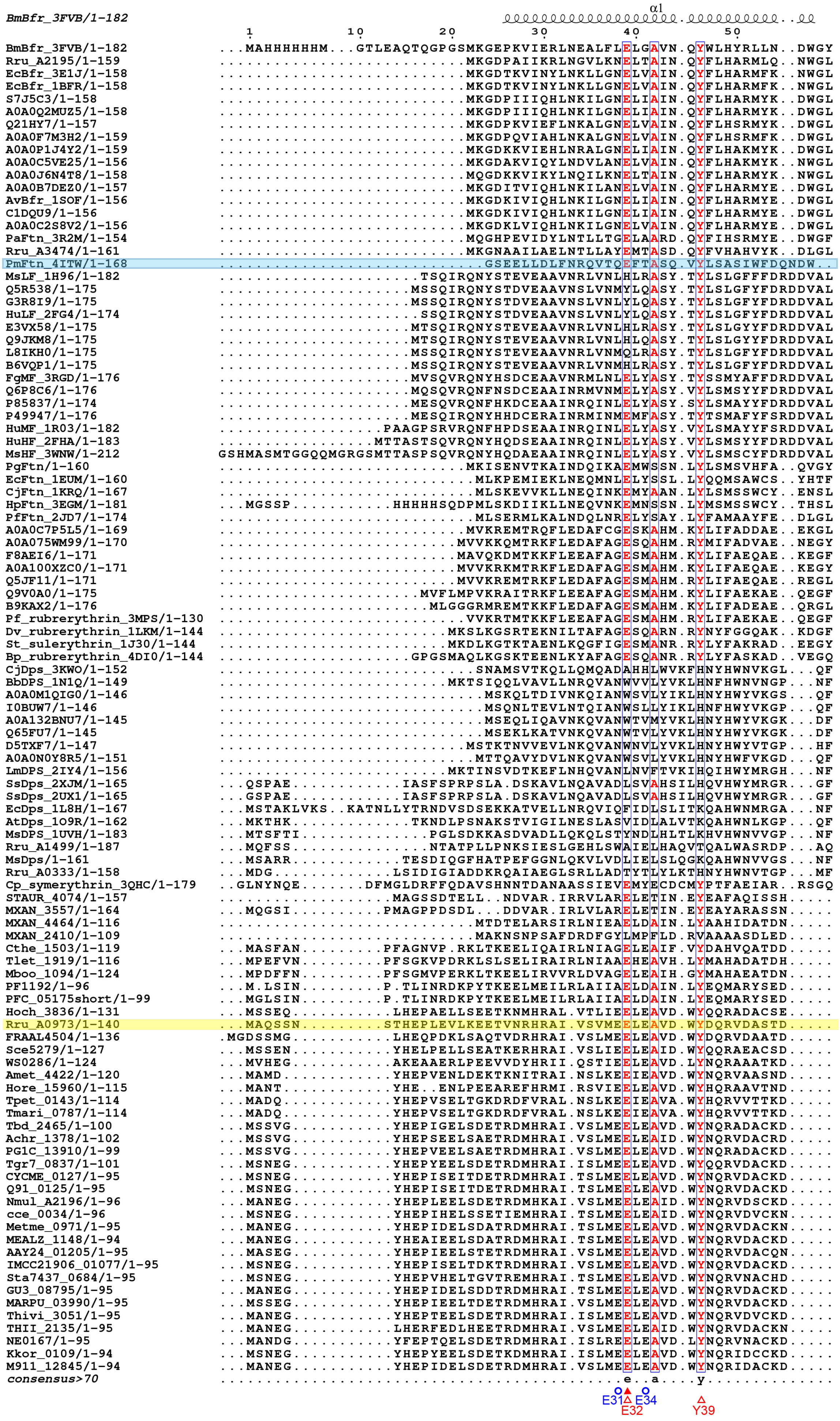
Supplementary file 1. Multiple sequence alignment



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BmBfr_3FVB/1-182                                                            α1
                               1          10        20        30        40         50
BmBfr_3FVB/1-182            ...MAHHHHHHM...GTLEAQTQGPGSMKGEPKVIERLNEALFLELGAVN.QYWLHYRLLN..DWGY
Rru_A2195/1-159             ...........................MKGDPAIIKRLNGVLKNELTAIN.QYFLHARMLQ..NWGL
EcBfr_3E1J/1-158            ...........................MKGDTKVINYLNKLLGNELVAIN.QYFLHARMFK..NWGL
EcBfr_1BFR/1-158            ...........................MKGDTKVINYLNKLLGNELVAIN.QYFLHARMFK..NWGL
S7J5C3/1-158                ...........................MKGDPIIIQHLNKILGNELIAIN.QYFLHARMYK..DWGL
A0A0Q2MUZ5/1-158            ...........................MKGDPIIIQHLNKILGNELIAIN.QYFLHARMYK..DWGL
Q21HY7/1-157                ...........................MKGDPKVIEFLNKALGNELVAIN.QYFLHSRMYK..DWGL
A0A0F7M3H2/1-159            ...........................MKGDPQVIAHLNKALGNELVAIN.QYFLHSRMFK..DWGL
A0A0P1J4Y2/1-159            ...........................MKGDKKVIEHLNRALGNELIAIN.QYFLHAKMYK..DWGL
A0A0C5VE25/1-156            ...........................MKGDAKVIQYLNDVLANELVAIN.QYFLHAKMYK..NWGL
A0A0J6N4T8/1-158            ...........................MQGDKKVIKYLNQILKNELTAIN.QYFLHARMYK..NWGL
A0A0B7DEZ0/1-157            ...........................MKGDITVIQHLNKILANELVAIN.QYFLHARMYE..DWGL
AvBfr_1SOF/1-156            ...........................MKGDKIVIQHLNKILGNELIAIN.QYFLHARMYE..DWGL
C1DQU9/1-156                ...........................MKGDKIVIQHLNKILGNELIAIN.QYFLHARMYE..DWGL
A0A0C2S8V2/1-156            ...........................MKGDKLVIQHLNKILGNELVAIN.QYFLHARMYE..DWGL
PaFtn_3R2M/1-154            ...........................MQGHPEVIDYLNTLLTGELAARD.QYFIHSRMYE..DWGF
Rru_A3474/1-161             ...........................MKGNAAILAELNTLLAYEMTASD.QYFVHAHVYK..DLGL
PmFtn_4ITW/1-168            .............................GSEELLDLFNRQVTQEFTASQ.VYLSASIWFDQNDW..
