

**Figure S2.** Sequence alignment of cysteine-rich C-terminal domains found among Aquatic clade homologs. Note the presence of 10 perfectly conserved cysteine residues per domain, along with a glycine-rich motif and conserved tyrosine at the C-terminal end (asterisks). Sequence names include an abbreviation for genus and species, preceded by a number to account for multiple homologs from a given species and a letter to account for multiple domains within a homolog, e.g. "b1\_Eurh\_ex" denotes the 2nd cysteine-rich C-terminal domain found in homolog 1 from *Eurhomalea exalbida*. The sequence names is also tagged with a protein or nucleotide identifier for the database source of the sequence.

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a1 Hola_du NIPMO1000167 IRTCDGGRKSGSIFGGGGGCIITR-LPP-AGYACKCT--YVFFKT--CK-GTVVNCSDPNSQDCTNPTPGPGACAAGGGDCGGY
a1 Laqu_ru BAS30476 VPPCDGNY-----HSGGCSISK-ASP-PGLACKCR--YAGWT--CR-GSIISCKKPSVSKCTPKTKSKCLEGGDCGGY
a1 Hydr_sy GCHW01001734 YESNCDY-----YSGGCKIEK-AAP-RGYACCT--YEGAWT--CH-GWVVLCSKDKSCKRNPDKSIESCREGRDCGAY
a2 Hydr_sy GCHW01017582 YESCDY-----FSGGCKIVK-KAP-KGMACQCD--YHFLWS--CR-GWVVLCSKSNRDKSCKSPDNKSKQSCLEGGDCGGY
a1 Podo_ca GBEH01026212 YESCNDYDGGG-SGV-SGGCKIQK-AAP-RGYACCT--YEGAWT--CH-GWVVLCSKDNRSKCRSPNTSKQSCVLEGGDCGGY
a2 Podo_ca GCHV01008176 STLCECTY-----SSGGCKVTK-RAP-NGLACCT--YVFLWT--CA-GWVVRCKDMNHSKCRNPDLKSSKCLQGRGDCGAY
a1 Turritopsis IAAF01047012 IPDCECRY-----SPGGCKITI-KAP-SGFACCT--YVFLWT--CA-GWVVSCLDTRSPKCNPNDLRLACLQGRGDCGGY
a3 Podo_ca GCHV01026281 YESCAEE-----KSNGCKITT-AAP-KGMACYCR--KDAEPP--CK-GYIVLCRDVSSSCHKPDTSIESCKEGRDCGGY
a1 Mill_al GFAS01197550 PYKRCCHY-----VNGGCKIVE-PAP-KGLACKCK--HSFIRT--CWGAKVVLCSMDHLKCNPDTSKEACILGRGNCKGY
a2 Mill_al GFAS01232024 PYSACKKI-----TWGGCYISK-PSP-RGLACRCG--NHVFW--CK-GASVLCNPNDAKCVNPNDKSEAEKTAGGDCGGY
a4 Podo_ca GBEH01012910 YESCDY-----YSGGCKIVK-PAP-KGMACQCE--YVALWS--CH-GWVVLCSKSNRDKSCKNADKSKQSCLEGGDCGGY
a1 Anur_ma GAUE_02011119 PHSDCGYRNDTFKLKGGGCIITN-APP-RNHACKCS--VNKPWI--CK-GEVVSCDKPSSSFKNPIDNKETCKQGNDCGGY
a1 Adin_CAWI020040641 PNKCSCEY-----ENGGCSISF-PAP-LKAACKCI--KVPIFPS--CI-GSVVSCDQSOAK-CIQSDASKAECQLGKNCAGY
a1 Rota_ta GDRK01009776 PNKCDY-----HKGCCISW-PAP-SLKACKCK--YKGAWT--CG-GSLVSC-DVSRSKRPEDEKAEACQLGGDCDAY
a2 Rota_so GDRH01012943 IDKCDY-----HPGGCIISW-PAP-SGKACCT--YKPLWT--CE-GSLVAC-DASLPKCSKPDSEKAECELGKDCGGY
