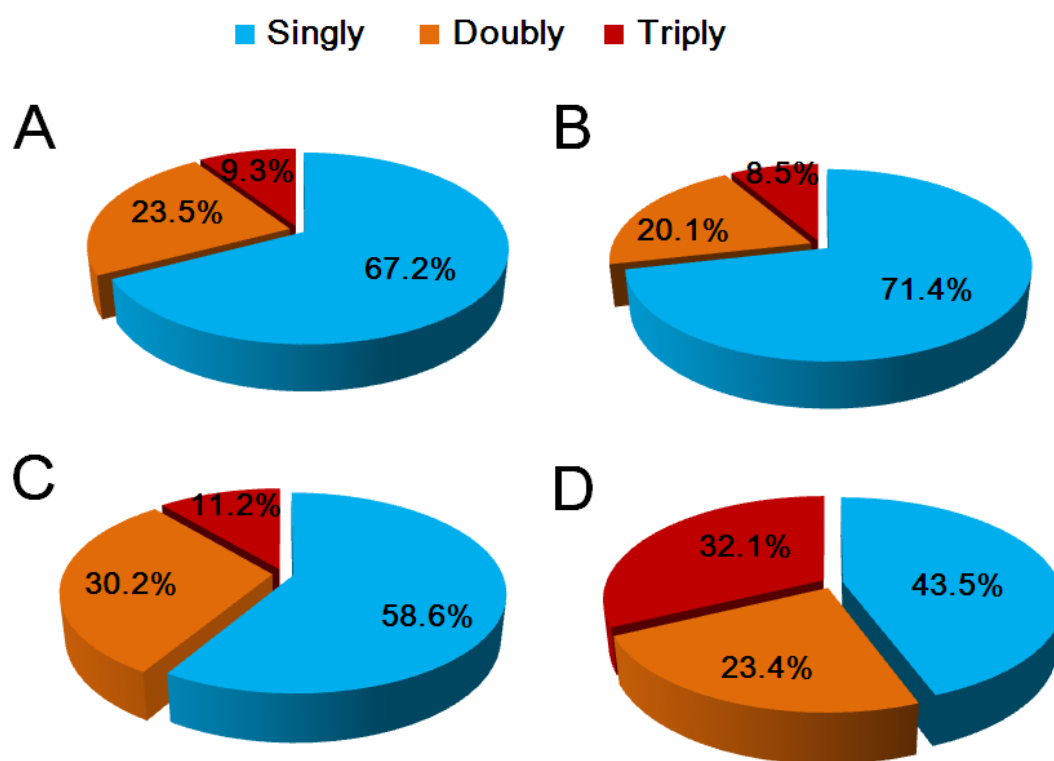
Supplemental Fig. 4 – The percentage of the multiply phosphorylated peptides throughout the 45 pooled fractions found in the first dimensional separation.



Supplemental Fig. 5 – The number of unique phosphopeptides and p-sites identified by the different types of mass spectra with a FDR<1% based on the classification filtering strategy.



Supplemental Fig. 6 – The distribution of the singly, doubly and triply phosphorylated peptides identified from the four different classes of mass spectra. (A) MS2/MS3; (B) Non-Neutral; (C) NeutralMS2; (D) NeutralMS3.



Supplemental Tables

Supplemental Table S1 – The statistical data on the experimentally identified p-sites collected in this study. a. Sub., the number of phosphorylated substrates.

Supplemental Table S2 – To evaluate the performance of iGPS, the testing data set containing 3,508 kinase-specific p-sites in 1,390 substrates. a. If a kinase-specific p-site is from *S. cerevisiae*, *C. elegans*, *D. melanogaster*, *M. musculus* or *H. sapiens*, the iGPS algorithm can be used to predict the potential ssKSRs. Since there are a number of kinase-specific p-sites from mammals as well as other species, we used the PPIs of either two (Human and mouse) or five (all species) to predict the ssKSRs.

Supplemental Table S3 – To compare iGPS with NetworkKIN (25, 26), we collected 1,701 kinase-specific p-sites in 830 substrates from Phospho.ELM 9.0 (released in September 2010) (17, 18) for twelve PK groups. We also manually collected 450 phosphoproteins with 1,193 kinase-specific p-sites from the scientific literature. After redundant clearing, the testing data set contains 2,894 kinase-specific p-sites in 1,280 proteins.

Supplemental Table S4 – Identified phosphopeptides classified in the MS2/MS3 group. The pS, pT, and pY indicate p-sites, while the character “*” indicates methionine oxidation with +16 Da modification. A total of 8,074 unique phosphopeptides were identified. Phosphopeptides with different methionine oxidation were listed but not repeatedly accounted.

Supplemental Table S5 – Identified phosphopeptides classified in the NoNeutral group. The pS, pT, and pY indicate p-sites, while the character “*” indicates methionine oxidation with +16 Da modification. A total of 4,437 unique phosphopeptides were identified. Phosphopeptides with different methionine oxidation were listed but not repeatedly accounted.

Supplemental Table S6 – Identified phosphopeptides classified in the NeutralMS2 group. The pS, pT, and pY indicate p-sites, while the character “*” indicates methionine oxidation with +16 Da modification. A total of 996 unique phosphopeptides were identified. Phosphopeptides with different methionine oxidation were listed but not repeatedly accounted.

Supplemental Table S7 – Identified phosphopeptides classified in the NeutralMS3 group. The pS, pT, and pY indicate p-sites, while the character “*” indicates methionine oxidation with +16 Da modification. A total of 114 unique phosphopeptides were identified. Phosphopeptides with different

methionine oxidation were listed but not repeatedly accounted.

Supplemental Table S8 – The detailed information on the 56 STK and 21 TK specific predictors in GPS 2.0 and their corresponding PKs.

Supplemental Table S9 – The detailed performance of the iGPS algorithm for the no PPI, STRING and experimental PPI (STRING & Exp. PPI), and only experimental PPI (Exp. PPI) information. The *Ac*, *Sn*, *Sp*, *MCC* and *Kpr* were extensively calculated for the three thresholds.

Supplemental Table S10 – To further evaluate the performance of the iGPS algorithm, the *Lpr* values were thoroughly calculated for each PK. *a*. Pre., predicted hits.

Supplemental Table S11 – The detailed data statistics for the prediction results of five eukaryotic phosphoproteomes.

Supplemental Table S12 – The number of p-sites for each PK in five eukaryotic PPNs. The top 10 PKs with the most p-sites are marked in yellow.

Supplemental Table S13 – The conserved KSRs were detected by the comparative analysis. *SC*, *S. cerevisiae*; *CE*, *C. elegans*; *DM*, *D. melanogaster*; *MM*, *M. musculus*; *HS*, *H. sapiens*.

Supplemental Table S14 – The number of p-sites for each PK in the human liver PPN. The top 10 PKs with the most p-sites are marked in yellow.

Supplemental Table S15 – All PKs with significantly over- or under-represented p-sites in the human liver PPN (*p*-value < 0.01).

Supplemental Table S16 – The number of PPIs for each PK. The top 10 PKs with the most PPIs are marked in yellow.

Supplemental Table S17 – The number of p-sites for each PK in the mouse liver PPN. The top 10 PKs with the most p-sites are marked in yellow.

Supplemental Table S18 – All PKs with significantly over- or under-represented p-sites in the mouse liver PPN (*p*-value < 0.01).

Supplemental Table S19 – The statistical data on the experimentally identified and pre-calculated PPI information.

Supplemental Table S20 – The distribution of the predicted kinase-specific p-sites with the source of the PPIs.

Supplemental Table S1 – The statistical data on the experimentally identified p-sites collected in this study. The reference numbers are according to the main text. *a.* Sub., the number of phosphorylated substrates.

P-sites data	<i>S. cerevisiae</i>		<i>C. elegans</i>		<i>D. melanogaster</i>		<i>M. musculus</i>		<i>H. sapiens</i>	
	Sites	Sub. ^a	Sites	Sub.	Sites	Sub.	Sites	Sub.	Sites	Sub.
PhosphoPep v2.0	8,998	2,039	4,911	2,045	10,309	2,900	0	0	3,901	1,818
Phospho.ELM 8.3	50	23	3	2	16	7	5,246	2,139	12,720	3,748
SysPTM 1.1	9,106	2,397	0	0	2,709	1,472	7,598	3,372	13,051	4,467
PhosphoSitePlus	0	0	0	0	16	1	47,304	8,536	52,377	9,188
HPRD 9.0	0	0	0	0	0	0	0	0	15,515	4,086
Tan <i>et al.</i>	4,078	1,500	4,471	2,103	12,318	3,840	0	0	23,395	6,351
Xu <i>et al.</i>	0	0	0	0	0	0	0	0	5	1
Steen <i>et al.</i>	0	0	0	0	0	0	8	7	0	0
Villen <i>et al.</i>	0	0	0	0	0	0	1,723	1,073	0	0
Li <i>et al.</i>	1,484	784	0	0	0	0	0	0	0	0
Matsuoka <i>et al.</i>	0	0	0	0	0	0	0	0	901	600
Total	14,534	2,812	5,555	2,307	15,622	4,273	49,119	8,812	60,816	10,253

Supplemental Table S8 – The detailed information on the 56 STK and 21 TK specific predictors in GPS 2.0 and their corresponding PKs.

Predictor	<i>S. cerevisiae</i>	<i>C. elegans</i>	<i>D. melanogaster</i>	<i>M. musculus</i>	<i>H. sapiens</i>
TKL/STKR			C5WLU3	Q61271	Q8NER5
TKL/STKR				O35607	Q16671
TKL/STKR				P27040	Q13873
TKL/STKR				P27038	Q13705
TKL/STKR				Q91YR0	Q04771
TKL/STKR				Q64729	P37023
TKL/STKR		Q09488	Q9VMT1	P36898	P36897
TKL/STKR			Q9VZI9	P37172	P36896
TKL/STKR		P50488	A1Z7L9	A2AJR4	P36894
TKL/STKR				Q91ZR8	P27037
TKL/STKR				Q8K592	D2JYI1
TKL/STKR		P20792	Q7JQ36	P36895	B4DSV1
TKL/RAF		Q07292	P11346	Q61097	Q8IVT5
TKL/RAF		Q19380	Q24171	Q3UVC0	Q6VAB6
TKL/RAF				P28028	P15056
TKL/RAF				P04627	P10398
TKL/RAF		Q8T4N7		Q99N57	P04049
TKL/MLK		Q9NF64	Q4V4A7	Q8VDG6	Q5TCX8
TKL/MLK		O17055	Q9V400	B2RTJ7	Q59H18
TKL/MLK		Q9TZC4	Q9VW24	O55222	Q13418
TKL/MLK		Q8T7Z0	Q9VCV0	Q60700	Q12852
TKL/MLK				Q3U1V8	Q02779
TKL/MLK		Q21982		Q66L42	P80192
TKL/MLK				Q923A8	O43318
TKL/MLK		O01700	Q95UN8	Q1HKZ5	O43283
TKL/MLK				Q9ESL4	B8ZZU2
TKL/MLK		Q9XTC6	Q9V3Q6	Q80XI6	B2RDI6
TKL/IRAK				Q8K4B2	Q9Y616
TKL/IRAK		Q9XU80	Q05652	Q8R4K2	Q9NWZ3
TKL/IRAK				Q62406	P51617
TKL/IRAK				Q8CFA1	O43187
TK/VEGFR			Q8IQ00	P35918	P35968
TK/VEGFR			Q95P10	P35917	P35916
TK/VEGFR				P35969	P17948
TK/Trk				P15209	Q16620
TK/Trk		Q0MQ66		Q3UFB7	Q16288
TK/Trk				Q6VNS1	P04629
TK/Tie				Q8BGI2	Q02763
TK/Tie				B1AWS8	P35590
TK/Tec				P35991	Q08881
TK/Tec				B1AUL6	Q06187
TK/Tec				Q3U436	P51813
TK/Tec				P42682	P42681
TK/Tec			P08630	Q03526	P42680
TK/Syk			Q24145	P48025	P43405
TK/Syk				P43404	P43403
TK/Src				Q64434	Q9H3Y6
TK/Src				Q0VBH4	Q13882

TK/Src			Q8K2M8	P51451
TK/Src	Q45539	Q9V9J3	Q922K9	P42685
TK/Src	Q8T6F8	P00528	P39688	P12931
TK/Src			P05480	P09769
TK/Src			P25911	P07948
TK/Src			Q04736	P07947
TK/Src	Q9N3S5		Q8BGM0	P06241
TK/Src			P06240	P06239
TK/Src			A2AMC5	A8K4G3
TK/Ret		Q7KA88	P35546	P07949
TK/PDGFR			Q3UEW6	P36888
TK/PDGFR			P26618	P16234
TK/PDGFR			Q8C8K9	P10721
TK/PDGFR			P05622	P09619
TK/PDGFR			P09581	P07333
TK/Met	Q22489		Q62190	Q04912
TK/Met	Q9XVQ7		P16056	P08581
TK/JakA		Q24592	Q62137	P52333
TK/JakA			Q3TXE3	P29597
TK/JakA			B1ASP2	P23458
TK/JakA			Q62120	O60674
TK/InsR	Q968Y9	P09208	Q9WTL4	P14616
TK/InsR			Q60751	P08069
TK/InsR			P15208	P06213
TK/FGFR		Q09147	Q7TSI8	P22607
TK/FGFR	Q10656	Q07407	Q03142	P22455
TK/FGFR			P21803	P21802
TK/FGFR			P16092	P11362
TK/Fer/Fer;	Q22243		P70451	P16591
TK/Fer/Fer;	Q9U2U8	P18106	P16879	P07332
TK/Fer/Fer;	Q23136			
TK/Fer/Fer;	Q23102			
TK/Fer/Fer;	Q22766			
TK/Fer/Fer;	Q22765			
TK/Fer/Fer;	O02064			
TK/Fer/Fer;	B1Q276			
TK/Fer/Fer;	O01798			
TK/Fer/Fer;	Q9TYX4			
TK/Fer/Fer;	Q21764			
TK/Fer/Fer;	Q18684			
TK/Fer/Fer;	P34265			
TK/Fer/Fer;	Q22245			
TK/Fer/Fer;	Q21292			
TK/Fer/Fer;	Q21299			
TK/Fer/Fer;	Q19726			
TK/Fer/Fer;	Q9U3B5			
TK/Fer/Fer;	Q22146			
TK/Fer/Fer;	P91360			
TK/Fer/Fer;	Q20933			
TK/Fer/Fer;	O01325			
TK/Fer/Fer;	Q9TXI2			
TK/Fer/Fer;	Q19704			
TK/Fer/Fer;	O17755			

TK/Fer/Fer;		Q18865			
TK/Fer/Fer;		O61767			
TK/Fer/Fer;		Q18142			
TK/Fer/Fer;		Q9GZG1			
TK/Fer/Fer;		Q9N4S6			
TK/Fer/Fer;		Q9XW34			
TK/Fer/Fer;		O01774			
TK/Fer/Fer;		Q23538			
TK/Fer/Fer;		Q23554			
TK/Fer/Fer;		Q9XXE5			
TK/Fak				P34152	Q658W2
TK/Fak			Q0E917	Q9QVP9	Q14289
TK/Eph				B9EIV2	Q9UF33
TK/Eph				Q8BYG9	Q5JZY3
TK/Eph				Q8BSU8	Q15375
TK/Eph				Q80VZ2	P54764
TK/Eph				Q8CBF3	P54762
TK/Eph				Q8C7S3	P54760
TK/Eph				Q60629	P54756
TK/Eph				Q91YS9	P54753
TK/Eph				A3KG00	P29323
TK/Eph				A3KG07	P29322
TK/Eph				Q8BRB1	P29320
TK/Eph				Q3UNI2	P29317
TK/Eph				Q60750	P21709
TK/Eph		O61460	Q9V4E5	O08644	D3DXD3
TK/EGFR		P24348	P04412	B2KGF6	Q15303
TK/EGFR				Q61526	P21860
TK/EGFR				P70424	P04626
TK/EGFR				Q01279	P00533
TK/Csk		Q9BL77	Q9VGK8	P41242	P42679
TK/Csk				Q8VCW1	P41240
TK/Axl				Q60805	Q12866
TK/Axl				P55144	Q06418
TK/Axl				Q80YQ3	P30530
TK/AIk				P97793	Q9UM73
TK/AIk		O76411	Q7KJ08	P08923	P29376
TK/Abl				Q4JIM5	Q59FK4
TK/Abl		P03949	P00522	P00520	P42684
STE/STE-Unique/NIK				Q9WUL6	Q99558
STE/STE-Unique/COT				Q07174	P41279
STE/STE7		Q21307		Q9WVS7	Q13163
STE/STE7	P08018	Q95YI9	O62602	Q9JJE1	Q02750
STE/STE7	P32491	O01706	O61444	P70236	P52564
STE/STE7	P32490	Q20347	Q23977	O09110	P46734
STE/STE7		Q8MPS3		P47809	P45985
STE/STE7	P06784	Q10664	Q24324	Q9D7B0	P36507
STE/STE7		Q9UAH1		Q8CE90	O14733
STE/STE7		Q58AU8			
STE/STE7		Q58AU7			
STE/STE7		Q9TYV7			
STE/STE20	P08458	Q9NB31	Q8T0S6	Q8BPM2	Q9Y4K4
STE/STE20		Q9XTC8	P83098	Q9R0G8	Q9UKE5

STE/STE20	Q03497	Q9GRY2	Q9VE62	Q6P9R2	Q9UEW8
STE/STE20				Q99JT2	Q9P289
STE/STE20				Q8C015	Q9P286
STE/STE20				Q3ULB5	Q9NQJ5
STE/STE20				Q8BYC6	Q9H2K8
STE/STE20				Q3UUJ4	Q9C0K7
STE/STE20	P38692	Q17850	P10676	P70218	Q92918
STE/STE20				Q8K3H5	Q8NEV4
STE/STE20		Q11112	Q9W179	Q5SXG0	Q8N4C8
STE/STE20	P48562	Q23356	Q7KV88	Q99JP0	Q8IVH8
STE/STE20		O17566	Q9VXE5	B9EKN8	Q7Z2Y5
STE/STE20				Q8K4T3	Q7RTN6
STE/STE20				Q5F2E8	Q7L7X3
STE/STE20				Q99KH8	Q5U0E6
STE/STE20		Q18637	Q9VEV1	B7ZNR8	Q53TX8
STE/STE20		P46549	Q0KHQ5	Q9JI10	Q13188
STE/STE20				Q8CIN4	Q13177
STE/STE20				O88643	Q13153
STE/STE20		Q22553	Q9VEN3	Q9JI11	Q13043
STE/STE20		Q9XWL8	B7Z0W0	Q61161	Q12851
STE/STE20				Q8BTW9	O96013
STE/STE20	Q12469	Q23290	A1ZBH7	Q9Z1W9	O95747
STE/STE20				O54988	O94804
STE/STE20				Q6IR17	O00506
STE/STE20				B1ATW8	D3DRA1
STE/STE20				Q1EG27	C9J3X5
STE/STE20				A3KGC1	B2RCU6
STE/STE20				Q6ZQ29	A7MCZ2
STE/STE11				Q61083	Q9Y2U5
STE/STE11				Q61084	Q99759
STE/STE11	P25390			O35099	Q99683
STE/STE11	P27636	Q21029	Q9VDS9	A2AQW0	Q6ZN16
STE/STE11	Q01389			Q3UVM5	Q56UN5
STE/STE11	P53599			P53349	Q13233
STE/STE11	P23561	O01837	Q95YH7	Q9WTR2	O95382
STE/STE11				Q6PDG6	B9EG75
Other/Wnk				Q80XP9	Q9H4A3
Other/Wnk		Q18657	Q9VP17	P83741	Q96J92
Other/Wnk				Q3UH66	B1AKG2
Other/Wnk				Q80UE6	A6PVR3
Other/PLK		Q20845		Q6P571	Q9NYY3
Other/PLK		P34331	O97143	Q4FZD7	Q9H4B4
Other/PLK	P32562	Q9N2L7	P52304	Q07832	P53350
Other/PLK				P53351	O00444
Other/PLK				Q64702	
Other/PEK	P15442	Q9XVY4	Q9V9X8	A2AUM0	Q9P2K8
Other/PEK		Q19192	Q9NIV1	Q69ZK8	Q9BQI3
Other/PEK				Q03963	P19525
Other/PEK		Q9NAK3		Q9Z2B5	B2RCU9
Other/NEK		Q6AW07		B2RXX0	Q96PY6
Other/NEK				Q9ES74	Q8TDX7
Other/NEK				Q8K1R7	Q8TD19
Other/NEK				Q8C0Q4	Q8NG66

Other/NEK				Q91ZR4	Q86SG6
Other/NEK		001775		Q3UGM2	Q6ZWH5
Other/NEK	P22209	P84199	Q9W3N8	Q7TSC3	Q6P3R8
Other/NEK				Q6GTE9	P51957
Other/NEK		Q19530	Q9VC32	Q9R0A5	P51956
Other/NEK				Q91Z18	P51955
Other/NEK				Q9ES70	B7Z2D9
Other/IKK			Q9VEZ5	Q8C2I3	Q9UHD2
Other/IKK			Q9V3Y8	Q5D0E0	Q14164
Other/IKK				Q9WUN2	O15111
Other/IKK				Q8CBT3	O14920
Other/CK2	P15790			Q61177	P68400
Other/CK2	P19454	P18334	P08181	O54833	P19784
Other/AUR/IPL1-yeast	P38991				
Other/AUR/AUR-B				Q8C6C1	C7G533
Other/AUR/AUR-A				P97477	O14965
Other/AUR		O01427	Q9VGF9	O88445	Q9UQB9
Other/AUR		Q21271	Q9VKN7		
CMGC/MAPK		Q8IG56		O54949	Q9UBE8
CMGC/MAPK	P36005	Q9XXC0	O62618	Q80Y86	Q8TD08
CMGC/MAPK	P32485	Q8WQG9	Q23993	Q61532	Q16659
CMGC/MAPK		Q17446		Q5U421	Q16539
CMGC/MAPK		Q8MXI4		Q569F1	Q15759
CMGC/MAPK	P16892	Q9U3L3	P83100	Q9WVS8	Q13164
CMGC/MAPK		Q9U9Y8		O08911	P53778
CMGC/MAPK		Q9XTI6		Q5NCK8	P45984
CMGC/MAPK	P14681	O44408	P92208	Q6P5G0	P31152
CMGC/MAPK	P41808	P39745	P40417	P63085	P28482
CMGC/MAPK	Q00772	Q11179	Q9W354	Q63844	P27361
CMGC/MAPK		O44514		Q9Z1B7	O15264
CMGC/MAPK		Q19243		Q91Y86	D3DX92
CMGC/MAPK		O44182	O61443	Q80W82	A8MTD8
CMGC/GSK	P38615	Q9N667	Q9VK37	Q9WV60	P49841
CMGC/GSK	P50873	Q9XX60	P18431	Q2NL51	P49840
CMGC/GSK	P21965	Q09595	P83101		
CMGC/GSK	Q12222	P91267			
CMGC/GSK		Q93372			
CMGC/GSK		Q93344			
CMGC/GSK		Q9U2Q9			
CMGC/DYRK	P14680	Q8WQL7	Q9VX06	Q9Z188	Q9Y463
CMGC/DYRK		Q966P6	P83102	Q8BI55	Q9NR20
CMGC/DYRK				A2AQH3	Q9H422
CMGC/DYRK				Q9QZR5	Q9H2X6
CMGC/DYRK		Q19632	Q9Y145	Q5U4C9	Q92630
CMGC/DYRK		Q19727		Q3V016	Q8NE63
CMGC/DYRK				A9R9X0	Q86Z02
CMGC/DYRK		Q9XTF3	Q9V3D5	Q61214	Q13627
CMGC/DYRK				C7G3P2	Q13523
CMGC/DYRK		Q966P5	Q9W0Q1	Q922Y0	O43781
CMGC/CDK/CDC2	P00546	O61847	P23573	P97377	Q00526
CMGC/CDK/CDC2		P34556	P23572	P11440	P24941
CMGC/CDK/CDC2					P06493
CMGC/CDK		Q09437	Q9VPC0	Q14AX6	Q9NYV4

CMGC/CDK		A4V4W9	Q9VP22	Q8BWD8	Q9BWU1
CMGC/CDK				Q3V3A1	Q96Q40
CMGC/CDK	P17157	Q9XTR1	A1Z840	Q9JHU3	Q8IZL9
CMGC/CDK	P06242	O18142	Q7K306	Q3UMM4	Q15131
CMGC/CDK		Q23357		Q69ZA1	Q14004
CMGC/CDK				Q8K0D0	Q00537
CMGC/CDK				Q04735	Q00536
CMGC/CDK	P43568	Q9TVL3	C9QP81	P49615	Q00535
CMGC/CDK	P39073	Q9Y0G1	P48609	Q64261	Q00534
CMGC/CDK		Q17794	Q7KM05	Q99J95	P50750
CMGC/CDK	Q03957	O17903	O17432	Q03147	P50613
CMGC/CDK		C8JQR0	Q9VD82	Q8R3L8	P49336
CMGC/CDK				P24788	P21127
CMGC/CDK	P23293	P90866	Q24216	P30285	P11802
CMGC/CDK				O35495	O94921
CMGC/CDK				Q04899	B4DK03
CMGC				Q9WVS4	Q9UQ07
CMGC				Q9JKV2	Q9UPZ9
CMGC				O54781	Q9UPE1
CMGC		P90932	Q8T3S1	O35493	Q9HAZ1
CMGC				O70551	Q96SB4
CMGC	Q03656	Q17917	Q9VL64	B1AU43	Q8IVW4
CMGC		Q03563		O35492	Q59FC5
CMGC	P32581	Q9BHM0	A4V3J9	Q3TZA2	Q2NME9
CMGC		Q20643	Q9VXN5	Q8CEQ0	Q00532
CMGC				O35491	P49760
CMGC				Q04859	P20794
CMGC	P32350	Q9U2H1	Q1RKV9	Q3UTQ8	O76039
CMGC				Q9Z0G2	C9JQJ0
CMGC		C0Z1Y5	Q9GSP5	Q9QUK0	B4DH08
CMGC				Q3UXB6	B4DFW7
CK1		Q93521	Q7JWT4	Q99K78	Q9Y6M4
CK1		P34635	Q9VQE3	Q6PCN3	Q9HCP0
CK1		Q22203	Q7KRY6	Q8BN21	Q99986
CK1	P29295	P42168	P54367	Q8BK63	Q8N752
CK1		Q21026			Q8IV63
CK1		O18107		Q8K3G5	Q86Y07
CK1		Q9NAP8	Q8IMC6	A2AW15	Q6IQ55
CK1		P34633	Q7KMI3	Q3UWH3	Q5TCY1
CK1		Q18189	Q9VYN5	Q6P2B2	P78368
CK1	P23292	Q8WQ99	O76324	Q9DC28	P49674
CK1	P39962	Q22518	Q9VEX2	Q8C4X2	P48730
CK1	P23291	Q20471	Q9VJC2	Q9JMK2	D3DQG1
CK1		Q22033			
CK1		Q3S1L3			
CK1		O45897			
CK1		O44751			
CK1		Q23103			
CK1		Q22573			
CK1		O44192			
CK1		Q22223			
CK1		Q9XVK4			
CK1		Q21590			

CK1	P34516
CK1	P91332
CK1	Q20018
CK1	Q9XVP6
CK1	Q19794
CK1	Q18984
CK1	Q18976
CK1	Q18882
CK1	O17693
CK1	Q18707
CK1	Q09503
CK1	Q17960
CK1	Q17651
CK1	Q17631
CK1	P42169
CK1	O01429
CK1	Q9N3T7
CK1	Q9N4H2
CK1	Q9N4E5
CK1	O01773
CK1	P91566
CK1	Q23566
CK1	Q19848
CK1	Q19798
CK1	Q19784
CK1	Q94277
CK1	O02157
CK1	Q95PZ9
CK1	Q966G1
CK1	Q966G2
CK1	O01899
CK1	Q9TXU0
CK1	Q20288
CK1	Q20160
CK1	O76711
CK1	O76712
CK1	O44777
CK1	Q18738
CK1	Q17853
CK1	Q18553
CK1	Q7KQ32
CK1	O44950
CK1	Q93288
CK1	O01733
CK1	Q17825
CK1	Q17448
CK1	O62426
CK1	Q9BHK8
CK1	Q9BL55
CK1	Q9N4Q0
CK1	P91571
CK1	Q23546
CK1	D0VWM6

CK1		Q20192			
CK1		Q20193			
CK1		Q19742			
CK1		Q21204			
CK1		Q19043			
CAMK/RAD53	P22216	A4F324	A4V0X0	Q9Z265	O96017
CAMK/RAD53	P39009	Q9U1Y5			
CAMK/PKD				Q62101	Q9BZL6
CAMK/PKD		O45818		Q8BZ03	Q1KKQ2
CAMK/PKD		Q9XUJ7	Q9VE91	Q5FWX6	O94806
CAMK/PHK				P07934	Q16816
CAMK/PHK		Q9N3L4	Q7K4Y9	A6H632	P15735
CAMK/MLCK		Q23260	A8DYP0	Q3UIZ8	Q9H1R3
CAMK/MLCK		Q23551	Q7KQP6	Q8VCR8	Q86YV6
CAMK/MLCK		Q8ISF7		B1B1A8	Q32MK0
CAMK/MLCK		O01761	A1ZA66	Q5SUV5	Q15746
CAMK/MLCK			A1Z7Y7		D3DPF9
CAMK/MAPKAPK		Q21360	P49071	O54992	Q8IW41
CAMK/MAPKAPK		Q9TZ16	Q9VGI4	Q3UMW7	Q16644
CAMK/MAPKAPK		Q22005		P49138	P49137
CAMK/MAPKAPK				Q3U1I8	B5BUJ6
CAMK/MAPKAPK				Q8CDB0	A4CYL7
CAMK/DAPK				Q8VDF3	Q9UIK4
CAMK/DAPK					Q9UEE5
CAMK/DAPK				Q80YE7	Q59H88
CAMK/DAPK				Q8BG48	O94768
CAMK/DAPK		O44997	Q0KHT7	O54784	O43293
CAMK/CAMKL/LKB		Q9GN62	Q8T9L5	Q9WTK7	Q15831
CAMK/CAMKL/CHK1	P38147	O44546	O61661	O35280	O14757
CAMK/CAMKL/CHK1		Q86S44			
CAMK/CAMKL/CHK1		Q9N3Z3			
CAMK/CAMKL/CHK1		Q9NF25			
CAMK/CAMKL/CHK1		Q59DM0			
CAMK/CAMKL/AMPK		P45894		Q5EG47	Q13131
CAMK/CAMKL/AMPK	P06782	Q95ZQ4	O18645	B1ASQ8	P54646
CAMK/CAMKL	Q03002	Q21017	Q95SH0	B7ZNH4	Q9Y2K2
CAMK/CAMKL	P13186	A7WK47	Q9V8V8	Q32M05	Q9P0L2
CAMK/CAMKL	P34244	Q9TW45	Q9VGQ0	A0AUV4	Q9NRH2
CAMK/CAMKL	P31374	Q19469	Q9W532	Q8C0V7	Q9H0K1
CAMK/CAMKL	P25389	D1MN54	Q9VUV4	Q3UTA8	Q96RG2
CAMK/CAMKL	Q01919	Q22855	Q7YU19	Q8C0X8	Q96L34
CAMK/CAMKL	Q12152	Q9TXI1	Q4QQA7	Q5RJI5	Q8TDC3
CAMK/CAMKL	Q12263	O17879	Q9VGP9	Q69Z98	Q8IY84
CAMK/CAMKL	P13185		Q9VPW3	B2RQ72	Q8IWQ3
CAMK/CAMKL	Q08217		Q0E981	A2AQX6	Q7KZI7
CAMK/CAMKL				Q3UT86	Q53GX0
CAMK/CAMKL				A0JLX3	P57059
CAMK/CAMKL				Q9QYZ6	P57058
CAMK/CAMKL				Q9QYZ3	P27448
CAMK/CAMKL				Q9QYZ5	O60285
CAMK/CAMKL				B9EKK5	B4E0Y5
CAMK/CAMKL				Q8C0N0	
CAMK/CAMKL				Q8CIP4	

CAMK/CAMKL				Q9JKE5	
CAMK/CAMKL				Q571J8	
CAMK/CAMKL				Q14DQ3	
CAMK/CAMKL				Q3TPU1	
CAMK/CAMKL				Q8BHI9	
CAMK/CAMKL				Q8BZN4	
CAMK/CAMKL				Q641K5	
CAMK/CAMKL				Q8CEE6	
CAMK/CAMKL				Q6P4S6	
CAMK/CAMKL				Q8CFH6	
CAMK/CAMKL				Q60670	
CAMK/CAMKL				B9EK90	
CAMK/CAMK2				Q80TN1	Q7LDD5
CAMK/CAMK2				Q6PHZ2	Q13557
CAMK/CAMK2		O62305	A4V133	Q923T9	Q13555
CAMK/CAMK2				Q5SVJ0	Q13554
CAMK/CAMK1	P38622			Q91VB2	Q96NX5
CAMK/CAMK1	P22517			Q8BW96	Q5SQQ7
CAMK/CAMK1	P38623	Q9TXJ0	Q7JMV3	Q8BGR3	Q16566
CAMK/CAMK1				Q91YS8	Q14012
CAMK/CAMK1	P27466			Q9QYK9	B4E1A6
CAMK		O61821		Q62070	Q9P1W9
CAMK	Q03533	Q20443	Q9V3Z1	Q9JLM8	Q9C098
CAMK	P28708	P54936	Q9VCL7	Q924X7	Q9BYT3
CAMK				Q9D411	Q9BXA7
CAMK				Q8C1R0	Q9BXA6
CAMK				A2AAJ9	Q96RU8
CAMK				Q8K4K3	Q96RU7
CAMK				Q91YA2	Q96QS6
CAMK				Q6P8M9	Q96PN8
CAMK				Q9D2E1	Q96PF2
CAMK				Q8K4K2	Q92519
CAMK		Q17737	Q9VE58	Q6PGN3	Q8N568
CAMK				Q8K4K4	Q8N2I9
CAMK		Q23128		P58750	Q86V86
CAMK				Q80YU1	Q6SA08
CAMK				Q0KL02	Q15772
CAMK				Q7TNL3	P11801
CAMK		O62424		Q8CFN8	P11309
CAMK				Q62407	O75962
CAMK				A2CG49	O60229
CAMK		O44747	Q8T4D4	Q8BWQ5	O15075
CAMK	P36003	Q95QC4	Q7PLI7	O70589	B7ZKY2
CAMK	P24719	Q19962	Q24210	Q3UHL1	B2RDF9
CAMK				Q925K9	A6NGQ3
Atypical/PIKK/FRAP	P32600	Q95Q95	Q9VK45	Q9JLN9	P42345
Atypical/PIKK/FRAP	P35169				
Atypical/PIKK/DNAPK				P97313	P78527
Atypical/PIKK/ATR	P38111	Q22258	Q9VXG8	Q9JKK8	Q13535
Atypical/PIKK/ATM	P38110	Q9N3Q4	Q5EAK6	Q62388	Q13315
Atypical/PIKK		Q6A4L2	A8DY44	Q3UH32	Q9Y4A5
Atypical/PIKK	P38811	O01510	Q70PP2	Q8BKX6	Q96Q15
Atypical/PDHK	P40530	Q02332		O70571	Q16654

Atypical/PDHK				Q9JK42	Q15119
Atypical/PDHK				Q3U5E5	Q15118
Atypical/PDHK	P53170		P91622	Q3UC13	O14874
Atypical/PDHK				Q922H2	B4DXG6
AGC/SGK				Q9WVC6	Q9HBY8
AGC/SGK		Q2PJ68		Q9QZS5	Q96BR1
AGC/SGK				Q9ERE3	O00141
AGC/RSK				A2CEE7	Q9UK32
AGC/RSK	P53739	Q9NAH6	Q9VR61	Q9Z1M4	Q9UBS0
AGC/RSK				Q810V8	Q15418
AGC/RSK				Q9WUT3	Q15349
AGC/RSK				P18654	P51812
AGC/RSK		Q21734		Q5SWG1	P23443
AGC/RSK	P38070	Q18846	Q9V3I5	Q3U3M8	O75676
AGC/RSK	P25341	Q86DC2	Q94533	Q8C050	O75582
AGC/PKG		O76360	P32023	Q61410	Q13237
AGC/PKG		Q8MQE4	Q9VL34	P0C605	A5YM56
AGC/PKG			Q03042		
AGC/PKC			A1Z9X0	P28867	Q05655
AGC/PKC				Q02956	Q05513
AGC/PKC		Q19266	P13678	Q02111	Q04759
AGC/PKC				P16054	Q02156
AGC/PKC				Q5DTK3	P41743
AGC/PKC				Q8K2K8	P24723
AGC/PKC		P34885	P83099	Q4VA93	P17252
AGC/PKC	P24583	P90980	P05130	P63318	P05129
AGC/PKC		P34722	P13677	P68404	D3DWF5
AGC/PKB	Q12236	Q9UA62	C7LAC8	Q9Z2A0	O15530
AGC/PKB	Q03407	Q9Y1J3			
AGC/PKB	Q03306				
AGC/PKA	P05986	Q7JP68	Q53XD8	P68181	P51817
AGC/PKA			P16912		P22694
AGC/PKA	P06244		Q9VA47	P05132	P22612
AGC/PKA					P17612
AGC/PKA	P06245	P21137	P12370	Q922R0	O43930
AGC/GRK				O70293	Q8WTQ7
AGC/GRK				Q9WVL4	Q15835
AGC/GRK				Q8VEB1	P43250
AGC/GRK		Q09639	P32865	Q3UYH7	P35626
AGC/GRK				Q3V151	P34947
AGC/GRK					P32298
AGC/GRK		Q09537	P32866	Q99MK8	P25098
AGC/DMPK;				P70335	Q13464
AGC/DMPK/ROCK					
AGC/DMPK;		P92199	Q9VXE3	P70336	O75116
AGC/DMPK/ROCK					
AGC/DMPK			Q9W1B0	B2RQQ7	Q9Y5S2
AGC/DMPK				Q80UW5	Q6DT37
AGC/DMPK				B2RXX8	Q5VT25
AGC/DMPK		O01583	Q9VTY8	P49025	Q2M5E1
AGC/DMPK				P54265	Q09013
AGC/AKT	P11792	Q9XTG7	Q8INB9	Q9WUA6	Q9Y243
AGC/AKT	P12688	Q17941		Q60823	P31751

AGC/AKT	P18961			Q6GSA6	P31749
AGC				Q8R2S1	Q9Y6S9
AGC	P53894	Q2L6W9	Q9NBK5	Q9R1L5	Q9Y2H9
AGC		Q20821	Q9VEA9	B2KFR4	Q9Y2H1
AGC				Q9JJX8	Q9NY57
AGC		Q21483	Q9VN23	Q7TSJ6	Q9NRM7
AGC				Q8BLK9	Q96S38
AGC				Q5SYL1	Q96LW2
AGC		B6VQ53	A1Z7T4	A2AQY2	Q96GX5
AGC				Q8BGW6	Q8WU08
AGC				Q8QZV4	Q86UX6
AGC				Q8K045	Q6P5Z2
AGC	P22204	O45797	Q24590	B1AST8	Q6P0Q8
AGC				Q3TBR3	Q16513
AGC				P70268	Q16512
AGC		Q8MYQ1	Q9VWQ2	Q91VJ4	Q15208
AGC				Q8BYR2	O95835
AGC	P32328	D3KFW7	Q95TN8	Q3U214	O60307
AGC	P43565	Q19858	Q9VUQ9	Q811L6	B5MCH9

Supplemental Table S9 – The detailed performance of the iGPS algorithm for the no PPI, STRING and experimental PPI (STRING & Exp. PPI), and only experimental PPI (Exp. PPI) information. The *Ac*, *Sn*, *Sp*, *MCC* and *Kpr* were extensively calculated for the three thresholds.

