

zf-NADH-PPase Domain

[A]

L. major; CAJ08548

AFNFCANCGTATDPTRDVGFSPK-----CKQHF

S. cerevisiae; AJS01736

AKYKF¹CPG²CSPLFP-V³E⁴AG⁵TKLO⁶CSN⁷E⁸N⁹RNVY¹⁰CNV¹¹RD¹²AR¹³INNVC¹⁴F

***M. oryzae*; ELQ65661**

D R N P F C S O C G O K T L P - V H A G A K R A C P P T D M A G G - - - - -

F. avenaceum; KIL95307

SRSPFCAGCGQPNL-SVHAGFKRVCPPADKKGGESSEPRADCPTRH

D. rerio; NP 001017675

SRYFCPTCGSNTRV-EDGGYKRTCLRAGCRS-----LOGVYNTCY

X. laevis; NP 001088355

SRYKFCPTCGSATII-EEGGYKRTCLKNECPS-----LRGIHNTSY

H. sapiens; NP 001287670

SR**Y**K**F**C**P**T**C**G**N**A**T**K-**I**E**E**G**G**Y**K**R**L**C**L**-----**K**E**D**C**P**S**L**N

[B]

L. major; CAJ08548

AFNRFCA^{*}NC^{*}GTATDPT^{*}RDVGF^{*}SRFC^{*}PKCRKQHF

Sphingomonas sp.; WP 009820466

ARHPFCSVCGGATOA V-KAGWSRRCE TCGAEHF

P. carotovorum; WP 039494831

RSRFCGYCGHEMVR S-KTELACLCHHCKERY

E. coli; ELD86860

RS**HKY**CGY**CGH**EM**YP**S-K**TEW**AM**LCS**H**CR**ERY**Y**

G. uraniireducens; WP 011940127

RNSAICSRCGGEHERI-PTWGKRCKSCRHEHY

M. tuberculosis; CNF29781

NTNRYCPRCGTETRVSSAGHVRVCPDGSQHF

Supplementary Table 3: Partial sequence alignment of zf-NADH-PPase Domain proteins. Partial amino acid sequence alignment of the **zf-NADH-PPase Domain** of *L. major* (Lmjf.31.2950; NCBI Accession: CAJ08548) and its comparison with different eukaryotic organisms **[A]** and bacteria **[B]**. Sequences Accession numbers for the sequences for each species are as shown in parenthesis. Conserved cysteine residues involved in zinc chelation are marked with red asterisk.