(a)

Tom7

```
CLUSTAL FORMAT: MUSCLE (3.7) multiple sequence alignment

                              CYTOSOL (out)                      transmembrane      IMS (in)

EctsiTom7        ---------MGEKIMRRRPRRKSAPLLPK-----------VLAVAKPIMRWGIMPAVLLMGM-RSE----PNPTLLEV--LYPL---  Stramenopiles
PhatrTom7        -MAVPRRRQSGGLVKFGKLSSRILSMLDV---------NYIFAKTRTLLLYGFAPAVVLIGL-RTE----PRPSPWDLVNIWE----  Stramenopiles
ChlreTom7        ------MNAITGPNGSNDLAKKLEQAVDV-----------IVTYGKPIVHWGFIPAVILVGMLTTK----PRPTLGQL--LWLG---  Plantae
ArathTom7-1      MESTISLKVNKGKGKGSKGASSSDDKSKF--DVVKEWTNWSLKKAKVVTHYGFIPLVIFVGM-NSD----PKPHLFQL--LSPV---  Plantae
SoltuTom7-1      -----MLKPKGKNTKKAAAADEDDGAVAVVGKFVKEWGTWTAKKAKVITHYGFIPLVIIIGM-NSE----PKPSLSQL--LSPV---  Plantae
VitviTom7        MASRVSVKGKGKSIKGSKDGSEGHSTAKC----LKDWSNWALKKAKVITHYGFIPMVIIIGM-NSE----PKPQLYQL--LSPV---  Plantae
RiccoTom7-1      MASRVSLKSKGKSSGGAKGSKAMEEKSTI--QCLKEWSTWTLKKAKVITHYGFIPLVVIIGM-NSE----PKPQLYQL--LTPV---  Plantae
SacceTom7        ----------MSFLPSFILSDESKERISK-----------ILTLTHNVAHYGWIPFVLYLGWAHTS----NRPNFLNL--LSPLPSV  Opisthokonts
NeucrTom7        ---------------MFALSEESKERIGK-----------LIDISRVVVHYGYLPLILYLGYTRSV----PRPSIIRL--LSPLS--  Opisthokonts
ApimeTom7        ----------------MAMCPRTKQKVAI-----------ILDVSKAIFHWGFIPAILFLGFRKGADPGMPQLSIINL--LWQ----  Opisthokonts
HomsaTom7        ---------------MVKLSKEAKQRLQQ-----------LFKGSQFAIRWGFIPLVIYLGFKRGADPGMPEPTVLSL--LWG----  Opisthokonts
                                                                .    :*  * :: :*                :  :
```

(b)

