

Supplementary material

Figure S1: Tree of life

Opisthokonta - Animalia - Vertebrata

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

Homo sapiens hydrogen voltage gated channel 1 (HVCN1), transcript variant 1, mRNA. NM_001040107

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGDDYHAWNINYKKWENEEE
EEEEEQPPPTPVSGEEGRAAPDVAPAPGPAPRAPLDFRGMLRKLFSSHR
FQV^{II}ICLVVL^DALLVLAELILD^LKII^QPDKNYAAMVFHYMSITILVFF
MMEIIFKLFVFRLEFFHHKFEILDAVVVVVSFILDIVLLFQEHQFEALGL
LILL^LLRVAR^IINGIISV^KTRSERQLRLKQMNVLAAKIQHLEFSCS
EKEQEIERLNKLLRQHGLLGEVN-

**voltage-gated hydrogen channel 1 [Xenopus laevis].
XP_018099695**

MAGCLRHF^TSVGDDTKKREWKEEDVEVAHEEEKKNTPHPF^IASYS^LRGAL
KWL^FSSHKFQ^IVI^ISLVIL^DALFVLVEVLLDLELLAEKVDHI^IPE^IFHYL
SVSVLSFFILEIA^GKLYAFRLEFFHHKFEVFDAAIVVISFIIDIVYISRE
DIFNA^VGLLILL^LLRVAR^IIVNGVIVSVK^SRAEEKIHKLEENQRSLL^EKV
TQLEQQSAQQEQEIARLQKLLKQHNVPDS-

**voltage-gated hydrogen channel 1 isoform X1 [Xenopus laevis].
XP_018104580**

MAGCLRHF^TSVGDDTKKREWQEDVEVAYEEPLKNTPHPF^IASYS^FRGAL
KWL^LSSHKFQ^IVI^ICLVIL^DALFVLVEVLLDLELLAEKVDHI^IPE^IFHYL
SISVLTFFILEIA^GKLYAFRLEFFHHKFEVFDAAIVVISFIIDIVYISRE
DIFNA^VGLLILL^LLRVAR^IIVNGVIVSVK^TRAEEKMHKLKEQKGSLL^EKV
AQLEQQCAQQEQEIGRLHKLLQEHNVFPAS-

Pan troglodytes XM_016924207
Macaca mulatta XM_028829869
Balaenoptera musculus XM_036823351
Mus musculus NM_028752
Rattus norvegicus XM_017598517
Danio rerio NM_001002346
Lacerta agilis XM_033159246
Gekko japonicus XM_015415738
Microcaecilia unicolor XM_030220075
Petromyzon marinus XM_032947247

Opisthokonta - Chordata - Tunicata

Eukaryota; Metazoa; **Chordata**; **Tunicata**; Ascidiacea; Phlebobranchia; Cionidae; Ciona.

Ciona intestinalis voltage-gated hydrogen channel 1 (hvcn1), mRNA.
NM_001078469

MEGDNCNKSRHKSHNMINPNYASVRCTQPLPSVIQLRSRNKMIGITEDPS
SDSEPVSSNQPLLLTNLSYEVHTFNDNNNHERPAPQEQSTQNTMISMQSE
QKSDRFTASNLGMFQYMKFEIGEDGDDHEEEAILTNREKLRHILHSKIP
VAIIIVLVVLDSFLVVGELLIDLKVIIVPHGNPAPEILHGFSLSILSIFMV
EIALKIIADHRHFIHHKVEVLDAVVVISFGVDIALIFVGESEALAAIGL
LVILFLWRVFRINGIIVTVKTKADDRVHEIKKKNSELELQIHNLEEKLS
QKEQDMSRLHEILRCNNIDIPPTVPLTTSVQIHSTTTASADV-

Ciona intestinalis voltage-sensor containing phosphatase (vsp),
mRNA. NM_001033826

MEGFDGSDFSPPADLVGVDGAVMRNVVDVTINGDVTAPPKAAPRKSESVK
KVHWNVDVQGPSEKPETRQEERIDIPEISGLWWGENEHGVDDGRMEIPTT
GVGRVQFRVRAVIDHLMGRVFGVFLIFLDIILMIIDLSIPGKSESSQSFY
DGMALALSCYFMLDLGLRIFAYGPKNFFTNPWEVADGLIIVVTFVVTIFY
TVLDEYVQETGADGLGRLVVLAFLLVVFLAIFYSHQMKASSRRTISQ
NKRRYRKDGFDLDTYVTDHVIAMSFSSGRQSLFRNPIGEVSRRFFKTKH
PDKFRIYNLCSERGYDETKFDNHVYRVMIDDHNVPTLVDLLKFIDDAKVW
MTSDPDHVIAIHCKGGKGRGTGLVSSWLLEDGKFDTAKEALEYFGSRRTD
FEVGDFVQGVETASQIRYVGYFEKIKKNYGGQLPPMKKLKVTGVTITAIQ
GVGRNGSDLSMQIVSERQEVLLCKFAEGYNALQYDATDDCVTCEVKNC
PVLAGDIKVRFMSTSKSLPRGYDNCPFYFWFNTSLVEGDHVTLKREEIDN
PHKKKTWKIYRDNFTVKLTFSDAEDI-

Polycarpa mytiligera GIUT01151021
Salpa thompsoni GFCC01108773
Oikopleura dioica GCJN01019160
Phallusia mammillata LR785897
Aplidium turbinatum OU964926
Ascidia mentula OX387201
Styela clava XM_039415523
Clavelina lepadiformis OX392441

Oikopleura dioica comp23289_c0_seq2 transcribed RNA sequence.
ACCESSION GCJN01027812

MSENSSVVESTPFLEILKSDMTCWEKTSRVVHKLLHSHTTQAILLFLVLV
DCAVIACEIVFDEKVKTHNDYCGANSTLCQEEIDNEQTKKWKKIYKALYY
TSLTLLSVFVVEFILKIVFSAKKFLKSWVHIFDALIVISSWILMLIMLNK
DVKNGMIAEFLIABVILIHGMKEALEEANELLHENMEEIHALKAENN
KLKEELLAVKDR-

Oikopleura dioica TRINITY_DN2869_c0_g1_i1, transcribed RNA
sequence. GKAI01006710

MDNRISKFFSSDTEAYLERTPVTISEKIAHFLHSSTCHLIVIVLVLVDC
FVLTELIFDGKLDTYAEYCDPTPSCSEQSHKLHHWEHVTHVIHICSIIVL
TIFMIEVILKVIYTREHFFSHKIEMIDGVVVLLSWILDLIMLNPNLVGKW
AEFIIIFRFLKINGMILSAKQAADKRVHEQKRKVQELEKELVDLKKQYE
TQNNQ-

Opisthokonta - Animalia - Cephalochordata

**Eukaryota; Metazoa; Chordata; Cephalochordata; Leptocardii;
Amphioxiformes; Branchiostomidae; Branchiostoma.**

**Branchiostoma belcheri voltage-gated hydrogen channel 1-like
(LOC109464640), transcript variant X1, misc_RNA. XR_002139895**

MDKLKNAFKFELFQNDSSSVITSSDATSSSGNAEPKTFREKLLHVLHST
EFQVAVVILVIVDCILVVFELLIDLGGIKLCEEAVRAECESAGTTATMTP
AEEAEKEAECDHPEILHYMSIAILTIIFLIEIMFKVYAYQKDYLKHKME
LFDADVVIISFCFDVAYANHEDAFDGIQLLVVLRLWRVTIINGILMSVQ
HTAEKKINAHKQARQEVQEELNKMIAHAHDLEKEIDLLRKTLRENGISVE
SIPRTPEVSSSQVKVEAEITPTTEYATPAHFSAFSGQDDTQA-

**Branchiostoma belcheri uncharacterized LOC109463761
(LOC109463761), mRNA. XM_019760615**

MTPCDGEKKPPPSGEATVGGIFPDEIAVIKKQAQNDKRRPLKIVIIAGVA
VMAVLAIGVLLITRPSRHGVVTCSLNFWTGKQLLHETVETDKDAETDAF
YTEGSRGEAAVMDHSSMMKAFKLSRSNKTCFIFEETQGEKNAVKKTAEE
LEEKQDGSLLQFAEYGGAMLMTVDTERPARPVLSQKLQNFCCGLEPRWAKL
TPATEEEQQGDRVEIIMPAEARDMGELAEMPVGPNGEKETPPTPSSTHPL
TESRDHHHDNQDCRHKLKHMLERQSVHIAIVVLIVLDTLIVIMELLIDVR
VIKLCPPDPDVCVPKAGHNGTTGLVTTGAPGHHVIDAGDHGTGGHEECHH
VLIEVLHVVSILILCIFVVEIALKIYVDRLEFFKNGFHVLDADVVLVSLG
LDIASLVRPSTFTDAGLLILLLWRITRIVNGIIISVEEEWEHKVNHLK
HEHQLVERERDRLLKENALLQKTLTNHGIDIPKLPPDSGDESTCEFEFE-

**Branchiostoma belcheri uncharacterized LOC109467017
(LOC109467017), transcript variant X1, mRNA. XM_019764911**

MPRFKGQQQHETCRHLAVEDVMVADELGLGMSSADLYNRNVEGDFLDLE
AAIFCDIEEEKTKQVRVQQLLDGPATQITIVLTSWLLSHVLLLFLVLDLS
AIFHHDKMVARIHVVGLGVLSVFTVEVLTRLVCHQMQFFDKKIEVLDL
AVVIIACVPMIVVSVELAPSTAWDGFSLVILRIWRCYRVVQGCVSPVRE
EASRKVHVLLQAQRRRAHQELQTLYLMHDENQEEIHRLRLLLGRREAEEDN
VSQQLQVALERKDSQYVAQLIHTIEQRQGRNKGRQRDGGDRDSPYSTIVVH
AHQLSDSNDVPSGTIASRLSESTTGDSGICEETRPQQQTNDSESRNHANS
GVTQLPKCGQQALTVEPRGSHQQHSNRSPCSNSKRNPVSSCDMDRIDV
IGSEIILQHRNDSTGKKFLDGKLPSNKDSRLLFRDNKSMPSNGKVSHSKN
KVSEIKVNKSLDDDHKKAVSMDNKTVSKNNTATAQTNGKVRKGKKKAGSG
DSYVNGALLLEMTLQQKGDTGYCNEIVIEQFYQNGNAPATAL-

Asymmetron lucayanum GETC01094801 GETC01046531
Branchiostoma lanceolatum JT904261
Branchiostoma floridae GESZ01013291

Opisthokonta - Animalia - Hemichordata

Eukaryota; Metazoa; Hemichordata; Enteropneusta; Harrimaniidae; Saccoglossus.

Saccoglossus kowalevskii voltage-gated hydrogen channel 1-like (LOC100367669), mRNA. XM_002734179

MWNFSKIHVPYIRNSCDCFSYHHYHKMDGFGFKRMQESKQDGQLRVITK
DDTSDSLASDSQDEATKKEFNNGFRGTCLAVMNHHCQVAIVVLVILDVIF
VLAALVLDQMSTPDCGNSTETQEFEEENTASAVLHYCSLTILSLFMIEI
SLRIYCMRLEFFKHKLEVFDVAVIVIIISFSFDVAYAISPDTFHDILGLLVI
FRLWVVRIFNGVLISVKNQNEKKLAAQRRKCSELEQELEKFRQYCTVQE
NEIELLRDELKKHGITLEAEKKERPQSLTQVDVIVEVNKVNEKTIESLD
RKDFKEDIDAVDYSVTPDPPSTETDKSPTRSTSSTIPESPQEPDYGSNC-

Saccoglossus kowalevskii voltage-gated hydrogen channel 1-like (LOC102802600), mRNA. XM_006812030

MAADEESHQGPVTIVRDGFENRSSTPRSFSTPDLITATHRRRPRPKYCMA
MERFINSVIVQVIILLMVVLICLIATTETLVAYRRLKFDSSSKTAE TVITV
LHYVCLFFFIVFVFEVIFRICAMGVEYFHQPMQIVDGLVVFLTFTLDVSL
WLAPVSHPALHTLSFLIII-MG-LHLIIKGITDRVREDADVQIELERIMR
RNIEACADKLQQQCDQQNKEIAFLKDLLQQHHIESLQSNQSVIHTDSETL
KKAESSSSSTAGTIDGSPIDKRKCSVDNIAVTNDHYATATSTAILQSAMD
DVINRSQNIENIEKDKDEVKTSQDNQNITIIETPATPLKECKAVSVSMP
QIGTAANPPIRYEDLDTLNLELAEIRRLSQEALLQDFTTPLEGINNNNIE
SIAIE-

Ptychodera flava GDGM01225783

Opisthokonta - Animalia - Arthropoda - Insecta

**Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
Zygentoma; Nicoletiidae; Nicoletia.**

**Nicoletia phytophila proton channel mRNA, complete cds.
KT780722**

MWLKMDAHKRLSEDLEKVIMKEDGNSSIMTEPDHNIQPSKTVRERLRKLL
HSHKFQISVITLVIIDCLLVITELLIDLEMHEEESLAQHVLHYCSITILS
IFIVEIFLKLYAFRQEFFKHRLEVFDAIIVIVSFALDIAFRNSRDALSGV
GLIIILRLWVAFLNGVVLVSKMQAEHQLEREKQRGMALEGELSRCRQV
CAAQQRELDVLRVAVLQHHGLDQQLPDGNRVDVVADVEKR-

Extatosoma tiaratum GAWG01024136
Aposthonia japonica GAWU01255994
Peruphasma schultei GAWJ01019192
Aretaon asperimus GAWC01068486
Medauroidea extradentata GAWD01057497
Ramulus artemis GAWF01048256
Sipyloidea sipylus GAWF01047109
Clitarchus hookeri GFVY01085196

Opisthokonta - Animalia - Arthropoda - Chelicerata
Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Chelicerata;
Merostomata; Xiphosura; Limulidae; Limulus.

Limulus polyphemus voltage-gated hydrogen channel 1-like
(LOC106464594), transcript variant X1, mRNA. XM_013924749

MEDTTEKTDGDSIATNLESDPDIQPLITFRERLTKLLHSYKFQVGVITL
VIVDCLLVISELLVDNLISVNSHSSAPHVLHYLSISILSLFIIIEIGAKL
YAFRLFFHHKLELFDAVIVLVSFALDITFRDKESAVSGVGLLIILRLWR
VARVLNGIVLSVKTQADHKLAKQKKRENLEQELARSRDYIAALEEEVET
LRRILKDNNIKELPPTVIDNGAFKCTTLNVVAEVNHMIT-

Limulus polyphemus transmembrane protein 266-like
(LOC106463214), mRNA. XM_022390662

MRNSDPLVWGLTGDTSLDDDGPTRLCEKIWATVNGKVFSAVIVTLVFEVFG
LVIFSELLIDFEVVDQPQWKTSLNCSANVSGLVFSSAGANSPKLMAKDI
LSYISIVILIIIFVFEVGFRLVSGRARYLIQGMETCDIAIVVLVAFGLDIAF
LTPPSKKGAGKEAAVLIILLRLWRILKRIQSVINDNTRLEMGHFLSICERE
KIQAEHKVDILILKVEDLEHEVAYLKEKLKKTEKESLYAKRQRKKDGYSS
TQHKHPTITIGVETSPARHPCTGTQTAIVICEQHIPEEKVTKEQVMDMRT
FADVTSTRIIADALCMVTGNPNQFLRSPTTGGSTVKDGTTSHCRIAGDFE
SGYISNVSGITWDKAASRIPTLGTTRTLKCPSSPESGYGSSSSARNPAA
SSVSPLDTGTETASTSTGSSKHTDTVFLFPDPTGQRREVELGVEMDILEE
ISEIERVKHIEFDPNKQDQDIPMTSL-

Limulus polyphemus uncharacterized LOC111087200
(LOC111087200), transcript variant X1, mRNA. XM_022393049

MRNFSMFNSKEELMRNSEPLVWSLTGDESLDDDDSTRLCERIWVSVNGK
VFNAVIVTMVFEVGLVVFSELLIDFEIVQDPHWKTIRNCSANVPALIFPS
SEAVSPNLRNTKDVLSYISIVILIIIFVFEIGCRLAVGRAKYLIQGIEICD
AAVVLVAFGLDIAFLTPPSKKGAGKEAAVLIILLRLWRILKRIQSVIDKT
RVEMGHFLSICEREKAQAEQKVDILILKVEDLEHEVAYLKEKLKKSEKES
LCAKRQRKKEGYSGIQKHPKITVGVETSPARHPCTGTQTARAICEGFIL
DEKATKRKVMIDITFAEITATRIIAKALCVASPDGQYVRFLATKDAVGI
SGTTLCRRIDGSFESGYGSNTSGMTLDKTTNCIPSVGIRRTVKCPSSPE
SGYGSSSSARNTVATSVSPLDIEMETTSVSTGSKQTDTVFLFPDSANQC
RKAERGVEMDILEELSEIERIKQVEFDPNKQDEDIPMTSL-

Parasteatoda tepidariorum XR_001584685 XM_043048148
Dermacentor andersoni XM_050188908 XM_050168704
Ixodes scapularis XM_029987868 XM_042290414
Varroa destructor XM_022812381 XR_002674557
Metaseiulus occidentalis XM_003738312
Tachypleus gigas GILM01000651
Carcinoscorpius rotundicauda GILQ01010360
Piratula clercki IBTM01003006
Pholcus opilionoides IALF01028455
Zoropsis spinimana ICQH01009853

Opisthokonta - Animalia - Arthropoda - Myriapoda

Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Myriapoda; Chilopoda; Pleurostigmophora; Scolopendromorpha; Cryptopidae; Scolopocryptops.

