

Supplemental Materials

Molecular Biology of the Cell

Holden et al.

Supplementary data for:

Involvement in surface antigen expression by a moonlighting FG-repeat nucleoporin in trypanosomes

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Supplementary figure legends

Figure S1: Locations of trypanosome nucleoporins during the cell cycle. A broad selection of trypanosome C-terminal GFP-tagged nuclear pore complex proteins were analysed for their locations at interphase and during late mitosis. Cells were fixed and counterstained with DAPI to visualize DNA. Note the clear essentially exclusive nuclear envelope localization for TbNup98, and the repositioning to the spindle anchor site for TbNup92 in mitosis. TbNup53B displays intranuclear puncta during both interphase and mitosis. Scale bar 2um.

Figure S2: Comparison of the distribution of the FG-repeats (red) and coiled-coil regions (blue) among Nup53b proteins of kinetoplastid flagellates. Panel A: The distribution of FG-repeats (red) and coiled-coil regions (blue) is shown for proteins of kinetoplastids. Predicted proteins were identified by BLAST, and where possible also by synteny. Panel B: Maximum likelihood phylogenetic tree of TbNup53b and TbNup53a homologs in eukaryotes. Iterative HMMER searches were used to identify both the human Nup58/45/yeast Nup49 and human Nup62/yeast Nsp1 as probable orthologs of TbNup53b as well as of TbNup53a, suggesting they are all members of a single family of related proteins. The phylogenetic analysis assigned TbNup53b to the human Nup58/45/yeast Nup49 clade and TbNup53a to the human Nup62/yeast Nsp1 clade. The numbers indicated by the arrow to the internode separating the two clades are the bootstrap/SI-like LRT branch support values for the monophyly between the two subgroups.

Figure S3: Impact of TbNup53b RNAi on PCF and BSF cells. Lower panels refer to BSF and upper to PCF throughout. (A) Quantitation of TbNup53b mRNA in uninduced versus TbNup53b knockdown cells in PCFs and BSFs. At 24h induction, ~90% and ~40% reduction in TbNup53b mRNA is observed in PCFs and BSFs respectively. (B) TbNup53b knockdown results in a gross growth defect over a seven-day period in BSFs but not PCFs. (C) At 0, 24, 48 and 72 hour time points post induction, cells were fixed and stained with DAPI to visualise DNA. This allowed categorisation of cells into distinct stages of the

cell cycle. 100 cells were recorded at each time point and the mean scores of triplicate experiments (i.e. n = 300) are shown. TbNup53 knockdown disrupts normal progression through the cell cycle in BSFs but not PCFs. An initial decrease in 2K1N cells is observed, followed by an increase in unusual cell types at 72 hours post induction.

Figure S4: TbNup53b knockdown impacts on correct nucleolar positioning and spindle microtubule formation in BSF cells. TbNup53b RNAi was induced in BSF cells. (A) Uninduced and induced cells were fixed and probed with anti- β tubulin antibody (KMX) and anti-NOG-1 antibody to highlight the spindle microtubules (red) and the nucleolar protein NOG-1 (green). DAPI was used to visualise DNA (blue). Scale bar: 2 μ m. NOG-1 appeared to have an unusual distribution in induced cells. Similarly, the spindle microtubules were often undetectable using the KMX antibody in induced cells. (B) The number of nucleoli and presence of the mitotic spindle were recorded in 1K1N, 2K1N and 2K2N cells. Mean scores from triplicate experiments are shown (n=300). The number of nucleoli increased in induced interphase and mitotic cells, whilst the mitotic spindle was undetectable in induced mitotic cells.

Figure S5: TbNup53b is not required for TSR1 distribution. TbNup53b RNAi was induced in PCF and BSF cells. Cells were fixed and probed with anti-TSR1 antibody and imaged by widefield microscopy. The distribution of TSR1 within the nucleoplasm was indistinguishable between uninduced and induced PCF and BSF cells indicating that TSR1 does not require TbNup53b for nucleoplasmic localization.

Figure S6: TbNup53b knockdown does not affect whole cistrons. Genome wide RNA-seq profiles following RNAi mediated knockdown were mapped at GeneDB for genes upregulated. The vast majority of genes are observed as singletons, indicating the absence of a significant impact on an overall PTU.

Figure S7: TbNup53b knockdown does not impact on the site of SL-RNA transcription. SNAP-42 was genetically tagged at the C-terminus with a 12xcMyc epitope in TbNup53b RNAi cells. The localization of SNAP42::cMyc (green) was monitored in uninduced (-Tet) and induced cells (+Tet -24h, -48h, -72h) by confocal microscopy. TbNup53b knockdown did not affect the localization of SL-RNA transcription in PCF cells. For all images, DAPI was used to visualize DNA (blue).

Figure S8: Expression of genes contained within the procyclin locus are not affected in TbNup53b knockdown BSF cells. The relative expression of genes contained within the procyclin locus following TbNup53b knockdown in BSFs were validated by qRT-PCR. The steady state of individual mRNAs was not altered following TbNup53b knockdown at 48h post induction. Expression levels were normalised to β -tubulin.

Figure S9: RNAseq profiles for selected loci demonstrate specific impact on the procyclin locus of Chr X. RNAseq read counts are shown mapped to the 427 genome, with control profiles at top in light blue and 12 and 48 hours post induction as middle and lower profiles (dark blue). Positions of ORFs are shown beneath each system, with the conventional top strand in blue and the lower strand in red. GeneDB accession numbers are also indicated.

Figure S10: Changes in the procyclin protein levels upon TbNup53b RNAi. 1×10^7 cells were extracted by 2% CHAPS (90s 100°C, 15min 12000g) prior to SDS-PAGE. Procyclins were detected by monoclonal anti-EP antibody (Cedarlane) or anti-GPEET antibody and the signal intensities were measured using ImageJ. Right: relative change in expression following 48h TbNup53b knockdown compared to uninduced cells (dashed line). The standard deviations were calculated from three independent experiments. The relative intensity of the entire Coomassie stained lanes were used to normalize the procyclin signals.

Figure S11: RNAseq map. Combined datasets for 0, 12 and 48 hour RNAi and singefungin-treated cells mapped to the *T. brucei* 427 genome, and corresponding to the data summarized in Table S2. Full dataset available to view or download at doi: 10.6084/m9.figshare.5017019.

Table S1: Sequences and accession numbers of proteins used for phylogenetic reconstruction of the ScNup49 and ScNsp1 families.

Table S2: Protein identifications for TSR1 affinity isolation. The top 25 hits were considered and colored as bold; affinity handle, green; GFP, red; possible splicing/mRNA processing factor, gray; likely contaminants, light gray; Obado keratin, black; others.

Table S3: RNAseq raw data. Sheared cDNA synthesised from RNA extracted from TbNup53b uninduced and induced (12h, 48h post-induction) cells were sequenced by 76bp paired end Illumina sequencing. Reads were mapped to the *T. brucei* 427 strain reference genome and aligned to annotated transcripts. The FPKM's of annotated transcripts is normalised by quantile normalisation and the statistical significance for transcript level changes is calculated based on (FPKM_{treat}/FPKM_{parental}) values against null distribution using *t*-test. In the filter column, '1' denotes a significant gene with p<0.05 and vice-versa.

Table S1. Protein sequences used in this study.

