

Table S3 The identified amino acid sequences of KRP in tomato, tobacco, *Arabidopsis*, capsicum and eggplant.

>SIKRP1

MRRKYKCKSKGIIGEVVIMEVAEVAVKMTREREVLEVVDTRKRKKRDGDLEMSPTVARV
RRNSVISESPASELSSQGNTVLCEPAVSSNFDNVASAGFGDNESSNTKGSSKFLDDEDSV
EIATSYSELRESREIILSSSKFKVEFQSTPKPQHAKSCRRLTEATMPSEAEVDVFFAAEKD
LHKHFAEKYNFDFAKEEPLGRYEWVRQ

>SIKRP2

MGKYLRKSGHVMESSSLGVRTRSTTLALQRLQSSSSSTPPPSLPSASDSCYLQLRSRRLHK
PPTPIPCPNSHPHSASGVSVDEISFPDNNLHFQHTHRSTRETPCSLVREVDEMVPNGSATR
RTTELNTTQRERRNFILRNIPSAHEIEEFFTFAEQQQQRLFMEKYNFDVVNDVPLSGRYEWIR
VNH

>SIKRP3

MGKYMRRKTKATGEVVAVLDVSPLGVRTRAKTLALKRLQKSSGGDGDDVGGGCYL
QLRSRRLERKPLVGFEKGRRKHPLKESKRQNRSRLRVREMKGQSWNNGSGEGEEKKEQVQ
ENQKEIDNNNGSFEVENLLEFDGRERTTRESTPCNLIRDPDSIPTPGSSTRANNASEGNGREP
TSAQRIIPTAHEMNDFFAGTEEKQQKQFIEKYNFDPVNDKPLPGRYKWVKVDR

>SIKRP4

MGKYIRKTRKTEDVSPLGVLTRAKALALNGGDGGSYLELRSSRLVKPFTVLEGRRQKNG
VPKNPNLVNPNNPQQIPNVCVNSEEKGKVKEMENQKEKEKSCLGPEDSFGENLLEFEGRK
RTTRESTPCSLIRDSDNIQTPGSSTRRTNANEANGRVPNSIQPTIPTDLEMEEFFTRAKEKEQQ
RKFIEKYNFDPVNEKPLPGRYEWVKVNH

>SIKRP5

MDVLLMMRKRKICDNYTPVVSSDKYEPDGSSMCCSSNSKSRDLDEKCGEVAEKEEKL
IEEEYESEKMPPVEEFDELESNEIEEFGKEMASVEEFDELELKEIEEFGEELDEMTSVEEF
DELEMNEMPSLEEVELDEMLFPLEEPEPPLIPTTEELEEFFTRHEQRISTRRLQNYNFDFE
KEEPLEGRFEWVPIRKMKF

>SIKRP6

MGEFLKKCEKINGGMVTELNGGLRIRDNDVEEVTSNCMSYSRKRRKFGSVDVDF
SENSASPATSVTHIPTNSQCSCYESGEVMMKSILKSLDLKAEGFTDNSASFNGGFSEN
FKPIDQPNPPSEHCGDSEDMESSTTKSSSSASAPRKQLSASKVPPEAEIEFFSAAEKRE
QKRFAEKYNYDIVKDAPLEGRYQWVSLKP RRINE

>OIT30955

MRRRYNKS SKKGIGEMTVMEVGKVEEVAVKMTASAEREVLEVADHAKKRKMC GDLE
MSPTVACVRSHSEDILVAQESLVTPTSELSSPKENAALSSNFDDALASCCASNGSSKSLDLE
EETVEIATSKSKERASLCSSIKAELRQMEPTRAHHPKSRRRLTAEKMPSETDLEEFFAAAE
KDILKRFTKKYNFDVKEDPLEGHYEWVRSTVKP

>OIT30650

MGKYMRSKTTGEVALLEVSHTQSSPLGVRTRAKTLALQRLQSNSTGNGGGDGDDGGGG
GGSYLNQLRSRRLEKPNKEGKRQKYPLKDPNLPNVKNNQSSKTSSTRLRQGHWSNSVSV
EERLGDEKKEEINLQETQNEIKDNSCGE GGVEASFGENLLEFEGRERTTRESTPCSLIRDAD
NIQTPGSSTRPTNATEDNSRVSNSTRRHIPTAREMNDFFGGPEEQQQRQFIEKYNFDPVND
KPLPGRYEWEKVDR

>OIT28532

MGRYMRKCKGIGEVTIMDVSDVDLDVPTMTTKRKLSSDGDVKLISPALLRCRSQSGV
GDAQAGSLVSPASSVNLNDASNLDQDLASCCSRNGSTEVTKSNAKSLDLNENNVAESAES
KEEKLSSERQRTPEKMPSEKEIEDFFAVRKKTIFKRFREKYNFDFEKEEPLEGRYEWVRIAS
>OIT19452

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>OIT07235

MGDFLRKCEKIREMKVMEIGHGGSRTREDVEVISSSLSSSKRRKFDAASNVDFSENSASPA
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NPPTEHCGDSEEMESLTTKKSSSAVSAHRKPPSAAKVPSEVEIEFFSVAEKREQKRFA
EKNYDYIAKDVPLKGRYQWVILKP

>OIT08281

MGKYMRAKAKITGDVAVMEVSQATPLGVRTRARTLALQRLHSSSTPPPPSSASASDSCYLQ
LRSRRLEKPPTPLSDPRTKNLLTEENPKSDSRFLVSGSGVSITQKDGLDVNEISFGENT
LDFEPRDRSTRETPCSLVREADATVNPGSATRRTNLNTTAQRTRDSILRNIPSAQEMEEFFT
FAEQQQQRLFMEKYNFDVVNDLPLPGRYEWIRVDY