MsLF_1H96/1-182             ......................TSQIRQNYSTEVEAAVNRLVNLHLRASY.TYLSLGFFFDRDDVAL
Q5R538/1-175                .....................MSSQIRQNYSTDVEAAVNSLVNMYLQASY.TYLSLGFYFDRDDVAL
G3R8I9/1-175                .....................MSSQIRQNYSTDVEAAVNSLVNLYLQASY.TYLSLGFYFDRDDVAL
HuLF_2FG4/1-174             ......................SSQIRQNYSTDVEAAVNSLVNLYLQASY.TYLSLGFYFDRDDVAL
E3VX58/1-175                .....................MTSQIRQNYSTEVEAAVNRLVNLHLRASY.TYLSLGYYFDRDDVAL
Q9JKM8/1-175                .....................MTSQIRQNYSTEVEAAVNRLVNLHLQASY.TYLSLGYYFDRDDVAL
L8IKH0/1-175                .....................MSSQIRQNYSTEVEAAVNRLVNMQLRASY.TYLSLGFYFDRDDVAL
B6VQP1/1-175                .....................MSSQIRQNYSTEVEAAVNRLVNMHLRASY.TYLSLGFYFDRDDVAL
FgMF_3RGD/1-176             .....................MVSQVRQNYHSDCEAAVNRMLNLELYASY.TYSSMYAFFDRDDVAL
Q6P8C6/1-176                .....................MQSQVRQNFNSDCEAAINRMVNMELYASY.VYLSMSYYFDRDDVAL
P85837/1-174                .....................MESQVRQNFHKDCEAAINRQINLELYASY.SYLSMAYYFDRDDVAL
P49947/1-176                .....................MESQIRQNYHHDCERAINRMINMEMFASY.TYTSMAFYFSRDDVAL
HuMF_1R03/1-182             ..................PAAGPSRVRQNFHPDSEAAINRQINLELYASY.VYLSMAYYFSRDDVAL
HuHF_2FHA/1-183             .................MTTASTSQVRQNYHQDSEAAINRQINLELYASY.VYLSMSYYFDRDDVAL
MsHF_3WNW/1-212             GSHMASMTGGQQMGRGSMTTASPSQVRQNYHQDAEAAINRQINLELYASY.VYLSMSCYFDRDDVAL
PgFtn/1-160                 ...........................MKISENVTKAINDQIKAEMWSSN.LYLSMSVHFA..QVGY
EcFtn_1EUM/1-160            ............................MLKPEMIEKLNEQMNLELYSSL.LYQQMSAWCS..YHTF
CjFtn_1KRQ/1-167            ............................MLSKEVVKLLNEQINKEMYAAN.LYLSMSSWCY..ENSL
HpFtn_3EGM/1-181            ...MGSSP...........HHHHHSQDPMLSKDIIKLLNEQVNKEMNSSN.LYMSMSSWCY..THSL
PfFtn_2JD7/1-174            ............................MLSERMLKALNDQLNRELYSAY.LYFAMAAYFE..DLGL
A0A0C7P5L5/1-169            ...........................MVKREMTRQFLEDAFCGESKAHM.KYLIFADDAE..EKGL
A0A075WM99/1-170            ..........................MVVKKQMTRKFLEDAFAGESQAHM.RYMIFADVAE..NEGY
F8AEI6/1-171                ..........................MAVQKDMTKKFLEEAFAGESMAHM.KYLIFAEQAE..KEGF
A0A100XZC0/1-171            ..........................MVVKRKMTRKFLEDAFAGESMAHM.KYLIFAEQAE..KEGY
Q5JF11/1-171                ..........................MVVKREMTRKFLEDAFAGESMAHM.RYLIFAEQAE..REGL
Q9V0A0/1-175                ......................MVFLMPVKRAITRKFLEEAFAGESMAHM.KYLIFAEKAE..QEGF
B9KAX2/1-176                .......................MLGGGRMREMTKKFLEDAFAGESMAHM.KYLIFADEAE..QRGL
Pf_rubrerythrin_3MPS/1-130  ...........................VVKRTMTKKFLEEAFAGESMAHM.RYLIFAEKAE..QEGF
Dv_rubrerythrin_1LKM/1-144  .........................MKSLKGSRTEKNILTAFAGESQARN.RYNYFGGQAK..KDGF
St_sulerythrin_1J30/1-144   .........................MKDLKGTKTAENLKQGFIGESMANR.RYLYFAKRAD..EEGY
Bp_rubrerythrin_4DI0/1-144  .....................GPGSMAQLKGSKTEENLKYAFAGESQANR.RYLYFASKAD..VEGQ
CjDps_3KWO/1-152            ............................SNAMSVTKQLLQMQADAHHLWVKFHNYHWNVKGL...QF
BbDPS_1N1Q/1-149            .........................MKTSIQQLVAVLLNRQVANWVVLYVKLHNFHWNVNGP...NF
A0A0M1QIG0/1-146            .............................MSKQLTDIVNKQIANWSVLYIKLHNYHWYVKGS...QF
I0BUW7/1-146                .............................MSQNLTEVLNTQIANWSLLYIKLHNFHWYVKGP...QF
A0A132BNU7/1-145            .............................MSEQLIQAVNKQVANWTVMYVKLHNYHWYVKGK...DF
Q65FU7/1-145                .............................MSEKLKATVNKQVANWTVLYVKLHNYHWYVKGK...DF
D5TXF7/1-147                ...........................MSTKTNVVEVLNKQVANWNVLYVKLHNYHWYVTGP...HF
A0A0N0Y8R5/1-151            ............................MTTQAVYDVLNKQVANWSVLYVKLHNYHWFVKGD...QF
LmDPS_2IY4/1-156            .........................MKTINSVDTKEFLNHQVANLNVFTVKIHQIHWYMRGH...NF
SsDps_2XJM/1-165            ...QSPAE............IASFSPRPSLA.DSKAVLNQAVADLSVAHSILHQVHWYMRGR...GF
SsDps_2UX1/1-165            ...GSPAE............IASFSPRPSLA.DSKAVLNQAVADLSVAHSILHQVHWYMRGR...GF
EcDps_1L8H/1-167            ...MSTAKLVKS..KATNLLYTRNDVSDSEKKATVELLNRQVIQFIDLSLITKQAHWNMRGA...NF
AtDps_1O9R/1-162            ...MKTHK.............TKNDLPSNAKSTVIGILNESLASVIDLALVTKQAHWNLKGP...QF
MsDPS_1UVH/1-183            ...MTSFTI..............PGLSDKKASDVADLLQKQLSTYNDLHLTLKHVHWNVVGP...NF
Rru_A1499/1-187             ...MQFSS...............NTATPLLPNKSIESLGEHLSWAIELHAQVTQALWASRDP...AQ
MsDps/1-161                 ...MSARR............TESDIQGFHATPEFGGNLQKVLVDLIELSLQGKQAHWNVVGS...NF
Rru_A0333/1-158             ...MDG.............LSIDIGIADDKRQAIAEGLSRLLADTYTLYLKTHNYHWNVTGP...MF
Cp_symerythrin_3QHC/1-179   ..GLNYNQE.......DFMGLDRFFQDAVSHNNTDANAASSIEVEMYECDCMYPTFAEIAR..RSGQ
STAUR_4074/1-157            ...................MAGSSDTELL..NDVAR.IRRVLARELETIN.EYEAFAQISSH.....
MXAN_3557/1-164             ...MQGSI..........PMAGPPDSDL...DDVAR.IRLVLARELETIN.EYEAYARASSN.....
MXAN_4464/1-116             ............................MTDTELARSIRLNIEAELDAIN.LYAAHIDATDN.....
MXAN_2410/1-109             ............................MAKNSNPSAFDRDFGYLMPFLD.RVAAAASDLED.....
Cthe_1503/1-119             ...MASFAN.........PFAGNVP.RKLTKEELIQAIRLNIAGELEAIF.VYDAHVQATDD.....
Tlet_1919/1-116             ...MPEFVN.........PFSGKVPDRKLSLSELIRAIRLNIAAEHEAVH.LYMAHADATDH.....
Mboo_1094/1-124             ...MPDFFN.........PFSGMVPERKLTKEELIRVVRLDVAGELEAIH.GYMAHAEATDN.....
PF1192/1-96                 ...M.LSIN.........P.TLINRDKPYTKEELMEILRLAIIAELDAIN.LYEQMARYSED.....
PFC_05175short/1-99         ...MGLSIN.........P.TLINRDKPYTKEELMEILRLAIIAELDAIN.LYEQMARYSED.....
Hoch_3836/1-131             ...MSSEQ...........LHEPAELLSEETKNMHRAL.VTLIEELEAVD.WYQQRADACSE.....
Rru_A0973/1-140             ...MAQSSN.........STHEPLEVLKEETVNRHRAI.VSVMEELEAVD.WYDQRVDASTD.....
FRAAL4504/1-136             .MGDSSMG...........LHEQPDKLSAQTVDRHRAI.VSLMEELEAVD.WYDQRVDAATD.....
Sce5279/1-127               ...MSSEN...........YHELPELLSEATKERHRAI.VSLIEELEAID.WYQQRAEACSD.....
WS0286/1-124                ...MVHEG...........AKEAAERLPEEVVDYHRII.QSTIEELEAVD.LYNQRAAATKD.....
Amet_4422/1-120             ...MAMD............YHEPVENLDEKTKNITRAI.NSLKEEIEAVD.WYNQRVAASND.....
Hore_15960/1-115            ...MANT............YHE..ENLPEEAREFHRMI.RSVIEELEAVD.WYHQRAAVTND.....
Tpet_0143/1-114             ...MADQ............YHEPVSELTGKDRDFVRAL.NSLKEEIEAVA.WYHQRVVTTKD.....
Tmari_0787/1-114            ...MADQ............YHEPVSELTGKDRDFVRAL.NSLKEEIEAVA.WYHQRVVTTKD.....
Tbd_2465/1-100              ...MSSVG...........YHEPIGELSDETRDMHRAI.VSLMEELEAVD.WYNQRADACKD.....
Achr_1378/1-102             ...MSSVG...........YHEPSEELSAETRDMHRAI.VSLMEELEAID.WYNQRVDACRD.....
PG1C_13910/1-99             ...MSSVG...........YHEPVEELSAETRDMHRAI.VSLMEELEAVD.WYNQRADACKD.....
Tgr7_0837/1-101             ...MSNEG...........YHEPYEELSDETRDMHRAI.ISLMEELEAVD.WYQQRVDACKD.....
