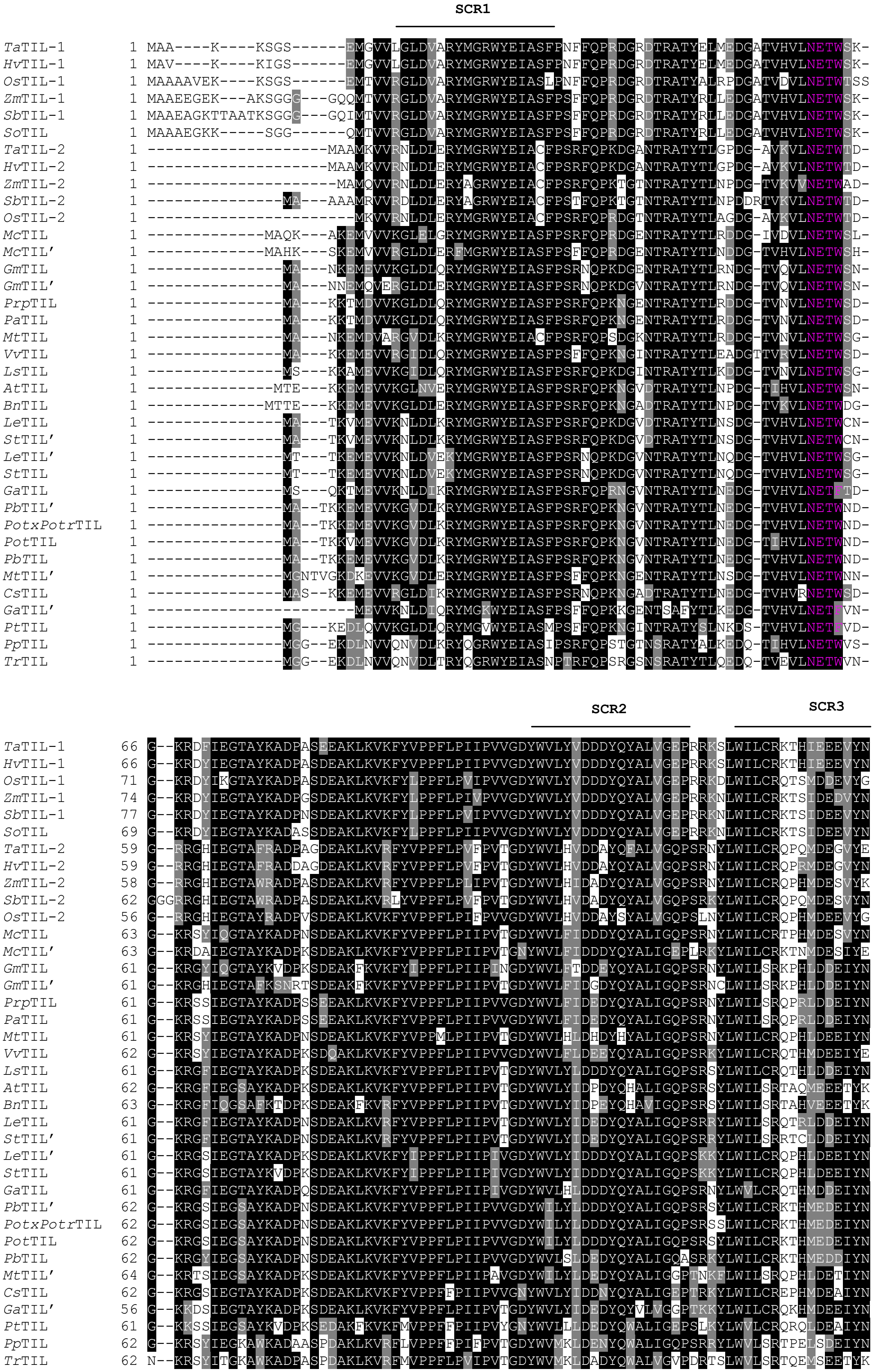

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HvTIL-1        1 MAV----K----KIGS------EMGVVLGLDVARYMGRWYEIASFPNFFQPRDGRDTRATYELMEDGATVHVLNETWSK-
OsTIL-1        1 MAAAAVEK----KSGS------EMTVVRGLDVARYMGRWYEIASLPNFFQPRDGRDTRATYALRPDGATVDVLNETWTSS
ZmTIL-1        1 MAAEEGEK---AKSGGG---GQQMTVVRGLDVARYMGRWYEIASFPSFFQPRDGRDTRATYRLLEDGATVHVLNETWSK-
SbTIL-1        1 MAAEAGKTTAATKSGGG---GQIMTVVRGLDVARYMGRWYEIASFPSFFQPRDGRDTRATYRLLEDGATVHVLNETWSK-
SoTIL          1 MAAAEGKK-----SGG------QMTVVRGLDVARYMGRWYEIASFPSFFQPRDGRDTRATYRLLEDGATVHVLNETWSK-
TaTIL-2        1 --------------------MAAMKVVRNLDLERYMGRWYEIACFPSRFQPKDGANTRATYTLGPDG-AVKVLNETWTD-
HvTIL-2        1 --------------------MAAMKVVRNLDLERYMGRWYEIACFPSRFQPKDGANTRATYTLGPDG-AVKVLNETWTD-
ZmTIL-2        1 ---------------------MAMQVVRNLDLERYAGRWYEIACFPSRFQPKTGTNTRATYTLNPDG-TVKVVNETWAD-
SbTIL-2        1 ---------------MA---AAAMRVVRDLDLERYAGRWYEIACFPSTFQPKTGTNTRATYTLNPDDRTVKVLNETWTD-
OsTIL-2        1 -----------------------MKVVRNLDLERYMGRWYEIACFPSRFQPRDGTNTRATYTLAGDG-AVKVLNETWTD-
McTIL          1 -------------MAQK---AKEMVVVKGLELGRYMGRWYEIASFPSRFQPRDGENTRATYTLRDDG-IVDVLNETWSL-
McTIL’         1 -------------MAHK---SKEMVVVRGLDLERFMGRWYEIASFPSFFQPRDGENTRATYTLNDDG-TVHVLNETWSH-
GmTIL          1 ---------------MA---NKEMEVVKGLDLQRYMGRWYEIASFPSRNQPKDGENTRATYTLRNDG-TVQVLNETWSN-
GmTIL’         1 ---------------MA---NNEMQVERGLDLERYMGRWYEIASFPSRNQPKDGVNTRATYTLRNDG-TVQVLNETWSN-
PrpTIL         1 ---------------MA---KKTMDVVKGLDLQRYMGRWYEIASFPSRFQPKNGENTRATYTLRDDG-TVNVLNETWSD-
PaTIL          1 ---------------MA---KKTMDVVKGLDLQRYMGRWYEIASFPSRFQPKNGENTRATYTLRDDG-TVNVLNETWSD-
MtTIL          1 ---------------MA---NKEMDVARGVDLKRYMGRWYEIACFPSRFQPSDGKNTRATYTLRDDG-TVNVLNETWSG-
VvTIL          1 ---------------MA---KKEMEVVRGIDLQRYMGRWYEIASFPSFFQPKNGINTRATYTLEADGTTVRVLNETWSD-
LsTIL          1 ---------------MS---KKAMEVVKGIDLQRYMGRWYEIASFPSRFQPKDGINTRATYTLKDDG-TVNVLNETWSG-
AtTIL          1 --------------MTE---KKEMEVVKGLNVERYMGRWYEIASFPSRFQPKNGVDTRATYTLNPDG-TIHVLNETWSN-
BnTIL          1 -------------MTTE---KKEMEVVKGLDLERYMGRWYEIASFPSRFQPKNGADTRATYTLNPDG-TVKVLNETWDG-
LeTIL          1 ---------------MA---TKVMEVVKNLDLKRYMGRWYEIASFPSRFQPKDGVDTRATYTLNSDG-TVHVLNETWCN-
StTIL’         1 ---------------MA---TKVMEVVKNLDLKRYMGRWYEIASFPSRFQPKDGVDTRATYTLNSDG-TVHVLNETWCN-
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StTIL          1 ---------------MT---TKEMEVVKNLDVEKYMGRWYEIASFPSRNQPKDGVNTRATYTLNQDG-TVHVLNETWSG-
GaTIL          1 ---------------MS---QKTMEVVKNLDIKRYMGRWYEIASFPSRFQPRNGVNTRATYTLNEDG-TVHVLNETFTD-
PbTIL’         1 ---------------MA--TKKEMEVVKGVDLKRYMGRWYEIASFPSRFQPKNGVNTRATYTLNEDG-TVHVLNETWND-
PotxPotrTIL    1 ---------------MA--TKKEMEVVKGVDLKRYMGRWYEIASFPSRFQPKNGVNTRATYTLNEDG-TVHVLNETWND-
PotTIL         1 ---------------MA--TKKVMEVVKGVDLKRYMGRWYEIASFPSRFQPKNGVNTRATYTLNEDG-TIHVLNETWND-
PbTIL          1 ---------------MA--TKKEMEVVKGVDLKRYMGRWYEIASFPSRFQPKNGVNTRATYTLNEDG-TVHVLNETWND-
MtTIL’         1 ---------------MGNTVGKDKEVVKGVDLERYMGRWYEIASFPSFFQPKNGENTRATYTLNSDG-TVHVLNETWNN-
CsTIL          1 ---------------MAS--KKEMEVVRGLDIKRYMGRWYEIASFPSRNQPKNGADTRATYTLNEDG-TVHVRNETWSD-
GaTIL’         1 -----------------------MEVVKNLDIQRYMGKWYEIASFPSFFQPKKGENTSAFYTLKEDG-TVHVLNETFVN-
PtTIL          1 ---------------MG---KEDLQVVKGLDLQRYMGVWYEIASMPSFFQPKNGINTRATYSLNKDS-TVHVLNETFVD-
PpTIL          1 ---------------MGG--EKDLNVVQNVDLKRYQGRWYEIASIPSRFQPSTGTNSRATYALKEDQ-TIHVLNETWVS-
TrTIL          1 ---------------MGG--EKDLNVVQNVDLTRYQGRWYEIASNPTRFQPSRGSNSRATYTLQEDQ-TVEVLNETWVN-

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HvTIL-1       66 G--KRDYIEGTAYKADPASDEAKLKVKFYVPPFLPIIPVVGDYWVLYVDDDYQYALVGEPRRKSLWILCRKTHIEEEVYN
OsTIL-1       71 G--KRDYIKGTAYKADPASDEAKLKVKFYLPPFLPVIPVVGDYWVLYVDDDYQYALVGEPRRKDLWILCRQTSMDDEVYG
ZmTIL-1       74 G--KRDYIEGTAYKADPGSDEAKLKVKFYLPPFLPIVPVVGDYWVLYVDDDYQYALVGEPRRKNLWILCRKTSIDEDVYN
SbTIL-1       77 G--KRDYIEGTAYKADPNSDEAKLKVKFYLPPFLPVIPVVGDYWVLYVDDDYQYALVGEPRRKNLWILCRKTSIDEEVYN
SoTIL         69 G--KRDYIEGTAYKADASSDEAKLKVKFYLPPFLPIIPVVGDYWVLYVDDDYQYALVGEPRRKNLWILCRKTSIDEEVYN
TaTIL-2       59 G--RRGHIEGTAFRADPAGDEAKLKVRFYVPPFLPVFPVTGDYWVLHVDDAYQFALVGQPSRNYLWILCRQPQMDEGVYE
HvTIL-2       59 G--RRGHIEGTAFRADDAGDEAKLKVRFYVPPFLPVFPVTGDYWVLHVDDAYQYALVGQPSRNYLWILCRQPRMDEGVYN
ZmTIL-2       58 G--RRGHIEGTAWRADPASDEAKLKVRFYVPPFLPLIPVTGDYWVLHIDADYQYALVGQPSRNYLWILCRQPHMDESVYK
SbTIL-2       62 GGGRRGHIEGTAWRADPASDEAKLKVRLYVPPFLPVFPVTGDYWVLHVDADYQYALVGQPSRKYLWILCRQPQMDESVYN
OsTIL-2       56 G--RRGHIEGTAYRADPVSDEAKLKVKFYVPPFLPIFPVVGDYWVLHVDDAYSYALVGQPSLNYLWILCRQPHMDEEVYG
McTIL         63 G--KRSYIQGTAYKADPNSDEAKLKVKFYVPPFLPIIPVTGDYWVLFIDDDYQYALIGQPSRNYLWILCRTPHMDESVYN
McTIL’        63 G--KRDAIEGTAYKADPKSDEAKLKVKFYVPPFLPIIPVTGNYWVLFIDDDYQYALIGEPLRKYLWILCRKTNMDESIYE
GmTIL         61 G--KRGYIQGTAYKVDPKSDEAKFKVKFYIPPFLPIIPINGDYWVLFTDDEYQYALIGQPSRNYLWILSRKPHLDDEIYN
GmTIL’        61 G--KRGHIEGTAFKSNRTSDEAKFKVKFYVPPFLPIIPVTGDYWVLFIDGDYQYALIGQPSRNCLWILSRKPHLDDEIYN
PrpTIL        61 G--KRSSIEGTAYKADPSSEEAKLKVKFYVPPFLPIIPVVGDYWVLFIDEDYQYALIGQPSRNYLWILSRQPRLDDEIYN
PaTIL         61 G--KRSSIEGTAYKADPSSEEAKLKVKFYVPPFLPIIPVVGDYWVLFIDEDYQYALIGQPSRNYLWILSRQPRLDDEIYN
MtTIL         61 G--KRSYIEGTAYKADPNSDEAKLKVKFYVPPMLPIIPVTGDYWVLHLDHDYHYALIGQPSRNYLWILCRQPHLDEEIYN
VvTIL         62 G--KRSYIEGTAYKADPKSDQAKLKVKFYVPPFLPIIPVVGDYWVLFLDEEYQYALIGQPSRKYLWILCRQTHMDEEIYE
LsTIL         61 G--KRGFIEGTAYKADPKSDEAKLKVKFYVPPFLPIIPVTGDYWVLYLDDDYQYALIGQPSRSYLWILCRQTHLDDEIYN
AtTIL         62 G--KRGFIEGSAYKADPKSDEAKLKVKFYVPPFLPIIPVTGDYWVLYIDPDYQHALIGQPSRSYLWILSRTAQMEEETYK
BnTIL         63 G--KRGFIQGSAFKTDPKSDEAKFKVRFYVPPFLPIIPVTGDYWVLYIDPEYQHAVIGQPSRSYLWILSRTAHVEEETYK
LeTIL         61 G--KRGFIEGTAYKADPNSDEAKLKVRFYVPPFLPIIPVTGDYWVLYIDEDYQYALIGQPSRRYLWILSRQTRLDDEIYN
StTIL’        61 G--KRGFIEGTAYKADPNSDEAKLKVRFYVPPFLPIIPVTGDYWVLYIDEDYQYALIGQPSRRYLWILSRRTCLDDEIYN
LeTIL’        61 G--KRGSIEGTAYKADPKSDEAKLKVKFYIPPFLPIIPIVGDYWVLYIDDDYQYALIGQPSKKYLWILCRQPHLDEEIYN
StTIL         61 G--KRGSIEGTAYKVDPKSDEAKLKVKFYIPPFLPIIPIVGDYWVLYIDDDYQYALIGQPSKKYLWILCRQPHLDEEIYN
GaTIL         61 G--KRGFIEGTAYKADPQSDEAKLKVKFYVPPFLPIIPIVGDYWVLHLDDDYQYALIGQPSRNYLWVLCRQTHMDDEIYN
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PotxPotrTIL   62 G--KRGSIEGSAYKADPNSDEAKLKVKFYVPPFLPIIPVVGDYWILYLDDDYQYALIGQPSRSSLWILCRKTHMEDEIYN
PotTIL        62 G--KRGSIEGSAYKADPNSDEAKLKVKFYVPPFLPIIPVVGDYWILYLDDDYQYALIGQPSRSYLWILCRKTHMEDEIYN
PbTIL         62 G--KRGYIEGSAYKADPNSDEAKLKVKFYVPPFLPIIPVVGDYWVLSLDEDYQYALIGQASRKYLWILCRKTHMEDDIYN
MtTIL’        64 G--KRTSIEGSAYKADPKSDEAKLKVKFYVPPFLPIIPAVGDYWILYLDEDYQYALIGGPTNKFLWILSRQPHLDETIYN
CsTIL         62 G--KRGSIEGTAYKADPKSDEAKLKVKFYVPPFFPIIPVVGNYWVLYIDDNYQYALIGEPTRKYLWILCREPHMDEAIYN
GaTIL’        56 G--KKDSIEGTAYKADPKSDEAKLKVKFYVPPFLPIIPVTGDYWVLYIDEDYQYVLVGGPTKKYLWILCRQKHMDEEIYN
PtTIL         61 G--KKSSIEGSAYKVDPKSEDAKFKVKFMVPPFFPIIPVYGNYWVLLLDEDYQWALIGEPSLKYLWVLCRQRQLDEAIYN
PpTIL         62 G--KRSYIEGKAWKADAASPDAKLKVRFLVPPFFPIFPVTGDYWVMKLDENYQWALIGQPSRRYLWVLSRTPELSDEIYN
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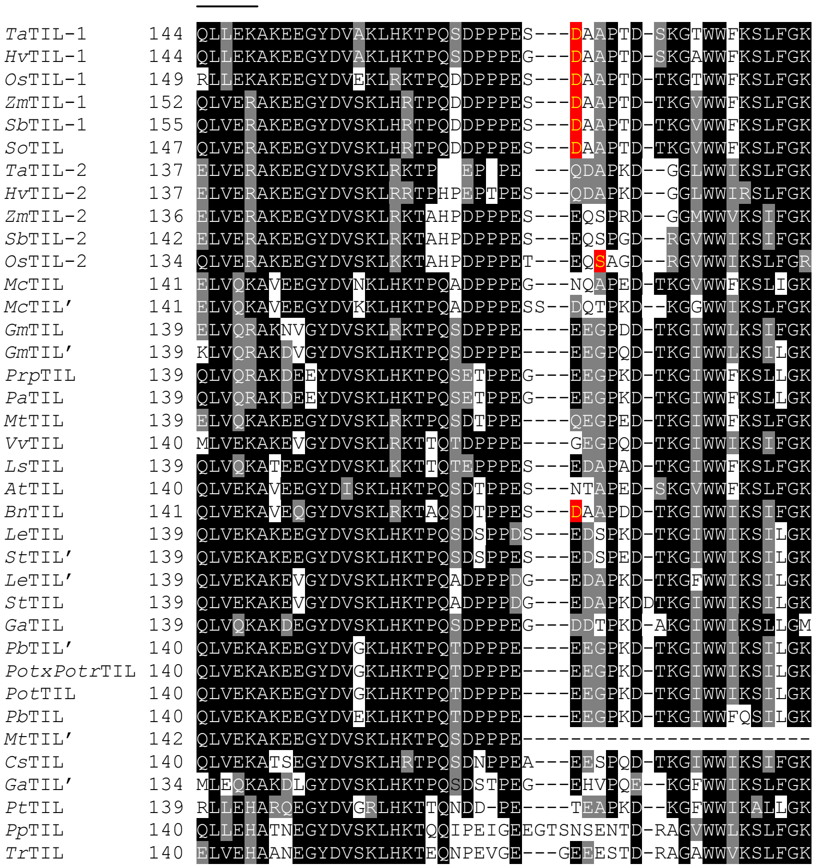

