Figure S1 Phylogenetic tree of Vps29

A phylogenetic tree (ClustalX, neighbour joining, corrections with multiple substitutions, random generator seed value 111, bootstrap trials 1000) of selected Vps29 amino acid sequences (including predicted sequences based on whole genome and EST sequences available in public databases) from various domains of life including metazoans, plants, fungi and protozoans is shown. Database entries are given in the FASTA definition line in the accompanying FASTA file (Figure S2 supplementary material). The Vps29 related archaeal metallo-phosphatase MJ0936 was used as an out-group to root the tree.

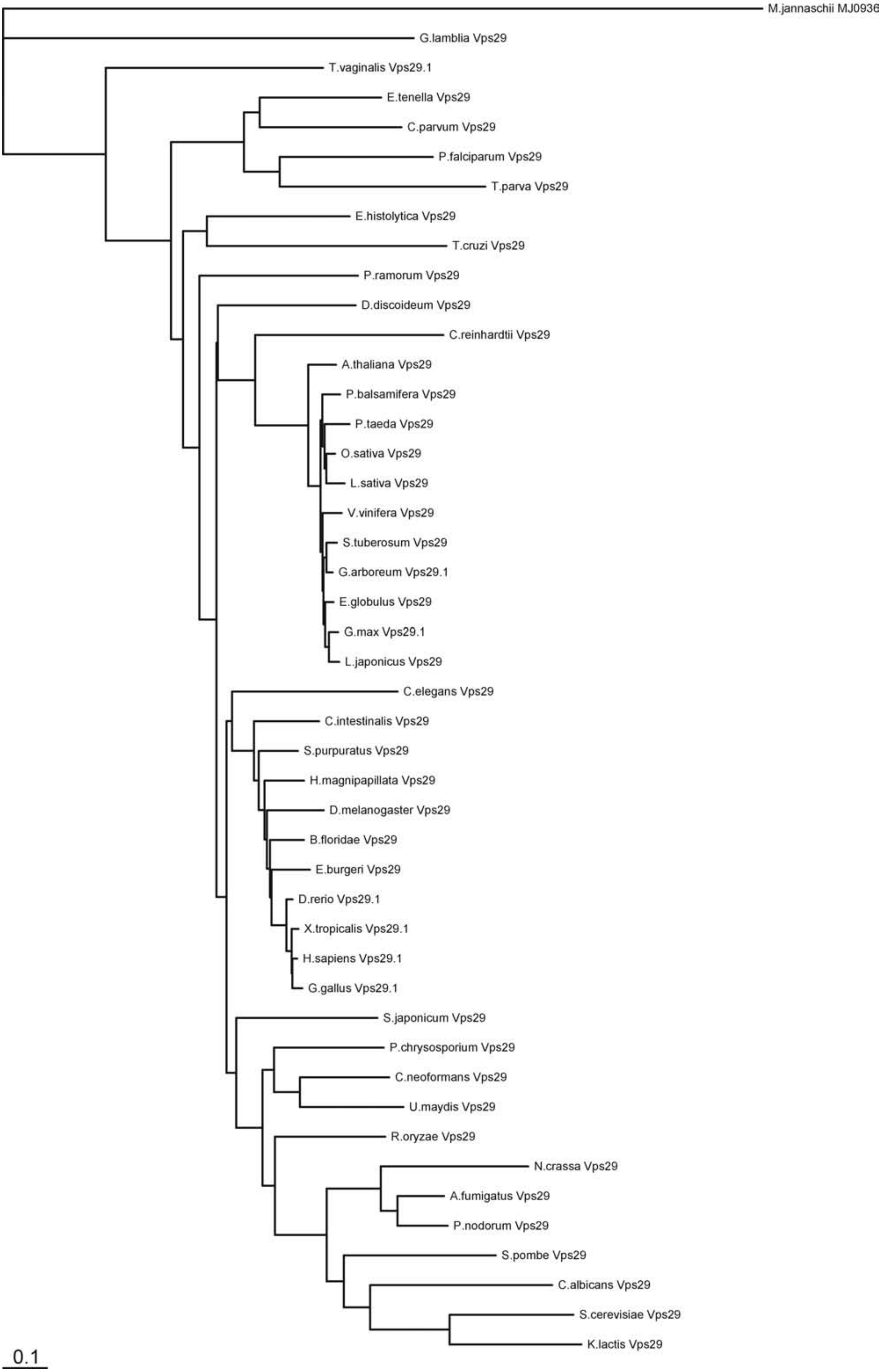
Figure S2 FASTA files of Vps29 amino acid sequences

FASTA files of Vps29 amino acid sequences used for the multiple sequence alignment (Figure S1 supplementary material) and the phylogenetic tree (Figure S3 supplementary material) construction of Vps29. NCBI database entry accession codes, whole genome sequence contigs, ESTs, or TIGR Clustered (TC prefix) EST sequences are given in the FASTA definition line. Protein sequences derived from nucleotide sequence entries were conceptually translated. It should be noted that conceptual translations of draft whole genome sequences must be considered preliminary.

