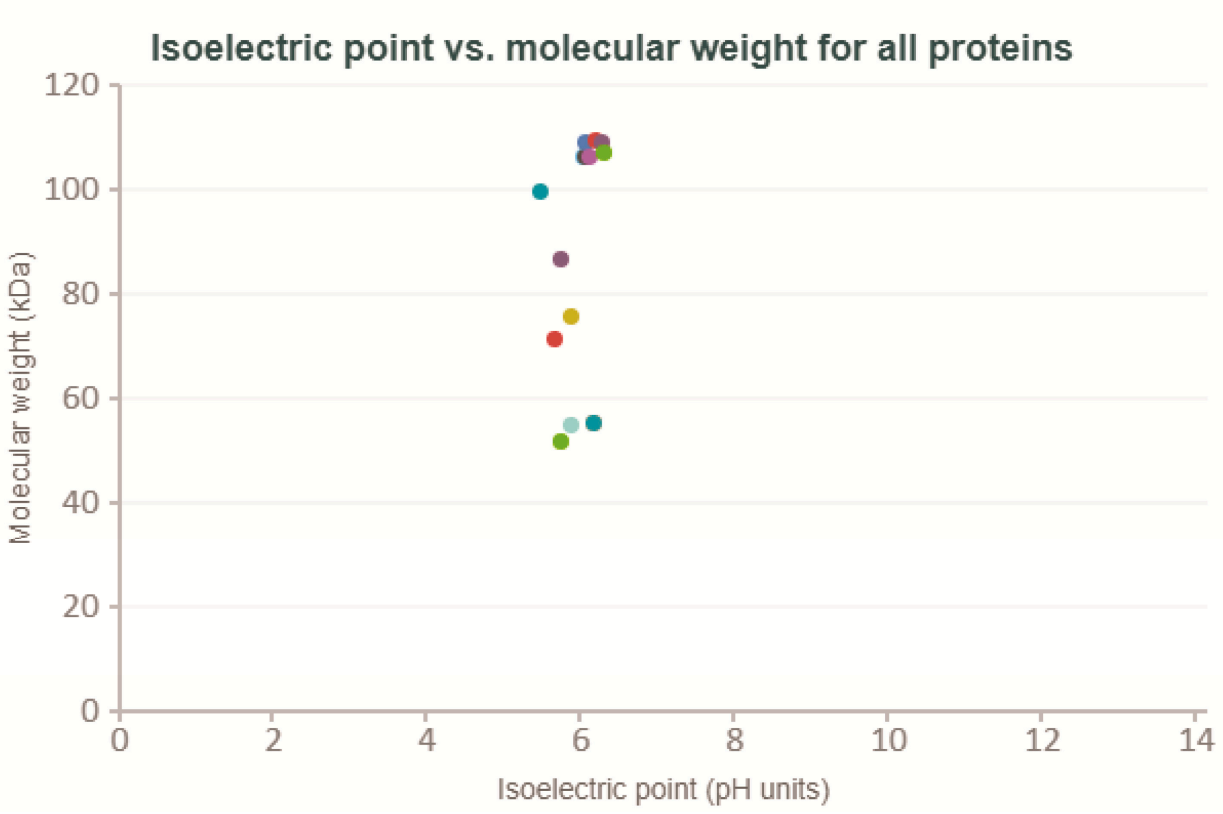


Figure S1. The molecular mass (kDa) and isoelectric point of plots of TaACO genes.

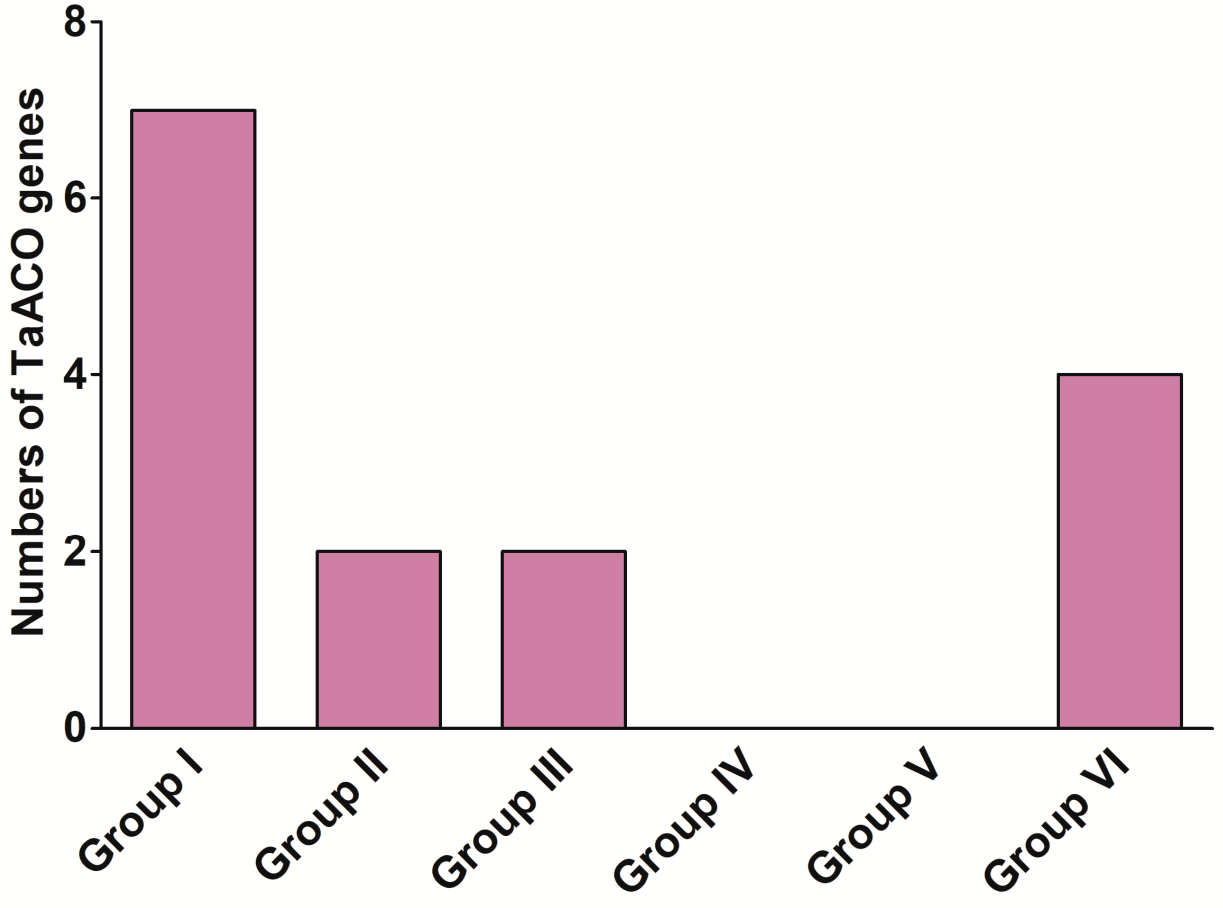


Figure S2. Dispersal of TaACOs in a different group of the phylogenetic tree.

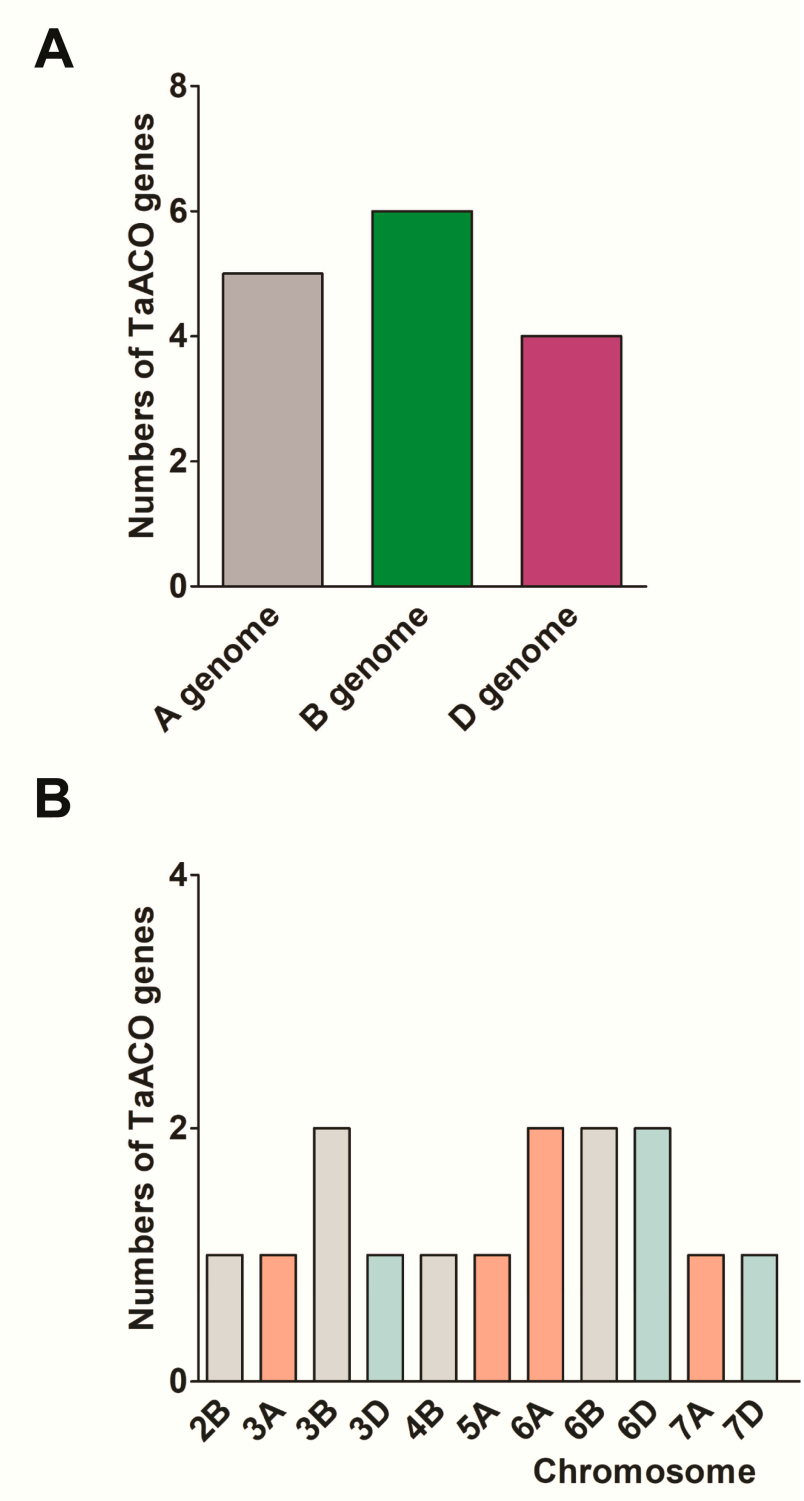


Figure S3. Chromosomal locations of identified ACO genes and on the three sub-genomes of (**A**) Dispersal of ACO genes in the A, B and D sub-genomes. (**B**) Dispersal of ACO genes on wheat chromosomes.

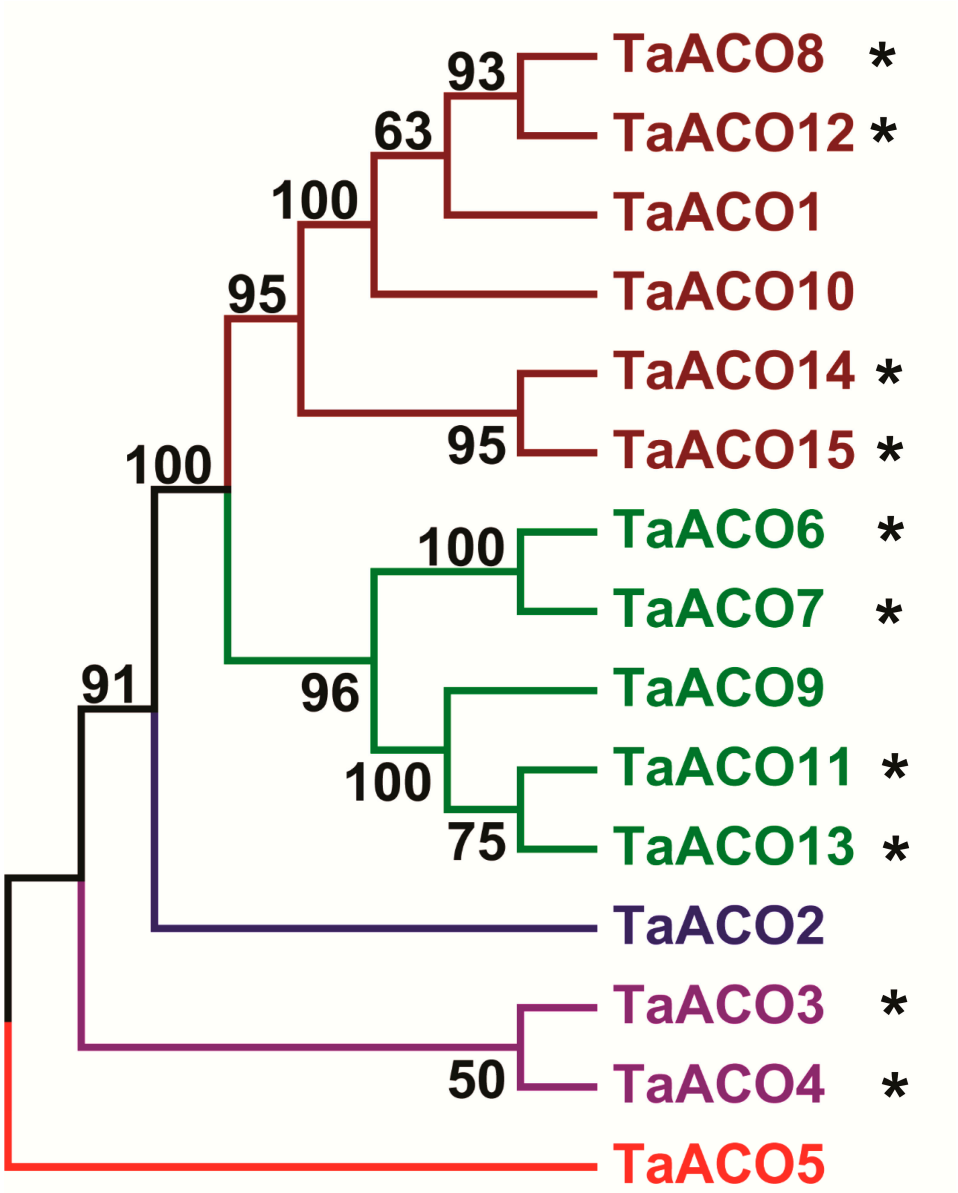


Figure S4. Evolutionary analysis of TaACO genes. A phylogenetic tree was produced using MEGA7 with the NJ method and 1000 bootstrap replications. A black asterisk denotes the duplicated gene pairs.

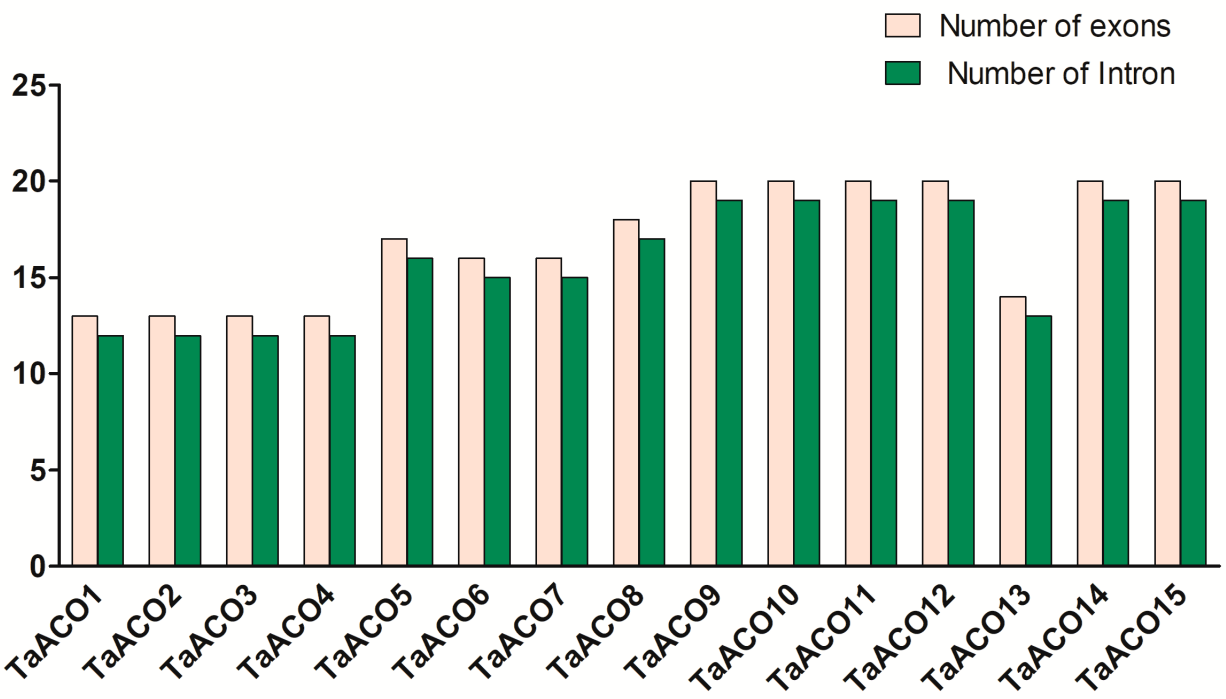


Figure S5. The different number of exons and introns in found in the TaACOs gene family.