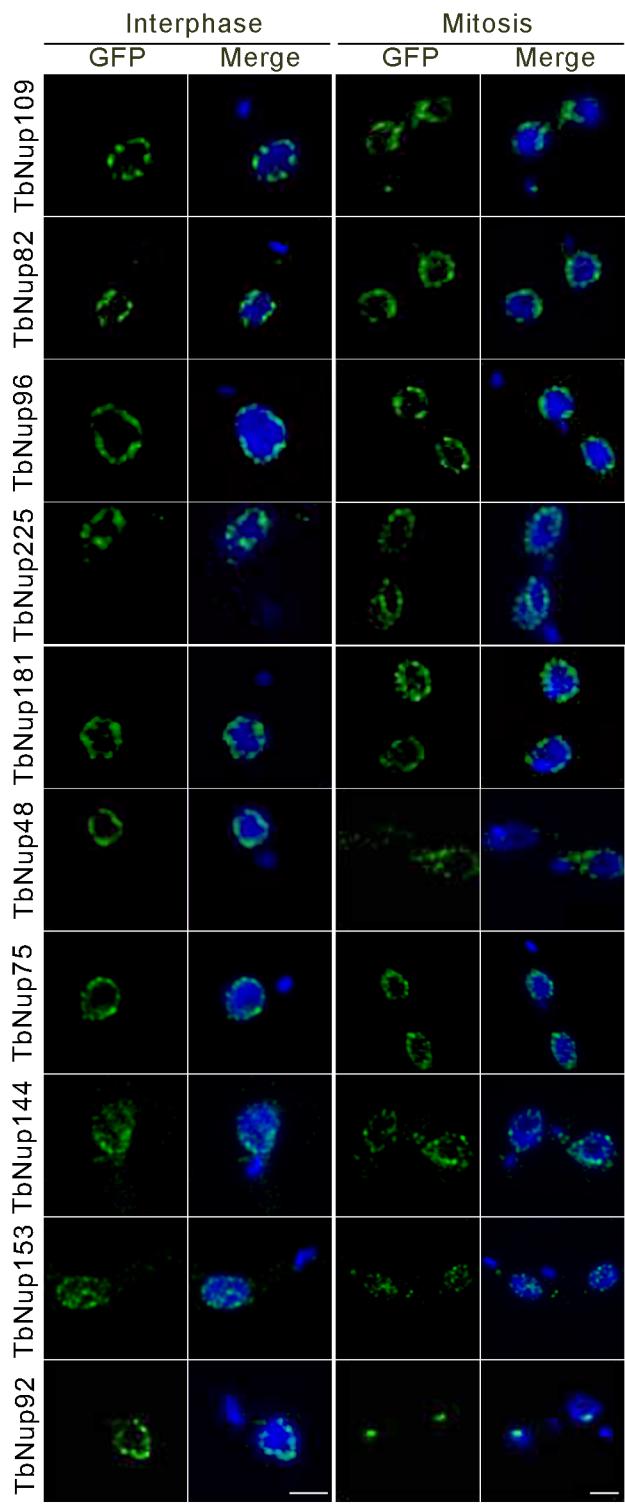
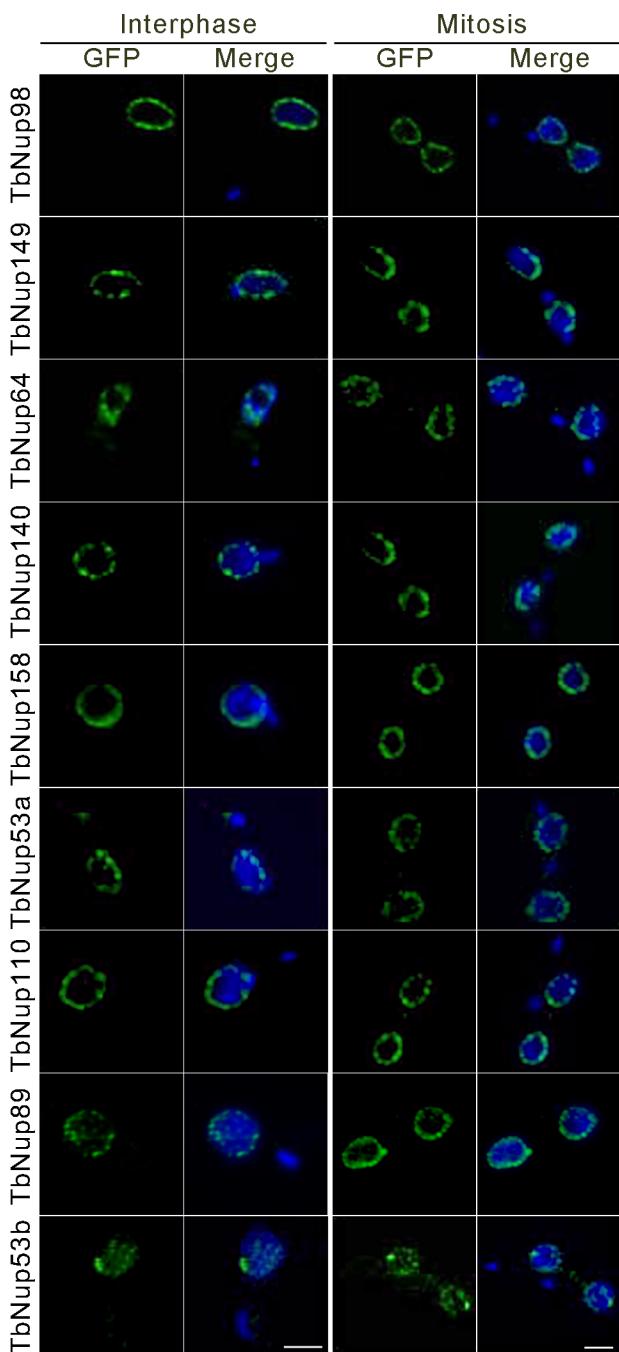
Species	Group	Source	Sequence
TbNup53b / ScNup49 / HsNup58/45:			
Trypano-soma brucei	Kinetoplastea	NCBI XP_843946	MMSMSTAPTGGGGFGAAAKGGFGAVTATGGTGFGTAAATGSTGNFGFGTATGSGF AAVTTTGTFGGFGAGKGFGTVAATPAOPHLPQYKGKGPGSTEWLHGVLNLSLIRD DVVFEDLPVPLQHQHDFHNFIQAEHDAKOVVFAFLTDSATPNATPAPSYRELVKKM NQLASGENAV/DGIRVECFEREVQAHRLGQTLDKCEDDILDMKNW/KPLSEIDFTQ RAGGNRPKPASEPFQRLREICGCMDAISAASVSELEAAVPPCGRVRGPVDDASR SNAEPEPPCASASEFTKLTKTGVLVPDVPPGGLGSAASAHPSRINASLSNQLTLL NLAATWLRLHTRADSARDLFVNHYGTSEAEFLLAQQHQQAESSAGRRPFLPPSST AAAAAEEVNQDTVGDIHRRSAFPHRSKALSNGERKMQYDVLLERKYQTAAPAAAPLS TATASGTASSVAGATLGTASSTSTIATGFGAPQSLGTIGGATIFGAGTSAADPRKTLN KTGRS
Trypano-soma congolense	Kinetoplastea	NCBI CCC89792	MSANVPVPGSADNRGASLGFGATPTAGMSGGGFFGLGVGMKTFGVNASSSTFGG ISINKFGVGPQAQPQIPPKYKGKGPGSTDWLQKVNVSSLRDVDLFGDPLPPLQQLH MEIHNFQIAEHAEAKQAVEAFLTDSTTRSIAGDAGYRKLVTLQSLQTLGGENAV/DAIRVD CFEREVQSHKLRSAMDRCDEEIDHNYMKQVWTPLSGLDFTLPIGCSRPRPSLEPFOR ALRETEECMKGSLSTTIAELKASVPGGHMCQRGIVDDKNNINSV/ADPSSSAASVHS RLTSLQPPHVPVLAGLGVSAHPVIRISSLNLARTLLNLARTLWLHTRADNARDIF VHYRGAPEAEILIFAGRQQEESSTDPRRPFLSSTAATSDAVKQDTIGDIHRRSACSH HSEALSDVGFIRMQYDVLLERSQQNSVPTATTAPATSSAGPVAPATTFGAATAPSPA VPGMGFAQTSSLGEARFGGRSSTSASKRTLTNGYRS
Trypano-soma cruzi	Kinetoplastea	NCBI XP_810452	MFKPGQASAGTGFAAAPAATAGKSASSGGGGANTVTGGGGNNSTVGFSFGA AKGKGFTAAAIQGQAQVPSYKGIKGPGFSTDWARSVNFSTFRDVLFEEPLPPQH LMELHNFQIAEHDAKRFVESFLDSIGTASAGDSSYMELOKKLVQTAGDNA/DAIR VDCFEREVQGQHGLMILLENCEEDVQYSKHWVWEPLAEQDFTQRLGGNRALPEP FOCKLREVQTRMEEAVLAVQPKRQKRTTNDKNTSNTTNEPASHF SRYTAEMKPLDTATGLRPTIASHPVQMNTTLSNELATLNLAAWTSLRHALADAAR DLFVHLYGSSEAEVLLAQHQWQMPVGPKRPFPLRSAEASSFSEPNDTIGDIHRRS VGLDRLGNSGERRMQYDVLLERQRQDSDAPASVGNTITGFAAPVAPAAAAVA SAVPLTAGTTTTASTAAAGFGASAPPATGTGGTTAFGAPGLGTASSTRANKK GRV
Trypano-soma vivax	Kinetoplastea	NCBI CCC47107	MMFGQSSQPAFSSAPGTNAGVATGATPFFGAVPPGVVGAGATSFGSGFNGKGF ATPQQGPQIPPKYKGKGPFSAEWRPLVNLNLDKRVFEDLPPPLQHHLIELHNFVQ AEHTAKQFVKSLADSVGPPEGAASYRSLSKNCRLLNKGNAVDGIRVDCFERES QSNRLGHILDKEEEEVHNYIKHWEPMSEEDFTQRRTPSGSESSEPPFSALCEIQTY MKEVAAEMKPLDTATGLRPTIASHPVQMNTTLSNELATLNLAAWTSLRHALADAAR CEASAGSGSPAITNPVAQVNSSLNNELTALLNLATWTLOLHSRAEDARDLPHSR VHMYG ASEAELFSQNQQRNAIGPKRFLPLRSAKAATKEDGHTTIDHRRSIGLDRALARVS SGERKMOYDVLDLQRHVPLVGAPPTAPAGLNPVASTAPAVTVGAAPTNFTAPA LLGSTATPSSRTGTGEFSRHRVGGKGRQ
Trypano-soma rangeli	Kinetoplastea	NCBI ESL12123	MFGLGQTSAGTGATAPAAATAGKSAPFSSVGTGATAAAGGGFGSGTNTTATGGF GTSTVGGFSASKGFTATAIAQPVQPPYKGKGPFSNDWSRSVNFTLDDA LFEELPPSLQHQHMLMELHNFQITEHEARLFVESFLADSVGAAA VSSYRELQKQLAQL TTGENADAVR/DCFCEVPLQPOLOQHMLMERSFMHAERDAAKVYLYFNESDDADSAAG AIATSATGSSPTASSSSYRQLLAQMAALKGGNRAVDLVAHNCNQHEGQTRQL QRLEKLEANIRDYERHVWEPLLEQQLPQLSSGMLLQGSMNAAGGGAYRPAVNSNGAASP ALVEELSHRMHDHVSSALTELEATLVPGRSLRGAGVGGCRGHINGRAISNDIAQIN AALVYELNQLRDSSVVAHLHSRTDIARELFTQYQGAEEADVLFADETEQRNRGMLT FRFRASPTFYDIPPLPQQSQSOSAASATTMGIATPATGFGAGTTSALGGGIGATS GGGAFGAAPAAAGAAGAATTGGFSAPATAAAAPAGGGVVGFFGFGATAPAAATGFGA AAGGTTSTPAAGLATAVGGFGAATAGFGAALASATAAAPAATGAPPFAPSLGPAA PGSATPVFNLLGGGAAATGTGGMAPGKSGIGGGDDDRPSRRAR
Leishmania braziliensis	Kinetoplastea	NCBI XP_001566 428	MSLGGFGTGANAGGGFGAKPAMATGFAATPSTGAGTGTGPGVNGGHRGGFGTSA AAAGGGFAPLSAPGGFAPAAATGFGAKPGFTAPATGGFGAGGGFGIGATTGGT GFGSTATSGVGRGGGGMAGGGFGSTTAPATAQYPPYQKGKGPGNATSWAR DIDFSQVTEQVRFEALPQLOQHMLMERSFMHAERDAAKVYLYFNESDDADSAAG AIATSATGSSPTASSSSYRQLLAQMAALKGGNRAVDLVAHNCNQHEGQTRQL QRLEKLEANIRDYERHVWEPLLEQQLPQLSSGMLLQGSMNAAGGGAYRPAVNSNGAASP ALVEELSHRMHDHVSSALTELEATLVPGRSLRGAGVGGCRGHINGRAISNDIAQIN AALVYELNQLRDSSVVAHLHSRTDIARELFTQYQGAEEADVLFADETEQRNRGMLT FRFRASPTFYDIPPLPQQSQSOSAASATTMGIATPATGFGAGTTSALGGGIGATS GGGAFGAAPAAAGAAGAATTGGFSAPATAAAAPAGGGVVGFFGFGATAPAAATGFGA AAGGTTSTPAAGLATAVGGFGAATAGFGAALASATAAAPAATGAPPFAPSLGPAA PGSATPVFNLLGGGAAATGTGGMAPGKSGIGGGDDDRPSRRAR
Phytom-nas sp. isolate EM1	Kinetoplastea	NCBI CCW59601	MSFTFAAAPAANQAGAAGKMLGFLSSPVAASSTPAMNTGFTNTGFMKPG TFTSGTGISNTATGVGNSAGGFPSTTGFSSITTFGNSTNLNTLPQLPPYKGKGP GYAKTWONTVDFSQINDYTLFDLSPPLQHMLMELYAFSSKEEESVRAVTVDLNIDIK PIHTGKGTANSKMDTNGSYRHSRQLAELKGGSASHAVPIVAVSCENHEKEAQFSQ LDHQFESIREYQHRVWEPLLASGNLTRAKNNSTNSLGSMSFDHNVNAKSPLL SIEELOGIMRTLSQIEELKMNVMPSLTPNHLVNAADSAKODRSLCNAYASNVYL VDGRTPLYRNTSLNNYNSNRCDRLQFCPTSPSLGTTVTGFGSALEGDPOTSSEVI PQINASLMSLFTSLMNLSSWAGHLHKRTDTARGIFTRQYQGYEADVLFKPPRSQET PLVPGLSAPVLPAAAPVAAAATTQMANFSVMMNTATNLQATAPATPVGGFGSG QGLVGSFGWKTNPVR
Crithidia fasciculata	Kinetoplastea	NCBI AODS0100 0155	MSFGGGFGAKPATAAATGFGAATAGGGFGSPAGGGFGSAGGGGGFGAAA TTGGFAPATAPAGGGFGASAAGGGFGAKPATAAAGPFGAPTTGGGGFGSSATG GGGGGGTSSGGFGAAPTGTGFGAPAGGGSGLATMTGGFGAGRGFFGVASTGSG GGMGAAPAAAPAAAPTAQYPPYKGKGPNSMSWAREVDFSQVTEQTPFESLPQPL QOHLIELRSFMHAERDATKKVVEYLNESDRSTSTQTSAAA AKAGAGDAATSYRGL LSKLADLKGSNCNAVDLVAHCNQHEGQARQLQRIERLEASVRYDYEHRVWEPL ERGLPQSTNGGTSGLRGGMYRPSASSDAASPPVALVEELSRRLDSVSEELGALEA TLVPPGRPLRGVGSGERAGHRRGGSAVPSDAAQINASLLYELNQLRDFSCVA SRDTDAARELFTQYQGAEEADVLFTDTEAQSRQGALFRRASPTYDIPPLPQLS VAAA AAAAA AAGGGFGAPAA PTATGGFGAGAGTGGFGFGT KPATAPAAA PATGGFG AKPSTATT ATAA PAGGGFG GAA PATAPGTT SAT PAA PAT MGFGAG PASGA

