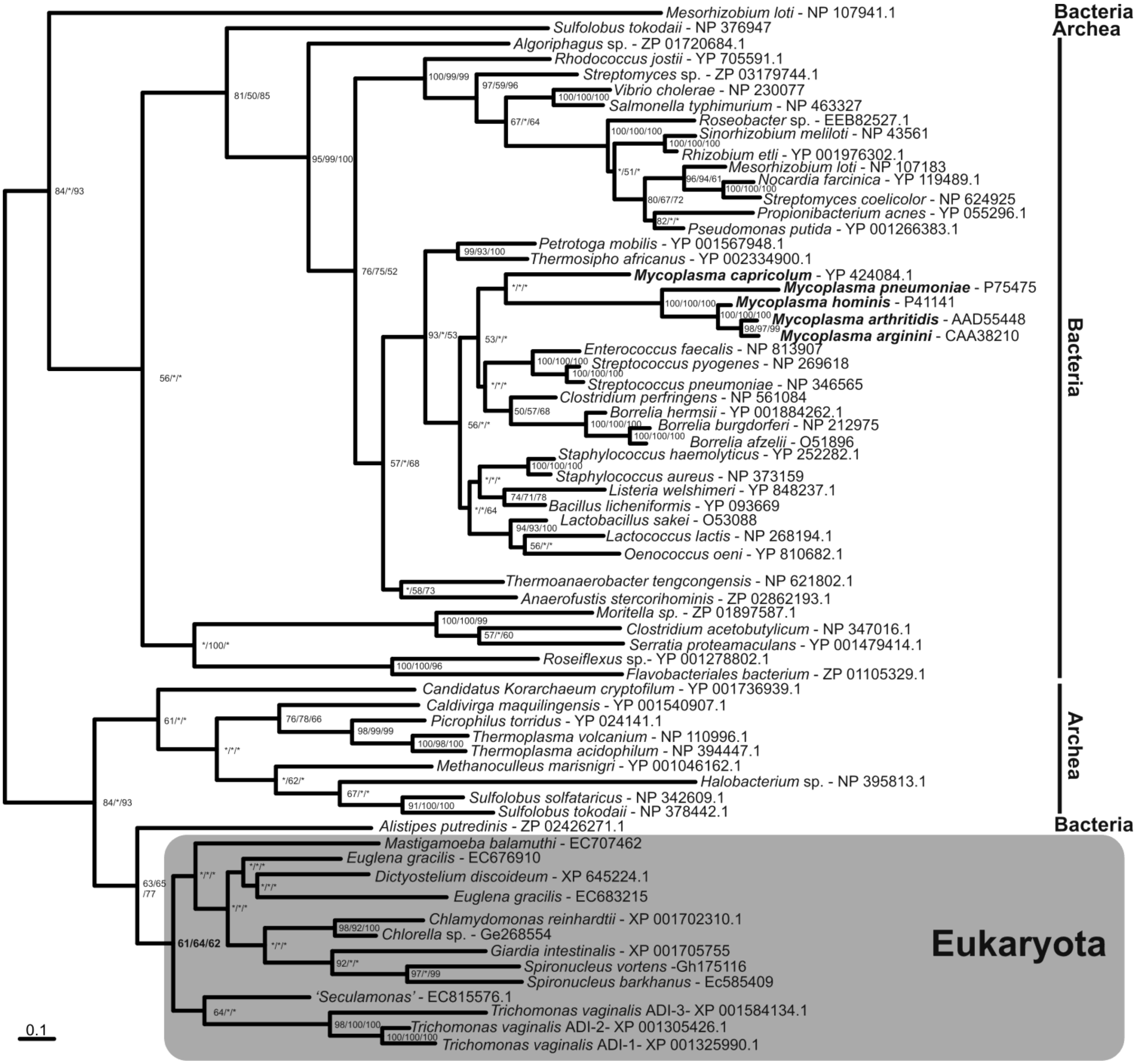
Fig.s1

```
                                                                       ▼
TvADI-1       MLASISRA SSSFRFPLVK SFNQVSEFDH PTDIITHCPG --IETRFPFH LSAFLYEHPP NPKKAVGCHN EFRKLLHEAC GARIWTVREI  86
TvADI-2     MLQSISRFSS NLQLKKPLVK SFSQISEFDH PTDIITHCPG --VETRFPFH LSAFLYENPP DPDKAVECHN LFRKALHDAC GAKVWTVREI  88
TvADI-3      MLCSIQRSI TKKVPKILAS SLRQISECDQ PTDIITHPPT --AATQFPFH LEAFLFDTPP DPAAAHLCHE SFQTALAQIS GAKVWNVIDV  87
Giardia             MT DFSKDKEKLA QATQGGENER AEIVVVHLPQ GTSFLTS-LN PEGNLLEEPI CPDELRRDHE GFQAVLKEK- GCRVYMPYDV  80
Mycoplasma             MSVFDSKFK GIHVYSEIGE LESVLVHEPG REIDYITPAR LDELLFSAIL ESHDARKEHK QFVAELKAN- DINVVELIDL   78
                         .             .*  .    ::.* *           .  .  * .     .      *:  *   *     . .:    ::  13
                                                                                                             ▼
TvADI-1     LKNME---TS ELRKALVNFT PVHFSLTPGI PSADTQTKLK QEYLDFSLSK LSKDHLIDLI FLHPTLIIDV NDKSSTGFHY DKIPLSPLAN  173
TvADI-2     LKEMP---VE KLRSTLIDFT DLQFDVVPGI PTEQMRKQIT KDYISYSLSR LSKDNLIDLI FMHPSVKIDV DKNSSTGFHY DKLPLLPLAN  175
TvADI-3     LKKLS---HK ELRAILMETC DIAFNVDTDI KIDPIAKEIS PEYIDYSLSQ LSKHDLLDLI LLNPSIRIKV D-KSSTGFSY KTIPVSPLSN  173
Giardia     LSEASPAERE VLMDQAMASL KYELHATGAR ITPKMKYCVS DEYKRKVLSA LSTRNLVDVI LSEPVIHLAP G-VRNTALVT NSVEIHDSNN  169
Mycoplasma  VAETY---DL ASQEAKDKLI EEFLEDSEPV LSEEHKVVVR ----NFLKAK KTSRELVEIM MAG~ITKYDL GIEADH---- -ELIVDPMPN  155
            : :      .               :               :   ::     :   .  .::    : .  : :   .          . : :    *  28
              ▼ ▼                     ▼                                   ▼ ▼                  ▼
TvADI-1     TVFTRDQQIT TAKGVVIGRF GAAQRRDEND LMSIVWP-QI GVNPVGRIEA PG---TIEGG DFIPLSKDCM LLGVGLRTNM NAAQQLMDKD  259
TvADI-2     TVFTRDQQIT TAKGVVIGRF GAQQRRDENK LMKVVWA-EL GIEPVGQING PG---TLEGG DFIPISEDYC MLGVGLRTNM TAAKQLMNQD  261
TvADI-3     MLFTRDQQIA TANGVVMGRF NAPQRTTEIA LMNQVMP-LL GVQPIGAIGD PG---HLEGG DFFPLGYDMS MLGVGLRTTA EAARQLMRND  259
Giardia     MVFMRDQQIT TRRGIVMGQF QAPQRRREQV LALIFWK-RL GARVVGDCRE GGPHCMLEGG DFVPVSPGLA MMGVGLRSTY VGAQYLMSKD  258
Mycoplasma  LYFTRDPFAS VGNGVTIHYM RYKVRQRETL FSRFVFSNHP KLINTPWYYD PSLKLSIEGG DVFIYNNDTL VVGVSERTDL QTVTLLAKNI  245
