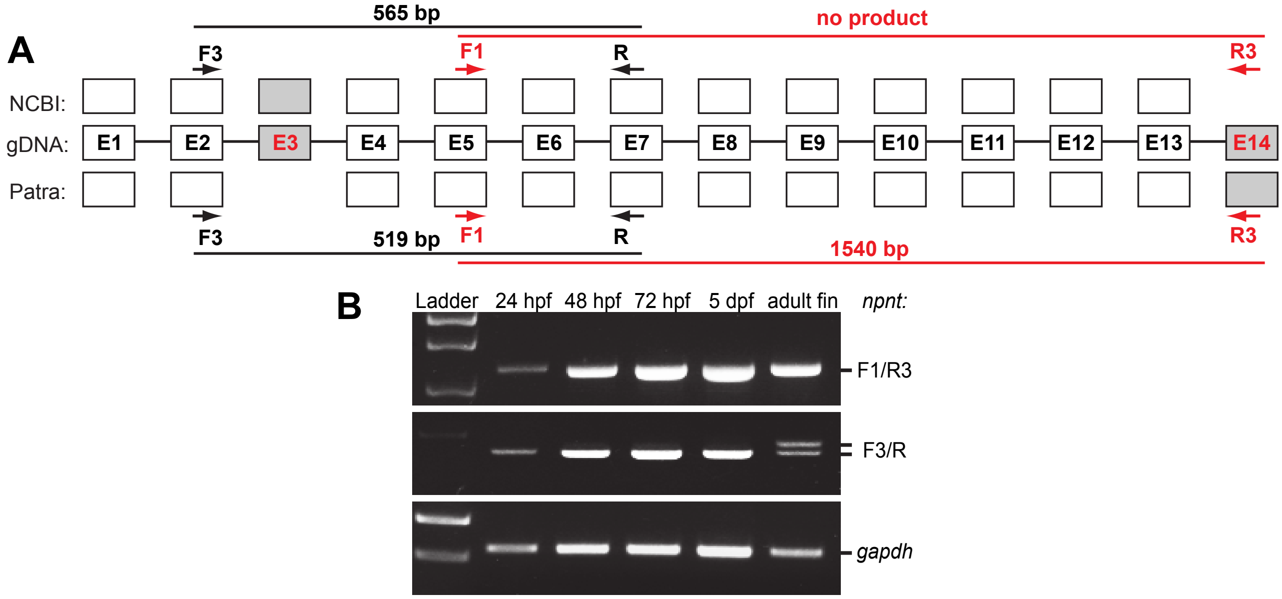

C

```
                                                   
NCBI   1     MWIIKFMLMWTCWIAVDADFDGRWSRQMSSSNGLCRYGGRIDCCWGWTRVSWGQCQPLYVLTRRVIGIRC  70
             MWIIKFMLMWTCWIAVDADFDGRWSRQMSSSNGLCRYGGRIDCCWGWTRVSWGQCQPL
Patra 1      MWIIKFMLMWTCWIAVDADFDGRWSRQMSSSNGLCRYGGRIDCCWGWTRVSWGQCQPL------------  68
                                EGF-like domain       EGF_CA         EGF-like domain
NCBI   71    QPQALCQHGCKHGECVGPNKCKCHPGYTGKTCNQDLNECGLKPRPCKHRCMNTFGSFKCYCLNGFMLLPD 140
                  CQHGCKHGECVGPNKCKCHPGYTGKTCNQDLNECGLKPRPCKHRCMNTFGSFKCYCLNGFMLLPD
Patra 99     -----CQHGCKHGECVGPNKCKCHPGYTGKTCNQDLNECGLKPRPCKHRCMNTFGSFKCYCLNGFMLLPD 123
                                                                EGF_CA
NCBI   141   GSCANARTCSMANCQYGCEVMKGEVRCQCPSPGLQLAPDGRTCVDVDECAAGLAVCPRFRKCINTFGSYI 210
             GSCANARTCSMANCQYGCEVMKGEVRCQCPSPGLQLAPDGRTCVDVDECAAGLAVCPRFRKCINTFGSYI
Patra 124    GSCANARTCSMANCQYGCEVMKGEVRCQCPSPGLQLAPDGRTCVDVDECAAGLAVCPRFRKCINTFGSYI 193
                                           EGF_CA
NCBI   211   CKCHDGFDLQYVNGKYQCTDVNECSLGQHQCGPYATCYNTPGSYKCKCKEDYRGVGYDCKPIPKVVIDPP 280
             CKCHDGFDLQYVNGKYQCTDVNECSLGQHQCGPYATCYNTPGSYKCKCKEDYRGVGYDCKPIPKVVIDPP
Patra 194    CKCHDGFDLQYVNGKYQCTDVNECSLGQHQCGPYATCYNTPGSYKCKCKEDYRGVGYDCKPIPKVVIDPP 263

NCBI   281   RPGKTTPSSNNNKGGNKIPGSDQKRTTTTVRPPVTAKRISPTITTTTTTTKPPPTKKITPPARVPVTTTR 350
             RPGKTTPSSNNNKGGNKIPGSDQKRTTTTVRPPVTAKRISPTITTTTTTTKPPPTKKITPPARVPVTTTR
Patra 264    RPGKTTPSSNNNKGGNKIPGSDQKRTTTTVRPPVTAKRISPTITTTTTTTKPPPTKKITPPARVPVTTTR 333
                                                                        RGD domain
NCBI   351   KPFIPTRKPPVLVTTKPKVPTHQHTTTKVPVVTAVVPFIPTRRPFTIPFVTPIDNSIKDITQKQRGDVHI 420