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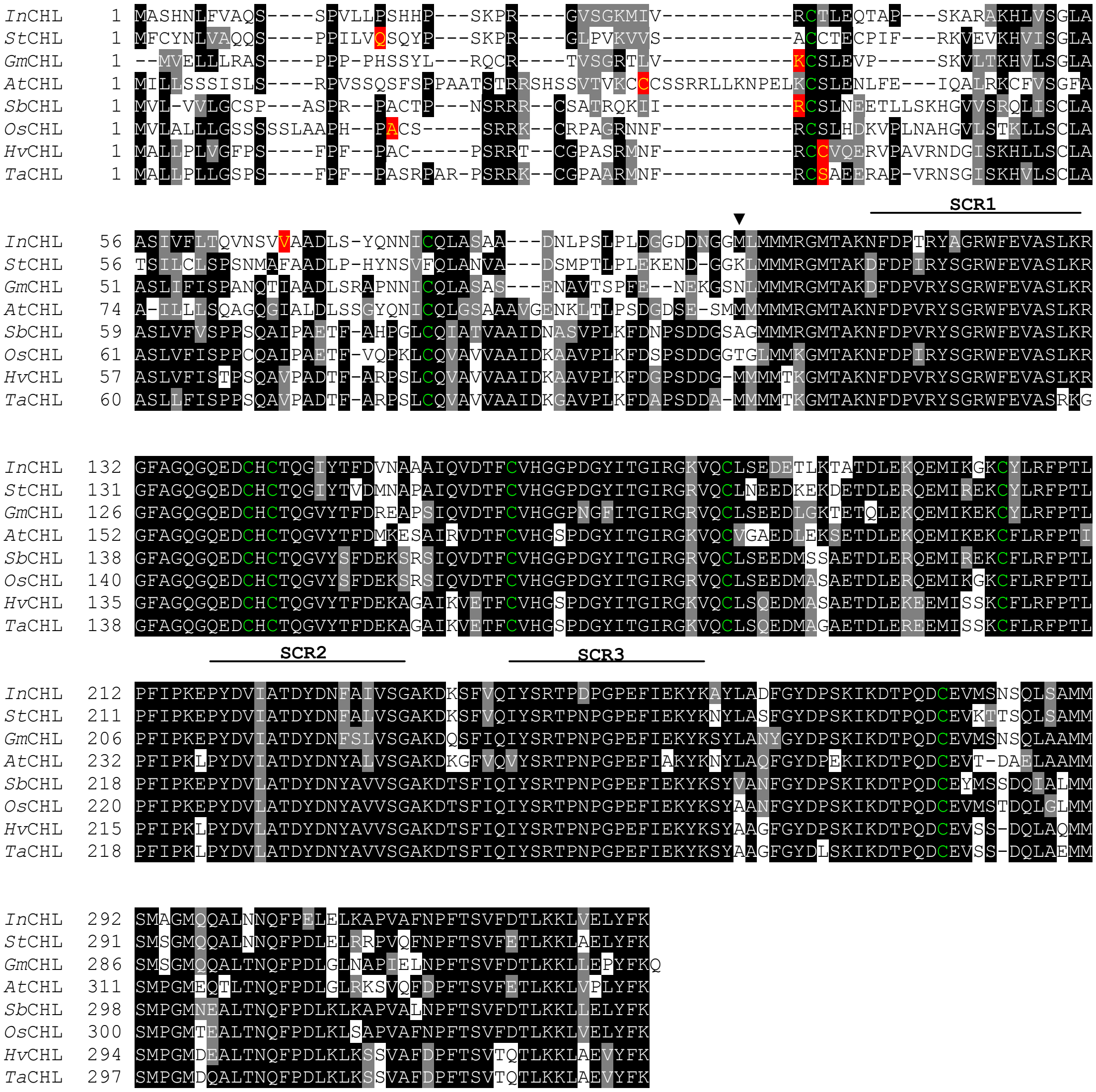
OsTIL-1      149 RLLEKAKEEGYDVEKLRKTPQDDPPPES---DAAPTD-TKGTWWFKSLFGK
ZmTIL-1      152 QLVERAKEEGYDVSKLHRTPQDDPPPES---DAAPTD-TKGVWWFKSLFGK
SbTIL-1      155 QLVERAKEEGYDVSKLHRTPQDDPPPES---DAAPTD-TKGVWWFKSLFGK
SoTIL        147 QLVERAKEEGYDVSKLHRTPQDDPPPES---DAAPTD-TKGVWWFKSLFGK
TaTIL-2      137 ELVERAKEEGYDVSKLRKTP  EP PE ---QDAPKD--GGLWWIKSLFGK
HvTIL-2      137 ELVERAKEEGYDVSKLRRTPHPEPTPES---QDAPKD--GGLWWIRSLFGK
ZmTIL-2      136 ELVERAKEEGYDVSKLRKTAHPDPPPES---EQSPRD--GGMWWVKSIFGK
SbTIL-2      142 ELVERAKEEGYDVSKLRKTAHPDPPPES---EQSPGD--RGVWWIKSIFGK
OsTIL-2      134 QLVERAKEEGYDVSKLKKTAHPDPPPET---EQSAGD--RGVWWIKSLFGR
McTIL        141 ELVQKAVEEGYDVNKLHKTPQADPPPEG---NQAPED-TKGVWWFKSLIGK
McTIL’       141 ELVQKAVEEGYDVKKLHKTPQADPPPESS--DQTPKD--KGGWWIKSLFGK
GmTIL        139 ELVQRAKNVGYDVSKLRKTPQSDPPPE----EEGPDD-TKGIWWLKSIFGK
GmTIL’       139 KLVQRAKDVGYDVSKLHKTPQSDPPPE----EEGPQD-TKGIWWLKSILGK
PrpTIL       139 QLVQRAKDEEYDVSKLHKTPQSETPPEG---EEGPKD-TKGIWWFKSLLGK
PaTIL        139 QLVQRAKDEEYDVSKLHKTPQSETPPEG---EEGPKD-TKGIWWFKSLLGK
MtTIL        139 ELVQKAKEEGYDVSKLRKTPQSDTPPE----QEGPED-TKGIWWFKSLFGK
VvTIL        140 MLVEKAKEVGYDVSKLRKTTQTDPPPE----GEGPQD-TKGIWWIKSIFGK
LsTIL        139 QLVQKATEEGYDVSKLKKTTQTEPPPES---EDAPAD-TKGIWWFKSLFGK
AtTIL        140 QLVEKAVEEGYDISKLHKTPQSDTPPES---NTAPED-SKGVWWFKSLFGK
BnTIL        141 QLVEKAVEQGYDVSKLRKTAQSDTPPES---DAAPDD-TKGIWWIKSIFGK
LeTIL        139 QLVEKAKEEGYDVSKLHKTPQSDSPPDS---EDSPKD-TKGIWWIKSILGK
StTIL’       139 QLVEKAKEEGYDVSKLHKTPQSDSPPES---EDSPED-TKGIWWIKSILGK
LeTIL’       139 QLVEKAKEVGYDVSKLHKTPQADPPPDG---EDAPKD-TKGFWWIKSILGK
StTIL        139 QLVEKAKEVGYDVSKLHKTPQADPPPDG---EDAPKDDTKGIWWIKSILGK
GaTIL        139 QLVQKAKDEGYDVSKLHKTPQSDPPPEG---DDTPKD-AKGIWWIKSLLGM
PbTIL’       140 QLVEKAKEEGYDVGKLHKTPQTDPPPE----EEGPKD-TKGIWWIKSILGK
PotxPotrTIL  140 QLVEKAKEEGYDVGKLHKTPQTDPPPE----EEGPKD-TKGIWWIKSILGK
PotTIL       140 QLVEKAKEEGYDVGKLHKTPQTDPPPE----EEGPKD-TKGIWWIKSILGK
PbTIL        140 QLVEKAKEEGYDVEKLHKTPQTDPPPE----EEGPKD-TKGIWWFQSILGK
MtTIL’       142 QLVEKAKEEGYDVSKLHKTPQSDPPPE-----------------------
CsTIL        140 QLVEKATSEGYDVSKLHRTPQSDNPPEA---EESPQD-TKGIWWIKSIFGK
GaTIL’       134 MLEQKAKDLGYDVSKLHKTPQSDSTPEG---EHVPQE--KGFWWIKSLFGK
PtTIL        139 RLLEHARQEGYDVGRLHKTTQNDD-PE----TEAPKD--KGFWWIKALLGK
PpTIL        140 QLLEHATNEGYDVSKLHKTQQIPEIGEEGTSNSENTD-RAGVWWLKSLFGK
TrTIL        140 ELVEHAANEGYDVSKLHKTEQNPEVGE---GEEESTD-RAGAWWVKSLFGK
```

Supplemental Figure 1. Alignment of the deduced amino acid sequences of TIL lipocalins. Identical residues are in black and similar residues are in grey. The three SCRs that provide a signature for the lipocalins are indicated above. Conserved N-glycosylation sites are in pink. Putative cleavage sites with a DGPI score over 0.700 are in red with yellow letters.



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StCHL    1 MFCYNLVAQQS----PPILVQSQYP---SKPR----GLPVKVVS-----------ACCTECPIF---RKVEVKHVISGLA
GmCHL    1 --MVELLLRAS----PPP-PHSSYL---RQCR----TVSGRTLV-----------KCSLEVP-----SKVLTKHVLSGLA
AtCHL    1 MILLSSSISLS----RPVSSQSFSPPAATSTRRSHSSVTVKCCCSSRRLLKNPELKCSLENLFE---IQALRKCFVSGFA
SbCHL    1 MVL-VVLGCSP---ASPR--PACTP---NSRRR--CSATRQKII-----------RCSLNEETLLSKHGVVSRQLISCLA
OsCHL    1 MVLALLLGSSSSSLAAPH--PACS-----SRRK--CRPAGRNNF-----------RCSLHDKVPLNAHGVLSTKLLSCLA
HvCHL    1 MALLPLVGFPS----FPF--PAC-----PSRRT--CGPASRMNF-----------RCCVQERVPAVRNDGISKHLLSCLA
TaCHL    1 MALLPLLGSPS----FPF--PASRPAR-PSRRK--CGPAARMNF-----------RCSAEERAP-VRNSGISKHVLSCLA

                                                                ▼             SCR1
InCHL   56 ASIVFLTQVNSVVAADLS-YQNNICQLASAA---DNLPSLPLDGGDDNGGMLMMMRGMTAKNFDPTRYAGRWFEVASLKR
StCHL   56 TSILCLSPSNMAFAADLP-HYNSVFQLANVA---DSMPTLPLEKEND-GGKLMMMRGMTAKDFDPIRYSGRWFEVASLKR
GmCHL   51 ASLIFISPANQTIAADLSRAPNNICQLASAS---ENAVTSPFE--NEKGSNLMMMRGMTAKDFDPVRYSGRWFEVASLKR
AtCHL   74 A-ILLLSQAGQGIALDLSSGYQNICQLGSAAAVGENKLTLPSDGDSE-SMMMMMMRGMTAKNFDPVRYSGRWFEVASLKR
SbCHL   59 ASLVFVSPPSQAIPAETF-AHPGLCQIATVAAIDNASVPLKFDNPSDDGSAGMMMRGMTAKNFDPVRYSGRWFEVASLKR
OsCHL   61 ASLVFISPPCQAIPAETF-VQPKLCQVAVVAAIDKAAVPLKFDSPSDDGGTGLMMKGMTAKNFDPIRYSGRWFEVASLKR
HvCHL   57 ASLVFISTPSQAVPADTF-ARPSLCQVAVVAAIDKAAVPLKFDGPSDDG-MMMMTKGMTAKNFDPVRYSGRWFEVASLKR
TaCHL   60 ASLLFISPPSQAVPADTF-ARPSLCQVAVVAAIDKGAVPLKFDAPSDDA-MMMMTKGMTAKNFDPVRYSGRWFEVASRKG

InCHL  132 GFAGQGQEDCHCTQGIYTFDVNAAAIQVDTFCVHGGPDGYITGIRGKVQCLSEDETLKTATDLEKQEMIKGKCYLRFPTL
StCHL  131 GFAGQGQEDCHCTQGIYTVDMNAPAIQVDTFCVHGGPDGYITGIRGRVQCLNEEDKEKDETDLERQEMIREKCYLRFPTL
GmCHL  126 GFAGQGQEDCHCTQGVYTFDREAPSIQVDTFCVHGGPNGFITGIRGRVQCLSEEDLGKTETQLEKQEMIKEKCYLRFPTL
AtCHL  152 GFAGQGQEDCHCTQGVYTFDMKESAIRVDTFCVHGSPDGYITGIRGKVQCVGAEDLEKSETDLEKQEMIKEKCFLRFPTI
SbCHL  138 GFAGQGQEDCHCTQGVYSFDEKSRSIQVDTFCVHGGPDGYITGIRGRVQCLSEEDMSSAETDLERQEMIREKCFLRFPTL
OsCHL  140 GFAGQGQEDCHCTQGVYSFDEKSRSIQVDTFCVHGGPDGYITGIRGRVQCLSEEDMASAETDLERQEMIKGKCFLRFPTL
HvCHL  135 GFAGQGQEDCHCTQGVYTFDEKAGAIKVETFCVHGSPDGYITGIRGKVQCLSQEDMASAETDLEKEEMISSKCFLRFPTL
TaCHL  138 GFAGQGQEDCHCTQGVYTFDEKAGAIKVETFCVHGSPDGYITGIRGKVQCLSQEDMAGAETDLEREEMISSKCFLRFPTL
                  SCR2                SCR3

InCHL  212 PFIPKEPYDVIATDYDNFAIVSGAKDKSFVQIYSRTPDPGPEFIEKYKAYLADFGYDPSKIKDTPQDCEVMSNSQLSAMM
StCHL  211 PFIPKEPYDVIATDYDNFALVSGAKDKSFVQIYSRTPNPGPEFIEKYKNYLASFGYDPSKIKDTPQDCEVKTTSQLSAMM
GmCHL  206 PFIPKEPYDVIATDYDNFSLVSGAKDQSFIQIYSRTPNPGPEFIEKYKSYLANYGYDPSKIKDTPQDCEVMSNSQLAAMM
AtCHL  232 PFIPKLPYDVIATDYDNYALVSGAKDKGFVQVYSRTPNPGPEFIAKYKNYLAQFGYDPEKIKDTPQDCEVT-DAELAAMM
SbCHL  218 PFIPKEPYDVLATDYDNYAVVSGAKDTSFIQIYSRTPNPGPEFIEKYKSYVANFGYDPSKIKDTPQDCEYMSSDQIALMM
OsCHL  220 PFIPKEPYDVLATDYDNYAVVSGAKDTSFIQIYSRTPNPGPEFIEKYKSYAANFGYDPSKIKDTPQDCEVMSTDQLGLMM
HvCHL  215 PFIPKLPYDVLATDYDNYAVVSGAKDTSFIQIYSRTPNPGPEFIEKYKSYAAGFGYDPSKIKDTPQDCEVSS-DQLAQMM
TaCHL  218 PFIPKLPYDVLATDYDNYAVVSGAKDTSFIQIYSRTPNPGPEFIEKYKSYAAGFGYDLSKIKDTPQDCEVSS-DQLAEMM

InCHL  292 SMAGMQQALNNQFPELELKAPVAFNPFTSVFDTLKKLVELYFK
StCHL  291 SMSGMQQALNNQFPDLELRRPVQFNPFTSVFETLKKLAELYFK
GmCHL  286 SMSGMQQALTNQFPDLGLNAPIELNPFTSVFDTLKKLLEPYFKQ
AtCHL  311 SMPGMEQTLTNQFPDLGLRKSVQFDPFTSVFETLKKLVPLYFK
SbCHL  298 SMPGMNEALTNQFPDLKLKAPVALNPFTSVFDTLKKLLELYFK
OsCHL  300 SMPGMTEALTNQFPDLKLSAPVAFNPFTSVFDTLKKLVELYFK
HvCHL  294 SMPGMDEALTNQFPDLKLKSSVAFDPFTSVTQTLKKLAEVYFK
TaCHL  297 SMPGMDQALTNQFPDLKLKSSVAFDPFTSVTQTLKKLAEVYFK
```
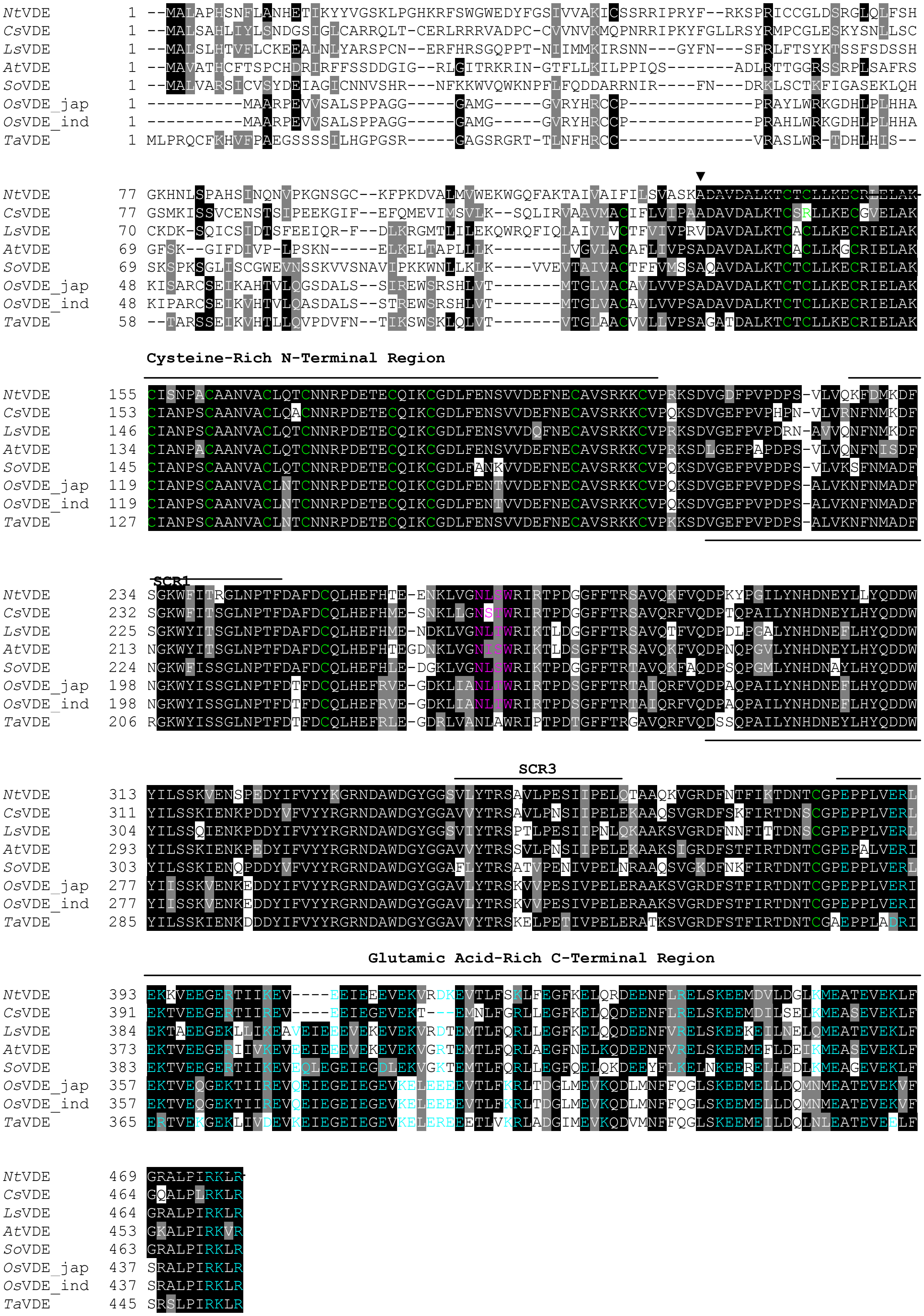

Supplemental Figure 2. Alignment of the deduced amino acid sequences of CHL lipocalins. Identical residues are in black and similar residues are in grey. The three SCRs that provide a signature for the lipocalins are indicated above. Conserved cysteine residues are in green. Putative chloroplastic transit peptide cleavage sites identified with Signal P / ChloroP software are in red with yellow letters. The triangle indicates the putative chloroplastic transit peptide cleavage site based on sequence comparison.