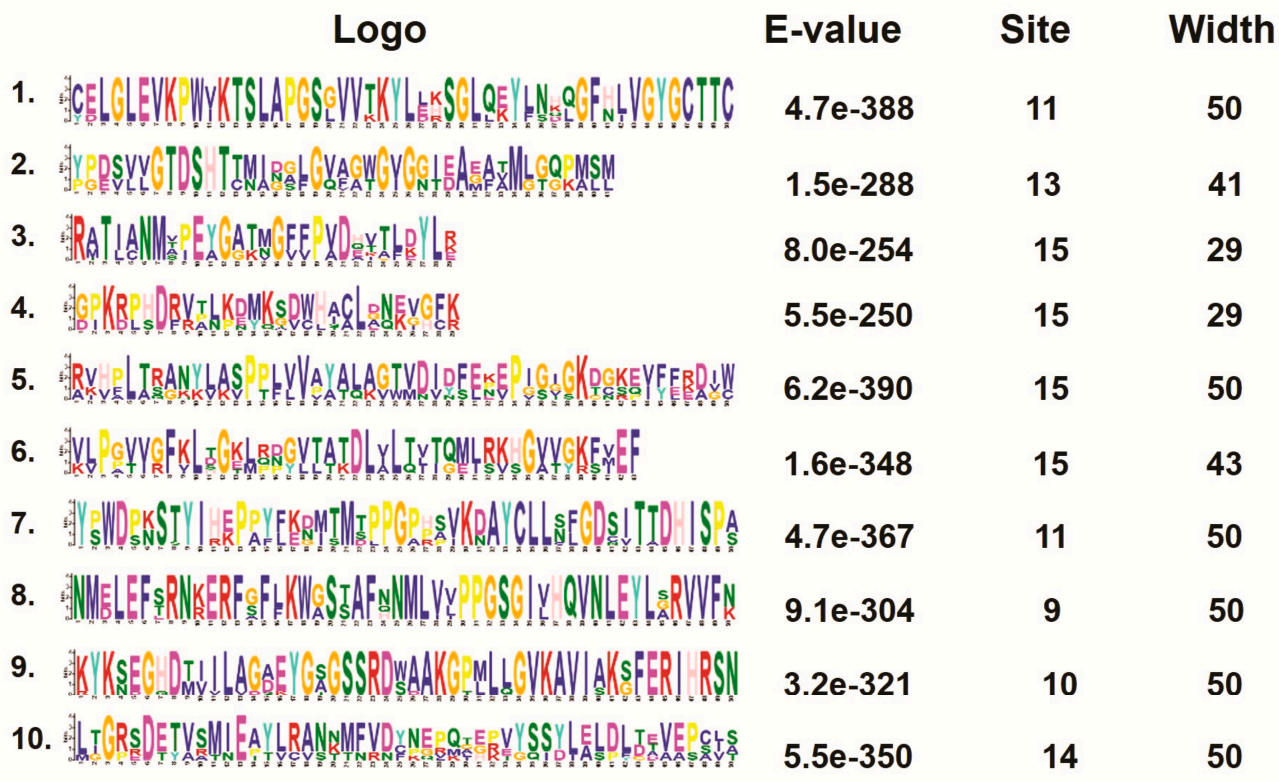
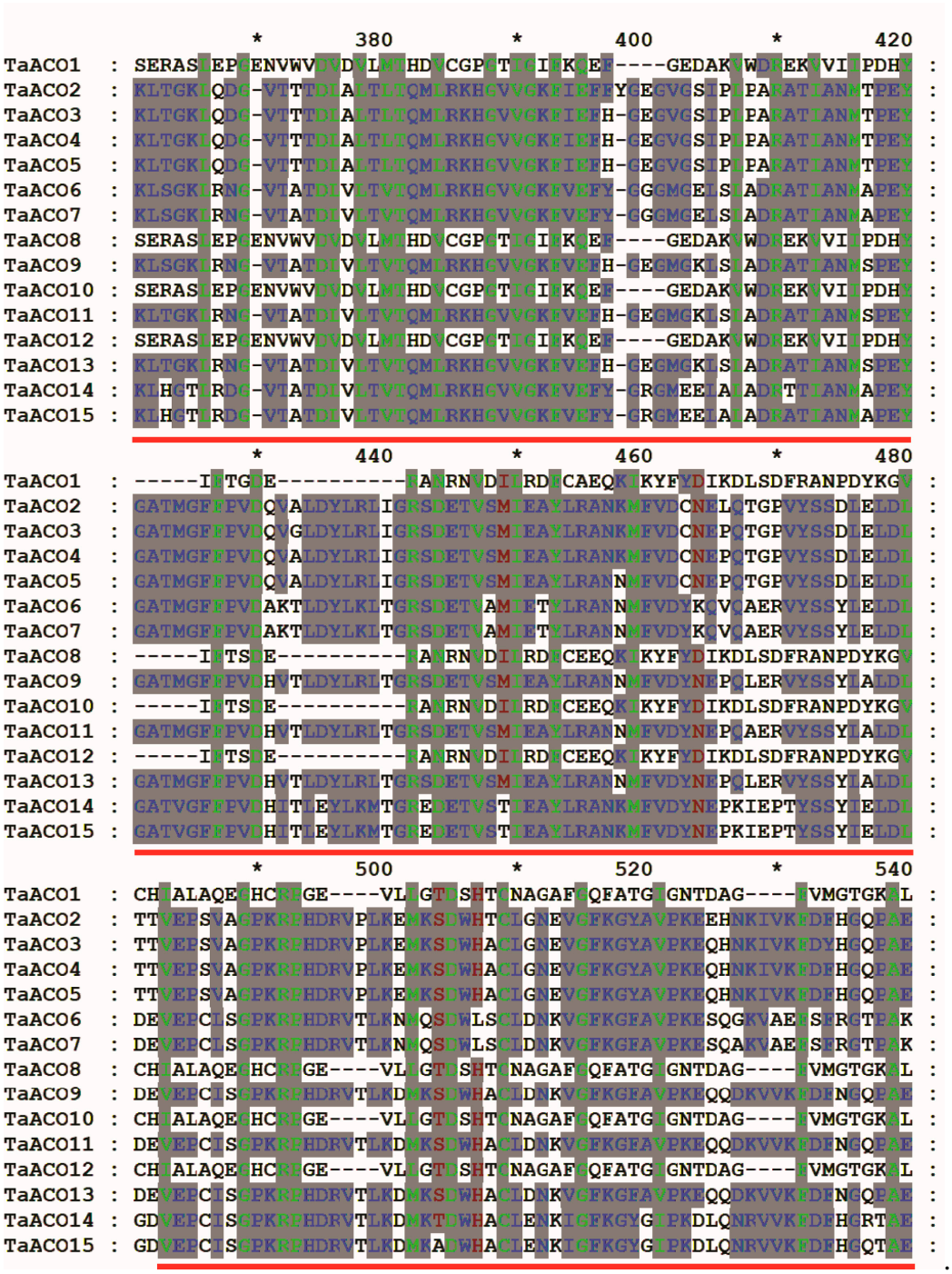


Figure S6. Sequence logo of TaACO motif and height of each mountain indicate the conservation at this position, whereas the height of the different letters represent the frequency of the corresponding amino acids.


TaACO1
TaACO2
TaACO3
TaACO4
TaACO5
TaACO6
TaACO7
TaACO8
TaACO9
TaACO10
TaACO11
TaACO12
TaACO13
TaACO14
TaACO15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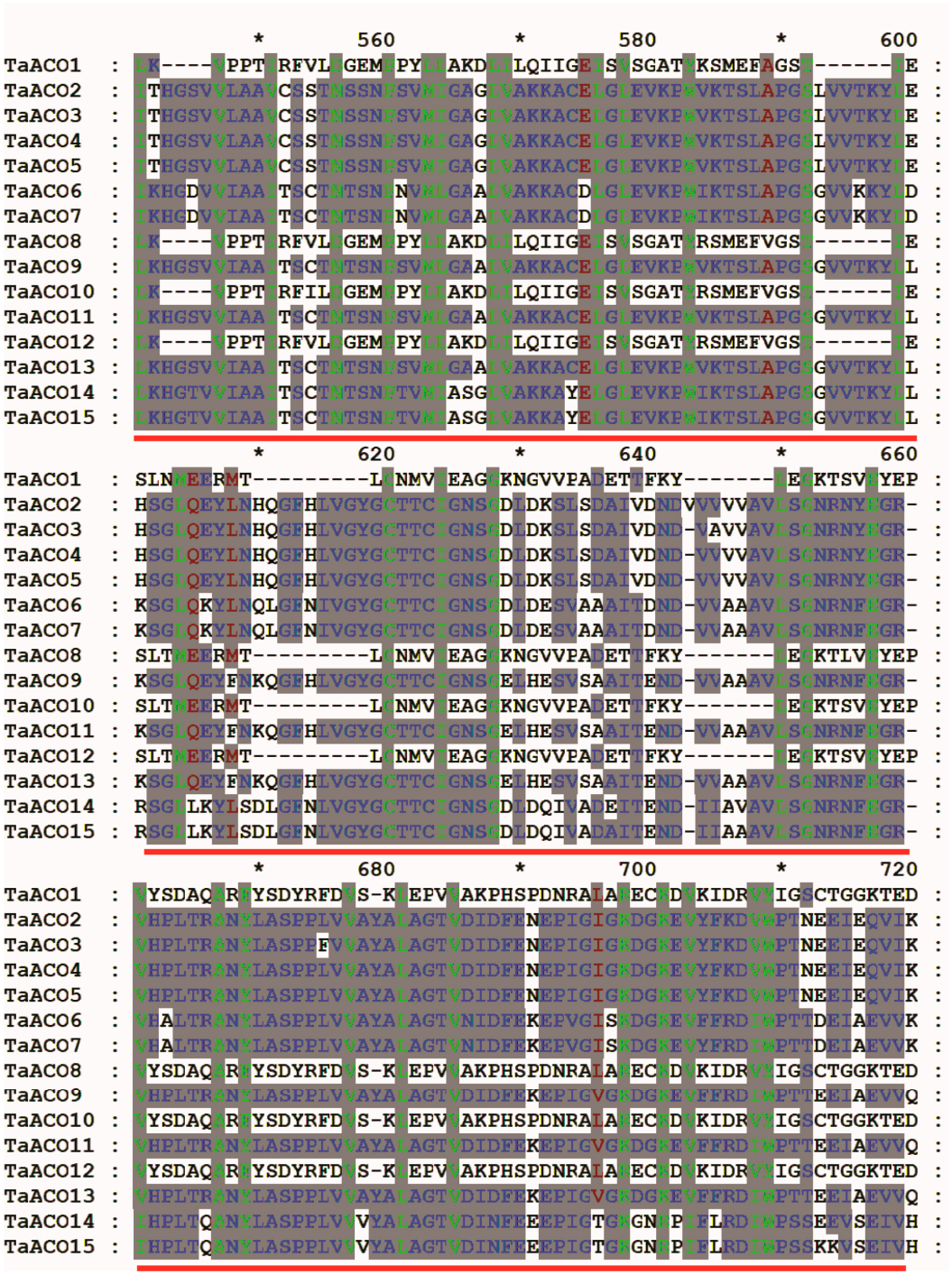
TaACO02
TaACO03
TaACO04
TaACO05
TaACO06
TaACO07
TaACO08
TaACO09
TaACO10
TaACO11
TaACO12
TaACO13
TaACO14
TaACO15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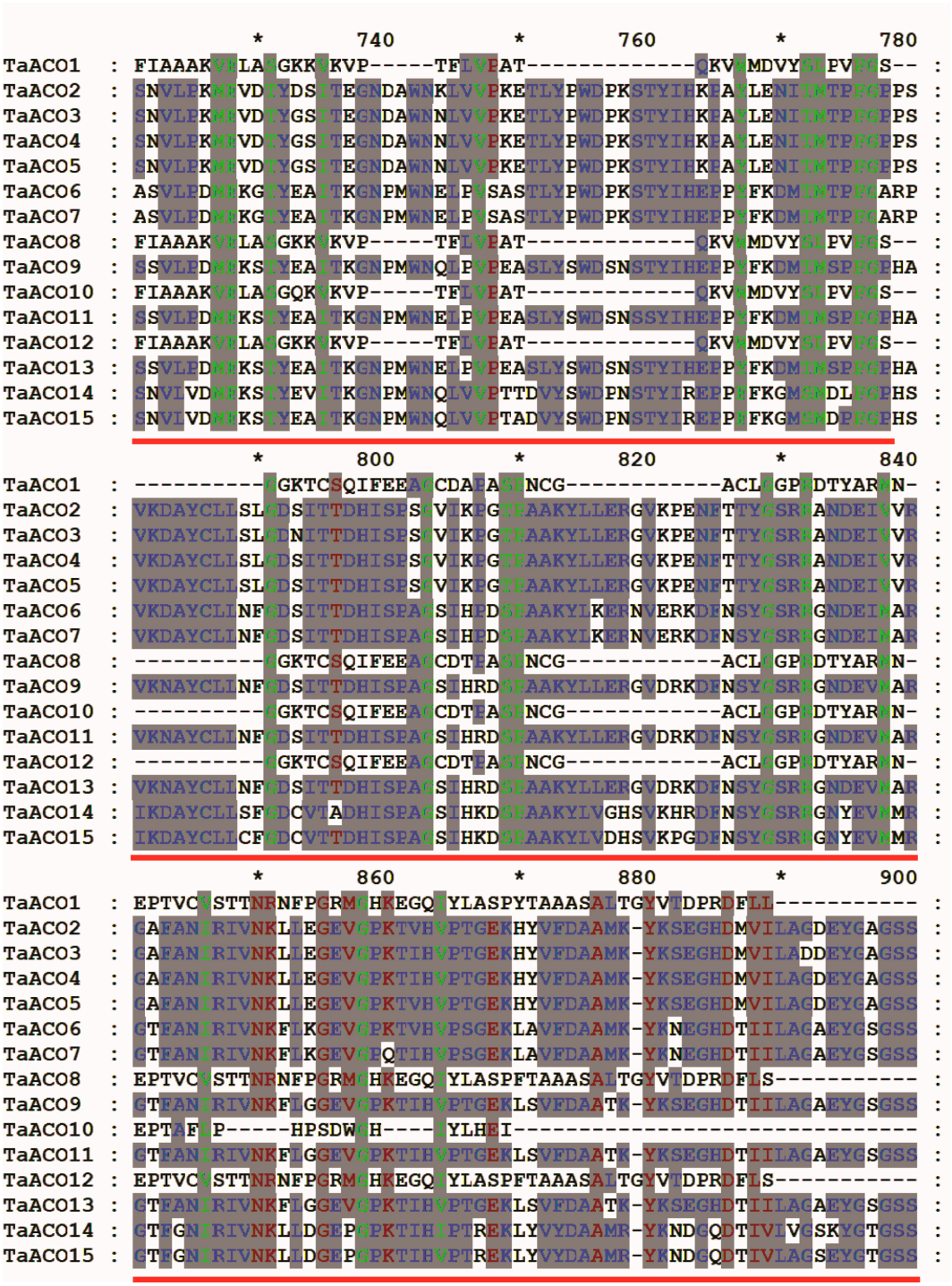
580
600
620
640
660
680
700
720
TaACO01
TaACO02
TaACO03
TaACO04
TaACO05
TaACO06
TaACO07
TaACO08
TaACO09
TaACO10
TaACO11
TaACO12
TaACO13
TaACO14
TaACO15