Scolopocryptops rubiginosus strain wildtype

C96881_a_4_0_1_1490, transcribed RNA sequence. GCIY01020623

MENHHKMSDDLERVIMKDDSSSSSVTEEDPQLQQFQTFRERLAHLLHSYK
FQVAIVGLVILDCLLVIGELLIDLRILEIQEHYDYGAGEADLSICHQVLHY
MGITILSMFVVEIIAKLYAFRLEFFHHKMEIFDAVVIIVSLSLDLAFLDK
HNALNGAELIILILFLWRTRILNGIVISVKTQAEHRLHRERRIKEALEQE
LAKYREYCTEQEQEIEALRGLLRKHGISENEIIESPMTLINQMDVIAEVN
HTNEQNDKLIA-

Scolopocryptops rubiginosus strain wildtype

s6321_L_19063_0_a_4_4_1_1908, transcribed RNA sequence. GCIY01027533

<YFSLTILSIFIEMLLRIVSGKVQFFKQCMELFDAMVVFAAFSLALSFL
TTPKDGRNVAIFVVLRLRVKLIVHSVHDTKRQMSHIINAYKRDKIQA
EHKVELLILKVEDLEHEVAYLKEKLKKTDEKAAQRKKHLRVSSQLAEFPI
TPQIEKYNPLFHNPILSQRPPPEGRTESPPRDQDVERLERFAECTVKAIL
RTASNELISKDRWQQKRQSQRRRSAGASDDIHEASSSSSNIIGASSSPTE
LRQLTDTDGAEGLLSNNSAACFRVAQSSQEELDELSEIERIKKIRFDPTK
EEKNIPVTAL-

Henia illyrica GESB01025859 GESB01004335

Schendyla carniolensis GESL01004004

Scolopendra cingulata GCAP01021964 GCAP01017169

Lithobius forficatus GCAY01038678

Cryptops iheringi GJOG01009205 GJOG01023410

Strigamia acuminata GESK01000419

Scutigera coleoptrata GCAQ01037316 GCAQ01012485

Polydesmus complanatus GESI01001010

Himantarium gabrielis GCIL01017378 GCIL01018683

Opisthokonta - Animalia - Arthropoda - Crustacea

Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Crustacea; Branchiopoda; Diplostraca; Cladocera; Anomopoda; Daphniidae; Daphnia.

Daphnia pulex voltage-gated hydrogen channel 1-like(LOC124207115), mRNA. XM_046604416

MESTKEMLLPRPEVDGIQQSQIEMVTVGQDPGMRLMNDQVDQQRDALLS
KDIVLHPSHVYASDPNLAAMPDSSSRARLRRILSSSHRFQVFVVSFVIVDC
MNVIAELLMDLRILGMMEEYGMKNRNKVSLEAHYIVPDVLHSISIAILAM
FLLETVIKIAAFGLSFLRMGWEIFDTVVICVTFVLDVLMQHSHSSTNGLG
LFIILLRLRVARILNGMVRSVRSQAVRHVECEKRRREVLEDELLKYRELC
QRQKKLLAEMENLLKNHNIPLPDNLVMLPSP-

Amphibalanus amphitrite XM_043361853
Pollicipes pollicipes XM_037237188
Homarus americanus XM_042376150
Eriocheir sinensis XM_050860406
Cherax quadricarinatus XM_053773827
Procambarus clarkii XM_045762000
Penaeus vannamei XM_027375813

Opisthokonta - Animalia - Nematoda

Eukaryota; Metazoa; Ecdysozoa; Nematoda; Chromadorea; Desmodorida; Desmodorina; Desmodoroidea; Desmodoridae; Stilbonematinae; Laxus.

Laxus oneistus TRINITY_DN84728_c0_g1_i3_9dedup, transcribed RNA sequence. GJNO01007626

MTGHVYKKKRPLSAHAAVGGAGREEECVIMNTEGDGSSSVTSESEHGNEH
QPPRILHGRSLREWLDVHLSTKFQVLIVCLVIFNCLVVIVGLLIDLKIF
ALERKNNVAAEILRYVGIVIVSLFVLEMALKVLVLGKRFFKHKMEMFDAV
VVILAFSLGLSFGGRENSADGFGLLIMLRLLWFSKILNSMITSVRKEAER
KMAKERRSRRALEREVAKLREYCLQQECELQMYRLLLQQNNIPEPTVLRP
PPAPRTL SVIAEVNELDPPGTATFLAPLSAPQSGTDDSSSTNSGSFEGPLC
SDRPPANG-

Trichinella spiralis GEBN01052808
Plectus murrayi GGJS01022439
Koerneria luziae GIUA01076674
Trichinella patagoniensis GECA01018136
Trichinella zimbabwensis GEBX01035233
Trichinella papuae GEBW01009651
Trichinella pseudospiralis GEBS01033974
Trichinella britovi GEBO01040153

Opisthokonta - Ecdysozoa - Priapulida

**Eukaryota; Metazoa; Ecdysozoa; Scalidophora; Priapulida;
Priapulimorpha; Priapulimorphida; Priapulidae; Priapulus.**

**Priapulus caudatus voltage-gated hydrogen channel 1-like
(LOC106809460), mRNA. XM_014812541**

MKGLGVQGFKKVSLEKVIIVRDDATSMSTVESEEDNFRTRMPLHDRVNA
LIHGQRFQIFIVVLVII DVLLVIAELLVDLKVFEMEPGDSGEDASESAIG
EVLHYASLAILSLFMVEIVVKLYAMRLSFFKHK LEMFDVVVVVAFSLDI
AFTTNKGGAVNGLNLLVILRLWFIARIVNGIILSMTAQAEKRLHREKRER
EAVEDELGKFRFCARQTQEIERLRDLLELNGISAHKVERTAFGSQQLQVV
AEVNDIITSKKLEADT-

Opisthokonta - Animalia - Lophotrochozoa - Mollusca

Eukaryota; Metazoa; Spiralia; Lophotrochozoa; Mollusca; Gastropoda; Heterobranchia; Euthyneura; Tectipleura; Aplysiida; Aplysioidea; Aplysiidae; Aplysia.

**Aplysia californica voltage-gated hydrogen channel 1-like
(LOC101848758) XM_005100609**

MKLDGLRKMQDDLKVIERRDDTSTVTSDSDETIARGPKTLRETLD~~DD~~VIHS
QKFMVFIIVLVVLDCLMVIAELLFDLEIVKLGEHHYIPKIFHYGSLGIL
SLFLIEIGLRIFVLRLDFFKHKLELFDVAVVIVSFILDIVFRDNEDAATG
VGLLIILRLWRVTIVNGIVLSVQKQAEKKIEREKHLREECEQELAKFRE
YCMAQEAEIEVLQGLLHKHNIEFTTNKITRPESRVQVDVVAEVNSMTAVA
ETDIPSPSPQGEQEISLSSGDNVTDVAVVVV-

**Aplysia californica uncharacterized LOC101850633_x1-x4
XM_005093050**

MRMSRSIEYPSEKNGEPSCIEAEQSRSGETKMLKSEQSQDEAETS~~DS~~WSENE
DSHSGKLDANSCKGKLAFLKTNLVQYSIIALVILDCLIIVMELLIDMNI
IVFPEDDPPHPPGEGSSHHPVAFASRSSNLTGDNHTVYPAAHHIHTHHDNS
SNLTMYGNDSAHAAPVHHHTNKEKAEHVLHALSLTILSIFMVEVCVKIYV
EGKHMLKQKAEVFDAIVVIVSFTLDITFSFVSVSKAASEAAGLMVILRL
RVTIINGVIMSVKLDANKKMEVHKKARRKLERENKRLQAKIERLREVA
TLKQKMATSSTPQMSFEMQSGLSVERSPSGEMRENSAQV-

**Aplysia californica uncharacterized LOC101855857
XM_005094218**

MGDAEPRAHPRPRGQASPFMPRLRKRGEKLLHSKYVVILVILTVTDCAL
VIAELILDLSSVKKTQGATEAMTLSFVEKIIKKYPDEVAPLHSLTDVFEE
LNHADIVWNNTNRSGHDLDPDLERNLHHHHHKNRDALHTSVTTPTSPVPV
VGGESVAEGWPLSSDTPLGVGNFSRALRTLWIQKRNYSNSRFRRSNRND
SLRDSSAVLSRLLERTRLEIEKVLSKLSRRRKRSEETGGLTAEYEATDS
GEAGDTSRNSQELEDEVLSNDDFFENNYGKNNGKTYLSSLTGLIVKILTMQ
SNETGPILGGPARYAEAPLTVESAGKGEGKGAHVSDQDILHKYRLEFHH
SEDMEIAKLHYASVAVVSILLIEVTMKIICAGSHFLKRKIEVFDAVIVV
ASVIVDLIFIKGLNQFPVDDSIFVLAFLLPLVISVVNSLMAVIDHEHV
KLRLLYSRKKKLDKTVETLRNEVDELKGMMDIRQFCIKEGIEASRIDSL
LGKFAPRRRKDSKFYTLVKLVNSTASINNNNNNDNSVSSSSMENDLRDYA
NRDSVLNEATSNTNTVTSKQYLSVPFFSGGNRSNTLDIESRGSGRSGGS
PSIYITSPASDDEAPVFSFDIADEDDVDMSNDQDDAGSQDDETSIQAGSD
AATIAVTSAEVNTVSPNVAFYVGSQSSLCSVHSQEDIRTVVDTNDNYERN
FPMC*GV*PCASGGEDLAAAALDDVISNSPTVNSNSWGPSRHYSRFLTVPCC
TSLSAVTNTTSTATSYPPSSNNTNNNSNSNNNNNNACAETHPLLGDPPP
GQNMTRSVDNCDVTATQYGARTCGGRYGSPVPMRRKPCLSEKRRSYARA
RSESIENQEFIPLMSQGANKGRVRHSDLEGRPSTRKDDLKRSRSHSPSP
MVLLGVPGQTKKYSDPPSYQAASRSMNDVSSAGKGQSGNPHANNLGKDG
RILRRSCLSLTSEGRKRRGKSPQRVSFKVS-

Aplysia californica uncharacterized LOC101862058
XM_013086351

MRQDVFTITPSTKAHGTQQVPPSPGGILKTPGKVSCNPNGKFRPGPQGAG
MRRSVSVESTSTFDPSLERPGNLSSRQRCQRRLSVLLHTHVVLILVCTL
AALDAVCVIGQLICDILIMREKLDHFEVIDDQLTDILFDHIPKLNQSLHP
KWNLDAILDVLGTGRDHHSNDGPVPTAPPLASNLSSLMSVVNSSVLQNFTH
MNQSALHHRVRAAKQEVPGHEVDHGLLYDLTHFLGSMVILSLLLLLET
LLKVFAMGKKLRHHKLEVFDAVVVAISWALDVAFWEGIWAHPGTAAATIL
IYMLPWRVVRIVNSFVLVIQEKDHVQLKIVKQRLRQSLKKSKEFTDKASS
YRHEVKALAGLCRKLGANESSEITACSPSGKACRRGSIHSLVLERAAASLTFI
STLSSMGSLPSLFDMGEMSSDEEDSRPQHQLDRTTSQAPTLKSAFSSTT
LDSGSVVLSIDNDTGGGMEHPVFDASNSSTKSSDVKHSADK GKREVERT
SSSDSAPPSYHIAVSKTDSNTRL-

Aplysia californica uncharacterized LOC101857936
XM_013080089

MRKITITSSKMPYRKKEIPKAWSMETLPPPGMVTSRPLRKKGLFHTQTC
MEGSWQVLAQTLKIASINGLGELDKLENELEDEIRYENRSPSKTAVGRL
RRQGQHQLHSKVLLLIVVVLNVIDCLLVMAELTDFHHVSHRLQNKLDML
ESFIYNMITKHAPVLDNIPRSPRKSNNVLLQKILDANVVWDTSQPNVTNFA
SNCAHLLKSTAENASQSLTGYSNMLNNSDWSEPNACFQPYMAAQNTTVN
SAAANQKMYLSTDGQTNEKLTIVAHKLHYISISILSVLVVILLKMICSG
KRFFRSRMQVFDGIVIIISFILDVFIIEGVITILKMDDFVLILTFLLPWRIL
LEVLNLSLIVAVLDKQRLNLKIIYTQKKKISRNLSEVNNKMEVMQRHIEVL
QNLCSRGLADGDVKKVLGRELSTASAKSGSSQKNGSSGGLAGMMALGKL
AFQAADAFAPITQGSRKSHTPKTTKQNKPALNGSAPNLLTPTEEDPPTPP
HLAHSMSQPQGESNTTSSNSHVNTVAADIEDTSRPSFTLHNETGSAEGTE
SGIGGSVGGGIDGSGVDDKTADKENTPPTPTPIPTHDTYLDIESQPNANT
GLETSDSSTGVNTNVATTTTSPDSVTVQIANGSGPPMDLDSNSNEERKTS
VSLPDFSDDIHLEDSDVVSR-

Aplysia californica uncharacterized LOC101852977
XM_013090418

MSPGILKGPSTPRVDRPPVTISTSVRLSAQHGHNRNGVGKQARMSTGLLTG
CRQRTLKCINCRPFLIAICALVVVECACVLAELMVDLQGIKFRFENELEE
IKRFVLHLRTKYPGAFSDDRARTMTDVINLLDQAIVLRTRQDLLTPPKAP
CFCPCANETSGPAAALRNSMSPAGSKQMKSHGKVQPLGVVDGGDLRVPR
QKAQPDKYDKTRQEMIFTTPNVELTHTQIDITSSSSSSSSSSSSSSSSSS
SSMSSPPSSALSSKLTTAQAGDVTGAGHDFGQAGSESRFRSSGNHDAPK
METVNTSGSKQMLLSRVASFSLNTPPPGDPLRLNWKGNHPVLSNTSEQ
SSGKSQFVFSFSQKIHRALREVGLQRLALGRRLMGVAIENDQPTPAGHPI
SNVISTHLPNHAMTTTEAEAVTISSPSLQSGFSAHKSTADPVKGWVQQT
TKDVTLGAITPESDSEDSLQNHNEGSSPSDVPTRTSVTDPPASPAPISKR
ATGTLTPDSQVFTKREDDIQNSNMKNRGRDPEGSLSRQQQAGEQFLNIQES
DIPESVDRNTSGNKSVSNASLSQRAPLPLPQNAAVHQFQDAPVPQSQNPP
SPQIENAPLPLSQKAPPPFSQSKPPNGSSSSPGTNHLTSLGDVFVLEINN
VIDSFLLVAEFLPDHHGSNDTKFIQYNSEYRKIYKTSKALHFISLSILSV
MVLETAVKLFCTGCGFFKKKFEVFD AFIVVSSFALDFVFLDSRWYETGKD
ATTILVLLLPRVVRIVNSFLMTMKHKKHLLQMMNMKRAKKKAEKLSAKLQ
TLLSEVRKDVQLLVALCRSHDIEEKDVQACLYGKGRRSVTL SAMSTCTSL
MLISTLGKDAIQEDDIYGKVFEALNEGDNAEIDTEIKQAEAAIDAAIE
LDEQIEARKKSRKYKSKALVKRSYTVPRRSASVEIPDPDINENNSNIFY
VNDGYLTAHASSPRNSELLMVESGGVAGVRSGLRGNFTLVGTPPPLPPS
GSSEENHRLSCSRVEEESSTDENSEDALSLTAVTTDLSPQQEQQQIQ>

