

Species [NCBI Accesion]	Code	NUDIX Domain	SQPWPYP Domain	PTS-1
<i>L. major</i> [CAJ08548]	LMPER	GFVLHG-ESAEETVRREVEEESGA	S-QPWPYP	SQL
<i>T. brucei</i> [Q57Z14]	TbNH2	GGVEEGDADIIRAAVREVHEEVGL	-	SSI
<i>S. cerevisiae</i> [AJS01736]	SCPER	GFMEPS-ETIEEACIREIWEETGI	S-QPWPYP	SHL
<i>M. oryzae</i> [ELQ65661]	MOPER	GFLEPG-ESIEEATRREVWEESGV	C-QPWPMP	PKI
<i>F. avenaceum</i> [KIL95307]	FAPER	GFLEPG-ESIEESVRREVWEESGV	S-QPWPYP	PKI
<i>D. rerio</i> [NP_001017675]	DRPER	GFIEPG-ECVEAAVRREVQEESGV	S-QPWPMP	ANL
<i>X. laevis</i> [NP_001088355]	XL12PER	GFIEPG-EIIEDAVRREVEEESGV	SCQPWPMP	ANL
<i>H. sapiens</i> [NP_001287670]	HS12PER	GFIEPG-ETIEDAVRREVEEESGV	ACQPWPMP	PNL
<i>H. sapiens</i> [NP_001099133]	HS7PER	GKRDPTDMDDAATALREAQEEVGL	-	SRL
<i>C. platini</i> [KKF95078]	CPPER	GKADTTSESPYEIARREAWEEIGL	-	AKM
<i>M. tuberculosis</i> [CNF29781]	MTB	GFVEPG-ESLEQAVAREVKKEEVGL	S-QPWPLP	None
<i>E. coli</i> [ELD86860]	EC	GFVEVG-ETLEQAVAREVLEESGI	S-QPWPFP	None

Supplementary Table 4: Partial sequence alignment of microbody located NUDIX domain proteins. Partial amino acid sequence alignment of the **NUDIX domain box**, consensus sequence **SQPWPYP** and C-terminal tripeptide (**peroxisomal targeting sequence** type-1) of *L. major* (Lmjf.31.2950; NCBI Accesion: CAJ08548) and its comparison with different organisms. Sequences highlighted in pink color are for peroxisomal NADH diphosphatase while with grey background belong to bacteria. Accession numbers for the sequences for each species are depicted in parenthesis.