```
Adi_EP-like-1      1 ----------------------------------------MGAARFLVQVTMLLAVKAALSAATNTTRM 29
Adi_EP-like-2      1 ---------------------------------------MCPGSRIFAKIVILLAVDSANSLQANTSTI 30
Ami_USOMP-5        1 ----------------------------------------MGAARFLVQVAIFLLVKPARSAPA-PMWK 28
Ean_EP             1 ------------------------------------------MKIAFVVLGLLMMIAASVA-------- 19
Gfa_EP             1 ------------------------------------------MKTAFVFLGLLLMIVAAVA-------- 19
Nve_248548         1 MQFGRISWKRVVNHFDTIDRTGFEANVENGIYFPNVLSDIHPTGKMYRFLAVLCLVACGYALDLDDQYC 69

Adi_EP-like-1     30 QANPAANTCSQAPTNNCHCQC-----------------------------------ELRPDSSTAIAV 62
Adi_EP-like-2     31 HSSPTSK-CSKPASNNCNCNC-----------------------------------NVHTSSISDPAL 62
Ami_USOMP-5       29 GNSTARKSCSQASINNCSCRC-----------------------------------ELSPASTTANAV 61
Ean_EP            20 --------------NGSGC-----------------------------------------CDKAI 29
Gfa_EP            20 --------------NGSGC-----------------------------------------CDHAI 29
Nve_248548        70 QHQETYYTIYQVPSHNCKCTAKQTGALRYKDGNLQVCNGNEYVNVGGNAGQEAPVGTETNPGKSCRNIL 138

Adi_EP-like-1     63 SA------------------------------------------------------------------ 64
Adi_EP-like-2     63 VT------------------------------------------------------------------ 64
Ami_USOMP-5       62 SA------------------------------------------------------------------ 63
Ean_EP            30 ET------------------------------------------------------------------ 31
Gfa_EP            30 TM------------------------------------------------------------------ 31
Nve_248548       139 TKRKDAKSGMYFIKPRDVVMKTYCYMGTLCGSNGWTMVMKIDGNKNTFRYDSKYWSNKQHYNVAGATGG 207

Adi_EP-like-1     65 ---LQDKIDQL--------------------------------------------------------- 72
Adi_EP-like-2     65 ---LEDKLDHI--------------------------------------------------------- 72
Ami_USOMP-5       64 ---LEDKIDQV--------------------------------------------------------- 71
Ean_EP            32 ---FERKMETL--------------------------------------------------------- 39
Gfa_EP            32 ---FEKKMETL--------------------------------------------------------- 39
Nve_248548       208 FNHVETKLDTYSHFPLSKLCLGLETKGKREWKEINYMAGSLYELIADGKFRETHYGRKFWKSMVPDSSL 276

Adi_EP-like-1     73 ---------------------------IALVNRT-----TPRHSAPVA---------------------- 88
Adi_EP-like-2     73 ---------------------------ISLVNKTGAIPQLPPTLIPAAA--------------------- 94
Ami_USOMP-5       72 ---------------------------IALANRT-----TPRHSAPVA---------------------- 87
Ean_EP            40 ---------------------------IAELKSS---CQSPP---------------------------- 51
Gfa_EP            40 ---------------------------VMELKSS---CRTPP---------------------------- 51
Nve_248548       277 QRNCGREGFNVVKITGSDKRNGFAKVRIGIIGNQENDCHTPDSRIGFGAMGNLCGQNNDNSAGNEARCS 345