CYCME_0127/1-95             ...MSNEG...........YHEPISEITDETRDMHRAI.TSLMEELEAVD.WYNQRVDACKD.....
Q91_0125/1-95               ...MSNEG...........YHEPISEITDETRDMHRAI.TSLMEELEAVD.WYNQRVDACKD.....
Nmul_A2196/1-96             ...MANEG...........YHEPLEELSDETRDMHKAI.VSLMEELEAID.WYNQRVDSCKD.....
cce_0034/1-96               ...MSNEG...........YHEPIHELSSETIEMHRAI.TSLMEELEAID.WYNQRVDVCKN.....
Metme_0971/1-95             ...MANEG...........YHEPIDELSDATRDMHRAI.TSLMEELEAVD.WYNQRVDACKN.....
MEALZ_1148/1-94             ...MANEG...........YHEAIEELSDATRDMHRAI.TSLMEELEAVD.WYNQRVDACKD.....
AAY24_01205/1-95            ...MASEG...........YHEPIEELSTETRDMHRAI.VSLMEELEAVD.WYNQRVDACQN.....
IMCC21906_01077/1-95        ...MSNEG...........YHEPISELTDKTRDMHRAI.VSLMEELEAVD.WYNQRVDACKD.....
Sta7437_0684/1-95           ...MSNEG...........YHEPVHELTGVTREMHRAI.TSLMEELEAVD.WYNQRVNACHD.....
GU3_08795/1-95              ...MANEG...........YHEPIDELSDDTRDMHRAI.TSLMEELEAVD.WYNQRVDACKD.....
MARPU_03990/1-95            ...MSSEG...........YHEPIEELTDETRDMHRAI.VSLMEELEAVD.WYNQRVDACKD.....
Thivi_3051/1-95             ...MANEG...........YHEPTEELSDETRDMHRAI.ISLMEELEAVD.WYNQRVDVCKD.....
THII_2135/1-95              ...MANEG...........LHERFEDLHEETRDMHRAI.VSLMEELEAID.WYNQRVDACKN.....
NE0167/1-95                 ...MANDG...........YFEPTQELSDETRDMHRAI.ISLREELEAVD.LYNQRVNACKD.....
Kkor_0109/1-94              ...MSNEG...........YHEPYEELSDETKDMHRAI.ISLMEELEAVD.WYNQRIDCCKD.....
M911_12845/1-94             ...MANEG...........YHEPIDELSDETRDMHRAI.VSLMEELEAVD.WYNQRIDACKD.....
consensus>70                ............................................e..a....y..............
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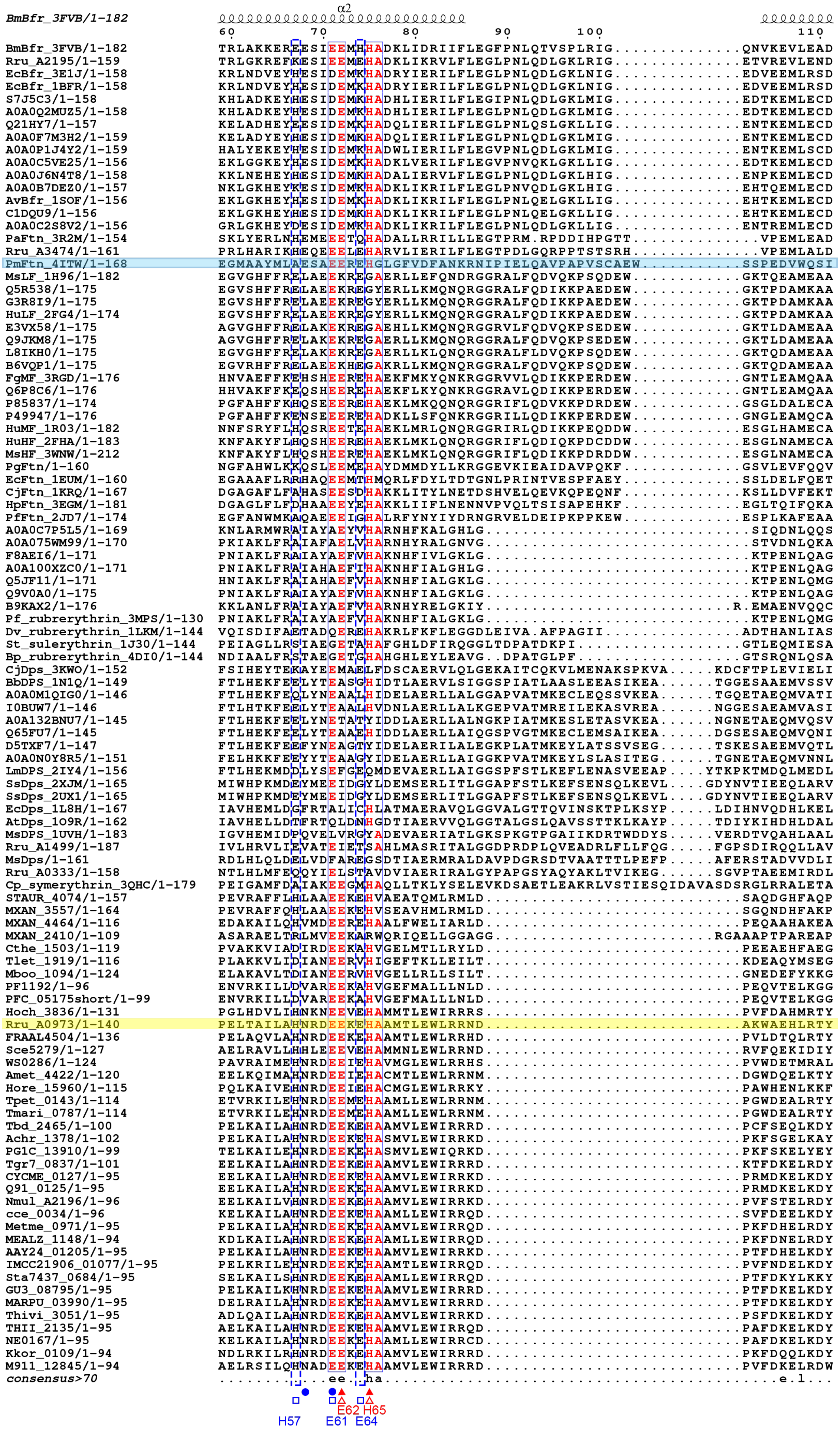

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BmBfr_3FVB/1-182            TRLAKKEREESIEEMHHADKLIDRIIFLEGFPNLQTVSPLRIG..............QNVKEVLEAD
Rru_A2195/1-159             TRLGKREFKESIEEMEHADKLIKRVLFLEGLPNLQDLGKLRIG..............ETVREVLEND
EcBfr_3E1J/1-158            KRLNDVEYHESIDEMKHADRYIERILFLEGLPNLQDLGKLNIG..............EDVEEMLRSD
EcBfr_1BFR/1-158            KRLNDVEYHESIDEMKHADRYIERILFLEGLPNLQDLGKLNIG..............EDVEEMLRSD
S7J5C3/1-158                KHLADKEYHESIDEMKHADHLIERILFLEGIPNLQDLGKLMIG..............EDTKEMLECD
A0A0Q2MUZ5/1-158            KHLADKEYHESIDEMKHADHLIERILFLEGLPNLQDLGKLMIG..............EDTKEMLECD
Q21HY7/1-157                KELADHEYEESIDEMKHADQLIERILFLEGLPNLQSLGKLLIG..............ENTKEMLECD
A0A0F7M3H2/1-159            KELADYEYHESIDEMKHADQLIERILFLEGLPNLQDLGKLMIG..............ENTKEMLECD
A0A0P1J4Y2/1-159            HALYEKEYHESIDEMKHADWLIERILFLEGVPNLQDLGKLMIG..............ENTKEMLSCD
A0A0C5VE25/1-156            EKLGGKEYHESIDEMKHADKLVERILFLEGVPNVQKLGKLLIG..............EDTKEMLECD
A0A0J6N4T8/1-158            KKLNEHEYHESIDEMKHADALIERVLFLEGLPNLQDLGKLHIG..............ENPKEMLECD
A0A0B7DEZ0/1-157            NKLGKHEYKESIDEMKHADKLIKRILFLEGLPNVQDLGKLHIG..............EHTQEMLECD
AvBfr_1SOF/1-156            EKLGKHEYHESIDEMKHADKLIKRILFLEGLPNLQELGKLLIG..............EHTKEMLECD
C1DQU9/1-156                EKLGKHEYHESIDEMKHADKLIKRILFLEGLPNLQELGKLLIG..............EHTKEMLECD
A0A0C2S8V2/1-156            GRLGKHEYDESIDEMKHADKLIKRILFLEGLPNLQDLGKLLIG..............ENTREMLECD
PaFtn_3R2M/1-154            SKLYERLNHEMEEETQHADALLRRILLLEGTPRM.RPDDIHPGTT..............VPEMLEAD
Rru_A3474/1-161             PRLHARIKHEQEEELEHARVLIERILFLEGTPDLGQRPPTSTSRH..............VPEMLALD
PmFtn_4ITW/1-168            EGMAAYMLAESAEEREHGLGFVDFANKRNIPIELQAVPAPVSCAEW...........SSPEDVWQSI
MsLF_1H96/1-182             EGVGHFFRELAEEKREGAERLLEFQNDRGGRALFQDVQKPSQDEW............GKTQEAMEAA
Q5R538/1-175                EGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAEDEW............GKTPDAMKAA
G3R8I9/1-175                EGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAEDEW............GKTPDAMKAA
HuLF_2FG4/1-174             EGVSHFFRELAEEKREGYERLLKMQNQRGGRALFQDIKKPAEDEW............GKTPDAMKAA
E3VX58/1-175                AGVGHFFRELAKEKREGAEHLLKMQNQRGGRVLFQDVQKPSEDEW............GKTLDAMEAA
Q9JKM8/1-175                AGVGHFFRELAKEKREGAERLLKMQNQRGGRALFQDVQKPSEDEW............GKTLDAMEAA
L8IKH0/1-175                EGVGHFFRELAKEKREGAERLLKLQNQRGGRALFLDVQKPSQDEW............GKTQDAMEAA
B6VQP1/1-175                EGVRHFFRELAEEKHEGAKRLLKMQNQRGGRALFQDVQKPSQDEW............GKTQDAMEAA
FgMF_3RGD/1-176             HNVAEFFKEHSHEEREHAEKFMKYQNKRGGRVVLQDIKKPERDEW............GNTLEAMQAA
Q6P8C6/1-176                HHVAKFFKEQSHEEREHAEKFLKYQNKRGGRAVLQDIKKPERDEW............GNTLEAMQAA
P85837/1-174                PGFAHFFKHQSEEEREHAEKLMKQQNQRGGRIFLQDVKKPDRDEW............GSGLDALECA
P49947/1-176                PGFAHFFKENSEEEREHADKLLSFQNKRGGRILLQDIKKPERDEW............GNGLEAMQCA
HuMF_1R03/1-182             NNFSRYFLHQSREETEHAEKLMRLQNQRGGRIRLQDIKKPEQDDW............ESGLHAMECA
HuHF_2FHA/1-183             KNFAKYFLHQSHEEREHAEKLMKLQNQRGGRIFLQDIQKPDCDDW............ESGLNAMECA
MsHF_3WNW/1-212             KNFAKYFLHQSHEEREHAEKLMKLQNQRGGRIFLQDIKKPDRDDW............ESGLNAMECA
PgFtn/1-160                 NGFAHWLKKQSLEEMEHAYDMMDYLLKRGGEVKIEAIDAVPQKF.............GSVLEVFQQV
EcFtn_1EUM/1-160            EGAAAFLRRHAQEEMTHMQRLFDYLTDTGNLPRINTVESPFAEY.............SSLDELFQET
CjFtn_1KRQ/1-167            DGAGAFLFAHASEESDHAKKLITYLNETDSHVELQEVKQPEQNF.............KSLLDVFEKT