Tuber melano-sporum	Fungi	tr D5GCV8	MSLFGRINTPTSGTPSLFGQQQQPQTPLFGSTTTSGSSGGPLGGASQPAAPA PAGLFCGGGQAQATPAIGTGCISGGAATPATSGGGGGGGFLGGALTPAATPA PASGLLFGFTPSITTPPTGAVPTGGLFGGAATQAAATSAQAGGLFGAGTAASASAPAT GGGLFGGGTSQPPPKPLFTGPSAATTSTGTGAFGSTATPRPGGLFGGTTPSTTQPQ QQSQQQQNVTVAATIDASKLIPTRFGDCHAEVQRILEGIEQEIQRIATELAHFP GHRATIDSIPSDTAVLTHKLATTKSFLAADDAAALARQHHNEDDAATLTSIRNVDF RVLPAQRSOYIAQQHNPQMRENDSITSKPMINVFDTQIAKMDQKLDLFLESVQEVEL SLRSVEEQTAMGSIGGENLTALGGVGRQDARRNLNTREFNDALKDVSGRIVDS KDGIRALRSR
Dactylellina haptotyla	Fungi	tr S8AK90	MSLFNRVSNTPSAINTSAAANTFGTASGAATGGIGGTAAPSLFGQSTASQAPASAGL FGGAPAAAPSGGLFGATANTTNAAPTAGLFGGAAQTAAPAAGGLFGAAPSITSA GAGTGFAAAATPSAPAAGGLFGAGQATAQAPAPSGFFGGGPAMQPQGATQGAAAG GGLFGGSTAGGSLFAQSCAQRFAGSMFGQQPAQCPNMFGQSSQAQCPQAVEM NFSNMRGTRYFEELHADVRNLDDYIQLKAIGISQELSARTVGHKETMESVDGDV EHVSRKLGFITFLNNDGHISQQLHNASSQLINTAALSTRTIDILRLPISQRSQYLSH HTSNPEYSLIPYFEEKAGELEGTKQNFLAAVEDEVKTLEAVERDVGVQVNMSAESKV EVVKAERVVFSGLMVAASKVASVNEDELVKU
Cryptococcus neoformans	Fungi	tr Q5KP67	MSFGGFKGNSSTTAPATGSAPTTSSPFSGNTSTSNAQPAAGASNTGGGMFGGF GQNNQQQQPQPAAGGGSLSFGAKPAAPAAAGTGTGGGLFGGASGQQQPPS GGGLFGGSTTQQPQGGNQPLGASTNTPFGASTTGFTSTLNQNTQNAQNTSQAKL LFGSTVQKPAQSGLFGSTTOPTQOSTIGLFGSTAQTAQQPASTGLFGSTTQQQP STSLFGQSTAQQLGGSSLFGQTTPQQPNQQQELKTSANPGANTGADKTTKFDLPEA AQKYKIMQLDIAKQKSIASTLQTEPLGRAWITSDLVKSATEEYSSISHTLKSLSKNYSIS QLRDKMIDQSRDVERIKEWDIYTSGEGRMGQIRLGAYPEFPEHEFFS TRYKKTTQLNRVVASLSSDQSSTSPQVIQONTINHHQQAIALAAQLDQLQVRMNGLK AEFTADWRDKTGSVRDPFEMAREERNVKV
Wallemia sebi	Fungi	tr I4Y9E0	MSLFGNNTSGGGGFNFQATAQPQQQASGGFGFGGGSNTQAQNTAAKPSLFGGA AAPATQQPATGFGFGQQTQQPQQNQQQQTQGTLFGQSQQQSTTGGTFGGF GGTQLLGFGSTTQQPQGGNQPLGASTNTPFGASTTGFTSTLNQNTQNAQNTSQAKL TRTTKFNDLPDAHRIEIDIDAHQGRSHIALALKEPLGKDVRSSVLLDQVSNDLMS LQGTLASTAASLSDSLNDTEQDVTALMTDRGTYRPPQESGAWLKTYRDFFHEFF AOTAVDLKDRANKYTGLEIEKHLSYLLTANAAGHTPSQIAQILQHQATFMSLASN VAELAAATTNLKDGYRDIWRSKTSKSYADPFALSNSVEM
Puccinia graminis	Fungi	tr E3L419	MFGASNPSSASAAPSSGGLFGSAKPNQNSGNIFGSSSTTSGGLFGASTTSTPQTTN LFGSSTSAAATTQTLFGSTTNQQAQTQGTSNLFGASSONTTSTNLFGSNNNATG GGTQLLGFGSTTQQPQGGNQPLGASTNTPFGASTTGFTSTLNQNTQNAQNTSQAKL NLNTSGVNLFGGNQNGNSAPLNGNSFGTKASSVPVTPAPSVSQSNPVFTRTFRNDL PEDAKKQLETIDAMQTQCRHSRDLTAKMLQGTEITEGTSSLRQVTSEMHTASAVKT SNLSDSIRQSIDGDVADLLNLAIVDAHHSQRMAVGSHNAESLPNPMKFOFFFS QKAADMEERVKRYRQTDYVELQLKGLFDRPSPASIVPALKAQYSTFMVLADKV AQTAVRNLRKEEYRDIWRHQTGSVRDPFAEIDQAFGLGSSTATFQAG
Homo sapiens	Metazoa	sp Q9BVL2	MSTGFSFGSGTGLGTTVAAGGSTGGVFSFGTGASSNPSVGLNFGNLGQSTSTPATT SAPSSGFGTGSKPKATLGLTGTNTGATTTTGLTGPATTSAAATTGFSLGFNFK PAASATPFLPITSTSAGLTLSSALTSTPAASTGFTLNLQGTTTATTASTGLSLGG ALAGLGGSLFQSTNTGSLGQNALGLTGTAAATSTAGNEGLGGIDFSSSSDKKS DKTGTRPEDSKALKDENLPPVCIQDVENLQKFVKEQKQVQEIESRMSSKAMLKVQE DIKALKQLLSSAANGIQRNNTNIQDLKIETAQELKNAEIALRTQKTPGQHLQEYAAPAD YFRILVQVQEFLVQYRQKQVQHNLATQANNHITPQDLMSAMQKQYQTFVALAA QLQSIHENKVULKVEQYLGYRKMFGLDADVFTERAAKKWVNTPRVTTGPTFEST MPNAAAAMAAATLTLQQQPATGPQPSLGSVFGTPFGSGIGTGLQSSGLGSSNLLG FGTSSGFGCCTGASTFGFTKPSGSLSAQGSSSTSGFNFSNPQGITASAGLTF GVSNPSAGFTGQQLLQKPPAGNKRGKR
Hymenolepis microstoma	Metazoa	NCBI CDS28776	MALLASLSNILDSDKQQKDQTVPEELTVVEELKYLAEQKKIRDEVAKTSNKQLDDLS TELQELQRQSVTCNLQSLRRONVKSSHLSSEEIQLERNTGIIQRSLDMSSDFAQNSPEI NEYFKLQNSFSNSRVTQYKQVEVLAIESLSSRAKSQNLTPKELSDILRKLDDTFMSLAA QLYSLNEQQLSVPAKHLRQYQSLDQSGQIESSTAAMSLFDEIIFSEKKSANTPYGP SPFSSVTVTGAQAAATATSGPLSLGLVLTQQPSTVTTSSAFSLSLAKPSSGASSFSL GGTTASALSFGLGGLAKASTSTPSTAFQSGNTLTASSGTTTNTSTFGGLST ASQGLSTGFGFTSLTATPTTTAFTGFGTGTGTSIFGSPATKPSLFGS
Hydra vulgaris	Metazoa	tr T2M6T6	KTESERKVMATSSGGFTGATNNNSNIFGAKTTTSTFSGTTAPAFSGFGLSNTSNASS TLAFGATTNTNPGFSFGGGFAGALTSTLPSSTSGLFGSKPATTGFSLFDTKSTTAT SLPFQLGVSATPSQLQSDSSFAKPLLENPKVEKVPAAEFVTYINETENYLTQRELK DEISRISQTVNEIQLDQLMNTMQIAIIANSLSLQRDKLAAEYLKNQVQGELKNTETARLI RDLPLSNLHDNFAPMQYFQLSLVLTQFQIRKKSQREIEELEVFLSSSSPSNQFTPQDLK VVLKRLKSESFLGLAAELCTVHEAVKMIKQKYLQFLRSTFDYSDPFTSRRLKKDLREK EPSDFNGSPFPPIQAGAGISGAFKIDNPKONLQYQNLRNNSAFFPKPSGTGLTRSLSD EIAKSTPFSVSTEGSNTNNNPLQGSPATSSSSNSFKLNRNPPNGKRGKLY
Ciona intestinalis	Metazoa	tr F6TX13	MAFKGFGTSNTGSGGGFSFGGASSSTAATKTTGFSGAPATASTGLGFGAKPT VSAPSLGANQSKPAATGFSLGSATTKPTLFGQQTASTASALTLGSTQPQTTKP KPTLTTSTTSLGGLFNTQTPAAKPGAGILGATTATGSGVFGTPATTQSTMGLGGVDPKT STTAAGGSAADPKAGDGKTLKQSKQVPPPEIVKTEDFKTYIKEEKTQVEGIRSMSCKP MYKVKQEDVASLQKOLLSIVSNGLQRNACAVEKLKEMTMQELKNAEMAQRTKDIQAGL QYENTAPTEYFQLRVENFETQMLSYRQOQETLEGHHLHSISQPSILSPEELVELLRLKH ETFIALLAQLHQVHEAVKTQKEHYLNRYKIFLHDTKNIFEREKKA/KPKVLPEHFGPK LVEELLRLHETFIALLAQLHQVHEAVKIIYGFSTAATTTTSSGFTGLNTATVRPLGF GTPAAPTITTPSLFGLGTPQVTPAFGTPQGFPSSAGGEQPFQLNKKPPGRTKLGFEI GICGSEAKYMFYF
Crassostrea gigas	Metazoa	tr K1QL21	MFGGKPNPTPGFTGATPSAGSTPATGGGSFGTPSTQATGNVSFSAAVGQTPAA GPTSSFSFGATPTASTGGFLQGLTPSFPSTQSSAAUTTGFTALGTSTASTQSGGF KLGTTLPPAFPGTSTAPGTTAVAPAMGCFAMPISSTATVGGGLGMGMGLGGA KPTLTTSTTSLGGLFNTQTPAAKPGAGILGATTATGSGVFGTPATTQSTMGLGGVDPKT STTAAGGSAADPKAGDGKTLKQSKQVPPPEIVKTEDFKTYIKEEKTQVEGIRSMSCKP MYKVKQEDVASLQKOLLSIVSNGLQRNACAVEKLKEMTMQELKNAEMAQRTKDIQAGL QYENTAPTEYFQLRVENFETQMLSYRQOQETLEGHHLHSISQPSILSPEELVELLRLKH ETFIALLAQLHQVHEAVKTQKEHYLNRYKIFLHDTKNIFEREKKA/KPKVLPEHFGPK LVEELLRLHETFIALLAQLHQVHEAVKIIYGFSTAATTTTSSGFTGLNTATVRPLGF GTPAAPTITTPSLFGLGTPQVTPAFGTPQGFPSSAGGEQPFQLNKKPPGRTKLGFEI GICGSEAKYMFYF

