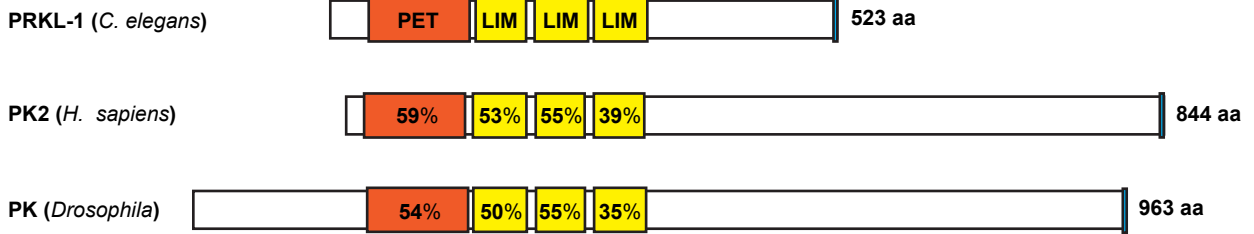


A



B

| | | |
|--------|---|-----|
| CePRKL | -----MSEIRRRRLEASEQFAPQLISSRRAQGGLSPASRIRIRIADAHRRHSISDDDSGCCALDEYAWVPSGLKPNMVHAYFACLPENKVPFIGSAGEKWRQORSRYQ | 101 |
| Dm PK | PGCSANPKYSNAQLPPPHHHHQLSPALSTPSPPSLLHHPAGGTSSASAHAPFLGGPHMDMOROSHSDDDSGCALEEYTWVPPGLRPDQVRLYFSQIPDDKVPYVNSPGEQYRVROLLHO | 240 |
| Dr PK2 | -----MPLEMEKTVTKLMYDFQRNSTSDDDSGCALEEYAWVPPGLKPEQVHQYSSLPEDKVPYVNSPGEKYRIKQLLHO | 75 |
| Mm PK2 | TGLGRIERGQPCNACGQCPCGFALHKWRKICLHCKCPCQEHMVTVMPEMEKTIKSLMDFQRNSTSDDDSGCALEEYAWVPPGLKPEQVHQYSSCLPEEKVPYVNSAGEKLRIRKQLLHO | 135 |
| Hs PK2 | -----MVTVMPEMEKTIKSLMDFQRNSTSDDDSGCALEEYAWVPPGLKPEQVHQYSSCLPEEKVPYVNSAGEKLRIRKQLLHO | 79 |
| CePRKL | LPEQDSVRYCEDLNAAEADTLRMFERTRKTECLGSGVYQAFEDTK---CEKPKRLEEGETISVMAARTGK--RYHSCFCRCQTCVDVLLVDLIYFAHDNQIYCGRHHABQVKKRCAACD | 216 |
| Dm PK | LPPHDNEVRYCHSLTDEERKELRFLSTQRKRDALGRGNVRQLMSARF---CDGDDLLSTGDIADFATRLGNASWHPACFACSVCRELLVDLIYFHRDGRMYCGRHHAETLKRCSACD | 357 |
| Dr PK2 | LPPHDNEVRFENSLDDEEKRELKLFENQRKRENLRGNVRPFVMTGAICEQGGQINGGDIADFASRAGHGVCWHPQCFVCSMCDLLVDLIYFYQDGKIFCGRHHAERLKRCSACD | 195 |
| Mm PK2 | LPPHDNEVRYCNSLDEEKRELKLFENQRKRENLRGNVRPFVMTGAICEQGGQIKGGDIADFASRAGHGVCWHPQCFVCTVCNELLVLDLIYFYQDGKIYCGRHHABCLKPRCAACD | 255 |
| Hs PK2 | LPPHDNEVRYCNSLDEEKRELKLFENQRKRENLRGNVRPFVMTGAICEQGGQINGGDIADFASRAGHGVCWHPQCFVCTVCNELLVLDLIYFYQDGKIYCGRHHABCLKPRCAACD | 199 |
| CePRKL | EVIFFGDECLEAEGRSWHFHFQCAQCNVLDADQYMQRANKPVCLKCFHSSSSTFSCTTCLRSFSSDTPHMSQGLHWHASAEFCFCCVCCKNLLGVKYSRVGESLFCGYQPCGGDEEEL | 336 |
| Dm PK | EIILADECTEAEGRWMMHMFACHECDKLGGRYIMREGKPYCLHCFDAMFAEY--CDYQGEAIVDQGGMSHDGQHWHATECFSCNTCRCLLGRAFLPRRGAIFCSIACSKGEPTTP | 476 |