HpFtn_3EGM/1-181            DGAGLFLFDHAAEEYEHAKKLIIFLNENNVPVQLTSISAPEHKF.............EGLTQIFQKA
PfFtn_2JD7/1-174            EGFANWMKAQAEEEIGHALRFYNYIYDRNGRVELDEIPKPPKEW.............ESPLKAFEAA
A0A0C7P5L5/1-169            KNLARMWRAIAYAEYVHARNHFKALGHLG.............................SIQDNLQQS
A0A075WM99/1-170            PKIAKLFRAIAFAELVHARNHYRALGNVG.............................STVDNLQKA
F8AEI6/1-171                PNIAKLFRAIAYAEFVHAKNHFIVLGKLG.............................KTPENLQAG
A0A100XZC0/1-171            PNIAKLFRAIAHAEFIHAKNHFIALGHLG.............................KTPENLQAG
Q5JF11/1-171                HNIAKLFRAIAHAEFVHAKNHFIALGKLG.............................KTPENLQMG
Q9V0A0/1-175                PNIAKLFRAIAYAEFVHAKNHFIALGKLG.............................KTPENLQAG
B9KAX2/1-176                KKLANLFRAIAYAEFVHARNHYRELGKIY...........................R.EMAENVQQC
Pf_rubrerythrin_3MPS/1-130  PNIAKLFRAIAYAEFVHAKNHFIALGKLG.............................KTPENLQMG
Dv_rubrerythrin_1LKM/1-144  VQISDIFAETADQEREHAKRLFKFLEGGDLEIVA.AFPAGII...............ADTHANLIAS
St_sulerythrin_1J30/1-144   PEIAGLLRSIAEGETAHAFGHLDFIRQGGLTDPATDKPI..................GTLEQMIESA
Bp_rubrerythrin_4DI0/1-144  NDIAALFRSTAEGETGHAHGHLEYLEAVG..DPATGLPF..................GTSRQNLQSA
CjDps_3KWO/1-152            FSIHEYTEKAYEEMAELFDSCAERVLQLGEKAITCQKVLMENAKSPKVA.....KDCFTPLEVIELI
BbDPS_1N1Q/1-149            FTLHEKFEELYTEASGHIDTLAERVLSIGGSPIATLAASLEEASIKEA......TGGESAAEMVSSV
A0A0M1QIG0/1-146            FTLHEKFEQLYNEAALHIDELAERLLALGGAPVATMKECLEQSSVKEA......TGQETAEQMVATI
I0BUW7/1-146                FTLHTKFEELYTEAALHVDNLAERLLALKGEPVATMREILEKASVREA......NGGESAEAMVASI
A0A132BNU7/1-145            FTLHEKFEELYNETATYIDDLAERLLALNGKPIATMKESLETASVKEA......NGNETAEQMVQSV
Q65FU7/1-145                FTLHEKFEELYTEAAEHIDDLAERLLAIQGSPVGTMKECLEMSAIKEA......DGSESAEQMVQNI
D5TXF7/1-147                FTLHEKFEEFYNEAGTYIDELAERILALEGKPLATMKEYLATSSVSEG......TSKESAEEMVQTL
A0A0N0Y8R5/1-151            FELHKKFEEYYTEAAGYIDELAERLLAIGGKPVATMKEYLSLASITEG......TGNETAEQMVNNL
LmDPS_2IY4/1-156            FTLHEKMDDLYSEFGEQMDEVAERLLAIGGSPFSTLKEFLENASVEEAP....YTKPKTMDQLMEDL
SsDps_2XJM/1-165            MIWHPKMDEYMEEIDGYLDEMSERLITLGGAPFSTLKEFSENSQLKEVL....GDYNVTIEEQLARV
SsDps_2UX1/1-165            MIWHPKMDEYMEEIDGYLDEMSERLITLGGAPFSTLKEFSENSQLKEVL....GDYNVTIEEQLARV
EcDps_1L8H/1-167            IAVHEMLDGFRTALICHLATMAERAVQLGGVALGTTQVINSKTPLKSYP.....LDIHNVQDHLKEL
AtDps_1O9R/1-162            IAVHELLDTFRTQLDNHGDTIAERVVQLGGTALGSLQAVSSTTKLKAYP.....TDIYKIHDHLDAL
MsDPS_1UVH/1-183            IGVHEMIDPQVELVRGYADEVAERIATLGKSPKGTPGAIIKDRTWDDYS.....VERDTVQAHLAAL
Rru_A1499/1-187             IVLHRVLIEVATEIETSAHLMASRITALGGDPRDPLQVEADRLFLLFQG.....FGPSDIRQQLLAV
MsDps/1-161                 RDLHLQLDELVDFAREGSDTIAERMRALDAVPDGRSDTVAATTTLPEFP.....AFERSTADVVDLI
Rru_A0333/1-158             NTLHLMFEQQYIELSTAVDVIAERIRALGYPAPGSYAQYAKLTVIKEG......SGVPTAEEMIRDL
Cp_symerythrin_3QHC/1-179   PEIGAMFDAIAKEEGMHAQLLTKLYSELEVKDSAETLEAKRLVSTIESQIDAVASDSRGLRRALETA
STAUR_4074/1-157            PEVRAFFLHLAAEEKEHVAEATQMLRMLD............................SAQDGHFAQP
MXAN_3557/1-164             PEVRAFFQHLAAEEKEHVSEAVHMLRMLD............................SGQNDHFAKP
MXAN_4464/1-116             EDAKAILQHVMDEEREHAALFWELIARLD............................PEQAAHAKEA
MXAN_2410/1-109             ASARAELTRLMVEEKARWQRIQELLGGAGG........................RGAAAPTPAREAP
Cthe_1503/1-119             PVAKKVIADIRDEEKAHVGELMTLLRYLD............................PEEAEHFAEG
Tlet_1919/1-116             PLAKKVLIDIANEERVHIGEFTKLLEILT............................KDEAQYMSEG
Mboo_1094/1-124             ELAKAVLTDIANEERVHVGELLRLLSILT............................GNEDEFYKKG
PF1192/1-96                 ENVRKILLDVAREEKAHVGEFMALLLNLD............................PEQVTELKGG
PFC_05175short/1-99         ENVRKILLDVAREEKAHVGEFMALLLNLD............................PEQVTELKGG
Hoch_3836/1-131             PGLHDVLIHNKNEEVEHAMMTLEWIRRRS............................PVFDAHMRTY
Rru_A0973/1-140             PELTAILAHNRDEEKEHAAMTLEWLRRND............................AKWAEHLRTY
FRAAL4504/1-136             PELAQVLAHNRDEEKEHAAMTLEWLRRHD............................PVLDTQLRTY
Sce5279/1-127               AELRAVLLHHLEEEVEHAMMNLEWLRRND............................RVFQEKIDIY
WS0286/1-124                PAVRAIMEHNRDEEIEHAVMGLEWLRRHS............................PVWDETMRAL
Amet_4422/1-120             EELKQIMAHNRDEEIEHACMTLEWLRRNM............................DGWDQELKTY
Hore_15960/1-115            PQLKAIVEHNRDEEIEHACMGLEWLRRKY............................PAWHENLKKF
Tpet_0143/1-114             ETVRKILEHNRDEEMEHAAMLLEWLRRNM............................PGWDEALRTY
Tmari_0787/1-114            ETVRKILEHNRDEEMEHAAMLLEWLRRNM............................PGWDEALRTY
Tbd_2465/1-100              PELKAILAHNRDEEKEHAAMVLEWIRRRD............................PCFSEQLKDY
Achr_1378/1-102             PELKAILAHNRDEEKEHASMVLEWIRRKD............................PKFSGELKAY
PG1C_13910/1-99             TELKAILEHNRDEEKEHASMVLEWIQRKD............................PKFSKELYEY
Tgr7_0837/1-101             EELKAILAHNRDEEKEHAAMVLEWIRRRD............................KTFDKELRDY
CYCME_0127/1-95             EELKAILAHNRDEEKEHAAMVLEWIRRKD............................PRMDKELKDY
Q91_0125/1-95               EELKAILAHNRDEEKEHAAMVLEWIRRKD............................PRMDKELKDY
