Figure S1. Phenotypic comparison of photoperiod-insensitive early flowering pea mutants.
A) Representative 7 week old wild type (WT) line NGB5839 compared to isogenic photoperiod-insensitive early flowering *sn-4*, *dne-1* and *ppd-3* mutants in 8h short day (SD) or 16h long day (LD) conditions.
B) The *ppd-3* is phenotypically similar to *ppd-1* and *ppd-2* in Borek background (compare Figure 1: all at 7 weeks and carry the *hr* mutation).
C) Mean node of flower initiation. Values represent mean ± SE for n = 5 to 6. Growth conditions as in Figure 1.
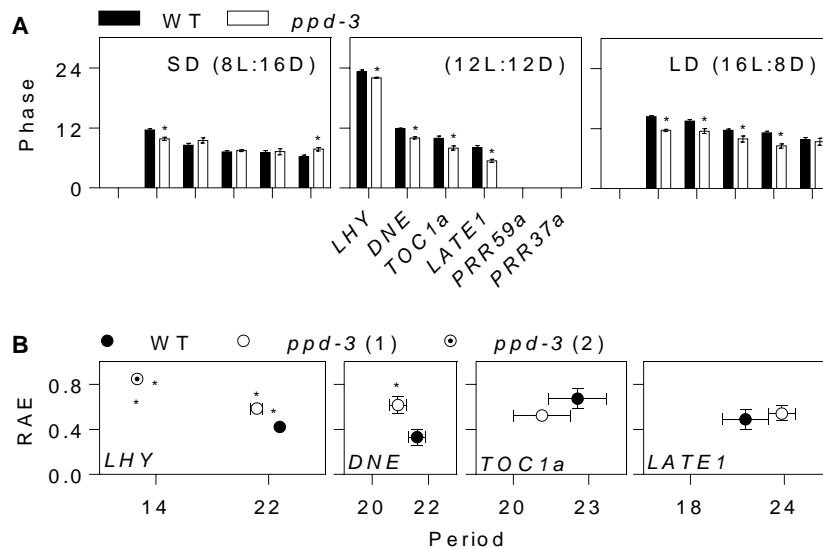
Figure S2. Circadian gene rhythms analysis

A) Circadian clock gene expression peak phase estimates form lights on (time = 0) under different entrainment conditions. Mean phase was estimated in BRASS using FFT-NLL or mFourfit using the data from SD and LD **Figure 3** and the entrainment cycle **Figure 4**. **B)** Period and relative amplitude error (RAE) estimates after transfer to constant dark. Mean period and RAE was estimated in BRASS using FFT-NLL from the data in **Figure 4** from ZT 12h to 72h except for *DNE* from ZT 24h to 72h. One and 2 in parenthesises following *ppd-3* indicate different primary and secondary periods over the analysed time window. Error bars are ± SEM. Asterisks indicate differences between WT and *ppd-3* mutant values of P<0.05. See the Materials and Methods for details of the analysis software.

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                                  *        20        *        40        *        60        *        80
PsEEC        : -----MKC-AIDEGKE---ISPMFPRLHVKDA-EKGG-PKAPPRNKMALYEQFSI----PSQS--FAAGGPGSGSLFSLP :  63
LcEEC        : -----MKC-EIDEGKD---ISPMFPRLHVKDA-EKGG-PKAPPRNKMALYEQFSI----PSQS--FAAGGPGSGSLFSLP :  63
MtEEC        : -----MKC-AIDEGKE---ISPMFPRLHVKDA-EKGG-PKAPPRNKMALYEQFSI----PSQS--FAS--SGSGSLFTLP :  61
CaEEC        : -----MKC-AIDEGKE---ISPMFPRLHVKDA-EKGG-PKAPPRNKMALYEQFSI----PSSG--HGS----GGSLFSLP :  59
PvEEC        : --MNRMRC-GIEESKE---ISPMFPRLHVKDA-EKGG-PKAPPRNKMALYEQFSI----PSQS--FAP---GSASLFPLP :  63
CcEEC        : --MNRMRC-EIEEGKE---ISPMFPRLHVKDA-EKGG-PKAPPRNKMALYEQFSI----PSQN--FAS--GSPSLFPLP :  63
GmEEC-1      : -MMNRTRC-GIEEGKE---ISPMFPRLHVKDA-EKRG-PKAPPRNKMALYEQFSI----PSQN--FAP---GSTSLFPLP :  64
GmEEC-2      : -MMNRMSC-GIEEDKE---ISPMFPRLHVKDA-ERGG-PKAPPRNKMALYEQFSI----PSQN--FAP---GSASLFPLP :  64
LaEEC        : -----MKC-IIDEGKE---ISPMFPRLHVKDA-EKGG-PKPPRNKMALYEQFNI----PSQS--IAS--GSTSLYPLP :  60
LjEEC        : -----MKC-AIGEGKEM--ISPMFPRLHVKDA-EKGG-PKAPPRNKMALYEQFSI----PSSQGQFASSESGSPSLFPLL :  66
AiEEC        : -MMKCAMIDEGKE---IIPMFPRLHVKDA-EKGG-PKAPPRNKMAIYQQFNINMHPSQN--YASG--SSTSLFPLH :  68
PsELF3b (PPD): ----MSRKG-DAEK---VCPMFPRLHVNDT-AEKGG-PRAPPRNKMALYEQFSV----PFQRFNP------NSNSNS-- :  58
LcELF3b      : ----MSGCKV-DAEK---VCPMFPRLHVNDT-AEKGG-PRAPPRNKMALYEQFSV----PFQRGN--------DPER-- :  55
MtELF3b      : -----MKRCKGGDDEK---VCPMFPRLHVNDT-TEKGG-PRAPPRNKMALYEQFSV----PFQRLNP------NSHSSS-- :  59
CaELF3b      : ----MKRCKCDDDDDEKVVGPMFPRLHVNDT-TEKGG-PRAPPRNKMALYEHFNV----PFQRFNN------NSNSSS-- :  63
GmELF3b-1    : ----MKRCNE--EEK---LGGPMFPRLHVNDI-AEKGG-PRAPPRNKMALYEQFSI----PSQKFNPRLLP--RKPNSS-- :  61
GmELF3b-2    : ----MKRCNE--EEK---VGPMFPRLHVNDG-HLP--RKPNSS-- :  60
CcELF3b      : ----MKRCSE--DDK---VVGPMFPRLHVNDT-AEKGG-PRAPPRNKMALYEQFSI----PSQRFNPRLLP--LNPNPS-- :  61
PvELF3b      : ----MKRCNE--DEK---VAGPMFPRLHVNDA-AEKGG-PRAPPRNKMALYEQLSV----PSQRFNPRLLP--LKPNSS-- :  61
AiELF3b      : --------------------MFPRLHVNDT-TEKGG-PRAPPRNKMALYEQFSV----PSQRFNN------QRLLP-- :  43
LaELF3b-1    : ----MKREKD--EEK---VVGPMFPRLHVNDT-TEKGG-PRAPPRNKMALYEQFSI----PSQNLNQ-------------- :  51
LaELF3b-2    : ----MKRCKA---EK---VGPMFPRLHVNDT-TEKGG-PRAPPRNKMALYEHFTI----PSR-------------- :  45
PsELF3a (HR) : ----MKRCND--DEK---MMCPLFPRLHVGDT-E-KGG-PRAPPRNKMALYEQFSI----PSQRFN---LP-LHPNTSN-- :  59
LcELF3a      : ----MKRCSD--DEK---MMCPLFPRLHVGDT-E-KGG-PRAPPRNKMALYEQFSI----PSQRFN---LP-LHPNNST-- :  59
MtELF3a      : ----MKRCND--DEK---VMCPMFPRLHVGDT-E-KGG-PRAPPRNKMALYEQFSI----PSQRFN---LP-LPPHHPNTSI-- :  60
CaELF3a      : ----MKRCKD--DEKM--MMCPMFPRLHVGDT-E-KGG-PRAPPRNKMALYEQFSI----PSQRFN---LP-LHPNTST-- :  60
LjELF3       : ----MKRCKD--DEK---VMCPMFPRLHVSDT-E-KGG-PRAPPRNKMALYEQFSI----PSQRFNQGLLPPTNTNTSS-- :  63
GmELF3a      : ----MKRCKD--DEK---VMCPMFPRLHVNDT-E-KGG-PRAPPRNKMALYEQFSI----PSQRFNSGVLP-LNPNISS-- :  62
CcELF3a      : ----MKRCKD--DEK---VMCPMFPRLHVNDT-E-RGG-PRAPPRNKMALYEQFSI----PSQRFNSGVLP-LNPNISS-- :  62
AiELF3a      : ----MKRCKD--DEK---VMCPMFPRLHVSDT-E-KGG-PRAPPRNKMALYEQFSI----PSQRFNSGVLP-LNPNTST-- :  62
LaELF3a      : ----MKRCKD--DEK---IVCPMFPRLHVDK-EDKGG-PRAPPRNKMALYEQLSI----PSQRFNHGVLL-QNPDTSS-- :  63
MdELF3-1     : ----MKRC---NEEK---VMCPMFPRLHVND-ADKGG-PRAPPRNKMALYEQLSI----PSQRFNPGVLP---LNSNN-- :  59
PbELF3-1     : ----MKRC--NEEK---VMCPMFPRLHVND-ADKGG-PRAPPRNKMALYEQLSI----PSQRFNPGVLP---LNSNN-- :  59
MdELF3-2     : ----MKRC--NEEK---VVCPMFPRLHVND-ADKGG-PRAPPRNKMALYEQLSI----PSQRFNPGVLP---LNSIN-- :  59
PbELF3-2     : ----MRRC--NEEK---VMCPMFPRLHVND-ADKGG-PRAPPRNKMALYEQLSI----PSQRFNPGVLP---LNSNN-- :  59
PmELF3       : ----MKRC---NEEK---VMCPMFPRLHVND-ADKGG-PRAPPRNKMALYEQLSI----PSQRFNPVVMP---LNPNS-- :  59
PpELF3       : ----MKRC---NEEK---VMCPMFPRLHVND-ADKGG-PRAPPRNKMALYEQLSI----PSQRFNPVVMP---LNPNN-- :  59
FvELF3       : ----MKRCGR-DDEK---VMCPMFPRLHVND-PDKGG-PRAPPRNKMALYEQLSI----PSQRSNHGAMP---LHQNS-- :  61
AtELF3       : ----MKRCKD--EEK---ILEPMFPRLHVND-ADKGG-PRAPPRNKMALYEQLSI----PSQRFGDHGTMNSRSNNTS-- :  63
HvELF3       : -MRRAGGCGGGGGGSGEDKVMGPLFPRLHVNDTTLKGG-PRAPPRNKMALYEQFSV----PSQRFAANTAPAAHRP----- :  70
ZmELF3-2     : -MRR---CATKDAAPDKVMGPLFPRLHVNDT-LKGG-PRAPPRNKMALYEQFSV----PSHRYSAAVPPAPSPAPPWGA :  70
OsELF3-1     : MATRGGGCGGGGKEAKGKVMGPLFPRLHVNDA-AKGG-PRAPPRNKMALYEQTV----PSHRFSGGGGG-GGVGGSP-A :  73
OsELF3-2     : --MRGGGCGGKEVEERGKVMGPLFPRLHVNDA-AKGG-PRAPPRNKMALYEQFTV----PSHRFSGGGGALASARGSL-A :  72
ZmELF3-1     : --MTRGGCGQGGGKEEPGKVMGPLFPRLHVSDA-AKGG-PRAPPRNKMALYEQTV----PSNRFSPAASARAAGASL-V :  72
PmEEC        : ---------MRGGKDEEHLISPVFPRRFHVNDT--DKCGPRPPRNKMALYEQFSIPS--QSFTSGGSASMLPLPHNDRR-L :  66
PpEEC        : ---------MRGGKDEEHLISPVFPRRFHVNDT--DKCGPRPPRNKMALYEQFSIPS--QSFTSGGSASMLPRPHNDRR-L :  66
FvEEC        : ---------------MSPIFSRLHVNET--EKGGLRGPPR-IMALYDQFSSPV--CSIT-----MLPPANNNSSSL :  51
AtEEC        : ------MCGMKDEAKR-ITIPLFPRVHVNDT-GRGGLSQQFDGKTMSLVSSKRP-------------------- :  47


                                  *        100       *        120       *        140       *        160
PsEEC        : LRNCTVPTSSSHLGYN-QSINFCSSKSNAISILSEKTQAYNSRKINLTKLTVSHDLEHMKPAKQITKVQQDNYINSSKSS : 142
LcEEC        : LRNCTVPSTSSHLGYN-QSIKFCSSKSNAISILSEKSQAYNSRKINLTKLTVSHDLEHMKPAKQITKVQQDNFINSSKSS : 142
MtEEC        : LRNCTVPTTSSHLGCG-QSIKFYSS--NASSILSEKTQAYNSRKINSTKLTASHDLEHMTPAKQVTKIQQDYFINNSKNS : 138
CaEEC        : LRNCTLSTTSTHLGCSTQSIKFCSS--NASSILSDKAQAYNSRMINSTKLMASRDFEHKKPAKQIT--KDNFIS-SKNS : 133
PvEEC        : LRNYTGPTSSSHISSN-QSIQF-TY--NAPSIMAEKSQAYNFRRSNLTKRT----------------QENFIN-SKNS : 120
CcEEC        : FRNYTGPTASSHISSS-QSIQFGTS--IAPSILPEKTQTYNSRRNNLTKFT----------------QEDFID-SKNS : 121
GmEEC-1      : LRNYTGPTSSSHISSN-QSIQFCTS--SMPSILAEKSQAYNSRKTNLTKFT----------------QDDFIN-SKNS : 122
GmEEC-2      : LRNYTGPTSSSHISSN-QSIQFCTS--SMPSILAEKSQTYNSRKTNLTKFM----------------QDDFIN-SKNS : 122
LaEEC        : LRKCTIPSTSSHVSSN-QTIQFCTS--SAASVVAENIQVYDSRKINLNKLM----------------QHNFIN-SKKS : 118
LjEEC        : LRNCTLPPTSTQPVRE-----------SSCGIIQ--------------------------------PDDFIN-TRCF :  89
AiEEC        : LRSFTPPSISPY--------------------------------------------------PDDFIN-TRCF :  90
PsELF3b (PPD): --SNSLPLTPSSNLGNDPERS-------------------YISHQSN-GANTHTLS----AQLEHRKKVDGDDSRA--YDH : 111
LcELF3b      : --SYIFPVCLPSQTEN---------------------YISHQSN-GA--HTLS----AQIEHKKKVDGDDSRA--YDC : 101
MtELF3b      : --SNSIPLTSSSTMGNDLERSNIFPVRLPSQADAHRAKSYISHQSN-GANLDTLS----TQLEQGKKVDGDDSRA--YDH : 130
CaELF3b      : ---NSHPLTPSSTLGNDPERSYIVPVNLPSQTATQRAESYTSHQSN-EANMDTLS----AQLGQRKKVDGDGSHA--YDH : 133
GmELF3b-1    : --SNIVP---PPTQGNGHERSYVYPVRFSSQTPTHRAESYISRQSDDGSRSNTSL----VQLERRKKVD-DDIHV--YTC : 129
GmELF3b-2    : --SNIVP---PPT--------------SSTEGNGRERSYISRQSDDGARSNTSL----VQLERRKKVD-DGIHV--YTC : 113
CcELF3b      : --SNKVSSSTPSTQGNGHERSHVYPVCLPSQTPSHRAESYISRQSD-GSRSNTSS----VQLERQKNVDEDDIHA--YIR : 132
PvELF3b      : --SNLVAPPVSSTQGNGHERSYAYPVRLPSQIPAHRAESYISRQSD-GSRSNTSS----VQLERRKRADEDDVHA--YIC : 132
AiELF3b      : --INHPSTPSSSSQGTGPERSYAFPVHKPSQASTRR-ESYSSRQYD-GANLNTPS----TQVEQGRKVDDDDFMVPVYVH : 115
LaELF3b-1    : ---------LGSSSQGTGSGRSYIIPCHLPSQMPTHRAEIYISHQSN-RARQNTSS----AHLEQRKNKVDEDDFMVPVYVD : 118
LaELF3b-2    : ---------GSSNKGTGSERSYIIPGNLPSQMPTQRAESYISHQFN-GASQNTSS----AQLEQRNKVDEDDFMVPVYVD : 111
PsELF3a (HR) : --NSVPP---ASSSQGTVHERNYVFPGHLTPETLIRQAGKH-LSRQTKGANLNASL----AQIEHRKKVDEDDFRVPVYVR : 130
LcELF3a      : --NSVPP---ASSSQGTVHERNYIFPGHLTPETLIRQAGKH-LSRQSKGANLNGSL----AQIEHRKKVDEDDFRVPVYVR : 130
MtELF3a      : --NTVPP---SSSSQGAVHERNYYVFPGHLTPETLTRQS---------EGKNLASL----SQLEQRKKIDEDDFRVPVYIR : 123
CaELF3a      : --NTVPP---SSSIQGTVLERNYVFRGHLTSQTPIHQAEKR-SSLQLEGVNLNTSL----SQLEQRKKVDEDDFMVPVYIR : 131
LjELF3       : --NTAPP---ASSSQGAVHERNYYVFPVQSPSQTPIRRAEKP-VSHQSEGANLNSSL----VQLEQRKKVDEDDFTVPIYIR : 134
GmELF3a      : --NTVPP---ASSSLRTVPERNCVYPVHLPPQRPIHRAEKC-NSRQSEGTNLSAS-------LEQRKKVDEDDFRVPVYFH : 130
CcELF3a      : --NTVPP---ASSSQGTVPERNHVFPVHLPPQNPIRRAEKC-ISRQSEGANLSAS----AQLEQRKKIDEDDFRVPVYIH : 130
AiELF3a      : --TNTPPPPPASSTQGTGPERNYAFPYQFPPQTPTRRAEKYSVSRQSEVANGNGSL----LQLEQRKKVDEDDFRVPVYVH : 136
LaELF3a      : --NNVPP---TSTSQGAGLERNYGFPAYLPSQTSTRRAEKY--TSRSYGANLNASP----VQFQEKRKKVDEDDFMVPVYVH : 133
MdELF3-1     : ------------QGSRSDGNLPFPLHGHPSTPTHQAEMLHGRQSDRANVNLPFE----QTNLTRKIGDEDDFSVPEFVQ : 122
PbELF3-1     : ------------QGSRSDGNLPFPLHGHPSTPTHQAEMLHGRQSDRANVNLPFE----QTKLTRKIGDEDDFSVPEFVQ : 122
MdELF3-2     : ------------QGSRSDGNLAFPLHGHPSTPTHQAVIFHGRQSDGANVNVPFG----QTDLRRKIGYEDDFSVPVFVQ : 122
PbELF3-2     : ------------QGSRSDGNLAFPLRGRTSTPTHQAVMFHGRQSDRANVNVPFE----HTDLRRKIGDEDDFSVPVFVQ : 122
PmELF3       : --TSSVVPSAFSSQGSRSEGNLPVPLHVRPSTPTRQAEMFHARQSDGANENTPLT----QPDQRKKVGEEDDFRVPVFVQ : 133
PpELF3       : --TSSVVPSAFSSQ-------------------------------------------------------------------- :  71
FvELF3       : --NSSMGSPALSNQGNGPERNLPFPVHARPAAPTH-----HSGQSDGVNVNTASV----QPQQRKRGGNEDDFMVPVF-Q : 129
AtELF3       : --TLVHP--GPSSQPCGVERN--LSVQHLDSSAANQATEKFVSQMSFMENVRSSA----QHDQRKMVREEEDFAVPVYIN : 133
HvELF3       : AASFAAVSSASAGQIGGIDRPLFPSFCVPSNEPVPLPQHINTNSSGHATSG---------RLSTQLKSKDAYAAGSTAE : 140
ZmELF3-2     : QRPASAVPSTSASQVGGGDRPIFPLFRVPSTEPVRSSDQTNANSNGQGANG---------TIAESGRQRQSTHLKS--K : 138
OsELF3-1     : HSTSAASQSQSQVYGRDSSLFQPFNVPSNRPGHSTEKINSDKINKKISGSRKE----LGMLSSQTKGMDIYASRSTAE : 149
OsELF3-2     : RSTSAASQSQ----VYGCDMPLFEPFNVPSNGPGQSVEKMNSNSVNRQINGSRKD----SGMLSTQPKGIDKYGSGSRAE : 144
ZmELF3-1     : PSTAAA-------QVYGYDRTLFQPFDVPSNEPPRSSEKFKGNTINGQSNSTRRE----PLRMSSQTKNKDVCASKSIAK : 141
PmEEC        : VPPTSWSDVSSNERNILTPPCNFLVVPSDPAEKIQSYDPTGANLNTMMADCERISTKP-SNYLNTTGPSSSAAKYDSFQP : 145
PpEEC        : IPPTSWSDVSSNERN--TPPCNFLVVPSDPAEKIQSYNSTGANLNTMMADCERISTKP-SNYLNTTGPSSSAAKYDSFQP : 143
FvEEC        : VSSTSWSDVGANQRSILTPYC-YSVVPSHPSEKIQSDSSTGPKLYTTMTDYERVSSKLNSQGFVSTGPSSSSANCDSFRS : 130
AtEEC        : ----NLPSPTNNISDSLSTFSLSLPPPPNNARLIDGPEKNQFSPIYNTKFEGKLN-------------KKGINYTSPKG : 109
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                              *       180       *       200       *       220       *       240
PsEEC       : LKTLDGE-DAFITPSSVHLKSSFYGGVVQNEKDEDKLARCNLSFSFKSLNSFRKVMNSSEAIVSFKSLNSFRKVMNSSEA : 221
LcEEC       : LKTLDGK-EAFITPSSVQVKSSFYGGVIQNEKDEDKLARCNLSFSFKSLN------------------SFRKMMNSSGA : 202
MtEEC       : LKTLDGE-DAFITSGSVHVKSNPS-----DKDEENKLARYNLNCSLKSLS------------------SFRKVMNSPGT : 193
CaEEC       : LKTIDGEEAAFITPGSVHVKSSCCGLIIQNDKE--KLTRENLSCSLKNLN------------------SFRKMMNSNGA : 192
PvEEC       : LKALDGE-DVFITSGSAHGKS----SSFQNNKDE---GGCNLSCSLKNLN------------------SFRKKVNSPGV : 173
CcEEC       : LKTLDGE-DSFVTSGPAYAKKSCC-SIIQNNKDEDKLARCNLSYSLKSLD------------------SFRKKVNSLGV : 180
GmEEC-1     : LKALDGE-DAFISSGSAHRKNSYC-SIIQNNKDEGKLSCSNLSCSHKRLN------------------SIR-KVNSPGA : 180
GmEEC-2     : LRTLDGE-DTFITCGSAHRKNSSC-SIIQNFKDEDKLSHSNLSGLKSPN------------------SFR-KVNSPGA : 180
LaEEC       : LKIFDGE-DISIASSSDFGKNSSC-----SMIQNDKLDNCNLIYPLKSPS------------------SLRKKVSSPET : 173
LjEEC       : --------------------------NDKDDDKLARNNLNCSLKSLH------------------SFRNKVNSSEA : 121
AiEEC       : LKTFDGE-----YAGSAHEGNSGC-NLKQNDKDEDK-------LPLKSLN------------------SFREKVNSLVT : 138
PsELF3b (PPD) : SRIGQSNDKTMKSFNGEIITPT--GS---RNFGCLVSGKNDSDKDQTQFG-----------------SLLVEMRKDVRN : 168
LcELF3b     : SRIGKSNDKTMKSFNGEKHTPT--GS---GNFGCLVSGKNDQTQFG------------------SLVVEMRKDVRN : 158
MtELF3b     : SRIGQSNHKMTNSFNGEKIT------------------------------------------------LVIP------- : 154
CaELF3b     : SRIGQSNNKTMKSFNGKKLTPV--GA---RNFCCSVAGENDGD----------------------------------- : 171
GmELF3b-1   : SGIDQSNDKTMESVDGKKLTPF--GA---RNFCYSVAVQNDGDKDPTQFSSC---------------SLPVDLRKDVRN : 188
GmELF3b-2   : SRIDQSNDKMLESFNGKKLTPF--GA---RNFCYSVAVQNDGDKDTTQFG------------------FLPADMRKDARK : 170
CcELF3b     : SRVGQPSDKTLESYKGKKFTTL--GS---RNVCFSVAVQNDGDKDLTQFG-----------------CVPVDMRKDVRS : 189
PvELF3b     : SRIGHSNDKTMKSFNGEKITPL--GA---RNFC-SVSVQDDGERGPTLFG-----------------SLPVDMRKHVRS : 188
AiELF3b     : SRNGQSNDETVQSSNGRHLTPM--VR---SERHPSIIS------------------------------------------- : 148