740
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TaACO3
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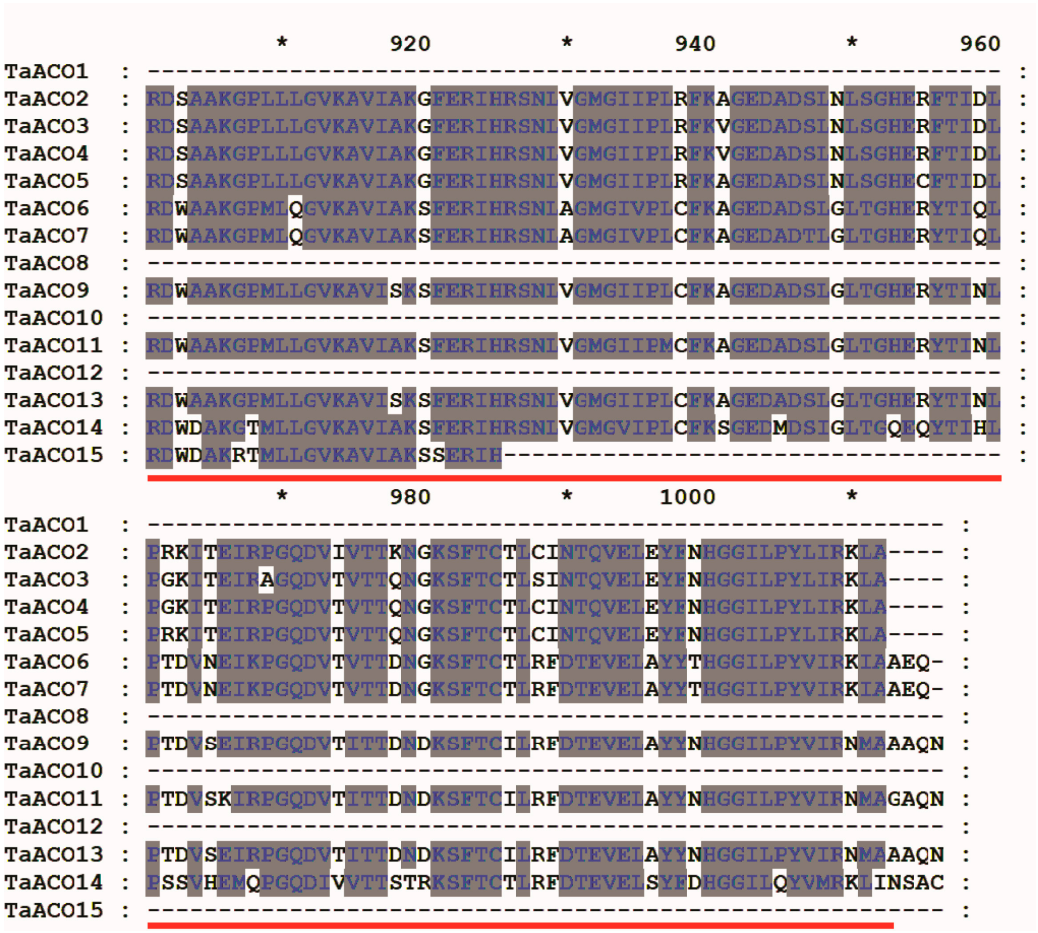
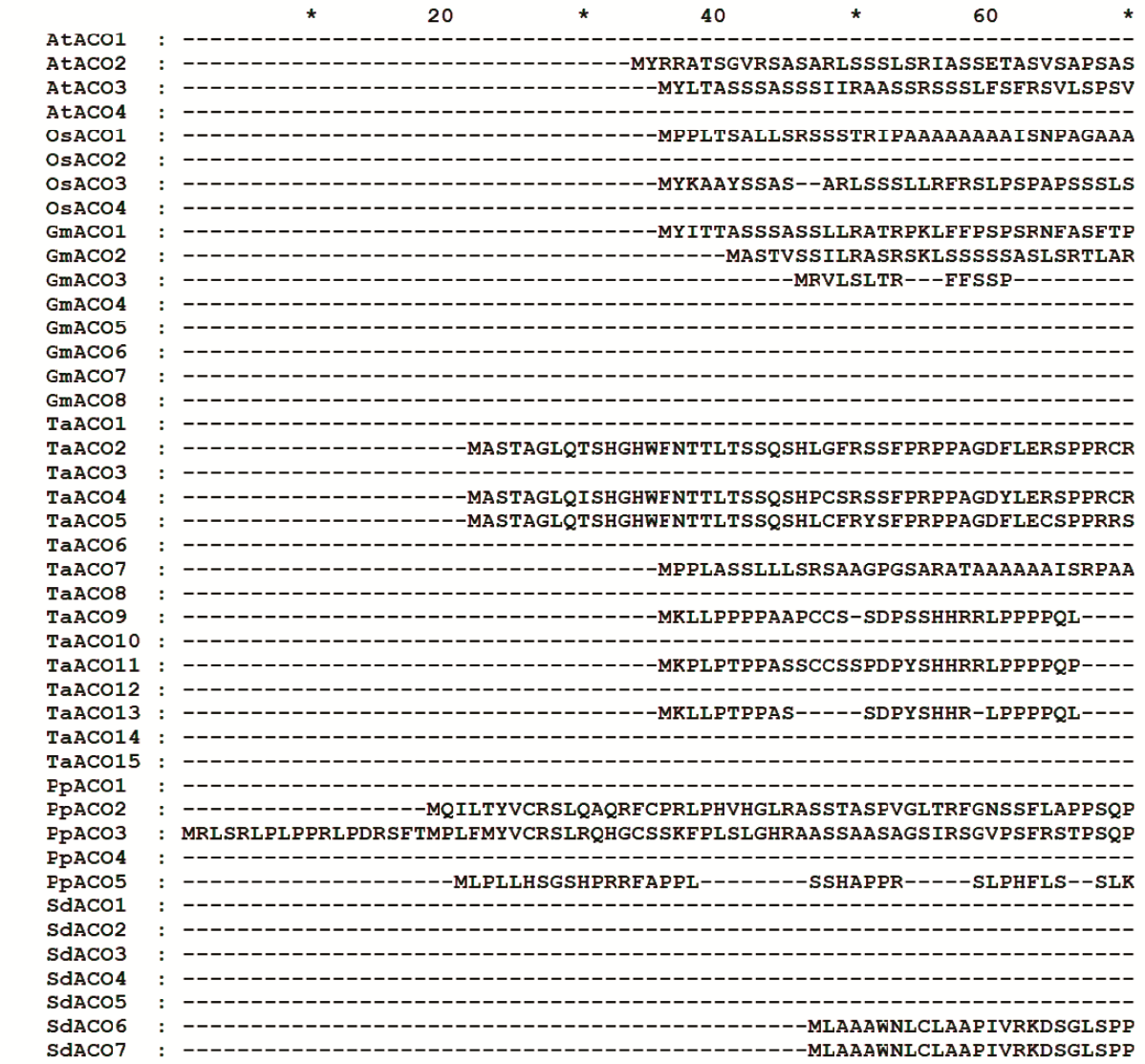


Figure S7. Alignment of the TaACO proteins and preserved aconitase domain is indicated with red color line. Amino acid residues conserved in all proteins were shaded blue and similar amino acids were gray shaded. Dashes denotes gaps led to exploit the alignment of the homologous region.

A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AtACO4 : ----------
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OsACO2 : ----------
OsACO3 : ----------MYKAAYSSAS--ARLSSSLLRFRSLPSPAPSSSLS :
OsACO4 : ----------
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GmACO2 : ----------MASTVSSILRASRSKLSSSSSASLSRTLAR :
GmACO3 : ----------MRVLSLTR---FFSSP---------
GmACO4 : ----------
GmACO5 : ----------
GmACO6 : ----------
GmACO7 : ----------
GmACO8 : ----------
TaACO1 : ----------
TaACO2 : ----------MASTAGLQTSHGHWFNTTLTSSQSHLGFRSSFPRPPAGDFLERSPPRCR :
TaACO3 : ----------
TaACO4 : ----------MASTAGLQISHGHWFNTTLTSSQSHPCSRSSFPRPPAGDYLERSPPRCR :
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TaACO6 : ----------
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TaACO8 : ----------
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TaACO10 : ----------
TaACO11 : ----------MKPLPTPPASSCCSSPDPYSHHRRLPPPPQP---- :
TaACO12 : ----------
TaACO13 : ----------MKLLPTPPAS-----SDPYSHHR-LPPPPQL---- :
TaACO14 : ----------
TaACO15 : ----------
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PpACO2 : ----------MQILTYVCRSLQAQRFCPRLPHVHGLRASSTASPVGLTRFGNSSFLAPPSQP :
PpACO3 : MRLSRLPLPPRLPDRSFTMPLFMYVCRSLRQHGCSSKFPLSLGHRAASSAASAGSIRSGVPSFRSTPSQP :
PpACO4 : ----------
PpACO5 : ----------MLPLLHSGSHPRRFAPPL--------SSHAPPR-----SLPHFLS--SLK :
SdACO1 : ----------
SdACO2 : ----------
SdACO3 : ----------
SdACO4 : ----------
SdACO5 : ----------
SdACO6 : ----------MLAAAWNLCLAAPIVRKDSGLSPP :
SdACO7 : ----------MLAAAWNLCLAAPIVRKDSGLSPP :