a3 Rota_ta GDRK01040881 IDKCDY-----HPGGCIISW-PAP-SGKACCT--YKPLWT--CE-GSLVAC-DASLPKCSKPDSEKAECELGKDCGGY
a1 Phys_po GDRG01010225 EGPDCDF-----DFPGCKVST-PAP-KFTACKC--SLSVFS--CN-AEVVSCDKPSSPLCANPDTSKQSCVLEGGDCGGY
a1 Daph_ma KZS200062 FWECDSY-----YRRTGGGCAITK-MAP-PNHACYCS--YKGAWS--CG-GQTVQCPDTEHFCRKPDLKSKAEACLLGGDCGGY
a3 Daph_pu EFX63581 FFECDY-----FYRISGGCAITK-SAP-PNHACRCT--YKGFWT--CG-GQTECDTNDRLCRPDVSKAEACLGGDCGGY
a2 Daph_pu EFX90329 FWECDY-----FYRIFGGGCAITK-MAP-PNHACEF--YKGAWS--CG-GQTIKCPDLNDRFCQSPDTSSEACILFGGGDCGGY
a2 Daph_ga HAFNO1026617 WVKDCNY-----RGKIFGGGCKISK-IAP-PNYACKCS--YKGAWT--CG-GTVVNCNKSQSLCKSPNAKAEACQLGGDCGGY
a2 Mega_ne GETT01014203 IGTCSCLY-----TVSGCKRISN-PAP-EYSACKCK--LWLWT--ICI-GDVVFCNPNQSPKCHKPDTTIGSCLRGGDCGGY
a2 Macr_li LFJF01005372 PNNCDY-----HWGGCTISS-PAP-PFKACRCK--YKGFWT--CG-GSVVSC-NSSHFKCRNPDKSKESKLLGGDCGGY
a1 Macr_li LFJF0102150 PNNCDY-----HWGGCTISS-PAP-PFKACRCK--YKGFWT--CG-GSVVSC-NSSHFKCRNPDKSKESKLLGGDCGGY
a3 Macr_li GFJZ01009867 PNKCDY-----KKGCCISF-PAP-LGKACKCS--MKFAWT--CG-GSVVDCNNSRCKSTPDASRACRLLGGDCGGY
a2 Macr_tu GFJZ01073267 EHRCDY-----HRGGCAISN-PAP-VGHACQCR--YMGFWT--CR-GALARC-NLSHGKCSKPDVSKAEACELGGDCGGY
a1 Rudi_ph GAEH01001910 KLECDY-----HPGGCSISR-PAP-SGMACQCE--YKGAWT--CG-GSVSHLCPNPNYCSNPDPVSHSCLGGDCGGY
a1 Beroe_sp pink comp12247_c0 IGVCDYRKLPSNGVNSGGCVITL-PPP-PFSSCHCT--LNRDQ--CW-GTVVGRDVLNKNCAVPDTSLTACLGGSGNCGY
a1 Eurh_ex GFAG01028535 GLDCDY-----HPGGCSISK-PAP-SGMACYCE--YKGAWT--CG-GNVAQCSNSASYYCTHDPDYVSVCLLGGDCGGY
a2 Rota_ta GDRK01010974 PHVDCSY-----NSDGCVISM-PPP-SMTACKC--YKGAWT--CD-GTVVCSNPNQSPKCHKPDTTIGSCLRGGDCGGY
a1 Amoe_pa GAKF01035315 GEGCEKYIQPV--KAGSGGCIIVTR-LPP-KGRACKCK--YIGFWA--CT-GSLVYCKDPOHPLCEDPEPFGVEMCVLGGDCGGY
a2 Amoe_pa GAKF01008738 LSGCECTYRPN--KHVGGCVITR-LPP-AGKACKCE--YKGMWT--CS-SSVVPCTNASSSELCKTPEPGETCLLGGDCGGY
a1 Vall_mu comp61091_c0 IGSDCY-----TSGGCRITYK-RAP-NYSACRNC--YDGGWA--CS-GQVVCDDITSEYCLNPNRDIIVSCVGGDCGGY
a1 Eupl_du comp44097_c0 IGTCSCEY-----HSGGCSIVV-AAP-VYSACRCL--YNGFWK--CS-GQVVGCDSDSSYXETPDTTISQSCVGGDCGGY
a1 Mnem_le AGCP01005106 RGTCTYCKR--NGTGCVIST-PAP-OHSACKCT--ENAEV--CV-GKVVGCKDLSDPHCLTPDVSLSCYQSLGDCGGY
a2 Pleu_ba AVPN01000039 IGTCDY-----SAGGCYIYT-PAP-AYSACRCI--YDGAWT--CS-GQVVCDDQDSEHCENPDKSIKSCVGGDCGGY