LaELF3b-1   : SRTGQCNDKRLESFDRKKLTSM--GS---RNFGCSLEVQKDGGRHLKQLG-----------------SPLTNMREDASS : 175
LaELF3b-2   : SRIGQYNDKRLVNFEMEKLTSM--SS---RNFGCSIEVQKDGGRHRKQLD-----------------SPPINIREDASS : 168
PsELF3a (HR) : SNIGQSNEKRIESFDGKRPPST--GS---RYFGFLKPGKSDRERDPRQHG-----------------SAVVNAVTDVRN : 187
LcELF3a     : SNIGQSNEKRPESFDGKRLPST--GS---RYFGFLKPGKIDRERELIQNG-----------------STVVNAGTDVRN : 187
MtELF3a     : SKIGQSNDKSHESFDGKKNLTSA-GS---RNFGFFKAGRINRERDLN-----------------------NPRTDVRN : 173
CaELF3a     : SKIGQSNDKSLESFDGKKLNST--RS---RYFGFSKAGKTDCERDPKQYG-----------------SHLVNTKIDVRN : 188
LjELF3      : SRTGQSSDR---SLDGKRL---------RYFGCSVAEQNDCERDLKQYA-----------------PSLVNKRRDVRS : 183
GmELF3a     : SRTGQCNDKSVESFNGKKLTPT--GS---RYFGGSISGQSDCERDPKQFG-----------------SSVVNMRKDVRS : 187
CcELF3a     : SRIGQCNNKSVESFDAKKLTPT--GF---RYFGGSVAGQSDCERDPKQFG-----------------SSLVNMRKDVRS : 187
AiELF3a     : SRIGLSNNKRRESLDGEKLVPS--SS---RYFGSSVAGQNDCVRNPKQLG-----------------SSLVNTRKDRRS : 193
LaELF3a     : SRTGQSNSKNLESFDWKKLTLAPKGC---RYIGCSTAGQNDFERDPKQFG-----------------SLFVNMRKDVRS : 192
MdELF3-1    : SRMGLGHSKTQIVSDKEKLTPISSP-----HSGHLVKVKNAAKKDPKQISSP---------------TLNLRREV--- : 177
PbELF3-1    : SRMGLCHSKTQIVSDKEKLTPISSP-----HSGHLVKVKNAAKKDPKQISSP---------------TLNLRREV--- : 177
MdELF3-2    : SRMGLGHSKTQIGSE-EKLTPISSP-----HSDHLVKVRNVGKKDPKQISSP---------------TLNLRRELRSE : 179
PbELF3-2    : SRMGLGHSKTPIGSE-EKLTSISSP-----HSDHLVKVRNVGKKDPKQISSP---------------TLNLTRELRSE : 179
PmELF3      : SRMGLCHSKTQIGIDKEKLAPIGPSHSGHTHSGHTVKLKNVGKNDPKQLSSP--------------TTFNLRRELRSE : 197
PpELF3      : -------------------------------------KDPKQLSSP---------------TTLNLRRELRSE : 92
FvELF3      : SRMGQCQSRTQNGGGKAKLTPFNQS-----HPDHGIIFKSATKKDQRQSSSP---------------SLNLRRESRRE : 187
AtELF3      : SRRSQSHGRTKSGIEKEKHTPMVAPS----------SHHSIRFQEVNQTG------------------------------- : 173
HvELF3      : CTSSHGRDNNAKNSSGNKLTNDDDFTVPSVFCSGVRPRSNHEEARIQENSTH---------------LPATSPYKSGPT : 204
ZmELF3-2    : DTNAAGPPAEGNNSVGKKLANDDDFTVPSVLYSGMPPHSS------QEKLTL---------------FPTTSPCKSVP- : 195
OsELF3-1    : -APQRRAENTIKSSSGKRLADDDEFMVPSVFNSRFPQYSTQENAGVQDQSTP---------------LVAANPHKSPST : 212
OsELF3-2    : CAPQQRVEKGIKSSGRKLADDDEFIVPSVFSARFPQYSTKERAGVQEESTP---------------LVALSPHKSPPA : 208
ZmELF3-1    : CTSQHRVGNTIMSS-GKKVVSDDEFMVPSICYPRFYRQSTQDHA---DKSKP---------------QSTTNPHKSP-A : 200
PmEEC       : KKTSHFRNFSLEKYGNEDYLKVPSPFQGTALQCRNSQQSKEKEKLPCLSSMEQLKS------------SCIKKINGSNT : 212
PpEEC       : KKTSNFRNFSLEKYGHEDYLKVPSPFQGTALQCRNSQQSKEREKLPCLSSMEQLRS------------SCIKKIS--NS : 208
FvEEC       : HTISNLRNFRSKKFGNEDEFQSPISSQVTTLHCRDSLRSKGKDNLHQSSYTLQKG------------DYIEKMNGSST : 197
AtEEC       : SSVTNTKPSSIKQNEYLKNLTS-----------------------------------------------LDSIKSPIVI : 141


                              *       260       *       280       *       300       *       320
PsEEC       : IDLKSSQYGKNRMEEHKDASQIDQKAKEKSPHSLNGFDDTTNES----------SNSSAKYTNSK-------SMKEEIKN : 284
LcEEC       : IELKSSQYGKNRMEEHKDASPIDQKAKEKSPHSLNGFDDTTTES----------SNSSAKYTNSK-------SMKDEIKN : 265
MtEEC       : IELKSAQYGKSLMKEHKDVRQIDQNAEEKPLHSLNGFNDTTNAS----------SNSSIKDRNSKSMNKEQRSLKEENRN : 263
CaEEC       : IELKSAQCGKIQMEEHKNSSQIDQKEEEGIPLSLNSFDDMTNAS----------SNSLVKDTNSKSMKKEHRSMKEETKN : 262
PvEEC       : VDPKSAQYGKIQMEELTKVSQNGQKPEE--VLSLDGFGDMTDTS----------LMSLVQ------------------ : 221
CcEEC       : VELKSAQYGKNQMAEHIEVSQIDQKIEEGLTHSLDGFGGMPDASS---------LISLVKGKNSISMNKENRSLKDEIRS : 251
GmEEC-1     : VDLMSEQYEKNQIEEHTEVSQIGQKPEEVLPHSLDGFGDMTDAS----------LISLEKGKNSKSMNKEHRSLKEENRS : 250
GmEEC-2     : VDLKSAQYGKNRMEDHTEVSQNGQKPEEVLPHSLDGFGDMTDAS----------LISLVKG------------------ : 231
LaEEC       : IALEFAQYGKNLMEEHFKMSRKGWKPEEESANPIDGFCGMADSS---------FLSLNKDKNFKSSMKEHRFLKEETTS : 243
LjEEC       : IDLNSAKYGKNQMEEPIVVRQIGLKPEEGPPHPLDGFGDMRDDES---------LNSLVKGRSSTSMKREHGSLKGEIRS : 192
AiEEC       : IELNSTQYEKNEREEE--VSQ----------------------------------------------------------- : 157
PsELF3b (PPD) : KGEVHLQESLSRQKTVMSVESIL-TGEIIDSSVRQAEKISDEED-----------Q-----------ND-ACLQQ---- : 219
LcELF3b     : KGEAHLQESLSRQKTVISVERIS-TGENIDSPVRQAEMISDEED-----------Q-----------SD-ACVQQ---- : 209
MtELF3b     : ---------SRQNTVISVKSAL-TGEIIDSRVRQGKKIPDEED-----------QECSVSNINFPQGD-SCTRQ---- : 207
CaELF3b     : ----------KDQTQFGSLLVKM-RKDVNKSRLHQGNACVQQXX-----------X----------------XQ---- : 207
GmELF3b-1   : GNEANPHVSSSRRKPKMSVKNNS-SGEIIDSLMMQAKVIPNLED-----------QDYSVPNISRLHQDD-TCLQKECVA : 255
GmELF3b-2   : GNEANPHVSSSRQKLKLSVKPKS-SGEIIDSLVMQAKVIPNQED-----------QDYSVPNINRLHQDD-ACLQKECVA : 237
CcELF3b     : GNEVHPQVSSSRQRKITVRNKS-SGEIIYSPVMQVKVIPNQED-----------QDYSVPNISRLHQDN-APPQQKCVA : 256
PvELF3b     : GNEAHPHVSSSRQQQKMSVKNKS-SGEVIDSLVMQAKVIPNQED-----------QDCSVPSLSRSHQDG-ACLQQECVA : 255
AiELF3b     : ----------NGQQPVMSCRDIS-SRETVNG-LSQTKTIPN--------------QNCFVSNISRSHHAD-ACLWPVSVA : 201
LaELF3b-1   : ESEGFAQVSPSRDPP---AKNIS-TVETTKSLVNQTKVIQYQDC-----------PASFVSSLC---QAD-DCLQQECVA : 236
LaELF3b-2   : ESEGLPQVSESRELH---VKNIS-TIETIKSLARQAKVIQNQEY------------------------------------- : 208
PsELF3a (HR) : DIDGPPQVSPNKEHPSSSARDGS-IGEHSDTLVRQKVTANQEV-----------QDRRVFKLSSLRQGD-ARLRQDCRA : 254
LcELF3a     : EIDGPPQVSPNKEHPVTSARNAS-TGERVDALVRQVKVTPNQEV-----------QDRRVFKHSSLRQGD-ARLRQDCRA : 254
MtELF3a     : EIDGPPQVSPNKEQPFTSARDTS-NGESSNTSVRQAKVIQNQEF-----------QDRAVFKLSSSRQGD-GCLHQDCRA : 240
CaELF3a     : EIDGPPQVSPNKEHPFTSVRDIS-TGESVDTLVRQAKVTLNQEF-----------SDCAVFKLSSLRQVD-ACSREECGT : 255
LjELF3      : ETDGLPPVSPNKEQPLIRARNTS-TGENIDTFKRQAKVTPNQEF-----------QDCTLSKPTRLQRDD-ACLRRDCEA : 250
GmELF3a     : EIDVLPQVSTSKEQASMSVRSIS-TRENIHTLLRQAKVTPNREF-----------QDCHVSKFNRLQQGE-TCLQLECGV : 254
CcELF3a     : EIDGLPQVSTRKEHPLMSVTSIS-TGENIDT-VKHAKVTPNQEF-----------QDCHVSKQNRLQQGD-ACLRHDCGV : 253
AiELF3a     : ETEGLPQVSTNKEQSVVFVRKISLTGENIDILARQSKVNPSQEF-----------QDSPLSKHSRLRQDG-ACTQREGRA : 261
LaELF3a     : ETKGLVQVTPSKEQPIKSVRDLSSTGENVDTLVRQAKVTPNQEF-----------RDSPASKHNMLHQGDDTFLQREREY : 261
MdELF3-1    : -----------------------------NASPNQED----------AECSVPRFNRLADSD-ACLQQVSRS : 209
PbELF3-1    : -----------------------------NASPNQED----------AECSVPRFNRLAESD-ACLQQESRS : 209
MdELF3-2    : REEDLINVSGLSKGHSGKFAAKISTLQKIDG-PVEANASPNQED-----------AECSVPRFNRLAESD-ACLQQESRX : 246
PbELF3-2    : REEDLIEVSGSSKGHSGKFAAKISTIQKIDG-PVEANASPNQED-----------AECSVPRFNRLAESD-ACLQQESRS : 246
PmELF3      : REEDLIKVSGPARDHSAKSATKISCRQKIDGPAEEVSASPNQEY-----------ADCPVPRFSRLSESD-ACLQQESRS : 265
PpELF3      : REEDLIKVSGPVRDHSAKSATKISTRQKIDGPAEEVSASPNQEY-----------ADYPVPRFSSLKSSD-ACLQQESRS : 160
FvELF3      : TEEDR-NASSPARDHSVKAATSISTRRERVD-IPMNANTSRNQEY----------EDHPVPTFNRSCDSD-ACLQQDSRS : 253
AtELF3      : ----------SKQNVCLATCSKPEVRDQVKANARSGGFVISLDV----------SVTEEIDLEKSASSHDRVNDYNASL : 232
HvELF3      : VSKPTAKFPNTDKRYLEGRNPSDTRSRDSPNIIRDKAPANTTTNFLEAEERTSSFQFSADKTMGKRDDKGSSYRDKPSSI : 284
ZmELF3-2    : -----AKYSSTDKRRLEGMDASDVKSK-GPSGIKKEPVQVRID-LEDKETTPSFQVLNDKTWSP-DPKLSSHMDR---- : 263
OsELF3-1    : VSKSSTKCYNTVSKKLERIHVSDVKSR-TPLKDKEMEAAQTSKN-VEVEKSSS--FHASKDMFESRHAKVYPKMDKTGII : 288
OsELF3-2    : VSKSPTKCYNTVSKNLERINVSDVKSR-GSQKDKFTGPAQTLKN-VEVEHFSS--FEASKDMFGSKHAKVCP---KTGTI : 281
ZmELF3-1    : MSKSSVECYSTVNKHLDKINEADRRLM-NSPKVKEKEAVQGSKA-VEVEKEKSS--SFQASEKFKDKYAKLCQMRNKASNI : 276
PmEEC       : IDLKLRQCGRNHEEENPKVSQTNEDPVERSVSLALAIVKDFANTSSSPSNTVKNSESLKRAHASLSQENRS-SVNDLSKL : 291
PpEEC       : IDLKLRQCGRNHEEGNPKVSQTNEDPVERSVSLALAIVKDFANTSSSPSNTVKNSESLKRAHVSLSQENRS-SVNDLSVL : 287
FvEEC       : VQLNSRQYLGNHNEESPKACQIIEDPVEKSISLTLARVREFENISSTPSQRVEHFESLKRKHESVSQESRSRSVTDFNKL : 277
AtEEC       : HSEIDPQANTDLSLQFCTSGSSKPGGEAVVGSKILLSERLEDEN----------------------------------- : 185
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                         *        340        *        360        *        380        *        400
PsEEC        : ISVDSLKALQGSNGHRHEDH-AAFVDKNKFRDHCMEKPTMSDVQKCSGELEIGRRSLHG-KRERSRDEETSRNYDA---- : 358
LcEEC        : ISVDSLKALQGSNGHRHEDH-AAFVDKSNFRDQYMEKPATSDVQKCSGELEIGRRSLHG-KRERSRDEETSRNYDA---- : 339
MtEEC        : ISVDSLKTLQGSNGHRYEDH-VAFADKINLRDHCSEKPTMSDFQKCSRELEIGTRSSHG-KRERSKDEETSKNYDA---- : 337
CaEEC        : ISIDSLKTLKGSNGNRHEDH-AGFVEKIKLKDHCMEKPAKSDVERILGELEIGRRSFFGGKRERSKDEETDRNYDA---- : 337
PvEEC        : ---DSLKTLQGSSVHTHEEH-ATFGDKFNSRDHHMEKPAAGDVHKCSGELEIGRRFFLD-KGAGNEDEETS--------- : 287
CcEEC        : ISVDSLKTLQGSSVHTHEDH-AAFGDKINSRDHHIEKPTASDVQKCPAELEIGRRFFLD-KGDRNEDEETNRHYGA---- : 325
GmEEC-1      : ISVDSLKTLQGSSVRTQEEL-AAFRDQIKSRDHHIEKPAASELHKCSGELEIGRRCFLD-KVNRNEDEETYSHYDA---- : 324
GmEEC-2      : -----------SSVRTHEEL-AVFEDQVNSRDHHIEKPTANDVHKCAGELEIGRRCFLD-KVDMNEDEETYRHSDA---- : 294
LaEEC        : ISKDCLKTLQGNNAEAREEHDEAFANIVDLQDNCMKKTADNDVYKCPDELEIGRRCLLS-KRDRNKDEETCRDYDA---- : 318
LjEEC        : ISVDSLKTLQGRNVHTHEEH-AAFED--------------------------------------NKDEEAYRDHDT---- : 229
AiEEC        : -----------KSQEDE---------------------------------------------------EKTYRHYNG-- : 172
PsELF3b (PPD): --ESNDIEHGGSLVDSAM--DMDNRNSLVLRGCFRSTVNQISVPEAADHTEYHDT-NIDSPIENGSSEGSDDLSKN---- : 290
LcELF3b      : --ESNNIEHGGSLVDSAM--DMDNRNSLVLRGCFRSSVNQTNVPETANHTEYHDT-NIDSPIENGNSEGSDDLSKN---- : 280
MtELF3b      : --ESNDIEHSDGLLDTAM--DMDNRNS------SFHSTVDRTMVLEAANDTEYHDA-NIDSPIQKGNSEGSGDLSNI---- : 272
CaELF3b      : --ESNDSEHGDGLIDSAM--DIDNRNSLVLRSCSHSTVDQTSVLEATNDTEYHDT-NIDSPMQKGNSEGSDDLSKT---- : 278
GmELF3b-1    : GSQSNDVEHGDDLLNSTR--DIDNGNALVPRGCFHSAANQTRPLEATNDAEYHDT-GTGGPIQKGNFDERDNISKI---- : 328
GmELF3b-2    : GSQSNDIEHGGDLLNSTR--DMDNGNALVPRGCFHSAANQTHPLEATNDAEYHDT-RTGGPIQKGNFDESDNISKI---- : 310
CcELF3b      : GSQSNDIEHCDVLLNSTRERDVDNGNALVPKGCFHSAVNQTRLLEATIDAEYHDA-GTGGPIQKGNFDESGDVSKI---- : 331
PvELF3b      : GPQSNDVEHRNGLLSSTR--DMDNGNALVPKSCFYSAANQTCPVEATGDVEYHDT-GTEGPMQKGIFDEIGDVSKI---- : 328
AiELF3b      : GSQSNDDEHDDILT----------------------ENQTSPQEDNNDPECQDT-QIGGPMQGENLDDSDDISKI---- : 253
LaELF3b-1    : GSQSNNIGHRHREVLLDSIGDTDKGNTTLPMGCFRSPTNQTSPVEAMHETEFDDTTRTASPVQKGSSDESDDVSKI---- : 312
LaELF3b-2    : ----------------------------------------QDSPVEATHDAEFHDT-RTGSLVQKGSSDDGDDVSKI---- : 244
PsELF3a (HR) : ESQSNGHGQSDSLLESTR--EVDKSNG--------PIVNQTSPTQAINGTEYHDT-GTGSPKQLGNSNKNDSISKI---- : 319
LcELF3a      : ESQSNGHGQSDGLLESTR--EVDTSNG--------PIVNQISPTQAINDTEYHDT-GTGSPKQLGNLNKNDSISKI---- : 319
MtELF3a      : ESQSNGTGQRDASVESTR--EIGKSND--------PIANQTSPTEAINGTEYHDT-GTGSPIHSGNLNKNDNISKI---- : 305
CaELF3a      : ESQSNGIRQSNTLVESTR--GVDKSND--------PIANQTSPTEAINGTEYKDT-WTGSPIQKGNLNRKDNISKI---- : 320
LjELF3       : VSQSNGIGQSGGLVESTP--ETDKRNA--------PTESQTSPGEAINDTEYQNT-RPGCPIRRGSLNKSGNVSKI---- : 315
GmELF3a      : ESRSNDIGDNGCLVESAR--ETDKGNA--------PTANQTSPADAINDTEHHDT-RMGSPIQRGNLNESDNASKI---- : 319
CcELF3a      : ASQSNDIGHNGCLVESAR--ETDKGNA--------PTVNKISPAEAINDTRHHGT-RTGSSIQRGNLNKSDNASKI---- : 318
AiELF3a      : GSQSNGIGHVDGVAESTR--ETDKGNV--------PTTNQTSPAEAINDTECRDT-RTGGATQKRNLNKSDNISKI---- : 326
LaELF3a      : GSQFNDTRQGDGLVEPTR--ETDNGNA--------AVSNQTTPTVAINDTEYHVI-RAG-------------------- : 309
MdELF3-1     : GSQPNVTGQGDGLVESSR--DVEKGTVSRERSVSCSXADPSSPNEADNDSEYRGD-RACISPQMGHVDKSDDASET---- : 282
PbELF3-1     : GSRPNVTGQGDGLVESSR--DVEKGTVSRERSVSCSRADPSSPNEPDNDSEYRGD-TACISPQMGHVDKGDDVSET---- : 282
MdELF3-2     : GSQPNVTGQGDGLVESSR--XVEKGTLSQEKSVSCSGADPTSPNEDPNDSEYRGD-RKCISPQTGHVDKSDDVSET---- : 319
PbELF3-2     : GSQPNVTGQGDGLVESSR--DVEKGTLSQEKSVSCSGADPTSPNDPDNDSEYRGD-RKCISLQMGHVDKSDDVSET---- : 319
PmELF3       : GSQPNITGQGDGLVECTR--DAEKGAVFQERSLSYSGEDPGGPNELDNDSEYRGD-RTCISPQMGHVDKSDDVSET---- : 338
PpELF3       : GSQPNITGQGDGLVECTR--DVEKGAVFQERSLSYSGEDPGGPNELDNDSEYRGD-RTCISPQMGHVDKSDDVSET---- : 233
FvELF3       : GTQLNDTRQGDGLLESTR--DVEKGTVSQARSISRFGENPSSPNEPDNDSEYR-----MWSPQRGNADKGDDVSET---- : 322
AtELF3       : RQESRNRLYRDGGKTRLK--DTDNGAESHLATENHSQEGHGSPEDIDNDREYSKS-RACASLQQINEEASDDVSDD---- : 305
HvELF3       : NVSDKQQSRNEGHQARTRNENAAESQNAPKAGN----GPYSTDIACNGASNLSEKGLRETGEKRKRSTGHHDVQR----- : 355
ZmELF3-2     : --LKKQHAEAESYQIRTRNENAVETQSPPKNGVSLLSKPYVDRREQNGDSDLLGHGLRETGVKRKRS--HHDVEQN---- : 335
OsELF3-1     : NDSDEPHGGNSGHQATSRNGGSMKFQNPPMRRNEISSNPSS--ENTDRHYNLPQGGIEETGTKRKRLLEQHDAEKSDDVS : 366
OsELF3-2     : NDLDEPHLENSEHQATSRNGGSVKFQNPPVRRNTISAKPSPGIENTNGHCNLPQGGLKEAGTKRKRLEAQDNAEK----- : 356
ZmELF3-1     : N-----HCDNNGCQPASVNGNFTEAKNPTAARNTSSCKPCTDVDSSNRKSNLLERSPREVGAKRKR--GHHNGEQ----- : 344
PmEEC        : CSSSARLHRESMTVHDRVALRDGILVQSRIGTAKEISSKVREKSCLTPSLVDDNRISGGLGNENECCEEKCGVAQVGNL- : 370
PpEEC        : CSSSARLHRESMTVHDRVALRDGILVQSRIGTAKEISAKVREKSCLTPSLVDDNRISGGLGNERECCEENCGVARVGNL- : 366
FvEEC        : HCPNAHFNTEHLLVHDREAIKDDSVMISRIAVA-EVSSKRVKESYTRSFLEDETKFPNGIENSSETSQENCEVVHVGSLN : 356
AtEEC        : --------------------------------QNGSPNVMKTQSYRRNFAEFNNETQKKPKTLPRREQVASN---- : 225


                         *        420        *        440        *        460        *        480
PsEEC        : -------------LNKSSSDCRFGVDIIPDVVGICGEXQFWRTRKTIINQQRNFMQVFELHRLIK--VQRLIACSENL : 423
LcEEC        : -------------LNKSSSECRFGVDILPDVIGICGEXQFWKTRTIISQQRIFFMQVFELHRLIK--VQRLIACSENL : 404
MtEEC        : -------------LNKSSSKCRFGVDISPDVVGICGEXQFWNTRRTIINQQRIFMQVFELHRLIK--VQRLIACSENL : 402
CaEEC        : -------------LNKPRSAYRFGVDISPDVVGICGDXQFWNTRKTIINQQRIFMQVFELHRLIK--VQRLIACSEHL : 402
PvEEC        : --------------------AVHISPDVVGAIGEQQFWKRRTIVQQKIFVMQVFELHRLIK--VQRLIACSPHI : 342
CcEEC        : ------------LNKVNSECTMVVDITPDVVEAIGVQQFWKRRTIINQQKIFVMQVFELHRLIKKQVQRLIACSPHI : 392
GmEEC-1      : ------------VNKYNSECTSVVDISPDVVGAIGEQQFWKVRRTIINQQKIFVQSELHRLIK--VQRLIACSEHV : 389
