

A szálkaperje (*Brachypodium distachyon*) A ,B és D típusú ciklinjeinek teljes hosszúságú aminosav-szekvenciái alapján készült szekvencia-illesztés
A szekvenciák 50-75% százalékában előforduló konszenzus aminosavak szürke, a szekvenciák több mint 75%-ában előforduló fekete háttérrel kerültek kiemelésre.

cycB2-2 (Bradi1g29830) 1 -----MEN-----RVHAMSSENTMEGVKFASETAANTNRRLRDIKNIIGNPHQLAVSKRG-----LLEKPAADPKNQRFAGHRVTRKFAATMATQPSA-PPAPVGS-----RQ-----KRNADTAFHTDMECT-----K--IS---DDSP-L
cycB2-3 (Bradi5g18397) 1 MER-----AREN-----RRPVVG-----KP-VPSVRDMGNRRRLDRDINNHHVGAQYPCAIKPK-----MLEKKRDE-----QKPAVPSRRVTRKFAASLNPGGE-----PVAPGVDP-----HN-----EPIPDGTTDDIESV-----D-----D-----
cycB1-3 (Bradi2g10890) 1 MASRR-----QAPARDVLAQEH-----KAGGDAARLARRTKSMVAQPAARTRRALVDVGNLINGRAALAA-----DKCGKAI-----R-----QHKENNRV-----K-----PELIVISSDSEKEKK-----IPGKRA--AS-----RRAP-I
cycB1-1 (Bradi2g52760) 1 MATRN-----QNVAAAPQLQON-----RAIGGGVHVLGKQVAMAGRPDKNRRALGDIGNVNVRAAEKGP-----QLQEQPAHRVTRNFGAQLLKDQAQAKKNPGARP-AVRLTRKEAPA-KFVPPPP-----EHVIEISSDSEVSTRKQSKGVS SVRK--GS-----RKEV-I
cycB1-5 (Bradi2g21330) 1 MATRH-----QNAAAAPQPAN-----RGAAVPAAKKAAAGRPEARNRRLGDIGNLVHPQALDC-----LKEGINRPI TRSFQAQLLKNQAANGAVANKVAIAPARQAAPKA-KKAPAK-----AKITTI P-----DQAKKPSAEVASSAQK--AS-----RKKV-V
cycA1-1 (Bradi2g31632) 1 -----MSTLV-AG-----RRSSVSKAEINIGARAAKLTAQDKKRVALGNLTIVVGGRAA-----ADVKLSSSNVAVSKGFSFAPVNVNWKSGSLTKTTS-----NQFDQAI SHHGNA LQKENLSCLPLDPMRTLAP---HRS--L SGLSD--SVSMEDDMLTNCNV--QSPDLEYLDNE-----GSSV-A
cycA1-1 (Bradi2g31626) 1 -----MAESAGGAKLVDPVAVQAKKRVALGNITNIAAGAMRGTCGKVAVATPGNARLHSTTSAAPVKKGS LASVQNAIANRSLAVKSAS-----TRPTPK-----AEDIVPPPKVPTVMPAIAASVIPCSCFAS PQHSED--SISTDETMSTSDSM--KSPDLEYIDNG-----DSLVL-L
cycA1-1 (Bradi2g07952) 1 -----MSSTAASRRLLSSSAAT-ATAKRPAEMAENAGGAKPGRMAAQPKRKRVALGNLTNVA-----ARLHSATSVPVKKGSLASARNVITNRGSAVKSVS-----TRPTPVTS CRGSTTQKEIVPPKLPAMPVIVAPPVPCSSFVSPRHSAD--SMSTDETMSTCDSM--KSPDFEYIDNG-----DSSV-L
cycA2-1 (Bradi4g06827) 1 MAARKDNPVLLACQAPSGRITRSQAANRKGFGMAHPVPSGKIERKPAVKRVKRGALDEN A--CASAATSAPQPKRR--AVLKDVNTISLANSSKN-CIAVT-----KLQSRPPQKVRILSKKKQSAK-----K-----VTKPSLLAVSGT SFVNSDNIIEAQTKL LAKPEPITLVGNT--GSPSLQNIERN-----RDSG-L
cycA3-1 (Bradi1g70627) 1 -----MEDKENAGSA-----APPAKRPRRERKALAE LPTG-----SATN-----SASAP-----P-----PSPQASKPRT-----RSQV-A
cycA3-1 (Bradi4g03470) 1 -----MSDKENVLPAAAAAAAGPRVTRAAAKRAA-----SSGASSSGAAKRKRVALGELPTL-----CNA A-----AVPGQ-----P-----SRPVKPAKPA-----A-----
