

Supplemental Information

Cell Host & Microbe, Volume 8

The Systematic Functional Analysis of *Plasmodium* Protein Kinases Identifies Essential Regulators of Mosquito Transmission

Rita Tewari, Ursula Straschil, Alex Bateman, Ulrike Böhme, Inna Cherevach, Peng Gong, Arnab Pain, and Oliver Billker

SUPPLEMENTAL EXPERIMENTAL PROCEDURES

Generation of Gene Knockout Parasites

Oligonucleotides used to amplify targeting sequences from *P. berghei* genomic DNA are described in “Table oligonucleotides”. Depending on construct design, restriction digests with KpnI/SacII or ApaI/XbaI were used to release the linear targeting vector from the cloning plasmid. Electroporated parasites were mixed immediately with 100 µl of reticulocyte-rich blood from a phenylhydrazine treated, naive mouse and incubated at 37°C for 15 minutes. Re-invaded parasites were injected intraperitoneally into naive mice. From day 1 post infection pyrimethamine was applied in the drinking water for four days. Mice were monitored for 15 days to allow any slow growing mutants to reach patency. Drug selection was repeated after passage to a second mouse, and resistant parasites were used for cloning by limiting dilution, and genotyping.

Genotype Analysis of Mutants.

Chromosomes of wild type and knockout parasites were separated by pulsed field gel electrophoresis (PFGE) on an LKB 2015 Pulsaphor system or CHEF DR III using a linear ramp of 60–500 s for 72 hr at 4V/cm. Gels were blotted and hybridized with a probe recognizing both the resistance cassette in the targeting vector and, more weakly, the 3'UTR of the *P. berghei dhfr/ts* locus on chromosome 7. Two diagnostic PCR reactions were used as illustrated in Fig. 2A. In one reaction primers 1 and 2 were used to determine correct integration of the selectable marker at the target locus. Primers 3 and 4 (Fig. 2A) verified deletion of the target gene. Sequences for the locus-specific primers (P1, P3, and P4) are given in Table S4. The generic primer P2 was either ol248 (5'-GATGTGTTATGTGATTAATTCATACAC-3') or ol539 (5'-CAATGATTCATAAATAGTTGGACTTG-3'), depending on whether the 5' or 3' end of the *tgdhfr/ts* cassette was used to verify integration. Having confirmed integration on one end by diagnostic PCR, we usually used Southern blot analysis to probe integration on the opposite end of the construct. Genomic DNA from wild type and mutant parasites was digested with diagnostic restriction enzymes cutting once within the knockout cassette, as illustrated in Fig. 2A. The fragments were separated on a 0.8% agarose gel, blotted onto a nylon membrane,

and probed with a PCR fragment homologous to the *P. berghei* genomic DNA just outside of the targeted region.

Phenotype Analysis

Infections for phenotype screens were initiated by the intraperitoneal injection of infected blood containing 5×10^6 parasites into mice that had been pretreated with 0.2 ml of 6 mg/ml phenylhydrazine in PBS intraperitoneally to induce reticulocytosis. Asexual stages and gametocyte production were monitored on Giemsa-stained blood films.

Exflagellation was examined on days 3-4 post infection. 5 μ l of gametocyte-infected blood were obtained from the tail with a heparinized pipette tip and mixed immediately with 40 μ l of ookinete culture medium (RPMI1640 containing 25 mM HEPES, 25% fetal bovine serum, 10 mM sodium bicarbonate, 50 μ M xanthurenic acid at pH 7.6). The mixture was placed under a Vaseline-coated cover slip and 10-20 min later exflagellation centers were counted by phase contrast microscopy in 12-15 fields of view using a 63x objective and 10x ocular lens.

Ookinete formation was assessed on the same day. 10 μ l of infected tail blood were obtained as above, mixed immediately with 40 μ l ookinete culture medium, and incubated for 1 h at 19°C to allow completion of gametogenesis and fertilisation. Each culture was then diluted with 0.4 ml of ookinete medium and transferred to a 24-well plate, which was incubated at 20°C for a further 21–24 h to allow ookinete differentiation. Cultures were pelleted for 2 min at 5000 rpm and then incubating for 5min on ice with 50 μ l of ookinete medium containing the DNA dye Hoechst 33342 to a final concentration of 5 μ g/ml and a Cy3-conjugated mouse monoclonal antibody 13.1, which recognizes the P28 protein on the surface of ookinetes and any undifferentiated macrogametes or zygotes. Labeled cultures were placed on a microscope slide under a Vaseline-rimmed cover slip and P28-positive cells counted with a Leica DMR fluorescence microscope. Ookinete conversion was expressed as the percentage of P28 positive parasites that had differentiated into ookinetes. *In vitro* cross fertilisation experiments with the *srpk* mutant were carried out by mixing 5 μ l volumes of tail blood containing equal number of either *srpk*, *cdpk4* or *nek-4* mutant gametocytes (Liu et al., 2008). Ookinete conversion was then determined as above.

For mosquito transmission experiments 50-100 *Anopheles stephensi* SD500 mosquito were allowed to feed for 20-30 min on anaesthetized mice that had been infected with wild type or mutant parasites 4-5 days earlier, had reached an asexual parasitaemia ~5-7% and were carrying comparable numbers of gametocytes as determined on Giemsa stained blood films. Unfed mosquitoes were removed the following day. On day 14 post feeding approximately 20 mosquitoes were dissected and oocysts on their midguts counted. DNA replication in the cysts was examined by staining with Hoechst 33342 for 10-15

minutes before guts were washed and mounted under Vaseline-rimmed cover slips. Images were recorded using a 63x oil immersion objective on a Leica DMR fluorescence microscope equipped with a Leica DC500 digital camera. On day 21 post feeding another 20 mosquitoes were dissected and their guts and salivary glands crushed separately in a loosely fitting homogenizer to release sporozoites, which were then quantified using a haemocytometer.

Due to day-to-day variations in transmission levels, all data were normalized to a matching number of wild type controls analyzed on the same day. Average total infection levels for wild type were as follows: 67.5 ± 7.0 % of female gametes transformed into ookinetes within 24 h *in vitro* (n = 25 cultures); 97.8 ± 55.4 wt oocysts were counted per infected mosquito midgut on day 14 p.i. (n = 43 experiments); 31,000 ± 7,400 sporozoites were obtained per mosquito midgut on day 21 p.i. (n = 34 experiments); 6,600 ± 2,800 sporozoites were recovered from salivary gland per mosquito on day 21 p.i. (n = 37 experiments).

All mutants with salivary gland infections were analysed for the infectivity of their sporozoites. 30-50 infected mosquitoes were allowed to feed for 20 min on 3 anesthetized naïve C57Bl/6 mice, which are highly susceptible to sporozoite challenge. Mice were monitored for blood stage infections from day 3 and until about day 15 post feeding.

Supplemental References

Edgar, R.C. (2004). MUSCLE: a multiple sequence alignment method with reduced time and space complexity. *BMC Bioinformatics* 5, 113.

Felsenstein, J. (1985). Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 39, 783-791.

Goodstadt, L., and Ponting, C.P. (2001). CHROMA: consensus-based colouring of multiple alignments for publication. *Bioinformatics* 17, 845-846.

Liu, Y., Tewari, R., Ning, J., Blagborough, A.M., Garbom, S., Pei, J., Grishin, N.V., Steele, R.E., Sinden, R.E., Snell, W.J., *et al.* (2008). The conserved plant sterility gene HAP2 functions after attachment of fusogenic membranes in *Chlamydomonas* and *Plasmodium* gametes. *Genes Dev* 22, 1051-1068.

Saitou, N., and Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol* 4, 406-425.

Tamura, K., Dudley, J., Nei, M., and Kumar, S. (2007). MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Mol Biol Evol* 24, 1596-1599.

Zuckerlandl, E., and Pauling, L. (1965). Evolutionary divergence and convergence in proteins. In *Evolving Genes and Proteins*, V. Bryson, and H.J. Vogel, eds. (New York, Academic Press), pp. 97-166.

Tewari et al., Figure S1 A (cont.)

	IVa	Vib catalytic aspartate HRDxxxN	VII Mg2+ binding aspartate D (FG)	VIII conserved glutamate APE	IX
PF1020c	---KIFKSRKKNKK---KLLFE---SKKLINL---	Q-AG-IC-HLDFLDN---	S-KN-GD---M-RIC-D	AKCTP (9) --KKMDSLCL	FQSCI-TTIGKYM---VYVPCWVDV (22) --EERKKYFF
PBANKA 141450	---RLKKQEKRR---ENNQ---ICLQIKN---	E-HN-VA-HRDLKPNL---	NLDTPD-IN---V-EIC-D	LRSAKK---VEKSI	SIPYI---CSRW-YRABE
MAL8P1.203	---YMKISNNEKS---FLLYQ---CLKLIIRL---	D-AG-LS-HLDFPENL---	S-DN-YE---L-RFC-D	LSKSTP (9) --KDMNRYL	FESCE-PTIARGA---YMPBCWKI (22) --EKRRQYFF
akt1	---RERVFSRDRAR---FYGAE---YVSAVDYL---	SEKN-VV-YRDLKLENL---	D-KD-GH---L-KIT-D	GLCKE---GIKDGAT	MKTFC---GTFPE-YLAPB
MAL13P1.278	---KKRRIPELAY---KYFCH---VWNGYYLN---	Q-MG-IF-HRDLKPNL---	D-HK-DN---A-KIS-D	LSAM---ILGKKS	HSSIC---GTLV-YFSEB
PBANKA 041040 gsk3	---NNQFLPFLVK---LVSYQ---LCRAIGYL---	S-KL-IC-HRDLKPNL---	D-PKT-HT---L-KIC-D	LSAKS---LISGQR	SVSYI---CSRW-YRABE
limk1	---MDSQYFWSQV---SFAKD---IASGMAYL---	S-MN-LI-HRDLKPNL---	R-EN-KN---V-VVA-D	LLARL (12) SLKPKPRK	RYTVV---GNPY-YRABE
PBANKA 112690 pk4	---GDKNTNHPLEF---DLFKQ---LKGKDDH---	S-TC-FI-HRDLKPNL---	D-LDT-YI---L-KIG-D	LLVRF (5) RENDLNIND	FKDNI (20) GTFPG-YRABE
zak	---RSEEMDMDHIM---TWATD---VAKGMHYL---	MEAPVKVI-HRDLKPNL---	A-AD-GV---L-KIC-D	MASRF---HNHTT	HMSLV---GTFPE-YRABE
PBANKA 144300 nek-1	---MFGKIEEHAIV---DITRQ---LHAAYCH---	GP-NGERVL-HRDLKPNL---	ST-GI (16) P-AKIG-D	LSKN---IGIESM	AHSCV---GTFPE-YRABE
PBANKA 080800 crk-4	---DMPSLTEMQTK---VITIQ---MLQGNHFF---	K-KF-LI-HRDLKPNL (10) NDS	KE-WI---V-KIA-D	GLGVY---DHFLEKTE	KDCNI---ITLQ-YRABE
PBANKA 092640	---RSIGVSENIFF---NIILO---MVHAYATH---	D-KD-VI-HRDLKPNL---	N-KD-GT---L-KIA-D	TSKD (116) RNYRKKT	FONYV---GTAN-YRABE
PBANKA 123020 crk-5	---NQAGLCLREAK---WLSFQ---LNGAYL---	N-NK-VC-HRDLKPNL---	Q (4) NK-YL---L-KIG-D	LLCRE---LKNDDG	MTPVY---CTIY-YRABE
PBANKA 094200	---YKXKVENVCK---YILMQ---LQAVNYL---	Y-HN-LI-HRDLKPNL (1) --	N-KK-RN (9) --	YDTQF (24) IKTIQNSK	TNNAF (10) GTIYG-YRABE
PF10_0380	---KETVVSVEEKK---KIMKE---CLKLIKLI---	N-AG-LA-HLDSPEL---	S-NN-SE---F-RIC-D	LAKSAP (9) --KGDEKSP	FQSYQ-PCIGKLT---CMPKWDI (22) --EERKKYFF
PBANKA 100820 pkg	---KLGLLRSQAQ---FYLGS---LILAEYEL---	E-RS-IV-YRDLKPNL---	D-KQ-GY---V-KIA-D	CAKK---IHRG	SYTLV---GTFPH-YRABE
PBANKA 130520	---NVLYLELSAQ---YFFRK---LIDGKYM---	S-NK-LA-HRDLKPNL---	C-KK-VLNO (16) EL	ACCF---NDASNK	HYDIV---GTLG-YRABE
PF0750w	---DQAGNLKEAK---WLSFQ---LNGAYL---	N-NK-VC-HRDLKPNL (10) QETS	N-HK-YL---L-KIG-D	LLCRE---LKNDDG	MTPVY---CTIY-YRABE
PBANKA 061670 nek-4	---QNTPIKEKRII---IWLQ---LITAKPFL---	S-NH-LI-HRDLKPNL---	D-SD-KR---V-RIC-D	LSKV---LENTLYE	ANTLI---GTFPE-YRABE
PF0420w cdpk3	---KKGCFVETFAF---FIMKQ---LPSVANYL---	I-RN-IC-HRDLKPNL---	PE-SL---L-KIA-D	LSAY---FTHNYYE	MTKA---GTFPE-YRABE
insr_1-276	---GRPPTLQEMI---QMAAE---IADGMAYL---	A-KK-FV-HRDLKPNL---	A-HD-FT---V-KIG-D	MTDR---IYEDYI	RKGGK---GLLPVR-YRABE
PBANKA 082690	---EKKVLSVDISL---KMCRO---LAAVNYL (4) NK	KN-VI-HRDLKPNL---	D-SD-WM---L-HIC-D	LDSE---TEDGN	VNVS---GATWI-YRABE
PBANKA 061520 cdpk4	---SRKRFVVDAA---RIIQQ---VLSGYTME---	K-NN-VI-HRDLKPNL---	E-TKN-KEDMI	LDSTH---FEYSKK	MKDKI---GTFPE-YRABE
PF10110c	---IYRDISENERK---KIIHE---WIKLSRI---	D-TG-LS-HLDSPEL---	G-EN-HK---M-RIC-D	AKSTP (9) --KPNGLK	FQSC-PTVGPKP---YAPB (22) --EERKKYFF
pf14_0423_1-361	---GFCRNEKLIW---ELIKQ---LILGASYL---	D-MK-IM-HRDLKPNL---	Q-IT-DN---L-LIAKIG-D	LTTR---IGDQ	INPSA---GTFPH-YRABE
PBANKA 082710	---KNVAYNLNFRV---LTLME---IANMSYIL---	KQTPNHEFYI-HRDLKPNL---	KN-KK---L-LIT-D	NLSRK---IDAEYIL	MQQC---GTFK-HLABE
PBANKA 112270 tk15	---NKNVHKKQRL---EWAIQ---SNIHHE---	S-NHPP-LI-HRDLKPNL---	N-NN-MD---L-VMC-D	KARF---KNSK	LNSNF---GTFPE-YRABE
PBANKA 091210 ck1	---CNRRFSLKTVL---MTADQ---MNRREYV---	S-KN-FI-HRDLKPNL---	GR-GK-KV-TL---	LIT	HTI---GTFAR-YASIN
PF0525c gsk3	---NNQALPFLVK---LVSYQ---LQAVNYL---	S-KF-IC-HRDLKPNL---	D-PRT-HT---	LSAKN---LLAGOR	SVSYI---CSRW-YRABE
PF0605w pk7	---YTCFPIQVIK---CIKIS---VNSFSYIL---	NEKN-IC-HRDLKPNL---	D-KN-GR---V-KIS-D	SEYI---MVDKK	IKGSR---GTFPE-YRABE
PBANKA 101980 cdlk	---KNKCLLESESI---QIVRQ---VCTEYEL---	S-NN-LI-HRDLKPNL---	K-NKN-TE (1) --	MAKT---VNCYD	LTEIC---GTFPH-YRABE
PF07_0072 cdpk4	---SRKRFVVDAA---RIIQQ---VLSGYTME---	K-NN-VI-HRDLKPNL---	E-TKN-KEDMI	LDSTH---FEYSKK	MKDKI---GTFPE-YRABE
raf1	---QETKQMFQLI---DIARQ---LQAGMDYL---	A-KN-LI-HRDLKPNL---	H-EG-LT---	LATV---KSRWSGQ	YQPTF---GTFPE-YRABE
PF0485w	---RNKCFNEEAR---YLFHQ---LILGAYL---	S-KK-VA-LRDLKPNL---	FEN-EKN-GE---	YVFIN	PLQALYFNKRNIVLE
PBANKA 113320 pk5	---CDGGLSHTAK---SFLQ---LNGAYCH---	E-RR-VI-HRDLKPNL---	N-RE-GE---	LARA---HDSATPTIDA	PHHRV---GTFPH-YRABE
PF11_0239 cdpk6	---NSESFNTEYIK---NIMFQ---LILGAYL---	S-NN-LA-HRDLKPNL---	K-EKG-DD (1) --	LAE	INKSEI---SKTAA---GTFPE-YRABE
PF13_0206 crk-6	---KKHNLNKEIK---YIIFE---LILGAYL---	S-NN-YI-HRDLKPNL---	T-SE-GE---	LMSVE---KSDH	MTPVY---GTFPE-YRABE
PBANKA 136210 tk13	---QNHLSRQVUV---KIFQQ---LAKGMYEL---	S-NH-FI-HRDLKPNL---	D-EN-KN---A-FIS-D	LSSTY---FSLNDS	AVAYI---GTFPE-YRABE
MAL7P1.100 nek-4	---QNTPIKEKRII---IWLQ---LITAKPFL---	S-NH-LI-HRDLKPNL---	D-SD-KR---V-RIC-D	LSKV---LENTLYE	ANTLI---GTFPE-YRABE
PF0045c	---RKPILKNRYAK---KKKIYD---SLNLIIRL---	D-AG-LI-HLDFPENL---	S-EN-NE---	LAKSTP (9) --QETKGLCL	FQSC-PTVGKSA---YMPBCWKI (22) --DERKKHYF
PF01165w	---GCGNNLEKAK---KILHE---SKKLITL---	E-TG-LS-HLDSPEL---	G-NN-CE---	LNSAP (11) NKRILYSS	YQPCI---SKVP-LILPCWNI (22) --EERKSYFF
PBANKA 146000 pkb	---KLTKEFTNIAR---FYISE---YIAGQYEL---	K-LN-LI-HRDLKPNL---	D-KN-GH---L-RIT-D	LSKE---CISDNNS	AKPIC---GTFPE-YRABE
PBANKA 080220	---SNENISPEKIK---DIIFQ---LISGASAL---	D-NF-LI-HRDLKPNL---	K-DK-NFEK---	DMSIY (113) NTLSDNNT	YTKR (74) GTFPE-YRABE
PF14_0227 cdlk	---KNKCLMESESA---LIVRQ (10) ---LCCALQYEL---	S-NN-FI-HRDLKPNL---	K-NKN-TK (1) --	MAKR---VNCYD	LTEIC---GTFPH-YRABE
PF03170w	---SDKMNHPLEF---DLFKQ---LKGKDDH---	A-TC-FI-HRDLKPNL---	D-PDT-YT---	LLVRF (5) REKDFNID	FKDNI (20) GTFPG-YRABE
tgfbr1	---NRYTVTVEGMI---KLALS---TAGSAHL (4) GT	QGKPAIARHLSKKNL---	K-KN-GT---	C-TIA	D
PBANKA 101330	---RADILEEVHKK---YIIFQ---LILGAYL---	S-G-LI-HRDLKPNL---	N-SE-CH---	LARS---ISTVHNKIPV	LIDYV---ATRW-YRABE
PF13_0258 tk13	---YAKSLTRPKLV---KIFQQ---VAGQMYIL---	TN-OCFHRDLKPNL---	D-EN-QN---A-VIS-D	LNSTN---FSSNDSP	AIVYI---GNIF-YRABE
PBANKA 146050 gsk3	---NKKDIKEFHI---KILKQ---LISGNYL---	T-QEIP-LI-HRDLKPNL---	D-KN-NV---Y-KIC-D	CSHTV (6) NDLKKNLNL	LKYEI-ERDTIYI---YRABE
PBANKA 113310	---KKRRIPELAY---KYFCH---VWNGYYLN---	Q-MG-IF-HRDLKPNL---	D-HK-DN---A-KIS-D	LSAM---ILGKKS	HSSIC---GTLV-YFSEB
PBANKA 122880 tk16	---GENFLYELRL---RMCYQ---LEAVNMYL---	EDKK-LV-HRDLKPNL---	D-DE-YN---	KTKM---LSDNTHVI	LEDNG---GTFPE-YRABE
MAL7P1.175	---RKKMFSIGRKK-KKKKLLY---CNLIRKLI---	N-AG-LS-HLDFPENL---	S-DK-HE---	L-KATP (9) --NNINGHS	FESCA-PCVGKIR---YMPBCWLI (21) --EERKPYFF
PBANKA 092550 cdpk6	---KQVIFSEYTIK---NIMFQ---LILGAYL---	S-NN-LA-HRDLKPNL---	K-TDG-YD (1) --	LAE	INKSEI---SKTAA---GTFPE-YRABE
PBANKA 131800 kin	---KNSINENIAK---RIIYQ---LILGAYL---	K-LN-VI-HRDLKPNL---	D-NN-NN---	LDSTI---YSKNNF	LQSC---GTFPE-YRABE
PBANKA 040110 SRPK	---DYKGIPIINLVR---KIATH---VILGQYEL---	DVCK-LI-HRDLKPNL (190) NT	NK-DN (16) DM	K(28) SINEN (141) YVDKDNK	FPIY (82) ESRY (7) YRABE
PBANKA 071730 crk-3	---NMNLFITGEIK---NIMLQ---LQAGYEL---	K-NN-VI-HRDLKPNL---	D-AN-GI---	LALRF---HDSFASN	MNRVR---ITLW-YRABE
PF0755c crk-4	---EMPSLTIQTK---VITIQ---MLQGNHFF---	K-KF-LI-HRDLKPNL (10) NDP	KE-WI---V-KIA-D	GLGVY---DHFLEKTE	KDCNI---ITLQ-YRABE
PF01130c	---MGTEWFEVVK---KILFK---SKKLIRL---	D-VG-LI-HLDFPENL---	T-KN-FD---	LKSAP (9) --KEMNML	FQSC-PTVGKSA---YMPBCWLI (22) --EERKPYFF
PF10115c	---KTYKFKNDKK---KIMLE---CLKLIKLI---	Q-VG-IC-HLDFPENL---	S-KN-GD---M-RIC-D	SKSTP (9) --KMKMLCL	FQSCI-PSVGKTR---YMPBCWLI (22) --EERKPYFF
PF0520w cdpk2	---ENGSLTEKNA---TIMKQ---LPSVANYL---	S-LN-LV-HRDLKPNL---	QSEN-KD-SL---	LSKN---LGTGEF	TITKA---GTFPE-YRABE
PF11_0488	---YHGPINELLAL---CNIRQ---LILGLYMK---	N-LPTGKVRHCDLKPNL---	KD-GI---	LAKL---ILPDTHQ	YVNGG---GTFPE-YRABE
map3k3	---AYGALTESVTR---KYTRQ---ILEGMSYL---	S-NN-MIVHRDLKPNL---	D-SA-GN---V-KIG-D	MASKR---LQICMSGTG	MRSVT---GTFPE-YRABE
PBANKA 124070 nek-2	---MKTIIIPENKIK---RWLQ---LITAKPFL---	E-KK-LI-HRDLKPNL---	D-EN-EK---	LAKL---LEKTDQ	TNTLC---GTFPE-YRABE
PBANKA 040740	---KHDFTKEQVA---LVVYQ---IADALSYL---	N-FN-LI-HRDLKPNL (11) NVS	KI-YKYGI---	LFCQ---LKNKROK	RSTFC---GTFPE-YRABE
csnk1g1	---CDRTFLKTVL---MIAIQ---LILGAYL---	S-KN-LI-HRDLKPNL---	GRQGNK-KE-HV---	LAK (4) ETKKHIPYRE	HSLT---GTFAR-YASIN
PBANKA 070970 pk1	---KKCFNENQVK---IYVYQ---LIRATLYL---	S-LC-LI-HRDLKPNL (226) DE	LDN-IY (16) YI	KIC	D
PBANKA 090380	---ENLNNMSEAF---LYFIQ---LQGMWYIL---	D-MN-LV-HRDLKPNL---	Y-SN-KK---	VIA	D
PBANKA_080560	---SISQYQNPVK---FIQIT---LAKIL---	N-GN-VI-HRDLKPNL---	RYSYIN-EN-E (16) EI	KICVI	D
dapkl	---EKESLTEEAT---EFLKQ---LNGYYEL---	S-LQ-LA-HRDLKPNL---	L-DRN-VBKPR---	LAKH---IDFGNE	FKNIF---GTFPE-YRABE
prkca	---QVGFKEPQAV---FYAAE---LILGAYL---	K-RG-LI-HRDLKPNL---	D-SE-GH---	LAKH---HMDGVT	TRTFC---GTFPE-YRABE
MAL13P1.109	---VSDISNEDKK---KILYN---SLNLIIRL---	D-RR-VI-HRDLKPNL---	S-PKN-YE---	LSQSTP (11) LNSIKPFS	FQPCI---GTFPE-YRABE
MAL13P1.279 pk5	---CEGGLSHTAK---SFLQ---LNGAYCH---	E-RR-VI-HRDLKPNL---	N-RE-GE---	LARA---FGI PVK	YTHEV---ITLW-YRABE
PBANKA 040820 cdpk3	---KKGFSVEMYS---FIMKQ---LPSVANYL---	I-RN-IC-HRDLKPNL---	YDKS-TE-SL---	LAAV---FNIDYE	MTKA---GTFPE-YRABE
PF11_0377 ck1	---CNRRFSLKTVL---MTADQ---MNRREYV---	S-KN-FI-HRDLKPNL---	GR-GK-KV-TL---	LIT	HTI---GTFAR-YASIN
PF0665w	---VPGSLDVEYIK---KIMKE---LPSVANYL---	S-NN-LI-HRDLKPNL (196) CS	LHN-YN (16) NM (8) SDIC	II	D
PF14_0320 tk14	---CKIKYIVLFI---LHIFQ---LIDKKNIL---	K-KG-LA-HRDLKPNL (41) HMN	HI-YN (16) SV	NIY	D
PF14_0294 map-1	---KADLLEIHKK---YIIFQ---LILGAYL---	S-GG-LI-HRDLKPNL---	N-SE-CH---	LARS---ISTVHNKIPV	LIDYV---ATRW-YRABE
PF14_0346 pkg	---KLGLLRSQAQ---FYLGS---LILAEYEL---	E-RN-IV-YRDLKPNL---	D-KQ-GY---	V-KIA	D
PF1285w	---KRTVYNLNFVR---LTLLE---IANMSYIL---	KPNIKQEFYI-HRDLKPNL---	KG-KK---	LIT	D
camk2a	---AREYVSEADAS---HCIOQ---LEAVLHCH---	Q-MG-IV-HRDLKPNL---	A-SKL-KG (2) --	V-KIA	D
PF0800c nek-3	---NNEIYSESEIF---NLLHQ---LNGNYL---	Q-NG-LI-HRDLKPNL---	KD-NK---	KIG	D
MAL13P1.196	---KKGLNMLVLL---DLRQ---KKGITL---	K-KG-LI-HRDLKPNL---	S-ST-TFFT---	V-RIG	D
PBANKA 031030 pk7	---ESYFIPVPIK---CMVKK---LKSILYV---	T-KN-IC-HRDLKPNL---	D-KN-GI---	KIN	D
MAL13P1.84	---RMKQKRENN---KND---LQAGYEL---	K-ND-FA-HRDLKPNL---	D-LDSN-IK---	EIC	D
PBANKA 071990 crk1	---KSPGFTVSELK---CLIKQ---LNGNYL---	T-NW-VI-HRDLKPNL---	S-NK-GI---	KIC	D
PBANKA 142160	---GFNILEKEVK---IVSQ---LILGAYL---	I-KG-LI-HRDLKPNL (38) KEN	IK-NN (9) --	V-KIC	D
PBANKA 083560 PKAcac	---RNKRFNDVGC---FYAAQ---YVLIYEL---	S-LN-LV-HRDLKPNL---	D-KD-GF---	L-KMT	D
PF14_0516 kin	---NNYINNNAR---RIIYQ---LILGAYL---	E-IK-LV-HRDLKPNL---	D-NN-NN---	V-KIA	D
PF14_0392	---NKLYLDEVSAQ---YFFRK---YVGGKYM---	K-NN-LA-HRDLKPNL---	CKIQ-IS (16) DL	KIG	D