**Aplysia californica uncharacterized LOC101854637
(LOC101854637), mRNA. XM_013082371**

MTMEDDSTKNSRSCECTSLQ**HSVCL****E**SMVITLTIVSALAVTGEMLLDFHF
FTVTETISQDNQSLAGEAPFREDKDVM DILDT**V****F****H**YTSLCIAGLFGLEIL
LKIA**F**L**R**M**R****F**L**R**H**P****W**QILDIFVVSGTLGVEIA**F**H**F**L**D**L**P**Y**D****S**LYAVSYVV
LL**S**L**L****W****F****V**P**F**V**C**N**I**RANLIREELEEDMELYRCGRQKAEERCSWLEENLNQQ
ANIIKGLEQTLLGLKPSSMEDEESSHAETQDNSQPSAAGSHVTTNYGQNG
PMMSEQPSVQSSRKDQ**N**Q**K**R**L**H**R**S**K**K**R**V**E**S**D**N**A**E**M**E**M**S**E**F**N**K**D**N**P**R**P**D**H**
ARKRENISSNFSES**G**T**K**R**E**L**K**D**K**D**S**K**A**E**H**I**D**T**S**E**V**Q**L**R**P**R**G**Y**S**D**N**M**L**
DFSNTNSLPRSEASLNSSSSTPRPGQINMRQ**R**K**R**S**S**T**S**E**Y**I**D**Y**S**N**L**S**S**P
EQDKVFYDDVKDKFSSCPSLDHSTQSGEKERSVK**S**P**E**L**W**T**G**K**K**E**V**I**E**G**G**
TDEVDGGTKEDADNGSIK**K**T**D**S**S**T**S**D**A**S**S**G**V**S**S**E**V**S**V**N**G**K**R**E**R**R**D**R**K**K**Y**K
RFTSCPEYVITQ**R**M**S**I**T**N**D**E**S**K**L**L**D**E**S**H**T**T**E**D**P**S**M**Y**D**N**M**A**F**L**N**E**D**E**T**G**L**H
VLA**E**F**D**G**S**K**T**Y**R**N**E**D**G**I**P**M**T**S**L**-

Crassostrea gigas XM_011420311 XM_011429833 XM_011440664 XM_011458201 XM_011454844
XM_020070532 XM_011450860 XM_011440929 XM_011436069
Mizuhopecten yessoensis XM_021517539 XM_021506621 XM_021506642 XM_021492263
XM_021492266 XM_021497401 XM_021497397 XM_021497398
XM_021512362 XM_021497391 XM_021497611
Lottia gigantea XM_009053636 XM_009064134 XM_009063093 XM_009055697 XM_009059372
Octopus bimaculoides XM_014933788 XM_014930220 XM_014931773 XM_014930385

**Limacina antarctica TR73269_c0_g1_i2 transcribed RNA sequence.
GDRM01043900**

MVT**T**H**E**R**G**G**E**G**S**V**G**G**A**S**E**D**T**S**H**A**T**L**K**A**T**N**S**R**Y**R**F**P**H**E**T**H**N**G**T**K**T**G**D**S**P**T**K**
K**P**R**R**H**I**G**D**G**G**L**I**S**I**L**A**A**Q**T**A**R**N**V**G**S**A**F**T**K**I**E**E**K**I**D**K**E**V**E**D**D**L**L**Y**E**K**R**E**L**K**
N**K**V**D**R**F**R**H**Q**V**E**A**F**T**H**S**K**P****V**L**L**L**V**V**F**L**N**V**I**D**C**I**F**V**G**L**E**L**V**F**D**F**L**Y**F**T**G**G**L**E
N**P**T**D**M**K**S**I**N**G**T**T**C**P**E**T**G**S**F**K**T**F**G**D**L**S****H**Y**F**H**Y**A**S**I**G**V**L**S**I**L**L**I**I**V**F**A**H**V**F**
G**S**G**K**R**F**F**K**H**K****L**H**T**C**D**F**I**V**I**I**A**A**W**V**L**D**V**V**L**Y**K**G**I**N**S**F**T**R**G**T**A**V**I**L**M**V**M**L**L**
L**R****V**L**F****V**L**N**S**L**V**V**I**L**V**D**G**Q**R**L**Q**I**R**V**M**Y**T**T**K**K**K**I**Q**A**E**L**D**D**S**K**A**K**G**G**D**F**K**Q**Q**L**
E**H**V**R**T**F**C**L**S**R**G**L**K**E**H**E**F**E**R**I**L**N**G**G**A**P**H**T**Y**T**N**G**D**L**N**G**N**V**Q**K**G**K**G**H**K**E**N**G**I**D**
G**T**P**P**R**H**G**N**V**I**S**R**Q**F**K**K**I**S**Q**V**M**A**P**A**R**R**S**V**S**E**D**V**S**S**P**T**S**S**N**G**L**S**N**G**L**S**N**G**L**S**-

Opisthokonta - Animalia - Lophotrochozoa - Brachiopoda/Phoronidae
Eukaryota; Metazoa; Lophotrochozoa; Brachiopoda; Linguliformea;
Lingulata; Lingulida; Linguloidea; Lingulidae; Lingula

Lingula anatina voltage-gated hydrogen channel 1-like
(LOC106176220), transcript variant X2, mRNA. XM_013558499

MDGFKKLHEDLEKVEIKDDSNSSTTTSEMEDPKHSKQTFRQKLRHILHTN
KFQIGVICLVILDCLLVIAELLIDLEVFEIGEAKDELGPAKVLHYMSITI
LSIFLIEIFTKIFAMGLDYFKNKLEVFDGIVVVVSFVLDVVFANQEGAYG
GIGLLIVLRRLWVTRILNGIIMSVKKQSEKRCRLRERMLKEAAEQELAKFR
EYCAAQEKEIEELQALLKKHGIDFPKIEKPVEVSTISVTAEVNEVDGYTK
RPDDNSA-

Lingula anatina uncharacterized LOC106178050 (LOC106178050), mRNA.
XM_013561049

MADRDDGSRRLHTIDNVENGTKKQTYQQWLDHYLHCQLANSVILVLVVL
DSLIIYMLLLIDIGIIHALCTCSLAEDNHSSTINGSSTAGFTNKVLPVPN
SQVNLAGEILHYISLCILCLFMLEVILKLVARSGAFFKYKLEVLDVAVLVT
LVFVIYVVYSFDIIPSTAKDGVGLLIVFRLLWRIKEVIRGAALRLRKEAIE
KFSRERKARIEAECKAVEAISQQEWDQREISSLKEKLSQYEDRLQPSTQA
PEIKSALKSKSSSTKKTEQGGGRFKKKPTSQPVFTDFHDDHDQHTDDHRI
SFDDKRRLSESKPKKYQPAITSTAFGYDNESYDGSLDAKEEEKDVDIPL
KXLQERNMGLTYSFNWQHSLEDFVRLLS-

Lingula anatina transmembrane protein C15orf27 homolog
(LOC106155662), transcript variant X3, mRNA. XM_013530614

MASLLWRNPASAANCNVKKKKKYQGYICLSSQFSFLRHKSFEQELEDNDID
DDILQTEIEAQAQAEKSCHEKLVEVLESNPIQVAICILVLIDAVLMVSLI
MLDVHIVQAKCNANQEDISKLIDAIDSRMPGALAHVHGADVTLSDIINSL
HGETNSSHGSSSHSVHKRDLSSVAHLLDAVQEGAETVMGSSSSSEGGIFLR
RLLYKEETQGDNDSTLEVHVSSDKLAANESHSHSKDAHGDGHGHS LIENVA
HALHISSIVILGIFLVEVILKCYALRLSYFRKKMELVDGIIIIISFTVDV
IFYDGLGGRSGVDAASLLIFFLMLRMLRVFNGFLVTSRKRLKFRLLTLQMR
ARKRAEAKISDLDVRIGFMEKELDSLRLASKYGAKNHEVLNCKPKASVH
KNVTAKEGISSMLCASMSMMHHFASKENVAKNEQMAQITESEEVEDDNS
NRINPFMLSPLKKGKASQMNTKDSKENETTVTGSVKPDPVDTNISSPSGQT
KEASALNDVKIDMEDHRENDADIVANPNGKNECSATDDKISSPAPPQPSP
QAQKSKTQDLNERNGTLPSSQSTRSRGALKRTSSVDDQNMSSCDDQGTLF
TSGEPTPAHPPGEVDGSENLQQKSDTQTPSDCNKLNNVAAKNATILTNGD
VISNGM-

Lingula anatina uncharacterized LOC106156217 (LOC106156217) , mRNA.
XM_013531343

METQIISRQDSVAMEKDKTWEKAAKVSFRKRLTKYLYSYP**LLMAISILSI**
ADAACVVGEVL**IDLT**L**T**NGKTEAAESYVTSIRQALYDRFPHLKSIIATESV
SDLIRKISNIHCPRPTTSESTVSHAPTQTEEPGVLYLNVLTGSLTKQAVP
GQPSNCSLPGDTDQCPHALEHVLKEIG**HVLHMLS**SLFILSSIVFVHCLRII
ATKRRFFQYKFQ**VFDA**AVVTISLVLDLAF**L**KGIWSDDTGE**AAVLVLVLVP**
WRVIFIVNSFVMTVKEKDHIAMKMVKSGRKKALKRVSDLIKQAERHKQEI
RALRGLCKKFEAPEDAINACKPQVGNNRFRRRSSGASLTMLASLAAFGS
LGLDPSKVHPSDDEESEDGSQPYLPTSLHEKSSSVNSETTENRAVDDDSP
SNNNFGDSFFSNDDDTDKNALDFYNENETCVELQSTRQEQQKENDKFALVE
LPEKKPRSFVSISIGTASSFLKSPIKRLRSLTYTEGNGADSEPRSSHTAT
LVDNMEIPNEQNEITHC-

Phoronis australis GFSC01012821 GFSC01079495 GFSC01010288 GFSC01051093
Phoronis muelleri GKAW01058824

Opisthokonta - Animalia - Lophotrochozoa - Annelida

Eukaryota; Metazoa; Spiralia; Lophotrochozoa; Annelida; Clitellata; Oligochaeta; Crassichelitellata; Lumbricina; Lumbricidae; Lumbricinae; Eisenia.

Eisenia fetida Ef_Cf_16012018_18296_c2_g1_i1, transcribed RNA sequence. GIKG01069578

MVQMRMEGFKKVKPSDDMERVIEKDDSNSSMTTEYDEGKAYPAAWRDHLS
LTLDSEIKFQIAVVCLVVLSSGLVVVAELLISLNVLELHMQSIVPQVLR^YI^V
IGILSVFVVEVVLKIFAWRLSYFRNKMELFDGAVVAVTFALSM^PFSSNSS
FHSSIGLLVLL^RL^W^RIV^KILNGIILSVKAQAERKLRHERHIREALEQELA
KFREYCASQEKEIELLQAVLRKHEINYPAEKPVAVETISVVAEVNSICE
DQQQQQQHEFHCEFAGR-

Eisenia fetida 59034, transcribed RNA sequence.
ACCESSION GIUK01058977

MVFSMHRVSQYGGRCDWLKNQFLRDLEGDSVDAEILDEELRLLQEQQPK
TCRGKTARVLETSPLQIAMCVLVLI^DAGVVIAEILL^DLHAMRSQQRAATS
DLVQAMVFLKDQYSADLGDYHGEIGIGYILDKIRLKQNPANGNSSTTAETN
VTRSKRHQTLQPDPKWTL^LLATSVPVMPTPFEVGLREKPSEPEPLESLYG
SSKVHKGPSFLDTKVPSFMPGHSRADVDPLSVGLARVSRRAVNGFSGLFE
PRRKRYIRQARHKNDQDNDFVIARVTRTPVVGSRDEGSSSSSRGFIYTEP
DSDAAAVKRS^AE^LA^SE^SV^VR^SH^DN^EE^DD^DY^EG^KA^DG^GD^HH^LT^ES^FT^IK^N
TYAEKLLKIAH^IL^HY^GS^IA^IL^GI^FV^IQ^VF^LK^IF^GM^GP^EF^FK^NK^LE^VF^DG^V
VVMASFTIDLIFV^EG^IT^GT^EG^EE^AI^AL^II^IF^LL^W^RIL^RVINGIMVTAKKR
QEFRIKLQKRACRRAEKKLECLDDELSWKEKEIHNLKNLCLRKGASEEDV
VRCRPKRSPFFAKMDTSAGLSSIASLSLGFTMSMRSSDSRMRLPIAHS^LV
SLSGHRQTVHDVHSSSLGNPSMSLNRSGQWPRSRKPSTSTVRSSDNQSLP
VSMRQLTESRSMEDIAERPKHQLDLSIMSSSTSMQSLAADSISNCCPVT
SGLGLLPSRSIANDRVAAAVSGLTACNSSRPQPSESGGGIPDICIVISD
ANGSTQVNSSRERKRSACQAASSSDSEGRPSPAESVLSNPDHGNNRTVQ
FYVETPTDMSMENIASTASTAGAANGDGRCANDFSSPSTSSQIVNGPAS
RLPSPPADTDRQQQQQQRESGGSLTSRWLSKLRRSSKSRSHHENQVASSS
DKVRRKPVWVSPFAQAKEKKTKETFL-

Glycera dibranchiata GASB01008782
Megasyllis nipponica ICSJ01060984 ICSJ01016660
Platynereis dumerilii HALR01262921
Notospermus geniculatus GFRY01018744
Alitta virens GINI01122785
Lumbricus rubellus GIKI01097867 GIKI01020978
Arenicola marina GJHO01023177
Paraescarpia echinospica GHDM01078138
Hirudo verbana GGIQ01040411 GGIQ01076257
Harmothoe impar OX381720

Opisthokonta - Animalia - Platyhelminthes

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

Schistosoma haematobium Voltage-gated hydrogen channel 1 mRNA.

XM_012937229

MDESNKELINNVPHSRAKTRPSGKCTLARKRLKQVFNMRY^YYLSVIGLT
G^FF^EALLVLCRVILETESLRLPPGNTQRLILEGQLALECLSLFTLT^LLFVV
EV^PPFKIWAMGIRQWGRQL^LLF^IIDGLVCAVCFSLDI^YNIYRHSSRPSRGI
TSSKVLELCNYLHITSQADTASTFAE^IFGLVIVY^RL^WY^IK^EF^IK^KTVFI
KSKQSIKRIQELQQVYGEADQRINQLENILQE^IDRKDNHRSISNVILD
NKQGQQQTTRPMSKVNYSNRPA^RQFSNIER-

Schistosoma haematobium hypothetical protein mRNA.

XM_012937230

MSMIENDERNFSTKKENTMKHKRRQISTESNQCQSDVTNGLLLPVNEII
EIIPIETILTPAPPPTPPPPPTTTTTTTTPTVTINTIQSCNEKYKLLFSR
ILDCKLFH^MIIVGLCAL^DGILVICMLLLEIESLKLKLTHLRYRLN^FTSF
^IFECISYTIILLFLIEI^PIKLWTFGYQFYQYQW^IELLDV^FVCIISFTVD
TYNIHRHIMETKLNKMNTMNEYTIDDNLEQTLHTTIADAAG^LLVLF^RL
^WR^VI^IIVNSIIVSV^TATHERNMKSLKEAHHISLKRIYELEQLLQDNGIS
IPSLTPKSQSILAKIF-

Schistosoma japonicum FN318210

Schistosoma mansoni XM_018790876

Opisthorchis viverrini XM_009166151

Heterobilharzia americana OX104105

Dicrocoelium dendriticum OX104059

Echinococcus granulosus XM_024492501

Spirometra erinaceieuropaei LN077116

Hymenolepis microstoma LR215995

Macrostomum poznanienae GIJT01038552

Opisthokonta - Animalia - Lophotrochozoa - Bryozoa

Dendrobeatia fruticosa db_e_tr88007_c2_g3_i4, transcribed RNA sequence. GJXY01266092

Eukaryota; Metazoa; Spiralia; Lophotrochozoa; Bryozoa; Gymnolaemata; Cheilostomatida; Flustrina; Buguloidea; Bugulidae; Dendrobeatia.

