

Supplementary material

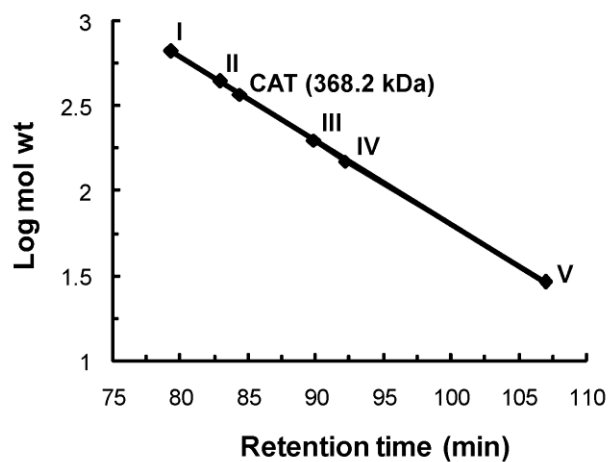


Fig. S1 Determination of molecular weight of native CAT isolated from *A. terreus* by SEC column (Hiprep Sephacryl S-300 HR, 1.6×60 cm, 50 μ m, GE). Molecular weight standards were: I. thyroglobulin (669 kDa), II. apoferritin (443 kDa), III. β -amylase (200 kDa), IV. alcohol dehydrogenase (150 kDa) and V. carbonic anhydrase (29 kDa) (Sigma)

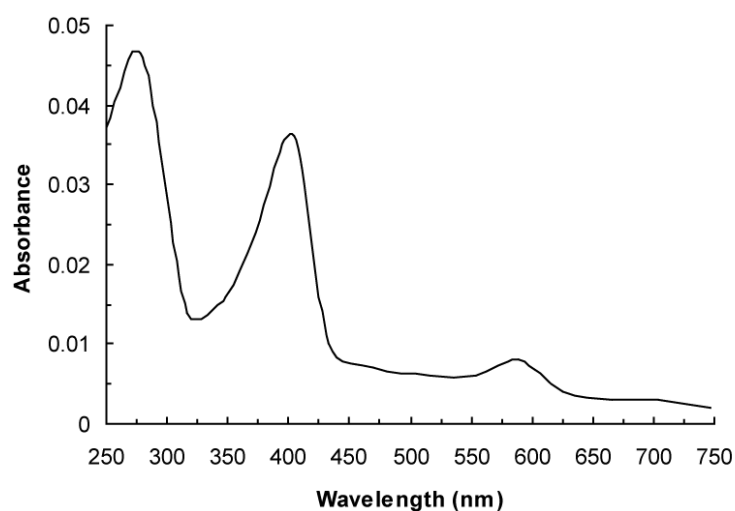


Fig. S2 UV-Vis spectra of purified CAT. The protein concentration was 15 μ g ml⁻¹ in 50 mM SPB (pH 7.5). The data was recorded at a scan rate of 100 nm min⁻¹

VATSAYANP_CATALASE_081908 #4248 RT: 41.77 AV: 1 NI · 4 00F6
T: + c NSI d Full ms2 1039.04@28.00 [275.00-2000.00]