Predictor	Threshold	No PPI					String & Exp. PPI					Exp. PPI				
		<i>Ac</i>	<i>Sn</i>	<i>Sp</i>	<i>MCC</i>	<i>Kpr</i>	<i>Ac</i>	<i>Sn</i>	<i>Sp</i>	<i>MCC</i>	<i>Kpr</i>	<i>Ac</i>	<i>Sn</i>	<i>Sp</i>	<i>MCC</i>	<i>Kpr</i>
AGC	High	97.04%	38.56%	98.26%	0.3347	16.89%	98.01%	15.88%	99.73%	0.2881	35.75%	97.96%	1.32%	99.98%	0.0877	64.94%
AGC	Medium	94.53%	54.73%	95.36%	0.3069	13.10%	97.84%	21.55%	99.44%	0.2998	30.16%	97.94%	1.80%	99.95%	0.0859	59.51%
AGC	Low	91.93%	64.65%	92.50%	0.2876	11.44%	97.67%	25.24%	99.19%	0.3037	26.64%	97.91%	2.08%	99.92%	0.0804	54.79%
AGC/AKT	High	98.04%	87.78%	98.16%	0.5544	20.12%	99.18%	82.22%	99.38%	0.7023	37.58%	99.19%	68.89%	99.54%	0.6595	69.60%
AGC/AKT	Medium	94.85%	91.11%	94.90%	0.3845	14.58%	98.52%	84.44%	98.69%	0.5962	30.08%	98.75%	70.00%	99.09%	0.5699	58.67%
AGC/AKT	Low	92.00%	95.56%	91.96%	0.3262	12.45%	98.16%	88.89%	98.27%	0.5711	25.45%	98.40%	71.11%	98.72%	0.5230	51.74%
AGC/DMPK	High	93.65%	89.74%	93.73%	0.4200	30.74%	98.33%	71.79%	98.83%	0.6136	51.03%	98.04%	46.15%	99.03%	0.4576	75.47%
AGC/DMPK	Medium	87.68%	92.31%	87.60%	0.3123	24.73%	96.90%	74.36%	97.32%	0.4939	45.36%	96.95%	46.15%	97.91%	0.3542	69.84%
AGC/DMPK	Low	80.53%	92.31%	80.30%	0.2407	21.19%	96.04%	74.36%	96.45%	0.4447	40.26%	96.42%	46.15%	97.37%	0.3230	66.67%
AGC/DMPK/ROCK	High	93.66%	89.47%	93.74%	0.4251	30.67%	98.23%	71.05%	98.76%	0.6046	50.35%	97.97%	47.37%	98.97%	0.4633	75.47%
AGC/DMPK/ROCK	Medium	85.75%	89.47%	85.68%	0.2835	24.89%	96.70%	71.05%	97.21%	0.4728	45.70%	96.81%	47.37%	97.78%	0.3585	70.97%
AGC/DMPK/ROCK	Low	80.27%	92.11%	80.04%	0.2420	21.33%	95.94%	73.68%	96.38%	0.4432	40.72%	96.10%	47.37%	97.05%	0.3193	67.65%
AGC/GRK	High	95.28%	66.67%	97.20%	0.6154	23.02%	96.25%	45.24%	99.68%	0.6248	64.29%	96.10%	42.86%	99.68%	0.6059	97.56%
AGC/GRK	Medium	94.01%	88.10%	94.40%	0.6458	16.08%	96.63%	57.14%	99.28%	0.6777	49.57%	96.63%	52.38%	99.60%	0.6713	94.12%
AGC/GRK	Low	92.28%	92.86%	92.25%	0.6123	11.83%	96.70%	60.71%	99.12%	0.6904	37.43%	96.78%	55.95%	99.52%	0.6899	89.66%
AGC/PKA	High	97.80%	64.99%	98.35%	0.4977	16.26%	98.59%	36.34%	99.64%	0.4704	34.36%	98.51%	23.87%	99.76%	0.3804	63.76%
AGC/PKA	Medium	95.24%	80.37%	95.49%	0.4145	12.47%	98.40%	43.50%	99.32%	0.4656	28.02%	98.35%	27.85%	99.53%	0.3646	58.16%
AGC/PKA	Low	92.06%	89.12%	92.11%	0.3573	11.18%	98.12%	47.75%	98.96%	0.4461	25.09%	98.14%	30.24%	99.28%	0.3436	53.89%
AGC/PKB	High	97.64%	88.89%	97.81%	0.6235	11.92%	98.79%	77.78%	99.22%	0.7140	20.11%	98.68%	66.67%	99.33%	0.6599	45.31%
AGC/PKB	Medium	94.56%	97.22%	94.51%	0.4908	9.77%	98.13%	86.11%	98.37%	0.6589	17.43%	98.02%	75.00%	98.49%	0.6031	41.03%
AGC/PKB	Low	90.71%	97.22%	90.58%	0.3884	9.16%	97.42%	86.11%	97.65%	0.5944	15.68%	97.36%	75.00%	97.81%	0.5423	36.26%
AGC/PKC	High	96.87%	39.24%	98.13%	0.3357	17.89%	98.05%	26.95%	99.61%	0.3939	41.83%	97.98%	18.20%	99.73%	0.3210	72.96%
AGC/PKC	Medium	94.34%	61.94%	95.05%	0.3430	14.58%	97.82%	41.84%	99.05%	0.4419	36.55%	97.76%	29.31%	99.26%	0.3589	67.33%
AGC/PKC	Low	91.81%	73.76%	92.20%	0.3304	12.87%	97.70%	50.59%	98.74%	0.4745	33.28%	97.68%	36.17%	99.03%	0.3918	63.21%
AGC/PKG	High	97.66%	85.71%	97.88%	0.5931	20.30%	98.94%	57.14%	99.70%	0.6600	42.98%	98.77%	45.24%	99.74%	0.5808	81.08%
AGC/PKG	Medium	94.04%	90.48%	94.11%	0.4280	15.74%	98.47%	59.52%	99.18%	0.5738	36.60%	98.38%	45.24%	99.35%	0.4947	75.00%
AGC/PKG	Low	90.60%	90.48%	90.60%	0.3454	12.87%	98.26%	59.52%	98.96%	0.5423	33.14%	98.21%	45.24%	99.18%	0.4665	69.77%
AGC/RSK	High	96.99%	80.65%	97.24%	0.4879	17.37%	98.35%	61.29%	98.92%	0.5248	31.16%	98.38%	33.87%	99.36%	0.3810	46.99%

AGC/RSK	Medium	94.11%	90.32%	94.17%	0.4002	13.78%	97.60%	67.74%	98.06%	0.4745	27.51%	97.82%	37.10%	98.75%	0.3286	41.75%
AGC/RSK	Low	91.57%	91.94%	91.56%	0.3433	11.66%	97.19%	69.35%	97.61%	0.4500	23.61%	97.46%	37.10%	98.38%	0.2971	37.72%
AGC/SGK	High	95.86%	89.29%	95.97%	0.4849	18.92%	98.23%	89.29%	98.39%	0.6543	41.61%	98.05%	42.86%	99.01%	0.4187	63.41%
AGC/SGK	Medium	91.22%	89.29%	91.26%	0.3459	12.92%	97.26%	89.29%	97.40%	0.5673	30.57%	97.50%	42.86%	98.45%	0.3603	56.25%
AGC/SGK	Low	87.02%	89.29%	86.98%	0.2820	10.77%	96.40%	89.29%	96.53%	0.5130	26.22%	96.95%	42.86%	97.89%	0.3197	55.10%
Atypical/PDHK	High	97.50%	100%	97.37%	0.8057	50.00%	100%	100%	100%	1.0000	100%	97.50%	50.00%	100%	0.6980	100%
Atypical/PDHK	Medium	88.75%	100%	88.16%	0.5208	19.05%	98.75%	100%	98.68%	0.8885	100%	96.25%	50.00%	98.68%	0.5585	100%
Atypical/PDHK	Low	80.00%	100%	78.95%	0.3974	12.50%	98.75%	100%	98.68%	0.8885	100%	96.25%	50.00%	98.68%	0.5585	100%
Atypical/PIKK	High	97.59%	65.96%	98.13%	0.4869	40.38%	98.61%	32.98%	99.73%	0.4655	50.00%	98.38%	4.26%	99.98%	0.1823	63.51%
Atypical/PIKK	Medium	93.55%	92.55%	93.56%	0.4103	26.32%	98.31%	54.26%	99.06%	0.5097	36.34%	98.36%	7.45%	99.91%	0.2044	52.88%
Atypical/PIKK	Low	89.89%	95.74%	89.79%	0.3423	19.24%	97.93%	56.38%	98.64%	0.4730	27.70%	98.34%	7.45%	99.89%	0.1959	46.33%
Atypical/PIKK/ATM	High	96.28%	96.49%	96.28%	0.5071	39.57%	98.74%	92.98%	98.83%	0.7040	51.52%	98.61%	82.46%	98.85%	0.6464	65.96%
Atypical/PIKK/ATM	Medium	94.79%	100%	94.71%	0.4557	25.30%	98.31%	96.49%	98.33%	0.6616	36.78%	98.23%	85.96%	98.41%	0.6116	55.83%
Atypical/PIKK/ATM	Low	94.46%	100%	94.38%	0.4439	17.85%	98.28%	96.49%	98.31%	0.6588	26.59%	98.20%	85.96%	98.39%	0.6088	49.63%
Atypical/PIKK/ATR	High	98.49%	100%	98.47%	0.6848	55.56%	99.31%	100%	99.30%	0.8136	63.89%	99.31%	90.00%	99.44%	0.7861	69.23%
Atypical/PIKK/ATR	Medium	97.11%	100%	97.07%	0.5596	38.03%	99.31%	100%	99.30%	0.8136	49.02%	99.31%	90.00%	99.44%	0.7861	62.50%
Atypical/PIKK/ATR	Low	96.70%	100%	96.65%	0.5332	28.13%	98.90%	100%	98.88%	0.7412	37.31%	98.90%	90.00%	99.02%	0.7068	57.14%
Atypical/PIKK/DNAPK	High	97.83%	100%	97.79%	0.6409	52.63%	99.33%	61.90%	99.92%	0.7552	70.00%	99.33%	61.90%	99.92%	0.7552	66.67%
Atypical/PIKK/DNAPK	Medium	94.30%	100%	94.21%	0.4516	32.09%	99.03%	61.90%	99.62%	0.6638	48.89%	99.03%	61.90%	99.62%	0.6638	60.87%
Atypical/PIKK/DNAPK	Low	91.45%	100%	91.32%	0.3769	25.14%	98.88%	61.90%	99.47%	0.6286	40.35%	98.88%	61.90%	99.47%	0.6286	50.00%
Atypical/PIKK/FRAP	High	96.97%	93.33%	97.08%	0.6709	32.81%	97.98%	93.33%	98.12%	0.7448	38.18%	97.98%	93.33%	98.12%	0.7448	64.29%
Atypical/PIKK/FRAP	Medium	92.73%	93.33%	92.71%	0.4939	26.52%	96.97%	93.33%	97.08%	0.6709	31.53%	96.97%	93.33%	97.08%	0.6709	46.51%
Atypical/PIKK/FRAP	Low	91.11%	93.33%	91.04%	0.4531	20.22%	96.77%	93.33%	96.88%	0.6584	26.09%	96.77%	93.33%	96.88%	0.6584	40.00%
CAMK	High	95.50%	58.48%	96.08%	0.3152	25.81%	98.33%	19.38%	99.56%	0.2740	42.48%	98.49%	3.46%	99.97%	0.1496	70.59%
CAMK	Medium	89.65%	77.16%	89.85%	0.2615	19.70%	97.90%	25.61%	99.03%	0.2625	35.12%	98.46%	4.84%	99.92%	0.1493	60.14%
CAMK	Low	83.90%	86.16%	83.86%	0.2281	16.88%	97.66%	30.45%	98.70%	0.2739	31.14%	98.44%	5.54%	99.89%	0.1505	55.66%
CAMK/CAMK1	High	96.17%	94.12%	96.18%	0.3795	27.59%	99.23%	76.47%	99.41%	0.6148	40.24%	99.37%	52.94%	99.73%	0.5604	80.00%
CAMK/CAMK1	Medium	88.32%	100%	88.23%	0.2331	21.43%	98.83%	76.47%	99.00%	0.5281	35.71%	99.23%	52.94%	99.59%	0.5106	71.43%
CAMK/CAMK1	Low	84.66%	100%	84.55%	0.2006	17.47%	98.51%	76.47%	98.68%	0.4809	31.45%	99.05%	52.94%	99.41%	0.4607	64.52%
CAMK/CAMK2	High	97.72%	57.45%	98.29%	0.4192	26.43%	98.56%	30.85%	99.52%	0.3761	46.71%	98.48%	9.57%	99.73%	0.1727	71.11%
CAMK/CAMK2	Medium	94.26%	89.36%	94.33%	0.3884	21.26%	98.45%	56.38%	99.04%	0.4976	40.34%	98.34%	18.09%	99.47%	0.2354	60.00%
CAMK/CAMK2	Low	90.26%	95.74%	90.19%	0.3215	18.42%	98.25%	59.57%	98.80%	0.4868	35.81%	98.19%	19.15%	99.31%	0.2232	56.79%
CAMK/CAMKL	High	95.35%	83.95%	95.48%	0.3725	29.03%	98.37%	49.38%	98.93%	0.4065	47.24%	98.39%	13.58%	99.37%	0.1569	68.57%
CAMK/CAMKL	Medium	89.24%	95.06%	89.18%	0.2774	22.20%	97.61%	55.56%	98.09%	0.3634	38.92%	97.96%	17.28%	98.89%	0.1519	59.34%

CAMK/CAMKL	Low	83.99%	96.30%	83.85%	0.2262	18.82%	96.93%	55.56%	97.41%	0.3197	35.19%	97.61%	17.28%	98.53%	0.1319	55.10%
CAMK/CAMKL/AMPK	High	96.79%	97.44%	96.78%	0.4587	30.48%	99.13%	51.28%	99.59%	0.5221	45.67%	99.06%	33.33%	99.68%	0.4037	61.29%
CAMK/CAMKL/AMPK	Medium	91.83%	100%	91.76%	0.3081	23.73%	98.65%	53.85%	99.07%	0.4313	38.65%	98.82%	35.90%	99.41%	0.3577	53.85%
CAMK/CAMKL/AMPK	Low	87.82%	100%	87.71%	0.2510	20.26%	98.50%	53.85%	98.93%	0.4101	35.68%	98.74%	35.90%	99.34%	0.3438	51.22%
CAMK/CAMKL/CHK1	High	94.54%	100%	94.39%	0.5548	32.39%	98.06%	53.33%	99.28%	0.5866	52.17%	97.89%	46.67%	99.28%	0.5346	72.73%
CAMK/CAMKL/CHK1	Medium	88.91%	100%	88.61%	0.4128	23.29%	97.36%	53.33%	98.55%	0.5028	40.00%	97.54%	46.67%	98.92%	0.4887	64.29%
CAMK/CAMKL/CHK1	Low	85.04%	100%	84.63%	0.3563	19.63%	97.18%	53.33%	98.37%	0.4866	34.67%	97.54%	46.67%	98.92%	0.4887	54.55%
CAMK/CAMKL/LKB	High	97.11%	88.24%	97.20%	0.4572	25.73%	99.10%	70.59%	99.39%	0.6161	52.00%	99.10%	11.76%	100%	0.3414	83.33%
CAMK/CAMKL/LKB	Medium	91.58%	88.24%	91.61%	0.2779	20.18%	98.32%	70.59%	98.60%	0.4849	45.16%	99.10%	11.76%	100%	0.3414	75.00%
CAMK/CAMKL/LKB	Low	88.57%	88.24%	88.57%	0.2360	17.69%	97.95%	70.59%	98.24%	0.4464	43.08%	99.04%	11.76%	99.94%	0.2774	75.00%
CAMK/DAPK	High	95.98%	79.31%	96.37%	0.5022	23.26%	98.42%	65.52%	99.19%	0.6471	32.48%	98.19%	31.03%	99.76%	0.4754	62.96%
CAMK/DAPK	Medium	91.33%	89.66%	91.37%	0.3953	16.57%	98.35%	72.41%	98.95%	0.6604	25.95%	98.19%	37.93%	99.60%	0.5026	55.88%
CAMK/DAPK	Low	87.16%	89.66%	87.10%	0.3243	14.88%	98.11%	72.41%	98.71%	0.6317	25.00%	98.19%	37.93%	99.60%	0.5026	54.29%
CAMK/MAPKAPK	High	96.62%	89.19%	96.77%	0.5447	27.59%	98.16%	48.65%	99.11%	0.4908	45.88%	98.11%	40.54%	99.22%	0.4407	80.65%
CAMK/MAPKAPK	Medium	92.78%	94.59%	92.75%	0.4180	19.42%	97.19%	51.35%	98.07%	0.4037	35.34%	97.19%	43.24%	98.23%	0.3580	65.22%
CAMK/MAPKAPK	Low	89.56%	94.59%	89.46%	0.3509	16.52%	96.72%	51.35%	97.60%	0.3721	30.30%	96.78%	43.24%	97.81%	0.3297	60.00%
CAMK/MLCK	High	98.08%	100%	97.96%	0.8571	18.18%	97.12%	50.00%	100%	0.6965	40.00%	95.19%	16.67%	100%	0.3982	100%
CAMK/MLCK	Medium	91.35%	100%	90.82%	0.6027	14.94%	97.12%	50.00%	100%	0.6965	40.00%	95.19%	16.67%	100%	0.3982	100%
CAMK/MLCK	Low	84.62%	100%	83.67%	0.4777	13.33%	97.12%	50.00%	100%	0.6965	40.00%	95.19%	16.67%	100%	0.3982	100%
CAMK/PHK	High	95.33%	100%	95.17%	0.6260	34.88%	96.73%	42.86%	98.55%	0.4462	60.00%	96.42%	33.33%	98.55%	0.3638	70.00%
CAMK/PHK	Medium	91.90%	100%	91.63%	0.5134	20.33%	96.57%	42.86%	98.39%	0.4329	31.03%	96.26%	33.33%	98.39%	0.3515	46.67%
CAMK/PHK	Low	87.23%	100%	86.80%	0.4207	16.67%	95.48%	42.86%	97.26%	0.3620	24.32%	95.33%	33.33%	97.42%	0.2944	35.00%
CAMK/PKD	High	95.71%	100%	95.63%	0.5467	21.97%	98.05%	40.00%	99.20%	0.4375	76.47%	97.86%	20.00%	99.40%	0.2731	100%
CAMK/PKD	Medium	91.23%	100%	91.05%	0.4069	19.08%	97.27%	40.00%	98.41%	0.3513	60.00%	97.47%	20.00%	99.01%	0.2265	100%
CAMK/PKD	Low	86.94%	100%	86.68%	0.3355	16.50%	97.08%	40.00%	98.21%	0.3361	55.17%	97.27%	20.00%	98.81%	0.2099	83.33%
CAMK/RAD53	High	97.76%	100%	97.71%	0.6793	28.22%	99.06%	76.47%	99.52%	0.7599	42.31%	99.06%	76.47%	99.52%	0.7599	81.25%
CAMK/RAD53	Medium	93.87%	100%	93.74%	0.4806	20.98%	98.00%	76.47%	98.44%	0.6090	34.00%	98.00%	76.47%	98.44%	0.6090	77.14%
CAMK/RAD53	Low	89.03%	100%	88.81%	0.3705	18.08%	97.52%	76.47%	97.95%	0.5647	28.80%	97.52%	76.47%	97.95%	0.5647	74.36%
CK1	High	92.73%	58.75%	93.68%	0.3182	28.77%	97.46%	21.25%	99.58%	0.3430	54.55%	97.16%	8.75%	99.62%	0.1745	68.42%
CK1	Medium	87.42%	73.75%	87.80%	0.2890	16.29%	97.43%	33.75%	99.20%	0.4146	39.56%	97.03%	15.00%	99.31%	0.2243	64.52%
CK1	Low	82.72%	76.25%	82.90%	0.2461	11.49%	97.03%	35.00%	98.75%	0.3763	29.01%	96.62%	15.00%	98.89%	0.1861	57.14%
CMGC	High	94.70%	59.05%	95.55%	0.3552	26.58%	97.52%	14.97%	99.50%	0.2398	36.54%	97.71%	2.14%	100%	0.1390	61.44%
CMGC	Medium	87.36%	86.02%	87.39%	0.3167	20.96%	97.29%	21.22%	99.11%	0.2647	30.45%	97.68%	2.30%	99.96%	0.1152	56.57%
CMGC	Low	79.37%	91.28%	79.08%	0.2545	17.22%	96.92%	22.37%	98.70%	0.2403	26.68%	97.66%	2.30%	99.94%	0.1016	53.03%

CMGC/CDK	High	95.63%	63.40%	96.31%	0.3945	28.67%	97.51%	39.48%	98.75%	0.3862	45.72%	97.40%	17.29%	99.11%	0.2124	66.93%
CMGC/CDK	Medium	90.86%	95.97%	90.75%	0.3955	23.56%	97.13%	62.82%	97.86%	0.4784	41.64%	97.15%	25.36%	98.68%	0.2574	60.81%
CMGC/CDK	Low	85.69%	98.56%	85.41%	0.3250	19.05%	96.57%	64.27%	97.26%	0.4475	36.57%	96.94%	25.94%	98.46%	0.2460	57.89%
CMGC/CDK/CDC2	High	95.77%	66.67%	96.35%	0.4048	31.34%	97.84%	59.82%	98.60%	0.5136	52.53%	98.18%	42.47%	99.29%	0.4715	78.79%
CMGC/CDK/CDC2	Medium	90.70%	98.63%	90.54%	0.3914	26.26%	97.21%	89.50%	97.36%	0.5903	47.76%	97.78%	60.73%	98.52%	0.5114	71.65%
CMGC/CDK/CDC2	Low	83.71%	99.09%	83.41%	0.2960	21.01%	96.24%	89.95%	96.37%	0.5325	41.95%	97.29%	61.19%	98.01%	0.4698	68.80%
CMGC/DYRK	High	90.72%	57.14%	91.27%	0.2077	29.46%	96.47%	38.10%	97.43%	0.2562	39.13%	97.55%	28.57%	98.67%	0.2606	63.16%
CMGC/DYRK	Medium	83.28%	66.67%	83.55%	0.1673	18.72%	95.71%	42.86%	96.57%	0.2513	30.30%	97.16%	28.57%	98.29%	0.2332	57.14%
CMGC/DYRK	Low	78.07%	71.43%	78.18%	0.1492	15.59%	94.94%	47.62%	95.71%	0.2506	28.00%	96.63%	33.33%	97.66%	0.2350	56.52%
CMGC/GSK	High	91.57%	77.65%	91.87%	0.3373	25.51%	97.28%	45.88%	98.37%	0.4011	35.88%	97.21%	24.71%	98.75%	0.2562	55.81%
CMGC/GSK	Medium	81.21%	89.41%	81.04%	0.2495	19.79%	96.45%	54.12%	97.35%	0.3881	23.60%	96.67%	28.24%	98.12%	0.2447	45.71%
CMGC/GSK	Low	77.17%	95.29%	76.78%	0.2386	15.90%	95.98%	60.00%	96.75%	0.3936	20.06%	96.25%	29.41%	97.67%	0.2308	40.24%
CMGC/MAPK	High	95.67%	60.40%	96.39%	0.3744	26.19%	98.03%	52.48%	98.96%	0.5062	34.37%	98.18%	40.59%	99.36%	0.4697	64.40%
CMGC/MAPK	Medium	90.93%	89.11%	90.97%	0.3641	20.53%	97.38%	73.93%	97.87%	0.5421	27.84%	97.69%	58.09%	98.50%	0.4953	60.33%
CMGC/MAPK	Low	86.31%	92.41%	86.18%	0.3053	17.03%	96.96%	76.90%	97.37%	0.5240	24.45%	97.34%	60.07%	98.10%	0.4731	56.11%
Other/AUR	High	95.81%	80.00%	96.30%	0.5517	24.68%	96.99%	8.00%	99.79%	0.2007	48.30%	96.86%	2.67%	99.83%	0.0871	66.25%
Other/AUR	Medium	90.72%	90.67%	90.72%	0.4346	17.30%	96.86%	9.33%	99.62%	0.1915	38.12%	96.74%	4.00%	99.66%	0.0944	58.33%
Other/AUR	Low	84.89%	96.00%	84.54%	0.3614	14.54%	96.42%	9.33%	99.16%	0.1402	31.73%	96.42%	4.00%	99.33%	0.0654	53.70%
Other/AUR/AUR-A	High	96.39%	100%	96.29%	0.6392	26.03%	98.96%	67.86%	99.80%	0.7786	45.28%	98.86%	64.29%	99.80%	0.7554	81.48%
Other/AUR/AUR-A	Medium	90.79%	100%	90.54%	0.4503	18.13%	98.29%	67.86%	99.12%	0.6698	32.00%	98.29%	64.29%	99.22%	0.6584	73.33%
Other/AUR/AUR-A	Low	85.94%	100%	85.56%	0.3689	14.73%	97.91%	67.86%	98.73%	0.6241	23.53%	97.91%	64.29%	98.83%	0.6103	66.67%
Other/AUR/AUR-B	High	95.87%	93.33%	95.95%	0.6139	24.73%	96.49%	50.00%	97.98%	0.4516	50.00%	96.90%	26.67%	99.15%	0.3509	54.05%
Other/AUR/AUR-B	Medium	89.99%	100%	89.67%	0.4602	17.47%	94.84%	53.33%	96.17%	0.3805	41.67%	96.39%	30.00%	98.51%	0.3244	50.00%
Other/AUR/AUR-B	Low	83.90%	100%	83.39%	0.3667	14.99%	93.29%	53.33%	94.57%	0.3270	36.84%	95.77%	30.00%	97.87%	0.2833	46.30%
Other/AUR/IPL1-yeast	High	94.62%	100%	94.39%	0.6384	22.08%	98.49%	84.21%	99.10%	0.8130	50.00%	98.06%	73.68%	99.10%	0.7470	63.64%
Other/AUR/IPL1-yeast	Medium	86.02%	100%	85.43%	0.4396	15.15%	97.63%	84.21%	98.21%	0.7375	43.24%	97.20%	73.68%	98.21%	0.6704	53.85%
Other/AUR/IPL1-yeast	Low	80.00%	100%	79.15%	0.3664	12.94%	96.77%	84.21%	97.31%	0.6784	40.00%	96.34%	73.68%	97.31%	0.6117	50.00%
Other/CK2	High	93.72%	72.90%	94.31%	0.4167	24.11%	97.32%	40.50%	98.93%	0.4445	57.25%	97.28%	33.96%	99.08%	0.4036	82.19%
Other/CK2	Medium	88.50%	81.31%	88.70%	0.3385	14.52%	96.79%	45.48%	98.25%	0.4229	38.97%	96.83%	38.01%	98.50%	0.3822	73.66%
Other/CK2	Low	84.30%	85.98%	84.25%	0.3016	10.39%	96.66%	48.60%	98.02%	0.4296	29.62%	96.72%	41.12%	98.30%	0.3925	63.64%
Other/IKK	High	97.08%	95.92%	97.11%	0.6706	17.74%	98.76%	87.76%	99.08%	0.7936	28.74%	98.60%	73.47%	99.31%	0.7351	53.95%
Other/IKK	Medium	92.64%	95.92%	92.55%	0.4849	10.71%	97.70%	87.76%	97.98%	0.6853	19.76%	97.81%	73.47%	98.50%	0.6422	42.27%
Other/IKK	Low	89.72%	97.96%	89.49%	0.4265	8.10%	97.08%	89.80%	97.28%	0.6469	15.36%	97.42%	75.51%	98.04%	0.6149	34.71%
Other/NEK	High	98.72%	100%	98.68%	0.8442	17.72%	97.45%	53.85%	98.94%	0.5724	27.59%	97.45%	53.85%	98.94%	0.5724	47.06%

Other/NEK	Medium	95.66%	100%	95.51%	0.6433	11.97%	96.43%	53.85%	97.89%	0.4829	18.60%	96.43%	53.85%	97.89%	0.4829	44.44%
Other/NEK	Low	93.62%	100%	93.40%	0.5653	9.33%	96.17%	53.85%	97.63%	0.4658	14.29%	96.17%	53.85%	97.63%	0.4658	38.10%
Other/PEK	High	99.56%	100%	99.53%	0.9678	43.18%	98.24%	75.00%	100%	0.8579	60.87%	98.24%	75.00%	100%	0.8579	73.68%
Other/PEK	Medium	96.04%	100%	95.73%	0.7828	22.47%	98.24%	75.00%	100%	0.8579	38.89%	98.24%	75.00%	100%	0.8579	66.67%
Other/PEK	Low	95.15%	100%	94.79%	0.7495	17.07%	97.80%	75.00%	99.53%	0.8210	28.00%	97.80%	75.00%	99.53%	0.8210	58.33%
Other/PLK	High	93.58%	97.67%	93.51%	0.4350	29.59%	98.68%	93.02%	98.78%	0.7235	61.63%	98.64%	48.84%	99.51%	0.5508	86.67%
Other/PLK	Medium	87.04%	100%	86.82%	0.3185	20.12%	97.81%	95.35%	97.85%	0.6370	50.00%	98.21%	48.84%	99.07%	0.4737	78.79%
Other/PLK	Low	81.98%	100%	81.66%	0.2663	15.57%	97.29%	95.35%	97.32%	0.5953	44.36%	97.93%	48.84%	98.78%	0.4380	74.29%
Other/Wnk	High	96.51%	66.67%	97.59%	0.5599	10.81%	98.26%	50.00%	100%	0.7008	33.33%	98.26%	50.00%	100%	0.7008	75.00%
Other/Wnk	Medium	95.35%	66.67%	96.39%	0.4944	8.00%	98.26%	50.00%	100%	0.7008	30.00%	98.26%	50.00%	100%	0.7008	75.00%
Other/Wnk	Low	93.02%	66.67%	93.98%	0.4069	5.88%	98.26%	50.00%	100%	0.7008	20.00%	98.26%	50.00%	100%	0.7008	75.00%
STE/STE11	High	95.42%	63.64%	95.84%	0.3139	28.30%	98.31%	45.45%	99.02%	0.4096	26.92%	98.43%	45.45%	99.14%	0.4273	43.75%
STE/STE11	Medium	90.83%	72.73%	91.08%	0.2459	18.39%	97.23%	54.55%	97.80%	0.3572	18.60%	97.83%	54.55%	98.41%	0.4049	33.33%
STE/STE11	Low	83.47%	72.73%	83.62%	0.1711	14.68%	96.26%	54.55%	96.82%	0.3051	16.67%	96.98%	54.55%	97.56%	0.3420	32.00%
STE/STE20	High	97.13%	75.00%	97.59%	0.5300	17.05%	98.30%	45.59%	99.39%	0.5180	32.41%	98.27%	25.00%	99.79%	0.4145	52.08%
STE/STE20	Medium	93.73%	85.29%	93.90%	0.4189	11.33%	97.97%	51.47%	98.93%	0.4969	24.67%	98.03%	26.47%	99.51%	0.3656	39.19%
STE/STE20	Low	91.04%	86.76%	91.13%	0.3591	9.03%	97.58%	51.47%	98.54%	0.4537	20.07%	97.76%	26.47%	99.24%	0.3221	35.80%
STE/STE7	High	97.08%	75.00%	97.86%	0.6311	35.48%	97.94%	65.00%	99.11%	0.6746	48.48%	97.77%	60.00%	99.11%	0.6394	77.78%
STE/STE7	Medium	94.33%	100%	94.13%	0.5960	25.23%	97.77%	90.00%	98.04%	0.7371	44.68%	97.77%	85.00%	98.22%	0.7208	76.00%
STE/STE7	Low	91.92%	100%	91.64%	0.5230	18.54%	97.59%	90.00%	97.86%	0.7239	36.84%	97.59%	85.00%	98.04%	0.7069	73.08%
STE/STE-Unique/COT	High	98.03%	100%	97.98%	0.7378	37.50%	99.01%	60.00%	100%	0.7707	36.36%	98.03%	20.00%	100%	0.4428	25.00%
STE/STE-Unique/COT	Medium	93.10%	100%	92.93%	0.4945	26.67%	98.52%	60.00%	99.49%	0.6635	28.57%	97.54%	20.00%	99.49%	0.3059	20.00%
STE/STE-Unique/COT	Low	90.15%	100%	89.90%	0.4240	20.34%	98.03%	60.00%	98.99%	0.5899	21.05%	97.54%	20.00%	99.49%	0.3059	16.67%
STE/STE-Unique/NIK	High	96.46%	100%	96.40%	0.5669	18.18%	99.12%	100%	99.10%	0.8128	40.00%	99.12%	100%	99.10%	0.8128	66.67%
STE/STE-Unique/NIK	Medium	92.92%	100%	92.79%	0.4308	11.76%	99.12%	100%	99.10%	0.8128	33.33%	99.12%	100%	99.10%	0.8128	50.00%
STE/STE-Unique/NIK	Low	80.53%	100%	80.18%	0.2585	5.88%	98.23%	100%	98.20%	0.7007	22.22%	98.23%	100%	98.20%	0.7007	50.00%
TK/Abl	High	91.81%	68.00%	94.14%	0.5569	28.04%	92.70%	54.00%	96.48%	0.5296	38.02%	91.81%	30.00%	97.85%	0.3775	50.75%
TK/Abl	Medium	85.77%	80.00%	86.33%	0.4759	22.64%	90.57%	64.00%	93.16%	0.5022	32.70%	90.57%	32.00%	96.29%	0.3333	43.37%
TK/Abl	Low	81.49%	82.00%	81.45%	0.4217	16.94%	88.97%	66.00%	91.21%	0.4711	26.63%	89.15%	32.00%	94.73%	0.2862	36.00%
TK/Alk	High	76.67%	100%	74.07%	0.4714	47.06%	78.33%	100%	75.93%	0.4897	80.00%	75.00%	66.67%	75.93%	0.2836	85.71%
TK/Alk	Medium	71.67%	100%	68.52%	0.4228	40.00%	76.67%	100%	74.07%	0.4714	66.67%	73.33%	66.67%	74.07%	0.2667	85.71%
TK/Alk	Low	68.33%	100%	64.81%	0.3944	32.00%	76.67%	100%	74.07%	0.4714	53.33%	73.33%	66.67%	74.07%	0.2667	85.71%
TK/Axl	High	91.43%	100%	90.82%	0.6303	32.35%	93.33%	100%	92.86%	0.6814	52.38%	94.29%	100%	93.88%	0.7110	78.57%
TK/Axl	Medium	86.67%	100%	85.71%	0.5345	26.83%	90.48%	100%	89.80%	0.6081	47.83%	91.43%	100%	90.82%	0.6303	78.57%

TK/Axl	Low	80.95%	100%	79.59%	0.4543	22.45%	88.57%	100%	87.76%	0.5686	42.31%	89.52%	100%	88.78%	0.5876	73.33%
TK/Csk	High	95.88%	100%	95.73%	0.6647	21.43%	98.82%	100%	98.78%	0.8607	30.00%	98.82%	100%	98.78%	0.8607	37.50%
TK/Csk	Medium	92.94%	100%	92.68%	0.5558	11.32%	97.65%	100%	97.56%	0.7651	17.65%	97.65%	100%	97.56%	0.7651	23.08%
TK/Csk	Low	90.00%	100%	89.63%	0.4836	10.34%	96.47%	100%	96.34%	0.6941	13.64%	96.47%	100%	96.34%	0.6941	22.22%
TK/EGFR	High	90.79%	84.85%	91.60%	0.6516	29.48%	92.96%	77.27%	95.08%	0.6851	36.06%	92.60%	66.67%	96.11%	0.6405	55.84%
TK/EGFR	Medium	86.46%	90.91%	85.86%	0.5884	21.95%	92.24%	83.33%	93.44%	0.6836	27.45%	91.70%	71.21%	94.47%	0.6254	48.11%
TK/EGFR	Low	79.96%	95.45%	77.87%	0.5142	17.74%	90.07%	87.88%	90.37%	0.6467	23.08%	89.71%	75.76%	91.60%	0.5889	42.47%
TK/Eph	High	91.78%	100%	91.25%	0.6213	35.29%	95.89%	77.27%	97.08%	0.6761	65.52%	96.16%	72.73%	97.67%	0.6760	94.74%
TK/Eph	Medium	87.40%	100%	86.59%	0.5293	23.30%	94.52%	77.27%	95.63%	0.6135	48.72%	94.79%	72.73%	96.21%	0.6067	85.71%
TK/Eph	Low	83.29%	100%	82.22%	0.4668	19.51%	93.70%	77.27%	94.75%	0.5822	40.43%	93.97%	72.73%	95.34%	0.5728	78.26%
TK/Fak	High	90.60%	92.31%	90.50%	0.5450	17.44%	94.87%	76.92%	95.93%	0.6109	35.14%	93.16%	46.15%	95.93%	0.3935	52.94%
TK/Fak	Medium	85.47%	92.31%	85.07%	0.4497	12.40%	91.88%	76.92%	92.76%	0.5079	25.49%	91.03%	46.15%	93.67%	0.3262	34.62%
TK/Fak	Low	77.78%	92.31%	76.92%	0.3575	11.76%	89.32%	76.92%	90.05%	0.4465	25.45%	89.32%	46.15%	91.86%	0.2870	34.62%
TK/Fer/Fer	High	92.00%	60.00%	95.56%	0.5556	20.00%	94.00%	60.00%	97.78%	0.6389	50.00%	90.00%	0%	100%	N/A	100%
TK/Fer/Fer	Medium	92.00%	80.00%	93.33%	0.6340	16.28%	94.00%	60.00%	97.78%	0.6389	40.00%	90.00%	0%	100%	N/A	100%
TK/Fer/Fer	Low	88.00%	80.00%	88.89%	0.5379	14.04%	94.00%	60.00%	97.78%	0.6389	31.58%	90.00%	0%	100%	N/A	100%
TK/Fer/Fes	High	93.59%	77.78%	95.65%	0.7017	36.00%	97.44%	77.78%	100%	0.8694	69.23%	97.44%	77.78%	100%	0.8694	90.00%
TK/Fer/Fes	Medium	91.03%	77.78%	92.75%	0.6245	18.87%	97.44%	77.78%	100%	0.8694	45.00%	97.44%	77.78%	100%	0.8694	69.23%
TK/Fer/Fes	Low	79.49%	88.89%	78.26%	0.4705	15.07%	92.31%	77.78%	94.20%	0.6607	34.62%	92.31%	77.78%	94.20%	0.6607	69.23%
TK/FGFR	High	88.89%	96.77%	87.74%	0.6695	34.78%	95.47%	74.19%	98.58%	0.7855	42.86%	95.47%	70.97%	99.06%	0.7830	61.54%
TK/FGFR	Medium	83.95%	96.77%	82.08%	0.5860	22.73%	94.65%	74.19%	97.64%	0.7506	30.28%	95.06%	70.97%	98.58%	0.7638	48.48%
TK/FGFR	Low	77.78%	96.77%	75.00%	0.5049	17.78%	94.24%	74.19%	97.17%	0.7344	23.74%	95.06%	70.97%	98.58%	0.7638	42.67%
TK/InsR	High	91.96%	87.88%	92.72%	0.7331	27.10%	93.38%	75.76%	96.64%	0.7428	39.18%	94.09%	74.24%	97.76%	0.7652	54.07%
TK/InsR	Medium	88.42%	90.91%	87.96%	0.6668	20.86%	92.43%	77.27%	95.24%	0.7164	31.08%	93.14%	75.76%	96.36%	0.7351	48.70%
TK/InsR	Low	83.45%	93.94%	81.51%	0.5960	16.91%	91.49%	78.79%	93.84%	0.6937	26.56%	92.20%	77.27%	94.96%	0.7094	44.32%
TK/JakA	High	96.43%	87.80%	97.24%	0.7924	33.58%	96.64%	80.49%	98.16%	0.7865	41.05%	96.43%	78.05%	98.16%	0.7707	59.68%
TK/JakA	Medium	90.76%	90.24%	90.80%	0.6175	21.43%	95.80%	82.93%	97.01%	0.7518	28.08%	95.59%	80.49%	97.01%	0.7359	46.43%
TK/JakA	Low	87.18%	90.24%	86.90%	0.5437	16.72%	94.96%	82.93%	96.09%	0.7168	22.78%	94.75%	80.49%	96.09%	0.7007	38.61%
TK/Met	High	95.06%	100%	93.94%	0.8612	30.86%	98.77%	100%	98.48%	0.9609	42.02%	98.77%	100%	98.48%	0.9609	72.58%
TK/Met	Medium	91.36%	100%	89.39%	0.7807	21.61%	98.15%	100%	97.73%	0.9426	30.91%	98.15%	100%	97.73%	0.9426	64.29%
TK/Met	Low	84.57%	100%	81.06%	0.6649	16.61%	96.30%	100%	95.45%	0.8919	24.06%	96.30%	100%	95.45%	0.8919	57.69%
TK/PDGFR	High	89.48%	90.91%	89.34%	0.6008	22.69%	93.81%	88.64%	94.33%	0.7041	29.12%	93.20%	79.55%	94.56%	0.6511	55.68%
TK/PDGFR	Medium	84.74%	95.45%	83.67%	0.5360	16.28%	92.78%	93.18%	92.74%	0.6902	21.15%	92.16%	84.09%	92.97%	0.6375	43.22%
TK/PDGFR	Low	78.97%	97.73%	77.10%	0.4704	12.87%	90.93%	95.45%	90.48%	0.6522	16.37%	90.31%	86.36%	90.70%	0.5994	36.36%

TK/Ret	High	96.30%	100%	95.52%	0.8869	31.48%	98.77%	92.86%	100%	0.9565	48.48%	98.77%	92.86%	100%	0.9565	88.89%
TK/Ret	Medium	92.59%	100%	91.04%	0.7983	22.37%	98.77%	92.86%	100%	0.9565	38.10%	98.77%	92.86%	100%	0.9565	69.57%
TK/Ret	Low	87.65%	100%	85.07%	0.7045	18.68%	97.53%	92.86%	98.51%	0.9136	34.78%	97.53%	92.86%	98.51%	0.9136	69.57%
TK/Src	High	91.15%	53.40%	94.58%	0.4542	18.34%	92.91%	42.52%	97.49%	0.4716	31.38%	92.57%	34.69%	97.83%	0.4174	52.34%
TK/Src	Medium	86.80%	63.61%	88.92%	0.4017	14.03%	91.63%	52.04%	95.23%	0.4635	25.27%	91.26%	42.18%	95.73%	0.3996	46.52%
TK/Src	Low	81.90%	70.75%	82.91%	0.3608	11.79%	90.47%	58.16%	93.41%	0.4576	21.81%	90.21%	46.60%	94.18%	0.3897	41.65%
TK/Syk	High	92.48%	89.23%	92.95%	0.7223	19.54%	93.07%	83.08%	94.55%	0.7193	34.48%	91.88%	72.31%	94.77%	0.6501	53.64%
TK/Syk	Medium	88.12%	96.92%	86.82%	0.6570	15.86%	91.68%	90.77%	91.82%	0.7077	30.25%	90.10%	76.92%	92.05%	0.6173	50.88%
TK/Syk	Low	82.18%	96.92%	80.00%	0.5627	13.40%	88.91%	90.77%	88.64%	0.6464	25.64%	87.52%	76.92%	89.09%	0.5590	44.44%
TK/Tec	High	95.97%	100%	95.61%	0.7984	27.46%	97.85%	93.33%	98.25%	0.8653	38.20%	97.85%	93.33%	98.25%	0.8653	79.07%
TK/Tec	Medium	89.78%	100%	88.89%	0.6262	19.12%	95.97%	93.33%	96.20%	0.7785	30.91%	95.97%	93.33%	96.20%	0.7785	68.00%
TK/Tec	Low	84.14%	100%	82.75%	0.5281	15.27%	94.62%	93.33%	94.74%	0.7285	26.12%	94.62%	93.33%	94.74%	0.7285	58.62%
TK/Tie	High	92.21%	100%	91.55%	0.6766	28.57%	94.81%	83.33%	95.77%	0.6950	33.33%	92.21%	0%	100%	N/A	N/A
TK/Tie	Medium	89.61%	100%	88.73%	0.6167	20.00%	94.81%	83.33%	95.77%	0.6950	23.81%	92.21%	0%	100%	N/A	N/A
TK/Tie	Low	83.12%	100%	81.69%	0.5079	14.29%	94.81%	83.33%	95.77%	0.6950	15.15%	92.21%	0%	100%	N/A	N/A
TK/Trk	High	98.78%	92.31%	100%	0.9539	20.69%	98.78%	92.31%	100%	0.9539	52.17%	91.46%	46.15%	100%	0.6473	85.71%
TK/Trk	Medium	92.68%	100%	91.30%	0.7904	14.94%	100%	100%	100%	1.0000	40.63%	91.46%	46.15%	100%	0.6473	66.67%
TK/Trk	Low	87.80%	100%	85.51%	0.6952	11.61%	100%	100%	100%	1.0000	30.23%	91.46%	46.15%	100%	0.6473	60.00%
TK/VEGFR	High	92.00%	100%	91.16%	0.7035	32.47%	94.50%	89.47%	95.03%	0.7367	47.92%	96.00%	89.47%	96.69%	0.7919	74.19%
TK/VEGFR	Medium	86.50%	100%	85.08%	0.5928	22.81%	94.50%	89.47%	95.03%	0.7367	35.82%	96.00%	89.47%	96.69%	0.7919	61.54%
TK/VEGFR	Low	82.00%	100%	80.11%	0.5261	17.81%	94.50%	89.47%	95.03%	0.7367	27.91%	96.00%	89.47%	96.69%	0.7919	48.98%
TKL/IRAK	High	99.00%	100%	98.98%	0.8123	21.05%	100%	100%	100%	1.0000	36.36%	100%	100%	100%	1.0000	57.14%
TKL/IRAK	Medium	95.50%	100%	95.41%	0.5418	11.43%	100%	100%	100%	1.0000	19.05%	100%	100%	100%	1.0000	44.44%
TKL/IRAK	Low	92.50%	100%	92.35%	0.4409	7.84%	100%	100%	100%	1.0000	17.39%	100%	100%	100%	1.0000	44.44%
TKL/MLK	High	91.98%	100%	91.81%	0.4426	43.66%	99.32%	100%	99.31%	0.8698	65.91%	98.51%	62.50%	99.31%	0.6379	78.26%
TKL/MLK	Medium	85.05%	100%	84.72%	0.3280	29.63%	98.78%	100%	98.75%	0.7950	52.73%	98.23%	62.50%	99.03%	0.5973	66.67%
TKL/MLK	Low	79.48%	100%	79.03%	0.2752	22.70%	98.37%	100%	98.33%	0.7496	44.62%	97.96%	62.50%	98.75%	0.5632	64.29%
TKL/RAF	High	97.77%	83.33%	98.17%	0.6701	29.17%	97.32%	16.67%	99.54%	0.2782	36.36%	97.32%	16.67%	99.54%	0.2782	50.00%
TKL/RAF	Medium	92.86%	83.33%	93.12%	0.4329	20.00%	96.88%	16.67%	99.08%	0.2212	28.57%	96.88%	16.67%	99.08%	0.2212	50.00%
TKL/RAF	Low	90.62%	83.33%	90.83%	0.3803	15.73%	95.98%	16.67%	98.17%	0.1621	22.22%	95.98%	16.67%	98.17%	0.1621	50.00%
TKL/STKR	High	94.17%	100%	93.93%	0.6199	16.67%	98.65%	66.67%	100%	0.8108	26.09%	98.65%	66.67%	100%	0.8108	46.15%
TKL/STKR	Medium	91.48%	100%	91.12%	0.5412	9.09%	98.21%	66.67%	99.53%	0.7471	19.35%	98.21%	66.67%	99.53%	0.7471	40.00%
TKL/STKR	Low	88.79%	100%	88.32%	0.4835	6.47%	97.31%	66.67%	98.60%	0.6526	13.33%	97.31%	66.67%	98.60%	0.6526	33.33%
STKs	High	94.02%	73.10%	94.60%	0.4227	35.95%	97.63%	49.25%	98.96%	0.5159	53.71%	97.58%	36.21%	99.27%	0.4460	76.83%

TKs	High	91.05%	76.54%	92.71%	0.5985	22.09%	93.53%	63.55%	96.95%	0.6334	44.59%	92.97%	52.37%	97.61%	0.5750	63.86%
All PKs	High	93.84%	73.80%	94.49%	0.4489	33.77%	97.37%	52.17%	98.84%	0.5437	51.31%	97.29%	39.51%	99.17%	0.4777	72.17%
STKs	Medium	87.16%	86.89%	87.17%	0.3367	28.96%	97.11%	60.28%	98.12%	0.5174	48.27%	97.24%	44.27%	98.70%	0.4486	72.67%
TKs	Medium	86.23%	82.26%	86.68%	0.5191	16.52%	92.59%	68.72%	95.31%	0.6145	37.08%	92.11%	56.28%	96.20%	0.5515	56.67%
All PKs	Medium	87.10%	85.95%	87.14%	0.3563	27.24%	96.82%	62.00%	97.96%	0.5393	45.62%	96.92%	46.72%	98.55%	0.4736	67.24%
STKs	Low	80.84%	90.94%	80.56%	0.2819	24.79%	96.64%	63.11%	97.56%	0.4963	43.47%	96.98%	46.67%	98.37%	0.4383	68.69%
TKs	Low	80.79%	85.34%	80.27%	0.4511	13.51%	91.33%	71.09%	93.64%	0.5838	31.72%	91.08%	58.52%	94.80%	0.5239	51.12%
All PKs	Low	80.84%	89.79%	80.55%	0.2985	23.25%	96.30%	64.74%	97.33%	0.5167	40.69%	96.61%	49.09%	98.16%	0.4606	62.65%

Supplemental Table S10 – To further evaluate the performance of the iGPS algorithm, the Lpr values were thoroughly calculated for each PK. a. Pre., predicted hits.