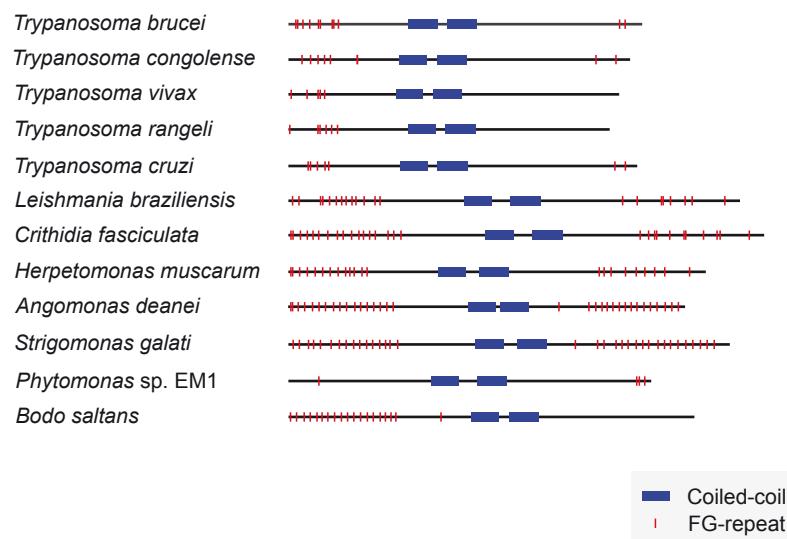
<i>Phytophthora parasitica</i>	Strameno-piles	tr V9EIM9	MAFSFGGTAAPAAASSGSFGSTPAAPAASSGSFGATSAAPAASSGSFGSSAA PAASSGSFGATPAAPAASSGSFGATPAAPAASSGSFGAKPASTGSTGSFAS TAPASTAPSFLFGTTGATTTPAPTCGFQFGFTGQPAATGGFFGFGTAOPAAATQP AGPPITLETAFEALPDDVKKNMTOQFHAFLKEDQDSDAFLKTVSPROMEVRENMAK LEQEVLARRNRNQRQTAAVQHVRQDVRQLLHQVDAATLTRRSLDSSNGGTPNMYH VMRRVEMPSPYWWELLDHYEQKMAAIAQIODEVAQFKPLYDGRSNANATGAGAP APAQLQQLAQNAALMQAARVAEVEHEKAEELRQLFLTKMREDLARHGKEKNPAAF QNPFDKRKKSEADKRAIDKIRFRTSVAPTTVTPQPAAPATGFGFTTSTATTP TSGFSFGSTAASAPAKTVSFNLTSTTATSVAPPATTSITAAPLATGFTAPTVATSGF GSSFLPSATDTSAAVGSKRSGRAKQMKR
<i>Albugo laibachii</i>	Strameno-piles	tr F0W7S3	MKTSRESMRCLCEAFKNNSVSTFCLENTICIASMSFSSTSPPNSSGFQFGNPNSSAAS PSGSALTSPKFAGSTWNANPATPTPAPTCGFQFGFTGQPAATGGFFGFGTAOPAAATQP LETLFEDLPNDVKENIIAQFOAFLPQDFQKLMQDLSLTLQMVQSRQ HILARQNTSAHHGKDVKHTVLQVDEASILRNSMDKONGSTTLVAQIARNVHTPSPF YWKLYESFENRMSHLQQIEELQLCIQSDMIRECNSPNDSNIIQSNTGQSISINTD SFHDIFVQGNAALMKVASLVAIHERNEKLDRFLANMVKMQDYIKHGDIAAEFTFKNPF EQSQKRNLAEQERRQMLDTIRKTTVAPSLVNSQPPAVNMIASTSNTNPSTTP NVFGVSAPTLPNPKHVTDFGTSAPAATTTPSFQFGTNPIGCTVPGAGSSSSS LFSSSLTDKSKRSRSTRSKTR
<i>Saprolegnia diclina</i>	Strameno-piles	tr T0S2F3	MAFSFGASGASAAPATGFSFGGASAAPASTGFSFGSTPAATSAAAPASTGGFSF GGSSGSSTTTAAPASTGFSFGGNSTPAAPAAASSTGFSFGGSSTPAAPASTGF SFGGSATPAPASTGFSFGGSNTTPAPASTGFSFGGASSTPAAAPASTGFNFGSTA AAPSTSFSGSAPAATPSSLGGAAPGNTKLEDFDLPAVDQKQLIEGFTFVKE QSREEASIRAVSSAKLTQLKESTTHLEGQAALVLQNIHARQAKNIGALKTVDKDLVVA EAESADQTHLHMSTETGIQRHEPMPSYVWSLQHESRLATLKGQMTDVHSQQLQGA KHDVSMDADEASTVHMTPRLVQETLQSNEAFMRAARADVHERADTLRDQYL SRQQAAPHGFGVLRNPFEEADRVQAEERRIVDRIRLSAACSTLPASSSTAVTTAA APTATASTLTSFGAATTPAPAAAPATGFSFGAAAATPAAPSAFGTSSFGAAATGA VPSLTKSFSFGSLGTQVTPDAGAFGANKSARRPKTKR
<i>Aphano-myces astaci</i>	Strameno-piles	tr W4FE99	MAFSFGGTTGAASTTAPAFNGBAAAPAAATPSFGFGFTASNAAPAATTSGFGAPA STGSTGTPAWNGLSSATPAATSTPSFSFGGATTTPAAAPTSFSFGSTQPATGF AA PASNAFSFGGTTNTAAAPSTGFSFGGFTGSSNTQSLFGKPATSGGGFGSFQAPSQF GVAAATPAQPPQPVVSLDRMFDALPPDVQTQKDFDHFLKEQSREEASIRVSQAQPL ADLQDATKOLEQVALVNRNIQTRQAKDQIOLLSKSDVKNVNSQAEADQIHHILTSDTGI QRTEDEMPSSAYWTLVQDFEQRQMTQLCKQMTDVHSQLQGLQQTTRPHMHQPTPQL QLQLQSCNDAFMNIAAHVATTHEAEVLRDQYLATLQHQQPDGGKVRNPFEEAAD RIQAEERRIVDRIRLSAAQVTFPAATPGTTAPASSFSFNTPAAAPATAAPAPSTFGT ATGGTSFSFPAPVSTAATTPSAFGGAQPPPTLTKSVSFAGLGNVAPSADNSAGA FGMPVVSNLPKSVRRKPSSTKRR
<i>Thalassiosira pseudonana</i>	Strameno-piles	tr B8BZW1	MAFSFGAPTAAPATLAASTTSFSFGATAAAAPAFGAPSSAAPSTSFGSTPAASTTAP STSLFGGTTPAPASGGGLFGSNSPVLFAFNISQAPAPSTSFGSTPAPSTGGLFGSTP AAPSTSLSFGPSSAVNSGGLFGSTQSAAPFGTAQPCQQQQQQQHQATPLS ANTPYSQLDPSAKTIDSYIOLMMHRRRTLSVKTMAPSSLRIEGQENIHSAASND NIPSSPADAAGFAKRSSSSKSKEPIDPSNMSLPLQQMNLHTQINTLRLSAEINMAE AQQLKSRAGNAACVAKMHGAWSVAVRQVALSSVRAVLGDRKDASSGRSDG TSALGGNGGTASSSTSSGGTPASSLNVSGMNNVDAVALQHMDVRAASVDRME TMPSPYLWEVHNFEERVAIVQRDVDAVKARLTIAEAERVQALGGSGMPLGDETA LLLSNNCFAAMASLMMYEGGGIQRQVPLCKSLASLRSQNEQFLRIAQARARVHEG LEEVKMRYRFFCENNTHYGGGGHEDPFLRADVEIRRELOQRRIEEQLATVSPVK TSFLFGAATPAPSTSFGSTPAPAPSTGGLFGSTPAAAPATGGLFGNPSPAPAT EGLFATPTTPAPTLAPRKPGSRSGGRR
<i>Thalassiosira oceanica</i>	Strameno-piles	tr K0TB43	MFLQKPYITNNLTRVQPROLEEAFSALLAMRRAFGAQRLVRNKKILRTQNNNDIPH NMKYCSYHLRPAPSAFGAAGPTKNAEFWSLSESITLQQPAAPAFGSAPOQQAOQSP VFSGNTPYSQLPDNAKRAIDQYQLMMQHRTLAVKTMAPALLADQSSCTDSMNE KVSPDAAAAGSPKRTTPQTDETLSQVM/GLNSQIQTLLQSAESNMITEAHQLKSRA EATAQAKLHGAWPVALSSVIREALLNDPSGEPSAGNSNGKPASSVNV SGMTNLDAILOQIMDIRASHDVRVEAMPSPYVEVHNFEQRVIAVQRDVAVRSR LAIAEEAERVQAAISGRRMGNDASLLSGGNANTMMMLYQNNQHGVPLPKLAS LARSHSDFAIQISAQARAHEGLVYQLRCLCQRQGYYDDPFLKADVEEISREER EMQHRIREEQIATAPPPEPKPAQAPSTGLFGAKSPAPATGGGLFGAPAPSGGGGLF GSTPTSKSLFSSSCQIPHLSSQLTCVPDEGGFLFGSTTSAAGGGLFGSTTPAPAA APAAGGGFLGSKAPGNNTSMRPFVIPHLVYLTQFLAAPAAGGGLFGSTTPGNHSW TCCCPVARLFLRFSPIPAAPAAGGLFLGSTPAAPAAAGGGLFGSTTPGTSDSSASA MHASPDSIVFLAAPAAGFGGKTSITHII
<i>Capsaspora owczarzaki</i>	Filasterea	tr E9BYV3	MQGYGYGQQQQQPGMGGMAGLAGMAGMGRGLGMGAAPGQPGMLGMGGQQM GMGGMGGQQLNPMQGQMGOMGHQCMQMGOMGPQQQMGQQQMGCMQ MGQQAGQMGAGAMATPAQQQQQQQQMGGYATPQQATGYPQQGAMNAGA VQQLQFTQPHQAVAGAGMGMATPTGALPGAMPAMPAGMLGAPKIGMGAAGM GAAGLPGGAATPGLGPMGAGLGLGAARPAGLGGIGGAAAGPAAAAA GGLGAVPAMGAMGALGAARPGLGAGLGAAPGAAAPGALGLLAAGGLGA ARPPGLGAARPPGLGVPGAAPAAAPVGAAPALGPVGPAVAATPALGAPAAA AGGLAGGLGVPRPTGLPAGVGLLAGAAGPAGLAGAAGPAGLGGALGAPRPLGA PGAALGAPGALGAPGVGLAGARPPGALGAVPGALGAPGAAGLGAPEGVGPAPQ SGFIISLSSAPTVMTKTFSELPEWDKRLKLDLEKSIATQKSASNEIANHTNARALNVA ARCKTLKQKAVALTIERDTVIVDRLKRDVQVLEKNAEMASRTLARLKMPIPASMQL EMASASDYFNHLTFNENRMONYRHIEELEAHLOSSISEREQMTQALSDIMRNQH ETFLALAAQVQLHDAVQEKEQFLSHSAGDPFAARKKAKEAQVKRIPAPASGGLTLE SSLRYYNTPAQPRAGPAGIPAGPMGGGLGVRPPGALGAPALGGLGAAAGGLGAYRP PGQLGAVGGLGAGAGLGGAGALGAAGALGGLGAPRPLGGLGOGPALGQPGALGQ GALGQPGALGQPGLLGAQPAAGGLGGMAGAMQVGAGVPPLNVAATGSDLARR MQNKV
<i>Naegleria gruberi</i>	Heterolobosea	tr D2V106	MSGFTFNFGGGGGATTQPASTTATTGGTTGGGGGFSFGANTQPATTTGGTT GGFNFGGTTNPTTGTATTGGTGGFSFTGTPSTTGGTTTQPTTGAGFNFGGTT TAPTTTGATGTTNTTAPTCGFNGGSTAPTTNTLTTNNNTTNTNATVTPQQPI TPKTOFQKLPSDQMVKQWEQEKEKETKRNAMDIVKQQENSSDLNLKQRIERVEK KINTSKVNITRAKDNVERIKHDLVLESKNAEQAGNNFNKLRSAYNTDPMNSSTYFIN TAQKLEQRMOEIWKQIEDVAQTLSHSEAYQLPFGQLLQQGTVISQQQAFFNAARLSV LHEKANELRDEIERTYQIRGDPFKEPSKTSKPSVSYNSKLSNSSSLPLGNIPPTQPTTS TTQPTNTSGFLGNTTNTGFLNTATTGTTGFTPTNTANTGTGPNFSTQ AGSSSNKRRM