GmEEC-2      : ------------VSKVNSECTLAVDISPDVVGAIGEQQFWKVRRTIINQQKIFVKQVFELHRLIK--VQRLIACSEHV : 359
LaEEC        : -------------LNRPTSECKVGTDISPDSVLGVIGLKFWKTRKTILQQRMFMQVFELHRLIK--VQKTIAASPHL : 383
LjEEC        : -------------LNKPSSECLFGRDISPDSVVGVIGEBFWKARRTIILQQRIFLMQVFELHRLIK--VQRLIAESPHL : 294
AiEEC        : -------------LNKPRLECKLGVDISPNLVLGVIGEXQFWKAFTTIINQQRIFLIQLSELHRLIE--VQKTIARSPHL : 237
PsELF3b (PPD): ----------------TLENMPSPRLSPDGVAELGQQLFWKARRTIIQQRMYAVQVFELHRLIK--VQHLIAESSNL : 352
LcELF3b      : ----------------TLENMPSPKLSPDGVVELGQQLFWKRRKITSQQRMYAVQVFELHRLIK--VQHLIAESSNL : 342
MtELF3b      : ----------------TIENLSSSKLSPDGVVQLGQQLFWKRRKITTQQRAFAVQVFELHRLIK--VQHLIACSSNL : 334
CaELF3b      : ----------------TLESLSSSELSPDGIVQLGQHFWKARRKITTQQRVFAVQVFELHRLIK--VQLIACSSDL : 340
GmELF3b-1    : ----------------TVTNLSSIVSPDIVVGLGQHFWKARRKIAQQSVFAVQVFELHRLIK--VQOLIAASFDV : 390
GmELF3b-2    : ----------------TVTNLSSIVSPDIVVGLGQHFWKARRKIAQQSVFAVQVFELHRLIK--VQOLIAASFDV : 372
CcELF3b      : ----------------TVTNLSSIVSPDIVVGLGQHFWKARRQIAQQRVFAVQVFELHRLIK--VQOLIAASFDV : 393
PvELF3b      : ----------------TVTNLSSQVVSPDIVVGLGQRFWKARRKIAQQRVFAVQVFELHRLIK--VQOLIASSFNV : 390
AiELF3b      : ----------------SIENSSTIRVSTDIVVGLGQHFFKARRETAQQRIFAVQVFELHRLIK--VQOLIACSEEL : 315
LaELF3b-1    : ----------------SIGNLSSIKASPDIVVGLGQRFWKARRKLAQQRVFAVQVFELHRLLK--VQHLIARSPDL : 374
LaELF3b-2    : ----------------STENLSSIKASPDIVVGLGQRFWKARRKFVQSVFAVQVFELHRLLK--VQKLIARSPDL : 306
PsELF3a (HR) : ----------------RVEDLSTVKISPDIVVAVIGQHFWKARKAIAQQRVFAVQVFELHRLIK--VQLIACSPDL : 381
LcELF3a      : ----------------RVENLSTVKISPDIVVAVIGQHFWKARKAIAQQRVFAVQVFELHRLIK--VQLIACSPDL : 381
MtELF3a      : ----------------RVEDLSTIKISPDIVVAIGQQFWKARKAIAQQRVFAVQVFELHRLIK--VQLIACSPDL : 367
CaELF3a      : ----------------GVENLSTIKISPDIVVAIGQHFWKRARKAIAQQRVFAVQVFELHRLIK--VQLIACSPDL : 382
LjELF3       : ----------------RVENLSTKVSPDIVVGLGQHFWKARRAIVQQRVFAVQVFELHRLIK--VQLIACSPDL : 377
GmELF3a      : ----------------RVENLSTVRISPDIVVGLGQHFWKARRAIAQQRVFAVQVFELHRLIK--VQLIACSPDL : 381
CcELF3a      : ----------------MVENLSTAKISPDIVVGLGQHFWKARRAIATQQRVFAVQVFELHRLIK--VQLIACSPDI : 380
AiELF3a      : ----------------SVVENLSTSDLSPDIVVGLGQHFFKARRAIAQQRVFAVQVFELHRLIK--VQKLIACSPDI : 388
LaELF3a      : ----------------KLESVSTIKVSPDIVVEILGQRFWKARKAIASQQRVFAVQVFELHRLIK--VQKLIACSPDL : 370
MdELF3-1     : ----------------GMVDSISGIDISPDIVVGIGQHFWTARKAIVQQRLFAVQVFELHRLIK--VQRLIACSPHL : 344
PbELF3-1     : ----------------GMVDSISGVDISPDIVVGIGQHFWKARKAIVQQRLFAVQVFELHRLVK--VQRLIACSPHL : 344
MdELF3-2     : ----------------GMVDSISGVDISPDIVVGIGQXFWKARKAIVQQRLFAVQVFELHRLIK--VQLIACSPHL : 381
PbELF3-2     : ----------------GMVDSISGVDISPDIVVGIGQHFWKARKAIVQQRLFAVQVFELHRLIK--VQRLIACSPHL : 381
PmELF3       : ----------------GMVDSVSGIDISPDIVVGIGQHFWKARKAIVQQRLFAVQVFELHRLIK--VQRLIAGAENL : 400
PpELF3       : ----------------GMVDSISGIDISPDIVVGIGQHFWKARKAIVQQRLFAVQVFELHRLIK--VQRLIACSPNL : 295
FvELF3       : ----------------GMVDSVSGIDISPDIVVGIGPHFWKARKAIVKQRLFAVQVFELHRLIK--VQRLIACSPHI : 384
AtELF3       : ----------------GMVDSISSIDISPDIVVGIGQHFWKARKAIAQQRVFAVQLFELHRLIK--VQLIAASPHL : 367
HvELF3       : ----------DDSSDSVESLPEIEISPDIVVGAIGPHFWKARKAIVQQRVFAVQVFELHRLIK--VQLIAASFHL : 422
ZmELF3-2     : ----------DDLSDSVESLPGVEISPDIVVGSAIGPHFWKARKAIVQQRVFAVQVFELHRLIK--VQKLIAASFHV : 402
OsELF3-1     : RLLEQHDAENIDDVSDSVECITGWEISPDIVVGICAHFWKARRAIIQQRVFAVQVFELHKLVK--VQKLIAASFHV : 444
OsELF3-2     : ----------IDDLSDSVECITAWEISPDEIVGAICAHFWKARRAIIQQRVFAAQVFELHKLVK--VQKLIAASFHV : 424
ZmELF3-1     : ----------NDDLSDSVECIPGGEISPDEIVAAIGPHFWKARRAIQQQRVFAVQVFELHKLVK--VQKLIAASFHL : 412
PmEEC        : -------CGHEDISDMIMDCNSAVDGISPHVGICAQFCEMRKAIVSQQRVFAAQVFELHRLIK--VQRLIACSEHL : 441
PpEEC        : -------CGHEDISDMIMDCNSAVDGISPHVGICAQFCEMRKAIVSQQRVFAAQVFELHRLIK--VQRLIACSEHL : 437
FvEEC        : -------CRRGDVSDMIMGESSTSIDISPDIVIGICDNQFCKTRKAIVQQRVFAMQVFELHRLIK--VQKLIACSPDL : 427
AtEEC        : --------------CIAIESLSGISASSYITARVIGERFWKMRTYMINQQKIFAGQVFELHRLIM--VQKMVAKSENL : 288
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                     *        500        *        520        *        540        *        560
PsEEC         : LFDNLVINKPPTKTSSPEKLQS-DFISEQPLTVFKHDSKSEKASTSEDVKNSAVG-NIP--FPCVNN--ISIEH-NRLS : 496
LcEEC         : LFDNLVINKPPTKTPSSEKLES-DFISEQPLTVFKHDSKSEKASTSEDVKNSAVG-NIP--FPCVNN--ISIEH-NRLS : 477
MtEEC         : LFDKLLINKPSVEASSNKLQS-DFISEQQPLTVFKIDSKSEKATTSEDVKNNAVG-KIS--LPFVNN--ISIEN-NQLS : 475
CaEEC         : LFPD----KSPIITSSPK---------------K-DDKSEKAATSDDIKNNVVG-NIH--LPSVNN--ITIEH-NHLP : 455
PvEEC         : LLIDNLLINKPPPKTSTTKKFQS-DFVGEKPSSVVKIDSKSVKAPTAEHATNSAVE-KIP--IPCFNN--ITIGHTNQPP : 416
CcEEC         : LLDNLLINKPPPKTSTTKKLQSDDFVGEKPSSVVKIDSKSGNAPPTEHVTNNAFG-KIP--IPCVNN--ITIGHANQLP : 467
GmEEC-1       : LLDNLLHNKPPQKTSTTQKFQS-DFAGKKPSSVVKIDNKSVKVNTDEKATNSAVG-KIP--IPCISN--ITIGHANQLP : 463
GmEEC-2       : LLDNLLINKPPPKTSTSKKFQS-DFASQKPSSVVKIDNKSVKVNTAEKATNSAVG-KIP--IPCISN--TTIGHANQLP : 433
LaEEC         : LLDNLVSNKQSLKPSAIKKIQS---DYQQTTSIVKINTKSEKPPTAEHAKNIAFR-KIPP-LPCLNN--ISISGL----- : 451
LjEEC         : LLGDNSMINKPQLKTSSTKKLP------SPSTVIKIESKSERTSTPEPAKNNAIG-MFP--LPSPINNISISHSNQLS : 365
AiEEC         : LLDIHVINRTLPKPSPFKRLQS-----------DYIADQSPAGKLANHSENIAIGGKIPLPPPCINN--ISIGHFN---- : 301
PsELF3b (PPD) : LPDTAAVIGKPLLQGSNSKS--L--------SFEEVIEPQA--QNHKQQDHSENQ----NHKLDYSTENGIGI-TSLSSQ : 415
LcELF3b       : LLDSAAIIGKSPLRGSNSKS--L--------SLEEVIEPQA--QNHKQQDHSENR----NHELDCSPVNGIEI-TSFSSQ : 405
MtELF3b       : MLDAAAIIEKFPLQEIIPKS--L--------SLEVVIESQT--KNHKQQDHSESL----NHRLDCSAEKGIEI-TSCSYQ : 397
CaELF3b       : LFDAAIIGKFPLQASTPKS--I--------SLEVIIEPPT--QNHKQQDHSEKL----NHKLEHSAENGIGI-TSFSSQ : 403
GmELF3b-1     : LDVAFIGKFPLTESPPKN-I--------SLEVVIEPQQ--QNPKRKNDSEKL----NHKTECSAENAIAI-RTSFSSP : 454
GmELF3b-2     : LLDGAFIGKFPLMGSPPKNKNI---------SLEVVI---------------------NHKTECSAENAIAI-KKSFSSP : 422
CcELF3b       : LLDGAFVENFPVPGSTPKN--L--------SLEVIIEPQQ--QNHKRKNDSEKP----NHKTECSAENAISI-KTSFSSP : 457
PvELF3b       : LLDGAFIGKFPLEGSTPKT--L--------SLQVVIEPQQ--QNPKRKNNSEKP----NHKTECSAENAIEI-KTSFSSP : 454
AiELF3b       : LLDAAFIGKIPLKGSTTKN--L--------SLEELIEPKR--QNLKRKDDSQKL----NHKMECSAENAIGI-ASFSSQ : 378
LaELF3b-1     : LLDGAFIGNSPPKRSTPNL----------TLEVVIKPQL--QNHKRKDDSEKLN--HNKMECSAENAIGI-RSCSTP : 437
LaELF3b-2     : LLDGSFIRNSLPKRSTPNL----------AVNVVIKPQI--QNLKRKDDSEKLN--HNKMEYSAENVIGI-RSCSIP : 369
PsELF3a (HR)  : LFDDGAFIGKSLPDGSTPKK--L--------SLEYVIKARL--QNLKRKVDSEKI----NQNMECSAENAIGI-TSISSV : 444
LcELF3a       : LFDDGAFIGKSLPDGSTPKK--L--------PLEYVIKTRL--QNLKRKVDSEKI----NQNMECSAENAIGI-TSISSV : 444
MtELF3a       : LFDGAFIGKSLPDGSTPKK--L--------ALEYVIKPRL--QNLKRKVDSENV----NQNMECSAENAIGI-TSISSV : 430
CaELF3a       : LFDGAYIGKSPPVGCTTKK--L--------SLEYVIKPRE--QNLKRKDSEKI----NQEMECSAENAIGI-TSISSV : 445
LjELF3        : MLVDGAFIRKSPPKGSTPKK--L--------SLEYVIKPLQ--ENLKRN-DSEKQ----NHKMECSAENAIGI-TSISSV : 439
GmELF3a       : LLDGAFIGKSPPKGSTPKK--L--------ALEYVIKPRQ--QNLKRKDDSEKL----NHKMECSAENAIGI-TSLSSV : 444
CcELF3a       : LVDGTFIGKSPAKESTPKK--L--------PLEYVIKPRQ--QNLKHKDDSEKL----NHKMECCAENAIGI-TSLSSV : 443
AiELF3a       : LLDAAFIGKSPPKGSTPKK--L--------AIEYVIKPRQ--PNLKRKDSEKL----HHKMECSAENAIGI-TSLSSV : 451
LaELF3a       : LLHAAFIGKSPLKGSTPKK--P--------ALEFVIKPQP--QTLKRKHESEKA----NHKMECSAENAIGI-TSLSPM : 433
MdELF3-1      : LLDTAFIGTSTLRGSPAKK--L--------SSEYVIKPLL--HVVKRKHXPEEP----NNKXECSAENAIGI-TSHSSV : 407
PbELF3-1      : LLDTAFIGTSTLRGSPAKK--L--------SSEYVIKPLL--HVVKRKHEPEEP----NNKMECSAENAIGI-TSHSSV : 407
MdELF3-2      : LLDTAFVGTSTLRGSPAKK--L--------SSEYVIKPLL--HIVKRKHEPEKP----NNKMECSAENAIGI-TSHNSV : 444
PbELF3-2      : LLDTAFIGTSTLRGSPATK--L--------SSEYVIKPLL--HVVKRKHEPEKP----NNKMECSAENAIGI-S----- : 439
PmELF3        : LLDTAFIGTSSLRGSPAKK--L--------SSEYVIKPLL--RVVKRKHEPEKP----NNKIECSAENAIGI-TSLSSV : 463
PpELF3        : LLDTAFIGTSSLRGSPAKK--L--------SSEYVIKPLL--RVVKRKHEPEKP----NNKIECSAENAIGI-TSLSSV : 358
FvELF3        : LLDSAFIGTS-LRRSPAKK--L--------PADYVIKPLL----LKRKHESEKS----NHKMECSAENAIGI----SV : 444
AtELF3        : LLDEISFIGKVSAKSYPVKK-LL--------PSEFLIKPPLPHVVVKQRGDSEKTD--QHKMESSAENVIGI-----LSN : 431
HvELF3        : LIIGDPCIGSALVTSKKKTAAAN--------VEKQLISAKS-KDDDDAQLTLQQVE---YSKDNTEGNQASPSQDNDLVE : 490
ZmELF3-2      : LIIGDPCIGKSLAVSKKR-LAGD--------VETQLIESAKN-DDG-----VRPTQLE--HSKEKTEANQPSPSQDE---- : 461
OsELF3-1      : LIISDPCIGNALLGSKNKLVEEN--------LKAQPILVAT-IDD--VEPSLQQPE---VSKENTEDSPPSP-HDTGLGS : 509
OsELF3-2      : LIISDPCIGNALLASKKKMAEEN--------LKAQPILVAT-NDD--VQPSLQQPE---LSKENSEENPPSP-RDTAPVS : 489
ZmELF3-1      : LIIGDPVIGNALTGKRNKLPKGN--------SKVQTISITN-KDD--IQPTLEQPE---LSKQDTEGNLLAHSHDDGLGD : 478
PmEEC         : LLDNDFISKPAIKVPPVKK----------VPLEHAIELPPLIVKPKDHPQKPHSS-GECVEENAVGKFPIPPVNNRTSS : 510
PpEEC         : LLDNDFISKSAIKVPPVKK----------VPLEHAIEPPP----PKDYPQKPHSS-GECVEENAVGKFPIPPVNNRTSS : 502
FvEEC         : FFKGKPLIKNPAVEISVLNN---------VPIERAQEPTPSIVKPKDYPQKPYSN-TECGEESTVGKFPIPFVYNDASS : 496
AtEEC         : FLISKLNGVKHGTMRISHQL------------------------AMAASKVR-----KPNTENHKPIPEEYPEHMK : 335


                     *        580        *        600        *        620        *        640
PsEEC         : YYGNHHLGNLTLVSADKSSSSICLSKQSSSIVIP-PEP-NQWLVPVMSPSEGLVYKPIIGECPPNAGGIMTPLYIACGAL : 574
LcEEC         : YYGNHHLGSLTLASADKNSNSISISKQSSSIVIP-PEP-NQWLVPVMSPSEGLVYKPIIGECPPNAGGIMTPLYITCGAL : 555
MtEEC         : NYGNHHLGNLALASADKSSN----AKHSPNIVIP-PEPPNQWLVPVMSPSEGLVYKPIIGECPPNSGGIMTPLYIGCSPM : 550
CaEEC         : NYVNHHLGNLALASNDIKNSN----SKQSPNIVIP-PEPPANQWLVPVMSPSEGLVYKPIIGECPPNS-LVAPLFIACSSL : 530
PvEEC         : NFG-HHLAKLPIASSDTN------SKQSPSYVIP-PEG-NQWLVPVMSPSEGLVYKPVLGECPPNAG-FMAPIYITCGSV : 486
CcEEC         : NYS-HHLGNLAVASADSN------SKQSPSYVIP-PEG-NQWLVPVMSPSEGLVYKPIIGECPPNAG-FMAPIYITCGTV : 537
GmEEC-1       : NYG-HHLNLALGSADSN------SKQPPSYVIP-PEG-NQWLVPVMSPSEGLVYKPIIGECPPNAG-FMAPIYISCGTM : 533
GmEEC-2       : NYG-HHLGNPALASADSN------SKQSPSYVIP-PEG-NQWLVPVMSPSEGLVYKPIIWECPPNAG-FMAPIYISCGTV : 503
LaEEC         : PYFVHDLRNPALCLPDIN------IKQSPSCVIP-PEG-NQWLVPVMSPSEGLVYKPMAGECPPNPGFMPPPVHNAFSTM : 523
LjEEC         : NYS-HHLD-----------------INSPSCVIPPVEPVNQWLVPVMSPLIEGLVYKPAIIAPI---NAG-FMAPPP------ : 417
AiEEC         : NHG-HYIGKPTLLTSLDSMN----TKNTLGCVIPTSQG-NQWLVPVMSPILEGLVYKPIIGECPPNPS-LITPIYICPYSPQ : 374
PsELF3b (PPD) : K-------------SNQAN-AGSQ------CINQPE-GHQWLIPVMSPSEGLIYKPYPGEAFPG-----AVYGICY-EPF : 467
LcELF3b       : KYGSHLSNYTPFSGNSDQAN-FGAH------SINQPE-GHQWLIPVMSPSEGLVYKPYPGEAFPG-----SVYGICY-EPF : 471
MtELF3b       : KYGSHLSNYTPFSGNSDQAN-VGSQ------YINQSE-GHQWLIPVMSPSEGLVYKPYPGEGYTG-----AVYGICY-RPF : 463
CaELF3b       : KYGSHLSNYTPFYGNPHQEN-VVSR------SINHSPIGYQWLIPVMSPSEGLVYKPYPGEGFTG-----PMYGIC-GPF : 469
GmELF3b-1     : KNGSHLANHTPFSGTPHQAN-VASDNKTSPWCINQTE-GHQWLIPVMSPSEGLVYKPYPGEGFKG-----TMHGICGGPF : 527
GmELF3b-2     : KNGSHHTNHTPFSGTPHQAN-EASDNKTSPWCINQAE-GHQWLIPVMSPSEGLVYKPYPGEGFMG-----TMNGICGGPF : 495
CcELF3b       : KNGSHLTNHTPFSGTPHQAN-VTSDNRTSPWCINQAE-GHQWLIPIMSPSEGLVYKPEEFTG-----TMHGICSVPF : 530
PvELF3b       : KNGSHLTNHSPFSGIPHQTD-VASDNGTSPWSINQSP-QHQWLIMSPSEGLIYKPYPRPEAFTG-----MMPAICGGPL : 527
AiELF3b       : KSGSHHLNYSSTPGDPHQAS-GAADNRMAPMCINPSP-GHQWLIPVMTPSEGLVYKPYPGEGFTG-----SFCGIF-GPL : 450
LaELF3b-1     : KNGSHHSNYTPFAGNLHQTE-AAADNRMGSWCINQSP-GHQWLIPVMTPSEGLVYKPYPGEAFPG-----TMCGIGCGPF : 510
LaELF3b-2     : ENGCHLSNYTSFSGTPHQTK-VAADNRMGSWGINHSP-GHQWLIPVMTPSEGLVYKPYPGEAFQE-----TMCGRGCEPF : 442
PsELF3a (HR)  : KNTSHLSSSMPFAGNPHQGN-VAADNGMGPWCINQSP-GHQWLIPVMSPSEGLVYKPYPGEGFTG-----TNFGIC-CGPY : 516
LcELF3a       : KNTSHLSSSMPFAGNPHQGN-MAADNGMGPWCINQSP-GHQWLIPVMSPSEGLVYKPYPGEGFTG-----TNFGIC-CGPY : 516
MtELF3a       : KNGSHLSSSTPFAGNPHHGN-MAAENGMGWGINQSP-GHQWLIPVMSPSEGLVYKPYPGEGFTG-----TNYGIC-SGPF : 502
CaELF3a       : KNGSYLSTATPFAGNPHQGN-MAADSGMGPWCINQSP-GHQWLIPVMSPSEGLVYKPYPGEGFTG-----TNCGEIC-GPI : 517
LjELF3        : KNGSHLSHHTPFPGNPQPN-VPADSGMSPWGIHQSP-GHQWLIPVMSPSEGLIYKPYPGEGYTG-----TNGGIC-CGPF : 511
GmELF3a       : KDGSHLSKCTPFPGNQHQTN-VAADSGMGPWCINQSPPGHEWLIPVMTPSEGLVYKPYPGEGFTG-----TGCGIGCGPF : 518
CcELF3a       : KNGSHLSNYTPFPGNPQQTN-VGADSGMGPWCIHQSP-GDQWLIPVMTPSEGLVYKPYPGEGFTG-----TGYGIC-CG-- : 513
AiELF3a       : KNGSHPSNYTPFAGNPYQTN-SAADSGMGPWGIHQSP-GHQWLIPVMSPSEGLVYKPYPGEGFTG-----TMCGIC-CGPF : 523
LaELF3a       : KNGSHHSNYTPFSRNQHTAN-VPADSGMPWCIHQSP-GHQWLIPIMSPSEGLVYKPYPGEGFTG-----TTCEIC--GY : 503
MdELF3-1      : RNGSQTSNYGPYIGNP-QPTPVATDNKANPWCIHQSP-GHQLLIPVMSPSEGLVYKPYNGEGYMG-----AVCGIC-CGPF : 479
PbELF3-1      : RNGSQTSNNGPYLGNP-QPTPVATDNKANPWCIHQSP-GHQLLIPVMSPSEGLVYKPYNGEGYMG-----AVCGIC-CGPF : 479
MdELF3-2      : KNGSQTSNYGPYLGNP-QPTLMASDNKASPWCIHQSX-GHQFLIPVMSPSEGLVIXKKPYNGEGFMG-----PVCGIC-CGPY : 517
PbELF3-2      : -----QSLVFPYLGNP-QPTPMASD-KASPWCIHQSP-GHQLLIPVMSPSEGLVYKPYNGEGFMGG-----PVCGIC-CGPY : 506
PmELF3        : KNGSQTSNYGPYVGNP-QPTPVGTDNKASPWCIHQSP-GHQLLIPVMSPSEGLVYKPYHGEGFVG-----PVCGIC-CGPF : 535
PpELF3        : KNGSQTSNYGPYVGNP-QPTPVGTDNKASPWCIHQSP-GHQLLIPVMSPSEGLVYKPYHGEGFMG-----PVCGIC-CGPF : 430
FvELF3        : KNCSQPSHHVPYVGNPPAPAPLPADNKAAPWCIHQPP-GHQYLIPVMSPSEGLITYRPYRGECPPTGG-FMPPIYI----- : 517
AtELF3        : QGHHQQSNYMPFANNPPASP--APNGYCFPPQPPPSGNHQQWLVPVMSPSEGLIYKPHPGMAHTG-----HYGICYGHY : 503
HvELF3        : VRHENQAASNGAVSSNPPAMPAPTDNKQNNW--CAPEPQNQWLVPVMSPSEGLVYKPYTGECPPAGSFLAP-FYASCAPL : 567
ZmELF3-2      : -----QAATNGDVAAS---MHTPSDNKQKSW--CIPAPPSQWLVPVMSPSEGLVYKPYTGHCPPVGSLLAPPFFASYPTS : 531
OsELF3-1      : -GQRDQAATNGVKSNRRATPVASDNKQNNWGVQLQPPQNQWLVPVMSPSEGLVYKPYSGECPPAGSILAP-FYANCTPL : 587