MKGIGSFGKAGPDDLERVVEKSDTSSSIVSDDIVKPPQTIREQIAEIIHS
RKFAQIVVICLVAIIDCLLVSELLIDLKAFEQEAQVGHDIKSTSSGGEHV
TNGEGSNVKKLEDAEKREKASLLAAEVLHYFSIAILSIFLLEICAKLFAM
GRQFFQHKMEIVDAVIVIVSFALDLAFIDHERLASAFGLLVILRLWRLGR
IVNGVVLVSVKTQAEKKIAKEKGLREATEAELVKFREYCTAQEREIEALQL
LLTQNKIEFTKMAKPSLPVSTIDVVAEVNQFIEATKLASGGGGEGGGDSS
VL-

Dendrobeatia fruticosa db_e_tr82209_c1_g1_i3, transcribed RNA sequence. GJXY01243660

MTGSELMEIDEKLSRALREDSVDPVAVVLEELKSLNDDVLDHSNTRCRVRL
ERVLESTPLEIFLVVLVIVDVIIILLAMLLMDLNVLLHLYLEDGNNAAASKLS
TALQTNCRGNPELNLYNKSNIITRHLEHDCIWDPHSTNYTISDSASS
EAQSPNHVTQHRRRRKRSAPPKEGSNPTIAILLEAGHILHITSVLILAI
MVVEVVLKIFALGAKYFKGKLEVIDGIVIIISFAMDLYFI DGIPSEGVNN
GATVLIIFLLRLILVFNALLVTAKKRLQFRIRVQKRMRSLEEKIENLN
DDITHYEDYIENLKRLAKRHNVPDYEMKACKPLVRQLKKANTSAGLASMM
QMSMGLMQGMNMMKVADKPRSRIVDNLRNPPTETVETDKESASAADVLVN
AMDATMAANSTVDVVDHDSQHILPVPMMTAMATSNQSVHRSRPHRSRPHRSR
RLPHTSTSVANGTRTIPSMFEKAVATGSPKSNEALLLNWNDKSDKENND
PNSNQNTSLS-

Dendrobeatia fruticosa db_e_tr59641_c0_g2_i1, transcribed RNA sequence. GJXY01200275

MTIPHDPVQRKPPAKKQKFHESLAKICVNHKFMLFVLIVSVGDALLVATE
LTVDILAIKIQKEEVCDTKEILKYLKREHSGQLDELFNNSIKAILYELK
TRNDHHYHHKRDVSAVLESEDIKVRKRAAPPKKGKGEIKESPLSSVLLF
EVAHACRYGSIALLSCMFLINIFRVYAMRKDFHLSKLQVLDIVVIISLL
LDISFLPQVWTFDTATLTAPIIIIGLSRVVIVINNSLINLHEKDKILLS
RETALLKDSEKRNRRHKHEIYNLRGLCRKLGAETDITACAKLVKTIKKK
RFSKISLASGIMSVNSLAFLGTLRSREKQPHEPNLDRVESFTKTDETKSDE
GFDTLQRSSEFLRRNQRGSSSNKIPARRAGSRMSNVSSIGSISMASFDR
DLDDIDNTSYERATETSDTDNDDSDGRGSKSDKSDKSQRKFF-

Terminoflustra membranaceotruncata GIMX01037542 GIMX01141019 GIMX01229943
Fredericella sultana GHLZ01039460 GHLZ01006033
Membranipora membranacea OU612068
Bugulina stolonifera OW285188

Opisthokonta - Animalia - Lophotrochozoa - Entoprocta
Eukaryota; Metazoa; Spiralia; Lophotrochozoa; Entoprocta;
Loxosomatidae; Loxomitra.

Loxomitra sp. KK-2020 isolate Shimoda Marine Station
tr115673_c0_g1_i2, transcribed RNA sequence. GIMU01079853

<VEKQLEEAADASRQEEIASGLRRKIHDLIHKRWFQIVVVTLVILDSL
IVVAELLIELNVLGDVMKKVCNGTGHEIEELNEEFLFAAEVLHFCSIGIL
SIFLVDLALKLYAMRLDILKHKMEVFDAFVVVVSFSLDVAFI GMEGGEAT
SLLIVLRRLWRVTIINGLSITMKSQADKKVRRLIKIKEALSLEVKQLRVD
LARSELLIKRMNKSLEQNGLEVPGVNENSVLRKSLLPVRTELYTDCSDV-

Loxomitra sp. KK-2020 isolate Shimoda Marine Station
tr112662_c0_g1_i1, transcribed RNA sequence. GIMU01076890

<VILFLFIIELLLLKLFVMRWEFFHHKMEVFDAVIVIVVSFSLDIAFINQEV
AQASSLLIILRLWRVTIINGFSLTIKTKSDREIHLRLTRIKDFLHTEVKR
LRMELARVESQNRKMIRVLRRHEIQTPILPTSEVISPK-

Loxomitra sp. KK-2020 isolate Shimoda Marine Station
tr203811_c0_g1_i1, transcribed RNA sequence. GIMU01203676

<AFEGINLLMILRLWRITRIVNGLIVSVKAETEEKYHHILHHKQAVIDSL
KSKLDRCQSLMVKHSVTIPEGLLHSMDELDAFFPAITPSTGNVCATCNI-

Pedicellina cernua GIMK01062983 GIMK01039117
Loxosomella nordgaardi GIMJ01039792
Barentsia gracilis GIMW01064503 GIMW01098986 GIMW01061213

Opisthokonta - Animalia - Lophotrochozoa - Nemertea
Eukaryota; Metazoa; Spiralia; Lophotrochozoa; Nemertea;
Pilidiophora; Heteronemertea; Lineidae; Notospermus.

Notospermus geniculatus TRINITY_DN199650_c0_g2_i7 transcribed
RNA sequence. GFRY01018746

MDGFKTFKKLDDDLQRVIEKEETSSSVTSESDETKHAMMDHREHLKHLH
TNKFQICVIILVILDCVIVIAELLIDLKVFEMEGGKNAHDSIAPHILHYI
SIAILSIFLVELGVKLYAFRLEFFKSKMEVFDAFVVVLSFALDIAFANDE
GIIGGLGLFIVLFLWVTSILNGIVLSVKIQAEKKLARERSSREAVEQEL
AKFREYCSAQEREIEILQGLLKKHGIEFQKMERPIVINKIDVVAEVNEYI
EKTNSENFSSA-

Notospermus geniculatus TRINITY_DN203828_c2_g3_i1 transcribed
RNA sequence. GFRY01079887

MKTSSSSGTVPISEEDTTESPVSPSPRLVRHESLDTGTPKQNGSVASSLH
VKFTVGASDDEDEPHYRRPRSRKNSSFGILDNLNEDWITRNHFLEKLEAD
SLQSDVIQAKLAEIAEDTVKEKETCRKLAKHMTTTAFTIFILVIALLD
TVTITAVILQIHSEHDEIIIVREQHKKFSKFTKLAYGNKVDLDNVLSGKE
MIDRVEKYLNKTQNASAAATKNIHKRDVSEEQQYYKTIEISRRGHGS
RQGRSAKGQGRKRSETADDDKDRGERVLVRRKRAAATAADGTPLFESKT
ALTLANVAHNHLYCSIALLSILLIEVFVKIFALGCEFFKSKVEVIDMIIV
SVAFFLDVYFI DGVMDNVAATILLFIWQMI VCTTILIQDRKRVDFLLDV
VRDSNDANKKKVQEQERNNSLETAVQRLTAVAKYNGATEAEIKRCVDII
VTVNKVEETKKSPPKPMFKSLQSVFTNVKKRRKKKAGFDLDQTESTDSKS
NPPKRRSLTDLNVQLVHRQRMASHANIHPKSKTHRSLHILHSLHHHRHDR
RRLHDTDDIKQNGDYHPEHSGEGSFRSPVNRRLHLLGGHTNLEHEEDL
TSPRFTFVSSFSAPAQSPSVSRTNSILKDCSSPRFKKKDVCSPNVSRS
SRSQNDSGFDNCGFSKADEHQERGKPSDIKGSVNGDVGIGDVRGNLPMNK
EGDTGVSSDGTGGKEGDSNDVTFKNSGDTKSERECERSRFSDSVTEALSP
QSNTNHMKTGDSCQKKLHGILKQPSFEVQPADNQNKPSDEAHSPTVDTAI
INDDDEDTGL-

Notospermus geniculatus TRINITY_DN198369_c0_g1_i2 transcribed
RNA sequence. GFRY01070393

MELMKIADNINNRRNARKPRLHPIRKEPERLTKIESLRRRINRFLNSHHVL
ILICALVVIDAAMSIGQLMIDLYMIREKFGKAEESLLHLVDILKKDYPYI
NAYQVNTIEDLLHAIDYGKRDLEKQTEKRTTRDAHVNLEAPPNELSSSV
SGLPQQMWNYKRRKREISPRSKDKRERRDDVTNPFFQTSAEKGSQSLRNI
LQTSSESQATGFHASVTMAVDDSLNHRTTSLPYTAVVINDKTKLPPKGGA
MKEIGGKSVDLDDPVIGYTVNKTIASDYMRSKTGNSSCDCSVVQEKNSTQ
LCHCEDDYHLLMEIAHSFHLGSLCILSLMTLEKFMKGLSQGKSFLKRKLE
IFDFTFVVISSFVLDIVFLQGIWSTA EKDAALFLVCLLPWVIVIVNCFVM
TMKQRHYIRMQLQKHARRKAQKKVKLFKKHLERLKRQIKSLKGLCRKHGA
EEREINACAFVFTESRRRKSSLPVNMSTMASLALIGVIGNDPHMPRQOD
DMEEVDLDTLDEKDEEIEELDEVENELMRIEEEPVDQGVQMNGNCHDR
KVSTISGTESIEISCGSVSFDDSGSPTMERRLSDDSIDVIGAISDDSYAD
TGDSDDGGRNKDEKILKSRRFSTTDFLYNSKKSFKRKKKK-

Opisthokonta - Animalia - Placozoa

Trichoplax adhaerens hypothetical protein (TRIADDRAFT_54341),
partial mRNA. XM_002110878

Eukaryota; Metazoa; **Placozoa**; Trichoplacidae; Trichoplax.

MIDDGDNNSETLFAVHGDNEGMNPPQSVTWRS DHRAKLRQLIYSHKVHIA
IVVLVILDALIVIAELLIDLSVIKVHHTSPLARAFHFTSIAILAIFLVEI
VLKLYASDLAFFLHYFEVFDALIVIVSFVLDIAYSNSEALSGVGLLVVL
LWRIARIVNGIISSVKSQANDKIHHLRRELEKTRSYLEQKLD RKEAEIQL
LKKVLTDRNIPIPKPLLEVLDLNGNSTAQANGSASEEITVVDIAGSSAKSTS
SAYIG-

Trichoplax adhaerens hypothetical protein (TRIADDRAFT_54343),
partial mRNA. XM_002110360

MSKKVKTEDKDSYIDILDEESASVRIDHANHTLQQNSDCLHKTEEIMEHP
ITQLILILLVFI²CGIVIAELLI²DRDAIRVEDVEDVKEAFHYTSIMILGI
FLFEVALKICVEGLAFFLHYIEVLDALVVIISFIVDIMSLVPYFYNHVFN
LICYARAAENKLRGIGLLIIL²LWRIARIVNGIIASVKKHMRKRLETITE
DRNRCRRKLNRAIKVARAKVEEIKLLEGILEKEGIEYRQIVAKTEQGDGD
PAEVKLVIEEDIIDDKDNLEEEHKSIDGKEESKSNQEEKSKSIDEKEEGK
GNQNEEGKSV²DHKEEDKSLETGQTEKSEKDAQEGDKRSSRGDSDAASHHS
ERKADDAKDNKEEVEPEVLVYT-

Opisthokonta - Animalia - Cnidaria

Actinia tenebrosa voltage-gated hydrogen channel 1-like
(LOC116299624), mRNA. XM_031708302

Eukaryota; Metazoa; Cnidaria; Anthozoa; Hexacorallia; Actiniaria;
Actiniidae; Actinia.

MDPDDQQLVGRLSFDELSTDTAEMEVGGAGDSNLEVPSTPWWKDNRAKL
RELLHSQKAQYTVVGLVVLDCIIVIAELIVDLQILKVHHDNPAPHILHYI
SIAILSIFLIELILKMYAMGLDFLRHKMEVFDGIVVVVSFALDIAFSGSE
SAAEGASLLVILFLWVTRIVNGIVMSVKIQAEKKIEQLTAENDELKEEI
IKIKTRNAELEKEISALKGQ-

Nematostella vectensis XR_007308022
Acropora millepora MZ029046
Pocillopora damicornis XM_027201316
Stylophora pistillata XM_022939457
Dendronephthya gigantea XM_028555994
Xenia sp. XM_047006720
Hydra vulgaris XM_047284425
Acropora digitifera XM_015907824

Opisthokonta - Echinodermata

Anneissia japonica voltage-gated hydrogen channel 1-like
(LOC117105210), transcript variant X1, mRNA. XM_033246280
Eukaryota; Metazoa; Echinodermata; Pelmatozoa; Crinoidea;
Articulata; Comatulida; Comatulidae; Comatulinae; Anneissia.

MDTKIDSTNDDTPFQETKKSGEVKGTDMGFLNLTGNSKSEDQENIVKNEN
IEVRTAPPNQPAVTESADTFRGKLQRTLHSHWFHGAIIALVLTDCILVIC
ELVLDLSAVENENKACEGEGDEHKEEDTAEKELTAALVLHYMSIAILSIF
MVEIVFKLYAFRLFFFKHKLEVFDAVIVIVSVFLDIVFLIYEETFMAVIQ
LLIFLRLWRIVRIVNGLVISVESKAHEKITAQKQLREEAEEEELEQLRKYC
DQQRQLELIMAEARKHGIVLNSISKLDPPKHRKQFKVDVDVNGPPLDST
TNKKSHQDGFTNVTFDIQDEPADGKTGIS-

Acanthaster planci XM_022240659
Strongylocentrotus purpuratus XM_030990962
Patiria miniata XM_038200083
Lytechinus variegatus XM_041600440
Asterias rubens XM_033772565
Paracentrotus lividus GCZS01131405
Echinarachnius parma GAVF01025219
Evechinus chloroticus GAPB01008884
Holothuria scabra GHHS01281259
Loxechinus albus GGVM01158715

Opisthokonta - Animalia - Porifera

Eukaryota; Metazoa; Porifera; Calcarea; Calcaronea; Leucosolenida; Sycettidae; Sycon.

Sycon ciliatum, transcript: scigl.0025458_3, transcribed RNA sequence. HBWS01076755

MDTDYQSYKKYEAKEKERNEEEDRVAENINLSIRSWRDLIDREHLKKFLT
YSQKVQIFIVVLVVLDCITIVLTELLIDLGIIVKNLCEHSDSDCPLLSISPN
GTINTTETEGYYKCFKNLEQTKCEFHGKKRCLSEDISPDIDPAYVLHIF
GIVVLALFLVEIILKLYALGLEFFHHKLEVFDAFIVIISFSLDVAVS
DAWEGVELLILLWVARIANGVVISVKKEAEKKAEHLQGKVEAFQEEV
RKLKEKLAELKGYTAYEDSDNEATPSSGGESQAQDLHVPYNAPGFVPA
TDTAEA-

Sycon ciliatum, transcript: scigl.0041756_2, transcribed RNA sequence. HBWS01116653

MADSDKEGGGAAANDSSITLETLHQQDSVGSPPSDTTTAASSASSHGRGV
DIKISVDDIDGPRENERPPSIEENTDAHHSNPGSALVPPNSADIKRVA
SVEIVPPEELPDIDDENFDELQHVYDDETUVQLKDAWRSRKHLANFLT
HYFHFVIVMVALVMVVLVELILDLELIRDNECRKDSDCPITRRSNLSD
TSSIQSCSYDTNFSHCIIYHGKHSQCLEETHHDIDPAEVFHYLGIAILSY
FNLEVLVKLFALDIKFFKHKLEVFDAIVVITSLVLDITI
LILLELRITRIENGITLAVEEREKEKRHLKHKDLALKDVDRLQKIVH
ELKVEIHEWRSRAHVEPTYKGLRHADELQSMIAEEEEKHHADGKHHGHHH
HHHHHHGKNHHGKNHHHGHKNHLHGNHMQAPSSDSNHSLSHGSQAQSA
AV-

Sycon ciliatum, transcript: scigl.0080075_3, transcribed RNA sequence. HBWS01098561

MSDVSAATEAGTPGLFEVLSDAEGARSSSGNTSRQEDTAKSASPTKSETS
SSGSATKSGTSSRGDPPAYDDDHAAAYIAQQKAAVHRTTFELDGRPLPDL
EHYYDEFHDPEPEDEPSHDFKDFWRSHENFKAYLTKNHHFHEFIAFLIV
LDILIVLGELILDLEILRADECAHDHDCPLVEATVNGSMWDCSFNSNYTT
CLYKGGRHTCVDEYTKADKDPSEILHKLSIAVLSCFVLESIVRLVVLQRE
FFKRKLEVFDSIVVTTALFLDIFVHHGAVALLLFVRLWVTRIINGIAI
AMESREEAKRHELKQNRCAHELVRKRETVHLLRIELMEWKKAAAVFHE
AEHFTVAAPMPTG-

Oscarella lobularis GIUN01026972
Hymeraphia stellifera GKDX01077406
Cymbastela stipitata GHWA01021218
Aplysina aerophoba HANI01325610
Leucetta chagosensis GIYV01003700 GIYV01008849
Eurypon sp. GKDW01052485
Dysidea avara HANJ01327516
Halichondria panicea HBWD01528479
Halisarca caerulea GFTQ01354451

Opisthokonta - Fungi

**Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
Eurotiomycetes; Eurotiomycetidae; Eurotiales; Trichocomaceae;
Talaromyces; Talaromyces sect. Bacillispori.**

**Talaromyces proteolyticus uncharacterized protein
(BGW36DRAFT_366576), mRNA. XM_046214761**

MASSADPSQPLLGDQQQIERRQQQQRSDDVTRKSSSPSASHDLLRRITES
HFIGNRMPSSWSSRGDGGEYGHRYHDYYNEYYPEPSSSIPRLRAKARSAL
SSKWGHYAVLFLVAVDVACIFAEFLIELHTCELRRERHQVVD RRWEIAQEA
LGLSGLIFSCLFMV ELIVTVLSFGLHYFKSKFHIFDAIVIVVAFVFDVAL
RGLVEELGSLVVILFLWRVFKIIIEEMSEVSAEMMEKYEDEIDKLKHENMK
LKRKLRGYGDEDDDDMEANAGGDEEEDNND-