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AtACO1  : ------------------------------------------------------------MASENPFRSI :
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AtACO3  : SSTSPSSLLARRSFGTISPAFRRWSHSFHSKPSPFRFTSQIRAV---SPVLDRLQRTFSSMASEHPFKGI :
AtACO4  : ----------------------------------------MASVISSSPFL---------CKSSSKS :
OsACO1  : SSSSPSPPPPSSRPR--------PASPFASGLAGRIFGGRRAAARSSSSAAAVFERRFASAAAKNSYDEI :
OsACO2  : ------------------------------------------------------------------- :
OsACO3  : RLLSLRARAFSRPSRGGWAAAGGWSGRASSSPVVGCGACRAQIGAVAPAVERVHRRMAATAAAEHPFKNI :
OsACO4  : ----------------------------------------MASISAASPVAG-------KAAAFAHK :
GmACO1  : CTS-----SFSATARSLLCSVPRWSHRLHSA-SPLTPRPRISAV---APLVERFHREIATMANENPFKGN :
GmACO2  : SAPRRSPGSSSAATRSFGSAVPRWSHGVDWR-SPLGLRPQIRAA---APLIERFHRRIATSATDNPFKGN :
GmACO3  : ------------------------------------------------------------------- :
GmACO4  : ----------------------------------------MRIYDEFK-----------EIVKIQK :
GmACO5  : ----------------------------------------MASSLLSPSFT---------SFPRIKK :
GmACO6  : ------------------------------------------------------------------- :
GmACO7  : ------------------------------------------------------------------- :
GmACO8  : ----------------------------------------MAFNSSP--------------FITCKK :
TaACO1  : --------------------------------------MNYSCIIREA---------SMRMINP :
TaACO2  : RRCSHAVAAAIVVEKLGQGRSVGPSLPVPRRSRDGFLARRGRQQPAAAPCGSAVEGAGAAAPATDRFANT :
TaACO3  : ------------------------------------------------------------------- :
TaACO4  : RRCSHAVAAAIVVEKLGQRRSVGPSLPVPRRSRDGFLARRGRQQPAAAPCGSAVEGAG-AAPATDRFAKT :
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TaACO6  : ------------------------------------------------------------------- :
TaACO7  : AEPAPCPSAPAPSPLHAARGGQGPRGAFASGLAGRLFGGRRAAARSSSSAAAVFERRFASAATKNSYDEI :
TaACO8  : ----------------------------------------MASISAAAKAT---------SAAFAHK :
TaACO9  : RRAAFPP-AASRPFAGLLRAAR---VRCSSS-TSGRGRG---------SVARFQRSSMAASGTEHAYNNI :
TaACO10 : ----------------------------------------MASISAAAKAT---------SAAFAHK :
TaACO11 : RRAAFPP-PAPRPFAGLLRAAR---ARCSPSPSATTGPA----------VERSQRSRMAASGTEHAYSNI :
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TaACO13 : RRASFPP-AASRPFAGLLRAAR---VRCSSSSAAGRGRGSVAP-----AVARFQRR-MAVSGTEHAYSNI :
TaACO14 : -MSTSSSNSNPFSFALR------------------------------------------------------ :
TaACO15 : ------------------------------------------------------------------- :
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PpACO2  : RL-SSPVINSRLFRTLAAASY-PDEHRPADFSVARS-----TKSTVGLRSTIPGARMASTQASENPFSSL :
PpACO3  : RL-SPDSAGSRLFRTIVSASYSADECRAAVASVGRSSPRALSPTMVPTTTTVPGSRMASTQASENPFSSL :
PpACO4  : ----------------------------------------MATTAVSVAHHPGISSALRDGASLASG :
PpACO5  : FL-CPASFHSVTILILLLSPP--------------------PPSPLPFP-----STMASSPASKNPFSNL :
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SdACO2  : -------MHSQELKYFSLDSF----------------------------------------FAANPYKNL :
SdACO3  : ------------------------------------------------------------------MEG :
SdACO4  : ------------------------------------------------------------------- :
SdACO5  : ------------------------------------------------------------------- :
SdACO6  : RLSCFHRVRSVHFRASIALRQ----------------------------------RQEIAMVSGHPFESI :
SdACO7  : RLSCFHRVRSVHFRASIALRQ----------------------------------RQEIAMVSGHPFESI :
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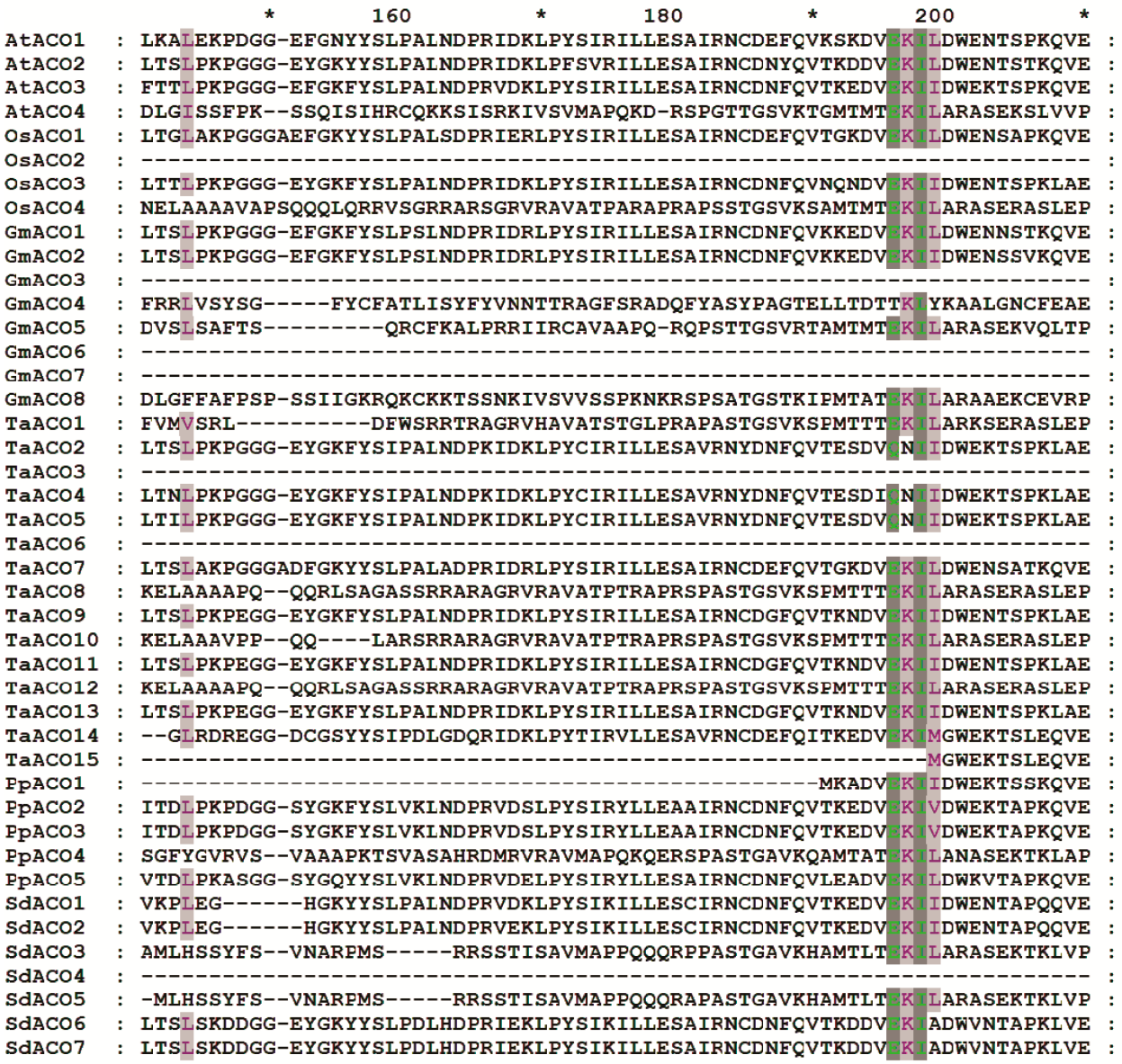
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GmACO4 : FRRLVSYSG-----FYCFATLISYFYVNNTTRAGFSRADQFYASYPAGTELLTDTTKVYKAALGNCFEAE :
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GmACO6 : ---------- :
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TaACO14 : --GLRDREGG-DCGSYYSIPDLGDQRIDKLPYTIRVLLESAVRNCDEFQITKEDVEKVMGWEKTSLEQVE :
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SdACO4 : ---------- :
SdACO5 : -MLHSSYFS--VNARPMS-----RRSSTISAVMAPPQQQRAPASTGAVKHAMTLTEKVLARASEKTKLVP :
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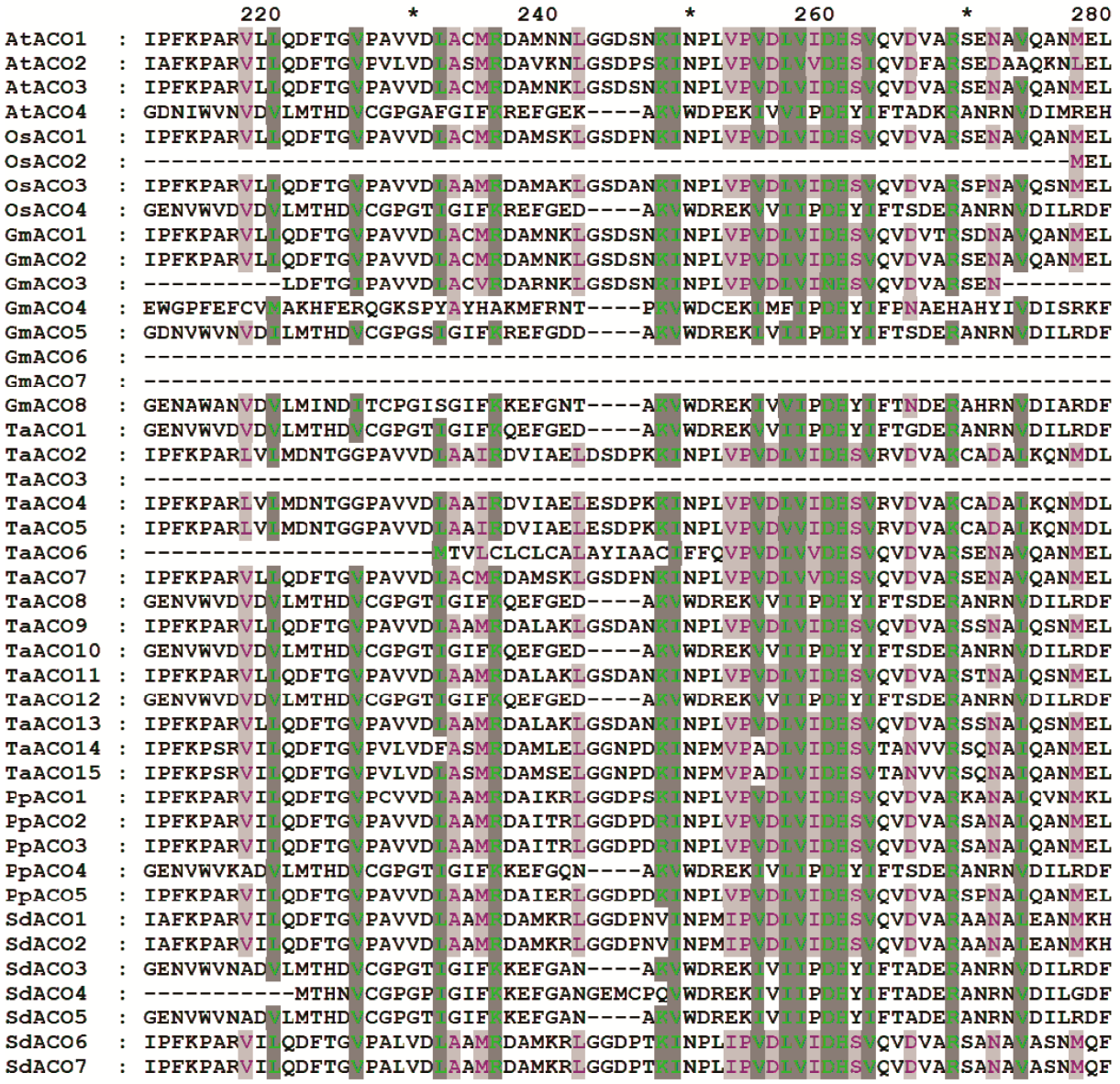
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OsACO2 : ----------MEL :
OsACO3 : IPFKPARVLLQDFTGVPAVVDLAAMRDAMAKLGSDANKINPLVPVDLVIDHSVQVDVAMSPNAVQSNMEL :
OsACO4 : GENVWVDVDVLMTHDVCGPGTIGIFKREFGED----AKVWDREKVVIIPDHYIFTSDEMANRNVDILRDF :
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GmACO3 : ----------LDFTGIPAVVDLACVRDARNKLGSDSNKINPLVPVDLVIDHSVQVDVAMSEN--------- :
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SdACO6 : IPFKPARVIMQDFTGVPALVDLAAMRDAMKRLGGDPTKINPLIPVDLVIDHSVQVDVAMSANAVASNMQF :
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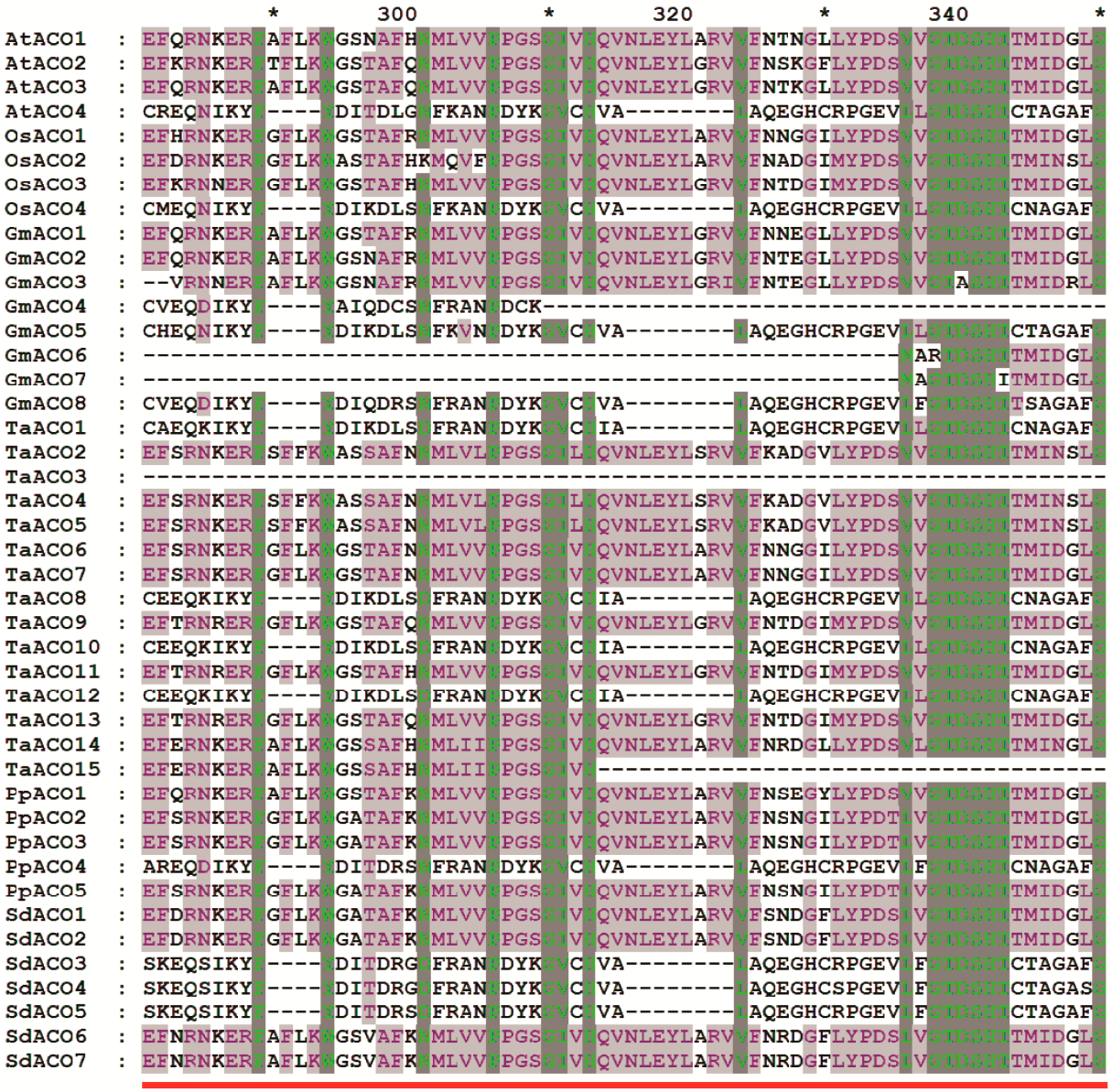
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AtACO4 : CREQNIKYT----YDITDLGWFKANPDYKGVCWVA--------IAQEGHCRPGEVLLGTDSHICTAGAFG :
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OsACO2 : EFDRNKERVGFLKWASTAFHKMQVFPPGSGIVEQVNLEYLARVVFNADGIMYPDSVVGTDSHITMINSLG :
OsACO3 : EFKRNNERVGFLKWGSTAFHYMLVVPPGSGIVEQVNLEYLGRVVFNTDGIMYPDSVVGTDSHITMIDGLG :
OsACO4 : CMEQNIKYT----YDIKDLSWFKANPDYKGVCWVA--------IAQEGHCRPGEVLLGTDSHICNAGAFG :
GmACO1 : EFQRNKERVAFLKWGSTAFRYMLVVPPGSGIVEQVNLEYLGRVVFNNEGLLYPDSVVGTDSHITMIDGLG :
GmACO2 : EFQRNKERVAFLKWGSNAFRYMLVVPPGSGIVEQVNLEYLGRVVFNTEGLLYPDSVVGTDSHITMIDGLG :
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GmACO4 : CVEQDIKYT----IAIQDCSWFRANPDCK--- :
GmACO5 : CHEQNIKYT----YDIKDLSWFKVNPDYKGVCWVA--------IAQEGHCRPGEVLLGTDSHICTAGAFG :
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GmACO8 : CVEQDIKYT----YDIQDRSWFRANPDYKGVCWVA--------IAQEGHCRPGEVLFGTDSHITSAGAFG :
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TaACO15 : EFERNKERVAFLKWGSSAFHYMLIIPPGSGIVE---------------------------------- :
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SdACO2 : EFDRNKERVGFLKWGATAFKYMLVVPPGSGIVEQVNLEYLARVVFSNDGFLYPDSIVGTDSHITMIDGLG :
SdACO3 : SKEQSIKYT----YDITDRGWFRANPDYKGVCWVA--------IAQEGHCRPGEVLFGTDSHICTAGAFG :
SdACO4 : SKEQSIKYT----YDITDRGWFRANPDYKGVCWVA--------IAQEGHCSPGEVLFGTDSHICTAGASG :
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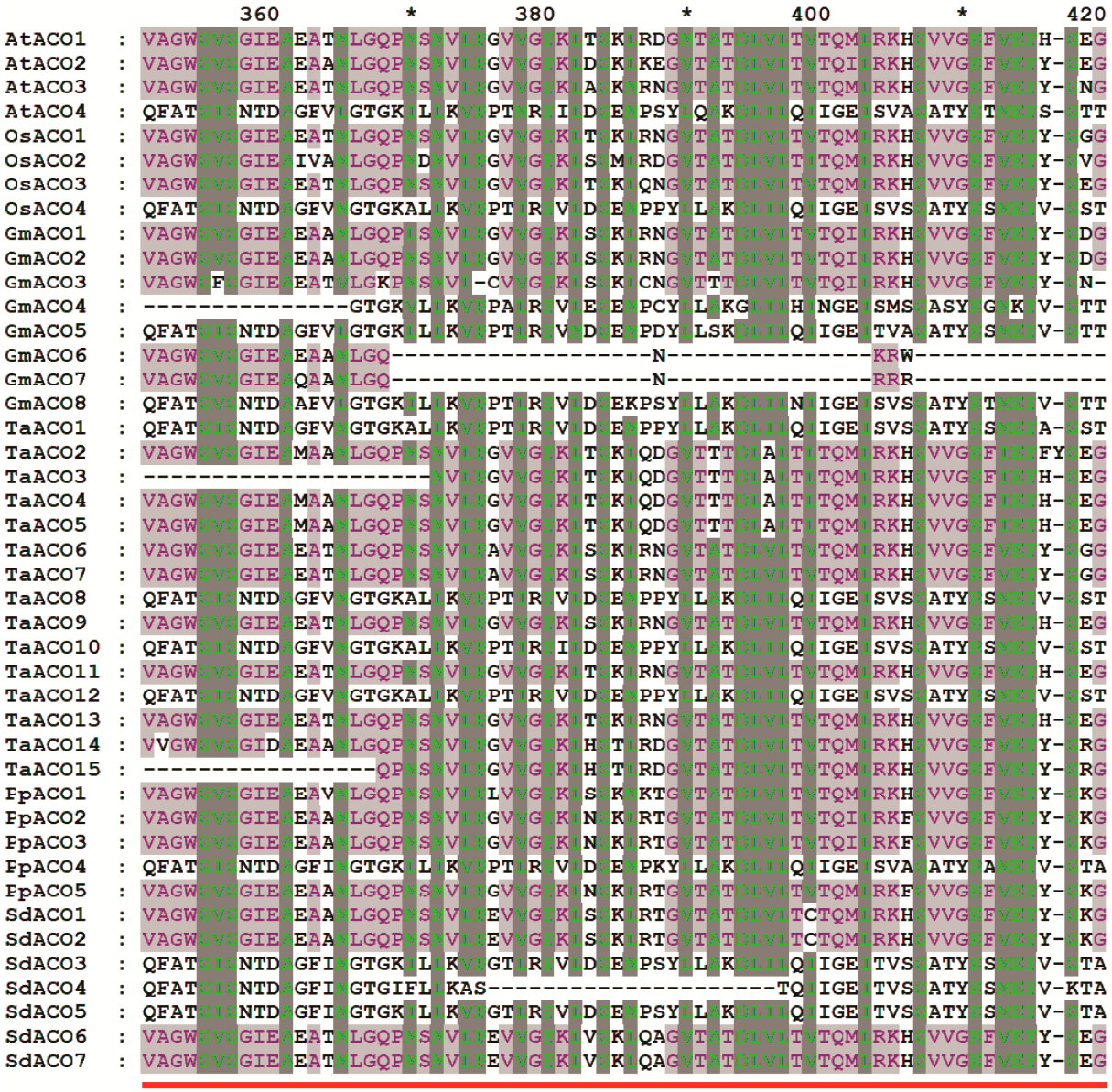
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AtACO2
AtACO3
AtACO4
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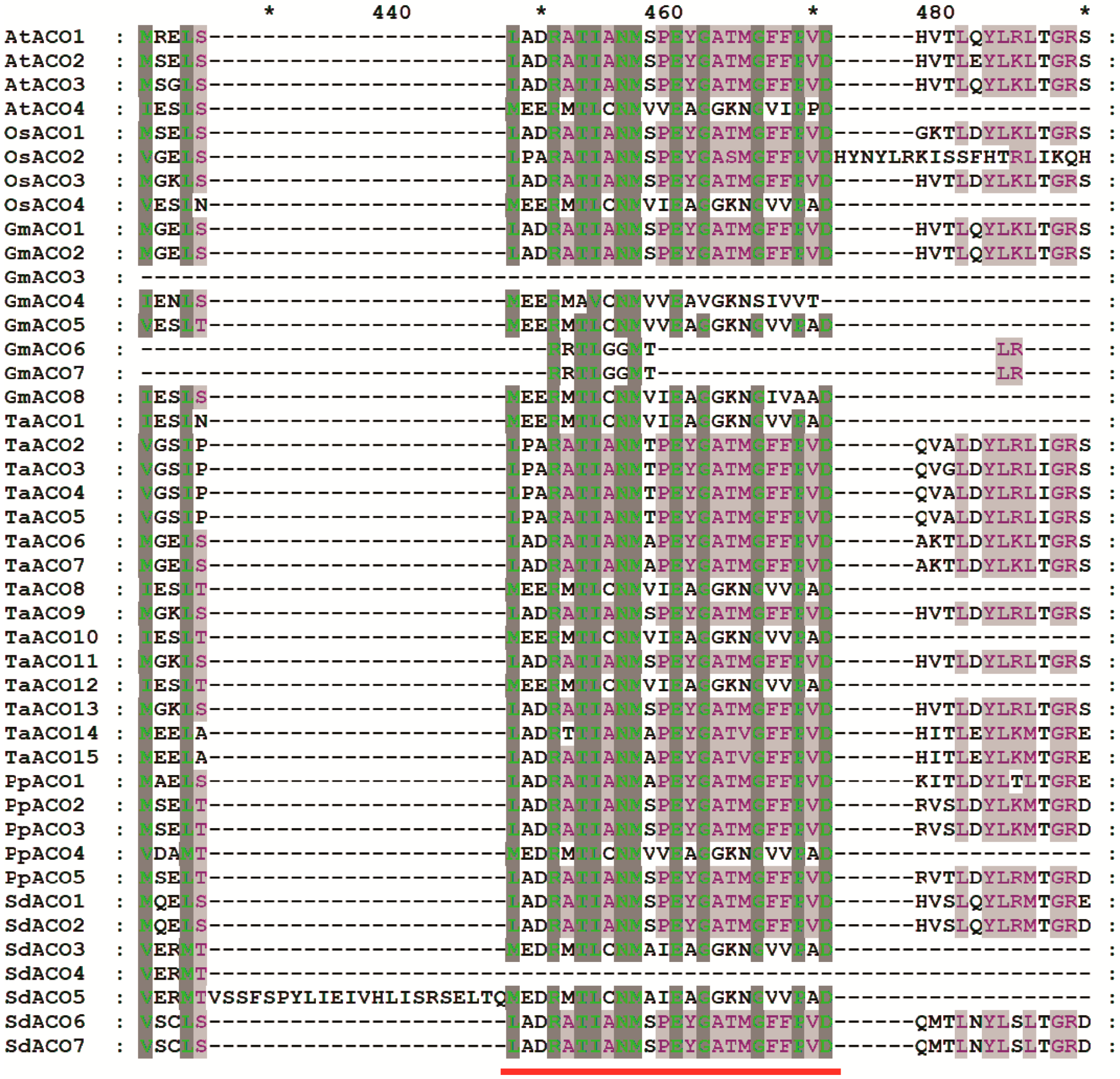
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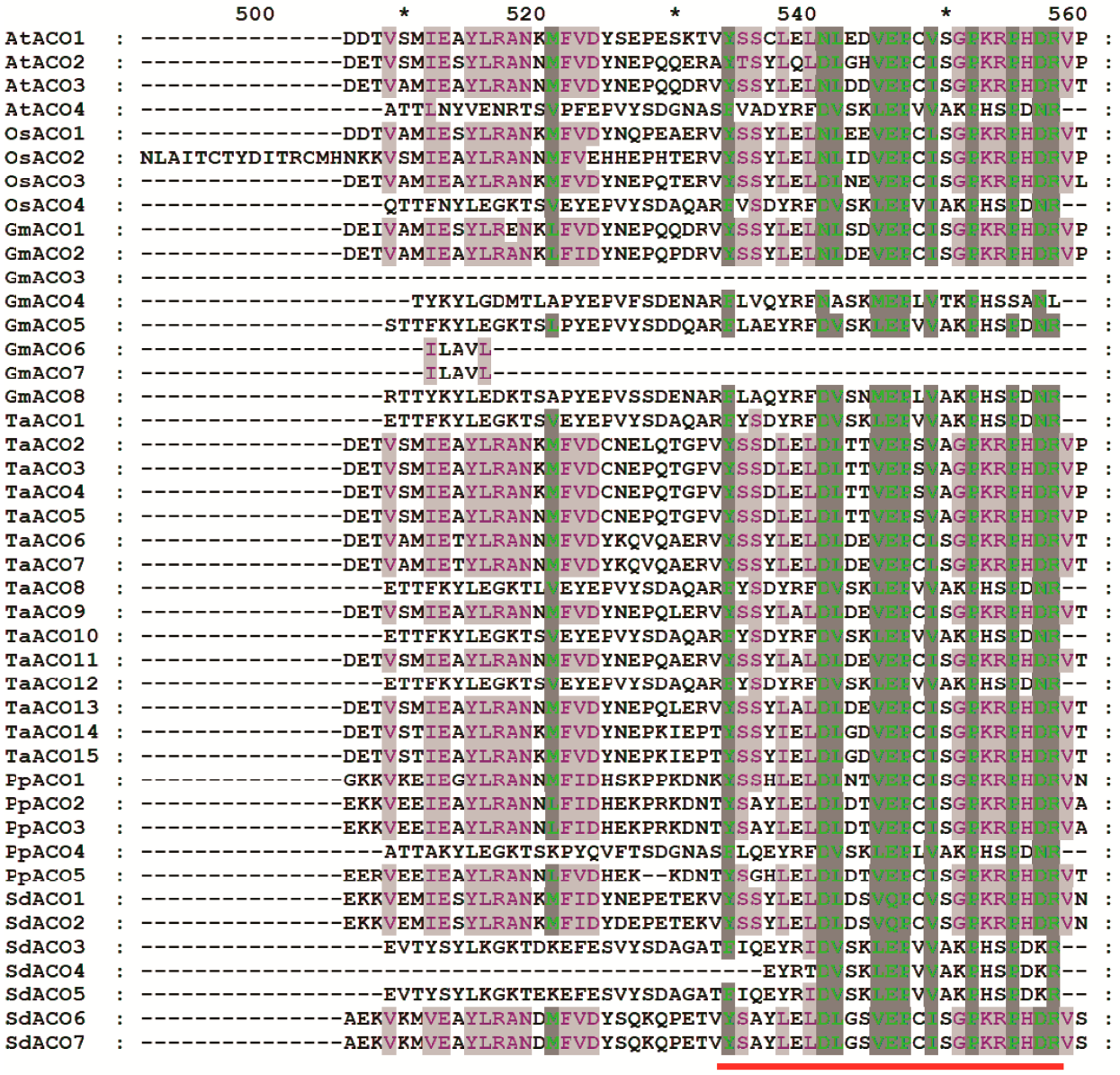
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AtACO3 : ---------------DETVAMIEAYLRANNMFVDYNEPQQDRVMSSYLELMLDDVEPCISGGKRPHDRVT :
AtACO4 : -------------------ATTLNYVENRTSVPFEPVYSDGNASEVADYRFQVSKLEPVVAKGHSPDMR-- :
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OsACO2 : NLAITCTYDITRCMHNKKVSMIEAYLRANNMFVEHHEPHTERVMSSYLELMLIDVEPCISGGKRPHDRVP :
OsACO3 : ---------------DETVAMIEAYLRANKMFVDYNEPQTERVMSSYLELDLNEVEPCISGGKRPHDRVL :
OsACO4 : -------------------QTTFNYLEGKTSVEYEPVYSDAQARGVSDYRFQVSKLEPVVAKGHSPDMR-- :
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GmACO2 : ---------------DETVAMIEAYLRANKLFIDYNEPQPDRVMSSYLELMLDEVEPCISGGKRPHDRVP :
GmACO3 : -- :
GmACO4 : --------------------TYKYLGDMTLAPYEPVFSDENARGLVQYRFMASKMEPLVTKGHSSAMLL-- :
GmACO5 : -------------------STTFKYLEGKTSLPYEPVYSDDQARGLAEYRFQVSKLEPVVAKGHSPDMR-- :
GmACO6 : ----------------------ILAVL-- :
GmACO7 : ----------------------ILAVL-- :
GmACO8 : -------------------RTTYKYLEDKTSAPYEPVSSDENARGLAQYRFQVSNMEPLVAKGHSPDMR-- :
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PpACO2 : ---------------EKKVEEIEAYLRANNLFIDHEKPRKDNTMSAYLELDLDTVEPCISGGKRPHDRVA :
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SdACO5 : -------------------EVTYSYLKGKTEKEFESVYSDAGATGIQEYRIQVSKLEPVVAKGHSPDKR-- :
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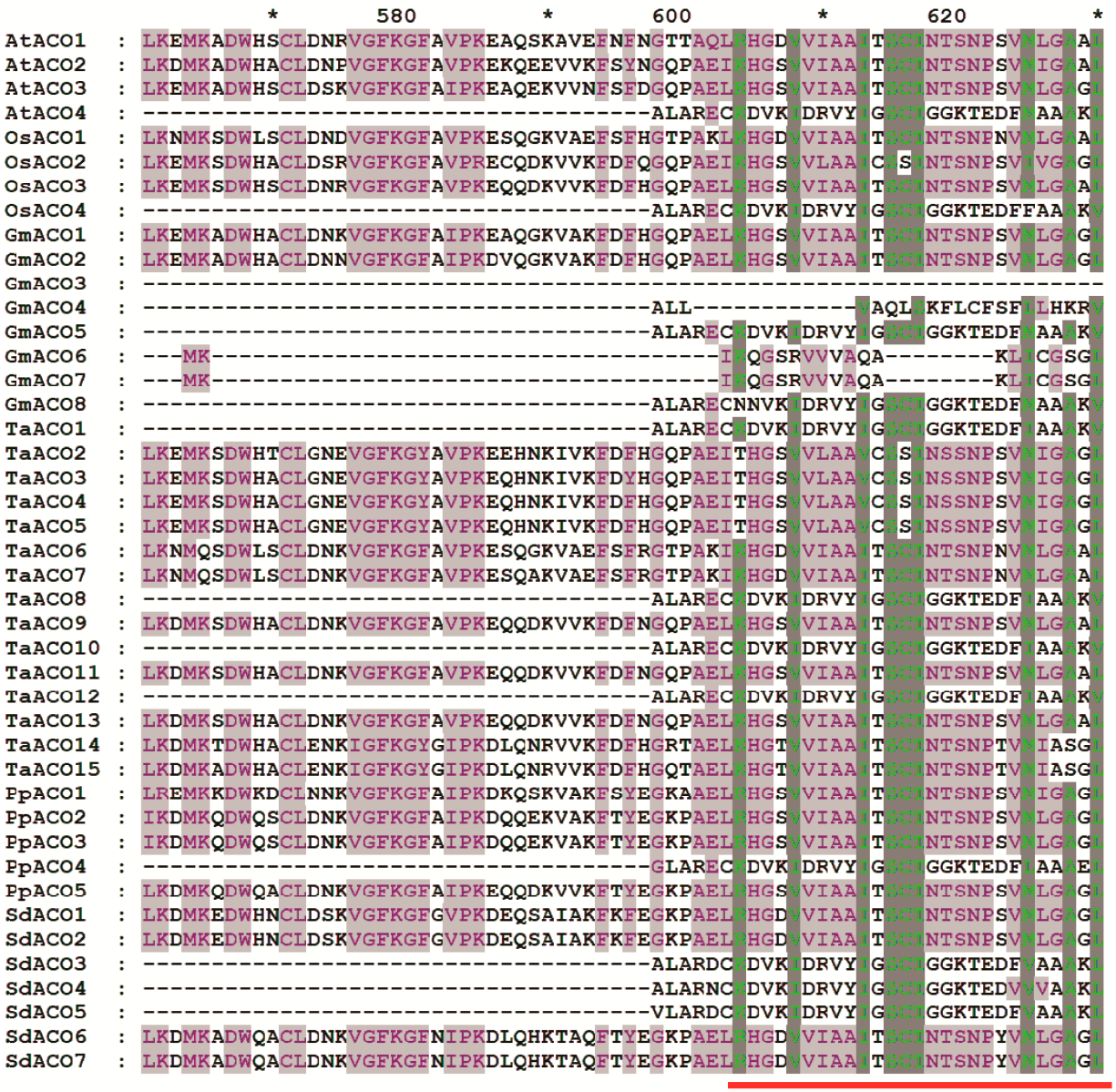
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AtACO3 : LKEMKADWHSCLDSKVGFKGFAIPKEAQEKVVNFSFDGQPAELPHGSWVIAAITSCTNTSNPSVMLGAGL :
AtACO4 : ----------ALARECPDVKIDRVYIGSCTGGKTEDFMAAAKL :
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OsACO2 : LKEMKSDWHACLDSRVGFKGFAVPRECQDKVVKFDFQGQPAEIPHGSWVLAAICSSINTSNPSVIVGAGL :
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GmACO3 : ---------- :
GmACO4 : ----------ALL----------VAQLPKFLCFSFILHKRV :
GmACO5 : ----------ALARECPDVKIDRVYIGSCTGGKTEDFMAAAKV :
GmACO6 : ---MK----------IPQGSRVVVAQA--------KLICGSGL :
GmACO7 : ---MK----------IPQGSRVVVAQA--------KLICGSGL :
GmACO8 : ----------ALARECNNVKIDRVYIGSCTGGKTEDFMAAAKV :
TaACO1 : ----------ALARECPDVKIDRVYIGSCTGGKTEDFIAAAKV :
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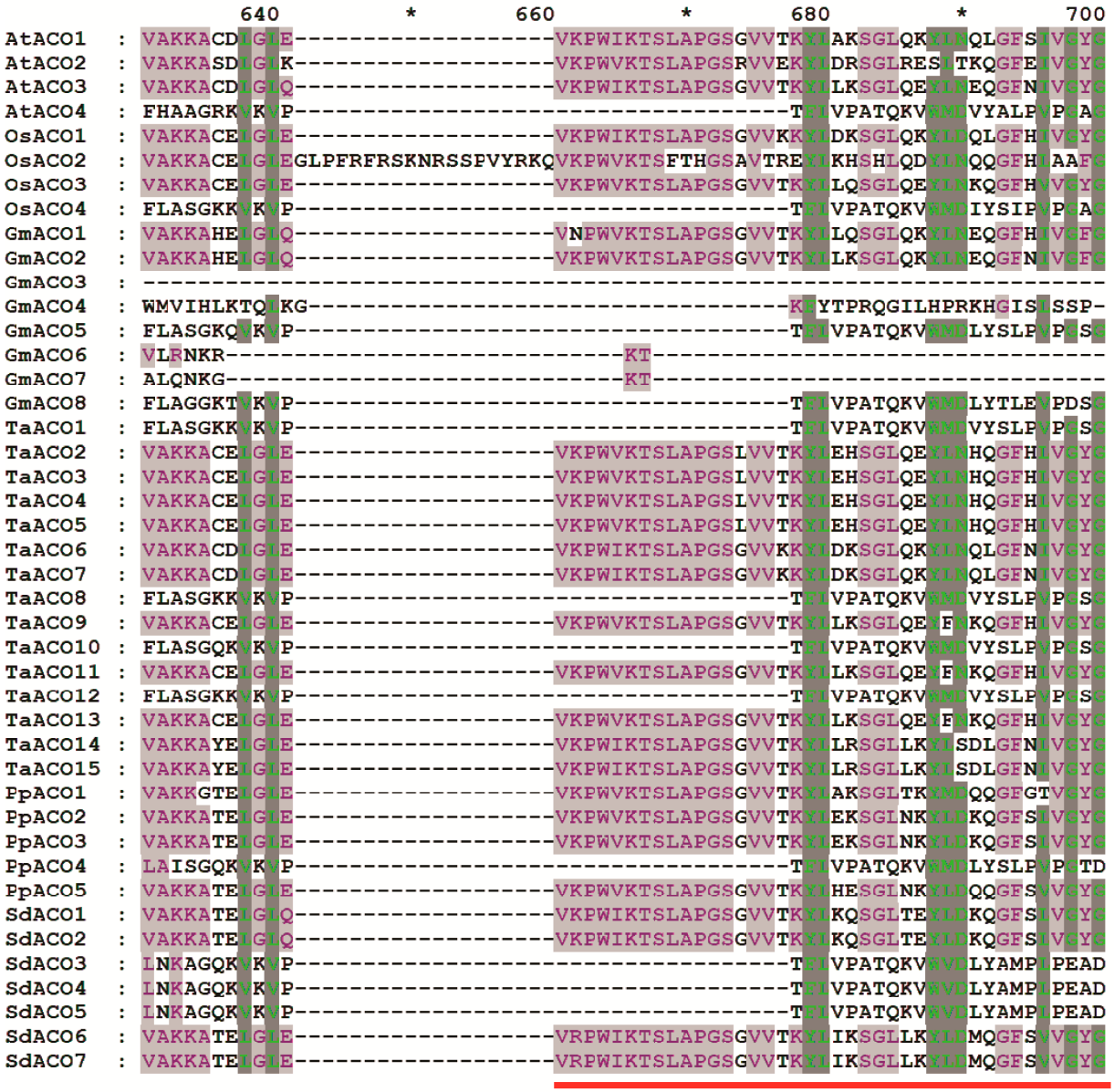
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AtACO2 : VAKKASDLGLK----------VKPWVKTSLAPGSRVVEKYLDRSGLRESLTKQGFEIVGYG :
