## **Supporting Information**



Figure S1 - **SEM** images from skeleton macro and microstructure. (A) Radial corallites arrangement with separate walls and internal septa, (B) Closer view into corallites showing different vestigial and complete septa. Polished and EDTA-etched sections from a longitudinal cut: (C) Fibrous microstructure, (D) Close-up showing evidence of crystalline fibers. The skeleton of *Acropora millepora* is composed exclusively of aragonite. Macroscopic views (Figure 1A) of the skeleton surface reveal cup-like rounded corallites separated by distinct walls and the highly porous coenosteum. The radial corallites are evenly distributed and of approximately equal size (Figure 1A), with complete and incomplete septa (Figure 1B). In longitudinal sections (Figure 1C), a rather uniform microstructure is evident, but with unevenly distributed porosity. At higher magnification (Figure 1D), individual needle-like fibers, constituting the basic units of the coral microstructure (Nothdurft and Webb 2006), are observed. These exhibit a discrete size with trabecular orientation (white arrows on Figure 1D) (Wendt 1990).

SAARP1/1-386	1 MA F V S C F H L R L L F L C L A L F MAA E C R P D E L N K K V D S D E T I S D D D V S A R V Q P N G G K I M I V R - D N D Y D A S I	D <mark>D</mark> 68
SAARP2/1-391	1 HCLPLE SIALFLV CLADEERKDDDNTKTIRGKNVSAKIFGRSCKIMIVRVDDEEDTH	KDTVD 62
SAARP1/1-386	69 NDNDNDDDDNNDNDNDNDDDNDVDRDNDVDRDNDDDDFDDSNDDMLSF	ELD S   117
SAARP2/1-391	63 R V S D K K D N V DD R R D N D D R E E S I D K K D T V D K K N P I D D K DD K DD K D D V D N D N D K - DD D F R D D D E D L L S F I	ELD EL 133
SAARP1/1-386	118 E EKDS DGNDVG ST EGHSV ESFEDRPFSLSSVDRNSNALGVAAINVNLSTKLEDSNADVD IMLYLFREI	DGT I S 189
SAARP2/1-391	134 K EV DADGDEVDDKHSVDSFDDVEFQLSHVRTASRFKGLAVI SVNLSTHLQNNKANVGIMVYLFLEF	PGSVT 203
SAARP1/1-386	190 FGNETFDVQAGTVKFNIKISNWDFCDCSAQDCSEAKAGEYLDVNIKFKSKDTPIEVTDEERKSQNKP	AVCKD 261
SAARP2/1-391	204 FGNETFNVKAGTVKFNIEVNNWDFCEGSSPACSSRKEGKFLDLTMKIKSKDSPTEVEDDDRKK	AVCND 271
SAARP1/1-386	262 KDTPDTDSDPDDSSDNANDGDDDDDDCPHIYNMGGDSEMLLNRGVM-NGDTYTAMPFGFPKVEIED	G E K K I 332
SAARP2/1-391	272 KDDDNDDDDVDDDDDDDDDDDDCPIIYSMGGDSEMLLNRGVMLDDDEYTAMPVGFPKLEIED	ETRK F 337
SAARP1/1-386	333 K FR V P K F D D N V N I D P S V T P G - R V P K NA S P S P A L C L K I H I L F I A L L Q A V T L F I N S W	386
SAARP2/1-391	338 V <mark>F R I P K F</mark> S K R A L V <mark>D P S V T P G</mark> E R T <b>P K</b> L <mark>A</mark> I S A G T W – L Q L N F L V T V L V Q I A V M F V F H –	390

Figure S2 - Pairwise sequence alignment of the secreted acidic Asp-rich proteins: SAARPs 1 and 2 (UniprotKB Ac. Nos.: B3EWY6, B3EWY8, respectively). Identical residues are dyed in blue. Sequence alignments were performed and visualized with Jalview (Waterhouse et al. 2009).