			TTTAAAGGGSGATTSATAAGGGSGATTSATAAVGGNLGNSAAAATSGTAMGTC KSAAAELKGKALFSILAQFDFKDFADYREFQKLSQHMLFRDRQIIDRGNELAYISHLD AAISSAEASKORLSELKSQGAIAAMMQRVEDAVQPIYAKVRPNFTKLDEQREATYT AVINLFDEVEAFRLRLSQSVAQHNRSLRQLRECDLTERMAGLVDQCLSLERCSKR AEELESEMLLGGNSAM
Trypano-soma vivax	Kinetoplastea	NCBI CCC54154	MLEPPMETQSTLYHPVNFMVTLASVAYFLTVQVQDVPPAVFFSFQRPPLSLPIHS PQAYGVHFARAQCVCYNGRVLFPFFASLVPSCPAGFGAVGAVSPAATFGFATTTP TTGFGSVPDATTGVTNMSADATARKELSGKMLSSILANFDKNSRTDYHDFIELSQL MMLRDRQIIDRGNELSHSSHLDSAIFEAQSLSAQOLKAKQNSISEMMQRLEDAD EPIYARVRPSFSKVDELREEAYASVLSLDETEALKRLRQECVQHQHRSRQLHECD DISKFVGLIDSQSAMEVCGQAAEELHOLLGKPDNV
Leishmania braziliensis	Kinetoplastea	NCBI XP_001567 611	MAFNAFASSATLGFGGGSTPAGGFQFCNLGSVASTAPPAGGFSATATSVPALGF NFSAGASTSAASAPAPTGTIGLGGFGAGNAAPSPGSASGFSATLQPPNAPATPF GTSGFSEAAASAAAPCTAATGFGATTTPAATGFGATTTPGATGFGATATPATGFGATATPG FTTGFGSVPDATTGVTNMSADATARKELSGKMLSSILANFDKNSRTDYHDFIELSQL MMLRDRQIIDRGNELSHSSHLDSAIFEAQSLSAQOLKAKQNSISEMMQRLEDAD EPIYARVRPSFSKVDELREEAYASVLSLDETEALKRLRQECVQHQHRSRQLHECD DISKFVGLIDSQSAMEVCGQAAEELHOLLGKPDNV
Phytomonas sp. isolate EM1	Kinetoplastea	NCBI CAVQ0100 01283	MINFGAPASGNVPSAPTAIFSGGGPANPPAGTGVPNPTNAPPITSWGAGFATTPL PASVPAATTAASPFQGVSGLATASPAAGGTTASATNAPFGSIPPAAPPTPTPSTA GGGGFCFTADPAKPGSPNPAQPGFGFCQAAAPPASTSTAPSPPATAAPMGSGT PFAAPIAAATSFQALPSTGAAPAPASTAAPASTAASTLFTGTAAPTSTEGSAP PLANGTSSTTAPISFGAPPSTGAAPTAAPSTAPSPPLPGSPNEGKPDATDFTGKPLS KILGAFDKHYHAQKDFTELAKHVVLDRHLLERKLDDLSISHTIKGALSVAHATKSTL RECGEKQKAMDRLRLLQDVALDRQNFADLARHVHVRDRQIMARGRELTEVGVSVVKDAL AAKSAEATLAECQKQRAVQLSEYLVQPVYQAWEQQQQHGSTDPRGVDDQQ RAVTYDNVIALLEEVQGVEEKVGRAIRQHNSRNELLGLSIEGTMRLIDGQLCALQ CCSALASALEELDRLLGKAA
Critidia fasciculata	Kinetoplastea	NCBI AODS0100 3144	TAPAPADGAKAAPAAPVASASSPGASPQSFEQAGTKLSSVLAKLDTYVAADQRHFAE LAQHVVARDRQIMTRGRELMVEQSVIKDAVTAAKSAEATLKECQKQRAALSDYLOA LEEKVQPRYEEWQQQQQQQQSHDTRGMQDRNVIAYDSVMTLLEEVQSVEDK VSRAVRQHNHARTELARSEVEGTMRMIDGQLLQCQSTLATEVELDRLLGKSE
Herpetomonas muscarum	Kinetoplastea	NCBI AUXJ01006 122	TAAGGAGGGFGKAPAAAGPAAAPAGGFAAPAAAAAPAAAAGGFGFKAP AAAATSAAAAPATAAAAGGFGSGAISTSATPAGAAAAAASAAALPSSAQEFAG KTЛААГКДЛКТЯАЕДКХАFTDVRVLQVARDNPKTQDQHRSRQIYADSVMTLLEEVQSVEDK AAALDDCHDKQQSITKTLDELDLEALVNPVYVSRAIAEAAGRAEGGTTTAAAAAALPAA DRTRIAAFDAAVALFDEVQALQQLRDAAVRQHRRHRRGMRAADGSGGEGRHSFGE LGGMIALSVQLSALCETCGMAESLERSLSDLLGKRP
Trypanoplasma borreli	Kinetoplastea	non-public	ATTPGFGSATDQVTSSKGTVTPQEVQEAMAELKGKTLGKILQEWDRFETDDYQNFH SAAIRVKGDRDIEVTDYGNAILSMTAQDLAAIESATATKNHFSSEIVAVNLNNLAVDVQKL TQSVEAEKSNSINTKDQYIDETNAKDGDRGRARYDEQEMTYRDVVRFLFDETQSLA HSLDQLVEQHNVNATARNEDCDRIVRVLQYQLTAVHDLYRKVADLEDIISTTYGL
Bodo saltans	Kinetoplastea	GeneDB scaffold458	CRIRRSSRSSSCNSTTAAPAAAGFASPAAAAGPSTGLAAPAADTKPTTHAAARAAL AALPTAAALLOEIQOGLHTSKVLDQWDKRFTEAHSFTETARSVSKDDTVLQYGNRI LSLKDALTYSIQFSKHTQQTWTKVDAVQQHAMSALKELEETVDPLFAKAQDRFEKTD ETRYDQYLNLTDEVNALAMRQAQRQVRRHNEALESRCSDVDRVLGVVDSQLSV LEVITKRAHQLDDELTLLGRSSY
Saccharomyces cerevisiae	Fungi	tr E7Q5J4	MRKRMAMPLNLPSPHFGAKSDEKKDXSSKPKAFSGAKPDEKKNDEXSKPKAFSGA KANEKKESDESKSASFSGSXPXTGKEEGDGTKAISFGAKPEEIQKSXDTSPKAFTFG AQKDNEKKEETSESTGKSTADVKSSDLSKLNQPKVLPKPSLDNKTLDLTVKWTNQ LTESASHFEQYTKKINSWDQVLVKGGEQISOLYSDAVMAEHQSQNQKIDSQYIEROQQ DELENFLNFETKTEALLSDVSTSGAANNNNDQKRXQAYKTAQTLDENLNSSLSS NLSSLIVEINNSNTFNKTTNDINNENEDIQILKILNNSHFDALRSDDNTSLEKQINSIK K
Schizosaccharomyces pombe	Fungi	sp Q10168	MSFNPGNNQNSGFSFGKPAQPNAAQGAATPAATGLFGNTNNNTSSTAPSGLFG SNNSAANTSAPSTFSFGKAATTGNTNSTNASTSSPFSGSTNTNTAGAKPLFGGLGST GSANSTGDKSKNTASSATGAAATTNPGSFTNFGSSNNSFNFQKPASTNTTTPAAA STGSLFGKPAATGTSNAPPSTSSTPATGSGGFSFGKPAISLGSNTNNASTSTTAN SGFSFGKPAITAPSNTVTPSSSITGNDSPKAASNTGSPATTGFSFGKPAQQA ASTATDKGTTTSSAGTGFSPKPATTEDTNPKTAPNSAFTKPATSTGDQNKPTFSFG NTSKPTENTSTTAPPLSNTKPAEAGNQTSGGSFQKPAITDTTSTSSTKQPLFG NKPADPSAKPGATASTTPSEPPSSIIKHTLQELNWKSTDLTQTEVFNKLCDQVS DWDRITLVDNAGALISKLYTETVEAEQMSNRIDDDLEYVSSSQELFKLDSYETQLET FDGRATSLNVERERAFGVADDLTSRDLRGEDLGTVINQMNDFSKPDDSIIEIVKVL NAQLASLGWVVENRIFQMEEKLDTIKKKNSDVL
Aspergillus flavus	Fungi	tr B8NLM8	MFGTSSATGGQGSTLFGGATGSAATPSSGTTAFTSGTQSKPAGTTQAPSLSFGSGS QTPKTNETPSSGQTPAGGLFGNAAKPAGGLFANATSTPGQSGGSISFGNTASTTPAG PPPQGGATGOPOSLFGQTAQKPGLFGVN/NTTSSSTTPTTATAPSTNPLFGGAP QTQTSQNGGGGLFGSNTQNTQQKPLFGSTPAAPAGGNLFGNANKPAESTTPTSA DTAPKPLFGAATPTSTGGTTSQAOTPSPFLQPKPAAGTDSAPKPAFSLGTTNTSAQPSST PAASSATQPKSLFPVIAIGTTSSTPSTTPAAPSQGMFSALGAAPKTGTTAPSTTAT APPATOPAAPTGGLFGNKPAGTASSQPSSTTSATPAAATDASKPSLTPSAPATSTA TGTGATGATSNATGGAALGASTAGPTPPAQSRLNKNTMDEIITRWATDLTKYQKDF KEQAEVWDRMLVENGTVKLYGTVDAERATQEVERQASVEQQQUELGS WLDRYEREVDEMMSKQVGPQGESLQGPQDQERERTYKLAEKLSERLDEMGKDLTSMI EEVNGASATLSKTNKADEPISQIVRLNSHLSLQLQVIDQGTSELQTKVSAAQKAGQSL SSRFGYGFSSSGMANSTAADDFYRSYMGRR