Tewari et al., Figure S1 A (cont.)

PFB0520w tk11	---YKINMKLQDII---KISKD---ITAFMSYFL---N-KG---IM-HCDLSSNLI---S---IT---RD---I---KIC---D---LALSVF---NKYNKPK---YLGIV---GTQY---WTAPE---VL---RSEG---Y---TK---EADYSP---VILWEMI---HR-KIPF---
PFL1370w nek-1	---MFGKIEBHAI---DITRQ---LHAAYCH(4)GP-NGERVL---HRDIPKPNIL---D---SD---GI(16)P---AKIG---D---LALSKN---IGIESM---AHSVY---GTPY---YAPPE---LL---LHETKS---Y---DD---KSDMAL---CITYELC---SG-KTFF---
PBANKA_101090 tk14	---NRIFYKIQLK(5)LNFIQ---IEQIYIV---K-KK---IT-HFDINTCNILI(93)MKK---KD---CQ(6)I---VHS---D---LRESKF---FLRDTDFIF---FRKNR---GNEI---LAAPB---LL(77)-DKIRILRY(6)KS(40)KSDIWSL---SLLYEMI---TN-ESLF---
PFL1280c	---DEKVLGIDISL---KMCRO---LAEVINFLR(4)NK-KN---VI-HRDIPKPNILI---D---SD---WN---I---HIC---D---LADAE---CEDGI---FNVVS---GATWI---YAPPE---LLTCHPLKQSSDYNF(6)SY---KWDIWSM---CVFORMM---NL-PSPF---
cdk2	---ALTGIFPLPLIK---SYLFO---LQGFAPCF---S-HR---VL-HRDIPKPNILI---N---TE---GA---I---KIA---D---LALARA---FGVPTV---YTHEV---VTLW---YRABE---IL---LGCK---Y---ST---AVDIWSL---CIFAEMV---TR-RALF(11)---
PBANKA_135090 crk-6	---KIYNLNKEVK---YIIFE---LLALCYLY---S-NN---YL-HRDIPKPNILI---N---SK---GE---I---KIG---D---LALSVF---KSDN---MTPSV---VTIW---YRABE---LL---LKQNN---Y---DQ---KIDIWSL---CIFAELI---TG-RPLF(8)---
PFL1415w	---NNRRKKEYKKK(11)EILRQ---LNVCLLY---R-NK---IF-HSDIKPSNIVI---N---KN---IH(16)YL(13)KI---D---LALSVF---KSDN---MTPSV---VTIW---YRABE---LL---LKQNN---Y---DQ---KIDIWSL---CIFAELI---TG-RPLF(8)---
PBANKA_130920 lammer	---DYNGFHIEDIK---LYCIE---LKAHYLYR---K-LK---IT-HRDIPKPNILI---D---DP---HF(16)QI(7)IKI---D---LALCATF---KSDN---MTPSV---VTIW---YRABE---LL---LKQNN---Y---DQ---KIDIWSL---CIFAELI---TG-RPLF(8)---
PFB0815w cdpk1	---NRHFKDECDAA---NIMKQ---LISGICYLY---K-HN---IV-HRDIPKPNILI---E---NKH---SL(2)I---KIV---D---LALSSF---FSKDNK---LRDLR---GTAY---YRABE---VL---RKK---Y---NE---KCDVWSC---VILYLLI---CG-YPPF---
mapk1_1-289	---KTQHLSDNDHC---YFLYQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1_0242 cdpk7	---AETRLSEIHAN---KIIQK---LKTAYLY---R-CG---LI-HRDIPKPNILI---TDKS---RD---AQ---I---KIT---D---LALSTL---CAPNEL---LKEPC---GTLA---YRABE---VI---TLQG---Y---NH---KVDWSI---LILYLLI---SG-KLFF---
PBANKA_030850 tk11	---KKTKIKILDII---KMCKD---LISGICYLY---N-KG---LV-HRDIPKPNILI---S---ES---GE---I---KIC---D---LALSIQ---NFDMPKPK---FGLIV---GTQY---WTAPE---IL---RCEG---Y---TK---KADIYSF---VILWEMI---HR-TIPF---
PFO8_0044 pk1	---KKSFLNENQIK---IYLYQ---LIRATLYLY---S-LC---IT-HRDIPKPNILI(245)ND---NT---DK---I(85)KIC---D---LALNTSIK---LKENYK---YFSYV---CSRY---YRABE---NE---LFGSNYV---SQ---ALDIWSI---CVMBELI---LG-KPLF(11)---
PBANKA_082960	---KTYVYVPEMIA---EILRQ---LKAACYLY---E-NQ---Y-HSDIKPSNIVA---N---KN---IK(16)YI(13)KI---D---LALSVF---KSDN---MTPSV---VTIW---YRABE---LL---LKQNN---Y---DQ---KIDIWSL---CIFAELI---TG-RPLF(8)---
MAL7P1.144	---TFLKTRRKDI---NILHA---CLKLIRIRL---D-AG---LC-HLDLTPDNILI---S---KS---MD---M---RJC---D---LALAKSTP(9)---KESEDSYK---FESYV---THVAKSA---YTPBCWEI(22)-ERRKQYF---DVA---CADKML---VFFFWIW---TN-GNLF---
PBANKA_093300 prk4	---NGHGLNAAAVH---CYTRQ---LFIARHMR---K-CR---IM-HADIPKPNILI---N---EK---FN---A---LKV---D---LALASAD---ISENE---ITSYL---VSRF---YRABE---II---LGFR---Y---DS---QIDVWSA---AATVPELA---TG-KILF(11)---
PBANKA_130690	---KKGKGLTLGLQ---QILTK---NLEGAAYLY---S-KN---IT-HCDIPKPNILI(30)DSN---EK(6)DN(16)KI---D---LALNSCIY---ESDK---LEMYV---QTRP---YRABE---VL---LQNN---Y---DR---KIDIWSL---CIFAELI---TG-KILF(31)---
PFL1_0060	---YKQVKNICK---YIILQ---LQGFAPCF---S-HR---VL-HRDIPKPNILI---N---TE---GA---I---KIA---D---LALARA---FGVPTV---YTHEV---VTLW---YRABE---IL---LGCK---Y---ST---AVDIWSL---CIFAEMV---TR-RALF(11)---
PFL10141 mrk	---RKIFLTDQSKK---CILLQ---LNGNLYLY---K-YF---IM-HCDIPKPNILI(36)NND---HK---TN(9)Y---KIC---D---LALSVK---CGNEFFP---YRGIK---GSGY---FLIAPB---LF---HECN---F---NN---KIDMAL---THERYV---F---
gsk3b	---AKQTLFVIYV---LYMYQ---LFRSAYLY---S-FG---IC-HRDIPKPNILI---D---PDT---AV---I---KIC---D---LALSAQ---LVGEPF---NVSIV---CSRY---YRABE---LI---FGATD---Y---TS---SIDIWSA---CVLAELI---LG-QPIF(11)---
map4k1	---VTGSLSELQIS---YVCRE---S-QK---KI-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1_0147 map-2	---TPIFLTEQHVK---TILYN---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL13_0085 pk9	---NNGRKKKEYKKK(11)EILRQ---LNVCLLY---R-NK---IF-HSDIKPSNIVI---N---KN---IH(16)YL(13)KI---D---LALSVF---KSDN---MTPSV---VTIW---YRABE---LL---LKQNN---Y---DQ---KIDIWSL---CIFAELI---TG-RPLF(8)---
MAL7P1.91 est	---NNGRKKKEYKKK(11)EILRQ---LNVCLLY---R-NK---IF-HSDIKPSNIVI---N---KN---IH(16)YL(13)KI---D---LALSVF---KSDN---MTPSV---VTIW---YRABE---LL---LKQNN---Y---DQ---KIDIWSL---CIFAELI---TG-RPLF(8)---
PFL0125c	---GYSTLGRKAKK---KIMLS---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1_0464	---ENLSSNMNEAF---LYFIQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_092700 tk12	---TFLFLSFTSRI---NILVO---LNVFCYLY---N-TSSP---LV-HRDIPKPNILI---D---DK---FN---A---KIG---D---LALSAQ---LVGEPF---NVSIV---CSRY---YRABE---LI---FGATD---Y---TS---SIDIWSA---CVLAELI---LG-QPIF(11)---
ck1	---GFLPFRDLHIR---KIMYQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFB0385c	---KKQPLNEEVA---LVYFQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
mapkapk2	---GDQAFTEREAS---EIMKS---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
csn1	---CSRKFLKTVL---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
pfc0105w srpk	---DYKGFPLNLRV---KATHV---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
pFA0380w eik2	---TRENMINRNRY---EIQM---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1685w PKAcat	---RNKRFPDVG---FYAQY---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_061580 est	---YNGOGLTESECK---FLYFQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1_0156 prk4	---NGHGLNAAAVH---CYTRQ---LFIARHMR---K-CR---IM-HADIPKPNILI---N---EK---FN---A---LKV---D---LALASAD---ISENE---ITSYL---VSRF---YRABE---II---LGFR---Y---DS---QIDVWSA---AATVPELA---TG-KILF(11)---
PFL1_0476	---INGSCHTSEAR---VIIIK---LKTAYLY---R-CG---LI-HRDIPKPNILI(1)---T---KD---NT(2)Y---VHS---D---LALAKI---TPSNQSVVK---SRVGV---GDFY---YRABE---II---KKNK---Y---GI---KIDIWSL---VLIFFII---TG-KVFF---
PBANKA_060060 nek-3	---NNEHYSSESEIF---NILNQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
MAL7P1.26	---KNVQYQ---NVPKS---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_031140	---VPGSLHYEIK---KIMKN---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL0105cpw	---LAIIDNNKKK---KYLIE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_093860 ck2	---PKFTDKDIR---YIYIQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_031420 cdpk1	---NRHFKDECDAA---NIMKQ---LISGICYLY---K-HN---IV-HRDIPKPNILI---E---NKH---SL(2)I---KIV---D---LALSSF---FSKDNK---LRDLR---GTAY---YRABE---VL---RKK---Y---NE---KCDVWSC---VILYLLI---CG-YPPF---
PBANKA_010410	---EHGPFSEKVA---TMLFE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
camk1	---EKGFYTERDAS---RLIFQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFD1175w	---EDTRVDRDCK---IMTPE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFB0150c	---NYGRISBELLV---YILDQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1885c pk2	---NNGPYEQVAK---KAMKR---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_092520 cdpk7	---SETRLSEIHAN---KIIQK---LKTAYLY---R-CG---LI-HRDIPKPNILI---TDKS---RD---AQ---I---KIT---D---LALSTL---CAPNEL---LKEPC---GTLA---YRABE---VI---TLQG---Y---NH---KVDWSI---LILYLLI---SG-KLFF---
prkaca	---IRGRFSEPHAR---FYAQY---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL0095c	---YPKVFNKSKK---KILFE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL13_0211 cdpk5	---KYGSFSEYAY---KIMKQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1290w nek-2	---LETPIFEKIK---RWLQY---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_040940	---NRKAFSEESR---YLYFQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
nek1	---KGVLFQDQIL---DMVQY---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
nek7	---QKRLIPERTVW---KYVQY---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_093370 MAP-2	---TPIFLTEQHVK---TILYN---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL0040c	---SDVRNDEFKK---ELLYK---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL10_0160	---IFALHSYMKR---KILFE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_135150 cdpk5	---KHGSFSEYAY---KIMKQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_145320 pk2	---NNGPYEQVAK---KAMKR---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_090110	---YHGFNELLAL---SWIKQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL2280w gsk	---NKDKKIEIIV---NILQD---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
MAL7P1.18	---SKENISPEKTK---SIIQK---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_020580 eik2	---RRTIRINIKRN---EIIIM---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1_0227	---RSVGVNEKITF---NIIILQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFB0260	---ENGPFCEKVA---EMLFE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_141360 pk9	---NNGYLSEKETY---FLFLQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1145c tk15	---NKNLHKKQRL---EMALQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1_0510	---NNNILSDREKK---KILYE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1_0220 tk12	---TPIFLTEQHVK---TILYN---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
rock1	---SNYDVEKWAR---FYTAE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
src	---TGKYLRLPQLV---DMAAQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFC0060c	---FNTFLNKKKK---KILYE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_122500 FIKK	---FNMKISNNEKS---YIYIQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
pak1	---TECMDGQIA---AVCRE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1_0431 lammer	---NYNGFHIEDIK---LYCIE---LKAHYLYR---K-LK---IT-HRDIPKPNILI---D---DP---YF(16)QI(7)IKI---D---LALCATF---KSDN---MTPSV---VTIW---YRABE---LL---LKQNN---Y---DQ---KIDIWSL---CIFAELI---TG-RPLF(8)---
PFL1_0408	---RKGLTLGLQ---QILTK---NLEGAAYLY---S-KN---IT-HCDIPKPNILI(111)NN---NN---NN(16)KI---D---LALNSCIY---ESDK---LEMYV---QTRP---YRABE---VL---LQNN---Y---DR---KIDIWSL---CIFAELI---TG-KILF(31)---
PFL2250c pbk	---KREFSEETAK---FYSSE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
egfr	---HKDNIGSQYLL---NWCQY---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFD0740w crk-3	---YANLFSIGEIK---NIFIQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
MAL7P1.73	---GFNLQEQVQ---IILQY---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_121280 mrk	---RKILLTDSQKK---CILLQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
map2k1	---KAGRFPEQILG---KVSIA---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFD0865c crk-1	---KSPFTISELK---CILLQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1_0733	---DDLVTVEEKK---SILYK---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL0100c	---KENLVITKRRK---KILFE---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_135260	---KKQNICMLVIK---DLMHQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_130840 eik1	---GFYKNEKLIW---ELIQY---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PFL1_0096 ck2	---LYPKFTDKDIR---YIYIQ---LQGFAPCF---S-AN---VL-HRDIPKPNILI---N---TT---CD---I---KIC---D---LALARV---ADPDHDTGF---LLEYV---ATRW---YRABE---IM---LNSKG---Y---TK---SIDIWSV---CILAEMI---SN-RPIF(11)---
PBANKA_131370	---INGSCHTSEAR---VIIIK---LKTAYLY---R-CG---LI-HRDIPKPNILI(1)---T---KD---NT(2)Y---VHS---D---LALAKI---TPSNQSVVK---SRVGV---GDFY---YRABE---II---KKNK---Y---GI---KIDIWSL---VLIFFII---TG-KVFF---
Consensus/80%bpb.....bh.p.....lh.sl.bh.....p.....lh.HpDIPKPNILI.....p.....pp.....l.....+lh.....D.....FG.T.....hps.h.....s*.....a.sPE.....l.....a.....s.....p.Dbashghhbbbbb.....a.....

Tewari et al., Figure S1 A (cont.)