Tom40

```
CLUSTAL FORMAT: MUSCLE (3.7) multiple sequence alignment

EctsiTom40      PQFPSGH------------YQGTLTVV---------GESE-T---MVRASMDAD-----CNVSMDAHAPLGMPGL-------------AGKLTVHQGKN------------DVIQGTALY
PhatrTom40      SMLPDGRTST---------YSFVTQVA----------DEA-G---FMMARWDPGQASVNGRVHRALLGGLAMGKL-------------QIGVSAE-GQN------------DTLLGEVDF
ThapsTom40      SMLPDGRTSS---------YGFTTQMN----------DEE-G---FCMARVDPERGTMDGRIHKALFGGVAMAKL-------------QVGTSSE-GSN------------DQLLGEIDL
PhyinTom40      PMIPGGL------------YQFGANVVMGDP-----MDPS-T---FLMSKITPD-GYLDARWNQKLSDNWKM-RV-------------KAQLKNE-EHG------------SQALADFDY
PhysoTom40      PMIPGGL------------YQFGANVVMGDP-----MDPS-T---FLMSKITPD-GYLDARWNQRLSGNWKM-RV-------------KSQLKNE-EHG------------SQALADFDY
PhyraTom40      PMIPGGL------------YQFGANVVMGDP-----MDPS-T---FLMSKITPD-GYLDARWNQRLSAKWKM-RV-------------KSQLKNE-EHG------------SQALADFDY
CyameTom40      QTTPG--------------YALSVNYI----------TNT-L---IAVSRMDMT-GRFNGRLFYTHTPRLIS-KLLVSRQPAEDPAAAAAMLAAA-TGGAAIQPPPPTSATTTVMYDLDY
ChlreTom40      MELQTGGRQ--IIKTPVGTYEFGATTV---------SESQNL---VLMGRLASD-GRLSGRIKYDVANWLGF-KV-------------QAQLANA-ANQ------------SQVMLDTDV
MicpuTom40      IEVPAQGNQ--IIKIPNATYEFGANVV----------DQK-Y---MLVGRALTD-GRLSGRLKYDFNDAISA----------------KIQTSKE-PGF------------SQVMMDLDY
OstluTom40      VEVPAQGQ---IVKLPTSTYEFGANVV----------DQD-Y---MLVGRILTD-GRVSGRVKYDLSDWLSL----------------KLQSTKE-PGF------------SQVMFDADF
ArathTom_2      TEVPNPTPSSEIIKIPTANYDFGAGFI----------DPK-L---YLIGRITTD-GRLNARAKFDLTDNFSV-KA-------------NALLTDE-EDK------------SQGHLVIDY
ArathTom_1      TEVPAQSPET-TIKIPTAHYEFGANYY----------DPK-L---LLIGRVMTD-GRLNARLKADLTDKLVV-KA-------------NALITNE-EHM------------SQAMFNFDY
PhypaTom40      VEVPSQGAQ--IIKVPAAHYEFGANLI----------DQRMM---MLIGRILTD-GRMSARIKYDFTDRFSV-KV-------------NAQLTNE-PHF------------SQGMFHFDY
CioinTom40      EGSS---------------YRFGSTYVGTKQ-----PSPT-EAYPVMIGEMSNE-GNLQAQFIHQVTSRFKA----------------KCIAQTLGSKL------------QSVQVGGDV
HydmaTom40      PQLTS--------------YHFGATYVGGSQ-----SNPA-EATPVILGDIDNS-GSLSAQIIHQFNKRIKG----------------KCVVQTQQKEF------------AMVQADVDY
HomsaTom40      IGESN--------------YHFGVTYVGTKQ-----LSPT-EAFPVLVGDMDNS-GSLNAQVIHQLGPGLRS----------------KMAIQTQQSKF------------VNWQVDGEY
SacceTom40      QALPK--------------YAFSALFA----------NDN-L---FAQGNIDND-LSVSGRLNYGWDKKNIS----------------KVNLQISDGQP------------TMCQLEQDY
NeucrTom40      RLNP---------------YAFAALYG--------------TNQIFAQGNLDNE-GALSTRFNYRWGDRTIT----------------KTQFSIG-GGQ------------DMAQFEHEH
DicdiTom40      PNENSRTPK----------YSNQNVYS---------KDST-----LLYGKIDSE-RRLFGRFDQGFFNNSIRVSL-------------TNMMDKSFKNN------------LAGELEFKL
PlafaTom40      TLREVGYL-----------YQFGANFT---N-----LDNS-L---LMISRINID-GSVNGRFCKKINNNIDC-KL-------------NFNTYAKNDTR------------NMYEMSLEV
ToxgoTom40      QSKEGGCS-----------YSFGPTLVIGEPDEAAQQEGQ-MPNFFGMARMNSD-GFLQARFIKAISKTFDI-KFNS-----------NSSISEDAKDK------------SMYEVSFDK
PermaTom40      SLSPNQYL-----------YQFGPTYA---------TDDGRT---VMVGRLGMD-GGVNARLMKKLFKGTDL-KI-------------NANSNLHDPQR------------NMYEFTVDQ
                                   *                          .           .
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```
EctsiTom40      HGDTCSGQISLGT------G----PTEISYNQAVTPHLSMGGQGQFSS----AQQAVGLLYGFKY--NTPSWA--------------VLGRLIG----------GGANVVTAQYLRRVVP
PhatrTom40      GGHSWMGNLRYGS---MG-G--GVVLGCNYMQALTPALHMGGDGMYVG----ANGSFQTNYALKY--TM-PALTGEEDLPTTTPAKPATGMETAGSSTLCAQFKPGQGMASLDYKRVVTP
ThapsTom40      GAQTWTANLKYGS---MG-G--GNVFGCNYFQSVTPRLAMGGEGMYIG----ANGNMMSSYTAKY--SFNPSN-------------SGDGD-------------ERQGMLSLNYKRAITP
PhyinTom40      TGEDFTWNMKVSN----G-P----LLGVSYLQSVTQNLALGGEAYYHG----KHRKVISAYAGKW--TDRDWV--------------GMATY------------GAMGTLQLAYLRKVGH
PhysoTom40      VGEDFTWNMKISN----G-P----LLGVSYLQSVTQNLALGGEAYYHG----KHRKVISAYAGKW--SERDWV--------------GMATY------------GAMGTFQLAYLRKVGH
PhyraTom40      AGDDFTWNMKVSN----G-P----LFGVSYLQSVTQNLALGGEAYYHG----KHRKVISAYAGKW--TDRDWV--------------GMATY------------GAMGTLQLAYLRKVGH
CyameTom40      RGSDYSANLKLGT----G-G----VISLAYMQSIVPSFSMGGEGFFQL----RNKFSALTAAARF--LTTDGI--------------FSATV------------ASFGPVVASYVHRVNP
ChlreTom40      KGGDWNAQLKLGA----P-G----FVGLNYFQSLTPKLSAGGEFFYLP----SNPKSGVGLALRH--QGDKHV--------------ATCQV------------ATTGLMNMQYTHKVTE
MicpuTom40      KGLDCQAQLKLGN----G-Q----FYGVNYLQSVSDALALGGEGFYLG----GQRKSGVGFAARY--NDDKTV--------------ATGQV------------ATTGLVSLTYTTKVSE
OstluTom40      KGLDYQAQLKYGS----G-K----FYGVNYLQSVTPTLSLGGEGFYLG----TQGKSGVGFAARY--ADDKTV--------------ATGQI------------ATTGLLSLTYCTKVSE
ArathTom_2      KGSDYRTQLQLGN----N-S----VYAANYIQHVTPHLSLGGEAFWLG----QQLMSGVGYAARY--ETDKTV--------------ASGQI------------ASTGVAVMNYVHKVSE
ArathTom_1      MGSDYRAQLQLGQ----S-A----LIGATYIQSVTNHLSLGGEIFWAG----VPRKSGIGYAARY--ETDKMV--------------ASGQV------------ASTGAVVMNYVQKISD
PhypaTom40      RGKDYQTQLQLGN----N-A----FYGFNYIQSVTPTVALGGEVFWLG----HQRKSGIGFAGRY--NTDKVV--------------ATGQF------------ASTGIVSLTYVQRVSD
CioinTom40      VFNDSTLSVVCADPDLLN-G--TGMLIVHYLQAITPKLSIGSELLYQR--GAARQQAIASIAGRY--KTENWQ--------------AAGTI-------------AAGGMHASFYRKANE
HydmaTom40      RGDDFTTTCTLGNIDILN-E--SGIIVAHYLQRVTDNIDIGTELLYHY--GQGQQSAILSLAGRY--SADKWV--------------AAAQI-------------NAGGWHASYYRKGND
HomsaTom40      RGSDFTAAVTLGNPDVLV-G--SGILVAHYLQSITPCLALGGELVYHR--RPGEEGTVMSLAGKY--TLNNWL--------------ATVTL-------------GQAGMHATYYHKASD
SacceTom40      QASDFSVNVKTLNPSFSEKGEFTGVAVASFLQSVTPQLALGLETLYSRTDGSAPGDAGVSYLTRYVSKKQDWI--------------FSGQL------------QANGALIASLWRKVAP
NeucrTom40      LGDDFSASLKAINPSFLD-GGLTGIFVGDYLQAVTPRLGLGLQAVWQRQGLTQGPDTAISYFARY--KAGDWV--------------ASAQL------------QAQGALNTSFWKKLTD
DicdiTom40      PFMNFCLKADTEN-----------QRGFSFLTSISKKLAIGYENSYLF--NHSQSIKQIQFFVNN--PLSTWS----------------LVV------------GNTAQIGSSYVYRQK-
PlafaTom40      NKPLYTYNFKSIW----Q-G--AWIFNTSYTQLLTKKLQAGVDLTYIA----SNCASIGSFGLRY--NHKNNV-LTMQIVRQPNFKSPEFML------------NQTHLYKIQYAKKISD
ToxgoTom40      MGSDWAANLKLAW----Q-G--TWILNGLFSQVITPKLQLGGELTWVA----ATGISMGSVGARY--GFNENNTVTCQIGVGPDFSSPMGFA------------NDVYSTKAQYVRKVTD
PermaTom40      QGEDWAASAKLAY----Q-G--TWISNVSFAQEVTNNLSLGGELTHVA----VNGVSIGGLGARY-----VWGPNYLSFALGRQPDFKQGPQ------------ANVHSAKMQYVRKVSD
                                             :   :   .  * :                     .

EctsiTom40      GRVTLGAEYQ---------A---------QLGAGSQMMVGAEFQLKQSK--MSASVDSNG KVDSTLELKCGTFPTLPVTLTISSSLDHSEDKQTFGLALTCGQ-----------------
PhatrTom40      NRVTLASSLEF--------S---------PLSLESQLLVAAEFKLSRST--LNLCVDGSG HLQSVLEAKLGMGQGSP-TINFSADMDHAKQQMRFGYGIKIEG-----------------
ThapsTom40      SRVNIGASLEC--------S---------PATLESQVMVGAEFNLTRSK--MNVCVDGTG RIQSTLEAKLGREQGSP-SLNFAAELDHGKSLMRFGYGLNIG-----------------
PhyinTom40      -RIRYGSELVY--------N---------HASGEAQTTCGVEMDLGQTR--FVSSVDSTF RVATSIESRVLPNF----VLTLSAEGFPLKDDFKFGYGAQLSF-----------------
PhysoTom40      -RIRYGSELVY--------N---------HASGEAQTTCGVEMDLGQTR--FVSSVDSTF RVATSIESRVLPNF----ALTLSAEGFPLKDDFKFGYGAQLSF-----------------
PhyraTom40      -RIRYGSELVY--------N---------HASGEAQTTCGVEMDLGQTR--FVSSVDSTF RVATSIESRVLPNF----VLTLSAEGFPLKDDFKFGYGAQLSF-----------------
CyameTom40      -RVSLAAELFW--------D***-------------------------------------------------------------------------------------------
ChlreTom40      -KVTLAADFMW--------H---------LLSRDVTATVGYDVVLRQCR--IRGKADTNG VITTLLEERFSPGI----NFVLSAEMDHWQSNYKFGFGIVAGE-----------------
MicpuTom40      -KAMLASDFMW--------N---------WNARQAQASVGYDYILRQSR--LRGRIDNTG VVSAFLEERLNAGF----TLTFSAEIDHANKNHKFGFGMTVGE-----------------
OstluTom40      -KAMLASDFLW--------N---------WNQRSAQASVGYDYILRQCR--IRGRIDNHG VVSTYLEERLNVGL----NLILSAEVDHFNKNHKFGFGMTVGE-----------------
ArathTom_2      -KLSFATDFIY--------N---------YLSRDVTASVGYDLITRQSR--LRGKVDSNG VVAAYLEEQLPIGL----RFLLSAEVDHVKKDYKFGFGVNAF-----------------
ArathTom_1      -KVSLATDFMY--------N---------YFSRDVTASVGYDYMLRQAR--VRGKIDSNG VASALLEERLSMGL----NFLLSAELDHKKKDYKFGFGLTVG-----------------
PhypaTom40      -KVSLASDFLY--------N---------WNSKEATTSVGYDYLLRQCR--LRGRLDTNG CIAAYLEERLNLGV----NFLLSAEIDHWKKDYKFGFGMTVGE-----------------
CioinTom40      -NVQVGVELEA--------S---------LKNKESVTTFAYQMDLPKMNLLFKGMLTSEW TIGSALEKRLQPLPI---TLNLTGTYNIKKDKVAVGIGAVLG-----------------
HydmaTom40      -NVQVGVDYEY--------N---------SRMQDSNVSLGYQIDIPKANVTFRGMVDTNW AVGGLFEKKLYPLPF---SFILSGKLDHLKNQSRFGFGLQIG-----------------
HomsaTom40      -QLQVGVEFEA--------S---------TRMQDTSVSFGYQLDLPKANLLFKGSVDSNW IVGATLEKKLPPLPL---TLALGAFLNHRKNKFQCGFGLTIG-----------------
SacceTom40      -NVEAGIETTLQAGMVPITDPLMGTPIGIQPTVEGSTTIGAKYEYRQSV--YRGTLDSNG KVACFLERKVLPTL----SVLFCGEIDHFKNDTKIGCGLQFETAGNQELLMLQQGLDADG
NeucrTom40      -RVQAGVDMTL--------SVAPSQSMMGGLTKEGITTFGAKYDFRMST--FRAQIDSKG KLSCLLEKRLGAAPV---TLTFAADVDHVTQQAKLGMSVSIEASDVDLQEQQEGAQSLNI
DicdiTom40      -NLHIGTDLVM--------G------ISQEGKFMSEYSFGVRYAFQQSL--VKFRADSHG SIFGSYDQMINSFT----KLNLSGSLNYFAQDYKFGLGLTFQK-----------------
PlafaTom40      -RLSLGTELEI--------T---------PQTKESAMRLGWDYSFRHAK--VQGSIDTSG KISVFTQDYSGFG--------VSGYIDYLNNDYKFGFMMHISPSQEQPQ------TAA--
ToxgoTom40      -RLSMGTELEF--------T---------HPDMSSAMRVGWQYLFRQAR--VQGLVDTAG RVSMFAQDYNGFG--------LSGMIDYWHGDYKFGFQMNVVPPPPQAE----QPPPM--
PermaTom40      -RLAIGSEFEY--------S---------QPEQESQLRLGYEYTFRHAR--VQGLLDTCG KVSCFVQDFMGFG--------ISGMVDFVKGDYRFGFMMHMVPQPEDAAAAGGAPTSA--
                 .   . .                                                                                  PoxGxxΦxΦ
```