Predictor	Threshold	No PPI			String & Exp. PPI			Exp. PPI		
		Total	Pre. ^a	Lpr	Total	Pre.	Lpr	Total	Pre.	Lpr
AGC	High	120,876	10,257	76.43%	12,740	970	73.73%	3,077	220	72.03%
AGC	Medium	120,876	18,974	61.78%	12,740	1,866	59.04%	3,077	430	57.07%
AGC	Low	120,876	25,450	52.50%	12,740	2,538	49.80%	3,077	573	46.30%
AGC/AKT	High	120,876	9,703	75.08%	19,784	1,494	73.52%	2,366	255	81.44%
AGC/AKT	Medium	120,876	19,223	62.27%	19,784	3,026	60.77%	2,366	428	66.83%
AGC/AKT	Low	120,876	26,341	54.11%	19,784	4,201	52.91%	2,366	554	57.29%
AGC/DMPK	High	120,876	5,441	55.57%	5,870	331	64.53%	413	44	81.23%
AGC/DMPK	Medium	120,876	12,362	41.33%	5,870	690	48.96%	413	80	69.03%
AGC/DMPK	Low	120,876	18,975	36.30%	5,870	1,009	41.82%	413	105	60.67%
AGC/DMPK/ROCK	High	120,876	5,354	54.85%	4,473	248	63.93%	327	37	82.32%
AGC/DMPK/ROCK	Medium	120,876	12,342	41.24%	4,473	492	45.45%	327	67	70.72%
AGC/DMPK/ROCK	Low	120,876	18,205	33.60%	4,473	725	38.30%	327	90	63.67%
AGC/GRK	High	120,876	6,364	62.01%	5,688	266	57.23%	474	62	84.71%
AGC/GRK	Medium	120,876	13,217	45.13%	5,688	567	39.81%	474	108	73.67%
AGC/GRK	Low	120,876	18,996	36.37%	5,688	827	31.22%	474	138	65.65%
AGC/PKA	High	120,876	10,563	77.11%	8,976	1,029	82.55%	3,978	492	83.83%
AGC/PKA	Medium	120,876	18,715	61.25%	8,976	1,650	67.36%	3,978	769	68.96%
AGC/PKA	Low	120,876	25,302	52.23%	8,976	2,140	58.06%	3,978	990	59.82%
AGC/PKB	High	120,876	2,051	-17.87%	4,323	167	48.23%	875	53	66.98%
AGC/PKB	Medium	120,876	7,643	5.11%	4,323	426	39.11%	875	127	58.66%
AGC/PKB	Low	120,876	16,471	26.61%	4,323	761	43.19%	875	191	54.19%
AGC/PKC	High	120,876	7,488	67.71%	14,874	961	69.04%	4,060	253	67.91%
AGC/PKC	Medium	120,876	15,470	53.12%	14,874	1,938	53.95%	4,060	528	53.86%
AGC/PKC	Low	120,876	21,835	44.64%	14,874	2,729	45.50%	4,060	742	45.28%
AGC/PKG	High	120,876	10,506	76.99%	2,154	222	80.59%	303	56	89.18%
AGC/PKG	Medium	120,876	20,271	64.22%	2,154	413	68.71%	303	81	77.56%
AGC/PKG	Low	120,876	27,293	55.71%	2,154	531	59.44%	303	99	69.39%
AGC/RSK	High	120,876	9,658	74.97%	9,669	750	74.22%	1,521	145	79.02%

AGC/RSK	Medium	120,876	18,124	59.98%	9,669	1,377	57.87%	1,521	251	63.64%
AGC/RSK	Low	120,876	24,349	50.36%	9,669	1,822	46.93%	1,521	315	51.71%
AGC/SGK	High	120,876	10,714	77.44%	4,574	456	79.94%	263	38	86.16%
AGC/SGK	Medium	120,876	20,052	63.83%	4,574	784	64.99%	263	53	70.23%
AGC/SGK	Low	120,876	27,121	55.43%	4,574	1,063	56.97%	263	71	62.96%
Atypical/PDHK	High	120,876	4,853	50.19%	2,628	119	55.83%	980	39	49.74%
Atypical/PDHK	Medium	120,876	11,745	38.25%	2,628	261	39.59%	980	95	38.11%
Atypical/PDHK	Low	120,876	23,277	48.07%	2,628	522	49.66%	980	205	52.20%
Atypical/PIKK	High	120,876	2,614	7.52%	6,950	199	30.15%	723	20	27.70%
Atypical/PIKK	Medium	120,876	8,816	17.73%	6,950	653	36.14%	723	72	39.75%
Atypical/PIKK	Low	120,876	15,983	24.37%	6,950	1,093	36.41%	723	107	32.43%
Atypical/PIKK/ATM	High	120,876	4,401	45.07%	10,537	594	64.52%	1,252	169	85.18%
Atypical/PIKK/ATM	Medium	120,876	5,447	-33.15%	10,537	772	18.11%	1,252	196	61.67%
Atypical/PIKK/ATM	Low	120,876	5,563	-117.29%	10,537	802	-31.38%	1,252	198	36.77%
Atypical/PIKK/ATR	High	120,876	2,047	-18.10%	2,371	101	53.05%	1,105	59	62.54%
Atypical/PIKK/ATR	Medium	120,876	3,179	-128.14%	2,371	142	-0.18%	1,105	81	18.15%
Atypical/PIKK/ATR	Low	120,876	3,784	-219.44%	2,371	158	-50.06%	1,105	92	-20.11%
Atypical/PIKK/DNAPK	High	120,876	3,166	23.64%	2,987	179	66.63%	593	58	79.55%
Atypical/PIKK/DNAPK	Medium	120,876	8,553	15.20%	2,987	356	49.66%	593	96	62.94%
Atypical/PIKK/DNAPK	Low	120,876	13,911	13.11%	2,987	479	37.64%	593	119	50.17%
Atypical/PIKK/FRAP	High	120,876	14,399	83.21%	9,166	1,071	82.88%	1,922	165	76.70%
Atypical/PIKK/FRAP	Medium	120,876	28,153	74.24%	9,166	2,073	73.47%	1,922	359	67.88%
Atypical/PIKK/FRAP	Low	120,876	34,938	65.40%	9,166	2,613	64.92%	1,922	451	57.38%
CAMK	High	120,876	16,721	85.54%	11,253	1,408	84.02%	1,759	215	83.64%
CAMK	Medium	120,876	30,521	76.24%	11,253	2,648	74.50%	1,759	410	74.26%
CAMK	Low	120,876	41,350	70.77%	11,253	3,632	69.02%	1,759	567	68.98%
CAMK/CAMK1	High	120,876	10,528	77.04%	4,518	520	82.62%	1,726	220	84.31%
CAMK/CAMK1	Medium	120,876	22,447	67.69%	4,518	950	71.47%	1,726	409	74.68%
CAMK/CAMK1	Low	120,876	29,761	59.38%	4,518	1,224	63.09%	1,726	520	66.81%
CAMK/CAMK2	High	120,876	11,415	78.82%	5,822	555	79.02%	635	70	81.86%
CAMK/CAMK2	Medium	120,876	22,355	67.56%	5,822	1,101	68.27%	635	139	72.59%
CAMK/CAMK2	Low	120,876	30,865	60.84%	5,822	1,496	61.08%	635	187	66.04%
CAMK/CAMKL	High	120,876	13,693	82.34%	10,507	1,237	83.01%	4,236	551	84.62%
CAMK/CAMKL	Medium	120,876	26,185	72.30%	10,507	2,300	72.59%	4,236	1,037	75.49%

CAMK/CAMKL	Low	120,876	34,829	65.29%	10,507	3,054	65.60%	4,236	1,343	68.46%
CAMK/CAMKL/AMPK	High	120,876	11,941	79.75%	4,579	568	83.88%	1,945	300	87.03%
CAMK/CAMKL/AMPK	Medium	120,876	21,921	66.92%	4,579	1,001	72.55%	1,945	506	76.94%
CAMK/CAMKL/AMPK	Low	120,876	29,454	58.96%	4,579	1,287	64.42%	1,945	636	69.42%
CAMK/CAMKL/CHK1	High	120,876	13,237	81.74%	5,976	567	78.92%	966	96	79.88%
CAMK/CAMKL/CHK1	Medium	120,876	25,125	71.13%	5,976	1,107	67.61%	966	185	68.67%
CAMK/CAMKL/CHK1	Low	120,876	32,448	62.75%	5,976	1,421	57.95%	966	232	58.36%
CAMK/CAMKL/LKB	High	120,876	2,926	17.38%	3,528	151	53.27%	163	15	78.27%
CAMK/CAMKL/LKB	Medium	120,876	8,127	10.76%	3,528	346	38.82%	163	22	55.55%
CAMK/CAMKL/LKB	Low	120,876	11,891	-1.65%	3,528	465	24.13%	163	27	39.63%
CAMK/DAPK	High	120,876	5,095	52.55%	3,948	161	50.96%	176	19	81.47%
CAMK/DAPK	Medium	120,876	10,877	33.32%	3,948	319	25.74%	176	28	62.29%
CAMK/DAPK	Low	120,876	16,202	25.39%	3,948	498	20.72%	176	36	51.11%
CAMK/MAPKAPK	High	120,876	12,736	81.02%	2,873	280	79.48%	513	67	84.69%
CAMK/MAPKAPK	Medium	120,876	24,948	70.93%	2,873	567	69.60%	513	118	73.92%
CAMK/MAPKAPK	Low	120,876	33,205	63.60%	2,873	773	62.83%	513	145	64.62%
CAMK/MLCK	High	120,876	4,965	51.31%	3,842	158	51.37%	229	7	34.57%
CAMK/MLCK	Medium	120,876	12,699	42.89%	3,842	395	41.64%	229	19	27.68%
CAMK/MLCK	Low	120,876	23,134	47.75%	3,842	750	48.77%	229	38	39.74%
CAMK/PHK	High	120,876	8,420	71.29%	423	42	79.86%	82	18	90.89%
CAMK/PHK	Medium	120,876	18,663	61.14%	423	62	59.06%	82	22	77.64%
CAMK/PHK	Low	120,876	26,332	54.10%	423	91	53.52%	82	30	72.67%
CAMK/PKD	High	120,876	7,350	67.11%	4,426	305	70.98%	374	20	62.60%
CAMK/PKD	Medium	120,876	15,929	54.47%	4,426	628	57.71%	374	42	46.57%
CAMK/PKD	Low	120,876	20,638	41.43%	4,426	818	45.89%	374	55	32.00%
CAMK/RAD53	High	120,876	7,781	68.93%	8,755	501	65.05%	2,813	158	64.39%
CAMK/RAD53	Medium	120,876	15,921	54.45%	8,755	1,090	51.81%	2,813	347	51.36%
CAMK/RAD53	Low	120,876	23,976	49.58%	8,755	1,658	47.20%	2,813	521	46.01%
CK1	High	120,876	11,966	79.80%	10,153	994	79.57%	3,855	408	81.10%
CK1	Medium	120,876	20,860	65.23%	10,153	1,788	65.93%	3,855	766	69.80%
CK1	Low	120,876	28,065	56.93%	10,153	2,421	58.06%	3,855	1,031	62.61%
CMGC	High	120,876	19,893	87.85%	7,601	1,191	87.24%	2,147	296	85.49%
CMGC	Medium	120,876	35,848	79.77%	7,601	2,196	79.23%	2,147	550	76.58%
CMGC	Low	120,876	46,800	74.17%	7,601	2,971	74.42%	2,147	771	72.15%

CMGC/CDK	High	120,876	17,272	86.00%	20,898	3,055	86.32%	5,486	808	86.42%
CMGC/CDK	Medium	120,876	32,345	77.58%	20,898	5,744	78.17%	5,486	1,442	77.17%
CMGC/CDK	Low	120,876	40,335	70.03%	20,898	7,268	71.25%	5,486	1,832	70.05%
CMGC/CDK/CDC2	High	120,876	18,239	86.75%	16,710	2,727	87.74%	4,442	867	89.75%
CMGC/CDK/CDC2	Medium	120,876	33,311	78.23%	16,710	4,956	79.77%	4,442	1,524	82.51%
CMGC/CDK/CDC2	Low	120,876	43,522	72.23%	16,710	6,429	74.01%	4,442	1,865	76.18%
CMGC/DYRK	High	120,876	21,018	88.50%	5,639	1,103	89.78%	890	193	90.78%
CMGC/DYRK	Medium	120,876	33,902	78.61%	5,639	1,701	80.11%	890	293	81.77%
CMGC/DYRK	Low	120,876	42,944	71.85%	5,639	2,118	73.38%	890	353	74.79%
CMGC/GSK	High	120,876	22,115	89.07%	10,794	1,911	88.70%	2,732	478	88.57%
CMGC/GSK	Medium	120,876	35,183	79.39%	10,794	3,108	79.16%	2,732	786	79.15%
CMGC/GSK	Low	120,876	43,605	72.28%	10,794	3,888	72.24%	2,732	990	72.40%
CMGC/MAPK	High	120,876	14,848	83.72%	24,857	2,967	83.24%	6,487	836	84.48%
CMGC/MAPK	Medium	120,876	30,635	76.33%	24,857	6,031	75.27%	6,487	1,704	77.16%
CMGC/MAPK	Low	120,876	37,949	68.15%	24,857	7,532	67.00%	6,487	2,084	68.87%
Other/AUR	High	120,876	9,360	74.17%	1,221	114	78.58%	146	11	73.45%
Other/AUR	Medium	120,876	19,760	63.30%	1,221	235	68.83%	146	23	61.91%
Other/AUR	Low	120,876	28,462	57.53%	1,221	342	64.30%	146	37	60.54%
Other/AUR/AUR-A	High	120,876	8,436	71.34%	2,749	152	63.83%	226	33	86.30%
Other/AUR/AUR-A	Medium	120,876	18,011	59.73%	2,749	355	53.54%	226	50	72.88%
Other/AUR/AUR-A	Low	120,876	25,263	52.15%	2,749	525	47.64%	226	63	64.13%
Other/AUR/AUR-B	High	120,876	7,702	68.61%	3,554	205	65.33%	210	25	83.20%
Other/AUR/AUR-B	Medium	120,876	15,717	53.86%	3,554	418	48.99%	210	36	65.00%
Other/AUR/AUR-B	Low	120,876	22,888	47.19%	3,554	612	41.93%	210	46	54.35%
Other/AUR/IPL1-yeast	High	120,876	8,396	71.21%	812	80	79.70%	428	46	81.39%
Other/AUR/IPL1-yeast	Medium	120,876	19,351	62.52%	812	170	71.34%	428	89	71.15%
Other/AUR/IPL1-yeast	Low	120,876	26,575	54.52%	812	230	64.70%	428	123	65.20%
Other/CK2	High	120,876	16,950	85.74%	8,785	1,975	91.10%	2,729	696	92.16%
Other/CK2	Medium	120,876	26,528	72.66%	8,785	2,788	81.09%	2,729	945	82.67%
Other/CK2	Low	120,876	33,511	63.93%	8,785	3,308	73.44%	2,729	1,100	75.19%
Other/IKK	High	120,876	6,968	65.31%	9,198	509	63.86%	1,242	88	71.77%
Other/IKK	Medium	120,876	15,509	53.24%	9,198	1,067	48.28%	1,242	166	55.11%
Other/IKK	Low	120,876	22,563	46.43%	9,198	1,545	40.47%	1,242	218	43.03%
Other/NEK	High	120,876	4,194	42.36%	4,011	177	54.68%	850	31	45.16%

Other/NEK	Medium	120,876	10,059	27.90%	4,011	350	31.24%	850	68	25.00%
Other/NEK	Low	120,876	17,826	32.19%	4,011	618	35.10%	850	117	27.35%
Other/PEK	High	120,876	2,117	-14.20%	7,774	132	-17.79%	736	28	47.43%
Other/PEK	Medium	120,876	5,853	-23.91%	7,774	403	-15.74%	736	61	27.61%
Other/PEK	Low	120,876	9,853	-22.68%	7,774	630	-23.40%	736	87	15.40%
Other/PLK	High	120,876	19,016	87.29%	9,314	1,328	85.97%	1,569	236	86.70%
Other/PLK	Medium	120,876	31,977	77.32%	9,314	2,262	75.29%	1,569	400	76.47%
Other/PLK	Low	120,876	41,418	70.82%	9,314	2,980	68.74%	1,569	525	70.11%
Other/Wnk	High	120,876	2,095	-15.39%	1,380	51	45.88%	110	9	75.56%
Other/Wnk	Medium	120,876	6,444	-12.55%	1,380	97	14.64%	110	11	40.00%
Other/Wnk	Low	120,876	12,506	3.35%	1,380	180	23.33%	110	17	35.29%
STE/STE11	High	120,876	4,445	45.61%	10,924	464	52.91%	4,338	209	58.49%
STE/STE11	Medium	120,876	13,086	44.58%	10,924	1,290	49.19%	4,338	517	49.66%
STE/STE11	Low	120,876	23,372	48.28%	10,924	2,281	52.11%	4,338	913	52.49%
STE/STE20	High	120,876	6,813	64.52%	16,030	916	65.00%	4,752	293	67.56%
STE/STE20	Medium	120,876	15,273	52.51%	16,030	2,000	51.91%	4,752	622	54.16%
STE/STE20	Low	120,876	20,947	42.29%	16,030	2,768	42.09%	4,752	864	45.00%
STE/STE7	High	120,876	7,904	69.41%	15,041	1,165	74.18%	2,726	196	72.18%
STE/STE7	Medium	120,876	16,343	55.62%	15,041	2,178	58.56%	2,726	365	55.19%
STE/STE7	Low	120,876	21,472	43.71%	15,041	2,810	46.47%	2,726	466	41.50%
STE/STE-Unique/COT	High	120,876	2,790	13.35%	2,107	86	51.00%	105	9	76.67%
STE/STE-Unique/COT	Medium	120,876	7,480	3.04%	2,107	211	40.09%	105	21	70.00%
STE/STE-Unique/COT	Low	120,876	9,967	-21.28%	2,107	264	20.19%	105	22	52.27%
STE/STE-Unique/NIK	High	120,876	8,908	72.86%	1,938	125	68.99%	160	13	75.38%
STE/STE-Unique/NIK	Medium	120,876	17,336	58.16%	1,938	240	51.55%	160	24	60.00%
STE/STE-Unique/NIK	Low	120,876	29,414	58.91%	1,938	447	56.64%	160	40	60.00%
TK/Abl	High	24,764	2,732	63.74%	2,543	357	71.51%	218	42	79.24%
TK/Abl	Medium	24,764	4,875	54.28%	2,543	605	62.17%	218	62	68.35%
TK/Abl	Low	24,764	7,036	47.21%	2,543	860	55.65%	218	85	61.53%
TK/Alk	High	24,764	1,344	26.30%	1,613	142	54.56%	272	32	66.00%
TK/Alk	Medium	24,764	2,731	18.39%	1,613	230	36.88%	272	49	50.04%
TK/Alk	Low	24,764	4,628	19.74%	1,613	326	25.78%	272	63	35.24%
TK/Axl	High	24,764	1,668	40.61%	1,405	104	45.96%	172	22	68.73%
TK/Axl	Medium	24,764	3,521	36.70%	1,405	214	40.91%	172	41	62.24%

TK/Axl	Low	24,764	5,247	29.21%	1,405	306	31.13%	172	55	53.09%
TK/Csk	High	24,764	1,278	22.49%	2,033	127	35.97%	298	29	58.90%
TK/Csk	Medium	24,764	2,727	18.27%	2,033	280	34.65%	298	53	49.40%
TK/Csk	Low	24,764	4,356	14.72%	2,033	444	31.32%	298	72	37.92%
TK/EGFR	High	24,764	2,685	63.11%	5,599	696	67.82%	1,032	174	76.28%
TK/EGFR	Medium	24,764	4,802	53.59%	5,599	1,233	59.13%	1,032	279	66.71%
TK/EGFR	Low	24,764	6,979	46.77%	5,599	1,776	52.71%	1,032	377	58.94%
TK/Eph	High	24,764	1,734	42.87%	3,200	307	58.31%	366	50	70.72%
TK/Eph	Medium	24,764	3,552	37.25%	3,200	564	48.94%	366	80	58.83%
TK/Eph	Low	24,764	5,396	31.16%	3,200	791	39.32%	366	100	45.10%
TK/Fak	High	24,764	2,742	63.87%	3,946	522	69.76%	770	117	73.68%
TK/Fak	Medium	24,764	4,943	54.91%	3,946	919	61.36%	770	194	64.28%
TK/Fak	Low	24,764	6,921	46.33%	3,946	1,316	55.02%	770	250	53.80%
TK/Fer/Fer	High	24,764	1,940	48.94%	1,741	164	57.54%	244	15	34.93%
TK/Fer/Fer	Medium	24,764	3,544	37.11%	1,741	281	44.24%	244	28	21.57%
TK/Fer/Fer	Low	24,764	5,037	26.25%	1,741	436	40.10%	244	42	12.86%
TK/Fer/Fes	High	24,764	1,995	50.35%	1,741	170	59.04%	244	20	51.20%
TK/Fer/Fes	Medium	24,764	3,514	36.57%	1,741	289	45.78%	244	33	33.45%
TK/Fer/Fes	Low	24,764	5,432	31.62%	1,741	449	41.84%	244	53	30.94%
TK/FGFR	High	24,764	2,334	57.56%	2,610	307	65.99%	241	46	79.04%
TK/FGFR	Medium	24,764	4,074	45.29%	2,610	471	50.13%	241	54	59.83%
TK/FGFR	Low	24,764	6,117	39.27%	2,610	697	43.83%	241	70	48.36%
TK/InsR	High	24,764	2,795	64.56%	3,613	485	70.20%	513	122	83.18%
TK/InsR	Medium	24,764	4,974	55.19%	3,613	810	59.86%	513	157	70.59%
TK/InsR	Low	24,764	7,069	47.45%	3,613	1,125	51.83%	513	201	61.72%
TK/JakA	High	24,764	1,827	45.78%	3,134	307	59.17%	833	121	72.46%
TK/JakA	Medium	24,764	3,623	38.48%	3,134	556	49.27%	833	193	61.16%
TK/JakA	Low	24,764	5,436	31.67%	3,134	798	41.09%	833	252	50.42%
TK/Met	High	24,764	2,123	53.34%	2,185	282	69.01%	299	54	77.85%
TK/Met	Medium	24,764	3,981	44.02%	2,185	457	56.97%	299	85	68.34%
TK/Met	Low	24,764	5,858	36.59%	2,185	652	49.73%	299	101	55.59%
TK/PDGFR	High	24,764	2,667	62.86%	4,043	535	69.77%	654	130	79.88%
TK/PDGFR	Medium	24,764	4,754	53.12%	4,043	864	57.89%	654	171	65.58%
TK/PDGFR	Low	24,764	6,811	45.46%	4,043	1,249	51.45%	654	236	58.43%

TK/Ret	High	24,764	1,674	40.83%	1,698	134	49.31%	170	18	62.22%
TK/Ret	Medium	24,764	3,219	30.76%	1,698	245	37.62%	170	24	36.25%
TK/Ret	Low	24,764	5,243	29.15%	1,698	406	37.27%	170	37	31.08%
TK/Src	High	24,764	3,262	69.63%	6,334	1,027	75.33%	2,130	385	77.87%
TK/Src	Medium	24,764	5,568	59.97%	6,334	1,657	65.60%	2,130	606	68.37%
TK/Src	Low	24,764	7,855	52.71%	6,334	2,287	58.46%	2,130	823	61.18%
TK/Syk	High	24,764	3,137	68.42%	2,512	480	79.07%	558	139	83.94%
TK/Syk	Medium	24,764	5,405	58.76%	2,512	738	69.37%	558	195	74.25%
TK/Syk	Low	24,764	7,618	51.24%	2,512	982	61.63%	558	246	65.98%
TK/Tec	High	24,764	2,582	61.64%	2,324	327	71.57%	542	104	79.15%
TK/Tec	Medium	24,764	4,632	51.88%	2,324	540	61.27%	542	157	68.93%
TK/Tec	Low	24,764	6,528	43.10%	2,324	761	54.19%	542	203	59.95%
TK/Tie	High	24,764	1,278	22.49%	1,412	86	34.33%	68	3	9.33%
TK/Tie	Medium	24,764	2,549	12.56%	1,412	141	9.87%	68	3	-104.00%
TK/Tie	Low	24,764	4,197	11.49%	1,412	262	19.16%	68	10	-2.00%
TK/Trk	High	24,764	1,807	45.18%	2,167	188	53.89%	238	26	63.38%
TK/Trk	Medium	24,764	3,552	37.25%	2,167	332	41.26%	238	40	46.45%
TK/Trk	Low	24,764	5,290	29.78%	2,167	493	34.07%	238	59	39.49%
TK/VEGFR	High	24,764	2,414	58.97%	2,177	297	70.68%	291	55	78.84%
TK/VEGFR	Medium	24,764	4,204	46.98%	2,177	461	57.50%	291	72	63.63%
TK/VEGFR	Low	24,764	5,927	37.33%	2,177	626	47.84%	291	99	55.91%
TKL/IRAK	High	120,876	2,331	-3.71%	3,253	75	13.25%	296	9	34.22%
TKL/IRAK	Medium	120,876	6,719	-7.94%	3,253	208	6.16%	296	26	31.69%
TKL/IRAK	Low	120,876	12,041	-0.39%	3,253	348	6.52%	296	46	35.65%
TKL/MLK	High	120,876	5,755	57.99%	9,382	489	61.63%	974	55	64.58%
TKL/MLK	Medium	120,876	12,672	42.77%	9,382	1,009	44.21%	974	100	41.56%
TKL/MLK	Low	120,876	19,506	38.03%	9,382	1,543	39.20%	974	153	36.34%
TKL/RAF	High	120,876	3,134	22.86%	11,457	325	29.50%	1,045	36	41.94%
TKL/RAF	Medium	120,876	10,346	29.90%	11,457	1,060	35.15%	1,045	112	44.02%
TKL/RAF	Low	120,876	13,895	13.01%	11,457	1,411	18.80%	1,045	147	28.91%
TKL/STKR	High	120,876	9,748	75.20%	9,051	725	75.03%	1,319	106	75.11%
TKL/STKR	Medium	120,876	18,932	61.69%	9,051	1,379	60.62%	1,319	208	61.95%
TKL/STKR	Low	120,876	25,859	53.26%	9,051	1,910	52.61%	1,319	278	52.55%
STKs	High	6,769,056	508,800	73.39%	422,847	38,651	78.12%	89,849	9,936	81.91%

TKs	High	520,044	46,018	54.80%	58,030	7,044	67.05%	10,153	1,704	76.17%
All PKs	High	7,289,100	554,818	71.85%	480,877	45,695	76.41%	100,002	11,640	81.07%
STKs	Medium	6,769,056	1,007,484	59.69%	422,847	73,244	65.36%	89,849	18,014	70.07%
TKs	Medium	520,044	84,744	44.77%	58,030	11,887	56.06%	10,153	2,576	64.53%
All PKs	Medium	7,289,100	1,092,228	58.53%	480,877	85,131	64.06%	100,002	20,590	69.38%
STKs	Low	6,769,056	1,402,437	51.73%	422,847	98,559	57.10%	89,849	23,565	61.87%
TKS	Low	520,044	124,981	37.59%	58,030	17,042	48.92%	10,153	3,434	55.65%
All PKs	Low	7,289,100	1,527,418	50.58%	480,877	115,601	55.89%	100,002	26,999	61.08%

Supplemental Table S11 – The detailed data statistics for the prediction results of five eukaryotic phosphoproteomes.

Organism	String & Exp. PPI					No PPI					Exp. PPI				
	PK	Sub.	Site	ssKSR	Ave	PK	Sub.	Site	ssKSR	Ave	PK	Sub.	Site	ssKSR	Ave
<i>S. cerevisiae</i>	91	1,598	7,041	20,909	3.0	91	2,658	12,889	145,409	11.3	91	1,395	6,049	14,648	2.4
<i>C. elegans</i>	110	272	544	867	1.6	302	2,153	5,112	107,738	21.1	32	78	156	183	1.2
<i>D. melanogaster</i>	140	888	2,697	6,191	2.3	172	3,896	13,656	236,780	17.3	66	180	444	594	1.3
<i>M. musculus</i>	358	2,349	11,191	45,032	4.0	415	8,219	43,131	1,588,383	36.8	128	235	935	1,254	1.3
<i>H. sapiens</i>	380	4,140	22,817	113,923	5.0	407	9,452	52,909	1,922,988	36.3	327	1,661	8,423	18,194	2.2
Total	1,079	9,247	44,290	186,922	4.2	1,387	26,378	127,697	4,001,298	31.3	644	3,549	16,007	34,873	2.2

Supplemental Table S12 – The number of p-sites for each PK in five eukaryotic PPNs. The top 10 PKs with the most p-sites are marked in yellow.

PK Name	Uniprot	Predictor	No PPI		String & Exp. PPI		Exp. PPI	
			Protein	Site	Protein	Site	Protein	Site
<i>Homo sapiens</i>								
Erk1	P27361	CMGC/MAPK	3,245	8,601	710	2,415	89	310
AKT1	P31749	AGC/AKT	2,393	4,797	901	2,377	101	319
Erk2	P28482	CMGC/MAPK	3,245	8,601	627	2,276	127	564
CDK2	P24941	CMGC/CDK/CDC2	3,417	9,226	488	2,270	76	372
CDC2	P06493	CMGC/CDK/CDC2	3,417	9,226	404	2,071	100	655
FRAP	P42345	Atypical/PIKK/FRAP	3,121	7,266	503	2,025	25	119
CK2a2	P19784	Other/CK2	2,390	6,632	405	1,934	58	265
p38a	Q16539	CMGC/MAPK	3,245	8,601	457	1,687	76	310
GSK3A	P49840	CMGC/GSK	3,511	11,376	316	1,635	20	117
CDK4	P11802	CMGC/CDK	3,372	9,005	364	1,504	33	135
CDK5	Q00535	CMGC/CDK	3,372	9,005	297	1,415	41	211
SRC	P12931	TK/Src	1,529	2,140	658	1,402	164	423
PLK1	P53350	Other/PLK	3,107	7,546	268	1,246	46	223
PKCa	P17252	AGC/PKC	2,158	4,281	417	1,166	107	288
MAP2K1	Q02750	STE/STE7	2,805	6,263	376	1,049	22	92
CDK9	P50750	CMGC/CDK	3,372	9,005	212	1,031	51	219
CDK6	Q00534	CMGC/CDK	3,372	9,005	216	944	14	53
p38b	Q15759	CMGC/MAPK	3,245	8,601	263	941	11	45
CaMK2g	Q13555	CAMK/CAMK2	2,915	6,151	326	930	21	79
EGFR	P00533	TK/EGFR	1,604	2,256	427	920	94	284
p38g	P53778	CMGC/MAPK	3,245	8,601	246	868	14	64
FYN	P06241	TK/Src	1,529	2,140	352	848	145	402
PKN1	Q16512	AGC	1,925	3,672	279	842	14	49
CHK1	O14757	CAMK/CAMKL/CHK1	3,553	8,439	244	841	22	111
CHK2	O96017	CAMK/RAD53	3,170	7,048	296	827	23	108
ROCK1	Q13464	AGC/DMPK; AGC/DMPK/ROCK	2,345	4,736	173	814	19	148
p38d	O15264	CMGC/MAPK	3,245	8,601	228	812	6	17

PKCb	D3DWF5	AGC/PKC	2,158	4,281	247	787	45	149
PKACa	P17612	AGC/PKA	2,246	4,393	271	750	120	371
p70S6K	P23443	AGC/RSK	2,368	4,849	281	706	26	79
CDK8	P49336	CMGC/CDK	3,372	9,005	144	699	30	165
CDK7	P50613	CMGC/CDK	3,372	9,005	159	698	25	100
ErbB2	P04626	TK/EGFR	1,604	2,256	305	694	36	125
RAF1	P04049	TKL/RAF	1,354	1,884	324	693	53	121
MAP3K1	Q13233	STE/STE11	2,828	6,056	253	691	46	128
LCK	P06239	TK/Src	1,529	2,140	286	689	72	238
FAK	Q658W2	TK/Fak	1,669	2,395	310	679	52	162
Trio	O75962	CAMK	2,822	5,881	181	669	4	11
IKKb	O14920	Other/IKK	1,500	2,712	263	667	42	125
IKKa	O15111	Other/IKK	1,500	2,712	252	662	38	114
CK1d	P48730	CK1	1,989	4,756	183	659	11	28
PKCe	Q02156	AGC/PKC	2,158	4,281	213	654	29	78
CK1e	P49674	CK1	1,989	4,756	186	650	12	50
SGK1	O00141	AGC/SGK	2,616	5,690	197	639	14	51
PKCd	Q05655	AGC/PKC	2,158	4,281	230	634	57	135
PKCg	P05129	AGC/PKC	2,158	4,281	229	633	31	86
MAP2K4	P45985	STE/STE7	2,805	6,263	234	613	16	57
HIPK2	Q9H2X6	CMGC/DYRK	4,033	11,983	132	604	14	53
CK2a1	P68400	Other/CK2	2,390	6,632	129	596	129	596
PDGFRb	P09619	TK/PDGFR	1,571	2,289	269	588	50	140
ROCK2	O75116	AGC/DMPK; AGC/DMPK/ROCK	2,345	4,736	123	583	2	18
PKD1	Q1KKQ2	CAMK/PKD	3,203	6,896	237	575	13	35
INSR	P06213	TK/InsR	1,586	2,310	268	566	47	134
AKT2	P31751	AGC/AKT	2,393	4,797	185	560	17	51
PKCz	Q05513	AGC/PKC	2,158	4,281	188	553	39	104
TGFbR2	D2JYI1	TKL/STKR	2,235	4,324	217	552	0	0
PYK2	Q14289	TK/Fak	1,669	2,395	245	551	46	155
PFTAIRe1	O94921	CMGC/CDK	3,372	9,005	113	536	4	24
RSK2	P51812	AGC/RSK	2,368	4,849	178	531	15	49
KIT	P10721	TK/PDGFR	1,571	2,289	242	529	39	101
SYK	P43405	TK/Syk	1,592	2,306	210	525	58	206

ABL1	Q59FK4	TK/Abl	1,666	2,390	229	505	0	0
TGFbR1	P36897	TKL/STKR	2,235	4,324	181	501	52	133
DYRK1A	Q13627	CMGC/DYRK	4,033	11,983	115	501	12	75
ATM	Q13315	Atypical/PIKK/ATM	1,418	1,980	265	499	46	171
PKACg	P22612	AGC/PKA	2,246	4,393	194	498	1	2
Trad	O60229	CAMK	2,822	5,881	128	495	1	5
PDGFRa	P16234	TK/PDGFR	1,571	2,289	223	493	18	68
MAP3K5	Q99683	STE/STE11	2,828	6,056	178	483	26	88
MAP2K2	P36507	STE/STE7	2,805	6,263	167	483	12	41
MARK2	Q7KZI7	CAMK/CAMKL	3,185	7,139	151	481	15	90
PKCt	Q04759	AGC/PKC	2,158	4,281	152	467	16	53
MAP2K6	P52564	STE/STE7	2,805	6,263	152	467	11	23
IGF1R	P08069	TK/InsR	1,586	2,310	209	465	30	106
DYRK2	Q92630	CMGC/DYRK	4,033	11,983	100	462	0	0
ZAP70	P43403	TK/Syk	1,592	2,306	178	460	37	130
PKCi	P41743	AGC/PKC	2,158	4,281	139	454	16	37
PCTAIRE1	Q00536	CMGC/CDK	3,372	9,005	84	453	7	24
CDKL2	B4DH08	CMGC	3,165	8,299	96	449	1	2
ErbB3	P21860	TK/EGFR	1,604	2,256	184	446	35	124
Erk5	Q13164	CMGC/MAPK	3,245	8,601	119	445	12	57
SMG1	Q96Q15	Atypical/PIKK	895	1,187	196	440	3	10
JAK2	O60674	TK/JakA	1,643	2,327	221	439	61	170
CLK1	B4DFW7	CMGC	3,165	8,299	46	432	7	100
CHED	Q14004	CMGC/CDK	3,372	9,005	84	425	2	8
FER	P16591	TK/Fer/Fer; TK/Fer/Fes	2,024	2,953	130	421	9	28
AurB	C7G533	Other/AUR/AUR-B	2,157	3,893	142	419	12	46
PKN2	Q16513	AGC	1,925	3,672	128	415	13	30
CDK3	Q00526	CMGC/CDK/CDC2	3,417	9,226	72	403	11	30
p70S6Kb	Q9UBS0	AGC/RSK	2,368	4,849	135	400	8	34
ILK	Q13418	TKL/MLK	1,733	2,502	183	398	21	51
BRAF	P15056	TKL/RAF	1,354	1,884	177	395	12	23
YES	P07947	TK/Src	1,529	2,140	132	391	22	77
MET	P08581	TK/Met	1,632	2,346	162	387	25	76
smMLCK	Q15746	CAMK/MLCK	3,090	6,693	149	387	10	21

CDK11	Q9BWU1	CMGC/CDK	3,372	9,005	64	387	5	13
PKG1	A5YM56	AGC/PKG	2,552	5,195	138	386	20	71
MSK1	O75582	AGC/RSK	2,368	4,849	123	381	16	47
CRK7	Q9NYV4	CMGC/CDK	3,372	9,005	45	381	4	71
PCTAIRE2	Q00537	CMGC/CDK	3,372	9,005	63	371	2	4
CDK10	Q15131	CMGC/CDK	3,372	9,005	74	368	1	1
PKCh	P24723	AGC/PKC	2,158	4,281	105	361	3	9
BMPR1A	P36894	TKL/STKR	2,235	4,324	126	358	3	3
AurA	O14965	Other/AUR/AUR-A	2,329	4,620	115	358	15	63
Erk3	Q16659	CMGC/MAPK	3,245	8,601	95	353	3	3
KDR	P35968	TK/VEGFR	1,667	2,456	169	351	33	81
ErbB4	Q15303	TK/EGFR	1,604	2,256	152	351	22	80
NIK	Q99558	STE/STE-Unique/NIK	3,526	8,508	143	349	17	39
BARK1	P25098	AGC/GRK	2,672	5,935	140	349	23	94
CaMK2d	Q13557	CAMK/CAMK2	2,915	6,151	109	349	10	47
FMS	P07333	TK/PDGFR	1,571	2,289	151	347	14	43
TRRAP	Q9Y4A5	Atypical/PIKK	895	1,187	129	347	7	22
MAP2K5	Q13163	STE/STE7	2,805	6,263	110	347	8	20
FGFR1	P11362	TK/FGFR	1,720	2,492	169	345	15	39
BTK	Q06187	TK/Tec	1,631	2,339	157	345	31	102
MAP3K3	Q99759	STE/STE11	2,828	6,056	129	345	68	209
JAK1	P23458	TK/JakA	1,643	2,327	158	343	51	131
PDK1	O15530	AGC/PKB	2,267	4,403	112	339	30	110
PKN3	Q6P5Z2	AGC	1,925	3,672	110	337	2	5
PKD3	O94806	CAMK/PKD	3,203	6,896	126	335	2	3
PCTAIRE3	B4DK03	CMGC/CDK	3,372	9,005	59	333	0	0
CSK	P41240	TK/Csk	1,619	2,287	186	331	35	65
PLK3	Q9H4B4	Other/PLK	3,107	7,546	63	330	6	32
FGFR2	P21802	TK/FGFR	1,720	2,492	156	326	2	11
MAPKAPK2	P49137	CAMK/MAPKAPK	3,279	7,555	92	320	20	94
LATS1	O95835	AGC	1,925	3,672	115	318	4	10
AKT3	Q9Y243	AGC/AKT	2,393	4,797	100	316	6	27
LKB1	Q15831	CAMK/CAMKL/LKB	3,373	7,717	145	315	13	26
FGR	P09769	TK/Src	1,529	2,140	132	315	11	33

PKD2	Q9BZL6	CAMK/PKD	3,203	6,896	116	314	7	17
DNAPK	P78527	Atypical/PIKK/DNAPK	1,190	1,638	104	306	40	119
FES	P07332	TK/Fer/Fer; TK/Fer/Fes	2,024	2,953	105	303	18	68
TYK2	P29597	TK/JakA	1,643	2,327	138	297	21	73
PIM1	P11309	CAMK	2,822	5,881	88	297	7	24
NEK2	P51955	Other/NEK	1,187	1,726	118	296	5	11
PKG2	Q13237	AGC/PKG	2,552	5,195	97	286	3	7
RSK1	Q15349	AGC/RSK	2,368	4,849	80	284	7	30
PAK2	Q13177	STE/STE20	2,705	5,739	101	281	33	112
FLT1	P17948	TK/VEGFR	1,667	2,456	140	279	13	45
JAK3	P52333	TK/JakA	1,643	2,327	132	279	27	71
RET	P07949	TK/Ret	1,641	2,323	144	277	15	37
MSK2	O75676	AGC/RSK	2,368	4,849	77	277	7	21
TAK1	O43318	TKL/MLK	1,733	2,502	111	274	24	55
Erk7	Q8TD08	CMGC/MAPK	3,245	8,601	72	273	4	23
PIM2	Q9P1W9	CAMK	2,822	5,881	85	265	3	7
MOK	Q9UQ07	CMGC	3,165	8,299	57	265	2	8
NRK	Q7Z2Y5	STE/STE20	2,705	5,739	115	263	1	1
Erk4	P31152	CMGC/MAPK	3,245	8,601	75	263	5	14
GSK3B	P49841	CMGC/GSK	3,511	11,376	39	251	39	251
TRKA	P04629	TK/Trk	1,691	2,439	137	248	21	52
RSK4	Q9UK32	AGC/RSK	2,368	4,849	66	247	0	0
SRPK1	Q96SB4	CMGC	3,165	8,299	44	247	15	104
BMPRI1B	B4DSV1	TKL/STKR	2,235	4,324	87	245	15	57
MAP3K4	B9EG75	STE/STE11	2,828	6,056	71	236	10	23
IKKe	Q14164	Other/IKK	1,500	2,712	101	235	26	58
ARAF	P10398	TKL/RAF	1,354	1,884	97	234	9	18
TEC	P42680	TK/Tec	1,631	2,339	99	232	23	70
BLK	P51451	TK/Src	1,529	2,140	88	232	7	24
MLK3	B2RDI6	TKL/MLK	1,733	2,502	94	231	10	19
DAPK3	O43293	CAMK/DAPK	2,959	6,253	100	228	7	20
LYN	P07948	TK/Src	1,529	2,140	73	228	73	228
MARK1	Q9P0L2	CAMK/CAMKL	3,185	7,139	56	227	1	14
CaMK4	Q16566	CAMK/CAMK1	3,314	7,523	72	226	6	17