SAARP1/1-386 SAARP2/1-390 CARP4_P2/1-311 CARP5_P15/1-258 P27/1-186	1 MAF VS CFHLRLLFLCLALFMAAE CRPDELNKK VDS DE TIS DDD VS AR VQPNGGK I MI VRDND YD AS DDNDNDNDDDD 1
SAARP1/1-386 SAARP2/1-390 CARP4_P2/1-311 CARP5_P15/1-258 P27/1-186	78 NNDNDNDNDDDNDVDRDNDNDDDD FDD SNDDML SFELD SIE EKD SDGND VGSTEGHSVESFED RPFSLSSV 80 REESID KKDT VDKKNPIDD KDD KDD KDD KDD KDD ND KDDD FRDDEDLLSFELD ELKEVD ADGDEVDDKHSVD SFDD VEFQLSHV 16DDKHSVD STDD VDDDDDDDD GVDDDDDDDD FSDD NEEMLSFEVD ELE EKD VDGNOVOTMQRHSVD SFDD VCFTFTKV 51 KDD
SAARP1/1-386 SAARP2/1-390 CARP4_P2/1-311 CARP5_P15/1-258 P27/1-186	149 DRN SN ALG VAAIN VNL ST KLED SN AD VDI MLYLFREDGTIS FGNE TFD VQAGT V K FNIKI SNWDFCDG SAQD CSEA KAGEYL 163 RT AS RFKGLAVIS VNL STH QNNKAN VGIM VYLFLEPGSVTFGNE TFN VKAGT V KFNIKI SNWDFCDG SSPACSSR KEGKFL 85 DTQAKYDGLP VTN VNLSAT PSS-SSLEI M VYLFRRAGKVTFGNE TFN VKAGT V KFNIKI SNWDFCDG SSPACSSR KEGKFL 120 NKKSTLDGIH VTT VNLSTYLDQKASLEI I VYLFRCAGSVRF
SAARP1/1-386 SAARP2/1-390 CARP4_P2/1-311 CARP5_P15/1-258 P27/1-186	231 D VN I K F K S KDT - P I E VTD E E R K S QN K P A V CKD KDT P D TD S D P DD S S DN ANDG D D D D D C P H T YN MG C D S EMLL N R C V-MNG D T YT AMP 245 D L TMK I K S KD S - P T E VE D D R K K A V CND K D D D D D D D D D D D D D D D D D D
SAARP1/1-386 SAARP2/1-390 CARP4_P2/1-311 CARP5_P15/1-258	318 FGFPKVE I EDGEKKI KFRVPKFDDNVN I DPSVTPGRVPKNASPSPALCL KI HILFI ALLQAVTLFI NSW 323 VGFPKLE I EDETRKFVFRI PKFSKRAL VDPSVTPGERTPKLAI SAGTWLQLNFL VTVL VQI AVMFVFH- 247 EGYPKFE VEDGEKKFVFRI PKFKKSVL VDPSVNVGRVNGVNSLAHANTGLAFLLFI AAFI VTNYV SRAHL

CRRPS p15/1-258 234 Figure S3 - Multiple sequence alignment of SAARPs 1 and 2 (UniprotKB Ac. Nos.: B3EWY6, B3EWY8), CARPs 4 and 5 (UniprotKB Ac. Nos.: M1SN56, M1RYM2) and P27 (M1TA76). Identical residues are dyed in blue. Sequence alignments were performed with MUSCLE (Edgar 2004) and visualized with Jalview (Waterhouse et al. 2009).

SAARP1/301-386	301 MLLNRGVM-NGDTYTAMPFGFPKVEIED-GEKKIKFR	V P K F D D N V N I D P S V T P G – 352
Uncharacterized_SOMP_4/136-204	136 MXXXHGVMLDDDEYTAMPVGFPKLEIED-ETRKFVFR	I P K F S K R A L V D P S V T P G E 189
SAARP2/305-391	305 MLLNRGVMLDDDEYTAMPVGFPKLEIED-ETRKFVFR	I P K F S K R A L V D P S V T P G E 358
Acidic_SOMP/271-359	271 MVLNKGVLVNNMDYVAMPQGFPNLEKTGMMQKKLTFR	L P K T P G S V I I D P S V N I G V 325
SAARP1/301-386 Uncharacterized_SOMP_4/136-204 SAARP2/305-391 Acidic_SOMP/271-359	353 RVPKNASPSPALCLKIHILFIALLQAVTLFINSW 190 RTPKLGNKCWNMAAA	386 204 390 359

Figure S4 - Multiple sequence alignment of the C-terminal from the secreted acidic Asp-rich proteins: SAARP1 and 2 with two related sequences: uncharacterized SOMP-4 and acidic SOMP (UniprotKB Ac. Nos.: B8UU74, B3EWY7, respectively). Conservation of residues is dyed by shades of blue: the darker the color, the more conserved the residue. Sequence alignments were performed with MUSCLE (Edgar 2004) and visualized with Jalview (Waterhouse et al. 2009).

