

Additional file 7

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R2-1_BMi -----KNTMFNITRPEDSQVDRV
R2-1_MLe KLHRCCPLFQEKDSGGLNRSASGVMSNTSHSKLNLKMDNKLKTSLETSPGVRADSIITRV
R2-1_PBa TL----PFLKLNMRNLNNEKNSGAVRSTEFs----VADNRPSQSLRTTESH-----
          . :. .

R2-1_BMi TIDAESGLPNHAGANLLQCEWCDRLCNKAAGLTLHCKACKNNPAVGSAGNTNDNRRINT
R2-1_MLe RTSSNRG-EHSNGVTYPRCE-----QGVAPLDTHGGICDAPPQVTVPATETDKQKK---
R2-1_PBa -----RCPNCRKLCRSGNGLALHMKHC-----AKCYQNGDNRQEPV
          :*      :. * * *      . :. :. :

R2-1_BMi PPTMRSLFNCEYCNCTGYGTDRLSAHISKKHIPEWNMIKMERFKADGPRQHVWREGDWEI
R2-1_MLe -----CEYCEFTYLKPRQIGTHMRKRHPQEWNDIKRTKFLSE-KRQKRWLDEDDEL
R2-1_PBa KPRME---CSICGLFFSGQRGVAIHKRKKHPAEWNETKRVEDTLS-RKKIRWTSGDREL
          * . * : * : * * : * * * * . . : : * . * * :

R2-1_BMi LCQGEHEHRLPSTAKNKLGVNMFIRASYFPQLTIQAISCQRKSPNFHRY--KNDRLQD
R2-1_MLe LCIGQEEYLVLSIGKGQKGINQYIQTKYFPTLSTDAIKSQKRSRRFSEYSEKRSRELQP
R2-1_PBa LHLGMIEWEASAKTHSQ----EDWVRDHKFPERTINSIKCQIRSKLFRRYVAARPRDEAP
          * * * . . : : : : * * : : * . * * : * :

R2-1_BMi PVTEPQELEPIPEIEIPAQASNPNTNPLEFTPLAEDIAEIRGKPLGPEILNVYRLLAQ
R2-1_MLe CNTSSDPE-----ELPNEAVT-ENSPLSFDPLDRDVVKIKSSKDHGQDILLVQEHILN
R2-1_PBa ---APTPE-AAIQEDEC-----AGSILC---LKDAAIRWLEKEPDGEEYLAITYERLQD
          . **      *      . . * *      : : * : * : . * :

R2-1_BMi AQFNEANDKSRFIDELAKDFTRLSTVPKQPTTSKNKNKKKVGKKRISQRPEKRLSPSK
R2-1_MLe GRYQEANTLAKAIFEKLSGKFPNLKTGDHRP--GKQQTARKVGKKRV--RGSGKKLSPSK
R2-1_PBa GRLGEAGERSRRKFDELASKYT-----PLAKSQPAKGRSKPVDLKSKTNGKLSPAK
          . : ** . : : * : * : . .      * . : : : *      : * * : *

R2-1_BMi AKRKELAYIVQKKWH-TKKRSSVIDTILRDSLQGV---REPAHTPEQLAEFWKGLFSRES
R2-1_MLe QNRRELYAIVQKQWR-TKKRSKVINQILTGNLNKE---QSYTHTPDQLAQFWSTLFGRVs
R2-1_PBa RRRRAKYGCQKEWHNNNQRSGLIRSILQKFGSKEVLKDPRETEETI-DFWSGIFNRDS
          . * : *      * * : * : : * * * * . . . . . : . * : : : * * : * * *

R2-1_BMi PPDNRPIPNRPEIPQLDNPILVSEVDSLKRATEKATGLDGVPLKHLREIGATALTILY
R2-1_MLe PRDDRPINHRRSVIPELDPLSVEEVEAALKGAKDAATGIDGVPISHLKLHLSAALTILY
R2-1_PBa TPDSREIENARETIGALDNMITVEEVAKALKGKSERARGPDGVPKCLKELGATKLAILY
          . * . * * : * * * * : * . * * : * * * * * . * : : : : * : * *

R2-1_BMi NGLYCKQLIPTSWKEARTVLIPKCDVPSSPGEYRPITISSYYYRIYSTIGRRLSDSVGL
R2-1_MLe NGLYVTGSIPDPWKRARTILIPKSNPPASPGDYRPISISSYFYRIYTSISKRLASAVSL
R2-1_PBa NGVFCTSEVPDSWREARTVLIPKKEPKGPADYRPITIGSYFYRAYTSVLGGRISDVVRP
          * * : . . * * . : * * : * * * * * : * * . : * * * * * . : . . *

R2-1_BMi SNRQKGFIKADGIRDNLILLLETIIEDSKKTSPLHMTFMDVKKAFDSVSHSIRRALEWA
R2-1_MLe DDRQKGFIKEDGIRDNLISLIDTLINETKAGSKSLFMTFMDVKKAFDSVSHYAIARSLEWA
R2-1_PBa SQRQKGfVRSDGIRDNLCLLDGLIYNSKNRVQPLHMSFMDVRKAFDSVSHFSIQRMRLWS
          . : * * * : : * * * * * * * * : * : * : * . . * . * : * * : * :