Trb3	Q96RU7	CAMK	2,822	5,881	57	223	14	41
PLK4	O00444	Other/PLK	3,107	7,546	71	221	2	8
ITK	Q08881	TK/Tec	1,631	2,339	89	220	20	73
Trb1	Q96RU8	CAMK	2,822	5,881	69	220	2	3
CaMK1a	Q14012	CAMK/CAMK1	3,314	7,523	75	218	8	19
MARK3	P27448	CAMK/CAMKL	3,185	7,139	58	218	12	47
PKR	P19525	Other/PEK	716	877	118	216	16	29
ALK1	P37023	TKL/STKR	2,235	4,324	78	211	3	7
PEK	B2RCU9	Other/PEK	716	877	103	210	4	5
CDKL5	O76039	CMGC	3,165	8,299	34	208	5	37
HIPK3	Q9H422	CMGC/DYRK	4,033	11,983	48	206	19	66
SGK3	Q96BR1	AGC/SGK	2,616	5,690	66	204	4	23
RSKL1	Q96S38	AGC	1,925	3,672	47	204	0	0
HGK	Q53TX8	STE/STE20	2,705	5,739	79	201	3	6
PAK4	O96013	STE/STE20	2,705	5,739	84	200	5	10
SRPK2	C9JQJ0	CMGC	3,165	8,299	30	200	3	22
TRKC	Q16288	TK/Trk	1,691	2,439	91	198	7	16
ALK	Q9UM73	TK/AIk	1,685	2,440	99	197	21	59
EphA1	P21709	TK/Eph	1,662	2,390	89	195	1	2
BMPR2	Q13873	TKL/STKR	2,235	4,324	89	195	9	19
NuaK1	O60285	CAMK/CAMKL	3,185	7,139	49	191	2	2
COT	P41279	STE/STE-Unique/COT	3,124	6,846	82	189	10	22
AMPKa2	P54646	CAMK/CAMKL/AMPK	3,325	7,645	60	187	7	21
MARK4	Q96L34	CAMK/CAMKL	3,185	7,139	43	187	13	89
PLK2	Q9NYY3	Other/PLK	3,107	7,546	49	183	0	0
SRM	Q9H3Y6	TK/Src	1,529	2,140	58	180	0	0
LATS2	Q9NRM7	AGC	1,925	3,672	64	179	2	3
QIK	Q9H0K1	CAMK/CAMKL	3,185	7,139	47	178	2	30
BARK2	P35626	AGC/GRK	2,672	5,935	69	176	4	17
TBK1	Q9UHD2	Other/IKK	1,500	2,712	78	175	17	51
IRAK1	P51617	TKL/IRAK	1,300	1,728	91	173	21	35
EphA2	P29317	TK/Eph	1,662	2,390	76	171	11	28
EphA4	P54764	TK/Eph	1,662	2,390	75	170	5	11
JNK2	P45984	CMGC/MAPK	3,245	8,601	33	170	33	170

EphB2	P29323	TK/Eph	1,662	2,390	90	169	10	24
GPRK5	P34947	AGC/GRK	2,672	5,935	52	169	11	54
NuaK2	B4E0Y5	CAMK/CAMKL	3,185	7,139	48	169	2	6
TAO1	Q7L7X3	STE/STE20	2,705	5,739	54	168	0	0
ALK2	Q04771	TKL/STKR	2,235	4,324	69	167	18	46
IRR	P14616	TK/InsR	1,586	2,310	54	166	1	6
SIK	P57059	CAMK/CAMKL	3,185	7,139	54	163	1	9
MELK	Q53GX0	CAMK/CAMKL	3,185	7,139	41	162	7	22
AXL	P30530	TK/Axl	1,696	2,460	67	154	12	40
PDHK4	Q16654	Atypical/PDHK	1,333	1,872	54	153	1	1
NIM1	Q8IY84	CAMK/CAMKL	3,185	7,139	52	151	0	0
ACTR2B	Q13705	TKL/STKR	2,235	4,324	61	149	4	6
MAP3K2	Q9Y2U5	STE/STE11	2,828	6,056	55	145	11	36
ICK	Q9UPZ9	CMGC	3,165	8,299	24	144	1	5
TIE2	Q02763	TK/Tie	1,643	2,292	103	142	1	1
ABL2	P42684	TK/Abl	1,666	2,390	55	140	16	48
DCLK1	O15075	CAMK	2,822	5,881	24	139	0	0
PDHK2	Q15119	Atypical/PDHK	1,333	1,872	46	138	6	11
skMLCK	Q9H1R3	CAMK/MLCK	3,090	6,693	59	135	2	6
MAPKAPK3	Q16644	CAMK/MAPKAPK	3,279	7,555	45	134	3	15
ALK4	P36896	TKL/STKR	2,235	4,324	53	133	6	13
AMPKa1	Q13131	CAMK/CAMKL/AMPK	3,325	7,645	38	133	15	74
NEK6	B7Z2D9	Other/NEK	1,187	1,726	48	132	13	34
DLK	Q12852	TKL/MLK	1,733	2,502	46	130	5	9
EphB4	P54760	TK/Eph	1,662	2,390	65	127	2	3
DYRK1B	Q9Y463	CMGC/DYRK	4,033	11,983	37	127	3	5
VRK1	Q99986	CK1	1,989	4,756	31	127	2	3
BRSK1	Q8TDC3	CAMK/CAMKL	3,185	7,139	32	126	2	7
RON	Q04912	TK/Met	1,632	2,346	57	123	13	40
HPK1	Q92918	STE/STE20	2,705	5,739	53	123	17	32
EphA3	P29320	TK/Eph	1,662	2,390	53	121	9	16
BMX	P51813	TK/Tec	1,631	2,339	50	121	12	35
TXK	P42681	TK/Tec	1,631	2,339	55	120	9	23
NEK3	P51956	Other/NEK	1,187	1,726	40	120	0	0

GCK	Q12851	STE/STE20	2,705	5,739	48	119	3	8
STLK5	Q7RTN6	STE/STE20	2,705	5,739	32	119	1	1
ACTR2	P27037	TKL/STKR	2,235	4,324	50	118	1	2
CK1a	D3DQG1	CK1	1,989	4,756	39	117	0	0
NEK1	Q96PY6	Other/NEK	1,187	1,726	31	116	3	26
STLK3	Q9UEW8	STE/STE20	2,705	5,739	48	115	5	9
BRK	Q13882	TK/Src	1,529	2,140	42	115	6	34
MINK	Q8N4C8	STE/STE20	2,705	5,739	36	115	9	40
PIM3	Q86V86	CAMK	2,822	5,881	35	113	1	5
PRKX	P51817	AGC/PKA	2,246	4,393	40	109	2	5
MNK2	A4CYL7	CAMK/MAPKAPK	3,279	7,555	36	109	4	11
PSKH1	P11801	CAMK	2,822	5,881	34	109	0	0
CLK2	P49760	CMGC	3,165	8,299	25	109	1	2
HIPK1	Q86Z02	CMGC/DYRK	4,033	11,983	24	108	3	23
TNIK	Q9UKE5	STE/STE20	2,705	5,739	25	107	3	10
PAK6	Q9NQU5	STE/STE20	2,705	5,739	44	105	3	4
CaMK1g	Q96NX5	CAMK/CAMK1	3,314	7,523	37	105	0	0
RHOK	Q15835	AGC/GRK	2,672	5,935	35	105	5	10
TYRO3	Q06418	TK/Axl	1,696	2,460	61	104	4	11
NDR1	Q15208	AGC	1,925	3,672	43	104	5	7
IRAK4	Q9NWZ3	TKL/IRAK	1,300	1,728	62	102	3	5
ALK7	Q8NER5	TKL/STKR	2,235	4,324	40	102	0	0
MST1	Q13043	STE/STE20	2,705	5,739	42	100	7	17
SPEG	Q15772	CAMK	2,822	5,881	19	99	0	0
EphB6	D3DXD3	TK/Eph	1,662	2,390	45	97	8	20
PRP4	Q13523	CMGC/DYRK	4,033	11,983	21	97	7	34
HRI	Q9BQI3	Other/PEK	716	877	50	96	4	6
MST2	Q13188	STE/STE20	2,705	5,739	46	95	6	13
OSR1	O95747	STE/STE20	2,705	5,739	36	94	4	19
DYRK3	O43781	CMGC/DYRK	4,033	11,983	18	94	0	0
PRKY	O43930	AGC/PKA	2,246	4,393	32	92	0	0
NLK	Q9UBE8	CMGC/MAPK	3,245	8,601	28	91	7	23
MLK2	Q02779	TKL/MLK	1,733	2,502	44	90	10	20
AurC	Q9UQB9	Other/AUR	1,911	3,321	28	90	2	32

LTK	P29376	TK/AIk	1,685	2,440	46	89	6	12
Wnk1	Q9H4A3	Other/Wnk	697	843	45	89	4	13
BRSK2	Q8IWQ3	CAMK/CAMKL	3,185	7,139	16	86	2	7
MRCKa	Q5VT25	AGC/DMPK	2,319	4,628	39	85	0	0
KSR1	Q8IVT5	TKL/RAF	1,354	1,884	32	85	0	0
IRAK2	O43187	TKL/IRAK	1,300	1,728	46	84	5	11
Wnk4	Q96J92	Other/Wnk	697	843	39	84	2	2
RSK3	Q15418	AGC/RSK	2,368	4,849	23	83	23	83
STK33	Q9BYT3	CAMK	2,822	5,881	23	83	0	0
caMLCK	Q32MK0	CAMK/MLCK	3,090	6,693	29	82	0	0
DRAK2	O94768	CAMK/DAPK	2,959	6,253	43	81	0	0
ATR	Q13535	Atypical/PIKK/ATR	1,118	1,494	36	77	25	57
MER	Q12866	TK/Axl	1,696	2,460	37	76	4	11
EphB3	P54753	TK/Eph	1,662	2,390	35	76	4	13
GPRK4	P32298	AGC/GRK	2,672	5,935	20	76	0	0
PAK5	Q9P286	STE/STE20	2,705	5,739	31	72	3	6
TIE1	P35590	TK/Tie	1,643	2,292	52	71	4	8
PHKg1	Q16816	CAMK/PHK	3,304	7,340	24	68	4	30
GCN2	Q9P2K8	Other/PEK	716	877	37	67	2	3
QSK	Q9Y2K2	CAMK/CAMKL	3,185	7,139	10	67	1	9
YSK1	O00506	STE/STE20	2,705	5,739	33	66	8	14
MYO3A	Q8NEV4	STE/STE20	2,705	5,739	28	64	2	3
LOK	O94804	STE/STE20	2,705	5,739	17	64	1	7
EphA7	Q15375	TK/Eph	1,662	2,390	27	62	3	8
MISR2	Q16671	TKL/STKR	2,235	4,324	27	58	0	0
NEK7	Q8TDX7	Other/NEK	1,187	1,726	19	58	1	5
VACAMKL	B2RDF9	CAMK	2,822	5,881	13	58	0	0
MLK4	Q5TCX8	TKL/MLK	1,733	2,502	18	54	0	0
VRK2	Q86Y07	CK1	1,989	4,756	14	54	3	13
Trb2	Q92519	CAMK	2,822	5,881	24	53	0	0
Wnk3	B1AKG2	Other/Wnk	697	843	24	52	1	1
KHS2	Q8IVH8	STE/STE20	2,705	5,739	16	51	3	3
DRAK1	Q9UEE5	CAMK/DAPK	2,959	6,253	31	50	0	0
EphA5	P54756	TK/Eph	1,662	2,390	23	50	1	1

CLK3	Q59FC5	CMGC	3,165	8,299	17	50	0	0
SgK085	Q86YV6	CAMK/MLCK	3,090	6,693	21	49	0	0
DAPK2	Q9UIK4	CAMK/DAPK	2,959	6,253	28	48	3	3
FRK	P42685	TK/Src	1,529	2,140	22	48	1	4
SGK2	Q9HBY8	AGC/SGK	2,616	5,690	13	48	1	6
MAP2K7	O14733	STE/STE7	2,805	6,263	12	47	12	47
KHS1	Q9Y4K4	STE/STE20	2,705	5,739	25	45	5	10
PHKg2	P15735	CAMK/PHK	3,304	7,340	22	45	1	2
DCLK3	Q9C098	CAMK	2,822	5,881	3	45	0	0
SSTK	Q9BXA6	CAMK	2,822	5,881	18	43	2	4
EphA6	Q9UF33	TK/Eph	1,662	2,390	16	43	0	0
PAK1	Q13153	STE/STE20	2,705	5,739	16	42	16	42
ZAK	B8ZZU2	TKL/MLK	1,733	2,502	16	42	3	4
STLK6	Q9C0K7	STE/STE20	2,705	5,739	15	40	2	5
MRCKb	Q9Y5S2	AGC/DMPK	2,319	4,628	11	39	0	0
PSKH2	Q96QS6	CAMK	2,822	5,881	10	39	0	0
PITSLRE	P21127	CMGC/CDK	3,372	9,005	7	39	7	39
NEK8	Q86SG6	Other/NEK	1,187	1,726	18	38	5	10
PDHK1	Q15118	Atypical/PDHK	1,333	1,872	15	38	8	23
CaMK1b	B4E1A6	CAMK/CAMK1	3,314	7,523	14	38	0	0
EphA8	P29322	TK/Eph	1,662	2,390	14	38	1	2
MAP3K6	O95382	STE/STE11	2,828	6,056	9	38	2	10
TSSK3	Q96PN8	CAMK	2,822	5,881	8	38	0	0
TAO3	Q9H2K8	STE/STE20	2,705	5,739	10	36	3	6
MAPKAPK5	Q8IW41	CAMK/MAPKAPK	3,279	7,555	8	36	8	36
MST4	Q9P289	STE/STE20	2,705	5,739	16	35	6	15
PASK	Q96RG2	CAMK/CAMKL	3,185	7,139	9	35	1	3
IRAK3	Q9Y616	TKL/IRAK	1,300	1,728	22	34	2	4
CDKL3	Q8IVW4	CMGC	3,165	8,299	11	32	0	0
TSSK1	Q9BXA7	CAMK	2,822	5,881	11	30	2	11
PAK3	B2RCU6	STE/STE20	2,705	5,739	7	29	7	29
MLK1	P80192	TKL/MLK	1,733	2,502	16	28	1	5
CK1g2	P78368	CK1	1,989	4,756	16	27	3	5
TRKB	Q16620	TK/Trk	1,691	2,439	10	27	10	27

CK1g3	Q9Y6M4	CK1	1,989	4,756	14	26	1	1
NEK9	Q8TD19	Other/NEK	1,187	1,726	11	26	4	10
MAP2K3	P46734	STE/STE7	2,805	6,263	9	26	9	26
YANK3	Q86UX6	AGC	1,925	3,672	5	26	0	0
DMPK1	Q09013	AGC/DMPK	2,319	4,628	7	25	7	25
MAK	P20794	CMGC	3,165	8,299	6	25	0	0
SNRK	Q9NRH2	CAMK/CAMKL	3,185	7,139	11	24	1	2
TTBK1	Q5TCY1	CK1	1,989	4,756	7	24	3	20
LZK	O43283	TKL/MLK	1,733	2,502	11	22	3	4
PDHK3	B4DXG6	Atypical/PDHK	1,333	1,872	9	22	1	1
VRK3	Q8IV63	CK1	1,989	4,756	6	22	1	1
TSSK2	Q96PF2	CAMK	2,822	5,881	7	21	0	0
NEK4	P51957	Other/NEK	1,187	1,726	7	21	0	0
NEK11	Q8NG66	Other/NEK	1,187	1,726	7	21	1	4
NDR2	Q9Y2H1	AGC	1,925	3,672	6	21	2	3
FGFR3	P22607	TK/FGFR	1,720	2,492	6	20	6	20
MAST2	Q6P0Q8	AGC	1,925	3,672	10	19	2	3
EphB1	P54762	TK/Eph	1,662	2,390	7	18	7	18
CK1g1	Q9HCP0	CK1	1,989	4,756	11	17	0	0
BCKDK	O14874	Atypical/PDHK	1,333	1,872	5	17	2	4
FLT3	P36888	TK/PDGFR	1,571	2,289	5	17	5	17
TSSK4	Q6SA08	CAMK	2,822	5,881	3	17	1	8
KSR2	Q6VAB6	TKL/RAF	1,354	1,884	6	16	4	8
GPRK7	Q8WTQ7	AGC/GRK	2,672	5,935	9	15	0	0
HH498	Q59H18	TKL/MLK	1,733	2,502	6	15	1	3
CLK4	Q9HAZ1	CMGC	3,165	8,299	2	15	1	12
YANK2	Q9NY57	AGC	1,925	3,672	7	13	0	0
TTN	D3DPF9	CAMK/MLCK	3,090	6,693	7	12	7	12
FLT4	P35916	TK/VEGFR	1,667	2,456	4	12	4	12
CK1a2	Q8N752	CK1	1,989	4,756	4	11	0	0
MASTL	Q96GX5	AGC	1,925	3,672	3	11	0	0
CTK	P42679	TK/Csk	1,619	2,287	4	10	4	10
FGFR4	P22455	TK/FGFR	1,720	2,492	4	10	4	10
SgK495	Q8N2I9	CAMK	2,822	5,881	3	8	1	3

HUNK	P57058	CAMK/CAMKL	3,185	7,139	6	7	1	1
GPRK6	P43250	AGC/GRK	2,672	5,935	3	7	3	7
HIPK4	Q8NE63	CMGC/DYRK	4,033	11,983	3	7	0	0
EphA10	Q5JZY3	TK/Eph	1,662	2,390	3	7	0	0
PKACb	P22694	AGC/PKA	2,246	4,393	2	7	2	7
DMPK2	Q6DT37	AGC/DMPK	2,319	4,628	3	6	1	1
DYRK4	Q9NR20	CMGC/DYRK	4,033	11,983	3	6	0	0
DAPK1	Q59H88	CAMK/DAPK	2,959	6,253	3	5	3	5
CaMK2b	Q13554	CAMK/CAMK2	2,915	6,151	2	4	2	4
PFTAIRE2	Q96Q40	CMGC/CDK	3,372	9,005	2	3	1	1
MAST3	O60307	AGC	1,925	3,672	2	2	0	0
SgK494	Q96LW2	AGC	1,925	3,672	1	1	0	0
SLK	D3DRA1	STE/STE20	2,705	5,739	1	1	1	1
<i>Mus musculus</i>								
ERK2	P63085	CMGC/MAPK	2,918	7,241	475	1,725	13	80
ERK1	Q63844	CMGC/MAPK	2,918	7,241	383	1,365	5	28
AKT1	Q6GSA6	AGC/AKT	2,201	4,246	462	1,197	1	2
CDC2	P11440	CMGC/CDK/CDC2	3,073	7,789	275	1,150	7	25
CDK2	P97377	CMGC/CDK/CDC2	3,073	7,789	281	1,058	4	10
GSK3B	Q9WV60	CMGC/GSK	3,185	9,577	245	1,038	4	14
p38a	Q5U421	CMGC/MAPK	2,918	7,241	280	866	0	0
CDK4	P30285	CMGC/CDK	3,025	7,575	199	747	2	3
CDK5	P49615	CMGC/CDK	3,025	7,575	193	707	3	27
JNK2	Q5NCK8	CMGC/MAPK	2,918	7,241	186	690	3	16
PLK1	Q07832	Other/PLK	2,832	6,336	168	577	1	11
MAP2K1	Q9JJE1	STE/STE7	2,561	5,353	187	551	4	17
PKACb	P68181	AGC/PKA	2,093	3,910	211	524	0	0
EGFR	Q01279	TK/EGFR	1,180	1,641	211	462	9	18
IKKa	Q8CBT3	Other/IKK	1,343	2,245	172	433	0	0
FYN	P39688	TK/Src	1,136	1,569	153	411	13	66
CK2a2	O54833	Other/CK2	2,229	5,562	108	400	0	0
CDK6	Q64261	CMGC/CDK	3,025	7,575	94	398	3	5
Trio	Q0KL02	CAMK	2,639	5,207	109	393	0	0
PYK2	Q9QVP9	TK/Fak	1,226	1,719	186	391	0	0

PLK3	Q6P571	Other/PLK	2,832	6,336	119	386	0	0
CaMK2a	Q80TN1	CAMK/CAMK2	2,722	5,454	127	384	10	40
ErbB2	P70424	TK/EGFR	1,180	1,641	153	342	2	6
ROCK1	P70335	AGC/DMPK; AGC/DMPK/ROCK	2,160	4,184	73	339	2	6
CHK2	Q9Z265	CAMK/RAD53	2,948	6,180	139	333	1	6
FAK	P34152	TK/Fak	1,226	1,719	144	325	9	32
PLK2	P53351	Other/PLK	2,832	6,336	110	322	0	0
p70S6K	Q5SWG1	AGC/RSK	2,174	4,248	136	319	0	0
PKCe	P16054	AGC/PKC	1,997	3,762	108	313	4	24
ERK5	Q9WVS8	CMGC/MAPK	2,918	7,241	81	311	0	0
Trad	A2CG49	CAMK	2,639	5,207	84	310	1	3
SGK1	Q9WVC6	AGC/SGK	2,436	5,023	91	309	0	0
BARK1	Q99MK8	AGC/GRK	2,435	5,086	120	306	0	0
INSR	P15208	TK/InsR	1,184	1,720	133	303	5	30
IKKb	Q5D0E0	Other/IKK	1,343	2,245	127	300	2	4
ABL1	P00520	TK/Abl	1,238	1,743	139	300	12	29
PDK1	Q9Z2A0	AGC/PKB	2,096	3,878	100	294	2	2
CHK1	O35280	CAMK/CAMKL/CHK1	3,301	7,388	112	276	0	0
MarkmA10	A0AUV4	CAMK/CAMKL	2,975	6,291	22	272	0	0
LCK	P06240	TK/Src	1,136	1,569	111	269	7	42
MAP2K5	Q9WVS7	STE/STE7	2,561	5,353	90	265	6	19
GSK3A	Q2NL51	CMGC/GSK	3,185	9,577	58	262	1	1
PITSLRE	P24788	CMGC/CDK	3,025	7,575	48	261	0	0
TAK1	Q923A8	TKL/MLK	1,506	2,078	127	258	0	0
TGFBR1	Q64729	TKL/STKR	2,014	3,726	84	257	22	44
MAP3K1	P53349	STE/STE11	2,542	5,216	97	256	3	9
MAP2K4	P47809	STE/STE7	2,561	5,353	83	252	2	14
RAF1	Q99N57	TKL/RAF	1,191	1,601	141	252	2	2
AKT2	Q60823	AGC/AKT	2,201	4,246	93	248	0	0
HIPK2	Q9QZR5	CMGC/DYRK	3,673	10,097	87	248	1	1
SGK3	Q9ERE3	AGC/SGK	2,436	5,023	79	247	0	0
SYK	P48025	TK/Syk	1,194	1,698	91	245	1	3
ROCK2	P70336	AGC/DMPK; AGC/DMPK/ROCK	2,160	4,184	51	241	0	0
ATM	Q62388	Atypical/PIKK/ATM	1,154	1,523	148	239	1	1

TRRAP	Q3UH32	Atypical/PIKK	700	879	81	234	0	0
PKCa	Q4VA93	AGC/PKC	1,997	3,762	97	233	0	0
KIT	Q8C8K9	TK/PDGFR	1,169	1,675	105	229	3	10
MAP2K2	Q9D7B0	STE/STE7	2,561	5,353	83	225	0	0
PKCd	P28867	AGC/PKC	1,997	3,762	76	220	0	0
ZAP70	P43404	TK/Syk	1,194	1,698	81	216	1	1
FGR	Q8BGM0	TK/Src	1,136	1,569	62	211	0	0
CASK	O70589	CAMK	2,639	5,207	49	205	0	0
PKACa	P05132	AGC/PKA	2,093	3,910	76	204	2	8
DYRK2	Q5U4C9	CMGC/DYRK	3,673	10,097	62	201	0	0
IGF1R	Q60751	TK/InsR	1,184	1,720	81	200	2	7
p38g	O08911	CMGC/MAPK	2,918	7,241	47	197	0	0
p38b	Q569F1	CMGC/MAPK	2,918	7,241	53	196	0	0
CDK9	Q99J95	CMGC/CDK	3,025	7,575	46	195	1	17
AurB	Q8C6C1	Other/AUR/AUR-B	1,982	3,354	80	193	0	0
JAK2	Q62120	TK/JakA	1,209	1,675	95	192	12	34
smMLCK	B1B1A8	CAMK/MLCK	2,889	5,880	82	191	0	0
ILK	O55222	TKL/MLK	1,506	2,078	70	188	0	0
ErbB3	Q61526	TK/EGFR	1,180	1,641	77	187	1	3
MET	P16056	TK/Met	1,213	1,714	81	187	1	10
FMS	P09581	TK/PDGFR	1,169	1,675	81	187	1	2
YES	Q04736	TK/Src	1,136	1,569	57	185	1	3
PKD1	Q62101	CAMK/PKD	2,962	6,072	63	183	1	4
KDR	P35918	TK/VEGFR	1,244	1,793	81	180	0	0
MAPKAPK2	P49138	CAMK/MAPKAPK	3,042	6,693	56	174	0	0
BRAF	P28028	TKL/RAF	1,191	1,601	77	174	2	2
DNAPK	P97313	Atypical/PIKK/DNAPK	941	1,218	70	173	0	0
AKT3	Q9WUA6	AGC/AKT	2,201	4,246	55	172	0	0
BTK	P35991	TK/Tec	1,215	1,696	79	168	8	15
AurA	P97477	Other/AUR/AUR-A	2,098	3,893	71	167	0	0
MAP2K7	Q8CE90	STE/STE7	2,561	5,353	59	166	1	3
BMPr1A	P36895	TKL/STKR	2,014	3,726	68	166	0	0
CRIK	P49025	AGC/DMPK	2,134	4,080	67	164	1	1
MARK2	Q571J8	CAMK/CAMKL	2,975	6,291	40	164	1	8

MAP2K3	O09110	STE/STE7	2,561	5,353	58	162	3	11
MOK	Q9WVS4	CMGC	2,837	6,985	32	158	0	0
CDK7	Q03147	CMGC/CDK	3,025	7,575	47	155	0	0
FES	P16879	TK/Fer/Fer; TK/Fer/Fes	1,499	2,172	49	155	0	0
PDGFRa	P26618	TK/PDGFR	1,169	1,675	72	155	0	0
CDK8	Q8R3L8	CMGC/CDK	3,025	7,575	37	148	0	0
SGK2	Q9QZS5	AGC/SGK	2,436	5,023	33	143	0	0
PCTAIRE1	Q04735	CMGC/CDK	3,025	7,575	30	140	0	0
MAP2K6	P70236	STE/STE7	2,561	5,353	51	140	1	1
PRKX	Q922R0	AGC/PKA	2,093	3,910	65	139	0	0
RSK2	P18654	AGC/RSK	2,174	4,248	55	139	2	9
PAK1	O88643	STE/STE20	2,468	4,948	53	139	5	19
PAK2	Q8CIN4	STE/STE20	2,468	4,948	54	139	0	0
p38d	Q9Z1B7	CMGC/MAPK	2,918	7,241	29	138	0	0
EphA5	Q60629	TK/Eph	1,232	1,749	69	135	0	0
CaMK4	Q8BGR3	CAMK/CAMK1	3,093	6,598	55	134	0	0
AMPKa2	B1ASQ8	CAMK/CAMKL/AMPK	3,090	6,698	37	133	0	0
p70S6Kb	Q9Z1M4	AGC/RSK	2,174	4,248	45	132	0	0
CK1a	Q8BK63	CK1	1,869	3,996	64	132	0	0
PLK4	Q64702	Other/PLK	2,832	6,336	52	132	2	4
FER	P70451	TK/Fer/Fer; TK/Fer/Fes	1,499	2,172	43	132	1	5
FGFR1	P16092	TK/FGFR	1,260	1,813	66	132	0	0
FGFR2	P21803	TK/FGFR	1,260	1,813	58	132	0	0
FLT1	P35969	TK/VEGFR	1,244	1,793	60	131	3	9
RET	P35546	TK/Ret	1,221	1,699	72	129	0	0
LKB1	Q9WTK7	CAMK/CAMKL/LKB	3,144	6,752	59	128	1	1
MLK2	Q66L42	TKL/MLK	1,506	2,078	53	127	0	0
MarkmA3	Q9QYZ5	CAMK/CAMKL	2,975	6,291	22	126	0	0
CK1e	Q9JMK2	CK1	1,869	3,996	46	126	2	9
CaMK2b	Q5SVJ0	CAMK/CAMK2	2,722	5,454	36	124	3	7
JAK1	B1ASP2	TK/JakA	1,209	1,675	62	124	0	0
PAK4	Q8BTW9	STE/STE20	2,468	4,948	41	123	0	0
PKCb	P68404	AGC/PKC	1,997	3,762	41	121	1	1
DAPK1	Q80YE7	CAMK/DAPK	2,754	5,513	36	116	0	0

MarkmD1	Q8C0X8	CAMK/CAMKL	2,975	6,291	15	112	0	0
CLK1	Q3UXB6	CMGC	2,837	6,985	15	112	0	0
MAP3K4	Q6PDG6	STE/STE11	2,542	5,216	38	112	0	0
AMPKa1	Q5EG47	CAMK/CAMKL/AMPK	3,090	6,698	34	110	1	8
ITK	Q03526	TK/Tec	1,215	1,696	40	102	0	0
CDKL5	Q3UTQ8	CMGC	2,837	6,985	16	101	0	0
ERK3	Q61532	CMGC/MAPK	2,918	7,241	25	101	0	0
BMPR1B	P36898	TKL/STKR	2,014	3,726	45	101	8	29
DYRK1A	Q61214	CMGC/DYRK	3,673	10,097	26	100	1	1
JAK3	Q62137	TK/JakA	1,209	1,675	53	100	1	2
DMPK1	P54265	AGC/DMPK	2,134	4,080	42	99	0	0
PKCt	Q02111	AGC/PKC	1,997	3,762	42	99	0	0
SMG1	Q8BKX6	Atypical/PIKK	700	879	39	98	0	0
NIK	Q9WUL6	STE/STE-Unique/NIK	3,230	7,255	38	98	1	1
PKR	Q03963	Other/PEK	609	719	67	97	0	0
ACTR2B	P27040	TKL/STKR	2,014	3,726	29	93	0	0
PFTAIRE1	O35495	CMGC/CDK	3,025	7,575	22	91	0	0
CDK11	Q8BWD8	CMGC/CDK	3,025	7,575	12	91	0	0
BMPR2	O35607	TKL/STKR	2,014	3,726	47	91	2	2
TRKB	P15209	TK/Trk	1,238	1,769	52	89	2	2
FLT4	P35917	TK/VEGFR	1,244	1,793	34	89	0	0
CSK	Q8VCW1	TK/Csk	1,173	1,645	53	88	2	5
TRKA	Q3UFB7	TK/Trk	1,238	1,769	54	88	1	1
ALK2	P37172	TKL/STKR	2,014	3,726	31	87	7	18
LATS2	Q7TSJ6	AGC	1,790	3,258	36	86	1	1
EphA1	Q60750	TK/Eph	1,232	1,749	36	85	1	1
PKN2	Q3TBR3	AGC	1,790	3,258	30	84	1	7
TAO2	Q6ZQ29	STE/STE20	2,468	4,948	33	83	0	0
TAO3	Q8BYC6	STE/STE20	2,468	4,948	32	82	0	0
HPK1	P70218	STE/STE20	2,468	4,948	30	81	3	11
MAP3K3	Q61084	STE/STE11	2,542	5,216	36	80	1	4
TAO1	Q5F2E8	STE/STE20	2,468	4,948	32	80	0	0
PIM2	Q62070	CAMK	2,639	5,207	23	79	0	0
PEK	Q9Z2B5	Other/PEK	609	719	43	79	1	2

ICK	Q9JKV2	CMGC	2,837	6,985	10	78	0	0
EphA4	Q80VZ2	TK/Eph	1,232	1,749	32	77	0	0
BLK	Q8K2M8	TK/Src	1,136	1,569	24	76	0	0
GPRK4	Q3V151	AGC/GRK	2,435	5,086	20	75	0	0
COT	Q07174	STE/STE-Unique/COT	2,862	5,818	36	75	0	0
KSR1	Q61097	TKL/RAF	1,191	1,601	35	73	1	1
MarkmA6	Q9QYZ6	CAMK/CAMKL	2,975	6,291	14	72	0	0
CaMK2g	Q923T9	CAMK/CAMK2	2,722	5,454	22	71	0	0
CaMK2d	Q6PHZ2	CAMK/CAMK2	2,722	5,454	17	69	2	18
ALK	P97793	TK/AIk	1,228	1,727	40	69	0	0
PKCi	Q5DTK3	AGC/PKC	1,997	3,762	22	67	0	0
RSK1	Q9WUT3	AGC/RSK	2,174	4,248	19	66	2	9
TBK1	Q9WUN2	Other/IKK	1,343	2,245	25	66	2	9
TIE2	B1AWS8	TK/Tie	1,197	1,663	52	66	2	2
MAP3K2	Q61083	STE/STE11	2,542	5,216	29	64	1	4
FGFR4	Q03142	TK/FGFR	1,260	1,813	26	64	0	0
IRAK4	Q8R4K2	TKL/IRAK	1,102	1,417	34	64	0	0
CAMK1g	Q91VB2	CAMK/CAMK1	3,093	6,598	23	63	0	0
QIK	Q8CFH6	CAMK/CAMKL	2,975	6,291	22	63	0	0
MARK1	Q14DQ3	CAMK/CAMKL	2,975	6,291	6	62	0	0
SIK	Q60670	CAMK/CAMKL	2,975	6,291	26	62	1	1
NLK	O54949	CMGC/MAPK	2,918	7,241	23	62	2	8
MSK1	Q8C050	AGC/RSK	2,174	4,248	29	61	1	2
MNK2	Q8CDB0	CAMK/MAPKAPK	3,042	6,693	14	61	0	0
SRPK1	O70551	CMGC	2,837	6,985	11	61	1	12
RON	Q62190	TK/Met	1,213	1,714	32	61	0	0
ARAF	P04627	TKL/RAF	1,191	1,601	34	61	1	1
MAPKAPK5	O54992	CAMK/MAPKAPK	3,042	6,693	23	60	2	5
DAPK3	O54784	CAMK/DAPK	2,754	5,513	29	59	2	7
Obscn	A2AAJ9	CAMK	2,639	5,207	10	57	1	5
MAPKAPK3	Q3UMW7	CAMK/MAPKAPK	3,042	6,693	23	57	0	0
BMX	B1AUL6	TK/Tec	1,215	1,696	23	57	0	0
TRKC	Q6VNS1	TK/Trk	1,238	1,769	36	57	1	1
CaMK1a	Q91YS8	CAMK/CAMK1	3,093	6,598	25	56	0	0

PKD3	Q5FWX6	CAMK/PKD	2,962	6,072	19	56	0	0
LYN	P25911	TK/Src	1,136	1,569	13	56	13	56
BRK	Q64434	TK/Src	1,136	1,569	20	55	1	2
IKKe	Q8C2I3	Other/IKK	1,343	2,245	23	54	0	0
YSK1	Q6IR17	STE/STE20	2,468	4,948	23	54	0	0
NIM1	Q8BHI9	CAMK/CAMKL	2,975	6,291	16	53	0	0
ALK1	Q91YR0	TKL/STKR	2,014	3,726	21	52	0	0
Wnk1	P83741	Other/Wnk	630	716	26	51	0	0
GCK	Q61161	STE/STE20	2,468	4,948	13	51	0	0
PAK5	Q8C015	STE/STE20	2,468	4,948	18	51	0	0
PSKH1	Q91YA2	CAMK	2,639	5,207	13	50	0	0
PAK6	Q3ULB5	STE/STE20	2,468	4,948	15	49	0	0
EphB4	Q8C7S3	TK/Eph	1,232	1,749	22	49	0	0
TEC	Q3U436	TK/Tec	1,215	1,696	19	49	0	0
ALK4	Q61271	TKL/STKR	2,014	3,726	19	48	0	0
MLK3	Q80XI6	TKL/MLK	1,506	2,078	18	47	1	2
PKG1	P0C605	AGC/PKG	2,347	4,535	13	46	3	23
DCLK3	Q8BWQ5	CAMK	2,639	5,207	9	46	0	0
PDHK1	Q3U5E5	Atypical/PDHK	1,142	1,587	14	45	0	0
EphA2	Q3UNI2	TK/Eph	1,232	1,749	18	45	0	0
EphB1	Q8CBF3	TK/Eph	1,232	1,749	17	45	1	1
EphB3	Q91YS9	TK/Eph	1,232	1,749	18	45	0	0
DLK	Q60700	TKL/MLK	1,506	2,078	18	43	1	2
ACTR2	P27038	TKL/STKR	2,014	3,726	15	43	0	0
DCLK1	Q9JLM8	CAMK	2,639	5,207	9	42	0	0
Trb3	Q8K4K2	CAMK	2,639	5,207	14	40	1	3
OSR1	Q6P9R2	STE/STE20	2,468	4,948	15	40	0	0
DRAK2	Q8BG48	CAMK/DAPK	2,754	5,513	20	39	0	0
Wnk4	Q80UE6	Other/Wnk	630	716	21	39	1	1
TIE1	Q8BGI2	TK/Tie	1,197	1,663	32	39	0	0
MarkmA5	Q9QYZ3	CAMK/CAMKL	2,975	6,291	15	38	0	0
PRP4	C7G3P2	CMGC/DYRK	3,673	10,097	6	38	1	11
MST1	Q9JI11	STE/STE20	2,468	4,948	19	38	2	2
EphB6	O08644	TK/Eph	1,232	1,749	15	38	0	0

PIM3	P58750	CAMK	2,639	5,207	13	37	0	0
PCTAIRE3	Q04899	CMGC/CDK	3,025	7,575	12	37	0	0
RSK4	A2CEE7	AGC/RSK	2,174	4,248	9	36	0	0
PASK	Q8CEE6	CAMK/CAMKL	2,975	6,291	15	36	0	0
EphA3	Q8BRB1	TK/Eph	1,232	1,749	17	35	0	0
MRCKa	B2RXX8	AGC/DMPK	2,134	4,080	14	34	0	0
HIPK1	A9R9X0	CMGC/DYRK	3,673	10,097	11	33	0	0
DYRK1B	Q9Z188	CMGC/DYRK	3,673	10,097	12	33	0	0
STLK3	Q9Z1W9	STE/STE20	2,468	4,948	17	33	2	2
MLK4	Q8VDG6	TKL/MLK	1,506	2,078	12	33	0	0
PKCh	Q8K2K8	AGC/PKC	1,997	3,762	10	32	0	0
SPEG	Q62407	CAMK	2,639	5,207	8	32	0	0
Wnk3	Q80XP9	Other/Wnk	630	716	16	32	1	1
RSKL1	Q8BLK9	AGC	1,790	3,258	7	31	0	0
CaMK1b	Q9QYK9	CAMK/CAMK1	3,093	6,598	14	30	0	0
RHOK	Q9WVL4	AGC/GRK	2,435	5,086	15	29	0	0
CDK10	Q3UMM4	CMGC/CDK	3,025	7,575	9	27	0	0
NEK6	Q9ES70	Other/NEK	1,083	1,498	11	27	1	1
EphA8	A3KG07	TK/Eph	1,232	1,749	10	27	0	0
TSSK1	Q80YU1	CAMK	2,639	5,207	9	26	0	0
NuaK1	Q641K5	CAMK/CAMKL	2,975	6,291	9	26	0	0
CLK2	O35491	CMGC	2,837	6,985	5	26	1	3
TNIK	B9EKN8	STE/STE20	2,468	4,948	5	26	0	0
EphA7	Q8BSU8	TK/Eph	1,232	1,749	10	26	0	0
MNK1	Q3U1I8	CAMK/MAPKAPK	3,042	6,693	9	25	0	0
AXL	Q80YQ3	TK/Axl	1,222	1,752	11	24	0	0
SRC	P05480	TK/Src	1,136	1,569	8	24	8	24
IRAK2	Q8CFA1	TKL/IRAK	1,102	1,417	16	24	1	5
TSSK2	Q6P8M9	CAMK	2,639	5,207	6	23	0	0
MarkmB1	Q8C0V7	CAMK/CAMKL	2,975	6,291	7	23	0	0
SRPK2	O54781	CMGC	2,837	6,985	4	23	1	12
GCN2	A2AUM0	Other/PEK	609	719	16	23	1	2
Wnk2	Q3UH66	Other/Wnk	630	716	11	23	0	0
ABL2	Q4JIM5	TK/Abl	1,238	1,743	11	23	0	0

PDHK4	O70571	Atypical/PDHK	1,142	1,587	13	22	0	0
DAPK2	Q8VDF3	CAMK/DAPK	2,754	5,513	11	22	1	1
ATR	Q9JKK8	Atypical/PIKK/ATR	882	1,118	13	21	1	1
MARK4	Q8CIP4	CAMK/CAMKL	2,975	6,291	6	21	0	0
MER	Q60805	TK/Axl	1,222	1,752	15	21	0	0
FRK	Q922K9	TK/Src	1,136	1,569	8	21	0	0
ZAK	Q9ESL4	TKL/MLK	1,506	2,078	9	21	0	0
STK33	Q924X7	CAMK	2,639	5,207	4	20	0	0
NuaK2	Q8BZN4	CAMK/CAMKL	2,975	6,291	7	20	2	7
KHS2	Q99JP0	STE/STE20	2,468	4,948	3	20	0	0
EPHA6	B9EIV2	TK/Eph	1,232	1,749	8	20	0	0
ALK7	A2AJR4	TKL/STKR	2,014	3,726	9	20	0	0
PCTAIRE2	Q8K0D0	CMGC/CDK	3,025	7,575	5	19	0	0
MLK1	Q3U1V8	TKL/MLK	1,506	2,078	8	19	0	0
CAMK1d	Q8BW96	CAMK/CAMK1	3,093	6,598	10	18	0	0
BRSK1	Q5RJI5	CAMK/CAMKL	2,975	6,291	4	18	0	0
MarkmA1	Q8C0N0	CAMK/CAMKL	2,975	6,291	8	18	0	0
DYRK3	Q922Y0	CMGC/DYRK	3,673	10,097	4	18	0	0
MISR2	Q8K592	TKL/STKR	2,014	3,726	10	18	0	0
MSK2	Q3U3M8	AGC/RSK	2,174	4,248	8	17	0	0
TSSK3	Q9D2E1	CAMK	2,639	5,207	5	17	0	0
VRK2	Q8BN21	CK1	1,869	3,996	6	17	3	13
AurC	O88445	Other/AUR	1,714	2,813	2	17	0	0
NEK7	Q9ES74	Other/NEK	1,083	1,498	5	17	0	0
MRCKb	B2RQQ7	AGC/DMPK	2,134	4,080	2	16	0	0
GPRK5	Q8VEB1	AGC/GRK	2,435	5,086	9	16	0	0
caMLCK	Q3UIZ8	CAMK/MLCK	2,889	5,880	9	16	0	0
BARK2	Q3UYH7	AGC/GRK	2,435	5,086	8	15	0	0
Trb1	Q8K4K4	CAMK	2,639	5,207	8	15	0	0
MAP3K6	Q9WTR2	STE/STE11	2,542	5,216	7	15	1	6
MarkmC2	Q3UT86	CAMK/CAMKL	2,975	6,291	7	14	0	0
MSSK1	Q9Z0G2	CMGC	2,837	6,985	3	14	0	0
CHED	Q69ZA1	CMGC/CDK	3,025	7,575	1	14	0	0
IRAK3	Q8K4B2	TKL/IRAK	1,102	1,417	10	14	0	0

MELK	Q3TPU1	CAMK/CAMKL	2,975	6,291	5	13	0	0
BRSK2	Q69Z98	CAMK/CAMKL	2,975	6,291	3	13	0	0
LOK	B1ATW8	STE/STE20	2,468	4,948	5	13	0	0
DCLK2	Q6PGN3	CAMK	2,639	5,207	3	12	0	0
SSTK	Q925K9	CAMK	2,639	5,207	5	12	0	0
MarkmC1	Q3UTA8	CAMK/CAMKL	2,975	6,291	6	12	0	0
QSK	Q6P4S6	CAMK/CAMKL	2,975	6,291	3	12	0	0
PHKg1	P07934	CAMK/PHK	3,079	6,479	8	12	0	0
CLK4	O35493	CMGC	2,837	6,985	2	12	0	0
Trb2	Q8K4K3	CAMK	2,639	5,207	5	11	0	0
PHKg2	A6H632	CAMK/PHK	3,079	6,479	8	11	0	0
TTBK1	Q6PCN3	CK1	1,869	3,996	2	11	0	0
JNK1	Q91Y86	CMGC/MAPK	2,918	7,241	2	11	2	11
PDHK3	Q922H2	Atypical/PDHK	1,142	1,587	5	10	0	0
TTBK2	A2AW15	CK1	1,869	3,996	1	10	0	0
MST2	Q9JI10	STE/STE20	2,468	4,948	6	10	0	0
CTK	P41242	TK/Csk	1,173	1,645	4	10	0	0
PDGFRb	P05622	TK/PDGFR	1,169	1,675	3	9	3	9
MarkmB2	B7ZNH4	CAMK/CAMKL	2,975	6,291	1	8	0	0
SgK085	Q5SUV5	CAMK/MLCK	2,889	5,880	6	8	0	0
PKN3	Q8K045	AGC	1,790	3,258	3	7	0	0
FRAP	Q9JLN9	Atypical/PIKK/FRAP	2,735	5,940	3	7	3	7
TSSK5	Q8C1R0	CAMK	2,639	5,207	3	7	0	0
CK1g3	Q8C4X2	CK1	1,869	3,996	1	7	0	0
NEK8	Q91ZR4	Other/NEK	1,083	1,498	6	7	1	1
STLK6	Q8K4T3	STE/STE20	2,468	4,948	4	7	0	0
MST4	Q99JT2	STE/STE20	2,468	4,948	5	7	0	0
MST3	Q99KH8	STE/STE20	2,468	4,948	5	7	0	0
YANK3	Q8QZV4	AGC	1,790	3,258	3	6	0	0
GPRK6	O70293	AGC/GRK	2,435	5,086	1	6	1	6
VACAMKL	Q3UHL1	CAMK	2,639	5,207	3	6	0	0
MarkmE2	A2AQX6	CAMK/CAMKL	2,975	6,291	2	6	0	0
CK1g2	Q99K78	CK1	1,869	3,996	4	6	0	0
CDKL2	Q9QUK0	CMGC	2,837	6,985	1	6	0	0