| Dr PK2 | EIILADECTEAEGRWMMHMFACHECDKLGGRYIMREGKPYCCCFESLYAEY--CDSQGEHIGIDQGGMTYDGOHWHATECFSCARCCKKSLLRPFLPKQGGIIFCSRACSVGDEQNG | 314 |
| Mm PK2 | EIIFADECTEAEGRWMMHMFACHECDKLGGRYIMKEGRPYCCCFESLYAEY--CDTCAOHIGIDQGGMTYDGOHWHATECFCCAHCCKKSLLRPFLPKQGGIIFCSRACSVGDEPNG | 374 |
| Hs PK2 | EIIFADECTEAEGRWMMHMFACHECDKLGGRYIMKEGRPYCCCFESLYAEY--CDTCAOHIGIDQGGMTYDGOHWHATECFCCAHCCKKSLLRPFLPKQGGIIFCSRACSVGDEPNG | 318 |
| CePRKL | LD--EDRLGSPHRKVTQKSTKVVRIIPASPRVAPRPHVVIQONLTTMTTIQKPSVVIQNRKPPQRAE----- | 402 |
| Dm PK | SDSSGTGMYTTPPTQVRVPHQAPLPAIPSSHASSPSPMSPOQQOQHATFNQAMYQMSQOQMEAAAGLVDSQKSYAASDSDAG-----VVKDLEHGCHMGGD | 578 |
| Dr PK2 | SDSSDAFQARSREARRSSSKS--NKSSITGGSGGDGHSQKASAMRFSADVPLSLQMDLLSLSSQTPSLNRESFVWKTQAEEMFYEGRNE--LSTNPLHLLSQCNIRTSYSSN--LSPGH | 430 |
| Mm PK2 | SDSSDAFQARAKESRRSAKIGKNGKTEEAMLNQHSQLOVSSNRLSADVPLSLQMDLLSLSSQTPSLNRD--PIWRSREPFHYGNKMEQNSQSPLOLLSQCNIRTSYSPGGQAGA | 493 |
| Hs PK2 | SDSSDAFQARAKESRRSAKIGKNGKTEEAMLNQHSQLOVSSNRLSADVPLSLQMDLLSLSSQTPSLNRD--PIWRSREPFHYGNKMEQNTQSPLOLLSQCNIRTSYSPGGQAGA | 437 |
| CePRKL | -----PPPESENIYETVLPCCSSN | 420 |
| Dm PK | LTFDFSGGRASSTSONLSPNSPGDFQPHLPPKPMELQRDGVYVNFNEMSSNLDAAWSAKPTNSYHLQRQLLENPHTASMPPELAGKLVAPPAHQHLSQLHAVSSHQFQOHEYADILHPPPP | 698 |
| Dr PK2 | LSDPRPKFASPKRPPVSALKGKSLNENWFQQGPEDYYPALRTOASFNEVPHNSFMDKR--SVSLHVQFQREKED--VGPQMSRSRNPISALGFSEQLTPLEQTPRGSMESLALSATG | 546 |
| Mm PK2 | QPDMMWAKHFNPKRSSSMALKHG--SFIQECREDDYYPGRMSQESYSMSQSFNETRGSIPVPKYEEEBEIEGGISTQCCRPRPLSSLYKYTEMDTPTTEQTPRGSMESLALSATG | 611 |
| Hs PK2 | QPEMWWKHFNSPKRSSLAMTCHAG--SFIKCECREDYYPGRMSQESYSMSQSFNETRGSIQVPKYEEEBEIEGGISTQCCRTRHPISSLYKYTEMDTPTTEQTPRGSMESLALSATG | 554 |
