```
CKL1            FRLGRKIGSGSFGEIYLGTNIHTNEELAIKLENVKTKHPQLLYESKLYRILQGGTGVPNV 60
CKL12           YRLGRKIGSGSFGEIYLGTHIQTNEEVAIKLENVKTKHPQLLYESKLYRILQGGTGVPNI 60
CKL2            FRLGRKIGGGSFGEIYLGTNIQTNEEVAIKLENVKTKHPQLLYESKLYKVLQGGTGVPNV 60
CKL5            FRLGRKIGSGSFGEIYLGTDVQTNEEVAIKLESVKTAHPQLSYESRIYRVLQGGTGIPNM 60
CK1d            YRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVKTKHPQLHIESKIYKMMQGGVGIPTI 60
CKL8            YKLGRKLGSGSFGELFLGVNVQTGEEVAVKLEPARARHPQLHYESKLYMLLQGGTGIPHL 60
CKL13           FKLGRKLGSGSFGEIFLGVNVQTGEEVAVKLEPLRARHPQLHYESKLYMLLQGGTGIPHL 60
CKL10           FKLGRKIGSGSFGELYIGINVQTGEEVALKLEPVKTKHPQLHYESKVYMLLQGGTGVPHI 60
CKL11           FKLGRKLGSGSFGELYLGINIQTGEEVAVKLEPVKTRHPQLQYESKIYMFLQGGTGVPHL 60
CKL7            FKLGKKIGSGSFGELYLGVNVQTGEEVAVKLENVKTKHPQLHYESKLYMLLQGGSGIPNI 60
CKL9            FKLGRKIGSGSFGELYLGINVQTGEEVAVKLESVKTKHPQLHYESKLYMLLQGGTGVPNL 60
CKL6            FKLGRKIGGGSFGELFLAVSLQTGEEAAVKLEPAKTKHPQLHYESKIYMLLQGGSGIPSL 60
CKL3            YKLGRKIGGGSFGEIFLATHVDTFEIVAVKIENSKTKHPQLLYEAKLYRILEGGSGIPRI 60
CKL4            YKLGRKIGGGSFGEIFLATHIDTFEIVAVKIENSKTKHPQLLYEAKLYRTLEGGSGIPRI 60
                ::**:*:*.****::::.  : : *  *:*:*  :: ****  *:::*  ::** *:* :

CKL1            KWFGVEGDYNVLVMDLLGPSLEDLFNFCSRKLSLKSVLMLADQMINRVEFFHSKSFLHRD 120
CKL12           KWFGVEGDYNTLVMDLLGPSLEDLFNFCSRKLSLKSVLMLADQMINRVEYFHSKSFLHRD 120
CKL2            KWYGVEGDYNVLVIDLLGPSLEDLFNFCSRKLSLKTVLMLADQMINRIEFVHQKSFLHRD 120
CKL5            KWYGVEGDYNVLVMDLLGPSLEDLFSYCKRQFSLKTVLMLADQMINRLEFIHSKSYLHRD 120
CK1d            RWCGAEGDYNVMVMELLGPSLEDLFNFCSRKFSLKTVLLLADQMISRIEYIHSKNFIHRD 120
CKL8            KWYGVEGEYNCMVIDLLGPSMEDLFNYCSRRFNLKTVLMLADQMINRVEYMHVRGFLHRD 120
CKL13           KWFGVEGEFNCMVIDLLGPSMEEFFNYCSRSFSLKTVLMLADQMINRVEYMHVKGFLHRD 120
CKL10           KWFGVEGNYNCMAIDLLGPSLEDLFNYCTRSFSLKTVLMLADQLINRVEYMHSRGFLHRD 120
CKL11           KWFGVEGEYSCMVIDLLGPSLEDLFNYCKRIFSLKSVLMLADQLICRVEYMHSRGFLHRD 120
CKL7            KWFGVEGDYSVMVIDLLGPSLEDLFNYCNRKLTLKTVLMLADQLLNRVEFMHTRGFLHRD 120
CKL9            KWYGVEGDYNVMVIDLLGPSLEDLFNYCNRKLSLKTVLMLADQLINRVEFMHTRGFLHRD 120
CKL6            KWFGVQGDYNAMVIDLLGPSLEDLFNYCNRRLTLKAVLMLADQLISRVEYMHSRGFLHRD 120
CKL3            KWFGVDGTENALVMDLLGPSLEDLFVYCGRKFSPKTVLMLADQMLTRIEFVHSKGYLHRD 120
CKL4            RWFGVDGTENALVMDLLGPSLEDLFVYCGRKFSPKTVLMLADQMLTRIEYVHSKGYLHRD 120
                :* *.:*  . :.::*****:*::* :* * :. *:**:****:: *:*:.* :.::***

CKL1            LKPDNFLMGLGRRANQVYIIDFGLAKKYRDSTTHQHIPYRENKNLTGTARYASMNTHLGI 180
CKL12           LKPDNFLMGLGRRANQVHIIDFGLAKKYRDNTTHQHIPYRENKNLTGTARYASMNTHLGI 180
CKL2            IKPDNFLMGLGRRANQVYVIDFGLAKKYRD-SNHQHIPYRENKNLTGTARYASMNTHLGI 179
CKL5            IKPDNFLMGLGRRANQVYIIDYGLAKKYRDSSTHRHIPYRENKSLIGTPRYASLNTHLGI 180
CK1d            VKPDNFLMGLGKKGNLVYIIDFGLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGI 180
CKL8            IKPDNFLMGLGRKANQVYIIDYGLAKKYRDLQTHRHIPYRENKNLTGTARYASVNTHLGI 180
