

Supplementary file 5. Amino acid sequences of putative PAC domains with only five Cys residues, more than six Cys residues, or no Gly upstream Cys1.

In the protein name, “.nd” means that the type of protein could not be determined because the amino acid sequence of the protein is not complete; “.1”, “.2”, “.3” or “.4” refers to the type of protein (see Figure 2).

Originally, the accession numbers originating from the onekp database were of the following type: #onekp:JVSZ_scaffold_2013751 Equisetum_hymale. They have been simplified for more convenience, as follows: >JVSZ_2013751_Equisetum_hymale.

Five Cys residues

>LOC_Os07g40100.1

GEVY**C**DT**C**RAGFVTNVTTAIQAARVRLE**C**RHYMSASGSVERSAEGTTDATGHYRMELVEV
DNRGAELV**C**AVALLSSPVTE**C**HEMEVGRDRAPVTLVQDVGLATMVRRANPLGFLQTMLAR
YADTDTRYVDTKMWHL

>Aco007813.2

GSVT**C**LD**C**TPHHNLSGVVAVK**C**AHMKLLPAVTNNEGYPFIVSIPATTPKSSPTLTPQ**C**FAR
LLGGREQLYAFERSMAASIVAVGRGSNGYDLASPLAYLSK**C**

Seven Cys residues

>JVSZ_2013751_Equisetum_hymale.2 (incomplete sequence)

GSVY**C**DQ**C**LQGHRTLWSTPLRGASVALE**C**MNSTAAGQKKAETDLLGMYAIRLEGSLDMQG
CIARLVSSPKGSSG**C**NLAGVASRPLKLTWKLFVSYTSDAL**C**

>IZGN_2005470_Dacrydium_balansae.2

GSVF**C**DK**C**SQHSLHLPPTYFIPDATVAVE**C**SLNRKARASIRVEGRTDQSGEFRIELPSSIYNT
YSG**C**SVEVINSPDGL**C**NVPSVNKLAFTMNGKHDSVY**C**AGILSYRPQVLPS**C**

>IZGN_2005471_Dacrydium_balansae.2

GSVF**C**DT**C**SHHSLHSPTTYFITDATVAVE**C**SLNRKARASIRVEGRTDQSGEFRIELPSSIYN
TYSG**C**SVEVINSPDGL**C**NVPSVNKLAFTMNGKHDSVY**C**AGILSYRPQVLPS**C**

>Spipo4G0058500.2

GTVF**C**DI**C**ANNSFSKHSYFLRGAKVRVE**C**SFKAAAAAREEITISVERTTDRFGVYRVDVPPV
DDFQ**C**REGREIESF**C**RANLVRSSSSM**C**NVPGLSISSEHVG**C**

>Spipo1G0064500.2

GTVF**C**DQ**C**LDGQRDLFDYPLYGARVAVV**C**TGGGDGQMALYGEATTNWFGVY**C**VQFDGG
PDLSS**C**SAQVVSQTQW**C**GGAAGPPGGLHLLFGLFGTAMYTADALLALPSKPAS**C**

>P.equestris_XP_020598742.1

GRVF**C**DT**C**RAGFETPATTYIEGAKVKVE**C**KAGDKI**C**SYDGVTDNSGTFNILVEDEHEHEI**C**E
AMLVSSPDTE**C**KTEVPGREKSRIVLSHNNGISSDTRFANALGFQKDTPLAF**C**

>GSMUA_Achr1T21560.1

GRVF**C**DT**C**RAGFETPVSTYTKGAKVRIE**C**RSKATGAKT**C**NFEGTTDHTGTYNILVADEHEH
EI**C**ESMLVSSPESR**C**KTPLQGRERARVFLSHNNGIASDTRYANSLGFQTDTPLSV**C**

>GSMUA_Achr11T13000.1

GRVF**C**DT**C**RAGFETPASTYIRGAKVSVE**C**RSRITGAKT**C**SFDGTTDHTGTYNILIADHDDH
EI**C**ESVLVSSPESG**C**KTVLRGRERARVFLSRNNGIASDTRFANSLGFTKDTPLS**C**

>GSMUA_AchrUnT14160.1

GRVF**C**DT**C**RAGFETPVSTYIQGATVRVE**C**RSEFTGAKT**C**SFEGTTDHTGTYNILVEGEHDD
HEI**C**ESLLVSSPESG**C**KTALQGRERAPVFLSHNNGIASDTRFANSLGFLKDTSLPV**C**