OsELF3-2      : -GHHDQTAKIGASKSNLRATPVASDNRQNNCGVQLQPPQNQWLVPVMSPSEGLVYKPYSGECPPAGSILAP-FYANCTPL : 567
ZmELF3-1      : -NHHNQAATNETFTSNPPAMHVAPDNKQNNW--CMNPPQNQWLVPVMSPSEGLVYKPFAGECPPVGNLLTP-FYANCAPS : 554
PmEEC         : RGLVTQQP---------------YSKPALWCLQPPE-GNMWFVPVTSSSEIAVIQPYTGECAPTGG-FMAPMYISCGPA : 572
PpEEC         : RGLVTQQSNYGQYSNKSPSASATTNSKPALWCLQPPE-GNMWFVPVTSSSEIAYKPYTGECAPTGG-FIAPMYISCGPA : 580
FvEEC         : RGLVIQKSNNGQYSRKTSPASEATYSKPASWCIQPPE-GNMWLVPVMSPSEGLITYRPYRGECPPTGG-FMPPIYI----- : 569
AtEEC         : PKLPLPSISKELVTPIWPQQ-------------LLPEPGNQWLVPVITDSDGLVYKPFPGECPPS-------------- : 387
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                      *         660         *         680         *         700         *         720
PsEEC        : SLNPGTKD-VLDPSLT-SFHQKIGILSGSSLP-----QLLEICVPSFMH--RSISASSIEQMGQSS-GPKNHHSYAELNS : 644
LcEEC        : SLNSGTKD-VLDPSLT-SFHQKIGILSGSSLP-----QLLEICVPSFMH--RSISASSIEQMGQSS-GPKNHHSYAELNS : 625
MtEEC        : SFNQGSKDV-MDPSLTTSFHQKIRLLSGSSLP-----QLLEICVPSFMH--RSISASSIEQMAQSN-GPKNHYSSAELNS : 622
CaEEC        : SLNPGNKD-VLDQSLGTNCHQKVGIFSSSSLP-----QLIE---TSFMH--RSISASAIEQMEQSNYGTKNHQSNAEF-- : 597
PvEEC        : SFNPLSKDVSSEAALAESSHQKFGILSGSSLP-----PPFIHNPSSISASAIEQMGQSN-GPENHNSCGEVNS : 557
CcEEC        : NFNPGSKDASLDAALAESSQKFGLLSGPSLP-----QILE---PPFVP-PSSISASAIEQMGQSN-GPENHHSCGEVNS : 607
GmEEC-1      : SFNPLSKDASSDATLAESSHQKLGIISGSSLS-----QLP-----SFMNHPSSISASAIEQMGQSN-GPENHHSCGEVNS : 602
GmEEC-2      : SFNPLSKDASSDAALAESSHQKLGILSGSSLP-----QSLE---PSFMNHPSSISASAIEQMGQSN-GPENHHSWGEVNS : 574
LaEEC        : AFNLGSKDATDAAALSSGSHQRTGIPSGSSLP-----NSLE---PPFMIP-PMLPVSAIEHIWQSN-GPE------EANS : 587
LjEEC        : ------------------TPPPPPIIASSLP-----QSLEI-PSLMH----HPSMSIEKMGQSNGPDQNHHSSGEVNS : 467
AiEEC        : HVQEVP------TLPPTNSHQRIGSLSDSFSP-----PMMH---PSIEHPNNNNNNNNNGHESH---HYSSSLGEVNS : 437
PsELF3b (PPD): GHSPPDGTFVNPAYGVENFHQAIAMSPFIPPSS---YAIFPEIQG-VPAMN-QSASGSVAEIVNQFVAQGSGDRNGNSSLV : 542
LcELF3b      : GHSPADGTFVNPAYGVENFHQAIAMSPFIPPSS---YAIFPEIHG-VPAMN-QSTSRSAAEIVNQFVAHGSRDRNNNSSLV : 546
MtELF3b      : GQGPPDVTFVNPAYGVEDFHQAIAVPPFIPPGG---YPIFPEIHG-VPAMY-QSASVSAIEQVNQFSAHGSRNQNGTSSLE : 538
CaELF3b      : GPGPPNGAFVNPAYGIEDFHQAVAVSFIPPGS---YAHFPEIHC-VPAMN-QSASGSVIEQANRFAAQVSHDSNGNSSLV : 544
GmELF3b-1    : GQAPLSATFVNPAYGFEASHPVVGVSPFVPPAS---HTIFAEIFG-MPVVN-QATSGSAIEQVNQFAAQGSHGQNGHSSVE : 602
GmELF3b-2    : GQAPLGATFVNPAYGFEASHPVVGVSPFVPPAS---HAIFPEISFG-MPVVN-QATSGSTIEQVNQFAAQGSHGQNGHSYIE : 570
CcELF3b      : GQAPIGTTFVNPAYGVEASHQVVGVSPFVPPAS---HAIFPEIYG-MPVVN-QAASGSAIEPVNQFAAQGSHGQNGHSSVE : 605
PvELF3b      : GQAPLGATFVNPAYGFEASHQVVGVSPFVSPAN---HTIFSEIYG-MPVVN-QAASGSAAEIHVNQFATQGSHGQNGHSSVE : 602
AiELF3b      : GPVPMSNTYVNPVGLEASHEAIGVPPYIPPGS---HAIFPEIYG-MPFMNNQAMSGSAIEQANQFMAQGSHLQNGHSSAD : 526
LaELF3b-1    : GPGPPGGTFVNPSYGVE---------PHISPGS---LTIFPEIYG-MPVMN-QAVSGSADEIVNHFAAQGSHDQNGHSLVE : 576
LaELF3b-2    : GPGPPGGTFVNPSYGVE---------PHIPPGS---LAIFHEIYG-MPVMN-QSVSGSADEIVNHLAAQGSRGQNGHSSIE : 508
PsELF3a (HR) : AAAPSGGTFVNPSYGIE-------PPPETPPGS---QAIFPEIYGGMPVMK-AAASESAIEHVNQFSAR---GQSRRLSED : 582
LcELF3a      : GASPSGGTFVNPSYGIE-------PPPETPPGS---HAIFPEIYGGMPFMK-AAASESAIEHVNQFSAH---GQNHRLSED : 582
MtELF3a      : GAPPSCGTFVNPSYGME-------PPPETPPGS---HAIYPEIYGSMPFMK-AAASESVIEHVNQFSAR---VQSRHLSEG : 568
CaELF3a      : GAAP----FVNPSYGME-------AAPETPPGS---HAIFPEIYGGMPVTK-AAVAESAIGHVNQFSAH---GQNDHLSEV : 579
LjELF3       : GPAPLGGTFVNAAYGIENSYQGIGVPPDAPPGS---HAIFPEIYG-MPTMN-AAMSESAIDQVNQFSALESRGQSGHISGR : 586
GmELF3a      : VPALLGGSFVNPGYGIETSHQGVGVPPDTHPGS---HGILPEIYG-MPVMN-SSMSESVIEQGNQFSALGSHGHNGHLPGG : 593
CcELF3a      : -PAPLGGAFVNPAYGIQTSHQGE---DTPPGS---HGIFPEIYG-MPFMN-AAMSESAIEQVNQFSALGSR---GHLSRG : 579
AiELF3a      : APAPMGGTFVNPAYGVETSNQVPGVPPETPPGS---HAIFPEIYG-LPVMT-KAMSESAIEQANQFSARGSQGQNDHSQGG : 598
LaELF3a      : GPTPLGGTFVNAAYVIEASHQENGVPKNTPPSS---HAIYPEIYR-MPVVN-AAMSESAIEQVKQFSEHASHGQNGHLNGR : 578
MdELF3-1     : GSTPMAGNFVKPTYGVE-SSHHQGMGVLPVPPSLG-HTIFPEIYG-MSVMN-PAMSTSAIEQMHWFAGPGSHGHTDQSSGG : 555
PbELF3-1     : GSTPMAGNFVKPTYGVE-SSHHQGMGVLPVPPSLG-HTIFPEIYG-MSVMN-PAMSTSPIEQMHWFAGPGSHGHTDQSSGG : 555
MdELF3-2     : GSTPMTGNFVKPSYGVE-SHHLQGMGVLPVPPSLGHT-FPEIYG-MSVMN-PGMPSSAIEQMHWFAGPVSHGHTNQSXGG : 594
PbELF3-2     : GSTPMMGNFVKPSYGVE-SHHLQGMGVLPVPPSLNGHT-FPEIYG-MSVMN-PAMPSSAIEQMHWFAGPVSHGHTDQSSGG : 583
PmELF3       : NSTPMTGNFVKPNYGVEASHHHQGTGVLPVPPPLG-HTIFPEIYG-MSVMN-PAMPSSGIEQMHWFAGPGSHGQIDQLSGG : 612
PpELF3       : NSTPMTGNFVKPNYGVEASHHHQGTGVLPAPPPLG-HTIFPEIYG-MSVMN-PAMPSSGIEQMHWFAGPGSHGQIDQLSGG : 507
FvELF3       : GSSPMTGNFVLKPAYGVE--GPHHQGMGVLPAP----HPTIFPEIYG-MSVMN-PTMSSSAIEQMNWFAGPGLHGSTDQLSG- : 589
AtELF3       : MPTPMVMPQYHPGMGFE-----------PPGN----G-FPEIYGMMPTIMNPYCSSQQQQQQQPNEQMNQFGHPGNLQNT : 567
HvELF3       : SLPSTAGEFVNSPYGLEMPHQPQHMGVGGPPAMP--PMVFPEIYG-MPVVN-PVVSSSAIEQVSRVAAARPN-THEHHSRS : 642
ZmELF3-2     : SSSTAGGDFVSS-------------ACGARLMSA--PVIFPSFS-MP-----AVSGSAIEQVSHVAAS-------QHKRN : 583
OsELF3-1     : SLPSTAGDFVNSAYGVEMPHQPQHMGAPGPPSMP--MNIFPEFS-IPVMN-PTAPAPVIEQGRHPSMPQPYGNFEQQSWI : 663
OsELF3-2     : RLPSTTGDFVNSAYGVEIPHQPQHMGAPGTPTMP--MNIFPEFS-MPVMN-PVALASAIEQGRHPSMPQPYGNLEQHSRM : 643
ZmELF3-1     : RLPSTP-------YGVEIPHQPQHMVPPGAPAMH--MNIFPEFS-MPVMN-PGTPASAIEQGSHAAAAPQPHGHMDQQSLI : 623
PmEEC        : SLNPGARDYVNATYSNESLYQQGMGIGTPPLLQ----TCFPEIYG-MPIINPSLSSSAIENMTPFSGGHSNWHENQLSFG : 646
PpEEC        : SLNPGARDYVNATSSNESLYQQGMGIGTPPLLQ----TIFPEIYG-MPIINPSLSSSAIENMTPFSGGHSNWHENQLSFG : 654
FvEEC        : SLDPGNKNYSNAAYGIELTYQQGMGIGTPPLLQ----TIFPTYT--PPVIN----------------HS-SHENPLSFG : 625
AtEEC        : -----SSAFVVPVYGQDSLETPFRFPVSSPFSH----SIFPEIPN----------ARITVDQTNPFG-------------- : 434

                      *         740         *         760         *         780         *         800
PsEEC        : AILYQSPS-NMSTQ--ISQVMSRNISTYQSLEDNKELQVSTASSP-SKRMKG-DELPLFPLAPTFWSSP----------- : 708
LcEEC        : AILYQSPS-NMSTQ--ISQVMSRNISTYQSLEDNKELQVSTASSP-SKRMKG-DELPLFPLAPTFWSSP----------- : 689
MtEEC        : TILYQSPS-NMSTQ--ISHVMARNFSPYQSLEDNKELQISIANSP-SKRMKGVDELPLFPVAPTLWPSS----------- : 686
CaEEC        : --MYQTPSSNMSTQ--ISQVMSRNISNYQSYEDNKELQISRASSP-SKRMKGVDELPLFPVAPTLWPSS----------- : 661
PvEEC        : AIIYQSSS-NISSP--TSQVMSRNIST-HHSPKDKEPQRSTASSP-SKRMSAAEVLPLFPLAPTFWQTE----------- : 621
CcEEC        : AILHQSSS-NISSP--TSQVMSINIST-YHSVKDKELQRSTASSP-SKRTSG-ELPLFPLAPTFCHTE----------- : 670
GmEEC-1      : AILHQSSS-NMSSP--TSQMMSRNISTYHHSLKDKELQRSTASSP-SKRMSG-EALPLFPLAPTFWQSE----------- : 666
GmEEC-2      : AILFQSSS-NMSSP--TSQVMPRNISTYHHSLQDKELHRSTASSP-SKRVSG-EALPLFPLAPTCWQSE----------- : 638
LaEEC        : AILYQSSS-NLSSQ--ASRALSRNVPTSHHSLKEKESQTSTATSP-PKRVKG-DVLPLFPVAPTLWPSTK---------- : 652
LjEEC        : AMLYRSSS-NLSTQ--TSRVMSRNILT-HHSVEDKELQRSTASSPPSKKMKG-DELPLFPVEPTSRLSA----------- : 531
AiEEC        : SILYKSPSSNIIENYHTSQIMPRTTNN-VRKDKDRSTTSSRSSSP-DVLPLFPVAPTFLASN----------- : 503
PsELF3b (PPD): -GADFDTH-NQSSCNFSNQKSGAVLHVTKSRPS-RERELASSPNEK----AQGIRI---EKSSEGRDAL----------- : 601
LcELF3b      : -GAGFDTH-NQSSCDFSNQKSGPILHVTKARPS-RERELASSPNEK----AQGIRI---EKSSEGRDAF----------- : 605
MtELF3b      : -EANFYTH-NQSSCNLTNQKNGATLHVRKPQPS-RERELESSPGEK----AQEIIK--EKSAEERDTL----------- : 597
CaELF3b      : -GASFNTH-NQSSCNLTNQKNGATLHITKFQPS-IERELQGIPTSRPN--EKEIRI---EKSAEGRDAL----------- : 605
GmELF3b-1    : -GADFNTHHNQSSNLPVQKNGARLHVKKSQAL-KERGLQGSTRSSPSEMAQGIRA---GKIADGSDAQ----------- : 666
GmELF3b-2    : -GTDFNTHHNQSSNLPVLKNGATLHVKKSQAS-KERGLQGSTISSPSEMAQGIRA---GKIAEGNDAH----------- : 634
CcELF3b      : -GANFNTHPNQSSNLPVQKNGATLHVKKSQAS-KERQLQGSTTSSPSEMAQGISA---GKIAEGSDAQ----------- : 669
PvELF3b      : -GANFNTHHNQSSNLPVQRSGAMSHVKKLQVS-KERQLQGSTASTASETPQRIKA---RNITEGSDAH----------- : 666
AiELF3b      : -RIDFPAH-NQSGSNQPVQRTGSASLAGKSRTP-KDSEFQGSSTNSPNETAQETRTT--QQVAEGREAN----------- : 590
LaELF3b-1    : -GANFNTH-NQVSNNSPVQRKGAISHVKKSHAS-KKSELQGSTASSPSEKAQGIRK---RQIADGRDAH----------- : 639
LaELF3b-2    : -EANFSTH-NQSYNLPAQKNKGAIFQKKAS-KKSEIQGSTASSLIEKAHGIRQ---RQIAEGRNAH----------- : 571
PsELF3a (HR) : -EADCNKH-NQSGYDLPVQRNGATSHVMYHQRS-KEFEVQMSTASSPSEMAQEMST--GQVAEGRDVL----------- : 645
LcELF3a      : -EDNCNKH-NQSSCNLPAQRNEDTSHVMYHQRS-KEFDLQMSTASSPSEMAQEMST--GQVAEGRDVL----------- : 645
MtELF3a      : -EADCNKH-NQSSCNLPVQRNGATTHVMHHQRS-KEFELQMSTASSPSEMTQGMST--GQVAEERDAL----------- : 631
CaELF3a      : -EANHNKH-NQIPCNLPAQRNGATSHVMNRQRH-KEFELQGSTASSPSEMAQGMSI--GQVSEGRDVL----------- : 642
LjELF3       : -EADHNTH-NQSCDVPVQGNGATSHVMYQQMY-KEFELQGSRTSSPSEMG--------QVAEGRDAL----------- : 643
GmELF3a      : GKANHNTN-NKSSCNLPVQRNGAISHVLKHQTS-KDFELQETSASSPSEMAQGLST---GQVAEGRDVL----------- : 657
CcELF3a      : -EGNLNTN-NQSSCNLPVQKNGAMSHALKYQTS-KDFDLQGSTASSPSEMAQGLST---GQHAEGRDVL----------- : 642
AiELF3a      : -DANPSTN-NQNSNNLPDPRNGTISNVMRYQVCSREVELQGSSATSPSETAQG-------RTDAGRDVL----------- : 658
LaELF3a      : -ETDINTN-NQSCDLPVQRNRAISHAMKKYQTSKEVELQGSTASSPSEMAQGIST---RQIAEGRDAL----------- : 642
MdELF3-1     : -GTNSNLQ-HQSSCNMPSRKNVTIPHAKKFQPS-NDSGLQGSTANSTGDRAPVRTN---QNAEGSDAL----------- : 617
PbELF3-1     : -GTNSNLQ-HQSSCNMPSRKNVTIPHAKKFQPS-NDSGLQGSTANSTGDRAPVRTN---QNAEGSDAL----------- : 617
MdELF3-2     : -GANSNLQ-HQSSCNMPSQKNVTIPHAKRLQPS-NDSGLQGSTANNTGDRAPMRTD---QNPEGSDAL----------- : 656
PbELF3-2     : -GANSNLQ-HQSSCNMP-QKNVTIPNAKRLQPS-NDSGLQGSTANNTGDRAPMRTD---QNPEGSDAL----------- : 644
PmELF3       : -GTNSNVQ-HQSSCNMPSQKSGAIPHAMMFQAS-NDSELQGSTTNSPDRARLGTD---RNAEGSDAL----------- : 674
PpELF3       : -GTNSNVQ-HQSSCNMPSQKSGAIPHAMMFQAS-NDSELQGSTANSPGDTARLGTD---QNAEGSDAL----------- : 569
FvELF3       : ---NSNLQ-HQSSCNMPTPKNAAIPHAMKSRAS-NPSELQGSTANSPGDRAPVVTD---QTAGESDAL----------- : 649
AtELF3       : QQQQQRSD-NEPAPQQQQQPTKSYPRARKSRQGSTGSSPSGPQGISGSKSFRPFAAVDEDSNINNAPEQ----------- : 635
HvELF3       : SCNMRNEAVSVGGVWRFHSSRGSELQGSSAASG--PFDRQQGQGEARGHAAAAPAAPLPTSSSAGNGN------------ : 708
ZmELF3-2     : SC---SEAVLA---------SRDSEVQGSSASS------------------PASS------------------- : 608
OsELF3-1     : SCN----MSHPSGIWRFHASRDSEAQASSASS---PFDRFQCSGSG-------PVSAFPTVSAQNNQP----------- : 717
OsELF3-2     : SCN----MSHPSGIWRFHASRDSEAQASSASS---PFDRLQCGGSG-------PVSAFPTASAQNTQP----------- : 697
ZmELF3-1     : SCN----MSHPSGVWRFLASRDSEPQASSATS---PFDRLQVQGDGS------APLSFFPTASAPNVQPPPSSGGRDRDQQ : 691
PmEEC        : --EINFTLPHQSSCNMSGQMSQVMPCYVGNIQASKGSEIQGTTASSPSDRTLGNALPLFPTAPQSQE------------ : 711
PpEEC        : --EINFTLPHQSSCNMASQMSQVMPCYVGNIQASKGSEIQGTTASSPSDRTLGNALPLFPMAPQSQE------------ : 719
FvEEC        : --ETNFTLPHQRSCNMSNQMREVMSYYMGNIPAPIVNELQGSTPNSPSDKTKGNVLPLFPTAPQGEEFA---------- : 692
AtEEC        : --------QFQRWSNTSSHMTQAIPFSLKKSQESNDSDIQGSTASSPPEKHKLEVLPLFPTEPTHQTDEYK--------- : 497
```

```
                            *       820       *       840       *       860
PsEEC        : -------------------DRD---SQVEHQSKVIKALPHN-KKSASESAAKIFMSIQDERKLL----- : 749
LcEEC        : -------------------DRD---SRVEHQPKVIKALPHN-KKSASESAAKIFMSIQDERKLL----- : 730
MtEEC        : -------------------DRDSIDEHQEHHSRVIKALPHN-PKSASESAARIFKSIQEERKFL----- : 730
CaEEC        : -------------------DRD---TRVENQSRVIKALPHN-AKSASESAARIFKSIQEERKLL----- : 702
PvEEC        : -------------------DRN---TQVELQPRVIKAMPHN-PKSASESAARIFRSIQEERKHL----- : 662
CcEEC        : -------------------DRS---TQVEQQPRVIKAMPHN-PKSATESAARIFRSIQEERKHL----- : 711
GmEEC-1      : -------------------DRN---TQVEHRPRVIKAMPHN-PKTASESAARIFRSIQEERKHL----- : 707
GmEEC-2      : -------------------DTN---TQVEQQPRVIKAMPHN-PKTASETAAKIFRSIQEERKHL----- : 679
LaEEC        : -------------------DKN---KNVENQPRIIKAMPHN-PKSATESAARIFRSIQEERKFL----- : 693
LjEEC        : -------------------EQN---TPVENLPRVIKALPHN-PKSATESAARIFRSLQEERKYL----- : 572
AiEEC        : -------------------NVD---HHHHHQAKVIKALPHN-PKSATESAARIFRSIQEERKYL----- : 544
PsELF3b (PPD): --------LSSFTVPLASDE-VFQSLETRQKPQVIRVVPHN-PRSATVSAARIFQSIQEERKQYDLF-- : 658
LcELF3b      : --------PSSFTVPLVSDE-VFQPLETRQKPQVIRVVPHN-PRSATVSAARIFQSIQEERKQYALF-- : 662
MtELF3b      : --------SSSFTVPIVSKE-VLKSLETRQKPQVIRVVPHN-PRSATVSAARIFQSIQEERKRYDLV-- : 654
CaELF3b      : --------SPSFTAPSVSEE-VFQSLETKQKPQVIRVVPHN-PRSASVSAARIFQSIQEERKQYDLV-- : 662
GmELF3b-1    : --------SLS-----------LHAVETRQQTQAIKVVPHN-RKSATESAARIFQSIQEERKQHDLV-- : 713
GmELF3b-2    : --------SLS-----------LQAVETRQQTQVIKVVPHN-RKSATESAARIFQSIQEERKQHDLV-- : 681
CcELF3b      : --------SLP-----------LPSVATRQQTQVIKVVPHN-RKSATESAARIFQSIQEERKQHV---- : 714
PvELF3b      : --------SLS-----------LHSVDARQQTQVIKVVPHN-GKSATESAARIFQSIQEERKQHDLV-- : 713
AiELF3b      : --------SPSLVDPVVVIDGANQSHETRSETRVIKVVPHN-RRSATESAARIFLSIQEERKRYDS--- : 647
LaELF3b-1    : --------SLSHVAALIPEG-DLQSLETRPQTRVIKVVPHN-RRSATESAARIFQSIQEERKQYDLM-- : 696
LaELF3b-2    : --------SLSHMATLIPEG-VLQPLETGKQTRVIKVVPHN-RRSATESAARIFQSIQEERKQCDLL-- : 628
PsELF3a (HR) : --------PLFPMVPVE-PESVPHSLETGQKTRVIKVVPHN-RRSATESAARIFQSIQEERKQYDAL-- : 702
LcELF3a      : --------PLFPMVSAE-PESVPHSLETGQQTRVIKVVPHN-RRSATESAARIFQSIQEERKQYDAP-- : 702
MtELF3a      : --------PLFPMVPVE-PEGVAQSIETGQQTRVIKVVPHN-RRSATESAARIFQSIQEERKQYDTL-- : 688
CaELF3a      : --------PLFPMVPLE-PEVVPQSPETRQQSRVIKVVPHN-RRTATESAARIFQSIQEERKQYESL-- : 699
LjELF3       : --------PLFPTVPVE-PEGAPQSLETGQQTRVIKVVPHN-RRSATESAARIFQSIQEGRKQYD---- : 698
GmELF3a      : --------PLFPMVPAE-PESVPQSLETGQHTRVIKVVPHN-RRSATASAARIFQSIQEGRKQNDSV-- : 714
CcELF3a      : --------PLFPMVSAE-PESAPQSLETGQQTRVIKVVPHN-RRSATESAARIFKSIQEERKQYDSV-- : 699
AiELF3a      : --------PLFPMGPVT-PEGAPQSLETGQQTRVIKVVPHN-RRTATESAARIFQSIQENERKQYESM-- : 715
LaELF3a      : --------PLFPMAPVAAPEEVPQSLETGQQPRAIKVVPHN-PRSASESAARIFQSIQNERKQHDLV-- : 700