AtACO3 : VAKKACDLGLQ----------VKPWIKTSLAPGSGVVTKYLLKSGLQEYLNEQGFNIVGYG :
AtACO4 : FHAAGRKVKVP----------TFLVPATQKVRMDVYALPVPGAG :
OsACO1 : VAKKACELGLE----------VKPWIKTSLAPGSGVVKKYLDKSGLQKYLDQLGFHIVGYG :
OsACO2 : VAKKACELGLEGLPFRFRSKNRSSPVYRKQVKPWVKTSFTHGSAVTREYLKHSHLQDYLNQQGFHLAAFG :
OsACO3 : VAKKACELGLE----------VKPWVKTSLAPGSGVVTKYLLQSGLQEYLNKQGFHVVGYG :
OsACO4 : FLASGKKVKVP----------TFLVPATQKVRMDIYSIPVPGAG :
GmACO1 : VAKKAHELGLQ----------VNPWVKTSLAPGSGVVTKYLLQSGLQKYLNEQGFHIVGFG :
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GmACO3 : ----------
GmACO4 : WMVIHLKTQLKG----------KFYTPRQGILHPRKHGISLSSP- :
GmACO5 : FLASGKQVKVP----------TFLVPATQKVRMDLYSLPVPGSG :
GmACO6 : VLRNKR----------KT---------- :
GmACO7 : ALQNKG----------KT---------- :
GmACO8 : FLAGGKTVKVP----------TFLVPATQKVRMDLYTLEVPDSG :
TaACO1 : FLASGKKVKVP----------TFLVPATQKVRMDVYSLPVPGSG :
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SdACO4 : LNKAGQKVKVP----------TFLVPATQKVRVDLYAMPLPEAD :
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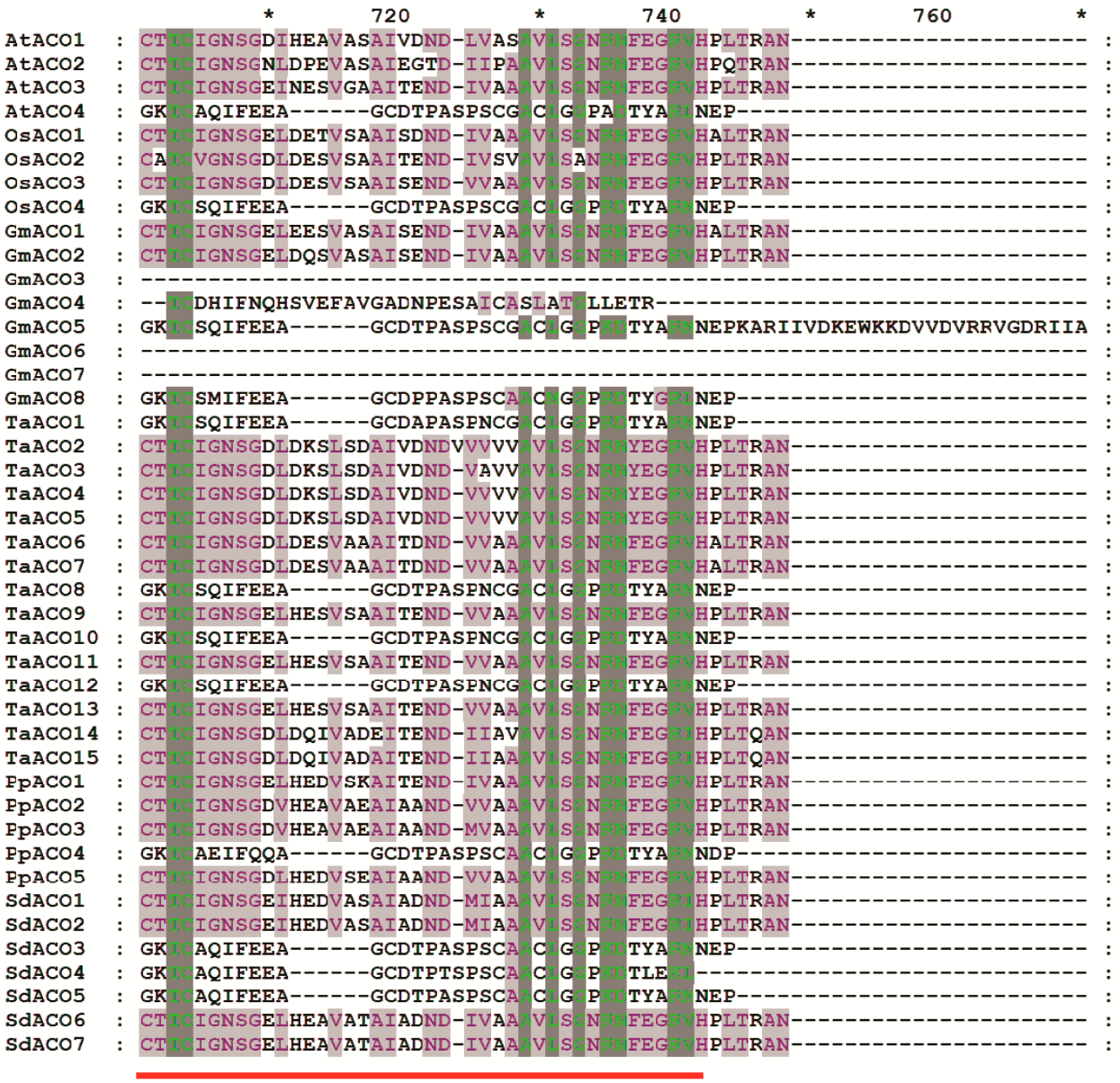
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740
760
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AtACO2
AtACO3
AtACO4
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OsACO2
OsACO3
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GmACO5
GmACO6
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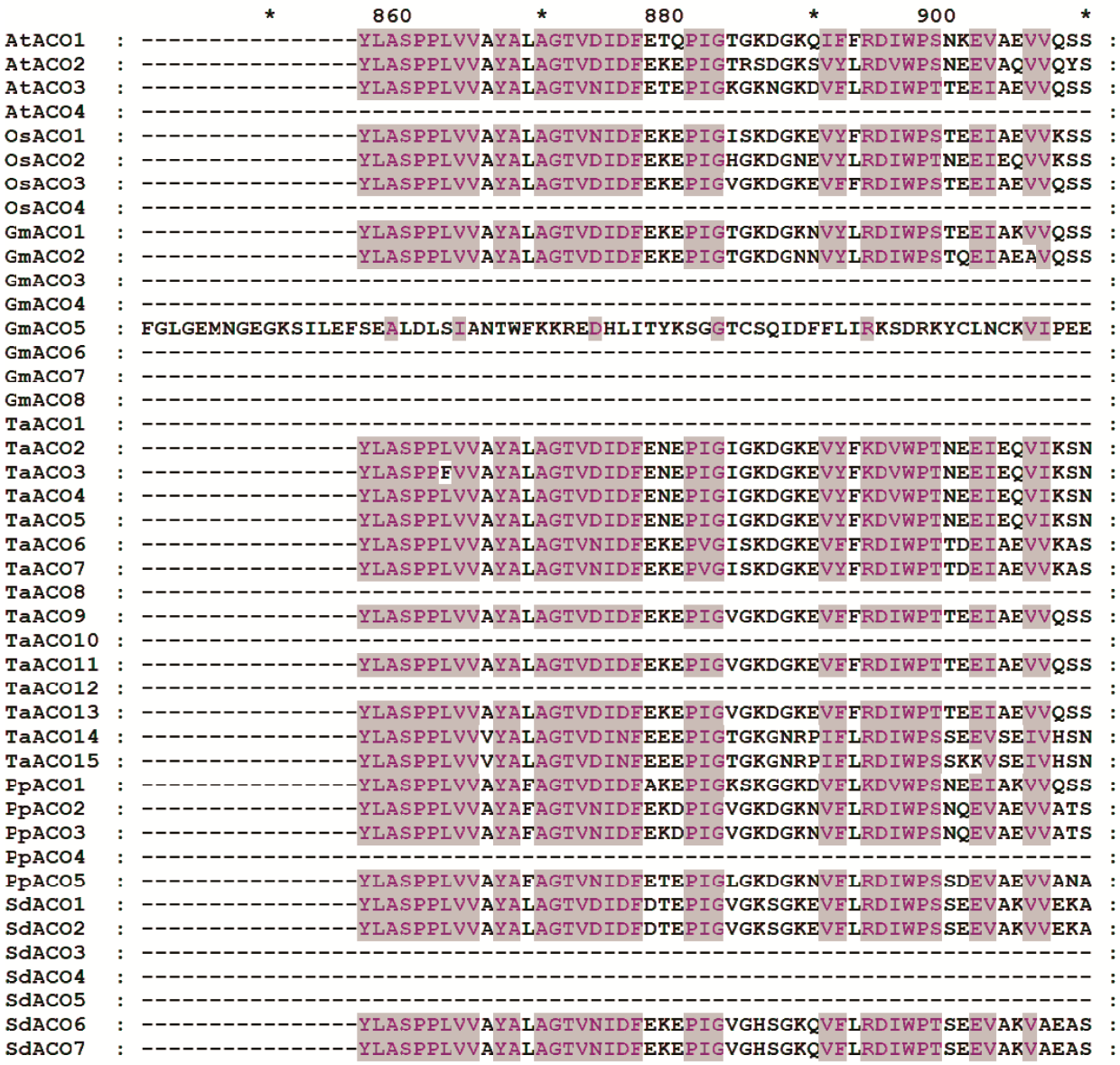
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AtACO3 : ----------YLASPPLVVAYALAGTVNIDFETEPIGKGKNGKDVFLRDIWPTTEEIAEVVQSS :
AtACO4 : ----------
OsACO1 : ----------YLASPPLVVAYALAGTVNIDFEKEPIGISKDGKEVYFRDIWPSTEEIAEVVKSS :
OsACO2 : ----------YLASPPLVVAYALAGTVDIDFEKEPIGHGKDGNEVYLRDIWPTNEEIEQVVKSS :
OsACO3 : ----------YLASPPLVVAYALAGTVDIDFEKEPIGVGKDGKEVFFRDIWPSTEEIAEVVQSS :
OsACO4 : ----------
GmACO1 : ----------YLASPPLVVAYALAGTVDIDFEKEPIGTGKDGKNVYLRDIWPSTEEIAKVVQSS :
GmACO2 : ----------YLASPPLVVAYALAGTVDIDFEKEPIGTGKDGNNVYLRDIWPSTQEIAEAVQSS :
GmACO3 : ----------
GmACO4 : ----------
GmACO5 : FGLGEMNGEGKSILEFSEALDLSIANTWFKKREDHLITYKSGGTCSQIDFFLIRKSDRKYCLNCKVIPEE :
GmACO6 : ----------
GmACO7 : ----------
GmACO8 : ----------
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SdACO4 : ----------
SdACO5 : ----------
SdACO6 : ----------YLASPPLVVAYALAGTVNIDFEKEPIGVGHSGKQVFLRDIWPTSEEVAKVAEAS :
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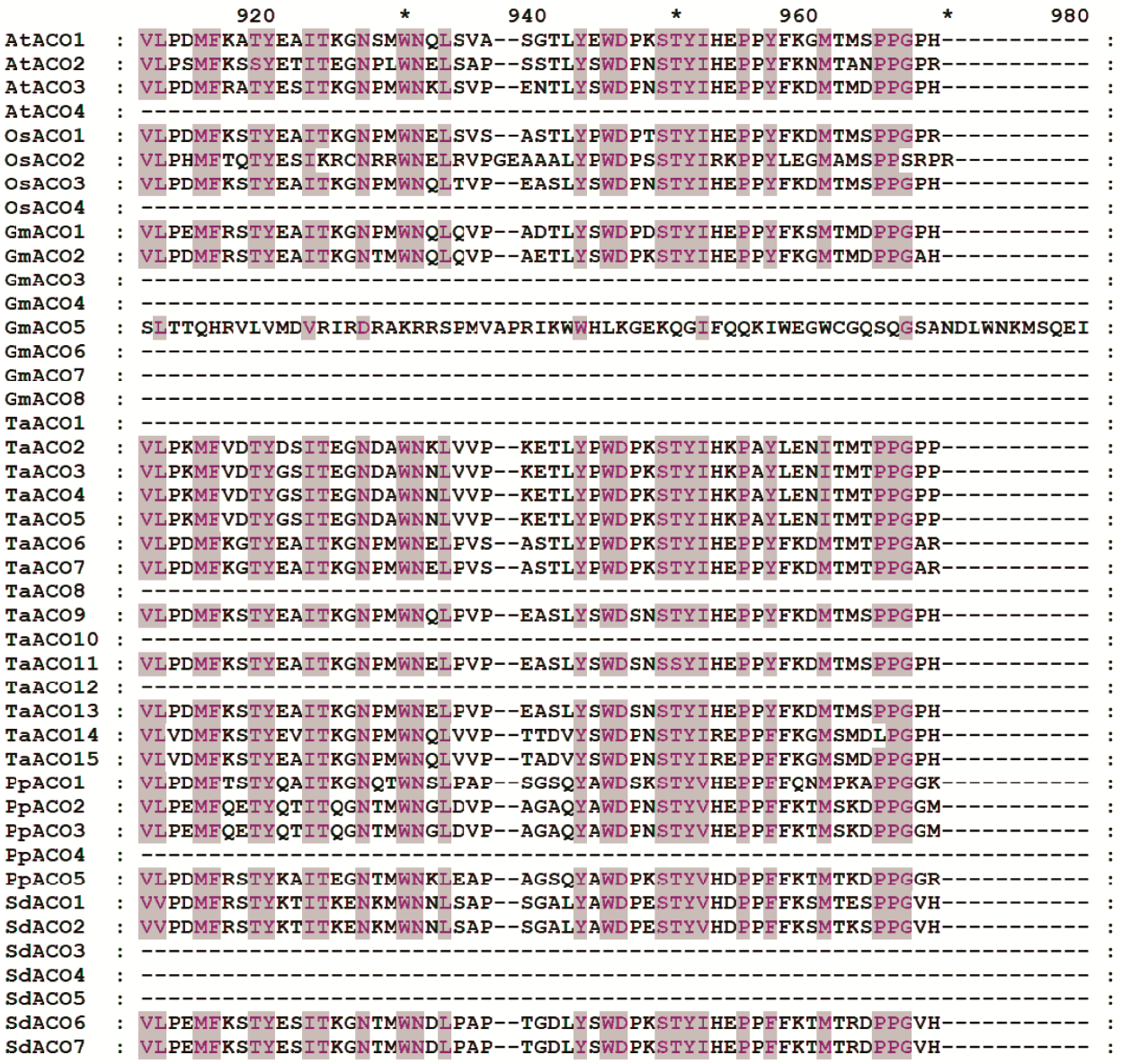
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AtACO3 : VLPDMFRATYESITKGNPMWNKLSVP--ENTLYSWDPNSTYIHEPPYFKDMTMDPPGPH- :
AtACO4 : ---------- :
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OsACO2 : VLPHMFTQTYESIKRCNRRWNELRVPGEAAALYPWDPSSTYIRKPPYLEGMAMSPPSRPR- :
OsACO3 : VLPDMFKSTYEAITKGNPMWNQLTVP--EASLYSWDPNSTYIHEPPYFKDMTMSPPGPH- :
OsACO4 : ---------- :
GmACO1 : VLPEMFRSTYEAITKGNPMWNQLQVP--ADTLYSWDPDSTYIHEPPYFKSMTMDPPGPH- :
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GmACO4 : ---------- :
GmACO5 : SLTTQHRVLVMDVRIRDRAKRRSPMVAPRIKWWHLKGEKQGIFQQKIWEGWCGQSQGSANDLWNKMSQEI :
GmACO6 : ---------- :
GmACO7 : ---------- :
GmACO8 : ---------- :
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TaACO9 : VLPDMFKSTYEAITKGNPMWNQLPVP--EASLYSWDSNSTYIHEPPYFKDMTMSPPGPH- :
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PpACO2 : VLPEMFQETYQTITQGNTMWNGLDVP--AGAQYAWDPNSTYVHEPPFFKTMSKDPPGGM- :
PpACO3 : VLPEMFQETYQTITQGNTMWNGLDVP--AGAQYAWDPNSTYVHEPPFFKTMSKDPPGGM- :
PpACO4 : ---------- :
PpACO5 : VLPDMFRSTYKAITEGNTMWNKLEAP--AGSQYAWDPKSTYVHDPPFFKTMTKDPPGGR- :
SdACO1 : VVPDMFRSTYKTITKENKMWNNLSAP--SGALYAWDPESTYVHDPPFFKSMTESPPGVH- :
SdACO2 : VVPDMFRSTYKTITKENKMWNNLSAP--SGALYAWDPESTYVHDPPFFKSMTKSPPGVH- :
SdACO3 : ---------- :
SdACO4 : ---------- :
SdACO5 : ---------- :
SdACO6 : VLPEMFKSTYESITKGNTMWNDLPAP--TGDLYSWDPKSTYIHEPPFFKTMTRDPPGVH- :
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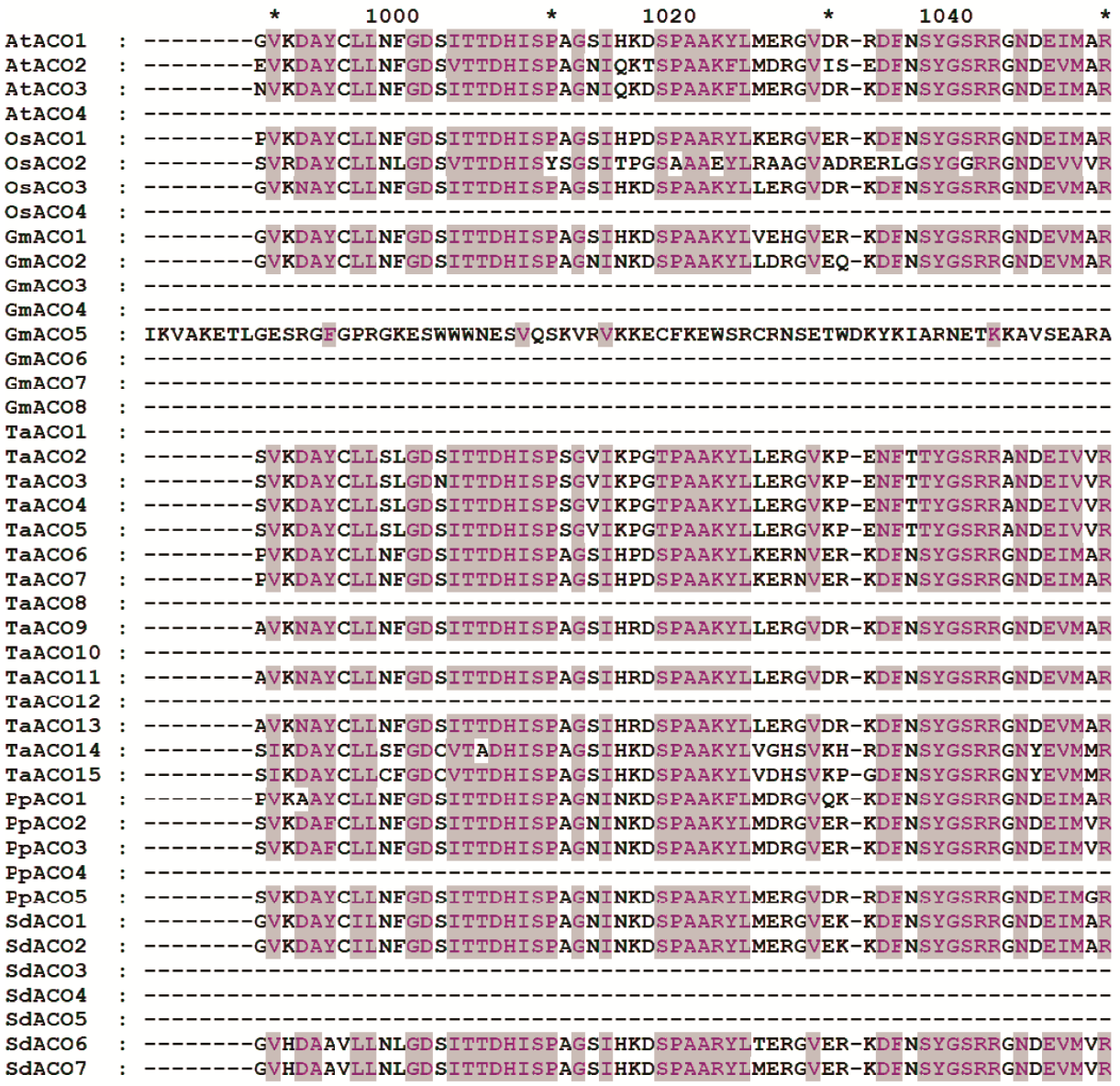
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AtACO4 : ---------- :
OsACO1 : --------PVKDAYCLLNFGDSITTDHISPAGSIHPDSPAARYLKERGVER-KDFNSYGSRRGNDEIMAR :
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OsACO4 : ---------- :
GmACO1 : --------GVKDAYCLLNFGDSITTDHISPAGSIHKDSPAAKYLVEHGVER-KDFNSYGSRRGNDEVMAR :
GmACO2 : --------GVKDAYCLLNFGDSITTDHISPAGNINKDSPAAKYLLDRGVEQ-KDFNSYGSRRGNDEVMAR :
GmACO3 : ---------- :
GmACO4 : ---------- :
GmACO5 : IKVAKETLGESRGFGPRGKESWWWNESVQSKVRVKKECFKEWSRCRNSETWDKYKIARNETKKAVSEARA :
GmACO6 : ---------- :
GmACO7 : ---------- :
GmACO8 : ---------- :
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TaACO9 : --------AVKNAYCLLNFGDSITTDHISPAGSIHRDSPAAKYLLERGVDR-KDFNSYGSRRGNDEVMAR :
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TaACO12 : ---------- :
TaACO13 : --------AVKNAYCLLNFGDSITTDHISPAGSIHRDSPAAKYLLERGVDR-KDFNSYGSRRGNDEVMAR :
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TaACO15 : --------SIKDAYCLLCFGDCVTTDHISPAGSIHKDSPAAKYLVDHSVKP-GDFNSYGSRRGNYEVMMR :
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PpACO3 : --------SVKDAFCLLNFGDSITTDHISPAGNINKDSPAAKYLMDRGVER-KDFNSYGSRRGNDEIMVR :
PpACO4 : ---------- :
PpACO5 : --------SVKDAYCLLNFGDSITTDHISPAGNINKDSPAARYLMERGVDR-RDFNSYGSRRGNDEIMGR :
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SdACO4 : ---------- :
SdACO5 : ---------- :
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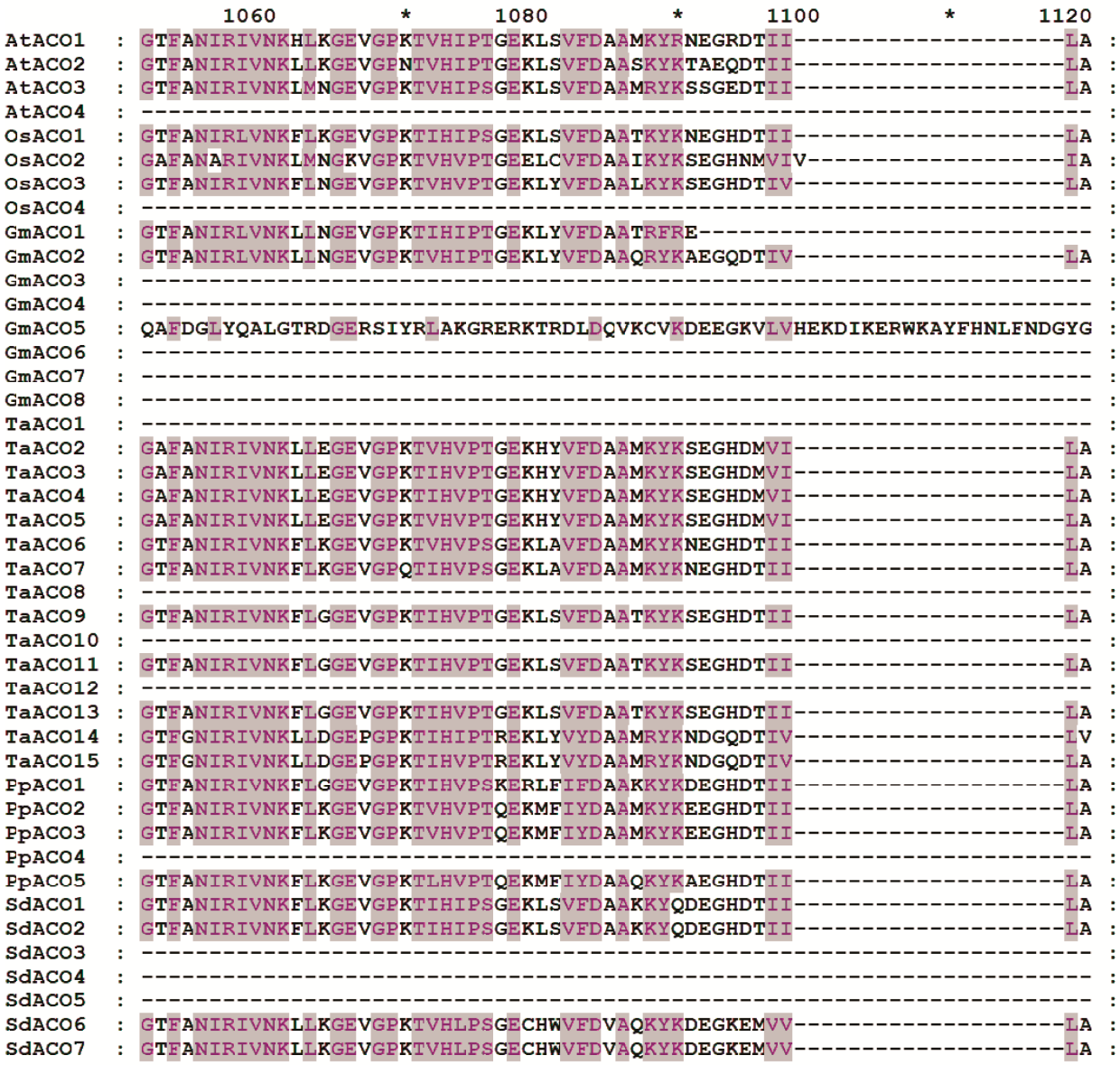
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AtACO3 : GTFANIRIVNKLMNGEVGPKTVHIPSGEKLSVFDAAMRYKSSGEDTII----------LA :
AtACO4 : ---------- :
OsACO1 : GTFANIRLVNKFLKGEVGPKTIHIPSGEKLSVFDAATKYKNEGHDTII----------LA :
OsACO2 : GAFANARIVNKLMNGKVGPKTVHVPTGEELCVFDAAIKYKSEGHNMVIV----------IA :
OsACO3 : GTFANIRIVNKFLNGEVGPKTVHVPTGEKLYVFDAALKYKSEGHDTIV----------LA :
OsACO4 : ---------- :
GmACO1 : GTFANIRLVNKLLNGEVGPKTIHIPTGEKLYVFDAATRFRE---------- :
GmACO2 : GTFANIRLVNKLLNGEVGPKTVHIPTGEKLYVFDAAQRYKAEGQDTIV----------LA :
GmACO3 : ---------- :
GmACO4 : ---------- :
GmACO5 : QAFDGLYQALGTRDGERSIYRLAKGRERKTRDLDQVKCVKDEEGKVLVHEKDIKERWKAYFHNLFNDGYG :
GmACO6 : ---------- :
GmACO7 : ---------- :
GmACO8 : ---------- :
TaACO1 : ---------- :
TaACO2 : GAFANIRIVNKLLEGEVGPKTVHVPTGEKHYVFDAAMKYKSEGHDMVI----------LA :
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SdACO2 : GTFANIRIVNKFLKGEVGPKTIHIPSGEKLSVFDAAKKYQDEGHDTII----------LA :
SdACO3 : ---------- :
SdACO4 : ---------- :
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AtACO3  : GAEYGSGSSRDWAAKGPMLQGVKAVIAKSFERIHRSNLVGMGIIPLCFKSGEDADTLG------------ :
AtACO4  : ---------------------------------------------------------------------- :
OsACO1  : GAEYGSGSSRDWAAKGPMLQGVKAVIAKSFERIHRSNLAGMGIIPLCFKSGEDADTLG------------ :
OsACO2  : GAEYGSGSSRDSAAKGPMLLMI------------------------------------------------ :
OsACO3  : GAEYGSGSSRDWAAKGPMLLGVKAVIAKSFERIHRSNLVGMGIIPLCFKAGEDADSLG------------ :
OsACO4  : ---------------------------------------------------------------------- :
GmACO1  : -CLYDKISSKCYICN--ISVYFPLCINYRVLFVQIDNTKGM---------------------------- :
GmACO2  : GAEYGSGSSRDWAAKGPMLLGVKAVIAKSFERIHRSNLVGMGIVPLCFKSGEDADTLG------------ :
GmACO3  : ---------------------------------------------------------------------- :
GmACO4  : ---------------------------------------------------------------------- :
GmACO5  : YDSSSLDTREEDRNYKYYRRIQKQEVKEALKRMSNGKAVGPDNIPIEVWKTLGDRGLEWLTKLFNEIMRS :
GmACO6  : ---------------------------------------------------------------------- :
GmACO7  : ---------------------------------------------------------------------- :
GmACO8  : ---------------------------------------------------------------------- :
TaACO1  : ---------------------------------------------------------------------- :
TaACO2  : GDEYGAGSSRDSAAKGPLLLGVKAVIAKGFERIHRSNLVGMGIIPLRFKAGEDADSLN------------ :
TaACO3  : DDEYGAGSSRDSAAKGPLLLGVKAVIAKGFERIHRSNLVGMGIIPLRFKVGEDADSLN------------ :
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TaACO15 : GSEYGTGSSRDWDAKRTMLLGVKAVIAKSSERIH---------------------------------- :
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PpACO3  : GAEYGSGSSRDWAAKGPYMQGVKAVIAKSFERIHRSNLVGMGLIPLCFKEGEDAETLG------------ :
PpACO4  : ---------------------------------------------------------------------- :
PpACO5  : GAEYGSGSSRDWAAKGPYLQGVKAVIAKSFERIHRSNLVGMGLIPLCFRNGEDADSLG------------ :
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SdACO4  : ---------------------------------------------------------------------- :
SdACO5  : ---------------------------------------------------------------------- :
SdACO6  : GAEYGSGSSRDWAAKGPFLQGVKAVISKSFERIHRSNLVGMSIIPLCYKNGEDAESLG------------ :
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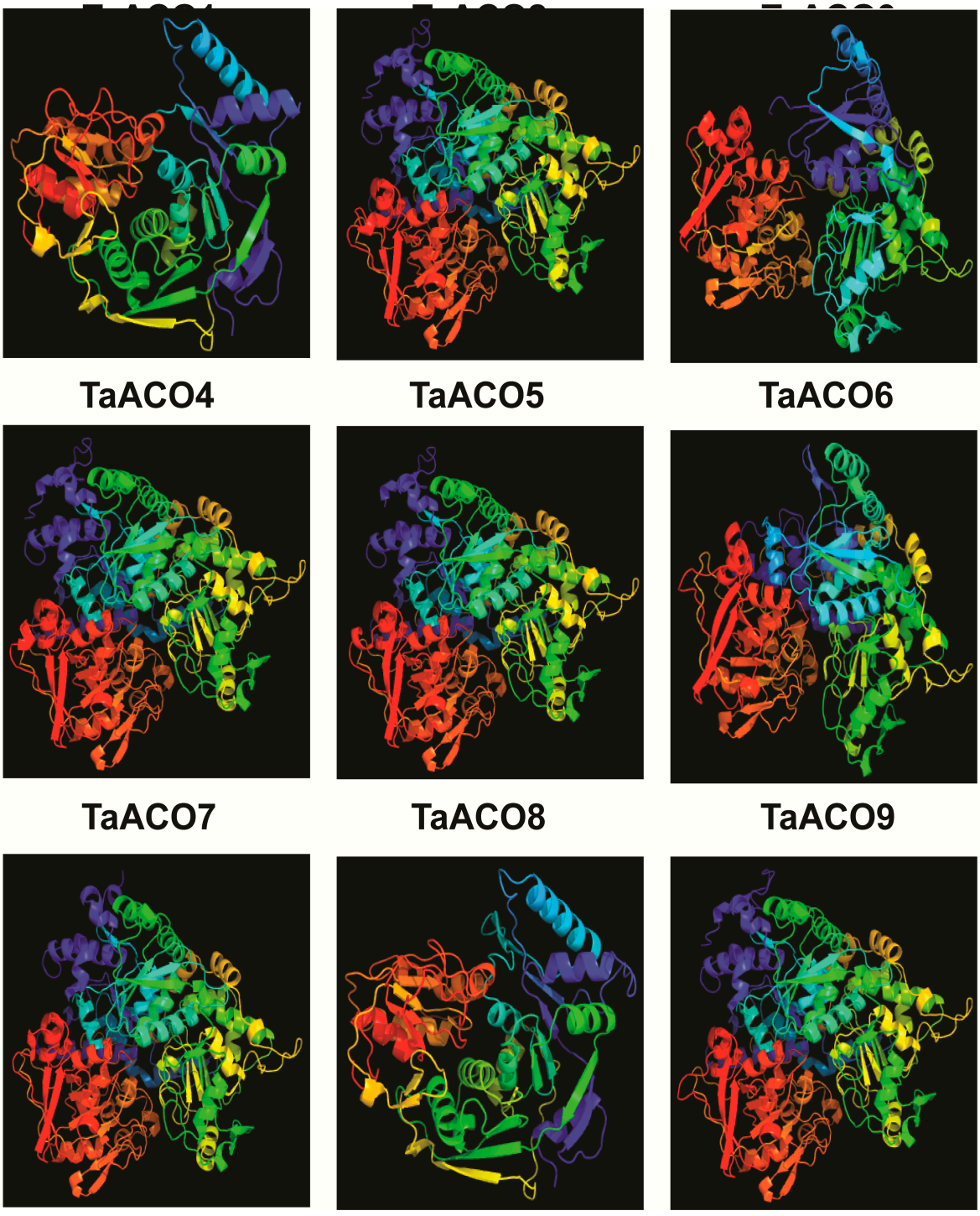