Figure S3 Multiple sequence alignment of Vps29

ClustalW multiple sequence alignment of selected Vps29 amino acid sequences (including predicted sequences based on whole genome and EST sequences available in public databases) from various domains of life including metazoans, plants, fungi and protozoans (from top to bottom) is shown. The alignment was exported to Microsoft WORD using the CHROMA sequence analysis software package. Database entries are given in the FASTA definition line in the accompanying FASTA file (Figure S2 supplementary material). The five sequence motifs (I-V) that lie in loops connecting the core secondary structure elements and contain active site residues are indicated. Active site residues are indicated by an asterisk. Amino acids are numbered according to the human Vps29 sequence.

Supplementary Figure 1



Supplementary Figure 2

Selected Vps29 sequences used for multiple sequence alignment and phylogenetic tree construction. NCBI database entry accession codes, whole genome sequence contigs, EST's, or TIGR Clustered (TC prefix) EST sequences are given in the FASTA definition line. Protein sequences derived from nucleotide sequence entries were conceptually translated.

```
>H.sapiens_Vps29.1 gi|7706441|ref|NP_057310.1| vacuolar protein sorting 29,
isoform 1; vacuolar protein sorting 29 (yeast homolog); vacuolar sorting
protein VPS29/PEP11; retromer protein; x 007 protein [Homo sapiens]
MLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHILCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVV
TVGQFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAFEHENKFYINPGSATGAYNALETNIIPSF
VLMDIQASTVVTYVYQLIGDDVKVERIEYKKP*

>X.tropicalis_Vps29.1 gi|52346072|ref|NP_001005079.1| MGC89642 protein
[Xenopus tropicalis]
MLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHILCTGNLCTKESFDYLKTLAGDVHIVRGDFDENLNYPEQKVV
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>G.gallus_Vps29.1 BU240962
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VLMDIQASTVVTYVYQLIGDDVKVERIEYKKS*

>D.rerio_Vps29.1 gi|41053315|ref|NP_956331.1| vacuolar protein sorting 29
[Danio rerio]
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VLMDIQASTVVTYVYQLIGDDVKVERIEYKKS

>E.burgeri_Vps29 BJ655784_BJ653486 hagfish
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>H.magnipapillata_Vps29 BP506496
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VTVGPFKIGLCHGHQIVPWGDPESLAMVQRQLDVDILITGHTHRFEAFEHENKFYVNPGSASGAYNPLDLNIVPS