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LsVDE          1 --MALSLHTVFLCKEEALNLYARSPCN--ERFHRSGQPPT-NIIMMKIRSNN---GYFN---SFRLFTSYKTSSFSDSSH
AtVDE          1 --MAVATHCFTSPCHDRIRFFSSDDGIG--RLGITRKRIN-GTFLLKILPPIQS-------ADLRTTGGRSSRPLSAFRS
SoVDE          1 --MALVARSICVSYDEIAGICNNVSHR---NFKKWVQWKNPFLFQDDARRNIR----FN---DRKLSCTKFIGASEKLQH
OsVDE_jap      1 ----------MAARPEVVSALSPPAGG-----GAMG-----GVRYHRCCP-------------PRAYLWRKGDHLPLHHA
OsVDE_ind      1 ----------MAARPEVVSALSPPAGG-----GAMG-----GVRYHRCCP-------------PRAHLWRKGDHLPLHHA
TaVDE          1 MLPRQCFKHVFPAEGSSSSILHGPGSR-----GAGSRGRT-TLNFHRCC--------------VRASLWR-TDHLHIS--

                                                                          ▼
NtVDE         77 GKHNLSPAHSINQNVPKGNSGC--KFPKDVALMVWEKWGQFAKTAIVAIFILSVASKADAVDALKTCTCLLKECRLELAK
CsVDE         77 GSMKISSVCENSTSIPEEKGIF--EFQMEVIMSVLK--SQLIRVAAVMACIFLVIPAADAVDALKTCSRLLKECGVELAK
LsVDE         70 CKDK-SQICSIDTSFEEIQR-F--DLKRGMTLILEKQWRQFIQLAIVLVCTFVIVPRVDAVDALKTCACLLKECRIELAK
AtVDE         69 GFSK--GIFDIVP-LPSKN-----ELKELTAPLLLK-------LVGVLACAFLIVPSADAVDALKTCACLLKGCRIELAK
SoVDE         69 SKSPKSGLISCGWEVNSSKVVSNAVIPKKWNLLKLK----VVEVTAIVACTFFVMSSAQAVDALKTCTCLLKECRIELAK
OsVDE_jap     48 KISARCSEIKAHTVLQGSDALS--SIREWSRSHLVT-------MTGLVACAVLVVPSADAVDALKTCTCLLKECRIELAK
OsVDE_ind     48 KIPARCSEIKVHTVLQASDALS--STREWSRSHLVT-------MTGLVACAVLVVPSADAVDALKTCTCLLKECRIELAK
TaVDE         58 --TARSSEIKVHTLLQVPDVFN--TIKSWSKLQLVT-------VTGLAACVVLLVPSAGATDALKTCTCLLKECRIELAK

                 Cysteine-Rich N-Terminal Region

NtVDE        155 CISNPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDVGDFPVPDPS-VLVQKFDMKDF
CsVDE        153 CIANPSCAANVACLQACNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPQKSDVGEFPVPHPN-VLVRNFNMKDF
LsVDE        146 CIANPSCAANVACLQTCNNRPDETECQIKCGDLFENSVVDQFNECAVSRKKCVPRKSDVGEFPVPDRN-AVVQNFNMKDF
AtVDE        134 CIANPACAANVACLQTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPRKSDLGEFPAPDPS-VLVQNFNISDF
SoVDE        145 CIANPSCAANVACLQTCNNRPDETECQIKCGDLFANKVVDEFNECAVSRKKCVPQKSDVGEFPVPDPS-VLVKSFNMADF
OsVDE_jap    119 CIANPSCAANVACLNTCNNRPDETECQIKCGDLFENTVVDEFNECAVSRKKCVPQKSDVGEFPVPDPS-ALVKNFNMADF
OsVDE_ind    119 CIANPSCAANVACLNTCNNRPDETECQIKCGDLFENTVVDEFNECAVSRKKCVPQKSDVGEFPVPDPS-ALVKNFNMADF
TaVDE        127 CIANPSCAANVACLNTCNNRPDETECQIKCGDLFENSVVDEFNECAVSRKKCVPKKSDVGEFPVPDPS-ALVKNFNMADF

                  SCR1
NtVDE        234 SGKWFITRGLNPTFDAFDCQLHEFHTE-ENKLVGNLSWRIRTPDGGFFTRSAVQKFVQDPKYPGILYNHDNEYLLYQDDW
CsVDE        232 SGKWFITSGLNPTFDAFDCQLHEFHME-SNKLLGNSTWRIRTPDGGFFTRSAVQRFVQDPTQPAILYNHDNEYLHYQDDW
LsVDE        225 SGKWYITSGLNPTFDAFDCQLHEFHME-NDKLVGNLTWRIKTLDGGFFTRSAVQTFVQDPDLPGALYNHDNEFLHYQDDW
AtVDE        213 NGKWYITSGLNPTFDAFDCQLHEFHTEGDNKLVGNISWRIKTLDSGFFTRSAVQKFVQDPNQPGVLYNHDNEYLHYQDDW
SoVDE        224 NGKWFISSGLNPTFDAFDCQLHEFHLE-DGKLVGNLSWRIKTPDGGFFTRTAVQKFAQDPSQPGMLYNHDNAYLHYQDDW
OsVDE_jap    198 NGKWYISSGLNPTFDTFDCQLHEFRVE-GDKLIANLTWRIRTPDSGFFTRTAIQRFVQDPAQPAILYNHDNEFLHYQDDW
OsVDE_ind    198 NGKWYISSGLNPTFDTFDCQLHEFRVE-GDKLIANLTWRIRTPDSGFFTRTAIQRFVQDPAQPAILYNHDNEFLHYQDDW
TaVDE        206 RGKWYISSGLNPTFDTFDCQLHEFRLE-GDRLVANLAWRIPTPDTGFFTRGAVQRFVQDSSQPAILYNHDNEYLHYQDDW

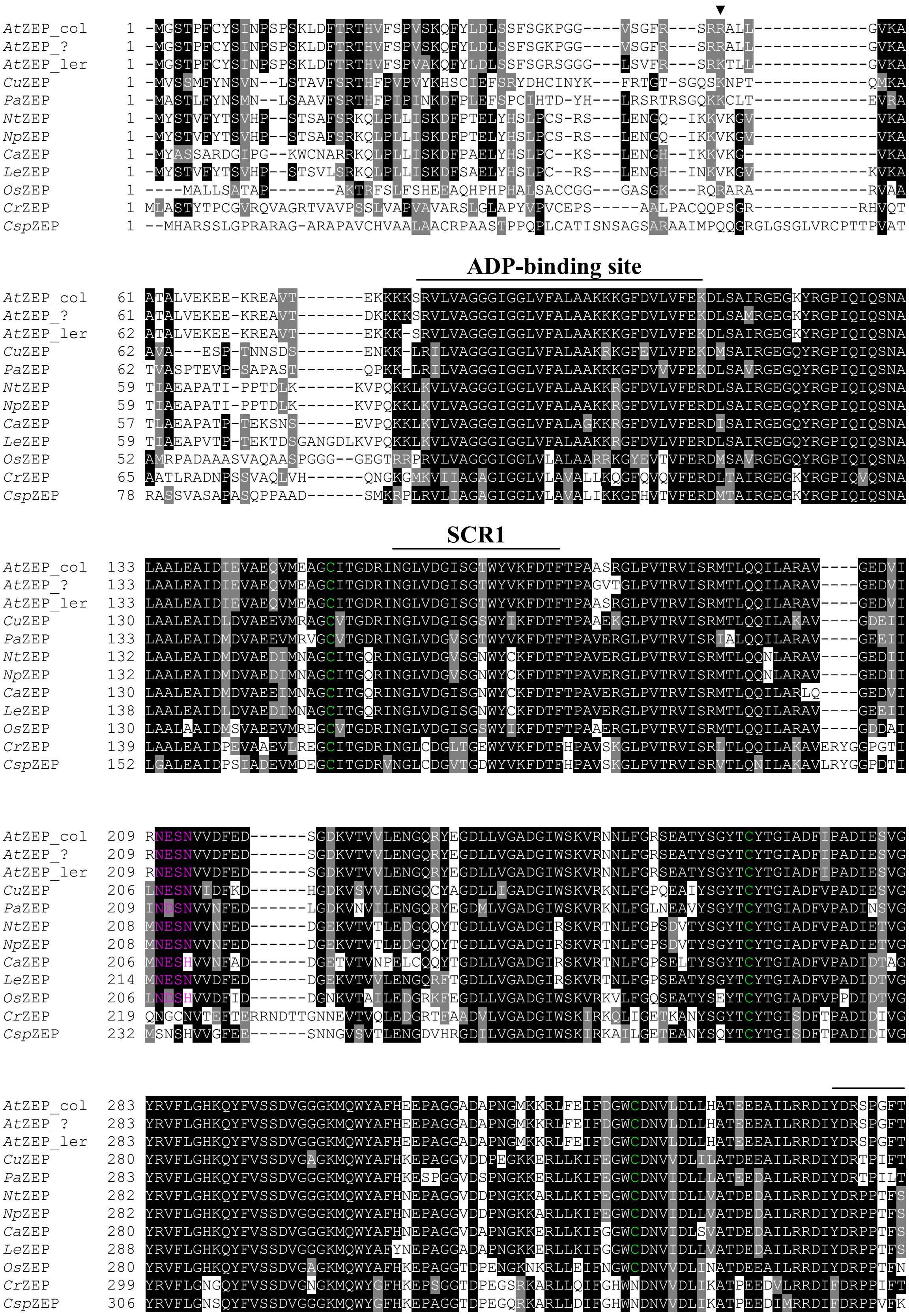
                                                   SCR3
NtVDE        313 YILSSKVENSPEDYIFVYYKGRNDAWDGYGGSVLYTRSAVLPESIIPELQTAAQKVGRDFNTFIKTDNTCGPEPPLVERL
CsVDE        311 YILSSKIENKPDDYVFVYYRGRNDAWDGYGGAVVYTRSAVLPNSIIPELEKAAQSVGRDFSKFIRTDNSCGPEPPLVERL
LsVDE        304 YILSSQIENKPDDYIFVYYRGRNDAWDGYGGSVIYTRSPTLPESIIPNLQKAAKSVGRDFNNFITTDNSCGPEPPLVERL
AtVDE        293 YILSSKIENKPEDYIFVYYRGRNDAWDGYGGAVVYTRSSVLPNSIIPELEKAAKSIGRDFSTFIRTDNTCGPEPALVERI
SoVDE        303 YILSSKIENQPDDYVFVYYRGRNDAWDGYGGAFLYTRSATVPENIVPELNRAAQSVGKDFNKFIRTDNTCGPEPPLVERL
OsVDE_jap    277 YIISSKVENKEDDYIFVYYRGRNDAWDGYGGAVLYTRSKVVPESIVPELERAAKSVGRDFSTFIRTDNTCGPEPPLVERI
OsVDE_ind    277 YIISSKVENKEDDYIFVYYRGRNDAWDGYGGAVLYTRSKVVPESIVPELERAAKSVGRDFSTFIRTDNTCGPEPPLVERI
TaVDE        285 YILSSKIENKDDDYIFVYYRGRNDAWDGYGGAVVYTRSKELPETIVPELERATKSVGRDFSTFIRTDNTCGAEPPLADRI

                                         Glutamic Acid-Rich C-Terminal Region

NtVDE        393 EKKVEEGERTIIKEV----EEIEEEVEKVRDKEVTLFSKLFEGFKELQRDEENFLRELSKEEMDVLDGLKMEATEVEKLF
CsVDE        391 EKTVEEGERTIIREV----EEIEGEVEKT---EMNLFGRLLEGFKELQQDEENFLRELSKEEMDILSELKMEASEVEKLF
LsVDE        384 EKTAEEGEKLLIKEAVEIEEEVEKEVEKVRDTEMTLFQRLLEGFKELQQDEENFVRELSKEEKEILNELQMEATEVEKLF
AtVDE        373 EKTVEEGERIIVKEVEEIEEEVEKEVEKVGRTEMTLFQRLAEGFNELKQDEENFVRELSKEEMEFLDEIKMEASEVEKLF
SoVDE        383 EKTVEEGERTIIKEVEQLEGEIEGDLEKVGKTEMTLFQRLLEGFQELQKDEEYFLKELNKEERELLEDLKMEAGEVEKLF
OsVDE_jap    357 EKTVEQGEKTIIREVQEIEGEIEGEVKELEEEEVTLFKRLTDGLMEVKQDLMNFFQGLSKEEMELLDQMNMEATEVEKVF
OsVDE_ind    357 EKTVEQGEKTIIREVQEIEGEIEGEVKELEEEEVTLFKRLTDGLMEVKQDLMNFFQGLSKEEMELLDQMNMEATEVEKVF
TaVDE        365 ERTVEKGEKLIVDEVKEIEGEIEGEVKELEREEETLVKRLADGIMEVKQDVMNFFQGLSKEEMEILDQLNLEATEVEELF

NtVDE        469 GRALPIRKLR
CsVDE        464 GQALPLRKLR
LsVDE        464 GRALPIRKLR
AtVDE        453 GKALPIRKVR
SoVDE        463 GRALPIRKLR
OsVDE_jap    437 SRALPIRKLR
OsVDE_ind    437 SRALPIRKLR
TaVDE        445 SRSLPIRKLR
```

Supplemental Figure 3. Alignment of the deduced amino acid sequences of VDE proteins. Identical residues are in black and similar residues are in grey. The SCRs that provide a signature for the lipocalins, the cysteine-rich N-terminal region and the glutamic acid-rich C-terminal region are indicated above. Conserved N-glycosylation sites are in pink. Conserved cysteine residues are in green. Conserved glutamic acid residues and other charged residues are in turquoise. The triangle indicates the chloroplastic transit peptide cleavage site.



```
                                                                                   ▼
AtZEP_col    1 -MGSTPFCYSINPSPSKLDFTRTHVFSPVSKQFYLDLSSFSGKPGG----VSGFR---SRRALL------------GVKA
AtZEP_?      1 -MGSTPFCYSINPSPSKLDFTRTHVFSPVSKQFYLDLSSFSGKPGG----VSGFR---SRRALL------------GVKA
AtZEP_ler    1 -MGSTPFCYSINPSPSKLDFTRTHVFSPVAKQFYLDLSSFSGRSGGG---LSVFR---SRKTLL------------GVKA
CuZEP        1 -MVSSMFYNSVN--LSTAVFSRTHFPVPVYKHSCIEFSRYDHCINYK---FRTGT-SGQSKNPT------------QMKA
PaZEP        1 -MASTLFYNSMN--LSAAVFSRTHFPIPINKDFPLEFSPCIHTD-YH---LRSRTRSGQKKCLT------------EVRA
NtZEP        1 -MYSTVFYTSVHP--STSAFSRKQLPLLISKDFPTELYHSLPCS-RS---LENGQ--IKKVKGV-------------VKA
NpZEP        1 -MYSTVFYTSVHP--STSAFSRKQLPLLISKDFPTELYHSLPCS-RS---LENGQ--IKKVKGV-------------VKA
CaZEP        1 -MYASSARDGIPG--KWCNARRKQLPLLISKDFPAELYHSLPC--KS---LENGH--IKKVKG--------------VKA
LeZEP        1 -MYSTVFYTSVHP--STSVLSRKQLPLLISKDFSAELYHSLPC--RS---LENGH--INKVKGV------------KVKA
OsZEP        1 ----MALLSATAP-------AKTRFSLFSHEEAQHPHPHALSACCGG---GASGK---RQRARA------------RVAA
CrZEP        1 MLASTYTPCGVRQVAGRTVAVPSSLVAPVAVARSLGLAPYVPVCEPS-----AALPACQQPSGR-----------RHVQT
CspZEP       1 --MHARSSLGPRARAG-ARAPAVCHVAALAACRPAASTPPQPLCATISNSAGSARAAIMPQQGRGLGSGLVRCPTTPVAT

                                              ADP-binding site
AtZEP_col   61 ATALVEKEE-KREAVT-------EKKKKSRVLVAGGGIGGLVFALAAKKKGFDVLVFEKDLSAIRGEGKYRGPIQIQSNA
AtZEP_?     61 ATALVEKEE-KREAVT-------DKKKKSRVLVAGGGIGGLVFALAAKKKGFDVLVFEKDLSAMRGEGKYRGPIQIQSNA
AtZEP_ler   62 ATALVEKEE-KREAVT-------EKKK-SRVLVAGGGIGGLVFALAAKKKGFDVLVFEKDLSAIRGEGKYRGPIQIQSNA
CuZEP       62 AVA---ESP-TNNSDS-------ENKK-LRILVAGGGIGGLVFALAAKRKGFEVLVFEKDMSAIRGEGQYRGPIQIQSNA
PaZEP       62 TVASPTEVP-SAPAST-------QPKK-LRILVAGGGIGGLVFALAAKKKGFDVVVFEKDLSAVRGEGQYRGPIQIQSNA
NtZEP       59 TIAEAPATI-PPTDLK------KVPQKKLKVLVAGGGIGGLVFALAAKKRGFDVLVFERDLSAIRGEGQYRGPIQIQSNA
NpZEP       59 TIAEAPATI-PPTDLK------KVPQKKLKVLVAGGGIGGLVFALAAKKRGFDVLVFERDLSAIRGEGQYRGPIQIQSNA
CaZEP       57 TLAEAPATP-TEKSNS------EVPQKKLKVLVAGGGIGGLVFALAGKKRGFDVLVFERDISAIRGEGQYRGPIQIQSNA
LeZEP       59 TIAEAPVTP-TEKTDSGANGDLKVPQKKLKVLVAGGGIGGLVFALAAKKRGFDVLVFERDLSAIRGEGQYRGPIQIQSNA
OsZEP       52 AMRPADAAASVAQAASPGGG--GEGTRRPRVLVAGGGIGGLVLALAARRKGYEVTVFERDMSAVRGEGQYRGPIQIQSNA
CrZEP       65 AATLRADNPSSVAQLVH------QNGKGMKVIIAGAGIGGLVLAVALLKQGFQVQVFERDLTAIRGEGKYRGPIQVQSNA
CspZEP      78 RASSVASAPASQPPAAD------SMKRPLRVLIAGAGIGGLVLAVALIKKGFHVTVFERDMTAIRGEGKYRGPIQIQSNA

                                        SCR1
AtZEP_col  133 LAALEAIDIEVAEQVMEAGCITGDRINGLVDGISGTWYVKFDTFTPAASRGLPVTRVISRMTLQQILARAV----GEDVI
AtZEP_?    133 LAALEAIDIEVAEQVMEAGCITGDRINGLVDGISGTWYVKFDTFTPAGVTGLPVTRVISRMTLQQILARAV----GEDVI
AtZEP_ler  133 LAALEAIDIEVAEQVMEAGCITGDRINGLVDGISGTWYVKFDTFTPAASRGLPVTRVISRMTLQQILARAV----GEDVI
CuZEP      130 LAALEAIDLDVAEEVMRAGCVTGDRINGLVDGISGSWYIKFDTFTPAAEKGLPVTRVISRMTLQQILAKAV----GDEII
PaZEP      133 LAALEAIDMDVAEEVMRVGCVTGDRINGLVDGVSGTWYVKFDTFTPAVERGLPVTRVISRIALQQILARAV----GEEII
NtZEP      132 LAALEAIDMDVAEDIMNAGCITGQRINGLVDGVSGNWYCKFDTFTPAVERGLPVTRVISRMTLQQNLARAV----GEDII
NpZEP      132 LAALEAIDMDVAEDIMNAGCITGQRINGLVDGVSGNWYCKFDTFTPAVERGLPVTRVISRMTLQQNLARAV----GEDII
CaZEP      130 LAALEAIDMDVAEEIMNAGCITGQRINGLVDGISGNWYCKFDTFTPAVERGLPVTRVISRMTLQQILARLQ----GEDVI
LeZEP      138 LAALEAIDLDVAEDIMNAGCITGQRINGLVDGISGNWYCKFDTFTPAVERGLPVTRVISRMTLQQILARAV----GEEII
OsZEP      130 LAALAAIDMSVAEEVMREGCVTGDRINGLVDGISGSWYIKFDTFTPAAERGLPVTRVISRMTLQQILARAV----GDDAI
CrZEP      139 LAALEAIDPEVAAEVLREGCITGDRINGLCDGLTGEWYVKFDTFHPAVSKGLPVTRVISRLTLQQILAKAVERYGGPGTI
CspZEP     152 LGALEAIDPSIADEVMDEGCITGDRVNGLCDGVTGDWYVKFDTFHPAVSKGLPVTRVISRVTLQNILAKAVLRYGGPDTI

AtZEP_col  209 RNESNVVDFED------SGDKVTVVLENGQRYEGDLLVGADGIWSKVRNNLFGRSEATYSGYTCYTGIADFIPADIESVG
AtZEP_?    209 RNESNVVDFED------SGDKVTVVLENGQRYEGDLLVGADGIWSKVRNNLFGRSEATYSGYTCYTGIADFIPADIESVG
AtZEP_ler  209 RNESNVVDFED------SGDKVTVVLENGQRYEGDLLVGADGIWSKVRNNLFGRSEATYSGYTCYTGIADFIPADIESVG
CuZEP      206 LNESNVIDFKD------HGDKVSVVLENGQCYAGDLLIGADGIWSKVRKNLFGPQEAIYSGYTCYTGIADFVPADIESVG
PaZEP      209 INDSNVVNFED------LGDKVNVILENGQRYEGDMLVGADGIWSKVRKNLFGLNEAVYSGYTCYTGIADFVPADINSVG
NtZEP      208 MNESNVVNFED------DGEKVTVTLEDGQQYTGDLLVGADGIRSKVRTNLFGPSDVTYSGYTCYTGIADFVPADIETVG
NpZEP      208 MNESNVVNFED------DGEKVTVTLEDGQQYTGDLLVGADGIRSKVRTNLFGPSDVTYSGYTCYTGIADFVPADIETVG
CaZEP      206 MNESHVVNFAD------DGETVTVNPELCQQYTGDLLVGADGIRSKVRTNLFGPSELTYSGYTCYTGIADFVPADIDTAG
LeZEP      214 MNESNVVDFED------DGEKVTVVLENGQRFTGDLLVGADGIRSKVRTNLFGPSEATYSGYTCYTGIADFVPADIDTVG
OsZEP      206 LNDSHVVDFID------DGNKVTAILEDGRKFEGDLLVGADGIWSKVRKVLFGQSEATYSEYTCYTGIADFVPPDIDTVG
CrZEP      219 QNGCNVTEFTERRNDTTGNNEVTVQLEDGRTFAADVLVGADGIWSKIRKQLIGETKANYSGYTCYTGISDFTPADIDIVG
CspZEP     232 MSNSHVVGFEE------SNNGVSVTLENGDVHRGDILVGADGIWSKIRKAILGETEANYSQYTCYTGISDFTPADIDIVG

