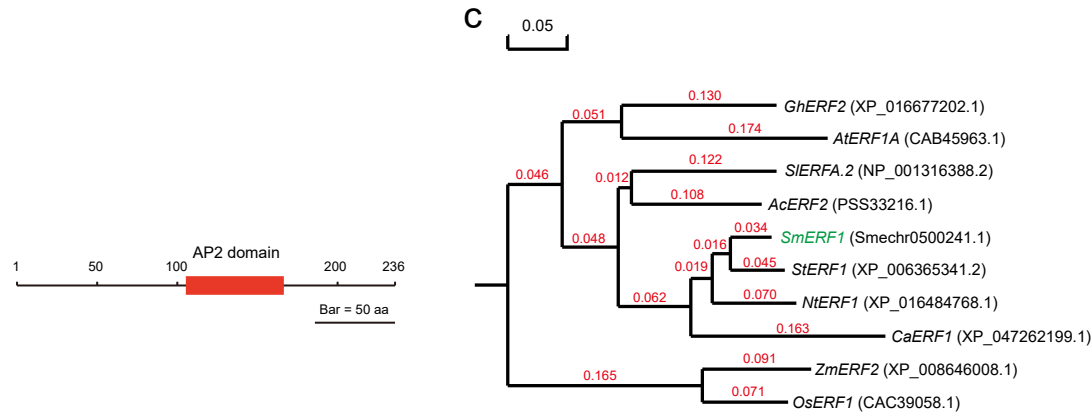


a

<i>SmERF1</i>MDQPISTELPPMNFPGDLEVYVNSSESRIPCLTETGA..LPLKVLSEDVYVGLKIFALSAGS.....	66
<i>SIERF1</i>MDQ.....QLLPTNFF.....VYVNSSESRIPCLTETGA..LPLKVLSEDVYVGLKIFALNVGHS.....	58
<i>NIERF1</i>MNQPISTELPPANFFGDFYVNSSESRIPCLTETGE..LPLKVLSEDVYVGLKIFALNVGHS.....	66
<i>SIERFA.2</i>MYGLPTSTELTFEFA..EFYVYVNSSESRIPCLTETGS..LPLKVLSEDVYVGLKIFALSAGT.....	65
<i>AcERF2</i>MYGQCETPVIFFASSSEFEFYVNSSESRIPCLTETGE..LPLKVLSEDVYVGLKIFALNVGHS.....	67
<i>CaERF1</i>MNQPISTELPPNFF.....VYVNSSESRIPCLTETGA..LPLKVLSEDVYVGLKIFALNVGHS.....	80
<i>GhERF2</i>	MEMYSTANESDLAMLDSIRCYLLSDSSDLRLTASTDFTSAP.....EMFCSSSESRIPYECITETGD..LPLKEDSEDVYVGLKIFALNVGHS.....	89
<i>ZmERF2</i>MLNLFACEAAAFMDISRHHLLDEFAAAATAAFA..FYVNSSESRIPCLTETGS..LPLKVLSEDVYVGLKIFALNVGHS.....	82
<i>AtERF1A</i>GOSIK.....FYVNSSESRIPYECITETGS..LPLKEDSEDVYVGLKIFALNVGHS.....	53
<i>OsERF1</i>MLNLPASREVAALDSIRHHLLDEEETPATAPATRRVYVNSSESRIPCLTETGS..LPLKVLSEDVYVGLKIFALNVGHS.....	84
Consensusr s f l w l p d d m l a g w	
AP2 domain		
<i>SmERF1</i>PENFTAG.....EVKSEPEEEIESA.....PELVPSFAVMAAF.....LPPRGGRGVGRVGRFWGKFAAEIRDPKNGARVWLGTETAEADAA	144
<i>SIERF1</i>PFSFTTG.....EVKSEPEEEIESA.....PEFVPSFAETIAAFV.....LPTPRGRGVGRVGRFWGKFAAEIRDPKNGARVWLGTETAEADAA	139
<i>NIERF1</i>PENFTAG.....EVKSELMEE.....EIVVSPADTTAAFA.....LPLPRGRGVGRVGRFWGKFAAEIRDPKNGARVWLGTETAEADAA	142
<i>SIERFA.2</i>PSENLTSE.....EVKLEPEEEIEP.....AMSTVSPPITVAF.....AALCPGRGVGRVGRFWGKFAAEIRDPKNGARVWLGTETAEADAA	144
<i>AcERF2</i>PENLTAN.....DVKPEPIDEFEP.....ATTISAGQLVESSEVTEVQTIAAARPPGRGRGVGRVGRFWGKFAAEIRDPKNGARVWLGTETAEADAA	154
<i>CaERF1</i>	EPTASPAKERYRGGVGFSEFTAG.....EVKSKPAPELMTLTADATVVPMLPASAEITKAA.....LALKDRGRGVGRVGRFWGKFAAEIRDPKNGARVWLGTETAEADAA	184
<i>GhERF2</i>PSDNST.....TNFALIKPE.PQEFLEQTS.....VEKMDTAERTVPA.....VVPARGGRGVGRVGRFWGKFAAEIRDPKNGARVWLGTETAEADAA	173