MdELF3-1     : --------QLLPMVPVIPDG-VPQSHDTDQPTRAIKVVPHN-PRTATASAARIFQSIQAERKQQDST-- : 674
PbELF3-1     : --------QLLPMVPVIPDG-VPQSHDTDQPTRAIKVVPHN-PRTATASAARIFQSIQAERKQQDST-- : 674
MdELF3-2     : --------QLFPMAXVIPDG-VPQSSDTGQPTRAIKVVPHN-PRTATASAARIFQSIQEERKQQVST-- : 713
PbELF3-2     : --------QLFPMAPVIPDG-VPQSHDIGQPMRAIKVVPHN-PRTATASAARIFQSIQEERKQQDST-- : 701
PmELF3       : --------QLFPMSPVIPGG-VAQPHDSGQPTRAIRVVPHN-PRTATASAARIFQSIQEERKQHDSI-- : 731
PpELF3       : --------QLFPMAPVIPEG-VAQPHDSGQPTRAIRVVPHN-PRTATASAARIFQSIQEERKQHDSI-- : 626
FvELF3       : --------QLFPTVPAVPER-VPQPHVTNQATRVIRVVPHN-PRSATASAARIFQSIQEERKQYD---- : 704
AtELF3       : --------TMTTTTTTTRTTVTQTTRDGGGVTRVIKVVPHN-AKLASENAARIFQSIQEERKRYDSSKP : 695
HvELF3       : --------GNAAQQPQVSSGSQENPVAAAAAARVIRVVPHT-ARTASESAARIFRSIQMERQQNGP--- : 765
ZmELF3-2     : -------------------------ETAAQPRVIRVVPHT-ARTASESAARIFRSIQMERKQNDP--- : 647
OsELF3-1     : --------------------QPSYSSRDNQTNVIKVVPHN-SRTASESAARIFRSIQMERQRDD---- : 760
OsELF3-2     : --------------------QPSSGSRDNQTNVIKVVPHNNSQTASESAARIFRSIQMERQQDDS--- : 742
ZmELF3-1     : NHVIRVVPRNAQTASVPKAQPQPSSGGRDQKNHVIRVVPHN-AQTASESAAWIPRSIQMERNQNDS--- : 756
PmEEC        : ----------------------PCKSEHQTRAIKVVPHN-TKSASESAARIFLSIQEERK------- : 748
PpEEC        : ----------------------PCQSEHQTRAIKVVPHN-TKSASESAARIFLSIQEERK------- : 756
FvEEC        : --------------------EIEQMSEHQSRAIKVIPHS-FRSATESAARIFLSIQEEK-------- : 730
AtEEC        : ----------------------QKQQPMLRAIKAVPHN-STSASESAARIFRFIQEERRDSDHMIS : 540
```

Figure S3. Alignment of selected ELF3-like protein sequences used to generate phylogenetic tree in **Figure 5B**. Sequence details are given in **Table S3.**

```
                                    Exon1   Exon2
                20        40        60      80
LaELF3a      : MKKGK---DDEK--IVGPMFPRLHVNDKEDKGGPRAPPRNKMALYEQLSIPSQRF-NHGVL--LQNPDTSSNNV--PPTSTSQCAGLERN :  80
AdELF3a      : MKRGK---DDEK--VMGPMFPRLHVNDT-EKGGPKAPPRNKMALYEQFSIPSQRF-NSGVL-PL-NPNTSTTNTPPPPASSTQCTGPERN :  81
AiELF3a      : MKRGK---DDEK--VMGPMFPRLHVNDT-EKGGPKAPPRNKMALYEQFSIPSQRF-NSGVL-PL-NPNTSTTNTPPPPASSTQCTGPERN :  81
CcELF3a      : MKRGK---DDEK--VMGPMFPRLHVNDT-ERGGPRAPPRNKMALYEQFSIPSQRF-NSGVL-PL-NPNISSNTV--PPASSSQCTVPERN :  79
GsELF3a      : MKRGK---DDEK--VMGPMFPRLHVNDT-EKGGPRAPPRNKMALYEQFSIPSQRF-NSGVL-PL-NPNISSNTV--PPASSSLGTVPERN :  79
GmELF3a      : MKRGK---DDEK--VMGPMFPRLHVNDT-EKGGPRAPPRNKMALYEQFSIPSQRF-NSGVL-PL-NPNISSNTV--PPASSLRTVPERN :  79
VaELF3a      : MKRRK---DDEK--VMGPMFPRLHVNDT-EKGGPRAPPRNKMALYEQFSIPSQRF-NSGVV-PL-NQNISSNTA--PPTSSSQCTVPERN :  79
VrELF3a      : MRRGK---DDEK--VMGPMFPRLHVNDT-EKGGPRAPPRNKMALYERFSIPSQRF-NSGVL-PL-NQNISSNTA--PPTSSSQCTVPERN :  79
LjELF3a      : MKRGK---DDEK--PLFPRLHVSDT-EKGGPRAPPRNKMALYEQFSIPSQRF-NQGLLPPT-NTNTSSNTA--PPASSSQCAVHERN :  80
CaELF3a      : MKRGK---DDEK-MMGPLFPRLHVGDT-EKGGPRAPPRNKMALYEQFSIPSQRF-N---L-PL-HPNTSTNTV--PPSSSIQCTVLERN :  77
TpELF3a      : MKRGN---DDDK-VMGPLFPRLHVGDT-EKGGPRAPPRNKMALYEQFSIPSQRF-N---L-PP-HPNTSTNTV--PPSSSSCAVTDRN :  76
MtELF3a      : MKRGN---DDEK--VMGPLFPRLHVGDT-EKGGPRAPPRNKMALYEQFSIPSQRF-N---L-PPHHPNTSINTV--PPSSSSCAVHERN :  77
MsELF3a      : MKRGN---DDEK--VMGPLFPRLHVGDT-EKGGPRAPPRNKMALYEQFSIPSQRF-N---L-PPHHP----NTV--PPSSSSCAVHERN :  73
VfELF3a      : MKRGN---DDEK-MVGPLFPRLHVGDT-EKGGPRAPPRNKMALYEQFSIPSQRF-N---L-PL-HPNTSGNSV-PPPASSSQCTVHERN :  77
LcELF3a      : MKRGS---DDEK-MMGPLFPRLHVGDT-EKGGPRAPPRNKMALYEQFSIPSQRF-N---L-PL-HPNNSTNSV--PPASSSQCTVHERN :  76
LsELF3a      : MKRGN---DDEK-MMGPLFPRLHVGDT-EKGGPRAPPRNKMALYEQFSIPSQRF-N---L-PL-HPNTLTNSV--PPASSSQCTVHERN :  76
PsELF3a (HR) : MKRGN---DDEK-MMGPLFPRLHVGDT-EKGGPRAPPRNKMALYEQFSIPSQRF-N---L-PL-HPNTSNNSV--PPASSSQCTVHERN :  76
PsELF3b (PPD): MSRGKG--DAEK---VGPMFPRLHVNDTAEKGGPRAPPRNKMALYEQFSVPFQRF-NP-------NSNSNSSNSLPLTPSSNLGNDPER- :  76
LsELF3b      : MSRGKG--DAEK---VGPMFPRLHVNDTAEKGGPRAPPRNKMALYEQFSVPFQRF-NP-------NSNSNSSNSLPLTRSSSLGNDPERS :  77
LcELF3b      : MSGGKV--DAEK---VGPMFPRLHVNDTAEKGGPRAPPRNKMALYEQFSVPFQR--------------------------GNDPERS :  56
VfELF3b      : MSRGNG--DAEK---VGPMFPRLHVNDTAEKGGPRAPPRNKMALYEQFSVPFQRF-NP-------N------SNSLPQTRSSSLGNDPERS :  72
MsELF3b      : MKRGKG-GDDEK---VGPMFPRLHVNDTTEKGGPRAPPRNKMALYEQFSVPFQRF-NP-------SSNSTSSNSIPLTSSSTMGNDLERS :  78
MtELF3b      : MKRGKG-GDDEK---VGPMFPRLHVNDTTEKGGPRAPPRNKMALYEQFSVPFQRL-NP-------NSHSSSSNSIPLTSSSTMGNDLERS :  78
TpELF3b      : MKRGKGDDDDEK--VGPMFPRLHVNDTTDKGGPRAPPRNKMALYEQFSVPFQRF-NP-------NSNS----------SNSLGNDPDRS :  69
CaELF3b      : MKRGKCDDDDDEKVVGPMFPRLHVNDTTEKGGPRAPPRNKMALYEHNFVPFQRF-NN-------NSNSS-SNSHPLTPSSTLGNDPERS :  81
VrELF3b      : MKRGN---DDEK--VAGPMFPRLHVNDT-AEKGGPRAPPRNKMALYEQLSVPSQRF-NPRLL-PL-KPNSSSNLV-APPTSSTQCSGHERS :  80
VaELF3b      : MKRGN---DDEK--VAGPMFPRLHVNDT-AEKGGPRAPPRNKMALYEQLSVPSQRF-NPRLL-PL-KPNSSSNLA-APPTSSTQCSEHGRS :  80
PvELF3b      : MKRGN---EDEK--VAGPMFPRLHVNDT-AEKGGPRAPPRNKMALYEQLSVPSQRF-NPRLL-PL-KPNSSSNLV-APPVSSTQCNGHERS :  80
GsELF3b-1    : MKRGN---EEEK--LGGPMFPRLHVNDT-AEKGGPRAPPRNKMALYEQFSIPSQKF-NPRLL-PR-KPNSSSNIV-PPP---TQCNGHERS :  77
GsELF3b-2    : MKRGN---EEEK--SAGPMFPRLHVNDT-AEKGGPRAPPRNKMALYEQFSIPSQKF-NPH-L-PR-KPNSSSNIV-PPPTSSTEGNGRGR- :  78
GmELF3b-1    : MKRGN---EEEK--LGGPMFPRLHVNDT-AEKGGPRAPPRNKMALYEQFSIPSQKF-NPRLL-PR-KPNSSSNIV-PPP---TQCNGHERS :  77
GmELF3b-2    : MKRGN---EEEK--SAGPMFPRLHVNDT-AEKGGPRAPPRNKMALYEQFSIPSQKF-NPH-L-PR-KPNSSSNIV-PPPTSSTEGNGRGR- :  78
CcELF3b      : MKRGS---EDDK--VVGPMFPRLHVNDT-EKGGPRAPPRNKMALYEQFSIPSQRF-NPRLL-PL-NPNPSSNKV-SSSTPSTQCNGHERS :  80
AiELF3b      : ------------------MFPRLHVNDT-EKGGPRAPPRNKMALYEQFSVPSQRF-NNQRLLPINHPST-------PSSSSQCTGPERS :  62
AdELF3b      : --------------------LHVNDT-EKGGPRAPPRNKMALYEQFSVPSQRF-NNQRLLPINHPST-------PSSSSQCTGPERS :  58
LaELF3b-1    : MKREK---DEEK--VVGPMFPRLHVNDT-EKGGPRAPPRNKMALYEQFSIPSQNL-N-------------------QLGSSSQCTGSGRS :  64
LaELF3b-2    : MKRGK----AEK---VGPMFPRLHVNDT-EKGGPRAPPRNKMALYEHFTIPSR--------------------GSSNKGTSSERS :  57
AkELF3-1     : MKRGK---DDEK--LLRPMFPRLHVNDK-EKGGPRAPPRNKMALYEQFSIPSQRF-NPGVQ-SL-NPVSSSNTV--SLASSSQCTAPERN :  79
AkELF3-2     : MKPGK---DDEK--FTVPMFPRLHVNDS-EKGGPRAPPRNKMALYEILSIPSQRF-KPGVL-PL-NPHGDCNTV--PPASSSQCTCPDRS :  79
CgELF3       : MKRGK---DDEK--VMGPMFPRLHVNDT-EKGGPRAPPRNKMALYEQLSIPSQFS-NPGVL-PL-NSNSANNTT--PPASSSQCAGPERN :  79
AtELF3       : MKRGK---DEEK--ILEPMFPRLHVND-ADKGGPRAPPRNKMALYEQLSIPSQRFGDHGTM----NSRSNNTSTLVHPGPSSQPCGVERN :  80
                        ----------Conserved block I----------
```

```
                100       120       140       160       180
LaELF3a      : YGFFAYLPSQTSTRRAEKY-TSR-S-YGANLNASPVQFCKRKKV-DEDDLRVPVYIHSRTGQSNSKNLESFDWKKLTLAPKGCRYIGCST : 166
AdELF3a      : YAFFYQFPQTPTRRAEKYSVSRQS-DVANGNGSLLQLEQRKKV-DEDDFRVPVYVHSRIGLSNNKRRESLDGEKLV--PSSSRYFGSSV : 167
AiELF3a      : YAFFYQFPQTPTRRAEKYSVSRQS-EVANGNGSLLQLEQRKKV-DEDDFRVPVYVHSRIGLSNNKRRESLDGEKLV--PSSSRYFGSSV : 167
CcELF3a      : HVFFVHLPQCNPIRRAEKC-ISRQS-EGANLSAS---LEQRKKI-DEDDFRVPVYIHSRIGQCNNKSVESFDAKKLT--PTGFRYFGGSV : 161
GsELF3a      : CVYFVHLPQCPIHRAEKC-NSRQS-EGTNLSAS---LEQRKKV-DEDDFRVPVYFHSRTGQCNDKSVESFNGKKLT--PTGSRYFGGSI : 161
GmELF3a      : CVYFVHLPQCPIHRAEKC-NSRQS-EGTNLSAS---LEQRKKV-DEDDFRVPVYFHSRTGQCNDKSVESFNGKKLT--PTGSRYFGGSI : 161
VaELF3a      : NVFFVHLPSQKPIRPVEKC-HSRQS-EEANLTCS---LEQRKKV-YEEDFRVPVYVHSRVGQCNDKSVETFDRKKIT--HTGTRYFGCSV : 161
VrELF3a      : HVFFVHMPSQKPIRPVEKC-HSRQS-EEANLTCS---LEQRKKV-YEEDFRVPVYVHSRVGQCNDKSVESFDRKKIT--HTGTRYFGCSV : 161
LjELF3a      : YVFFVQSPSQTPIRRAEKP-VSHQS-EGANLNSSLVQLEQRKKV-DEDDFTVPIYIRSRTGQSSDR---SLDGKRL------RYFGCSV : 157
CaELF3a      : YVFRGHLTSQTPIHQAEKR-SSLQL-EGVNLNTSLSQLEQRKKV-DEDDFMVPVYVRSKIGQSNDKSLESFDGKKLN--STRSRYFGFSK : 162
TpELF3a      : YVFFGHLTPETLIRQAGKH-ISHQS-EGGNLNASLAQLEQRKKA-DEDDFRVPVYVSNIGQSNDK---------LT--SAGSRNFGFFK : 152
MtELF3a      : YVFFGHLTPETLT---------RQS-EGKNLNASLSQLEQRKKI-DEDDFRVPVYIRSKIGQSNDKSHESFDGKNLT--SAGSRNFGFFK : 154
MsELF3a      : YVFFGHLTPETLTRQAEKH-ISRQS-EGENLNASLSQLEQRKKV-DEDDFRVPVYIRSKIGQSNDKSHESFDGKKLT--SAGSRNFGFFK : 158
VfELF3a      : YVFFGHLTPETLIRQAGKH-LSRQ------------LEHRKKV-DEDDFRVPVYVRSNIGQSNEKRPESFDGKRPF--PTGSRYSGFLK : 150
LcELF3a      : YIFFGHLTPETLIRQAGKH-LSRQS-KGANLNGSIAQLEHRKKV-DEDDFRVPVYVRSNIGQSNEKRPESFDGKRLP--STGSRYFGFLK : 161
LsELF3a      : YVFFGHLTPETLIRQAGKH-LTRQA-KGANLNASLAQLEHRKKV-DEDDFRVPVYVRSNIGQSNEKRIESFDGKRPP--STGSRYFGFLK : 161
PsELF3a (HR) : YVFFGHLTPETLIRQAGKH-LSRQT-KGANLNASLAQIEHRKKV-DEDDFRVPVYVRSNIGQSNEKRIESFDGKRPP--STGSRYFGFLK : 161
PsELF3b (PPD): ------------------SY-ISHQS-NGANTHTLSAQLEHRKKV-DGDD--SRAMDHSRIGQSNDKTMKSFNGEIIT--PTGSRNFGCLV : 142
LsELF3b      : YIFFEVCLPSQT-----ESY-ISHQS-NGANMHTLTARIEHRKKV-DGDD--SHAYDRSRIGQSNDKTMKSFNGEKHT--PMGSGNFGCSV : 155
LcELF3b      : YIFFEVCLPSQT-----ENY-ISHQS-NGA--HTLSAQIBHKKKV-DGDD--SRAMDCSRIGKSNDKTMKSFNGEKHT--PTGSGNFGCLV : 132
VfELF3b      : YIFFEVCLSSQT-----ESY-ISHQS-NVANMDALSA-LEHRKKV-DGDD--SRAYDRKRIGQSNDKTMKSFNGETLT--PTGSGNFGCLV : 149
MsELF3b      : NVFFEVRLPSQAGTHRAKSY-ISHE--NGANLDTLSTQLEHRKKV-DGDD--SRAYDHSRIGQSNDKMTNGFNGEKIT-------------- : 150
MtELF3b      : NIFFEVRLPSQADAHRAKSY-ISHQS-NGANLDTLSTQLEQGKKV-DGDD--SRAYDHSRIGQSNHKMTNSFNGEKIT-------------- : 150
TpELF3b      : CIFFEVRLPSQTDIHRAESD-ISHQS-NGANLDTMSAQIEQRKNV-RK------------------------------------------- : 113
CaELF3b      : YIVFVNLPSQTATQRAESY-TSHQS-NEANMDTLSAQLGQRKKV-DGDG--SHAYDHSRIGQSNNKTMKSFNGKKLT--PVGARNFCCSV : 164
VrELF3b      : YGYFVRLPSQTPAHRAESY-VSRQS-DGSRSNTSLVQLEBRRKRA-DEDD--VHAYICSRIGHSND---KAINRKKFT--PLGGGNFC-SV : 159
VaELF3b      : YGYFVRLPSQTPAHRAESY-ISRQS-DGSRSNTSSVQLEBRRKRA-DEDD--VHAYICSRIGHSND---KAINRKKFT--PLGGSNFR-SV : 159
PvELF3b      : YAYFVRLPSQIPAHRAESY-ISRQS-DGSRSNTSSVQLEBRRKRA-DEDD--VHAYICSRIGHSNDKTMKSFNGEKIT--PLGARNFC-SV : 162
GsELF3b-1    : YVYFVRFSSQTPTHRAESY-ISRQS-DDDGSRSNTSLVQLEBRRKKV-D-DD--IHVYTCSGIDQSNDKTMESVDGKKFT--PFGARNFCYSV : 160
GsELF3b-2    : ------------------SY-ISRQS-DDGARSNTSLVQLEBRRKKV-D-DG--IHVYTCSGIDQSNDKMLESFNGKKLT--PFGARNFCYSV : 144
GmELF3b-1    : YVYFVRFSSQTPTHRAESY-ISRQS-DDDGSRSNTSLVQLEBRRKKV-D-DD--IHVYTCSGIDQSNDKTMESVDGKKFT--PFGARNFCYSV : 160
GmELF3b-2    : ------------------SY-ISRQS-DDGARSNTSLVQLEBRRKKV-D-DG--IHVYTCSGIDQSNDKMLESFNGKKLT--PFGARNFCYSV : 144
CcELF3b      : HVYFVCLPSQTPSHRAESY-ISRQS-DGARSNTSSVQLEQRKNV-DEDD--IHAYIRSRVGQPSDKTLESYKGKKFT--TLGSRNVCFSV : 163
AiELF3b      : YAFFVHKPSQASTRR-ESY-SSRCY-DGANLNTPSTQVEQGRKV-DDDDFMVPVYVHSRNGQSNDETVQSSNGRHLT--PM--------- : 137
AdELF3b      : YAFFVHKPSQASTRR-ESY-SSRCY-DGANLNTPSTQVEQRKV-DDDDFMVPVYVHSRNGQSNDETVQSSNGRHLT--PM--------- : 133
LaELF3b-1    : YIIFCHLPSQOMPTHRAEIY-ISHQS-NRARQNTSSAHLEQRKKV-DEDDFMVPVYVDSRTGQCNDKRLESFDRKKIT--SMGSRNFGCSL : 149
LaELF3b-2    : YIIFGNLPSQMPTQRAESY-ISHCF-NGASQNTSSAQLEQRNKV-DEDDFMVPVYVDSRIGQYNDKRLVNFEMEKLT--SMSSRNFGCSI : 142
AkELF3-1     : YILFVHLPEQAPTYQVENN-ISHQS-DAANLNLLVKKFERRKKV-DEDDFRVPIYMNSRVGQSNDKTQKIFDGKKFA--NIGPRYFDCTI : 164
AkELF3-2     : YTFFEV---PQTPTYGARKN-ISHLS-DRTNLNTSFAQLEQRKKV-DEDDFRVPVYVHSRIGQSNHKTQKSFDGKKIT--PMGSGDFASSV : 161
CgELF3       : YIFFEVHLPLQTPTYRAEKH-ISRQS-DGANLNTSLAQLEQRKKV-DEDDFRVPVYVHSRIGQSHDKIQKSFDGKKFT--PVGSSYFGCTV : 164
AtELF3       : LSVQ-HLDSSAANQATEKF-VSQMS-FMENVRSS-AQHDQRKMVREEEDFAVPVYINSRRSQSHGRTKSGIEKEKHT--PMVAPSSHHSI : 164
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                         200        220        240        260
LaELF3a       : AG--QNDFERDPKQFG--SLFVNMRKDVR-SETKGLVQVTPSKEQPIKSVRDLSSTGENVDTLVRQAKVTPNQEFRD--SPASKHNMLHQ : 249
AdELF3a       : AG--QNDCVRNPKQLG--SSLVNTRKDRR-SETEGLPQVSTNKEQSVVFVRKISLTGENIDILARQSKVNPSQBFQD--SPLSKHSRLRQ : 250
AiELF3a       : AG--QNDCVRNPKQLG--SSLVNTRKDRR-SETEGLPQVSTNKEQSVVFVRKISLTGENIDILARQSKVNPSQBFQD--SPLSKHSRLRQ : 250
CcELF3a       : AG--QSDCERDPKQFG--SSLVNMRKDVR-SEIDGLPQVSTRKEHPLMSVTSIS-TGENIDT-VKHAKVTPNQEFQD--CHVSKQNRLRQ : 242
GsELF3a       : SG--QSDCERDPKQFG--SSVVNMRKDVR-SEIDVLPQVSTSKEQASMSVRSIS-TRENIHTLLRQAKVTPNRBFQD--CHVSKFNRLQQ : 243
GmELF3a       : SG--QSDCERDPKQFG--SSVVNMRKDVR-SEIDVLPQVSTSKEQASMSVRSIS-TRENIHTLLRQAKVTPNRBFQD--CHVSKFNRLQQ : 243
VaELF3a       : AG--QSDCERVPKQFG--SSHV--RKDAR-CETDGLPQVSTSKDQPLTSVRSIS-TRENIDTLVRQAKVTPNQEFQD--CHVSKRNRFRQ : 241
VrELF3a       : AG--QSDCERVPKQFG--SSHV--RKDAR-CETDGLPQVSTSKDQPLTSVRSIS-TRENIDTLVRQAKVTPNQEFQD--CHVSKRNRFRQ : 241
LjELF3a       : AE--QNDCERDLKQYA--PSLVNKRRDVR-SETDGLPPVSPNKEQPLIRARNTS-TGENIDTFKRQAKVTPNQEFQD--CTLSKPTRLQR : 239
CaELF3a       : AG--KTDCERDPKQYG--SHLVNTKIDVR-NEIDGPPQVSPNKEHPFTSVRDIS-TGESVDTLVRQAKVTLNQEFSD--CAVFKFSSLRQ : 244
TpELF3a       : PG--RIGRERDPKQYA--SPLVNTGTDVR-NEIDGPPQVSPNKEQSFTSARDIS-TGEHIDTLVRQAKATPNQEFQD--RAVFKLSSSRQ : 223
MtELF3a       : AG--RINRERDLN---------NPRTDVR-NEIDGPPQVSPNKEQPFTSARDTS-NGESSNTSVRQAKVIQNQEFQD--RAVFKLSSSRQ : 229
MsELF3a       : AG--RINRERDLN---------NLRTDVR-NEIDGPPQVSPNKEQPFTSARDTS-NGESIDTSVRQAKVIQNQQFQD--RAVFKLSSSRQ : 233
VfELF3a       : PG--KVDWERELKQHG--SAVVNAGTDVR-NEIDGPPQVSPNKEHPFSSARDES-TGERIDTLLRQAKVTPNQEVQD--CRVFKNSSLRQ : 232
LcELF3a       : PG--KIDRERELIQNG--STVVNAGTDVR-NEIDGPPQVSPNKEHPVTSARNAS-TGERVDALVRQVKVTPNQEVQD--RRVFKHSSLRQ : 243
LsELF3a       : PG--KIDRERDPKQFG--SAVVNAGTDVR-NEIDGPPQVSPNTEHPFTSARDES-IGERSDTLVRQGKVTANQDVQD--RRVFKLDSLRQ : 243
PsELF3a (HR)  : PG--KSDRERDPRCHG--SAVVNAVTDVR-NDIDGPPQVSPNKEHPSSSARDGS-IGEHSDTLVRQGKVTANQEVQD--RRVFKLSSLRQ : 243
PsELF3b (PPD) : SG--KNDSDKDQTCFG--SLLVMRKDVR-NKGEVHLQESLSRQKTVMSVESIL-TGEIIDSSVRQAEKISDEEDQN------------- : 213
LsELF3b       : SG--KNDGDKDQTCFG--SLVIKMRKDVR-NKGEAHLQESLSRQKTVISVERIL-TGENIDSPVRQAKMISDEEDQS------------- : 226
LcELF3b       : SG--KNDGDKDQTCFG--SLVVEMRKDVR-NKGEAHLQESLSRQKTVISVERIS-TGENIDSPVRQAEMISDEEDQS------------- : 203
VfELF3b       : SG---NVGDKDQTCFG--SLLVKMRKDVR-NKGEAHLQESLSTQKTVMPVERLS-TGEIIDSPVRQAEKISDEEDQR------------- : 219