Amil_sap1_CT			
Adig_sap1	1	MARDLLLVVFFACLLQSFWGLPLPLKNENAIVDGDGTSVVTTKEDASTIFERDPNPANQVSALVTGVILDENGDPGESDES	81
Amil_sap1_NT	1	MARDLLLVVFFACLLQSFWGLPLPLKNENAIVDGDGTSVVTTKEDASTIFERDPNPANQVSAMVTGVILDENGDPGESDES	81
Amil_sap1_CT			
Adig_sap1	82	VDNDG EGGD KDDD KNGDDND L DN K EH E E E KGDDD S GDD E E EDD AE DD ADD S GDDDD S GDDDD D S GDDDD S GDDDD S GD	159
Amil_sap1_NT	82	VEN VDNDG EGGD KDDD KNG E DND LDN KEH E E E KGDDD RGDD E E EDD AE GDND SNDN EG DDDDDDDD SGDDDD VD E SGA	158
Amil_sap1_CT			
Adig_sap1	160	DDD S G D DDD S G D DDD S G D ADD S G D E E DDD S G D A E N DD S G DDDD S G DDDD S G D DDD S G D DDD S G DDDD S G DDD S G DDDD S G DDD S G DD S G D S G D S G D S G D S G D S G D S G D S G D S G D S G	240
Amil_sap1_NT	159	DEDDDDDSGD	168
Amil_sap1_CT			
Adig sap1	241	GDNDDEDNDDDSGDDEDDDSGDDDDDSGDDDDDSGDDDDDSGDDDDDDSGDDDDDD	321
Amil_sap1_NT			
Amil_sap1_CT	1	SDDESGDDENGDDKDGDDDDKEEDGEDVSEEDEKADVGDDGDDDDNETGGNSDTNDDVDYGDGNDEAREIGDH	73
Adig sap1	322	VDGNGDDDSDDESGDDENGDDKDG DKEEDGEDVSEEDEEADVGDDGDDDDNETGGNGDTDDDVDYGDGNDEAGEIGD-	398
Amil_sap1_NT			
Amil_sap1_CT	74	SIQDIRDLILDAIHNKDGGEMDADNPLQNLPYGPDKLKELYLRSGGSHFKGQLLNITLGLGFCILFLLL	142
Adig sap1	399	- IQDIRDLILDAIHNKDGGEMDADNPLQNLPYGPDKLKELYLRSGGSYFKGQLLNMTLGLGFCILFLLL	466
Amil_sap1_NT			

Figure S5 – Mapping of the two protein fragments from Amil-sap1 (UniprotKB Ac. Nos.: B3EWZ0 (N-terminal) and B3EWZ1 (C-terminal)) with corresponding ortholog from *A. digitifera* (Adi-sap1). Mapping was visualized with Jalview (Waterhouse et al. 2009). Identical residues are shaded in blue.