<i>ZmERF2</i>DGSFAAVKFEFLAFDPSFYERGSPYCLGFFLLAEGPTEPTETATTPGSEE.....EAAAVSRGRGVGRVGRFWGKFAAEIRDPKNGARVWLGTETAEADAA	181
<i>AtERF1A</i>BSSSSDEDRSFFSVRIETPFESFAAVDS.....VVPVKKETSPVSA.....VTIARGGRGVGRVGRFWGKFAAEIRDPKNGARVWLGTETAEADAA	142
<i>OsERF1</i>DGSFAAVKFEQDSYDGSIGSGLASSSSSEAGTGPETVSTETATVTGIREG.EGEAVASRGGRGVGRVGRFWGKFAAEIRDPKNGARVWLGTETAEADAA	186
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<i>SmERF1</i>LAYDCAAMRVGRSKALNFFHRRIGLNEEFPVRVTAR.....RRAS.....PELAT.....SSSENGSEPRRRKAVRK.....CDVEVESKSS.VMVGCGCIEQLTR.....GHQILV	235
<i>SIERF1</i>LAYDCAAMRVGRSKALNFFHRRIGLNEEFPVRVTAR.....RRAS.....PE.PV.....SSSENGSEPRRRKAVRK.....CDGVEVESRSS.VMVGCGCIEQLTG.....VHQILV	229
<i>NIERF1</i>LAYDCAAMRVGRSKALNFFHRRIGLNEEFPVRVTAR.....RRAS.....PE.PA.....SSSENGSEPRRRKAVRK.....GAVEVESKSN.VLVCVCQVEILLR.....GHQILV	235
<i>SIERFA.2</i>LAYDCAAMRVGRSKALNFFHRRIGLNEEFPVRVTAR.....RRAS.....ESASSSVSASESGSEPRRRKGV.VAAKQ.AELDEVESRGENVMVGCGCIEQFV.....GEQILV	241
<i>AcERF2</i>LAYDCAAMRVGRSKALNFFHRRIGLNEEFPVRVTAR.....RRSP.....EPTS.....PSSESGSEPRRRKGVFAAKQ.AELGV.ESSVCVCQVEILLV.....GEQILV	247
<i>CaERF1</i>LAYDCAAMRVGRSKALNFFHRRIGLNEEFPVRVTAR.....RRVL.....HE.RD.....SPLNDLARRRGENGV.....EKCESSR.....SVEQLTG.....GEQILV	265
<i>GhERF2</i>LAYDCAAMRVGRSKALNFFHRRIGLNEEFPVRVTAR.....RSSP.....EP.....SSSGSENASEPRRRKGVFAAGVHAGLIVGAG..LDENVYKVTSCAR.....GEQILV	267
<i>ZmERF2</i>LAYDCAAMRVGRSKALNFFHRRIGLNEEFPVRVTAR.....EPTASSDSPPASSATPRRRKGVFAAATMAMALVFPFPP..AACGAFVQLTLPARPFWAAGPVCGV	293
<i>AtERF1A</i>LAYDCAAMRVGRSKALNFFHRRIGLNEEFPVRVTAR.....RSS.....FSSSNGEAPRRRTVAAGG.....GMPKGL.....TVKCEVPEAR.....GDRILV	224
<i>OsERF1</i>LAYDCAAMRVGRSKALNFFHRRIGLNEEFPVRVTAR.....SSSGSSSSSSSSSGSGSEPRRRKGVFAAASPMAMALVFPFPP.FACGAFVQLALGAPFWAAGPVCGV	302
Consensus	ayd aa r rg a l n p k	lv

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