Adi_EP-like-1     89 ------------------------------PISSCKEQFDKNNSSPSQVYELTF-GSQVVSVYCHMGNF 126
Adi_EP-like-2     95 -----------------------------DPVFSCKDQFDKDNSSQSKVYELTF-GSQKLPVYCHMGNF 133
Ami_USOMP-5       88 ------------------------------SISSCKEQFDKNNSSPSQVYELTF-GSQVVPVYCHMGNF 125
Ean_EP            52 -------------------------------VASSCQELHEKDPSLESGVYKLVL-GTQKIPVYCHMGNF 89
Gfa_EP            52 -------------------------------VASSCQELHKKDPSLHSGVYELVF-GLQKLPVYCHIGNF 89
Nve_248548       346 PDNGDKTIKSFGYIFAQERQEDALLGSFDKPAKSCKEIVAARPDAKNGVYYLNLRDAPHTRVYCHMTEI 414

Adi_EP-like-1    127 GCGNGGWTLAMKMDGTKTTFHYDSLLWSAQSSYNPAAGKTG-FDMLETKLPTYWSTPFDKVCLGMRVGG 194
Adi_EP-like-2    134 GCGQGGWTLAMKTDGTKSTFHFNSHVWTDKYSFNPEGGKTG-FDSSETKLPTYWSTPFSKVCLGMKRIG 201
Ami_USOMP-5      126 GCGNGGWTLAMKMDGTKTTFHYDSLVWSAQSSYNPAAGKTG-FDMLETKLPTYWSTPFDKVCLGMRLGQ 193
Ean_EP            90 GCGDGGWTPVMKIDGTKLTFLYDSGFWTNKTVYNSEGGMTGFFDLKETMLPSYWTTPLSKICLGMMIHG 158
Gfa_EP            90 GCGDGGWTPVMKIDGKKLTFVYDSGFWSNKTVFNSEGGMTG-FDQKETMLPSYWSTPLSKICLGMMIHG 157
Nve_248548       415 -CGSRGWTIIMKIDGRKTTFKYESSYWKNHNVYNTESIADG-LDNSDMKLHTYSKLPFEKLCLGMRVGG 481

Adi_EP-like-1    195 QQLNFVVLN--MTANSLFSLIADGRYRATSLGRNTWKSLIGTQASLQRNCNREGF--NVRSGYRSNSKA 259
Adi_EP-like-2    202 QKINFIVIR--KNATSLFSLIADGIYRATSLGRDKWKSLIGTDASLQLHCDKEGF--NTVGFRAETAKA 266
Ami_USOMP-5      194 Q-LNFVVLN--MTANSLFSLIADGLYRATSLGRNTWKSLIGAQASLQRNSIEKGS--TP---------- 247
Ean_EP           159 Q-IKFVVLD--KKASSLHSLIADGQYRATSLGRNQWKTLIGSDASLQRNCNKEGF--NPVP--ETWRRV 220
Gfa_EP           158 K-VNYVVIN--KSASSLHSLIADGVYRATSLGRDKWKSLIGSEASLQRNCNKEGF--NPVP--ETWRKT 219
Nve_248548       482 S-LEWLPVNMGKKVDSLFSVIAPGKYVATHISKNEWRKLV-PGSSLQRNCNMQGFNNNPVP-SQPAAKV 547

Adi_EP-like-1    260 RIGIIGNQENNCRSCDSRIGFGTGG--IPDNSNSCGNHAIQS-GDNGRKRIETMGYILVQ          316
Adi_EP-like-2    267 RIGFLGNNQNHCGLCDSRIGFGTGG--TPDDSGTCGNEAADRYSDNGPKSIKTMGYILVQ          324
Ami_USOMP-5      248 -------------------GLVVIG--MPG------------------------------          256
Ean_EP           221 RIGFVANQENDCRTCDSYVGFGSRG------DMSCGNYAAWG-GDNGNRHTTAMGYILVQ          273
Gfa_EP           220 RIGYVANQENNCDTCDSYVGFDSKG------DMSCGNYASYD-ADNGDRRTTTMGYILVQ          272
Nve_248548       548 RIGFVANQENDCGSPDSRIGFGGSGNYCGQSSYSAGNEARCD-GDNGNKSVAGYGYILAQ          606
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S17 Fig. Sequence alignment of coral egg proteins, EP-like proteins, and a similar protein of *Nematostella*. Local sequence similarity is found in middle of the proteins. Conserved positions are shaded in blue. Gene model IDs and NCBI accession IDs of the proteins are as follows: *A. digitifera* EP-like-1 (aug_v2a.22918.t1), EP-like-2 (aug_v2a.00002.t1), *A. millepora* USOMP-5 (B8VIU6.1), *Euphyllia ancora* egg protein (AGO04749.1), *Galaxea fascicularis* egg protein (BAE94663.1), and *N. vectensis* (Nemve1|248548).