X XI

PFI0120c -LWYISDPIIDINY (2) --YKKNMNFNKIWTLEW-----PKKIK--RIIR--QLLDL-DRRKNLN--LN--DLIN--DPWFTR-
PBANKA 141450)LIEVLGSPNINFY---ENIKDYTSTKNTSLIKEL-CELDIPPLSWD---HIG--NLIKEDPNEIK--ID--EVLN--NSYF-
MAL8P1.203 -LWKCSDPLQDEDF (2) --FVKCDMNFDFELTKNW-----PNEIK--DIK--QLLHV--RQRKLN--LK--DLA--HPW-
Hs akt1 -----YNQDH-----EKLFEILMEEIRFPRT-----LQPEAK--SLLS--GLLKK--DPKQLG (5) AK--EIMQ--HRFF-
MAL13P1.278 -----DGTQTQI-----VESIFSCNLKFPDF-----VNPLAI--DLK--KTLVV--DVNKRIR--LC--ELSS--DPWM-
PBANKA 041040 gsk3)IIQILGTPTEDEQ---KVMNPNYADVFPNVKPKD (5) PKGTPNNAI--NFVS--QFLKY--EPLKRLN--AI--EALA--DPFF-
Hs limk1 -----LPRTMDF-----GLNVRGFLDRYCPNCC-----PPSFF--PITV--RCDDL--DPKRRPS-----FVKL--EHWL-
PBANKA 112690 pk4 -NTIMERYKTLNDF-----RNYTVPDYVKIHLNFW-----YILM--LQMSKPNPADRPS--AA--DLVN--KI-
Hs rak -----KGLEGLQV-----ANLVVEKNERLTIPISSC-----PRSA--ELH--QWRA--DAKRRPS--FK--OITS--IL-
PBANKA 144300 nek-1 -----HKANN-----FSQLISELKKGPPELPK-----GSKSELN--FLK--NLNL--SAKERPS--AL--CCLG--YQIT-
PBANKA 080800 crk-4)VFRGIPDQNFNRL---LKKELVGGELPKFKVDRI (13) RILNDRGL--DLID--QFLSY--DYKNRIT--AN--EALK--HEWF-
PBANKA 092640 -----DGSSTEW-----FYNKIKKREINYPPII-----PLDLV--DLTE--KLVVI--NPKRIG (4) CE--DILQ--HPYF-
PBANKA 123020 crk-5)IVNSLGGPNNDEL---EYFSDSRFPYFKDDF (17) GKIDELGI--DLIV--KMLKY--NPNDRIT--AA--DALG--HPWF-
PBANKA 094200 PMSFMNRYNRTKDI (2) --KKEKKGINFNLSFNNY-----PLAK--DLQ--QFLQF--DPKRRIK (5) SY-----HPWL-
PFI0_0380 -IWKRADPSKDKIF (2) --LLNYNMDINSLAEADW-----PKGLK--NIN--KLLDL--ESRKRIN--LD--DLVK--HPWFY-
PBANKA 100820 pkg -----GNDQEDQ---LEIFRDLTGLTQTFPDY-----VTDTSI--NLK--RLCR--LPQGRIG (5) FK--DIKE--NSFF-
PBANKA 130520 -----DNEEKDI---KEAHNEIVNKKIIFPKN--RINRCSNNVK--NLI--GMNI--NPNNLS--LD--QVIN--DPW-
PFI0750w)IVNSLGGPNKDEL---EFFSNSRFPYKDEDF (17) GRIDELGI--DLIV--KMLKY--NPNDRIT--AA--DALG--HPWF-
PBANKA 061670 nek-4 -----HSTKGIQ---QLCYNIRYAPLPDLNPI-----YSKELN--NIYK--SMIR--EPNYRVT--VO--QLLV--SDIV-
PFC0420w cdpk3 -----FGSDHE---ILSMVKKGYQFKGKWF-----NNISEAK--DLK--RCLTM--DADKRIC--AS--EALQ--HPWF-
insr 1-276 -----QGLSNEQ---VLKFMVMDGGYLDQPDNC-----PERVT--DLMR--MCMQF--NPKRPT--FLBIVNLLKDDLHPSF-
PBANKA 082690 --OHYIISFDESQD---IYKLVVDVTKKLPKPI--HSKIDNSPFA--DIK--LCLNY--DPNLRPT--AK--EIVD--LL-
PBANKA 061520 cdpk4 -----NGSNEYD---ILKQVETGKYTFDLQPF-----KKISDKAK--DLK--KMLMY--TSAVVIS--AR--DALE--HEWI-
PFI0110C -LWKNKADSLDNDF (2) --FKENMMMLDIPPTQTW-----PEELK--YIS--QLLVL--ETRKNLQ--FK--DLIN--HPWFS-
pfl4_0423_1-361 --STSMERSITLSN---LLKGIYPEYMKADNKKF-----QFLS--SLAI--NPOECC--AY--NLH--ESVL-
PBANKA 082710 ----- (2) --YDNYKIDLKHFEIQDF-----LI--NLIL--VQDE--SPFMRPS--FS--EIR--LL-
PBANKA 112270 tk15 -----YNSKNTK---IRHELIVNKRPHIPSPF-----LPNSIK--KCLQ--KCFSF--NPKRPS--AY--EM--YKAL-
PBANKA 091210 ckl QGLKAI SKDKYDK---IMKKISTSVVLCRNT-----SFEFV--TYLN--YCRSL--RFEDRPPDYTLR--RLK--DLFI-
PFC0525c gsk3)IIQVLTGTPTEDEQ---KEMNPNYADIKFPDVKSKD (5) PKGTPDEAI--NLIT--QFLKY--EPLKRLN--PI--EALA--DPFF-
PFI0605w pk7 -SLVELFNIRTKNI---EYPLDRNHFLYPLTKNK (4) NNFLSNEDI--DFLK--LPLRK--NPAERIT--SE--DALK--HEWL-
PBANKA 101980 cdlk -----EGKNTQK---IVDEILNKNINWKNDF-----SSLSVEAI--DFLK--KLLER--NERKRLT--AF--EALN--HPWI-
PFI07_0072_cdpk4 -----NGSNEYD---ILKQVETGKYTFDLQPF-----KKISDKAK--DLK--KMLMY--TSAVVIS--AR--DALE--HEWI-
raf1 ---SHINNRDQII (2) --VGRGYASPLDSKLYKNC-----PKAMK--RLVA--DCVKK--VKEERPL--FP--QILS--SIEL-
PFC0485w -----KCSLDKDI---YKMFKNKNYKQLLKEK--KGLHLSKQVI--DLIF--NCLHP--NFNIYRN--IN--EALN--HDWF-
PBANKA 113320 pk5)IFKILGTPNSQNW--PDVFKLKYDFNFPVYNPLPWEFTIKGLDQDGI--DLIS--KMLK--DPNCRIT--AK--QATE--HPYF-
PFI1_0239_cdpk6 -----GNTYDEVK---QSIFRDEDPYKSLKSKL-----SQTAL--HMLK--LMLQK--DYNKRPM--AS--VLLH--HPWF-
PFI3_0206_crk-6)IYLLGDKDKLTT---VKERKDMFPYFIEINLI--KDAIDDEHTL--DLIS--KMLY--DPNCRIS--SK--EALK--HPCF-
PBANKA 136210 tk13 -----DGLSSSET---FCKISSGELHLPDPNDI-----PKDLS--DLK--SVLEY--DFTKRFLEVDIA--RKLE--HIWE-
MAL7P1.100 nek-4 -----HSTKGIQ---QLCYNIRYAPLPDLNPI-----YSKELN--NIYK--SMIR--EPNYRAT--VO--QLLV--SDIV-
PFE0045C -IWHCSDASTDENF (2) --FEKCDMSLDVDFQLTSTW-----PSGLK--NIN--ELLHI--EKRRMLV--LR--NLS--YFWFTK-
PFD1165W -IWEKADSNDRKF (2) --FVKCGMDLYNYELTYNW-----PDDLK--DIIN--QLLPL--ENRAQLS--LK--ELCK--HPWWSN-
PBANKA 146000 pkb -----NGSRDL---LFEINIKYKIKISNRL-----SPEVV--DLK--KLLQK--NPKRIG (5) AE--EIKK--HPFF-
PBANKA 080220 -LFEEISIDKWEDE (2) --NKNKEIIVFPFSLFHNV (40) KFDPRKIR (9) EIR--KALSL--DVCDQYS--NVS--QIME--SSIF-
PFI4_0227_cdlk -----EGKNTPKVVVL---QLKHTKLDIENLNKNIN (4) FSSLSIEAV--DFLK--RLLER--NEKRLT--AY--QALH--HPWI-
PFI1370w -TTIMERYKRLNDF-----RNYTVPDYVKIHLNFW-----YILM--LQMSKPNPADRPS--AA--DV--YSKI-
tgfbr1 -YDLVSPDSVEEM---RKVVCEQKLRPNIPNRW-----QSCEALRMA--KIMR--EOWYA--NGAARIT (5) KTLSQLSQ--QEGI-
PBANKA 101330)IEIVGKPNKKDI (10) IISFADTGRKKKFKFSEI---FHKASQDSI--DLLE--KLLQF--NPKRIT--AE--MALK--HKYV-
PFI3_0258_tk13 -----DGISASEV---FCKISSGELFLPDKDI-----PMELS--ELK--SMLEY--DFTKRFPL--FN--VIK--KLEQI-
PBANKA 146050 gak)NDENVNINFSNNS---FLSILNGSFVPHVTKY-----SKRII--SILL--MTLDK--NPKRIS--SS--TLL--IL-
PBANKA 113310 -----DGTQTQI-----VQSISYCNLNFNPF-----INPLAI--NLK--KALVV--DVNKRIR--LS--EIAS--DPWM-
PBANKA 122880 tk16 -----QNIKEKED---IVVELLVNKKKPNIPKW-----FNPEFT--EIK--RSFST--NPKRPS--CK--EYLN--LL-
MAL7P1.175 -LWKRSDPSYDLQY (2) --FEQFDMILDQPKTKRW-----PKELK--NIK--QLLHM--DYRKNLN--LN--DLSK--NPKWSS-
PBANKA 092550 cdpk6 -----TNTYEVK---QNIENSEPPYQFLKLMK-----SKPAL--HLK--LMLK--DYRKRPM--AA--VLLH--HPWF-
PBANKA 131800 kin -----NHNDI---NKLQOIKGLMQFEPH-----VSNAK--NLQ--NMNV--NCKNRYN--LN--QIKN--HIWF-
PBANKA 040110 SRPK)IEVLGNIPIKSMI (7) KYFNKNYKRLKNKIKKRY (8) KYGLPEKEINPLCSPLL--PMISI--DPQTRPS--AY--TMLQ--HPWL-
PBANKA 071730 crk-3)IVNKIGVFNNDY---KFLKRLPLWKKIKFNPI (23) NGVGEIGL--DLK--KLLK--DPLERIS--AH--DALG--HPWF-
PFC0755c crk-4)VFRGIPNENFDDL---LKEFELGELPKFKIDRL (13) RILSDEGL--DLID--QFLSY--DYKNRIT--AN--EALK--HKWF-
PFA0130C -LWDSAMEEDDYS---KFKVSDMNFDSFELTKSW-----PEGLK--VILK--QLLDE--NRRKNLN--FN--DLVI--HPWWSY-
PFI0150c -LWYKSDPLQDKDY (2) --YKSNMNFNFKWTFW-----PKELK--IIL--RLDL--EKRKNLN--LN--DLIS--HPWFSK-
PFI0520w cdpk2 -----YDGTDNE---VLKVKKGEFCFYENDW-----GSISSDAK--NLIT--KLLTY--NPNRCT--IE--EALN--HPWI-
PFI1_0488 -QFNYLEKCSKELL---VNMKNGLTYPKINQKI-----SNATL--SYIQ--YLNLF--DYELRPS--IE--EALS--YPIF-
map3k3 -----AEYEAM (2) --IFKIATQPTNPQLPSHI-----SEHGR--DFLR--RIFV--EAKRPS--AE--ELLT--HHPA-
PBANKA 124070 nek-2 -----KSKNGNM (2) --IVQKVCEQDPPLPSIY-----SKDLR--NLCY--WMSK--CSEKRP--VY--DIIG--TEYF-
PBANKA 040740 -----TDNSQ---ERIFEQIKKEDFHPKKT-----VSQAR--ELL--RLCSR--SSEKIS--AE--EVKS--HPWI-
csnk1g1 QGLKADTLKERYQK---IGDTRKNTPIEALCENF-----PEEMA--TYLR--YVRL--DFEKPDP-----YEXL (4)
PBANKA 070970 pk1)IIKILGTPNDEDF (2) --FRSIYKNVFPNPKIPIT (5) SNNSKESI--DLID--KLLQF--NPKRIR--LC--SALL--HNYF-
PBANKA 090380 -VECSKVAQIILKTV (2) --LRYSKPSPFRFRENKAW-----DLFV--KLTSS--NPNRIS--LQ--NVLD--HPWV-
PBANKA 080560 -----PKLEEDI---LLGYETQSNPF-----LLEIR--KLETV--KQRGRK-----RPMV-
dap1 -LGDTHQE---TLANVSANVEFEDEYF-----SNTSALAK--DFLR--RLLVK--DPKRRMT--IQ--DSLQ--HPWI-
prka -----DGEDEDE---LQSIMHNSVSPKS-----LSKEAV--SICK--GLMTK--HPAKRLG (5) ER--DVRE--HAPP-
MAL13P1.109 -IWKSDPIQDKIF (2) --FMKSNMDLNFIMTKSW-----PHELN--NLNVIIYKLLHM--BHRKTVK--LS--DLR--HPWSS-
MAL13P1.279 pk5)IFRILGTPNSKNW--PNVTELPKYDFNFTYEPLEPWESEFLKGLDESGI--DLIS--KMLK--DPNCRIT--AK--QATE--HAYF-
PBANKA 040820 cdpk3 -----YGESDHE---ILSMVKKGYNFKGKRW-----NNISEAK--DLK--RCLTI--DSGKRIN--AS--EALK--HPWF-
PFI1_0377_ck1 QGLKAI SKDKYDK---IMKKISTSVVLCRNT-----SFEFV--TYLN--YCRSL--RFEDRPPDYTLR--RLK--DLFI-
PFI0665w -----EINNYMPIHL---KKILMENKPKFEPFIW-----KQHTDLL--DLCL--RLIDP--NPNTIQ--NA--EALI--HYSF-
PFI4_0320_tk14 -NFLYIKLYKRDLL---KNIINNDIQHFYIKY-----LLEY--NTINP--NIKRRS--LN--DLRR--QT-
PFI4_0294_map-1)IIQVIGKPNKKDI (4) SPFAEKISSFVLDLKKKMLKDCYKASNESL--DLLE--KLLQF--NPKRIS--AE--NALK--HKYV-
PFI4_0346_pkg -----GNDEEDQ---LEIFRDLTGLTQTFPDY-----VTDTSI--NLK--RLCR--LPQGRIG (5) FK--DIKE--NSFF-
PFI1285w -----FSDHMYDINLSHFEPQDEF-----LI--NLIL--ACIDD--NPKRPT--FE--EI--SRLL-
camk2a --WDEDQRLYQOI-----KAGAYDFSPSEW-----DVTPEAK--DLIN--KMLTI--NPKRIT--AA--EALK--HPWI-
PFI0080c nek-3 -----ISLFDKKNYSYIINKI---SSIYSQKLV--NVIS--KLLSL--NTELE (5) NL--ETQ--HVLH-
MAL13P1.196)PWWKSTHNLRL (53) SLYTNNNNFIMNKKY (33) PLCSGDMC (69) DLAR--QLLNF--DYERIT--AE--QALN--HPWF-
PBANKA 031030 pk7 GLNINLQEIKAEEI---KYHIDRNYFLKVRKGA (5) HDLSNDDI--NFLK--IFKK--KPTERT--AE--EALD--HKWL-
MAL13P1.84)LIEVIGSPQMSFF---ENIKDHTSKNLLIKEL--CELNLIKPLCWD---ELG--NLI--EENPNERLN--ID--AVLS--NPFY-
PBANKA 071990 crk1)ILNLLGLPKETY (15) -FKKKIKMNVNRRSHF (8) GLVLSDIGL--DLK--KLLHP--NPQDRMS--AS--DALK--HPYF-
PBANKA 142160 -----YPCSRFEKVI FHERYW-----HNSPEAK--NFKQ--SLEI--DPFKRN--VI--EAMD--HPW-
PBANKA 083560 PKAcat -----YANEP---LLIYKILEGIYFFKPF-----LDNCK--HMK--KLSH--DLTKRYG (5) AQ--SVKE--HPWF-
PFI4_0516_kin -----NNSDM---NKLFTQIKGLIYFQPY-----VSKAK--HLQ--NMNV--NPKRPT--MN--KIKN--HIWF-
PFI4_0392 -DSEDKDV---KEAYNEIHKKIVFPKN--RVNKFSTSVR--SLL--AMNI--NPKRIS--LD--EVMK--HEWL-
PFI0520w tk11 -----SDMNPLDI---IAHVGANIKLSTVTKN--IPDLK--YILH--SCHK--NTHKRS-----FLW--SEYF-

Tewari et al., Figure S1 A (cont.)

PFL1370w nek-1 -----HKANN-----FAQLISELKRGPPELPIK-----GKSKEIN---LLK---NLNL-SAKEPS--AL--OCLG--YQII---
PBANKA_101090 tk14 NYYNFYIKYIEKK-----ELLNELNKKIKTQF-----KELK---YFFN---FFQF-DLKKRD--VY--EYK(5)YNFY---
PFI1280c_1-286 --QHYITTFDESQ---IYKLVDFVTKKLPPTC---HSKIENSPA---DITR---LCLNY-DPNLRPT--AS--EIVQ---LL---
cdk2)IFRTLGTDPDEVV-----PGVTSMPDYKPSFPPK(8)VPPLDEDR---SLIS---QMLHY-DPNKRIS--AK--AALA---HPFF---
PBANKA_135090 crk-6 LDLIYATLGNKTEI-----AMDNIERYNSFPYEEHILKSMISDESVC---DLIS---KMLTY-DPYFRIS--SK--EALK--HSCF---
PFI1415w ---SKINNDVHIY---FILSNKFKIKRKLKKY-----HYLSQPCK---DLK---KMLTY-NYENRIS--FI--QVFK--HSFT---
PBANKA_130920 lammer)LMENIIEPIPKMLYEATKTNGYKIDKNDLKLAW(24)---HDLFC---DFLY---TLIRI-DPTLRAS--PV--DLLK---HEFL---
PFB0815w cdpk1 ---GGQNDQD---IKKVEKGYKDFDFNDW-----KNISEAK---ELK---LMLTY-DYNKRIT--AK--EALN--SKWI---
mapk1_1-289)ILGILGSPSQEDL(4)NLKARNYLLSLPHKKNVFNRLFPNADSKAL---DLID---KMLTY-NPHKRIS--VE--CALA--HPYL---
PFI1_0242 cdpk7 ---PINKNT---EMNIQKNYVLSFKDYIW-----KSISSAK---DLIS---KLEL-NVEKRIS--AN--EALN--HIWV---
PBANKA_030850 tk11 ---NDLKHPLDI---IAQVGLYNQLIINNNI-----NNKLL---YVLT---SCHK-DKRKRIS--FF--EALN--SEYF---
PFB08_0044 pk1)IIKILGTNDQEDF(2)---FRSVYKNIKFPDKPIT(5)RHNCSESL---DLIS---ELIQF-NPQKRIS--LC--HALL--HNYF---
PBANKA_082960 ---SSINNDMHVL---FLIQNKNFIDIKNSFSKY-----SYFSHSFK---DLIQ---KMLKY-EYQKRIS--FF--DLFF--HPFV---
MAL7P1.144 ---LWVCSDDLQDDYF(2)---LMSKDMFNFPSCSNW-----PHGLK---HFK---QLLHM-KYRKLN--LN--ILGI--HPWYK---
PBANKA_093300 PRK4)MMEYKGFSSHMI(4)FYSQHFNDLDFIYVDRDH(40)KKIKQLG---DLIE---KCLIL-DPSKRYT--PD--QALQ--HPYL---
PBANKA_130690)IYYNDDDYFKE---DPIDEIEDEPVIYFNKND(40)TFLENNQ(7)---NFL---SLQI-DPCKRLN--SK--EALD--HPWL---
PFI1_0060)MCLMINKYKTKDI(2)---KKEKGINFNLLSFHNY-----PIAK---DLCE---QLQF-DPNKRIS--NTV--CAAN--HPWL---
gsk1_0141 mrk)IFLLGTPTNENNW---PEALCLPLYTEFKATKDFKTYFKIDDDDCI---DLIT---SFLK-NAHERIS--AE--DAMK--HRYF---
gsk3b)IIVLGTPTREQT---REMNPNYTEFKFPIKAHPW(18)PRTPEAI---ALCS---RLLEY-TPTARLT--PL--EACA--HSFF---
map4k1 ---FDVHPLRVLFL---MTKSGYQPPRLKKEKGGK-----SAAFH---NFK---VTLTK-SPKRRPS--AT--KMLS--HQLV---
PFI1_0147 map-2)IFNVIPTPEEDL---KCIKQEVIKYKLFPTPR(8)YSSISKEGI---DLIE---SMURF-NAQKRIT--ID--KALS--HPYL---
PFI3_0085 pk9 ---KYMKEKEL-----KNFESMTLNYANDI-----SDDLK---DLIS---LMLNY-DPNKRPI--IV--EILN--HRWF---
MAL7P1.91 est)DYDIVSLQWGD(227)FKMNVQNDMMNPNKDYW(38)LNYSDEYW---DLIT---NLLNY-VPSEKRL--AC--EVLG--HDFE---
PFI0125C ---FWNKADASVDKEY(2)---FARNMDFHKVEKTYHW-----PDGK---FLIQ---QLLHF-ESRKNLD--LN--DLIN--HPWFT---
PFI1_0464)IECSKVAQTILKTV(2)---LRHSKPPSFRFRENKAW-----DLFV---KLTSS-NPIEELS--LQ--NVLD--HPWV---
PBANKA_092700 tk12)VFDYLVNHNINND---YKSIYSILDYVNFDFP---LVEKLT---KLSF---LCLNF-NIKNRP--SKLV--NLIL---
c1k1)MMERILGLPLPKHM---IQTRKRYFHHDRLDW(24)DVEHERLF---DLIQ---KMLTY-DPAKRIT--LR--EALK--HPFF---
PFC0385c ---TDDTQ---ERIPDQIKELNHFHFKS-----VSLAQ---ELIL---KLSR-TAEERIS--AD--EVKS--HPWI---
mapkapk2 ---YSHGLAISFGM---KTRIRMQYFEPFNPW-----SEVSEEVK---MLR---NLKT-EPTQRYT--IT--EFMN--HPWI---
csn1)QGLKAATKRQYER---ISEKMSSTIEVLCKGY-----PSEFA---TYLN---FCRSL-RFDKPD--PD--YSYL--RQLF---
pF0105w srpk)IIEVLGNIPKHM(7)KYFNKNYRLKRNIRIKKY(8)KYNLPEKISPLCSFL---PMLSV-DPQTRPS--AY--TMLQ--HPWL---
pFA0380w eik2 ---ERMKI---LCNARHRIPLDLIKKH-----POVA---KLCQ---NLSL-DYHLRWT--SE--ELKPKKNIYI---
PFI1685w PKAcat ---YANEP---LLIYQKILEGIIYFPKP---LDNCK---HLMK---KLSH-DLTKRYG(5)AQ--NVKE--HPWF---
PBANKA_061580 est)NYDILSLQWDD(234)FKANIQRDYMGNKEYW(38)LNYSDDYW---NLIA---DLIY-MPEKRL--AC--EVLG--HDFE---
PFI1_0156 prk4)MMEYKGFSSHMI(4)FYSQHFNDLDFIYVDRDH(40)KKIKQLG---DLIE---KCLIL-DPSKRYT--PD--QALQ--HPYL---
PFI4_0476 ---TGKNANEL---YNNILKANIPPELLSKEK---SLNIQGLK---NLE---NLIVH-DPEKRF--CA--DILN--HRWI---
PBANKA_060060 nek-3 ---SANNINDM---IRLFEDKKNYKNEIINKI---SSFYSIQLV---DLIS---KLSL-MALDRLQ---VTSN--YNIVRN---
MAL7P1.26 ---ALLEEDILAGYTKSNNF-----DEIK---KLEIVKQKRRK-----FMVG---
PBANKA_031140 ---EYNTMPTYL---KIKLIRYTPNFDPPFIW---QESPLL---DLCL---RLDP-NPLTRIQ--NAK--EALI--HCCF---
PFI0105c ---LWDKATASQDEIF(2)---IVEKGMNLKALELTRKW---PRELK---SILK---NLSL-ESRKSFN--LK--DLID--HPWFTN---
PBANKA_093860 ck2)IAKVLGTEDLHAY(5)IKLPHYLNILGEYERKFW(8)MDIAKDEVI---DLID---KMLTY-DPAKRIT--PK--EAME--HPYF---
PBANKA_031420 cdpk1 ---GGQNDQD---IKKVEKGYKDFDFNDW-----KNISEAK---ELK---LMLTY-DYNKRIT--AE--EALN--SRWI---
PBANKA_010410 ---GSTNEERED---IMNRIQDYHWSQLFSEK(5)IDKLSPEFK---NFLN---LCLDK-NPKKRPT--AE--ELIQ--HPFI---
camk1 ---YDENDAK---LFEQILKAEYFDFSPYW---DDISDSAK---DFIR---HLMK-DPEKRF--CE--QALQ--HPWI---
PFI1175w ---IWKRADPPNDRTF(2)---FLKYNLNIWVQLAKQW---PKGLK---DITN---KLSL-ESRMTD--LN--ELTE--HPWIN---
PFB0150c ---KRNQSFENY---IKTIINSSPKINITEGY---SKHLC---YFVE---KCLQK-KPENRGN--VK--DLIN--HKFL---
PFI1885c pk2 ---RGNVKE---IFKKNMRCHISFNTKHW---LNKSEVVK---EITL---WMCK-NPDDRCT--AL--QALG--HWF---
PBANKA_092520 cdpk7 ---PINKNT---EMNIQKTYVLSFRDNIW---KTISSAK---DLIS---KLEL-NADKRIS--AS--EALN--HIWI---
prkaca ---FADQPT---QIYEKIVSGKVRFPSPHF---SSDLK---DLIR---NLQV-DLTKRFG(5)VN--DINK--HKWF---
PFI0095C ---LWECSDPLTKNY(2)---FEKNMSLDTFRVTKSW---PEDIK---IMTK---NLID-KYRKNIK--LK--NLK--HPWFK---
PFI3_0211 cdpk5 ---NGKNND---ILKVEKGEFVFDNSYW---ARVSDAK---DLIC---QCLNY-NYKRID--VE--QVLK--HRWF---
PFE1290w nek-2 ---KSNNSNM(2)---VAQKICEDEPDLPSDF---SKDLI---NLGY---WMLK-DWDRPT--IV--DIIS--TDYI---
PBANKA_040940 ---RSSVEKDIYWNML---VHKNYRELLTDKNGIHL---SNDV---DLIF---HCLDP-NFQTRYS--IN--QVLS--HTWF---
nek1 ---EAGSMKNL---VLKIIISGFPVPSLHY---SYDLR---SLVS---QLFK-NPRDRPS--VN--SILE--KGF---
nek7 ---YGDKNLYS---LCKIEQCYDPPPLSDH---YSEELR---QLVN---MCLNF-DPEKRF--VT--YVVD--VAKR---
PBANKA_093370 MAP-2)IFNIIPTPTEDDL---KNINKPEVIKYLFPFR(8)YPSISDDGI---NLE---SMURF-NPNKRIT--ID--QALD--HPYL---
PFI0040C ---MNTSFPSESVMF(2)---FLENMNLSCYPTKSW---PSDFK---FIVK---ELMNE-ECRKLIN--LK--NLMT--HPWFNE---
PFI0_0160 ---LWKSDDIEQDIDF(2)---VSECDMDIDVPELRTW---PYELK---KIQ(8)NKLQ-T-EGRKNLN--LN--ELCA--HPWFS---
PBANKA_135150 cdpk5 ---NGKNND---ILKVKKGEFVFDNSYW---SKISLDAK---ELIC---ECLNY-NYKRID--VH--KIVN--HKWF---
PBANKA_145320 pk2 ---RGNVKE---IFKKNMRCHISFNTKHW---LTKSENVK---EITL---WMCK-NPDDRCT--AI--QALG--HPWF---
PBANKA_090110 ---QFNYLEKCSKEL---VNMKMRGLSPKINQHI---SKITL---NYTE---YLNLF-DHECRPS--IE--EALS--YPIF---
PFI2280w gak ---QNNN---FLSINASFTPYCTKY---SKRII---SILL---MTLNK-NPQKRID--TS--TLFF--IL---
MAL7P1.18 ---LFDIISIRKWEHF(2)---NKNRNILIPFSFLFHN(1)---CSYFI---KLM---TYLI-MNNIYFS--KN--SYLL--DNKF(4)---
PBANKA_020580 eik2 ---IKTETNMERTQT---LCNARERILPDLIKKH---PNVA---SLCK---KMLSL-DYKSRPT-----SAQL--YNKI---
PFI1_0227 ---DGSTEW---FIYNKIKRRELKYPISII---PELTI---DLIE---KLTIM-NPEERIG(4)CE--EILE--HLVF---
PFI0260 ---GSTNEERENV---IMNRIQDYHWSQLFSEK(5)IDKLSPEFK---DFLN---LCLDK-NPKKRPT--AE--SLIQ--HPFI---
PBANKA_141360 pk9 ---IDVGKDIKYFEQSTLKY---SNDISDDLK---DLIS---LMLNY-DPNKRPI--IV--EILN--HRWF---
PFI1145c tk15 ---YNLTKNVK---IRHELLVKNKTPHINPF---LPNSIK---KLIQ---KCFSE-QPEDRPT--AY--EM--YKSL---
PFI1_0510 ---WLIANIEEDLNF(2)---IFEADMNFDFKFIKAW---PKEFK---KIQ---QLLHM-TSRKNLS--LK--ELSK--NPWKE---
PFI1_0220 tk12)VFDYLVNHLNMSD---YKSIYSILDYVNFDFP---LVEKLT---KLSF---LCLNF-NIKNRP--SKLV--NLIL---
rock1 ---YADSLVGTYS---KMNHNKNSLTFPPDNDI---SKEAK---NLIC---AFIT---DREVLGRNGVE--EIKR--HLFF---
src ---PGMVRN---VLDQVERGYRMPCEPEC---PESLH---DLMC---QWRK-EPEERPT-----FEYL--QAFI---
PFC0060C ---LMSRSDPEQDHVF(2)---LSQADMNFNMLERTKWK---PDDFK---FIK---KLLHM-EHRRNLD--LK--DLCK--HPWFTS---
PBANKA_122500 FIKK ---KCSDDLQDEDF---FVFKCDMMFDFKELTRKW---PSELK---SILK---GLLHA-ETRKLIN--LK--DMIM--HPWV---
pak1 ---LNENFLRAL---YLIATNGTPELQNPKEK---SAIFR---DFLN---RCLDM-DVEKRG--AK--ELIQ--HOFI---
PFI4_0431 lammer)MMESIQPIPKMLYEATKTNGSKYVKNDELKLAW(21)IHKHELF---DFLY---SLQI-DPTLRPS--PA--EALK--HKFL---
PFI4_0408)IFTKHGLIILKKE(13)---QLNQEDDEEIVFNSNDF(40)YPSDNLK(11)DFLS---SLQI-DPSKRCN--AM--EALK--HPWL---
PFI2250c pkb ---NNTNRNV---LFESIKYQKLNYPKNI---SPRAV---DLIT---KLFK-NPKRIG(5)AQ--EIKK--HPFF---
egfr ---DGIPASE---ISSILEKGERLPQPIC---TIDVY---MIMV---KCMWI-DADSRPK--FR--ELII--EF---
PFI0740w crk-3)IVNKLGFNERDI(13)---LNPHPNNHNNINHNK(11)PGVGLGL---DLIK---KPLK-NPYERIT--AS--DALN--HPWF---
MAL7P1.73 ---NT---SSEAK---DFIQ---SLQI-NPEKRLN--VI--EATE--HPCI---
PBANKA_121280 mrk)IFLLGTPTNENNW---PEAKHLPLTDFPKSNK(6)IKIEDDCI---DLIT---SLKLN-NSHERIT--AE--EALK--HRYF---
map2k1)MFGCQVEGDAAET(13)---YGMDSRPFMAIFELLDY(11)GVFLEFQ---DFVN---KCLIK-NPAERAD--LK--QLVW--HAFI---
PFI0865c crk-1)ILCLGLDPKESY(15)---FKKKIKMNVNRRSHF(8)GLYLSDNL---DLIQ---KMLHY-NPQKRIS--AQ--EALN--HPYF---
PFI4_0733 ---LWDCSDPSKDEIF(2)---INECEMDLKDCLTDNW---PEGLK---AMK(22)RLNF-ESRKEIN--LK--DITV--DPWST---
PFI0100c ---LWGNFDMQSNF(2)---FVNSDMNDFLFPPTREW---PEGLK---YIIR---KLDY-ESRSLD--LN--ELIE--HPWST---
PBANKA_135260)FVWSQTPDRMLSL(51)NKYNSLISLSPSPVCPNW(40)NCCDEQF(20)DLR---RLDF-DYNTNIT--SE--EALK--HAWF---
PBANKA_130840 eik1 ---STSMERSI---VLSNLLKCIYSPESIRS---DNKIF---QFLL---SLLEI-DPQNRIS--AY--SLH--ENFF---
PFI1_0096 ck2)IAKVLGTEDLHAY(5)IKLPHYLNILGEYERKFW(8)MDIAKDEVI---DLID---KMLTY-DPAKRIT--PK--EAME--HPYF---
PBANKA_131370 ---TGKNANEL---YNNILKANIPPELLSKEK---SLNIQGLK---NLE---NLIVH-DPEKRF--CS--DILN--HRWI---
Consensus/80%b.....b.....s.h.....pb1.....hlp.p.ppr.s.....phb.....p.bb.....