Nmul_A2196/1-96             EELKAILVHNRDEEKEHAAMVLEWIRRKD............................PVFSTELRDY
cce_0034/1-96               KELKAILAHNRDEEKEHAAMLLEWIRRQD............................SVFDEELKDY
Metme_0971/1-95             PELKAILAHNRDEEKEHAAMVLEWIRRQD............................PKFDHELRDY
MEALZ_1148/1-94             KDLKAILAHNRDEEKEHAAMLLEWIRRQD............................PKFDNELRDY
AAY24_01205/1-95            PELKAILAHNRDEEKEHAAMVLEWIRRKD............................PTFDHELKDY
IMCC21906_01077/1-95        PELKRILEHNRDEEKEHAAMTLEWIRRQD............................PVFNDELKDY
Sta7437_0684/1-95           SELKAILSHNRDEEKEHAAMLLEWIRRQD............................PTFDKYLKKY
GU3_08795/1-95              PELKAILKHNRDEEKEHAAMVLEWIRRRD............................PTFDKELKDY
MARPU_03990/1-95            DELRAILAHNRDEEKEHAAMVLEWIRRRD............................PTFDKELKDY
Thivi_3051/1-95             ADLQAILAHNRDEEKEHAAMVLEWIRRKD............................PSFDKELKDY
THII_2135/1-95              AELKAILAHNRDEEKEHAAMVLEWIRRQD............................PAFDKELKDY
NE0167/1-95                 KELKAILAHNRDEEKEHAAMLLEWIRRCD............................PAFDKELKDY
Kkor_0109/1-94              NDLRKILRHNRDEEKEHAAMVLEWIRRRD............................PKFDQQLKDY
M911_12845/1-94             AELRSILQHNADEEKEHAAMVLEWIRRRD............................PVFDKELRDW
consensus>70                ............ee..ha...........................................e.l...
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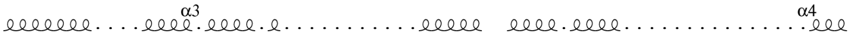
BmBfr_3FVB/1-182



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                                      120                    130         140
BmBfr_3FVB/1-182            LKGEYDA....RASY.KESR.E...........ICDKLGDYVSK.QLFD................ELL
Rru_A2195/1-159             LALELAA....RDTL.VEGV.A...........EAEAAQDFVSR.QILD................EIL
EcBfr_3E1J/1-158            LALELDG....AKNL.REAI.G...........YADSVHDYVSR.DMMI................EIL
EcBfr_1BFR/1-158            LALELDG....AKNL.REAI.G...........YADSVHDYVSR.DMMI................EIL
S7J5C3/1-158                LKLELSA....IPDL.RDAI.A...........YAEDIRDYVSR.DLFQ................DIL
A0A0Q2MUZ5/1-158            LKLELAA....IPDL.RDAI.A...........YAEDIRDYVSR.DLFQ................DIL
Q21HY7/1-157                LKLEMKA....IPDL.RDGI.E...........YAESVRDYISR.DLLQ................SIL
A0A0F7M3H2/1-159            LSLELKA....VPDL.KDGI.K...........HCESVADYGSR.ELLE................EIL
A0A0P1J4Y2/1-159            LKLEHLA....VPDL.REAM.A...........YCESVQDYVSR.DLFR................RIL
A0A0C5VE25/1-156            LKLENMA....VPVL.REAI.A...........YCESVQDYVSR.DLLE................DIL
A0A0J6N4T8/1-158            LKLEMDA....LPVL.REAI.A...........YCESAKDYVTR.DLLE................DIL
A0A0B7DEZ0/1-157            LRIEKTG....HADL.KAAI.A...........HCETVGDFGSR.ELLE................DIL
AvBfr_1SOF/1-156            LKLEQAG....LPDL.KAAI.A...........YCESVGDYASR.ELLE................DIL
C1DQU9/1-156                LKLEQAG....LPDL.KAAI.A...........YCESVGDYASR.ELLE................DIL
A0A0C2S8V2/1-156            LKLEQSG....IADL.KVAI.A...........YCESVGDYGSR.ELLE................DIL
PaFtn_3R2M/1-154            LKLERHV....RAAL.AKGI.A...........LCEQHKDFVSR.DILKA...............QLA
Rru_A3474/1-161             LDTERTV....VTNL.RRVI.K...........LCEAEKDYVTR.QALLP...............LLN
PmFtn_4ITW/1-168            LELEQAN....TRSL.LNLA.E...........AASTCHDFAVM.AFLN................PFH
MsLF_1H96/1-182             LAMEKNL....NQAL.LDLH.A...........LGSARADPHLC.DFLES...............HYL
Q5R538/1-175                MALEKKL....NQAL.LDLH.A...........LGSAHTDPHLC.DFLET...............HFL
G3R8I9/1-175                MALEKKL....NQAL.LDLH.A...........LGSARTDPHLC.DFLET...............HFL
HuLF_2FG4/1-174             MALEKKL....NQAL.LDLH.A...........LGSARTDPHLC.DFLET...............HFL
E3VX58/1-175                LALEKNL....NQAL.LDLH.A...........LGSAKTDPHLC.DFLEN...............HFL
Q9JKM8/1-175                LTLEKSL....NQAL.LDLH.A...........LGSAKTDPHVC.DFLEN...............HFL
L8IKH0/1-175                LLVEKNL....NQAL.LDLH.G...........LASARGDPHIC.DFLEN...............HFL
B6VQP1/1-175                IKMEKNL....NEAL.LDLH.A...........LACARADPHLC.DFLES...............HFL
FgMF_3RGD/1-176             LQLEKTV....NQAL.LDLH.K...........LATDKVDPHLC.DFLES...............EYL
Q6P8C6/1-176                LQLEKTV....NQAL.LDLH.K...........LASDKTDPHLC.DFLES...............EYL
P85837/1-174                LQLEKNV....NQSL.LDLH.K...........VCSEHNDPHMC.DFLET...............HYL
P49947/1-176                LQLEKNV....NQAL.LDLH.K...........IASDKVDPHLC.DFLET...............HYL
HuMF_1R03/1-182             LLLEKNV....NQSL.LELH.A...........LASDKGDPHLC.DFLET...............YYL
HuHF_2FHA/1-183             LHLEKNV....NQSL.LELH.K...........LATDKNDPHLC.DFIET...............HYL
MsHF_3WNW/1-212             LHLEKSV....NQSL.LELH.K...........LATDKNDPHLC.DFIET...............YYL
PgFtn/1-160                 YEHECKV....TEMI.EAVV.R...........AASEAGDMASQ.DFFW................KYI
EcFtn_1EUM/1-160            YKHEQLI....TQKI.NELA.H...........AAMTNQDYPTF.NFLQ................WYV
CjFtn_1KRQ/1-167            YEHEQFI....TKSI.NTLV.E...........HMLTHKDYSTF.NFLQ................WYV
HpFtn_3EGM/1-181            YEHEQHI....SESI.NNIV.D...........HAIKSKDHATF.NFLQ................WYV