FVLMDIQAGIVVAYVYQLHGDDVKVDRIEYKK

>S.purpuratus_Vps29 AAGJ01182906 DN585406
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TVGQFRVGICHGHQVIPWGDVESLSMVQRQLDVDILISGHTHKFEAYEHEGKFYINPGSATGAYSALDANTVPSF
VLMDIQASTVVTYVYQLMGDDVKVERIEYKKN

>D.melanogaster_Vps29 gi|7296116|gb|AAF51410.1| CG4764 gene product
[Drosophila melanogaster]
MLVLVLGDLHIPHRCSSLPAKFKKLLVPGRIHHILATGNICTKESYDYLKSLANDVHIVRGDFDENLTYPEQKVV
TVGQFRIGLCHGHQVVPRGDPEALALIQRQLDVDILITGHTYKFEAYEHGNKFYINPGSATGAFNPLDTNVVPSF
VLMDIQSTTVVTYVYQLIGDEVKVERIEYKKI
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VTVGQFRIGMCHGHQICPWGDTESLAMLQRQLNVDILIFGHTHKFEAYEHESHFYINPGSITGAFSPTASEVIPS
FVLMDIQASTVVTYVYQLQANDVKVERIEYQKS

>S.japonicum_Vps29 gi|29841378|gb|AAP06410.1| similar to NM_019780 vacuolar
protein sorting 29 [Schistosoma japonicum]
MLVLVIGDFHIPDRKRCLHPAFKTLLAPGKIQHILCTGNLTSKHMLDYLKLICGDVHVVKGDFDEGLDFPLTKVL
SVGNFKIGLIHGHQVVPWGDQKSLAMLQRELNVDILISGHTHKFEAYEYAGHFYINPGSATGAYSPFEKNPQPSF
VLLDIQETVIQLYIYTLVNDEHKVSRIEYQKNKHT

>C.elegans_Vps29 gi|30424354|emb|CAA87426.2| Hypothetical protein ZK1128.8a
[Caenorhabditis elegans]
MLVLLIGDFNLPHRAANISPKFRKLLVPNKMQHVLCTGNLCSRETFDYLRTLSSDVHIVRGEFDDETLKYPDTKV
VTVGQFRIGVCHGHQIIPWGDQRMLELLARQLDVDILVTGNTYECSAVEKNGRFFVDPGSATGSFSVTKTEPTTP
SFALLDVQADNVVTYLYRLIDDAVKVDRIIYKKSKTT

>O.sativa_Vps29 AP004683
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LTIGQFKLGLCHGHQVVPWGDLDSLAMLQRQLDVDILVTGHTHQFKAYKHEGGVVINPGSATGAYSSITYDVNPS
FVLMDIDGLRVVVYVYELIDGEVKVDKIDFKKTATMHA*

>L.sativa_Vps29 TC14228 ORF 156..721 frame +3
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FVLMDIDGLRVVVYVYELIDGEVKVDKIDFKKTSTATI

>E.globulus_Vps29 BF707478
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LTIGQFKLGLCHGHQAIPWGDLDSLAMLQRQLDVDILVTGHTHQFTAYKHEGGVVINPGSATGAYSSITYDVNPS
FVLMDIDGLRVVVYVYELIDGEVKVDKIDFKKTTTTTAH

>S.tuberosum_Vps29 TC125942 ORF 154..722 frame +1
MVLVLALGDLHIPHRAADLPAKFKSMLVPGKIQHVICTGNLCIKEVHDYLKTLCPDLHITRGEYDEDTRYPETKT
LTIGQFKLGLCHGHQVIPWGDLDSLAMLQRQLDVDILVTGHTHQFTAYKHEAGVVINPGSATGAYSSITYDVNPS
FVLMDIDALRVVVYVYELIDGEVKVDKIDFKKTTTQSAN

>G.arboreum_Vps29.1 TC32658 ORF 136..710 frame +1
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LTIGQFKLGLCHGHQVIPWGDLDSLAMLQRQLDVDILVTGHTHQFTAYKHEGGVVINPGSATGAYSSITYDVNPS
FVLMDIDGLRVVVYVYELIDGEVKVDKIDFKKTPATTHSAH

>P.balsamifera_Vps29 BU870410
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FVLMDIDGLRVVVYVYELIDGEVKVDKIDFKKTTAATHSTH*

>G.max_Vps29.1 TC205293 ORF 191..762 frame +2