Tewari et al., Fig. S1B

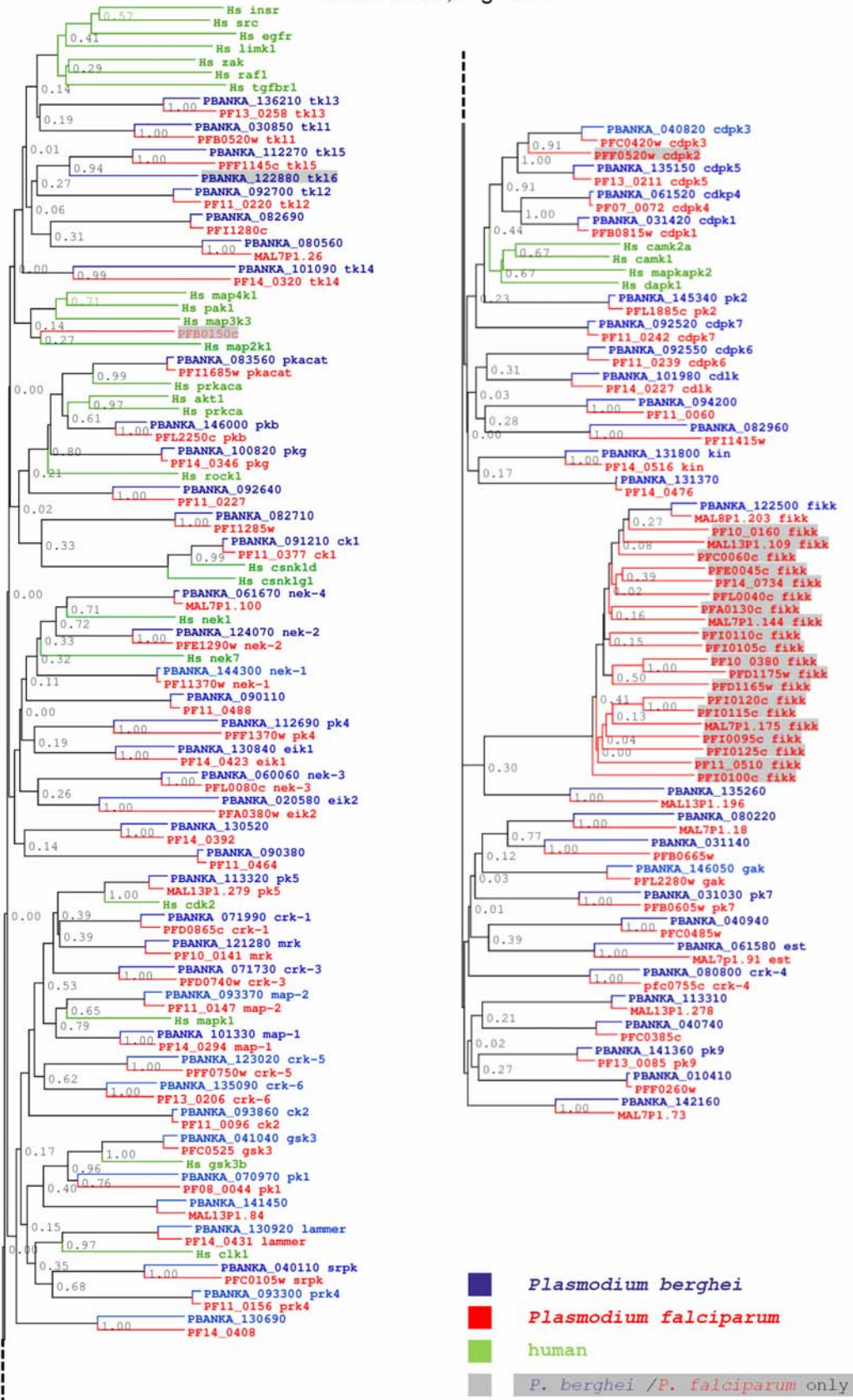
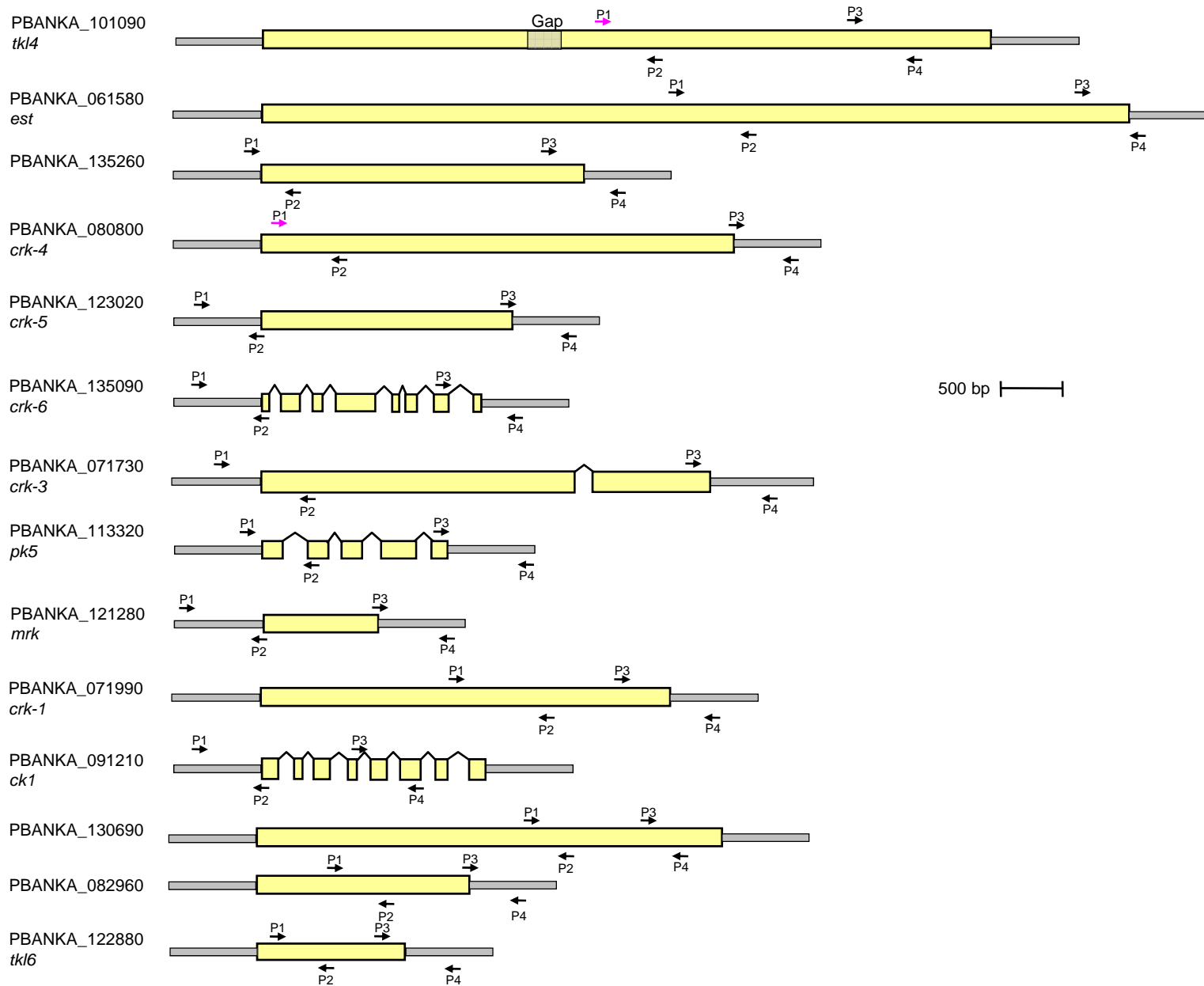


Figure S1 (relates to Figure 1). Comparative Analysis of Kinase Domain Sequences from *P. berghei* and *P. falciparum*

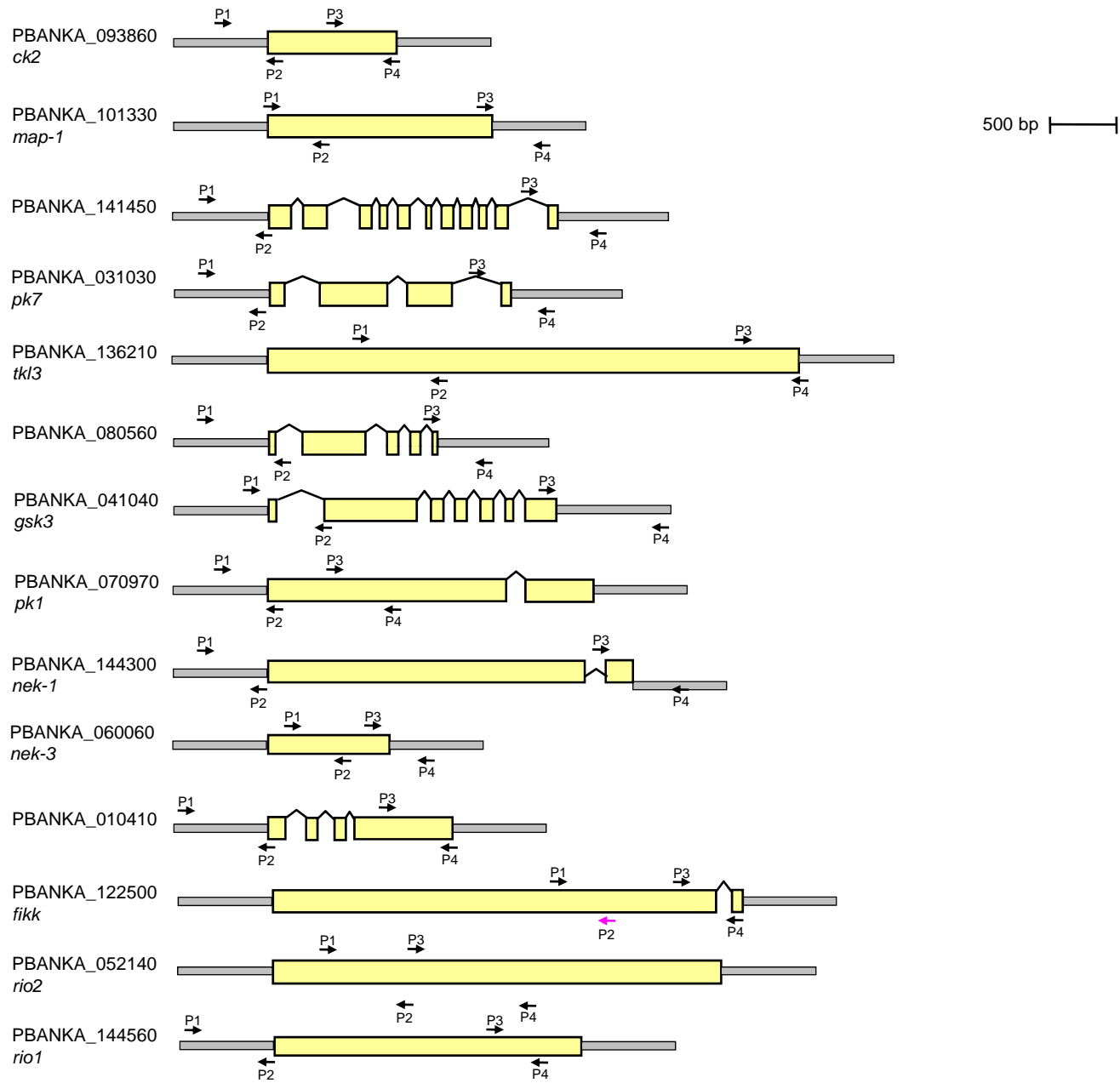
(A) Multiple sequence alignment of *Plasmodium* kinase domains. The alignment was generated using the MUSCLE software (Edgar, 2004) and coloured using the CHROMA software to highlight conserved residues (Goodstadt and Ponting, 2001). Kinase domain sequences for *P. falciparum* were taken from Ward et al., (2004), those from *P. berghei* are contained in a supplemental text file entitled “Pb kinase domain sequences”.

(B) Evolutionary relationships of *Plasmodium* and selected human kinase domains. The evolutionary history was inferred from the alignment in Figure S1 using the Neighbor-Joining method (Saitou and Nei, 1987). The optimal tree with the sum of branch length = 72.77107574 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (500 replicates) are shown next to the branches (Felsenstein, 1985). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Poisson correction method (Zuckerkandl and Pauling, 1965) and are in the units of the number of amino acid substitutions per site. All positions containing alignment gaps and missing data were eliminated only in pairwise sequence comparisons (Pairwise deletion option). There were a total of 4009 positions in the final dataset. Phylogenetic analyses were conducted in MEGA4 (Tamura et al., 2007).