PfFtn_2JD7/1-174            YEHEKFI....SKSI.YELA.A...........LAEEEKDYSTR.AFLE................WFI
A0A0C7P5L5/1-169            IEGENFE....VQEM.YPVYNN...........AAKFQNENEAV.RTTH................FAL
A0A075WM99/1-170            IEGESYE....VEEM.YPVFNN...........AAKFQGESEAE.KSTY................YAL
F8AEI6/1-171                IEGETYE....VEEM.YPVFKN...........TAELQGEKEAV.RSTH................YAL
A0A100XZC0/1-171            IDGETYE....VEEM.YPVFKN...........AAEFQGEKDAI.RTTH................YAL
Q5JF11/1-171                IEGETFE....VEEM.YPVYKN...........SAEFQEEKDAV.RTTH................YAL
Q9V0A0/1-175                IEGETYE....VEEM.YPVFNK...........TAEFQGEKDAV.RTTH................FAL
B9KAX2/1-176                IDGETFE....IEEM.YPVYNT...........VAQFQQEKGAE.RSTK................FAW
Pf_rubrerythrin_3MPS/1-130  IEGETFE....VEEM.YPVYNK...........AAEFQGEKEAV.RTTH................YAL
Dv_rubrerythrin_1LKM/1-144  AAGEHHE....YTEM.YPSFAR...........IAREEGYEEIA.RVFA................SIA
St_sulerythrin_1J30/1-144   IAGETYE....WTQM.YPGFAK...........VAREEGFPEVA.EWFE................TLA
Bp_rubrerythrin_4DI0/1-144  IAGETHE....YTDM.YPGMAK...........TARDEGFEEIA.NWFE................TLA
CjDps_3KWO/1-152            KQDYEYL....LAEF.KKLN.E...........AAEKESDTTTA.AFAQ................ENI
BbDPS_1N1Q/1-149            VNDFVDL....VGEL.KVAR.D...........VADEADDEATA.DMLD................AIE
A0A0M1QIG0/1-146            VSDFETM....IEEL.KEGM.K...........IADEVGDETTG.DMLL................GIH
I0BUW7/1-146                VSDFGIV....IGEL.KEGM.A...........LAEKVGDETTG.DMLL................AIH
A0A132BNU7/1-145            YDDFTVI....AEEL.KSGM.D...........LADEVGDETTG.DMLL................AIH
Q65FU7/1-145                YNDFLTV....AEEL.KSGM.E...........LADEVNDETTG.DMLL................AIH
D5TXF7/1-147                VNDYSAL....IQEL.KEGM.E...........VAGEAGDETSA.DMLL................AIH
A0A0N0Y8R5/1-151            ITDFNTL....VDEL.KQGI.D...........IADQAGDESTA.DMLT................HIR
LmDPS_2IY4/1-156            VGTLELL....RDEY.QQGI.E...........LTDKEGDNVTN.DMLI................AFK
SsDps_2XJM/1-165            VEVFRYL....AALF.QKGF.D...........VSDEEGDSVTN.DIFN................VAK
SsDps_2UX1/1-165            VEVFRYL....AALF.QKGF.D...........VSDEEGDSVTN.DIFN................VAK
EcDps_1L8H/1-167            ADRYAIV....ANDV.RKAI...............GEAKDDDTA.DILT................AAS
AtDps_1O9R/1-162            IERYGEV....ANMI.RKAI.D...........DSDEAGDPTTA.DIFT................AAS
MsDPS_1UVH/1-183            DLVYNGV....IEDT.RKSI.............EKLEDLDLVSQ.DLLI................AHA
Rru_A1499/1-187             AASLAAF....GHSL.REAI.R...........QAVSIDDAPTA.HLFI................ELS
MsDps/1-161                 TTRINAT....VDTI.RRVH.............DAVDAEDPSTA.DLLH................GLI
Rru_A0333/1-158             ARDQEAV....TRTA.RSIF.P...........VADEAADEPTA.DLLT................QRM
Cp_symerythrin_3QHC/1-179   LEVETIE....SQKT.YPAFAK...........LAAEQGNMEVA.TAFE................AIV
STAUR_4074/1-157            IAPGHFQKVLSAPPA.PPAPASPSPAP......AGPEQTRAPPVIEPISHLPPQRVVYGVPAP.PST
MXAN_3557/1-164             FVPGHFQ....AAEAPAPATVH.VPTPDGPAFSVNGRNGRLPSE.PPTS.LPPQRLLYGLPAPPPAV
MXAN_4464/1-116             VEKYRLI....TSGA.SHEAVE...........AVGKEGAAPS.........PA...........DVT
MXAN_2410/1-109             AEAPRLA....RGSA.DELH.E...........AAP...........FA...................
Cthe_1503/1-119             EQEVKEM....LEQL..............................NITPK...............PLS
Tlet_1919/1-116             AKEVEEM..........................................................MVE
Mboo_1094/1-124             TLEVDTL...........................AGQIGAAGAA.....................APV
PF1192/1-96                 FEEVQGA.............................................................
PFC_05175short/1-99         FEEVKEL.....TGI.E................A..................................
Hoch_3836/1-131             LFTERPI.....LEL.EEEDTG...........SSSSVAASPT......................SAP
Rru_A0973/1-140             LFTEGPI.....TAI.EAADTA...........GEGSGGDAAKG....................ATAQ
FRAAL4504/1-136             LFTSGPV.....TEV.EEETMD.....R....GGSGDPDAVTE...................RQAAGP
Sce5279/1-127               LNSQGPI.....TEV.EAAE.............EAAKLGATAKT....................GAMA
WS0286/1-124                LFKEGEI.....ISH.EQAFTG...........KTGEVASALG.........................
Amet_4422/1-120             LFTTGSI.....LEA.EMGA.............ETGTETETVV.........................
Hore_15960/1-115            LFSEGDI.....ASL.EEEE.............ENQENTETTD.........................
Tpet_0143/1-114             LFTDKPI.....TEI.EEET.............SGGSENT............................
Tmari_0787/1-114            LFTDKPI.....TEI.EEET.............SGGSENT............................
Tbd_2465/1-100              LFTDKAI.....A...HEAKKD...........S..................................
Achr_1378/1-102             LFREGPI.....N...HEDDAQ...........ASG................................
PG1C_13910/1-99             LFTKKTI.....A...HRPDDA..............................................
Tgr7_0837/1-101             LFTDKPI.....AGLEHEHKG...............................................
CYCME_0127/1-95             LFTDKPI.....A...HK..................................................
Q91_0125/1-95               LFTDKPI.....A...HK..................................................