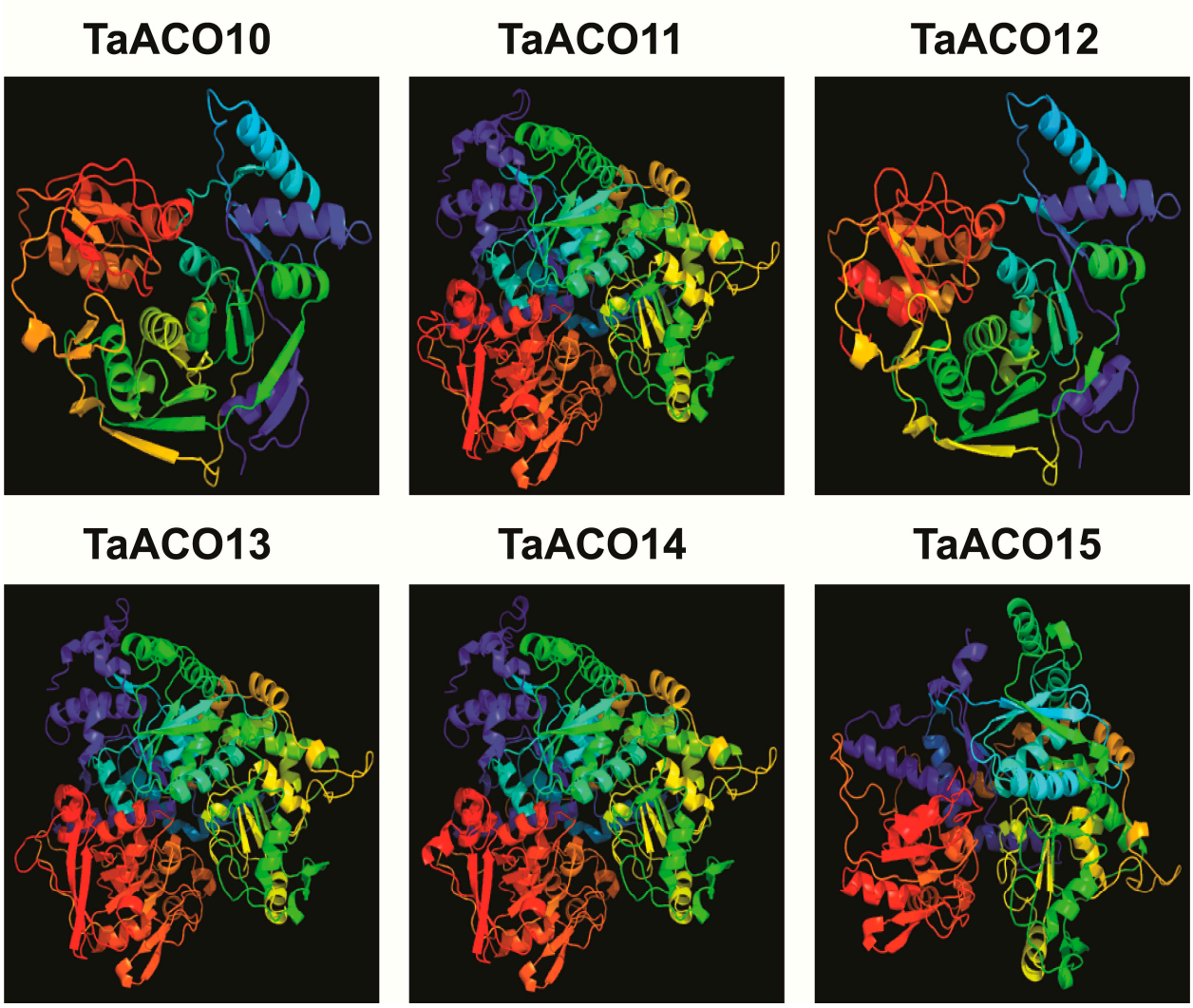
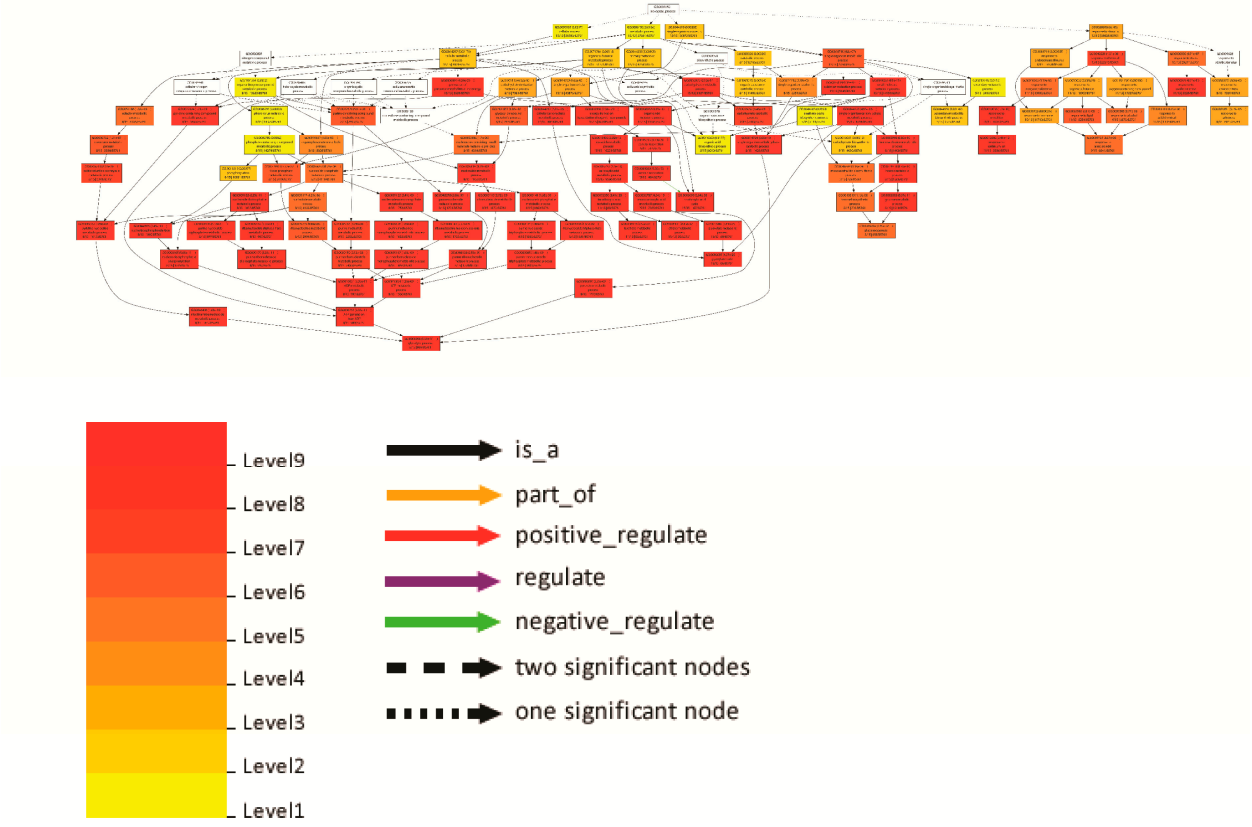