	1 10	20	30	40	50	60
Amil-Galaxin/1-338 Adi-Galaxin/1-338 Gfas-Galaxin/1-343 Amil-Galaxin2/1-275 Adi-Galaxin2/1-275 Nemvo_11144/1-259 Nemvo_1957/1-278 Hmag_228867/1-342	MKPSGAFLSLCVVI MKPSGAFLSLCVVI MSPT.VSICFCSAL MTRF.TSIGLCAVI MTRL.TSIGLCAVI MDTFLI	LSLATHCFSFI LSLVTYCFSFI FAVFSSCATIC LFNVCSCATIC LFNVCSCATIC MAC SC	SDSLRRDAHSD SDSLRRDAHSD NDTLSADSENU KDTIASMLKKG KDAIASMLKKE KDAIASMLKKE	TNALKSRDRRÇ INALKSRDRRÇ PNKLETRYRRÇ KSPRVTRQRRÇ KSPRVTRQRRÇ	APAPQLS. APAPQLS. APVPPVVSY LPSP FKPEKYSQC	CGGVLYNPAA CGGVSYNPAA CGGAPFSTAT CGSLQ CGSLQ IRVENVALVV CGRQTYDNRR CGTKAYTPTK
Amil-Galaxin/1-338 Adi-Galaxin/1-338 Gfas-Galaxin/1-343 Amil-Galaxin2/1-275 Adi-Galaxin2/1-275 Nemve_11144/1-259 Nemve_1957/1-278 Hmag_228867/1-342	70 EMCCHGNVEPRV.G HICCNGNAEPKT.G LLLCLANSQALLMS YICCSGRVVLRRYG QICCGGEVFKKT.D	80 ASPMCCESSS STPMCCDSNS PGQLCCDSNS PGQLCCDSYK PGQLCCDSYK VSQCKTSRSHD KNTSCCRYTP INSGCCYNQY	90 DPST DPLS NPVT NPVT DPREPCGGLPR: DPREPCGGLPR: OKGQ	LOQ QMCCEGTV QMCCEGTV QCCEGTV QCCEGTV SSPDICCEGRF KICCYPNI KQCCGRQI	SNKPPGI SNKPPGI SHKATSPGA LKRTGGL LPRRYGV VDI	110 AMCCGSEA MPCCGSEA .MPACCASDG 
Amil-Galaxin/1-338 Adi-Galaxin/1-338 Gfas-Galaxin/1-343 Amil-Galaxin2/1-275 Adi-Galaxin2/1-275 Nemve_11144/1-259 Nemve_1957/1-278 Hmag_228867/1-342	120 13 YDANSO CONGNIN YDANSO CONGNIN YDMSTO CONDNYA 	144 ITKATGPTAOPO ITKATGPKAOPO IKKPTGPTAIPO VKPASPTAIPO UKKPGSINT ILRRYGKNT.S I.PILTFNETE	150 CCGEFSIDAAS CCGEFSIDAS( CCGDBSVDASV CCDQSAVDRNT CCDQSAVDRNT .RWNSV CCRYTFYNPLT CCGTTLINPVN	160 DLCCDSHPV DLCCDSH.VPP LLCCDSNVVPP HLCCDATLSPE HLCCDATLSPE KICCYPNILPF EICCAEISSPE	17 'LMVGSLPSG 'LMVGSLPSG 'IM.GSLSAG IPPATTLPAG  'R.YGVYTSG (L.HGTFTKG	CCRNGYDANT CCRNGYDANT CCRNSYDTNT CCPVVYDSSV CCPVVYDSSV CCPVVYDSSV CCSQTFDRT CCSQTFDRT CCSQFFDSOK
1 Amil-Galaxin/1-338 Gfas-Galaxin/1-343 Amil-Galaxin2/1-275 Adi-Galaxin2/1-275 Nemve_1957/1-278 Hmag_228867/1-342	SO 190 SLCCGDNNVAFVSG TLCC.DSNVAFVSG N	200 P.QAACCGDMG P.QAACCGDMG P.QAQCCGSQC  PGNSFCCGGVT K.NTSCCRYTT I.LDQCCNGKI	210 SYNRNTHICCDS YSRNTHICCDS STOCCAS STOCCAS YDCQITCCAG YDCQITCCAG YDCQITCCGRG	220 N. VIPMPA. VIPKPGA A. VINKPVG A. VINKPVG TIRLISETGG N. IIPRRYG Z. VRPLMFG	MGACCG. MGACCG. VPRALCCG. VPRALCCG. VRSTFCCG. VRSTFCCG. NQHTGCCRI	230 
Amil-Galaxin/1-338 Adi-Galaxin/1-338 Gfas-Galaxin/1-343 Amil-Galaxin2/1-275 Adi-Galaxin2/1-275 Nemve_211144/1-259 Nemve_221144/1-258 Hmag_228867/1-342	240 QTHLCCECVQLYE. THLCCECVQLYE. DTHLCCECVQLYE. THLCCECVILLE THLCCECVILLE TOVCCMCFPVPHA NTQVCCMCFPVPHA RTHLCCECNVLER RTHMCCLN.KLSKI	250 GMNTGCC GMSTA.CCC GMSFA.CCC GPNATSICC GPNATSICC GSDMTSFCC FCKESG.CCI	260 SAVGYNQVNSLC SAVGYNQVNSLC SASYNQSSLC PFFYDISTQMC BFFYDISTQMC EKTYDSRSEIC LDKVYDLSTHIC	270 EGTÜVPKSPS GATUVPKSPS NGNIALKSAT NGNIALKSAT ARKILKRNSI YPNILPRRYG DGILHKKTLM	280 KPV. CCGTI KFV. CCGTI KFV. CCGST HTH. CCGMF HTH. CCGMF NTS. CCRYI MISERCCGEF	290 SYNPLTELCC SYNPLTELCC SPNPATHICS SPNPATHICS SPNPATHICS CVYNPLTKICS VYNPLTKICS
Amil-Galaxin/1-338 Adi-Galaxin/1-338 Gfas-Galaxin/1-343 Amil-Galaxin2/1-275 Adi-Galaxin2/1-275 Nemve_211144/1-259 Nemve_1957/1-278 Hmag_22867/1-342	300 DGIAFFKTGFIRF DGHAFFKTGFIRF DGHVGTRAGLTSFI NGYPYPKLGFISF RSKTVKKF YPNISRRYGVTS DKQLHREPFLHEW	310 CCGGAIYDA CCGGAIYDA CCGSLVYD CCGSLVYD GFLWYL CGRQTYD WYCCGRQTYD	320 TVARCCDG ATAKCCDG LTMRCCDGSHV WNFLKCF RKYICCSG RIWECKKDNK.	330 VPTYNVASCA VPTYNVASCA VPTYNVASCA JLITPNQDPCA JLITPNQDPCA LISSRGFSPIT	IGLA IGLA IGLA INLA INLA INLA INLA INLA	

Figure S6 - Multiple sequence alignment showing the sequence similarities between galaxins from *Acropora millepora* (Amil), *Acropora digitifera* (Adi), *Galaxea fascicularis* (Gfas) and the detected homologues from *Nematostella vectensis* (Nemve) and *Hydra magnipapillata* (Hmag). Amil-Galaxin (Uniprot Ac. No.: D9IQ16), and Gfas-Galaxin (Uniprot Ac. No.: Q8I6S1) correspond to the same form of galaxin and are grouped together with Adi-Galaxin (predicted from Adi transcriptome: EST\_assem\_14006). Subsequentely the Amil-Galaxin 2 (Uniprot Ac. No.: B8UU51) and Adi-Galaxin 2 (predicted from Adi transcriptome: EST\_assem\_8935) are shorter lacking the segments in the positions 60-77, 93-120 and 181-206 of the alignment. Finally the distantly related sequences from Nematostella (Nemve\_211144 (GI:156374951); Nemve\_1957 (GI: 156377965)) and Hydra (GI:221103149) show the conservation of nine double-Cys residues and the presence of other identical residues dyed in red (**A**). Regions with high frequency of semi-conserved substitutions are also indicated (A). Sequence alignments were performed with MUSCLE (Edgar 2004) and visualized with Espript 2.2 (Gouet et al. 2000).