>OIS96940

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GRKRTTRESTPCSLIRDSDNMQTPGSSTRRINATSVPNLLRTNIPTAHEMDEFFTSAAEQQQ
RRRFIEKYNFDPLNEKPLPGRYEWVKVDC

>AtKRP1

MVRKYRKAKGIVEAGVSSTYMQLRSRRIVYVRSEKSSSVVGNDNGVSSCSGSNEYKK
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CCSGRKTMEETVTAEEEKAJLMTEMPESEIEDFFVEAEKQLKEFKKKYNFDFEKEKP
LEGRYEWVKLE

>AtKRP2

MAAVRRRERDVVEENGVTTTVKRRKMEEVDLVESRIILSPCVQATNRGGIVARNSAGA
SETSVVIVRRRDSPVEEQCQIEEDSSVCCSTSEEKSRRIEFVDLEENNNGDDRETETSWI
YDDLNKSEESMNMDSSSVAVEDVESRRRLRKLHETVKEAELEDFFQVAEKDLRNKLLEC
SMKYNFDFEKDEPLGGGRYEWVKLNP

>AtKRP3

MGKYMKKSKITGDISVMEVKATAPSPGVRTRAAKTLALKRLNSSAADSALPDNDSCYLQ
LRSRRLEKPSSLIEPKQPPRVHRSGIKESGSRVDSVNSVPVAQSSNEDECDFNFVSVQVS
CGENSLGFESRHRFVVFFFFLFFMFPLLVCSTRETPCNFVEDMEIMVTPGSSTRSMCRATK
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>AtKRP4

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NFFDLEEEHTQSFNRTTRETPCSLIRRPEIMTPGSSTKLNICVSESNQREDSLRSRSHRRP
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>AtKRP5

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DCNFGDKGFDLESENRSMISDSKSIQSEIEDFFASAEQQQQRFFIQKYNFDIVSDNPLPGRY
EWVKVMP

>AtKRP6

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GGEESDQSSSISSGCFTSESKEIAKNSSSGVDLEDHQIETETSTFITSNFRKETSPVSEGL
GETTTEMESSSATKRKQPGVRKPTAAEIEDLFSELESQDDKKQFIEKYNFDIVNDEPLEG
RYKWDR

>AtKRP7

MSETKPKRDSEYEGSNIKRMRLDDDDVLRSPTRTLSSSSSLAYSVSDSGFCVALSEE
EDDHLSSSISSGCSSETNEIATRLPFSDEAHEISETEISTLLTNFRKQGISSENLGETAEM
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RYQWVSLKP

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FFTFAEQQQQRLFMDKYNFDVANDPLSGRYEWIRVNH

>SMEL_001g118310

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NGAFSSENFKPIDQLNPPSEHCGDSEDMESSTTKSYSDSAHRKQPPASKVPPEAEIEE
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>SMEL_002g167200

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RPAPSIPQSFSFSSPFIEDKASFRSRTTVSRKFVKELHKLESTPRPQHAKSCRRLIEAKMPS
EAELTDFFAAAEKDLHKHFAEKYNDFAKEEPLLEGRYKWVRQ

>SMEL_003g173930

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KEALEGRYKWVQIHEN

>SMEL_005g241220

MGKYIRKGKKAGEVVAVLDVSSFGVLTRAKTLALQKSTGGGGGGGGSGDGGCYL
QLRSRRLKPLVGFEKKRKHPLKESNRSLRVREMKGQSWNSGDGEGEEEKKEETQNEA
NNNGSCEGENLLEGRNTRESTPCNLIRDADNIQTSSSIRPNNAEANGGGPHSPQLVIPTE
QELSRVFRTNEKQQKEFMEKYNFDVVNDKPLPGRYKWVKIDD

>SMEL_009g334280

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QQRRFIEKYNFDVPNDKPLPGRFEWVKVDP

>PHT72728.1

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CSVVREADAMVNPGSATRLADSSATAQITRNSILSNIPSAHEIEEFFTFAEQQQQRLFMEKY
NFDVANDLPLSGQYEWIRVNH

>PHT78525.1

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DNVSREDEHVIPENIENGDQANYGELSQSDDSASNNADGGECPYDSSSSDGVRFNSRQRS
MSISPYPKQESIPQTSMQRPTSMSQSNNRPRFYSNEVLFLDHFQEAPDVFMKDHENNFVPT
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EWYNFDPVNEKPLRGCYEWVKIDP

>PHT85361.1

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>XP_047259206.1

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DMNDFFAGPEEKQQREFIEKYNFDPVNEKPLPGRYEWVKIDP

>PHT91594.1

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LKVELHKLEATPQQQLAKCRCRRSNTEAKMPSEAEELDEFFVAAEKDLHKQFAEKYNNLS
FFTHLSLFSIFYSARKTVFTIHEFACGNRYNFDFAKEEPLGRYKWVRQ

>XP_016539606.1

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PATSVTSVDIPANSQFSSCYESGEVIMMKKNILKSSDLKAEEFETDNSASFNGGFSENFKQI
DQQNLTEHTGDSEEMESSSTTKKSSSSGSDDPRKLPSAAKFPEAEIEFFAEAEKREQK
RFAEKYNYDIVKDAPLEGARYQWVILKP