Aspergillus ibericus XM_025718342
Botrytis fragariae XM_037341616
Aplosporella prunicola XM_033538120
Grosmanina clavigera XM_014317838
Hyaloscypha bicolor XM_024883444
Phaeoacremonium minimum XM_007913592
Penicillium zonata XM_022728519
Lachnellula hyalina XM_031151652
Venustampulla echinocandica XM_032013960
Sporothrix schenckii XM_016736437

Opisthokonta - Choanoflagellates

**Eukaryota; Choanoflagellata; Craspedida; Salpingoecidae;
Salpingoeca.**

**Salpingoeca urceolata comp17136_c0_seq4 transcribed RNA
sequence. GGOY01009290**

MATKADDPFSASASIGRSTLTTLAMSALGVSNAAEVYIRTFPIGAVPRVLS
GPAKSFRQRVHDWLERKHHVHN**FLLFLIALDVLIVLAELLLEFEDCRLELH**
DLEHDSHSNEGKIERIKKA**EKGLRIVTLIIILSIFMIEVAAKVYVLRQTLF**
RHK**LELFDVIVVIVSFCIEVFLKGFERRAASIVVIFRIWELTRIINGVAV**
ALELRMEEKVTMLKHAVDFRQKFSVAEHLASLRAQLANVQAQAASHLQ
DEVAEMQSTTRRVQRLLETPVVSEETVLSTSGRFKAQEGYVPPGNSL
LVSGHGPDPPLAPYRAKSSPGPTNTLNKSRVTWQVTDSDDENGD AEHVYRA
RSLPTHDLPTPQDSVELHADTNTQDDPESPQPGQSPDVGWASKV-

Salpingoeca dolichothecata GGOK01012774

Salpingoeca kjevrii GGOX01017848

Salpingoeca punica GGOZ01029229

Didymoeca costata GGOQ01021484

Stephanoeca diplocostata GGOS01015804

Opisthokonta - Ichtyosporea

**Eukaryota; Ichthyosporea; Ichthyophonida; Amoebidiaceae;
Amoebidium.**

**Amoebidium parasiticum JAP-7-2 G13375_050632 transcribed RNA
sequence. GAKF01050632**

MVYGNHLQRHQTRVAGGFHITPHLVLKEPQFEKAEGKHWRNQLRDFIHSK
RVHTIMLVLLVLDVMLVITGIALEIQNLSGALHLCESTVESCVAKESCTM
RDFENHALVTAEHWTAYLSLAIIAIFIENLLLIVALGPIGYFSNLLYAL
DFVVVITSFVLETLEIDKPEEGLLVLYRVWRFVRIAHTFYETNVDEELER
VKHAIKQAERELLAMSLTPEAQKEAHEALAKRMAESYPDAAGAILSAAIH
YAEHNKHGKTPQSDPMEVKSSTEGEEEATVQQ RTP-

Archaeplastida - Chloroplastida/Chlorophyta/Charophyta
Eukaryota; Viridiplantae; Chlorophyta; core chlorophytes;
Chlorodendrophyceae; Chlorodendrales; Chlorodendraceae; Tetraselmis.

Tetraselmis striata, TRINITY-DN8512-c0-g1-i1, transcribed RNA
sequence. HBPS01066517

MERSGSSAKAIKPVRLDRKSMTVLDRLSIALKREQSTKRLQQQQSGGRP
AKEQPEGKGAVEGAEEEEVKHHWRRRLHFLHIRWVHTTMTALLILDIT
VVTSLLEIQIQSSQKKGQAKSICLHEYETGHAMPTYMENNTTCNPDGLHAC
DYTEQEPYHMAHTLHSAELGLAYISIAILSTFLENLAMVAALGWNFFRH
FFFVLDIVVAVSLALEIVAVASAHLELTVGNILIVARMWFFSVAHGIY
FLEHSEEA AHEVDDKDAGDSMGKKQSQVENGTTV-

Ulva lactuca GFUR01058327
Ettlia oleoabundans GFXW01038773
Chlorella sp. GGGA01109849
Nephroselmis pyriformis HBHO01063905
Chara braunii GGXX01073780
Chlorella sorokiniana GAPD01037882

Archaeplastida - Chloroplastida/Embryophyta

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta; Bryophytina; Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrium.

**Physcomitrella patens voltage-gated hydrogen channel 1-like
(LOC112276685), mRNA. XM_024508236**

MDAHGRTDLEGADWDDSATALLPEREPQDAGDGEMPDGPDASSLGSALQ
EVSKAWRKRTQAQRLSAQRWIEQETHVPRRARWREELAEALEATWTHVAI
VVLILLV¹DLAATAIDILKTMHNKSHDL²DVCVDLVESCQGCIGHFEHSAEWK
WTYWTSIVILVILMLNVGLIVAFGRSFFLHP³LYVLDLVVVSTALGLEVL
LDADTAGLIIILTL⁴WRIV⁵RV⁶VAHGIFEVTD⁷EAWEKSIRELETQVKGVQDAY
ERAQEALQEKNRELGEKDGRIAELEARLESGSTPF-

**Physcomitrella patens uncharacterized LOC112285145 (LOC112285145),
mRNA. XM_024525718**

<LNDCIAMVESCTSCGSYFERREEWKWTYW¹TSVAILSL²LLLN³VFGLIVAF
GMA⁴FFLHPLYVLDLIV⁵CTAPV⁶LELT⁷LHTDTAGVIIM⁸TL⁹WRIV¹⁰RV¹¹VAHGI
FEVT¹²DEAWEKDIHRL¹³ETQVQAVQSACDEEQVLLQERDQQIAELEARLREL
TVIET-

**voltage-gated hydrogen channel-like protein [Arabidopsis thaliana].
NP_001321473**

MNIINTGTVDNVEFSIQNLIKSWCRRRKWRQLCNFSPKQQQEELISINQQ
WRITLSNFLESYQVH¹LFTIFLLSL²DIILTSLELSSSL³LSCTSVKKTETEN
EWF⁴RWGG⁵TVILSILAVKSMALVVAMGKSFFKQPGCVMDG⁶TLAIVALILQV⁷
LLEKKGTG⁸FIVVVSL⁹WRIV¹⁰RV¹¹VETAFELS¹²DEAIEVQIDGIISQFQALSKE
NRTLLET¹³LAEKDEVIKMLEEELNRFKENG¹⁴DIPFVKP-

Selaginella bryopteris GEMU01010353
Bryum argenteum GCZP01005159
Sphagnum palustre ICRE01047567
Triticum polonicum GEDT01074033
Ginkgo biloba GHLL01415143
Marchantia polymorpha GEFO01020457
Selaginella sellowii GIMF01015262
Dicranum scoparium HANF01033133
Isoetes echinospora GGKY01088505
Lygodium japonicum FX959670
Pinus sylvestris GHKW01007963

Archaeplastida - Rhodophyta

**Eukaryota; Rhodophyta; Florideophyceae; Rhodymeniophycidae;
Gracilariales; Gracilariaceae; Gracilaria.**

**Gracilaria vermiculophylla Cluster-14487.30734, transcribed
RNA sequence. GILD01028259**

MATDQQEAAAAAKIGCAPLKQANLQQPQPMRRPSLASSSRGSLSTNSM
YFGIPTTADAEDHAEERHGTHSWRYRVVAFHLHKPRVQKIVMGLLLTDVIL
LFVELFLLATFPHCSIIERDGLSCVPANGTTIAAAAAAAAAAEQEEVEHR
WLLVAATRFLAGGGGSGDDHGDGSAICEEGYEWNGLEAGCDEYKWSVVHT
LETFIFSLTVIILSLFFIELTVEMLALTPQIFFRQFWFLLDYVIISISLA
LEIAFRVKREDVYQSFAGLLVVVRIWRFVRIHGIVEVTHENEENGMRRL
FQYVQQLEGLLQTNLDIALPGCAQHIIHHVHHDHAQHLLDVIEGSAKQTPS
RVRFAGEDSDIIMDEEGKGDDDESSAADPEKRWDTTSL-

Rhodella violacea HBJD01001165
Timpurckia oligopyrenoides HBFP01003029
Madagascaria erythrocladioides HBNE01039390
Devaleraea ramentacea GFTF01008765
Devaleraea mollis GFTE01010127
Laurencia pacifica GFZU01160101
Erythrolobus australicus HBGI01005155
Rubrointrusa membranacea GFTD01034059
Kappaphycus alvarezii GGUP01041343

Sar - Alveolata

Eukaryota; Sar; Alveolata; Dinophyceae; Gymnodiniales; Kareniaceae; Karlodinium.

Karlodinium veneficum voltage-gated proton channel kHv1 mRNA, complete cds. JN255155

MDRILHHAVHTVHTSKSARDAEGHGTWQSKLNEALNSSKVHTILNVLLIC
DLMTVIIGMLLEQYYSDSQVQGLTEAFKDCLEKRTFCPDPSHLAHYGNHD
LHEWAERMEYASLAILLIFLLENMLLVLANGCRFFANPFHILDIVVVVVS
VGFEIQGILGEGHDAGIGLVVFATWRFIRLGHGIHEMHEEHEAEDHGEH
RVSDAAGSLEAPLQKGSFEQHAAGTSGVHHARSQASSNREGREGCCVQ-

Karlodinium veneficum, TRINITY-DN53119-c1-g1-i1, transcribed RNA sequence. HBOS01067516

MWRTASATGTKKSKIRRVPHILDEISHEATHFRRLLLHSKPVHFTILVL
LIAGLICLTCGVLEAHYHLHGKSDDCQNYVNKCLIHHRRLVNWPGRPELE
LPSWLRSPWMSDAGAEAEWASNAELLLDEEFQDDQAPRMLSGSASSSSAS
STGSSASSSSSGSHGSSGSHSSASSSSSGSHGSSSGECAGHPHFGDHTLHDI
EIIILAYISVGILSLFLVEQVLLIVDLGKEYLKPMFILDVIVVSSLLIEI
LVVNMIGGLLVLAFTWRFARVGHGVFEAKEMIEEMIGEDDDTVKNMMDA
WKELTPERWEEILHSGSAEILRESGVTPAEIKLGEALGNPAVAMRALAF
ARGWKQKLDKKKAKRLSGSNPKRQMPGASLQTTATVGKGHSEH-

Alexandrium monilatum, TRINITY-DN21304-c0-g1-i2, transcribed RNA sequence. HBNR01032293

MLAQGRCVHSRVGGQPCLRTLAAHARSAGGAMGHEHQSEGEDDILAAGSLI
ALPLRFMNSTAGHLLFFLLVLVMIVVASGFLDTQYLLSQTKDCKGYVT
ACTNHSRRLGNDGREEQHARLRLASSGGGSSAPVDCSADPHFGDHGL
HDAEVILAYISIGILGVFLIEQMLRVVSGCRYLAKPLHVLDICVITLSL
VLEVLVTHLPLAGLLVLGRVWFARTGYTTAEGLHDIHKVRPAFGSMAHG
AIEAVWPRLPEHRWKALASRSSMELDLEMMEVNLAETIAKTS PGFVLHAL
ARENERLRTPRSNPAVLTEMTDATEAS-

Karenia mikimotoi isolate RCC1513 Kmik_DN141715_c0_g1_i1, transcribed RNA sequence. GJRC01038612

MSGKVHPMAVSGESQQVDTVKAQEVQEVKEATLDDEATLDDDAYNEREDK
ETNRLKQVLEQMRRENEADRLQAQRRALFVKAKDEEKEMGHDHGKHSW
QTRLHLRLHHHYFQGFLLICLLLLDVVVVVVELFLEAQYPDCDIKRDVAVS
CVPIACAPSTHGSTSSHSSSSATTSSHSSSTSSGSSSSSHGRRIAGMEEGD
WEYGQDAWSWPAEEPLGLLSWESRGRLLSGDSHGPTCKDSHLYSPMESAK
ATCDEHKYGLWHTVHHLLVGVSVFILGVFFVELILLFTCLGCGFFKNPLY
IADLFIVSVSLILEFLLMSFTEQSLVSLMLFAFWRFVVAHGLITSVHE
PMSHKCEHMEDIVEQLNARNEKLARAERHMKMIDFLLKDSKDPKAAKAA
ALKAACAAMAIEYPQAPDHDGRGPRESARAPEGDAAPFLAEHSER-

Scrippsiella hangoei, TRINITY-DN19376-c0-g2-i1, transcribed RNA sequence. HBPM01014491

MSLCRTHCSWKLSDRRLRSGWRKTLGEAVEGTVMAMAVCLLLFVDLICTFI
DEIIQNTDLLNPKYEDQGEGVAKWCEHISLVVLVLFMLELSLGVVAFGKR
FFSHIWYLLDFGVVLSLICEIVSRFYDTDGAQLLAGILILLRANKFFAF
GFDILMLRHKVHEFEEHNVNNGNEPTPAPALAEELDQENRT-

Karenia mikimotoi GISR01074873
Breviolum minutum GICE01010199
Pelagodinium beii HBNF01018002
Symbiodinium sp. HBTG01074859
Durusdinium trenchii ICPJ01008996
Lingulodinium polyedrum JO744110
Selenidium pygospionis GHVN01105692
Gonyaulax spinifera HBNG01058504
Prorocentrum donghaiense GHMW01205561
Dinophysis ovum GKBT01018307

Sar - Stramenopiles

Eukaryota; **Sar**; **Stramenopiles**; Ochrophyta; Bacillariophyta;
Mediophyceae; Biddulphiophycidae; Eupodiscales; Odontellaceae;
Odontella.

Odontella aurita strain CCMP816 TRINITY_DN47737_c0_g1_i1,
transcribed RNA sequence. GHBW01044937

MSTTPMKQKSTLKRLLQEEEEAGITTTIRCFVPEKEEVWFVDHNTKEGNW
RRKLIRIVHSTNAQ LILGFLLLLDVVFLFTQVFL DAHFPPCYAIIGKAEC
SQGELICNPKPSG IIVDQILYIGSVSILCVFLELGLLFFVCL QIQFFRN
CGY WLD FVIVLTS LILELVL HGSSDASAASVVI I ARIWRLLI IGHGIFNS
KRRQIIARMLADEEDLYIHDHEPYEDSSDEEDYPDKEEEYGSDKVIIRRLS
HRIVKRRSYLAKQEDKENGPHL>

Odontella aurita strain CCMP816 TRINITY_DN117390_c0_g1_i6,
transcribed RNA sequence. GHBW01194335

MAPQEQGDHVFDESETPSSHSHKVGRPPVHIPTDEEVETHVQELHGHDDWR
SKTLHVLHAKP ITFTLLGLLVLD VFILFAELYL GAEPSPCTIIERDAISC
CPAEEGAGGDHGGGTHRWLQEMQEIVSDKGFYRDAADKWT SIGSSGKDWS
RALAEETHDDHADGSHAEAEVERLFHDEEDGHGDDHGDEHGDDHGDHGD
GHSVASASGHGAHGDGHHASHYCTNGLTDMDPAKYPAACDPHKYEALHHA
HHVLFWLTIAILGTFFLELSIMIVCLGCTFF TKPFY VLDL FVVTTSLLLE
LTFHFV DQESLASLAGLLILA FLWR FV RIGH GLVEST NKWQAQKHERLLK
YIDQLEGLCKDNGVELPDRQSIRNLKLLNDEESSTE-

Odontella aurita strain CCMP816 TRINITY_DN105452_c0_g1_i4,
transcribed RNA sequence. GHBW01145983

MSPHDSRDSATDVPARPTMQLAGTTS DRKADAKVTALSRFSVSFNEDPS
EDSNGCFGRKTRRFKPAIPTSEEELDKVEERCGQNSWQMKAVKFINS GPL
QK LLLVSLLLC VIILFIELYLDASY PSCHTVSRDAISCCPAGCSEKGYV
DKYDDHKDEYDDGHRFLGGSGYGYCEYPLEDTHHPAACDDHKYEGVHKAH
TILFAMTITILSFFMIEILVLIVCL GPMLFFGR FLYVLD FV VIGSSLSLE
IVFATM DDAAAAD VAGLLVVF FLWR FV RIGH GLVAST HEMATHKMNKLKK
YTRALEEEVIRCGGVLPEKWSLGLLEETASNHLSSGGDSTSVKKISVEL
GGRVVNTEHLVSKRH TTAGSAEDTERETSSSDVDTKDAFVDNALAA-

Odontella aurita strain CCMP816 TRINITY_DN85551_c0_g1_i1,
transcribed RNA sequence. GHBW01102851

<GGASAGHGYCEYPLEDTHYPASCDDHKYEGVHKAH TVLWGITIAILSFF
LLEILTLMVCL GPRTFFCR FLYVLDL FVITSSLALEITFATL DDRKAADI
AGLIVVF SVWR FV RIGH GLVAST HEMAAHKMKKLK KYTRSLEQEVIHCGG
NIPESKWSSQRTLQQLSDNSTTVRDTMPSEDSGREA-

Phaeomonas parva HBGJ01043600 HBGJ01042220
Aplanochytrium stocchinoi HBIN01016972
Thraustochytrium sp. HBSU01005162
Nitzschia palea GJPG01004537
Navicula sp. HBQT01027484
Grammatophora oceanica HBGK01048152
Heterosigma akashiwo ICRV01078048
Chattonella subsalsa HBNW01021031
Thalassionema frauenfeldii HBL01017232
Licmophora paradoxa HBMT01029076

Sar - Rhizaria

**Eukaryota; Sar; Rhizaria; Cercozoa; Chlorarachniophyceae;
Amorphochlora.**

**Amorphochlora amoebiformis, MMETSP0042-doi:10.5281-zenodo.249982-
Transcript-23202, transcribed RNA sequence. HBEM01014674**

MLGGPRTTNLQHASSDITAYGHQGGMKPEDEENTKVSRAHTQPMVGRERQ
YRRPRRRAPFQSPDGKWRGEIRNDFALGHPILKHFIRPPGRLEGHHGEDW
HHKLNRFLLHHHRTHLVLNILLIVDVVLIIIAIELEFAFKNSEIQDLEHAC
EEVEAMHAGASCPSPHGDKSLEDGVRGVEYASVGILCIFAIDNLLLLLLAN
GKEFFRNPLYLDDAVVVYLAIIFFETVLSGDGGLAGGIIIIIVFAWRFRIG
HGIYETTHDSPQKQDEKSRDITLKRASIGSAPDQKTSPDVENAVKT-

**Amorphochlora amoebiformis, MMETSP0042-doi:10.5281-zenodo.249982-
Transcript-22745, transcribed RNA sequence. HBEM01014165**

<AGSPGRMAVDPFLLQATTPLVRPDAKKNVSICSCCMYATSYHTKADHMG
DCWQRSLLRFLHNAAVQDFLTFLLLLDIICVVSEILIEHYSQEGIEVPED
LELGLKYTSLSILITFCVEIFLYIVAKGLDFFTEPLEVFDMFIVAGSLYQ
DVVYEEATGGLLMLLVWRFGRIFGVWATEHERCATRIRQLESKVRYL
KKNKQLESQKVNLLHHEMYSDDGGSSKAGTMERL-

Bigelowiella longifila HBMK01033472
Lotharella globosa HBIV01019936
Chlorarachnion reptans HBKK01013759
Lotharella oceanica HBHP01002709
Bigelowiella natans HBQC01075387

Haptista - Haptophytes

Eukaryota; Haptista; Haptophyta; Prymnesiophyceae; Isochrysidales; Noelaerhabdaceae; Emiliana.

