AtAAC2 AtAAC1 RcAAC LcAAC1 ZmANT	MVEQTQHPTILQKVSGQLLSSSVSQDIRGY	28 30 62
AtAAC2 AtAAC1 RcAAC LcAAC1 ZmANT	ASASKRPATYQKHAAYGNYSNAAFQYPLVAASQIATTTSPVFVQAPGEKGFTNFAI -VGYQRPSMYQRHATYGNYSNAAFQFPPTSRMLATTASPVFVQTPGEKGFTNFAL DGSLQRPALYQRR-AYGNYTNAAFQYPMGCADLSVVPTTASSVCVQAPSEKGFAGFAI DGAFNRPALYQRR-TYGNYSNAAFHPVVRACGATSDMSMVASTASPVFVQAPSEKGFAGFAI RNICPSVSSYERRFATRNYMTQSLWGPSMSVSGGINVPVMQTPLCANAPAEKGGKNFMI	82 87 123
AtAAC2 AtAAC1 RcAAC LcAAC1 ZmANT	DFMMGGVSAAVSKTAAAPIERVKLLIQNQDEM <mark>L</mark> KAGRL <mark>T</mark> EPYKGIRDCF <mark>G</mark> RTIRDEG <mark>I</mark> GSLW DFLMGGVSAAVSKTAAAPIERVKLLIQNQDEMIKAGRLSEPYKGIGDCF <mark>G</mark> RTIKDEGFGSLW DFLMGGVSAAVSKTAAAPIERVKLLIQNQDEMIKSGRLSEPYKGIGDCFKRTIKDEGFGSLW DFLMGGVSAAVSKTAAAPIERVKLLIQNQDEMIKTGRLSEPYKGIGDCFKRT <mark>M</mark> KDEG <mark>IV</mark> SLW DFMMGGVSAAVSETAAAPIERVKLLIQNQDEMIKSGRLSEPYKGIVDCFKRTIKDEGFSSLW	144 149 185
AtAAC2 AtAAC1 RcAAC LcAAC1 ZmANT	RGNTANVIRYFPTQALNFAFKDYFKRLFNFKKDKDGYWKWFAGNLASGGAAGASSLLFVYSL RGNTANVIRYFPTQALNFAFKDYFKRLFNFKKDRDGYWKWFAGNLASGGAAGASSLLFVYSL RGNTANVIRYFPTQALNFAFKDYFKRLFNFKKDKDGYWKWFAGNLASGGAAGASSLLFVYSL RGNTANVIRYFPTQALNFAFKDYFKRLFNFKKDKDGYWKWFAGNLASGGAAGASSLLFVYSL RGNTANVIRYFPTQALNFAFKDYFKRLFNFKKDRDGYWKWFAGNLASGGAAGASSLFFVYSL	210 206 211 247 213
AtAAC2 AtAAC1 RcAAC LcAAC1 ZmANT	DYARTRLAND <mark>S</mark> K <mark>S</mark> AKKGG <mark>G</mark> ERQFNGLVDVY <mark>K</mark> KTLKSDGIAGLYRGFNISC <mark>A</mark> GIIVYRGLYFG DYARTRLANDAKAAKKGG <mark>G</mark> RQF <mark>D</mark> GLVDVYRKTLK <mark>T</mark> DGIAGLYRGFNISCVGIIVYRGLYFG DYARTRLANDAKAAKKGG-ERQFNGLVDVYRKTLASDGIAGLYRGFNISCVGIIVYRGLYFG DYARTRLANDAKAAKKGG-ERQFNGLVDVYRKTMKSDGIAGLYRGFNISCVGIIVYRGLYFG DYARTRLANDAKAAK <mark>G</mark> GG-ERQFNGLVDVYRKTLKSDGIAGLYRGFNISCVGIIVYRGLYFG	272 308
AtAAC2 AtAAC1 RcAAC LcAAC1 ZmANT	LYDSVKPVLLTGDLQDSFFASFALGWLITNGAGLASYPIDTVRRRMMMTSGEAVKYKSS <mark>F</mark> DA LYDSVKPVLLTGDLQDSFFASFALGW <mark>V</mark> ITNGAGLASYPIDTVRRRMMMTSGEAVKYKSSLDA MYDSLKPVVLTGNLQDSFFASFALGWLITNGAGLASYPIDTVRRRMMMTSGEAVKY <mark>RG</mark> SLDA MYDSLKPVVLTGSLQDSFFASFALGWLITNGAGLASYPIDTVRRRMMMTSGEAVKYKSSLDA LYDSIKPVVLTGNLQDNFFASFALGWLITNGAGLASYPIDTVRRRMMMTSGEAVKYKSSLDA	330 334 370
AtAAC2 AtAAC1 RcAAC LcAAC1 ZmANT	FSQI <mark>V</mark> KK <mark>EGAKSLFKGAGANILRAVAGAGVLAGYDKLQLIVFGKKYGSGGA- FKQILKNEGAKSLFKGAGANILRAVAGAGVL<mark>S</mark>GYDKLQLIVFGKKYGSGGA- FSQILKNEGAKSLFKGAGANILRAVAGAGVLAGYDKLQLIVFGKKYGSGGA- FSQILKNEGAKSLFKGAGANILRAVAGAGVLAGYDKLQLIVFGKKYGSGGGA- FQQILKKEGPKSLFKGAGANILRAIAGAGVLSGYDQLQILFFGKKYGSGGA-</mark>	385 381 385 422 387