ERK7	Q80Y86	CMGC/MAPK	2,918	7,241	1	6	0	0
NEK10	Q3UGM2	Other/NEK	1,083	1,498	3	6	0	0
NEK11	Q8C0Q4	Other/NEK	1,083	1,498	2	6	0	0
KHS1	Q8BPM2	STE/STE20	2,468	4,948	2	6	0	0
CLK3	O35492	CMGC	2,837	6,985	2	5	0	0
HIPK4	Q3V016	CMGC/DYRK	3,673	10,097	3	5	0	0
MAP3K5	O35099	STE/STE11	2,542	5,216	2	5	2	5
EphA10	Q8BYG9	TK/Eph	1,232	1,749	2	5	0	0
HH498	B2RTJ7	TKL/MLK	1,506	2,078	1	5	0	0
BCKDK	Q3UC13	Atypical/PDHK	1,142	1,587	2	4	0	0
MarkmD3	Q32M05	CAMK/CAMKL	2,975	6,291	1	4	0	0
VRK1	Q3UWH3	CK1	1,869	3,996	1	4	1	4
CDKL4	Q3TZA2	CMGC	2,837	6,985	2	4	0	0
LZK	Q1HKZ5	TKL/MLK	1,506	2,078	4	4	0	0
MAST1	Q9R1L5	AGC	1,790	3,258	2	3	0	0
SNRK	B9EK90	CAMK/CAMKL	2,975	6,291	2	3	0	0
PKD2	Q8BZ03	CAMK/PKD	2,962	6,072	2	3	0	0
MAK	Q04859	CMGC	2,837	6,985	1	3	0	0
CDKL1	Q8CEQ0	CMGC	2,837	6,985	1	3	0	0
MAST2	B1AST8	AGC	1,790	3,258	1	2	0	0
YANK1	Q8BGW6	AGC	1,790	3,258	2	2	0	0
DYRK4	Q8BI55	CMGC/DYRK	3,673	10,097	1	2	0	0
NEK4	Q6GTE9	Other/NEK	1,083	1,498	2	2	0	0
HRI	Q69ZK8	Other/PEK	609	719	1	2	1	2
MYO3A	Q8K3H5	STE/STE20	2,468	4,948	2	2	1	1
NDR2	B2KFR4	AGC	1,790	3,258	1	1	0	0
PDHK2	Q9JK42	Atypical/PDHK	1,142	1,587	1	1	1	1
VRK3	Q8K3G5	CK1	1,869	3,996	1	1	0	0
CCRK	Q9JHU3	CMGC/CDK	3,025	7,575	1	1	0	0
ERK4	Q6P5G0	CMGC/MAPK	2,918	7,241	1	1	0	0
FGFR3	Q7TSI8	TK/FGFR	1,260	1,813	1	1	1	1
IRAK1	Q62406	TKL/IRAK	1,102	1,417	1	1	1	1

Drosophila melanogaster

cdc2	P23572	CMGC/CDK/CDC2	1,271	2,390	117	319	8	39
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cdc2c	P23573	CMGC/CDK/CDC2	1,271	2,390	106	279	8	35
bsk	P92208	CMGC/MAPK	1,169	2,132	131	255	15	35
polo	P52304	Other/PLK	1,127	1,972	94	244	9	21
Akt1	Q8INB9	AGC/AKT	1,132	1,926	85	179	11	37
SAK	O97143	Other/PLK	1,127	1,972	78	178	7	15
aur	Q9VGF9	Other/AUR	971	1,521	73	162	1	1
FRAP	Q9VK45	Atypical/PIKK/FRAP	1,022	1,664	80	144	4	5
Cdk5	P48609	CMGC/CDK	1,257	2,338	70	141	8	11
sgg	P18431	CMGC/GSK	1,308	2,692	55	138	5	11
rok	Q9VXE3	AGC/DMPK; AGC/DMPK/ROCK	1,152	1,936	32	133	4	22
mbt	Q9VXE5	STE/STE20	1,159	1,920	61	126	2	3
rl	P40417	CMGC/MAPK	1,169	2,132	48	125	18	47
Ckl1alpha	P08181	Other/CK2	935	1,875	44	122	1	1
Cdk9	O17432	CMGC/CDK	1,257	2,338	54	120	1	2
Cdk7	Q24216	CMGC/CDK	1,257	2,338	52	120	1	8
ial	Q9VKN7	Other/AUR	971	1,521	43	108	0	0
CG8878	Q7KMI3	CK1	664	1,135	31	99	0	0
wt5	Q24590	AGC	947	1,531	40	88	1	1
dco	O76324	CK1	664	1,135	49	87	0	0
SNF1A	O18645	CAMK/CAMKL/AMPK	1,620	2,983	47	82	0	0
grp	O61661	CAMK/CAMKL/CHK1	1,724	3,289	40	81	8	10
Pak	B7Z0W0	STE/STE20	1,159	1,920	43	77	3	6
Mpk2	O62618	CMGC/MAPK	1,169	2,132	42	76	1	2
trc	Q9NBK5	AGC	947	1,531	28	71	0	0
ird5	Q9VEZ5	Other/IKK	604	814	40	71	0	0
put	C5WLU3	TKL/STKR	806	1,158	34	66	2	3
phl	P11346	TKL/RAF	558	650	40	65	4	8
tkv	Q9VMT1	TKL/STKR	806	1,158	30	64	0	0
CG17528	Q7PLI7	CAMK	1,405	2,448	29	62	0	0
SAX	Q7JQ36	TKL/STKR	806	1,158	35	62	1	1
Ckl1alpha	P54367	CK1	664	1,135	25	59	0	0
gskt	P83101	CMGC/GSK	1,308	2,692	30	58	0	0
KP78b	Q9VGQ0	CAMK/CAMKL	1,553	2,824	15	57	7	44
Dsor1	Q24324	STE/STE7	1,132	1,905	36	55	6	10

CG11489	Q8T3S1	CMGC	1,133	2,044	17	53	11	32
Cdk4	Q7K306	CMGC/CDK	1,257	2,338	31	53	10	15
S6kII	Q94533	AGC/RSK	1,149	1,944	29	52	4	7
ball	Q7KRY6	CK1	664	1,135	24	52	0	0
aPKC	A1Z9X0	AGC/PKC	1,017	1,720	29	51	0	0
CG11228	Q8T0S6	STE/STE20	1,159	1,920	25	51	5	12
JIL1	Q9V3I5	AGC/RSK	1,149	1,944	29	49	0	0
Ilk	Q9V400	TKL/MLK	619	781	22	49	0	0
CG10522	Q9VTY8	AGC/DMPK	1,135	1,896	26	47	0	0
Pka-C1	P12370	AGC/PKA	1,168	1,967	25	44	7	10
Src64B	P00528	TK/Src	146	175	24	43	4	6
Nek2	Q9W3N8	Other/NEK	330	391	17	40	1	1
trbl	Q9V3Z1	CAMK	1,405	2,448	24	39	4	10
Strn-Mlck	A1ZA66	CAMK/MLCK	1,527	2,707	22	37	0	0
Caki	Q24210	CAMK	1,405	2,448	19	36	2	3
MAPk-Ak2	P49071	CAMK/MAPKAPK	1,518	2,803	16	35	2	3
PKA-C3	P16912	AGC/PKA	1,168	1,967	22	34	1	2
Pk92B	Q9VDS9	STE/STE11	1,135	1,859	19	34	0	0
Pak3	Q9VEV1	STE/STE20	1,159	1,920	17	34	1	1
Egfr	P04412	TK/EGFR	145	170	19	33	2	2
Pkg21D	Q03042	AGC/PKG	1,247	2,134	17	32	0	0
CG7597	Q9VP22	CMGC/CDK	1,257	2,338	7	32	0	0
fray	Q9VE62	STE/STE20	1,159	1,920	13	31	0	0
Cdk8	C9QP81	CMGC/CDK	1,257	2,338	11	28	2	5
Pk34A	Q9VK37	CMGC/GSK	1,308	2,692	16	28	0	0
Fps85D	P18106	TK/Fer/Fer; TK/Fer/Fes	184	227	15	28	1	2
wit	Q9VZI9	TKL/STKR	806	1,158	8	28	0	0
Pkc98E	P13678	AGC/PKC	1,017	1,720	21	27	0	0
Gcn2	Q9V9X8	Other/PEK	201	223	17	27	0	0
CG8485	Q0E981	CAMK/CAMKL	1,553	2,824	8	26	0	0
Lk6	Q9VGI4	CAMK/MAPKAPK	1,518	2,803	12	26	3	5
ninaC	P10676	STE/STE20	1,159	1,920	12	25	0	0
Tak1	Q9V3Q6	TKL/MLK	619	781	11	25	2	8
smi35A	Q9V3D5	CMGC/DYRK	1,567	3,128	14	24	0	0

lic	O62602	STE/STE7	1,132	1,905	19	24	0	0
CG7236	Q1RKV9	CMGC	1,133	2,044	9	23	0	0
hep	Q23977	STE/STE7	1,132	1,905	17	23	5	6
Src42A	Q9V9J3	TK/Src	146	175	11	23	2	7
CG4549	Q70PP2	Atypical/PIKK	187	200	16	22	0	0
CG9374	Q8T9L5	CAMK/CAMKL/LKB	1,614	2,948	16	22	0	0
Abl	P00522	TK/Abl	157	186	11	22	2	8
Pk61C	C7LAC8	AGC/PKB	1,057	1,716	17	21	4	6
p38b	O61443	CMGC/MAPK	1,169	2,132	12	20	4	7
PEK	Q9NIV1	Other/PEK	201	223	14	20	0	0
S6k	Q9VR61	AGC/RSK	1,149	1,944	11	18	4	6
CG17309	Q9VGK8	TK/Csk	150	175	10	18	1	1
gek	Q9W1B0	AGC/DMPK	1,135	1,896	10	17	0	0
slpr	Q95UN8	TKL/MLK	619	781	6	17	0	0
CG4290	Q9W532	CAMK/CAMKL	1,553	2,824	4	16	0	0
CG7125	Q9VE91	CAMK/PKD	1,606	2,937	10	16	0	0
Mkk4	O61444	STE/STE7	1,132	1,905	12	16	0	0
Fak56D	Q0E917	TK/Fak	153	176	10	16	0	0
btl	Q09147	TK/FGFR	169	197	13	16	0	0
CG6535	Q5EAK6	Atypical/PIKK/ATM	331	369	14	15	0	0
Pitslre	Q9VPC0	CMGC/CDK	1,257	2,338	5	15	0	0
STLK	P83098	STE/STE20	1,159	1,920	6	15	0	0
htl	Q07407	TK/FGFR	169	197	8	15	0	0
gwl	Q95TN8	AGC	947	1,531	5	14	0	0
CG14305	Q9VE58	CAMK	1,405	2,448	13	13	0	0
KP78a	Q9VGP9	CAMK/CAMKL	1,553	2,824	8	13	0	0
pII	Q05652	TKL/IRAK	425	506	10	13	0	0
Pkc53E	P05130	AGC/PKC	1,017	1,720	7	12	0	0
hop	Q24592	TK/JakA	149	177	10	12	1	1
CG8789	Q9VW24	TKL/MLK	619	781	7	12	0	0
Pk17E	Q9VWQ2	AGC	947	1,531	9	11	9	11
CG12069	Q9VA47	AGC/PKA	1,168	1,967	7	11	0	0
CG7028	Q9Y145	CMGC/DYRK	1,567	3,128	5	11	0	0
ksr	Q24171	TKL/RAF	558	650	9	11	1	1

CG4629	Q9VPW3	CAMK/CAMKL	1,553	2,824	8	10	0	0
inaC	P13677	AGC/PKC	1,017	1,720	6	9	1	1
CG9222	Q8T4D4	CAMK	1,405	2,448	7	9	0	0
Doa	A4V3J9	CMGC	1,133	2,044	3	9	3	9
InR	P09208	TK/InsR	161	193	8	9	2	2
CG7156	Q9VEA9	AGC	947	1,531	4	8	0	0
CG8565	Q9VXN5	CMGC	1,133	2,044	2	8	0	0
CG17090	Q9W0Q1	CMGC/DYRK	1,567	3,128	2	8	0	0
Btk29A	P08630	TK/Tec	163	189	8	8	3	3
CG10177	Q9VCL7	CAMK	1,405	2,448	7	7	0	0
CaMKI	Q7JMV3	CAMK/CAMK1	1,580	2,912	7	7	0	0
P38c	P83100	CMGC/MAPK	1,169	2,132	3	7	0	0
Tak1	Q4V4A7	TKL/MLK	619	781	6	7	0	0
CG6498	Q9VUQ9	AGC	947	1,531	4	6	1	1
CG15072	Q4QQA7	CAMK/CAMKL	1,553	2,824	5	6	0	0
CG6800	Q9VD82	CMGC/CDK	1,257	2,338	5	6	2	3
CG2309	Q9W354	CMGC/MAPK	1,169	2,132	5	6	2	3
shark	Q24145	TK/Syk	162	191	3	6	0	0
mei-41	Q9VXG8	Atypical/PIKK/ATR	234	256	5	5	1	1
CaMKII	A4V133	CAMK/CAMK2	1,446	2,559	2	5	2	5
CG6114	Q9VUV4	CAMK/CAMKL	1,553	2,824	4	5	0	0
cdc2rk	A1Z840	CMGC/CDK	1,257	2,338	4	5	0	0
CG5169	Q9VEN3	STE/STE20	1,159	1,920	4	5	0	0
PDK	P91622	Atypical/PDHK	468	562	2	4	1	2
CG12147	Q7JWT4	CK1	664	1,135	3	4	0	0
CG7094	Q9VJC2	CK1	664	1,135	3	4	0	0
CG9962	Q9VQE3	CK1	664	1,135	3	4	0	0
CG2577	Q9VYN5	CK1	664	1,135	3	4	0	0
Eph	Q9V4E5	TK/Eph	150	176	3	4	0	0
Gprk1	P32865	AGC/GRK	1,254	2,194	2	3	0	0
CG3277	Q8IQ00	TK/VEGFR	147	180	2	3	0	0
BABO	A1Z7L9	TKL/STKR	806	1,158	2	3	2	3
PKCdelta	P83099	AGC/PKC	1,017	1,720	1	2	1	2
CG14217	Q0KHQ5	STE/STE20	1,159	1,920	1	2	1	2

CG4527	Q9W179	STE/STE20	1,159	1,920	2	2	0	0
mnb	Q9VX06	CMGC/DYRK	1,567	3,128	1	1	1	1
Alk	Q7KJ08	TK/Alk	153	181	1	1	0	0
<i>Caenorhabditis elegans</i>								
cdk-1	P34556	CMGC/CDK/CDC2	656	1,092	45	98	0	0
kin-3	P18334	Other/CK2	571	1,015	31	58	0	0
mpk-1	P39745	CMGC/MAPK	608	1,016	21	50	15	29
par-1	Q9TW45	CAMK/CAMKL	1,014	1,528	15	26	0	0
spk-1	Q03563	CMGC	589	979	12	23	5	9
pkc-3	Q19266	AGC/PKC	645	895	8	21	2	3
zyg-8	Q95QC4	CAMK	942	1,375	9	21	8	19
pmk-1	Q17446	CMGC/MAPK	608	1,016	9	20	6	15
air-2	O01427	Other/AUR	513	677	13	19	1	1
lin-2	P54936	CAMK	942	1,375	10	16	7	13
air-1	Q21271	Other/AUR	513	677	13	16	3	3
C45B11.1	Q18637	STE/STE20	636	945	9	15	0	0
let-502	P92199	AGC/DMPK; AGC/DMPK/ROCK	686	967	5	14	0	0
M04C9.5	P90932	CMGC	589	979	11	13	0	0
lit-1	Q9U9Y8	CMGC/MAPK	608	1,016	3	13	3	13
sax-1	Q2L6W9	AGC	622	839	2	12	0	0
T01C8.1	Q95ZQ4	CAMK/CAMKL/AMPK	1,037	1,576	6	12	1	1
ttn-1	Q8ISF7	CAMK/MLCK	984	1,472	1	12	0	0
akt-2	Q9XTG7	AGC/AKT	739	1,055	5	11	3	8
F28B12.3	Q19848	CK1	383	612	6	11	0	0
cdk-4	Q9XTR1	CMGC/CDK	643	1,065	6	11	0	0
akt-1	Q17941	AGC/AKT	739	1,055	6	10	3	6
W10G6.2	Q2PJ68	AGC/SGK	784	1,175	6	10	4	7
unc-43	O62305	CAMK/CAMK2	966	1,421	7	10	2	2
ZK617.1a	Q23551	CAMK/MLCK	984	1,472	3	10	0	0
cmk-1	Q9TXJ0	CAMK/CAMK1	1,013	1,537	4	9	0	0
chk-2	Q9U1Y5	CAMK/RAD53	1,001	1,501	5	9	0	0
nsy-1	Q21029	STE/STE11	597	867	6	9	0	0
pak-1	Q17850	STE/STE20	636	945	7	9	0	0
mkk-4	Q20347	STE/STE7	584	878	3	9	1	1

kin-29	Q21017	CAMK/CAMKL	1,014	1,528	3	8	1	4
B0495.2	Q09437	CMGC/CDK	643	1,065	3	8	1	5
pat-4	Q9TZC4	TKL/MLK	303	359	5	8	0	0
F32D8.1	Q19962	CAMK	942	1,375	5	7	0	0
F23C8.8	Q9TXI1	CAMK/CAMKL	1,014	1,528	5	7	0	0
Y43D4A.6	Q9NF25	CAMK/CAMKL/CHK1	1,089	1,697	5	7	0	0
C44C8.6	Q9TZ16	CAMK/MAPKAPK	1,025	1,557	5	7	0	0
Y42A5A.4	Q9U2H1	CMGC	589	979	3	7	0	0
plk-1	P34331	Other/PLK	606	985	5	7	2	2
mig-15	Q23356	STE/STE20	636	945	5	7	5	7
mek-2	Q10664	STE/STE7	584	878	3	7	1	4
sma-6	Q09488	TKL/STKR	358	463	7	7	6	6
F47F2.1	Q7JP68	AGC/PKA	728	1,004	4	6	0	0
B0261.2	Q95Q95	Atypical/PIKK/FRAP	500	766	6	6	0	0
F49C5.4	O17879	CAMK/CAMKL	1,014	1,528	4	6	0	0
aak-1	P45894	CAMK/CAMKL/AMPK	1,037	1,576	3	6	0	0
chk-1	Q9N3Z3	CAMK/CAMKL/CHK1	1,089	1,697	5	6	0	0
T08D2.7	A4F324	CAMK/RAD53	1,001	1,501	4	6	0	0
H25P06.2	Q9TVL3	CMGC/CDK	643	1,065	4	6	3	5
F14H12.4	Q9NB31	STE/STE20	636	945	5	6	0	0
F31E3.2	Q8MYQ1	AGC	622	839	2	5	1	4
R06A10.4	O44747	CAMK	942	1,375	3	5	0	0
sad-1	Q19469	CAMK/CAMKL	1,014	1,528	4	5	0	0
R02C2.2	O44546	CAMK/CAMKL/CHK1	1,089	1,697	3	5	0	0
C03C10.1	P42168	CK1	383	612	3	5	0	0
K04C1.5	Q21204	CK1	383	612	3	5	0	0
cdk-5	O18142	CMGC/CDK	643	1,065	4	5	0	0
mbk-1	Q8WQL7	CMGC/DYRK	824	1,417	5	5	1	1
F55G1.8	Q20845	Other/PLK	606	985	5	5	0	0
M03C11.1	Q21483	AGC	622	839	3	4	0	0
egl-4	O76360	AGC/PKG	799	1,140	2	4	0	0
T01H8.1a	Q21734	AGC/RSK	727	1,047	2	4	0	0
pdhk-2	Q02332	Atypical/PDHK	225	254	1	4	0	0
B0511.4	O61821	CAMK	942	1,375	2	4	0	0

R02C2.1	Q86S44	CAMK/CAMKL/CHK1	1,089	1,697	3	4	0	0
jnk-1	Q8WQG9	CMGC/MAPK	608	1,016	3	4	1	1
jkk-1	Q9UAH1	STE/STE7	584	878	1	4	1	4
F33E2.2	O01700	TKL/MLK	303	359	2	4	1	3
F46F6.2	B6VQ53	AGC	622	839	2	3	0	0
kin-1	P21137	AGC/PKA	728	1,004	2	3	0	0
pdk-1	Q9Y1J3	AGC/PKB	659	899	1	3	0	0
kin-13	P34885	AGC/PKC	645	895	3	3	0	0
pkc-2	P90980	AGC/PKC	645	895	2	3	1	2
T25E12.4	O45818	CAMK/PKD	1,007	1,492	2	3	0	0
Y18D10A.5	Q9U2Q9	CMGC/GSK	686	1,285	2	3	0	0
T07A9.3	O44408	CMGC/MAPK	608	1,016	3	3	0	0
ZC581.1	O01775	Other/NEK	143	168	3	3	0	0
Y59A8B.23	Q9GRY2	STE/STE20	636	945	3	3	0	0
K08B12.5	O01583	AGC/DMPK	679	949	2	2	0	0
Y47D3A.16	Q9NAH6	AGC/RSK	727	1,047	1	2	0	0
Y38H8A.3	O62426	CK1	383	612	2	2	0	0
F52B5.2	Q20643	CMGC	589	979	2	2	0	0
K03E5.3	O61847	CMGC/CDK/CDC2	656	1,092	2	2	0	0
mbk-2	Q9XTF3	CMGC/DYRK	824	1,417	2	2	0	0
C05D10.2	Q11179	CMGC/MAPK	608	1,016	1	2	0	0
mek-1	Q21307	STE/STE7	584	878	2	2	0	0
daf-2	Q968Y9	TK/InsR	35	39	2	2	1	1
lin-45	Q07292	TKL/RAF	208	236	2	2	0	0
ksr-1	Q19380	TKL/RAF	208	236	2	2	0	0
daf-4	P50488	TKL/STKR	358	463	1	2	1	2
W04B5.5	Q9UA62	AGC/PKB	659	899	1	1	0	0
tpa-1	P34722	AGC/PKC	645	895	1	1	0	0
smg-1	O01510	Atypical/PIKK	76	80	1	1	0	0
K12C11.4	O44997	CAMK/DAPK	963	1,427	1	1	0	0
Y50D7A.3	Q9N3L4	CAMK/PHK	1,030	1,554	1	1	0	0
F36H12.9	O76711	CK1	383	612	1	1	0	0
E02H4.6	Q19043	CK1	383	612	1	1	0	0
F46F2.2	Q20471	CK1	383	612	1	1	0	0

Y106G6E.6	Q8WQ99	CK1	383	612	1	1	0	0
E02H4.3	Q17917	CMGC	589	979	1	1	0	0
F39H11.3	P90866	CMGC/CDK	643	1,065	1	1	0	0
pmk-2	Q8MXI4	CMGC/MAPK	608	1,016	1	1	1	1
plk-2	Q9N2L7	Other/PLK	606	985	1	1	0	0
VZC374L.1	O01706	STE/STE7	584	878	1	1	0	0
sek-1	Q95YI9	STE/STE7	584	878	1	1	1	1
vab-1	O61460	TK/Eph	32	32	1	1	0	0
R05H5.4	Q21764	TK/Fer/Fer; TK/Fer/Fes	47	48	1	1	0	0
C24A1.3	O17055	TKL/MLK	303	359	1	1	0	0
mom-4	Q9XTC6	TKL/MLK	303	359	1	1	0	0
ksr-2	Q8T4N7	TKL/RAF	208	236	1	1	0	0

Saccharomyces cerevisiae

CDC28	P00546	CMGC/CDK/CDC2	978	1,889	298	1,062	220	874
SNF1	P06782	CAMK/CAMKL/AMPK	1,200	2,531	244	787	163	547
YCK1	P23291	CK1	795	1,467	221	720	165	550
MCK1	P21965	CMGC/GSK	985	2,312	179	665	129	511
TPK1	P06244	AGC/PKA	687	1,166	192	567	171	521
CKA1	P15790	Other/CK2	935	1,866	155	533	104	355
SLT2	Q00772	CMGC/MAPK	897	1,667	169	530	128	419
PHO85	P17157	CMGC/CDK	962	1,831	162	521	123	437
YCK2	P23292	CK1	795	1,467	146	513	123	431
CKA2	P19454	Other/CK2	935	1,866	146	482	79	265
RAD53	P22216	CAMK/RAD53	1,110	2,116	163	405	131	342
SSN3	P39073	CMGC/CDK	962	1,831	127	389	76	232
CLA4	P48562	STE/STE20	754	1,272	160	376	135	310
BCK1	Q01389	STE/STE11	789	1,283	145	366	114	301
FUS3	P16892	CMGC/MAPK	897	1,667	107	347	77	222
TOR1	P35169	Atypical/PIKK/FRAP	837	1,365	135	346	97	240
HOG1	P32485	CMGC/MAPK	897	1,667	128	339	81	220
CMK1	P27466	CAMK/CAMK1	1,191	2,425	118	338	83	231
HSL1	P34244	CAMK/CAMKL	1,163	2,366	117	336	92	249
GIN4	Q12263	CAMK/CAMKL	1,163	2,366	83	335	56	231
RIM11	P38615	CMGC/GSK	985	2,312	76	334	39	187

YAK1	P14680	CMGC/DYRK	1,220	2,679	101	331	39	124
IME2	P32581	CMGC	861	1,586	90	327	56	195
CDC5	P32562	Other/PLK	1,088	2,177	108	315	81	229
STE20	Q03497	STE/STE20	754	1,272	123	307	82	207
KSS1	P14681	CMGC/MAPK	897	1,667	102	297	68	166
MEK1	P24719	CAMK	1,003	1,810	94	295	67	194
PKC1	P24583	AGC/PKC	616	1,071	118	291	73	177
CTK1	Q03957	CMGC/CDK	962	1,831	123	284	97	220
DBF2	P22204	AGC	577	957	119	280	102	247
TOR2	P32600	Atypical/PIKK/FRAP	837	1,365	98	261	61	140
TPK2	P06245	AGC/PKA	687	1,166	92	258	45	154
SKY1	Q03656	CMGC	861	1,586	76	242	69	228
SGV1	P23293	CMGC/CDK	962	1,831	88	242	62	166
HRR25	P29295	CK1	795	1,467	78	241	61	202
IPL1	P38991	Other/AUR/IPL1-yeast	801	1,445	90	230	54	123
CHK1	P38147	CAMK/CAMKL/CHK1	1,281	2,757	93	215	53	111
PBS2	P08018	STE/STE7	716	1,131	90	204	62	134
SCH9	P11792	AGC/AKT	737	1,287	68	199	34	107
RCK2	P38623	CAMK/CAMK1	1,191	2,425	44	198	40	187
CDC15	P27636	STE/STE11	789	1,283	69	195	46	129
TPK3	P05986	AGC/PKA	687	1,166	69	194	44	110
CAK1	P43568	CMGC/CDK	962	1,831	70	190	49	120
STE11	P23561	STE/STE11	789	1,283	65	190	36	103
KIN2	P13186	CAMK/CAMKL	1,163	2,366	51	189	45	173
YOL045W	Q08217	CAMK/CAMKL	1,163	2,366	50	189	40	120
SSK2	P53599	STE/STE11	789	1,283	72	189	51	135
CMK2	P22517	CAMK/CAMK1	1,191	2,425	57	186	22	55
YPL141C	Q03002	CAMK/CAMKL	1,163	2,366	46	181	44	172
RIM15	P43565	AGC	577	957	63	179	44	119
DUN1	P39009	CAMK/RAD53	1,110	2,116	98	176	70	126
KIN28	P06242	CMGC/CDK	962	1,831	72	176	19	41
CBK1	P53894	AGC	577	957	51	172	37	122
FUN31	P31374	CAMK/CAMKL	1,163	2,366	45	166	34	139
KCC4	P25389	CAMK/CAMKL	1,163	2,366	38	164	17	87

YGL059W	P53170	Atypical/PDHK	458	578	46	151	45	150
PRR1	P28708	CAMK	1,003	1,810	39	149	23	106
YPK2	P18961	AGC/AKT	737	1,287	39	129	16	40
KIN1	P13185	CAMK/CAMKL	1,163	2,366	35	129	20	76
KIN4	Q01919	CAMK/CAMKL	1,163	2,366	46	123	44	120
SMK1	P41808	CMGC/MAPK	897	1,667	35	120	19	58
YPL150W	Q12152	CAMK/CAMKL	1,163	2,366	52	112	50	105
STE7	P06784	STE/STE7	716	1,131	48	111	11	22
RCK1	P38622	CAMK/CAMK1	1,191	2,425	41	106	41	106
TRA1	P38811	Atypical/PIKK	241	268	64	104	47	75
YKL161C	P36005	CMGC/MAPK	897	1,667	26	93	7	26
MKK2	P32491	STE/STE7	716	1,131	47	90	17	31
YPK1	P12688	AGC/AKT	737	1,287	29	87	19	48
KIN82	P25341	AGC/RSK	742	1,262	33	85	22	61
YCK3	P39962	CK1	795	1,467	31	83	18	55
MKK1	P32490	STE/STE7	716	1,131	44	82	19	37
GCN2	P15442	Other/PEK	186	213	56	81	30	49
SPS1	P08458	STE/STE20	754	1,272	34	77	16	38
YMR291W	Q03533	CAMK	1,003	1,810	15	76	13	71
YOL128C	Q12222	CMGC/GSK	985	2,312	16	74	10	42
YKL171W	P36003	CAMK	1,003	1,810	27	70	26	68
KIC1	P38692	STE/STE20	754	1,272	20	66	12	37
DBF20	P32328	AGC	577	957	24	65	15	46
YNR047W	P53739	AGC/RSK	742	1,262	23	64	19	53
KNS1	P32350	CMGC	861	1,586	26	64	21	54
PKH1	Q03407	AGC/PKB	706	1,184	27	61	17	39
SKM1	Q12469	STE/STE20	754	1,272	32	60	27	54
SSK22	P25390	STE/STE11	789	1,283	22	56	17	47
MEC1	P38111	Atypical/PIKK/ATR	303	348	46	55	25	33
MRK1	P50873	CMGC/GSK	985	2,312	17	55	12	25
TEL1	P38110	Atypical/PIKK/ATM	411	484	34	49	19	26
KIN3	P22209	Other/NEK	323	411	17	39	14	33
PKH2	Q12236	AGC/PKB	706	1,184	21	33	14	20
YDR466W	Q03306	AGC/PKB	706	1,184	16	30	16	30

YBR028C	P38070	AGC/RSK	742	1,262	10	20	6	14
YIL042C	P40530	Atypical/PDHK	458	578	6	16	6	16

Supplemental Table S13 – The conserved KSRs were detected by the comparative analysis. SC, *S. cerevisiae*; CE, *C. elegans*; DM, *D. melanogaster*; MM, *M. musculus*; HS, *H. sapiens*.

Conservation	String & Exp. PPI					Exp. PPI				
	PK	Sub.	Site	ssKSR	Ave	PK	Sub.	Site	ssKSR	Ave
In Five organisms										
SC	1	1	1	1	1.0	1	1	1	1	1.0
CE	1	1	1	1	1.0	0	0	0	0	N/A
DM	1	1	8	8	1.0	0	0	0	0	N/A
MM	1	1	11	11	1.0	0	0	0	0	N/A
HS	1	1	11	11	1.0	1	1	11	11	1.0
In Four organisms										
SC-CE-DM-MM										
SC	1	1	1	1	1.0	1	1	1	1	1.0
CE	1	1	1	1	1.0	0	0	0	0	N/A
DM	1	1	8	8	1.0	0	0	0	0	N/A
MM	1	1	11	11	1.0	0	0	0	0	N/A
SC-CE-DM-HS										
SC	2	4	23	23	1.0	2	3	17	17	1.0
CE	2	4	14	14	1.0	0	0	0	0	N/A
DM	2	4	21	21	1.0	0	0	0	0	N/A
HS	3	5	82	95	1.2	2	3	45	45	1.0
SC-CE-MM-HS										
SC	9	8	25	26	1.0	6	5	13	13	1.0
CE	9	8	17	19	1.1	1	1	1	1	1.0
MM	8	8	46	50	1.1	0	0	0	0	N/A
HS	11	8	47	64	1.4	8	6	39	44	1.1
SC-DM-MM-HS										
SC	11	19	56	71	1.3	10	17	50	63	1.3
DM	12	20	49	73	1.5	0	0	0	0	N/A
MM	12	24	92	140	1.5	1	1	17	17	1.0
HS	15	24	98	180	1.8	7	10	53	94	1.8
CE-DM-MM-HS										
CE	3	3	3	3	1.0	0	0	0	0	N/A
DM	3	3	11	11	1.0	0	0	0	0	N/A
MM	4	3	13	14	1.1	0	0	0	0	N/A
HS	3	3	14	14	1.0	1	1	11	11	1.0
In three organisms										
SC-CE-DM										
SC	4	6	30	30	1.0	2	3	17	17	1.0
CE	4	6	16	16	1.0	0	0	0	0	N/A
DM	4	6	23	23	1.0	0	0	0	0	N/A
SC-CE-MM										
SC	10	9	27	28	1.0	6	5	13	13	1.0
CE	10	9	18	20	1.1	1	1	1	1	1.0
MM	9	9	51	55	1.1	0	0	0	0	N/A
SC-CE-HS										
SC	12	16	56	58	1.0	8	8	31	31	1.0
CE	12	16	36	39	1.1	1	1	1	1	1.0
HS	14	17	147	195	1.3	9	11	89	95	1.1
SC-DM-MM										

SC	11	21	59	74	1.3	10	17	50	63	1.3
DM	12	22	57	87	1.5	0	0	0	0	N/A
MM	12	26	105	153	1.5	1	1	17	17	1.0
SC-DM-HS										
SC	17	41	160	193	1.2	14	30	108	127	1.2
DM	17	42	113	156	1.4	2	2	2	2	1.0
HS	21	50	261	440	1.7	11	19	115	165	1.4
SC-MM-HS										
SC	26	52	167	217	1.3	21	40	116	135	1.2
MM	30	60	246	371	1.5	2	2	18	18	1.0
HS	34	63	282	483	1.7	22	31	170	255	1.5
CE-DM-MM										
CE	3	3	3	3	1.0	0	0	0	0	N/A
DM	3	3	11	11	1.0	0	0	0	0	N/A
MM	4	3	13	14	1.1	0	0	0	0	N/A
CE-DM-HS										
CE	8	14	27	27	1.0	1	1	1	1	1.0
DM	9	13	38	43	1.1	1	1	1	1	1.0
HS	9	14	110	132	1.2	3	5	58	58	1.0
CE-MM-HS										
CE	17	18	29	33	1.1	2	2	2	2	1.0
MM	19	18	86	100	1.2	0	0	0	0	N/A
HS	20	21	97	120	1.2	10	8	60	65	1.1
DM-MM-HS										
DM	39	82	179	293	1.6	9	11	25	34	1.4
MM	43	91	371	565	1.5	8	9	50	52	1.0
HS	47	93	376	709	1.9	32	46	204	308	1.5
In two organisms										
SC-CE										
SC	18	24	78	84	1.1	11	12	41	44	1.1
CE	18	23	46	52	1.1	3	2	3	5	1.7
SC-DM										
SC	19	62	227	285	1.3	16	42	147	168	1.1
DM	19	62	166	227	1.4	2	2	2	2	1.0
SC-MM										
SC	29	69	213	279	1.3	25	47	134	157	1.2
MM	33	77	311	453	1.5	2	2	18	18	1.0
SC-HS										
SC	35	130	446	653	1.5	32	92	295	360	1.2
HS	45	144	724	1,291	1.8	34	61	327	446	1.4
CE-DM										
CE	22	26	55	67	1.2	1	1	1	1	1.0
DM	24	25	90	129	1.4	3	2	22	43	2.0
CE-MM										
CE	20	22	36	41	1.1	2	2	2	2	1.0
MM	22	22	112	134	1.2	1	1	12	12	1.0
CE-HS										
CE	26	42	75	83	1.1	3	4	4	4	1.0
HS	30	45	264	348	1.3	13	16	125	137	1.1
DM-MM										
DM	52	104	245	471	1.9	13	15	33	45	1.4

<i>MM</i>	59	116	493	850	1.7	10	12	63	65	1.0
<i>DM-HS</i>										
<i>DM</i>	55	163	407	715	1.8	14	22	39	55	1.4
<i>HS</i>	65	179	885	1,750	2.0	43	78	382	520	1.4
<i>MM-HS</i>										
<i>MM</i>	242	1,213	5,606	15,960	2.8	70	116	461	551	1.2
<i>HS</i>	243	1,218	6,366	19,320	3.0	172	472	2,490	4,219	1.7

Supplemental Table S14 – The number of p-sites for each PK in the human liver PPN. The top 10 PKs with the most p-sites are marked in yellow.