SOMP_similar_to_cephalotoxin/1-473	1 RWLGWQ K FCW I S C L F S S I S S G L D FG E Q A K Y T T A L D TAQ FA I NA I NE E Y LAQA KA I E E A L K Y S TQA RSAD
SE-cephalotoxin/1-1052	1 V I L L FA L L WAANAA P E I H T T R PN Y FE I K R PN S TE I E T PA Y K QL E T P S I F L L T T L E VA EA D V D S T L E T M K D
SOMP_similar_to_cephalotoxin/1-473	70 L L R R Q T = E L A K F G S K V G KA L KA VQA A S A I A S F V F T F F M P S E L D V I T S I N E R F N E VNA KLD R I D E KLD E ME K S
SE-cephalotoxin/1-1052	74 R N K K N S A K L S K I G N N M K S L L S V F S V F G G F L S L L S V V T T T S D L Q V I S D M = F T G V N R KLD Q I N D KLD K
SOMP_similar_to_cephalotoxin/1-473	142 KADTA FN VFL SAWI KWEYKVINGA KKL SDI RKAMGTKTOR I DOVKLA E E YVK VYETN L DGN VLSL YRMAAL
SE-cephalotoxin/1-1052	145 VELQG-L LINYI PWOYSVING I EKLI ETYKKMVE ETDMNKR RLMA EN FLAFFENROI ESNI NNLIKLTT
SOMP_similar_to_cephalotoxin/1-473	215 PESITQRNIFDRIA GFCCDITKLSE MLVONIMTS CQQKLTYYYFKGDQSRANSSFKDIOMYFFKIRQGF
SE-cephalotoxin/1-1052	212 TDAVHQNMLFNELLDAGCDIIRLTRIYMHVIRIFYQ TQLVLAYNSFK - QMDPPEMKKYLNALIF- RNMY
SOMP_similar_to_cephalotoxin/1-473	288 D D R VWHC R RN S L D YA K RDAN K I L KNMRG SS R ES I V RA I FN EL KV KY PWY TWA VAA V K SD R P R I RGL EL RG STY
SE-cephalotoxin/1-1052	282 O S R VWHC K ET T I AQS K CD I KD I V K TNAK FG I TT V L R K I NS EL S R KY PWY SW SI V T V K KM LA NORN STL – G NQ F
SOMP_similar_to_cephalotoxin/1-473	361 FR LEDRS DAKKVKGYFVYEDTRSSASCSDITOAKTLLVFKKCDGCNSDYIYAADNILSKKRCGESTLERLVD
SE-cephalotoxin/1-1052	354 YEME AVCPHCSNFVVIWQCFKEHSQCEDIQ KANTIAVLTICKSCIQSHVFTPSNMLNKNTCPNNQYPQVKA
SOMP_similar_to_cephalotoxin/1-473	434 F KQQC P V CH RWP Y S I TC YCA N R V KQD SQ NMGL Y CI S SQHH
SE-cephalotoxin/1-1052	425 F I DR R F P R D E I O R K K SD V F W V A / C F K

Figure S7 - Pairwise sequence alignment between the cephalotoxin-like SOMP (Uniprot Ac. No.: B7W114) and the SE-cephalotoxin from *Sepia esculenta* (Uniprot Ac. No.: B2DCR8). Identical residues are dyed in blue. Conserved and semi-conserved substitutions are dyed in shades of grey. Sequence alignments were performed and visualized with Jalview (Waterhouse et al. 2009).