CKL13           IKPDNFLMGLGRKANQVYIIDYGLAKKYRDLQTHKHIPYRENKNLTGTARYASVNTHLGI 180
CKL10           IKPDNFLMGLGRKANQVYIIDYGLAKKYRDLQTHKHIPYRENKNLTGTARYASVNTHLGI 180
CKL11           IKPDNFLMGLGRRANQVYIIDYGLAKKYKDLQTQKHIPYRENKNLTGTARYASVNTHLGI 180
CKL7            IKPDNFLMGLGRKANQVYIIDFGLGKKYRDLQTHKHIPYRENKNLTGTARYASVNTHLGV 180
CKL9            IKPDNFLMGLGRKANQVYIIDFGLGKKYRDLQTHRHIPYRENKNLTGTARYASVNTHLGV 180
CKL6            IKPDNFLMGLGRKANQVYIIDFGLAKKYRDLQTHRHIPYRENKNLTGTARYASVNTHLGV 180
CKL3            IKPDNFLMGLGRKANQVYLIDFGLAKRYRDANTNRHIPYRENKNLTGTARYASCNTHLGI 180
CKL4            IKPDNFLMGLGRKANQVYLIDFGLAKRYRDANTNRHIPYRENKNLTGTARYASCNTHLGI 180
                :**********::.* *::**:**.*:*:*  .::********.* **.**** *****:

CKL1            EQSRRDDLESLGYILMYFLKGSLPWQGLKAGTKKQKYERISEKKVSTSIEALCRGYPSEF 240
CKL12           EQSRRDDLESLGYILMYFLKGSLPWQGLKAGTKKQKYERISEKKVSTSIESLCRGYPSEF 240
CKL2            EQSRRDDLESLGFVLMYFLKGSLPWQGLKAGNKKQKYEKISEKKVSTSIEALCRGYPSEF 239
CKL5            EQSRRDDIESLGYILMYFLKGSLPWQGLKAGNKKQKYDKISEKKVSTSIETLCRGHPTEF 240
CK1d            EQSRRDDLESLGYVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEF 240
CKL8            EQSRRDDLESLGYVLMYFLRGSLPWQGLRAGTKKQKYDKISEKKRLTPVEVLCKSFPPEF 240
CKL13           EQSRRDDLESLGYLLMYFLRGSLPWQGLRAGTKKQKYDKISEKKRLTPVEVLCKNFPPEF 240
CKL10           EQSRRDDLESLGYVLMYFIRGSLPWQGLKAGTKKQKYEKISEKKMLTPVEVLCKSYPSEF 240
CKL11           EQSRRDDLESLGYVLMYFLRGSLPWQGLKAGTKKQKYDKISEKKMLTSVETLCKSYPSEF 240
CKL7            EQSRRDDLESLGYVLMYFLKGSLPWQGLKAGTKKQKYDRISEKKVSTPIEVLCKNQPSEF 240
CKL9            EQSRRDDLEALGYVLMYFLKGSLPWQGLKAGTKKQKYDRISEKKVATPIEVLCKNQPSEF 240
CKL6            EQSRRDDLESLGYVLMYFLRGSLPWQGLKAGTKKQKYDRISEKKVSTPIEVLCKSYPPEF 240
CKL3            EQSRRDDLESLGYVLLYFLRGSLPWQGLKAVDKKQKYDKICEKKISTPIEVLCKNHPVEF 240
CKL4            EQGRRDDLESLGYVLLYFLRGSLPWQGLKAVDKKQKYDKICEKKISTPIEVLCKSHPVEF 240
                **.****:*:**::*:**  ********:*  *:***::*.***  *.:* **:. * **

CKL1            ASYFHYCRSLRFDDKPDYAYLKRIFRDLFI 270
CKL12           ASYFHYCRSLRFDDKPDYGYLKRIFRDLFI 270
CKL2            ASYFHYCRSLRFDDKPDYAYLKRLFRDLFI 269
CKL5            ASYFHYCRSLRFDDKPDYAYLKRLFRNLFI 270
CK1d            ATYLNFCRSLRFDDKPDYSYLRQLFRNLF- 269
CKL8            TSYFLYVRSLRFEDKPDYPYLKRLFRDLFI 270
CKL13           TSYFLYVRSLRFEDKPDYSYLKRLFRDLFI 270
CKL10           TSYFHYCRSLRFEDKPDYSYLKRLFRDLFI 270
CKL11           TSYFHYCRSLRFEDKPDYSYLRRLFRDLFI 270
CKL7            VSYFHYCRSLRFDDKPDYSYLKRLFRDLFI 270
CKL9            VSYFRYCRSLRFDDKPDYSYLKRLFRDLFI 270
CKL6            VSYFQYCRSLRFEDKPDYSYLKRLFRDLFI 270
CKL3            ASYFHYCHTLTFDQRPDYGFLKRLFRDLF- 269
CKL4            ASYFHYCHTLTFDQRPDYGFLKRLFRDLF- 269
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Supplemental Figure 1. Alignment of kinase domains of Arabidopsis CKL and human CK1delta (CK1d). Leu 85 and Ile 148 that are crucial for B-AZ binding (Figure 4) are marked in orange.