(c)

Tom22

CLUSTAL FORMAT: MUSCLE (3.7) multiple sequence alignment

```
                                                                                CYTOSOL (out)                                                                                transmembrane
EctsiTom22      ---------------------------------------------MAK--KLTFNDEKRDNGPGVLQ--TLVVTGRSLGVA-----GFGWAQWAAKKTGRTGWVLLTTAVVTLVPLVFE
PhatrTom22      ---------------------------------------------MTKEP--KSSGGLKGLLQRTGKFFYTTGVYARDKGSTA---------FKWGYQVGGQVAFAVATTSMVMLMPLLFE
PhyinTom22      -------------------------------MSAIGALRELEKDKKGP--KNAGIKELFLNLPSRIRQSGPVKGGINFAVK------------SWKTSGRWLWVLSTTLLVTLVPLSIE
ArathTom22_1    ---------------------------------------------MAP--KKIGAGKGDSSILAKISNYDIVSQGRRAACD-----AVYVSKKLLKSTGKAAWIAGTTFLILAVPLILE
ArathTom22_2    ---------------------------------------------MAAKRIGAGKSGGGDPNILARISNSEIVSQGRRAAGD-----AVEVSKKLLRSTGKAAWIAGTTFLILVVPLIIE
OstluTom22      ---------------------------------------------MEIT--PDYGAEEAKSAKPVRLGWADASRLTRKLAVH----------------TGKAAWTFGTSFLVLIVPLIVQ
MicpuTom22      ---------------------------------------------MEIT--P--APDATCNSQMSSLG--DSARVGKKLIWH----------------TGKAAWVFGTSFLLLVVPLIVQ
SacceTom22      MVELTEIKDDVVQLDEPQFSRNQAIVEEKASATNNDVVDDEDDSDSDFE--DEFDENETLLDRIVALK--DIVPPGKRQTISNFFGFTSSFVRNAFTKSGNLAWTLTTTALLLGVPLSLS
NeucrTom22      -------------MVQLTEVEDEHFQQPQVGPEEDDEDFTDTDSEISVD--SDYESQETFTDRLYALR--DMVSPTTRGWFYHKYSTTTNFVKSTLSFAGRAAWAVSVSGLLIGVPFAIA
HomsaTom22      ----------------MAAAVAAAGAGEPQSPDELLPKGDAEKPEEELE--EDDDEELDETLSERLWGLTEMFPERVRSAAGATFDLSLFVAQKMYRFSRAALWIGTTSFMILVLPVVFE
DromeTom22      ----------MDSDPEIEFIEKDSGMSSLGGSKDETPERRAVAATSNDPQRENYDDEPDETASERFWGLTEMFPEPVRNAVGAVSSATVKSVKGFYSFSCNASWIFFTSAVILFAPVIFE
                                                                                                                                                                                  :   .: ::   *. .

                                                IMS (in)
EctsiTom22      ITREAQLIEQEKI-----HINALLAEGKTRQEIAQMGLYSAL--DPNVMGPEAS--     stramenopiles
PhatrTom22      IAREGQMLESERA-----QVKDYKGRGYSDRQLQELGFSEAALHTPSVASLNKK--     stramenopiles
PhyinTom22      MLREEQTNEVVK---------ELVSKGFSYNQIQGMGYMVSQPQSTLSTPAEGATQ     stramenopiles
ArathTom22_1    LEQDHRLGEIDF------EQASLLG-TP----------------PVGAML-----     Plantae
ArathTom22_2    MDREAQINEIEL------QQASLLGAPPS----------------PMQRGL-----     Plantae
OstluTom22      LHREEQLIELEK------EQLGVLN--------------------QPTGLQAE--     Plantae
MicpuTom22      LHREEQMAAAEQ------EQLGVLNLGSS-----------SLMTNAVPVQ------     Plantae
SacceTom22      ILAEQQLIEMEKTFDLQSDANNILAQGEK---------------DAAATAN-----     Opisthokonts
NeucrTom22      FAEDQNYAAMEQEARMRELGSDVLTAGGEGQAGTAEKTLAAIGGEGARPAL-----     Opisthokonts
HomsaTom22      TEK-LQMEQQQQLQ----QRQILLGPNTG---------LSGGMPGALPSLPGKI--     Opisthokonts
DromeTom22      TER-AQMEELHKSQ----QKQVLLGPGSA-----------MGPGGPSPSLPLIR--     Opisthokonts
                     .
```

(d)

Mia40

```
ThapsMia40      SIETVDR----------EDCPLC-KKFGSGP-CGKVFQQWLSCTDANPGKDESGEPLHLTKCAIFAEKLAVCIDTN
PhyraMia40      DATTGECLAPK------AECGFC-KFMKAGP-CGREFSAWEACLDRCKKSGDD----FIDTCGPQTLALRDCVDAN
PhysoMia40      DTTAGECLAPK------AECGFC-KFMKAGP-CGKEFTAWEACLDRCKKSGDD----FIEKCGPQTLALRDCVDAN
PhatrMia40      -----------------DSCPLC-RQFRQGP-CAAPFNSWYACTERANAASQD----HVAVCSESFAAFHACVASN
DicdiMia40      -----------------ADCPPCIRRMANSQYCGDELVKSYLCFQESNKNGTS-----VESCAGSFNKLKDCMVKY
OstluMia40      -----------------LAC-PCVADLRQSS-CGTSFDEALTCFMLAKDEEKG------KKCVEEFVSLHACMVKN
MicpuMia40      DAIKAA-----------MEC-PCVADLKNSA-CGEAFAGALGCFMSADAEERG------SKCVKEFVAMHACMVEN
ArathMia40      GEDDNENESLEAKAQRALDC-PCIADLRNGS-CGSQFSEAFLCFLKSTAEEKG------SDCVNPFVALQSCINAN
PhypaMia40      -----------------LKC-DCVAELRDGP-CGSQFKEAFYCFLTSTAEEQG------SDCTKSFIAMQTCMTAN
CyameMia40      -----------------LNC-PCVESLKEGS-CGGAFIAAYRCFLESEAEPRG------SDCYEVFQRMQDCMLAH
HomsaMia40      N----------------WNC-PCLGGMASGP-CGEQFKSAFSCFHYSTEEIKG------SDCVDQFRAMQECMQKY
SacceMia40      EEVQHEGAYNPDTGEINWDC-PCLGGMAHGP-CGEEFKSAFSCFVYSEAEPKG------IDCVEKFQHMQDCFRKY
                -------------------CXXC---------C---X9----C------------------C---X9----C----
```