M_musculus/1-1159 H_sapiens/1-1159 Ap_pallida/1-1121 Ac_millepora/1-1114 H_magnipapillata/1-714	-MFLKQPGGCILL -MPRKQPAGCIFL MSFLVYLTMFVLA -MMDRSNAAFVLT 4-MLFKGTVLILL	Q - F LG	L LG L VGA VTR L SG L VG TVTR NAH S KGG I TR L I CH VAA I TR VIA I E I P LD Y	TYYIGIVEEY	WNYVPQGKDV WNYVPQGKNV WDYAPSGFNN WDYAPSGYNK CEFWLEIKEKLTM	I TG KS FS ED KLATL FL I TG KS FTED KLATL FL ANG I KLDND SDAS VF T I KG VKLEDD SDATV FA I YKKNLLYS SGGSLFL	ERC PNRIGCI ERC PNRIGSI VRCDTTIGKV TKCAHRIGRI YNESPC PNATKIP	72 73 81 75 78
M_musculus/1-1159 H_sapiens/1-1159 Ap_pallida/1-1121 Ac_millepora/1-1114 H_magnipapillata/1-71-	YKKA VYRH FTDGS YKKA VYRRFTDGT YKKVIYREYTDGT YDKVLYREYEDAS 4LDDVISADGENRM	YSTEIPKPPWLC YSIEIPKPPWLC FTSEKTHPKHLC FTKEKPHPKYLC IVIVINGTLP	F L G P I L R A E V F L G P I L R A E V I L G P V L Y G E V F L G P I L K G E I G P P I V V Y E	GDVIVIHLMNF GDVIVIHLKNF GDVIRVIFKNK GDTIVVHFKNN HQNLIIHVKNM	- A S R P F S L H PHG V - A S R P Y S L H PHG V - A T R R Y S V H PHG T - G S R V Y S MH PHG V L L S D V T T L H WHG L	FYDKDSEGALYPDGTS FYNKDSEGALYPDGTS FYKKNAEGALYEDETS FYSKDSEGALYEDNTK HQKGTPFMDGVC	GRNKEDDMVPPGK GRNKNDDMVPPGK QEDKHDDHVPPGE GKFKKDDKVPPGG WISQCPISAGQ	159 160 168 162 155
M_musculus/1–1159 H_sapiens/1–1159 Ap_pallida/1–1121 Ac_millepora/1–1114 H_magnipapillata/1–714	NYTYVWPVREEYA NYTYVWPVREEYA TYTYTWEVKPNHG THTYSWHLTQSHA 4TFTYKF	PAPADANCLTW PTPADANCLTW PTKADSNCLTW PADQEDKCITW KAEPKGTFW-	YHSHIDAPKD YHSHIDAPKD YHSHLEPGKD YHSHVVPSKD YHSHVGSQR-	ICSGLIGPLLV ICSGLIGPLLV INTGLIGPLIT INTGLLGIMLI -TNGAYGAFIII	KEG VLN RYSGMR KEG I LN RYSG TR KKDTFDS – NG KR RKGA LN – – QGQQ KEREKVN – – TEK I	TD VD REFVIMFTLVDE ND VD REFVIMFTLVDE KD VD QDFFLLFSVFDE SG VD KEFVALFTVLDE TD V IMTVGD	NQSWYLDDNIKQF NQSWYLNENIKHF NASWLLDENIDRF NESWLLSKNIER- 	247 248 255 247 212
M_musculus/1-1159 H_sapiens/1-1159 Ap_pallida/1-1121 Ac_millepora/1-1114 H_magnipapillata/1-714	C TN PNSVDKSD C TN PDSVDKKD C SN P TKA KN SKEK C SD P TKVN PDD 4KTSE	A V F Q R S N K MHA L A V F Q R S N K MHA L E D F Q E A N K MHA I E D F K E S N K MHA I E V Y	NG F L F G NMP E NG Y L F G N F P E NG Y F Y G N L P G NG Y F Y G N L P G	PEMCVGESVSW PDMCVGESVSW LKLCVHKTISW LDMCYGDSVKW LKMVYGNFIGM	HLFGMGNEIDIHS HLFGMGNEIDIHS HLFGIGNEVDIHT HLAGIGNEVDIHT KPFNVSQTVDG	I YF YGNTF I TRGH RAD I YF YGNTF I SRGH RTD A YFHGQTVD I NSH RKD A YFHGQSFT I DGH RKD G LF SG VPWV	VVNLFPATFLTTE VVNLFPATFLTTE IASLLPATFVTAT VASLLPATFVTAS	333 334 343 333 251
M_musculus/1–1159 H_sapiens/1–1159 Ap_pallida/1–1121 Ac_millepora/1–1114 H_magnipapillata/1–714	MIVEN PG KWMITC MIAEN PG KWMITC MRAHN PG TWMVNC MKALN PG KWMLNC 4ALIEG KG RYID	QVSDHLQAGMLC QVSDHLQAGMLC VVDDHYNAGMYA LVNDHYNAGMYA	QYS VGNC RGN QYN VDNC KSD L FN VSSC SRQ L FN VTKC PG K	A – PH P K VQ – GQ( I – F Y P KM K – GQ( – – A S PQ V R S G K VG VA P S V S G G K – – PN TG KDN GA	QRRYFIAAEKVLW QRRYFIAAEKILW TRTYYITAEEVIW KRTYFIAANEVEW PLTWYTVKHGLKY	D YG PQG YD KF TG F P LN D YA PQG YN KF SG L P LN D YG P SGMN KY KGG E LN N YG P TG YNG MDGQS L I R F	ITSGSDSAVYFTQA IASGSDSDLYFTQG IASGSDSAVFFDRG APGSDSAVFFAQN	419 420 429 421 286