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>L.japonicus_Vps29 TC15081 ORF 211..770 frame +1
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>V.vinifera_Vps29 TC39978 ORF 52..626 frame +1
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>A.thaliana_Vps29 gi|15228262|ref|NP_190365.1| putative protein
[Arabidopsis thaliana]
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LTIGQFKLGLCHGHQVIPWGDLDSLAMLQRQLGVDILVTGHTHQFTAYKHEGGVVINPGSATGAYSSINQDVNPS
FVLMDIDGFRAVVYVYELIDGEVKVDKIEFKKPPTTSSGP

>C.reinhardtii_Vps29 C_370066 [chlre2:164094] BE238177_TC29021
MVLVLCIGDLHIPHRAPDLPAKFKELLKPGKIHSTICVGNVCSKVFLDYLRTISGELHVVSGDFDEFAAPEQLVL
DIAGFRVGVCHGHQIVPWGDADAISLLQRQMGADILVTGNTHKFEARKAGSCLALNPGSATGAFSVSAAGTSQPA
PTPSFVLMDLDGQKVTVYVYQLVDGEVRVEKIDYNKAA

>S.cerevisiae_Vps29 gi|6321800|ref|NP_011876.1| Endosomal protein that is a
subunit of the membrane-associated retromer complex essential for endosome-
to-Golgi retrograde transport; forms a subcomplex with Vps35p and Vps26p
that selects cargo proteins for endosome-to-Golgi retrieval; Vps29p
[Saccharomyces cerevisiae]
MLLLALSDAHIPDRATDLPVKFKKLLSVPDKISQVALLGNSTKSYDFLKFVNQISNNITIVRGEFDNGHLPSTKK
DKASDNSRPMEEIPMNSIIRQGALKIGCCSGYTVVPKNDPLSLLALARQLDVDILLWGGTHNVEAYTLEGKFFVN
PGSCTGAFNTDWPIVFDVEDSDEAVTSEVDKPTKENQSEDDDAKGGSTGKEQPGSYTPKEGTAGERENENESNVK
PENQFKEDEVDMSDSDINGSNSPSFCLLDIQGNTCTLYIYLYVNGEVKVDKVVYEKE

>K.lactis_Vps29 gi|50308195|ref|XP_454098.1| unnamed protein product
[Kluyveromyces lactis]
MLLLALSDAHIPERAIDVPLKFRKLLNVPNKIQQVTLLGNCTKSASFLKFVNTISENIVFVRGEFDPATVSTTKN
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>C.albicans_Vps29 gi|68473870|ref|XP_719038.1| hypothetical protein
CaO19_6076 [Candida albicans SC5314]
MLTLAIGDLFVPERAVDLPSKFRKLLAPQPNNTPSNSKINQVICLGNITNSSTILQFLTNISPQFNLVKGEFDNP
VVLSQQLSSLNKSSNIPLYNRFVHDNLKIGYTNGFQVIPRGDPLALSAFARELDVDVLIWGGTHKVEAYTLDGKF
FINPGSATGAFNFDWPENDEEEREEADKSQDDDEATDKESHDTEEAEPKVENETSTSASDDFKQTLHEVSEINSN
IPSFCLLDTHGSTCILYIYTQIDGEVKVDKVTYTKD

>S.pombe_Vps29 gi|19115219|ref|NP_594307.1| similar to yeast vacuolar
sorting protein VPS29/PEP11 [Schizosaccharomyces pombe]
MLVLVIGDFHIPDRAPKLSEKFRQLLIPGKISQIICLGNLTSTSVYEYLKHVCSDLKLVKGAFDISSKAPIAGKI
TLGSFKIGYTNGHLVVPQDSPEALSILAREMDADILLFGGTHKFAAYELDGCFFVNPGSATGAPNVSAVEDDEKI
VPSFVLMDVQGAVLILYVYRIFDGEVRVEKMQYRKPE

>A.fumigatus_Vps29 contig4873 modified from gi|66849950|gb|EAL90277.1|
vacuolar protein sorting 29, putative [Aspergillus fumigatus Af293]
MTSRLVLVIGDLFIPDRAPDLPAKFRKLLTPGKIGQILCLGNLTDRETFEFLRQVAPDLQLVKGDFDVDSPNLPL