              * **   : . .*:.:  :     *  *   :   .                  .    :*** *..  .   :  :**  *:        *   :  53
                                    ▼▼ ▼▼
TvADI-1     LLG--CDRFV VVEDKVDCNQ QRMHLDTFFN VASEKLCVCV DKIAQDD--- ---------P QYVRIAHEYV KR-EEGYVEE KTMPFGQWLK  334
TvADI-2     LLG--TKRFI VVEDLYDKNQ QRMHLDTYFN VASEKLCVCV DKIAEDD--- ---------P KYIRIAREFV RDGVNSYKEV SQLPFGKWLK  337
TvADI-3     LVG--TQKFV VVEDTHDRNP TRAHLDTVFN VIDEKTCICL DAIADDA--- ---------P DFMRTARVYV KH-DSHYVEE EKMPFGKFLV  334
Giardia     LLG--TRRFA VVKDCFDQHQ DRMHLDCTFS VLHDKLVVLD DYICSGMGLR YVDEWIDVGA DAVKKAKSSA VTCGNYVLAK ANVEFQQWLS  346
Mycoplasma  VANKECEFKR IVAINVPKWT NLMHLDTWLT MLDKDKFLYS -PIANDV--- ---------F KFW--DYDLV NGGAEPQPVE NGLPLEGLLQ  320
                       :*            * **  ::      :                                                             62
                                                                                                 ▼    ▼
TvADI-1     -----KEKFE VVEATFKQQE DYFINLLHLG K-----TPLG KDRVFAINPE VEKALVQHGY D--GHVYYMD FSQITAMYGG AHCATQVLRS  412
TvADI-2     -----KEGFE VVPASFKQQE DYFINLLHLG K-----NKNG KDIVFAINPE VEKALKQRGF D--GEVHYLD FHEITAMYGG AHCASQVLRQ  415
TvADI-3     -----KEGFK VVKCSMKQQA EYVPNFINLG K-----DSHG KARILINNTE LQTLLKANDV NI--NCYDID FAAISSMSGG PRSSTFVLRA  412
Giardia     -----ENGYT IVRIPHEYQL AYGCNNLNLG NNCVLSVHQP TVDFIKADPA YISYCKSNNL PNGLDLVYVP FRGITRMYGS LHCASQVVYR  431
Mycoplasma  SIINKKPVLI PIAGEGASQM EIERETHFDG TN---YLAIR PGVVIGYSRN EKTNAALEAA --GIKVLPFH GNQLSLGMGN ARCMSMPLSR  405
                 :      :      *      :    *                                                ::   *  : :  :      73

TvADI-1     QK                                                                                                414
TvADI-2     HK                                                                                                417
TvADI-3     ESK                                                                                               415
Giardia     TPLAPAAVKA CEQEGDGIAA IYEKNGEPVD AAGKKFDCVI YIPSSVDDLI DGLKINLRDD AAPSREIIAD AYGLYQKLVS (AA)59        580
Mycoplasma  KDVKW                                                                                             410
```


Mesorhizobium loti - NP 107941.1
Bacteria
Sulfolobus tokodaii - NP 376947
Archea
Algoriphagus sp. - ZP 01720684.1
Rhodococcus jostii - YP 705591.1