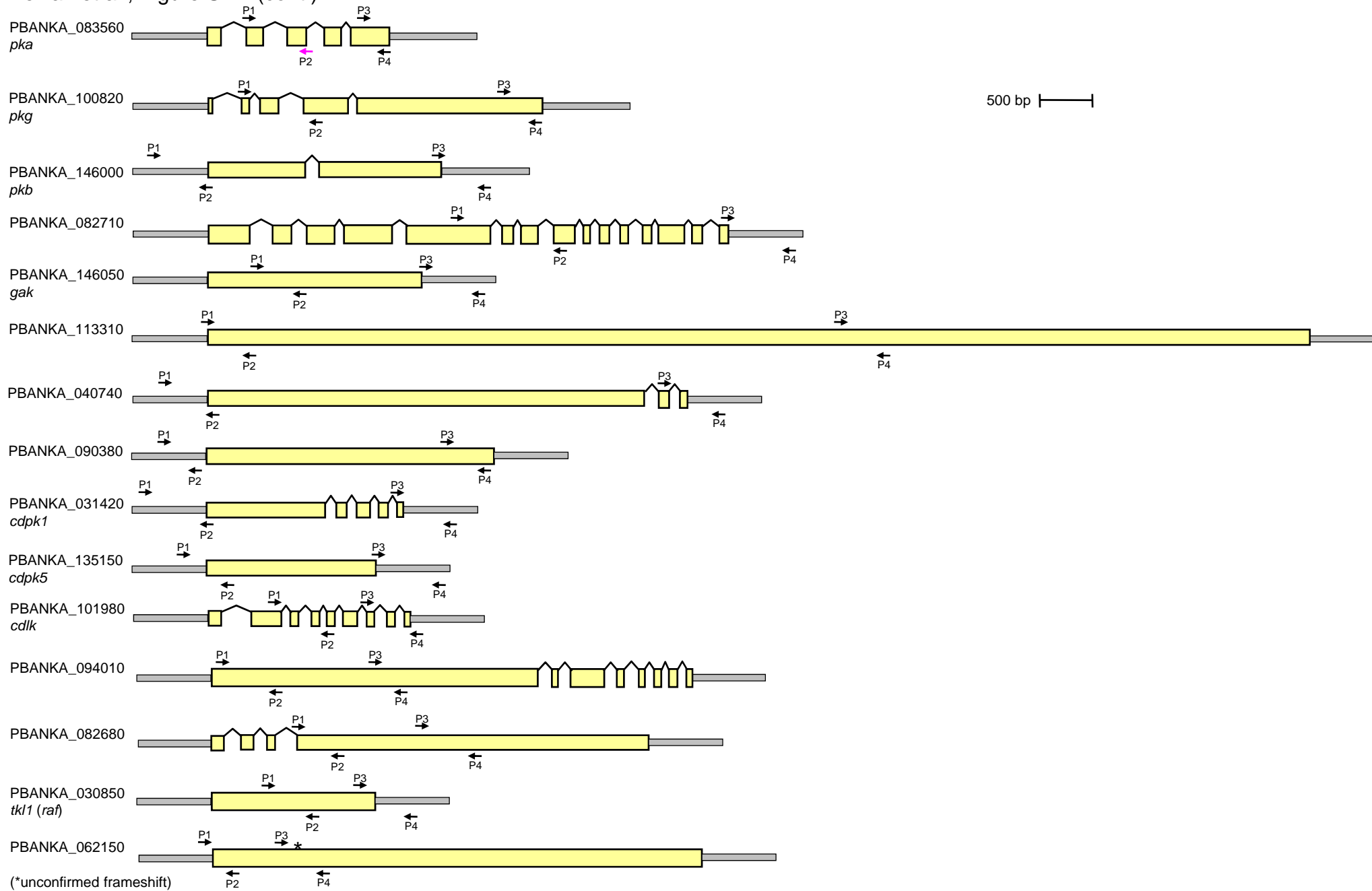
Tewari et al., Figure S2 A (top)



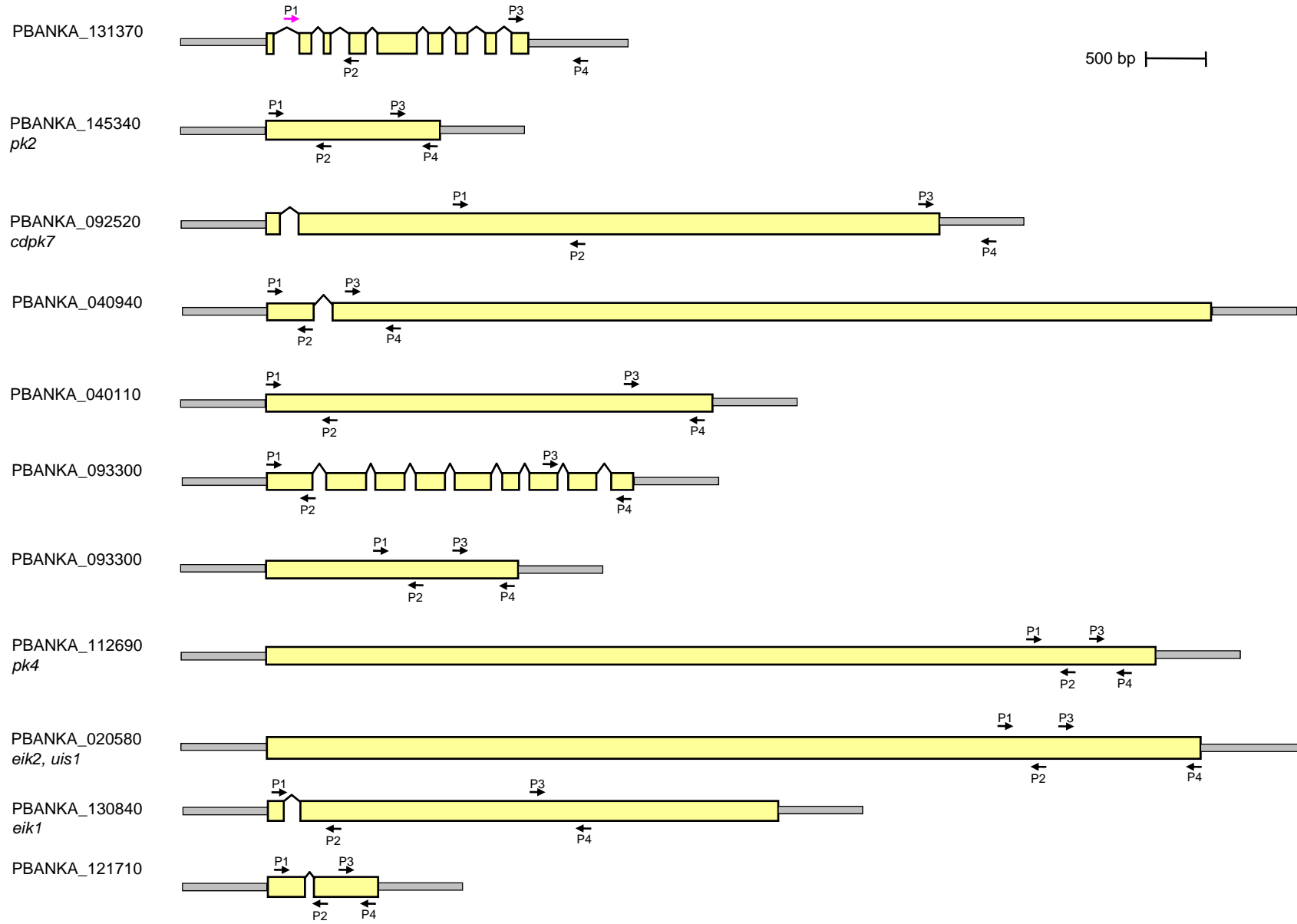
Tewari et al., Figure S2 A (cont.)



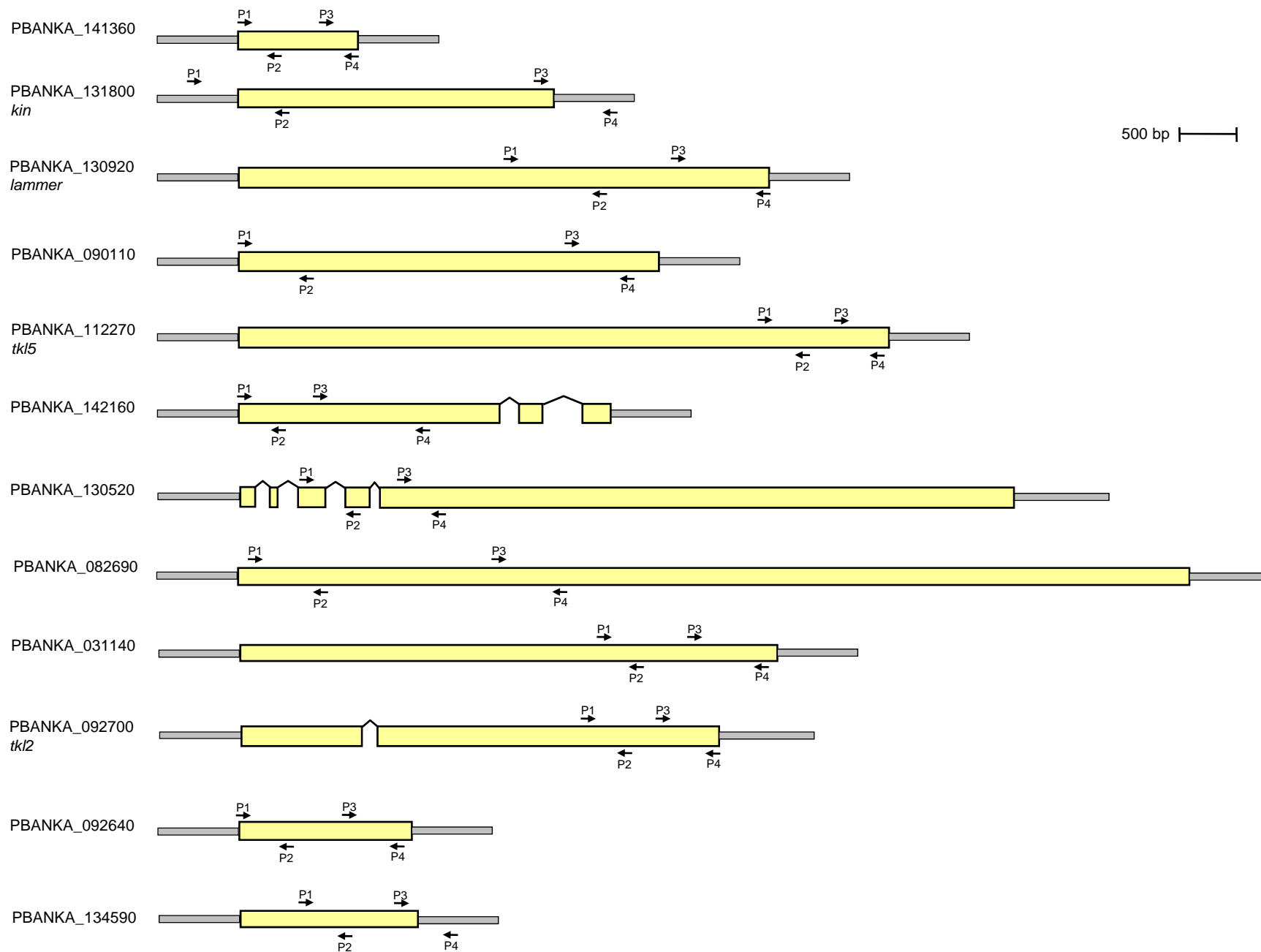
Tewari et al., Figure S2 A (cont.)



Tewari et al., Figure S2 A (cont.)



Tewari et al., Figure S2 A (cont.)



Tewari et al., Figure S2B

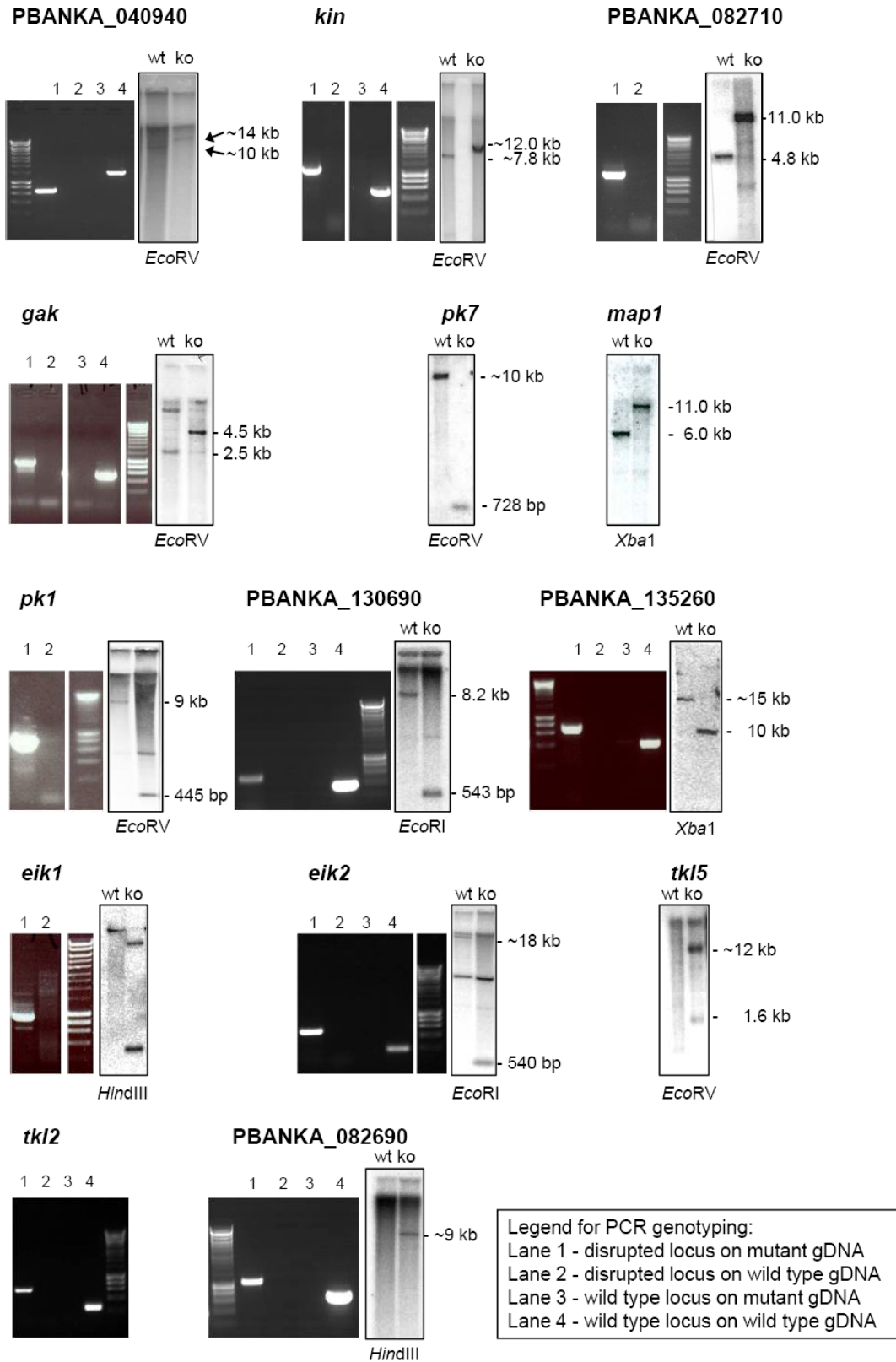


Figure S2 (relates to Figure 2). Vector Designs and Genotyping Data

(A) Description of gene targeting vectors. Gene models are shown as predicted in the May 2010 assembly of the *P. berghei* ANKA genome and have not been verified experimentally.

(B) PCR and Southern hybridisations confirming the disruption of 14 ePK genes. PCR genotyping (on the left) used the same rationale as illustrated in Figure 2. Southern blots (on the right) were routinely probed with gene-specific probes flanking the integration site. Diagnostic bands confirming correct integration are indicated by arrows. In a few cases evidence from only one method of genotyping was obtained. Additional details are available from the authors on request.

Table S1 (relates to Fig.1): List of all *P. berghei* kinase-like genes and their *P. falciparum* orthologs. Gatekeeper residues are taken from the multiple sequence alignment in Fig. S1, or from a manual alignment where indicated. Also shown are the total number of knock out attempts and how many of these led to deletion of the target as confirmed by genotype analysis. "p" gives an estimate for the likelihood of error for "possibly essential" genes. It is calculated from the average technical failure rate (0.248 per attempt for redundant genes in this study) to the power of n, where n is the total number deletion attempts for the gene. * = genes for which no mutant clones were obtained despite positive genotyping

Gene name	<i>P. berghei</i> ID	<i>P. falciparum</i> ortholog	Group	Gatekeeper	Total	Successful	Outcome	p	
									Knock out attempts
<i>cdpk1</i>	PBANKA_031420	PFB0815w	CaMK	T	6	0	Possibly essential	0.00024	
<i>cdpk2</i>	no ortholog	PFF0520w	CaMK				n/a		
<i>cdpk3</i>	PBANKA_040820	PFC0420w	CaMK	M	4	3	KO confirmed		
<i>cdpk4</i>	PBANKA_061520	PF07_0072	CaMK	S	7	7	KO confirmed		
<i>cdpk5</i>	PBANKA_135150	PF13_0211	CaMK	L	6	0	Possibly essential	0.00024	
<i>cdpk6</i>	PBANKA_092550	PF11_0239	CaMK	M	16	12	KO confirmed		
<i>cdpk7</i>	PBANKA_092520	PF11_0242	CaMK	M	5	0	Possibly essential*	0.00095	
<i>cdlk</i>	PBANKA_101980	PF14_0227	CaMK	L	11	8	KO confirmed		
<i>pk2</i>	PBANKA_145340	PFL1885c	CaMK	L	4	0	Possibly essential	0.00382	
	PBANKA_040940	PFC0485w	CaMK	M	5	3	KO confirmed		
	PBANKA_094200	PF11_0060	CaMK	M			Not done		
	PBANKA_082960	PFI1415w	CaMK	?	5	0	Possibly essential	0.00095	
	PBANKA_031140	PFB0665w	CaMK	M	5	0	Possibly essential	0.00095	
	PBANKA_080220	MAL7P1.18	CaMK	M			Not done		
	<i>kin</i>	PBANKA_131800	PF14_0516	CaMK, Snf1-like	L	4	3	KO confirmed	0.00382
		PBANKA_131370	PF14_0476	CaMK, Snf1-like	L	4	0	Possibly essential	0.00382
		PBANKA_141360	PF13_0085	CaMK, Snf1-like	M	9	0	Possibly essential	3.6E-06
	<i>pka</i>	PBANKA_083560	PFI1685w	AGC	L	3	0	Possibly essential	0.01535
<i>pkg</i>	PBANKA_100820	PF14_0346	AGC	T	3	0	Possibly essential	0.01535	
<i>pkb</i>	PBANKA_146000	PFL2250c	AGC	L	6	0	Possibly essential	0.00024	
	PBANKA_092640	PF11_0227	AGC	M	8	0	Possibly essential	1.5E-05	
	PBANKA_040740	PFC0385c	AGC	L	3	0	Possibly essential	0.01535	
	PBANKA_082710	PFI1285w	AGC	L	3	3	KO confirmed		
	PBANKA_113310	MAL13P1.278	orphan	L	4	0	Possibly essential	0.00382	
	PBANKA_090380	PF11_0464	orphan	Q	5	0	Possibly essential	0.00095	
	PBANKA_010410	PFF0260w	orphan	M	8	0	Possibly essential	1.5E-05	
	<i>gak</i>	PBANKA_146050	PFL2280w	GAK	M	4	3	KO confirmed	
	<i>pk7</i>	PBANKA_031030	PFB0605w	orphan	N	9	5	KO confirmed	
	<i>est</i>	PBANKA_061580	MAL7P1.91	orphan	I (ma	4	0	Possibly essential	0.00382
<i>ck1</i>	PBANKA_091210	PF11_0377	CK1	L	4	0	Possibly essential	0.00382	
<i>pk5</i>	PBANKA_113320	MAL13P1.279	CMGC, CRK	F	2	2	KO confirmed		
<i>mrk</i>	PBANKA_121280	PF10_0141	CMGC, CRK	M	6	0	Possibly essential	0.00024	
<i>crk-1</i>	PBANKA_071990	PFD0865c	CMGC, CRK	M	3	0	Possibly essential	0.01535	
<i>crk-3</i>	PBANKA_071730	PFD0740w	CMGC, CRK	F	4	0	Possibly essential	0.00382	
<i>crk-5</i>	PBANKA_123020	PFF0750w	CMGC, CRK	Y	5	0	Possibly essential	0.00095	
<i>crk-6; PK6</i>	PBANKA_135090	MAL13P1.185	CMGC, CRK	F	6	0	Possibly essential	0.00024	
<i>map-1</i>	PBANKA_101330	PF14_0294	CMGC, MAPK	F	2	2	KO confirmed		
<i>map-2</i>	PBANKA_093370	PF11_0147	CMGC, MAPK	L	4	3	KO confirmed		
<i>ck2</i>	PBANKA_093860	PF11_0096	GMGC, CK2	F	4	0	Possibly essential	0.00382	
<i>gsk-3</i>	PBANKA_041040	PFC0525c	CMGC, GSK3	M	9	0	Possibly essential	3.6E-06	
<i>pk1</i>	PBANKA_070970	PF08_0044	CMGC, GSK3	M (ma	4	3	KO confirmed		
	PBANKA_141450	MAL13P1.84	CMGC, GSK3	F	5	0	Possibly essential	0.00095	
<i>lammer</i>	PBANKA_130920	PF14_0431	CMGC, SRPK	F	3	0	Possibly essential	0.01535	
<i>srpk</i>	PBANKA_040110	PFC0105w	CMGC, SRPK	F	5	4	KO confirmed		
<i>prk4</i>	PBANKA_093300	PF11_0156	CMGC, SRPK	F	4	0	Possibly essential	0.00382	
<i>crk-4</i>	PBANKA_130690	PF14_0408	CMGC, SRPK	T	3	3	KO confirmed		
	PBANKA_080800	PFC0755c	CMGC	? (po	4	0	Possibly essential	0.00382	
	no ortholog	PFB0150c	CMGC				n/a		
<i>nek-2</i>	PBANKA_135260	MAL13P1.196	CMGC	F	2	2	KO confirmed		
	PBANKA_124070	PFE1290w	CMGC, NEK	M	7	6	KO confirmed		

<i>nek-4</i>	PBANKA_061670	MAL7P1.100	CMGC, NEK	M	2	2	KO confirmed	
<i>nek-1</i>	PBANKA_144300	PFL1370w	CMGC, NEK	M	8	0	Possibly essential	1.5E-05
<i>nek-3</i>	PBANKA_060060	PFL0080c	CMGC, NEK	I	7	0	Possibly essential	5.9E-05
<i>eik1</i>	PBANKA_130840	PF14_0423	CMGC, ELK	M	4	2	KO confirmed	
<i>eik2; uis1</i>	PBANKA_020580	PFA0380w	CMGC, ELK	M	5	3	KO confirmed	
<i>pk4</i>	PBANKA_112690	PFF1370w	CMGC, ELK	M	3	0	Possibly essential	0.01535
	PBANKA_090110	PF11_0488	orphan	M	9	0	Possibly essential	3.6E-06
	PBANKA_130520	PF14_0392	orphan	M	6	0	Possibly essential*	0.00024
	PBANKA_142160	MAL7P1.73	orphan	L	3	0	Possibly essential	0.01535
<i>tkl6</i>	PBANKA_122880	no ortholog	TKL	L	5	0	Possibly essential	0.00095
<i>tkl5</i>	PBANKA_112270	PFF1145c	TKL	L	3	3	KO confirmed	
<i>tkl2</i>	PBANKA_092700	PF11_0220	TKL	Y	4	1	KO confirmed	
<i>tkl1 (raf)</i>	PBANKA_030850	PFB0520w	TKL	L	3	0	Possibly essential	0.01535
<i>tkl3</i>	PBANKA_136210	PF13_0258	TKL	L	5	0	Possibly essential*	0.00095
<i>tkl4</i>	PBANKA_101090	PF14_0320	TKL	M	3	0	Possibly essential	0.01535
	PBANKA_082690	PFI1280c	orphan	T	3	2	KO confirmed	
	PBANKA_080560	MAL7P1.26	orphan	F	5	0	Possibly essential	0.00095
	PBANKA_121710	PFC0945w	pseudokinase	n.d.	5	0	Possibly essential	0.00095
	PBANKA_094010	PF11_0079	pseudokinase	n.d.	4	0	Possibly essential	0.00382
	PBANKA_082680	PFI1275w	pseudokinase	n.d.	4	0	Possibly essential	0.00382
	PBANKA_134590	PF13_0166	pseudokinase	n.d.	3	0	Possibly essential	0.01535
	PBANKA_062150	MAL7P1.127	pseudokinase	n.d.	5	0	Possibly essential	0.00095
<i>rio1</i>	PBANKA_144560	PFL1490w	aPK, RIO		3	0	Possibly essential	0.01535
<i>rio2</i>	PBANKA_052140	PFD0975w	aPK, RIO		4	0	Possibly essential	0.00382
<i>fikk</i>	PBANKA_122500	MAL8P1.203	FIKK, ancestral	S	5	0	Possibly essential	0.00095
	no ortholog	MAL7P1.144	FIKK				n/a	
<i>R45</i>	no ortholog	PFD1175w	FIKK				n/a	
	no ortholog	PFI0095c	FIKK				n/a	
	no ortholog	PFI0100c	FIKK				n/a	
	no ortholog	PFI0105c	FIKK				n/a	
	no ortholog	PFI0110c	FIKK				n/a	
	no ortholog	PFI0115c	FIKK				n/a	
	no ortholog	PFI0120c	FIKK				n/a	
	no ortholog	PFI0125c	FIKK				n/a	
	no ortholog	PFL0040c	FIKK				n/a	
	no ortholog	PFD1165w	FIKK				n/a	
	no ortholog	PFE0045c	FIKK				n/a	
	no ortholog	PFC0060c	FIKK				n/a	
	no ortholog	PF14_0734	FIKK				n/a	
	no ortholog	PFA0130c	FIKK				n/a	
	no ortholog	PF11_0510	FIKK				n/a	
	no ortholog	PF10_0160	FIKK				n/a	
	no ortholog	MAL7P1.175	FIKK				n/a	
	no ortholog	PF10_0380	FIKK				n/a	
	no ortholog	MAL13P1.109	FIKK				n/a	

sum: 0.23139

Table S2. Unique ePKs of *P. berghei*/*P. falciparum* and Their Distribution across Other *Plasmodium* Genomes

	<i>P. berghei</i>	<i>P. yoelii</i>	<i>P. chabaudi</i>	<i>P. vivax</i>	<i>P. knowlesi</i>	<i>P. falciparum</i> 3D7	<i>P. reichenowi</i>	<i>P. gallinaceum</i>
<i>tkl6</i>	PBANKA_122880	<u>PY04849</u> <u>PY04848</u>	<u>PCAS_122950</u>	<u>PVX_093670</u>	<u>PKH_011700</u>	—	—	Pgal0325e01.p1k Pgal0616c03.p1k Pgal0616c03.q1k Pgal0489d11.p1k
PFB0150c	—	—	—	<u>PVX_003590</u>	<u>PKH_041680</u>	PFB0150c	3502696.c000217971. Contig1	gal28a.d0000062 93. Contig1
<i>cdpk2</i>	—	—	—	—	—	PFF0520W	3502696.c000218538. Contig1	gal28a.d0000019 39. Contig1
Ancestral <i>fikk</i>	PBANKA_122500	<u>PY03326</u>	<u>PCAS_122560</u>	<u>PVX_088265</u>	<u>PKH_011260</u>	MAL8P1.203	3502696.c000024654. Contig1	gal28a.d0000159 42. Contig1
<i>fikk</i> expansion	none	none	none	none	none	20	yes	none

Table S3 (relates to Fig. 3). Data from phenotyping 23 mutants. All data are given as percentage of wild type controls studied in parallel. SD = standard deviation. n = number of replicate experiments.