             KPFIPTRKPPVLVTTKPKVPTHQHTTTKVPVVTAVVPFIPTRRPFTIPFVTPIDNSIKDITQKQRGDVHI
Patra 334    KPFIPTRKPPVLVTTKPKVPTHQHTTTKVPVVTAVVPFIPTRRPFTIPFVTPIDNSIKDITQKQRGDVHI 403
                                                              MAM domain
NCBI   421   PRNHGKNNVLGIDLDIELGNTEEELKDDPESGYLSCSFDHGLCGWIQRREGDLHWETSEDPSGGRYLTIS 490
             PRNHGKNNVLGIDLDIELGNTEEELKDDPESGYLSCSFDHGLCGWIQRREGDLHWETSEDPSGGRYLTIS
Patra 404    PRNHGKNNVLGIDLDIELGNTEEELKDDPESGYLSCSFDHGLCGWIQRREGDLHWETSEDPSGGRYLTIS 473

NCBI   491   EGGEKRGGRGAQLILPLKTPWNEGNLCLAFRHNMAGHHVGMLQVFVQKGRQHSPAVWGRTGGNGWRSTQI 560
             EGGEKRGGRGAQLILPLKTPWNEGNLCLAFRHNMAGHHVGMLQVFVQKGRQHSPAVWGRTGGNGWRSTQI
Patra 474    EGGEKRGGRGAQLILPLKTPWNEGNLCLAFRHNMAGHHVGMLQVFVQKGRQHSPAVWGRTGGNGWRSTQI 543

NCBI   561   TLWGNGLESVIVKGERRRGRKGEIALDDMSLKRGSCQEEHNLRRL 605
             TLWGNGLESVIVKGERRRGRKGEIALDDMSLKR   ++   L
Patra 544    TLWGNGLESVIVKGERRRGRKGEIALDDMSLKREDSRKMDTLWKGTWPSVSPDMVMVHFLSGCKCMSQLNRVR 616
```

D

Motif Scan results:

List of matches

ASX_HYDROXYL:	120-131, 202-213, 247-258
CYS_RICH:	70-258
EGF_1:	91-102
EGF_2:	91-102, 129-143
EGF_CA:	105-129, 185-211, 230-256
EGF_3:	66-103, 105-144, 185-223, 230-270
MAM_2:	454-598
PRO_RICH:	332-402
THR-RICH:	306-377

Frequent patterns:

AMIDATION:	578-581
C_tripleX:	71- 87
CAMP_PHOSPHO_SITE:	304-307, 317-320, 336-339, 592-595
CK2_PHOSPHO_SITE:	182-185, 401-404, 406-409, 441-444, 477-480, 488-491, 595-598
EGF_alliinase:	90-109
MYRISTYL:	79- 84, 125-130, 141-146, 207-212, 237-242, 252-257, 497-502
PKC_PHOSPHO_SITE:	62- 64, 98-100, 126-128, 253-255, 309-311, 315-317, 329-331, 335-337, 348-350, 356-358, 364-366, 376-378, 391-393, 406-408, 411-413, 590-592
RGD:	415-417
Transglut_C:	519-538
TIL:	166-189
TYR_PHOSPHO_SITE:	446-453