Figure S8. Alignment and 3-dimensional structure of the TaACO protein sequences. **A.** The aconitase domain is underlined with red color. Colored and shaded amino acids are chemically similar residues. Dashes indicate gaps introduced to maximize the alignment of the homologous region. **B.** Predicted 3D structures TaACO proteins.

A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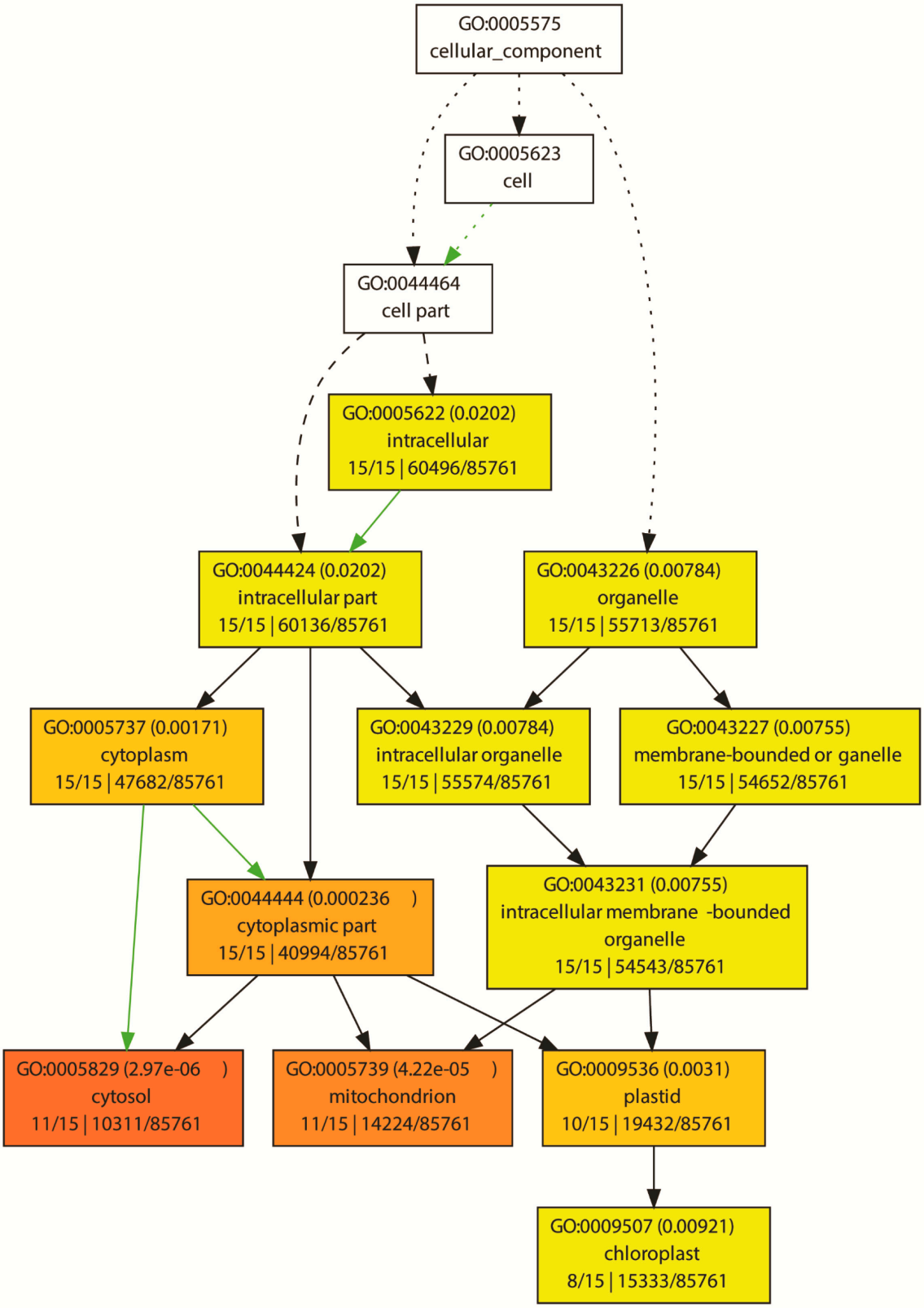
Level1
is_a
part_of
positive_regulate
regulate
negative_regulate
two significant nodes
one significant node