SKVVTHGSLRIGFTHGHTIIPPGDADALLIAARQMDVDILLWGGTHRFEAFEMEGRFFVNPGSATGAMSTGYWPE
GEEPVPSFCLMDIQGDVLVLYVYQLKTDANGVETVAVEKVSFRKNNIPSS*
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>P.nodorum_Vps29 gi|62183417|gb|AAGI01000106.1| Phaeosphaeria nodorum SN15
cont1.106, whole genome shotgun sequence
MASRLVLVLGDLFIPDRAADIPTKFKKLLAPGKIGQILCLGNITDRETYEFLRAIAPDLQIVKGDFDVEAPNLAL
SKVVTHGSLRIGFTHGHTIIPPGDGDSLLIAARQMDVDVLLWGGTHKFEAYEMEGKFFVNPGSATGAMTTGWWTE
DEDPTPSFVLMDVQGDVLVLYVYQLRKDAEGNENVAVEKVSFRKNGGGVS

>N.crassa_Vps29 gi|32415565|ref|XP_328261.1| hypothetical protein
[Neurospora crassa]
MAFLILVIGDLHIPDRALDIPAKFKKLLAPGKISQTLCLGNLTDRSTYEYLRTIAPDLKIVRGRMDVEATSLPLT
SVVTHGNLRIGFLEGFTLVSNEPDLLLAEANRLDVDVLCWGGTHKFECFEYMDKFFVNPGSATGAFTTTAASWAV
NLGSNGEGQKEQDKGFDEDEEVVPSFCLMDVQGISLTLYVYQLRKDEKGVENVAVEKVTYTKPVEPTGAGGAAAG
AGAAASGAASVSSS

>C.neoformans_Vps29 gi|58258243|ref|XP_566534.1| retrograde transport,
endosome to Golgi-related protein, putative [Cryptococcus neoformans var.
neoformans JEC21]
MVLVLVIGDLHIPNLVHDLPAKFKKLLVPGKIGQIICTGNVCDKETYDYLRTTAPEVHVVRGEFDENPHFPLSLI
IQHQSLRIGVVHGQQVVPAGDPDMLAALARQMDVDVLISGGTHRFESFEFEGRFFVNPGSATGAWSSLWNGEVTP
SFALMDIQGPVIVTYVYQLVDGEVKVDKVEYRKPDPTSEIQSQSTRSEVAARW

>U.maydis_Vps29 gi|49072008|ref|XP_400293.1| hypothetical protein UM02678.1
[Ustilago maydis 521]
MLVLVIGDLHIPFRAHDLPAKFKKLLVPGKIQQIICTGNVCNTDYLHYLRTIAGDVHLVKGDYDDNPHFPSSLIL
NHPPLRIGVLHGHQVVPAGDTQSLAAVARAMDVDILLTGHTHRFEAFELEGRFFVNPGSATGAWHPTWPLRDPAS
LAALSERTAAKTKEDATIADKKADEPKPKKGAKTSDNKKNDDSAKDKPSASELKDANKDAESNKDGDEEEEEAKE
AAAPVPSFALLDIQGAVVVTYVYQLIDGDVKVEKIEYRKNLDSNSLALQRGASGNAVAVGASATNYGQYGGR

>P.chrysosporium_Vps29 gi|46851680|gb|AADS01000252.1| Phanerochaete
chrysosporium RP-78 White_Rot252, whole genome shotgun sequence
MVLVLVIGDLHIPHRIHDLPAKFKKLLVPGKIQQILCTGNLCDRETYEYLRSVSPDVHVVRGDYDESALPLSVTV
THSPIRIGVIHGHQCVPGGDLDSLSAIARQMDVDVLVSGHTHVFQAVEYDNRFFVNPGSATGAWIGNINGEPTPT
FALMDIQGPVVVTYVYQLIEGEVRVEKIEYRKDIETAKEPPRSMPQSIPNSPPPQQQAVW*

>R.oryzae_Vps29 gi|61601706|gb|AACW01000352.1| Rhizopus oryzae RA 99-880
cont1.77, whole genome shotgun sequence
MLVLVIGDLHIPQRAHDLPLKFKKLLIPGKIQKIICTGNITDKSTLDYLRSIAGDITVVKGDNDQDMQLPQTKVL
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FVLMDIQASVVVTYVYKLINDEVKVEKIEFTKHLDANKIL

>E.histolytica_Vps29 gi|13276202|emb|CAC34071.1| putative vacuolar sorting
protein [Entamoeba histolytica]
MLVLVIGDFHVPHRSAAIPQVFLDRLNTGRIQTVLCTGNLCGKETYDILRTLAREVHVVKGDFDEMQGLNETEVI
KIGNFKIGLMHGHQVIPWGDREALAIYQRQLDVDILITGHTHKLETKEVGGKYFLNPGSATGAYSPLVDNPVPSF