R2-1_BMi GVPLGLRNVIAIDLYKDCSTRIGLSDIKVTRGVKQGDPLSSILFNLVEMALSKIPDRLGI
R2-1_MLe GVPDGMRSVIAIDLYQDCTTDICGRSVKVTGKQGDPLSSTLFNLVIEMVMSNVPERLGI
R2-1_PBa GIPPLLRsVINDLYIGATTsVLGKTVPVKVGVKQGDPLSSILFNLVLDMALDGLTDELGV
          * : * : * . * * * * . : * : : * . * * * * * * * * * : * . . : . : * :

R2-1_BMi GYLGHRLFYMAFADDLVILSRSQLTNQTLVDRVTEQLGLVGLLHPNCKSVAVRADAKR
R2-1_MLe QFQGHRLFYLAFAADDLVLLTRGPTANQKLVSLEHQLARVGLLHPGCKSIAIMADPKR
R2-1_PBa SYLGERLCWMAFADDLVILAPSRA TLQELISNITDRLKRVGLVMNGDKCKSLSICADGKR
          : * . * * : : * * * * * : . : * * . : : * * * * : * * *

R2-1_BMi KTTFVDSTQTIRVNGSEIPALNSEGWYKYLGIKVSSSGMPQGGYTDKILLERVTRAPL
R2-1_MLe KTTFVDQGSsVLIGGEPVSSLGPQEWYKYLGIKLGSGGMPQGIYRDQADLLAKTDSAPL
R2-1_PBa KRTYVDTSQKLYIEGNMLDSMSITDYTYLIGINGARGVKKENLHSEWKTLLERTDKAPL
          * * : * * . . : : * . : : . : * . * * * . : : * * : . * *

R2-1_BMi KPHQRMFILRTHILPRFNHRMMFEKVACKTLTEIDILVREVVRRWLKLPKDVPVAAFYTD
R2-1_MLe KPQQLYILRSHILPKFNHRLMFERVTCQTLEGLDKLIRTHVRKWLKLPKDTGPAFYAD
R2-1_PBa KPHQKLYVVKHAYPTLQHKCSFYASKKCLTELDKLTTRYVVRKMMWL PQDTTIEAFYAS
          * * : * : : * * : * : * : * : * : * : * : * : * : * : * :

R2-1_BMi VPSGGLGLLSLRLTRIPLLKQRTERMAESSDPIRLLVHQEPSKTRLTIGKKRCRIFGKN
R2-1_MLe KGSGLGLLITLRYRVPLLLKRRHKMADSPDPVIRLIPNAEPTISLLARWTMCSLYGKQ
R2-1_PBa VEDGGLQLPSFRIYVPLNKFRRLLCKMRTSEDPLVRKLANAEPAKTIDNAKKLCVVDGNS
          . * * * * : * * : * * : * * * * : * : * : : . * * : * :

R2-1_BMi YHSKSQLASITREKFWSTCDGKGLRTEVPINTSKSSFKLLSDDRTSLKAAQYLGAISVRL
R2-1_MLe YQHSSELSKIIRDKYWTMCDGKGLRTEVPPDTAKKTLsLLFEDRTPLKPGQLIGAIGVRL
R2-1_PBa IENKSQLKSRVDRDAYKWSYDGRGLRTE-PQVQKRGNFQQLQGA VTTLSTRNLVGAWNIRL
          . * * : * . * : * . * * : * * * * * : . : * * * . : : * * : * *

R2-1_BMi NCLGTPLRNNRGGMKPAI---HNLCDKCPGQKFASLGHSIQTCPATHGLRVKRHDKVVTR
R2-1_MLe NTLGTPARNNRAKGYsPE---ANICDKCPGNRQATLGHISQTCPATHGRRVKRHDKIVNR
R2-1_PBa NTTQTTPARKNRAGGAGGAGDSASTCDKCPNGRLATLGHISQSCPETHGSRTKRHDVVDH
          * * * * * : * . * * * . * * * * . * * * * * : * * * * : * :

R2-1_BMi LAKHFGKENTLTVLVEPQLKYGNLPMQKPDLVINTGSTVEIIDIQIKADQGIPRDEDID
R2-1_MLe IAKALKERGSVKNILTEPHLRHDKLPLRKPDLIVHTEKSVEIIDVQVVDQGISRHEDED
R2-1_PBa LQSALLNAQGVTSVLKEPEIRPKGSYCKPDLVAMAERVVVVDVQITS DGGIEDLEGV-
          : . : . . : * * * : . * * * : . * : * : * : * * * .

R2-1_BMi ETVKKDKYDTQECRAAYLALGVTPGSLPCNVNAFTLTWRGNPAPHYSKLARRLGFTSIM
R2-1_MLe QQKKIVKYDVGDKYKRAAYKMLGIDYGSIPCNVSFAFTITWRGNLAPHSLKLASRLQFSPVL
R2-1_PBa AKRRTDKYGSPEILKATLLHLGL-PSDTPISVHAFSITWRGNTLRHsLETASTLVGTHIL
          * * * . : : * * : * * : * * * * : * * * * * : * : : :

R2-1_BMi KYLIADALVDTWGMFVVWNCTS-----
R2-1_MLe KYIVADSLVDTWGAFLIWGKTS-----
R2-1_PBa PRVTTDLVDTYRMFLGWASGRRCVPNKKSTLK
          : : * * * : * : * .

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Figure S7: Multiple sequence alignment of Ctenophora B N-terminal architecture sequences: *Bolinopsis microptera*, *Pleurobrachia bachei*, *Mnemiopsis leidyi* (re-curated, first found Kojima 2016). CXXC residues in the ZnFs are highlighted in green.