100/99/99
Streptomyces sp. - ZP 03179744.1
97/59/96
Vibrio cholerae - NP 230077
100/100/100
Salmonella typhimurium - NP 463327
81/50/85
67/*/64
Roseobacter sp. - EEB82527.1
100/100/100
Sinorhizobium meliloti - NP 43561
100/100/100
Rhizobium etli - YP 001976302.1
95/99/100
/51/
Mesorhizobium loti - NP 107183
96/94/61
Nocardia farcinica - YP 119489.1
100/100/100
84/*/93
Streptomyces coelicolor - NP 624925
80/67/72
Propionibacterium acnes - YP 055296.1
82/*/*
Pseudomonas putida - YP 001266383.1
Petrotoga mobilis - YP 001567948.1
99/93/100
Thermosipho africanus - YP 002334900.1
76/75/52
Mycoplasma capricolum - YP 424084.1
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Mycoplasma hominis - P41141
100/100/100
Mycoplasma arthritidis - AAD55448
98/97/99
Mycoplasma arginini - CAA38210
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53/*/*
Enterococcus faecalis - NP 813907
100/100/100
Streptococcus pyogenes - NP 269618
100/100/100
Bacteria
56/*/*
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Streptococcus pneumoniae - NP 346565
Clostridium perfringens - NP 561084
50/57/68
Borrelia hermsii - YP 001884262.1
100/100/100
Borrelia burgdorferi - NP 212975
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100/100/100
Borrelia afzelii - O51896
Staphylococcus haemolyticus - YP 252282.1
100/100/100
57/*/68
Staphylococcus aureus - NP 373159
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Listeria welshimeri - YP 848237.1
74/71/78
Bacillus licheniformis - YP 093669
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Lactobacillus sakei - O53088
94/93/100
Lactococcus lactis - NP 268194.1
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Thermoanaerobacter tengcongensis - NP 621802.1
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Anaerofustis stercorihominis - ZP 02862193.1
Moritella sp. - ZP 01897587.1
100/100/99
Clostridium acetobutylicum - NP 347016.1
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Serratia proteamaculans - YP 001479414.1
Roseiflexus sp.- YP 001278802.1
100/100/96
Flavobacteriales bacterium - ZP 01105329.1
Candidatus Korarchaeum cryptofilum - YP 001736939.1
Caldivirga maquilingensis - YP 001540907.1
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Picrophilus torridus - YP 024141.1
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Thermoplasma acidophilum - NP 394447.1