MLLEINDSELTIYEYTLVDGSVKCERVDFNKKQQQ

>T.cruzi_Vps29 gi|70883998|gb|EAN96879.1| vacuolar sorting protein,
putative [Trypanosoma cruzi]
MVLVLVVGDLHIPQRAAAIPEEFTQMFSPGRINIVLITGNVGCREMYDYFRTVAPEVYCAKGEFDQWSHTQLKEI
HVITVEDLKIGLVHGHQVVPCGDRDSLAILQRKLDVDVLVSGATHHCKTFEFDGHLFINPGSITGAFTPAHLDVT
PTFVLLDIKEKTVTSFSYVYTRREGAAGGENFTIKRKVWTKE

>E.tenella_Vps29 contig177
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LDFPEYKILQFGEFKVALLHGHQVVPWGDADALLQWQRRLDCDIVVSGHTHSNSVREVEGCFFINPGSATGAYQP
WAPSPTPSFMLMALQGASVVLYIYEERDGKAEVVMSEFTKPAKK*

>P.falciparum_Vps29 gi|23509285|ref|NP_701952.1| vacuolar protein sorting
29, putative [Plasmodium falciparum 3D7]
MSGKLEDIGELVLLIGDFHSPIRNLGLPDCFKELLKTDKIKHVLCTGNVGCNENLELLKNIADSVHITKGDMDDN
FDFPEDITLCIGDFKISLIHGHQIIPWGDMNALLQWQKKYDSDIIISGHTHKNSIVQYEGKYFINPGSVTGAFQP
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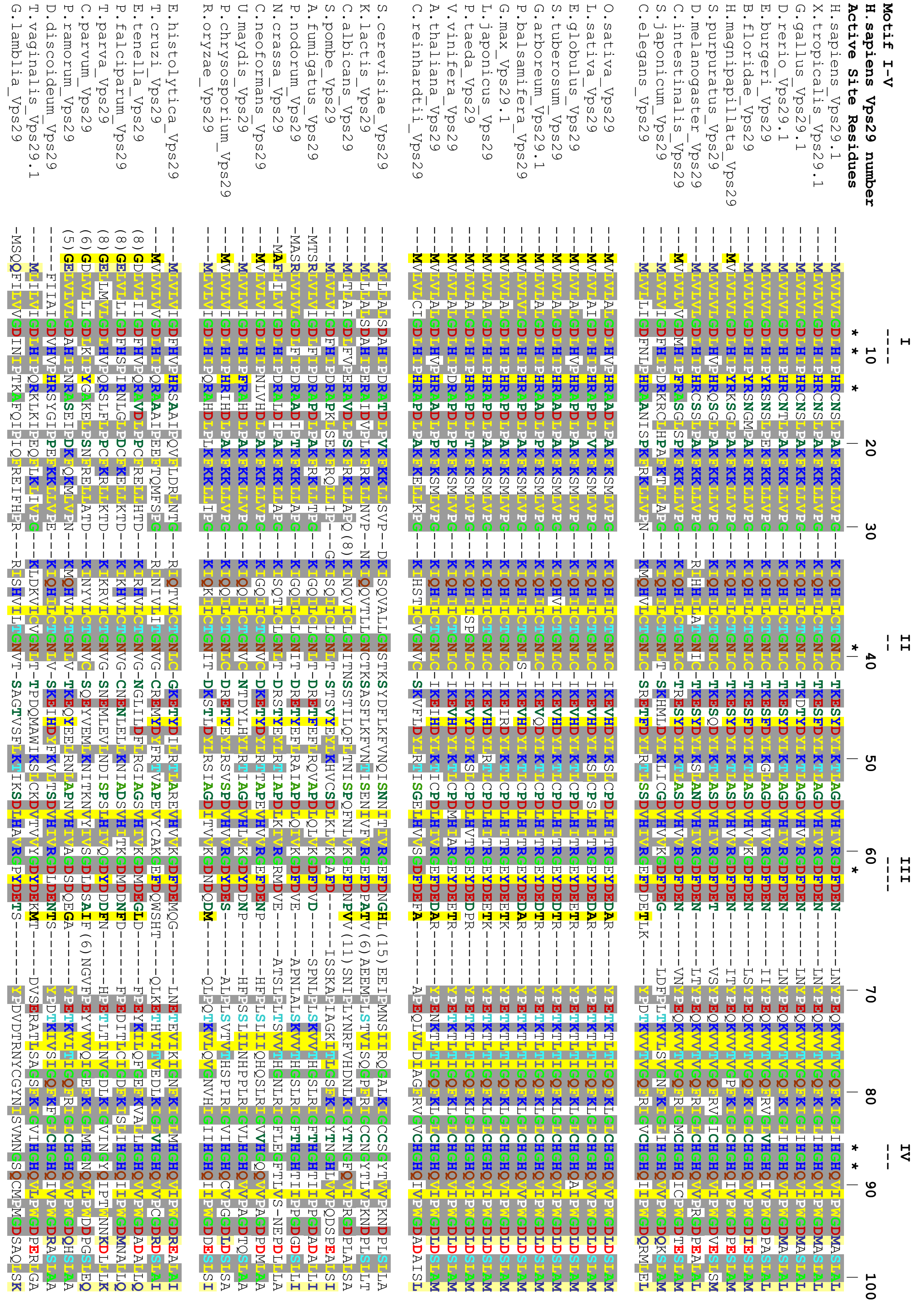
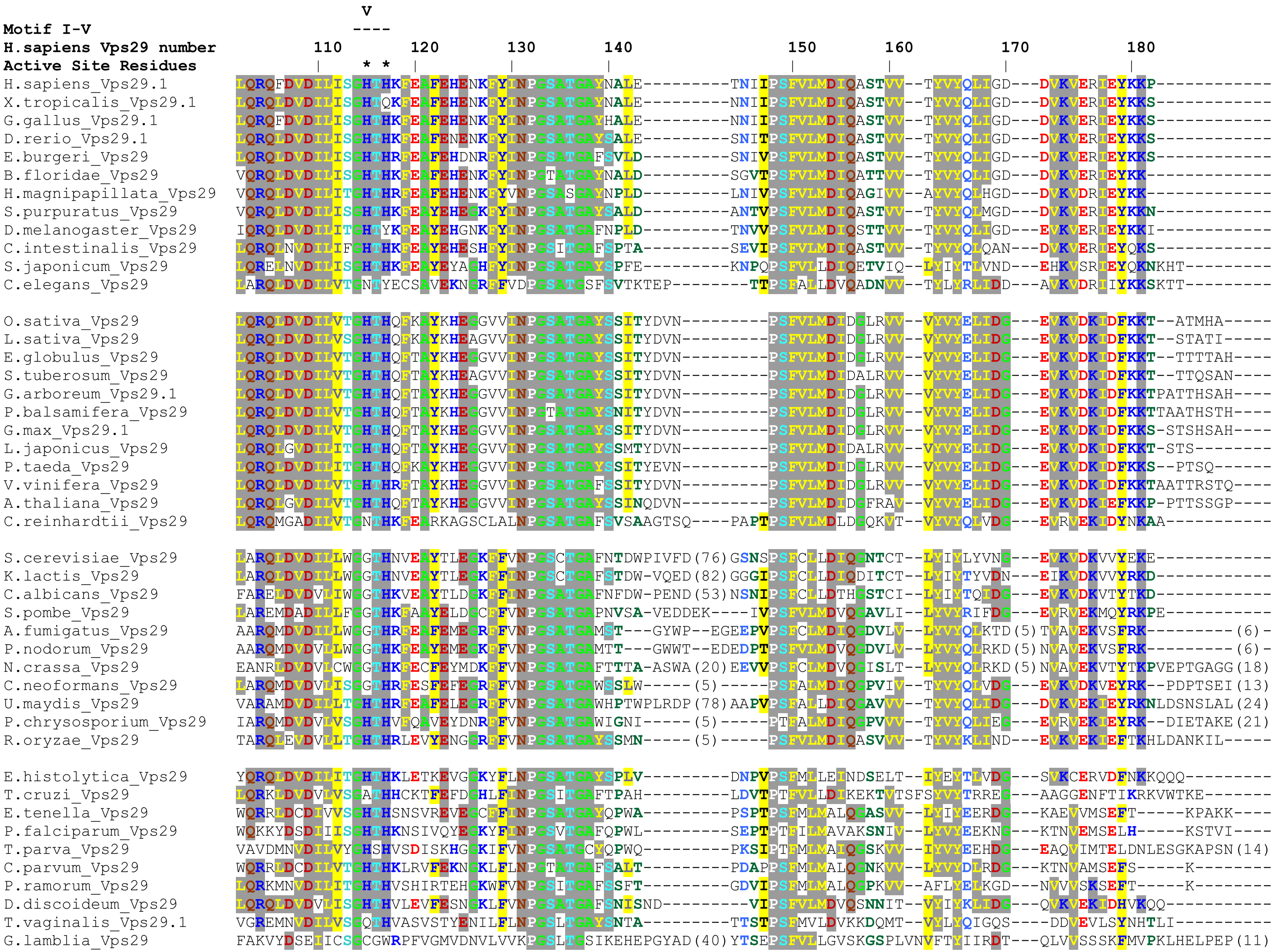
Supplementary Figure 3





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                                       V
Motif I-V                             ----
H.sapiens Vps29 number           110       120       130       140                150       160         170          180
Active Site Residues              |    * *  |         |         |                  |         |           |            |
H.sapiens_Vps29.1         LQRQFDVDILISGHTHKFEAFEHENKFYINPGSATGAYNALE---------TNIIPSFVLMDIQASTVV--TYVYQLIGD---DVKVERIEYKKP------------
X.tropicalis_Vps29.1      LQRQLDVDILISGHTQKFEAFEHENKFYINPGSATGAYNALE---------NNIIPSFVLMDIQASTVV--TYVYQLIGD---DVKVERIEYKKS------------
G.gallus_Vps29.1          LQRQFDVDILISGHTHKFEAFEHENKFYINPGSATGAYHALE---------NNIIPSFVLMDIQASTVV--TYVYQLIGD---DVKVERIEYKKS------------
D.rerio_Vps29.1           LQRQLDVDILISGHTHKFEAFENENKFYINPGSATGAYSALE---------SNITPSFVLMDIQASTVV--TYVYQLIGD---DVKVERIEYKKS------------
E.burgeri_Vps29           LQRQLDVDILISGHTHRFEAFEHDNRFYINPGSATGAFSVLD---------SNIVPSFVLMDIQASTVV--TYVYQLIGD---DVKVERIEYKKS------------
B.floridae_Vps29          VQRQLDVDILISGHTHKFEAFEHENKFYINPGTATGAYNALD---------SGVTPSFVLMDIQATTVV--TYVYQLIGD---DVKVERIEYKK-------------
H.magnipapillata_Vps29    VQRQLDVDILITGHTHRFEAFEHENKFYVNPGSASGAYNPLD---------LNIVPSFVLMDIQAGIVV--AYVYQLHGD---DVKVDRIEYKK-------------
S.purpuratus_Vps29        VQRQLDVDILISGHTHKFEAYEHEGKFYINPGSATGAYSALD---------ANTVPSFVLMDIQASTVV--TYVYQLMGD---DVKVERIEYKKN------------