AtZEP_col  283 YRVFLGHKQYFVSSDVGGGKMQWYAFHEEPAGGADAPNGMKKRLFEIFDGWCDNVLDLLHATEEEAILRRDIYDRSPGFT
AtZEP_?    283 YRVFLGHKQYFVSSDVGGGKMQWYAFHEEPAGGADAPNGMKKRLFEIFDGWCDNVLDLLHATEEEAILRRDIYDRSPGFT
AtZEP_ler  283 YRVFLGHKQYFVSSDVGGGKMQWYAFHEEPAGGADAPNGMKKRLFEIFDGWCDNVLDLLHATEEEAILRRDIYDRSPGFT
CuZEP      280 YRVFLGHKQYFVSSDVGAGKMQWYAFHKEPAGGVDDPEGKKERLLKIFEGWCDNVVDLILATDEEAILRRDIYDRTPIFT
PaZEP      283 YRVFLGHKQYFVSSDVGGGKMQWYAFHKESPGGVDSPNGKKERLLKIFEGWCDNVIDLLLATEEDAILRRDIYDRTPILT
NtZEP      282 YRVFLGHKQYFVSSDVGGGKMQWYAFHNEPAGGVDDPNGKKARLLKIFEGWCDNVIDLLVATDEDAILRRDIYDRPPTFS
NpZEP      282 YRVFLGHKQYFVSSDVGGGKMQWYAFHNEPAGGVDDPNGKKARLLKIFEGWCDNVIDLLVATDEDAILRRDIYDRPPTFS
CaZEP      280 YRVFLGHKQYFVSSDVGGGKMQWYAFHNEPAGGVDAPNGKKERLLKIFGGWCDNVIDLSVATDEDAILRRDIYDRPPTFS
LeZEP      288 YRVFLGHKQYFVSSDVGGGKMQWYAFYNEPAGGADAPNGKKERLLKIFGGWCDNVIDLLVATDEDAILRRDIYDRPPTFS
OsZEP      280 YRVFLGHKQYFVSSDVGAGKMQWYAFHKEPAGGTDPENGKNKRLLEIFNGWCDNVVDLINATDEEAILRRDIYDRPPTFN
CrZEP      299 YRVFLGNGQYFVSSDVGNGKMQWYGFHKEPSGGTDPEGSRKARLLQIFGHWNDNVVDLIKATPEEDVLRRDIFDRPPIFT
CspZEP     306 YRVFLGNSQYFVSSDVGGGKMQWYGFHKEPAGGTDPEGQRKARLLDIFGHWNDNVVDLIKATPEEDIMRRDIFDRPPVFK
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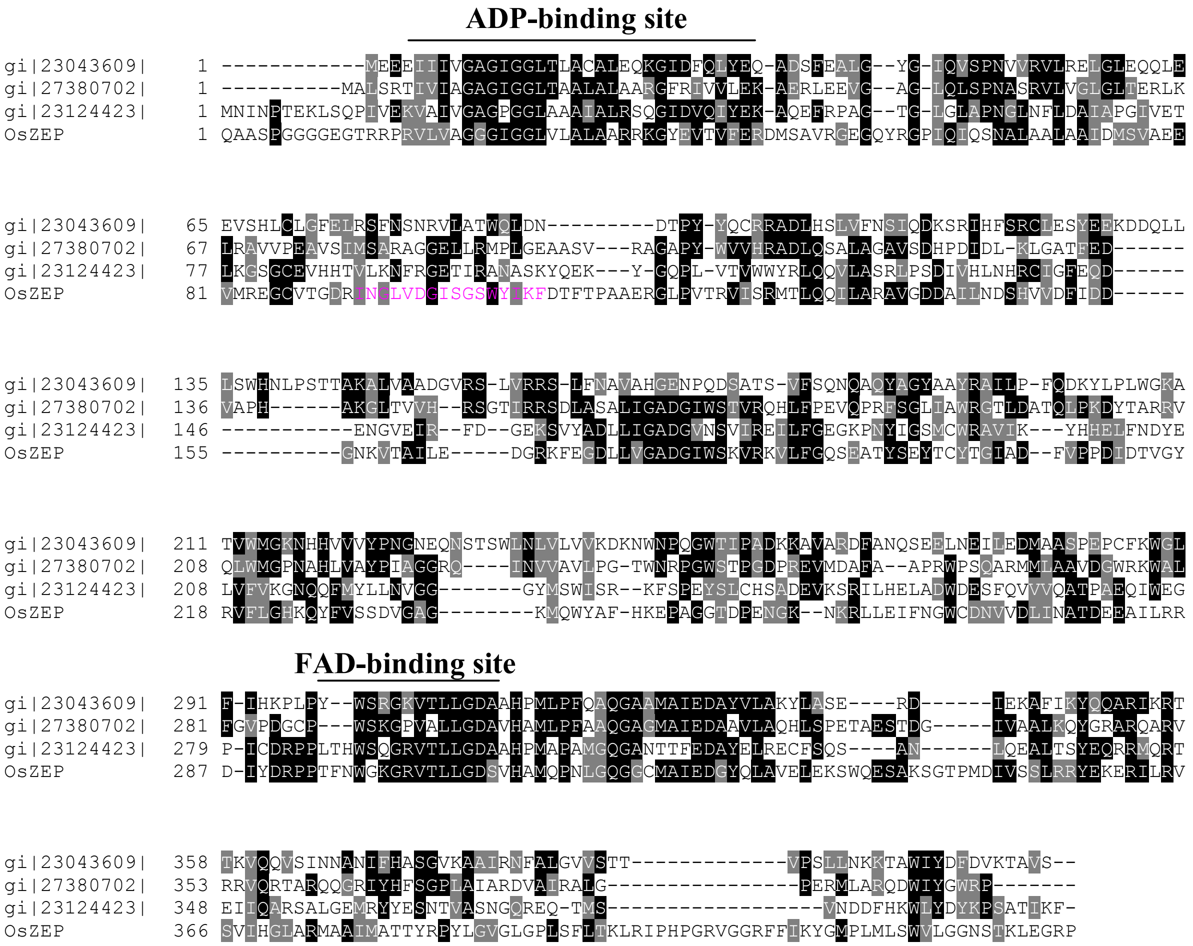
FAD-binding site

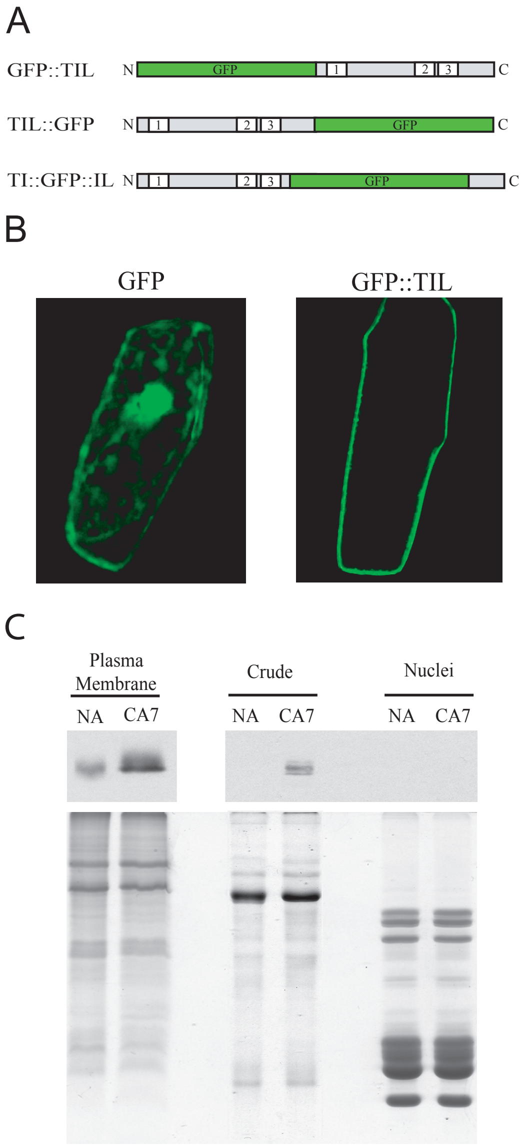
```
AtZEP_col  363 WGKGRVTLLGDSIHAMQPNMGQGGCMAIEDSFQLALELDEAWKQSVETTTPVDVVSSLKRYEESRRLRVAIIHAMARMAA
AtZEP_?    363 WGKGRVTLLGDSIHAMQPNMGQGGCMAIEDSFQLALELDEAWKQSVETTTPVDVVSSLKRYEESRRLRVAIIHAMARMAA
AtZEP_ler  363 WGKGRVTLLGDSIHAMQPNMGQGGCMAIEDSFQLALELDEAWKQSVETTTPVDVVSSLKRYEESRRLRVAIIHAMARMAA
CuZEP      360 WGRGRVTLLGDSVHAMQPNLGQGGCMAIEDGYQLAVELEKACKKSNESKTPIDIVSALKSYERARRLRVAVIHGLARSAA
PaZEP      363 WGKGHVTLLGDSVHAMQPNMGQGGCMAIEDGYQLALELDKAWKKSSETGTPVDVASSLRSYENSRRLRVAIIHGMARMAA
NtZEP      362 WGKGRVTLLGDSVHAMQPNLGQGGCMAIEDSYQLALELDKALSRSAESGTPVDIISSLRSYESSRKLRVGVIHGLARMAA
NpZEP      362 WGKGRVTLLGDSVHAMQPNLGQGGCMAIEDSYQLALELDKALSRSAESGTPVDIISSLRSYESSRKLRVGVIHGLARMAA
CaZEP      360 WGKGRVTLLGDSVHAMQPNLGQGGCMAIEDSYQLALELEKAWSRSAESGSPMDVISSLRSYESARKLRVGVIHGLARMAA
LeZEP      368 WGRGRVTLLGDSVHAMQPNLGQGGCMAIEDSYQLALELEKACSRSAEFGSPVDIISSLRSYESARKLRVGVIHGLARMAA
OsZEP      360 WGKGRVTLLGDSVHAMQPNLGQGGCMAIEDGYQLAVELEKSWQESAKSGTPMDIVSSLRRYEKERILRVSVIHGLARMAA
CrZEP      379 WSKGRVALLGDSAHAMQPNLGQGGCMAIEDAYELAIDLSRAVSDKAGNAAAVDVEGVLRSYQDSRILRVSAIHGMAGMAA
CspZEP     386 WSEGRTVLLGDSVHAMQPNLGQGGCMAIEDAYELANNLSDGMDAAGQQPAHLDVKKAFSTYQSHRMIRASAIHGMAGMAA


AtZEP_col  443 IMASTYKAYLGVGLG-PLSFLTKFRVPHPGRVGGRFFVDIAMPSMLDWVLGGNSEKLQ-GRPPSCRLTDK----ADDRLR
AtZEP_?    443 IMASTYKAYLGVGLG-PLSFLTKFRVPHPGRVGGRFFVDIAMPSMLDWVLGGNSEKLQ-GRPPSCRLTDK----ADDRLR
AtZEP_ler  443 IMASTYKAYLGVGLG-PLSFLTKFRVPHPGRVGGRFFVDIAMPSMLDWVLGGNSEKLQ-GRPPSCRLTDK----ADDRLR
CuZEP      440 VMASTYKAYLGVGLG-PLSFLTKFRIPHPGRVGGRFFIDLAMPLMLSWVLGGNSSKLE-GRSPCCKLSDK----ASDNLR
PaZEP      443 LMASTYKAYLGVGLG-PLSFLTKFRIPHPGRVGGRVFIDKAMPLMLSWVLGGNSSKLE-GRSPSCRLSDK----ASDQLR
NtZEP      442 IMASTYKAYLGVGLG-PLSFLTKFRIPHPGRVGGRFFIDLGMPLMLSWVLGGNGEKLE-GRIQHCRLSEK----ANDQLR
NpZEP      442 IMASTYKAYLGVGLG-PLSFLTKFRIPHPGRVGGRFFIDLGMPLMLSWVLGGNGEKLE-GRIQHCRLSEK----ANDQLR
CaZEP      440 IMASAYKAYLGVGLG-PLSFITKFRIPHPGRVGGRFFIDLGMPLMLSWVLGGNGEKLE-GRIQHCRLSEK----ANDQLR
LeZEP      448 IMASTYKAYLGVGLG-PLSFLTQYRIPHPGRVGGRVFIDLGMPLMLSWVLGGNGDKLE-GRIKHCRLSEK----ANDQLR
OsZEP      440 IMATTYRPYLGVGLG-PLSFLTKLRIPHPGRVGGRFFIKYGMPLMLSWVLGGNSTKLE-GRPLSCRLSDK----ANDQLR
CrZEP      459 FMASTYKCYLGEGWS---KWVEGLRIPHPGRVVGRLVMLLTMPSVLEWVLGGNTDHVAPHRTSYCSLGDKPKAFPESRFP
CspZEP     466 FMASTYKAYLGEGLPGPLQQLTKLKIHHPGRVVGRLVMNLTMPQVLGWVLGGNTENLDKSRVGHCRIADQPKAFHESQFS


AtZEP_col  517 EWFEDDDALERTIKGEWYLIPH---GDDCCV-------SETLCLTKDEDQ-PCIVGSEPDQDFP----------GMRIVI
AtZEP_?    517 EWFEDDDALERTIKGEWYLIPH---GDDCCV-------SETLCLTKDEDQ-PCIVGSEPDQDFP----------GMRIVI
AtZEP_ler  517 EWFEDDDALERTIKGEWYLIPH---GDDCCV-------SETLCLTKDEDQ-PCIVGSEPDQDFP----------GMRIVI
CuZEP      514 TWFRDDDALERAMNGEWFLVPS---GSENVV-------SQPIYLSGSHENEPYLIGSESHEDFP----------RTSIVI
PaZEP      517 NWFEDDDALERAIDGEWYLIPC---GQDNDA-------SQLICLNRDEKN-PCIIGSAPHGDVS----------GISIAI
NtZEP      516 NWFEDDDALERATDAEWLLLPA---GNSNAA-------LETLVLSRDE-NMPCNIGSVSHANIP----------GKSVVI
NpZEP      516 NWFEDDDALERATDAEWLLLPA---GNSNAA-------LETLVLSRDE-NMPCNIGSVSHANIP----------GKSVVI
CaZEP      514 NWFEDDDALERATDAEWLLLPA---GNSNAA-------LETLVLSRDE-NMPCTIGSVSHANIP----------GKSVVI
LeZEP      522 KWFEDDDALERATDAEWLLLPA---GNGSSG-------LEAIVLSRDE-DVPCTVGSISHTNIP----------GKSIVL
OsZEP      514 RWFEDDDALEQAMGGEWYLLPT---SSGD---------SQPIRLIRDEKK-SLSIGSRSDPSNS----------TASLAL
CrZEP      536 EFMNNDASIIRSSHADWLLVAERDAATAAAANVNAATGSSAAAAAAADVNSSCQCKGIYMADSAALVGRCGATSRPALAV
CspZEP     546 YLMENDEAIIQSSHADWMLMTSREAGSGSSD-------SNARVDATADATSTSECKGIYIGDEPSIIGRK--SESADLSI


AtZEP_col  576 PSSQVSKMHARVIY------------------KDGA----------------FFLMDLRSEHGTYVTDNEGRRYRATPNF
AtZEP_?    576 PSSQVSKMHARVIY------------------KDGA----------------FFLMDLRSEHGTYVTDNEGRRYRATPNF
AtZEP_ler  576 PSSQVSKMHARVIY------------------KDGA----------------FFLMDLRSEHGTYVTDNEGRRYRATPNF
CuZEP      574 PSAQVSKMHARISY------------------KDGA----------------FYLIDLQSEHGTYVTDNEGRRYRVSSNF
PaZEP      576 PKPQVSEMHARISY------------------KDGA----------------FYLTDLRSEHGTWIADIEGKRYRVPPNF
NtZEP      575 PLPQVSEMHARISY------------------KGGA----------------FFVTDLRSEHGTWITDNEGRRYRASPNF
NpZEP      575 PLPQVSEMHARISY------------------KGGA----------------FFVTDLRSEHGTWITDNEGRRYRASPNF
CaZEP      573 PLSQVSDMHARISY------------------NGGA----------------FLGTAFRSDHGTWFIDNEGRRYRVSPNF
LeZEP      581 PLPQVSEMHARISC------------------KDGA----------------FFVTDLRSEHGTWVTDNEGRRYRTSPNF
OsZEP      571 PLPQISENHATITC------------------KNKA----------------FYVTDNGSEHGTWITDNEGRRYRRTSEL
CrZEP      616 DDVHVAESHAQVWRGLAGLPPSSSSASTAAASASAASSAASGTASTLGSSEGYWLRDLGSGRGTWVN---GK--RLPDGA
CspZEP     617 NDGQVAPQHARVWR-------------TETSSVSGRDVVAY----------EYHVQDLGSDAGTWLN---GR--PMPRGG


AtZEP_col   622 PARFRSSDIIEFGSD-KKAAFRVKVIRKTPKSTRKNESNNDKLLQTA---------------------------
AtZEP_?     622 PARFRSSDIIEFGSD-KKAAFRVKVIRKTPKSTRKNESNNDKLLQTA---------------------------
AtZEP_ler   622 PARFRSSDIIEFGSD-KKAAFRVKVIRKTPKSTRKNESNNDKLLQTA---------------------------
CuZEP       620 PARFRPSDTIEFGSD-KKAIFRVKVIGTPPNNN-SERKEAGEILQAV---------------------------
PaZEP       622 PARFRPSDAIEIGS--QKVAFRVKVMKSSPG---SVEKEG--ILQAA---------------------------
NtZEP       621 PTRFHPSDIIEFGSD-KKAAFRVKVMKFPPKTAAK-EERQ--AVGAA---------------------------
NpZEP       621 PTRFHPSDIIEFGSD-KKAAFRVKVMKFPPKTAAK-EERQ--AVGAA---------------------------
CaZEP       619 PMRFHSSDVIVFGSD-K-AAFRIKAMKFAPKTAAK-EDRQ--AVGAA---------------------------
LeZEP       627 PTRFHPSDVIEFGSD-K-AAFRVKAMKFPLKTSERKEERE--AVEAA---------------------------
OsZEP       617 PCPF-PS----LGCH-----------------------------------------------------------
CrZEP       691 TVQLWPGDAVEFGRHPSHEVFKVKMQHVTLRSDELSGQAYTTLMVGKIRNN-DYVMPESRPDGGSQQPGRLVTA
CspZEP      669 TCQLHAGDVLEFGQSPSKEVYRVKMQHVSLRNDKLNGHAFTTLVVGAHEGHGDKHMIMA---------------
```

Supplemental Figure 4. Alignment of the deduced amino acid sequences of ZEP proteins. Identical residues are in black and similar residues are in grey. The SCRs that provide a signature for the lipocalins and other conserved motifs are indicated above. Conserved N-glycosylation sites are in pink. Conserved cysteine residues are in green. The triangle indicates the chloroplastic transit peptide cleavage site.



```
                                ADP-binding site
gi|23043609|    1 ------------MEEEIIIVGAGIGGLTLACALEQKGIDFQLYEQ-ADSFEALG--YG-IQVSPNVVRVLRELGLEQQLE
gi|27380702|    1 ----------MALSRTIVIAGAGIGGLTAALALAARGFRIVVLEK-AERLEEVG--AG-LQLSPNASRVLVGLGLTERLK
gi|23124423|    1 MNINPTEKLSQPIVEKVAIVGAGPGGLAAAIALRSQGIDVQIYEK-AQEFRPAG--TG-LGLAPNGLNFLDAIAPGIVET
OsZEP           1 QAASPGGGGEGTRRPRVLVAGGGIGGLVLALAARRKGYEVTVFERDMSAVRGEGQYRGPIQIQSNALAALAAIDMSVAEE

gi|23043609|   65 EVSHLCLGFELRSFNSNRVLATWQLDN---------DTPY-YQCRRADLHSLVFNSIQDKSRIHFSRCLESYEEKDDQLL
gi|27380702|   67 LRAVVPEAVSIMSARAGGELLRMPLGEAASV---RAGAPY-WVVHRADLQSALAGAVSDHPDIDL-KLGATFED------
gi|23124423|   77 LKGSGCEVHHTVLKNFRGETIRANASKYQEK---Y-GQPL-VTVWWYRLQQVLASRLPSDIVHLNHRCIGFEQD------
OsZEP          81 VMREGCVTGDRINGLVDGISGSWYIKFDTFTPAAERGLPVTRVISRMTLQQILARAVGDDAILNDSHVVDFIDD------

gi|23043609|  135 LSWHNLPSTTAKALVAADGVRS-LVRRS-LFNAVAHGENPQDSATS-VFSQNQAQYAGYAAYRAILP-FQDKYLPLWGKA
gi|27380702|  136 VAPH------AKGLTVVH--RSGTIRRSDLASALIGADGIWSTVRQHLFPEVQPRFSGLIAWRGTLDATQLPKDYTARRV
gi|23124423|  146 -----------ENGVEIR--FD--GEKSVYADLLIGADGVNSVIREILFGEGKPNYIGSMCWRAVIK---YHHELFNDYE
OsZEP         155 ----------GNKVTAILE-----DGRKFEGDLLVGADGIWSKVRKVLFGQSEATYSEYTCYTGIAD--FVPPDIDTVGY

gi|23043609|  211 TVWMGKNHHVVVYPNGNEQNSTSWLNLVLVVKDKNWNPQGWTIPADKKAVARDFANQSEELNEILEDMAASPEPCFKWGL
gi|27380702|  208 QLWMGPNAHLVAYPIAGGRQ----INVVAVLPG-TWNRPGWSTPGDPREVMDAFA--APRWPSQARMMLAAVDGWRKWAL
gi|23124423|  208 LVFVKGNQQFMYLLNVGG-------GYMSWISR--KFSPEYSLCHSADEVKSRILHELADWDESFQVVVQATPAEQIWEG
OsZEP         218 RVFLGHKQYFVSSDVGAG--------KMQWYAF-HKEPAGGTDPENGK--NKRLLEIFNGWCDNVVDLINATDEEAILRR

                       FAD-binding site
gi|23043609|  291 F-IHKPLPY--WSRGKVTLLGDAAHPMLPFQAQGAAMAIEDAYVLAKYLASE----RD------IEKAFIKYQQARIKRT
gi|27380702|  281 FGVPDGCP---WSKGPVALLGDAVHAMLPFAAQGAGMAIEDAAVLAQHLSPETAESTDG-----IVAALKQYGRARQARV
gi|23124423|  279 P-ICDRPPLTHWSQGRVTLLGDAAHPMAPAMGQGANTTFEDAYELRECFSQS----AN------LQEALTSYEQRRMQRT
OsZEP         287 D-IYDRPPTFNWGKGRVTLLGDSVHAMQPNLGQGGCMAIEDGYQLAVELEKSWQESAKSGTPMDIVSSLRRYEKERILRV

gi|23043609|  358 TKVQQVSINNANIFHASGVKAAIRNFALGVVSTT-------------VPSLLNKKTAWIYDFDVKTAVS--
gi|27380702|  353 RRVQRTARQQGRIYHFSGPLAIARDVAIRALG----------------PERMLARQDWIYGWRP-------
gi|23124423|  348 EIIQARSALGEMRYYESNTVASNGQREQ-TMS------------------VNDDFHKWLYDYKPSATIKF-
OsZEP         366 SVIHGLARMAAIMATTYRPYLGVGLGPLSFLTKLRIPHPGRVGGRFFIKYGMPLMLSWVLGGNSTKLEGRP
```

Supplemental Figure 5. Alignment of *Os*ZEP with mono-oxygenases and related FAD-dependent oxydases from bacteria and cyanobacteria. Identical residues are in black and similar residues are in grey. Two conserved motifs are indicated above. The *Os*ZEP SCR1 is indicated by pink letters.