PK Name	Uniprot	Predictor	String & Exp. PPI		Exp. PPI	
			Protein	Site	Protein	Site
AKT1	P31749	AGC/AKT	244	428	33	60
CK2a2	P19784	Other/CK2	123	420	13	34
Erk1	P27361	CMGC/MAPK	138	285	15	24
CDK2	P24941	CMGC/CDK/CDC2	98	278	9	17
FRAP	P42345	Atypical/PIKK/FRAP	126	265	11	17
Erk2	P28482	CMGC/MAPK	112	230	25	41
GSK3A	P49840	CMGC/GSK	80	229	7	14
p38a	Q16539	CMGC/MAPK	92	209	18	35
CDC2	P06493	CMGC/CDK/CDC2	84	198	16	35
PKCa	P17252	AGC/PKC	91	182	18	40
CDK4	P11802	CMGC/CDK	75	153	8	12
PKN1	Q16512	AGC	80	151	3	7
PLK1	P53350	Other/PLK	61	147	11	23
CDK5	Q00535	CMGC/CDK	58	145	5	14
CDK9	P50750	CMGC/CDK	61	143	21	48
CLK1	B4DFW7	CMGC	21	141	6	34
p70S6K	P23443	AGC/RSK	76	137	8	23
PKACa	P17612	AGC/PKA	75	136	38	74
CK1d	P48730	CK1	42	129	0	0
Trio	O75962	CAMK	61	129	1	2
CaMK2g	Q13555	CAMK/CAMK2	80	129	4	9
PKCb	D3DWF5	AGC/PKC	57	126	7	8
p38g	P53778	CMGC/MAPK	57	126	4	13
p38b	Q15759	CMGC/MAPK	58	125	3	11
MAP2K1	Q02750	STE/STE7	63	125	8	12
CK1e	P49674	CK1	43	123	1	1
PKCd	Q05655	AGC/PKC	57	109	11	16
SGK1	O00141	AGC/SGK	48	109	7	15
ROCK1	Q13464	AGC/DMPK; AGC/DMPK/ROCK	41	109	6	25
IKKb	O14920	Other/IKK	66	107	13	24
PKCe	Q02156	AGC/PKC	49	106	4	6
IKKa	O15111	Other/IKK	64	106	9	16
RSK2	P51812	AGC/RSK	48	103	5	10
p38d	O15264	CMGC/MAPK	50	102	2	5
CHK1	O14757	CAMK/CAMKL/CHK1	50	98	4	9
PKCg	P05129	AGC/PKC	53	97	4	8
MSK1	O75582	AGC/RSK	44	96	5	11
Trad	O60229	CAMK	46	94	1	1
PKN2	Q16513	AGC	43	93	7	7
AKT2	P31751	AGC/AKT	46	93	4	10
PKCi	P41743	AGC/PKC	39	92	3	5
CDK6	Q00534	CMGC/CDK	47	92	2	3
PKD1	Q1KKQ2	CAMK/PKD	55	88	3	5
CK2a1	P68400	Other/CK2	35	88	35	88
CHK2	O96017	CAMK/RAD53	52	88	3	7
CDK8	P49336	CMGC/CDK	30	87	9	34
PKCt	Q04759	AGC/PKC	39	83	3	7

PKCz	Q05513	AGC/PKC	45	83	6	11
p70S6Kb	Q9UBS0	AGC/RSK	37	82	3	6
PKACg	P22612	AGC/PKA	48	78	0	0
TGFbR2	D2JY11	TKL/STKR	39	76	0	0
ROCK2	O75116	AGC/DMPK; AGC/DMPK/ROCK	30	76	1	2
MARK2	Q7KZI7	CAMK/CAMKL	40	75	8	15
MSK2	O75676	AGC/RSK	28	72	2	4
CDK7	P50613	CMGC/CDK	34	71	7	14
RSK4	Q9UK32	AGC/RSK	25	69	0	0
RSK1	Q15349	AGC/RSK	27	68	2	8
DYRK1A	Q13627	CMGC/DYRK	27	68	7	20
PAK2	Q13177	STE/STE20	34	63	14	31
TGFbR1	P36897	TKL/STKR	36	62	11	18
MAP3K1	Q13233	STE/STE11	43	62	8	10
HIPK2	Q9H2X6	CMGC/DYRK	30	62	1	1
PKG1	A5YM56	AGC/PKG	36	61	9	14
SRPK1	Q96SB4	CMGC	18	60	10	38
RAF1	P04049	TKL/RAF	45	60	6	6
PIM1	P11309	CAMK	21	59	2	7
PKD2	Q9BZL6	CAMK/PKD	32	59	2	5
PKD3	O94806	CAMK/PKD	32	59	1	1
PKN3	Q6P5Z2	AGC	28	59	0	0
BARK1	P25098	AGC/GRK	33	59	5	18
CDKL2	B4DH08	CMGC	27	58	0	0
PKCh	P24723	AGC/PKC	26	57	1	1
LATS1	O95835	AGC	25	56	0	0
CaMK2d	Q13557	CAMK/CAMK2	27	56	3	16
IKKe	Q14164	Other/IKK	29	55	9	22
NRK	Q7Z2Y5	STE/STE20	30	53	0	0
AKT3	Q9Y243	AGC/AKT	28	53	3	6
TRRAP	Q9Y4A5	Atypical/PIKK	28	53	1	2
SRPK2	C9JQJ0	CMGC	13	52	1	1
MOK	Q9UQ07	CMGC	13	52	0	0
MAP3K3	Q99759	STE/STE11	31	52	25	45
RSKL1	Q96S38	AGC	15	50	0	0
PKG2	Q13237	AGC/PKG	24	50	2	3
smMLCK	Q15746	CAMK/MLCK	35	49	2	2
MAP2K4	P45985	STE/STE7	36	49	3	3
MAP3K5	Q99683	STE/STE11	32	47	5	6
MAP2K2	P36507	STE/STE7	28	46	5	6
CRK7	Q9NYV4	CMGC/CDK	10	45	3	19
Trb3	Q96RU7	CAMK	20	44	3	6
PIM2	Q9P1W9	CAMK	19	44	2	5
MAPKAPK2	P49137	CAMK/MAPKAPK	26	43	6	15
HIPK3	Q9H422	CMGC/DYRK	14	42	7	18
MARK1	Q9P0L2	CAMK/CAMKL	15	42	1	1
MAP2K6	P52564	STE/STE7	28	42	1	1
AurB	C7G533	Other/AUR/AUR-B	24	42	1	2
ILK	Q13418	TKL/MLK	33	42	4	7
Erk3	Q16659	CMGC/MAPK	19	40	1	1
AMPKa2	P54646	CAMK/CAMKL/AMPK	23	39	2	4
PLK3	Q9H4B4	Other/PLK	11	39	0	0
DYRK2	Q92630	CMGC/DYRK	20	39	0	0

BMPR1A	P36894	TKL/STKR	25	39	0	0
Erk5	Q13164	CMGC/MAPK	23	37	2	2
SMG1	Q96Q15	Atypical/PIKK	25	37	0	0
NIK	Q99558	STE/STE-Unique/NIK	25	36	5	5
PAK4	O96013	STE/STE20	22	35	1	1
MLK3	B2RDI6	TKL/MLK	21	35	0	0
PDHK4	Q16654	Atypical/PDHK	18	34	1	1
BARK2	P35626	AGC/GRK	14	33	1	5
BMPR1B	B4DSV1	TKL/STKR	19	33	4	6
LKB1	Q15831	CAMK/CAMKL/LKB	29	33	3	3
GSK3B	P49841	CMGC/GSK	13	32	13	32
Trb1	Q96RU8	CAMK	10	31	1	1
BRAF	P15056	TKL/RAF	23	31	3	3
PDK1	O15530	AGC/PKB	21	31	5	5
AMPKa1	Q13131	CAMK/CAMKL/AMPK	17	30	8	17
CaMK1a	Q14012	CAMK/CAMK1	19	30	2	3
TAK1	O43318	TKL/MLK	19	30	3	4
Erk7	Q8TD08	CMGC/MAPK	13	30	2	7
GPRK5	P34947	AGC/GRK	12	29	2	7
FAK	Q658W2	TK/Fak	22	29	7	10
CDK3	Q00526	CMGC/CDK/CDC2	9	29	1	1
NDR1	Q15208	AGC	14	28	0	0
PKR	P19525	Other/PEK	23	28	4	4
CaMK4	Q16566	CAMK/CAMK1	17	28	2	4
CDK11	Q9BWU1	CMGC/CDK	12	28	1	1
SPEG	Q15772	CAMK	7	27	0	0
MARK4	Q96L34	CAMK/CAMKL	15	27	5	14
MARK3	P27448	CAMK/CAMKL	13	27	2	2
MAP3K4	B9EG75	STE/STE11	14	27	0	0
RSK3	Q15418	AGC/RSK	8	26	8	26
TBK1	Q9UHD2	Other/IKK	19	26	5	6
HGK	Q53TX8	STE/STE20	15	26	2	2
AurA	O14965	Other/AUR/AUR-A	19	26	3	5
SGK3	Q96BR1	AGC/SGK	18	25	3	3
MAP2K5	Q13163	STE/STE7	19	25	2	4
DAPK3	O43293	CAMK/DAPK	16	25	0	0
PRP4	Q13523	CMGC/DYRK	10	24	4	8
TNIK	Q9UKE5	STE/STE20	9	24	2	2
PCTAIRE1	Q00536	CMGC/CDK	15	24	1	1
ALK1	P37023	TKL/STKR	11	24	0	0
PEK	B2RCU9	Other/PEK	19	24	0	0
MINK	Q8N4C8	STE/STE20	11	23	5	12
STLK5	Q7RTN6	STE/STE20	13	23	0	0
TAO1	Q7L7X3	STE/STE20	13	23	0	0
BMPR2	Q13873	TKL/STKR	15	23	2	5
PFTAIRE1	O94921	CMGC/CDK	18	23	0	0
ATM	Q13315	Atypical/PIKK/ATM	19	23	4	4
Erk4	P31152	CMGC/MAPK	11	23	0	0
GCK	Q12851	STE/STE20	13	22	1	1
PAK5	Q9P286	STE/STE20	15	21	1	2
MNK2	A4CYL7	CAMK/MAPKAPK	12	21	1	3
PDHK2	Q15119	Atypical/PDHK	13	21	2	4
LATS2	Q9NRM7	AGC	16	21	1	1

SRC	P12931	TK/Src	19	21	7	9
PAK6	Q9NQU5	STE/STE20	14	20	0	0
ACTR2B	Q13705	TKL/STKR	12	20	2	2
IRAK1	P51617	TKL/IRAK	19	20	4	4
STLK3	Q9UEW8	STE/STE20	11	19	1	1
ACTR2	P27037	TKL/STKR	8	19	0	0
PYK2	Q14289	TK/Fak	14	19	6	9
CDK10	Q15131	CMGC/CDK	9	19	0	0
DYRK3	O43781	CMGC/DYRK	2	18	0	0
RHOK	Q15835	AGC/GRK	8	18	0	0
HIPK1	Q86Z02	CMGC/DYRK	7	18	3	5
PIM3	Q86V86	CAMK	9	18	1	4
NEK2	P51955	Other/NEK	15	18	0	0
OSR1	O95747	STE/STE20	11	17	2	5
VRK1	Q99986	CK1	6	17	1	2
ALK4	P36896	TKL/STKR	9	17	2	2
MAPKAPK3	Q16644	CAMK/MAPKAPK	11	17	1	2
CHED	Q14004	CMGC/CDK	11	17	0	0
PCTAIRE3	B4DK03	CMGC/CDK	7	17	0	0
PLK4	O00444	Other/PLK	11	17	0	0
NuaK2	B4E0Y5	CAMK/CAMKL	12	17	0	0
ALK2	Q04771	TKL/STKR	8	17	1	3
SIK	P57059	CAMK/CAMKL	10	17	0	0
PCTAIRE2	Q00537	CMGC/CDK	8	16	0	0
ARAF	P10398	TKL/RAF	12	16	0	0
JNK2	P45984	CMGC/MAPK	8	16	8	16
DRAK2	O94768	CAMK/DAPK	6	15	0	0
NEK1	Q96PY6	Other/NEK	9	15	2	5
HPK1	Q92918	STE/STE20	10	15	5	6
CDKL5	O76039	CMGC	8	15	1	4
NuaK1	O60285	CAMK/CAMKL	14	15	1	1
QIK	Q9H0K1	CAMK/CAMKL	9	15	1	5
caMLCK	Q32MK0	CAMK/MLCK	10	14	0	0
STK33	Q9BYT3	CAMK	6	14	0	0
MST2	Q13188	STE/STE20	11	14	1	1
HRI	Q9BQI3	Other/PEK	10	14	0	0
DNAPK	P78527	Atypical/PIKK/DNAPK	12	14	6	6
PLK2	Q9NYY3	Other/PLK	7	14	0	0
MRCKb	Q9Y5S2	AGC/DMPK	5	13	0	0
PITSLRE	P21127	CMGC/CDK	4	13	4	13
Wnk4	Q96J92	Other/Wnk	10	13	0	0
CSK	P41240	TK/Csk	13	13	1	1
MAP3K2	Q9Y2U5	STE/STE11	9	13	2	3
DCLK1	O15075	CAMK	5	13	0	0
YANK3	Q86UX6	AGC	1	12	0	0
PAK1	Q13153	STE/STE20	8	12	8	12
Wnk1	Q9H4A3	Other/Wnk	9	12	2	2
ALK7	Q8NER5	TKL/STKR	5	12	0	0
FES	P07332	TK/Fer/Fer; TK/Fer/Fes	8	12	1	1
ICK	Q9UPZ9	CMGC	4	12	0	0
PSKH1	P11801	CAMK	9	12	0	0
NDR2	Q9Y2H1	AGC	3	11	0	0
KHS2	Q8IVH8	STE/STE20	5	11	1	1

YSK1	O00506	STE/STE20	9	11	3	3
FYN	P06241	TK/Src	9	11	4	5
COT	P41279	STE/STE-Unique/COT	8	11	0	0
MELK	Q53GX0	CAMK/CAMKL	8	11	2	3
DLK	Q12852	TKL/MLK	8	11	1	1
DYRK1B	Q9Y463	CMGC/DYRK	7	11	0	0
BRK1	Q8TDC3	CAMK/CAMKL	9	11	0	0
TAO3	Q9H2K8	STE/STE20	5	10	1	1
PHKg1	Q16816	CAMK/PHK	8	10	3	5
BRK2	Q8IWQ3	CAMK/CAMKL	8	10	0	0
LCK	P06239	TK/Src	8	10	3	4
PDGFRb	P09619	TK/PDGFR	9	10	2	2
skMLCK	Q9H1R3	CAMK/MLCK	10	10	1	1
MST1	Q13043	STE/STE20	8	10	1	1
NLK	Q9UBE8	CMGC/MAPK	3	10	1	1
AurC	Q9UQB9	Other/AUR	6	10	1	2
MYO3A	Q8NEV4	STE/STE20	6	9	0	0
EGFR	P00533	TK/EGFR	8	9	3	3
FER	P16591	TK/Fer/Fer; TK/Fer/Fes	7	9	1	1
YES	P07947	TK/Src	7	9	3	3
NIM1	Q8IY84	CAMK/CAMKL	9	9	0	0
CLK2	P49760	CMGC	5	9	0	0
CaMK1g	Q96NX5	CAMK/CAMK1	8	9	0	0
MAPKAPK5	Q8IW41	CAMK/MAPKAPK	4	8	4	8
STLK6	Q9C0K7	STE/STE20	6	8	1	1
SSTK	Q9BXA6	CAMK	5	8	1	2
Wnk3	B1AKG2	Other/Wnk	5	8	0	0
LOK	O94804	STE/STE20	5	8	1	2
SYK	P43405	TK/Syk	6	8	2	2
ABL1	Q59FK4	TK/Abl	4	8	0	0
KDR	P35968	TK/VEGFR	7	8	2	2
BTK	Q06187	TK/Tec	6	8	1	1
NEK6	B7Z2D9	Other/NEK	7	8	3	3
PRKX	P51817	AGC/PKA	7	8	2	2
MRCKa	Q5VT25	AGC/DMPK	8	8	0	0
PAK3	B2RCU6	STE/STE20	5	7	5	7
PASK	Q96RG2	CAMK/CAMKL	4	7	0	0
Trb2	Q92519	CAMK	6	7	0	0
FLT1	P17948	TK/VEGFR	6	7	2	2
IRAK4	Q9NWZ3	TKL/IRAK	7	7	0	0
PRKY	O43930	AGC/PKA	6	7	0	0
IRAK2	O43187	TKL/IRAK	6	7	0	0
DMPK1	Q09013	AGC/DMPK	5	6	5	6
PHKg2	P15735	CAMK/PHK	5	6	0	0
SGK2	Q9HBY8	AGC/SGK	4	6	1	1
ErbB2	P04626	TK/EGFR	6	6	0	0
INSR	P06213	TK/InsR	6	6	2	2
PDGFRa	P16234	TK/PDGFR	5	6	1	1
ZAP70	P43403	TK/Syk	4	6	1	1
MET	P08581	TK/Met	6	6	1	1
NEK3	P51956	Other/NEK	6	6	0	0
CK1a	D3DQG1	CK1	6	6	0	0
MLK2	Q02779	TKL/MLK	5	6	1	1

VRK2	Q86Y07	CK1	5	6	2	2
TSSK2	Q96PF2	CAMK	3	5	0	0
PDHK3	B4DXG6	Atypical/PDHK	4	5	1	1
CK1g3	Q9Y6M4	CK1	4	5	0	0
PDHK1	Q15118	Atypical/PDHK	3	5	2	2
ZAK	B8ZZU2	TKL/MLK	2	5	0	0
RET	P07949	TK/Ret	5	5	2	2
EphA2	P29317	TK/Eph	5	5	0	0
KSR1	Q8IVT5	TKL/RAF	5	5	0	0
GCN2	Q9P2K8	Other/PEK	5	5	0	0
QSK	Q9Y2K2	CAMK/CAMKL	4	5	0	0
DAPK2	Q9UIK4	CAMK/DAPK	3	5	0	0
KSR2	Q6VAB6	TKL/RAF	4	4	2	2
KIT	P10721	TK/PDGFR	4	4	2	2
JAK2	O60674	TK/JakA	4	4	1	1
SRM	Q9H3Y6	TK/Src	2	4	0	0
EphB2	P29323	TK/Eph	4	4	1	1
GPRK4	P32298	AGC/GRK	3	4	0	0
MISR2	Q16671	TKL/STKR	3	4	0	0
CLK3	Q59FC5	CMGC	3	4	0	0
DRAK1	Q9UEE5	CAMK/DAPK	3	4	0	0
KHS1	Q9Y4K4	STE/STE20	3	4	1	1
NEK8	Q86SG6	Other/NEK	3	4	0	0
CLK4	Q9HAZ1	CMGC	1	3	1	3
GPRK7	Q8WTQ7	AGC/GRK	2	3	0	0
BCKDK	O14874	Atypical/PDHK	2	3	1	2
TSSK4	Q6SA08	CAMK	1	3	0	0
NEK9	Q8TD19	Other/NEK	2	3	1	1
IGF1R	P08069	TK/InsR	3	3	2	2
FMS	P07333	TK/PDGFR	3	3	1	1
FGFR1	P11362	TK/FGFR	3	3	0	0
JAK1	P23458	TK/JakA	3	3	0	0
FGFR2	P21802	TK/FGFR	3	3	0	0
FGR	P09769	TK/Src	3	3	0	0
TYK2	P29597	TK/JakA	3	3	1	1
TRKA	P04629	TK/Trk	3	3	1	1
ITK	Q08881	TK/Tec	3	3	1	1
TIE2	Q02763	TK/Tie	3	3	0	0
BRK	Q13882	TK/Src	3	3	0	0
NEK7	Q8TDX7	Other/NEK	3	3	1	1
VACAMKL	B2RDF9	CAMK	2	3	0	0
PSKH2	Q96QS6	CAMK	3	3	0	0
IRAK3	Q9Y616	TKL/IRAK	3	3	0	0
PKACb	P22694	AGC/PKA	1	2	1	2
TTN	D3DPF9	CAMK/MLCK	2	2	2	2
ErbB3	P21860	TK/EGFR	2	2	0	0
JAK3	P52333	TK/JakA	2	2	0	0
BLK	P51451	TK/Src	2	2	0	0
EphA1	P21709	TK/Eph	2	2	0	0
EphA4	P54764	TK/Eph	2	2	0	0
IRR	P14616	TK/InsR	2	2	0	0
AXL	P30530	TK/Axl	2	2	1	1
ABL2	P42684	TK/Abl	2	2	1	1

EphB4	P54760	TK/Eph	2	2	0	0
BMX	P51813	TK/Tec	2	2	1	1
EphB6	D3DXD3	TK/Eph	2	2	1	1
ATR	Q13535	Atypical/PIKK/ATR	2	2	2	2
MER	Q12866	TK/Axl	2	2	0	0
MLK4	Q5TCX8	TKL/MLK	2	2	0	0
SgK085	Q86YV6	CAMK/MLCK	2	2	0	0
MAP2K7	O14733	STE/STE7	2	2	2	2
TSSK3	Q96PN8	CAMK	2	2	0	0
MST4	Q9P289	STE/STE20	2	2	2	2
CK1g2	P78368	CK1	2	2	0	0
MAP2K3	P46734	STE/STE7	2	2	2	2
MAK	P20794	CMGC	2	2	0	0
TTBK1	Q5TCY1	CK1	1	2	1	2
PFTAIRES2	Q96Q40	CMGC/CDK	1	1	0	0
HUNK	P57058	CAMK/CAMKL	1	1	1	1
ErbB4	Q15303	TK/EGFR	1	1	0	0
TRKC	Q16288	TK/Trk	1	1	0	0
ALK	Q9UM73	TK/Alk	1	1	0	0
RON	Q04912	TK/Met	1	1	0	0
EphA3	P29320	TK/Eph	1	1	0	0
TXK	P42681	TK/Tec	1	1	1	1
TYRO3	Q06418	TK/Axl	1	1	0	0
EphB3	P54753	TK/Eph	1	1	1	1
EphA7	Q15375	TK/Eph	1	1	1	1
EphA5	P54756	TK/Eph	1	1	0	0
EphA6	Q9UF33	TK/Eph	1	1	0	0
CaMK1b	B4E1A6	CAMK/CAMK1	1	1	0	0
EphA8	P29322	TK/Eph	1	1	0	0
TSSK1	Q9BXA7	CAMK	1	1	0	0
TRKB	Q16620	TK/Trk	1	1	1	1
SNRK	Q9NRH2	CAMK/CAMKL	1	1	0	0
NEK11	Q8NG66	Other/NEK	1	1	0	0
NEK4	P51957	Other/NEK	1	1	0	0
FGFR3	P22607	TK/FGFR	1	1	1	1
CK1g1	Q9HCP0	CK1	1	1	0	0
HH498	Q59H18	TKL/MLK	1	1	0	0
YANK2	Q9NY57	AGC	1	1	0	0

Supplemental Table S15 – All PKs with significantly over- or under-represented p-sites in the human liver PPN (p-value < 0.01).

PK Name	Uniprot	Predictor	String & Exp. PPI				
			Protein	Site	E-ratio	χ^2	p-value
<i>PKs with over-represented p-sites</i>							
CK2a2	P19784	Other/CK2	123	420	1.87	154.92	1.46E-35
CLK1	B4DFW7	CMGC	21	141	2.82	127.27	1.63E-29
AKT1	P31749	AGC/AKT	244	428	1.55	80.41	3.04E-19
MSK1	O75582	AGC/RSK	44	96	2.17	49.46	2.02E-12
RSK4	Q9UK32	AGC/RSK	25	69	2.41	44.96	2.01E-11
MSK2	O75676	AGC/RSK	28	72	2.24	39.80	2.81E-10
PKN2	Q16513	AGC	43	93	1.93	34.87	3.52E-09
p70S6K	P23443	AGC/RSK	76	137	1.67	32.18	1.40E-08
CK1d	P48730	CK1	42	129	1.69	31.24	2.28E-08
RSK1	Q15349	AGC/RSK	27	68	2.07	30.51	3.31E-08
Trio	O75962	CAMK	61	129	1.66	29.52	5.53E-08
SRPK2	C9JQJ0	CMGC	13	52	2.24	28.63	8.78E-08
SRPK1	Q96SB4	CMGC	18	60	2.10	27.91	1.27E-07
CK1e	P49674	CK1	43	123	1.63	26.11	3.22E-07
PKN1	Q16512	AGC	80	151	1.55	25.76	3.86E-07
PKCi	P41743	AGC/PKC	39	92	1.75	24.99	5.76E-07
PKACa	P17612	AGC/PKA	75	136	1.56	24.26	8.40E-07
RSK2	P51812	AGC/RSK	48	103	1.67	23.94	9.94E-07
RSKL1	Q96S38	AGC	15	50	2.12	23.75	1.10E-06
PAK2	Q13177	STE/STE20	34	63	1.93	23.47	1.27E-06
p70S6Kb	Q9UBS0	AGC/RSK	37	82	1.77	23.12	1.52E-06
IKKe	Q14164	Other/IKK	29	55	2.02	23.12	1.52E-06
RSK3	Q15418	AGC/RSK	8	26	2.70	21.19	4.15E-06
Trad	O60229	CAMK	46	94	1.64	20.07	7.45E-06
NDR2	Q9Y2H1	AGC	3	11	4.52	19.56	9.76E-06
YANK3	Q86UX6	AGC	1	12	3.98	18.14	2.05E-05
NDR1	Q15208	AGC	14	28	2.32	16.60	4.62E-05
SPEG	Q15772	CAMK	7	27	2.35	16.48	4.92E-05
PKCd	Q05655	AGC/PKC	57	109	1.48	15.06	1.04E-04
PKCa	P17252	AGC/PKC	91	182	1.35	14.82	1.18E-04
PIM1	P11309	CAMK	21	59	1.71	14.79	1.20E-04
PAK5	Q9P286	STE/STE20	15	21	2.52	14.79	1.20E-04
SGK1	O00141	AGC/SGK	48	109	1.47	14.48	1.42E-04
NRK	Q7Z2Y5	STE/STE20	30	53	1.74	13.96	1.87E-04
PKCt	Q04759	AGC/PKC	39	83	1.53	13.33	2.61E-04
MOK	Q9UQ07	CMGC	13	52	1.69	12.43	4.22E-04
PDHK4	Q16654	Atypical/PDHK	18	34	1.92	12.22	4.72E-04
PKD2	Q9BZL6	CAMK/PKD	32	59	1.62	11.95	5.47E-04
PKCb	D3DWF5	AGC/PKC	57	126	1.38	11.84	5.81E-04
MRCKb	Q9Y5S2	AGC/DMPK	5	13	2.88	11.80	5.91E-04
PITSLRE	P21127	CMGC/CDK	4	13	2.88	11.80	5.91E-04
PRP4	Q13523	CMGC/DYRK	10	24	2.14	11.57	6.72E-04
AMPKa2	P54646	CAMK/CAMKL/AMPK	23	39	1.80	11.50	6.97E-04
HIPK3	Q9H422	CMGC/DYRK	14	42	1.76	11.48	7.04E-04
AMPKa1	Q13131	CAMK/CAMKL/AMPK	17	30	1.95	11.25	7.95E-04
Trb3	Q96RU7	CAMK	20	44	1.70	10.70	1.07E-03

AKT2	P31751	AGC/AKT	46	93	1.43	10.67	1.09E-03
PKCe	Q02156	AGC/PKC	49	106	1.40	10.65	1.10E-03
IKKb	O14920	Other/IKK	66	107	1.38	10.11	1.47E-03
IKKa	O15111	Other/IKK	64	106	1.38	9.90	1.65E-03
PKD3	O94806	CAMK/PKD	32	59	1.52	9.01	2.68E-03
TNIK	Q9UKE5	STE/STE20	9	24	1.94	8.83	2.97E-03
PKN3	Q6P5Z2	AGC	28	59	1.51	8.76	3.08E-03
LATS1	O95835	AGC	25	56	1.52	8.54	3.48E-03
PAK1	Q13153	STE/STE20	8	12	2.47	8.02	4.62E-03
MARK1	Q9P0L2	CAMK/CAMKL	15	42	1.60	7.93	4.86E-03
GSK3A	P49840	CMGC/GSK	80	229	1.21	7.79	5.26E-03
BARK1	P25098	AGC/GRK	33	59	1.46	7.36	6.67E-03
PKG2	Q13237	AGC/PKG	24	50	1.51	7.35	6.71E-03
PKCg	P05129	AGC/PKC	53	97	1.32	6.77	9.25E-03
<i>PKs with under-represented p-sites</i>							
SRC	P12931	TK/Src	19	21	0.13	128.44	8.99E-30
EGFR	P00533	TK/EGFR	8	9	0.08	91.75	9.84E-22
FYN	P06241	TK/Src	9	11	0.11	79.07	5.98E-19
ErbB2	P04626	TK/EGFR	6	6	0.07	70.10	5.63E-17
LCK	P06239	TK/Src	8	10	0.13	61.82	3.76E-15
INSR	P06213	TK/InsR	6	6	0.09	54.70	1.41E-13
KIT	P10721	TK/PDGFR	4	4	0.07	54.19	1.82E-13
PDGFRb	P09619	TK/PDGFR	9	10	0.15	49.85	1.66E-12
IGF1R	P08069	TK/InsR	3	3	0.06	48.53	3.25E-12
ErbB3	P21860	TK/EGFR	2	2	0.04	48.29	3.68E-12
SYK	P43405	TK/Syk	6	8	0.13	46.07	1.14E-11
PDGFRa	P16234	TK/PDGFR	5	6	0.11	46.01	1.18E-11
ABL1	Q59FK4	TK/Abi	4	8	0.14	43.72	3.79E-11
JAK2	O60674	TK/JakA	4	4	0.08	43.45	4.35E-11
ZAP70	P43403	TK/Syk	4	6	0.11	42.11	8.62E-11
ErbB4	Q15303	TK/EGFR	1	1	0.02	39.02	4.20E-10
FMS	P07333	TK/PDGFR	3	3	0.07	34.51	4.24E-09
FGFR1	P11362	TK/FGFR	3	3	0.08	34.27	4.79E-09
JAK1	P23458	TK/JakA	3	3	0.08	34.04	5.40E-09
MET	P08581	TK/Met	6	6	0.13	33.56	6.92E-09
FER	P16591	TK/Fer/Fer; TK/Fer/Fes	7	9	0.18	32.22	1.38E-08
FGFR2	P21802	TK/FGFR	3	3	0.08	32.03	1.51E-08
PYK2	Q14289	TK/Fak	14	19	0.30	31.07	2.49E-08
FAK	Q658W2	TK/Fak	22	29	0.37	30.88	2.75E-08
FGR	P09769	TK/Src	3	3	0.08	30.74	2.95E-08
YES	P07947	TK/Src	7	9	0.20	28.81	8.00E-08
TYK2	P29597	TK/JakA	3	3	0.09	28.63	8.77E-08
JAK3	P52333	TK/JakA	2	2	0.06	28.46	9.56E-08
KDR	P35968	TK/VEGFR	7	8	0.20	25.94	3.52E-07
BTK	Q06187	TK/Tec	6	8	0.20	25.26	5.00E-07
PFTAIRe1	O94921	CMGC/CDK	18	23	0.37	24.08	9.26E-07
BLK	P51451	TK/Src	2	2	0.07	22.94	1.67E-06
TRKA	P04629	TK/Trk	3	3	0.10	22.90	1.70E-06
RET	P07949	TK/Ret	5	5	0.16	22.63	1.96E-06
TRKC	Q16288	TK/Trk	1	1	0.04	20.94	4.74E-06
ALK	Q9UM73	TK/Alk	1	1	0.04	20.82	5.04E-06
CHED	Q14004	CMGC/CDK	11	17	0.35	20.59	5.68E-06
ATM	Q13315	Atypical/PIKK/ATM	19	23	0.40	20.40	6.28E-06

ITK	Q08881	TK/Tec	3	3	0.12	19.65	9.28E-06
FLT1	P17948	TK/VEGFR	6	7	0.22	19.49	1.01E-05
EphA1	P21709	TK/Eph	2	2	0.09	18.63	1.59E-05
PCTAIRE2	Q00537	CMGC/CDK	8	16	0.37	16.43	5.05E-05
CSK	P41240	TK/Csk	13	13	0.34	16.28	5.47E-05
EphA4	P54764	TK/Eph	2	2	0.10	15.72	7.33E-05
IRR	P14616	TK/InsR	2	2	0.10	15.26	9.36E-05
PCTAIRE1	Q00536	CMGC/CDK	15	24	0.46	14.91	1.13E-04
FES	P07332	TK/Fer/Fer; TK/Fer/Fes	8	12	0.34	14.74	1.23E-04
AXL	P30530	TK/Axl	2	2	0.11	13.88	1.95E-04
SRM	Q9H3Y6	TK/Src	2	4	0.19	13.34	2.60E-04
CDK10	Q15131	CMGC/CDK	9	19	0.45	12.60	3.86E-04
DNAPK	P78527	Atypical/PIKK/DNAPK	12	14	0.39	12.51	4.05E-04
ABL2	P42684	TK/Abl	2	2	0.12	12.27	4.61E-04
RON	Q04912	TK/Met	1	1	0.07	12.18	4.83E-04
EphB2	P29323	TK/Eph	4	4	0.20	12.11	5.02E-04
EphA3	P29320	TK/Eph	1	1	0.07	11.95	5.47E-04
TXK	P42681	TK/Tec	1	1	0.07	11.83	5.82E-04
PCTAIRE3	B4DK03	CMGC/CDK	7	17	0.44	11.59	6.63E-04
EphB4	P54760	TK/Eph	2	2	0.14	10.78	1.03E-03
EphA2	P29317	TK/Eph	5	5	0.25	10.76	1.04E-03
TIE2	Q02763	TK/Tie	3	3	0.18	10.75	1.04E-03
BMX	P51813	TK/Tec	2	2	0.14	10.09	1.49E-03
TYRO3	Q06418	TK/Axl	1	1	0.08	9.98	1.58E-03
BRK	Q13882	TK/Src	3	3	0.23	7.75	5.37E-03
EphB6	D3DXD3	TK/Eph	2	2	0.18	7.38	6.59E-03
NEK2	P51955	Other/NEK	15	18	0.52	7.34	6.73E-03
CDC2	P06493	CMGC/CDK/CDC2	84	198	0.83	7.34	6.74E-03
EphB3	P54753	TK/Eph	1	1	0.11	6.75	9.36E-03

Supplemental Table S16 – The number of PPIs for each PK. The top 10 PKs with the most PPIs are marked in yellow.

PK Name	UniProt	Predictor	String & Exp. PPI	Exp. PPI
<i>Homo sapiens</i>				
AKT1	P31749	AGC/AKT	3196	159
SRC	P12931	TK/Src	2779	321
Erk1	P27361	CMGC/MAPK	2427	133
EGFR	P00533	TK/EGFR	2279	185
Erk2	P28482	CMGC/MAPK	1969	186
ErbB2	P04626	TK/EGFR	1528	68
PKCa	P17252	AGC/PKC	1512	185
ATM	Q13315	Atypical/PIKK/ATM	1469	72
FYN	P06241	TK/Src	1438	311
FRAP	P42345	Atypical/PIKK/FRAP	1352	43
MAP2K1	Q02750	STE/STE7	1352	44
p38a	Q16539	CMGC/MAPK	1349	109
CDK2	P24941	CMGC/CDK/CDC2	1297	114
INSR	P06213	TK/InsR	1287	83
FAK	Q658W2	TK/Fak	1279	104
RAF1	P04049	TKL/RAF	1268	125
KIT	P10721	TK/PDGFR	1241	62
PDGFRb	P09619	TK/PDGFR	1154	71
JAK2	O60674	TK/JakA	1125	103
LCK	P06239	TK/Src	1086	124
IKKb	O14920	Other/IKK	1057	86
IGF1R	P08069	TK/InsR	1034	58
CK2a2	P19784	Other/CK2	1002	84
CDC2	P06493	CMGC/CDK/CDC2	994	141
CDK4	P11802	CMGC/CDK	989	58
FGFR1	P11362	TK/FGFR	987	43
PDGFRa	P16234	TK/PDGFR	973	28
GSK3A	P49840	CMGC/GSK	935	27
PYK2	Q14289	TK/Fak	931	77
RET	P07949	TK/Ret	930	35
TGFbR1	P36897	TKL/STKR	925	199
KDR	P35968	TK/VEGFR	924	48
IKKa	O15111	Other/IKK	919	71
TGFbR2	D2JY11	TKL/STKR	899	0
SYK	P43405	TK/Syk	893	85
CHK2	O96017	CAMK/RAD53	892	40
FGFR2	P21802	TK/FGFR	879	9
MET	P08581	TK/Met	868	52
ABL1	Q59FK4	TK/Abl	859	1
p70S6K	P23443	AGC/RSK	848	46
CaMK2g	Q13555	CAMK/CAMK2	848	29
PKN1	Q16512	AGC	843	30
PKCb	D3DWF5	AGC/PKC	828	69
PKCd	Q05655	AGC/PKC	826	108
ErbB3	P21860	TK/EGFR	819	57
PKCe	Q02156	AGC/PKC	806	53
TRKA	P04629	TK/Trk	780	48

MAP2K4	P45985	STE/STE7	775	30
JAK1	P23458	TK/JakA	775	77
CDK5	Q00535	CMGC/CDK	771	60
ZAP70	P43403	TK/Syk	765	51
PKCg	P05129	AGC/PKC	764	49
PKR	P19525	Other/PEK	738	43
CSK	P41240	TK/Csk	737	55
PKD1	Q1KKQ2	CAMK/PKD	735	27
MAP3K1	Q13233	STE/STE11	731	105
FLT1	P17948	TK/VEGFR	715	24
FMS	P07333	TK/PDGFR	712	19
PKACa	P17612	AGC/PKA	706	165
p38b	Q15759	CMGC/MAPK	701	17
CHK1	O14757	CAMK/CAMKL/CHK1	687	36
PLK1	P53350	Other/PLK	680	85
BRAF	P15056	TKL/RAF	676	22
BARK1	P25098	AGC/GRK	671	44
SMG1	Q96Q15	Atypical/PIKK	663	8
ErbB4	Q15303	TK/EGFR	657	44
BTK	Q06187	TK/Tec	655	64
p38g	P53778	CMGC/MAPK	654	19
RSK2	P51812	AGC/RSK	646	26
TYK2	P29597	TK/JakA	641	30
ROCK1	Q13464	AGC/DMPK; AGC/DMPK/ROCK	635	29
p38d	O15264	CMGC/MAPK	629	12
PKCz	Q05513	AGC/PKC	624	78
JAK3	P52333	TK/JakA	618	37
SGK1	O00141	AGC/SGK	617	33
MAP3K5	Q99683	STE/STE11	606	50
TIE2	Q02763	TK/Tie	603	7
ILK	Q13418	TKL/MLK	596	51
ALK	Q9UM73	TK/Alk	588	49
NIK	Q99558	STE/STE-Unique/NIK	582	43
CDK6	Q00534	CMGC/CDK	574	28
MAP2K2	P36507	STE/STE7	571	15
Trio	O75962	CAMK	569	7
TRKC	Q16288	TK/Trk	558	19
IRAK1	P51617	TKL/IRAK	557	46
MARK2	Q7KZI7	CAMK/CAMKL	556	30
PEK	B2RCU9	Other/PEK	551	6
CDK9	P50750	CMGC/CDK	546	94
CK1e	P49674	CK1	536	25
BMPR1A	P36894	TKL/STKR	528	20
BMPR2	Q13873	TKL/STKR	524	55
CK1d	P48730	CK1	519	20
AKT2	P31751	AGC/AKT	513	27
PKG1	A5YM56	AGC/PKG	506	25
LKB1	Q15831	CAMK/CAMKL/LKB	500	27
MAP2K6	P52564	STE/STE7	490	19
EphB2	P29323	TK/Eph	489	17
NRK	Q7Z2Y5	STE/STE20	483	1
PKCt	Q04759	AGC/PKC	482	28
TRRAP	Q9Y4A5	Atypical/PIKK	480	30

FGR	P09769	TK/Src	476	21
BMPR1B	B4DSV1	TKL/STKR	467	78
ALK1	P37023	TKL/STKR	458	9
LATS1	O95835	AGC	455	5
FER	P16591	TK/Fer/Fer; TK/Fer/Fes	446	16
PKACg	P22612	AGC/PKA	436	1
smMLCK	Q15746	CAMK/MLCK	432	18
AurB	C7G533	Other/AUR/AUR-B	430	18
ALK2	Q04771	TKL/STKR	426	77
ROCK2	O75116	AGC/DMPK; AGC/DMPK/ROCK	419	7
DAPK3	O43293	CAMK/DAPK	419	10
YES	P07947	TK/Src	415	39
TAK1	O43318	TKL/MLK	407	58
p70S6Kb	Q9UBS0	AGC/RSK	405	10
EphA1	P21709	TK/Eph	405	3
CDK7	P50613	CMGC/CDK	398	43
AurA	O14965	Other/AUR/AUR-A	398	37
PKCi	P41743	AGC/PKC	397	35
TEC	P42680	TK/Tec	391	39
EphA4	P54764	TK/Eph	379	16
DNAPK	P78527	Atypical/PIKK/DNAPK	377	79
MSK1	O75582	AGC/RSK	364	30
MAP3K3	Q99759	STE/STE11	356	165
FES	P07332	TK/Fer/Fer; TK/Fer/Fes	356	26
CDK8	P49336	CMGC/CDK	354	42
PKN2	Q16513	AGC	353	14
TBK1	Q9UHD2	Other/IKK	345	33
ARAF	P10398	TKL/RAF	344	27
IKKe	Q14164	Other/IKK	343	61
PKD3	O94806	CAMK/PKD	337	6
TYRO3	Q06418	TK/Axl	337	7
IRAK4	Q9NWZ3	TKL/IRAK	335	10
Trad	O60229	CAMK	333	5
MAP2K5	Q13163	STE/STE7	332	11
EphA2	P29317	TK/Eph	331	22
ACTR2B	Q13705	TKL/STKR	330	17
PDK1	O15530	AGC/PKB	327	48
TIE1	P35590	TK/Tie	327	8
AXL	P30530	TK/Axl	324	21
PKCh	P24723	AGC/PKC	312	8
COT	P41279	STE/STE-Unique/COT	311	19
PKD2	Q9BZL6	CAMK/PKD	310	20
HIPK2	Q9H2X6	CMGC/DYRK	310	26
ITK	Q08881	TK/Tec	308	29
ACTR2	P27037	TKL/STKR	307	21
BARK2	P35626	AGC/GRK	306	7
PAK2	Q13177	STE/STE20	297	50
NEK2	P51955	Other/NEK	295	10
EphB4	P54760	TK/Eph	295	3
MAPKAPK2	P49137	CAMK/MAPKAPK	286	25
MLK3	B2RDI6	TKL/MLK	286	24
ALK4	P36896	TKL/STKR	286	18
DYRK1A	Q13627	CMGC/DYRK	281	17

PIM2	Q9P1W9	CAMK	278	9
LATS2	Q9NRM7	AGC	276	2
PIM1	P11309	CAMK	274	18
HGK	Q53TX8	STE/STE20	270	9
IRAK2	O43187	TKL/IRAK	266	17
AKT3	Q9Y243	AGC/AKT	264	7
MER	Q12866	TK/Axl	264	8
PKN3	Q6P5Z2	AGC	262	4
Erk5	Q13164	CMGC/MAPK	262	16
BLK	P51451	TK/Src	262	12
CaMK2d	Q13557	CAMK/CAMK2	255	15
CDKL2	B4DH08	CMGC	254	1
PAK4	O96013	STE/STE20	249	15
TXK	P42681	TK/Tec	249	10
RON	Q04912	TK/Met	248	20
PFTAIRe1	O94921	CMGC/CDK	243	15
EphA3	P29320	TK/Eph	243	18
Erk3	Q16659	CMGC/MAPK	238	4
PKG2	Q13237	AGC/PKG	235	4
GPRK5	P34947	AGC/GRK	230	21
EphB6	D3DXD3	TK/Eph	227	10
HRI	Q9BQI3	Other/PEK	225	5
IRAK3	Q9Y616	TKL/IRAK	223	6
DYRK2	Q92630	CMGC/DYRK	221	4
RSK1	Q15349	AGC/RSK	209	13
LTK	P29376	TK/AIk	207	7
ALK7	Q8NER5	TKL/STKR	207	2
EphB3	P54753	TK/Eph	204	8
MSK2	O75676	AGC/RSK	198	9
Trb1	Q96RU8	CAMK	196	4
IRR	P14616	TK/InsR	195	2
PDHK4	Q16654	Atypical/PDHK	194	4
CK2a1	P68400	Other/CK2	194	194
PLK3	Q9H4B4	Other/PLK	192	10
CaMK4	Q16566	CAMK/CAMK1	189	8
MAP3K4	B9EG75	STE/STE11	188	20
MLK2	Q02779	TKL/MLK	186	25
PLK4	O00444	Other/PLK	185	7
CaMK1a	Q14012	CAMK/CAMK1	183	10
ABL2	P42684	TK/Abl	183	19
MOK	Q9UQ07	CMGC	182	4
PCTAIRe1	Q00536	CMGC/CDK	178	13
SRM	Q9H3Y6	TK/Src	177	0
MISR2	Q16671	TKL/STKR	177	3
PLK2	Q9NYY3	Other/PLK	175	2
RSK4	Q9UK32	AGC/RSK	174	2
RHOK	Q15835	AGC/GRK	171	10
Erk4	P31152	CMGC/MAPK	171	5
MYO3A	Q8NEV4	STE/STE20	169	3
MARK1	Q9P0L2	CAMK/CAMKL	166	3
Trb3	Q96RU7	CAMK	162	29
AMPKa2	P54646	CAMK/CAMKL/AMPK	162	11
MARK3	P27448	CAMK/CAMKL	161	31

CK1a	D3DQG1	CK1	160	0
CDK10	Q15131	CMGC/CDK	159	1
Erk7	Q8TD08	CMGC/MAPK	159	7
GCN2	Q9P2K8	Other/PEK	159	4
CDK3	Q00526	CMGC/CDK/CDC2	158	17
DLK	Q12852	TKL/MLK	158	16
SIK	P57059	CAMK/CAMKL	155	3
MRCKa	Q5VT25	AGC/DMPK	154	2
MAP3K2	Q9Y2U5	STE/STE11	151	17
STLK3	Q9UEW8	STE/STE20	151	15
CHED	Q14004	CMGC/CDK	150	3
HPK1	Q92918	STE/STE20	148	24
Wnk1	Q9H4A3	Other/Wnk	147	8
MAPKAPK3	Q16644	CAMK/MAPKAPK	146	6
SGK3	Q96BR1	AGC/SGK	143	7
skMLCK	Q9H1R3	CAMK/MLCK	143	6
BMX	P51813	TK/Tec	142	23
Wnk4	Q96J92	Other/Wnk	140	7
BRK	Q13882	TK/Src	140	6
NDR1	Q15208	AGC	138	9
GCK	Q12851	STE/STE20	137	5
PAK6	Q9NQU5	STE/STE20	136	6
TAO1	Q7L7X3	STE/STE20	136	2
PDHK2	Q15119	Atypical/PDHK	134	10
ATR	Q13535	Atypical/PIKK/ATR	134	49
MST2	Q13188	STE/STE20	134	6
NEK6	B7Z2D9	Other/NEK	131	33
CDK11	Q9BWU1	CMGC/CDK	127	12
MINK	Q8N4C8	STE/STE20	124	14
CLK1	B4DFW7	CMGC	122	16
EphA7	Q15375	TK/Eph	122	8
FRK	P42685	TK/Src	122	1
PCTAIRE3	B4DK03	CMGC/CDK	121	0
HIPK3	Q9H422	CMGC/DYRK	121	29
MST1	Q13043	STE/STE20	121	16
TNIK	Q9UKE5	STE/STE20	121	7
YSK1	O00506	STE/STE20	121	22
LYN	P07948	TK/Src	118	118
PCTAIRE2	Q00537	CMGC/CDK	115	5
GPRK4	P32298	AGC/GRK	114	1
DRAK2	O94768	CAMK/DAPK	110	2
PAK5	Q9P286	STE/STE20	110	15
NEK1	Q96PY6	Other/NEK	108	13
NuaK1	O60285	CAMK/CAMKL	106	8
QIK	Q9H0K1	CAMK/CAMKL	106	2
NEK3	P51956	Other/NEK	106	3
MELK	Q53GX0	CAMK/CAMKL	104	12
SRPK1	Q96SB4	CMGC	104	22
MARK4	Q96L34	CAMK/CAMKL	102	28
PIM3	Q86V86	CAMK	101	1
MNK2	A4CYL7	CAMK/MAPKAPK	100	9
RSKL1	Q96S38	AGC	98	4
KSR1	Q8IVT5	TKL/RAF	97	2

NEK8	Q86SG6	Other/NEK	95	9
NIM1	Q8IY84	CAMK/CAMKL	93	0
DRAK1	Q9UEE5	CAMK/DAPK	92	1
VRK1	Q99986	CK1	92	7
PRKX	P51817	AGC/PKA	91	3
CDKL5	O76039	CMGC	91	5
DYRK1B	Q9Y463	CMGC/DYRK	90	11
AurC	Q9UQB9	Other/AUR	90	2
EphA5	P54756	TK/Eph	90	1
OSR1	O95747	STE/STE20	89	10
CRK7	Q9NYV4	CMGC/CDK	87	6
NuaK2	B4E0Y5	CAMK/CAMKL	86	4
STLK5	Q7RTN6	STE/STE20	84	2
AMPKa1	Q13131	CAMK/CAMKL/AMPK	83	20
DAPK2	Q9UIK4	CAMK/DAPK	83	4
ICK	Q9UPZ9	CMGC	81	1
PHKg1	Q16816	CAMK/PHK	79	5
PRKY	O43930	AGC/PKA	75	0
PRP4	Q13523	CMGC/DYRK	74	13
ZAK	B8ZZU2	TKL/MLK	73	8
NLK	Q9UBE8	CMGC/MAPK	72	14
CaMK1g	Q96NX5	CAMK/CAMK1	69	0
PHKg2	P15735	CAMK/PHK	68	1
LOK	O94804	STE/STE20	66	1
DCLK1	O15075	CAMK	65	0
caMLCK	Q32MK0	CAMK/MLCK	64	0
CLK2	P49760	CMGC	64	3
SRPK2	C9JQJ0	CMGC	64	3
EphA8	P29322	TK/Eph	64	6
KHS1	Q9Y4K4	STE/STE20	63	9
GSK3B	P49841	CMGC/GSK	61	61
Trb2	Q92519	CAMK	60	1
MLK4	Q5TCX8	TKL/MLK	60	0
PSKH1	P11801	CAMK	59	1
HIPK1	Q86Z02	CMGC/DYRK	58	8
Wnk3	B1AKG2	Other/Wnk	56	1
MST4	Q9P289	STE/STE20	56	19
PDHK3	B4DXG6	Atypical/PDHK	55	2
MLK1	P80192	TKL/MLK	55	2
STLK6	Q9C0K7	STE/STE20	54	5
JNK2	P45984	CMGC/MAPK	49	49
MAST2	Q6P0Q8	AGC	47	13
BRK1	Q8TDC3	CAMK/CAMKL	47	4
EphA6	Q9UF33	TK/Eph	47	0
CK1g2	P78368	CK1	45	4
MRCKb	Q9Y5S2	AGC/DMPK	44	6
CLK3	Q59FC5	CMGC	44	3
NEK7	Q8TDX7	Other/NEK	44	2
Sgk085	Q86YV6	CAMK/MLCK	43	0
VRK2	Q86Y07	CK1	43	7
SSTK	Q9BXA6	CAMK	42	3
FGFR3	P22607	TK/FGFR	42	42
TTBK1	Q5TCY1	CK1	41	8