D.melanogaster_Vps29      IQRQLDVDILITGHTYKFEAYEHGNKFYINPGSATGAFNPLD---------TNVVPSFVLMDIQSTTVV--TYVYQLIGD---EVKVERIEYKKI------------
C.intestinalis_Vps29      LQRQLNVDILIFGHTHKFEAYEHESHFYINPGSITGAFSPTA---------SEVIPSFVLMDIQASTVV--TYVYQLQAN---DVKVERIEYQKS------------
S.japonicum_Vps29         LQRELNVDILISGHTHKFEAYEYAGHFYINPGSATGAYSPFE---------KNPQPSFVLLDIQETVIQ--LYIYTLVND---EHKVSRIEYQKNKHT---------
C.elegans_Vps29           LARQLDVDILVTGNTYECSAVEKNGRFFVDPGSATGSFSVTKTEP--------TTPSFALLDVQADNVV--TYLYRLIDD---AVKVDRIIYKKSKTT---------

O.sativa_Vps29            LQRQLDVDILVTGHTHQFKAYKHEGGVVINPGSATGAYSSITYDVN---------PSFVLMDIDGLRVV--VYVYELIDG---EVKVDKIDFKKT--ATMHA-----
L.sativa_Vps29            LQRQLDVDILVSGHTHQFKAYKHEAGVVINPGSATGAYSSITYDVN---------PSFVLMDIDGLRVV--VYVYELIDG---EVKVDKIDFKKT--STATI-----
E.globulus_Vps29          LQRQLDVDILVTGHTHQFTAYKHEGGVVINPGSATGAYSSITYDVN---------PSFVLMDIDGLRVV--VYVYELIDG---EVKVDKIDFKKT--TTTTAH----
S.tuberosum_Vps29         LQRQLDVDILVTGHTHQFTAYKHEAGVVINPGSATGAYSSITYDVN---------PSFVLMDIDALRVV--VYVYELIDG---EVKVDKIDFKKT--TTQSAN----
G.arboreum_Vps29.1        LQRQLDVDILVTGHTHQFTAYKHEGGVVINPGSATGAYSSITYDVN---------PSFVLMDIDGLRVV--VYVYELIDG---EVKVDKIDFKKTPATTHSAH----
P.balsamifera_Vps29       LQRQLDVDILVTGHTHQFTAYKHEGGVVINPGTATGAYSNITYDVN---------PSFVLMDIDGLRVV--VYVYELIDG---EVKVDKIDFKKTTAATHSTH----
G.max_Vps29.1             LQRQLDVDILVTGHTHQFTAYKHEGGVVINPGSATGAYSSITYDVN---------PSFVLMDIDGLRVV--VYVYELIDG---EVKVDKIDFKKS-STSHSAH----
L.japonicus_Vps29         LQRQLGVDILITGHTHQFTAYKHEGGVVINPGSATGAYSSMTYDVN---------PSFVLMDIDALRVV--VYVYELIDG---EVKVDKIDFKKT-STS--------
P.taeda_Vps29             LQRQLDVDILITGHTHQFKAYKHEGGVVINPGSATGAYSSITYEVN---------PSFVLMDIDGLRVV--VYVYELIDG---EVKVDKIDFKKS--PTSQ------
V.vinifera_Vps29          LQRQLDVDILVTGHTHRFTAYKHEGGVVINPGSATGAFSSITYDVN---------PSFVLMDIDGLRVV--VYVYELIDG---EVKVDKIDFKKTAATTRSTQ----
A.thaliana_Vps29          LQRQLGVDILVTGHTHQFTAYKHEGGVVINPGSATGAYSSINQDVN---------PSFVLMDIDGFRAV--VYVYELIDG---EVKVDKIEFKKP-PTTSSGP----
C.reinhardtii_Vps29       LQRQMGADILVTGNTHKFEARKAGSCLALNPGSATGAFSVSAAGTSQ----PAPTPSFVLMDLDGQKVT--VYVYQLVDG---EVRVEKIDYNKAA-----------

S.cerevisiae_Vps29        LARQLDVDILLWGGTHNVEAYTLEGKFFVNPGSCTGAFNTDWPIVFD(76)GSNSPSFCLLDIQGNTCT--LYIYLYVNG---EVKVDKVVYEKE------------
K.lactis_Vps29            LARQLDVDILLWGGTHNVEAYTLEGKFFINPGSCTGAFSTDW-VQED(82)GGGIPSFCLLDIQDITCT--LYIYTYVDN---EIKVDKVVYRKD------------
C.albicans_Vps29          FARELDVDVLIWGGTHKVEAYTLDGKFFINPGSATGAFNFDW-PEND(53)NSNIPSFCLLDTHGSTCI--LYIYTQIDG---EVKVDKVTYTKD------------