Emiliana huxleyi, TRINITY-DN7767-c11-g4-i1, transcribed RNA sequence. HBNU01018021

MAEIQTLQPPPTSRLGGRVKEVHSPEKLERKLLKANPRENTLRKRQAVY
AAMDALAAAGASEVTSPKTRYGARAFGKPLKAQLLSARAEVEKAHAHGA
DSWQRRCLHLLHSHRVQLFFILLLLVLDMLIVITEICLDLEYPSCRLAKRD
TVSCCAAGEEGEHHTLRYLAEEHGGHSLCGKGTVEGPHGVGCDEHAHP
AVHTAHAVLTWASVAILSLFEIELLTLLAASGLRDFFSNVYYVLDIVIVS
ASLVLECVFYNTAGLSDLIGLVMFLRLWRLLRIGHAMFASTERASSTDNL
KEVVRELRAELDLLSEWAEERASARAPPDDPGVDDIG-

Emiliana huxleyi strain CCMP3266 Ehux3266_tr10784, transcribed RNA sequence. GIZZ01010784

MQSQQRRGAKWVSADSEARALSSRRGSYAWQTKLLAFLHSPRLQALLTLL
LVCDVIAVFGELFI DAEFPSCMYVLRDAIPCCDSGCIGAGDYSAAAADA
IQTILSLGKSVQGDHLHLEHDETRAEICAGQGSHLDSTGRIGCDSHKHD
AHKFHKFLFRVSLTVLVVFELELLGLIASLDRAFFRNPLYVLDLIVITVS
LGLETVFRVFSMPEQDLAMALIIVRLWRFLRIGHGIFASTHSVAKESDK
LHAEIRALEEEYTRALNQAASLATTTTRPTRLASAPSSTSGSPSATRPPPF
RGRSASEASAATHDLQGAGGEKLDGVAAALSQRSNTPTSPVGAPAMRRP
PAAAPLGAHRAHQLGPPSSAARTGMPGVGTRMGAGEAAAERQAPPAAE
PEPAEGAAAESVELELDALDMST-

Calcidiscus leptoporus HBER01001684
Gephyrocapsa muelleriae HBRT01056448 HBRT01109117
Coccolithus braarudii HBEY01039257
Scyphosphaera apsteinii HBMI01021482
Gephyrocapsa oceanica HBTM01082732 HBON01067641
Prymnesium parvum GBYI01026351
Phaeocystis sp. HBQW01022812
Phaeocystis globosa HBRY01039040

Haptista - Centrohelida

Eukaryota; Haptista; Centroplasthelida; Pterocystida; Raphidista; Choanocystis.

Choanocystis sp. FB-2015 c53027_g1_i1 transcribed RNA sequence. GDKX01062209

MEHNPQRDSL RQPISEKYAAKRASHGSLEARLVDTFKMLDRNANGLVNVN
ELRVLVNTYLET PLETEEIVDTLQQLLPDKGLAPDPHKS IKLNRDDFLKA
MIHFREQNSFPT PLMTRLHSDPITFNGRSALSTSKPCLSERQEHHVNVIS
ASNPNLEEHRQM TRKSTRQRLSRALLNLPDDLYVSGETTLP SKSQSGRSS
HSASLAELVEEP ENPKQEAKIENRDRSARVALAQHLNSTAMQ VLVVFLVL
VDAFVVIAELMVLS MPCHVPEPCGLSNFNATETLDGFGQCLSKYEHTCES
FHSLMSVLRWSSKG ILMFFLAQIICLALCVGWRFFKQPPFFVMDLLVSSA
MALEFSVSLRGG RMIVFVLLWFEVIAHALATTI DIHISNMERRVMRQTG
ADVRAASTLQRE IRSHQQTNRVAMERI QANSNRIANEEEFIESLKMEELR
DMILRERNHTSEV KQRVKELQEILTVVQGHMEAKRSQFKNRHIKHQARQH
PGLAVQYSTSSRSV STAGTIHHRDPVV-

Choanocystis sp. FB-2015 c20243_g1_i1 transcribed RNA sequence. GDKX01034169

MWVEGKGVESLE GR LKETFKMLDKDSDGHVDVHDIKV LLELRDQQPRTDA
EVIAI INRILPGKTHLAALTRKGKVTVSEEEFVLAMLHFLSNEATERAID
HDDLHNAFIDHLLDLPESDQSVTIDVDKSSKASRKSFAAARKSFAHAGQA
VKQARKSFANMALATRD AELDS DRAKAAGLAGFLNARVVVASRLNSTPMQ
ALIVLLVILDAFAVAMEIVLLGV QCKTPSECYAPSAEVHHKAGGGVVTDG
SKYDATTC LHKFDHVCHAVHQIEYILKWISKG ILLFFIAQISILAVSIGI
RSFLRQPFFVLDFVVVSVALGLEFGLKNAGGALLGFVMLWFLIRIVHAF
TTLDVHKGTVERHILRQEAEAKEALQIQRAIQEHRKLGQPLVNAIRHKT
IRRIEKRSALGKSPRLSAMTNESGLAATPVSHNMSVSSATTLPDISITLV
ETEPEVRDEEYWMGRVATLEAELKEDKVHVRELESKFVDIQNTLT TVYAH
LEGKKQRFLEKVLKQNQALNIPARGSLLEFTKEMQQIQPK-

Amoebozoa - Discosea

Eukaryota; Amoebozoa; Discosea; Flabellinia; Dactylopodida; Paramoebidae; Paramoeba.

Paramoeba aestuarina, MMETSP0161-doi:10.5281-zenodo.249982-Transcript-29362, transcribed RNA sequence. HBKR01021517

MGVIKGGLYSTEGMWKHNSTKRDKVLHVIHHKYTHFFITALLVIDLCVVI
TSISLEIEYLTSEVTDLEECVHECFFGDEHDEEHRSLTQQSFRQSNHETQ
EKNTNEALKRREEREREREYRESRQNDSDHDEEKSEKFLECEATAMFE
DDDDNWGNGNLKEAEALAYVSIAILCVFIIEHMILFGAMRMDYLRSPIL
IFDFFVIAVSLALEIIFQQQPEAGLLIVARAWRFIRILHGFHESTSDEVV
KETVHALNSKREDILNIYAALDDRLLVGASKKEAMENVAEQYPETIFEIL
QILGHHFQDKDKQEHLEHIKDTIEHRMHPTPSRTHL-

Balamuthia mandrillaris strain CDC-V039 BamaA010555t1, transcribed RNA sequence. GISS01003879

MAEHGDATPLLPSHGREAIGNGNHSRWRWLLDYPHQKVKRETAAGPPSG
LRALRLSMARFLEGRFMQYFLLALLVLDVVLVVELGIMEASCESGKEKS
DHTFHIIEQVLRVYVTLISILSIFAFELLLLLLALGLDFLKHPLYIVEVAII
ATAFVLEIGLRHLQAISGLLVIFELWRLRLVHGVITAQQDLHRNTKQNL
EESRARVHELEQEVERLRRRGSIRD-

Balamuthia mandrillaris strain CDC-V039 BamaA008510t1, transcribed RNA sequence. GISS01013796

MTTRRTSSGRREKDEGAHELERIDHHHQEEEEKGESSEGKDDEAVNPLGK
TKQKHLREQHHKYQHCKHPHHHLLLETTRGLVGKFGWLLGTHKYPHQKK
RERLEKAEHFPKIHRIRVKIAQFLEDPRFQYFLVALLLVVVILVVELLL
LERTCEGEEENEEEDHAVHVVEEVLFWFTVTILSIFALELLTLFFALGLD
FIRHPLYVVDALIVAAAFVIEVVLRTLAGSLLMLRLWRIRIAHGIIT
AHQELHHQTKKDLHVALHRINELEKLLAEA>

Paramoeba pemaquidensis GEWA01008129
Balamuthia mandrillaris GISS01013796
Tubulinea HBYL01016471
Acanthamoeba sp. IACY01017688
Acanthamoeba castellanii GJZG01027302
Vannella HBXS01019840

Amoebozoa – Mycetozoa

**Eukaryota; Amoebozoa; Evosea; Eumycetozoa; Dictyostelia;
Dictyosteliales; Raperosteliaceae; Raperostelium.**

**Raperostelium potamoides strain FP1A RPO_TRIN_CL14637,
transcribed RNA sequence. GIOX01005152**

MALVKGRYKFPFHFAKNSPRHKARRLWRRKLGSFLESNRVQIAIVALIFL
DLIIIVIIELFLEEHHYKSQCAEEHEIPHVIHRLLENALGIITLVLLGIFEFE
ILLLLFAFGRDFFKHPLYVFDAIVITVSIIVEVVFRDTAGALLVVFRLWR
VVRIIGHGIAISVETHDKKKYKELKSRYRKVEDNKVYLNQINVLRNRMGE
IAISPPNLSEVSANTSSIFSPSRSENIQSPNSTTPINEIKDDISDLSADS
DEDNFNEKLKINSNNNP-

Hagiwaraea rhizopodium GIOY01027566
Raperostelium gracile GIOO01028008
Physarum polycephalum GDRG01015357
Heterostelium gloeosporum GIPA01000642
Cavenderia multistipes GIOI01021321
Tieghemostelium menorah GIPF01006404
Cavenderia bifurcata GIOH01013395

Cryptista

**Eukaryota; Cryptophyceae; Pyrenomonadales; Chroomonadaceae;
Chroomonas.**

**Chroomonas sp. Dc01 RNA, 13hcomp50078_c1_seq1.p1, mRNA
sequence. ICPR01036203**

MMNAPYFPQVGMGFGQHPPPFGLSVDGGEKHEHHAEAQA AHDAAESLVHK
LRTHGERLLKSGARRFRPIRSYWL TADQERDRVIEKHGEDSWQAKVVDFI
QSRSVQA **LLISLLIL** **DVIIVAIELF** LEAEYPPCVIVKRDAVSCFNATALV
GMSAAALESSTHARAKILSPRGEGTLKHAAAATRTEALHTHTPENGTVHE
GVVEGGEHHDVCEEAGLISTGFEASCDKHKWSRVHDTHTT **FLWISVAILV**
AFLT **TELLALLACLA** **FDVRNP** **LYLFDLVIVLVSLVLEIVL** **EHVGEVQLSA**
LSGLLVFA **RIWR** **FV** **IAHGLATSV** HESEAASHEEITKQAEELHKQVVELR
AKLAGSARRGLMAR-

Geminigera cryophila HBHS01020640

Teleaulax amphioxeia GKBS01005298

Discoba - Euglenozoa

Eukaryota; Discoba; Euglenozoa; Euglenida; Spirocuta;
Euglenophyceae; Euglenales; Euglenaceae; Euglena.

Euglena gracilis comp31701_c0_seq1 transcribed RNA sequence.
GDJR01054876

MSYFDDTFVGGAPAPSVEATKVEDGCPIDCHKLASPSKAPTLRQKVHHFLS
CRPFKIFMMALLLLDLILVMASVLEETGSLQVSLDECERSIHDCEHICSN
STDFTATATNYCTNTHGQTCHYNHPSLATALHLAEKVLAYISIGLLSFFL
LERLVGIIICEGLKFFSCAFKVFDFVVIIVSLVLEILFLGQPGVGLIAIGF
FWRFFVRIGHGFHEAEELTHPVDEFVKEHKAALFALHRRLLGVPGLYGTEG
AVLAENAAAVREALALLEQDGFGLLLGIADAAVAGHRQHQEKEQLHYWK
LQ-

Euglena longa GG0E01032297
Neobodo designis HBGF01052964

Figure S2. Alignment of H_v1 and H_v2 from Xenopus.

Query	1	MAGCLRHTSVGDDTKKREWKEEDVEVAHEEEKKNTPHPFIASYSYSLRGALKWLFSSHKFQ	60
		MAGCLRHTSVGDDTKKREW+EDVEVA+EE KNTPHPFIASYS RGALKWL SSHKFQ	
Sbjct	1	MAGCLRHTSVGDDTKKREWQEDVEVAYEEPLKNTPHPFIASYSFRGALKWLLSSHKFQ	60
Query	61	IVIISLVILDALFVLVEVLLDLELLAEKVDHIIPEIFHYLSVSVLSFFILEIAGKLYAFR	120
		IVII LVILDALFVLVEVLLDLELLAEKVDHIIPEIFHYLS+SVL+FFILEIAGKLYAFR	
Sbjct	61	IVIICLVILDALFVLVEVLLDLELLAEKVDHIIPEIFHYLSISVLTFFILEIAGKLYAFR	120
Query	121	LEFFHHKFEVFDAAIVVISFIIDIVYISREDIFNAVGLLILLRLWRVARIVNGVIVSVKS	180
		LEFFHHKFEVFDAAIVVISFIIDIVYISREDIFNAVGLLILLRLWRVARIVNGVIVSVK+	
Sbjct	121	LEFFHHKFEVFDAAIVVISFIIDIVYISREDIFNAVGLLILLRLWRVARIVNGVIVSVKT	180
Query	181	RAEEKIHKLEENQRSLEKVTQLEQQSAQQEQEIARLQKLLKQHNVPFDS	230
		RAEEK+HKL+E + SLLEKV QLEQQ AQEQEI RL KLL++HNVFP S	
Sbjct	181	RAEEKMHKLKEQKGSLEKVAQLEQQCAQQEQEIGRLHKLLQEHNVFPAS	230

Figure S3. Cephalochordata sequences

Opisthokonta - Animalia - Cephalochordata

Eukaryota; Metazoa; Chordata; Cephalochordata; Leptocardii;
Amphioxiformes; Branchiostomidae; Branchiostoma.