Nmul_A2196/1-96             LFTDKPI.....A...HES.................................................
cce_0034/1-96               LFTEKTI.....A...HES.................................................
Metme_0971/1-95             LFTDKTI.....A...HE..................................................
MEALZ_1148/1-94             LFTDKPI.....A...H...................................................
AAY24_01205/1-95            LFTEKPI.....A...HE..................................................
IMCC21906_01077/1-95        LFTDKPI.....A...HK..................................................
Sta7437_0684/1-95           LFTSQPI.....A...HK..................................................
GU3_08795/1-95              LFTSGPL.....G...HH..................................................
MARPU_03990/1-95            LFTEKQI.....A...HH..................................................
Thivi_3051/1-95             LFTDKVI.....A...HH..................................................
THII_2135/1-95              LFTNKSI.....A...HE..................................................
NE0167/1-95                 LFTNKPI.....A...HE..................................................
Kkor_0109/1-94              LFTEDEI.....G...H...................................................
M911_12845/1-94             LFTDKKL.....D...H...................................................
consensus>70                ...e................................................................
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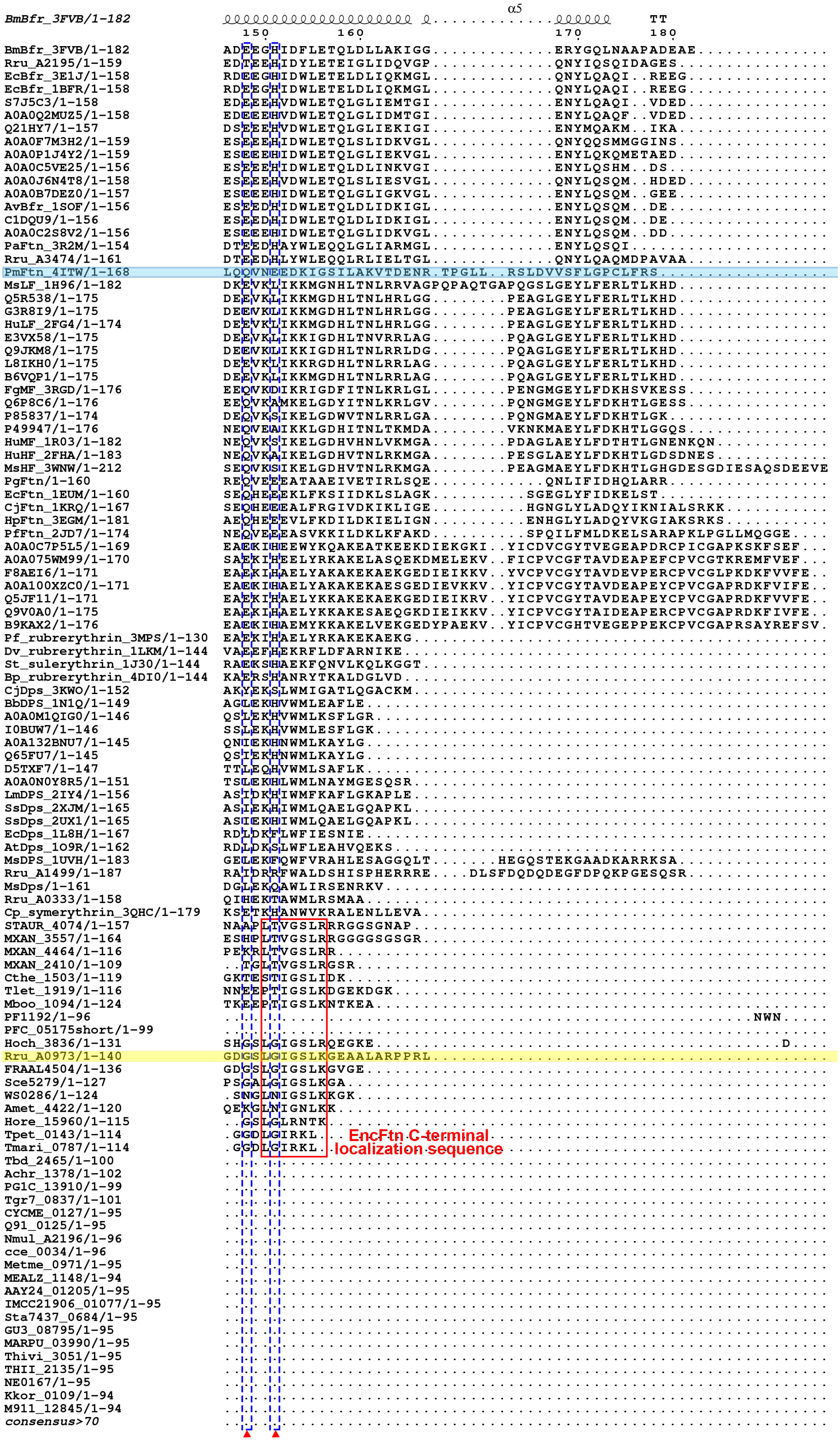

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                                                          α5
BmBfr_3FVB/1-182                                                         TT
                              150       160                    170       180
BmBfr_3FVB/1-182            ADEEGHIDFLETQLDLLAKIGG.............ERYGQLNAAPADEAE..............
Rru_A2195/1-159             EDTEEHIDYLETEIGLIDQVGP.............QNYIQSQIDAGES................
EcBfr_3E1J/1-158            RDEEGHIDWLETELDLIQKMGL.............QNYLQAQI..REEG...............
EcBfr_1BFR/1-158            RDEEGHIDWLETELDLIQKMGL.............QNYLQAQI..REEG...............
S7J5C3/1-158                EDEEEHVDWLETQLGLIEMTGI.............ENYLQAQI..VDED...............
A0A0Q2MUZ5/1-158            EDEEEHVDWLETQLGLIDMTGI.............ENYLQAQF..VDED...............
Q21HY7/1-157                DSEEEHVDWLETQLGLIEKIGI.............ENYMQAKM..IKA................
A0A0F7M3H2/1-159            ESEEEHIDWLETQLSLIDKVGL.............QNYQQSMMGGINS................
A0A0P1J4Y2/1-159            ESEEEHIDWLETQLGLIEKVGL.............ENYLQKQMETAED................
A0A0C5VE25/1-156            ESEEEHIDWLETQLDLINKVGI.............ENYLQSHM..DS.................
A0A0J6N4T8/1-158            ESEEEHVDWLETQLSLIESVGL.............QNYLQSQM..HDED...............
A0A0B7DEZ0/1-157            ESEEEHIDWLETQLGLIGKVGL.............ENYLQSQM..GEE................
AvBfr_1SOF/1-156            ESEEDHIDWLETQLDLIDKIGL.............ENYLQSQM..DE.................
C1DQU9/1-156                ESEEDHIDWLETQLDLIDKIGL.............ENYLQSQM..DE.................
A0A0C2S8V2/1-156            ESEEEHIDWLETQLGLIDKVGL.............ENYLQSQM..DD.................
PaFtn_3R2M/1-154            DTEEDHAYWLEQQLGLIARMGL.............ENYLQSQI.....................
Rru_A3474/1-161             DTEEDHLYWLEQQLRLIELTGL.............QNYLQAQMDPAVAA...............
PmFtn_4ITW/1-168            LQQVNEEDKIGSILAKVTDENR.TPGLL..RSLDVVSFLGPCLFRS..................
MsLF_1H96/1-182             DKEVKLIKKMGNHLTNLRRVAGPQPAQTGAPQGSLGEYLFERLTLKHD................
Q5R538/1-175                DEEVKLIKKMGDHLTNLHRLGG........PEAGLGEYLFERLTLKHD................
G3R8I9/1-175                DEEVKLIKKMGDHLTNLHRLGG........PEAGLGEYLFERLTLKHD................
HuLF_2FG4/1-174             DEEVKLIKKMGDHLTNLHRLGG........PEAGLGEYLFERLTLKHD................
E3VX58/1-175                DEEVKLIKKIGDHLTNVRRLAG........PQAGLGEYLFERLTLKHD................
Q9JKM8/1-175                DEEVKLIKKIGDHLTNLRRLDG........PQAGLGEYLFERLTLKHD................
L8IKH0/1-175                DEEVKLIKKRGDHLTNLRRLAG........PQAGLGEYLFERLTLKHD................
B6VQP1/1-175                DEEVKLIKKMGDHLTNLRRLAG........PQAGLGEYLFERLTLKHD................
FgMF_3RGD/1-176             EEQVKDIKRIGDFITNLKRLGL........PENGMGEYLFDKHSVKESS...............
