

A

Peptides identified by tandem mass spectrometry in the purified rCaEno1:

SIVPSGASTGVHEALELR

[MW + H]⁺ = 1822.8105

LGANAILGVSLAAANAAAAAQGIPLYK

[MW + H]⁺ = 2509.4063

VNQIGTLTESIQAANDSYAAGWGMVSHR

[MW + H]⁺ = 3075.2451

SGETEDTFIADLSVGLR

[MW + H]⁺ = 1809.7429

>CaEno1

MSYATKIHARYVYDSRGNPTVEVDFTTDKGLFR**SIVPSGASTGVHEALELR**DGDGKSKW
LGKGV LKAVANVNDIIPALIKAKIDVVDQAKIDFLSLDGTNPKSK**LGANAILGVSLAA**
ANAAAAAQGIPLYKHIANISNAKKGKFLVLPVPFQNVLNNGGSHAGGALAFQEFMIAPTG
VSTFSEALRIGSEVYHNLKSLTKKKYQGSAGNVGDEGGVAPDIKTPKEALDLIMDAIDKA
GYKGVGIAMDVASSEFYKDGKYDLDFKNPESDPSKWLSGPQLADLYEQLISEYPIVSI
EDPFAEDDWDAWVHFFERVGDKIQVGGDLTVTNPTRIKTAIEKKAANALL**KVNQIGTL**
TESIQAANDSYAAGWGMVSHRSGETEDTFIADLSVGLRSGQIKTGAPARSERLAKLN
QILRIEEELGSEAIYAGKDFQKASQL

B

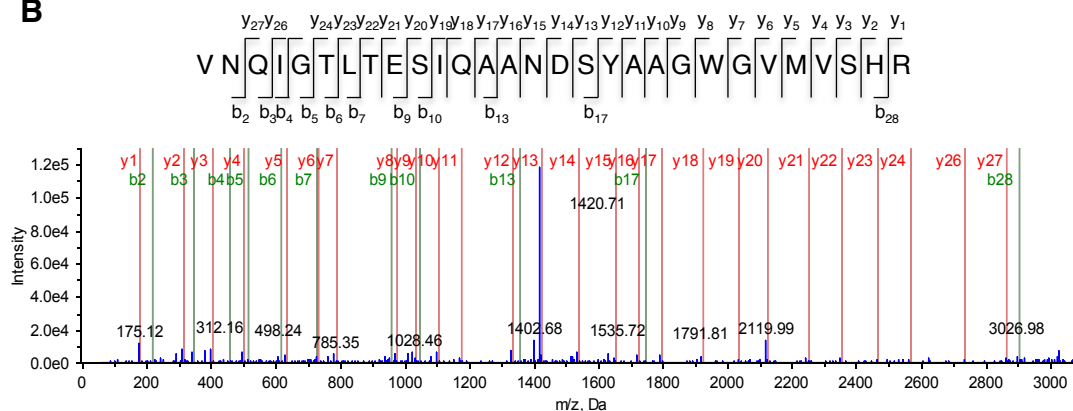


Figure S7. Identification of the recombinant *C. albicans* enolase 1 (rCaEno1) by tandem mass spectrometry. *A*, amino acid sequences are shown for the peptides identified (bold letters) by mass spectrometry with more than 95% in confidence, covering 20.68% of the total CaEno1 amino acid sequence. The m/z ratios for the corresponding precursor ions are shown. *B*, mass spectrum of the QIGTLTESIQAANDSYAAGWGMVSHR peptide is shown as an example.