Supplemental Figure 6. Cellular localization of the plant TIL lipocalins.

A. Schematic representation of GFP fusions used in the transient expression experiments.

B. Transient expression assays of GFP-TIL fusions. Plasmids carrying the fusions were transformed into onion epidermal cells by microprojectile bombardment. Confocal images of GFP fluorescence were captured 20 hours after transformation. Only the GFP::*At*TIL data is shown since the three constructs gave the same fluorescence pattern.

C. Biochemical fractionation analysis. Wheat protein extracts were prepared and subjected to SDS-PAGE and western blot analyses. Upper panels, western blot results obtained using the anti-*Ta*TIL antibody (dil. 1/25,000, 10 sec. exposure for the plasma membrane fractions; dil. 1/2,500, 5 min. exposure for the other fractions). Lower panel, Coomassie Brilliant Blue-stained gel showing the quality of the preparations. Typical protein patterns are observed for each fraction.

```
Mmus.a1GP       ---------QNPEHVNITIGDPITNETLSWLSDKWFFIGAAVLNPDYRQ----EIQKTQM
Rnor.a1GP       ---------IQNPEPANTLGIPITNETLKWLSDKWFYMGAAFRDPVFKQ----AVQTIQT
Hsap.a1GP       ----------QIPLCANLVPVPITNATLDQITGKWFYIASAFRNEEYNK----SVQEIQA
Ocun.a1GP       ----------QDPACANFSTSPITNATLDQLSHKWFFTASAFRNPKYKQ----LVQHTQA
Hsap.RBP        -----------ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPE------GLFL---QDN
Ggal.RBP        -----------ERDCRVSSFKVKENFDKNRYSGTWYAMAKKDPE------GLFL---QDN
Xlae.RBP        -----------EKNCRVDNFEVMKDFNKERYAGVWYAVAKKDPE------GLFL---LDN
Omyc.RBP1       ------------SDCQVSNIQVMQNFDRSRYTGRWYAVAKKDPV------GLFL---LDN
Ggal.Purp       ------------QTCAVDSFSVKDNFDPKRYAGKWYALAKKDPE------GLFL---QDN
TaTIL-1         ----------MAAKKSGSEMGVVLGLDVARYMGRWYEIASFPNF-----FQPRD---GRD
AtTIL           ----------MTEKK---EMEVVKGLNVERYMGRWYEIASFPSR-----FQPKN---GVD
TaTIL-2         ----------MAAMK------VVRNLDLERYMGRWYEIACFPSR-----FQPKD---GAN
AtZEP           -----------------CITGDRINGLVDGISGTWYVKFDTFTPAASRG-LPVTRVISRM
OsZEP           -----------------CVTGDRINGLVDGISGSWYIKFDTFTPAAERG-LPVTRVISRM
TaVDE           ----------------PDPSALVKNFNMADFRGKWYISSGLNPT-----FDTFD-----C
AtVDE           ----------------PDPSVLVQNFNISDFNGKWYITSGLNPT-----FDAFD-----C
TaCHL           ---------------MMTKGMTAKNFDPVRYSGRWFEVASRKGG-----FAGQGQEDCHC
AtCHL           --------------MMMMRGMTAKNFDPVRYSGRWFEVASLKRG-----FAGQGQEDCHC
Mmus.ApoD       ---------QNFHLGKCPSPPVQENFDVKKYLGRWYEIEKIPAS-----FEKG----N-C
Hsap.ApoD       ---------QAFHLGKCPNPPVQENFDVNKYLGRWYEIEKIPTT-----FENG----R-C
Sscr.VEG        -----------------AQEFPAVGQPLQDLLGRWYLKAMTSDP-EIP-----GKKPESV
Cfam.f1p        ------------------QDTPALGKDTVAVSGKWYLKAMTADQ-EVP------EKPDSV
Rnor.VEG2       ------------------AQAFPTTEENQDVSGTWYLKAAAWDK-EIFT-PDKKFGSVSV
Hsap.VEG        -----------------AHHLLASDEEIQDVSGTWYLKAMTVDR-EFPE-----MNLESV
Mmus.VNSP1      ------------------QDSSFLAFNNGNFSGKWFLKALVSED-DIPI--------NKV
Mmus.VNSP2      ---------------LQTYDDLPFISEEDKLSGVWFIKATVSQRRE--------VEGETL
Mmus.MUP4       --------------HAEEATSKGQNLNVEKINGEWFSILLASDKREKIE----EHGSMRV
Mmus.MUP5       ----------------EEASSERQNFNVEKINGKWFSILLASDKREKIE----EHGTMRV
Mmus.MUP        --------------HAEEASSTGRNFNVEKINGEWHTIILAFDKREKIE----DNGNFRL
Mmus.mMUP       --------------HAEESSSMERNFNVEQISGYWFSIAEASYEREKIE----EHGSMRA
Rnor.a2g1       --------------HAEEASSTRGNLDVDKLNGDWFSIVVASDKREKIE----ENASMRV
Rnor.a2g3       --------------HAEEASFERGNLDVDKLNGDWFSIVVASDKREKIE----ENGSMRV
Hsap.Lcn9       -------------QEFDPHTVMQRNYNVARVSGVWYSIFMASDDLN----RIKENGDLRV
Cfam.f2p        ----------------QEGNHEEPQGGLEELSGRWHSVALASNK--SDL--IKPWGHFRV
Tvul.Lip        --------LQPECSRSEEDLSDEKERKWEQLSRHWHTVVLASSD--RSL--IEEEGPFRN
Ccri.Aphr       -------------------------QDFAELQGKWYTIVIAADNLEKIE----EGGPLRF
Rnor.OBP1       -------------------HHENLDISPSEVNGDWRTLYIVADNVEKVA----EGGSLRA
Mmus.Pbas       -----------------------VMSLKKKIDGPWQTIYLAASTMEKIN----EGSPLRT
Rnor.Pbas       --------------------MMTDKNLKKKIEGNWRTVYLAASSVEKIN----EGSPLRT
Btau.alle       ------------------AQETPAEIDPSKIPGEWRIIYAAADNKDKIV----EGGPLRN
Btau.BLB        ----------------LIVTQTMKGLDIQKVAGTWYSLAMAASD--ISL-LDAQSAPLRV
Sscr.BLB        ----------------VEVTPIMTELDTQKVAGTWHTVAMAVSD--VSL-LDAKSSPLKA
Hsap.PP14       -------------VPAMDIPQTKQDLELPKLAGTWHSMAMATNN--ISL-MATLKAPLRV
Mmus.A1mg       ----------DPASTLP-DIQVQENFSESRIYGKWYNLAVGSTCPWLSR----IKDKMSV
Hsap.A1mg       -----------PVPTPPDNIQVQENFNISRIYGKWYNLAIGSTCPWLKK----IMDRMTV
Xlae.A1mg       -----------SPIQPEDNIQIQENFDLQRIYGKWYDIAIGSTCKWLKH----HKEKFNM
Ssal.A1mg       -----------VPVLPEPLFPIQDNFDLTKFMGKWHDIAIGSTCPWMQR----HKGDAAI
Ppla.A1mg       -----------LPVLPEPLYPTQENFDLTRFVGTWHDVALTSSCPHMQR----NRADAAI
Hsap.C8GC       ----QKPQRPRRPASPISTIQPKANFDAQQFAGTWLLVAVGSACRFLQ----EQGHRAEA
Ocun.C8GC       ----RWAQKPRGAPSAISAIQPKANFDAQQFAGTWLLAAVGSACHFLQ----EQGHRAEA
Xlae.cpl1       ------------SLWVGAEVQVQPDFQKEKVLGKWYGIGLASNSNW----FKDRKSHMKM
Bmar.lip        ------------------DVPIQPDFQEDKILGKWYGIGLASNSNW----FQSKKQQLKM
Mmus.PGDS       ------------QTPAQGHDTVQPNFQQDKFLGRWYSAGLASNSSW----FREKKAVLYM
Hsap.PGDS       ------------QAAPEAQVSVQPNFQQDKFLGRWFSAGLASNSSW----LREKKAALSM
Mmus.NGAL       ----QDSTQNLIPAPSLLTVPLQPDFRSDQFRGRWYVVGLAGNAV-----QKKTEGSFTM
Hsap.NGAL       ----QDSTSDLIPAPPLSKVPLQQNFQDNQFQGKWYVVGLAGNAI-----LREDKDPQKM
Hsap.Lcn12      ------KVLQAQTPTPLPLPPPMQSFQGNQFQGEWFVLGLAGNSF-----RPEHRALLNA
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Mmus.Lcn12      ------QILESQISAMSQGFPQMTSFQSDQFQGEWFVLGLADNTFR-----REHRALLNF
DhLip           -------------KKE--EMPVVEKIELDKYLGKWYEIARKPFL-----FQKKC---YSN
Cfre.OML        ----------CSSPTPPKGVTVVNNFDAKRYLGTWYEIARFDHR-----FERG----LDK
Ecol.OML        ----------CSSPTPPRGVTVVNNFDAKRYLGTWYEIARFDHR-----FERG----LEK
Vcho.Lpro       ----MEILIGATCLGMPESVKPVSDFELNNYLGKWYEVARLDHS-----FERG----LSQ
Ddis.Lip        ILGGVTYAYNSFKRYIPEGVHAVKPFYPEKYVGKWYEIARLYTY-----FEKD----LDK
Dmel.Lip        --AVWVAHAQVPFPGKCPDVKLLDTFDAEAYMGVWYEYAAYPFA-----FEIG----KKC
Gmel.Gall       -----------VHEGKCPDFKPVDNFNLTAYQGVWYEISKTPND-----AEKNG---K-C
Pbra.Bbp        ---------NVYHDGACPEVKPVDNFDWSNYHGKWWEVAKYPNS-----VEKY----GKC
Msex.IcyA       --------GDIFYPGYCPEVKPVDDFDLSAFAGAWHEIAKLPLE-----NENE----GKC
Hgam.CRC2       -----DGIPSFVTAGKCASVANQDNFDLRRYAGRWYQTHIIENA-----YQPV----TRC
Hgam.CRC1       DKIPDFVVPGKCASVDRNKLWAEQTPNRNSYAGVWYQFALTNNP-----YQLI----EKC
Mmus.Lcn13      -------------------AQEAPPDDLVDYSGIWYAKAMVHNG-------TLPSHKIPS
Tvul.BL         -------------IQAIENIHSKEELVVEKLIGPWYRVEEAKAM----------EFSIPL
Mmus.Lcn11      ----------------------LQDFHPEQVTGPWHTLKLASTDRSLIE----EGGAYRC
GvBLC           ---------------DSQPIETVAEVDFNRYDGRWYELARTPNIF---------QIGCTC
Btau.OBP        ----------------KNAQEEEAEQNLSELSGPWRTVYIGSTNPEKIQ----ENGPFRT
MgLip           DTSSVPNTVPSLWDGECFYPTPDIGFDTKSYLGRWYQVAGTVAP---------FTASCKC
Same.Laz        ----------AQETMGCADRSAINDFNATLYMGKWYEYAKMGSMPYEEG--------GVC
Tvul.LLP        ------------------DDVAFSAFTPSE--GTYYVQVIAVDKEFPEE-----EIPRDM
Ecab.p19p       -----------RRPHALHMGPGDPNFDEKLVKGKWFSVALASNE--------PKF-IAKD
Ggal.QS-21      ---------------------AATVPDSSEVAGKWYIVALASNT---DS-FLREKGKMKM
Hsap.Lcn5       ------------------QAVWLGRLDPEQLLGPWYVLAVASREK----GFAMEKDMKNV
Mmus.Lcn8       -------------------ESTRVELVPEKIAGFWKEVAVASDQ-------KLVLKAQRR
Mmus.ERBP       -----------------TEAAVVKDFDVNKFLGFWYEIALASKMG------AYGLAHKEE
Lviv.ESP        ------------------DIPVVPNFDAQKTVGKWHPIGMASKLP------EVPEYEQKI
PyLip           --------------RKCPNPATVPALDVAAYTGRWYQIGVTAEFAE------RQEDNKPC
                                                  :

Mmus.a1GP       VFFNLTPN---LINDTMELREYHTI-----DDHCVYNSTHLGIQRE--------------
Rnor.a1GP       EYFYLTPN---LINDTIELREFQTT-----DDQCVYNFTHLGVQRE--------------
Hsap.a1GP       TFFYFTPN---KTEDTIFLREYQTR-----QDQCIYNTTYLNVQRE--------------
Ocun.a1GP       AFFYFTAI---KEEDTLLLREYITT-----NNTCFYNSSIVRVQRE--------------
Hsap.RBP        IVAEFSV----DETGQMSATAKGRVR---LLNNWDVCADMVGTFTDTE------------
Ggal.RBP        VVAQFTV----DENGQMSATAKGRVR---LFNNWDVCADMIGSFTDTE------------
Xlae.RBP        IAANFKI----EDNGKTTATAKGRVR---ILDKLELCANMVGTFIETN------------
Omyc.RBP1       VVAQFSV----DESGKVTATAHGRVI---ILNNWEMCANMFGTFEDTP------------
Ggal.Purp       ISAEYTV----EEDGTMTASSKGRVK---LFGFWVICADMAAQYTVPDPT----------
TaTIL-1         TRATYELM---EDGATVHVLNETWS-----KGKRDFIEGTAYKADPASEE----------
AtTIL           TRATYTLN---PD-GTIHVLNETWS-----NGKRGFIEGSAYKADPKSDE----------
TaTIL-2         TRATYTLG---PD-GAVKVLNETWT-----DGRRGHIEGTAFRADPAGDE----------
AtZEP           TLQQILAR----AVGEDVIRNESNVVD--FEDSGDKVTVVLENGQRYEGDLLVGADGI--
OsZEP           TLQQILAR----AVGDDAILNDSHVVD--FIDDGNKVTAILEDGRKFEGDLLVGADGI--
TaVDE           QLHEFR-----LE-GDRLVANLAWRIP--TPDTGFFTRGAVQRFVQDSSQPAILYN----
AtVDE           QLHEFH-----TEGDNKLVGNISWRIK--TLDSGFFTRSAVQKFVQDPNQPGVLYN----
TaCHL           TQGVYT-----FDEKAGAIKVETFCVHGSPDGYITGIRGKVQCLSQEDMAGAETDLEREE
AtCHL           TQGVYT-----FDMKESAIRVDTFCVHGSPDGYITGIRGKVQCVGAEDLEKSETDLEKQE
Mmus.ApoD       IQANYSL----MENGNIEVLNKEL-S---PDGTMNQVKGEAKQSNVSEP-----------
Hsap.ApoD       IQANYSL----MENGKIKVLNQEL-R---ADGTVNQIEGEATPVNLTEP-----------
Sscr.VEG        TPLILKA----LEGGDLEAQITFLI-----DGQCQDVTLVLKKTN---------------
Cfam.f1p        TPMILKA----QKGGNLEAKITMLT-----NGQCQNITVVLHKTSE--------------
Rnor.VEG2       TPMKIKT----LEGGNLQVKFTVLI-----SGRCQEMSTVLEKTDE--------------
Hsap.VEG        TPMTLTT----LEGGNLEAKVTMLI-----SGRCQEVKAVLEKTD---------------
Mmus.VNSP1      SPMLILV----LNNGDIELSITHMI-----YDQCLEVTTILEKTD---------------
Mmus.VNSP2      VAFPIKFTC--PEEGTLELRHTLAS-----KGECINVGIRLQRTEE--------------
Mmus.MUP4       FVEHIHV----LEN-SLAFKFHTVI-----DGECSEIFLVADKTEK--------------
Mmus.MUP5       FVEHIDV----LEN-SLAFKFHTVI-----DEECTEIYLVADKTEK--------------
```

```
Mmus.MUP        FLEQIHV----LEN-SLVLKFHTVR-----DEECSELSMVADKTEK--------------
Mmus.mMUP       FVENITV----LEN-SLVFKFHLIV-----NEECTEMTAIGEQTEK--------------
Rnor.a2g1       FMQHIDV----LEN-SLGFKFRIKE-----NGECRELYLVAYKTPE--------------
Rnor.a2g3       FVQHIDV----LEN-SLGFTFRIKE-----NGVCTEFSLVADKTAK--------------
Hsap.Lcn9       FVRNIEH----LKNGSLIFDFEYMV-----QGECVAVVVVCEKTEK--------------
Cfam.f2p        FIHSMSA-----KDGNLHGDILIPQ-----DGQCEKVSLTAFKTAT--------------
Tvul.Lip        FIQNITV-----ESGNLNGFFLTRK-----NGQCIPLYLTAFKTEE--------------
Ccri.Aphr       YFRHIDCY---KNCSEMEITFYVIT-----NNQCSKTTVIGYLKG---------------
Rnor.OBP1       YFQHMECG---DECQELKIIFNVKL-----DSECQTHTVVGQKHE---------------
Mmus.Pbas       YFRHICVG---RRSNQVYLYFFIKK-----GTKCQLYKVIGRKK----------------
Rnor.Pbas       YFRRIECG---KRCNRINLYFYIKK-----GAKCQQFKIVGRRS----------------
Btau.alle       YYRRIECI---NDCESLSITFYLKD-----QGTCLLLTEVAKRQ----------------
Btau.BLB        YVEELKPT---PEG-DLEILLQKWE-----NGECAQKKIIAEKT----------------
Sscr.BLB        YVEGLKPT---PEG-DLEILLQKRE-----NDKCAQEVLLAKKT----------------
Hsap.PP14       HITSLLPT---PED-NLEIVLHRWE-----NNSCVEKKVLGEKT----------------
Mmus.A1mg       QTLVLQEG---ATETEISMTSTRWR-----RGVCEEITGAYQKTD---------------
Hsap.A1mg       STLVLGEG---ATEAEISMTSTRWR-----KGVCEETSGAYEKTDT--------------
Xlae.A1mg       GTLELSDG---ETDGEVRIVNTRMR-----HGTCSQIVGSYQKTET--------------
Ssal.A1mg       GTLELQAS---GTEDKVSMTRSMKK-----HGKCEQISGDYELTAT--------------
Ppla.A1mg       GKLVLEK----DTGNKLKVTRTRLR-----HGTCVEMSGEYELTS---------------
Hsap.C8GC       TTLHVA-----PQGTAMAVSTFRKL-----DGICWQVRQLYGDTG---------------
Ocun.C8GC       TALHVA-----PQGAAMAVSTFRKL-----DGICWQVSQRYGATG---------------
Xlae.cpl1       CTTIITP----TADGNLEVTATYPK-----MDRCETKSMTYFKT----------------
Bmar.lip        CTTVITP----TADGNLDVVATFPK-----LDRCEKKSMTYIKT----------------
Mmus.PGDS       CKTVVAP----STEGGLNLTSTFLR-----KNQCETKIMVLQPA----------------
Hsap.PGDS       CKSVVAP----ATDGGLNLTSTFLR-----KNQCETRTMLLQPA----------------
Mmus.NGAL       YSTIYEL----QENNSYNVTSILVRD---QDQGCRYWIRTFVPS----------------
Hsap.NGAL       YATIYEL----KEDKSYNVTSVLFR-----KKKCDYWIRTFVPG----------------
Hsap.Lcn12      FTATFEL----SDDGRFEVWNAMTR-----GQHCDTWSYVLIPAAQ--------------
Mmus.Lcn12      FTTLFEL----KEKSQFQVTNSMTR-----GKHCNTWSYTLIPATK--------------
DhLip           VSAKYSLN---DN-ANINVDNSCYSK----DGKLRQAIGEAFTQNPPFN-----------
Cfre.OML        VTATYSLR----DDGGINVINKGYNP---DREMWQKTEGKAYFTGDPS------------
Ecol.OML        VTATYSLR----DDGGLNVINKGYNP---DRGMWQQSEGKAYFTGAPT------------
Vcho.Lpro       VTAEYRVR----NDGGISVLNRGYSE---EKGEWKEAEGKAYFVNGST------------
Ddis.Lip        ITAEYSIN----KDGSITVVNSGYNY---KKKKRENAKGIAYFVNGSD------------
Dmel.Lip        IYANYSL----IDNSTVSVVNAAINR---FTGQPSNVTGQAKVLGPGQ------------
Gmel.Gall       GQAEYKL-----EGEVVKVKNSHV-----VDGVQKYVEGTAKFAEDANKSA---------
Pbra.Bbp        GWAEYTP-----EGKSVKVSNYHV-----IHGKEYFIEGTAYPVGDSKIGK---------
Msex.IcyA       TVAEYKY-----DGKKASVYNSFV-----INGVKEYMEGDLEIAPDAKLTK---------
Hgam.CRC2       IHSNYEYS---TNDYGFKVTTAGFNP----NDEYLKIDFKVYPTKEFP------------
Hgam.CRC1       VRN--EYS---FDGKQFVIKSTGIAY----DGNLLKRNGKLYPNPFGEP-----------
Mmus.Lcn13      IVFPVRIIA--LEEGDLETTVVFWN-----NGHCREFKFVMKKTEE--------------
Tvul.BL         FDMNIKEVN-RTPEGNLELIV-LEQ-----TDSCVEKKFLLKKT----------------
Mmus.Lcn11      FMTDIVL----LDNGNLNVTYFHRK-----DGKCVKEFYIAEKTDT--------------
GvBLC           VTANYSV----LSESSISVFNTCNRFR--PRGNLVTIDGVAVVADPN-------------
Btau.OBP        YFRELVFD---DEKGTVDFYFSVKR-----DGKWKNVHVKATKQ----------------
MgLip           IYAQYAL----NDNGTIQVNNTCEAG-----GRAVNILGTAEPADPGYG-----------
Same.Laz        VTAEYS-----MSSNNITVVNSMKDN---TTHEVNTTTGWAEFASELHT-----------
Tvul.LLP        SPLTIMY----LDDGKMEARFTMKK-----DDNCEEINIMLEKTAD--------------
Ecab.p19p       TDMKFFIHKIQVTPESLQFHFHRKV-----RGMCVPTMMTAHKTKK--------------
Ggal.QS-21      VMARISF----LGEDELEVSYAAPS-----PKGCRKWETTFKKTS---------------
Hsap.Lcn5       VGVVVTL----TPENNLRTLSSQHG-----LGGCDQSVMDLIKRNS--------------
Mmus.Lcn8       VEGLFLT----FSGGNVTVKAVYNS-----SGSCVTESSLGSERDT--------------
Mmus.ERBP       KMGAMVVE---LKENLLALTTTYYN-----EGHCVLEKVAATQVDG--------------
Lviv.ESP        SPMDHMVE---LTDGDMKLTANYMD------GVCKEATAMLKHTDK--------------
PyLip           VTADYRLTG--PTVEVINCKQDVPANR--SSGAIVGCAQAVAFPGKKED-----------
```

```
Mmus.a1GP       --NGTLSKYVGGVK----------------------------IFADLIVLKMHGA------
Rnor.a1GP       --NGTLSKCAGAVK----------------------------IFAHLIVLKKHGT------
Hsap.a1GP       --NGTISRYVGGQE----------------------------HFAHLLILRDTKT------
Ocun.a1GP       --NGTLSKHDGIRN----------------------------SVADLLLLRDPGS------
Hsap.RBP        -DPAKFKMKYWGVASFLQ---------------------KGNDDHWIVDTDYDT-------
Ggal.RBP        -DPAKFKMKYWGVASFLQ---------------------KGNDDHWVVDTDYDT-------
Xlae.RBP        -DPAKYRMKYHGALAILE---------------------RGLDDHWVVDTDYTT-------
Omyc.RBP1       -DPAKFKMRYWGAASYLQ---------------------TGNDDHWVIDTDYDN-------
Ggal.Purp       -TPAKMYMTYQGLASYLS---------------------SGGDNYWVIDTDYDN-------
TaTIL-1         ---AKLKVKFY--VPPFLPII------------------PVVGDYWVLYVDDD--------
AtTIL           ---AKLKVKFY--VPPFLPII------------------PVTGDYWVLYIDPD--------
TaTIL-2         ---AKLKVRFY--VPPFLPVF------------------PVTGDYWVLHVDDA--------
AtZEP           -WSKVRNNLFGRSE-ATYSGYTCYTGIADFIPADIESVG--YRVFLGHKQYFVSSDVGGG
OsZEP           -WSKVRKVLFGQSE-ATYSEYTCYTGIADFVPPDIDTVG--YRVFLGHKQYFVSSDVGAG
TaVDE           -HDNEYLHYQDDWY----------------ILSSKIE-NKDDDYIFVYYRGRNDAWD-GYG
AtVDE           -HDNEYLHYQDDWY----------------ILSSKIE-NKPEDYIFVYYRGRNDAWD-GYG
TaCHL           MISSKCFLRFPT-----LPF-------------------IPKLPYDVLATDYDN-------
AtCHL           MIKEKCFLRFPT-----IPF-------------------IPKLPYDVIATDYDN-------
Mmus.ApoD       ---AKLEVQFFP----LMP----------------------PAPYWILATDYEN-------
Hsap.ApoD       ---AKLEVKFSW----FMP----------------------SAPYWILATDYEN-------
Sscr.VEG        -QPFTFTAYDGK------------------------------RVVYILPSKVKDH------
Cfam.f1p        --PGKYTAYEGQR------------------------------VVFIQPSPVRDH------
Rnor.VEG2       --PGKYTAYSGKQ----------------------------VFTVYSIPSAVEDH------
Hsap.VEG        -EPGKYTADGGK------------------------------HVAYIIRSHVKDH------
Mmus.VNSP1      -VPGQYLAFEGKT------------------------------HLQVQLSSVKGH------
Mmus.VNSP2      --PGQYSAFWGHT------------------------------LFYIYDLPVKDH------
Mmus.MUP4       --AGEYSVMYDGFN-----------------------------TFTILKTDYDN-------
Mmus.MUP5       --AGEYSVTYDGFN-----------------------------TFTILKTDYDN-------
Mmus.MUP        --AGEYSVTYDGFN-----------------------------TFTIPKTDYDN-------
Mmus.mMUP       --AGIYYMNYDGFN-----------------------------TFSILKTDYDN-------
Rnor.a2g1       --DGEYFVEYDGGN-----------------------------TFTILKTDYDR-------
Rnor.a2g3       --DGEYFVEYDGEN-----------------------------TFTILKTDYDN-------
Hsap.Lcn9       --NGEYSINYEGQN-----------------------------TVAVSETDYRL-------
Cfam.f2p        --SNKFDLEYWGHN-----------------------------DLYLAEVDPKS-------
Tvul.Lip        --ARQFKLNYYGTN-----------------------------DVYYGSSKPNE-------
Ccri.Aphr       --NGTYQTQFEGN-----------------------------NIFQPLYITSD--------
Rnor.OBP1       --DGRYTTDYSGRN-----------------------------YFHVLKKTDD--------
Mmus.Pbas       --QEVYYAQYEGS------------------------------IAFMLKMVNEK-------
Rnor.Pbas       --QDVYYAKYEGS------------------------------TAFMLKTVNEK-------
Btau.alle       -EGYVVYVLEFYGTN----------------------------TLEVIHVSEN--------
Btau.BLB        KIPAVFKIDALNE-----------------------------NKVLVLDTDYKK-------
Sscr.BLB        DIPAVFKINALDE-----------------------------NQLFLLDTDYDS-------
Hsap.PP14       GNPKKFKINYTVAN-----------------------------EATLLDTDYDN-------
Mmus.A1mg       -IDGKFLYHKSKWN--------------------------ITLESYVVHTNYDE-------
Hsap.A1mg       --DGKFLYHKSKWN--------------------------ITMESYVVHTNYDE-------
Xlae.A1mg       --PGKFDYFNARWG--------------------------TTIQNYIVFTNYNE-------
Ssal.A1mg       --PGRLTYHIAKWG--------------------------ADVDAYVVDTNYDE-------
Ppla.A1mg       -TPGRIFYHIDRWD--------------------------ADVDAYVVHTNYDE-------
Hsap.C8GC       -VLGRFLLQARGAR--------------------------GAVHVVVAETDYQS-------
Ocun.C8GC       -VPGRFLLPARGPR--------------------------GAVHVVAAETDYHS-------
Xlae.cpl1       EQLGGFRAKSPRYG--------------------------SEHDMRVVETNYDE-------
Bmar.lip        EQPGRFLSKSPRYG--------------------------SDHVIRVVESNYDE-------
Mmus.PGDS       GAPGHYTYSSPHSG--------------------------SIHSVSVVEANYDE-------
Hsap.PGDS       GSLGSYSYRSPHWG--------------------------STYSVSVVETDYDQ-------
Mmus.NGAL       SRAGQFTLGNMHRYP-----------------------QVQSYNVQVATTDYNQ-------
Hsap.NGAL       CQPGEFTLGNIKSYP-----------------------GLTSYLVRVVSTNYNQ-------
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Hsap.Lcn12      --PGQFTVDH-GVEPG----------------------ADREETRVVDSDYTQ-------
Mmus.Lcn12      --PGQFTRDNRGSGP----------------------GADRENIQVIETDYIT-------
DhLip           ---SKLKVSFLPKAIRFLP-------------------IGRGDYWILKIDDN--------
Cfre.OML        --TAALKVSFFG------P--------------------FYGGYNVIALDRE--------
Ecol.OML        --RAALKVSFFG------P--------------------FYGGYNVIALDRE--------
Vcho.Lpro       --DGYLKVSFFG------P--------------------FYGSYVVFELDREN-------
Ddis.Lip        --EGMLKVSFFG------P--------------------FYSGYNVIAIDPD--------
Dmel.Lip        -----LAVAFYP----TQP-------------------LTKANYLVLGTDYES-------
Gmel.Gall       --KLLVTLTYGAVNR-------------------------ESPLNVIATDYQN-------
Pbra.Bbp        ---IYHKLTYGGVTK-------------------------ENVFNVLSTDNKN-------
Msex.IcyA       QGKYVMTFKFGPR-------------------------VVVQVPWVLATDYKN-------
Hgam.CRC2       --AAHMLIDAPSVF--------------------------AAPYEVIETDYET-------
Hgam.CRC1       ----HLSIDYENS--------------------------FAAPLVILETDYSN-------
Mmus.Lcn13      --PGKYTAFHNTK-----------------------------VIHVEKTSVNEH------
Tvul.BL         EKPAEFEIYIPSES-------------------------ASYTLSVMETDYDN-------
Mmus.Lcn11      --PGQYTFEYQGRN----------------------------SLTFVHVTED--------
GvBLC           -APGKLLITFEGSP-------------------------VAEDYWIIDLVEDPNNSAG--
Btau.OBP        -DDGTYVADYEGQN----------------------------VFKIVSLSRT--------
MgLip           -AKGALRVQFPGQPGP-----------------------ACSGPNYVVQDYTG-------
Same.Laz        --DGKLSVHFPN-----SPS--------------------VGNYWILSTDYDN-------
Tvul.LLP        --PRKITMNRRLR----------------------------YTCAAVRTSKQK-------
Ecab.p19p       --KFQYTVNHSG----------------------------HKTIFLEKVDPKH-------
Ggal.QS-21      -DDGELYYSEEA----------------------------EKTVEVLDTDYKS-------
Hsap.Lcn5       ----GWVFENPSIG--------------------------VLELWVLATNFRD-------
Mmus.Lcn8       --VGEFAFPGNRE------------------------------IHVLDTDYER-------
Mmus.ERBP       --SAKYKVTRISGEK---------------------------EVVVVATDYMT-------
Lviv.ESP        --PGVFKFTGGEIR-------------------------------MMDIDYEK-------
PyLip           --PGKLGVQFPGAP-------------------------FPAPYWVINLAGSKEDG---Y


Mmus.a1GP       -FMLAFDLKDEKK--------------------------------RGLSLN-AKRPDIT-
Rnor.a1GP       -FMLAFNLTDEN---------------------------------RGLSFY-AKKPDLS-
Hsap.a1GP       -YMLAFDVNDEKN--------------------------------WGLSVY-ADKPETT-
Ocun.a1GP       -FLLVFFAGKEQD--------------------------------KGMSFY-TDKPKAS-
Hsap.RBP        -YAVQYSCR-------------------------LLNLDGTCADSYSFVFS--RDPNGL-
Ggal.RBP        -YALHYSCR-------------------------ELNEDGTCADSYSFVFS--RDPKGL-
Xlae.RBP        -YAITYACR-------------------------RRNLDGTCRDSYSFVFS--RDINGL-
Omyc.RBP1       -YAIHYSCR-------------------------EVDLDGTCLDGYSFIFS--RHPTGL-
Ggal.Purp       -YAITYACR-------------------------SLKEDGSCDDGYSLIFS--RNPRGL-
TaTIL-1         -YQYALVGEP--------------------------------RRKSLWILC--RKTHIE-
AtTIL           -YQHALIGQP--------------------------------SRSYLWILS--RTAQME-
TaTIL-2         -YQFALVGQP--------------------------------SRNYLWILC--RQPQMDS
AtZEP           -KMQWYAFHEEPAGGADAPNGMKKRLFEIFDGWCDNVLDLLHATEEEAILR--RDIYDR-
OsZEP           -KMQWYAFHKEPAGGTDPENGKNKRLLEIFNGWCDNVVDLINATDEEAILR--RDIYDRP
TaVDE           -GAVVYTRSKELPETIVPEL---------------ERATKSVGRDFSTFI---RTDNTCG
AtVDE           -GAVVYTRSSVLPNSIIPEL---------------EKAAKSIGRDFSTFI---RTDNTCG
TaCHL           ---YAVVSGAK-------------------------------DTSFIQIYS--RTPNPG-
AtCHL           ---YALVSGAK-------------------------------DKGFVQVYS--RTPNPG-
Mmus.ApoD       -YALVYSCT------------------------TFFW---LFHVDFFWILG--RNPYLP-
Hsap.ApoD       -YALVYSCT------------------------CIIQ---LFHVDFAWILA--RNPNLP-
Sscr.VEG        -YILYCEGELDG------------------------------QEVRMAKLV-GRDPENN-
Cfam.f1p        -YILYCEGELHG------------------------------RQIRMAKLL-GRDPEQSQ
Rnor.VEG2       -YIFYYEGKIHR------------------------------HHFQIAKLV-GRNPEINQ
Hsap.VEG        -YIFYCEGELHG------------------------------KPVRGVKLV-GRDPKNNL
Mmus.VNSP1      -YMLYCDGEIEG------------------------------MRFLMTQLI-GRDPQENL
Mmus.VNSP2      -YIIYCESHPFQ------------------------------KISQFGYLI-GKYPEENQ
Mmus.MUP4       -YIMFHLINEKDG-----------------------------KTFQLMELY-GRKADLNS
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Mmus.MUP5       -YIMFHLINKKDE-----------------------------ENFQLMELF-GREPDLSS
Mmus.MUP        -FLMAHLINENDG-----------------------------ETFQLMGLY-GREPDLSS
Mmus.mMUP       -YIMIHLINKKDG-----------------------------KTFQLMELY-GREPDLSL
Rnor.a2g1       -YVMFHLINFKNG-----------------------------ETFQAMVLY-GRTKDLSS
Rnor.a2g3       -YVMFHLVNVNNG-----------------------------ETFQLMELY-GRTKDLSS
Hsap.Lcn9       -FITFHLQNFRNG-----------------------------TETHTLALY---------
Cfam.f2p        -YLILYMINQYND-----------------------------DTSLVAHLM-VRDLSRQQ
Tvul.Lip        -YAKFIFYNYHDG-----------------------------KVNVVANLF-GRTPNLSN
Ccri.Aphr       -KIFFTNKNMDRAG----------------------------QETNMIVVA-GKGNALTP
Rnor.OBP1       -IIFFHNVNVDES-----------------------------GRRQCDLVA-GKREDLNK
Mmus.Pbas       -ILLFHYFNKNRR----------------------------NDVTRVAGVL-AKG-KLNK
Rnor.Pbas       -ILLFDYFNRNRR----------------------------NDVTRVAGVL-AKGRQLTK
Btau.alle       -MLVTYVENYDGE-----------------------------RITKMTEGL-AKGTSFTP
Btau.BLB        -YLLFCMENSAE-----------------------------PEQSLACQCL-VRTPEVDD
Sscr.BLB        -HLLLCMENSAS-----------------------------PEHSLVCQSL-ARTLEVDD
Hsap.PP14       -FLFLCLQDTTTP-----------------------------IQSMMCQYL-ARVLVEDD
Mmus.A1mg       -YAIFLTKKSSHH----------------------------HGLTITAKLY-GREPQLRD
Hsap.A1mg       -YAIFLTKKFSRH----------------------------HGPTITAKLY-GRAPQLRE
Xlae.A1mg       -YVIMQMRKKKGS-----------------------------ETTTTVKLY-GRSPDLRP
Ssal.A1mg       -YAIVMLSKQKTG----------------------------GEKTKSAKLY-SRTMELPP
Ppla.A1mg       -YAIIIMSKQKTS----------------------------GENSTSLKLY-SRTMSVRD
Hsap.C8GC       -FAVLYLERAG---------------------------------QLSVKLY-ARSLPVSD
Ocun.C8GC       -FAVLYLERAR---------------------------------QLSVKLY-VRSLPVSD
Xlae.cpl1       -YILMYTVKTKGS-----------------------------ETNQIVSLF-GRDKDLRP
Bmar.lip        -YTLMHTIKTKGN-----------------------------EVNTIVSLF-GRRKTLSP
Mmus.PGDS       -YALLFSRGTKGP----------------------------GQDFRMATLY-SRTQTLKD
Hsap.PGDS       -YALLYSQGSKGP----------------------------GEDFRMATLY-SRTQTPRA
Mmus.NGAL       -FAMVFFRKTSEN-----------------------------KQYFKITLY-GRTKELSP
Hsap.NGAL       -HAMVFFKKVSQN-----------------------------REYFKITLY-GRTKELTS
Hsap.Lcn12      -FALMLSRRHTSR-----------------------------LAVLRISLL-GRSWLLPP
Mmus.Lcn12      -FALVLSLRQTSS-----------------------------QNITRVSLL-GRNWRLSH
DhLip           -YQTVLVGGP--------------------------------SRKYMWILS--RSQNHDE
Cfre.OML        -YRHALVCGP--------------------------------DRDYLWILS--RTPTISD
Ecol.OML        -YRHALVCGP--------------------------------DRDYLWILS--RTPTISD
Vcho.Lpro       -YSYAFVSGP--------------------------------NTEYLWLLS--RTPTVER
Ddis.Lip        -YKYALIAGQ--------------------------------SFDYMWILS--KEPTIPE
Dmel.Lip        -YAVVYSCT------------------------SVTP---LANFKIVWILT--RQREPSA
Gmel.Gall       -YAIAYTCK-------------------------YDEK-SKSHNDSIWILS--RAKKLEG
Pbra.Bbp        -YIIGYYCK-------------------------YDE-DKKGHQDFVWVLS--RSKVLTG
Msex.IcyA       -YAINYNCN-------------------------YHP-DKKAHSIHAWVLS--RNKVLEG
Hgam.CRC2       -YSCVYSCI------------------------TTDN----YKSEFAFVFS--RTPQTSG
Hgam.CRC1       -YACLYSCI-------------------------DYN--FGYHSDFSFIFS--RSANLAD
Mmus.Lcn13      -YIFYCEGRHNG-----------------------------TSSFGMGKLMG-RDSGENP
Tvul.BL         -YILGCLENVNYR------------------------------EKMACAHY-ERRIE-EN
Mmus.Lcn11      -FAIMDLENQSEG---------------------------------------------GT
GvBLC           DYAFAAIGG--------------------------------PNRDFIFIIS--RKPALET
Btau.OBP        -HLVAHNINVDKHG----------------------------QTTELTGLF--VKLNVED
MgLip           DFALVQTYN----------------------------------FSTLFVLS--RNQHPEE
Same.Laz        -YSIVWSCVKRP--------------------------DSAASTEISWILL--RSRNSSN
Tvul.LLP        HWILVCPREFQG------------------------------ETIRMAKLVG-PNTDKNP
Ecab.p19p       -FVIFCAHSMKHG-----------------------------KETVVVTLFS-RTPTVSP
Ggal.QS-21      -YAVIFATRVKDG-----------------------------RTLHMMRLYS-RSREVSP
Hsap.Lcn5       -YAIIFTQLEFGD-----------------------------EPFNTVELYS-LTETASQ
Mmus.Lcn8       -YTILKLTLLWQG-----------------------------RNFHVLKYFT-RSLENED
Mmus.ERBP       -YTVIDITSLVAG-----------------------------AVHRAMKLYS-RSLDNNG
Lviv.ESP        -YLIMYMKKSTFE---------------------------------AMYLS-ARGSDVGD
PyLip           RVAVVYSCTSTG------------------------------SFFSQGLFLLSRTPKLRY
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Mmus.a1GP       PEL-REVFQKAVTHVGMDESEIIFV--------DWKKDRCSQQEKQQLELEKETKKDPEE
Rnor.a1GP       PEL-RKIFQQAVKDVGMDESEIVFV--------DWTKDKCSEQQKQQLELEKETKKETKK
Hsap.a1GP       KEQ-LGEFYEALDCLRIPKSDVVYT--------DWKKDKCEPLEKQHEKERKQEEGES--
Ocun.a1GP       PEQ-LEEFYEALTCLGMNKTEVVYT--------DWTKDLCEPLEKQHEEERKKEKAES--
Hsap.RBP        PPE-AQKIVRQRQEELCLARQ--YRLIVH-------NGYCDGRSERNLL-----------
Ggal.RBP        PPE-AQKIVRQRQIDLCLDRK--YRVIVH-------NGFCS-------------------
Xlae.RBP        PSE-SQRIVRRRQEQLCLDRK--YRVVVH-------NGYCETN-----------------
Omyc.RBP1       RPE-DQKIVTDKKKEICFLGK--YRRVGH-------TGFCESS-----------------
Ggal.Purp       PPA-IQRIVRQKQEEICMSGQ--FQPVLQ-------SGAC--------------------
TaTIL-1         EEVYNQLLEKAKEEGYDVAKL--HKTPQS-----DPPPESDAAPTDSKGTWWFKSLFGK-
AtTIL           EETYKQLVEKAVEEGYDISKL--HKTPQS-----DTPPESNTAPEDSKGVWWFKSLFGK-
TaTIL-2         EGVYEELVERAKEEGYDVSKL--RKTPHP-----EPTPESQDAPKDG-GLWWIKSLFGK-
AtZEP           PGFTWGKGRVTLLGDSIHAMQPNMGQG-----GCMAIEDSFQLALELDEAWKQSVETTTP
OsZEP           PTFNWGKGRVTLLGDSVHAMQPNLGQG-----GCMAIEDGYQLAVELEKSWQESAKSGTP
TaVDE           AE-PPLADRIERTVEKGEKLIVDEVKEIEG----EIEGEVKELEREEETLVKRLADGIME
AtVDE           PE-PALVERIEKTVEEGERIIVKEVEEIEE----EVEKEVEKVGRTEMTLFQRLAEGFNE
TaCHL           PEF-IEKYKSYAAGFGYDLSKI-KDTPQD----CEVSSDQLAEMMSMPGMDQALTNQFP-
AtCHL           PEF-IAKYKNYLAQFGYDPEKI-KDTPQD----CEVTDAELAAMMSMPGMEQTLTNQFP-
Mmus.ApoD       PET-ITYLKDILTSNGIDIEK--MTTTDQ--------ANCPDFL----------------