a2 Pleu_pileus comp47111_c2 IGTCDY-----SSGGCYIYT-PAP-AYSACRCI--YDGAWT--CS-GQVVCDDQDSEHCENPDKSIKSCVGGDCGGY
a1 Coel_comp37501_c0 IGTCDY-----KPGGCRITYK-PAP-KYSACRCI--YDGAWO--CS-GQVVGCDNIQTKECLEPDKGIISCVGGDCGGY
a2 Mnem_le AGCP01011369 LGECDEY-----SAGGCSYIK-AAP-EFSACRCV--YDGAWS--CS-GQVVCDDQTEHPLCENPDKSIKSCVGGDCGGY
a2 EuplokamisSp-Gulf-2_15383 IGTCDY-----SAGGCYIYT-PAP-AYSACRCI--YDGAWT--CS-GQVVCDDQDSEHCENPDKSIKSCVGGDCGGY
a1 EuplokamisSp-Gulf-2_14984 IGTCSCEL-----EGEDNCKISK-PAP-SLSACOCYLSNNSNT--CR-GKVVGCDYDNTSPQCTITPDTTIESCILGSGOCTGY
a1 Pleu_pileus comp47659_c2 AGHCSEL-----VGENNCKIST-PAP-SLSACOCYLSNNSNT--CR-GKVVGCDYDNTSPQCTITPDTTIESCILGSGOCTGY
a1 Pleu_ba AVPN01007659 AGYCSCEL-----EGDGCKISK-PAP-SLSACOCYLSNNSNT--CR-GKVVGCDYDNTSPQCTITPDTTIESCALGSGOCTGY
a3 Mnem_le MLRB042621 VDGCGDK-----SSEGRIDE-VAVVPGSACRCVKGWFW--CK-GDVVGRDITAPHCVSPOQSVESCRGGDCGGY
a1 Dryo_gl comp14322_c0 VDGCGEK-----NNGGCKIDDEVSVEGTACRCKQYFFWAG--CR-GDVVGCVDITSEDCLEPGGSRMCTIGGGDCGGY
b1 Eurh_ex GFAG01028535 --ATCDY-----HRGGCTISQ-VPP-NTACYCS--YKGAWT--CG-GRIRCKDFNSYCTNPDSSINTCYIGRGGDCGGY
b2 Rota_ta GDRK01010974 --SCDQYIVKG--LLKPSGCKIIEK-AMI-SNLACRCH--RDSIWS--CS-GYPVSC-DTSNPKCANPDLKSKESCLGGDCGGY
b1 Amoe_pa GAKF01035315 --PTCDNYVRKG--L-DSGGCVLSM-TPK-NGTACKCK--YKGAWT--CG-GVRVAC-DLAEMCRNPVSKETCVLGGDCGGY
b2 Amoe_pa GAKF01008738 --PTCDY-----HSGGCSISV-TAP-VGYACECR--YRGLWT--CG-GTAKRC-DLNQAKCTPDVTKAEACVGGDCGGY
b1 Vall_mu comp61091_c0 --KSCDY-----GLGGCTIYQ-AAP-PGFACKCS--YDEFWM--CS-GSVKCRDRPHSKYCTSPDKSIFSCVGGDCGGY
b1 Eupl_du comp44097_c0 --LSCDQW-----GQGGCSVYN-PAP-AGYACKCS--YDFWFM--CS-GSLGCRDRHSEFCSPDASISCLQKGNCGAY
b1 Mnem_le AGCP01005106 --NTECTH-----ENDGCKVSK-AAN-YGKACRCT--LVKNGEKRFS--GEVVECRDPDSHYCTNST-SIQSCLOGGDCGGY
b2 Pleu_ba AVPN01000039 --LSCDY-----SLGGCTVYT-PAP-PGYACQCS--YDEFWM--CS-GTVTKCRDPFVSHCAIPDKSIKSCVGGDCGGY
b2 Pleu_pileus comp47111_c2 --LSCDQY-----YLGGCTVYT-PAP-PGYACQCS--YDEFWM--CS-GTVTKCRDPFVSHCAIPDKSIKSCVGGDCGGY
b1 Coel_comp37501_c0 --ISCDY-----SSGGCSIHD-PAP-AGYACKCS--YDELWM--CS-GSVTKCRDPHFKCNPKPDKSIFSCVGGDCGGY
b2 Mnem_le AGCP01011369 --LSCDQY-----SWGGCTVYD-PAP-AGYACQCS--YDEFWM--CS-GTITSCRDPHSEFCSPDTSIFSCVGGDCGGY
b2 EuplokamisSp-Gulf-2_15383 --LSCDQY-----HLGGCTVYT-PAP-PGYACQCS--YDFWFM--CS-GTVTKCRDPFVSHCAIPDKSIKSCVGGDCGGY
b1 EuplokamisSp-Gulf-2_14984 --STCTCY-----NNGGCTVITGPEG-VGEACRCV--KDSKGV--CE-SEVVRCDPSSPQCTSPKSTLLSCLGGDCGGY
