

[illegible]

Limnoperla for tunei NFUK01006104

Haliotis rufra Q9JH01001142

Haliotis rufescens QGM001000565

Pinctada imbricata NJ0101048221

Bathymodiolus platifrons MJUT01033839

Modiolus chilipapenae MJUL01021410

Pomacea scalaris Psc4690

Nia ampullacea Plab2769

Marisa cornuarietis Mcs2027

Lanistes nyassanus Ln24710

Asolene platæ A152885

Pomacea canaliculata Psc5338

Glossogobex pallidus TSA_GBIL01075477

Pygospio elegans TSA_GFLP01035490

Lingula anatina XP_013395432

Lingula anatina XP_013379610

Phoronis australis g9986.t1

Phoronis australis g16048.t1

Psychodera flava LD343027_4153450098

Psychodera flava LD343027_5100746347

Psychodera flava PFL3_pfl_40x0_9_20150316_1g6997.t1

Saccoglossus kowalevskii XP_006816582

Saccoglossus kowalevskii XP_006816581

Saccoglossus kowalevskii XP_006819810

Ephydatia muelleri m_29963.g.29963

Amphimedon queenslandica XP_013851448

Xestospongia testudinaria gnl|JBL_ORD_ID|61299

Haliciona tubifera TSA_GFAV01017079

Trichoplax adhaerens XP_002114911

Amphidiscus feneer after evm.m.model.scaffold_206.7

Discomoma sp. evm.m.model.scaffold_6.33

Orbicella faveolata XP_020628431

Sychocadylla hellebrandi TSA_GGNV01117022

Syllophora pisticulata XP_022802004

Exapatasia pallida XP_020895894

Lactinella veratr a c86768.g1_11

Actinia tenerosa TSA_GEVO10039432

Porites rus OHRP01000157

Pocillopora damicornis pdam_00006209-PA

Pachyseris speciosa Sc0001227

Nematostella vectensis XP_001629956

Fungia sp. flunt.m.4.16656.m.1

Goniastrea aspera a gsp1.m.3.6500.m.1

Anthopleura elegantissima TSA_GBYC01063006

Calliactis polypus c66498.g1_1

Nemanthus ananensis TR26025|c0_g2_13

Rentlia rentlii mis FXA011159338

Dicystostellum discoidium XP_640516

Polysiphonium pallidum XP_020429468

Cerithium ocella castellanum XP_004368209

Monoecia brevicollis XP_001742116

Salpingoeca rosea XP_004988636

Paramecium tetra aurelia XP_001462315

Tetrahymena thermophila XP_001020855

Thraustotheca clavata A1G55673

Saprodiegma declina XP_008694251

Leucamonas trahens XP_013759880

Naegleria gruberi XP_002676377

Aspergillus fumigatus XP_751813

Aspergillus oryzae XP_001821436

Aspergillus niger XP_001394335

Fusarium verticillioides AA.Z73168

Fusicoccum sp. AB-548762

Chaetomium globosum XP_001219963