Hsap.ApoD       PET-VDSLKNILTSNNIDVKK--MTVTDQ--------VNCPKLS----------------
Sscr.VEG        PEA-LEEFKEVARAKGLNP-DIVR---------PQQSETCSPGGN---------------
Cfam.f1p        EA-LEDFREFSRAKGLNQ-EILE---------LAQSETCSPGGQ----------------
Rnor.VEG2       EA-LEDFQNAVRAGGLNP-DNIFTFI------PKQSETCPLGSN----------------
Hsap.VEG        EA-LEDFEKAAGARGLST-ESIL--I------PRQSETCSPGSD----------------
Mmus.VNSP1      EA-LEEFKVFTQIKGLVA-ENLV--I------LEQMEKCEPESFYELPSRPSE-------
Mmus.VNSP2      DT-LEVFKEFIQHKGFLQ-EKIG--V------PEQRDRCIPIHDSAHQDHKC--------
Mmus.MUP4       DI-KEKFVKLCEEHGIIK-ENIID--------LTKTNRCLKARE----------------
Mmus.MUP5       DI-KEKFAKLCEEHGIVR-ENIID--------LSNANRCLQARE----------------
Mmus.MUP        DI-KERFAQLCEKHGILR-ENIID--------LSNANRCLQARE----------------
Mmus.mMUP       DI-KEKFAKLCEEHGIIR-ENIID--------LTNVNRCLEARE----------------
Rnor.a2g1       DI-KEKFAKLCEAHGITR-DNIID--------LTKTDHCLQARG----------------
Rnor.a2g3       DI-KEKFAKLCVAHGITR-DNIID--------LTKTDRCLQARG----------------
Hsap.Lcn9       --------ETCEKYGLGS-QNIID--------LTNKDPCYSKHYRSPPRPPMRW------
Cfam.f2p        DF-LPAFESVCEDIGLHK-DQIVV--------LSDDDRCQGSRD----------------
Tvul.Lip        EI-KKRFEEDFMNRGFRR-ENILD--------ISEVDHC---------------------
Ccri.Aphr       EE-NEILVQFAHEKKIPV-ENILN--------ILATDTCPE-------------------
Rnor.OBP1       AQ-KQELRKLAEEYNIPN-ENTQH--------LVPTDTCNQ-------------------
Mmus.Pbas       EE-MTEFMNLVEEMGIEE-ENVQR--------IMDTDNCPSKIRISITD-----------
Rnor.Pbas       DE-MTEYMNFVEEMGIED-ENVQR--------VMDTDTCPNKIRIR--------------
Btau.alle       EE-LEKYQQLNSERGVPN-ENIEN--------LIKTDNCPP-------------------
Btau.BLB        EA-LEKFDKALKA--LPMHIRLSFNP------TQLEEQCHI-------------------
Sscr.BLB        QI-REKFEDALKT--LSVPMR--ILP------AQLEEQCRV-------------------
Hsap.PP14       EI-MQGFIRAFRP--LPRHLWYLLDL------KQMEEPCRF-------------------
Mmus.A1mg       SL-LQEFKDVALNVGISENSIIFMP---------DRGECVPGDREVEPTSIAR-------
Hsap.A1mg       TL-LQDFRVVAQGVGIPEDSIFTMA---------DRGECVPGEQEPEPILIPRV------
Xlae.A1mg       TL-VDEFRQFALAQGIPEDSIVMLP---------NNGECSPGEIE---------------
Ssal.A1mg       TI-LEDFRRLVREQGMADDTIIIKQ---------NKGECVPGTEPVAAEPQPEITAP---
Ppla.A1mg       TV-LDDFKTLVRHQGMSDDTIIIKQ---------NKGDCIPGEQVEEAPSQPEPK-----
Hsap.C8GC       SV-LSGFEQRVQEAHLTEDQIFYFP---KYGFCEAADQFHVLDEVRR-------------
Ocun.C8GC       SV-LGAFEQRVAQANLTQDQVLFFP---TYGFCEAADQFHILDEVRR-------------
Xlae.cpl1       EL-LDKFQNFAKSQGLADDNIIILP---------HTDQCMTEA-----------------
Bmar.lip        EL-LDKFQQFAKEQGLTDDNILILP---------QTDSCMSEV-----------------
Mmus.PGDS       EL-KEKFTTFSKAQGLTEEDIVFLP---------QPDKCIQE------------------
Hsap.PGDS       EL-KEKFTAFCKAQGFTEDTIVFLP---------QTDKCMTEQ-----------------
Mmus.NGAL       EL-KERFTRFAKSLGLKDDNIIFSV---------PTDQCIDN------------------
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Hsap.NGAL       EL-KENFIRFSKSLGLPENHIVFPV---------PIDQCIDG------------------
Hsap.Lcn12      GT-LDQFICLGRAQGLSDDNIVFPDV---TGNMVHLQACWAVGTGPAGMSLVDPRGAGPS
Mmus.Lcn12      KT-IDKFICLTRTQNLTKDNFLFPDL---SDWLPDPQVC---------------------
DhLip           IV-VQDYLDYAKEIGFDVSDI-IMTKQT--------NE----------------------
Cfre.OML        EM-KQQMLAIATREGFEVNK--LIWVKQ--------PGA---------------------
Ecol.OML        EV-KQEMLAVATREGFDVSK--FIWVQQ--------PGS---------------------
Vcho.Lpro       GI-LDKFIEMSKERGFDTNR--LIYVQL--------Q-----------------------
Ddis.Lip        KI-KNSYLELAKSVGYDITK--LIWSKQ-------NENEN--------------------
Dmel.Lip        EA-VDAARKILEDNDVSQAF--LIDTVQ--------KNCPRLDGNGTGLAGEDGLDVDDF
Gmel.Gall       DA-KTAVDNYLKEHAKEIDA--SKLVQT----DFSEEACKFTSTSAVTEPQTKKQ-----
Pbra.Bbp        EA-KTAVENYLIG-SPVVDSQ--KLVYS----DFSEAACKVNN-----------------
Msex.IcyA       NT-KEVVDNVLKTFSHLIDA--SKFMSN----EFSEAACQYSTTYSLTGPDRH-------
Hgam.CRC2       PA-VEKTAAVFNKNGVEFSK--FVPVSH-------TAECVYRA-----------------
Hgam.CRC1       QY-VKKCEAAFKNINVDTTR--FVKTVQ-------GSSCPYDTQKTL-------------
Mmus.Lcn13      EA-MEEFKNFIKRMNLRLENMFVP---------EIGDKCVESD-----------------
Tvul.BL         KG-MEEFKKIVRT--LTIPYTM--------IEAQTREMCRV-------------------
Mmus.Lcn11      TIVIEFHGRSLSTDELG-------------------------------------------
GvBLC           YQDVLAYQGIVKRLQAQHFPVDALNSTP------QPTSCTYKSQSLPGGL----------
Btau.OBP        ED-LEKFWKLTEDKGIDKKNVVNFLEN--------EDHPHPE------------------
MgLip           AV-LDAWIKRAGALGSDLSDVIKND----------QTNCSFT------------------
Same.Laz        MT-LERVEDELKNLQLDLNK-YTKTEQS-------AKYCA--------------------
Tvul.LLP        KA-LEDFYRFIYRERFDK-RRIIT--------PKQTEACAPEHA----------------
Ecab.p19p       DV-MWMFKKYCKTHGIHTSNIVDLT---------QTDRCLHARH----------------
Ggal.QS-21      TA-MAIFRKLARE--RNYTDEMVAVLPS-------QEECSVDEV----------------
Hsap.Lcn5       EA-MGLFTKWSRSLGFLSQ-----------------------------------------
Mmus.Lcn8       EPGFWLFREMTADQGLYMLARHGR----------CAELLKEGLV----------------
Mmus.ERBP       EA-LNNFQKIALKHGFSETDIHILKHD-----LTCVNALQSGQI----------------
Lviv.ESP        DI-KEKFKKLVLEQNFPEAHIKYFN----------AEQCTPTAA----------------
PyLip           GVFEAVYWYVRVLARGIRFQKGNEFKLTP-----QGKSCTYRGDEGAKVVFQ--------


Mmus.a1GP       GQA---------------------------------------------------------
Rnor.a1GP       DP----------------------------------------------------------
Hsap.a1GP       ------------------------------------------------------------
Ocun.a1GP       ------------------------------------------------------------
Hsap.RBP        ------------------------------------------------------------
Ggal.RBP        ------------------------------------------------------------
Xlae.RBP        ------------------------------------------------------------
Omyc.RBP1       ------------------------------------------------------------
Ggal.Purp       ------------------------------------------------------------
TaTIL-1         ------------------------------------------------------------
AtTIL           ------------------------------------------------------------
TaTIL-2         ------------------------------------------------------------
AtZEP           VD------VVSSLKRYEESRRLRVAIIHAMARMAAIMASTYKAYLGVGLGPLSFLTKFRV
OsZEP           MD------IVSSLRRYEKERILRVSVIHGLARMAAIMATTYRPYLGVGLGPLSFLTKLRI
TaVDE           VKQDV------MNFFQGLSKEEMEILDQLNLEATEVEELFSRSLPIRKLR----------
AtVDE           LKQDE------ENFVRELSKEEMEFLDEIKMEASEVEKLFGKALPIRKVR----------
TaCHL           ---DLKLKSSVAFDPFTSVTQTLKKLAEVYFK----------------------------
AtCHL           ---DLGLRKSVQFDPFTSVFETLKKLVPLYFK----------------------------
Mmus.ApoD       ------------------------------------------------------------
Hsap.ApoD       ------------------------------------------------------------
Sscr.VEG        ------------------------------------------------------------
Cfam.f1p        ------------------------------------------------------------
Rnor.VEG2       ------------------------------------------------------------
Hsap.VEG        ------------------------------------------------------------
Mmus.VNSP1      ------------------------------------------------------------
Mmus.VNSP2      ------------------------------------------------------------
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Mmus.MUP4       ------------------------------------------------------------
Mmus.MUP5       ------------------------------------------------------------
Mmus.MUP        ------------------------------------------------------------
Mmus.mMUP       ------------------------------------------------------------
Rnor.a2g1       ------------------------------------------------------------
Rnor.a2g3       ------------------------------------------------------------
Hsap.Lcn9       ------------------------------------------------------------
Cfam.f2p        ------------------------------------------------------------
Tvul.Lip        ------------------------------------------------------------
Ccri.Aphr       ------------------------------------------------------------
Rnor.OBP1       ------------------------------------------------------------
Mmus.Pbas       ------------------------------------------------------------
Rnor.Pbas       ------------------------------------------------------------
Btau.alle       ------------------------------------------------------------
Btau.BLB        ------------------------------------------------------------
Sscr.BLB        ------------------------------------------------------------
Hsap.PP14       ------------------------------------------------------------
Mmus.A1mg       ------------------------------------------------------------
Hsap.A1mg       ------------------------------------------------------------
Xlae.A1mg       ------------------------------------------------------------
Ssal.A1mg       ------------------------------------------------------------
Ppla.A1mg       ------------------------------------------------------------
Hsap.C8GC       ------------------------------------------------------------
Ocun.C8GC       ------------------------------------------------------------
Xlae.cpl1       ------------------------------------------------------------
Bmar.lip        ------------------------------------------------------------
Mmus.PGDS       ------------------------------------------------------------
Hsap.PGDS       ------------------------------------------------------------
Mmus.NGAL       ------------------------------------------------------------
Hsap.NGAL       ------------------------------------------------------------
Hsap.Lcn12      V-YPGSSA---PACAQGSPGSWVPVLNPGSEPPPAAPGPLSWATSSHPGSPVPGHLLPPQ
Mmus.Lcn12      ------------------------------------------------------------
DhLip           ------------------------------------------------------------
Cfre.OML        ------------------------------------------------------------
Ecol.OML        ------------------------------------------------------------
Vcho.Lpro       ------------------------------------------------------------
Ddis.Lip        ------------------------------------------------------------
Dmel.Lip        VSTTVPNAIEKA------------------------------------------------
Gmel.Gall       ------------------------------------------------------------
Pbra.Bbp        ------------------------------------------------------------
Msex.IcyA       ------------------------------------------------------------
Hgam.CRC2       ------------------------------------------------------------
Hgam.CRC1       ------------------------------------------------------------
Mmus.Lcn13      ------------------------------------------------------------
Tvul.BL         ------------------------------------------------------------
Mmus.Lcn11      ------------------------------------------------------------
GvBLC           ------------------------------------------------------------
Btau.OBP        ------------------------------------------------------------
MgLip           ------------------------------------------------------------
Same.Laz        ------------------------------------------------------------
Tvul.LLP        ------------------------------------------------------------
Ecab.p19p       ------------------------------------------------------------
Ggal.QS-21      ------------------------------------------------------------
Hsap.Lcn5       ------------------------------------------------------------
Mmus.Lcn8       ------------------------------------------------------------
Mmus.ERBP       ------------------------------------------------------------
Lviv.ESP        ------------------------------------------------------------
```

```
PyLip           ------------------------------------------------------------


Mmus.a1GP       ------------------------------------------------------------
Rnor.a1GP       ------------------------------------------------------------
Hsap.a1GP       ------------------------------------------------------------
Ocun.a1GP       ------------------------------------------------------------
Hsap.RBP        ------------------------------------------------------------
Ggal.RBP        ------------------------------------------------------------
Xlae.RBP        ------------------------------------------------------------
Omyc.RBP1       ------------------------------------------------------------
Ggal.Purp       ------------------------------------------------------------
TaTIL-1         ------------------------------------------------------------
AtTIL           ------------------------------------------------------------
TaTIL-2         ------------------------------------------------------------
AtZEP           PHPGRVGGRFFVDIAMPSMLDWVLGGNSEKLQGRPPSCRLTDKADDRLREWFEDDDALER
OsZEP           PHPGRVGGRFFIKYGMPLMLSWVLGGNSTKLEGRPLSCRLSDKANDQLRRWFEDDDALEQ
TaVDE           ------------------------------------------------------------
AtVDE           ------------------------------------------------------------
TaCHL           ------------------------------------------------------------
AtCHL           ------------------------------------------------------------
Mmus.ApoD       ------------------------------------------------------------
Hsap.ApoD       ------------------------------------------------------------
Sscr.VEG        ------------------------------------------------------------
Cfam.f1p        ------------------------------------------------------------
Rnor.VEG2       ------------------------------------------------------------
Hsap.VEG        ------------------------------------------------------------
Mmus.VNSP1      ------------------------------------------------------------
Mmus.VNSP2      ------------------------------------------------------------
Mmus.MUP4       ------------------------------------------------------------
Mmus.MUP5       ------------------------------------------------------------
Mmus.MUP        ------------------------------------------------------------
Mmus.mMUP       ------------------------------------------------------------
Rnor.a2g1       ------------------------------------------------------------
Rnor.a2g3       ------------------------------------------------------------
Hsap.Lcn9       ------------------------------------------------------------
Cfam.f2p        ------------------------------------------------------------
Tvul.Lip        ------------------------------------------------------------
Ccri.Aphr       ------------------------------------------------------------
Rnor.OBP1       ------------------------------------------------------------
Mmus.Pbas       ------------------------------------------------------------
Rnor.Pbas       ------------------------------------------------------------
Btau.alle       ------------------------------------------------------------
Btau.BLB        ------------------------------------------------------------
Sscr.BLB        ------------------------------------------------------------
Hsap.PP14       ------------------------------------------------------------
Mmus.A1mg       ------------------------------------------------------------
Hsap.A1mg       ------------------------------------------------------------
Xlae.A1mg       ------------------------------------------------------------
Ssal.A1mg       ------------------------------------------------------------
Ppla.A1mg       ------------------------------------------------------------
Hsap.C8GC       ------------------------------------------------------------
Ocun.C8GC       ------------------------------------------------------------
Xlae.cpl1       ------------------------------------------------------------
Bmar.lip        ------------------------------------------------------------
Mmus.PGDS       ------------------------------------------------------------
Hsap.PGDS       ------------------------------------------------------------
```

```
Mmus.NGAL       ------------------------------------------------------------
Hsap.NGAL       ------------------------------------------------------------
Hsap.Lcn12      VPCPGPPPPAPPAPGPLSRPTSSHPGSPVLGYLLPPQVPCPGPSPPSGSPVLGHLLPSPI
Mmus.Lcn12      ------------------------------------------------------------
DhLip           ------------------------------------------------------------
Cfre.OML        ------------------------------------------------------------
Ecol.OML        ------------------------------------------------------------
Vcho.Lpro       ------------------------------------------------------------
Ddis.Lip        ------------------------------------------------------------
Dmel.Lip        ------------------------------------------------------------
Gmel.Gall       ------------------------------------------------------------
Pbra.Bbp        ------------------------------------------------------------
Msex.IcyA       ------------------------------------------------------------
Hgam.CRC2       ------------------------------------------------------------
Hgam.CRC1       ------------------------------------------------------------
Mmus.Lcn13      ------------------------------------------------------------
Tvul.BL         ------------------------------------------------------------
Mmus.Lcn11      ------------------------------------------------------------
GvBLC           ------------------------------------------------------------
Btau.OBP        ------------------------------------------------------------
MgLip           ------------------------------------------------------------
Same.Laz        ------------------------------------------------------------
Tvul.LLP        ------------------------------------------------------------
Ecab.p19p       ------------------------------------------------------------
Ggal.QS-21      ------------------------------------------------------------
Hsap.Lcn5       ------------------------------------------------------------
Mmus.Lcn8       ------------------------------------------------------------
Mmus.ERBP       ------------------------------------------------------------
Lviv.ESP        ------------------------------------------------------------
PyLip           ------------------------------------------------------------


Mmus.a1GP       ------------------------------------------------------------
Rnor.a1GP       ------------------------------------------------------------
Hsap.a1GP       ------------------------------------------------------------
Ocun.a1GP       ------------------------------------------------------------
Hsap.RBP        ------------------------------------------------------------
Ggal.RBP        ------------------------------------------------------------
Xlae.RBP        ------------------------------------------------------------
Omyc.RBP1       ------------------------------------------------------------
Ggal.Purp       ------------------------------------------------------------
TaTIL-1         ------------------------------------------------------------
AtTIL           ------------------------------------------------------------
TaTIL-2         ------------------------------------------------------------
AtZEP           TIKGEWYLIPHGDDCCVSETLCLTKDEDQPCIVGSEPDQDFPGMRIVIPSSQVSKMHARV
OsZEP           AMGGEWYLLPT--SSGDSQPIRLIRDEKKSLSIGSRSDPSNSTASLALPLPQISENHATI
TaVDE           ------------------------------------------------------------
AtVDE           ------------------------------------------------------------
TaCHL           ------------------------------------------------------------
AtCHL           ------------------------------------------------------------
Mmus.ApoD       ------------------------------------------------------------
Hsap.ApoD       ------------------------------------------------------------
Sscr.VEG        ------------------------------------------------------------
Cfam.f1p        ------------------------------------------------------------
Rnor.VEG2       ------------------------------------------------------------
Hsap.VEG        ------------------------------------------------------------
Mmus.VNSP1      ------------------------------------------------------------
```

```
Mmus.VNSP2      ------------------------------------------------------------
Mmus.MUP4       ------------------------------------------------------------
Mmus.MUP5       ------------------------------------------------------------
Mmus.MUP        ------------------------------------------------------------
Mmus.mMUP       ------------------------------------------------------------
Rnor.a2g1       ------------------------------------------------------------
Rnor.a2g3       ------------------------------------------------------------
Hsap.Lcn9       ------------------------------------------------------------
Cfam.f2p        ------------------------------------------------------------
Tvul.Lip        ------------------------------------------------------------
Ccri.Aphr       ------------------------------------------------------------
Rnor.OBP1       ------------------------------------------------------------
Mmus.Pbas       ------------------------------------------------------------
Rnor.Pbas       ------------------------------------------------------------
Btau.alle       ------------------------------------------------------------
Btau.BLB        ------------------------------------------------------------
Sscr.BLB        ------------------------------------------------------------
Hsap.PP14       ------------------------------------------------------------
Mmus.A1mg       ------------------------------------------------------------
Hsap.A1mg       ------------------------------------------------------------
Xlae.A1mg       ------------------------------------------------------------
Ssal.A1mg       ------------------------------------------------------------
Ppla.A1mg       ------------------------------------------------------------
Hsap.C8GC       ------------------------------------------------------------
Ocun.C8GC       ------------------------------------------------------------
Xlae.cpl1       ------------------------------------------------------------
Bmar.lip        ------------------------------------------------------------
Mmus.PGDS       ------------------------------------------------------------
Hsap.PGDS       ------------------------------------------------------------
Mmus.NGAL       ------------------------------------------------------------
Hsap.NGAL       ------------------------------------------------------------
Hsap.Lcn12      PAHKELGLIPGGALDLSSLPWVAAPA----------------------------------
Mmus.Lcn12      ------------------------------------------------------------
DhLip           ------------------------------------------------------------
Cfre.OML        ------------------------------------------------------------
Ecol.OML        ------------------------------------------------------------
Vcho.Lpro       ------------------------------------------------------------
Ddis.Lip        ------------------------------------------------------------
Dmel.Lip        ------------------------------------------------------------
Gmel.Gall       ------------------------------------------------------------
Pbra.Bbp        ------------------------------------------------------------
Msex.IcyA       ------------------------------------------------------------
Hgam.CRC2       ------------------------------------------------------------
Hgam.CRC1       ------------------------------------------------------------
Mmus.Lcn13      ------------------------------------------------------------
Tvul.BL         ------------------------------------------------------------
Mmus.Lcn11      ------------------------------------------------------------
GvBLC           ------------------------------------------------------------
Btau.OBP        ------------------------------------------------------------
MgLip           ------------------------------------------------------------
Same.Laz        ------------------------------------------------------------
Tvul.LLP        ------------------------------------------------------------
Ecab.p19p       ------------------------------------------------------------
Ggal.QS-21      ------------------------------------------------------------
Hsap.Lcn5       ------------------------------------------------------------
Mmus.Lcn8       ------------------------------------------------------------
Mmus.ERBP       ------------------------------------------------------------
```

```
Lviv.ESP        ------------------------------------------------------------
PyLip           ------------------------------------------------------------


Mmus.a1GP       ------------------------------------------------------------
Rnor.a1GP       ------------------------------------------------------------
Hsap.a1GP       ------------------------------------------------------------
Ocun.a1GP       ------------------------------------------------------------
Hsap.RBP        ------------------------------------------------------------
Ggal.RBP        ------------------------------------------------------------
Xlae.RBP        ------------------------------------------------------------
Omyc.RBP1       ------------------------------------------------------------
Ggal.Purp       ------------------------------------------------------------
TaTIL-1         ------------------------------------------------------------
AtTIL           ------------------------------------------------------------
TaTIL-2         ------------------------------------------------------------
AtZEP           IYKDGAFFLMDLRSEHGTYVTDNEGRRYRATPNFPARFRSSDIIEFGSDKKAAFRVKVIR
OsZEP           TCKNKAFYVTDNGSEHGTWITDNEGRRYRRTSELPCPFPSLGCH----------------
TaVDE           ------------------------------------------------------------
AtVDE           ------------------------------------------------------------
TaCHL           ------------------------------------------------------------
AtCHL           ------------------------------------------------------------
Mmus.ApoD       ------------------------------------------------------------
Hsap.ApoD       ------------------------------------------------------------
Sscr.VEG        ------------------------------------------------------------
Cfam.f1p        ------------------------------------------------------------
Rnor.VEG2       ------------------------------------------------------------
Hsap.VEG        ------------------------------------------------------------
Mmus.VNSP1      ------------------------------------------------------------
Mmus.VNSP2      ------------------------------------------------------------
Mmus.MUP4       ------------------------------------------------------------
Mmus.MUP5       ------------------------------------------------------------
Mmus.MUP        ------------------------------------------------------------
Mmus.mMUP       ------------------------------------------------------------
Rnor.a2g1       ------------------------------------------------------------
Rnor.a2g3       ------------------------------------------------------------
Hsap.Lcn9       ------------------------------------------------------------
Cfam.f2p        ------------------------------------------------------------
Tvul.Lip        ------------------------------------------------------------
Ccri.Aphr       ------------------------------------------------------------
Rnor.OBP1       ------------------------------------------------------------
Mmus.Pbas       ------------------------------------------------------------
Rnor.Pbas       ------------------------------------------------------------
Btau.alle       ------------------------------------------------------------
Btau.BLB        ------------------------------------------------------------
Sscr.BLB        ------------------------------------------------------------
Hsap.PP14       ------------------------------------------------------------
Mmus.A1mg       ------------------------------------------------------------
Hsap.A1mg       ------------------------------------------------------------
Xlae.A1mg       ------------------------------------------------------------
Ssal.A1mg       ------------------------------------------------------------
Ppla.A1mg       ------------------------------------------------------------
Hsap.C8GC       ------------------------------------------------------------
Ocun.C8GC       ------------------------------------------------------------
Xlae.cpl1       ------------------------------------------------------------
Bmar.lip        ------------------------------------------------------------
Mmus.PGDS       ------------------------------------------------------------
```