MsELF3b       : ------------------------------LVIPSRQKTVISVKSAL-TGEIIDGPARQAKIVNEEDQE-CSVSNINRFPQ : 200
MtELF3b       : ------------------------------LVIPSRQKTVISVKSAL-TGEIIDSRVRQGKIPDEDQE-CSVSNINRFPQ : 200
TpELF3b       : ------------------------------KGEGHLQVSSRQKTGMSVESIL-TGEIIDSPVRQTNKILDEEDQH-CSVSNI--LHK : 167
CaELF3b       : AG--ENDGDKDQTCFG--SLLVKMRKDVN-------------------------------------------------KSRLHQ : 195
VrELF3b       : SV--QNDGERDPACFG--SLPVDMRKHVR-SGNETHPHVSSSRQQPKMSVKNKS-SGEVIDSLVMQAKVIPNQBDQD--CSVPSISRLHQ : 241
VaELF3b       : SV--QNDGERDPACFG--SLPVDMRKHVR-RGNETHPHVSSSRQQPKMSVKNKS-SGEVIDSLVMQAKVIPNLEDQD--CSVPSIGRLHQ : 241
PvELF3b       : SV--QDDGERGPTLFG--SLPVDMRKHVR-SGNEAHPHVSSSRQQQKMSVKNKS-SGEVIDSLVMQAKVIPNQBDQD--CSVPSLSRSHQ : 244
GsELF3b-1     : AV--QNDGDKDPTCFSSCSLPVDLRKDVR-NGNEANPHVSSSRRKPKMSVKNNS-SGEIIDSLMMQAKVIPNLEDQD--YSVPNISRLHQ : 244
GsELF3b-2     : AV--QNGGDKDTTCFG--FLPADMRKDAR-KGNEANPHVSSSRQKLKLSVKPKS-SGEIIDSLMMQAKVIPNQBDQD--YSVPNINRLHQ : 226
GmELF3b-1     : AV--QNDGDKDPTCFSSCSLPVDLRKDVR-NGNEANPHVSSSRRKPKMSVKNNS-SGEIIDSLMMQAKVIPNLEDQD--YSVPNISRLHQ : 244
GmELF3b-2     : AV--QNGGDKDTTCFG--FLPADMRKDAR-KGNEANPHVSSSRQKLKLSVKPKS-SGEIIDSLMMQAKVIPNQBDQD--YSVPNINRLHQ : 226
CcELF3b       : AV--QNDGDKDLTCFG--CVPVDMRKDVR-SGNEVHPQVSSSRQQRKITVRNKS-SGEIIYSPVMQVKVIPNQBDQD--YSVPNISRLHQ : 245
AiELF3b       : ----------------------------VRSERHPSLISNGQQPVMSCRDIS-SRETVNGL-SQTKTIPNQN-----CFVSNISRSHH : 190
AdELF3b       : ----------------------------VRSERHPSLISNGQQPVMSCRDIS-SRETVDGL-SRTKTIPNQD-----CFVSNISRSHH : 186
LaELF3b-1     : EV--QKDGGRHLKCLG--SPLTNMREDAS-SESEGFAQVSPSRDPP---AKNIS-TVETTKSLVNQTKVI---QYQD--CPASFVSSLCQ : 225
LaELF3b-2     : EV--QKDGGRHRKCLD--SPPINIREDAS-SESEGLPQVSESRE---LHVKNIS-TIETIKSLARQAKVIQNQEYQD------------- : 210
AkELF3-1      : QV--QNDCDRDPKCFV--SPYVNIRKYMR-CESNSVFPNGSPSRDKPVKPARNIS-NGENLDNIASKDNAILNQEHQDWNCPGLRVGRLHH : 248
AkELF3-2      : DV--LNNCDRDPKCIG--SPHVSMRKDVR-SSDREGLPKVSPSRDQA-KSARNIA-KGENTDSLVWQAKVTPNQ---D--CSLASLSRLHQ : 240
CgELF3        : EGNVQNDCDKDPKCFG--SPHVSMRKDVR-SESEGLPKVSPIKEQPVKSAWNIS-NEENIDSLVWQAKVTPNQBYQD--CPVADLSRLRQ : 248
AtELF3        : RF--QEVNQTGSKQNV--CLATCSKPEVR-DQVK-----ANARSGGFVISLDVS-VTEIDLE---------------KSASSHDRVND : 227


                         280        300        320        340        360
LaELF3a       : GDDTFLQREREYGSQFNDT--RQGDGLVEPT--RETDNGNAA--------VSNQTTPTVAIN--DTEYLV-IRAG--------------- : 309
AdELF3a       : D-GACTQREGRAGSQSNGI--GHVDGIAESR--RETDKGNVP--------TTNQTSPABAIN--DTECHD-TRTGGATQKRNLNKSDNIS : 324
AiELF3a       : D-GACTQREGRAGSQSNGI--GHVDGVAEST--RETDKGNVP--------TTNQTSPABAIN--DTECRD-TRTGGATQKRNLNKSDNIS : 324
CcELF3a       : G-DACLRHDCGVASQSNDI--GHNGCLVESA--RETDKGNAP--------TVNKISPABAIN--DTRHEG-TRTGSSIQRGNLNKSDNAS : 316
GsELF3a       : G-ETCLQLECGVESRSNDI--GDNGCLVESA--RETDKGNAP--------TANQTSPADAIN--DTEHHD-TRMGSPIQMGNLNESDNAS : 317
GmELF3a       : G-ETCLQLECGVESRSNDI--GDNGCLVESA--RETDKGNAP--------TANQTSPADAIN--DTEHHD-TRMGSPIQRGNLNESDNAS : 317
VaELF3a       : D-DGYLRQDCGVGSQSNDI--GHSGSLVQSS--RKLGNGNAA--------TANQTNLABAIN--DTGHHD-TIGMGSLIRGGKLNGSDNAS : 315
VrELF3a       : D-DACLRQDCGVGSQSNDI--GHSGSLVQSS--RKIGNGNAA--------TANKTNPABAIN--DTGHHD-TGTGSLIQGGKLNGSDNAS : 315
LjELF3a       : D-DACLRRDCEAVSQSNGI--GQSGGLVEST--PETDKRNAP--------TESQTSPGBAIN--DTEYQN-TRPGCPIRRGSLNKSGNVS : 313
CaELF3a       : V-DACSREECGTESQSNGI--RQSNTLVEST--RGVDKSNDP--------IANQTSPTEAIN--GTEYKD-TWTGSPIQKGNLNRKDNIS : 318
TpELF3a       : -----------------------------RETNKSNGP--------TTTHTSPNEAMD--GTKYHD-TGTVSPIQRGNLNINDNIS : 269
MtELF3a       : G-DGCLHQDCRAESQSNGT--GQRDASVEST--REIGKSNDP--------IANQTSPTEAIN--GTEYHD-TGTGSPIHSGNLNKNDNIS : 303
MsELF3a       : G-DGCLRQDCRAESQSNGT--GQRDASLEST--RETGKSNDP--------IANQTSPSEAIG--GTEYHD-TGTGSPIHSGNLNKNDNIS : 307
VfELF3a       : G-DARLRQDCRAESQSNGH--GQSDGLLEST--REVDKSDGP--------IVNQTRLTEAID--DTEYHD-TGTGSLKQLGNLNKNDNIS : 306
LcELF3a       : G-DARLRQDCRAESQSNGH--GQSDGLLEST--REVDTSGP--------IVNQISPTEAIN--DTEYHD-TGTGSPKQLGNLNKNDNIS : 317
LsELF3a       : G-DSRLRQDCRAESQSNGHGNGQSDLLES---REVDKSPGP--------IVNQTSPTQAVN--GTKYHD-TGTGSPKQL---------- : 308
PsELF3a (HR)  : G-DARLRQDCRAESQSNGH--GQSDSLLEST--REVDKSNGP--------IVNQTSPTEAIN--GTEYHD-TGTGSPKQLGNSNKNDSIS : 317
PsELF3b (PPD) : --DACLQQE------SNDI--EHGGSLVDSA--MDMDNRNSLVLRGCFRSTVNQISVPEAAD--HTEYHD-TNIDSPIENGSSEGSDDIS : 288
LsELF3b       : --DACIQQE------SNNI--EHGGSLVDSA--MDTDNRNSLVLRGCFRSTVNQTSVPETAD--HTEYHD-TNIDSPIENGNSEGSDDIS : 301
LcELF3b       : --DACVQQE------SNNI--EHGGSLVDSA--MDMDNRNSLVLRGCFRSTVNQTNVPETAN--HTEYHD-TNIDSPIENGNSEGSDDIS : 278
VfELF3b       : --DACLQQE------SNYV--EHGGSLIDSA--MDMDNRNSLVLRGCFRSTVNQTSVLEAAN--HTEYHD-TNIDSPIDNGTSEGSDDVS : 294
MsELF3b       : G-DSCTRQE------SNDI--EHSDGLIDTT--MDMDNRNS------FHSTVDRTMVLEAAS--DTEYHD-TNIDSPIEKGNSEGSGDIS : 270
MtELF3b       : G-DSCTRQE------SNDI--EHSDGLIDTA--MDMDNRNS------FHSTVDRTMVLEAAN--DTEYHD-ANIDSPIQKGNSEGSDDIS : 270
TpELF3b       : G-DACVRQE------SNDI--EHSDDLI-----------------------------------------------------NSEGSDDIS : 195
CaELF3b       : G-NACVQQX-XXXQESNDS--EHGDGLIDSA--MDIDNRNSLVLRSCSHSTVDQTSVLEATN--DTEYHD-LNIDSPMQKGNSEGSDDIS : 276
VrELF3b       : D-GGCLQQECVAGHQSADV--D----LINST--RDMDNGNALVPKSCFSAVNQTCPVEVTDGVDVEYHD-VGTEGPLQKGNFDGSGDVS : 321
VaELF3b       : D-GACLQQECGAGPQSGDV--D----LIKST--RDMDNGNALVPKSCFSAVNQTCPVEVTLDVDVEYHD-VGTEGPLQKGNFDGSGDVS : 321
PvELF3b       : D-GACLQQECVAGPQSNDV--EHRNGLLSST--RDMDNGNALVPKSCFYSAANQTCPVEATG--DVEYHD-IGTEGPMQKGNIFDEIGDVS : 326
GsELF3b-1     : D-DTCLQKECVAGSQSNDV--EHGDLINST--RDIDNGNALVPRGCFHSAANQTRPLBATN--DAEYHD-TGTGGPIQKGNFDERDNIS : 326
GsELF3b-2     : D-DACLQKECVAGSQSNDI--EHGGDLINST--RDMDNGNALVPRGCFHSAANQTHPLBATN--DAEYHD-TRTGGPIQKGNFDESDNIS : 308
GmELF3b-1     : D-DTCLQKECVAGSQSNDV--EHGDDLINST--RDIDNGNALVPRGCFHSAANQTRPLBATN--DAEYHD-TGTGGPIQKGNFDERDNIS : 326
GmELF3b-2     : D-DACLQKECVAGSQSNDI--EHGGDLINST--RDMDNGNALVPRGCFHSAANQTHPLBATN--DAEYHD-TRTGGPIQKGNFDESDNIS : 308
CcELF3b       : D-NAPPQQKCVAGSQSNDI--EHCDVLINSTRERDVDNGNALVPKGCFHSAVNQTRLLBATI--DAEYHD-AGTGGPIQKGNFDESGDVS : 329
AiELF3b       : A-DACLWPVSVAGSQSNDD--EHDDIL----------------------TENQTSPQEDNN--DPECQD-TQIGGPMQGENLDDSDDIS : 251
AdELF3b       : A-DACLWPVSVAGSQTNDD--EHGDIL----------------------TENQTSPQEDNN--DPECQD-TQIGGPMQGGNLDDSDDIS : 247
LaELF3b-1     : A-DDCLQQECVAGSQSNNIGHRHREVLIDSI--GDTDKGNTTLPMGCFRSPTNQTSPVBAMH--ETEFDD-TRTASPVQKGSSDESDDVS : 310
LaELF3b-2     : ------------------------------------------------------SPVBATH--DAEFHD-TRTGSLVQKGSSDDGDDVS : 242
AkELF3-1      : I-DACLEQDHEAGPLCNNT--RNRGGLVYPS--SDTEKGDVLSPRGFFHSTABQNSPVEAI---DTDCHD-TRSTGPLER-NWDKSDNVS : 328
AkELF3-2      : G-DACIEPECGAGSQSNDT--GHGEGLVEST--RDTDTGNVPSPRGCFHSTADKNGPMEPIN--NIECHD-TRTDGPIQNGHIERSENFP : 322
CgELF3        : G-DACLPQQSGVGSQSNDT--GYGDGLVEST--RDTAKGNVPLPRSYFHSTSNQSSPLETIN--GTAYLH-ARTGRSAHKGNFDKSDNVS : 330
AtELF3        : Y-NASLRQE------SRNR--LYRDGGKTRL--KDTDNGAESHLATENHSQEGHGSPEDIDN--DREYSK-SRACASLQQINEEASDDVS : 303
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Exon2 ↓ Exon3   Exon3 ↓ Exon4

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                        380            400           420              440
LaELF3a        : ---KLESVSTLKVSPDDVVEIIGQKRFWKARKAIASQQRLFAVQVFELHRLIKVQKLIAGSPDLLLEH-AAFLGKSPLKGSTP--KKPAL : 393
AdELF3a        : KISVVENLSTSDLSPDDVVGIIGQKHFWKARRAIANQQRVFAVQVFELHRLIKVQQLIAGSPDILIED-AAFLGKSPPKGSTP--KKLAI : 411
AiELF3a        : KISVVENLSTSDLSPDDVVGIIGQKHFWKARRAIANQQRVFAVQVFELHRLIKVQQLIAGSPDILIED-AAFLGKSPPKGSTP--KKLAI : 411
CcELF3a        : KISMVENLSTAKISPDDVVGIIGQKHFWKARKAIATQQRVFAVQVFELHRLIKVQQLIAGSPDILVED-GTFLGKSPAKESTP--KKLPL : 403
GsELF3a        : KISMVENLSTVRISPDDVVGIIGQKHFWKARRAIANQQRVFAVQVFELHRLIKVQQLIAGSPDILLED-GAFLGKSPPKGSTP--KKLAL : 404
GmELF3a        : KISMVENLSTVRISPDDVVGIIGQKHFWKARRAIANQQRVFAVQVFELHRLIKVQQLIAGSPDILLED-GAFLGKSPPKGSTP--KKLAL : 404
VaELF3a        : KISVVDNLSPVNISPDDVVGIIGQKQFWKARRAI-NQQRVFAVQVFELHRLIKVQQLIAGSPEVLLED-GTFLGKSTPEGSTP--KKLSL : 401
VrELF3a        : KISPVDNLSPVNISPDDVVGIIGQKQFWKARRAIANQQRVFAVQVFELHRLIKVQQLMAGSPEVLLED-GTFLGKSIPKGSTR--KKLSL : 402
LjELF3a        : KISRVENLSTLKVSPDDVVGIIGQKHFWKARRAIVNQQRVFAVQVFELHRLIKVQQLIAGSPDLMLVD-GAFLRKSPPKGSTP--KKLSL : 400
CaELF3a        : KISGVENLSTLKIAIIGQKHFWKARKAIANQQRVFAVQVFELHRLIKVQQLIAGSPDLLFED-GAYLGKSPPVGCTT--KKLSL : 405
TpELF3a        : KTSRVENLSTLKVSPDDVVAIIGQKHFWKARKEIANQQRVFAVQVFELHRLIKVQQLIAGSPDLLFGD-AAFLGKSIPDGSTP--KKLPI : 356
MtELF3a        : KISRVEDLSTLKISPDDVVAIIGQKQFWKARKAIANQQRVFAVQVFELHRLIKVQQLIAGSPDLLFED-GAFLGKSLPDGSTP--KKLAL : 390
MsELF3a        : KISRVEDLSTLKISPDDVVAIIGQKHFWKARKEIANQQRVFAVQVFELHRLIKVQQLIAGSPDLLFED-GAFLGKSLPDGSTP--KKLAL : 394
VfELF3a        : KISRVEDLSTVKFFPDDVVAVIGQKHFWKARKEIANQQRVFAVQVFELHRLIKVQQLIAGSPDLLFDD-GAFLGKSLPDGSTP--KKLSL : 393
LcELF3a        : KISRVENLSTVKISPDDVVAVIGQKHFWKARKEIANQQRVFAVQVFELHRLIKVQQLIAGSPDLLFDD-GAFLGKSLPDGSTP--KKLPL : 404
LsELF3a        : -----EHLSTVKISPDDVVAVIGQKHFWKARKEIANQQRVFAVQVFELHRLIKVQQLIAGSPDLLFDD-GAFLGKSLPDGSTP--KKLSL : 390
PsELF3a (HR)   : KISRVEDLSTVKISPDDVVAVIGQKHFWKARKEIANQQRVFAVQVFELHRLIKVQQLIAGSPDLLFDD-GAFLGKSLPDGSTP--KKLSL : 404
PsELF3b (PPD)  : KNSTLENMPSPRLSPDGVAEILGQQLFWKARRKITNQQRMYAVQVFELHRLIKVQHLIAESSNLLPDT-AAVLGKPLLQGSNS--KSLSF : 375
LsELF3b        : KNSTLENMPSPKLSPDGVVEILGQQLFWKARRKISNQQRMYAVQVFELHRLIKVQHLIAESSNLLPDA-AAILGKSPLQGSNS--KSLSL : 388
LcELF3b        : KNSTLENMPSPKLSPDGVVEILGQQLFWKARRKITSQQRMYAVQVFELHRLIKVQHLIAESSNLLLDS-AAILGKSPLRGSNS--KSLSL : 365
VfELF3b        : KNSTLENMPSPKLSPDGVVEILGQQHFWKARRKITNQQRMYAVQVFELHRLIKVQHLIAESSNLLLDA-AAILGKSPLQGSNS--KSLSL : 381
MsELF3b        : NISTLENLSSLKLSPDGVVQILGQQLFWKARRKITNQQRAFAVQVFELHRLIKVQHLIAGSSNLMDV-AAILEKFPLQESIP--KSLSL : 357
MtELF3b        : NISTIENLSSLKLSPDGVVQILGQQLFWKARRKITNQQRAFAVQVFELHRLIKVQHLIAGSSNLMLDA-AAILEKFPLQESIP--KSLSL : 357
TpELF3b        : KISTLENLSSLKLSPDGVAQILGQQLFWKARRRITNQQRMYAVQVFELHRLIKVQQLIAGSSDLLEDAAAILGKFPLQESTP--KSLSL : 283
CaELF3b        : KTSTLESLSSSMELSPDGIVQILGQKHFWKARRKITQQRVFAVQVFELHRLIKVQQLIAGSSDLLFED-AAILGKFPLQASTP--KSISL : 363
VrELF3b        : KISTVTNLSSLIVSPDDVVGVLGQKHFWKARRKIANQQRVFAVQVFELHRLIKVQQLIASSPDVLLED-GAFLGKFPLEGSTP--KTISL : 408
VaELF3b        : KISMVTNLSSLIVSPDDVVGVLGQKHFWKARRKIANQQRVFAVQVFELHRLIKVQQLIASSPDVLLED-GAFLGKFPLEGSTP--KTISL : 408
PvELF3b        : KISTVTNLSSQVVSPDDVVGILGQKRFWKARRKIANQQRVFAVQVFELHRLIKVQQLIASSPNVLIED-GAFLGKFPLEGSTP--KTISL : 413
GsELF3b-1      : KISTVTNLSSLIVSPDDVVGILGQKHFWKARRKIANQQSVFAVQVFELHRLIKVQQLIAASPDVLLED-VAFMGKFPLTESPP--KNISL : 413
GsELF3b-2      : KISTVTNLSSLIVSPDDVVGILGQKHFWKARRKIANQQSVFAVQVFELHRLIKVQQLIAASPDVLLED-GAFMGKFPLMGSPPKNKNISL : 397
GmELF3b-1      : KISTVTNLSSLIVSPDDVVGILGQKHFWKARRKIANQQSVFAVQVFELHRLIKVQQLIAASPDVLLED-VAFMGKFPLTESPP--KNISL : 413
GmELF3b-2      : KISTVTNLSSLIVSPDDVVGILGQKHFWKARRKIANQQSVFAVQVFELHRLIKVQQLIAASPDVLLED-GAFMGKFPLMGSPPKNKNISL : 397
CcELF3b        : KISTVTNLSSLIVSPDDVVGILGQKHFWKARRQIANQQRVFAVQVFELHRLIKVQQLIAASPDVLLED-GAFVENFPVPGSTP--KNISL : 416
AiELF3b        : KISSIENSSTLRVSTDDVVGILGQKHFFKARREIANQQRIFAVQVFELHRLIKVQQLIAGSPELLIED-AAFIGKIPLKGSTT--KNISL : 338
AdELF3b        : KISSIENSSTLRVSTDDVVGILGQKHFFKARREIANQQRIFAVQVFELHRLIKVQQLIAGSPELLIED-AAFIGKIPLKGSTT--KNISL : 334
LaELF3b-1      : KISSIGNLSSLKASPDDVVGVLGQKHFWKARRKIANQQRVFAVQVFELHRLLKVQHLIARSPDLLED-GAFMGNSPPKRSTP---NITL : 396
LaELF3b-2      : KISSTENLSSLKASPDDVVGILGQKHFWKARR---NQQSVFAVQVFELHRLLKVQHLIAGSP-GSFMRNSLPKRSTP---NLAV : 325
AkELF3-1       : KISTVDRLISQKISTDDVVEIIGQKHFWKARSIINQQRVFAVQVFELHRLMKVQQLIAGSPDILLDG-GAFLGKSSLTGSPP--KKHTL : 415
AkELF3-2       : KTSMVDNLSSIKISPDDVVEIIGQKHFWKARTAIVNQQRVFAVQVFELHRLMKVQQLIAGSPDILLDG-GAFLGKSPPKGSPP--KKLPL : 409
CgELF3         : KISVVDNLSLKVSPDDVVEIIGQKHFWKARRAIVNQQRVFAVQVFELHRLMKVQQLIAGSPDILLED-AAFLGKSPLKGSSP--KKLSL : 417
AtELF3         : DDSMVDSISSIDVSPDDVVGILGQKRFWRARKAIANQQRVFAVQLFELHRLIKVQKLIAASPDLLLDE-ISFLGKVSAK-SYPVKKLLPS : 391

                 ----------------Conserved block II---------------
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                      460           480           500           520          540
LaELF3a        : EFVVKPQPQT--LKRKHESEKANH-KMECSAENAVG-KISLSPMKNGSH-HSNYTPFSRNQHTANVPADSGMPPWCFQQS-P----GHQW : 473
AdELF3a        : EYVVKPRQPN--LKRKDESEKLHH-KMECSAENAVG-KISLSSVKNGSH-PSNYTPFACNPYCTNSAADSGMGLWGFHQS-P----GHQW : 491
AiELF3a        : EYVVKPRQPN--LKRKDESEKLHH-KMECSAENAVG-KISLSSVKNGSH-PSNYTPFACNPYCTNSAADSGMGPWGFHQS-P----GHQW : 491
CcELF3a        : EYVVKPRQQN--LKHKDDSEKLNH-KMECCAENAVG-KISLSSVKNGSH-LSNYTPFCNPQCTNVGADSGMGPWCFHQS-P----GDQW : 483
GsELF3a        : EYVVKPRQQN--LKRKDDSEKLNH-KMECSAENAVG-KISLSSVKDGSH-LSKCTPFPCNQHCTNVAADSGMGPWCFNQS-PP--GHPW : 485
GmELF3a        : EYVVKPRQQN--LKRKDDSEKLNH-KMECSAENAVG-KISLSSVKDGSH-LSKCTPFPCNQHCTNVAADSGMGPWCFNQS-PP--GHPW : 485
VaELF3a        : EYVVKPWQQN--LMRKDDSEKLNH-KMECSAENAVG-KISLSSVKNDSH-LSNYTPFSRNPQCANVAADSGMGPWCFHQS-A----GHQW : 481
VrELF3a        : EYVVKPWQQT--LKRKDDSEKLNH-KMECSAENAVG-KISLSSVKNDSH-LSNYTPFPRNPQCANVAADSGMGPWCFQQS-A----GHQW : 482
LjELF3a        : EYVVKPLQEN--LKR-NDSEKQNH-KMECSAENAVG-KISISSVKNGSH-LSHHTPFPCNPPQCPNVPADSGMSPWGFHQS-P----GHQW : 479
CaELF3a        : EYVVKPREQN--LKRKDDSEKINQ-EMECSAENAVG-KISISSVKNGSY-LSTATPFACNPHCGNMAADSGMGPWCFNQS-P----GHQW : 485
TpELF3a        : EYVVKARLQN--LKRKVDSEKIDQ-NMECSAENAVG-KISISSVKNGSH-LSSSMPFACNPHCGNMTAENGMGPWGFNQS-T----GHQW : 436
MtELF3a        : EYVVKPRLQN--LKRKVDSENVNQ-NMECSAENAVG-KISISSVKNGSH-LSSSTPFACNPHHGNMAAENGMGPWGFNQS-P----GHQW : 470
MsELF3a        : EYVVKPRLQN--LKRKVDSENVNQ-NMECSAENAVG-KISISSVKNGSH-FSSSLPFACNPHHGNMAAENGMGPWGFNQS-P----GHQW : 474