Gene name	<i>P. berghei</i> ID	Ookinete conversion			Oocyst numbers			Oocyst prevalence			Oocyst sporozoites			Salivary gland sporozoites			Transmission by mosquito bite
		% of control	SD	n	% of control	SD	n	% of control	SD	n	% of control	SD	n	% of control	SD	n	
<i>cdpk3</i>	PBANKA_040820	94.65	6.97	3	3.30	2.79	8	n.d.			n.d.			0.00	0.00	2	n.d.
<i>cdpk4</i>	PBANKA_061520	0.00	0.00	4	0.00	0.00	4	0.00	0.00	4	n.d.			0.00	0.00	4	n.d.
<i>cdpk6</i>	PBANKA_092550	90.41	11.70	3	91.20	11.94	3	98.35	5.79	3	152.22	19.18	3	28.35	44.69	3	transmitted (delayed)
<i>cdlk</i>	PBANKA_101980	84.90	7.63	6	104.66	17.48	3	102.79	13.03	3	41.66	18.50	3	4.16	1.70	3	transmitted
	PBANKA_040940	70.59	14.26	3	49.04	23.30	6	97.36	16.94	6	132.61	18.13	3	9.98	2.11	6	no transmission (0/3)
<i>kin</i>	PBANKA_131800	89.00	6.76	3	105.28	29.73	3	103.85	0.00	3	148.56	27.35	3	4.65	1.03	3	delayed to 15d
	PBANKA_082710	97.11	7.82	2	91.58	2.23	2	95.56	6.29	2	52.93	0.27	2	51.24	16.37	2	transmitted
<i>gak</i>	PBANKA_146050	4.62	1.54	3	3.28	3.60	6	47.98	32.20	6	0.00	0.00	3	0.00	0.00	3	n.d.
<i>pk7</i>	PBANKA_031030	8.92	3.70	8	8.88	5.59	4	63.45	8.63	4	0.00	0.00	7	0.00	0.00	3	n.d.
<i>pk5</i>	PBANKA_113320	87.37	14.24	3	56.43	2.28	3	94.44	9.62	3	107.63	18.95	3	65.27	16.06	3	transmitted
<i>map-1</i>	PBANKA_101330	93.68	15.82	3	63.33	23.43	3	87.72	12.15	3	92.97	18.31	3	101.53	23.25	3	transmitted
<i>map-2</i>	PBANKA_093370	0.00	0.00	3	0.00	0.00	3	0.00	0.00	3	n.d.			0.00	0.00	3	n.d.
<i>pk1</i>	PBANKA_070970	98.40	8.84	3	87.36	31.51	3	104.00	6.97	3	98.82	13.24	3	104.79	25.44	3	transmitted
<i>srpk</i>	PBANKA_040110	0.00	0.00	3	0.00	0.00	3	0.00	0.00	3	n.d.			n.d.			n.d.
	PBANKA_130690	98.50	9.17	3	106.15	15.51	3	100.00	6.66	3	128.00	45.67	3	124.94	16.37	3	transmitted
	PBANKA_135260	95.79	10.15	3	57.46	9.47	3	103.70	8.49	3	136.00	28.09	3	66.41	6.58	3	transmitted
<i>nek-2</i>	PBANKA_124070	0.00	0.00	3	0.00	0.00	3	0.00	0.00	3	n.d.			n.d.			n.d.
<i>nek-4</i>	PBANKA_061670	0.00	0.00	3	0.00	0.00	3	0.00	0.00	3	n.d.			n.d.			n.d.
<i>eik1</i>	PBANKA_130840	84.47	11.65	3	109.68	55.03	3	102.44	26.38	3	108.54	11.61	3	94.40	26.16	3	transmitted
<i>eik2; uis1</i>	PBANKA_020580	51.87	19.40	3	19.86	15.46	3	64.22	44.57	3	n.d.			14.89	10.80	3	transmitted (4/4)
<i>tkl5</i>	PBANKA_112270	83.08	11.10	3	77.46	36.88	3	100.00	5.97	3	144.73	26.40	3	102.34	19.33	3	transmitted
<i>tkl2</i>	PBANKA_092700	79.45	13.07	3	124.24	15.96	3	121.46	2.53	3	92.46	5.29	3	83.12	10.89	3	transmitted
	PBANKA_082690	83.11	3.45	3	84.21	9.25	3	94.83	7.90	3	84.55	11.57	3	81.98	8.77	3	transmitted

Table S4. *P. berghei* Protein Kinase Domain Sequences Used in This Study

>PBANKA_101090 PbtKL4
ITFLKKINEHGNGKIFLCSYNI FNNKFFI I KLIDIANNINENYIFKNIFNEVKCLLTFQNSKKGICQMYSYGIIP
NCNNGFTYYLLMKYYEGNLKDLMNHYAHISYLKEIKKIRNNAKQFFLPVCKKRTEEIILNFKIAKITKKITKRC
KGNFIFCYKYLCRYTNVYSCYTMILKNRIYIKI IQLKFI LFI LNIFIQI IEQI IYVHKKKI IHFDINTCNILINF
KKTYP LLM SKKYKIKKNNY INNCNTKQTLKNIQSQIVMRDDFVENERKIYLNFI PPSYQINNSIYKKQNKFYNNF
DTSMASFHYRQYFKIIMKKKDCQHIAIPSIVISDFGESKFFLRD TDFIFFRKNRGNEILAAPELLINKNKYIYSK
NKYKIEKKNGKEDTEIKSRKAIQDSFYFENIPQNIIFQNEQSEMNYFYSTITCFENCKKFSCLNTKNDKIRILRY
NNINMKKSLRKNSIVSLEFYKYLKKIKMLIKKKGNGKLLQKKNINMSKSDIWSLGSLLYEMITNESLFNYNFI
YIKIYEKKELLNELINKKIKTQFKELKYFFNFFFQFDLKKRKDVYEIYKESIKIYNFY

>PBANKA_061580 PbEST
LKLMIHIFGKKYKCYKNENDKMCIGLCYEKLLKIKIKLNNSVIEIKYKPFDIYIDNIKAYNCGLTESECKFLFFQ
IVNGISFLQTCYQSNIRLTDIKLQNILVFTDIYNVYNPIKWHLCISDFGCSAMEYATFYLENSKNIYINAKTLL
NQWKYQFKNQLSSYFQGTVYTMapeGLCYDHMGNFQSKYNKLIYFYEQNFQNIEDRFQELQMP LVS IKNSINNF
NILNVNSSNFHFLEKKGKYE MNNTYNDMDADKNGSEVCKGETNKNKSKKSTNKNVKANESANSNGNNTSSKKK
GKVEEENNDK KETS DKINLTENNMN SSPEYLPFDVRSDSWSLGIILADLGKCGIGSYEYMISEKGNNGNNSK
NIIDLNNIILNDLNI LDDEENFYLYQYIMNYDILSIQW DNDIEIENDQVNKNADRNNKRDNSEMENKRNNDNSNN
GCTNNNSYKSKQKNKSL ENNSKEDVPGNCFVIDNANESISNEVSFCCKDPNAHNNNYDIKEETNNKNNAVLNNQ
IKSTLNFDECNKIKGNNDNSMKSLELFTKYYSFILKYKYDIKIDKIGYIKNEFVKYKLYKHHMMNENNIERILL
LLFLIIINNLTYNSCETQSFLKIELTIKNIGSGIFKFRNKKEKERYLQEFKANI QKDYMTGNKEYWNSRLTNKY
LAVILKDV CYDNFANRRKGIKKCFNKFEYPLNYSDDYWNLLADLLNMPYERLLACEVIGHDF

>PBANKA_135260
YSIQNKL GAGAYGEI WYGINLNKNVFPQNVVLK KIFIKKSVDESEQNLDNDEREKEYE IYAMREYVYFGEIFKNCD
NISRYIEHFKESETSENNKEHITFIWIVFANE GYSLSQHLFETDKNNSGMIIPKLWWSIKKQNI GMLVIKDLMHQ
LLNGINIAHKKHITHRDIK MENIFVSPNTPFTVRIGDWGSAVEYKNSFFFTPSMEEETE GYQPPELFGHMKN
FMRLPYDMWIGIGILFLQFVLGTKNPLEIKNKRNEMLKRIYSKSKDILKEVIFIQGLSDLCLIPWVSQTPDRL
MSLYDMKNNEKNSLQYSS IYGRNLI INKLEYFAITKNLIEIKRKRYNLINNMMSNKYNSLISLPNSPVC PNWKCL
HKYDEQANYNNKYNNTFDKIQNKFLQKKENYTFFKNNCDDEQFQKILQERDPSGVGLPDKNARDLLRRLDFD
YNTRITSEEALKHAWF

>PBANKA_080800 PbCRK-4
YKIVKKLGE GYVYKVFKAESLEDSYLNFAVKVLR YFWPNFKYKFGSEEF AINEFNI MRILFHPNVVCLLDSFRVH
TYRKNKIKNHRGQKTRCETLSAEYDFSFQRHRRMEKVQYSPSRETIERNNKYRNI VSKSCLTIEELEKNLVLNSF
DKEATI QDKGNLYNNHTGKVD ETSTIFSNNNCVKVLNYDEENNNLDNNKSNVLS SKMQORDIKRERSGDIFQYYP
KKMKTSNYKNGRNEAVKVMNKSIDKLFKFKHKKLKKIENKNDYIENWDLFLVIEKDCSLNDILNKAKKKH
FSFIQDIKDDTTKCLP SERIDLSYDHLHNYVYVYLP LKKIENRYFY PDMPSLTEMQTKVI IYQMLQGINHFHK
FI IHRDIKPANTLIKNIQYLS DGLNDSKEWIVKIADFGLVYDHF LKTETKDCNIITLQYRPPEILCNSTLYNYS
VDIWSIGITMCELLGFVPVTSKFESSVLFKILVFRGIPDQNF DNLLKELV GELPKFKVDRIKMLEIIFTDIYG
RRILNDKGLDLIDQFLSYDYKNRITANEALKHEWF

>PBANKA_123020 PbCRK-5
VSL EEKLG GGT YG DVYKGVKVN NNNSDLYQNTNYLPYDYTTDEFIIFRKNIYAIKFFKDDLRTINEEGISCTT
LREL SCLKNIGRHPNII LRLIDVTIDRQKGI SEYINRQILQHYSNYYHHQVKIDMVPLSLDQKFI FAAYEYCDGGD
LKKLIQKTKISENQAGLCLKEAKWLSFQLLNGLAYLHNNKMCHRDLK PENVMLQYTHNNKYLLKIGDLGLCRELK
NDGDMTP TVCTIYYRPLEVLLSKFDRSKTRSGKNGVKNKSGSGS SAKNGSVKNGSVKNGSVKNGSVKNGS
VKNGSVKNGSVKNGS IKNGS IKNGS IKNGS IKNGS GRCS EGRSDDAYMGDEAF EKDYESFNDRDFQYGLNVDI
W SAACIICELIIGKPLFRGVTEFDLIIRIVNSL GKPNNDELEYFSDSRFY PFKDDFFNIKIKNRKDALNVI TNGKI
DELGIDL LKMLKYNPNDRITAADALSHPW

>PBANKA_135090 PbCRK-6
FDFMDIIGKGT YGVVYKAIDKKENKIVA I KKI INLCDHNYGISKIILRELSILQKINHKNIIVLRNIFYGKDIEQ
KLIGENLENSCLYLTFEYCDIDLNF TKIYNLNIKEVKYIIFEILLALCYLHSNNYLHRDIK PENIFINSKGEIK
LGDLGLSVEKSDNMTPSVVTI WYRSP ELLKQNNYDQKIDIWSL GCLFVELITGRPLFP GKNDQS QLDLIYATLG
NKTEIAMDNIERYSFPYEEHILKSMISDESVC DLISKMLIYDPYFRISSKEALKHSCF

>PBANKA_071730 PbCRK-3
IVKIHQVGGAGYGDVWMAEDIENNKRIALKKLKLNGNKEGLAKTYIREISILNSLQHKNVVELIGVIRTNIIP EE
IKSNNI LYNFEKKQLLNQVVKDKSIDSYIMPDRALKKKLAKCSSIYQSSESESESSSSDSSDGI SCDSDSCL
CNKNPLNKKVNSCASIWMVF EYVPFDLSGYS ELLREERQKDRYKNMNLFTIGE IKNIMLQLFQALEYCHKNNVI
HRDIKIANLLIDANGILK LADFGLARFHIDSFASNMTRN VITLWYRPP ELLLGSENYSSSVDMWSCGCVL GELLT
SNPLFTADNESDILKTI VNKIGV PNNNDYKFLKRLPLWNKIKFNPIHPSNINNLNQTKKIETEYI IKNLNGVGEI
GLDLLKLLKWDPLERISAHDALSHPW

>PBANKA_113320 PbPK5

YHGLEKIGEGTYGVVYKAQNSDGESEFALKKIRLEKEDEGIPSTAIRESISILKELRHSNIVKLYDVIHAKKRLILV
FEHLDDQLKKLIDVDCDGLLESVTAKSFLQLLNGIAYCHEHRVLRDLKPQNLLINREGELKIADFGLARAFGIP
ARRYTHERVVTLWYRAPDILMGSKKYSTPIDIWSVGCIFAEMVNGRPLFPGASETDQLMRIFKILGTPNSQNWPDV
FKLPKYDPNFPVYNPLPWETFIKGLDDTGIDLLSKMLKLDPNQRITAKQAI EHPYF

>PBANKA_121280 PbMRK

IFKPNFLGEGSYGKVYKAYDVTVLKKEVAIKMKLNKISNYIDECGINFLILREIKIMKEIKHKNVMNALDLYCEK
DYINLVMEIMDYDLAKLINRKILLTDSQKCCILLQILNGLNTLHKYFMHRDLSPANIFINKKGEVKIADFGLSS
KYAFDMHSGKMANDKYSKRALNLTSKVVTLWYRAPELLMGSNKYNSSIDMWSFGCIFAELLQLKALFPGENEIDQ
LGKIFFLLGTPNENNWPEAKHLPYTDFTKSNKKLNKNIKIEDDDCIDLLTSLKLNLSHERITAEALKHRYF

>PBANKA_071990 PbCRK-1

YKLNKI SEGTYGTVFRAQNKTKKI IALKQLKFNFSNIRHEGFAITSLREINILLQLDHENILSIKEVIVGKHLN
DIYLVMEYIEHELKMLLDNKSFGFTVSELKCLLQQLLNGVNYLHTNWMHRDLKPTNLLYSNKGILKICDFGMAR
KFSHVDNPNFTKNVVTWYRAPELLLGEKCYTNKIDMWSIGCIFAEMILKKPLFLGENEVDQMWKILNLLGLPDK
ETYPKFYEYSFISKNKDLFKKKKIKMNVNIRSHFPNIASQFSGLYLSDIGLDDLKLLHFNPDQRMSASDALKH
PYF

>PBANKA_091210 PbCK1

YALGKKLGSGSFGDIYVAKDIVTMEEFVAVKLESTRSKHPQLLYESKLYKILGGGIGVPKVYWYGIEGDFTIMVLD
LLGPSLEDLFTLCNRKFSKTVLMTADQMLNRIEYVHSKNF IHRDIKPDNFLIGRGGKVTLIHIIDFGLAKKYRD
SRSHTHIPYKEGKNTGTARYASINTHLGIEQSRDDIEALGYVLMYFLRGSPLWQGLKAI SKKDKYDKIMEKKI
STSVEVLCRNTSFEFVTYLNYCRSLRFEDRDPDYTYLRRLKDLFI

>PBANKA_093860 PbCK2

YEILKKVGRGKYSEVFNQYDTEYNRLCAIKVLKPKVKKKIKREIKILQNLHGGPNI IKLLDIVKDPVTKTPSLIF
EYINNIDFKTLYPKFTDKDIRYYIYQILKALDYCHSQGIMHRDVKPHNIMIDHENKQIRLIDWGLAEFYHPGQY
NVRVASRYKGPPELLIDLQLYDYSLDIWSLGCMLAGMIFKKEPFFCGHDNYDQLVKIAKVLGTEDLHAYLKKYNI
KLKPHYLNILGEYERKPWSHFLNQSNMDIAKDEVIDLIDKMLIYDHAKRIAPKEAMEHPYF

>PBANKA_101330 PbMAP-1

YDI IKKIGKAYGIVFKARCRKYKIVAVKKIFGAFQNSTDAQRTFREIMFLHQLNGHDNI IKLLDVMRAKNDQD
IYLVFEYMETDLHEVIRADILEEVHKKYI IYQLLRALKYMHSGLLHRDIKPSNILLNSECHLKICDFGLARSIS
TEVNENKIPVLTDYVATRWYRAPDILLGSTNYTEGVMWSLGCIMAELLGKPLFRGNSTMNQLEKIEI EIVGKPN
KKDIEDIKSPYAETI ISSFADTGKKKKFFSEIFHKASQDSIDLLEKLLQFNPTKRITAEMALKHKYV

>PBANKA_093370 PbMAP-2

YI IKHLIGRGSYGVYLAIDKNTKNAIKKVNRMFEDLIDCKRILREITILNRLKSDYIIRLYDLIIPDDLKLF
DELYIVLEIADSDLLKFKTPIFLTEEHIKTILYNLLGENFIHESGIIHRDLKPANCLLNQDCSVKVCDFGLAR
TINSEKDTNIVNDLEENEPEGPHNKNLKKQLTSHVVTRWYRAPELILLQENYTKSIDIWSTGCI FAELLNMLQSH
INDPTNRFPLFPGSSCFPLSPDRNSKKVHEKSNRDLNII FNIIIGTPTEDDLKNINKPEVIKIKLFPHRKPINL
KQKYPISDDGINLLESMLKFNPNKRITIDQALDHPYL

>PBANKA_141450

YKLIKLI GKGTFGKYYAIDLSTQEPVAIKRSPKWRNKVSREVDLLKMMNYSKNIVNTKSI FYTTTDDKGFRIQNI
VPKYMTYSLGKFI RLKKQEKRENNQICLGIKNLHEHVAHRDLKPDNIIINLDTPDINVEICDLGSAKKVEKSI I
SIPYICSRWYRAPELLCGSMYYTTDVLWLSLGCIFELINLCPLFPKGKFKDEYSEECQIVNLI EVLGSPNINF
YENIKDYTSTKNTSLIKELCELDIPPLSWDHILGNILEKEDPNERLKIDEVLDNSYF

>PBANKA_031030 PbPK7

YKIVKTIHEGKYSKIIMCDKDGELYALKKYEKVFLEKKREFQKKTCDNKVI IKT KYDDLKNEKLIITDIKNEYCL
SCKEIIITNNDEVYIVNKYMNESILKYDHCFFIFHPNESYFIPPIPKVMKNILKSLLYVHTKKNICHROVKPS
NILLDKNGI IKLNDFGDSEYMINKKIKGTRGTYKFMPEFFVNTKCYGKVDIWSLGCICYALFYKVLFPFNKS
GLINLQFQEI AKKEIKYHIDRNYFLLKVRKGATKSSHDSLSNDDINFLKIFLKKKPTERCTAEAELEHKWL

>PBANKA_136210 PbTKL3

IIILNKIGGGSYAQVFRGKYGKTVACKLFLYNTKDLSEESYCESYISTPRSTHQYIFPKIFKSMTSAESEIGDV
NHDIEDNINFEKYVNSIKSYTEVSEKNDANISEEVLTNLCTLQRNKKIKKMANLEIFRYFPTPIKYRNYEAKILY
SLQNCHEVILKLVGCSLRQGEESLILQYCSGGSLEKYIYDERKKINKQNKHLSRPQVVKIFQQIAKGMYEIHSN
NFFHRDIKLSNILLDENKNAFISDFGLSTYFSLNDSPSAYAIYGNIFYAAPEVLKGGFFKESDVWSFGVSLWEA
LTKKIAYDGLSSSETFCKISSGELHLPINNDIPKDLSDLLKSVLEYDFTKRPLFDVIARKLEHIWE

>PBANKA_080560

MNYTLISAGSDAIYKCDFIGKEAIAKKVIYRKYRHHKIDSKIRKLRISNEIKFTKKLASLNIDVPYLYFVDTKE
KSLYFEYVNGCTINNIKLSISQYQPNIPKFIGITLAKIHNGNVIHGDFTTSNLILRYSYINENEIFNNLNAPYE
LNDIKEIKLCVIDFGLSFLSASVEDKAVDLFVLLKAIKSFHSEFPKLEEDILLGYETQSNNFDLIRKKLETVKQR
GRKRPMV

>PBANKA_041040 PbGSK3

YKLGNIIGNGSFGVVEATCIDTSEKVAIKKVLQDPQYKRELMMKNLNLNLI IYLDKDYTYTEAIKKNKKNVFL
NVVMEYIPQTVHKYMKYYLRNNQFLPIFLVKLYSYQLCRALGYLHSLKLIHRDLKPDNLLIDPKTHTLKLCDGFS

AKSLISGQRSVSYICSRFYRAPELMLGSTNYTTHIDLWSLGCIIAEMVLGYPIFSGQSSVDQLVRIIQIILGTPTE
DQMKVMNPNYADVDFPNVKPKDLKKVFPKGTNNAINFVSOFLKYEPLKRLNAIEALADPFF