(e)

Erv1

```
CLUSTAL FORMAT: MUSCLE (3.7) multiple sequence alignment

EctsiErv1       --------------MPSSRRRSKDPADCEDPACADMADLLRKGRALAAKNKQKAASNTATDGKAAGSQAQPSSSAAETDEHAA-------------SSSRNDGCPLDKGELGAATWGLIH
PhyraErv1       ------------------MVAAKSDPNCVEPACADKMDFFKSSMG-------KRVTTPAMQPK-------------------------------------DCPLDRQELGNATWGLLH
PhyinErv1       ------------------MVATKSDPNCVEPACADKMDFFKSSMG-------KKTKKTATQPKPAT-----------------------------------DCPLDRQELGNATWGLLH
PhysoErv1       ------------------MVATKSDPNCVEPACADKMDFFKSSMG-------KKATKPAAQPKPAT-----------------------------------DCPLDRQELGNATWGLLH
ThapsErv1       ------------------------------------------------------------------------------------------------------***CPPTRDEIGVSTWSLLH
PhatrErv1       ------------------------------------------------------------------------------------------------------***PPSSASLGNSSWTLLH
CyameErv1       ------------------------------------------------------------------------------------------------------***PPTRAELGRAGWTLLH
ChlreErv1       -----MPNAAAAVSEAAATPAARKLSDCKSRACS-------------------------------------------------------------------CPPDTWELGRATWTFLH
ArathErv1       ---------MGEKPWQPLLQSFEKLSNCVQTHLSNFIGIKNTPPSSQSTIQNPIISLDSSPPIATNSSSLQKLPLKDKSTG----------------------PVTKEDLGRATWTFLH
HomsaALR        ----------MAAPGERGRFHGGNLFFLPGGARSEMMDDLATDAGPGRGAERRGRLGLDASPGADLRFSCRRGRLPEAACRACVDFKTWMRTQQKRDTKFREDCPPDREELGRHSWAVLH
SacceErv1       MKAIDKMTDNPPQEGLSGRKIIYDEDGKPCRSCNTLLDFQYVTGKISNGLKNLSSNGKLAGTGALTGEASELMPGSRTYRKVD---------------------PPDVEQLGRSSWTLLH
                                                                                                                        *    .:*   * .:*

EctsiErv1       TTAAHYPEKPSKETQDQARALVTGLAGLYPCTYCRKDFREEVRKLPPDVSSRVALSLWACQQHNLVNEKIGKPTFGCT-LPALDERWKKGKPSCW--EGGAEGV---------------
PhyraErv1       SMGIYYPDKPSAEYQAKTKTFIEALALMYPCVHCADDFQKEIAKSPPCVESRTTFSMWLCEQHNIVNRKIHKPVFECT-MEKLEERWRKGKPSCWGEDGDEDSAKESLG----------
PhyinErv1       SMGIYYPDKPSPEYQAKAKTFIEALALMYPCVHCAEDFQKEVAISPPRVESRTTFSMWLCEQHNIVNRKIHKPVFECT-MEKLEERWRKGKPACWGEDGDEDSAQDSLH----------
PhysoErv1       SMGIYYPDKPSPEYQAKAKTFIEALALMYPCVHCADDFQKEIAKSPPRVESRTTFSMWLCEQHNIVNRKIHKPLFECT-MEKLEERWRKGKPSCWGEDGDEESAQDALG----------
ThapsErv1       SMAAWYPNQPSSQDEQFMSDFMKALARFYPCTWCASDFQRNIELSPPKTETREDLCIWICEQHNIVNEKLGKPLFQCT-MDKLDERWKK---------SSDPKCQK-------------
PhatrErv1       TMAAWYPDKPTTEDRSYITGFMNALARFYPCPWCAKDFRHNIEEKPVQTSSREALCTWLCEQHNIVNQKLGKPQYACD-IQTLDERWRK---------SSKDACQSGSH----------
CyameErv1       SIAANYPEVATPEMQTHARQFIASFAALYPCPTCREHFQGYVRTHPPALESREQFVKWCCRAHNAVNLRLGKPTIPCTDLQLLDKRWRDCH-------CDEQEPQNMIRAARRLIESRR
ChlreErv1       SVAAGYPESPSERQQGLMRGMVEGLAEFYPCEVCREHLREQVAARPPQVGSARELNMWLCGLHNEVNEMLGKPLFDCA---RVGERWRE---------GPADGSCD-------------
ArathErv1       TLAAQYPEKPTRQQKKDVKELMTILSRMYPCRECADHFKEILRSNPAQAGSQEEFSQWLCHVHNTVNRSLGKLVFPCE---RVDARWGKL--------ECEQKSCDLHGTSMDF-----
HomsaALR        TLAAYYPDLPTPEQQQDMAQFIHLFSKFYPCEECAEDLRKRLCRNHPDTRTRACFTQWLCHLHNEVNRKLGKPDFDCS---KVDERWRD---------GWKDGSCD-------------
SacceErv1       SVAASYPAQPTDQQKGEMKQFLNIFSHIYPCNWCAKDFEKYIRENAPQVESREELGRWMCEAHNKVNKKLRKPKFDCN---FWEKRWKD---------GWDE----------------
                : .  **  .:         ::  :: :***  * . :   :        :   :  * *   ** **  : *    *        ** .
                                          YPCXXC                        ______CX16C______

*** : incomplete sequences
```

(f)

Hot13

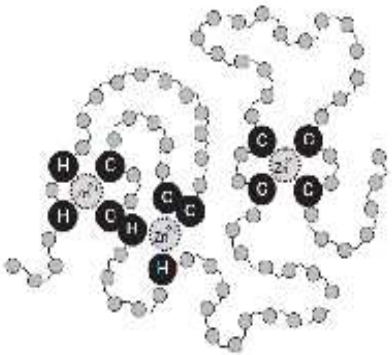
Panel 1

```
CLUSTAL FORMAT: MUSCLE (3.7) multiple sequence alignment


EctsiHot13      --------------------MLVPGQVSIQFPCCKRWYECPECHDERENHPQRI-----S TKNVAFACKTCRKIFVKDLSIYGTEDSA--CPHCETVFV----------LPAVTPEAKV-
PhyinHot13      -----------------MCKHIPNAQVSFQTPCCNRWFDCGECHFELSDHRQQP------ AAEMAFVCKQCRNPFRKDLTAFDEEDES--CPHCGNGLV----------QPVADLRA---
PhyraHot13      -----------------MCKHIPNAQVSFRAPCCNRWFDCSECHFELSDHRQQA------ ADEMAFVCKQCRNPFRKDLTAFDEEDEN--CPHCGNELI----------QSA--------
PhysoHot13      -----------------MCKHIPNAQVSFRAPCCSRWFDCSECHFELSDHRQQA------ AAEMAFVCKQCRNPFRKDLTAFDEEDES--CPHCGNMLV--------------------
CyameHot13      ----------------------------***PCCQVYYTCRLCHDEVNDHVMDR------ YAVERILCMRC----------LTEQAPAEVCSSCGERFXXXXXXXXNVSEPCTTFRIHVK
SacceHot13      MIETAIYGKTVDDQSRCVHWHLPKDVIAIRFKCCDKYYACFECHQELSSHPLEKYDLLDD ANKHLIICGVCRHEM--TFAEYYDYNSNLICPNCRSPFN---------------PGCKLH
NeucrHot13      -----------------MCKHVLNAQVSIRSPCCRKWFDCPECHAESESHPLKK------ TLEMTFACKKCKKCFRKDATEFEDSDEY--CPHCDNHYI----------IEAVTPKAALR
                                                **  :: *  ** * ..*               : *  *                  *. *

EctsiHot13      -----AQLALSILAAEVSAEVSKF-----------------
PhyinHot13      -----ATPAEANHRNELVVERAMP-----------------
PhyraHot13      ----------------------------------------
PhysoHot13      ----------------------------------------
CyameHot13      SVYHTSDLSLKHCHSRFL-----------------------
SacceHot13      YHLYFQNPPPAMC----------------------------
NeucrHot13      VEGEDARMDARMLKDERVKQTKKTMNQISIFDPDVDADKLG
```

Panel 2



Model of zinc-ion coordination by conserved Cys and His residues within SacceHot13
(Mesecke et al., 2008)