VfELF3a        : EYVVKTQLQN--LKRKVDSEKINQ-NMECSAENAVG-KISISSVKNTSH-LSNSMPFACNPHCGNMAADSGMGPWCYNQS-P----GHQW : 473
LcELF3a        : EYVVKTRLQN--LKRKVDSEKINQ-NMECSAENAVG-KISISSVKNTSH-ISSSMPFACNPHCGNMAADNGMGPWCFNQS-P----GHQW : 484
LsELF3a        : EYVVKDRLQN--LKRKVDSEKINQ-NLECSAENAVG-KISISSVKNTSH-ISSSMPFACNPHCGNMAADNGMGPWCFNQS-P----GHQW : 470
PsELF3a (HR)   : EYVVKARLQN--LKRKVDSEKINQ-NMECSAENAVG-KISISSVKNTSH-LSSSMPFACNPHCGNVAADNGMGPWCFNQS-P----GHQW : 484
PsELF3b (PPD)  : EEVVEPQAQN--HKQQDHSENQNH-KLDYSTENGVG-KISLSSQK-----------------SNCANAGSQ------CFNQS-P----GHQW : 435
LsELF3b        : EEVVEPHTQN--HKQQDHSENQNH-KLDCSTENGVG-KISLSSQK---------------SNCANAGSQ------FFNQS-P----GHQW : 448
LcELF3b        : EEVDEPQAQN--HKQQDHSENRNH-ELDCSPVNGVE-KISFSSQKYGSH-LSNYTPFSCNSDCANFGAH------CFNQ---PP--GHQW : 439
VfELF3b        : EEVVEPQAQN--HKQQDHSENQNH-KLDCSAENGVE-KISFSSQKYGSH-LSNYTSFPCNSDKTNVGAQ------CFNQS-P----GHQW : 455
MsELF3b        : EVVVEPQTQN--HKQQDHSESLNH-RLDCSAEKGVE-KISFSYQKYGSH-LSNYTRFSCISDCANVGSQ------CFNQS-P----GHQW : 431
MtELF3b        : EVVVESQTKN--HKQQDHSESLNH-RLDCSAEKGVE-KISCSYQKYGSH-LSNYTPFSCNSDCANVGSQ------YFNQS-P----GHQW : 431
TpELF3b        : EVVVEPQTQN--HKQQDHSENLNR-KSECSAENGVG-KISFTYQSYGSH-LSNYTPFPCNPQCENAGTQ------SFNPS-P----GHQW : 357
CaELF3b        : EVIVEPPTQN--HKQQDHSEKLNH-KLPHSAENGVG-KISFSSQKYGSH-LSNYTPFYCNPHQENVVSR------SFNHS-P----GYQW : 437
VrELF3b        : QVVVNPQQQT--PKQKNNSEKQNL-KTECSAENAVE-KKISFSSPKNGSH-LTNHTPFSCIPHQADVASDNRTSPWSFNQS-P----QHQW : 489
VaELF3b        : QVVVDPKQQT--PKQKNNSEKQNL-KTECSAENAVE-KKISFSSPKNGSH-ITNHTPFSCIPHQTDVASDNRTSPWSFNQS-P----QHQW : 489
PvELF3b        : QVVVEPQQQN--PKRKNNSEKPNH-KTECSAENAVE-KKISFSSPKNGSH-LTNHSPFSCIPHQTDVASDNGTSPWSFNQS-P----QHQW : 494
GsELF3b-1      : EVVVEPQQQN--PKQKNDSEKLNH-KTECSAENAVAKRISFSSPKNGSH-LANHTPFSCTPHQANVASDNKTSPWCFNQT-P----GHQW : 494
GsELF3b-2      : EVVVEPQQQN--PKQKNDSEKLNH-KTECSAENAVAKKKISFSSPKNGSH-HTNHTPFSCTPHQANEASDNKTSPWCFNQA-P----GHQW : 478
GmELF3b-1      : EVVVEPQQQN--PKRKNDSEKLNH-KTECSAENAVAKRISFSSPKNGSH-LANHTPFSCTPHQANVASDNKTSPWCFNQT-P----GHQW : 494
GmELF3b-2      : EVV----------------LNH-KTECSAENAVAKKKISFSSPKNGSH-HTNHTPFSCTPHQANEASDNKTSPWCFNQA-P----GHQW : 462
CcELF3b        : EVIVEPQQQN--HKRKNDSEKPNH-KTECSAENAVSRKISFSSPKNGSH-LTNHTPFSCTPHQANVTSDNRTSPWCFNQS-P----GHQW : 497
AiELF3b        : EELVEPKRQN--LKRKDDSQKLNH-KMECSAENAVG-RASFSSQKSGSH-HLNYSSTPCDPHQASGAADNRMAPMCFNPS-P----GHQW : 418
AdELF3b        : EELVEPKRQN--LKRKDDSQKLNH-KMECSAENAVG-KASFSSQKSGSH-HLNYSSTPCDPHQASGAADNRMAPMCFNPS-P----GHQW : 414
LaELF3b-1      : EVVVKPQLQN--HKRKDDSEKLNHNKMECSAENAVG-KRSCSIPKNGSH-HSNYTPFACNLHCTEAAADNRMGSWGFNQS-P----GHQW : 477
LaELF3b-2      : NVVVKPQIQN--LKRKDDSEKLNHNKMEYSAENAVG-KRSCSIPENCCH-LSNYTSFSCTPHCTKVAADNRMGSWGFNHS-P----GHQW : 406
AkELF3-1       : EYVSKPQHQN--LKCKGDSEKPSH-KMECSAENAVG-KISLSSMKNGSQ-LPNDTPFFCNSHQVN-------NPWHLHQS-P----GHQW : 488
AkELF3-2       : EYVQEPRQEN--RKRKDDSEKLNQ-KLECSAENAVG-KISASSVKNGSH-LSNYTPFSCNPQCANVAADSKMGPWHFHQS-P----G-LW : 488
CgELF3         : EYVVKPQQQN--LKRKNDSEKVNH-KMECSAENAVD-KISLSSVKNGSH-ISNYTPFSCNPQCANVAADNRMGPWCFQQS-P----GHQW : 497
AtELF3         : EFLVKPPLPHVVVKQRGDSEKTDQHKMESSAENVVG-RIS----NQCHEQQSNYMPFANNPPASPAPNG-----YCFPPQPPPSGNHQW : 471
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                                   560        580        600        620
LaELF3a       : LIPIMSPSEGLVYKPYPGPGFTGTTCEGGYG----PTPLGGTFMNAAYVIPASHQENGVPKNTPPSSHAYYPPYR-MP--VVNAAMSESAV : 557
AdELF3a       : LIPVMSPSEGLVYKPYPGPGFTGTMY-GGCG-PFAPAPMGGPFMNPAYGVPTSNQVPGVPPDTPPGSHAFFPPNG-LP--VMTKAMSESAV : 577
AiELF3a       : LIPVMSPSEGLVYKPYPGPGFTGTMC-GGCG-PFAPAPMGGTFMNPAYGVPTSNQVPGVPPETPPGSHAFFPPYG-LP--VMTKAMSESAV : 577
CcELF3a       : LIPVMTPSEGLVYKPYPGPGFTGTGY-GGCG----PAPLGGAFMNPAYGIQTSHQG-----DTPPGSHGYFPPYG-MP--FMNAAMSESAV : 561
GsELF3a       : LIPVMTPSEGLVYKPYPGPGFTGTGCGGGCG-PFVPALLGGSFMNPGYGIPTSHQGVGVPPDTHPGSHGYLPPYG-MP--VMNSSMSESVV : 572
GmELF3a       : LIPVMTPSEGLVYKPYPGPGFTGTGCGGGCG-PFVPALLGGSFMNPGYGIPTSHQGVGVPPDTHPGSHGYLPPYG-MP--VMNSSMSESVV : 572
VaELF3a       : LVPVMTPYDGLVYKPYPRPGFTETDG-GGCG----PSPFGGNFMNPAYGIPNSLQGVGVSPQTPPGSLAYFPPYG-MT--VMNATISESAV : 564
VrELF3a       : LVPVMTPYDGLVYKPYPRPGFTGTDG-GGCG----PAPFGGNFMNPAYGIPTSHQGVGVSPQTPPGSLAYFPPYG-MT--VMNATMSESAV : 565
LjELF3a       : LIPVMSPSEGLIYKPYPGPGYTGTNG-GGCG-PFGPAPLGGTFMNAAYGINSYQGIGVPPDAPPGSHAYFPPYG-MP--TMNAAMSESAV : 565
CaELF3a       : LIPVMSPSEGLVYKPYPGPGFTGTNC-GGEYG-PIGAAP---FMNPSYGMPA-------PPETPPGSHAYFPPYGGMP-VTKAAVAESAV : 561
TpELF3a       : LIPVMSPSEGLVYKPYPGPGFTGTNL-GGCG-PFGSAPSGGAFMNPSYGIPP-------PPETPPGSHPYFPPYGGMP-FMKAAASESVV : 516
MtELF3a       : LIPVMSPSEGLVYKPYPGPGFTGTNY-GGSG-PFGAPPSCGTFMNPSYGMPP-------PPETPPGSHAYYPPYGSMP-FMKAAASESVV : 550
MsELF3a       : LIPVMSPSEGLVYKPYPGPGFTGTNY-GGCG-PFGAPPSGGTFMNPSYGMPP-------PPETPPGSHAYFPPYGSMP-FMKAAASESAV : 554
VfELF3a       : LIPVMSPSEGLVYKPYPGPGFTGTNF-GGCGPPFGAAPSGGTFMNPSYGIPP-------PPETPPGSHPYFPPYGSMP-VMKAAGSESAV : 554
LcELF3a       : LIPVMSPSEGLVYKPYPGPGFTGTNF-GGCG-PYGASPSGGTFMNPSYGIPP-------PPEIPPGSHAYFPPYGGMP-VMKAAASESAV : 564
LsELF3a       : LIPVMSPSEGLVYKPYPGPGFTGTNF-GGCG-PYGAAPSGGTFMNPSYGIPP-------PPETPPGSQAYFPPYGGMP-VMKAAASESAV : 550
PsELF3a (HR)  : LIPVMSPSEGLVYKPYPGPGFTGTNF-GGCG-PYAAASGGTFMNPSYGIPP-------PPETPPGSQAYFPPYGGMP-VMKAAASESAV : 564
PsELF3b (PPD) : LIPVMSPSEGLIYKPYPGPGFPGAVY-GGYE-PFGHSPPDGTFMNPAYGVPNFHQAIAMSPFIPPSSYAYFPPQG-VP-AMNQSASGSVA : 521
LsELF3b       : LIPVMSPSEGLIYKPYPGPGFPGAVY-GGYE-PFGHSPPDGTFMNPAHGVPNFHQAIAMSPFIPPSSYAYFPPHG-VP-AMNQSAS--VA : 532
LcELF3b       : LVPVMSPSEGLVYKPYPGPAFPGSVY-GGYE-PFGHSPADGTFMNPAYGVPNFHQAIAMSPFIPPSSYAYFPPHG-VP-AMNQSTSRSAA : 525
VfELF3b       : LIPVMSPSEGLVYKPYPGPGFPGAVY-G---------PDGTFMNPAYGVPNFHQAIAVSPFIPPSSYAYFPPPG-MP-AMNQSVSGSVA : 533
MsELF3b       : LIPVMSPSEGLVYKPYPGPGYTGAVY-GGYR-PFGQGPDVTFMNPTYGVPDFHQAIAVPPFIPPGGYPYFPPHG-VP-AVYQSAVSAV : 517
MtELF3b       : LIPVMSPSEGLVYKPYPGPGYTGAVY-GGYR-PFGQGPDVTFMNPAYGVPDFHQAIAVPPFIPPGGYPYFPPHG-VP-AMYQSASVSAV : 517
TpELF3b       : LIPVMSPSEGLVYKPFPGPGFNGPVY-VCCG-PFGQGPLDGTVMNPTYGVPNFHQAIAVSPFIPPSSYAYFPPHG-VPAAINQPTSGVV : 444
CaELF3b       : LIPVMSPSEGLVYKPYPGPGFPMY-GGCG-PFGQGPNGAFMNPAYGIPDFHQAVAVSPFIPPGSYAHFPPHC-VP-AMNQSASGSVV : 523
VrELF3b       : LIPIMSPSEGLVYKPYPGPGTFTRTNP-ACCGG-PFGQAPLGATFMNPAFQFPASHQVVGVSPFVSLPNHTYFSPEYG-MQ--VVNQAATGSAV : 576
VaELF3b       : LIPVMSPSEGLVYKPYPGPGAFTRTNP-ACCGG-PFGQAPLGATFMHPASQFPASHQVVGVSPFVSLPNHTYFSPSG-VP--VVNQAASGSAV : 576
PvELF3b       : LIPIMSPSEGLIYKPYPRPAFTGMMP-ACCGG-PLGQAPLGATFMNPAYQFPASHQVVGVSPFVSPANHTYFSPYG-MP--VVNQAASGSAA : 581
GsELF3b-1     : LIPVMSPSEGLVYKPYPGPGFKGTMH-GCCGG-PFGQAPLSATFMNPAYQFPASHPVVGVSPFVPPASHTYFAPPG-MP--VMNQATSGSAV : 581
GsELF3b-2     : LIPVMSPSEGLVYKPYPGPGFMGTMN-GCCGG-PFGQAPLGATFMNPAYQFPASHPVVGVSPFVPPASHAYFSPG-MP--VVNQATSGSTV : 565
GmELF3b-1     : LIPVMSPSEGLVYKPYPGPGFMGTMH-GCCGG-PFGQAPLGATFMNPAYQFPASHPVVGVSPFVPPASHTYFAPPG-MP--VVNQATSGSAV : 581
GmELF3b-2     : LIPVMSPSEGLVYKPYPGPGFMGTMN-GCCGG-PFGQAPLGATFMNPAYQFPASHPVVGVSPFVPPASHAYFPSPG-MP--VVNQATSGSTV : 549
CcELF3b       : LIPIMSPSEGLVYKPYPGPEFTGTGCCSVPFGQAPIGATFMNPAYQFPASHQVVGVSPFVPPASHAYFPPYG-MP--VMNQAASGSAV : 584
AiELF3b       : LIPVMTPSEGLVYKPYPGPGFTGSFC-GGFG-PLGPVPMSNTYMNPVYGLPASHEAIGVPPYIPPGSHAYFPPYG-MPFMNNQAMSGSAV : 505
AdELF3b       : LIPVMTPSEGLVYKPYPGPGFTGSFC-GGFG-PLGPVPMSNTYMNPVYGLPASHEAIGVPPYIPPGSHAYFPPYG-MPFMNNQAMSGSAV : 501
LaELF3b-1     : LIPVMTPSEGLVYKPYPGPAFPGTMCG-GGCG-PFGPGPPGGTFMNPSYGVP---------PHISPGSLTYFPPYG-MP-VMNQAVSGSAD : 555
LaELF3b-2     : LIPVMTPSEGLVYKPYPGPAFQETMCGRGCE-PFGPGPPGGTFMNPSYGVP---------PHIPPGSLAYFHPYG-MP-VMNQSVSGSAD : 484
AkELF3-1      : LIPVMSPSEGLVYKPYAGPGFTGTTC-GGYG-PFGPGPLGAGFMSPAYGVPASHQGFGVPTGTPPSSHAYFPHYD-MP-VMAPAMSGSIA : 574
AkELF3-2      : LIPVKSPSEGLVYKPYPGPG-----------------PSGGNFMNPAYGVPASNQGIGILPDTSPPSYPYFAPYG-MP-VMNPAMSGSAV : 559
CgELF3        : LIPVMSPSEGLVYKPYPGPGFAGTAC-GGCG-PFGPAPMGGTFMNPAYGVPASHQGI-----TPPGSHAYFPPYG-MP-VMNPAMSGSAV : 578
AtELF3        : LIPVMSPSEGLIYKPHPGMAHTCHY-GGYYGHYMPTPMVMPQYHPGMGFP-----------PPGN-GYFPPYGMMPTIMNPYCSSQQQ : 546
              Conserved block III

                                   640        660        680        700        720
LaELF3a       : ------EQVKQFSEHASHGQNGHLNG-RETDINTN-N---QSSCDL-PVQRNRAI--SHAMKKYQTSKEVELQGSTASSPSEMAQGISTR : 633
AdELF3a       : ------EQANQFSARGSQGQGNDHSQG-GDANPSTN-N---QSSNNL-PGPRNGTI--SNVMRYQACSREVELQGSASSPSEMAQ----G : 649
AiELF3a       : ------EQANQFSARGSQGQGNDHSQG-GDANPSTN-N---QNSNNL-PDPRNGTI--SNVMRYQVCSREVELQGSATSPSETAQ----C : 649
CcELF3a       : ------EQVNQFSALGSR---GHLSR-GEGNLNTN-N---QSSCNL-PVQKNGAM--SHALKYQT-SKDFDLQGSTASSPSEMAQGISTG : 633
GsELF3a       : ------EQGNQFSALGSHGHNGHLPGGGKANHNTN-N---KSSCNL-PVQRNGAI--SHVLKHQT-SKDFELQETSASSPSEMAQGISTG : 648
GmELF3a       : ------EQGNQFSALGSHGHNGHLPGGGKANHNTN-N---KSSCNL-PVQRNGAI--SHVLKHQT-SKDFELQETSASSPSEMAQGISTG : 648
VaELF3a       : ------DQVNQFSSLGSHRYNGHLPG-GEADHITN-N---QSSRNL-PTPRKGAF--SHVLKYQT-SKDFELQGSTASSPSEMAQGISTG : 639
VrELF3a       : ------DQVNQFSSLGSHRYNGHLPG-GESNHITN-N---QSSRNL-PTPRNGAS--SHVLKYQT-SKDFELQGSTASSPDEMAQALSTG : 640
LjELF3a       : -----DQVNQFSALESRGQSGHISG-READHNTH-N---QSSCDV-PVQGNGAT--SHVMYQQM-YKEFELQGSRTSSPSEM------G : 634
CaELF3a       : ------GHVNQFSA---HGQNDHLSE-VEANHNKH-N---QIPCNL-PAQRNGAT--SHVMNRQR-HKEFELQGSTASSPSEMAQGMSIG : 633
TpELF3a       : ------EQVNQLSA---GGQNRHLSE-VEADCSKH-N---QSSCNL-PVQRNGAT--SNVMYRQR-SKEFDLQMSTASSPSEMAQEMSTG : 588
MtELF3a       : ------EHVNQFSA---RVQSRHLSE-GEADCNKH-N---QSSCNL-PVQRNGAT--THVMHHQR-SKEFELQMSTASSPSEMTGMSTG : 622
MsELF3a       : ------EHVNQFSA---RVQSRHLSE-GEGDCNKH-N---QSSCNL-PVQRNGAT--THVMHCQR-TKEFELQMSTASSPSEMTQGMSTG : 626
VfELF3a       : ------EHVNQFSA---RGONRRLSE-DEADCNKH-N---QNSCNL-PVQRNGTT--SHVMYHQR-SKDFELQMSTASSPGEMAQEISTA : 626
LcELF3a       : ------EHVNQFSA---HGQNHRLSE-DEDNCNKH-N---QSSCNL-PAQRNEDT--SHVMYHQR-SKEFDLQMSTASSPSEMAQEMSTG : 636
LsELF3a       : ------EHVNQFSA---RGONCRLSE-DEADCNKH-N---QNSCNL-PVQRNGTT--SHVMYHQR-SKELEVQMSTASSPSEMVLEMSTG : 622
PsELF3a (HR)  : -----EHVNQFSA---RGQSRRLSE-DEADCNKH-N---QSSYDL-PVQRNGAT--SHVMYHQR-SKEFEVQMSTASSPSEMAQEMSTG : 636
PsELF3b (PPD) : ------EQVNQFVAQGSGDRNGNSSL-VGADFDTH-N---QSSCNF-SNQKSAV--LPVTKSRP-SREREL----ASSPNEKAQGIRIE : 592
LsELF3b       : ------EQVNQFVAQGSRDRNGNSSL-VGADFDTH-N-------------------SGAV-LHVTKSRP-SREREL---VSSPNKKAHGIRIE : 593
LcELF3b       : ------EQVNQFVAHGSRDRNNNSSL-VGAGFDTH-N---QSSCDF-SNQKSGPI--LPVTKARP-SREREL----ASSPNEKAQGIRIE : 596
VfELF3b       : ------EQVNQFVAQGSCERNSNSSL-VGADFDTH-N---QSSRNF-SNQNSGAI--SHVTKSRP-SREREL---ACSPNEEAQGIRIE : 604
MsELF3b       : ------EQVNQFAAHGSRNQNGNSSL-EEANFNTR-N---QSSCNL-TNQKNGAT--LHVRKPQP-SREREL----ESSPGEKAQEIIKE : 588
MtELF3b       : ------EQVNQFSAHGSRNQNGTSSL-EEANFYTH-N---QSSCNL-TNQKNGAT--LHVRKPQP-SREREL---ESSPGEKAQEIIKE : 588
TpELF3b       : ------EQATQFVAHGSHDQNNNSSL-VGAGFDTH-N---QTPCNL-SNQKFGTI--SHVTKSRP-IRERGL----AGSPGEKAPGIRIE : 515
CaELF3b       : -----EQANRFAAQVSHDSNGNSSL-VGASFNTH-N---QSSCNL-TNQKNGAT--LHITKFQP-SIERELQGIPTSRPNEK--EIRIE : 596
VrELF3b       : ------EHVNQYAGGSHVQNGHSSV-EGASFNTQHN---QSSCNL-PVQRNGAV--SHVKKLRV-SKERRLQGSTASTPSETPQEIRTG : 652
VaELF3b       : ------EHVNQFAGQGSHGQNGHSSV-EGANFNTQHN---QSSSNL-PVQRNGAM--SHVKKLRV-SKERRLQGSTASTPTETPQGIRAG : 652
PvELF3b       : ------EHVNQFATQGSHGQNGHSSV-EGANFNTHHN---QSSSNL-PVQRSGAM--SHVKKLQV-SKERQLQGSTASTASETPQRIKAR : 657
GsELF3b-1     : ------EHVNQFAAQGSHGQNGHSSV-EGADFNTHHN---QSSSNL-PVQKNGAR--LHVKKSQA-LKERGLQGSTRSSPSEMAQGIRAG : 657
GsELF3b-2     : ------EQVNQFAAQGSHGQNGHSYI-EGTDFNTHHN---QSSSNL-PVLKNGAT--LHVKKSQA-SKERGLQGSTISSPSEMAQGIRAG : 641
GmELF3b-1     : ------EHVNQFAAQGSHGQNGHSSV-EGADFNTHHN---QSSSNL-PVQKNGAR--LHVKKSQA-LKERGLQGSTRSSPSEMAQGIRAG : 657
GmELF3b-2     : ------EQVNQFAAQGSHGQNGHSYI-EGTDFNTHHN---QSSSNL-PVLKNGAT--LHVKKSQA-SKERGLQGSTISSPSEMAQGIRAG : 625
CcELF3b       : -----EPVNQFAAQGSHGQNGHSSV-EGANFNTHPN---QSSSNL-PVQRNGAT--LHVKKSQA-SKERQLQGSTTSSPSEMAQGISAG : 660
AiELF3b       : ------EQANQFMAQGSHLQNGHSSA-DRIDFPAH-N---QGSSNQ-PVQRTGSA--SLAGKSRT-PKDSEFQGSTNSPNETAQETRTT : 580
AdELF3b       : ------EQANQFMAQGSHLQNGHSSA-DRIDFPAH-N---QGSSNQ-TVQRTGSA--SHAGKSRT-PKDSEFQGSTNSPNETAQQTRTT : 576
LaELF3b-1     : ------EQVNHFAAQGSHDQNGHSLV-EGANFNTH-N---QVSNNS-PVQRKGAI--SHVKKSHA-SKKSELQGSTASSPSEKAQGIRKR : 630
LaELF3b-2     : ------EQVNHLAAQGSRGQNGHSSI-EEANFSTH-N---QSSYNL-PAQKNGAI--SHVKKFQA-SKKSEIQGSTASSLIEKAHGIRQR : 559
AkELF3-1      : ------EQKNQFAGPDPHGKNGHLSG-KETNCNSNNNSHIQSSCNLPPVQKSRTISQSQVKKFQA-SKASELQGSTASSPGEMAHGISRT : 656
AkELF3-2      : ------EQTNHFAA---PGSNGHLSG-VGANFNTNHN---QGSCSF-PVQRNESM--SNVMKIHA-PKGRELQRSTASSPSELAQGTSTD : 632
CgELF3        : ------EQMNQFGRSDSNDQNGHLSC-GGANFNSH-N---QSSNNL-PVQKNGAI--SQVMKFQA-SKKSELQRSTASSPSELAEGISTG : 653
AtELF3        : QQQQQPNEQMNQFGHPG-NLQNTQQQQ-------------QRSDNE-PAPQQQ----QQPTKSYP-RARKSRQGSTGSSPSG-PQGISGS : 614
```
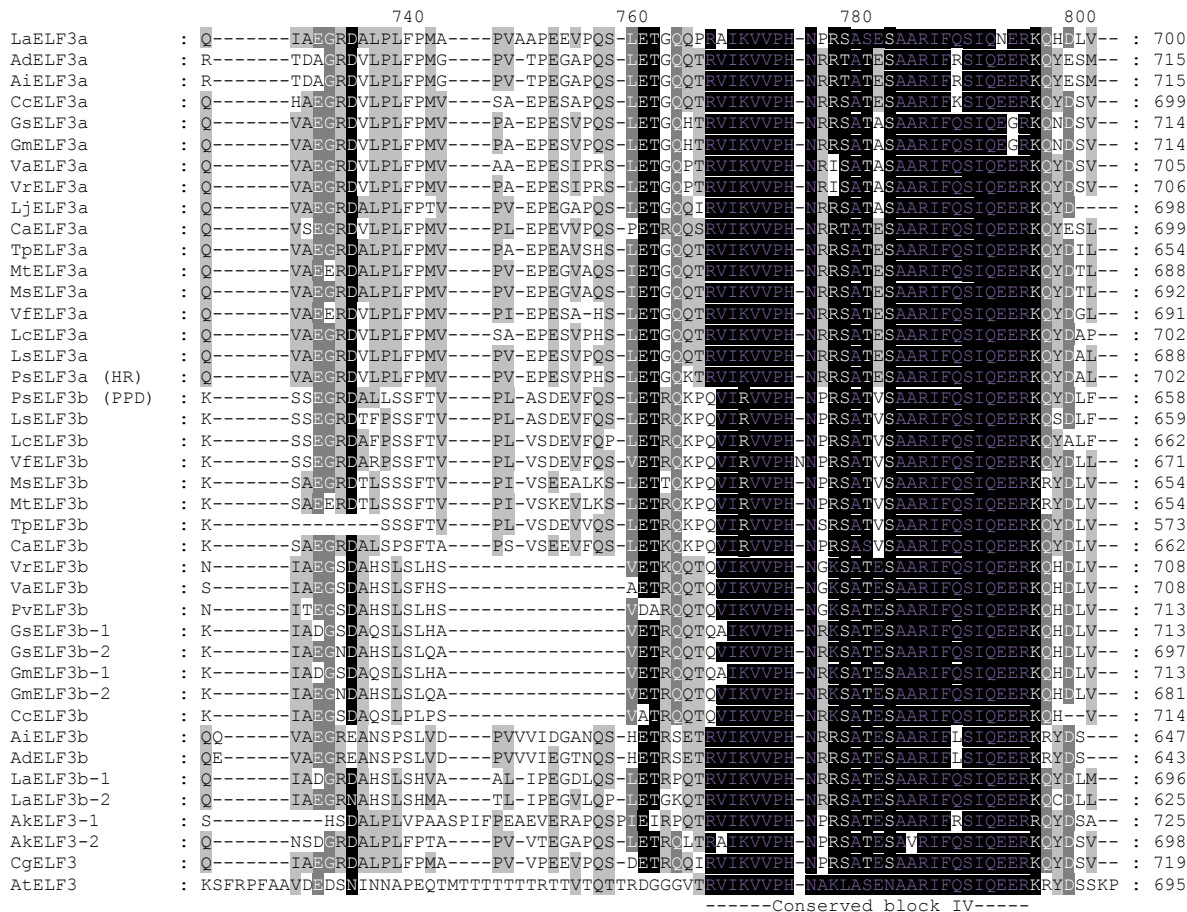
Figure S4. Alignment of ELF3-like protein sequences from 20 legume species with Arabidopsis ELF3. Sequence details are given in **Table S3.** Sequences were manually curated and mRNA transcripts translated at http://biotools.umassmed.edu/cgi-bin/biobin/transeq and splice site prediction by http://genes.mit.edu/GENSCAN.html. Deduced protein sequences were aligned in Geneious (FFT-NS-ix 1000 default settings) and conservation shaded in GeneDoc (black to grey shading scale showing conservation of 90%, 80%, 50% and <50% with similar amino acids residues shaded together). Coloured shading indicates ELF3 conserved motifs labelled according to Liu et al. (2001). Red background or red text indicates *ppd-1* and *ppd-3* allele mutations respectively. Arrows indicate splice sites in the corresponding pea ELF3 genes.