>GSMUA_Achr8T21210.1

GMVY**C**QK**C**KYVGSWNLDGARPLPSAKVSII**C**KDHHKRVIFYDSAETDRNGYFYKLLDGAHL
RSATFDPVTA**C**TARLLASPDAS**C**NRLTNVNYGIQGAKLRDESKTNSGEH**C**ETELYAAGPLAF
KPVH**C**

>Oropetium_21061A.1

GRVW**C**DT**C**RAGFETPASTYIAGAKVRVD**C**KSSTTGEKT**C**SFEGHTDRTGTYNILVADEHEH
EL**C**ESTLVSSPDT**C**AKAVAGRERAPVFLTNNNGVASNVRLMANALGFKKDVALPE**C**

>Oropetium_08744A.1

GRVY**C**DT**C**RAGFETNVTEYMKGAKVRLE**C**RHFGTGAVERAVDGVTDETGTYRIELEGNHV
EDI**C**EVTLVQSPRAD**C**AEVEQHRDRARVVLTTDGGI**C**DALRLANPLGYLKDAPLPV**C**

>Oropetium_24235A.2

GSVY**C**DA**C**SNNTFSKHSFFLKGAKVLIQ**C**NFKVNSTASEELSLAAERTTDQNGVYKLDVPTV
AGFA**C**REGHELRS**C**RATLVRSSSA**C**CNVPGLTRGSTQHVALRSRATNA**C**

>Oropetium_26560A.2

GTVF**C**DA**C**SSSSFSNHSYFLPGVKVRLD**C**CMVKVNSNSREEIKITAEKVTNSYGAYRLDIPAI
GFE**C**AATAAEAL**C**CRAAVLDNPSEL**C**CNVPVTTTTVRHVSFPTPNAASG**C**

>Bradi2g03930.1

GLIL**C**QP**C**AHRNSQ**C**LDAATPIPNAQVTVT**C**RDPKNRVKTSRVAKADAQGYFLAEIGVADGK
QEFYEGDPSKA**C**FVRLSSPDKG**C**NDLTNVRYGIEGAELRDEGKRWWADGVENVVYAAGP
LAFRPR**C**

>Bradi2g31950.1

GRVY**C**DT**C**RAGFETNASHSIPGAVVQME**C**RHFETNELHHKAEATTTDAQGWWYKMEVGEDH
QEEI**C**EVALLRSPEKD**C**AEIEKSRDR**C**RVPLTRNNGIKQSGVRYANPIAFFRKEPLAN**C**

>Bradi3g00370.2

GMVF**C**DQ**C**KDGARGLFDYPLYGARVAIQ**C**GGGETPLTVRE**C**CNTNWFGGFSVRMEGSPDM
NR**C**TARLIQGT**C**PH**C**PGGGSTAAPQQRDLTAFRMLGLALYTVQPLL**C**SHPDHPMD**C**

>Bradi2g48680.3

GVIY**C**KP**C**RSRRYSRDMASPLQGATAQLV**C**YGREVVNVTGTVTDERGYFLVMFYDLGNF
HPRN**C**KL_YLGTSPTTL**C**CNPVYPPN**C**KWIGLSLVRETRTTPPEGLQGIY**C**CPTSVLFYGP**C**TAGQ
K**C**

>LOC_Os04g32680.1

GRVY**C**DT**C**RAGFETNVTEYIKGAKVRLE**C**KHFGTDKVERAIDGVTDETGTYKIELKDSHEED
I**C**EVVLVHSPLAN**C**SEIEAERDRARVLLTRNVGI**C**CNLRLANPLGYLKDIPL**C**

>LOC_Os10g13914.1

GQVA**C**EL**C**LCPGSDLLTFELPGAKVEVA**C**ETEGPNTQANSVFTATDEFGNFTFHLPSRLHA
TPSLEN**C**AVVKVLQ**C**LPDS**C**AGLRHRPAASYRIRPSSSLSSSADGFRAYTAGVIRLQHGGTP
SGE**C**