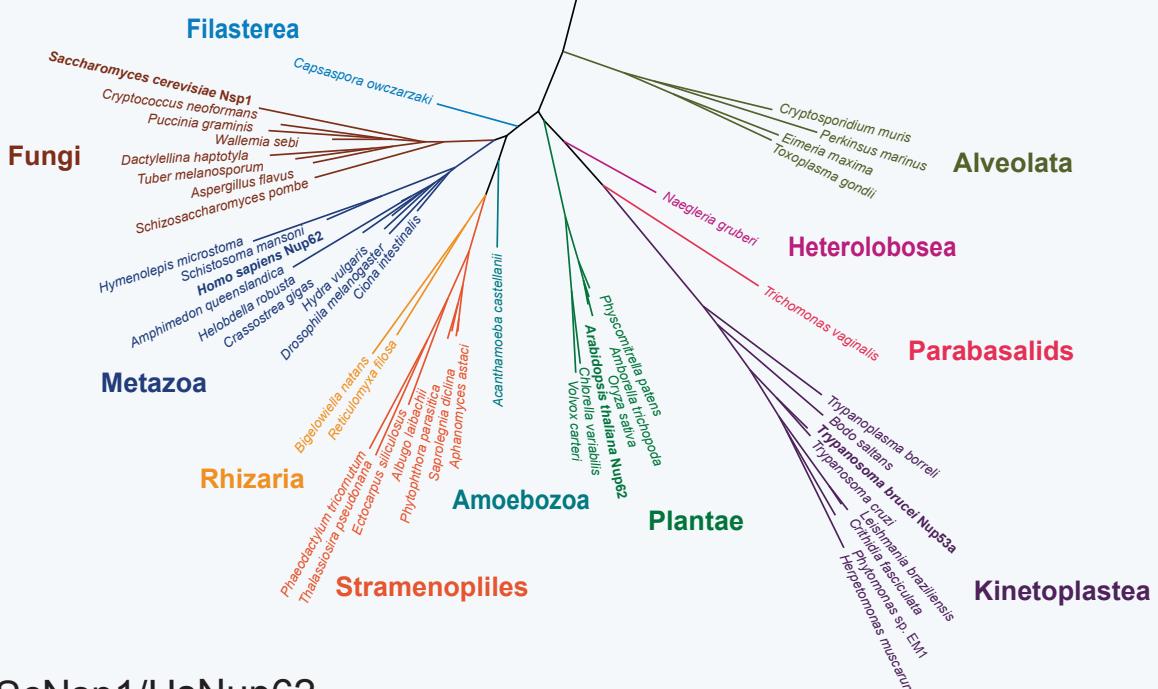
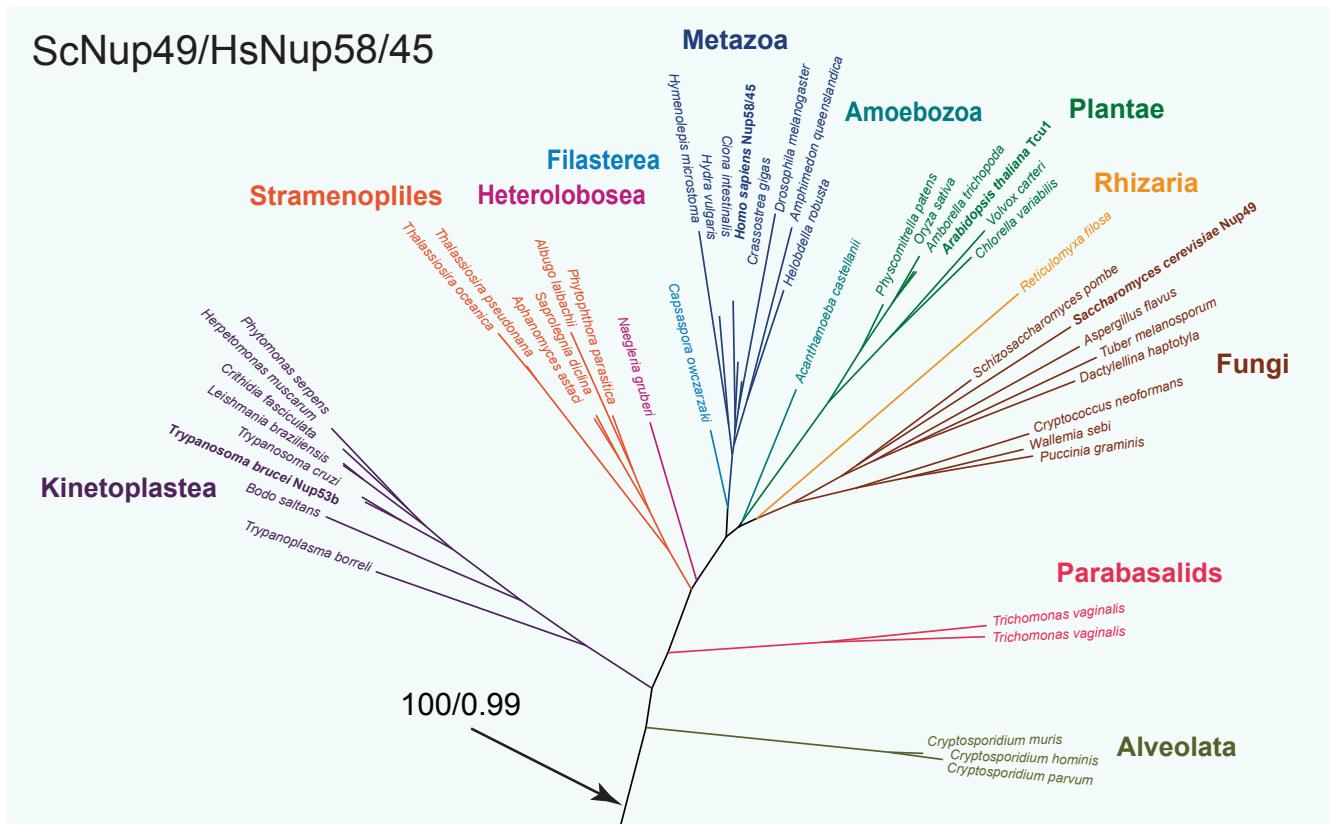
Cryptosporidium muris	Alveolata	tr B6AK04	MFGSTNNNTNIFGNTSLNTSSDNKTPFNFGTNAVSNASSTSIFGTANQSSTSNTLF GNIGANSSLNLQNLGGGLGSNLNSTLASTGQQQQKGQLNFGQQKSPGLGLOSTNTSS QISAISSMMNPMTSNTGTTVDNNIKPSLQQGQSTLNNQAGTSIGTNIPFGSTNNVQNV GTLNSGNNLFGGSNLSTSNSNSFSNSLNVNGINNKALPDPTVISSNDPSSSLNNPT SNLFGQSNSTAALNNKIDONSLFTGPNTKSLSGDSYATTGLPSASTNSESNKLVSGNS NLFSSTLSGTSQIESQAKSESTKDIAPINTKNDTNTNTQGTSNSGQLSTALQLDV STAASLQHERVDDVLKSWESRLAKQVKLFNKASSDVLAVDKAIITYTLLYSIRSDQQ EMKIRQETMDNRIDQIAQQONSLASMLRNIEELSRLKLETNLGSGVSTDTSNAQYQN VRISAARANALSTELQEIEGQVNDLMRHLSNVHEKIYPNPLNQIVKLNHLHQLTLQSIE DEAMNLKQKLTIAEDCLVRR
Toxoplasma gondii	Alveolata	tr V5BLS9	MFGNTATTSSAASGGGGGGFLGSTSSPFASSSSSLFGGSGTSKPGLFGAAPAG SGTATPSLFGGTTGGASFGLGAESTSIVSSGQTLSSPSTGSGLFGSASAACKPSLFGST VPATPSLFGGTTGGASFGLGAESTSIVSSGQTLSSPSTGSGLFGSASAACKPSLFGST AAAATTAAAGTGLFGATSSASOPSTAGTGLFGATSSASOPSTAGTGLFGAASSASQPSTA QPSTAGTGLFGAASSSSQPSTAAGTGLFGAASSASQPSTAAGTGLFGAASSASQPSTA GTGLFGAASSASQPSTAAGTGLFGAASSASQPSTAAGTGLFGAAGGGTGGSTAGTGLF GAASSSSQPSTAAGTGLFGAACKGAACTAEKQATAKCTEAPAFAASAPAEKTAT GGATGLLGGDTKAASASSTGATTSLGAAAGAAAAGGATGTPKAGDGSASS SVSAPFGAGLGLASSTANSGSSGNAAGGLFGAAAAGSASKAPEKLQGASGPAGATA SGATTAAETLPPQQVQALETLQHERVEEVLAKEWKRLLQRVRFRNEVAEEVGVEKA MIEESKKLHALREEQIIEKRQTICDFIDLERQQRDLTLLASVEASVLRQIPQDNG DPTGAAGGDAALAQRVQREWEAESFGHSSEEEALSRLRNIDEQLNDVGLALSEAT ERFPQGPLGTVAQVLGIHQALQASWRQASELQQRMDALQRLTSDAKHGE
Eimeria maxima	Alveolata	tr U6MA41	MLGGAGSSLFGNMSGSTAQTTPATSGTLFGSTGQAPGASTTSSIFGNAAPGSLF GAPTAACAAAGPATGGTASATAPKGDSLFGSSSSAPSSGGFLSSGTGMPSTSSG GLLGSNATSGVSGGSVASGATGLFGNTTALSNTQNAPOQGLFGVSAGAASGL SNATKSGLFGGATASNKPNELGKPAGLFLGGSLSTTGSTGEAPKGGLFGSSSTAATTS GKDPSSSGGFLGSSAAAEPATSPQAGPSSGGHSSAGTALTGTGTLPGAVAGSSQPSTAGTGLF GDASKGTGLFGSLGSDATKTASGGSLFANAASAVAAGVAVSGGSDGKGSGLFGTPS GASAAPQHSOTGGQANTAGPKSLFGFAASGSSGTTGLLSSGPAKVSEANSQK GSEEAPQHSPPSSATEQSTTGTGQANTAGPKSLFGFAASGSSGTTGLLSSGPAKVSEANSQK ESNTSPATGPVRSTPVPEVALETMQHERMDLLTNWEKRLQRKVGEFDELA QEVAAVEALITQSRLATIREEQRVHRRQLFVGETIDMIEQQQNDISNLLASIEGSL LAKLSPQEOIRSICSTVEQSMERVLIDDAQMDLSDAIAQAAARTQPDPAVVAISQVL AVHQAALAESATQQCAKLEQCLKSLQRFRV
Perkinsus marinus	Alveolata	tr C5LD28	MASKRESFSPMKSKRLEDEKTTLQELNNRLEMVLRKEVQDSRDVAEKELETIRER MQMDLSMTKTRLSKELEDTRKLFEEIDQKTRQVLEQFHTELVLRQVKEFCIDI RVELEQVQAALEAKEKSSAAKEALALQITSLQSAKRLKLDLKENRKLTSLSDT NELDQLKQKTSSEFSLRTDTEITLVRKEMENAKHEALAAWRRESEERLHSVEAEVRRAH FEQQEQLRQDEVNLELDSTVYERYTANDYDESLKIRQSLTDLSTIETQYRNER KFKFQEDRKMYEANIDNARQARLAKETEFNDLMDIKIALDAEISAYRSILDREESRVGID QANHSKRRKASLTPVKSSTTRQHKRRKSHSTGVLRITYLNLEQGRITLENTGSDALS LSGWQVSSKATVNVPQAFPEDYVQCPGRVSVQSRNAAPTEEKEMSDFYVIKKAM WNTQADVAQLTNPSGDVVSSYAEQMVYDDDVAADTPAKDCCGIM