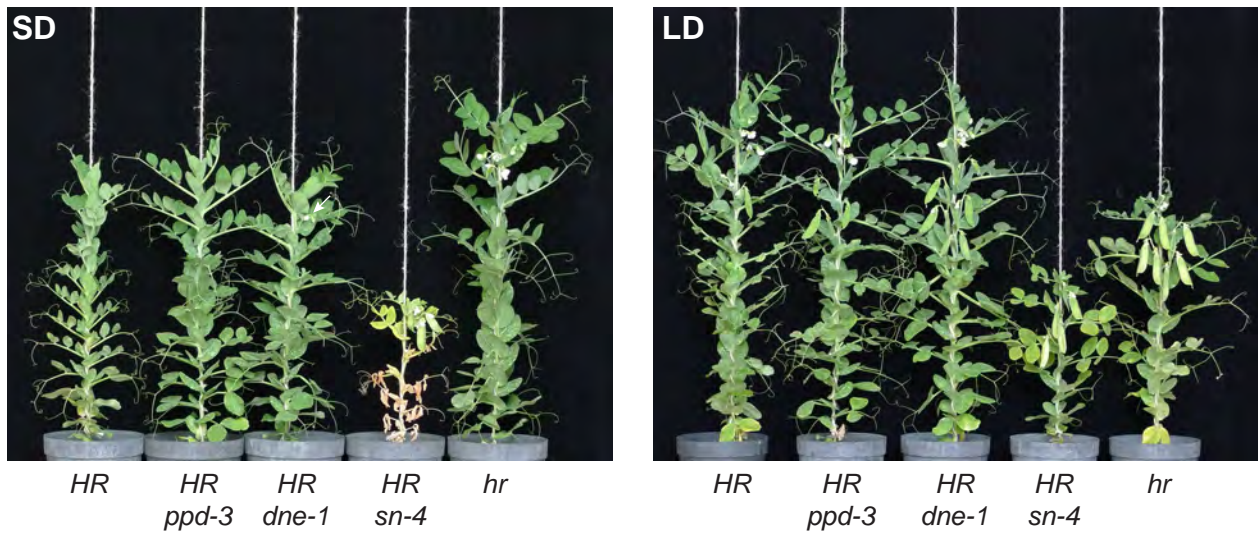
Figure S5. Phenotypic comparison of mutants for pea "evening complex" genes.
Representative ten-week-old plants grown under short days or long day conditions.
All plants are near isogenic to WT (*hr*). Growth conditions as in Figure 6
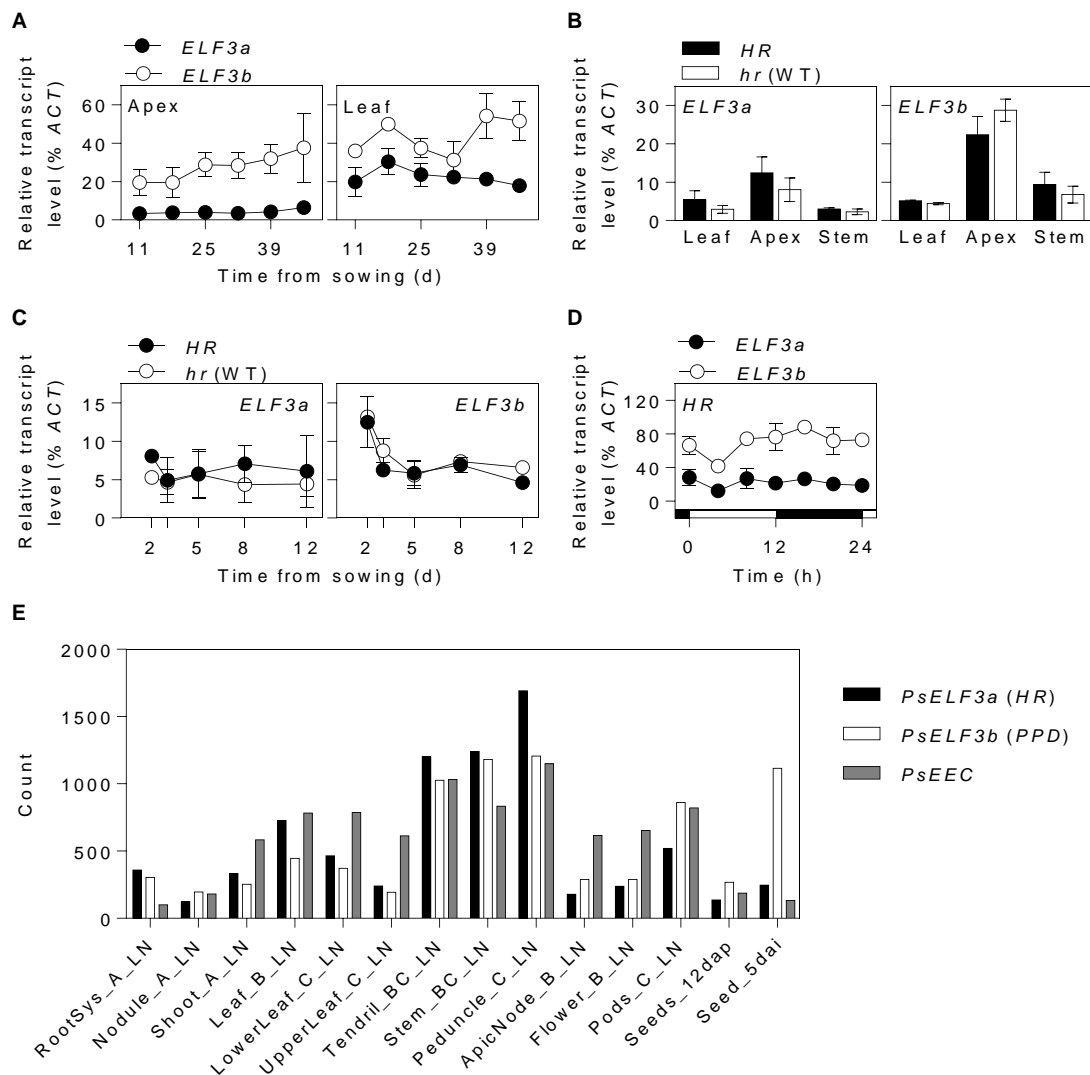
Figure S6. Comparison of pea *ELF3a* and *ELF3b* gene expression.

A) Developmental regulation of pea *ELF3* gene expression in the *hr* (WT) line NGB5839 under 8-h SD conditions (experiment also shown in **Figure 2**). **B)** Expression of *ELF3* genes in different tissues of *hr* (WT) and a near-isogenic *HR* line. Plants were grown for two weeks from sowing under LD conditions in the glasshouse before harvesting at 8h after lights-on. Leaf and apex tissues were harvested as described in the legend of **Figure 2**, and stem tissue consisted of the uppermost expanded internode and petiole of the subtending leaf. **C)** Developmental regulation in continuous darkness. Samples consisted of the entire shoot, excised at the cotyledonary node **D)** Diurnal timecourse of expression in leaflet tissue from three-week-old plants grown under a 12-h light/12-h dark cycle at 20°C. Light and dark periods are represented by white and black bars respectively. **A to D**). Values are normalized to *ACTIN* and represent mean ± se for 2 biological replicates. All harvests consisted of pooled material from two plants. **E)** Tissue distribution of *ELF3* gene expression in cultivar Cameor (*hr*) in various tissues, as presented in the pea gene expression atlas (Alves-Carvalho et al. 2015; bios.dijon.inra.fr/FATAL/cgi/PsUniLowCopy.cgi?). LN - low nitrogen, dap – days after pollination, dai – days after imbibition. A, B and C refer to different developmental stages.
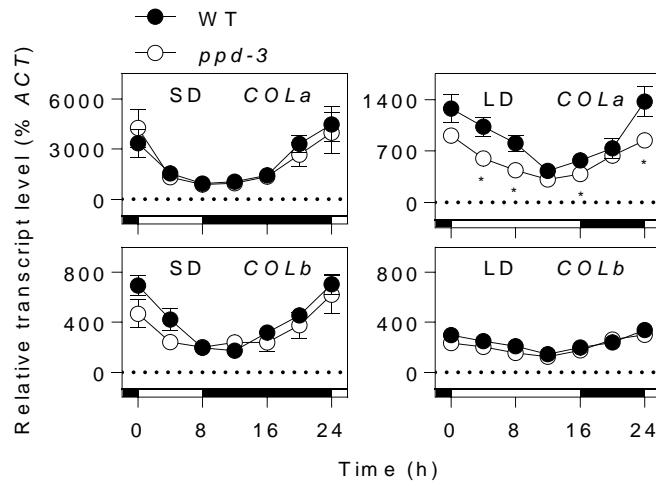
Figure S7. Diurnal regulation of group Ia *CO-like* genes in the *ppd-3* mutant.

Growth conditions and expression analysis as in **Figure 3**.

Table S1. SNPs in *PsELF3b* coding sequence in selected *P. sativum* lines. All accessions are var. *sativum* except 1794 (JI1794) which is var *humile*. CAM - cv. Cameor, BOR – cv. Borek.

Coding region	Cultivar sequenced	Mutation (relative to ATG)	
		cDNA	Protein
ELF3b exon1	5839, CAM, BOR, 1794, 1771	no mutations	
ELF3b exon2	5839, CAM, BOR	no mutations	
	1794	G339A	silent
	1794	A368G	K123R
	1794, 1771	G481A	E161K
	1771	G566A	S189N
ELF3b exon3	5839, CAM, BOR, 1794, 1771	no mutations	
ELF3b exon4	5839, CAM, BOR	no mutations	
	1771	A1066G	T356A
	1794, 1771	C1087T	P363S
	1794, 1771	T1125G	F375L
	1771	G1146C	Q382H
	1771	G1147A	A383T
	1771	A1287G	silent
	1771	C1329T	silent
	1771	T1356C	silent
	1771	T1399A	F467I
	1771	G1521C	Q507H
	1771	G1569A	silent
	1794, 1771	G1597C	G533R
	1771	A1653G	silent
	1771	A1654G	S552G
	1771	G1690A	V564I
	1771	C1797T	silent

Table S2. Primer and marker details.

Gene	Primer	Sequence (5' to 3')	Purpose	Tm (⁰C)	Enzyme	Population
COLb	COLb-F4	GGAAATATGGGCCTTTTGG	PCR and sequencing	55		
	COLb-R4	TGGTTGGATTGGTAGTGTGG	PCR and sequencing	58		
	COLb-F5	TCAAGTCAATGAATTTTGTTGC	PCR and sequencing	55		
	COLb-R5	TCGGCATATCTTGTCAAAAGC	PCR and sequencing	58		
	CO1P-2F	AGGTTCGAGAAGACAATTCG	PCR and sequencing	58		
	CO1P-1R	ACCGGCACAACTCCGTCTGC	PCR and sequencing	58		
DNE/*ELF4*	ELF4-GSP1	TCAGTCGGTGCTTGACAGGAACAGAGC	genotyping/HRM	58		
	ELF4-GSP2	TGAGATCAGAATAAAGAGAAGCAACCTTTG	genotyping/HRM			
HR/*ELF3a*	ELF3-HR-F	ACTAACACTTTATTGGCAAGTG	genotyping/HRM	58		
	ELF3-HR-R	GCGGAAAGTATCGTCATTTTG	genotyping/HRM			
PepTrans	PEPTRANS-F1	GCCGTGATTCGGATCTGATGG	Mapping/CAPs	60	*PciI*	Torsdag x Térèse
	PEPTRANS-R1	CGGTCGTATAAAGGAATGACTAC	Mapping/CAPs		*PciI*	Torsdag x Térèse
PPD/*ELF3b*	ELF3b-F2	CAAGCCCGAGACTTTCTCC	gene expression /qRT-PCR	62		
	ELF3b-R2	CTGTGCAATTCAAACACTTGG	gene expression /qRT-PCR			
	ELF3b-ppd1-HRM-F	AAGGGTGATGCCGAGAAGG	genotyping/HRM	60 | 62		
	ELF3b-ppd1-HRM-R	TCTTATTCCTCGGTGGTGCT	genotyping/HRM			
	ELF3b-ppd3-HRM-F	AGGCAAGCCGAGAAGATTTCA	genotyping/HRM			
	ELF3b-	CGCGGAGTCAACGAGACTT	genotyping			

	ppd3-HRM-R		g/HRM			
	ELF3b-ppd-3-HRM-2R	TCATTGGATTCCTGCTGTAAG	genotypin g/HRM			
	EFL3b-F1	AATGACACGGCAGAGAAAGG	PCR and sequencin g	58		
	ELF3b-R1	AATTCCTGGAGCCCGTAGG	PCR and sequencin g	60		
	ELF3b-F2	CAAGCCCGAGACTTTCTCC	PCR and sequencin g	60		
	ELF3b-R2	CTGTGCAATTCAAACACTTGG	PCR and sequencin g	57		
	ELF3b-F3	GGTCCAAGTGTTTGAATTGC	PCR and sequencin g	56		
	ELF3b-R3	CCCTGCAGAAGAGGTTTTCC	PCR and sequencin g	60		
	ELF3b-R4	CTGCTTGGAGGAATGAATGG	PCR and sequencin g	58		
	ELF3b-F5	AGAACCACACCAGAGAGG	PCR and sequencin g	56		
	ELF3b-R5	TCAACTCAAAGGTTACACATCC	PCR and sequencin g	58		
	ELF3b-F6	AACACGCACACTTTGTCAGC	PCR and sequencin g	58		
	ELF3b-R6	GTATGATCGGCAGCTTCAGG	PCR and sequencin g	60		
	ELF3b-F7	AATCTTTTGCCCGATACTGC	PCR and sequencin g	56		
	ELF3b-R7	ACTGTGAACCAGCATTTGCC	PCR and sequencin g	58		
	ELF3b-F8	TTCATGAATCCTGCCTATGG	PCR and sequencin g	56		
	ELF3b-I2-1F	ATGCTTCCTGTTGGAGTCTCG	PCR and sequencin g	61		
	ELF3b-F6	AACACGCACACTTTGTCAGC	genotypin g/CAPs	58	*AlwI*	NGB5839 x *ppd-3*

	ELF3b-R6	GTATGATCGGCAGCTTCAGG	genotyping/CAPs		AlwI	NGB5839 x *ppd-3*
ThiolP	ThiolP-F	CCGAAGAGGATTACCCCTAYCGTGC	Mapping/CAPs	55	*MboII*	Torsdag x Térèse
	ThiolP-R	GCTTCTCCCCAGCTACCACCCC	Mapping/CAPs		*MboII*	Torsdag x Térèse

Table S3. Sequence details

Family	Species	Protein name	Accession
Brassicaceae	*Arabidopsis thaliana*	AtELF3	AT2G25930
		AtEEC	AT3G21320
Fabaceae	*Acacia koa*	AkELF3-1	GBYE01012597.1
		AkELF3-2	GBYE01021588.1
		AkEEC (partial)	GBYE01064612.1
	Arachis duranensis	AdELF3a	|gb|JQIN01001261.1|A08:17057456..17061006
		AdELF3b	|gb|JQIN01001121.1|A06:109327377..109332334
		AdEEC	|gb|JQIN01001303.1|A09:4426999..4429737
	Arachis ipaensis	AiELF3a	|gb|JQIO01000312.1|B07:125055854..125059332
		AiELF3b	|gb|JQIO01000276.1|B06:133911868..133916526
		AiEEC	|gb|JQIO01000364.1|B09:5640632..5643286
	Cajanus cajan	CcELF3a	|gb|AGCT01007375.1|LG03:1360-5896
		CcELF3b	|gb|AGCT01015227.1|LG09:39494-44466
		CcEEC	|gb|AGCT01008553.1|LG11:1305-6005
	Cercis gigantea	CgELF3	Cgm40592_c0.4
		CgEEC	Cgm39860_c0.3
	Cicer arietimum	CaELF3a	LOC101489432
		CaELF3b	LOC101488316
		CaEEC	LOC101495393
	Glycine max	GmELF3a	Glyma.04G050200.1
		GmELF3b-1	Glyma.17G231600.1
		GmELF3b-2	Glyma.14G091900.1
		GmEEC-1	Glyma.08G197500.1
		GmEEC-2	Glyma.07G013500.1
	Glycine soja	GsELF3a	|gb|KHN29734.1|
		GsELF3b-1	|gb|KHN37008.1|
		GsELF3b-2	|gb|KHN17209.1|
		GsEEC-1	|gb|KHN11326.1 (with FAR1-RELATED SEQUENCE)
		GsEEC-2	|gb|KHN39274.1|
	Lathyrus sativus	LsELF3a	GBSN01007972
		LsELF3b	GBSN01012791
		LsEEC	GBSN01020173
	Lens culinaris	LcELF3a	Lc38669: |gb|JX946295.1|
		LcELF3b	Lc20598: LcChr5:249280295..249285299
		LcEEC	Lc31587: LcChr7:28615590..28620454
	Lotus japonicus	LjELF3a	Lj1g3v1785530.1
		LjEEC	Lj3g3v2719920.1
	Lupinus angustifolius	LaELF3a	Lup030650: NLL-03:23827343..23830452
		LaELF3b-1	Lup000361: Scaffold_1_1096:96100..101281
		LaELF3b-2	Lup012006: NLL-10:6040433..6045113

		LaEEC	Lup013664: NLL-09:12303329..12307096
	Medicago sativa	MsELF3a	GAFF01064723
		MsELF3b	GAFF01106657
		MsEEC	GAFF01066064
	Medicago truncatula	MtELF3a	Medtr3g103970.1
		MtELF3b	Medtr1g016920.1
		MtEEC	Medtr8g015480.1
	Phaseolus vulgaris	PvELF3b	Phvul.001G032900.1
		PvEEC	Phvul.010G142900.1
	Pisum sativum	PsELF3a (HR)	PsCam034343_1: |gb|JN983406.1|
		PsELF3b (PPD)	PsCam054737_1
		PsEEC	PsCam045014_1
	Trifolium pratense	TpELF3a	ASHM01006086.1
		TpELF3b	ASHM01002847.1
		TpEEC	ASHM01006217.1
	Vicia faba	VfELF3a	CSVX01003282.1
		VfELF3b	CSVX01003283.1
		VfEEC	CSVX01029249.1
	Vigna angularis	VaELF3a	|gb|JZJH01056101.1|
		VaELF3b	|gb|JZJH01047989.1|
		VaEEC	|gb|JZJH01050188.1|
	Vigna radiata	VrELF3a	|gb|JJMO01000121.1|Vr05_20836600-20840972
		VrELF3b	|gb|JJMO01000122.1|Vr06_33808491-33812872
		VrEEC	|gb|JJMO01000129.1|Vr09_1574582-1578437
Poaceae	*Hordeum vulgare*	HvELF3	|gb|JN180296.1: Chr1 (463,461,979-463,463,725)
	Oryza sativa	OsELF3-1	Os06g0142600
		OsELF3-2	Os01g0566100
	Zea mays	ZmELF3-1	LOC100383534
		ZmELF3-2	LOC103630791
Rosaceae	*Fragaria vesca*	FvELF3	mrna02656.1 LG2:18150208..18153629
		FvEEC	mrna22895.1 LG4:23802802..23805586
	Malus domestica	MdELF3-1	XP_008357349.1
		MdELF3-2	XP_008351957
	Prunus mume	PmELF3	LOC103320523
		PmEEC	LOC103342866
	Prunus persica	PpELF3	1G416000.1_v2.0
		PpEEC	3G054300.9_v2.0
	Pyrus bretschneideri	PbELF3-1	LOC103929644
		PbELF3-2	LOC103951808