Phanerochaete chrysosporium |GI Phc2r 2983917

Laccaria bicolor XP_001888631

450 460 470 480 490 500 510 520 530 540 550 560

ARK---TTRVDLLMAKN-Q-----RKIFADHDLLESRGEGSGLLVALTINVGRGV---LRKSLSHLAILEDQ---YVSAF---DTRVKRSLIIRDGSFENVLDGGMQVFMV
FRE---TVHVDLITARN-Q-----RTIIADRDLLWESRGEGSGLLVALTINVAGRVR---MQATIRHLRLSDIDQ---YVSVL---DSKVRISM--RNGTALADDDGGMQVFMV
ARK---ATRVDMMAKN-Q-----RRIIFADHDLLESRGEGSGLLVALTINVGRGV---LRKSLRLAVODDE---YVSVMF---DSKVHLSIR--RGDSFENVLDGGMQVFMV
FRE---AVHVDLITARN-Q-----RTIVADRDLLLESRGEGSGLLVALTINVGRGHN---LQTSIKRLRLQDAD---YVSVL---DSKVHLSIR--RDAALVMVDNGIPQIF
ARR---ATRVDMMAKN-Q-----RRIIFADHDLLESRGEGSGLLVALTINVGRGV---LRKSLRLAVODDE---YVSVMF---DSKVRISM--RDSGLIEVLDGGMQVFMV
ARK---ATRVDMMAKN-Q-----RRIIFADHDLLESRGEGSGLLVALTINVGRGV---LRKSLRLAVODDE---YVSVMF---DSKVRISM--RDSGLIEVLDGGMQVFMV
FRE---NLILSTVISTTT-Q-----EELIYADDDTLVETRGIL---NOTIVVTNLGTGSS---QOKSFAVAQODIT---EYENLH---DSDBVILIR--RNGHLETTIENNGQPKVY
VRK---ENIGKILDAE-Q-----REBVVSDSLVESRGH---HVKLVGAVINVGTGDDSFVTYTFSETDNVEGR---DFINAF---DADDVIRV--TNNELPITIMGPKVMY
FRE---KLGSAFYDQA-Q-----NEIRWRDSFYAFITRGH---GEVLVGVSNVGGSGST---EQRDIGDLPYHDBIT---TEKNIL---DTSBKLTAT--NGKYSININNGQPKVY
LRL---SHLSHEVLDQD-Q-----REBVAANDFEVETRGK---ENQFVLVETNRGNTSG---TLVEMOVVPVIAKCT---YVVMF---DETDTVM--NGETLKLITLGLPKVFMV
YRL---GNPNIDGIG-Q-----EELIYAFQSKMVLGRVDAAGRKLLAVIRKSRNGGQLVLAKGSRKYNVDKNRIVYVMF---NSDITMV--GNCAFDMWMCFIIFMHR
FRK---SLGTGEFFESK-Q-----QERLVDDDFLVTIRGT---DEKVVVALIRNGSGSQ---LQRTIPNLPHNDIT---KELNIF---DPSDQITC--TQKQITMSITINNGQPKVY
FRE---SLGSDLYEAD-Q-----REBVLVDDDFLVTIRGT---DEKVVVALIRNGSGSQ---LQRTIPNLPHNDIT---KELNIF---DPSDQITC--TQKQITMSITINNGQPKVY
FRS---SLGDFPINS-E-----TESLYSDPFYSITRT---TFLVLENGSGAS---YVQTLIRKIDSEFVLANVL---DPSDKVIR--ADGKFTTIRTERGEPKIVY
WRG---VLGTSRTAAD-Q-----VETRVDDDFYSITRGD---AMKCAIKLGEFGN---LSRRSYHNPIIT---VLVNIY---NTNDRVTI--QSYGIDISITGEPKIVY
FSR---SLGQNFIDSD-Q-----TETTYDDEFYSITRDL---TILVALSNKGSQTV---VERTITGHEGSGND---VETNIL---DHSDDTVI--TNDVMTITISNGEPKIVY
FRS---SLGQNFIDSD-Q-----TETTYDDEFYSITRDL---TILVALSNKGSQTV---VERTITGHEGSGND---VETNIL---DHSDDTVI--TNDVMTITISNGEPKIVY
FRD---LLGANFLINAD-Q-----IERVQDSSFATIRHD---MLVCSTINIGDNNN---LQRTITYHDTVTGT---VVLNLY---DENDRVTV--DTSQITNILEISGEKIVY
FRIT---EQGSSLYEAA-Q-----VERVVDQFVFAITRGH---VFVATSNIGTGQS---LSRPIITYHPYSDGT---TEVNIL---DSDBKVTI--DSDQFENIENNGQPKVY