M_musculus/1–1159 H_sapiens/1–1159 Ap_pallida/1–1121 Ac_millepora/1–1114 H_magnipapillata/1–714	DN R I GG K YWKA RY DN R I GG K YWK V RY AH R I GG RY K KA L Y AQR I GG TY L KA I Y 4	TEYVDATFSRR TEFVDATFTKR FEYTDSSFTVK EQYTDARFSTK	MPSDSEAHLG RLSAEEAHLG NSSIHLG PKPEHLG RSINVG	I LG P V I KA E VGI I LG P V I KA E VGI F LG P V I RA E VGI F LG P V I RA E VNI T I Y PMR I S VDGI	DILL VTFAN KADK DTLL VTFAN KADK DTVR VVF KN LAS R DIIE VVF KNNARF HEIS VVASD	VYSILPHGVFYDKASC VYSILPHGVIYDKASC SYSINAHGVFFNKSNE NFSIQPHGVFFNKSNE GYDIKPYSAE	AAPN VDG F L K AAPN LDG F V K G S L YND F TS A K G AL Y EDG TS RAQ K S V I VH PG E R	504 505 512 506 331
M_musculus/1–1159 H_sapiens/1–1159 Ap_pallida/1–1121 Ac_millepora/1–1114 H_magnipapillata/1–714	PGAHVKPGETFTY PGAHVKPGETFTY QDDIVKPNTTYVY ADDNVQPGQTFTY 4FDFILNANKTIDN	RWTVPESVSPTC KWTVPESVSPTA TWTVPEDSGPAR RWTVPEEVGPTR YWIRTESMEDGY	EDPPCLTYLY GDPPCLTYLY EDTQCVTWAY (SDAACITWVY (QNHSVQAILH	F SA VQP I KDTS F SA VDP I KDTS Y SSLDP V KDTY H SS VDP V KDTY Y EGA SNN E PTT	A G L VG P L L VC K KG S G L VG P L L VC K KG S G L I G P L L TC R KG S G L F G P L L TC K KG S KQ V C L KG	TLNADGTQKGIDKEFY VLNADGTQKGIDKEFY TLNAEGEQNNIDKEFI TLNNDNTRKDTDKEFY SSCKVVNCPF	LLFTVFDENFSSY LLFTVFDENLSRY LMLMVSDESMSWY LLFTVTDESESWY	592 593 600 594 397
M_musculus/1–1159 H_sapiens/1–1159 Ap_pallida/1–1121 Ac_millepora/1–1114 H_magnipapillata/1–714	LDENIKKFTWHPF FDENIQKFIWHPF HEENKRMFCTDPS HEKNKEMKANAIL 4FPEHLNLDCVL	S VD KED KEFVKS S ID KED KEFVKS G I T - EN ED YLES IND - DD ED YKES MSD LQNADD ED F	N RMHA VNG YM N RMHA VNG YM N KMHG I NG RL N KMHG I NG FL S P TF TAD S KE	YGSQPGLSMCKI YGNQPGLNMCKI YANLDGLEMCTI YANLPGLEMCLO	KD R VS WH L I G MG T RD R VS WH L I G L G T FD K VS WH L I G FG N GD T I S WH V I G L G N FL N FA -	D TDMHG VY FQGN T I H L D TDMHG I V FQG N T I H L E VDMH T I A F YG Q T V VE E VDMH T A Y F YG N T F TH 	RG TH RD S LA L F PH RG TH RD S LA L F PH NHN R KD T VS L L PG QG S V KD T VS L L PG PG	680 681 687 681 445
M_musculus/1-1159 H_sapiens/1-1159 Ap_pallida/1-1121 Ac_millepora/1-1114 H_magnipapillata/1-714	MA TTA YMQ PDH SG MA TTA FMQ PDH AG TF TTA TMT PDN KG VFG TL TMT PDN AG 4A VN	I F K V F C S T L PH F I F R V F C A TMPH L EWA L I C K T T DH F DWA L V C R TN DH Y	TRGMGQIYEI SRGMGQIYEV SAGMQAKFKV SAGMQAKYKV GRKFEF	S S C G N RD P S E P I S S C D N RD P S E Q I N E C - NQ P S T E I N T C - N R N P E L K P G V N S L T (	PYGML RTFFIAAE RYGMI RTFYIAAE SGKKTRRYYIAAV TSGKTRDYYIAAF QGDEIDSYDCNKH	E VEWD YA PN KNWEFEK E VEWD YA PN KNWEFEK E VDWD YA PTG KD ILGN EMEWD YA PTG LDA LDG DCG LD	CQH LDAGG E RHGD I CQH VDA RG E RHGD I IKTLEE – - SEHA KT KKLDQ – - SEEA KV	768 769 772 766 479
M_musculus/1–1159 H_sapiens/1–1159 Ap_pallida/1–1121 Ac_millepora/1–1114 H_magnipapillata/1–71-	FMNHTENWIGSQY FMNRTENWIGSQY FTINSNNRIGRVY FTVTSDKRIGRKY 4	RKVVYREYTNGE KKVVYREYTDGE KKAVYREFTDDT VKAVYREFTNDC - KVCYCHY	F VE I KA R P PQ F VE I KA R P P R F T KE K K R T D R F NQQKL R T PA E L K I P R	EEHLQLLGPMII EEHLELLGPMII DKYLGVLGPIV EEHLGILGPMLI DKTIQMII	HAEVGDSILIIFK HAEVGNTVLIIFK YAEVGDIIEIVFK HAEVGDTIKVVFK FTNIG	N KA S R P Y S I AAQG V N KA S R P Y S I SAQG V N KA S R D Y S VH PHG V FN NNAN RN Y S VH PHG L Y Y SGAGWGH P I H L HG	EDSN EEMD INKLNEGSDYMDGS SKAHEGSDYNDGT	845 846 860 854 517