cycA3-1 (Bradi1g14820) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD7-1 (Bradi3g06910) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD3-2 (Bradi4g08357) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD5-3 (Bradi1g70907) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD5-2 (Bradi4g03121) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD5-1 (Bradi1g14606) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD6-1 (Bradi1g24990) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD1-1 (Bradi4g29467) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD3-1 (Bradi3g58300) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD4-1 (Bradi4g32556) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD4-2 (Bradi3g38417) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD2-3 (Bradi1g60647) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD2-2 (Bradi1g21230) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----
cycD2-2 (Bradi1g21237) 1 -----MADKEN-----SAFASAPRLTRASAKRAA--AVT--AVAVAAKRKRVALSELPTL-----PNAV-----VQSH T-----K-----PKKSSHV-S-----K-----

cycB2-2 (Bradi1g29830) 123 PMLF-----EMDDLMS-SE-LKEIEMEDSEEV-----APDIDSCDA-----GNSLAVVEYVDEY SFYR-KTDL-----SCVSPITVSRN-----DIN--EKVRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycB2-3 (Bradi5g18397) 108 -----NDMD-----EEOENNVDES-----LMDIDSADL-----GNPLAATEYVDFYKFKR--NEPT--SCVHPDVS-S-SE-----DIN--EKVRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycB1-3 (Bradi2g10890) 108 HTLT-----SILTKCS-RASDQVSSPKKAPA-----TVDIDASDA-----QDEFAVYVVDIYRFYK--STGCT--CRFLCSMVS-S-SEA-----DIN--EKVRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycB1-1 (Bradi2g52760) 150 NTLT-----SVLTARS-KVAAGIDKPLE-----VIDIKLDG-----DNQLAVVYVTDIYVNFYK--VANE--CFE--CDTPE--S-V-----DIN--SKVRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycB1-5 (Bradi2g21330) 139 DTLT-----KVLTARS-KVACGLTRPKPE-----VEDIDELDK-----NNELAVVYVTDIYVNFYK--TAOHE--SRF--VDFG--N-D-----DIN--PKVRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycA1-1 (Bradi2g31632) 160 RATPLHCCANDKLHISDGRDV-TVTNLRKQGSTPMEIDS-----TFPIDINCE-----DPQLCATLADLYKMR--EATK--KFSPTVYKATN-----DID--TSRRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycA1-1 (Bradi2g31626) 1 -----MSTLV-AG-----RRSSVSKAEINIGARAAKLTAQDKKRVALGNLTIVVGGRAA-----ADVKLSSSNVAVSKGFSFAPVNVNWKSGSLTKTTS-----NQFDQAI SHHGNA LQKENLSCLPLDPMRTLAP---HRS--L SGLSD--SVSMEDDMLTNCNV--QSPDLEYLDNE-----GSSV-A