Branchiostoma belcheri voltage-gated hydrogen channel 1-like
(LOC109464640), transcript variant X1, misc_RNA. XR_002139895

MDKLKNAFKFELFQNDSSSVITSSDATSSSGNAEPKTFREKLLHVLHST
EFQVAVVILVIVDCILVVFELLIDLGGIKLCEEAVRAECESAGTTATMTP

AEEAEKEAECDHPAPEILHYMSIAILTI FLIEIMFKVYAYQKDYLKHKME
LFDVVVIISFCFDVAYANHEDAFDGI GLLVVLILWVTIINGILMSVQ
HTAEKKINAHKQARQEVQEELNKMIAHAHDLEKEIDLLRKT LRENGISVE
SIPRTPEVSSSQVKVEAEITPTTEYATPAHFSAFSGQDDTQA-

Gene:

Branchiostoma belcheri isolate BF01 breed outbred unplaced genomic scaffold, Haploidv18h27 scaffold1, whole genome shotgun sequence.
NW_017802379

**Branchiostoma belcheri uncharacterized LOC109463761
(LOC109463761), mRNA. XM_019760615**

MTPCDGEKKPPPSGEATVGGIFPDEIAVIKKQAQNDKRRPLKIVIIAGVA
VMAVLAIGVLLITRPSRHGVVTC SLNFWTGKQLLHETVETDKDAETDAF
YTEGSRGEAAVMDHSSMMKAFKLSRSNKTCFIFEETQGEKNAVKKTAEE
LEEKQDGS LQFAEYGGAMLMTVDTERPARPVLSQKLQNF CGQLEPRWAKL
TPATEEEQQGDRVEIIMP AEARDMGELAEMPVGP GNEKETPPTPSSTHPL
TESRDHHHDNQDCRHKLK HMLERQSVHIAIVVLIVLDTLIVIMELLIDVR
VIKLCPPDPDVCVPKAGHNGTTGLVTTGAPGHHVIDAGDHGTGGHEECHH
VLIEVLHVVSILILCIFVVEIALKIYVDRLEFFKNGFHVLDVVVLVSLG
LDIASLV RPSAFTDAGGLLILLWRITRIVNGIISV EEEWEHKVNHLK
HEHQ LVERERDRLLKENALLQKTLTNHGIDIPKLPPDSGDESTCEFEFE-

Gene:

Branchiostoma belcheri isolate BF01 breed outbred unplaced genomic scaffold, Haploidv18h27 scaffold1, whole genome shotgun sequence.
NW_017802379

**Branchiostoma belcheri uncharacterized LOC109467017
(LOC109467017), transcript variant X1, mRNA. XM_019764911**

MPRFKGQQQHETCRHLAVEDVMVADELGLGMSSADLYNRNVEGDFLDLE
AAIFCDIEEEKTKQRVQQLLDGPATQITIVLT SWLLSHVLLL ELLVDLS
AIFHFDKCMVARI IHVWGLGVLSVFTVEVLTRLVCHQM QFFDKKIEVLDL
AVVIIACVPMIVSV ELAPSTAWDGFSLVIL IWR CYRVVQGCVSPVRE
EASRKVHVLLQAQRRAHQELQTL YLMHDENQEEIHRLRLLLGRREAEEDN
VSQQLQVALERKDSQYVAQLIHTIEQRQGRNKGRQRDGG RDSPYSTIVVH
AHQLSDSNDVPSGTIASRLSESTTGDSGICEETRPQQQTND ESRNHANSS
GVTQLPKCGQQALT VVEPRGSHQQHSNRSPCSNSKRNP AVSSCDMDRIDV
IGSEIILQHRNDSTGKKFLDGKLP SNKDSRLLFRDNKSMPSNGKVSHSKN
KVSEIKVNKSLDDDHKKAVSMDNKT VSKNNTATAQTNGKVRKGKKKAGSG
DSYVNGALLLEMT ELQQKGDTGYCNEIVIEQFYQNGNAPATAL-

Gene:

Branchiostoma belcheri isolate BF01 breed outbred unplaced genomic scaffold, Haploidv18h27 scaffold173, whole genome shotgun sequence.
ACCESSION NW_017803191

Figure S4. Chelicerata sequences

Eukaryota; Metazoa; Ecdysozoa; Arthropoda; **Chelicerata**;
Merostomata; Xiphosura; Limulidae; Limulus.

Atlantic horseshoe crab

Hv1:

Limulus polyphemus voltage-gated hydrogen channel 1-like
(LOC106464594), transcript variant X1, mRNA. XM_013924749

MEDTTEKTGDSTSIATNLESDPDIQPLITFRERLTKLLHSYKFQVGVITL
VIVDCLLVISELLVDLNLVSVNSHSSAPHVLHYLSISILSLFIIIEIGAKL
YAFRLEFFHHKLELFDVIVLVSFALDITFRDKESAVSGVGLLIILRLWR
VARVLNGIVLSVKTQADHKLAKEQKKRENLEQELARSRDYIAALEEEVET
LRRILKDNNIKELPPTVIDNGAFKCTTLNVVAEVDNHMIT-

Gene:

Limulus polyphemus unplaced genomic scaffold, Limulus_polyphemus-2.1.2
Scaffold1698 Sequence ID: NW_013667308.1

Hv2:

Limulus polyphemus transmembrane protein 266-like
(LOC106463214), mRNA. XM_022390662

MRNSDPLVWGLTGDTSLDDGPTLCEKIWATVNGKVFSAVIVTLVVFVEG
LVIFSELLIDFEVVQDPQWKTSLNCSANVSGLVFSSAGANSPKLMAKDI
LSYISIVILIIIFVFEVGFRLVSGRARYLIQGMEICDAIVVLVAFGLDIAF
LTPPSKKGAGKEAAVLIILLRLWRILQSVI DNTRLEMGHFLSICERE
KIQAEHKVDILILKVEDLEHEVAYLKEKLKKTEKESLYAKRQRKKDGYSS
TQHKHPTITIGVETSPARHPCTGTQTAIVICEQHIPEEKVTKEQVMDMRT
FADVTSTRIIADALCMVTGNPNQFLRSPTTGGSTVKDGTTSHCRIAGDFE
SGYISNVSGITWDKAASRIPTLGTTRTLKCPESPESGYGSSSSARNPAA
SSVSPLDTGTETASTSTGSSKHTDTVFLFPDPTGQRREVELGVEMDILEE
ISEIERVKHIEFDPNKQDQDIPMTSL-

Gene:

Limulus polyphemus unplaced genomic scaffold, Limulus_polyphemus-2.1.2
Scaffold1350 Sequence ID: NW_013666960.1

Hv3:

Limulus polyphemus uncharacterized LOC111087200
(LOC111087200), transcript variant X1, mRNA. XM_022393049

MRNFSMFFNSKEELMRNSEPLVWSLTGDESLDDDDSTRLCERIWVSVNGK
VFNAVIVTMVFEGLVVFSELLIDFEIVQDPHWKTIRNCSANVPALIFPS
SEAVSPNLRNTKDVLSYISIVILIIIFVFEIGCRLAVGRAKYLIQGIEICD
AAVVLVAFGLDIAFLTTPPSKKGAGKEAAVLIILLRLWRILQSVIDKT
RVEMGHFLSICEREKAQAEQKVDILILKVEDLEHEVAYLKEKLKKSEKES
LCAKRQRKKEGYSGIQKHPKITVGVETSPARHPCTGTQTARAICEGFIL
DEKATKRKVMIDITFAEITATRIIAKALCVASPDGQYVRFLATKDAVGI
SGTTLCCRIDGSFESGYGSNTSGMTLDKTTNCIPSVGIRRTVKCPESP
SGYGSSSSARNTVATSVSPLDIEMETTSVSTGSKQTDTVFLFPDSANQC
RKAERGVMEDILEELSEIERIKQVEFDPNKQDEEDIPMTSL-

Gene:

Limulus polyphemus unplaced genomic scaffold, Limulus_polyphemus-2.1.2
Scaffold1865 Sequence ID: NW_013667475.1

Figure S5. Sequence alignment of two putative *Oikopleura dioica* Hv channels with *Ciona intestinalis* Hv1

	10 20 30 40 50
CiintHv1	MEGDNCNKSR HKSHNMINPN YASVRCTQPL PSVIQLRSRN KMIGITEDPS
OidioHvL1	-----
OidioHvL2	-----

	60 70 80 90 100
CiintHv1	SDSEPVSNNQ PLLLTNLSYE VHTFNDNNNH ERPAPQEQST QNTMISMQSE
OidioHvL1	-----MS
OidioHvL2	-----MD

	110 120 130 140 150
CiintHv1	QKSDRFTASN LGMFQYMKFE IGEDGDDHEE EAILTNREKL RHILHSPKPIH
OidioHvL1	ENSSVVESTP ----- -FLEILKSDM TCWEKTSRVV HKLLHSHTTQ
OidioHvL2	NRISKFFSS- ----- ---DTEAYLE RTPVTISEKI AHFLHSSTCH

	160 170 180 190 200
CiintHv1	VAIIIVLVVLD SFLVVGELLI DLKVIIVPHG -----
OidioHvL1	AILLFLVLVD CAVIACEIVF DEKVKTHNDY CGANSTLCQE EIDNEQTKKW
OidioHvL2	LIVIVLVVLD CAFVLTELIF DGKLDTYAEY C---DPTPSC SEQSHKLHHW

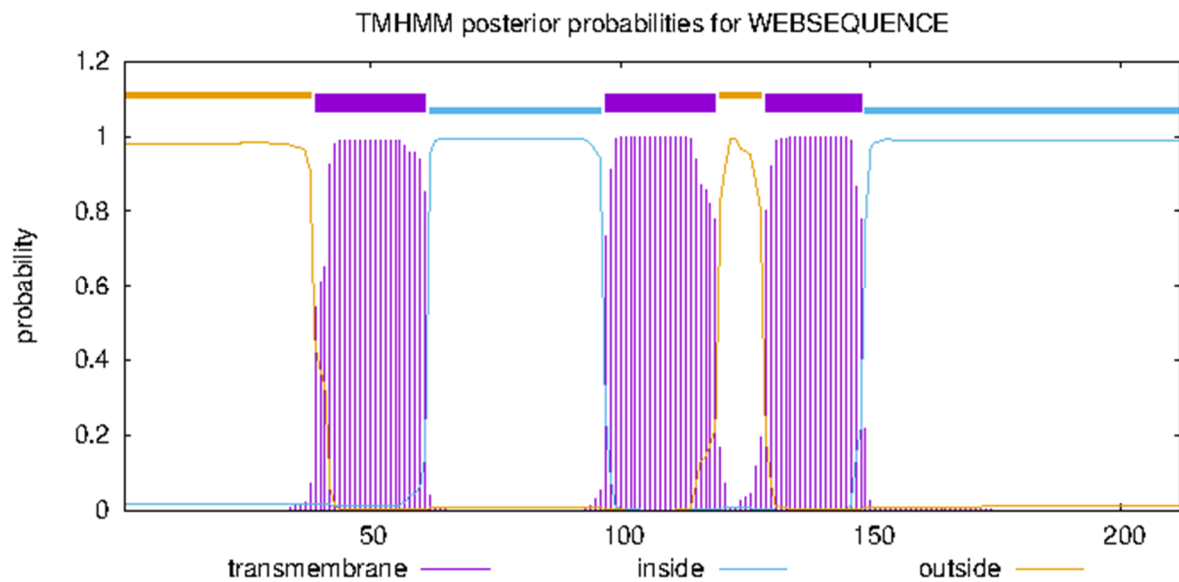
	210 220 230 240 250
CiintHv1	NPAPFILHGF SLSILSIFMV EIALKIIADH RHFIHHKVEV LDAVVVVISE
OidioHvL1	KKIYKALYYT SLTLLSVFV VEFILKIVFSA KKFLKSWVHI FDALIVISSW
OidioHvL2	EHVTHVIHIC SIIVLTIFMI EVILKVIYTR EHFFSHKIEI IDGVVVLVLSW

	260 270 280 290 300
CiintHv1	GVDIALIFVGES-EALAAIG LLV---ILRLVVFRIINGIIVTVKTKADDRVH
OidioHvL1	ILMLIMLNKDVKNGMIAEFL IAF-----FVIFLIHGMKEALEEANELLHE
OidioHvL2	ILDLIMLNP NLV-GKWAEFI IIF-----FFLFLINGMILSAKQAADKRVH
CiintVSP	VVTIFYTVLDEYVQETGADG LGRLVVVLARLLRVVVLARIFYSHQQMKASSRRT

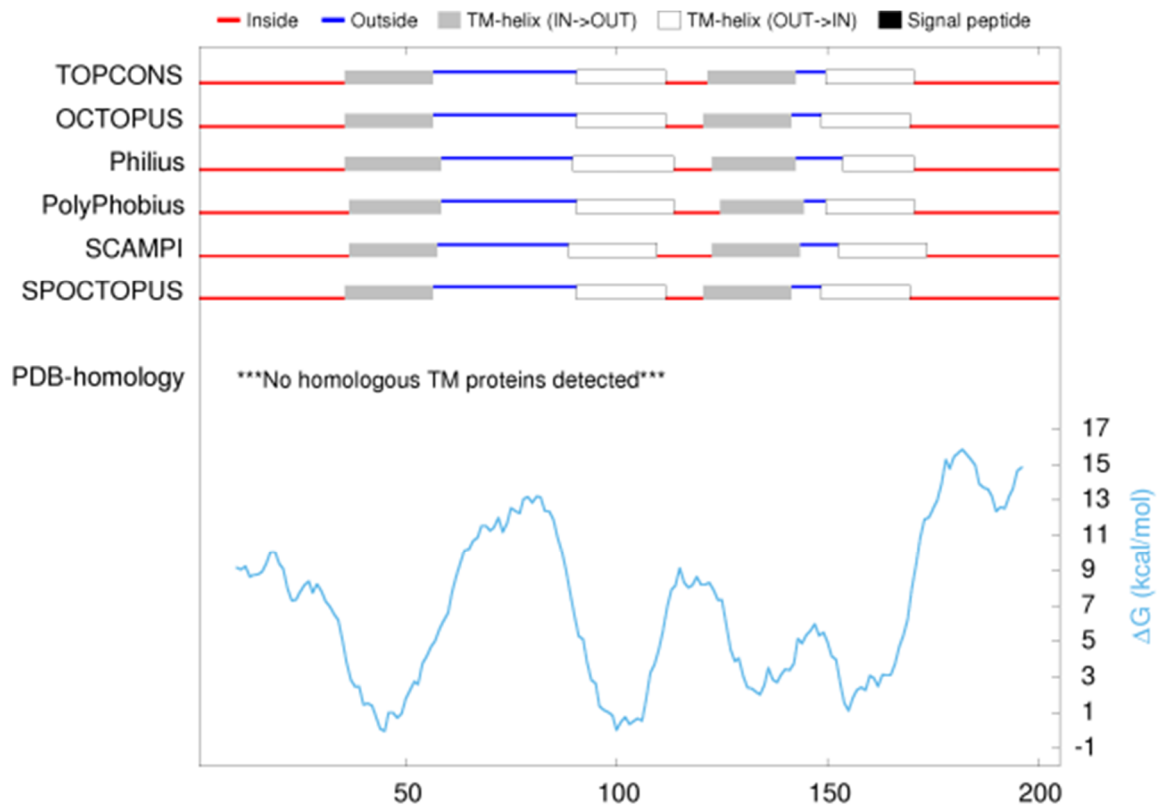
	260 270 280 290 300
CiintHv1	GVDIALIFV GES-EALAAI GLLVILRLWR VFRIIN--GI IVTVKTKADD
CiintVOSP	VVTIFYTVL DEYVQETGAD GLGRLVVLAR LLRVVRLARI FYSHQQMKAS
OidioHvL1	ILMLIMLNK DVKNGMIAEF -----LIAFR VIRLIH--GM KEALEEANEL
OidioHvL2	ILDLIMLNP NLV-GKWAEF -----IIIFR FLRLIN--GM ILSAKQAADK

	310 320 330 340 350
CiintHv1	EIKKKNSELE LQIHNLEEKL SQKEQDMSRL HEILRCNNID IPPTVPLTTS
OidioHvL1	NMEEEIHALK AENNNKKEEL LAVKDR-----
OidioHvL2	EQKRKVQELE KELVDLKKQY ETQNNQ-----

.....|.....|.....
360
CiintHv1 VQIHSTTTAS ADV-
OidioHvL1 -----
OidioHvL2 -----

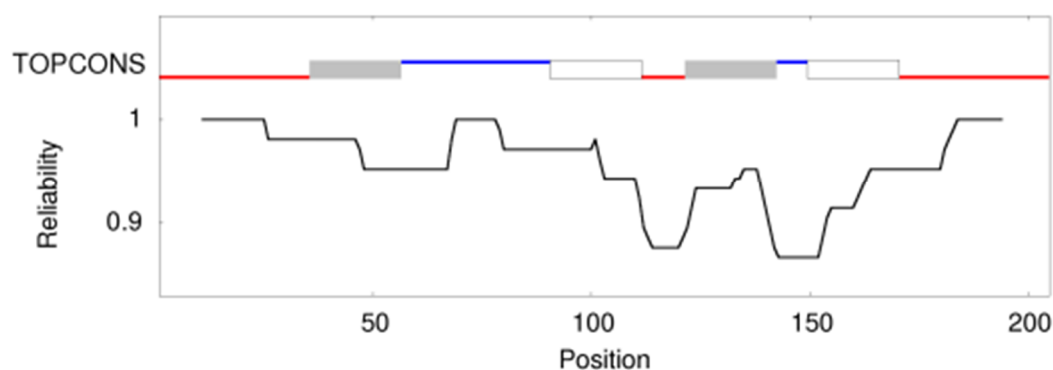


Transmembrane prediction using TMHMM of *Oikopleura dioica* sequences identified only three transmembrane spanning segments.



