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                                                                                Motif 1
CaEno1     1  MSYATKIHARYVYDSRGNPTVEVDFTTDKGLFRSIVPSGASTGVHEALELRDGDKSKWLG
ScEno      1  -MAVSKVYARSVYDSRGNPTVEVELTTEKGVFRSIVPSGASTGVHEALEMRDGDKSKWMG
                                                                                Motif 2
CaEno1    61  KGVLKAVANVNDIIAPALIKAKIDVVDQAKIDEFLLSLDGTPNKSKLGANAILGVSLAAA
ScEno     60  KGVLHAVKNVNDVIAPAFVKANIDVKDQKAVDDFLISLDGTANKSKLGANAILGVSLAAS
                                                                                Motif 3
CaEno1   121  NAAAAAQGIPLYKHIANISNAKKGKFVLPVPFQNVLNGGSHAGGALAFQEFMIAPTGVST
ScEno    120  RAAAAEKNVPLYKHLADLSKSKTSPYVLPVPFLNVLNGGSHAGGALALQEFMIAPTGAKT

CaEno1   181  FSEALRIGSEVYHNLKSLTKKKYGQSAGNVGDEGGVAPDIKTPKEALDLIMDAIDKAGYK
ScEno    180  FAEALRIGSEVYHNLKSLTKKRYGASAGNVGDEGGVAPNIQTAEEALDLIVDAIKAAGHD

CaEno1   241  GKVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLSGPQLADLYEQLISEYPIVSIEDPF
ScEno    240  GKVKIGLDCASSEFFKDGKYDLDFKNPNSDKSKWLTGPQLADLYHSLMKRYPIVSIEDPF
                                                                                Motif 4                                Motif 5
CaEno1   301  AEDDWDAWVHFFERVGDKIQIVGDDLTVTNPTRIKTAIEKKAANALLLKVNQIGTLTESI
ScEno    300  AEDDWEAWSHFFKTAG--IQIVADDLTVTNPKRIATAIEKKAADALLLKVNQIGTLSESI
                                                                                Motif 6                                PS00164
CaEno1   361  QAANDSYAAGWGVMVSHRSGETEDTFIADLSVGLRSGQIKTGAPARSERLAKLNQILRIE
ScEno    358  KAAQDSFAAGWGVMVSHRSGETEDTFIADLVVGLRTGQIKTGAPARSERLAKLNQLLRIE

CaEno1   421  EELGSEAIYAGKDFQKASQL
ScEno    418  EELGDNAVFAGENFHHGDKL
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Figure S9. Clustal Omega alignment of *C. albicans* enolase 1 and *S. cerevisiae* enolase 1 amino acid sequences. Identical residues are highlighted in black and conserved residues are highlighted in gray. Residues in rectangles correspond to Motifs 1-6 found in enolase family (PRINTS code: PR00148). Underlined residues correspond to PS000164 PROSITE conserved motif found in enolase. According to cd03313 conserved protein domain family: circles, metal-binding residues; triangles, substrate-binding residues; asterisks, catalytic-site residues.