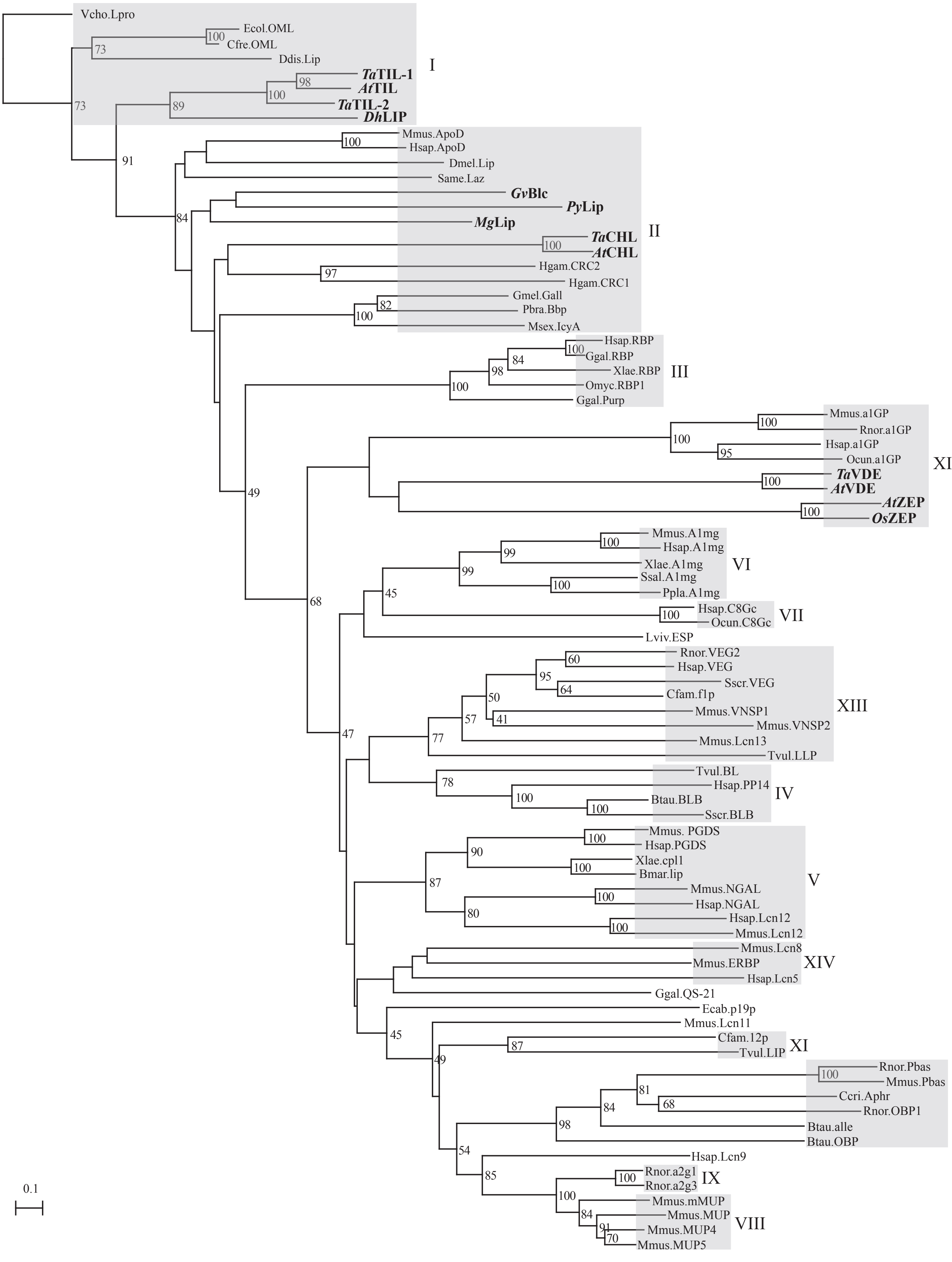
```
Hsap.PGDS       ------------------------------------------------------------
Mmus.NGAL       ------------------------------------------------------------
Hsap.NGAL       ------------------------------------------------------------
Hsap.Lcn12      ------------------------------------------------------------
Mmus.Lcn12      ------------------------------------------------------------
DhLip           ------------------------------------------------------------
Cfre.OML        ------------------------------------------------------------
Ecol.OML        ------------------------------------------------------------
Vcho.Lpro       ------------------------------------------------------------
Ddis.Lip        ------------------------------------------------------------
Dmel.Lip        ------------------------------------------------------------
Gmel.Gall       ------------------------------------------------------------
Pbra.Bbp        ------------------------------------------------------------
Msex.IcyA       ------------------------------------------------------------
Hgam.CRC2       ------------------------------------------------------------
Hgam.CRC1       ------------------------------------------------------------
Mmus.Lcn13      ------------------------------------------------------------
Tvul.BL         ------------------------------------------------------------
Mmus.Lcn11      ------------------------------------------------------------
GvBLC           ------------------------------------------------------------
Btau.OBP        ------------------------------------------------------------
MgLip           ------------------------------------------------------------
Same.Laz        ------------------------------------------------------------
Tvul.LLP        ------------------------------------------------------------
Ecab.p19p       ------------------------------------------------------------
Ggal.QS-21      ------------------------------------------------------------
Hsap.Lcn5       ------------------------------------------------------------
Mmus.Lcn8       ------------------------------------------------------------
Mmus.ERBP       ------------------------------------------------------------
Lviv.ESP        ------------------------------------------------------------
PyLip           ------------------------------------------------------------


Mmus.a1GP       --------------------
Rnor.a1GP       --------------------
Hsap.a1GP       --------------------
Ocun.a1GP       --------------------
Hsap.RBP        --------------------
Ggal.RBP        --------------------
Xlae.RBP        --------------------
Omyc.RBP1       --------------------
Ggal.Purp       --------------------
TaTIL-1         --------------------
AtTIL           --------------------
TaTIL-2         --------------------
AtZEP           KTPKSTRKNESNNDKLLQTA
OsZEP           --------------------
TaVDE           --------------------
AtVDE           --------------------
TaCHL           --------------------
AtCHL           --------------------
Mmus.ApoD       --------------------
Hsap.ApoD       --------------------
Sscr.VEG        --------------------
Cfam.f1p        --------------------
Rnor.VEG2       --------------------
Hsap.VEG        --------------------
```