cycA1-1 (Bradi2g07952) 158 DS--LQRRANANRRISESDV-EGTKWKKDATTPEIDN-----ISDVDDNYK-----DPQLCATLPSDIYHMR--EATR--KRPASDPEYK-----DIN--PSRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycA1-1 (Bradi2g07946) 171 DS--LQRRANANRRISESDV-EGAKWKKDATTPEIDT-----ICDVDDNYE-----DTQLCATLPSDIYHMR--EATR--KRPATDPEYK-----DIN--PSRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycA2-1 (Bradi4g06827) 181 HEAF-----F-QGRKIRDKSETADSKTGDASVSN-----IVDIDKDN G-----NPQMCVSYAABVYTNM--ASEPT--RRPKSNYEALQO-----DIT--KGRRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycA3-1 (Bradi1g70627) 57 REAT-----AA-EGEDA-----RKRKGS A-DVTRPV-----VSGQPDAGA-----AQSGSVYPIGDHRYRSLVRQS--RRPDDVYGTIK-----DIN--AKVRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycA3-1 (Bradi4g03470) 77 -----VEEEA-----HVDEGMCAPTTPA-----ASEEASGGG-----DPQLCGTYASDIYVSRMSVPA--RRAADYETVCT--DVT--ANRSILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycA3-1 (Bradi1g14820) 66 -----RKKPL-----PVREPTT--APVP-----VPADEIG-----DPQLCAYASDIYVSRMSVPAK--RRAADYETVCT--DVT--SLVRAILLDWLVVHY--KLELGEPLLVVHIDRFLAQENV-----KHLQVGRVRLAQEVEEYVFWDDIILCD-----RAT--TRADLEMBRITDITFENYV
cycD7-1 (Bradi4g29467) 16 SNDLLYCEAPFAEDDF-----SPVPPAAA-----IVDCDAVDEIMREYK--AKRRCFA-PAAGGGYRRLHDCGGGGGGSSSVSSARSAKHTNAYG--RLGAAARANANRRISESDV--WELWAWVAVACSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD3-2 (Bradi4g08357) 7 FA-DSLYCPEEHLDLQFPAE-E-----EELQVAVVM-----EDE--VRA-----LEAER--GKBEEL-----MSMA--PE-VVGGGGY--EEGRBAAGMAGAAA--RLGFSALAAATATAGCFLPLRRL--DGRFWMARLAVACSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD5-3 (Bradi1g70907) 12 PT-STLICLEDGNDLFVDD--D-----GDSFAAADL-----RLAAGDDD-----ARLLLDTDYVALDL--SKEGGGC-GAGG-----EETMDWT--KAARAAGDWTAKTNA--RGLFSGNAAVAVYDRFLAQRRDT--G-QGWAELAVACSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD5-2 (Bradi4g03121) 18 GG-FSLTCQEDGADLGDGVVD--D-----GDLFLLYSA--A-----AAAAGDDYVEQV--SKETSGF-FSDSGDAAE--CS-SAASEWLF--LEARLASRMLQTRG--CGFAHRRAVLAHADRFLRRRDR--AAMPWAARLAVACSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD5-1 (Bradi1g14606) 10 CS-FSLMCQEDGADLGDGFTS-D-----DGGEMFFMH--N-----AANENDEPYMEHV--SKETSFC-SSFC--SSA--PS-IAGSEWLF--QCTRRATVWILQTRG--HGFCHRRVAVVAVDRFLRRRDR--SVMPWATRLAVACSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD6-1 (Bradi1g24990) 1 -----MMDA-----GEE-----EYAYEYFD-----LENPTSPADPIASLL--AGCP--HSPSVSA--A-----ASSARQAAGFISKRYDGLLAVRVAVLAHADRFLRRRDR--EHKWAPRLAVACSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD1-1 (Bradi4g29467) 4 DA-SYLLCAEDAAGA AFFLDA-G-----AST-CTAEND-----GYWCS-GAA-----YSPRSVDPDOR-----SRSD--PAARADSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD3-1 (Bradi3g58300) 8 AA-SVLLCAEDNTA I L GDDE-V-----GDECSWAAATPRRHATAAAA-ADG--FLMDYVQSGCIATAP--EPEE--HMKEGYPQDRRL--GELD--LAARADSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD4-1 (Bradi4g32556) 8 AA-SILLCAEDSSSILGFGE-E-----EAAAVKAASW-----SPYS-GDV-----FAADLPLSECVARV--ETAE--HMREDVAQR--AGGD--LLRFDADSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD4-2 (Bradi3g38417) 9 AA-SMLLCAEDNVSI MFDPEA-E-----VEEPIAA--A-----ADP--GADLFPQSGCVAGV--EPEE--HMREDVAQR--AGGD--LLRFDADSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD2-3 (Bradi1g60647) 8 SS-SILLCTEDSATLWG-DDG-E-----VTE--GAE-----LVH-DYS--GFGSQPLESDIVESM--AKRRLTGTATGLYERIS--HGGE--LSCRNADSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD2-2 (Bradi1g21230) 17 SL-TLA-----RMD-----CLGDRE-----VGH-GAT--GD-LFPVDTAVGLM--RMD--HRNDSYKRE--QGGF--SSWRKADSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC
cycD2-2 (Bradi1g21237) 9 SS-SLLFAEDMSSVLGRD G-E-----VAAAGRGGLD-----FLD-AAA-----GA-VFPVDSMVRLLM--RMD--YRKDYMERK--QGGF--SSWRKADSWAKRDEMNIPFHHQMEEV--LRHSFRASVTRMELTILKALQWELAC

cycB2-2 (Bradi1g29830) 296 PFTFC-----FRRFLKAMQ-----SDKKMELLSFFTELVSMEMLKQPSMIAAAAVTQCTNG-----FKSNKCELHRYSEQLQMSRMVVEHQGAHGKLTGVH-----RKYSTFKYCAAKSE-----A-G-LLDA
cycB2-3 (Bradi5g18397) 272 PFTV-----FRRFLKAMQ-----SDKCELVSFFMELCQMKRPSMIAAAAVTQCAANH-----CRHTKICELHRSYRQCLIECSNMVQFHQAGGGKLTGVH-----RKYSTLKFCAAKVE-----A-V-LLL
cycB1-3 (Bradi2g10890) 282 PAVM-----FVRFLKAMD-----GDKEENMAYFYAELAVCSMGLNSPMTIAAAAVVARRCTDV-----CPLSDTQHHGLSEBELCCARRVSHSTAAASKQVYV-----NRYTDPKLGAVLYSE-----S-KKLLPVSDSD
cycB1-1 (Bradi2g52760) 319 PRAV-----FVRSKAMSSSDLKNDKEMTSFFFAELAMGQLQCRPSIAAASSVWARLTKR-----TPLTDTAYHGFTEQSMCKAKIVTVAHATAPESKLRVYV-----KRYSNELGEVSLRPE-----A-LFCK-
cycB1-5 (Bradi2g21330) 310 PFTV-----FVRSKAMG-----NDKELHMVFFFAEMAKENNMGLCSLVAASVWARCTKK-----SPIITGTLEHHTFNETQLLEPAKVVNAHAAAPESKLRAY-----KRYATEQFGRVALHPE-----A-VAAQGV-
cycA1-1 (Bradi2g31632) 335 -----GSCFVSPVPE-----
cycA1-1 (Bradi2g31626) 3 ICYKYLFDNRREFAQVCHERPALHESLASYAELSLVLSLQVPSLVAASSVPLNFIKIP-----TRNPTNSIYHAYQKPSHCVKVIHLFRVPGSNLPAIR-----EYYSQHKYKFAKKYCPSPV-EFQDTRY-
cycA1-1 (Bradi2g07952) 342 PAKC-----FRRVFAQVCEDEDPALHESLACYTELSLVLSLVAASSVPLSKFIQOP-----TKSPNSTAHAYQKASECCVKEQRFCVAPGSKLPAIR-----EYYSQHKYKFAKKYCPSPV-EFQDTRY-
cycA1-1 (Bradi2g07946) 355 PAKC-----FRRVFAQVCEDEDPALHESLASYAELSLVLSLVAASSVPLSKFIQOP-----TKSPNSTAHAYQKASECCVKEQRFCVAPGSKLPAIR-----EYYSQHKYKFAKKYCPSPV-EFQDTRY-
cycA2-1 (Bradi4g06827) 357 PAKC-----FRRVFAQVCEDEDPALHESLASYAELSLVLSLVAASSVPLSKFIQOP-----TKSPNSTAHAYQKASECCVKEQRFCVAPGSKLPAIR-----EYYSQHKYKFAKKYCPSPV-EFQDTRY-
cycA3-1 (Bradi1g70627) 231 PAKR-----FRRVFAQVCEDEDPALHESLASYAELSLVLSLVAASSVPLSKFIQOP-----TKSPNSTAHAYQKASECCVKEQRFCVAPGSKLPAIR-----EYYSQHKYKFAKKYCPSPV-EFQDTRY-
cycA3-1 (Bradi4g03470) 246 PAKC-----FRRVFAQVCEDEDPALHESLASYAELSLVLSLVAASSVPLSKFIQOP-----TKSPNSTAHAYQKASECCVKEQRFCVAPGSKLPAIR-----EYYSQHKYKFAKKYCPSPV-EFQDTRY-