(g)

Small Tims

Panel 1

```
EctsiTim9       -------MTPVQQQDFLQH-------------------------------------LESQ
EctsiTim13      ---MDGQASAEQQQAIIQQ-------------------------------------LQEQ
EctsiTim8       MSWFRGKKEPEPESTPEPTFSSDTSAFEGSTNFASGPPSRGGGGATSAGMGDLQAAMQIE
EctsiTim10      MSWF-GNSEPEPPSGPSPM-------------------------------------DLAK


EctsiTim9       QRKDSL-AMYNNLVFRCFDECSKSFRSKR-LDDGETKCINVCAEKFIKLTSRVALRFQDI
EctsiTim13      VQAKALQELMTQMTDQCFNRCAKTSSGDR-INSSEQGCLAMCMDRYMDT-------MGLV
EctsiTim8       QQKAQMQAIVSRLTDLAFTKCIQKPSSS--LSSSEQSCINATVLKYFDTSEFV---LGRL
EctsiTim10      QEVDMYSDLFTKMSGLCFKKCVVKMHGESDLNVGEMSCVDRCVSKYMEAQEKVGVILKRA
                                CFxxC                   CxxxC

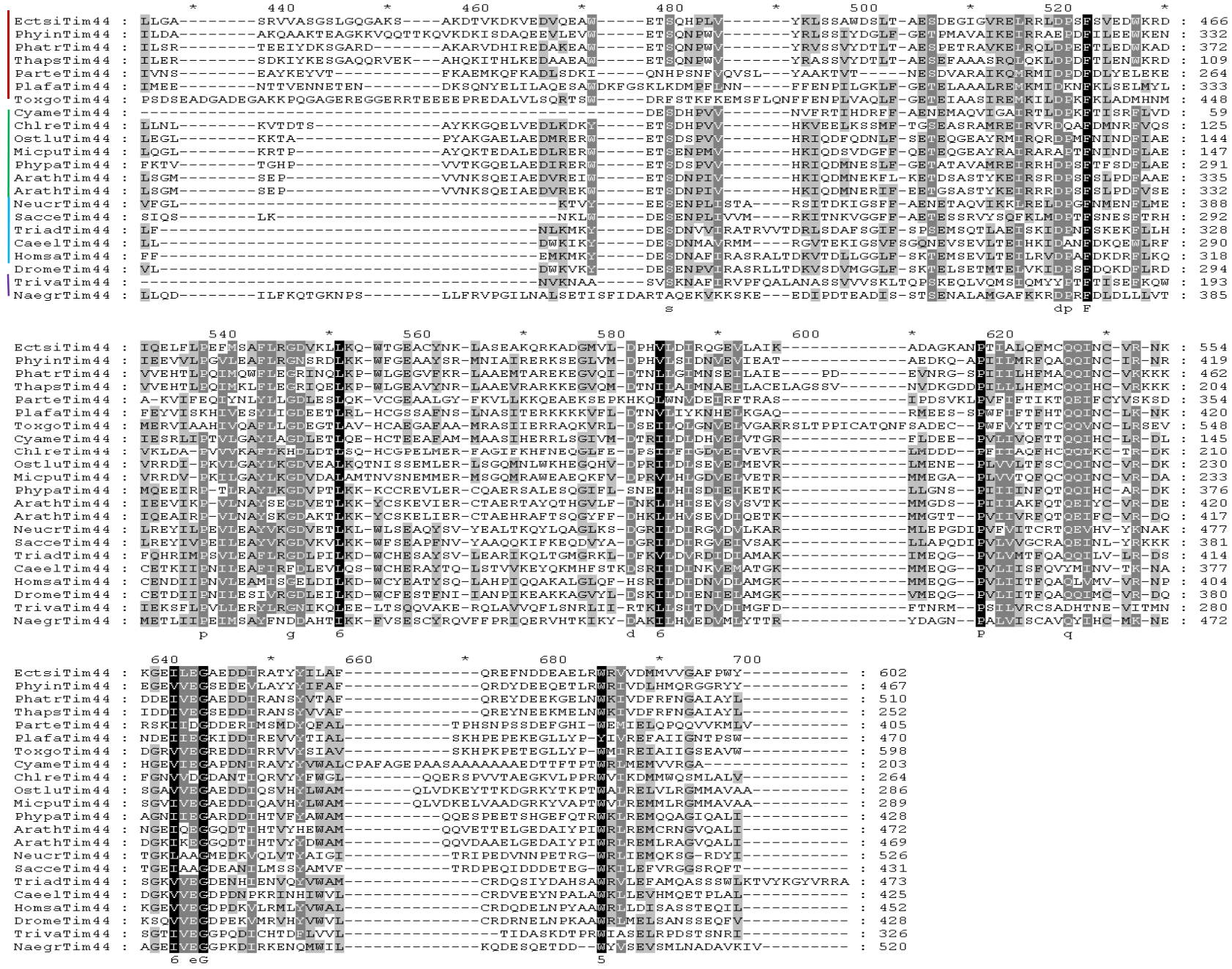
EctsiTim9       QQQKAKDEAA-------GVQR----
EctsiTim13      NKAMVAKANR---------------
EctsiTim8       MKSQQGGGDI---------------
EctsiTim10      EESLAAQQGGVGGPAAGGVPGVPGR
```

Panel 2

```
SacceTim9       NLVERCFTD
NeucrTim9       NLVDNCFTA
OrysaTim9       SLVERCFTD
HomsaTim9       KLTETCFLD
DromeTim9       KLSETCFTD
EctsiTim9       NLVFRCFDE
                .*. .**.
```

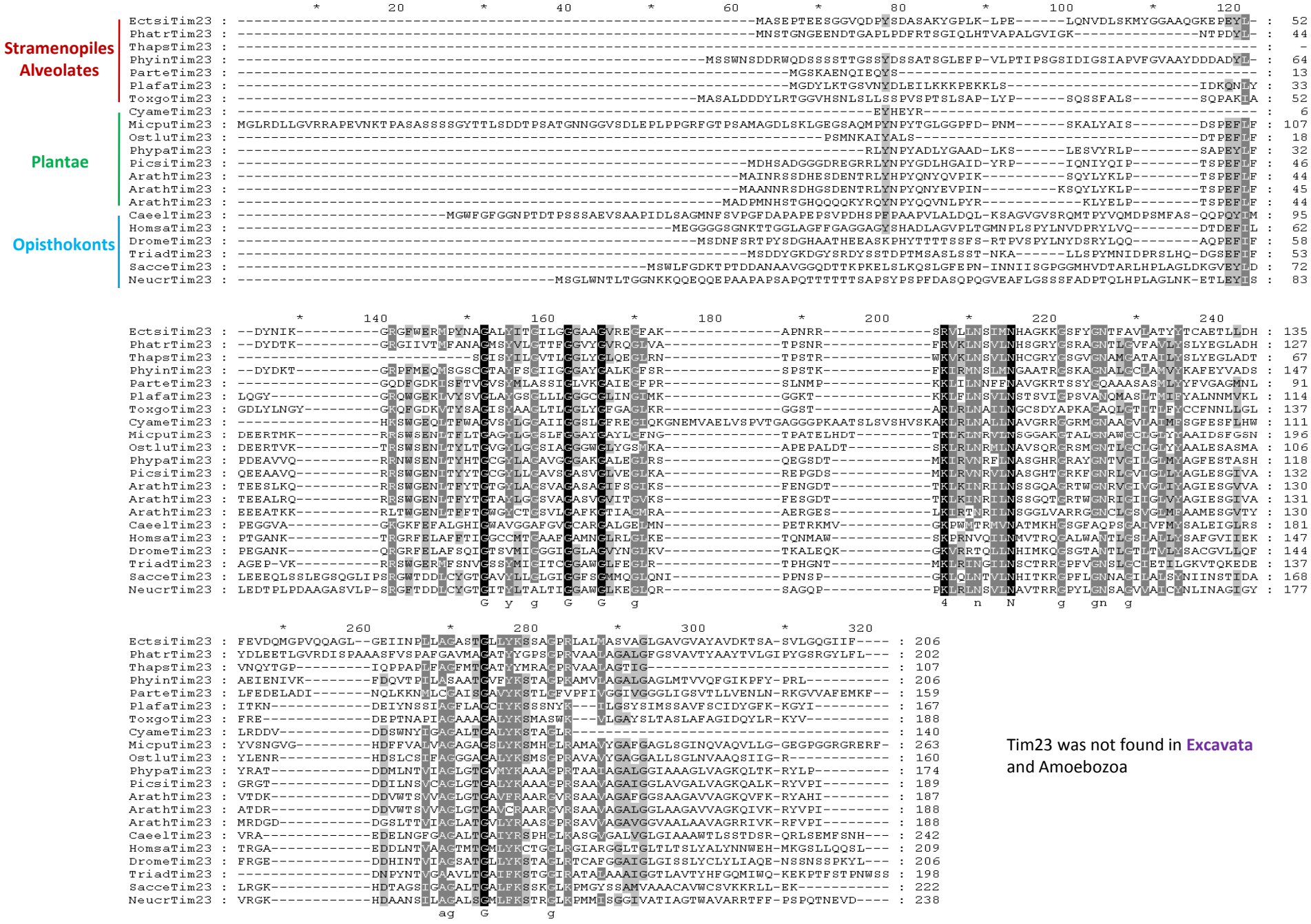
(h)