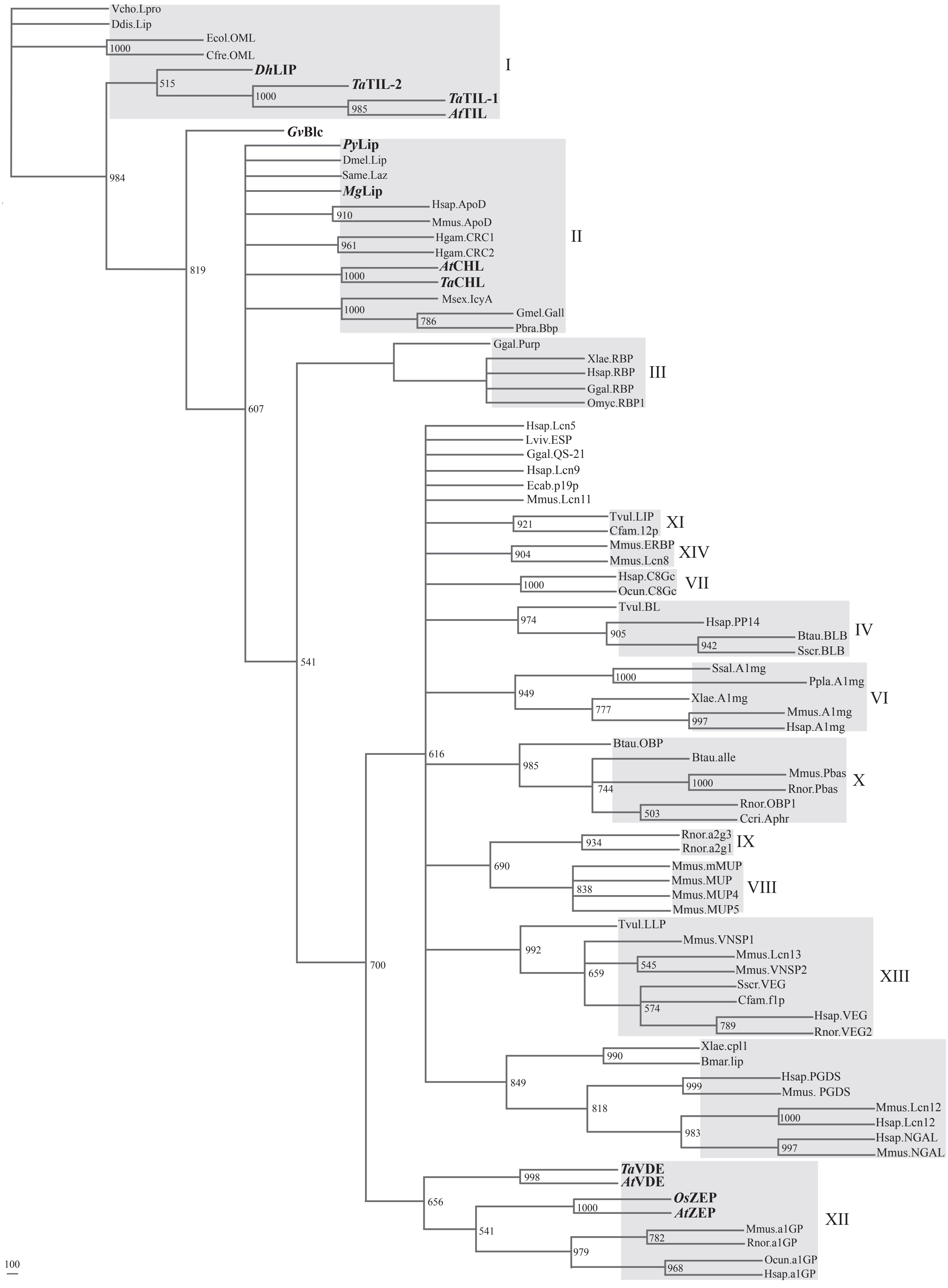
```
Mmus.VNSP1      --------------------
Mmus.VNSP2      --------------------
Mmus.MUP4       --------------------
Mmus.MUP5       --------------------
Mmus.MUP        --------------------
Mmus.mMUP       --------------------
Rnor.a2g1       --------------------
Rnor.a2g3       --------------------
Hsap.Lcn9       --------------------
Cfam.f2p        --------------------
Tvul.Lip        --------------------
Ccri.Aphr       --------------------
Rnor.OBP1       --------------------
Mmus.Pbas       --------------------
Rnor.Pbas       --------------------
Btau.alle       --------------------
Btau.BLB        --------------------
Sscr.BLB        --------------------
Hsap.PP14       --------------------
Mmus.A1mg       --------------------
Hsap.A1mg       --------------------
Xlae.A1mg       --------------------
Ssal.A1mg       --------------------
Ppla.A1mg       --------------------
Hsap.C8GC       --------------------
Ocun.C8GC       --------------------
Xlae.cpl1       --------------------
Bmar.lip        --------------------
Mmus.PGDS       --------------------
Hsap.PGDS       --------------------
Mmus.NGAL       --------------------
Hsap.NGAL       --------------------
Hsap.Lcn12      --------------------
Mmus.Lcn12      --------------------
DhLip           --------------------
Cfre.OML        --------------------
Ecol.OML        --------------------
Vcho.Lpro       --------------------
Ddis.Lip        --------------------
Dmel.Lip        --------------------
Gmel.Gall       --------------------
Pbra.Bbp        --------------------
Msex.IcyA       --------------------
Hgam.CRC2       --------------------
Hgam.CRC1       --------------------
Mmus.Lcn13      --------------------
Tvul.BL         --------------------
Mmus.Lcn11      --------------------
GvBLC           --------------------
Btau.OBP        --------------------
MgLip           --------------------
Same.Laz        --------------------
Tvul.LLP        --------------------
Ecab.p19p       --------------------
Ggal.QS-21      --------------------
Hsap.Lcn5       --------------------
Mmus.Lcn8       --------------------
```

```
Mmus.ERBP       --------------------
Lviv.ESP        --------------------
PyLip           --------------------
```

Supplemental Figure 7. Multiple sequence alignment of plant lipocalins, plant lipocalin-like proteins and other selected lipocalins. The alignment was generated using CLUSTAL X v.1.83.



Supplemental Figure 8. Phylogenetic analysis of selected lipocalins using the Neighbor-Joining method.



Supplemental Figure 9. Phylogenetic analysis of selected lipocalins using the maximum likelihood method.