FRN---SLGSOLYNAQ-Q-----IERVVDQFVFAITRGH---VFVATSNIGTGQS---LSRPIITYHPYSDGT---TEVNIL---DSDBKVTI--DSDQFENIENNGQPKVY
FRK---SYGSALEYAD-Q-----VQRVVDQFVFAITRGH---VFVATSNIGTGQS---LSRPIITYHPYSDGT---TEVNIL---DSDBKVTI--DSDQFENIENNGQPKVY
FRN---SRGSDLYEAD-Q-----VERVVDQFVFAITRGH---VFVATSNIGTGQS---LSRPIITYHPYSDGT---TEVNIL---DSDBKVTI--DSDQFENIENNGQPKVY
YRK---TV--INNGQA-Y-----VERVVDQFVFAITRGH---VFVATSNIGTGQS---LSRPIITYHPYSDGT---TEVNIL---DSDBKVTI--DSDQFENIENNGQPKVY
FRK---SLGDANWLHO-Q-----VERHVDPVDAFESRGD---VLVVVVICQDATVH---LTIQDHPVQPID---KITNVL---NARETFEWSGDQR
FRK---SLGDANWLDE-Q-----VERHVDPVDAFESRGD---VLVVVVICQDATVH---LTIQDHPVQPID---KITNVL---NARETFEWSGDQKLTMTMEMGEPLILL
FRK---ALGKEWLRK-Q-----VERHVSDVDAFESRGK---VLVITITQNTTVK---KITNTPVPEPN---TEKNVL---NPTEKFMSLDGSLPITNIGDPLVL
VIN---AQGDSWLKSD-Q-----IERHVSPVNVYESRGK---VLVITITQNTTVK---KITNTPVPEPN---TEKNVL---NPTEKFMSLDGSLPITNIGDPLVL
FRR---SLGNEVHEK-Q-----MERHVQTDVAFESRGK---ALVITITNLDTSIN---LSIRDTPYQPID---TEGNIL---NPSETLTSVSDGSLMTLSGDPLVL
VRK---SQGKSWLNSN-Q-----IERHVDAKVDVAFESRQN---VLVVITITNMSIT---RVLKSHPEKADQ---EVKNIL---DVKQKFKMSNEGLKMTLIDGELILL
VIN---AQGDSWLKSD-Q-----IERHVSPVNVYESRGK---VLVITITQNTTVK---KITNTPVPEPN---TEKNVL---NPTEKFMSLDGSLPITNIGDPLVL
VRK---DQGDNDWLKTD-Q-----IERVYTPNVVYESRGK---VLVITITANTTTT---AKIQSHQVSKBK---NEKNIL---NOKQMFKMSNGELVATVQDGEPLVL
FRR---SLGDDWLQNR-QVTVERYLLPLIERHVQSNVAYAFESRGQ---IMVVTISQEKTLN---LTIHSPVKPIOT---TERNAL---NFDEKFNMSDSSRLRILNSGEPLVL
FRR---SLGNEVQDK-Q-----VERHVQADVAFESRGK---VLVVITNLDTSIN---LSIRDTPYQPID---TEGNIL---NPSETLTSVSDGSLMTLSGDPLVL
FRIT---SLGDFWQK-Q-----VERHVQADVAFESRGK---VLVVITNLDTSIN---LSIRDTPYQPID---TEGNIL---NPSETLTSVSDGSLMTLSGDPLVL
FRS---SLGQPFVSSP-Q-----IEQHVPEVDAFESRGK---VLVVITITRVTTAS---TLIQSHPENEGE---KVVNVL---NMTOTFLDAKGRLEAKMVSGEPVL
FRK---ALGNKWLQEK-Q-----VERHVQADVAFESRGK---VLVVITITQNTTVK---KITNTPVPEPN---TEKNVL---NPTEKFMSLDGSLPITNIGDPLVL
FRK---ALGKEWLRQE-Q-----VERHVSDVDAFESRGK---VLVITITQNTTVK---KITNTPVPEPN---TEKNVL---NPTEKFMSLDGSLPITNIGDPLVL
VRK---DQGDNDWLKTD-Q-----IERHVDPVNVYESRGK---VLVITITANTTTT---TLIQSHPEKSGQ---HUKNVL---NOKQTFKMSNGVLIARQDGEPLVL
VRK---SMSVDWLKKP-Q-----IERHVSDVDAFESRGK---VLVITITSETKNTS---RTVQSHPEADANK---VKNLNL---DSTQMTFKSEKGLTVMKIDGEPVL
IRK---AMRAGWLKSP-Q-----IERHVQGEVAFESRGK---VLVVITITSETKNTS---RTVQSHPEADANK---VKNLNL---DSTQMTFKSEKGLTVMKIDGEPVL