>LOC_Os10g39890.1

GSVL**C**QD**C**TKSWNAYAYNAKPIPGSMVGIT**C**LDKETGRTVYHGTDKTDDKGMFNIEVPYTV
GSAHLHPSA**C**LVRLASSGDHG**C**AVFTNFNGGKTGERP**C**CRPSHVYPGRVTYSAGPFYFTLS
Q**C**

>LOC_Os10g22590.1

GRVW**C**DT**C**LAGFETPASTYIAGAKVKVE**C**RSKSTGAKT**C**SFEGQTDHTGTYNIPVNDEHEH
EL**C**ESVLVSSPDAK**C**GKIVAGRERAPVFLTNNNGVTSNVRLANALGFQKDAPLA**C**

>LOC_Os09g32988.2

GSVY**C**DA**C**SNNTFSKHSFFLKGARVLIQ**C**SFKVNSTMAEELSLEAERTTDQNGVYKLDVPA
AGGFD**C**REGHDLRS**C**RATLVRSSSA**C**CNVPGLRGSTQHIALRSRATNA**C**

>LOC_Os02g01190.2

GMVF**C**DQ**C**KDGARGLFDYPLYGARVAIE**C**GGGESPVTVRE**C**CNTNWFGGFSVRMEGTPEM
NR**C**TARVVQATGH**C**GAAIPTAPRDLTAFRMLGLALYTVPPLLSQPLRPMDF**C**

>LOC_Os01g52660.3

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>Sobic_009G082900.1

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>Sobic_003G059000.3

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>Zm00008a036634.1

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DTPSDRC

>Zm00008a025512.1

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>Aco000299.1

GRVVCDVCDADAAIGPEDHVLEDCLMLASENIFEYSPLRTGAEVAVLCITKSGEVLNYQAFTD
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>Aco003633.2

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>Aco006667.2

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>Aqcoe6G061600.1

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>Aqcoe5G346000.2

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>Aqcoe1G261600.3

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>Aqcoe3G160500.1

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>Lsat_1_v5_gn_5_42161.1

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>Lsat_1_v5_gn_6_28201.1

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GKQVKPESCFTRLVSSPDV CNIPTDFAGGKSGVKLGPRTMVYRDTIKHVLGPFYTTPMC

>Potri.006G119100.1

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GKQLKEKKCSVRLVSSPDPS CNILTDFAAGKSGVKLKRPTSVYRDTVKYMLTPFYFTSPMC

>Eucgr.K02418.1

GRVL**C**QD**C**TKGYDEWVKGGSPIKGAKVSLT**C**MDQRYRVIFYGSDDTDGTGQFNMIVDKYIN
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>Eucgr.D00613.3
GVVY**C**KS**C**KYSGVETLLGATPVLRS**C**RFDDEVSSFFAGAVVKLE**C**NNTKYRPTVQTAKTDKN
GYFFLKAPKTITTYAFHK**C**MASLASSPVPS**C**QKPSALHGGTVGAVLRPEKPVMIDKLPTYTF
TVGPFAFEPQ**C**
>AYMT_2115347_Eucalyptus_leucoxydon.nd
GMVY**C**DI**C**FNNTFSRHSYFLPGAQEVKID**C**KFEAVSPKTTEQISFSVKRTTNRYGVYKLEIPAV
DGIE**C**AKDSAIVSF**C**ASLMGISSDS**C**NPVPGYRTTTDQIAFKSKQANL**C**
>Gorai.010G248800.1
GTVL**C**EA**C**HQRRRRDPQPELRSWPISGALVSVK**C**ETP**C**KTSGTTPATTDEYGDFMIDLPS
HLHGVAIDLQKI**C**TVKVIGIPKESM**C**RPAFVKKHEHLRLSSVGNIGRTYTAGRIRFQDIMSKPS
KS**C**