Archea
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Halobacterium sp. - NP 395813.1
84/*/93
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Sulfolobus solfataricus - NP 342609.1
91/100/100
Sulfolobus tokodaii - NP 378442.1
Alistipes putredinis - ZP 02426271.1
Bacteria
Mastigamoeba balamuthi - EC707462
Euglena gracilis - EC676910
//*
//*
Dictyostelium discoideum - XP 645224.1
63/65
/77
//*
Euglena gracilis - EC683215
//*
Chlamydomonas reinhardtii - XP 001702310.1
98/92/100
Chlorella sp. - Ge268554
Eukaryota
61/64/62
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Giardia intestinalis - XP 001705755
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Spironucleus vortens -Gh175116
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Spironucleus barkhanus - Ec585409
'Seculamonas' - EC815576.1
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Trichomonas vaginalis ADI-3- XP 001584134.1
0.1
98/100/100
Trichomonas vaginalis ADI-2- XP 001305426.1
100/100/100
Trichomonas vaginalis ADI-1- XP 001325990.1

Fig. s2

Fig. s1. Genome sequence for ADI from *T. vaginalis*. Sequences were obtained by BLAST search in *T. vaginalis* genome database TrichoDB (http://trichdb.org/trichdb/) using the *G. intestinalis* ADI sequence (accession number XP_001705755) as query. Three *T. vaginalis* sequences (TVAG_467820, TVAG_344520 and TVAG_183850) were aligned with *G. intestinalis* and *Mycoplasma arginini* (accession number CAA38210) using ClustalX [15] and manually edited with BioEdit software. Putative mitochondrial targeting sequences (underlined) were predicted using the program PSORT II (http://psort.hgc.jp/). Arrowheads indicate conserved residues involved in substrate binding and reaction mechanisms [2].

Fig. s2. Phylogenetic analyses. The 52 prokaryotic and 14 eukaryotic (8 of them partial) sequences of arginine deiminase were aligned using ProbCons [4] and ClustalX [15]. The alignment was manually edited and 288 unambiguously aligned positions were used for phylogenetic reconstruction. Maximum likelihood tree was constructed using PROTGAMMAWAG model implemented in RAxML [13]. The bootstrap support (100 replicates) was calculated using RAxML, using maximum parsimony in PAUP [14] and using distance method (neighbor joining, LogDet distances) in PAUP.