TbNup62 / ScNup57 / HsNup54:			
Trypanosoma brucei	Kinetoplastea	NCBI XP_844668	MSVLGSGFGRGAPGGFAPACSTAGFGSGFTATTGGFAGANTATTGGFAGA ANTATTGGFAGANTVTGGFAGANTATTGGFAGANTVTGGFAGANTATTGGFAGA GAGANTATTGGFAGANTATTGGFAGANTATTGGFAGANTATTGGFAGANTATTGGFAGA NTATTGGFAGANTVTGGFAGANTATTGGFAGANTATTGGFAGANTATTGGFAGANT ATTGGFAGANTATTGGFAGANTATTGGFAGANTATTGGFAGANTATTGGFAGANT GGFGAGPNTAGGFTGATSVFSGSTAAGAESPNAVGASQQVINCQSAVGRYLLEI DHAYNAMHPNCRFRSFLYNVCAPGQSQIMAVERERLYAAAGGECKEEDDLLRAQQRN PDGVHLYPTRVHFMQELKNRVEKOKELEAMSRHVDSLATKADHFRELDEANAAQY RELQQEQAMLQRWVSYLMLKVTLRQLGLPAAESRMGGIASTLSAQLSAPGMYKT ALTELPQFLDAESSTTSFLRRNSVGSEGAICTPSEGVTGTLRNNRVDQALLRDWAR FAERIQQCVEGLSELLERADAADMRAIYQRVMS
Saccharomyces cerevisiae	Fungi	tr E7Q443	MFGFSGSNNNGFNKPGAGSTGFGFQGNNNNTNQPSASGFQGGSQPNSTGTTG GFGANQATNTFGSNQSQSTGGGLFGNKPALGSLSGSSSTASGTTAACGTGLFGQQT AQOPQQSTIGGGFLFGNKPPTTGGFLGSNAQNSNTTSGGLFGNKGVGSTGSLMGNS TQNTSNMNAAGGLFGAKPQNTTATGGFLGSKPGSTNTGGFLGSQGTQNNNTLGG GGLFGQSQQPQTNTAPGLGNTVSTOPSFAWSPKSTGSNQQQQQQQIQVPLCQ TOAIAQQQQSLNVPQQIQQVLCKCESWDPTTQLKRAFYVNKVNETEAILYTKPG HVLQEEWQDMAKEKKPSPTQIPIQYFEGLNQRNQVQTEVNAQARIILNHILEKSQL QOKHELDTASRILKAQOSRNVEIEKRLKLGTLQLATLKNRGLPLGIAEEKMMWSQFOTLL QRSEDPAGLGKTNELWARLAIKERAKNISSQSLKLMVFNDDTKNQDSMSKGTKGE ESNDRINKIVEILTNQRGITYLNEVLEKDAIAVKKI
Homo sapiens	Metazoa	tr Q53H29	MAFNFGAPSGTSGTAATAAAPAGGGGGFTTSTAGSAFSAPNTGTTGLFGGT QNKGFGFTGFTGTTGTTGTTGLGTLGFTGFFNTQQQQQQTTLGGFLSPQPTQA PTPNQSLNTASLASAPTLGGDERDALWKNQLQAFWGTGKGYFNNNIPPVEFTQE NPFCRFKAVGYSQCMPSNKDEDGLVLFVNKKETEIRSQQQQVLVESLHKVLGNNQTL TVNVEGTKTLPDDQTEVVYVVERSPNGTSRRVPATTLYAHFEQANIKTQLQQLGV LSMTRTELSPAQIKOLLONPPAGVDPIIWEQAKVNDPDESEKLIPIPVMVGFKELLRRLK VQDMQMTKQHQTDLIISEDISELQKNTQTSVAKIAQYKRKLMDLSHRTLQVLIKQEQI RKSGYAIQADEEQLRVQLDTIQGELNAPTFQFKGRNLNELMQSIRMQNHFGAVRSEER YYIDADLLREIKQHLLQQQQEGLSHLISIICKDDLEDIKLVHGLNETIHIRGGVFS
Arabidopsis thaliana	Plantae	sp Q8GYF7	MFGTPSSSPSFGTTPSSTPAFGTSSPAGFTPSATPAFGTPSNPSFSSGGFGSSLFSS PFSSQQPQQQQQQQQQQQQPSSLFQQQPGSSNFGQSPFNNTAQQQQQTTPFPNAQ LTTQMAPVAPIYSLADRDVQAAIEKADPNTPKYAFQHLLFSVTEPVQYRVPAAVS DIMWAÆAMSKEGLMDSTERERLWPQLVQGFKDLSQRKLQDDEVLSDRDRIKTTQS NVKMLQRHLCASTFPSIERLROKEQSLQRRLMRVMRIIEGLEGKGRPLPTKGEAEL SEKLTAITROVKGPGAEELSRRVQOSLOTISRAOANSIAAGSSLYPGSTKIDEQSLIDM QEVLQQETEAIRGLGNVILKRDMEIMVADETEMALDS