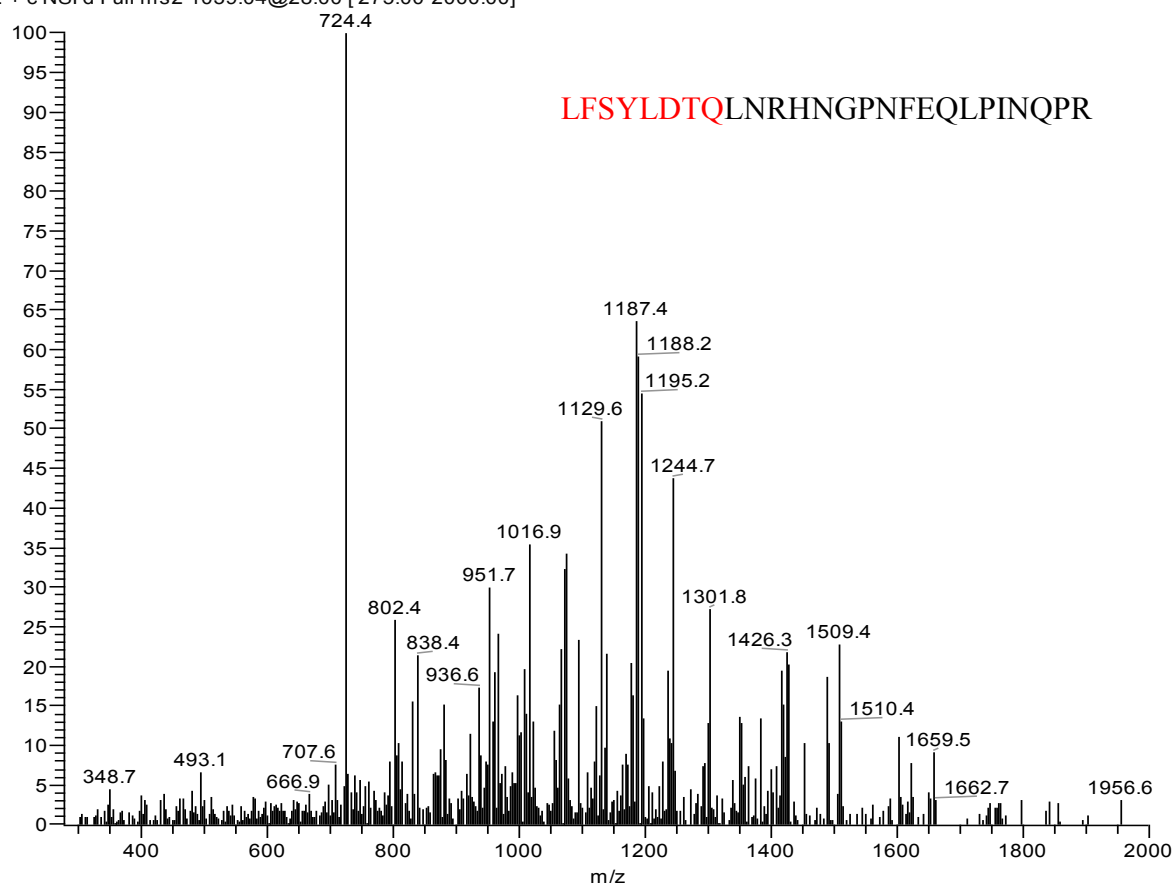


Fig. S3 LC-MS/MS tandem mass spectra of “LFSYLDTQLNRHNGPNFEQLPINQPR” peptide. The eight amino acid sequences from left belong to the proximal heme binding domain of the CAT. The first residue “R” in the left is missed here due to tryptic digestion, which is however, identified by the overlapping of spectra. The detailed description of proximal heme binding domain is given in the manuscript

VATSYAYANP_CATALASE_081908 #4222 RT: 41.37 AV: 1 NI · 7 10F6
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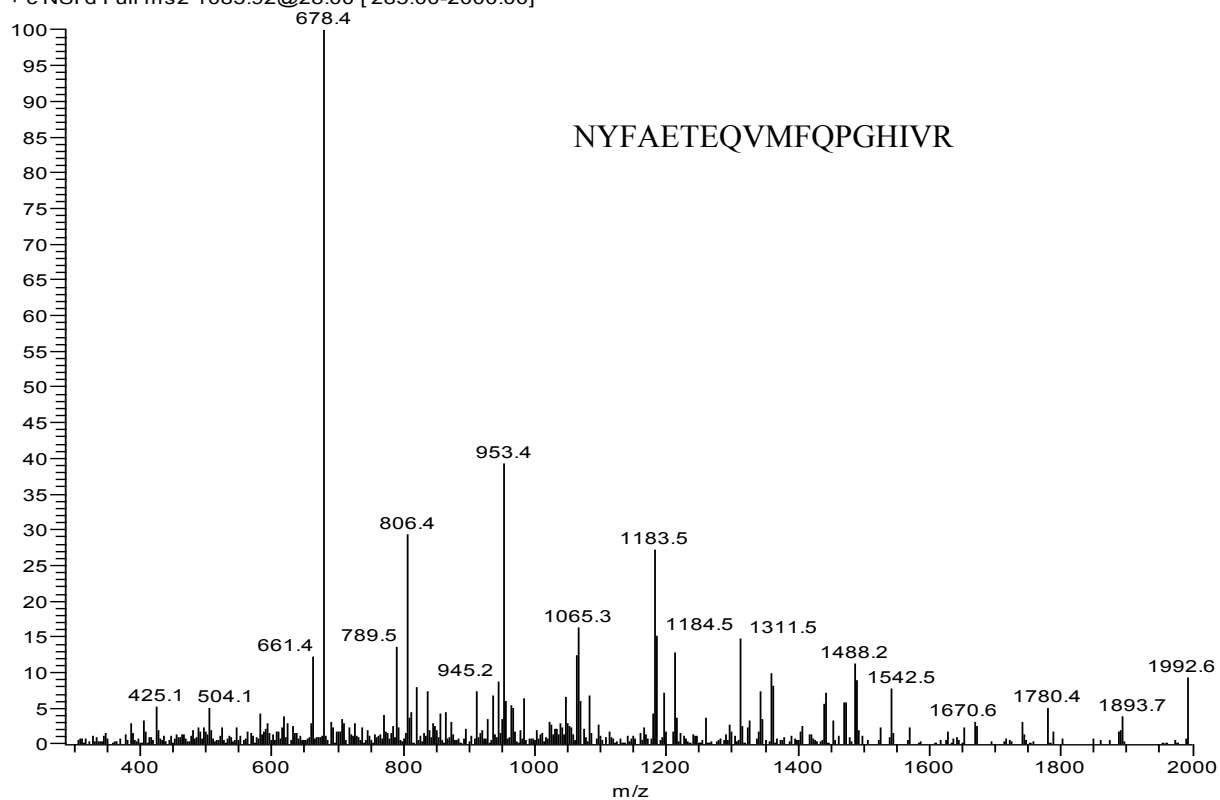


Fig. S4 LC-MS/MS tandem mass spectra of “NYFAETEQVMFQPGHIVR” peptide which belong to the tetramer interface domain of the CAT