cycA3-1 (Bradi1g14820) 232 PAKC-----FRRVFAQVCEDEDPALHESLASYAELSLVLSLVAASSVPLSKFIQOP-----TKSPNSTAHAYQKASECCVKEQRFCVAPGSKLPAIR-----EYYSQHKYKFAKKYCPSPV-EFQDTRY-
cycD7-1 (Bradi3g06910) 199 VFPFSLHPLTASPLD-----RSLCTRLRLCSHSPFEDSVMIAAAARCTTAAASNLTPA-----PLSTQLGYDQAEQFKMKKALLELDSSNSSSSQREQNYTAENANHLQGTIGSTPISVTD-----QNTTEDDRSCSTSS-----TVNNRSSAVIGRRRLFGAPDIEFHEVDV-
cycD3-2 (Bradi4g08357) 186 VFPFSLHPLTASPLD-----RCEAALAAPIRRWRHFPSSMAAAALATTATGDD-----DAQLLALINAPEVSNHIEAETAKIINGDNNNRK--LRTAAG--FSPPLS--SGVTSAAFSSE-----SSADS-----WFPASASSPGRTRPLKRAAPDDAWP
cycD5-3 (Bradi1g70907) 191 GPFVYVCGANRRLD-----RKAIVLGAVRCFASIKAMSSVQPSPIPLSLVLCANANKEEQTSPVDDELKALLGSSQQLHTCHYSYRVYIREEDRSMQ--QS-S-RE--VASSGCVSAHGMSSDSSSVMAGMNNNNNNNSNATF-----STEATPDKRKRHSP-
cycD5-2 (Bradi4g03121) 195 VFPDMLPCSSSLDHEGGCHD--PARNAIKSIGFPAAQASSVDVPSPIAAAALASCGALLTQEALE--AEMGYSPSICIEKHHAGYMYVGLKNRMS-----N--G--KSLPCS-----EDSNEAATSTVDSVDDVADTAAS-----A-AVSETNKRIRLELPGIR-----
cycD5-1 (Bradi1g14606) 188 VFPDMLPCSSSLDHEGGCHD--AGAKVKAASVPSPIAAAALASCGALLTQEALE--AEMGYSPSICIEKHHAGYMYVGLKNRMS-----N--G--KSLPCS-----EDSNEAATSTVDSVDDVADTAAS-----A-AVSETNKRIRLELPGIR-----
cycD6-1 (Bradi4g24990) 155 VFLAELGFGSECFPPRHPL--LAANKARAVDLRAQVVKMAEFPSPVAAASLAAAGEVAG-QALL--AOGAAGACPFVNSKRGSEAAACACGWPFAAM-----SADTSTVGHGHRASSESDRTVGSV--ANG-----ADAKKRCMCPSPQW-
cycD1-1 (Bradi4g29467) 196 VFPFSLHPLTASPLD-----YARATQVLAHILKFDHCPSPVAAASLAAAGEVAG-QALL--AOGAAGACPFVNSKRGSEAAACACGWPFAAM-----SADTSTVGHGHRASSESDRTVGSV--ANG-----ADAKKRCMCPSPQW-
cycD3-1 (Bradi3g58300) 201 VACSPIDYFHHNDRDAPSM--LAYSRSSDLSLAKGADPVEPSEPAASVALASFGECNS-S-VLE--R--ATTSCYINKRRLRQYELQDNTMG--NI-VLKS--AGSSIFS--VQSGEGVTRACLSQSDDTTAG-----SPATCYQN--SSASKRRRIGR-
cycD4-1 (Bradi4g32556) 190 VFPFSLHPLTASPLD-----SAVRSABELRISRGTDCEPSPVAAAATVAGECT-V-DI--D--MARCCVDPKRLRHEAQAQ--DLMPVAKT-ARRG--RASSVSS--APRFVGVDA--ACLSCRSDTTTAAAS--SPASSAFDSSPVCKRRKISR-----
cycD4-2 (Bradi3g38417) 193 VFPFSLHPLTASPLD-----CMLFRSABELCAAKGTGCEPSPVAAAATVAGECT-V-DI--D--MARCCVDPKRLRHEAQAQ--DLMPVAKT-ARRG--RASSVSS--APRFVGVDA--ACLSCRSDTTTAAAS--SPASSAFDSSPVCKRRKISR-----
cycD2-3 (Bradi1g60647) 154 VFPFSLHPLTASPLD-----YARATQVLAHILKFDHCPSPVAAASLAAAGEVAG-QALL--AOGAAGACPFVNSKRGSEAAACACGWPFAAM-----SADTSTVGHGHRASSESDRTVGSV--ANG-----ADAKKRCMCPSPQW-
cycD2-2 (Bradi1g21230) 181 VFPFSLHPLTASPLD-----YARATQVLAHILKFDHCPSPVAAASLAAAGEVAG-QALL--AOGAAGACPFVNSKRGSEAAACACGWPFAAM-----SADTSTVGHGHRASSESDRTVGSV--ANG-----ADAKKRCMCPSPQW-
cycD2-2 (Bradi1g21237) 189 VFPFSLHPLTASPLD-----YARATQVLAHILKFDHCPSPVAAASLAAAGEVAG-QALL--AOGAAGACPFVNSKRGSEAAACACGWPFAAM-----SADTSTVGHGHRASSESDRTVGSV--ANG-----ADAKKRCMCPSPQW-