S.pombe_Vps29             LAREMDADILLFGGTHKFAAYELDGCFFVNPGSATGAPNVSA-VEDDEK----IVPSFVLMDVQGAVLI--LYVYRIFDG---EVRVEKMQYRKPE-----------
A.fumigatus_Vps29         AARQMDVDILLWGGTHRFEAFEMEGRFFVNPGSATGAMST---GYWP--EGEEPVPSFCLMDIQGDVLV--LYVYQLKTD(5)TVAVEKVSFRK---------(6)-
P.nodorum_Vps29           AARQMDVDVLLWGGTHKFEAYEMEGKFFVNPGSATGAMTT---GWWT--EDEDPTPSFVLMDVQGDVLV--LYVYQLRKD(5)NVAVEKVSFRK---------(6)-
N.crassa_Vps29            EANRLDVDVLCWGGTHKFECFEYMDKFFVNPGSATGAFTTTA-ASWA(20)EEVVPSFCLMDVQGISLT--LYVYQLRKD(5)NVAVEKVTYTKPVEPTGAGG(18)
C.neoformans_Vps29        LARQMDVDVLISGGTHRFESFEFEGRFFVNPGSATGAWSSLW-----(5)-----PSFALMDIQGPVIV--TYVYQLVDG---EVKVDKVEYRK--PDPTSEI(13)
U.maydis_Vps29            VARAMDVDILLTGHTHRFEAFELEGRFFVNPGSATGAWHPTWPLRDP(78)AAPVPSFALLDIQGAVVV--TYVYQLIDG---DVKVEKIEYRKNLDSNSLAL(24)
P.chrysosporium_Vps29     IARQMDVDVLVSGHTHVFQAVEYDNRFFVNPGSATGAWIGNI-----(5)-----PTFALMDIQGPVVV--TYVYQLIEG---EVRVEKIEYRK--DIETAKE(21)
R.oryzae_Vps29            TARQLEVDVLLTGHTHRLEVYENGGRFFVNPGSATGAYSSMN-----(5)-----PSFVLMDIQASVVV--TYVYKLIND---EVKVEKIEFTKHLDANKIL-----

E.histolytica_Vps29       YQRQLDVDILITGHTHKLETKEVGGKYFLNPGSATGAYSPLV---------DNPVPSFMLLEINDSELT--IYEYTLVDG---SVKCERVDFNKKQQQ---------
T.cruzi_Vps29             LQRKLDVDVLVSGATHHCKTFEFDGHLFINPGSITGAFTPAH---------LDVTPTFVLLDIKEKTVTSFSYVYTRREG---AAGGENFTIKRKVWTKE-------
E.tenella_Vps29           WQRRLDCDIVVSGHTHSNSVREVEGCFFINPGSATGAYQPWA---------PSPTPSFMLMALQGASVV--LYIYEERDG---KAEVVMSEFT-----KPAKK----
P.falciparum_Vps29        WQKKYDSDIIISGHTHKNSIVQYEGKYFINPGSVTGAFQPWL---------SEPTPTFILMAVAKSNIV--LYVYEEKNG---KTNVEMSELH-----KSTVI----
T.parva_Vps29             VAVDMNVDILVYGHSHVSDISKHGGKIFVNPGSATGCYQPWQ---------PKSIPTFMLMAIQGSKVV--IYVYEEHDG---EAQVIMTELDNLESGKAPSN(14)
C.parvum_Vps29            WQRRLDCDILVTGHTHKLRVFEKNGKLFLNPGTATGAFSALT---------PDAPPSFMLMALQGNKVV--LYVYDLRDG---KTNVAMSEFS-----K--------
P.ramorum_Vps29           LQRKMNVDILITGHTHVSHIRTEHGKWFVNPGSITGAFSSFT---------GDVIPSFMLMALQGPKVV--AFLYELKGD---NVVVSKSEFT-----K--------
D.discoideum_Vps29        LQRQLDVDVLISGHTHVLEVFESNGKLFVNPGSATGAFSNISND---------VIPSFVLMDVQSNNIT--VYIYKLIDG---QVKVEKIDHVKQQ-----------
T.vaginalis_Vps29.1       VGREMNVDILVSGQTHVASVSTYENILFLNPGSLTGAYSNTA---------TTSTPSFMVLDVKKDQMT--VYLYQIGQS----DDVEVLSYNHTLI----------
G.lamblia_Vps29           FAKVYDSEIICSGCGWRPFVGMVDNVLVVKPGSLTGSIKEHEPGYAD(40)YTSEPSFVLLGVSKGSPLVNVFTYIIRDT---QLVVSSSKFMVPKLHELPEP(11)
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