M_musculus/1–1159 H_sapiens/1–1159 Ap_pallida/1–1121 Ac_millepora/1–1114 H_magnipapillata/1–714	NG KL LN VP VT KPG SG KQ FQ VPMT KPG NGAA KNDN R I KPS SGAD KLDNA I QPG 4	EIKTYRWN VPK EVKTYRWN IPK TKYTYTWS VPE KTYTYIWK VPE -HSF	SGPGPSDPNC SGPGPSDPNC AGPDSQDTRC AGPGKDGPAC	I PWVYFSTANF I PWVYYSTVNF L TWAYYSDVDS A TWAYYSDVNP YVL KMDY/	VKD TYSGLMGPLI VKD TYSGLMGPLI VKDAN TGL VGPLI I KD TN SGL IGPLI APQN I T TA KLI	TC REG VLNE – KG RRST TC RKG VLNE – KG RRST VC KRG TL TA – EG KPK I C KKG KL KEG TE ERST NA TEN – – – – – – – – K	VDYEFALLFLVFN VDYEFALLFLVFN VNEDFALLFTVMD VDREFVLMFTVLD IDCGFG	932 933 947 942 551
M_musculus/1-1159 H_sapiens/1-1159 Ap_pallida/1-1121 Ac_millepora/1-1114 H_magnipapillata/1-714	ENESWYLDDNIKK ENESWYLDDNIKK ENKSWYLDDNIKK ENESWYLDENIKK 4QK	YLN KD P RD F H YLN KD P RD F H YC TA R VD KD YC KN P G D K E T L H F C N E P KWK	HTDDFEESNK RTDDFEESNR - DEDFQESNK ADDDFMESNK - NKQWDN	MHAING KIFGN MHAING KIFGN MHVING FVFGN MHGING FVFGN	L PGL I MT ED SMTN LHGL I MN ED TMTN I PGL EMVYGDN VS L KGL KMYQD E K VD I PGLNL I NPP	WYLLGIGSEVDIHTIH WYLLGIGSEVDIHTIH WYLLGLGNEVDMHTVH WLLLGIGNEVDMHTVH	YHAESFLFKIDKS YHAESFLFKIDKS FHGQTFVQKSSSY FHGQSFLRKQVSY	1018 1019 1031 1030 579
M_musculus/1–1159 H_sapiens/1–1159 Ap_pallida/1–1121 Ac_millepora/1–1114 H_magnipapillata/1–71-	Y RED VYDL F Y RED VYDL F H PEGMRGD VYDL F H RED VYDL F 4 RKD TL I I P	PGTFQTIELFA PGTFQTIELFA PGVFATVKMVP PGVFATVEMVP TGGYAVLRFKS	H PG TWL LHCH H PG TWL LHCH S I G VWMLHCH S TG DWL LHCH N PG KWF LHCH	VSDHIHAGMET VSDHIHAGMET VNDHMDAGMEA VNDHMVAGMET IEVHALDGMAM	TYTVL RN I DN R I P TYTVL RN I DN R I P RFA VR LYSVL	YSTKTPSGAGSHAVT YSTTSP-GVASHPAT EKPTV 	P S Q E Q P G K E P S N E R P G K E S T T H K P P K G K T T P K P I T A IN E A P K P P K G F P V C	1098 1098 1097 1090 639
M_musculus/1–1159 H_sapiens/1–1159 Ap_pallida/1–1121 Ac_millepora/1–1114 H_magnipapillata/1–71-	ELYFF QLYFF QAYKP ASSF 4NN FYNDLS RDYFY	GKNLRPRGA KAA GKNLGPTGA KAA 	LVILFI LVILFI IFVLMI IFIYLS AKIYLATAIA	LGLLLL VA T IGLLLL I TT MA TLLL I VV FPVLAM LLKA LSVLLFVNVVT	VVLALRLRSSRRQ VILSLRLCSAMKQ A	MAYREVQSCALPTDAL TDYQQVQSCALPTDAL KLNHGKDVGTVLNENI		1159 1159 1121 1114 714

Figure S8 - Multiple sequence alignment showing the sequence similarities between hephaestin-like proteins from *Acropora millepora* (Uniprot Ac. No.: B3EWZ9), *Aiptasia pallida* (NCBI GI: 387005847), *Homo sapiens* (Uniprot Ac. No.: Q6MZM0), *Mus musculus* (Uniprot Ac. No.: Q3V1H3) and the cupredoxin-domain containing protein from *Hydra magnipapillata* (NCBI GI: 221113181). Conservation of residues is dyed by shades of blue: the darker the color, the more conserved the residue among the five species. Sequence alignments were performed with MUSCLE (Edgar 2004) and visualized with Jalview (Waterhouse et al. 2009).

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