| CePRKL | NSPNFDKYSHELTP-----TSNHHNYSKTPNNLLTGYPEMDG----- | 459 |
| Dm PK | PPGEIPELPTPNLSVASITALPPELMGSPTHSAGDRSLNTPMSQASASHAPHPVSVILSGASSSSPMSGEPAKKKGVRFEGIPDTLPRSRYSYG-----NGAGTSGGGERERDRDK | 808 |
| Dr PK2 | TSADGGSKRQEHLSRFSMPDLSDKSGMNVSEK--SNMGTLNSSVQEHSSSELRSLSNSAQPLLELAPVQVRFVQVPREPSGINALPPGFAYQEDRVSLLVSNANNARLPMSERTRRRSI | 665 |
| Mm PK2 | LSAEGGAKRQEHLSRFSMPDLSDKSGMNVSEKLSNMGTLNSSVQFRSAESVRSLSAQYQEMEGNLHQLSNPLGYRDLQSHGRMHQSFDFDGIASSKLPQGEVGHVQPMSETRRRRTT | 731 |
| Hs PK2 | LSADGGAKRQEHLSRFSMPDLSDKSGMNVSEKLSNMGTLNSSVQFRSAESVRSLSAQYQEMEGNLHQLSNPIGYRDLQSHGRMHQSFDFDGMAGSKLPQGEVGHVQPMSETRRRRTT | 674 |
| CePRKL | -----YSTSSSSDSD | 470 |
| Dm PK | DKEGGGRHGHSRRRRRRKSSSS-----SSHRRSGSHRSHSTTRADTYAPAQLSSSYQGPPSVLQAANLVHESPSRQORERERERESEESVDCSTCSSSSSSS | 913 |
| Dr PK2 | DHEPRRRHHHRRRRRRSRSDNALNLVAER--RPALK--RSQLHAREDYDQFLPGRSRTYSSGRLRQPPFRPCPTTSDLTLQNALHRHQGPYSWDQYDYDDWCSTCSSSSSESD | 782 |
| Mm PK2 | SRDD-NRRFRPHRRRRRRSRSDNALHLASEREVIARLKERPLRAREDYDQFMQRQSFQESLGGQ--SRDLVYQCPRTVSDLALQNAFGER-----WGPYFTEYDWCSTCSSSSSESDN | 843 |
| Hs PK2 | SRDD-NRRFRPHRRRRRRSRSDNALHLASEREVIRLKERPLRAREDYDQFMQRQSFQESMGHG--SRDLVYQCPRTVSDLALQNAFGER-----WGPYFTEYDWCSTCSSSSSESDN | 786 |
| CePRKL | EQLYISN-IMAAASLRVPAKSSSRKSKK---NEPMMMSGGVMAKSKKSRCTVS | 523 |
| Dm PK | EDYMMYQLPQRHYGGVRSYVFN-----DALAYDRKRKPSLGGDKKNCIIS | 963 |
| Dr PK2 | EGYFLGEPITPPIQLRHMTSEELLRKYNSSGLGASGQFSGRQLHMRKRRKSKNCIIS | 840 |
| Mm PK2 | EGYFLGEPITPPIQLRHMTSEELLRKYNSSGLGASGQFSGRQLHMRKRRKSKNCIIS | 901 |
| Hs PK2 | EGYFLGEPITPPIQLRHMTSEELLRKYNSSGLGASGQFSGRQLHMRKRRKSKNCIIS | 844 |