IRN---KFPKSWLKSP-Q-----IEQVYSNVVAFESRDE---TLITITITEKKEIT---VITKSHPEADQ---VEKNIL---NPHTHTKSKENEKLTMTYGEPLVF
FRA---NITEDTLIAQ-Q-----VQRYSDNGFYAFITRGH---AFVALTNGGSGNEV---QTSRNTIYHPYLEBT---TECNIFY---PTEDCKV--AGGAFVYLDIGESKIVY
F---VKQSLYQYP-Q-----IQRYADDSFYAFITRGH---TFVALTNGGSGNG---QISRTITYOPQDGT---TECNIFW---PTEDCKV--VQGFVYLDIGENESKIVY
YRK---QACQVQVYP-Q-----VQRYSDDTFYAFITRGH---TFVALTNGGSGNG---QISRTITYOPQDGT---TECNIFW---PTEDCKV--VQGFVYLDIGENESKIVY
YRN---TLPPDSFQAE-Q-----IEKVVMDLIVVVRGQ---VLVATITNGNGHS---TSASMDLPFANGT---REIDIV---AGKDALT--NNGTADIVLDGACVCEL
ART---KLPLASRYSSQ-Q-----YKCVVLNLIYVETRGH---VLVATITNGGCGAQ---TGASMDLPFANGT---REIDIV---AGKDALT--NNGTADIVLDGACVCEL
ARK---AVNAGQAE-Q-----VQRYADDDFYAFITRGH---LFAAFETSYDROV---IRKITYHPEADIT---VEKNVL---PTGDCLTV--QNGSFQYIRNVEVCHF
AKN---ITNAGLOG-Q-----IEKVVMDLIVVVRGQ---VLVATITNGGCGAQ---TGASMDLPFANGT---REIDIV---AGKDALT--NNGTADIVLDGACVCEL
QRK---KSKIWNPW-Q-----VERYSNPNFYVESRGEG---FLVALTNSNDQOH---FKMTYHPKDGQ---VKNIFY---PTSDCOTV--NGQVQVYLLNGESKIVY
QRK---KSKIWNPW-Q-----VERYSNPNFYVESRGEG---FLVALTNSNDQOH---FKMTYHPKDGQ---VKNIFY---PTSDCOTV--NGQVQVYLLNGESKIVY
QRK---KSKIWNPW-Q-----VERYSNPNFYVESRGEG---FLVALTNSNDQOH---FKMTYHPKDGQ---VKNIFY---PTSDCOTV--NGQVQVYLLNGESKIVY
LBK---NTTANVSFPQ-Q-----VQRYSDNFVAFESRGK---FLVALTNSGASF---ISITYSYPTKADV---VEKNIL---AVPADSDCLVTGASAFVYNGEPLKIVY
FRN---THFQEFLLNPLQ-Q-----VERVYANFVAFESRGN---VFVATITNVGSSYG---RLQYTIITYHPYSDGT---VECDIFW---GNNDCETV--NGQFTVILLNGESKIVY
IRSHAIKDPGVYTYK-N-----NPIKMDSTTIAMRGSDGAGITVLNLSNLGASGS---SYTSLGGTGAEAGQ---QTEMF---SCTTMTGSDKPKMPPMAGSLPRV
IRVYAIKSDGTGEVYK-N-----WPIKMDSTTIAMRGSDGAGITVLNLSNLGASGS---SYTSLGGTGAEAGQ---QTEMF---SCTTMTGSDKPKMPPMAGSLPRV
IRKLAISADSAVITYA-N-----DAFMTDSNTIAMRGSGTSQVITVLSNKGSGS---SYTSLGGSGTSGT---KELIAY---TCTSYTDSGSDIPMPMAGSLPRV
ARS---AVGGLGNDH-Q-----KHLMSQDSAYAMRSHAD---GDLMLTLTLNRGGYS---GQYCVNTGKNKN---TWMRF---GSQGTMTSGDNGKPMPPMAGSLPRV
IRVRAVADATIEVYK-N-----WPIKMDSTTIAMRGSDGAGITVLNLSNLGASGS---SYTSLGGTGAEAGQ---QTEMF---SCTTMTGSDKPKMPPMAGSLPRV
IRKSAISQDDGYLYK-S-----NPIKMDSTTIAMRGSDGAGITVLNLSNLGASGS---SYTSLGGTGAEAGQ---QTEMF---SCTTMTGSDKPKMPPMAGSLPRV
ARKAAASANSEFYATP-V-----KFPVYSTSQMAYSP-P---LUALILNNGSSSS---PQVMTSAGVDANE---ELIDMV---SCTKITADNGGYSITTAQGLASPLV
ARKAAAAANSTELTTLK-----FVTQDPSLLAVSP-P---LUALILNNGSSNSA-KSSTWASGVASANE---VVDVL---SCAIVKADGSGGSPMPPMAGSLPRV