B


GO:0005575
cellular_component
GO:0005623
cell
GO:0044464
cell part
GO:0005622 (0.0202)
intracellular
15/15 | 60496/85761
GO:0044424 (0.0202)
intracellular part
15/15 | 60136/85761
GO:0043226 (0.00784)
organelle
15/15 | 55713/85761
GO:0005737 (0.00171)
cytoplasm
15/15 | 47682/85761
GO:0043229 (0.00784)
intracellular organelle
15/15 | 55574/85761
GO:0043227 (0.00755)
membrane-bounded or ganelle
15/15 | 54652/85761
GO:0044444 (0.000236)
cytoplasmic part
15/15 | 40994/85761
GO:0043231 (0.00755)
intracellular membrane -bounded
organelle
15/15 | 54543/85761
GO:0005829 (2.97e-06)
cytosol
11/15 | 10311/85761
GO:0005739 (4.22e-05)
mitochondrion
11/15 | 14224/85761
GO:0009536 (0.0031)
plastid
10/15 | 19432/85761
GO:0009507 (0.00921)
chloroplast
8/15 | 15333/85761

C

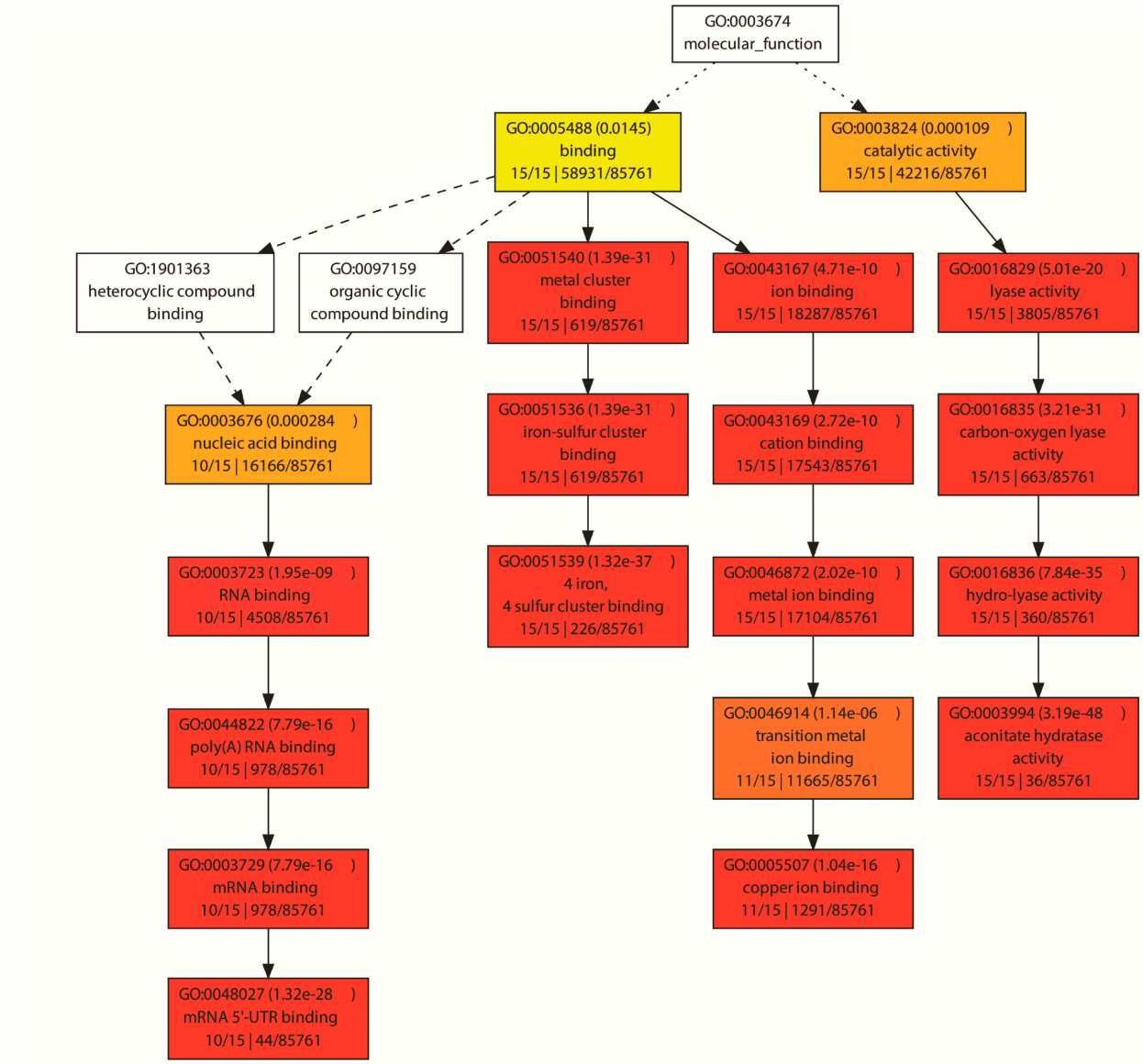


Figure S9. The predicted GO term of TaACO gene family using AgriGO **A.** Biological Process. **B.** Cellular component. **C.** Molecular function.

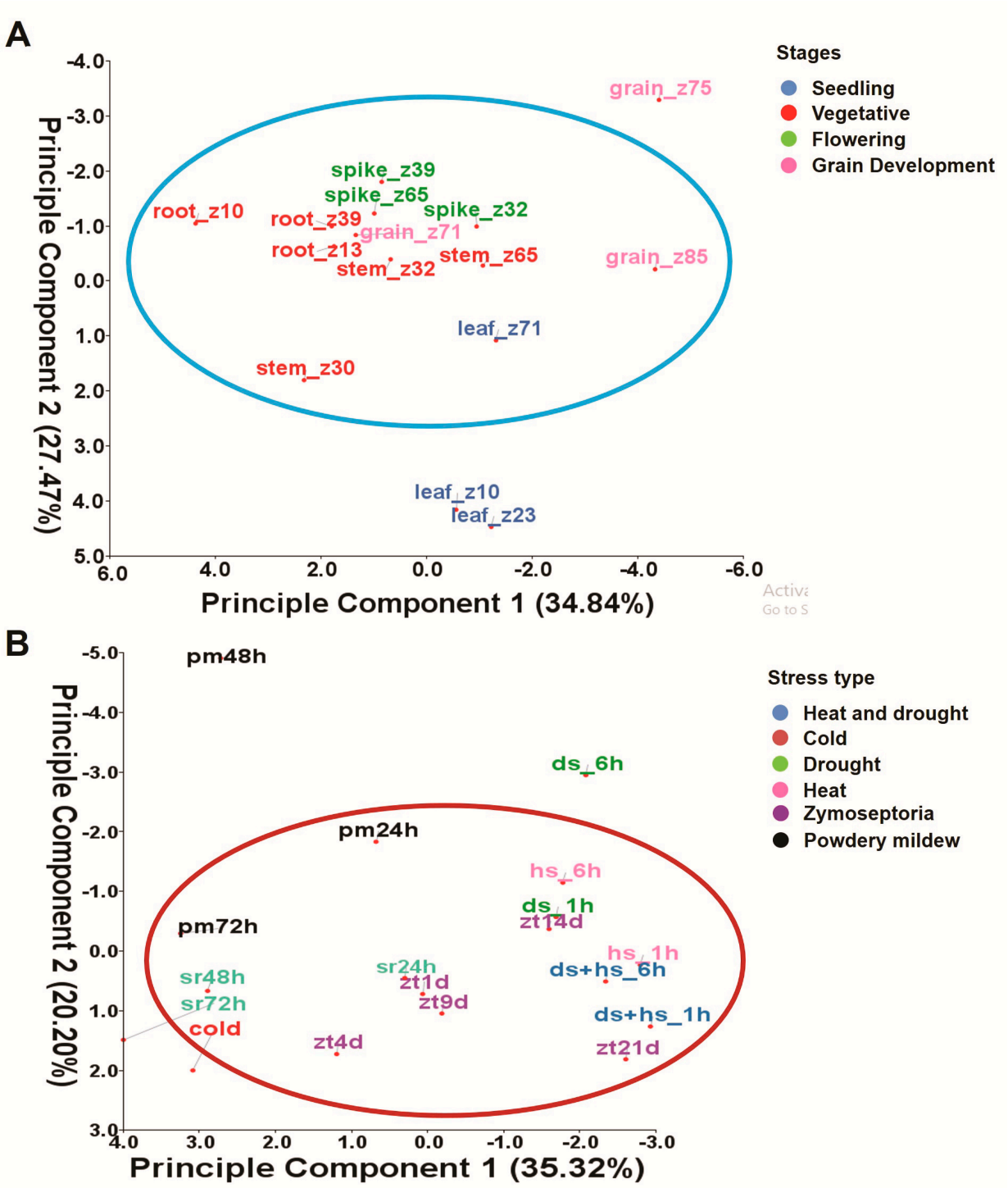


Figure S10. PCA plots displaying grouping of different (A) Different tissues and developmental stages (B) Diverse stress conditions based on the TaACO expression profiles. HS: Heat stress, DS: Drought stress, DS+HS: Combined drought and heat stress; PM: Powdery mildew; SR: Stripe rust, Zt: *Zymoseptoria tritici*, d: days and h: hour.

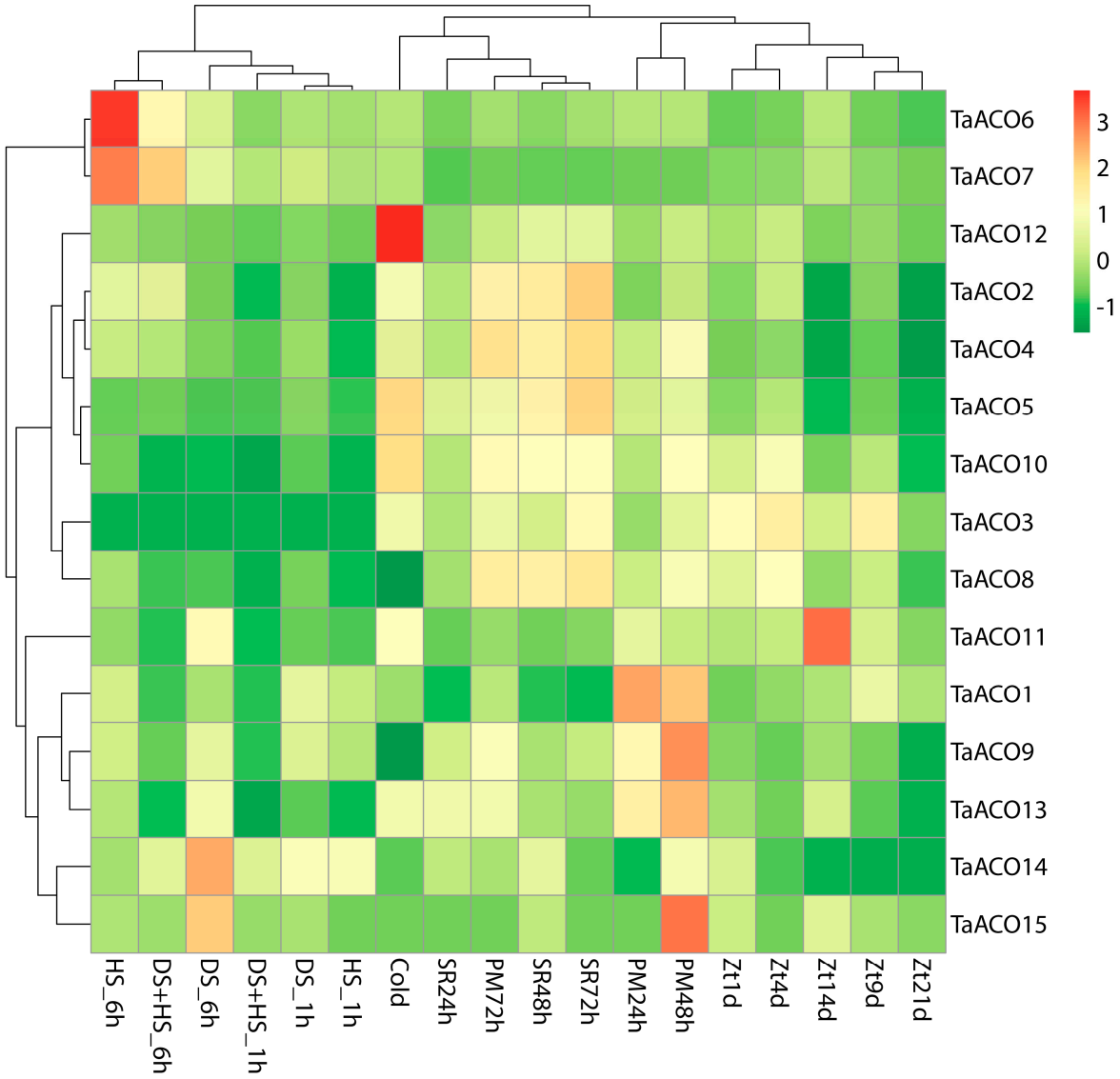


Figure S11. Heatmaps signifying the expression profile of *TaACO* genes in biotic and abiotic stress conditions. TPM values were directly used to produce the heatmaps. HS: Heat stress, DS: Drought stress, DS+HS: Combined drought and heat stress; PM: Powdery mildew; SR: Stripe rust, Zt: *Zymoseptoria tritici*, d: days and h: hour.