Tim44


Stramenopiles
Alveolates
Plantae
Opisthokonts
Excavata
EctsiTim44
PhyinTim44
PhatrTim44
ThapsTim44
ParteTim44
PlafaTim44
ToxgoTim44
CyameTim44
ChlreTim44
OstluTim44
MicpuTim44
PhypaTim44
ArathTim44
ArathTim44
NeucrTim44
SacceTim44
TriadTim44
CaeelTim44
HomsaTim44
DromeTim44
TrivaTim44
NaegrTim44

(i)

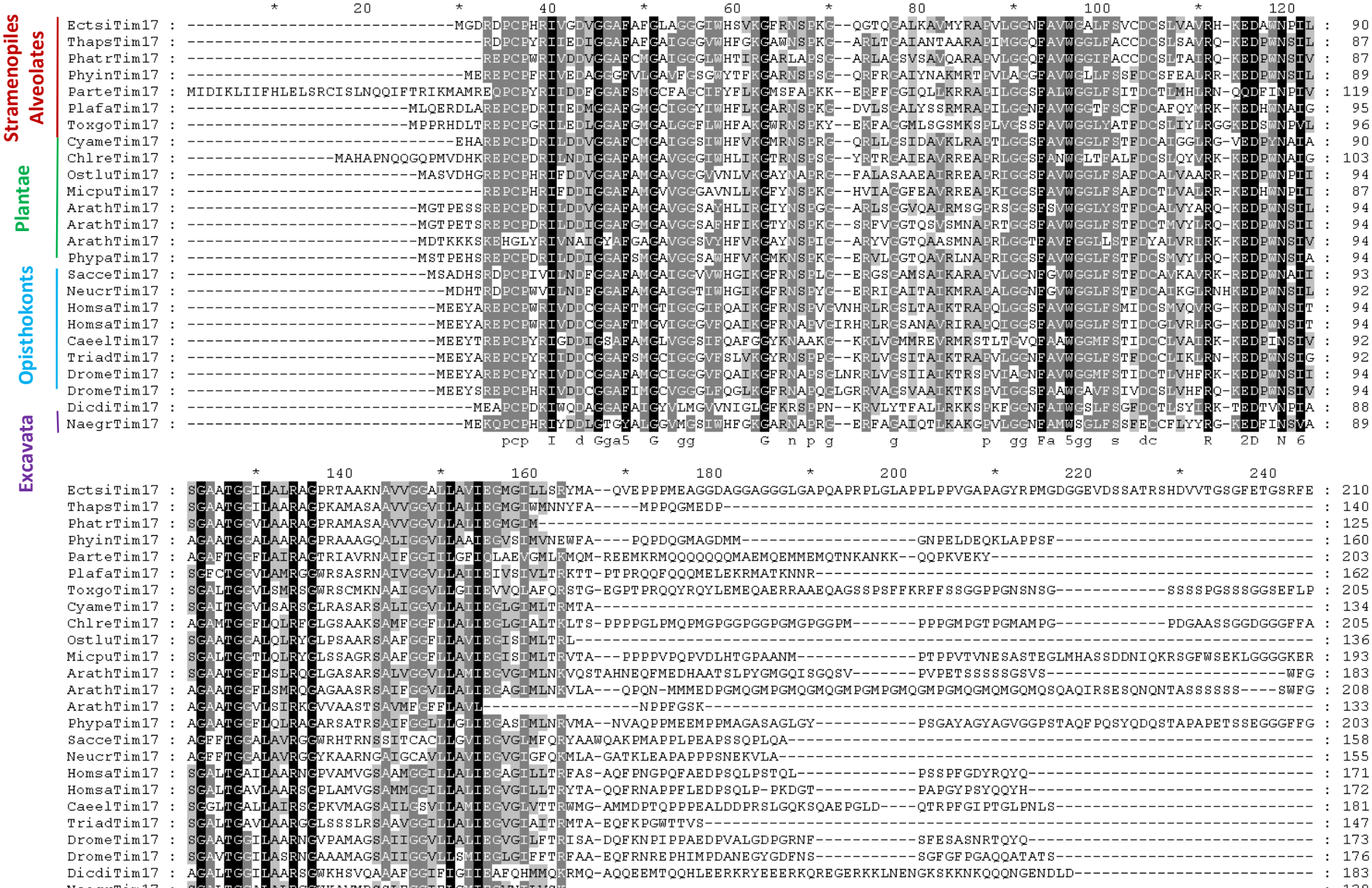
Tim23



Tim23 was not found in Excavata and Amoebozoa

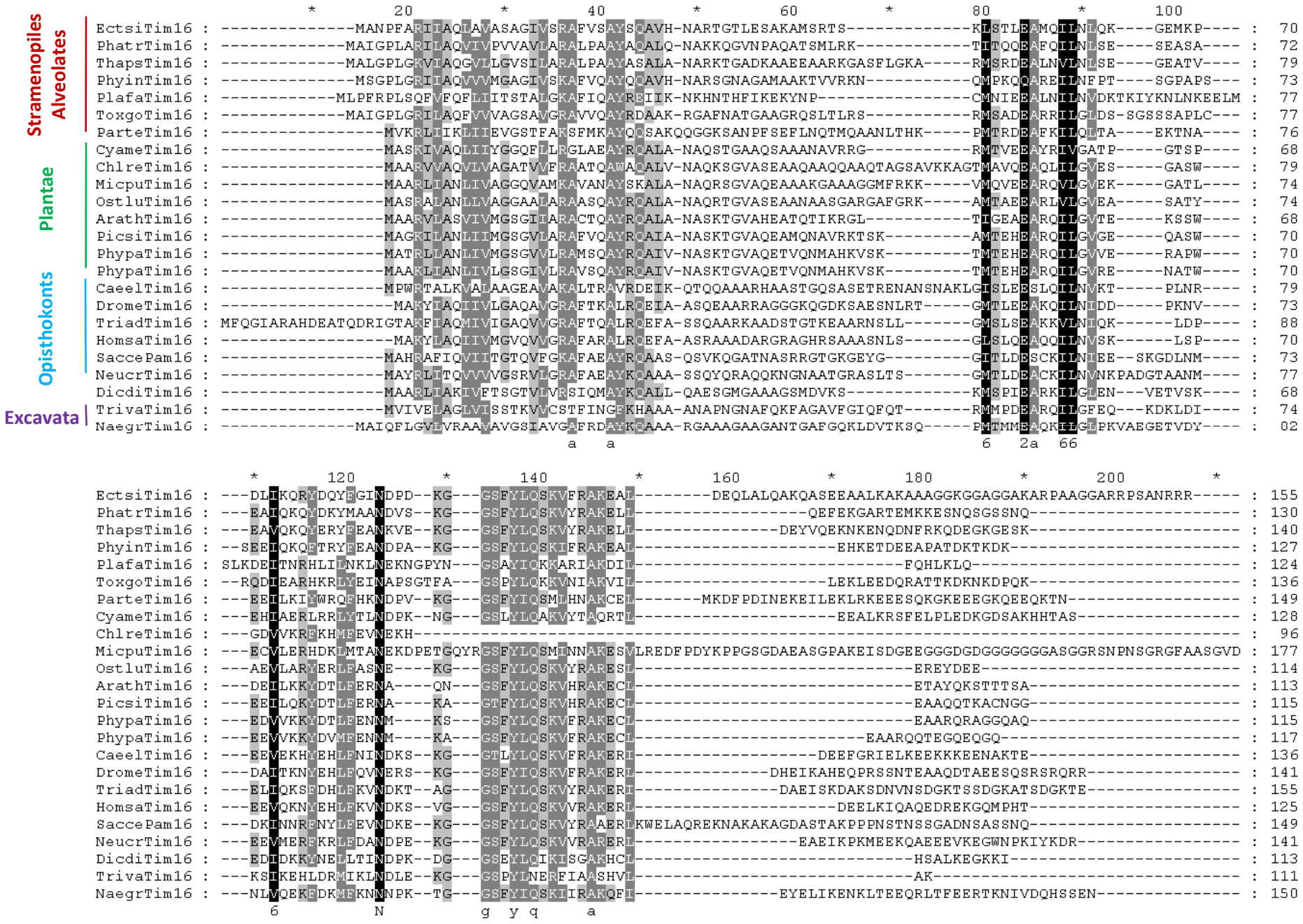
(j)