b1 Pleu_pileus comp47659_c2 --STCTCY-----NNGGCTVITGPEG-VGEACRCV--KDSKGV--CE-SEVVRCDPSSPQCTSPKSTLLSCLGGDCGGY
b1 Pleu_ba AVPN01007659 --STCTCY-----NNGGCTVITGPEG-VGEACRCV--KDSKGV--CE-SEVVRCDPSSPQCTSPKSTLLSCLGGDCGGY
c1 Vall_mu comp61091_c0 DYTCECTY-----GAGGCTVTK-PSP-RNTACQCV--YKGAWT--CS-AVITCRHDEAEKCNPNPDKSIFSCVGGDCGGY
c2 Pleu_pileus comp47111_c2 DYTCECTY-----GAGGCTVTK-PAP-SGTACRCV--YKGAWT--CS-GTIVSCRHDDAVACTDPTTIESCLEGGDCGGY
c1 Coel_comp37501_c0 DYTCECTY-----GSGGCVINK-AAP-SKTACQCS--YKGAWT--CS-GMITCRNDQAEKCRNPDKSIFSCVGGDCGGY
c2 Mnem_le AGCP01011369 DYTCECTY-----GKGGCTVTK-PAP-PGTACRCV--YEGAWT--CS-GTIVTKNDQAVDCLEPSTSIKSCVGGDCGGY
c2 EuplokamisSp-Gulf-2_15383 DYTCECTY-----GAGGCTVTK-AAP-AGTACRCV--YKGAWT--CR-GTIVSCRHDDAVACTDPTTIESCLEGGDCGGY
c1 EuplokamisSp-Gulf-2_14984 DENCKCEK-----EGDGCKITS-PSP-NSTACHCR--RYANGQ--CR-GHSLCPTQOS--CATPDTSLTSLVGGDCGGY
c1 Pleu_pileus comp47659_c2 DENCKCEK-----ESDGCKITS-PSP-NSTACHCR--RYSSGQ--CR-GHTLCPSPLOS--CTAPDTSILSCLGGDCGGY
c1 Pleu_ba AVPN01007659 DENCKCGK-----EGDGCKITS-PSP-NSTACHCR--RYTNGQ--CR-GHSLCPTSTP--QSCATPDTSLSCLGGDCGGY
d1 Vall_mu comp61091_c0 GDTCECTV-----QANGGCKVTK-PAP-KDTACMCT--YVD--FPYVSCD-AKVVPYCGIYHAQTCQNPDTSIDSCVGGDCGGY
d1 Eupl_du comp44097_c0 EETCDCKA-----VGNGCVISK-PSP-AQYACKCH--MDSLWKNKCY--GEIVMCGIIPSDTCDKPDRSLDSCVGGDCGGY
d1 Mnem_le AGCP01005106 PGGCECY-----VNA-GCRISK-AAP-AGSACRCV--SWW--FFGNSCY--GEVVGCGNLVSDKCNPNPDKSIFSCVGGDCGGY
d2 Pleu_ba AVPN01000039 POTCECEK-----KRE-GCVVSS-SAP-AGTACRCV--YVD--WPYVCF-AEIVGCVSPYSDTCMLPDTTIVSCLGGDCGGY
d2 Pleu_pileus comp47111_c2 POTCECKK-----NND-GCVVSS-AAP-ASTACRCV--YVD--FPYVCF-AEIVGCAVPYSDTCMLPDTTIVSCLGGDCGGY
d1 Coel_comp37501_c0 HEKCEGV-----QDNGGCKITK-AAP-RNTACKCT--YVG--WPYVSCS-AEIVGCVYSSCTQNPDLTIDACLGGDCGGY
d2 Mnem_le AGCP01011369 PDRCKCGV-----RDNGGCKITA-PAP-AHTACNRY--YHS--FPYFCT--GYVACGVYHSACTLEPDTTIVSCLGGDCGGY
d2 EuplokamisSp-Gulf-2_15383 POTCECKK-----KRO-GCVVSS-PAP-SGTACRCS--YVD--FPYVCF-AEIVGCVSPYSETCLOPDTTIVSCLGGDCGGY
d1 EuplokamisSp-Gulf-2_14984 GEECECEH-----HSH-GCRVKK-AAP-SGSACRCV--TESS-WFKTYCY--GDVVGCANDSEKCTPDTTIVSCLGGDCGGY
d1 Pleu_pileus comp47659_c2 GEECECEH-----HSG-GCRVKT-PAP-SGSACRCV--TESS-WFKTYCY--GDVVGCANDSEKCTPDTTIVSCLGGDCGGY
1.....10.....20.....30.....40.....50.....60.....70.....80.....

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