GPRK7	Q8WTQ7	AGC/GRK	40	1
VACAMKL	B2RDF9	CAMK	40	2
SPEG	Q15772	CAMK	39	0
RSK3	Q15418	AGC/RSK	37	37
NEK9	Q8TD19	Other/NEK	37	10
HH498	Q59H18	TKL/MLK	37	8
SNRK	Q9NRH2	CAMK/CAMKL	36	4
DYRK3	O43781	CMGC/DYRK	36	0
PDHK1	Q15118	Atypical/PDHK	35	13
CK1g3	Q9Y6M4	CK1	35	1
STK33	Q9BYT3	CAMK	34	0
TAO3	Q9H2K8	STE/STE20	32	4
PASK	Q96RG2	CAMK/CAMKL	30	5
KHS2	Q8IVH8	STE/STE20	30	5
LZK	O43283	TKL/MLK	30	5
CK1g1	Q9HCP0	CK1	29	0
KSR2	Q6VAB6	TKL/RAF	29	5
BRK2	Q8IWQ3	CAMK/CAMKL	28	3
PAK1	Q13153	STE/STE20	28	28
SGK2	Q9HBY8	AGC/SGK	27	1
MAP3K6	O95382	STE/STE11	27	3
QSK	Q9Y2K2	CAMK/CAMKL	26	2
CDKL3	Q8IVW4	CMGC	25	0
CaMK1b	B4E1A6	CAMK/CAMK1	23	0
TTN	D3DPF9	CAMK/MLCK	23	23
YANK3	Q86UX6	AGC	22	0
MAP2K7	O14733	STE/STE7	22	22
BCKDK	O14874	Atypical/PDHK	21	7
DAPK1	Q59H88	CAMK/DAPK	20	20
MAPKAPK5	Q8IW41	CAMK/MAPKAPK	20	20
YANK2	Q9NY57	AGC	19	0
TSSK1	Q9BXA7	CAMK	19	3
TSSK2	Q96PF2	CAMK	19	6
VRK3	Q8IV63	CK1	18	2
PITSLRE	P21127	CMGC/CDK	18	18
FGFR4	P22455	TK/FGFR	18	18
TSSK3	Q96PN8	CAMK	17	2
MAK	P20794	CMGC	17	0
MAP2K3	P46734	STE/STE7	17	17
TRKB	Q16620	TK/Trk	17	17
NDR2	Q9Y2H1	AGC	16	4
CK1a2	Q8N752	CK1	16	1
TSSK4	Q6SA08	CAMK	15	3
HUNK	P57058	CAMK/CAMKL	15	1
NEK11	Q8NG66	Other/NEK	15	2
PSKH2	Q96QS6	CAMK	14	0
DMPK2	Q6DT37	AGC/DMPK	13	6
NEK4	P51957	Other/NEK	13	0
MAST3	O60307	AGC	12	1
EphB1	P54762	TK/Eph	12	12
FLT3	P36888	TK/PDGFR	12	12
DMPK1	Q09013	AGC/DMPK	11	11
PAK3	B2RCU6	STE/STE20	11	11

EphA10	Q5JZY3	TK/Eph	11	0
MASTL	Q96GX5	AGC	9	1
DCLK3	Q9C098	CAMK	9	0
CLK4	Q9HAZ1	CMGC	9	4
PFTAIRE2	Q96Q40	CMGC/CDK	9	1
NEK10	Q6ZWH5	Other/NEK	9	0
SgK495	Q8N2I9	CAMK	8	2
MAST1	Q9Y2H9	AGC	7	4
GPRK6	P43250	AGC/GRK	7	7
HIPK4	Q8NE63	CMGC/DYRK	7	0
CTK	P42679	TK/Csk	6	6
FLT4	P35916	TK/VEGFR	6	6
DYRK4	Q9NR20	CMGC/DYRK	5	0
PKACb	P22694	AGC/PKA	4	4
CaMK2b	Q13554	CAMK/CAMK2	2	2
CDKL1	Q00532	CMGC	2	2
MAST4	B5MCH9	AGC	1	0
SgK494	Q96LW2	AGC	1	0
CaMK2a	Q7LDD5	CAMK/CAMK2	1	1
TTBK2	Q6IQ55	CK1	1	1
JNK3	A8MTD8	CMGC/MAPK	1	1
Wnk2	A6PVR3	Other/Wnk	1	1
MAP3K7	Q6ZN16	STE/STE11	1	0
MAP3K8	Q56UN5	STE/STE11	1	0
SLK	D3DRA1	STE/STE20	1	1
RSKL2	Q9Y6S9	AGC	0	0
YANK1	Q8WU08	AGC	0	0
CRIK	Q2M5E1	AGC/DMPK	0	0
CASK	B7ZKY2	CAMK	0	0
DCLK2	Q8N568	CAMK	0	0
Obscn	A6NGQ3	CAMK	0	0
CaMK1d	Q5SQQ7	CAMK/CAMK1	0	0
MNK1	B5BUJ6	CAMK/MAPKAPK	0	0
CDKL4	Q2NME9	CMGC	0	0
MSSK1	Q9UPE1	CMGC	0	0
CCRK	Q8IZL9	CMGC/CDK	0	0
JNK1	D3DX92	CMGC/MAPK	0	0
NEK5	Q6P3R8	Other/NEK	0	0
MST3	Q5U0E6	STE/STE20	0	0
MYO3B	C9J3X5	STE/STE20	0	0
TAO2	A7MCZ2	STE/STE20	0	0
HCK	A8K4G3	TK/Src	0	0

Mus musculus

AKT1	Q6GSA6	AGC/AKT	2030	4
ERK2	P63085	CMGC/MAPK	1876	15
ERK1	Q63844	CMGC/MAPK	1570	5
EGFR	Q01279	TK/EGFR	1459	11
PYK2	Q9QVP9	TK/Fak	1089	2
p38a	Q5U421	CMGC/MAPK	1080	0
ErbB2	P70424	TK/EGFR	997	2
ATM	Q62388	Atypical/PIKK/ATM	972	1
CDK2	P97377	CMGC/CDK/CDC2	899	4
INSR	P15208	TK/InsR	889	6

IKKa	Q8CBT3	Other/IKK	885	0
GSK3B	Q9WV60	CMGC/GSK	881	7
RAF1	Q99N57	TKL/RAF	865	7
ABL1	P00520	TK/Abl	782	22
CDC2	P11440	CMGC/CDK/CDC2	776	9
MAP2K1	Q9JJE1	STE/STE7	761	5
BARK1	Q99MK8	AGC/GRK	740	0
JAK2	Q62120	TK/JakA	732	20
PKACb	P68181	AGC/PKA	721	0
KIT	Q8C8K9	TK/PDGFR	719	4
FMS	P09581	TK/PDGFR	692	2
FAK	P34152	TK/Fak	664	17
TAK1	Q923A8	TKL/MLK	657	1
IKKb	Q5D0E0	Other/IKK	655	3
RET	P35546	TK/Ret	649	0
FGFR1	P16092	TK/FGFR	642	3
CDK4	P30285	CMGC/CDK	631	7
FYN	P39688	TK/Src	627	30
LCK	P06240	TK/Src	613	17
KDR	P35918	TK/VEGFR	608	1
JNK2	Q5NCK8	CMGC/MAPK	572	3
CDK5	P49615	CMGC/CDK	568	3
IGF1R	Q60751	TK/InsR	563	5
PKR	Q03963	Other/PEK	542	0
CHK2	Q9Z265	CAMK/RAD53	537	1
FGFR2	P21803	TK/FGFR	537	1
MET	P16056	TK/Met	508	4
PDGFRa	P26618	TK/PDGFR	492	0
TRKA	Q3UFB7	TK/Trk	489	4
CaMK2a	Q80TN1	CAMK/CAMK2	473	19
JAK3	Q62137	TK/JakA	470	1
TGFBR1	Q64729	TKL/STKR	469	127
PLK1	Q07832	Other/PLK	466	1
ZAP70	P43404	TK/Syk	432	1
ErbB3	Q61526	TK/EGFR	430	2
DNAPK	P97313	Atypical/PIKK/DNAPK	424	0
JAK1	B1ASP2	TK/JakA	415	0
PKCe	P16054	AGC/PKC	412	8
SYK	P48025	TK/Syk	411	3
TRKB	P15209	TK/Trk	408	5
FLT1	P35969	TK/VEGFR	407	5
p70S6K	Q5SWG1	AGC/RSK	405	2
TIE2	B1AWS8	TK/Tie	404	6
EphA5	Q60629	TK/Eph	398	0
PDK1	Q9Z2A0	AGC/PKB	391	15
BRAF	P28028	TKL/RAF	390	7
BTK	P35991	TK/Tec	387	27
BMPT1A	P36895	TKL/STKR	387	4
PKCa	Q4VA93	AGC/PKC	380	0
CHK1	O35280	CAMK/CAMKL/CHK1	369	2
MAP2K4	P47809	STE/STE7	363	2
TRRAP	Q3UH32	Atypical/PIKK	342	1
PKCd	P28867	AGC/PKC	337	3

PLK3	Q6P571	Other/PLK	332	0
MAP2K2	Q9D7B0	STE/STE7	331	0
SGK1	Q9WVC6	AGC/SGK	325	0
PEK	Q9Z2B5	Other/PEK	323	1
MAP3K1	P53349	STE/STE11	317	4
CK2a2	O54833	Other/CK2	316	2
PKD1	Q62101	CAMK/PKD	312	1
AKT2	Q60823	AGC/AKT	309	3
PLK2	P53351	Other/PLK	309	0
BMPR2	O35607	TKL/STKR	307	23
TRKC	Q6VNS1	TK/Trk	298	1
Trio	Q0KL02	CAMK	296	0
CDK6	Q64261	CMGC/CDK	296	4
MAP2K5	Q9WVS7	STE/STE7	293	13
KSR1	Q61097	TKL/RAF	291	8
ALK	P97793	TK/Alk	287	0
MLK2	Q66L42	TKL/MLK	284	0
ROCK1	P70335	AGC/DMPK; AGC/DMPK/ROCK	282	4
SGK3	Q9ERE3	AGC/SGK	276	0
AurA	P97477	Other/AUR/AUR-A	275	0
CK1a	Q8BK63	CK1	270	0
COT	Q07174	STE/STE-Unique/COT	267	1
ILK	O55222	TKL/MLK	265	0
smMLCK	B1B1A8	CAMK/MLCK	262	0
AurB	Q8C6C1	Other/AUR/AUR-B	261	1
TIE1	Q8BGI2	TK/Tie	259	0
BMPR1B	P36898	TKL/STKR	257	56
LKB1	Q9WTK7	CAMK/CAMKL/LKB	256	1
CRIK	P49025	AGC/DMPK	254	1
MAP2K3	O09110	STE/STE7	253	7
FLT4	P35917	TK/VEGFR	251	0
FGR	Q8BGM0	TK/Src	247	0
PKCt	Q02111	AGC/PKC	240	0
DAPK1	Q80YE7	CAMK/DAPK	240	0
EphA1	Q60750	TK/Eph	227	4
FES	P16879	TK/Fer/Fer; TK/Fer/Fes	225	0
PKACa	P05132	AGC/PKA	222	8
GSK3A	Q2NL51	CMGC/GSK	217	2
MAP2K6	P70236	STE/STE7	217	1
ALK2	P37172	TKL/STKR	211	45
IRAK4	Q8R4K2	TKL/IRAK	208	0
FGFR4	Q03142	TK/FGFR	207	0
EphA4	Q80VZ2	TK/Eph	204	0
MARK2	Q571J8	CAMK/CAMKL	201	1
ERK5	Q9WVS8	CMGC/MAPK	201	0
CK1e	Q9JMK2	CK1	200	6
HIPK2	Q9QZR5	CMGC/DYRK	197	5
DMPK1	P54265	AGC/DMPK	196	0
RSK2	P18654	AGC/RSK	196	5
YES	Q04736	TK/Src	196	2
MAP2K7	Q8CE90	STE/STE7	194	2
DAPK3	O54784	CAMK/DAPK	192	7
PAK1	O88643	STE/STE20	190	12

CSK	Q8VCW1	TK/Csk	190	3
Trad	A2CG49	CAMK	187	1
NIK	Q9WUL6	STE/STE-Unique/NIK	181	3
PRKX	Q922R0	AGC/PKA	177	0
ITK	Q03526	TK/Tec	173	4
PAK2	Q8CIN4	STE/STE20	171	2
CaMK4	Q8BGR3	CAMK/CAMK1	168	0
FER	P70451	TK/Fer/Fer; TK/Fer/Fes	166	1
MAPKAPK2	P49138	CAMK/MAPKAPK	163	0
SMG1	Q8BKX6	Atypical/PIKK	162	0
ARAF	P04627	TKL/RAF	161	3
ACTR2B	P27040	TKL/STKR	160	6
RON	Q62190	TK/Met	156	0
ROCK2	P70336	AGC/DMPK; AGC/DMPK/ROCK	155	0
LATS2	Q7TSJ6	AGC	154	1
ACTR2	P27038	TKL/STKR	150	5
PLK4	Q64702	Other/PLK	148	6
AKT3	Q9WUA6	AGC/AKT	147	0
RHOK	Q9WVL4	AGC/GRK	146	0
DYRK2	Q5U4C9	CMGC/DYRK	144	0
ALK4	Q61271	TKL/STKR	144	3
EphA3	Q8BRB1	TK/Eph	143	0
CDK7	Q03147	CMGC/CDK	141	0
ALK1	Q91YR0	TKL/STKR	141	0
p38b	Q569F1	CMGC/MAPK	138	0
TBK1	Q9WUN2	Other/IKK	137	5
IRAK2	Q8CFA1	TKL/IRAK	135	2
PAK4	Q8BTW9	STE/STE20	131	0
CASK	O70589	CAMK	130	1
EphB4	Q8C7S3	TK/Eph	129	0
CDK9	Q99J95	CMGC/CDK	125	2
IRAK3	Q8K4B2	TKL/IRAK	124	0
p70S6Kb	Q9Z1M4	AGC/RSK	122	0
p38g	O08911	CMGC/MAPK	122	1
AXL	Q80YQ3	TK/Axl	118	0
PKCb	P68404	AGC/PKC	111	2
MOK	Q9WVS4	CMGC	111	0
MAP3K4	Q6PDG6	STE/STE11	111	0
EphB3	Q91YS9	TK/Eph	111	0
PKCi	Q5DTK3	AGC/PKC	109	1
EphA2	Q3UNI2	TK/Eph	109	0
MSK1	Q8C050	AGC/RSK	108	1
MAP3K3	Q61084	STE/STE11	106	2
IKKe	Q8C2I3	Other/IKK	105	0
GPRK4	Q3V151	AGC/GRK	104	0
PITSLRE	P24788	CMGC/CDK	98	0
CaMK2b	Q5SVJ0	CAMK/CAMK2	97	3
AMPKa2	B1ASQ8	CAMK/CAMKL/AMPK	97	1
TAO2	Q6ZQ29	STE/STE20	93	0
BRK	Q64434	TK/Src	93	1
GCN2	A2AUM0	Other/PEK	92	2
HPK1	P70218	STE/STE20	91	4
MER	Q60805	TK/Axl	90	0

CDK8	Q8R3L8	CMGC/CDK	89	0
ERK3	Q61532	CMGC/MAPK	88	0
TAO1	Q5F2E8	STE/STE20	88	0
TAO3	Q8BYC6	STE/STE20	88	0
PCTAIRE1	Q04735	CMGC/CDK	87	0
p38d	Q9Z1B7	CMGC/MAPK	87	0
Wnk1	P83741	Other/Wnk	86	0
AMPKa1	Q5EG47	CAMK/CAMKL/AMPK	85	4
BMX	B1AUL6	TK/Tec	85	0
PDHK4	O70571	Atypical/PDHK	84	0
MAP3K2	Q61083	STE/STE11	84	3
DYRK1A	Q61214	CMGC/DYRK	82	1
MISR2	Q8K592	TKL/STKR	82	0
EphB1	Q8CBF3	TK/Eph	81	2
SGK2	Q9QZS5	AGC/SGK	80	0
PFTAIRE1	O35495	CMGC/CDK	80	1
NLK	O54949	CMGC/MAPK	77	3
CaMK1a	Q91YS8	CAMK/CAMK1	76	0
Wnk4	Q80UE6	Other/Wnk	75	2
PIM2	Q62070	CAMK	73	0
PKD3	Q5FWX6	CAMK/PKD	72	0
YSK1	Q6IR17	STE/STE20	69	0
EphA7	Q8BSU8	TK/Eph	69	0
GPRK5	Q8VEB1	AGC/GRK	68	1
CaMK2g	Q923T9	CAMK/CAMK2	67	1
SIK	Q60670	CAMK/CAMKL	67	1
MAPKAPK3	Q3UMW7	CAMK/MAPKAPK	67	0
ABL2	Q4JIM5	TK/Abi	66	1
MLK3	Q80XI6	TKL/MLK	65	1
PKN2	Q3TBR3	AGC	64	1
MAPKAPK5	O54992	CAMK/MAPKAPK	64	2
CDKL5	Q3UTQ8	CMGC	64	0
NEK8	Q91ZR4	Other/NEK	64	2
STLK3	Q9Z1W9	STE/STE20	64	4
MNK2	Q8CDB0	CAMK/MAPKAPK	63	6
ATR	Q9JKK8	Atypical/PIKK/ATR	62	1
MRCKa	B2RXX8	AGC/DMPK	60	0
RSK1	Q9WUT3	AGC/RSK	58	3
BLK	Q8K2M8	TK/Src	58	2
EphB6	O08644	TK/Eph	57	0
DRAK2	Q8BG48	CAMK/DAPK	56	0
DLK	Q60700	TKL/MLK	54	2
PKG1	P0C605	AGC/PKG	52	4
CaMK2d	Q6PHZ2	CAMK/CAMK2	52	4
ALK7	A2AJR4	TKL/STKR	52	0
MarkmD1	Q8C0X8	CAMK/CAMKL	51	0
TEC	Q3U436	TK/Tec	51	0
CAMK1g	Q91VB2	CAMK/CAMK1	50	0
QIK	Q8CFH6	CAMK/CAMKL	49	0
GCK	Q61161	STE/STE20	48	0
TSSK1	Q80YU1	CAMK	47	0
Wnk3	Q80XP9	Other/Wnk	47	1
EphA8	A3KG07	TK/Eph	46	0

MST1	Q9JI11	STE/STE20	45	3
BARK2	Q3UYH7	AGC/GRK	42	0
MarkmA5	Q9QYZ3	CAMK/CAMKL	41	0
MNK1	Q3U1I8	CAMK/MAPKAPK	41	0
ICK	Q9JKV2	CMGC	41	0
MLK4	Q8VDG6	TKL/MLK	41	0
FRK	Q922K9	TK/Src	40	0
CLK1	Q3UXB6	CMGC	39	0
OSR1	Q6P9R2	STE/STE20	39	0
PAK5	Q8C015	STE/STE20	39	0
PDHK1	Q3U5E5	Atypical/PDHK	38	0
DCLK1	Q9JLM8	CAMK	38	0
DAPK2	Q8VDF3	CAMK/DAPK	38	1
NEK6	Q9ES70	Other/NEK	38	3
PKCh	Q8K2K8	AGC/PKC	37	0
Trb2	Q8K4K3	CAMK	37	1
DYRK1B	Q9Z188	CMGC/DYRK	37	0
PAK6	Q3ULB5	STE/STE20	37	0
PIM3	P58750	CAMK	36	0
Trb3	Q8K4K2	CAMK	35	2
MarkmA10	A0AUV4	CAMK/CAMKL	35	0
PASK	Q8CEE6	CAMK/CAMKL	35	0
STLK6	Q8K4T3	STE/STE20	35	0
CDK10	Q3UMM4	CMGC/CDK	33	0
Wnk2	Q3UH66	Other/Wnk	32	0
MarkmA3	Q9QYZ5	CAMK/CAMKL	31	0
LOK	B1ATW8	STE/STE20	31	0
TSSK2	Q6P8M9	CAMK	30	0
NIM1	Q8BHI9	CAMK/CAMKL	30	0
SRPK1	O70551	CMGC	28	1
ZAK	Q9ESL4	TKL/MLK	28	0
CaMK1b	Q9QYK9	CAMK/CAMK1	27	0
PHKg1	P07934	CAMK/PHK	27	0
PCTAIRE3	Q04899	CMGC/CDK	27	0
MSK2	Q3U3M8	AGC/RSK	26	0
RSK4	A2CEE7	AGC/RSK	26	0
HIPK1	A9R9X0	CMGC/DYRK	26	2
PRP4	C7G3P2	CMGC/DYRK	25	1
MST3	Q99KH8	STE/STE20	25	0
Trb1	Q8K4K4	CAMK	24	0
CDK11	Q8BWD8	CMGC/CDK	23	0
MST4	Q99JT2	STE/STE20	23	0
EPHA6	B9EIV2	TK/Eph	23	0
MLK1	Q3U1V8	TKL/MLK	23	0
CAMK1d	Q8BW96	CAMK/CAMK1	22	0
DCLK3	Q8BWQ5	CAMK	21	0
PSKH1	Q91YA2	CAMK	21	0
MarkmA6	Q9QYZ6	CAMK/CAMKL	21	0
MELK	Q3TPU1	CAMK/CAMKL	21	0
NuaK2	Q8BZN4	CAMK/CAMKL	21	4
PHKg2	A6H632	CAMK/PHK	21	0
Obscn	A2AAJ9	CAMK	19	1
caMLCK	Q3UIZ8	CAMK/MLCK	19	0

CTK	P41242	TK/Csk	19	0
CLK2	O35491	CMGC	18	1
LYN	P25911	TK/Src	18	18
SPEG	Q62407	CAMK	17	0
NuaK1	Q641K5	CAMK/CAMKL	17	0
NEK7	Q9ES74	Other/NEK	17	0
MST2	Q9JI10	STE/STE20	17	0
RSKL1	Q8BLK9	AGC	16	0
VRK2	Q8BN21	CK1	16	3
SRPK2	O54781	CMGC	16	1
PCTAIRE2	Q8K0D0	CMGC/CDK	16	1
DYRK3	Q922Y0	CMGC/DYRK	16	0
TNIK	B9EKN8	STE/STE20	16	0
TSSK5	Q8C1R0	CAMK	15	2
MarkmA1	Q8C0N0	CAMK/CAMKL	15	0
MarkmC2	Q3UT86	CAMK/CAMKL	15	0
SSTK	Q925K9	CAMK	14	0
MAP3K6	Q9WTR2	STE/STE11	14	3
IRAK1	Q62406	TKL/IRAK	14	14
VACAMKL	Q3UHL1	CAMK	13	0
CK1g2	Q99K78	CK1	13	0
MAST2	B1AST8	AGC	11	0
MarkmC1	Q3UTA8	CAMK/CAMKL	11	0
SgK085	Q5SUV5	CAMK/MLCK	11	0
NEK4	Q6GTE9	Other/NEK	11	0
SRC	P05480	TK/Src	11	11
MAST1	Q9R1L5	AGC	10	3
STK33	Q924X7	CAMK	10	0
MARK4	Q8CIP4	CAMK/CAMKL	10	0
MarkmB1	Q8C0V7	CAMK/CAMKL	10	0
VRK3	Q8K3G5	CK1	10	0
YANK3	Q8QZV4	AGC	9	0
PDHK3	Q922H2	Atypical/PDHK	9	0
TSSK3	Q9D2E1	CAMK	9	2
CLK4	O35493	CMGC	9	0
MSSK1	Q9Z0G2	CMGC	9	0
HH498	B2RTJ7	TKL/MLK	9	0
PKN3	Q8K045	AGC	8	0
YANK1	Q8BGW6	AGC	8	0
BCKDK	Q3UC13	Atypical/PDHK	8	0
BRK1	Q5RJI5	CAMK/CAMKL	8	1
MARK1	Q14DQ3	CAMK/CAMKL	8	0
TTBK1	Q6PCN3	CK1	8	0
AurC	O88445	Other/AUR	8	0
EphA10	Q8BYG9	TK/Eph	8	0
QSK	Q6P4S6	CAMK/CAMKL	7	0
PKD2	Q8BZ03	CAMK/PKD	7	0
ERK7	Q80Y86	CMGC/MAPK	7	0
NEK11	Q8C0Q4	Other/NEK	7	0
LZK	Q1HKZ5	TKL/MLK	7	0
MRCKb	B2RQQ7	AGC/DMPK	6	0
MarkmB2	B7ZNH4	CAMK/CAMKL	6	0
SNRK	B9EK90	CAMK/CAMKL	6	0

CLK3	O35492	CMGC	6	0
HIPK4	Q3V016	CMGC/DYRK	6	0
NEK10	Q3UGM2	Other/NEK	6	0
KHS1	Q8BPM2	STE/STE20	6	0
KHS2	Q99JP0	STE/STE20	6	0
PDGFRb	P05622	TK/PDGFR	6	6
FRAP	Q9JLN9	Atypical/PIKK/FRAP	5	5
DCLK2	Q6PGN3	CAMK	5	0
MarkmE2	A2AQX6	CAMK/CAMKL	5	0
TTBK2	A2AW15	CK1	5	0
CDKL1	Q8CEQ0	CMGC	5	2
MAK	Q04859	CMGC	5	0
MYO3A	Q8K3H5	STE/STE20	5	1
MASTL	A2AQY2	AGC	4	0
NDR2	B2KFR4	AGC	4	0
MarkmD3	Q32M05	CAMK/CAMKL	4	0
CDKL4	Q3TZA2	CMGC	4	0
CHED	Q69ZA1	CMGC/CDK	4	0
JNK1	Q91Y86	CMGC/MAPK	4	4
SRM	Q0VBH4	TK/Src	4	0
YANK2	Q9JJX8	AGC	3	0
BRK2	Q69Z98	CAMK/CAMKL	3	0
CDKL2	Q9QUK0	CMGC	3	0
CCRK	Q9JHU3	CMGC/CDK	3	0
DYRK4	Q8BI55	CMGC/DYRK	3	0
MAP3K5	O35099	STE/STE11	3	3
PKCg	P63318	AGC/PKC	2	2
PKCz	Q02956	AGC/PKC	2	2
PDHK2	Q9JK42	Atypical/PDHK	2	2
CK1d	Q9DC28	CK1	2	2
CK1g3	Q8C4X2	CK1	2	0
MYO3B	Q1EG27	STE/STE20	2	0
MAST3	Q3U214	AGC	1	0
SgK494	Q5SYL1	AGC	1	0
GPRK6	O70293	AGC/GRK	1	1
VRK1	Q3UWH3	CK1	1	1
ERK4	Q6P5G0	CMGC/MAPK	1	0
CK2a1	Q61177	Other/CK2	1	1
HRI	Q69ZK8	Other/PEK	1	1
PAK3	A3KGC1	STE/STE20	1	1
FGFR3	Q7TSI8	TK/FGFR	1	1
KSR2	Q3UVC0	TKL/RAF	1	0
TGFBR2	Q91ZR8	TKL/STKR	1	1
LATS1	Q8BYR2	AGC	0	0
MAST4	Q811L6	AGC	0	0
NDR1	Q91VJ4	AGC	0	0
PKN1	P70268	AGC	0	0
RSKL2	Q8R2S1	AGC	0	0
DMPK2	Q80UW5	AGC/DMPK	0	0
PKG2	Q61410	AGC/PKG	0	0
RSK3	Q810V8	AGC/RSK	0	0
PIM1	Q8CFN8	CAMK	0	0
SgK495	Q7TNL3	CAMK	0	0

TSSK4	Q9D411	CAMK	0	0
HUNK	B2RQ72	CAMK/CAMKL	0	0
MARK3	Q9JKE5	CAMK/CAMKL	0	0
MarkmA2	B9EKK5	CAMK/CAMKL	0	0
MarkmA8	A0JLX3	CAMK/CAMKL	0	0
skMLCK	Q8VCR8	CAMK/MLCK	0	0
CK1g1	Q6P2B2	CK1	0	0
CDKL3	B1AU43	CMGC	0	0
CRK7	Q14AX6	CMGC/CDK	0	0
PFTAIRe2	Q3V3A1	CMGC/CDK	0	0
HIPK3	A2AQH3	CMGC/DYRK	0	0
JNK3	Q80W82	CMGC/MAPK	0	0
NEK1	B2RXX0	Other/NEK	0	0
NEK2	Q91Z18	Other/NEK	0	0
NEK3	Q9R0A5	Other/NEK	0	0
NEK5	Q7TSC3	Other/NEK	0	0
NEK9	Q8K1R7	Other/NEK	0	0
PLK5	Q4FZD7	Other/PLK	0	0
MAP3K7	A2AQW0	STE/STE11	0	0
MAP3K8	Q3UVM5	STE/STE11	0	0
HGK	B7ZNR8	STE/STE20	0	0
MINK	Q5SXG0	STE/STE20	0	0
NRK	Q9R0G8	STE/STE20	0	0
SLK	O54988	STE/STE20	0	0
STLK5	Q3UUJ4	STE/STE20	0	0
LTK	P08923	TK/AIk	0	0
TYRO3	P55144	TK/Axl	0	0
ErbB4	B2KGF6	TK/EGFR	0	0
EphB2	A3KG00	TK/Eph	0	0
IRR	Q9WTL4	TK/InsR	0	0
TYK2	Q3TXE3	TK/JakA	0	0
FLT3	Q3UEW6	TK/PDGFR	0	0
HCK	A2AMC5	TK/Src	0	0
TXK	P42682	TK/Tec	0	0

Drosophila melanogaster

bsk	P92208	CMGC/MAPK	625	49
Egfr	P04412	TK/EGFR	577	74
cdc2c	P23573	CMGC/CDK/CDC2	426	55
cdc2	P23572	CMGC/CDK/CDC2	422	39
Akt1	Q8INB9	AGC/AKT	409	54
btl	Q09147	TK/FGFR	369	10
polo	P52304	Other/PLK	348	29
dco	O76324	CK1	338	4
phl	P11346	TKL/RAF	333	44
SAK	O97143	Other/PLK	323	54
sgg	P18431	CMGC/GSK	318	19
mbt	Q9VXE5	STE/STE20	318	18
wtS	Q24590	AGC	311	3
FRAP	Q9VK45	Atypical/PIKK/FRAP	295	7
Cdk5	P48609	CMGC/CDK	289	47
Pak	B7Z0W0	STE/STE20	285	36
SNF1A	O18645	CAMK/CAMKL/AMPK	280	2
aur	Q9VGF9	Other/AUR	279	2

CG14305	Q9VE58	CAMK	269	0
CG10177	Q9VCL7	CAMK	263	1
InR	P09208	TK/InsR	230	10
CG6535	Q5EAK6	Atypical/PIKK/ATM	227	0
Src64B	P00528	TK/Src	227	56
htl	Q07407	TK/FGFR	221	10
rl	P40417	CMGC/MAPK	217	50
hop	Q24592	TK/JakA	214	7
ball	Q7KRY6	CK1	213	7
Cdk4	Q7K306	CMGC/CDK	199	77
ird5	Q9VEZ5	Other/IKK	199	2
CklIalpha	P08181	Other/CK2	198	22
Dsor1	Q24324	STE/STE7	196	25
tkv	Q9VMT1	TKL/STKR	196	0
Fak56D	Q0E917	TK/Fak	192	4
Cdk9	O17432	CMGC/CDK	191	1
Abl	P00522	TK/Abl	188	15
rok	Q9VXE3	AGC/DMPK; AGC/DMPK/ROCK	184	9
put	C5WLU3	TKL/STKR	184	9
aPKC	A1Z9X0	AGC/PKC	183	13
Cdk7	Q24216	CMGC/CDK	182	7
CG7094	Q9VJC2	CK1	180	1
SAX	Q7JQ36	TKL/STKR	176	1
Cklalpha	P54367	CK1	175	2
Src42A	Q9V9J3	TK/Src	175	29
CG8878	Q7KMI3	CK1	173	1
gskt	P83101	CMGC/GSK	172	0
ial	Q9VKN7	Other/AUR	172	2
CG7236	Q1RKV9	CMGC	167	0
grp	O61661	CAMK/CAMKL/CHK1	165	39
CG2309	Q9W354	CMGC/MAPK	162	4
S6klI	Q94533	AGC/RSK	160	11
CG10522	Q9VTY8	AGC/DMPK	157	2
Gcn2	Q9V9X8	Other/PEK	143	1
Mpk2	O62618	CMGC/MAPK	140	2
CG11228	Q8T0S6	STE/STE20	134	40
Pkg21D	Q03042	AGC/PKG	128	0
mei-41	Q9VXG8	Atypical/PIKK/ATR	128	12
hep	Q23977	STE/STE7	124	21
CG12147	Q7JWT4	CK1	118	0
Ilk	Q9V400	TKL/MLK	116	0
Pkc98E	P13678	AGC/PKC	115	14
PEK	Q9NIV1	Other/PEK	115	1
PKA-C3	P16912	AGC/PKA	111	4
Pka-C1	P12370	AGC/PKA	110	14
Btk29A	P08630	TK/Tec	109	12
Nek2	Q9W3N8	Other/NEK	107	8
Fps85D	P18106	TK/Fer/Fer; TK/Fer/Fes	105	5
trbl	Q9V3Z1	CAMK	104	17
Strn-Mlck	A1ZA66	CAMK/MLCK	104	2
CG9374	Q8T9L5	CAMK/CAMKL/LKB	102	0
fray	Q9VE62	STE/STE20	101	2
Pk61C	C7LAC8	AGC/PKB	99	14

CG17528	Q7PLI7	CAMK	99	3
trc	Q9NBK5	AGC	98	2
Pk92B	Q9VDS9	STE/STE11	96	3
Tak1	Q9V3Q6	TKL/MLK	96	8
CG4549	Q70PP2	Atypical/PIKK	94	0
JIL1	Q9V3I5	AGC/RSK	92	1
MAPk-Ak2	P49071	CAMK/MAPKAPK	91	3
lic	O62602	STE/STE7	90	3
ninaC	P10676	STE/STE20	87	3
p38b	O61443	CMGC/MAPK	86	12
CG17309	Q9VGK8	TK/Csk	85	10
CG4290	Q9W532	CAMK/CAMKL	81	3
Pak3	Q9VEV1	STE/STE20	81	2
pII	Q05652	TKL/IRAK	77	2
wit	Q9VZI9	TKL/STKR	74	2
Pk17E	Q9VWQ2	AGC	73	68
KP78b	Q9VGQ0	CAMK/CAMKL	73	19
Eph	Q9V4E5	TK/Eph	72	1
CG8565	Q9VXN5	CMGC	69	0
Pk34A	Q9VK37	CMGC/GSK	69	0
CG9222	Q8T4D4	CAMK	64	0
slpr	Q95UN8	TKL/MLK	63	4
inaC	P13677	AGC/PKC	62	6
smi35A	Q9V3D5	CMGC/DYRK	62	0
ksr	Q24171	TKL/RAF	61	9
shark	Q24145	TK/Syk	60	1
CG11489	Q8T3S1	CMGC	58	44
Alk	Q7KJ08	TK/Alk	57	0
Caki	Q24210	CAMK	56	9
CG7125	Q9VE91	CAMK/PKD	56	0
Lk6	Q9VGI4	CAMK/MAPKAPK	55	20
Mkk4	O61444	STE/STE7	54	2
KP78a	Q9VGP9	CAMK/CAMKL	51	0
S6k	Q9VR61	AGC/RSK	49	11
Cdk8	C9QP81	CMGC/CDK	49	3
Pkc53E	P05130	AGC/PKC	45	1
CG5169	Q9VEN3	STE/STE20	42	4
CaMKI	Q7JMV3	CAMK/CAMK1	39	0
CG15072	Q4QQA7	CAMK/CAMKL	35	3
STLK	P83098	STE/STE20	35	0
CG4629	Q9VPW3	CAMK/CAMKL	34	0
mnb	Q9VX06	CMGC/DYRK	34	12
Gprk2	P32866	AGC/GRK	33	3
cdc2rk	A1Z840	CMGC/CDK	33	0
CG12069	Q9VA47	AGC/PKA	31	0
TakI1	Q4V4A7	TKL/MLK	28	0
CG6800	Q9VD82	CMGC/CDK	27	14
CG8789	Q9VW24	TKL/MLK	27	0
gwl	Q95TN8	AGC	24	2
Gprk1	P32865	AGC/GRK	24	1
gek	Q9W1B0	AGC/DMPK	22	0
Pitslre	Q9VPC0	CMGC/CDK	21	0
CG3277	Q8IQ00	TK/VEGFR	17	0

CG7156	Q9VEA9	AGC	16	4
PDK	P91622	Atypical/PDHK	16	4
CG7028	Q9Y145	CMGC/DYRK	16	2
CG7597	Q9VP22	CMGC/CDK	15	0
P38c	P83100	CMGC/MAPK	15	0
PKCdelta	P83099	AGC/PKC	14	2
CG8485	Q0E981	CAMK/CAMKL	13	0
CG2577	Q9VYN5	CK1	13	0
CG17090	Q9W0Q1	CMGC/DYRK	12	0
CG14217	Q0KHQ5	STE/STE20	11	4
CG18020	A8DYP0	CAMK/MLCK	10	7
CG6114	Q9VUV4	CAMK/CAMKL	9	0
CG4527	Q9W179	STE/STE20	9	0
CG6498	Q9VUQ9	AGC	8	1
CaMKII	A4V133	CAMK/CAMK2	8	8
Dyrk3	P83102	CMGC/DYRK	8	0
BABO	A1Z7L9	TKL/STKR	8	8
PhK_	Q7K4Y9	CAMK/PHK	7	7
CG9818	Q9VN23	AGC	5	1
CG9962	Q9VQE3	CK1	5	0
CG10951	Q9VC32	Other/NEK	5	0
CG7177	Q9VP17	Other/Wnk	5	2
CG7097	A1ZBH7	STE/STE20	4	0
Doa	A4V3J9	CMGC	3	3
ik2	Q9V3Y8	Other/IKK	3	3
Tak12	Q9VCV0	TKL/MLK	3	0
CG3105	Q95SH0	CAMK/CAMKL	1	1
Par-1	Q9V8V8	CAMK/CAMKL	1	1
CG11533	Q8IMC6	CK1	1	0
nmo	Q23993	CMGC/MAPK	1	1
CG2049	A1Z7T4	AGC	0	0
Pka-C2	Q53XD8	AGC/PKA	0	0
for	P32023	AGC/PKG	0	0
CG4839	Q9VL34	AGC/PKG	0	0
CG2905	A8DY44	Atypical/PIKK	0	0
CG11870	Q7YU19	CAMK/CAMKL	0	0
CG1760	Q0KHT7	CAMK/DAPK	0	0
bt	Q7KQP6	CAMK/MLCK	0	0
CG1776	A1Z7Y7	CAMK/MLCK	0	0
lok	A4V0X0	CAMK/RAD53	0	0
gish	Q9VEX2	CK1	0	0
CG4588	Q9VL64	CMGC	0	0
SRPK	Q9GSP5	CMGC	0	0
Eip63E	Q7KM05	CMGC/CDK	0	0
Mekk1	Q95YH7	STE/STE11	0	0
msn	Q7KV88	STE/STE20	0	0
Ret	Q7KA88	TK/Ret	0	0
Pvr	Q95P10	TK/VEGFR	0	0
<i>Caenorhabditis elegans</i>				
daf-2	Q968Y9	TK/InsR	430	163
egl-15	Q10656	TK/FGFR	325	145
cdk-1	P34556	CMGC/CDK/CDC2	296	3
let-23	P24348	TK/EGFR	260	108

kin-3	P18334	Other/CK2	241	1
sma-6	Q09488	TKL/STKR	177	82
mpk-1	P39745	CMGC/MAPK	176	66
air-1	Q21271	Other/AUR	174	18
air-2	O01427	Other/AUR	120	8
vab-1	O61460	TK/Eph	113	41
Y38H8A.3	O62426	CK1	105	0
spk-1	Q03563	CMGC	101	33
M04C9.5	P90932	CMGC	97	0
lin-45	Q07292	TKL/RAF	90	20
lit-1	Q9U9Y8	CMGC/MAPK	85	43
zyg-8	Q95QC4	CAMK	82	41
pmk-1	Q17446	CMGC/MAPK	81	30
C45B11.1	Q18637	STE/STE20	81	0
F55G1.8	Q20845	Other/PLK	76	4
F52B5.2	Q20643	CMGC	64	0
Y18D10A.5	Q9U2Q9	CMGC/GSK	64	20
mek-1	Q21307	STE/STE7	64	8
mkk-4	Q20347	STE/STE7	63	7
par-1	Q9TW45	CAMK/CAMKL	60	1
chk-1	Q9N3Z3	CAMK/CAMKL/CHK1	58	13
lin-2	P54936	CAMK	56	22
plk-1	P34331	Other/PLK	56	18
let-502	P92199	AGC/DMPK; AGC/DMPK/ROCK	55	12
B0261.2	Q95Q95	Atypical/PIKK/FRAP	55	0
daf-4	P50488	TKL/STKR	55	16
mek-2	Q10664	STE/STE7	54	4
pak-1	Q17850	STE/STE20	52	4
sek-1	Q95YI9	STE/STE7	52	10
K04C1.5	Q21204	CK1	51	1
ZC581.1	O01775	Other/NEK	51	8
chk-2	Q9U1Y5	CAMK/RAD53	49	1
akt-1	Q17941	AGC/AKT	48	9
pat-4	Q9TZC4	TKL/MLK	46	2
T01C8.1	Q95ZQ4	CAMK/CAMKL/AMPK	45	9
mig-15	Q23356	STE/STE20	45	20
jnk-1	Q8WQG9	CMGC/MAPK	44	3
unc-43	O62305	CAMK/CAMK2	43	7
F36H12.8	O76712	CK1	42	0
ksr-1	Q19380	TKL/RAF	40	8
Y43D4A.6	Q9NF25	CAMK/CAMKL/CHK1	39	0
nsy-1	Q21029	STE/STE11	38	6
cdk-5	O18142	CMGC/CDK	37	0
F14H12.4	Q9NB31	STE/STE20	33	0
ZK593.9	Q23538	TK/Fer/Fer; TK/Fer/Fes	33	0
W10G6.2	Q2PJ68	AGC/SGK	32	6
K03E5.3	O61847	CMGC/CDK/CDC2	32	0
spe-8	O01798	TK/Fer/Fer; TK/Fer/Fes	32	0
akt-2	Q9XTG7	AGC/AKT	31	13
F49C5.4	O17879	CAMK/CAMKL	31	0
F28B12.3	Q19848	CK1	31	0
mbk-2	Q9XTF3	CMGC/DYRK	31	4
C44C8.6	Q9TZ16	CAMK/MAPKAPK	30	1

kin-1	P21137	AGC/PKA	29	2
aak-1	P45894	CAMK/CAMKL/AMPK	29	0
mbk-1	Q8WQL7	CMGC/DYRK	29	4
F23C8.8	Q9TXI1	CAMK/CAMKL	28	0
F46F2.2	Q20471	CK1	28	8
smg-1	O01510	Atypical/PIKK	27	0
R02C2.1	Q86S44	CAMK/CAMKL/CHK1	27	0
C03C10.1	P42168	CK1	27	1
F31E3.2	Q8MYQ1	AGC	26	8
T08D2.7	A4F324	CAMK/RAD53	26	0
F36H12.9	O76711	CK1	26	0
T07A9.3	O44408	CMGC/MAPK	26	7
F47F2.1	Q7JP68	AGC/PKA	25	0
E02H4.6	Q19043	CK1	25	0
C39H7.1	Q18553	CK1	25	0
ZK617.1a	Q23551	CAMK/MLCK	24	0
pkc-3	Q19266	AGC/PKC	23	3
R02C2.2	O44546	CAMK/CAMKL/CHK1	23	0
abl-1	P03949	TK/Abl	23	9
pkc-2	P90980	AGC/PKC	22	7
cmk-1	Q9TXJ0	CAMK/CAMK1	22	2
H25P06.2	Q9TVL3	CMGC/CDK	22	8
daf-1	P20792	TKL/STKR	22	1
pdk-1	Q9Y1J3	AGC/PKB	21	5
kin-13	P34885	AGC/PKC	21	3
F32D8.1	Q19962	CAMK	21	0
R06A10.4	O44747	CAMK	21	0
plk-2	Q9N2L7	Other/PLK	21	2
mom-4	Q9XTC6	TKL/MLK	20	6
M03C11.1	Q21483	AGC	19	0
B0511.4	O61821	CAMK	19	0
pmk-3	O44514	CMGC/MAPK	19	0
C36B1.10	Q93344	CMGC/GSK	18	1
W02B3.2	Q09639	AGC/GRK	17	1
W04B5.5	Q9UA62	AGC/PKB	17	1
Y106G6E.6	Q8WQ99	CK1	16	4
Y42A5A.4	Q9U2H1	CMGC	16	0
jkk-1	Q9UAH1	STE/STE7	16	7
F11E6.8	Q9XVQ7	TK/Met	16	0
cdk-4	Q9XTR1	CMGC/CDK	15	0
B0495.2	Q09437	CMGC/CDK	15	2
F39H11.3	P90866	CMGC/CDK	14	2
kin-22	O45539	TK/Src	14	3
egl-4	O76360	AGC/PKG	13	0
K12C11.4	O44997	CAMK/DAPK	13	0
cdk-7	Q9Y0G1	CMGC/CDK	13	0
F19H6.1	Q19530	Other/NEK	13	1
VZC374L.1	O01706	STE/STE7	13	0
M176.9	Q22243	TK/Fer/Fer; TK/Fer/Fes	13	1
sax-1	Q2L6W9	AGC	12	0
W02B12.12	Q23128	CAMK	12	0
kin-29	Q21017	CAMK/CAMKL	12	1
pmk-2	Q8MXI4	CMGC/MAPK	12	2