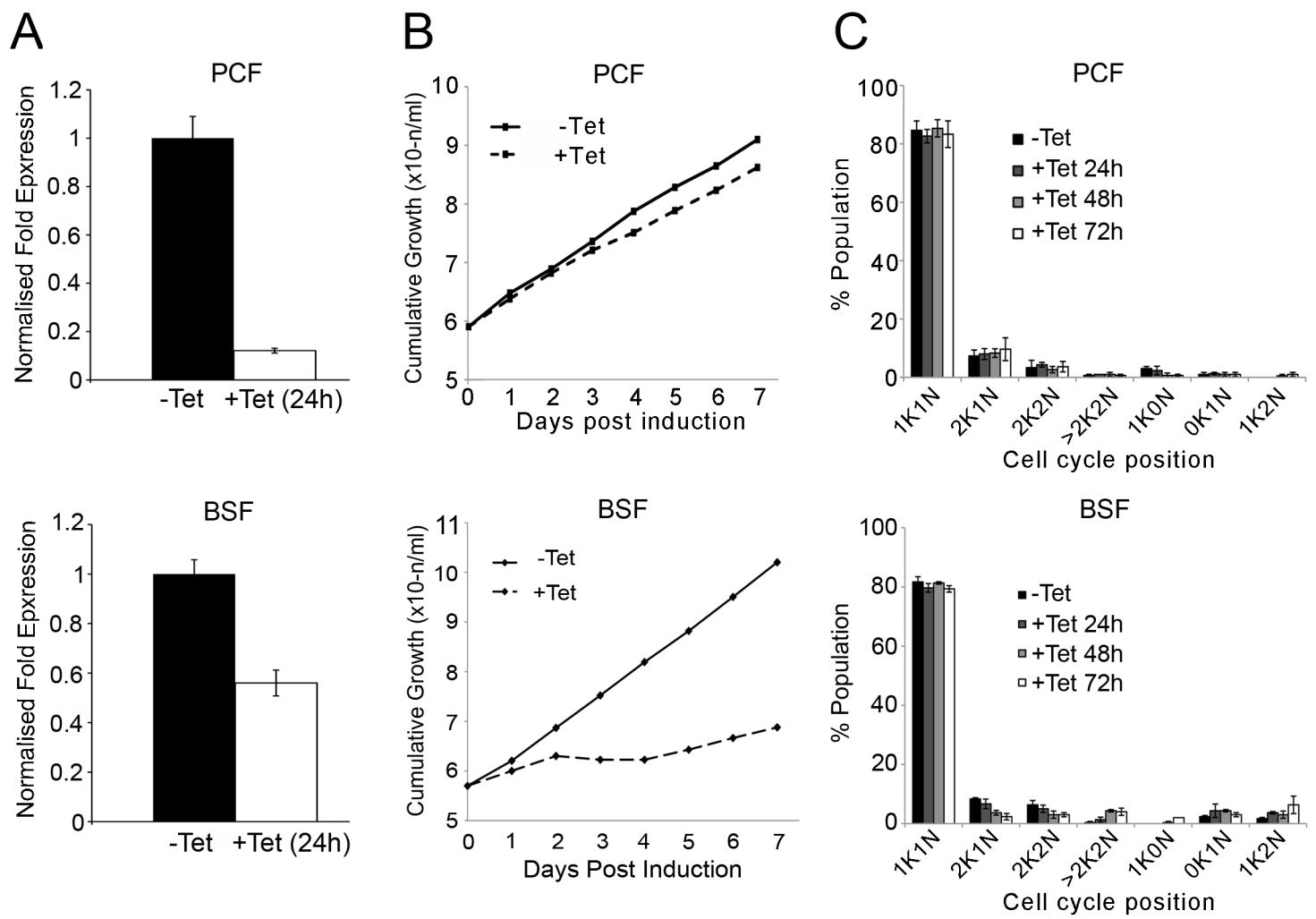
Nup53b ortholog

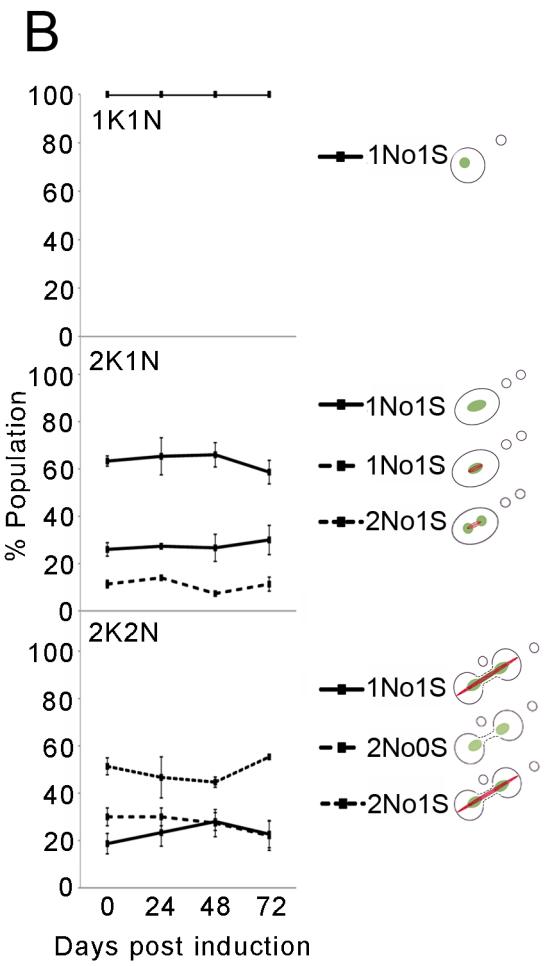
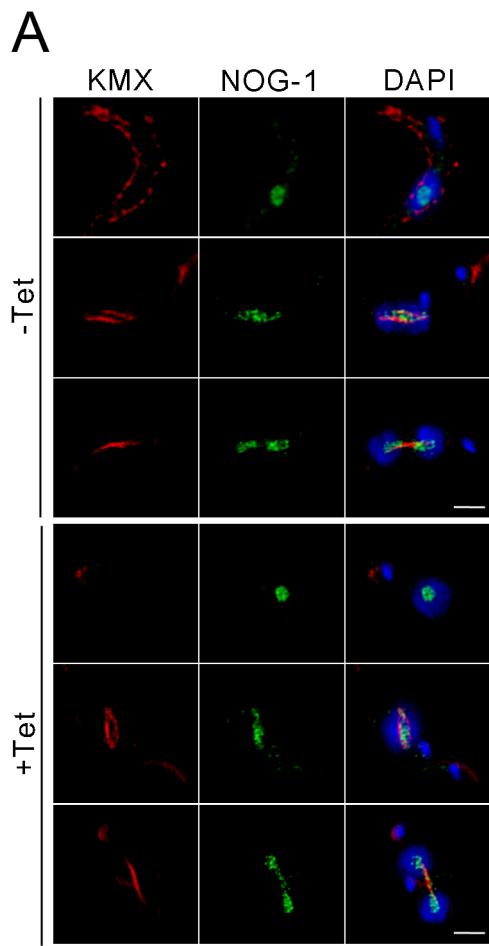


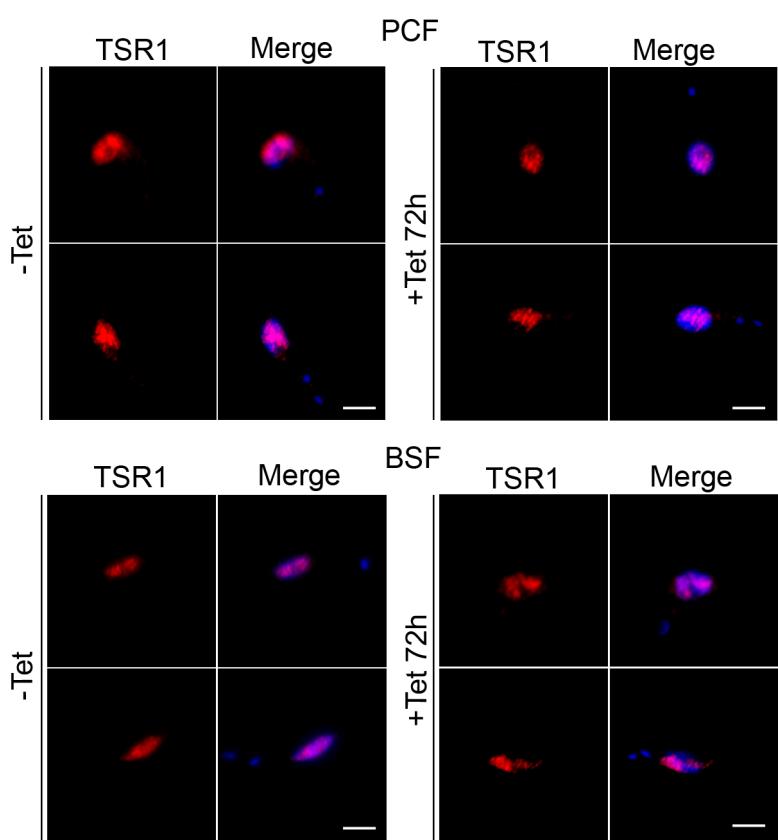
ScNup49/HsNup58/45



ScNsp1/HsNup62







█ Genes on forward strand;
█ Genes on reversed strand;

Sequence	Organism	Chromosome	#Genes	Length	Gene Locations
Tb427_10_v5	<i>Trypanosoma brucei Lister strain 427</i>	10	19	4145152	
Tb427_03_v4	<i>Trypanosoma brucei Lister strain 427</i>	3	11	1654840	
Tb427_11_01_v4	<i>Trypanosoma brucei Lister strain 427</i>	11	11	4977113	
Tb427_09_v4	<i>Trypanosoma brucei Lister strain 427</i>	9	9	3058680	
Tb427_02_v4	<i>Trypanosoma brucei Lister strain 427</i>	2	8	1194715	
Tb427_07_v4	<i>Trypanosoma brucei Lister strain 427</i>	7	8	2206643	
Tb427_01_v4	<i>Trypanosoma brucei Lister strain 427</i>	1	7	1064569	
Tb427_08_v4	<i>Trypanosoma brucei Lister strain 427</i>	8	7	2482252	
Tb427_05_v4	<i>Trypanosoma brucei Lister strain 427</i>	5	4	1609320	
Tb427_04_v4	<i>Trypanosoma brucei Lister strain 427</i>	4	1	1591669	
Tb427_06_v4	<i>Trypanosoma brucei Lister strain 427</i>	6	1	1619978	