Tim17


Stramenopiles
Alveolates
Plantae
Opisthokonts
Excavata
EctsiTim17
ThapsTim17
PhatrTim17
PhyinTim17
ParteTim17
PlafaTim17
ToxgoTim17
CyameTim17
ChlreTim17
OstluTim17
MicpuTim17
ArathTim17
ArathTim17
ArathTim17
PhypaTim17
SacceTim17
NeucrTim17
HomsaTim17
HomsaTim17
CaeelTim17
TriadTim17
DromeTim17
DromeTim17
DicdiTim17
NaegrTim17

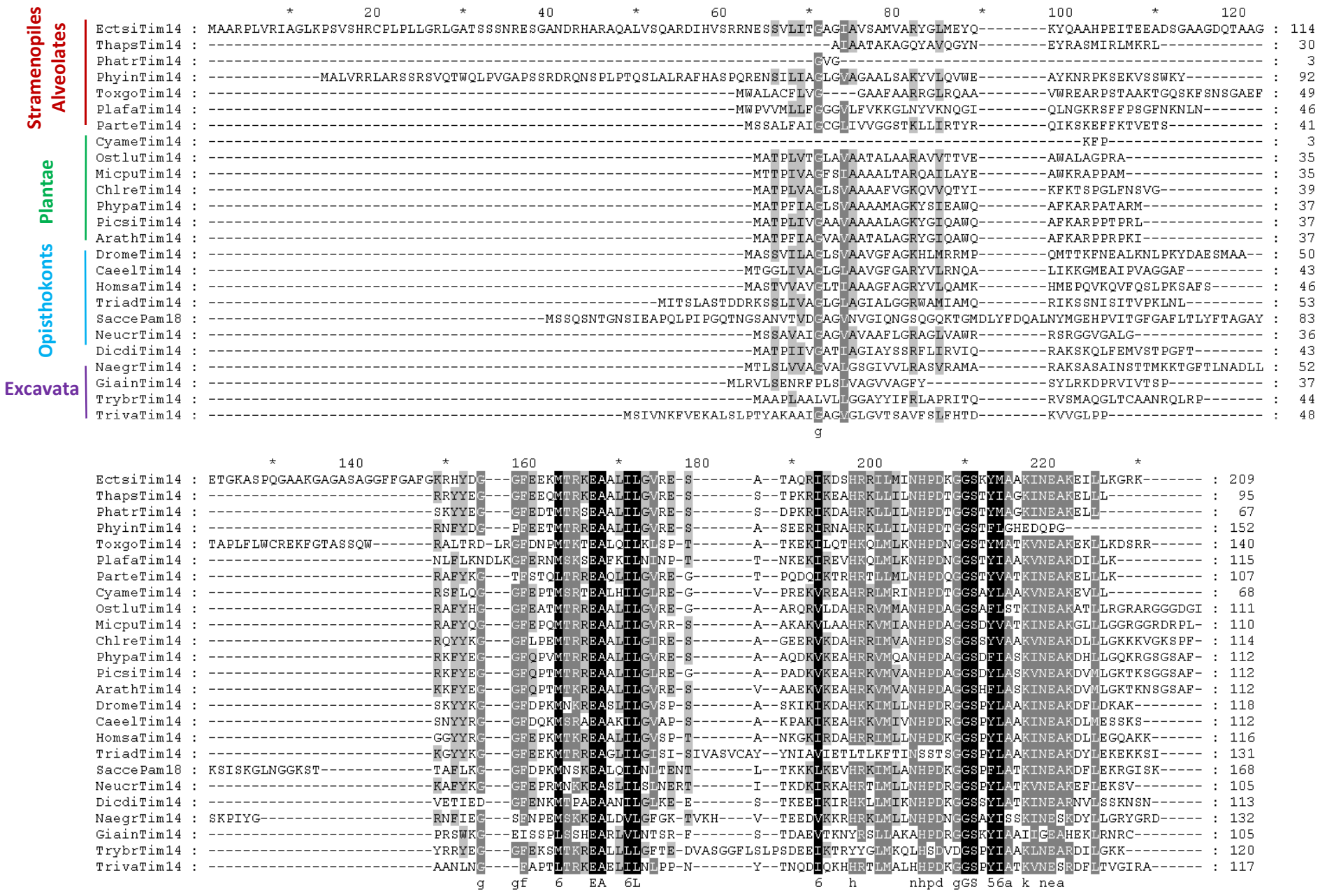
(k)

Tim16


Stramenopiles
Alveolates
Plantae
Opisthokonts
Excavata
EctsiTim16
PhatrTim16
ThapsTim16
PhyinTim16
PlafaTim16
ToxgoTim16
ParteTim16
CyameTim16
ChlreTim16
MicpuTim16
OstluTim16
ArathTim16
PicsiTim16
PhypaTim16
PhypaTim16
CaeelTim16
DromeTim16
TriadTim16
HomsaTim16
SaccePam16
NeucrTim16
DicdiTim16
TrivaTim16
NaegrTim16

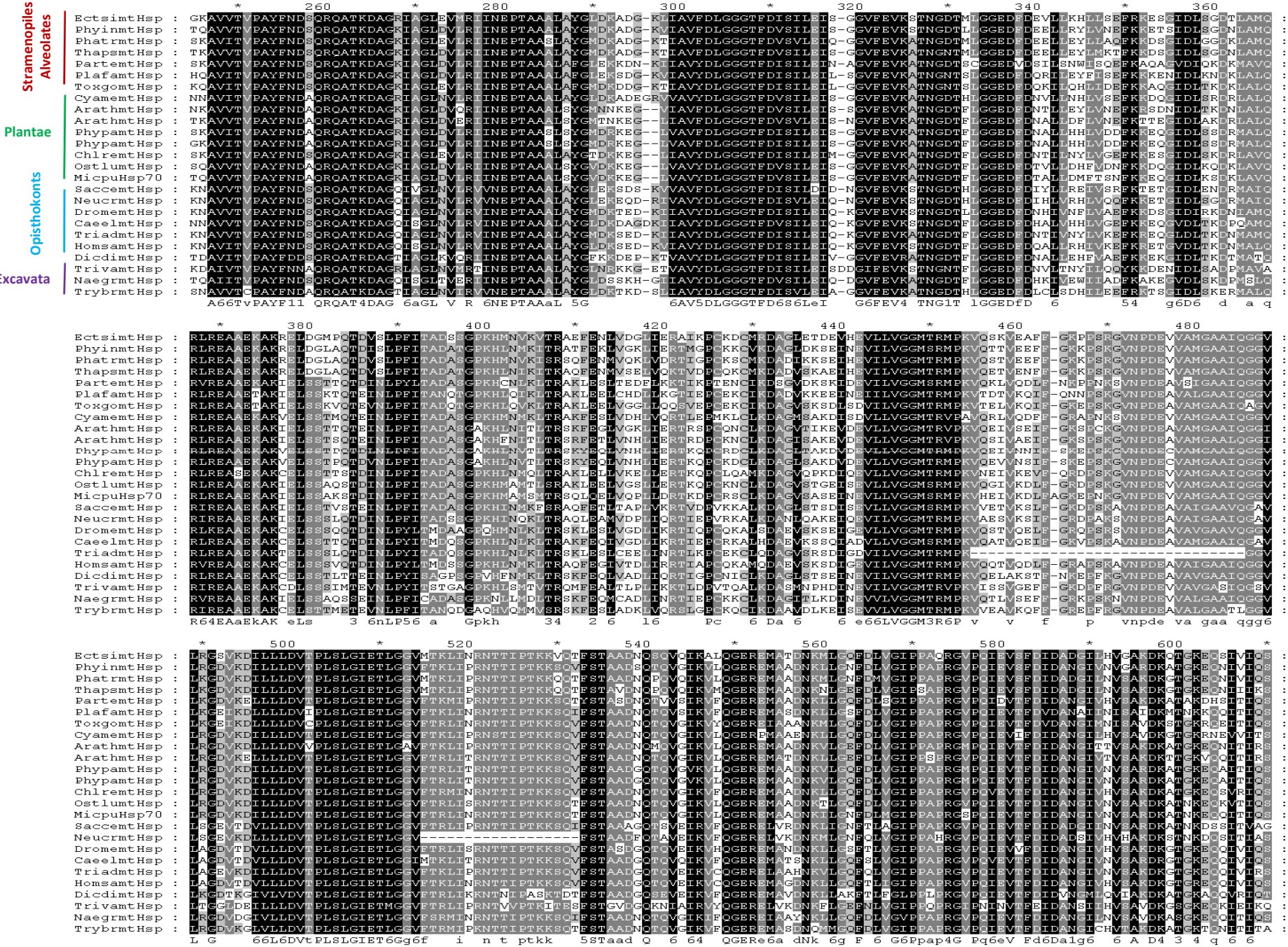
(I)