>PBANKA_070970 PbPK1

YKISHIIIGNVYGVVYKADCLENGNVVALKQTYQKSAKYFKEIEIMKKLKHPIVVKLKHAFYTLCPNGGIYVHMV
MEYGNTDLATSLYIITIKNSEHVNTYKNINNSKYIKNDKNDVVKLNDCTNFIASEENAKCVNNNNINSINESE
NKENLEKLQMNKCNENCMNVHDPNYNEMTKNLNSENKCNENKIDVNSYNNTEKEINSSNNNNVKSSENDCLNTYG
NIINNFNINMLQENINNICSCHNLSDYIKKCFNENQVKIYLYQLIRATLYLHSLCITHRDIKPQNILIFLNKPN
NNTDNSHENEKTQNKKCVVCIHNSVKFKCIMNKRNMNKSLENNNSNVNIKNSIVNNDCCNNNEYVVNNSNALLNED
IEKYHKNYTSKFNSINENNDIKKVNKENGYYNCCSTPISMLSEKKNNSNIKHAREKRSMSFSNTYTFKNSDNEHF
DYMDNSNKNDFKALKRSKTDLVIISLKMNTNTFNEKKEKTLPLSDVDKCCIDSCENVKEKNEITNFNDELND
IYNENNLDKIYMNSIVYKIKLCDFNTSTKLKENYKLSYVCSRYRAPELLFGSNYYSHAIDTWSIGCVMGELI
LGKPLFLGDCASDQVLEIKILGTPNDEDFLSFRSIVKYNVFPNIKPIITLKKLISNNSKESIDLLDKLLQFNPK
KRIKLC SALLHNYF

>PBANKA_144300 PbNEK-1

YEVIKKIGNRFGVEVFLVKHKRTQEFFCWKAISYRGLKEREKSQLVIEVNVNRELKHKNIIVRYIDRFLNKANQKL
YILMEFCDAGDLRNQIKCYKMFQKIEEHAIVDITRQLLHALAYCHNLKDGPNGERVLRDLKPNIFLSTGIRH
IGKITAQANLNKPIAKIGDFGLSKNIGIESMAHSCVGTPIYWSPELLLHETKSYDDKSDMWALGCIIEYELCSG
KTPFHKANNFSQLISELKKGPPELPIKGSKELNFLIKNLLNSAKERPSALQCLGYQII

>PBANKA_124070 PbNEK-2

YDVVKSIGRSGFIVTAVKNEQGEIFVVKQLDISCMNYKEKMNVINELKALIEVSTHPPFIVKYKEAFIEDGTYLV
AMDVCSKGDLLKYIKRAKEMKTIIPENKIKRWLLQIITAIFKIEHKKLIHRDLKCNIFLDENEKAKIGDFGLAK
LLEKTDQNTLTCGTVGYMAPEVCKNVPYSFSADIWSIGVILYELIALRHPFKSKNGNMLSIVQKVCEEQPDPLPS
IYSKDLRNL CYWMSKCEKRPTVYDIIGTEYF

>PBANKA_061670 PbNEK-4

YEKIRDIGKGNYGNTIILVRDKNDHYVMKIIINISQMSQKEKRQCLKEVELLSKLNHPFIVKYIESYIEGETLRIV
MKHCKGGDLYHYIQNKKKQNTPIKEKRILIWLTQILLTALKFLHSNHILHRDMKSLNILIDSDKRVRLCDFGISKV
LENTLDYANTLIGTPYYLSPCLCKDKKYSWPSDVWAIGCLIELATFRTPPFHSTKGIQQLCYNIRYAPIPDLPLNI
YSKELNNIYKSMILIREPNRYVTVQQLLVSDIV

>PBANKA_060060 PbNEK-3

YKFETVLEIMTSNSEIHLVKSLEDTNETFISKVYDLYGINENDLKNYMNELYIMKKLENCENIVKIVDFIKKNDL
SFIIEFCNQGDLYSDILRRKINNEHYSESEIFNINLQILNGLSSIHKNGI IHGDLKSTNIFIKDDKIKIGDFGIS
QKGSNKNLGTNLNLSYESIKLNKTNKLSDLFQVGCILYELVTLSSPFSANNINDMIRLFEDKNYKNEI IKNISSF
YSIQLVDIISKLLSLNALDRLQVISNYNIVRN

>PBANKA_010410 PbNEK-5

FDIAGFLGDGAHGSVFLACERRTNFICVLKCKISKSHLVKSTQEALLRKEIELQAHLKHPHIACMYTWFHTSSHVF
FVMEYCSNGDLFTYLNEHGPFSEKKVATMLFEI IWAIRTCHDKRIAHLDLKPENLVNHEEKCKLADFLSAHIG
SKHKKKGISHYRGTHDYWSPEQCARHQKKNFGEFDQKTDIWTGLILAFELKFGRPFFGSTNEEREDIIMNRIQ
DYHWSQLFSEKVKQDLIDKLSPEFKNFLNLCLDKNPKKRPTAEELIQHPFI

>PBANKA_083560 PbPKAcat

FNFIRTLGTGSFGRVILATYKNEDLPPVAIKRFEKSKI IKQKQVDHVF SERKILNYISHPFCVNLYGSFKDESYL
YLVLEFVIGGEFFTLRRNKRFPNDVGC FYAAQIVLIFEYLQSLNIVYRDLKPENLLLDKDGFIKMTDFGFAKVV
NTRYTLGTPPEYIAP EILLNAGHGKAVDWWTLGIF IYEILVGYPFYANEPLLIYQKILEGIIYFPKFLDNCK
HLMKKLLSHDLTKRYGNLKKGAQSVKEHPWF

>PBANKA_100820 PbPKG

LLTERIIGRGTFGIVKLVLHEPTKIRYALKCVSKSIIELNQONNIKLEREITAENDHPFIIIRLVRTFKDSKYFY
FLTELVTGGELYDAIRKLGLLSRSQAQFYLSII LAIEYLHERSIVYRDLKPENILLDKQGYVKLIDFGCAKKIH
GRSYTLVGTPHYMAPEVILGKGYGCTVDI WAFWGVCLYEFICGPLPFGNDQEDQLEIFRDILTGLTLFPDYVTDTD
SINLIKRLLCRLPQGRIGCSINGFKDIKENSFF

>PBANKA_146000 PbPKB

FNFLKVIKGSYGVKLVKHTQSNKLYAMKILKKNIIISQNFQEHKVEKNILKCVSHPFIVKMYYSFQTSKKLY
FILEYCPGGELFFHLSKLTFTENIARFYISEIIIALQYLHKLNI IYRDLKPENVLLDKNGHIRLTDGFLSKECI
SDNNSAKSLCGTPEYLSPEI IHQTGHGKSADWWSLGVMLYEMVTGQLPFGKSRDLLFENIKYKIKISNRLSPE
VVDLLKLLQKNPQKRLGSGITDAEEIKKHPFF

>PBANKA_082710

FTLKKKLGIGGFGEVWSVLSKSDIEENSSFFFFSIKKTSHFALKIMDINEFNLNESIIMREKAHINVINFCVFK
GYQLLNRQHEKERKESFCFLLELADTSLEKVFSDKNVAYNLNFVRLTLMELIANIMSYIHKQTPNHEFYIYRDLK
PDNLIKNNKILLTDFNLSRKIDADFEYLSQCCGTKGHLAPEQKSLVYDQKIDIWAFSIIIAKFLKHKNFNYFS
YDNYKIDLKHFEIQDKFLINLLVCVDESPFMRPFSSEIFRLL

>PBANKA_146050 PbGAK

IKEDNLI SEGAYSFVYLANDLNTNKIYTIKKTICQNEKLEMAKKEINILKSLPPHKNIVQYYGSTIINENNYKI
VIMLMEYCEGRNLLNIFEKNKDIKEFHIIKILKDIISGLNFLTHTQEIPIIHRDIKLENILCDKNNVYKICDFCS

HTVSNSFFPNDLKKNELNLLKYEIERDTTIYRPPPELIDLYSNGEISTKVDMMVGCVLVLLLFGFHFPQGTVST
KIIRRNDENVNDINPSNNSFLSILNGSFVIPHVTKYSKRIISILLMTLDKNPQIRISSSTLLLLIL
>PBANKA_113310
FSDAGNIGEGGFVVTMRFSLFPQYYAIKKISKDHIKKSQAAGQAYLEAKYHSHVNVKMYGCMQDDNYIY
HVLEYPKGSISYSISKNFKKRIIPEELAYKYFCNVVNGLYLQMGIFHRDIKMENVLVDHKDNAKLSDFGLSAM
ILGEKSHSSLCGLTVYFSPEIINGEGYDWRSDIWSLIGILLYEMLVGDVDFDGTQIVQSIYSCNLFNPNFINPL
AINLIKALVVDVNRKIKLSEIASDPWM
>PBANKA_040740
IVDKHPIGNRTGLVFKAIIRKENLQVALKVMADTILSLKIERQVLKEIIQSSSLKHINILDLIAYFEDKTRLF
LVLEIANGGSIRNKMMLKHDTFKEEQVALYVYQIADALSYLHNFNIIHRDLKPDNIIHYSDSDVYSDENVSKIY
KYGIKIADFGFSCQLKNRQKRSTFCGTVDYMPPEIINQIPYGCNADLWCLGIVIFELLVGFPPFTDNSQERIF
EQIKEFDHFPKTVSQMARELILRLCSRSEERISAEVVKSHPW
>PBANKA_090380
YIVLNNLKGKTYAEVWVKHKVTNEIFAALLQPNQFPKESFNRIVEMFTKEIINLSICQCPGVIKLHKVIGGKE
GWILIQDYANDGTLWKENLSNNMSEAFLYFIQLLQGMWYIQDMNIVHRDLKPTNIIHRYSNKKIIVADFGWSEHID
SCNLHPNEWPGTLEINPPEVLRNTGPMTEKIDNYALGMNMLFISGRFVCRQKGVESCKVAQIILKTVHNLRYSK
PPSRFRENKAWDLFVKLTSNPNERLSLQNVLDHPWV
>PBANKA_031420 PbCDPK1
YFKVRKLGSGAYGEVLLCKEKNGHSEKAIKVIKKSQFDKGRYSDDNKNIKPFHEEYNEISLLKSLDHPNIIKLF
DVFEDKKYFYLVTEFYEGGELFEQIINRHKFDECDANIMKQILSGICYLHKHNIVHRDIKPENILLENKNSLLN
IKIIVDFGLSFFSKDYKLRDLGTAYYIAPEVLKKKYNEKCDVWSCGVIMYILLCGYPPFGGQNDQDIKKEVEKG
KYYFDFNDWKNISDEAKELIKMLTYDYNKRCTAEALNSRWI
>PBANKA_040820 PbCDPK3
YNLSEPLGKGTGTYGCVYKATDKLLKIQRVAVKVVSKKLLKNIIPFRQEQIDIMKNLDHPNVIKLLETFEDEEQIYLI
MDLCTGGELFDKIIKKGFSFVEMYASFIMKQIFSVLNYLHIRNICHRDIKPENFLFYDKSTESLIKIIDFGLAAYF
NDIDYEMKTKAGTPYYVAPQVLTGCYDYKCDLWSAGVLFYIILCGYPPFYGESDHEILSMVKKGKYNFKGKEWNN
ISEEAKDLIKRCLTIDSGKRINASEALKHPWF
>PBANKA_061520 PbCDPK4
YKGIKILGKGSFGEVILSKDKHTGHEYAIKVISKHKVVRKTKDQSLLEVEILLKMLDHINIMKLYEFFEDNNYYY
LVSDVYSGGELFDEIISRKRFEVDAAARIKQVLSGITYMHKNNVHRDLKPENILLETKNKEDMIKIIDFGLS
THFEYSKMKDKIGTAYYIAPDVLHGTYDEKCDIWSGCVILYILLSGCPPFNGSNEYDILKKVETGKYTFDLPOF
KKISDKAKDLIKMLMYTSAVRISARDALEHEWI
>PBANKA_135150 PbCDPK5
YELDKYKLGKGSYGNVVKAINKKTGQAKAIKIDKKRINNIERLREILIMKQMDHPNIIKLYEVYEDNEKLYLV
LELCTGGELFDKIVKHGFSFSEYETYKIMKQIFALAYCHSKNIIHRDLKPENILYVDSDDSPIQIIDWGFASKC
MNNHNLKSVVGTPTYIAPAILKGYDKKCDIWSGVMYIMYILLCGYPPFNGKNNDDILKVKVKGFEVFDNSYWSKI
SLDAKELICECLNINYKERIDVHKIVNHKW
>PBANKA_092550 PbCDPK6
LSFKKILGCGAFGEVHLVEDNICLYKVVILKKKMKNIKVNNEINVLIYLDHPNIIKIFDVYESVNTYIVME
LCEGGELMNKIKKQIFSETYIKNIMFQILCAIAYMHSNIIAHKDLKPENILFKTDGYDTLKIIDFGLAELINKS
EGISKTAAGTVLYMAPEVFKKFTIKCDIWSAGVIMYFLFTKSLPFTGNTYEEVKQNI FNSEPDYQFLKLMKSKP
ALHLLKMLLEKDYSRPMAAVLLHHPWF
>PBANKA_101980 PbCDLK
YKFGKILGCGSFGVVRECTNKKTNEIYAVKIIKHKKHKKNSNFEEKMVKNEINYLSIMSHENIIKLDKDFEDKKN
FYIVLEKCEGGELFYKIVKNKCLLESESIQIVRQVCTLEYLHNSNIIHRDIKAENFLFKNKNTENIKLIDFGMA
KTVNCEYLTELCSPHYISPILIRKKYTMSSDIWALGVMVFFMLTGKYPFEGKNTQKIVDEILNKNINWKDNEFS
SLSVEAIDFLKLLERNERKRLTAFEALNHPWI
>PBANKA_131370
YKIINKIGDNFSKVFCCRGENKCKCAMKLMCCPLKKTSHYCNCFKRELFIMKTINNKHPYIVKILDYHEKIWKKY
YIVKLILEYCEGNLFYIKINGSCTHSEARVIIKLAQTIQYINSLKIMHRDIKPENILLRTKDNISVVLSDF
GLAKITPSNQSVVKSRSVCGSDFYLAPEIKNKEYGKIDIWSLGVLIFFIITGKVPFTGKNANELYNNILKANI
PELLSKEKSLNIQPLKNLLENILVHDPEKRFSCSDILNHRWI
>PBANKA_145340 PbPK2
YVLNKKIGKGSFNSVYIGTNIYGNRVVVVEVDKSKVKESNVYTEIEVLRKIMHKYIIKLIISAYEQEGYVYLVLE
YLKGGELFEYINNNNGPYSEQLAKKAMKRVLIALEALHNSGVVHRDLKMNMLLENVNDPSSLKIIDFGLASFLNS
PMSMRGCGSPGYVAPEILRYSSYGTKVDIFSLGVILYNICGYPPFRGNNVKEIFKKNMRCHISFNTKHWLTKSE
NVKEIILWMCSKNPDDRCTAIQALGHPWF
>PBANKA_092520 PbCDPK7
YEIHEQLGQKFSKVYRGINKQTNSEFAIKVINNRSVSIEKELLRSEISILRLLRHPNIVFLKEIINTKETLYI
SMELVKGGELYDFLLSETRLSEIHANKIISQLIKTVAYLHKCGIHRDIKPENILLTDKSKDAQIKLTDGGLSTL

CAPNELLKEPCGTLAYVAPEVITLQGYNHKVDAWSIGVILYLLLSGKLPFPINKNTEMNIQKTYVLSFRDNIWKT
ISSSAKDLISKLLELNADKRISASEALEHIWI

>PBANKA_040940

YKLLKVLQSAIYGTVYLSEIIEEDVNKKLINTKKAIKILSKHLIEMAKERIQEDPLSEYYYRDSMSGHSNIIICDS
IFDDAAAYIYVMVMPFAMHGDLFEVMKNRNKAFFSEESRYLFYQILLAIKFLHSKEMALRDISLENVLLFENETNGL
IYPVLNDPGQALHFVNKNNEVILEEYTKTFGKIFRPPEIHAKCKYDPTKVDVFCVGYILYFCLTKQELFRSSVE
KDIYWNMLVHKNYRELLTDKNGIHLSDAVDLIFHCLDPNFQTRYSINQVLSHTWF

>PBANKA_040110 PbSRPK

YRIEGLGWGHFSTVWIATDLKSKPLKFVAIKIQGSETYTESAKCEINYLKTVKINSFDSSWVEFKEQQRERLF
HYNMTKGVVVSFIDSEHKGPNGTHVCMVFEYMGPNLLSLIKHYDYKGIPINLVRKIATHVLIGLQYLHDVCKIIH
SDIKPENVVVSTLTNI PKPRDYTKSKLANNDTNIKNVTKNHCTSPSRPEQENNINTEKDFDKVEPQIDETKQG
ETEQQDTESNATAVKEQNEFDNVDWNKLTKNEKKLKRKKKKMFKKERLKMNEANNTEKNQQTNEAKINNLSHA
EDNRQFKKEDNENFRNIECIKTDDISLEQIQISTKMTFNNSMNPANPKVNINTNKNSTISGDCNNQNLNENSDMK
LCKDETKMDSKQIISNTVGGKLSFVNANMDNFSINENKLSDSLKEETKENTKCSIIEEDNEKNKIDNNNNLNKIKK
KKKKINEPPYVKHRLKPSNSDPSLLTTYNIHAIQETLTRKPYHYNNYFLNNPEKFGYDKSPQLLRRLPIDYLRN
DSSLEASNNSCNDNNTNDTYSEKSEIYVDKANKFPIYCGMFNHLIHPEAMKLNHESNKKKNIYSEVPNENQSL
GNNKNTNKVVYIKTEEGDYCIRPYDPTVYVYHEKSCYKICDLGNSLWIDESRYAEIQTRQYRAPEVILKSGFNETA
DIWSFACMVFEVLTGDFLFPQKSDIYDKNEEHLSFIEVLGNIPKSMIDSGYNSHKYFNKNTYKLNKIKNIKRY
GLYKILKYKYLPEKEINPLCSFLLPMLSIDPQTRPSAYTMLQHPWL

>PBANKA_093300 PbPRK4

SVVCELVGKGVFSNVLCYDMTNKIHVAIKVIRDNHMMHKAEEKEISILKLLNDYDKDNKKHIIIRLLRSVKYKNH
LCLIFEWMMGNLRIALKKYGNHGLNAAAVHCYTKQLFIALRHMRKCRIMHADLKPNDILINEKFNALKVCDLGS
ASDISENEITSYLVSRFYRAPEIILGFYRYSQIDVWSAAATVFELATGKILFPGKSNNHMIKLMMEYKGFSHKM
IKGGQFYSQHFNDNLDIYVDRDHYTKKEVVRISDLRPTKNITCDLLEHQYWLKGNSPKMQFLKKIKQLGDL
EKCLMLDPSKRYTPDQALQHPYL

>PBANKA_030850 PbTKL1

IWLLKLIIGRGGYNNVYKCLYINNIKKCRNYKMSNYRNFNINHSINNIALKICIDKKYSYDFFSELKILSILRHPN
VSLFLGGIRDPAIALEYIPYGSIFDILHKKTKIKILDIKMKCKDITSFMSFLHNKGILHCDLKSNNILLSESG
EIKICDFGLS IQNFDNPKPYLGI VGTYQWTAPEILRGEYTKKADIYSFGVILWELLHRTIPFNDLKHPLDIAIQ
VGYLNKQLIINNINNNKLLVLTSLCHKDKRKRKSFFFWSEYF

>PBANKA_112690 PbPK4

FQNIISLIGQGGFGSVYKVSHRLEPGSPTYAVKFIYLVKSSLDNVNSRRYFREIAANRDIYSKHVRYTWWCEEP
QFLPMDIIPKEIQNTLKKNKDPFKKVCNKNKNDNDYSSDCTVSSGENNKFDLKNYKQVITKKNSPKLFYSDNDT
PYNKRKNINQKNSFLNDKNLSDNIIYIENNNKKKKKKKKKKKIIYKEKKKGNIGINEDNKYSTFYEQNNPNPNS
TLQEQYDFPGYGLSENERDLIVFADNDESNKSGHKKNDNDRKSLNNQNGIYNTGGDI SKNGNVIHDDSNMLAC
QQSDKNSMTIKNTQGTSTINGTINRNTISDEGTGTQGTNNPNPKYSIDYHIDAIVKPKGESFTWVEKSPSNKYKDSL
DIINRNRKLIIEKNKKEKQGEKEKYKLMNGELEKKNANKIKYKKNVGPPEFSIVLLLQMEFCGFTLRRLD
RSSRSDKPLYFTYGDKNTHPLEFDLQKLIKGLKDIHSTCFIHRDLKPENIFVDLDTYILKIGDLGLVRFIEEK
KRENDLNNIDNFKDNIYTEINHNTITSQISLKGQMITPGYTAPEGGALCDEKADIYSAALILLELLCPRFNTIM
ERYKTLNDFRNYTVPDYVKIHLNPWYILMLQMSKPNPADRPSAADLYNKI

>PBANKA_130840 PbeIK1

FIFMYLIAAGGFSCVYKIKKKKSNKFYALKKIKFSANESNYEKKVLLNLREIECLRKLKNHPNIVSMNDFWLEVV
QTLSSKSKRERRGRKEQQREQMGDKRREKRQQRREKRKEQNTNTKKRVLITLSDHKKKKLHLSCPENALNISN
ITNNERNVLKKNWKNLILLKNFKKEKHNYFNHQLIELNKNYIMCLWKILNQMCVCKNEKKNIESLPEQLIKNF
KNFLFEKYILAIYDDCSYLNKNKNTFIFFNNLGNILHYLWWSYLGKNGKEKKNIDFKLLKYVSDNIKDNNTL
YNIILEFRHSLIELSRFSPNELGNVILNMRIPNGSCELSEYISNMAKINKLEIYRNKNTLEKFIKINCNMFDV
YKMWINFKNDIIEYEGKDVYKEHRKINLKRKIKKKDIWIKGKKEKHLKNTIGNKCIKKINIYKEPIHVFVYKSL
TYKRQKHHKLWRKHYNKKNWYCLNKHENSKKYILFSKICRLMKTQMNKFKREKFEKFKKAIATNIKVNYNDF
EQDISSFNIIQIYNKKNQQLINRIKEQYEQLSISLNPYKLYENENILRYNEHNYLFLGLKNDNEKENIYNAIYFL
NFYIWRREINEYAIISKKRQICQNSRNYQSKKKFYIKRHNQKTYFFENIFFYHYIMLFLDIEKYKKNFVSLFQ
YNLYRKLKISKRIVLMHR IETNVICIFLLKHFEYDFIRKGIHIVQDKSDRSNKGDEIGIHKMVKIWKSMIAIS
LIFGKKMYKKKNIFNFIEFLNINIINIFKKFEILYLIIFYFNYFEKSKQFDIEGIGDIYVWLSLINLFYDD
KGCIKILSKIFAKLNKLYVYWGKLYIIMNWTIVDTIFIRNVLSINREGNYWVIIVLKMINYFVNVAYTLT
RMDIFFIKVMIKFYTRIGSAAATNSVSKNSYNEIFNIFTLNFMYI IYNSYFENEKKNYDIYTKYAILFYCFI
IQAYYFDTLFNIRSLESNEIANLFPGYNSYKNILLFYERLGRVINKSNNTKICKYMWKRFINMWSNSIVIKEN
IISCLTTSRHIYFNILMNFMKIYCLDNILHIKKKKKKMNTPIVLTSKNDLKKWKDCELTKNPKSVKKGILIKKN
RNNKYYKKLKEKTHFIYNIKKVLFKLVNINIETILYEQNGQCYILVFGSVIKKKNQIKVKDTKIVRDINIIR
DYRIYFYNLEYFYKNNNAHISDNINLIYARKWPYNNKNAVKQFCPYFDKIKDGNRKDIVSLYGNKILVKQNFSKI
GNKIKNKNLCKKMRQTQKSIYNSNYWREKKNKLLNGNVNIKKYKSEKIKKKELENFFDNIVYSSENDDFKI
IFENATNSNACSTVDLAPNELNTRNNINKKLFKFKHKNKSKQKNYKNHSHKKIFFKSVNNANRFVTVNVEP
NPIMSNHQIADSNDIYNNFSIQKKYENHKNCGNIYNTKDCDENDSSYICFLINEHEGQVLSHRHKEYLNMLG