Y59A8B.23	Q9GRY2	STE/STE20	12	1
T01H8.1a	Q21734	AGC/RSK	11	1
C53A5.4	O17693	CK1	11	0
C44H4.6	Q93372	CMGC/GSK	11	0
C05D10.2	Q11179	CMGC/MAPK	11	0
K08B12.5	O01583	AGC/DMPK	10	1
T19D12.5	Q22573	CK1	10	1
pik-1	Q9XU80	TKL/IRAK	10	4
F46F6.2	B6VQ53	AGC	9	1
sad-1	Q19469	CAMK/CAMKL	9	0
T25E12.4	O45818	CAMK/PKD	9	0
R13H9.5	Q966G2	CK1	9	0
src-1	Q8T6F8	TK/Src	9	0
Y47D3A.16	Q9NAH6	AGC/RSK	8	0
Y38H8A.4	O62424	CAMK	8	0
W06F12.3	O45897	CK1	8	2
F22D6.5	Q19727	CMGC/DYRK	8	0
ZC416.4	O44182	CMGC/MAPK	8	0
C49C3.10	Q9U3L3	CMGC/MAPK	8	0
F35C8.1	Q58AU7	STE/STE7	8	0
kin-5	Q18684	TK/Fer/Fer; TK/Fer/Fes	8	0
F57B9.8	Q20933	TK/Fer/Fer; TK/Fer/Fes	8	1
F33E2.2	O01700	TKL/MLK	8	3
atl-1	Q22258	Atypical/PIKK/ATR	7	3
C03C10.2	P42169	CK1	7	0
H01G02.2	O17903	CMGC/CDK	7	0
pqn-25	P84199	Other/NEK	7	0
scd-2	O76411	TK/Alk	7	2
C25A8.5	Q18142	TK/Fer/Fer; TK/Fer/Fes	7	0
ksr-2	Q8T4N7	TKL/RAF	7	0
C54G4.1	Q18846	AGC/RSK	6	2
pdhk-2	Q02332	Atypical/PDHK	6	1
C50F4.10	Q18738	CK1	6	0
ZK354.6	P91566	CK1	6	0
E02H4.3	Q17917	CMGC	6	0
pek-1	Q19192	Other/PEK	6	0
Y52D3.1	Q9XTC8	STE/STE20	6	1
Y48G1C.2	Q9BL77	TK/Csk	6	1
kin-26	Q22245	TK/Fer/Fer; TK/Fer/Fes	6	0
K11D12.10	Q8T7Z0	TKL/MLK	6	1
atm-1	Q9N3Q4	Atypical/PIKK/ATM	5	0
R13H9.6	Q966G1	CK1	5	0
K06H7.8	P34516	CK1	5	0
F35C8.2	Q58AU8	STE/STE7	5	0
ZC449.6	Q8MPS3	STE/STE7	5	0
C35E7.10	O61767	TK/Fer/Fer; TK/Fer/Fes	5	0
C24A1.3	O17055	TKL/MLK	5	0
T20F10.1	O45797	AGC	4	1
C27D8.1	Q93288	CK1	4	0
spe-6	Q95PZ9	CK1	4	0
F09C12.2	Q19243	CMGC/MAPK	4	0
C46C2.1	Q18657	Other/Wnk	4	0
frk-1	Q22146	TK/Fer/Fer; TK/Fer/Fes	4	0

R05H5.4	Q21764	TK/Fer/Fer; TK/Fer/Fes	4	0
C55C3.4	Q18865	TK/Fer/Fer; TK/Fer/Fes	4	0
Y43C5B.2	Q9XXE5	TK/Fer/Fer; TK/Fer/Fes	4	2
T14E8.1	Q22489	TK/Met	4	3
ZK666.8	Q23566	CK1	3	2
C25H3.1	Q18189	CK1	3	0
ZK596.2	Q23546	CK1	3	2
F22F1.2	Q19742	CK1	3	1
Y39G8C.2	Q9BHK8	CK1	3	0
K11C4.1	Q94277	CK1	3	0
Y81G3A.3	Q9XVY4	Other/PEK	3	1
kin-18	P46549	STE/STE20	3	0
F23C8.7	Q9TXI2	TK/Fer/Fer; TK/Fer/Fes	3	0
F19C6.1	Q09537	AGC/GRK	2	0
tpa-1	P34722	AGC/PKC	2	0
prk-1	Q17737	CAMK	2	1
W03G1.6	A7WK47	CAMK/CAMKL	2	0
par-4	Q9GN62	CAMK/CAMKL/LKB	2	0
K08F8.1	Q21360	CAMK/MAPKAPK	2	1
C24G7.5	O01761	CAMK/MLCK	2	1
ttn-1	Q8ISF7	CAMK/MLCK	2	0
W09C5.5	Q9XUJ7	CAMK/PKD	2	0
H05L14.1	O18107	CK1	2	1
C08F8.6	Q17825	CK1	2	0
T15B12.2	Q22518	CK1	2	1
T05C12.1	Q22223	CK1	2	0
C38C3.4	Q7KQ32	CK1	2	0
gck-1	Q22553	STE/STE20	2	1
ZC404.9	Q23290	STE/STE20	2	0
C04A11.3	O17566	STE/STE20	2	1
E02D9.1	Q9TYV7	STE/STE7	2	1
F22B3.8	Q19704	TK/Fer/Fer; TK/Fer/Fes	2	1
Y52D5A.2	Q9N4S6	TK/Fer/Fer; TK/Fer/Fes	2	1
kin-21	Q21299	TK/Fer/Fer; TK/Fer/Fes	2	1
R11E3.1	Q9TYX4	TK/Fer/Fer; TK/Fer/Fes	2	1
W03A5.1	Q23136	TK/Fer/Fer; TK/Fer/Fes	2	1
Y47G6A.5	Q9N3S5	TK/Src	2	1
C09G4.2	Q8MQE4	AGC/PKG	1	0
prk-2	Q20443	CAMK	1	0
Y50D7A.3	Q9N3L4	CAMK/PHK	1	0
ZC581.2	O01773	CK1	1	0
F41G3.5	Q20288	CK1	1	0
C16A11.3	C0Z1Y5	CMGC	1	0
C03B1.5	Q11112	STE/STE20	1	0
ZC581.7	O01774	TK/Fer/Fer; TK/Fer/Fes	1	0
ZK622.1	Q23554	TK/Fer/Fer; TK/Fer/Fes	1	0
F55C5.7	Q20821	AGC	0	0
kin-4	D3KFW7	AGC	0	0
F28C10.3	Q19858	AGC	0	0
R04A9.5	Q86DC2	AGC/RSK	0	0
C47D12.1	Q6A4L2	Atypical/PIKK	0	0
unc-82	D1MN54	CAMK/CAMKL	0	0
ZK524.4	Q22855	CAMK/CAMKL	0	0

DC2.7a	Q59DM0	CAMK/CAMKL/CHK1	0	0
R166.5	Q22005	CAMK/MAPKAPK	0	0
ZC373.4	Q23260	CAMK/MLCK	0	0
F39F10.3	Q20192	CK1	0	0
F39F10.2	Q20193	CK1	0	0
T11F8.4	O44192	CK1	0	0
F59A6.4	Q21026	CK1	0	0
D2045.5	Q18984	CK1	0	0
D2024.1	Q18976	CK1	0	0
C34B2.3	O44950	CK1	0	0
F16B12.5	Q93521	CK1	0	0
Y65B4A.9	Q9BL55	CK1	0	0
C04G2.2	Q17631	CK1	0	0
F25F2.1	Q19784	CK1	0	0
C45G9.1	Q09503	CK1	0	0
C49C8.1	Q18707	CK1	0	0
F59E12.3	O01899	CK1	0	0
C55B7.10	O02157	CK1	0	0
C09B9.4	Q17853	CK1	0	0
Y69F12A.1	Q9N4Q0	CK1	0	0
C56C10.6	Q18882	CK1	0	0
F38E1.3	Q20160	CK1	0	0
F35C11.3	Q20018	CK1	0	0
T01H10.4	D0VWM6	CK1	0	0
W09C3.1	Q3S1L3	CK1	0	0
F53C3.1	Q9TXU0	CK1	0	0
Y71F9AL.2	Q9N4H2	CK1	0	0
W03G9.5	O44751	CK1	0	0
C09D4.3	O01733	CK1	0	0
Y47G6A.13	Q9N3T7	CK1	0	0
C05C12.1	Q17651	CK1	0	0
Y73B6A.2	Q9N4E5	CK1	0	0
B0218.5	Q17448	CK1	0	0
W01B6.2	Q23103	CK1	0	0
R10D12.10	Q9XVK4	CK1	0	0
F54H5.2	P91332	CK1	0	0
F33D11.7	O44777	CK1	0	0
F26A1.4	Q19794	CK1	0	0
F26A1.3	Q19798	CK1	0	0
F32B6.10	Q9XVP6	CK1	0	0
M7.7	Q21590	CK1	0	0
B0207.7	O01429	CK1	0	0
ZK507.1	P34633	CK1	0	0
ZK507.3	P34635	CK1	0	0
R90.1	Q22033	CK1	0	0
C14A4.13	Q17960	CK1	0	0
K09E4.1	Q9NAP8	CK1	0	0
T05A7.6	Q22203	CK1	0	0
ZK354.2	P91571	CK1	0	0
Y111B2A.1	Q9BHM0	CMGC	0	0
ZC504.3	Q23357	CMGC/CDK	0	0
B0285.1	C8JQR0	CMGC/CDK	0	0
pct-1	Q17794	CMGC/CDK	0	0

ZC123.4	A4V4W9	CMGC/CDK	0	0
C36B7.2	Q966P6	CMGC/DYRK	0	0
C36B7.1	Q966P5	CMGC/DYRK	0	0
hpk-1	Q19632	CMGC/DYRK	0	0
R03D7.5	Q09595	CMGC/GSK	0	0
Y106G6E.1	Q9N667	CMGC/GSK	0	0
Y106G6D.4	Q9XX60	CMGC/GSK	0	0
F21F3.2	P91267	CMGC/GSK	0	0
Y51B9A.9	Q9XXC0	CMGC/MAPK	0	0
C04G6.1	Q8IG56	CMGC/MAPK	0	0
W06B3.2	Q9XTI6	CMGC/MAPK	0	0
Y39G10AR.4	Q6AW07	Other/NEK	0	0
Y38E10A.8	Q9NAK3	Other/PEK	0	0
B0414.7	O01837	STE/STE11	0	0
Y38F1A.10	Q9XWL8	STE/STE20	0	0
aSWK454	Q9U3B5	TK/Fer/Fer; TK/Fer/Fes	0	0
F59A3.8	P91360	TK/Fer/Fer; TK/Fer/Fes	0	0
kin-24	Q21292	TK/Fer/Fer; TK/Fer/Fes	0	0
T08G5.2	B1Q276	TK/Fer/Fer; TK/Fer/Fes	0	0
kin-14	Q19726	TK/Fer/Fer; TK/Fer/Fes	0	0
Y116A8C.24	Q9U2U8	TK/Fer/Fer; TK/Fer/Fes	0	0
T25B9.4	Q22765	TK/Fer/Fer; TK/Fer/Fes	0	0
T25B9.5	Q22766	TK/Fer/Fer; TK/Fer/Fes	0	0
W01B6.5	Q23102	TK/Fer/Fer; TK/Fer/Fes	0	0
Y69E1A.3	Q9XW34	TK/Fer/Fer; TK/Fer/Fes	0	0
C18H7.4	Q9GZG1	TK/Fer/Fer; TK/Fer/Fes	0	0
F01D4.3	O17755	TK/Fer/Fer; TK/Fer/Fes	0	0
T21G5.1	O02064	TK/Fer/Fer; TK/Fer/Fes	0	0
F26E4.5	O01325	TK/Fer/Fer; TK/Fer/Fes	0	0
kin-31	P34265	TK/Fer/Fer; TK/Fer/Fes	0	0
D1073.1	Q0MQ66	TK/Trk	0	0
Y105C5A.24	Q9NF64	TKL/MLK	0	0
zak-1	Q21982	TKL/MLK	0	0
<i>Saccharomyces cerevisiae</i>				
CDC28	P00546	CMGC/CDK/CDC2	885	370
SNF1	P06782	CAMK/CAMKL/AMPK	742	319
MCK1	P21965	CMGC/GSK	685	323
CLA4	P48562	STE/STE20	664	332
SLT2	Q00772	CMGC/MAPK	642	361
YCK1	P23291	CK1	621	391
RAD53	P22216	CAMK/RAD53	608	301
BCK1	Q01389	STE/STE11	510	305
PKC1	P24583	AGC/PKC	507	252
TOR1	P35169	Atypical/PIKK/FRAP	478	243
STE20	Q03497	STE/STE20	474	208
DBF2	P22204	AGC	467	314
PHO85	P17157	CMGC/CDK	463	243
SSN3	P39073	CMGC/CDK	453	175
TPK1	P06244	AGC/PKA	446	325
CKA2	P19454	Other/CK2	446	172
MEC1	P38111	Atypical/PIKK/ATR	438	153
CKA1	P15790	Other/CK2	435	186
DUN1	P39009	CAMK/RAD53	415	214

FUS3	P16892	CMGC/MAPK	409	194
HOG1	P32485	CMGC/MAPK	408	165
PBS2	P08018	STE/STE7	399	237
CTK1	Q03957	CMGC/CDK	390	203
YCK2	P23292	CK1	386	277
CDC5	P32562	Other/PLK	368	163
TOR2	P32600	Atypical/PIKK/FRAP	361	171
KSS1	P14681	CMGC/MAPK	339	174
HSL1	P34244	CAMK/CAMKL	324	194
TPK2	P06245	AGC/PKA	295	90
CHK1	P38147	CAMK/CAMKL/CHK1	295	133
HRR25	P29295	CK1	294	163
TRA1	P38811	Atypical/PIKK	292	161
GCN2	P15442	Other/PEK	291	135
TPK3	P05986	AGC/PKA	286	133
IPL1	P38991	Other/AUR/IPL1-yeast	283	114
CMK1	P27466	CAMK/CAMK1	268	176
SCH9	P11792	AGC/AKT	261	82
SGV1	P23293	CMGC/CDK	261	107
CAK1	P43568	CMGC/CDK	252	112
MEK1	P24719	CAMK	250	142
IME2	P32581	CMGC	250	139
RIM15	P43565	AGC	238	134
TEL1	P38110	Atypical/PIKK/ATM	238	75
STE11	P23561	STE/STE11	234	77
SKY1	Q03656	CMGC	230	149
KIN28	P06242	CMGC/CDK	227	50
RIM11	P38615	CMGC/GSK	225	85
YAK1	P14680	CMGC/DYRK	216	83
SSK2	P53599	STE/STE11	216	135
GIN4	Q12263	CAMK/CAMKL	215	109
CDC15	P27636	STE/STE11	203	91
CBK1	P53894	AGC	187	96
YGL059W	P53170	Atypical/PDHK	179	112
YPL150W	Q12152	CAMK/CAMKL	164	117
MKK2	P32491	STE/STE7	164	68
RCK1	P38622	CAMK/CAMK1	158	121
STE7	P06784	STE/STE7	158	21
MKK1	P32490	STE/STE7	158	64
YOL045W	Q08217	CAMK/CAMKL	151	87
KIN2	P13186	CAMK/CAMKL	151	83
CMK2	P22517	CAMK/CAMK1	140	48
SPS1	P08458	STE/STE20	139	62
SKM1	Q12469	STE/STE20	137	70
KIN82	P25341	AGC/RSK	126	85
KIN4	Q01919	CAMK/CAMKL	126	92
FUN31	P31374	CAMK/CAMKL	125	62
PRR1	P28708	CAMK	117	58
YPL141C	Q03002	CAMK/CAMKL	111	88
YPK1	P12688	AGC/AKT	109	44
KCC4	P25389	CAMK/CAMKL	109	42
RCK2	P38623	CAMK/CAMK1	108	61
YKL171W	P36003	CAMK	105	77

SMK1	P41808	CMGC/MAPK	102	42
PKH1	Q03407	AGC/PKB	100	31
YPK2	P18961	AGC/AKT	96	31
KIN3	P22209	Other/NEK	95	52
YCK3	P39962	CK1	93	39
KNS1	P32350	CMGC	89	50
YNR047W	P53739	AGC/RSK	88	51
KIN1	P13185	CAMK/CAMKL	88	37
KIC1	P38692	STE/STE20	83	32
SSK22	P25390	STE/STE11	82	41
PKH2	Q12236	AGC/PKB	77	28
DBF20	P32328	AGC	71	39
YOL128C	Q12222	CMGC/GSK	63	27
YKL161C	P36005	CMGC/MAPK	62	16
MRK1	P50873	CMGC/GSK	52	26
YBR028C	P38070	AGC/RSK	47	21
YDR466W	Q03306	AGC/PKB	41	23
YMR291W	Q03533	CAMK	36	22
YIL042C	P40530	Atypical/PDHK	33	17

Supplemental Table S17 – The number of p-sites for each PK in the mouse liver PPN. The top 10 PKs with the most p-sites are marked in yellow.

PK Name	Uniprot	Predictor	String & Exp. PPI		Exp. PPI	
			Protein	Site	Protein	Site
ERK2	P63085	CMGC/MAPK	96	167	4	9
AKT1	Q6GSA6	AGC/AKT	106	164	0	0
ERK1	Q63844	CMGC/MAPK	73	120	1	3
CDC2	P11440	CMGC/CDK/CDC2	52	116	1	1
GSK3B	Q9WV60	CMGC/GSK	45	91	0	0
p38a	Q5U421	CMGC/MAPK	57	88	0	0
CDK2	P97377	CMGC/CDK/CDC2	36	72	0	0
JNK2	Q5NCK8	CMGC/MAPK	43	70	2	4
Trio	Q0KL02	CAMK	34	63	0	0
CDK5	P49615	CMGC/CDK	37	62	1	4
PKACb	P68181	AGC/PKA	35	59	0	0
SGK1	Q9WVC6	AGC/SGK	24	57	0	0
PLK1	Q07832	Other/PLK	30	55	0	0
CK2a2	O54833	Other/CK2	23	52	0	0
CDK4	P30285	CMGC/CDK	29	51	0	0
IKKa	Q8CBT3	Other/IKK	31	49	0	0
Trad	A2CG49	CAMK	26	48	0	0
p70S6K	Q5SWG1	AGC/RSK	30	48	0	0
MAP2K1	Q9JJE1	STE/STE7	31	46	0	0
PLK3	Q6P571	Other/PLK	20	44	0	0
PITSLRE	P24788	CMGC/CDK	11	43	0	0
IKKb	Q5D0E0	Other/IKK	28	43	0	0
MarkmA10	A0AUV4	CAMK/CAMKL	9	40	0	0
PLK2	P53351	Other/PLK	17	36	0	0
ROCK1	P70335	AGC/DMPK; AGC/DMPK/ROCK	13	36	0	0
PKCe	P16054	AGC/PKC	15	35	1	1
BARK1	Q99MK8	AGC/GRK	20	33	0	0
CHK2	Q9Z265	CAMK/RAD53	23	33	0	0
PKCd	P28867	AGC/PKC	18	32	0	0
AKT2	Q60823	AGC/AKT	22	32	0	0
CDK6	Q64261	CMGC/CDK	20	32	0	0
PYK2	Q9QVP9	TK/Fak	25	32	0	0
CaMK2a	Q80TN1	CAMK/CAMK2	20	32	1	1
SGK3	Q9ERE3	AGC/SGK	19	31	0	0
PDK1	Q9Z2A0	AGC/PKB	23	31	0	0
GSK3A	Q2NL51	CMGC/GSK	15	30	0	0
ABL1	P00520	TK/Abl	24	30	2	3
FYN	P39688	TK/Src	22	28	4	6
HIPK2	Q9QZR5	CMGC/DYRK	19	27	0	0
MAP2K4	P47809	STE/STE7	17	27	0	0
AMPKa2	B1ASQ8	CAMK/CAMKL/AMPK	13	26	0	0
TRRAP	Q3UH32	Atypical/PIKK	18	26	0	0
FAK	P34152	TK/Fak	22	26	4	4
MAP2K5	Q9WVS7	STE/STE7	16	26	3	3
EGFR	Q01279	TK/EGFR	23	25	3	3
INSR	P15208	TK/InsR	18	25	2	5
MarkmD1	Q8C0X8	CAMK/CAMKL	4	24	0	0

PAK1	O88643	STE/STE20	19	24	2	3
MOK	Q9WVS4	CMGC	7	24	0	0
TGFB1	Q64729	TKL/STKR	16	24	5	7
ROCK2	P70336	AGC/DMPK; AGC/DMPK/ROCK	11	24	0	0
PKCa	Q4VA93	AGC/PKC	14	24	0	0
AKT3	Q9WUA6	AGC/AKT	15	23	0	0
MAPKAPK2	P49138	CAMK/MAPKAPK	15	23	0	0
ERK5	Q9WVS8	CMGC/MAPK	17	23	0	0
TAK1	Q923A8	TKL/MLK	19	23	0	0
p70S6Kb	Q9Z1M4	AGC/RSK	13	22	0	0
PAK2	Q8CIN4	STE/STE20	18	22	0	0
SGK2	Q9QZS5	AGC/SGK	13	22	0	0
MARK2	Q571J8	CAMK/CAMKL	12	22	1	2
MAP2K2	Q9D7B0	STE/STE7	15	22	0	0
ErbB2	P70424	TK/EGFR	15	21	0	0
CASK	O70589	CAMK	10	21	0	0
MarkmA3	Q9QYZ5	CAMK/CAMKL	9	20	0	0
MAP2K7	Q8CE90	STE/STE7	12	20	0	0
PKD1	Q62101	CAMK/PKD	14	20	1	1
ILK	O55222	TKL/MLK	18	20	0	0
RAF1	Q99N57	TKL/RAF	17	20	0	0
DAPK1	Q80YE7	CAMK/DAPK	8	19	0	0
CDK7	Q03147	CMGC/CDK	12	19	0	0
PKACa	P05132	AGC/PKA	13	19	0	0
smMLCK	B1B1A8	CAMK/MLCK	15	19	0	0
RSK1	Q9WUT3	AGC/RSK	7	18	1	4
PAK4	Q8BTW9	STE/STE20	14	18	0	0
CRIK	P49025	AGC/DMPK	12	18	0	0
SYK	P48025	TK/Syk	15	18	0	0
FGR	Q8BGM0	TK/Src	13	18	0	0
p38b	Q569F1	CMGC/MAPK	11	18	0	0
CDK9	Q99J95	CMGC/CDK	13	18	1	2
PLK4	Q64702	Other/PLK	6	17	0	0
DYRK2	Q5U4C9	CMGC/DYRK	11	17	0	0
p38g	O08911	CMGC/MAPK	8	17	0	0
DYRK1A	Q61214	CMGC/DYRK	8	16	0	0
RSK2	P18654	AGC/RSK	12	16	1	4
MAP2K6	P70236	STE/STE7	11	16	1	1
AurA	P97477	Other/AUR/AUR-A	10	16	0	0
BMPr1A	P36895	TKL/STKR	7	16	0	0
FES	P16879	TK/Fer/Fer; TK/Fer/Fes	8	16	0	0
TBK1	Q9WUN2	Other/IKK	7	15	1	1
AMPKa1	Q5EG47	CAMK/CAMKL/AMPK	10	15	1	2
LKB1	Q9WTK7	CAMK/CAMKL/LKB	13	15	0	0
FER	P70451	TK/Fer/Fer; TK/Fer/Fes	8	15	0	0
AurB	Q8C6C1	Other/AUR/AUR-B	13	15	0	0
MET	P16056	TK/Met	12	15	0	0
YES	Q04736	TK/Src	10	15	0	0
CDK8	Q8R3L8	CMGC/CDK	6	15	0	0
MarkmA6	Q9QYZ6	CAMK/CAMKL	7	14	0	0
ALK2	P37172	TKL/STKR	8	14	3	4
PKCb	P68404	AGC/PKC	9	14	0	0
CHK1	O35280	CAMK/CAMKL/CHK1	9	14	0	0

IGF1R	Q60751	TK/InsR	9	14	0	0
MAP2K3	O09110	STE/STE7	10	14	1	1
PKN2	Q3TBR3	AGC	10	13	1	2
NIK	Q9WUL6	STE/STE-Unique/NIK	7	13	0	0
PKCt	Q02111	AGC/PKC	8	13	0	0
CDKL5	Q3UTQ8	CMGC	4	13	0	0
MAP3K1	P53349	STE/STE11	9	13	1	1
KIT	Q8C8K9	TK/PDGFR	12	13	2	2
JAK2	Q62120	TK/JakA	12	13	3	3
ErbB3	Q61526	TK/EGFR	9	13	1	1
RET	P35546	TK/Ret	8	13	0	0
MLK2	Q66L42	TKL/MLK	10	13	0	0
ERK3	Q61532	CMGC/MAPK	5	12	0	0
CLK1	Q3UXB6	CMGC	6	12	0	0
LCK	P06240	TK/Src	12	12	2	2
KDR	P35918	TK/VEGFR	8	12	0	0
PCTAIRE1	Q04735	CMGC/CDK	6	12	0	0
PRKX	Q922R0	AGC/PKA	9	12	0	0
ZAP70	P43404	TK/Syk	11	11	0	0
CaMK4	Q8BGR3	CAMK/CAMK1	7	11	0	0
PAK6	Q3ULB5	STE/STE20	6	10	0	0
PKD3	Q5FWX6	CAMK/PKD	6	10	0	0
CaMK2g	Q923T9	CAMK/CAMK2	6	10	0	0
GPRK4	Q3V151	AGC/GRK	4	10	0	0
TAO1	Q5F2E8	STE/STE20	8	10	0	0
TAO2	Q6ZQ29	STE/STE20	8	10	0	0
PFTAIRE1	O35495	CMGC/CDK	4	10	0	0
FMS	P09581	TK/PDGFR	9	10	0	0
FGFR2	P21803	TK/FGFR	6	10	0	0
FLT1	P35969	TK/VEGFR	7	10	0	0
CaMK2b	Q5SVJ0	CAMK/CAMK2	8	10	0	0
MarkmA5	Q9QYZ3	CAMK/CAMKL	8	9	0	0
PAK5	Q8C015	STE/STE20	7	9	0	0
Wnk1	P83741	Other/Wnk	7	9	0	0
IKKe	Q8C2I3	Other/IKK	5	9	0	0
YSK1	Q6IR17	STE/STE20	8	9	0	0
Obscn	A2AAJ9	CAMK	5	9	1	2
MNK2	Q8CDB0	CAMK/MAPKAPK	5	9	0	0
MARK1	Q14DQ3	CAMK/CAMKL	3	9	0	0
PKCi	Q5DTK3	AGC/PKC	4	9	0	0
ALK	P97793	TK/Alk	7	9	0	0
MAP3K3	Q61084	STE/STE11	6	9	0	0
TAO3	Q8BYC6	STE/STE20	7	9	0	0
LATS2	Q7TSJ6	AGC	6	9	0	0
ATM	Q62388	Atypical/PIKK/ATM	8	9	0	0
DNAPK	P97313	Atypical/PIKK/DNAPK	6	9	0	0
PDGFRa	P26618	TK/PDGFR	8	9	0	0
p38d	Q9Z1B7	CMGC/MAPK	4	9	0	0
FGFR1	P16092	TK/FGFR	6	9	0	0
PKR	Q03963	Other/PEK	8	9	0	0
SRPK2	O54781	CMGC	4	8	1	2
PKCh	Q8K2K8	AGC/PKC	3	8	0	0
Wnk4	Q80UE6	Other/Wnk	6	8	0	0

DCLK1	Q9JLM8	CAMK	4	8	0	0
GCK	Q61161	STE/STE20	4	8	0	0
MAPKAPK5	O54992	CAMK/MAPKAPK	5	8	1	2
CAMK1g	Q91VB2	CAMK/CAMK1	7	8	0	0
CaMK2d	Q6PHZ2	CAMK/CAMK2	5	8	1	1
BRAF	P28028	TKL/RAF	7	8	0	0
BTK	P35991	TK/Tec	7	8	0	0
CK1a	Q8BK63	CK1	4	8	0	0
CK1e	Q9JMK2	CK1	5	8	0	0
JAK1	B1ASP2	TK/JakA	8	8	0	0
SMG1	Q8BKX6	Atypical/PIKK	5	8	0	0
BMPR2	O35607	TKL/STKR	5	8	0	0
PDHK1	Q3U5E5	Atypical/PDHK	4	7	0	0
CaMK1a	Q91YS8	CAMK/CAMK1	4	7	0	0
MAPKAPK3	Q3UMW7	CAMK/MAPKAPK	4	7	0	0
SRPK1	O70551	CMGC	4	7	1	2
QIK	Q8CFH6	CAMK/CAMKL	4	7	0	0
TIE2	B1AWS8	TK/Tie	6	7	0	0
JAK3	Q62137	TK/JakA	7	7	0	0
HPK1	P70218	STE/STE20	3	7	0	0
DYRK3	Q922Y0	CMGC/DYRK	2	6	0	0
MARK4	Q8CIP4	CAMK/CAMKL	3	6	0	0
ABL2	Q4JIM5	TK/Abl	5	6	0	0
Wnk3	Q80XP9	Other/Wnk	4	6	0	0
DYRK1B	Q9Z188	CMGC/DYRK	2	6	0	0
PCTAIRE3	Q04899	CMGC/CDK	3	6	0	0
MST1	Q9JI11	STE/STE20	5	6	0	0
DRAK2	Q8BG48	CAMK/DAPK	6	6	0	0
DCLK3	Q8BWQ5	CAMK	5	6	0	0
ACTR2B	P27040	TKL/STKR	2	6	0	0
CDK11	Q8BWD8	CMGC/CDK	4	6	0	0
TRKB	P15209	TK/Trk	5	6	0	0
CSK	Q8VCW1	TK/Csk	6	6	0	0
KSR1	Q61097	TKL/RAF	4	6	0	0
MAP3K2	Q61083	STE/STE11	5	6	0	0
DAPK3	O54784	CAMK/DAPK	4	6	0	0
CLK2	O35491	CMGC	3	5	1	1
NuaK1	Q641K5	CAMK/CAMKL	5	5	0	0
MRCKa	B2RXX8	AGC/DMPK	2	5	0	0
RSK4	A2CEE7	AGC/RSK	4	5	0	0
TIE1	Q8BGI2	TK/Tie	4	5	0	0
OSR1	Q6P9R2	STE/STE20	3	5	0	0
Trb3	Q8K4K2	CAMK	4	5	1	1
ACTR2	P27038	TKL/STKR	1	5	0	0
MAP3K4	Q6PDG6	STE/STE11	4	5	0	0
DMPK1	P54265	AGC/DMPK	4	5	0	0
TRKA	Q3UFB7	TK/Trk	5	5	0	0
PIM2	Q62070	CAMK	3	5	0	0
MSK1	Q8C050	AGC/RSK	4	5	0	0
LYN	P25911	TK/Src	5	5	5	5
BRK	Q64434	TK/Src	4	5	0	0
NIM1	Q8BHI9	CAMK/CAMKL	4	5	0	0
PSKH1	Q91YA2	CAMK	5	5	0	0

ALK4	Q61271	TKL/STKR	3	5	0	0
GPRK6	O70293	AGC/GRK	1	4	1	4
FRAP	Q9JLN9	Atypical/PIKK/FRAP	2	4	2	4
MarkmB2	B7ZNH4	CAMK/CAMKL	1	4	0	0
MarkmC1	Q3UTA8	CAMK/CAMKL	3	4	0	0
PHKg1	P07934	CAMK/PHK	4	4	0	0
MarkmC2	Q3UT86	CAMK/CAMKL	3	4	0	0
BARK2	Q3UYH7	AGC/GRK	2	4	0	0
caMLCK	Q3UIZ8	CAMK/MLCK	3	4	0	0
MarkmA1	Q8C0N0	CAMK/CAMKL	3	4	0	0
PCTAIRE2	Q8K0D0	CMGC/CDK	2	4	0	0
MarkmB1	Q8C0V7	CAMK/CAMKL	3	4	0	0
Wnk2	Q3UH66	Other/Wnk	3	4	0	0
CDK10	Q3UMM4	CMGC/CDK	1	4	0	0
NEK6	Q9ES70	Other/NEK	4	4	0	0
RSKL1	Q8BLK9	AGC	2	4	0	0
HIPK1	A9R9X0	CMGC/DYRK	3	4	0	0
MLK4	Q8VDG6	TKL/MLK	3	4	0	0
STLK3	Q9Z1W9	STE/STE20	3	4	0	0
PRP4	C7G3P2	CMGC/DYRK	2	4	0	0
BMPR1B	P36898	TKL/STKR	3	4	1	2
FLT4	P35917	TK/VEGFR	3	4	0	0
PEK	Q9Z2B5	Other/PEK	4	4	0	0
FGFR4	Q03142	TK/FGFR	2	4	0	0
IRAK4	Q8R4K2	TKL/IRAK	3	4	0	0
TRKC	Q6VNS1	TK/Trk	4	4	0	0
MST3	Q99KH8	STE/STE20	3	3	0	0
MST4	Q99JT2	STE/STE20	3	3	0	0
STLK6	Q8K4T3	STE/STE20	2	3	0	0
PDHK3	Q922H2	Atypical/PDHK	1	3	0	0
JNK1	Q91Y86	CMGC/MAPK	1	3	1	3
PHKg2	A6H632	CAMK/PHK	3	3	0	0
DCLK2	Q6PGN3	CAMK	2	3	0	0
MSSK1	Q9Z0G2	CMGC	1	3	0	0
AurC	O88445	Other/AUR	1	3	0	0
NuaK2	Q8BZN4	CAMK/CAMKL	3	3	0	0
FRK	Q922K9	TK/Src	3	3	0	0
DAPK2	Q8VDF3	CAMK/DAPK	3	3	0	0
GCN2	A2AUM0	Other/PEK	3	3	0	0
AXL	Q80YQ3	TK/Axl	3	3	0	0
IRAK2	Q8CFA1	TKL/IRAK	2	3	0	0
TNIK	B9EKN8	STE/STE20	1	3	0	0
EphA5	Q60629	TK/Eph	3	3	0	0
EphA1	Q60750	TK/Eph	2	3	0	0
BLK	Q8K2M8	TK/Src	3	3	0	0
COT	Q07174	STE/STE-Unique/COT	3	3	0	0
NLK	O54949	CMGC/MAPK	3	3	0	0
ARAF	P04627	TKL/RAF	3	3	0	0
RON	Q62190	TK/Met	3	3	0	0
ALK1	Q91YR0	TKL/STKR	3	3	0	0
PKG1	P0C605	AGC/PKG	2	3	1	1
EphA2	Q3UNI2	TK/Eph	2	3	0	0
SPEG	Q62407	CAMK	2	3	0	0

CaMK1b	Q9QYK9	CAMK/CAMK1	3	3	0	0
DYRK4	Q8BI55	CMGC/DYRK	1	2	0	0
MarkmE2	A2AQX6	CAMK/CAMKL	2	2	0	0
VACAMKL	Q3UHL1	CAMK	1	2	0	0
TTBK2	A2AW15	CK1	1	2	0	0
TTBK1	Q6PCN3	CK1	1	2	0	0
QSK	Q6P4S6	CAMK/CAMKL	1	2	0	0
LOK	B1ATW8	STE/STE20	1	2	0	0
CHED	Q69ZA1	CMGC/CDK	1	2	0	0
IRAK3	Q8K4B2	TKL/IRAK	1	2	0	0
MRCKb	B2RQQ7	AGC/DMPK	1	2	0	0
MISR2	Q8K592	TKL/STKR	2	2	0	0
MLK1	Q3U1V8	TKL/MLK	1	2	0	0
ITK	Q03526	TK/Tec	2	2	0	0
EphA4	Q80VZ2	TK/Eph	2	2	0	0
SIK	Q60670	CAMK/CAMKL	2	2	0	0
EphB4	Q8C7S3	TK/Eph	2	2	0	0
MLK3	Q80XI6	TKL/MLK	2	2	0	0
RHOK	Q9WVL4	AGC/GRK	2	2	0	0
TSSK1	Q80YU1	CAMK	1	2	0	0
TSSK2	Q6P8M9	CAMK	1	2	0	0
PDHK4	O70571	Atypical/PDHK	1	2	0	0
MER	Q60805	TK/Axl	2	2	0	0
KHS2	Q99JP0	STE/STE20	1	2	0	0
CCRK	Q9JHU3	CMGC/CDK	1	1	0	0
MAST1	Q9R1L5	AGC	1	1	0	0
MAP3K5	O35099	STE/STE11	1	1	1	1
NEK10	Q3UGM2	Other/NEK	1	1	0	0
NEK11	Q8C0Q4	Other/NEK	1	1	0	0
YANK3	Q8QZV4	AGC	1	1	0	0
NEK8	Q91ZR4	Other/NEK	1	1	0	0
PKN3	Q8K045	AGC	1	1	0	0
SgK085	Q5SUV5	CAMK/MLCK	1	1	0	0
PDGFRb	P05622	TK/PDGFR	1	1	1	1
BMX	B1AUL6	TK/Tec	1	1	0	0
TEC	Q3U436	TK/Tec	1	1	0	0
EphB1	Q8CBF3	TK/Eph	1	1	0	0
EphB3	Q91YS9	TK/Eph	1	1	0	0
DLK	Q60700	TKL/MLK	1	1	0	0
PIM3	P58750	CAMK	1	1	0	0
PASK	Q8CEE6	CAMK/CAMKL	1	1	0	0
ZAK	Q9ESL4	TKL/MLK	1	1	0	0
BRSK1	Q5RJI5	CAMK/CAMKL	1	1	0	0
MSK2	Q3U3M8	AGC/RSK	1	1	0	0
NEK7	Q9ES74	Other/NEK	1	1	0	0
TSSK3	Q9D2E1	CAMK	1	1	0	0
VRK2	Q8BN21	CK1	1	1	1	1
GPRK5	Q8VEB1	AGC/GRK	1	1	0	0
CTK	P41242	TK/Csk	1	1	0	0

Supplemental Table S18 – All PKs with significantly over- or under-represented p-sites in the mouse liver PPN (p-value < 0.01).

PK Name	Uniprot	Predictor	String & Exp. PPI				
			Protein	Site	E-ratio	χ^2	p-value
<i>PKs with over-represented p-sites</i>							
SGK1	Q9WVC6	AGC/SGK	24	57	1.76	16.05	6.18E-05
RSK1	Q9WUT3	AGC/RSK	7	18	2.60	13.82	2.01E-04
AKT1	Q6GSA6	AGC/AKT	106	164	1.30	11.44	7.19E-04
MarkmD1	Q8C0X8	CAMK/CAMKL	4	24	2.04	10.49	1.20E-03
GPRK6	O70293	AGC/GRK	1	4	6.34	10.46	1.22E-03
Trio	Q0KL02	CAMK	34	63	1.53	10.15	1.44E-03
SRPK2	O54781	CMGC	4	8	3.31	9.40	2.17E-03
FRAP	Q9JLN9	Atypical/PIKK/FRAP	2	4	5.44	8.92	2.82E-03
AMPKa2	B1ASQ8	CAMK/CAMKL/AMPK	13	26	1.86	8.68	3.21E-03
PITSLRE	P24788	CMGC/CDK	11	43	1.57	7.73	5.44E-03
MarkmB2	B7ZNH4	CAMK/CAMKL	1	4	4.76	7.65	5.68E-03
TBK1	Q9WUN2	Other/IKK	7	15	2.16	7.59	5.88E-03
DYRK4	Q8BI55	CMGC/DYRK	1	2	9.52	7.16	7.45E-03
<i>PKs with under-represented p-sites</i>							
CDK2	P97377	CMGC/CDK/CDC2	36	72	0.65	14.19	1.66E-04
EGFR	Q01279	TK/EGFR	23	25	0.51	11.23	8.06E-04
ATM	Q62388	Atypical/PIKK/ATM	8	9	0.36	10.10	1.48E-03
CDK4	P30285	CMGC/CDK	29	51	0.65	9.60	1.95E-03
LCK	P06240	TK/Src	12	12	0.42	9.11	2.54E-03
EphA5	Q60629	TK/Eph	3	3	0.21	8.64	3.29E-03
CHK1	O35280	CAMK/CAMKL/CHK1	9	14	0.48	7.51	6.14E-03
MAP3K1	P53349	STE/STE11	9	13	0.48	6.93	8.46E-03
ITK	Q03526	TK/Tec	2	2	0.19	6.93	8.50E-03

Supplemental Table S19 – The statistical data on the experimentally identified and pre-calculated PPI information. *a* . All Exp., all experimental PPIs after redundant clearing.

Database	<i>S. cerevisiae</i>		<i>C. elegans</i>		<i>D. melanogaster</i>		<i>M. musculus</i>		<i>H. sapiens</i>	
	PPI	Protein	PPI	Protein	PPI	Protein	PPI	Protein	PPI	Protein
Biogrid	151,559	5,662	6,587	3,484	24,471	7,181	1,567	1,276	29,556	8,438
HPRD									38,660	9,594
DIP	22,048	4,968	3,904	2,545	21,797	6,995	582	634	1,928	1,535
MINT	20,281	5,131	5,158	3,115	16,166	5,810	1,837	1,574	9,330	4,706
Intact	8,364	3,046	2,141	1,470	3,027	3,270	1,076	1,124	7,078	3,969
All Exp.^a	165,012	6,020	9,559	4,246	32,533	8,324	4,740	3,244	59,481	12,221
STRING	239,330	5,949	147,413	8,425	374,633	11,389	709,610	15,438	1,212,607	16,523

Supplemental Table S20 – The distribution of the predicted kinase-specific p-sites with the source of the PPIs.

Data set	Exp.	String & Exp.	String	Total
Test	441	768	1,949	3,158
<i>S. cerevisiae</i>	6,280	8,368	6,261	20,909
<i>C. elegans</i>	31	152	684	867
<i>D. melanogaster</i>	187	407	5,597	6,191
<i>M. musculus</i>	590	664	43,778	45,032
<i>H. sapiens</i>	5,089	13,105	95,729	113,923