Tim14


Stramenopiles
Alveolates
Plantae
Opisthokonts
Excavata
EctsiTim14
ThapsTim14
PhatrTim14
PhyinTim14
ToxgoTim14
PlafaTim14
ParteTim14
CyameTim14
OstluTim14
MicpuTim14
ChlreTim14
PhypaTim14
PicsiTim14
ArathTim14
DromeTim14
CaeelTim14
HomsaTim14
TriadTim14
SaccePam18
NeucrTim14
DicdiTim14
NaegrTim14
GiainTim14
TrybrTim14
TrivaTim14

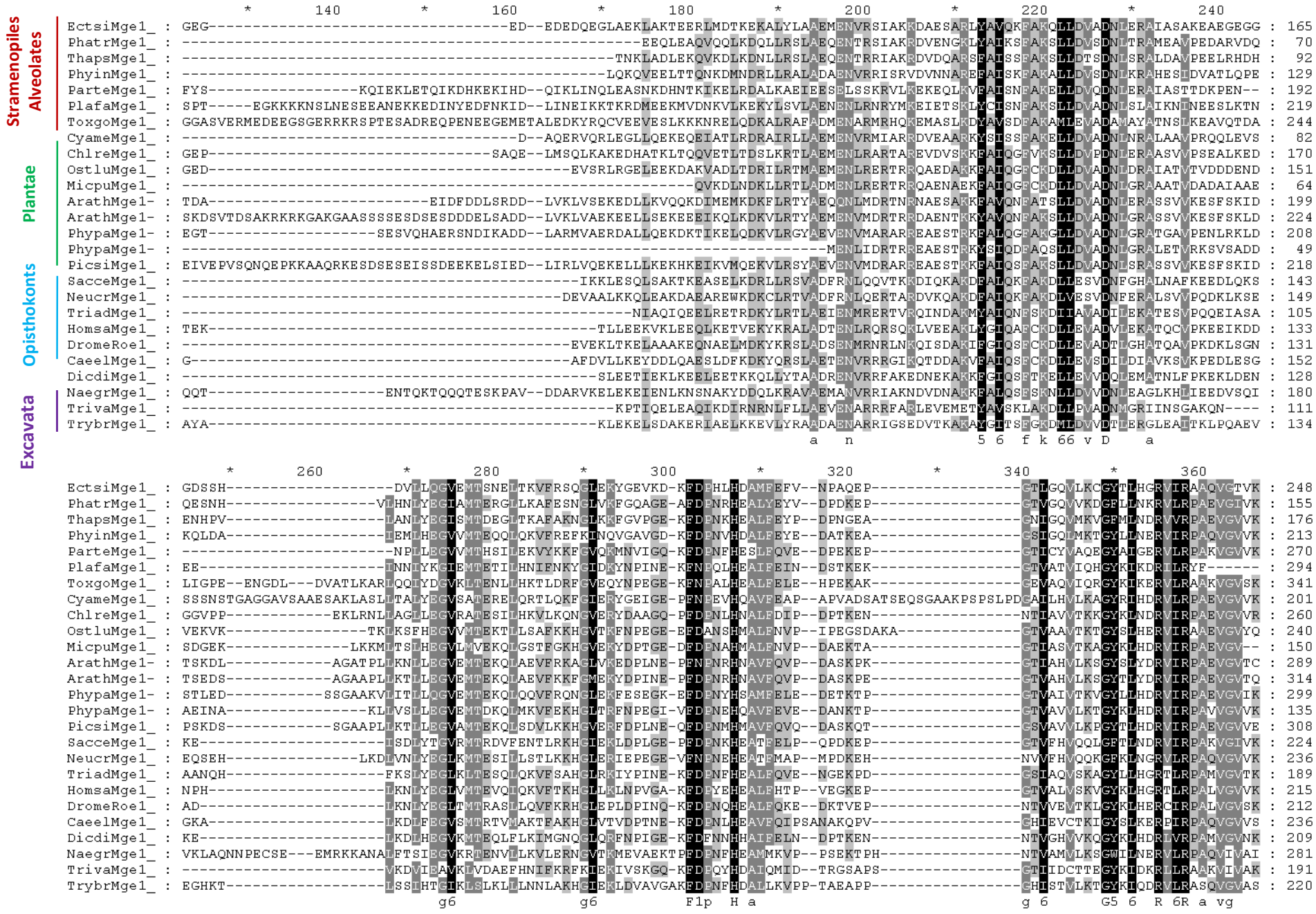
(m)

mtHsp70


Stramenopiles
Alveolates
Plantae
Opisthokonts
Excavata
EctsimtHsp
PhyinmtHsp
PhatrmtHsp
ThapsmtHsp
PartemtHsp
PlafamtHsp
ToxgomtHsp
CyamemtHsp
ArathmtHsp
ArathmtHsp
PhypamtHsp
PhypamtHsp
ChlremtHsp
OstlumtHsp
MicpuHsp70
SaccemtHsp
NeucrmtHsp
DromemtHsp
CaeelmtHsp
TriadmtHsp
HomsamtHsp
DicdimtHsp
TrivamtHsp
NaegrmtHsp
TrybrmtHsp

(n)

Mge1


Stramenopiles
Alveolates
Plantae
Opisthokonts
Excavata
EctsiMge1_
PhatrMge1_
ThapsMge1_
PhyinMge1_
ParteMge1_
PlafaMge1_
ToxgoMge1_
CyameMge1_
ChlreMge1_
OstluMge1_
MicpuMge1_
ArathMge1-
ArathMge1-
PhypaMge1-
PhypaMge1-
PicsiMge1_
SacceMge1_
NeucrMge1_
TriadMge1_
HomsaMge1_
DromeRoe1_
CaeelMge1_
DicdiMge1_
NaegrMge1_
TrivaMge1_
TrybrMge1_

(o)

Tim22

Stramenopiles
Alveolates
Plantae
Opisthokonts
Excavata
EctsiTim22
PhatrTim22
ThapsTim22
PhyinTim22
PhyinTim22
ParteTim22
PlafaTim22
ToxgoTim22
CyameTim22
CyameTim22
OstluTim22
MicpuTim22
ChlreTim22
ChlreTim22
ArathTim22
ArathTim22
ArathTim22
PhypaTim22
PhypaTim22
PhypaTim22
PicsiTim22
PicsiTim22
SacceTim22
NeucrTim22
CaeelTim22
DromeTim22
HomsaTim22
DicdiTim22
NaegrTim22
TrybrTim22