Eight Cys residues

>Zosma169g00070.2
GTVF**C**DI**C**SKNTFTKHSYFLPGTKVEVQ**C**NFKVINSTSKEEISITVDRKTDRIYGIYRVDVPPV
DGFE**C**RQGREIQSF**C**RARLIQSSSSL**C**NPVGLSTSVEHLAMKFSQSNL**C**IYNLNALNYKPSK
KNLAL**C**
>P.equestris_XP_020589188.2
GTVF**C**DA**C**SENTFSKHSYFLQGATVQIS**C**KFSTETTSCEEISINTKRTTDKFGIYKLEIPPVDG
FQ**C**SEGRALQSF**C**KASLVQSPSPL**C**NIPSLSSSKQHAFKAGGFNS**C**IYDLNALSYPKAQRD
SSF**C**
>GSMUA_Achr9T29260.2
GTVF**C**DA**C**ANNNFQHSYFLEGVKVRVQ**C**VLRVNETSAGEMRVAVDRTTDRFGVYKLDIP
PVDGFE**C**REGRGVDSF**C**ASLAESPSSL**C**DVPGLSSSTEHVAVRGGEGL**C**LYNLNALNY
RPSKKDADL**C**
>Bradi3g32620.1
GTVL**C**QD**C**TKNWNAYAYNAKPIPGSGVAVT**C**LEKKGKVAFYGKDETNEGVFSVEVPYEP
GSGAG**C**RLLDPSE**C**LVRLVASEDKG**C**SVLTNFNGGRSGQRPFPSKV**C**PTEVVYNVGPYYA
TLPQ**C**
>Aco011770.1
GKVL**C**QD**C**SKGWNQWAHGATPIIGSKVGVT**C**MGPQARVLLHKSDA**C**DRRGEFDVVVDKY
VNGVEVNPEE**C**TVRLVSSG**C**QNC**C**TVMTNFNGGKDGVRSLRPSTVYPGRIAYKVGPFYFTT
PK**C**
>Lsat_1_v5_gn_0_3380.1
GVVY**C**DA**C**SNNSFSTHSYFLPGAQEVRI**C**KFKAASPRTEQISFSVNRTTNKHGVYKLEIPS
VDGIN**C**AKEEVQVLNT**C**ASLIRSTSPA**C**NPVAFITTSNQFSVKSKQANL**C**IYSLYALSFRPS
KKDLA**C**
>Lsat_1_v5_gn_4_186081.1
GMVY**C**DV**C**SNNSFNNNHSYFLSGAEVRID**C**KFNAVSPRTAEQISVSVNKTNNRYGVYRLDI
PSVDGIY**C**ASESAVMNT**C**ASLIASSSPQ**C**NPVPGFITTSDEFSLKSQHANL**C**IYSMFALSFRP
FKKDLT**C**
>Lsat_1_v5_gn_4_2141.2
GSVF**C**DV**C**YSNLFTRYSYFLPGADVHVQ**C**KFQGNAPSTKEQISFSVNRTTNRYGVYRLDIP
SVEGVD**C**VEGPAIQSL**C**EA**C**TLIKSSVPG**C**NPVPGVSTTTKEITVSKSTNV**C**VYSVSALSYP
QINSTL**C**
>GSVIVT01033047001.1
GIVY**C**DI**C**SNNTFSRNSYFLPGVEVNIE**C**KFQAISPRTEQISFSVTRTTDKFGVYKLEIPSVE
GIE**C**ASDSAIESS**C**QASLMWSSSSS**C**NPVPGHKTTTDEIAIKSKQANV**C**IYSLNALNYPSE
RDTAL**C**

>AT3G26960.1

GFVYCDVCSKNSFSKHSYFMSGVEVRIVCRFKAASSTTTETITFSANRTTNEFGLYKVAISSL
DCADVDSLASSCQASLIGRKNFSDSSCNIPGYRTTTDQVLFKSQQSNSCVYGFNALNFRPF
KRDALC

Nine Cys residues

>GSMUA_Achr9T01210.1

GTVFCDAANNVFSEHSYFLAGVRVRVQCMRLRVTNSTSREEMSITVDRTTDKFGVYKLDIP
PVEGFECREGVVMDSCCRASLLGSPSSLCDVPGLNSSTGHVAVRGGEKRCLYNLNALNY
RPSKKDANLC

No Gly upstream Cys1

>AmTr_v1.0_019.68.1

DQISCCLDKTKHQAHGVLVIKCDSEKPILAVTDRTGSFKAIEITTSKTSAPLEDTCYASLLGPR
NKLCSFKNNQASKFVKSAKYHKDPSSSYALFTPLSFSSSDC

>Gorai.002G165500.1.

TLLDCYLCPKSFKGLQNVFYSSARARERERELLYPGACGGGGWGWISQGIASYGTGHGTRE
TCALHTARLSCDTLVDFWSALGEETRESLLRMKEEDFIERLIYRC