[High-resolution image](#)

Consensus prediction (TOPCONS):



[High-resolution image](#)

Predicted signal peptide and TM-helix positions (position starting from 1):

TOPCONS	TM1: 36-56, TM2: 91-111, TM3: 122-142, TM4: 150-170
OCTOPUS	TM1: 36-56, TM2: 91-111, TM3: 121-141, TM4: 149-169
Philius	TM1: 36-58, TM2: 90-113, TM3: 123-142, TM4: 154-170
PolyPhobius	TM1: 37-58, TM2: 91-113, TM3: 125-144, TM4: 150-170
SCAMPI	TM1: 37-57, TM2: 89-109, TM3: 123-143, TM4: 153-173
SPOCTOPUS	TM1: 36-56, TM2: 91-111, TM3: 121-141, TM4: 149-169
PDB-homology	***No homologous TM proteins detected***

Sequence and predicted topologies: (i: inside the membrane, o: outside of the membrane, M: membrane region, u: non-membrane region but location unknown)

Seq.	1	MDNRISKFFS	SDTEAYLERT	PVTISEKIAH	FLHSSTCHLI	VIVLVLVDC	41
TOPCONS		iiiiiiiiiii	iiiiiiiiiii	iiiiiiiiiii	iiiiiiMMMM	MMMMMMMMMM	
OCTOPUS		iiiiiiiiiii	iiiiiiiiiii	iiiiiiiiiii	iiiiiiMMMM	MMMMMMMMMM	
Philius		iiiiiiiiiii	iiiiiiiiiii	iiiiiiiiiii	iiiiiiMMMM	MMMMMMMMMM	
PolyPhobius		iiiiiiiiiii	iiiiiiiiiii	iiiiiiiiiii	iiiiiiMMMM	MMMMMMMMMM	
SCAMPI		iiiiiiiiiii	iiiiiiiiiii	iiiiiiiiiii	iiiiiiMMMM	MMMMMMMMMM	
SPOCTOPUS		iiiiiiiiiii	iiiiiiiiiii	iiiiiiiiiii	iiiiiiMMMM	MMMMMMMMMM	
PDB-homology							
Seq.	51	FVLTELIFDG	KLDTYAEYCD	PTPSCSEQSH	KLHHWEHVTH	VIHICSIIVL	91
TOPCONS		MMMMMMoooo	oooooooooooo	oooooooooooo	oooooooooooo	MMMMMMMMMM	
OCTOPUS		MMMMMMoooo	oooooooooooo	oooooooooooo	oooooooooooo	MMMMMMMMMM	
Philius		MMMMMMMMMo	oooooooooooo	oooooooooooo	oooooooooooo	MMMMMMMMMM	
PolyPhobius		MMMMMMMMMo	oooooooooooo	oooooooooooo	oooooooooooo	MMMMMMMMMM	
SCAMPI		MMMMMMMMMo	oooooooooooo	oooooooooooo	oooooooooooo	MMMMMMMMMM	
SPOCTOPUS		MMMMMMoooo	oooooooooooo	oooooooooooo	oooooooooooo	MMMMMMMMMM	
PDB-homology							
Seq.	101	TIFMIEVILK	VIYTREHFFS	HKIEMIDGVV	VLLSWILDLI	MLNPNLVGKW	141
TOPCONS		MMMMMMMMMM	Miiiiiiiiii	iMMMMMMMMM	MMMMMMMMMM	MMooooooooM	
OCTOPUS		MMMMMMMMMM	Miiiiiiiiii	MMMMMMMMMM	MMMMMMMMMM	MoooooooooMM	
Philius		MMMMMMMMMM	MMiiiiiiiiii	iMMMMMMMMM	MMMMMMMMMM	MMoooooooooo	
PolyPhobius		MMMMMMMMMM	MMiiiiiiiiii	iiiiiiMMMMM	MMMMMMMMMM	MMMMMooooooM	
SCAMPI		MMMMMMMMMM	iiiiiiiiiii	iMMMMMMMMM	MMMMMMMMMM	MMMoooooooo	

amHv1	TRRSSMDDQL	PADELKEMGQ	PGTTAAVMAS	TVCLTEDDTE	CPANKNHREK
kvHv1	LHHAVHTVHT	SKSARDAEG-	-----	-----	---HGTWQSK
kvHv2	RTASATGTKK	SKIRRIVP--	-----	-----HIL	DEISHEATHF
ehHv1	EAAGASEVTS	PKTRYGARAF	GKPLKAQLLS	ARAEVEKAHA	EHGADSWQRR
ehHv2	QRRGAKWVSA	DSEARALS--	-----	-----S	RRGSYAWQTK
egHv1	DDTFVGAPAP	SVEATKVEDG	CP-----	--IDCHKLAS	PSKAPTLRQK

	160	170	180	190	200
hsHv1	LRKLFSSHRF	QVIIICLVVL	DALLVLAELI	ID-----	-----
ciHv1	LRHILHSPKI	HVAIIVLVVL	DSFLVVGELL	ID-----	-----
npHv1	LRKLLHSHKF	QISVITLVII	DCLLVITELL	ID-----	-----
etHv1	AKLLLESPPK	HIVVLTLVII	ELTMVVAELM	ID-----	-----
spHv1	LHEIMETQKF	HIAILVLVVI	DCILVIVELV	IDFEVLSANN	HVPEAGCAHP
acHv1	LDDVIHSQKF	MVFIIIVLVVL	DCLMVIAELL	FD-----	-----
acHv2	LAAFLKTNLV	QYSIIALVIL	DCLIIVMELL	IDMNIIVFPE	DDPHHPPGEG
cgHv4	MRKVFHNPIT	HLIIIAFIVL	DIAILLVVLL	VDINVIQVRA	ETEED-----
aoHv1	ARDFLSSRRG	HYLVLLLVSV	DVACTFADFL	IELHVCELT-	-----
amHv1	LNELLHGDKI	QYAIVVLVII	DIIIVIAELV	ID-----	-----
kvHv1	LNEALNSSKV	HTILNVLLIC	DLMTVIIIGML	LEQYYSDSQV	QGLTEAFKDC
kvHv2	RRLLLHSPKV	HFTILVLLIA	DGLICLTCGV	LEAHYLGKKS	DDCQNYVNKC
ehHv1	CLHLLHSHRV	QLFFILLLLV	DMLIVITEIC	LDLEYPSCLR	AKRDTVSCCA
ehHv2	LLAFLHSPRL	QALLTLLLV	DVIAVFGELF	IDAEFPSCMY	VLRDAIPCCD
egHv1	VHHFLSCRPF	KIFMMALLLL	DLILVMASVL	LETGSLQVSL	DECERSIHDC

	210	220	230	240	250
hsHv1	-----	-----	-----	-----	-----
ciHv1	-----	-----	-----	-----	-----
npHv1	-----	-----	-----	-----	-----
etHv1	-----	-----	-----	-----	-----
spHv1	QE-----	-----	-----	-----	-----
acHv1	-----	-----	-----	-----	-----
acHv2	SSHHPVAFAS	RSSNLTGDNH	TVYPAHHIH-	-----	THHDNSSNLT
cgHv4	-----	-----	-----	-----	-----
aoHv1	-----	-----	-----	-----	-----
amHv1	-----	-----	-----	-----	-----
kvHv1	LEKRTFCP--	-----	-----	-----	-----
kvHv2	--100aa--	-----	-----	-----	-----
ehHv1	AGEEGEHHTL	RYLAEEHGG	HHSLCG----	-----	-----KG
ehHv2	SGCIGAGDYS	AAAAADAIQT	ILSLGKSVQG	DLHLEHDETR	AEICAGQGHS
egHv1	EHICSNSTDF	TATATNYCTN	THG-----	-----	-----

	260	270	280	290	300
hsHv1	-----L	KIIQPDKNY	AAMVFHYMSI	TILVFFMMEI	IFKLFVFRL-
ciHv1	-----L	KVIIIVPHGNP	APEILHGFSL	SILSIFMVEI	ALKIIADHR-
npHv1	-----LE	MH---EEESL	AQHVLHYCSI	TILSIFIVEI	FLKLYAFRQ-
etHv1	-----AS	GVEKSEALET	VEIALKFISI	SILSIFVIEN	LFTMYVLR-
spHv1	---EGQC	ETDKEEKEVT	AANVLHYISI	GILSIFMIEL	LKIPVFRM-
acHv1	-----LE	IVKLGEHHY	IPKIFHYGSL	GILSLFLIEI	GLRIFVLR-
acHv2	MYGNDSAHAA	PVHHHTNKEK	AEHVLHALSL	TILSIFMVEV	CVKIYVEGK-
cgHv4	-----	---EEHLREE	LEDGLHYAAL	TIISLFVVEV	VIKIYIEGK-
aoHv1	-----KH	GSHVAIGWGV	TQKVLAIIVGL	VFSCLFMLEL	MVTVFSFGK-
amHv1	-----L	RAGSEHHDNS	ASHVLHYISI	AILSVFMIEL	LLKIYAMGF-
kvHv1	-----DPSHL	AHYGNHDLHE	WAERMEYASL	AILLIFLLEN	MLLVLANGC-
kvHv2	----GECAGH	PHFGDHTLHD	IEIILAYISV	GILSLFLVEQ	VLLIVDLGK-
ehHv1	TVEGPHGVGC	DEHAHPAVHT	AHAVLTWASV	AILSLFEIEL	LTLAASGLR
ehHv2	HLDSTGRIGC	DSHKHDLAHK	FHKFLFRVSL	TVLVVFELEL	LGLIASLDR-
egHv1	----QTCHYN	HPSLATALHL	AEKVLAYISI	GLLSFFLLER	LVGIICEGL-


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          310          320          330          340          350
hsHv1  EFFHHKFEIL DAVVVVVSFI LDIVLLFQ-- -EHQFEALGL LILLFLWFWA
ciHv1  HFIHHKVEVL DAVVVVISFG VDIALIFVGE -SEALAAIGL LVILFLWFWF
npHv1  EFFKHRLEVF DAIIVIVSFA LDIAFRNS-- -RDALSGVGL IILFLWFWA
etHv1  EFFHKCLEVF DSIVIFTSLV LEVIFLNH-- -HDAATGVGI LIGFLWFWIV
spHv1  EFFRSKLEVF DGIIIVISFV LDVVSLIY-- -EEQFAVLQL LVLLFLWFWIV
acHv1  DFFKHKLELF DAVVVIVSFI LDIVFRDN-- -EDAATGVGL LIILFLWFWT
acHv2  HMLKQKAEVF DAIVVIVSFT LDITFSFVSV SKAASEAAGL MVILFLWFWT
cgHv4  HFFSDKWEVF DAIVIFVTFG LDLALAFSPV SSAVRDSVAL LVFLFLWFWV
aoHv1  GYFSSKFHVF DALVIIVAFG VDVALHGI-- ---EEELGSL IVVLFLWFWF
amHv1  TFFKHKMEVF DGFVIIVSFA LDIAFSNE-- -QGGVDGVSL IVLLFLWFWT
kvHv1  RFFANPFHIL DIVVVVSVSG FELQGILG-- -EGHDAGIGL VVFARTWFFI
kvHv2  -EYLKPMFIL DFVVIVSSLL IEILVVNM-- -----TIGGL LVLAFTWFFA
ehHv1  DFFSNVYYVL DIVIVSASLV LECVFYNT-- -AGLSDLIGL VMFLFLWFL
ehHv2  AFFRNPLYVL DLIVITVSLG LETVFRVFS- -MPEQDLAMA LIIVFLWFEV
egHv1  KFFSCAFKVF DFVVIIVSLV LEILFLGQ-- -----PGVGL IAIGFTWFEV

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          360          370          380          390          400
hsHv1  RIINGIIISV KTRSERQLLR LKQMNVLAA KIQHLEFS-C SEKEQEIERL
ciHv1  RIINGIIIVTV KTKADDRVHE IKKKNSELEL QIHNLEEK-L SQKEQDMSRL
npHv1  RVLNGVVLVS KMQAQEHQLER EKQRGMALEG ELSRCRQV-C AAQQRELDVL
etHv1  RVINGIAVTV AAQSEKKLEE EKDLREEIEM ELNKCVD-RS KKQQCYILFL
spHv1  RVVNGVILSV ETQAKKKIEQ QKHLRAEVEH EMEKFRRY-C AAQEKEIEVL
acHv1  RIVNGIVLSV QKQAEKKIER EKHLREECEQ ELAKFREY-C MAQAEIEVL
acHv2  RIINGVIMSV KLDANKKMEV HKKARRKLER ENKRLQAK-I ERLEREVATL
cgHv4  KIMTEIQYCV RREVPEAIDK EKLAQEKADW LARRQGHT-K V-----
aoHv1  KIIEELQSAN EDTLEEYEHE IERLRQENTY LRQRLNVS-L SNADPMD---
amHv1  RIVNGIILSV QMRAEKKVQA VMKENAELQK ELEQLKSK-C AQLESELTTL
kvHv1  RLGHGIHEMH EEHEAEDHGE HRVSDAAGSL EAPLQKGS-F EQHAKGTSGV
kvHv2  RVGHGVFEAK EMIEEMIGED DDTVKNMMDA WKELTPERWE EILHSGSAEI
ehHv1  RIGHAMFAST ERASSTDNLK EVVRELRAEL DLLSEWAE-- ---EEERASA
ehHv2  RIGHGIFAST HSVAKEKSDK LHAEIRALEE EYTRALNQAA SLATTTRPTR
egHv1  RIGHGFHEAE ELTHPVDEFV KEHKAALFAL HRRLLGVPGL YGTEGAVLAE

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          410          420          430          440          450
hsHv1  NKLLRQHGLL GEVN----- - - - - -
ciHv1  HEILRCNNID IPPTVPLTTS VQIHSTTTAS ADV----- - - - - -
npHv1  RAVLQHHGLD QQLPDGNR-- - - - - -VDVV ADVEKR---- - - - - -
etHv1  QKFIQSNGLE IPPHSSCPSR - - - - - ---NSSEGH- - - - -
spHv1  RNTLNQHGIQ IDDDYVAKKP QFSLNQLNVV VEMNSADKHD TGEDEGE GEE
acHv1  QGLLHKHNIE FTTNKITRPE --SRVQVDVV AEVNSMTAVA ETDIPLSPSQ
acHv2  KQKMATSSTP QMSFEMQSGL SVERSPSGEM RENSAQV--- - - - - -
amHv1  KQS----- - - - - -
kvHv1  HHARSQASSN REGREGCCVQ - - - - -
kvHv2  LRESGVTPAE IKLGEALGNS PAVAMRALAF ARGWKQKLDK KKAKRLSGSN
ehHv1  RAPPDDPGVD DIG----- - - - - -
ehHv2  LASAPSSTSG SPSATRPPPF RGRSASEASA ATHDLQGAGG EKLADGVAAA
egHv1  NAAAVREALA LLEQDGFGG L LGIADAABA GHRQHQEKEQ LHYWKLQ---

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	460	470	480	490	500
spHv1	GGGDGNTRRH	EKEREALGEH	TITLTTDDNV	NTIQADYHPQ	DTTFT-----
acHv1	PGEQEISLSS	GDNVTDVAVV	V-----	-----	-----
kvHv2	PKRQMPGASL	QTTATVGKGH	SEH-----	-----	-----
ehHv2	LSQRSNTPTS	PVGAPAMRRP	PAAAPLGAAH	RALQLGPSSS	AARTGMPGVG

	510	520	530	540	
ehHv2	TRMGAGEAAA	AERQAPPAAE	PEPAEGAAAA	ESVELELDAL	DMST-

Hv sequences were used from *Homo sapiens* (hsHv1, NM_001040107, Ramsey et al. 2006), *Ciona intestinalis* (ciHv1, NM_001078469, Sasaki et al. 2006), *Nicoletia phytophila* (npHv1, KT780722, Chaves et al. 2016), *Extatosoma tiaratum* (etHv1, GAWG01024136, Chaves et al. 2022), *Strongylocentrotus purpuratus* (spHv1, XM_030990962, Sakata et al. 2016), *Aplysia californica* (acHv1 & acHv2, XM_005100609 & XM_005093050, Chaves et al. 2023a), *Crassostrea gigas* (cgHv1, XM_011429833, Chaves et al. 2023b), *Aspergillus oryzae* (aoHv1, XM_001825513, Zhao & Tombola 2021), *Acropora millepora* (amHv1, MZ029046, Rangel-Yescas et al. 2021), *Karlodinium veneficum* (kvHv1 & kvHv2, JN255155 & HBOS01067516, Smith et al. 2011), *Emiliana huxleyi* (ehHv1 & ehHv2, HBNU01018021 & GIZZ01010784, Taylor et al. 2011), *Euglena gracilis* (egHv1, GDJR01054876). Transmembrane regions are shown in yellow, the totally conserved tryptophan residue within S4 in red, selectivity filter residues in light (D) or dark (E)purple, voltage-sensor positively charged residues in dark (R) or light (K)blue.