MERGNILYRDNACKLKDDFSLHDQCDNSMIKACGTNELIKESTKIKRENMDKINKMNEVNQHISLETLYKCSF
KKIDKNLIQNKKKIIIRKICQINKTFYFKYKINDKKRIYFDSVLCKSERHKTYKKRNENIKVILLKTLKGSNE
VYLTYLTYLTIYSDNINDPFENSRRKKINSNEIFYQKTFDMYCIEDGEVEYEEQKRVNKNKKKKYINEMIKMDTIR
TDFEDNFTNSYNKKCNILKMASNINNNKNSGKKERDIKRQFLITNKKKHENNIKIFYNLFKLEESNVNSNPQTNP
YYETVIHDNEDNIFYCYLYYIQQQVYRYCNCIDIDEYTSNCIDKNVKNWEWYGFIKENENYDKIKTEINSNSFYNC
REKHNICNSYNSVYQLEFRKLGNASKEKNFEKKKIKIEFRKSFNNFKLPSSLCLILKWDNFFKPHFIIRCDNFL
HTYNIYFDFILLMNLFHKGEGSNLYRFNSNKSIIYNPYLHQIYMVTKYFISNVHKINNKLPIHLENDILEIYS
YNRFLTIPNKCSFKNCGNDNNYDQRSKKHFTKCGILNTEKVKPSKRRIGWDGQRQRKRKDIINTLNEENQNM
FCKNKEKKEENYKIDTNISQFSEKNPVSNDNEKNKQNFIKNKYKFNLYIRMEYCKDTIENYINRRTRINIKR
NIEINMIIMGLNYIHNNMIMHRDLKPSNIFISNNDIVKIGDFGLASYDYLDHDKINTTKEEEIQKDLINKNCD
KIFFCNKKLFNSYNSVFPLENGQISDVHNTKGDYNESSISKSKKFAIQKNRNLRSCKRIFQWWSITIGELNLS
KNRRRLTKFKSGSNTIHIRKSTLDENIIVRHANKCHNLFSQNRHIDRNRMKKCNIIKNHIIKSNKSEKMNISM
NVFLRCTKTRRYFTDEDKSVETRKKCSKTSEEENGNICDTYKKNNDIGEKMKNKIAAQKKKKKENKHPIGRRS
TNSSISSAIVVKNAYCRLEIEKYFLSKSFQNCRSNKKKKYINIKTIKNKFCASANKNFGAKWMRIYRGLHDD
IQEKADQTTQMGCCNKTVASDFSSNLKNKESINHTLIGITKLYSAPEQLEGNKYTKSVDIFSLGLIIDLFI
KTETNMERTQILCNARERILPDLLIKHPNVAASLCKMMLSLDYKSRPSTSAQLYKNI

>PBANKA_020580 PbeIK2

FSEESVLGCGGFGYVMKVNKKFNIAVKKITLSSYCPNKRGNDELNVKNYNNHIKKNKSKHNDIEPMISGSFSS
GNNIMNENSLIMEEVIMIAKLQHENIVRYDADWVENNIDYFLKEIENNYKYVVKKNKGNKKNIIYIDEISNI
RNYNKNKNENIKINEKYLILMEYCPGKTLREADICGFYKNEKLIWELIKQILKGIYYIHDMMKMRDIPKSN
IFLQINDDILSAKIGDFLTKIDNTQINPSAGTVNYSPEQLNGEHFDQKADIFSLGVVFFEMFHEPSTSMER
SIVLSNLLKCIYSPESIRSDNKIFQFLLSLEIDPQNRLSAYSLLHENF

>PBANKA_141360 PbpK9

YIVEKRIGSGGFGIVFQGIHIQTKQKVALKFIPKSNFLDVTDVHRVFIIEIQTLRGLIHKNIKMYDVNHFQNYVC
LIMEYAVNSDLKYYILKNNGYLSEKETYFLFLQIVKGVYCHSKHIVHRDLKLENILLDENMTCKIADFGLSDFV
NVDQNIKTEAGTKLYIAPEIIFNQTTNYSVFKLDIWSLGIILFIMTQGYPPFIDVGKDIKYFEQSTLKYSDISD
DLKDLISLMLNVDPNKRPIIVEILNHRWF

>PBANKA_131800 PbkIN

YIIKNIKIGKTFGKVCGLMHTYTYEIVAIIKILNKKLLRIISYDKILREIKIHKKIDHNIICRFYEVHENKNIY
MILEYLGNGDLLTYICKNSINENIARIAKILYQLISAIYELHKNINIVHRDLKPENILLDHNNIKLIDFGLSTIYS
KNNFLQTSKSPFYTPPEILLGKKYNPELTDVWSLGIILFLLNKKLPFNHNDINKLQIQIKGLMQFEPHVSIN
AKNLIQNMLNVNCKNRYNLNQIKNHIWF

>PBANKA_130920 PblAMMER

YKVMRKMGGDTFGRVLLCQHIVNKKYAVKVVNRVVKYTKSAKIEADILKKIQSNDIKNNNIVRYHGKFMYDHM
CLIFEPGLPSLYEIIITKNDYNGFHIEDIKLYCIEILKALHYLRKLLKLTHTDLKPENILLDDPHFEKKIVTVKRV
DGKKIQIYRSKSKGIKIDFGCATFKTDYHGSIIINTRQYRAPEVILNLGWDVSSDMWSFGCILAELYTGNNLFT
HEHLEHLALMENIEPIPKMLYEATKTNGYKIDKNDLKLAWPENASSIDSIKHVKSLPLYKIIKHDLFCDFL
YTILRIDPTLRASPVDLLKHEFL

>PBANKA_090110

IRMNLIIRGGFAEVWEVFDNINLEMYAAKIHKIEPSMTNEIKNKIIQRAENEINIIHCHRHFIVKLEFFFFV
GSATNLLVGMELCDVDLDKYIKYHGPINELLALSWIKQILLGLLYMKNLPTGKVHHCCLKPANLLIKDGIKISD
FGLAKLILPDTYQYNGGTYQPECLPKPRNLLITDKIDIWSLGCILYEMIFCERPFQFNYLEKCSKELLVN
KMKRGLSYPKINQHISKITLNYIEYLLNFDHECRPSIEEALSYPIF

>PBANKA_112270 PbtLK5

IKIQSYLSKGGFGVYKIGILLKKNVYEEICDQNSKYTSDFHNGLDDGNSVEKEYNNIEEKEEICDQDVKIKRKK
MLINKQKENNDKIIAIIQDDNCNENVKQKNEREKEIHNKDFENPNSEQNNFRRLYAEVMKVNKNNSNHCNMNT
KKEYNMRINLKEDNKSVEINILKKKKIINEYNNNGNDKNGVNYSEQANKDINEIFGEQINEDNRSINSNGENKFK
LLNFPFFFGNMEKKKKNYDIEEELKNLTFNGDNMYQNEHVKKNEQYSHECHKGNVLPQQCLHSEEIKELKKS
MLNFIYGNKCCDDIVIEKNCFINEAEKINKLQSNKDLNKKYNDIEISYLLVEIYHNNIVYNNNLSFLCIKSKN
IITFSLNKDYLYIFDSQNIHYYSKSIKIVFIDDYKILNKYKHFTVFNILLNDKVLKNSSILKREINKHKNGL
NKLSIIPFSLNMLNLVNALIFGFLKFIINLRKKYHTIKKDCYCSLCKNPKNTNFMNIIASFSDRGSNPNDYDQN
FDDLESILLQNKINILDELICINSNNNDENIFSYPKNKNTTFRNSNLNHPPEESINDDNNAHIIDKEKTNF
RGNDNSIYHIVNTSDSGTKNNISNVNINIKNNLNKPNIAQNDEVQLNGNKGKIINSSNQGLGDSSTLLNSNTDEC
KTTIILNLSKNKNVSKDYINEKEYNNYVSKIKNNEKNKEEEDDEGNTSNMKNHDKKTYIQEKLKINCENSEN
KNREGNDFETPDNEEREVNEEEENGNKDGVEYMQIPVAIKIHDLKDSKNLKNFLREIEIYKNLQRSNICKFYGIC
IKHNKMLLLEYYAKGNLNFNFKNKNKIHKKQRLWAIQMCSIVHELHSHNPPINGDIKSNILINNMDLVMC
DFGARFKNSKLYSNFGSYRYMAPETFSCSTSEVTEKIDISLACCIVEIFCSKYPYNFNFKSNTKIRHELIVNKRT
PHIPSFLPNSIKKCLQKCFNPEERPSAYEMYKAL

>PBANKA_142160

NKKDRTLDNNGLYKKNIIQLVVKIKHKELYSKINECNKITEVEIHKKLLKHCNII LNMILSAEDEKYICVFLEYSSI
GDLYSFVGFNLIKKEVEKIVSQILFALYYLHIKGIHCDLKLLENLLLFNFDEESFLFESNLLSDIKMCHISQFK
KLNAKKLVHSIKENIKNNPNIKVFYKIVKLCDFGLSVKCEFDFKFPFNGIRGSYGFIAPELFFQECFNNKIDMWA
LGIISFLLGGYKPFYPCSRFEKVI FHERYWHNISPEAKNF IQSLEIDPFKRMNVI EAMDHPW

>PBANKA_130520

YIILEKINTGVSQVHLALDKKQVIFIVFSKAIDKSTVQGEGLFQKLDKDEIIVSCRMNHPVVKTIINILETRDK
IIQIMEYCDGGDLISYVRNVLYLEELSAQYFFRKILDGLKYMHSNKIAHRDLKPENIFLCKKVLNQEKTIRGK
LPSCFEYELKIGDFGACCFNDASNKLHYDIVGTLSYAAPEVLGCDKNNGYDSEKADIWSLGIILYAMLFGLLPFD
NEEKDIKEAHNEIVNKKIIFPKNRINRCSNNVKNLLIGMLNINPINRSLDQVINDPWV

>PBANKA_080220

LIKDNTINFLYKCYDIKNNKNVVIKCVNKEKQLS IMSYNTYTNIIYKIIKKIDNENIIKIYDVLENQSHFFIIMEL
CEGTDLVVDYVSNENISFEKIKDII FQLLSGISALHDNFI IHRDIKLDNLMFKDKNFELVIIDFDMSIYICAKDQ
IYPSKSDCIYTSETKNTIYDNKFDENYMNMCNSDQLFSKKIGISGNFNTEFSEKSKNNICEENNAATSNFTFDY
ANQGKHENPNKMHDSMNKNSCLYKNEPNMNTLDSNNTYTNKVTENDRKCNSLNSWHFSNSYDIKKNKTHN
KKSTSLDYNYIRKIEENNFLSTNTRDIQKPFINNEKIIYNDLIIGTKEYMSPHCLKGMYSTKTDIYVGVTFIL
IFKSFPYLFEEISIDKWEDEIINKNKEIIVIPFSFLFHNVNCTYFIKLMDLHLINNNIYFCNDSCLLDDNLKEIAK
IRGIKFDKIKINQKNIYLVEILRKALSLDVCDQYSNVSQIMESSLF

>PBANKA_082690

SLKYTVIEEGSFGVVYKGYKNMHVAVKVPVEKMKVQDPYGLTKRSINWKILSKCEHPNIIKLHGGIIHSYFDI
LWVTKLINGSDLHTIKNNMNKEEKVLSVDISLKMCRQLAAVINFLHTPIKNKKNVI IHRDIKPENLII DSDWNIH
LCDFGDESEETEDGNVSNVSGATWIYAPPELLTCHPLKQSSDYNFLDYAQLSYKWDIWSMGCVFQEMMNLSPFQ
YIISFDESQIYEKLVDFTKKLPCCIHISKIDNSPFADI IKLCLNYDPNLRPTAKEIVDLL

>PBANKA_031140

YYIIGLIYYGYSQVYKICINIKDKKTYAMKVV LKERENYEMVKNELNIDKFMKYMFLKKNPHKNIPIYDIFSD
NNYNFIIMEFCKGSTLLDYFMSLVPGLSLHIYEIKKIMKNIFLALDFLHSRGLIHRDIKLENIMFTKKKMRNFNYK
QCDNFDLNNTDFFLFEKGTCTNRGIVRNSVLKCESKIDLNNKQDNDLFLKKEEIDTIHKVDVDCWNSNGN
IEYEIDSDTSSSDNIEWNNIWCDDRYQDESSYNCELEEFNFENSSNNISEIRKKPRSFDAYNNLFGNLDAYNCD
DSSNIENNSLDNVMGRNLVNI LDNSYNFKLGKIYKNGSTIQIINKNNFQKKNII IKKNSSLTAIKSKRSEEKYL
NSEKVKYRDTENRNNCRKNNDKKSFFKRRKYFPCNLVDNLCIDMMDMEDI SNMNPKNKKNQNIICGTASYMS
PESFDGILSASNDI WACGVILYALMDGRFPYEIYNTMPNYLKKKILRYTKPNFDPFIWQESPDLLDLCLRLDPN
PLTRIQNAKEALIHCCF

>PBANKA_092700 PbtKL2

FSEENKIAKGGNGIVYKGI LKNCINVAIKVLKKNENNGFENELIIMSRYRHNNI LSLGAMNTNYFYLIYEYVS
LGDRLTLFFNHYYFYNSQNKENIDFNNLSNMKLNYYNNIPKNKYITSLNNYTNLNYSKTSNLSNQTPFLFSFST
RINILVQIINVLCYLHTSSPIVYHRDLKSANILIDEKFNALGDFGLSFIYINNNNIFNLTTGGTGPYADPYIST
HEINEQTEIYSFGALILEMLVSKSPAIVHGKNYSYCYTRNEKCPIHCHRDKNDNDNVFDYLIINHINTNDYKSIY
SILDYSVNFDFLVEKLTKLSFLCLNPNIKNRPSKLVNLIL

>PBANKA_092640

FELYMHIGSGNFSDFVMVKLKNDP SKIYSLKIFSKKEKVMRMKNVNSVLTEKKVMIKLNTPGHLNVIKLIS TFKDK
ENVYLLY EYADYELWEFLKTRSIGVSENITFNII LQMVHALAYIHDKDV IHRDVKCNFLINKDGTIKLIDFGTS
KDLDHIPMENNKNECTIKDELSKFSLKKNNNINKNLKNESEENTSMLRDESSNNYVLDNDSNEELD KISNNDIS
KNCRLEKPEQYNESFKYDDKNTIKCNDNLDNLDLDTIHLININKRNYRKKTFDNVYGTANFMPPEALINKCSGKV
RDFWSLGCTIYQLVCTIIPFDGSTEFIYNKIKKREINYPPIIPLDLVDLIEKLI VINPECRLGFKNGCEDILQH
PYF

>PBANKA_094200

AVLLNVIDKQNNTEKIIKIINKKKTLTAFGETWENMIEYI LSINQHKNLMKLYDIYDDGKNFYLIMEKLRGKELF
TFLVYKVKVENVCKYIILMQILQAVNYLHYHNI IHRDIKPENLMFRNQKRKDKNYEYNYELVLIDYDTCQFIKPO
TRFNLFPTSIYNCKHVNL TNIKTIQNSKDINNAFLNKSKHIKLVGTYGYIAPEI IKGLNYSISSDIWSIGIILYI
LITGVTPLP MCFMINYRNTKDILIKKEKGINFNLLSFNNYPLAKDLCQQFLQFDPKKRIKNTIIASYHPWL

>PBANKA_130690

YKIIKVLSKTTTFSTTLKCLNLDYKNSIKNGEDSSNLLTKEKVSELESVCKKSKILSDNPNMSFTQNLKDLNKNYP
FDISSIKKNSSEYIRNSTNNKNGIKKKYKYVCLKVMKKGKNYFDQGLFELTILNMLSEESINQTSMGNNKSN
DITGSNII TNKNI IQLYDYFYLGHLIIVTEYME SLYNYFIKKGKGLTGLQLQILTKNLLQGLAYIHSKLIHC
DLKPENIMINIKKKKKKKYPQHPTGNNNDETSNVQISHDSNEKNKYFSNDNDFDKNRENIFSSDQFSKIKI ID
NSSIFEFDKLEMYVQTRPYRSPEVLLQHNYSKIDMWSLGCILFEFLT KILFDHKNIYRFIYSIASYIGSFPHY
MIITCKIPYIFTKHGYMILKIIYYSNDDDPKEDPIDEIEDEPVI FNKNDFCLNKKCHQNDLLKIKNQPKFV
HKQTNHKVYDICYSSNTPLENNFQIDDLLFINFLSLLQIDPCKRLNSKEALDHPWL

>PBANKA_082960

YNGKIMTFYKYGGNSLMQWDKETRFQYKVKVYTVNEKKKKYIIFDKKMAENKKEYEYDKIWNPRINNDNNDN
ISNKRTRKREKTYVYPEYMAEILRQLLACFYLYENQIYHSDIKPSNIVAKNIKKKNLNIIFCKKEKKWYIKKY

GKIKKNKILIKIIDFEYSQKCYGEEANVGGTTSLFKPLENFRKKKINIFSKMVWIIIGITIFILSTGTHPFSSINN
DMHVLFLIQKNKFDIKNSFSKYSYFSHSFKDLLQKMLKVEYTORISFFDLFFHFPV

>PBANKA_122880 PbTKL6

LEIMEFISEGSFGAIYKAMWNNQIIALKKFSSMTLEGMRSIAREINAYRSISHKYIVKYGVCSDFIGIILE
YFSKKGKIFDTHLKGFEFNLTVELRLRMCTQLAEVMNYLHEDKKLVRDLKTSNILFDDEYNIKVCDGFKTMKLSDN
GTVILEDNNGSIGYMAPECFIEGNTITEKSDIWGLSCCFIEIFFNQVPFQNIKEKEDIVVEILVNKKKPNIPKWF
NPEFTEIIKRSFSTNPSKRPSCKEYLNLL

>PBANKA_122500 PbFIKK

FICIPITLGFSSNRVQQMYKAIIPSKDGNKNDVKLFIKKIPIYIWKQFNLMTFEDGGEYVTDGENFVMEASL
AFLSEYHPRIAPKLHKILYEVDNTNLDGSSNNIPPEMFSNLTVFNNVLEERLKNNINGNIVLVSEFFSEDILDF
IDRRQKNFNMKISNNEKSYILYQCLKLLIRLHDAGLSHLDLTPENILISDNYEMRLCDLSKSTPIYTYNLRHIKD
VNRLYLFESCEPTIAKGAYMPPECWKIYWKYDTMKIKNPLRDLKSITDQEKRKQFYFDVANADKFMGLGVFFFWIW
TNGNLWKCSDPLQDEDFYFVKCDMNFDKFELTRKWPSELKSIKGLLHAETRKKLNLDKMDMHPWW

>PBANKA_121710

MRILYSSKEKYTKYFHRGYLIKSDTNVNDTTLKLYPCVFLKSGEKRLVKKIDKNIFKGEILNALLKLRTYTYKNS
SLPKYLLKTYNIYEDDKFSYVIFENCAGGFFFDILKDNVINENILAEWFYQILTALNFLEKTNIYHGNLNGYCI
HFKDKTRKEIRVSLLSINNNDNIDEKGDLYGLYIRSPQEIKKLYHDKNNSWYVGMMLLYFILHGSYPFINNNVL
VNYNIVQNNIPFTALKLDHKNYTNLMYDFLKSALFKDYDMRPSVEGLLNHPWI

>PBANKA_094010

RVFRGRYMGKDVAIKVLVGNIKNFTKFHKVLYKLYILRHTNIALIMGVSIYFPVFIIEYIKNLCLFSYLHCVK
YKHIYVSKLLKYYQKFINQNFQQNNTMSSDRKYISNDNEKINFDNRNILRNKLEIKCKNNAKNI TEKNL
KDEQIYSSSTSISLSDTSSNMNNTKLNINFNKNRYINKIHSFRNKNNILCGNYYYLFRKKKNNISISHEHKN
SDRTIFTNESQNLKNIKISQKKINKKLNFKAKIKINRPYAFPPLQEDFNFYLEKKKKKKILFSYLKTHSYFKSK
KCDSRKNKLSHQIMKIIMDITLACSYLEKQKVRWINLKPTNILLDGSNAKISDFGIKEIEQCLDINIDYSYIV
FPNNVIFKFNKHFKNKIKKIKIVNKGSEDMHVFSSKNHIYKYNTREINVSSNTHNSSVFFWTSPEILKKGQSPS
LYSDVYAYGIIWELMTNSVFPNYRFSHLLASVGYAKESLPPFQNIIPFIKNIKSCINRNKYKRPTFDRILIEI

>PBANKA_082680

YKNVHKYMKQISRRICFIEHFIMSRLRHPNIVEYIGNIITWKKNKNKEIRENFGLVFEYIKGRLYDILYNKK
KGNKNEKENEKYYTHKNSKDNLYNGYKQWKLNNKFILKVLKICVTLHYLHEKNIYHGINSKNLFI TKNGNVKI
CNFKNAHIQNYDYKTDIQNRSECSEKNNIYYNLANNFIPFPYITYINYTKQDTKYIDEITSTPFFLYTNIFN
LKLMDHRNVYTAPEVLRGEEYTNKSDIYSFGIMYELIFETLPPFNKYNNNFNFFLSILISTCYFQNYIYFDIN
QLINKINNNIMFHIFINITILIKSCLNPDPSNRPTSKYLYYYF

>PBANKA_134590

YNKNRVGKTKHNENKKGYSYLYNIKVIECDETI VGGHEFIFSEDNSNNIKINKLIKEGKHINKSIYEYKEYCKD
MDNYEENKEPYFEEKNNLNSKHRKGYKGNKISINSKNNNDYEVTYETLGVVPYSDIIVLNKKELDKQNKQ
VAGFVTPFMLNGNIKKMIENINPNKYKFNDEMIFKSLCNIKVMNYLEEKNIHVGNIKPNNLFI SNNGFNILIG
NFVPKIKLSNYYFYVINKTRTRMKYISPELLLYIKRKTNQLKKNINKNKIVS IENYHLIKNDIFCLGLSFYYIVS
MNEDILNYIDDRYVQYKVDNIRDYIQKPELFFLLKNLLIYDHMYRPNWSDLSNLI

>PBANKA_062150

KSSEFLLGVQKYSLCEKGLNEKCGKDKIKNGEYNAKNYVQNEYNMIAASKFEKIKKLNHPNICRYININRKN
DYIFSEYYSLSLYDILNGENKNI AHFKCLRKIFGIKSQENNTKPSKMCVNMNEKLDGQTKIINHIVLKKIIEYI
LKGVEYLHASKNIHFLNITPYNILITSGKIKLHNYCISYLFDNYEYNSKKKNEFFSKKFLDHIMSMENMIKE
SKLSSVRNIQYPKYFLDLSENCEERILNSPLASLNDKIERKKKKKKYIFIENYFKYYNFSEDMLYFGPFFIFL
NLFENQKIKISYDLYKHIDIFSVGIVIIQIINGLIDFQFIIDIFFSNFFCSKVSEVINSEQTEFTKINNQCSDS
FEQNKKTDRYIRKYKINKIYESFKVVKNILQQRMSEKNMNKSEENYDKQKQLKFFVSSLLKDDVINRIENIFI