Q6P8C6/1-176                EEQVKAMKELGDYITNLKRLGV........PQNGMGEYLFDKHTLGESS...............
P85837/1-174                DEQVKSIKELGDWVTNLRRLGA........PQNGMAEYLFDKHTLGK.................
P49947/1-176                NEQVEAIKKLGDHITNLTKMDA........VKNKMAEYLFDKHTLGGQS...............
HuMF_1R03/1-182             NEQVKSIKELGDHVHNLVKMGA........PDAGLAEYLFDTHTLGNENKQN............
HuHF_2FHA/1-183             NEQVKAIKELGDHVTNLRKMGA........PESGLAEYLFDKHTLGDSDNES............
MsHF_3WNW/1-212             SEQVKSIKELGDHVTNLRKMGA........PEAGMAEYLFDKHTLGHGDESGDIESAQSDEEVE
PgFtn/1-160                 REQVEEEATAAEIVETIRLSQE............QNLIFIDHQLARR.................
EcFtn_1EUM/1-160            SEQHEEEKLFKSIIDKLSLAGK..........SGEGLYFIDKELST..................
CjFtn_1KRQ/1-167            SEQHEEEALFRGIVDKIKLIGE..........HGNGLYLADQYIKNIALSRKK...........
HpFtn_3EGM/1-181            AEQHEEEVLFKDILDKIELIGN..........ENHGLYLADQYVKGIAKSRKS...........
PfFtn_2JD7/1-174            NEQVEEEASVKKILDKLKFAKD..........SPQILFMLDKELSARAPKLPGLLMQGGE....
A0A0C7P5L5/1-169            EAEKIHEEWYKQAKEATKEEKDIEKGKI..YICDVCGYTVEGEAPDRCPICGAPKSKFSEF...
A0A075WM99/1-170            SAEKIHEELYRKAKELASQEKDMELEKV..FICPVCGFTAVDEAPEFCPVCGTKREMFVEF...
F8AEI6/1-171                EAEKIHAELYAKAKEKAEKGEDIEIKKV..YVCPVCGYTAVDEVPERCPVCGLPKDKFVVFE..
A0A100XZC0/1-171            EAEKIHAELYAKAKEKAESGEDIEVKKV..YICPVCGYTAVDEAPEYCPVCGAPRDKFVIFE..
Q5JF11/1-171                EAEKIHAELYKKAKEKAEKGEDIEIKRV..YICPVCGYTAVDEAPEYCPVCGAPRDKFVVFE..
Q9V0A0/1-175                EAEKIHAELYKKAKESAEQGKDIEIKKV..YICPVCGYTAIDEAPERCPVCGAPRDKFIVFE..
B9KAX2/1-176                EAEKIHAEMYKKAKELVEKGEDYPAEKV..YICPVCGHTVEGEPPEKCPVCGAPRSAYREFSV.
Pf_rubrerythrin_3MPS/1-130  EAEKIHAELYRKAKEKAEKG............................................
Dv_rubrerythrin_1LKM/1-144  VAEEFHEKRFLDFARNIKE.............................................
St_sulerythrin_1J30/1-144   RAEKSHAEKFQNVLKQLKGGT...........................................
Bp_rubrerythrin_4DI0/1-144  KAERSHANRYTKALDGLVD.............................................
CjDps_3KWO/1-152            AKYEKSLWMIGATLQGACKM............................................
BbDPS_1N1Q/1-149            AGLEKHVWMLEAFLE.................................................
A0A0M1QIG0/1-146            QSLEKHVWMLKSFLGR................................................
I0BUW7/1-146                SSLEKHVWMLESFLGK................................................
A0A132BNU7/1-145            QNIEKHNWMLKAYLG.................................................
Q65FU7/1-145                QSIEKHNWMLKAYLG.................................................
D5TXF7/1-147                TTLEQHVWMLSAFLK.................................................
A0A0N0Y8R5/1-151            TSLEKHLWMLNAYMGESQSR............................................
LmDPS_2IY4/1-156            ASIDKHIWMFKAFLGKAPLE............................................
SsDps_2XJM/1-165            ASIEKHIWMLQAELGQAPKL............................................
SsDps_2UX1/1-165            ASIEKHIWMLQAELGQAPKL............................................
EcDps_1L8H/1-167            RDLDKFLWFIESNIE.................................................
AtDps_1O9R/1-162            RDLDKSLWFLEAHVQEKS..............................................
MsDPS_1UVH/1-183            GELEKFQWFVRAHLESAGGQLT.......HEGQSTEKGAADKARRKSA................
Rru_A1499/1-187             RAIDRRFWALDSHISPHERRRE....DLSFDQDQDEGFDPQKPGESQSR...............
MsDps/1-161                 DGLEKQAWLIRSENRKV...............................................
Rru_A0333/1-158             QIHEKTAWMLRSMAA.................................................
Cp_symerythrin_3QHC/1-179   KSETKHANWVKRALENLLEVA...........................................
STAUR_4074/1-157            NAAPLTVGSLRRRGGSGNAP............................................
MXAN_3557/1-164             ESHPLTVGSLRRGGGGSGSGR...........................................
MXAN_4464/1-116             PEKRLTVGSLRR....................................................
MXAN_2410/1-109             ..TGLTVGSLRGSR..................................................
Cthe_1503/1-119             GKTESTIGSLIDK...................................................
Tlet_1919/1-116             NNEEPTIGSLKDGEKDGK..............................................
Mboo_1094/1-124             TKEEPTIGSLKNTKEA................................................
PF1192/1-96                 ........................................................NWN.....
PFC_05175short/1-99         ................................................................
Hoch_3836/1-131             SHGSLGIGSLRQEGKE...........................................D....
Rru_A0973/1-140             GDGSLGIGSLKGEAALARPPRL..........................................
FRAAL4504/1-136             GDGSLGIGSLKGVGE.................................................
Sce5279/1-127               PSGALGIGSLKGA...................................................
WS0286/1-124                .SNGLNIGSLKKGK..................................................
Amet_4422/1-120             QEKGLNIGNLKK....................................................
Hore_15960/1-115            ..GSLGLRNTK.....................................................
Tpet_0143/1-114             .GGDLGIRKL......................................................
Tmari_0787/1-114            .GGDLGIRKL......................................................
Tbd_2465/1-100              ................................................................
Achr_1378/1-102             ................................................................
PG1C_13910/1-99             ................................................................
Tgr7_0837/1-101             ................................................................
CYCME_0127/1-95             ................................................................
Q91_0125/1-95               ................................................................
Nmul_A2196/1-96             ................................................................
cce_0034/1-96               ................................................................
Metme_0971/1-95             ................................................................
MEALZ_1148/1-94             ................................................................
AAY24_01205/1-95            ................................................................
IMCC21906_01077/1-95        ................................................................
Sta7437_0684/1-95           ................................................................
GU3_08795/1-95              ................................................................
MARPU_03990/1-95            ................................................................
Thivi_3051/1-95             ................................................................
THII_2135/1-95              ................................................................
NE0167/1-95                 ................................................................
Kkor_0109/1-94              ................................................................
M911_12845/1-94             ................................................................
consensus>70                ................................................................
```

Amino acid sequences of ferritin family proteins were aligned progressively using EMBL-EBI web services[1,2] Clustal Omega[3], T-Coffee[4] and MAFFT[5]. Protein names were adapted from either UniprotKB[6], KEGG[7] database or common name with PDB entry code[8]. Sequences were sorted in an order corresponding to the clades in phylogenetic tree (Figure 13). The alignment was edited by Espript 3.0 web server[9]. The *Rhodospirillum rubrum* EncFtn (Rru_A0973) sequence was highlighted in yellow. The ferroxidase centre (FOC) of *Pseudo-nitzschia multiseries* ferritin (PmFtn_4ITW) (highlighting in blue) consists of Fe_A site (E16, E49, E52) and Fe_B site (E49, E95, E131, Q128) which were labelled with solid red triangles[10]. Another iron binding site in PmFtn_4ITW (the gateway site or Fe_C site[11]) consisted of E48, E45 and E131 which are marked with solid blue circles[10]. The FOC of *R. rubrum* EncFtn was labelled with empty red triangles as E32, E62, H65 and Y39; and the iron entry site was marked with empty blue circles including E31 and E34.The putative iron exit site was marked with empty blue squares including H57, E61 and E64. The C-terminal localization sequences common to the encapsulin associated ferritins were highlighted within the red rectangle.

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