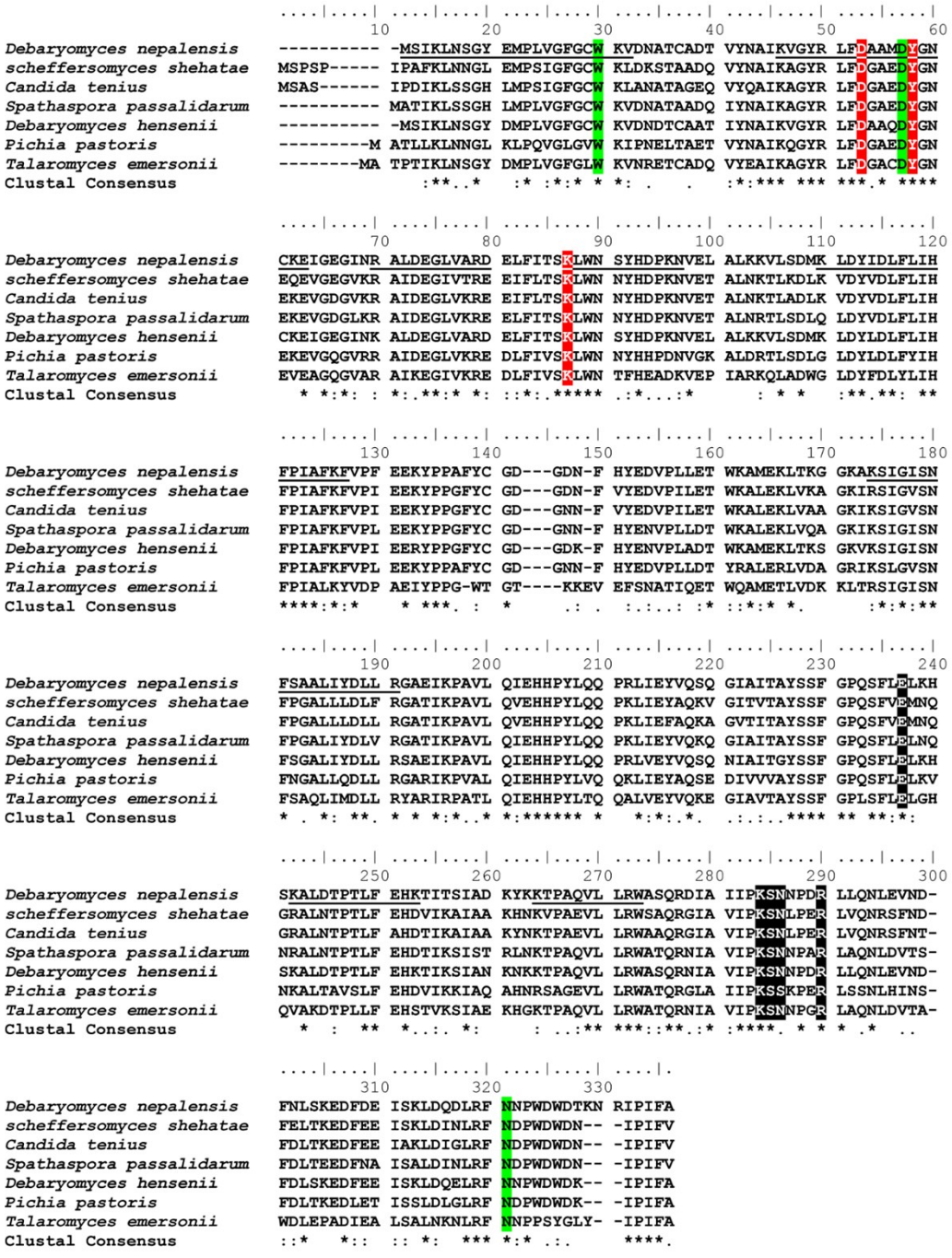

Fig. S1. Multiple alignments of *Dn*AR and six other aldose (xylose) reductases. Sequences were aligned using ClustalW and were rendered using BioEdit 7.0.0. The residues involving in substrate binding (green), catalysis (red) as well as the important residues for cosubstrate binding (black) are highlighted. The clustal consensus is given below the alignments. Asterisks indicate high conservation of residues, whereas double and single dots represent decreasing conservation consecutively. Underlined regions indicate determined peptide sequences of *Dn*AR by peptide mass fingerprinting using LC-MS.

Mass spectroscopy (LC-MS) analysis of purified *Dn*AR

The pH of the purified protein sample was adjusted to ~8.5 using 50 mM ammonium carbonate. To this sample (2 ml), ice cold trypsin (0.2 U/µl) was added in 1:30 (enzyme:protein) ratio and incubated at 55 °C for 2 h. The digested peptides were vacuum dried and reconstituted in 15 µl of 2% (v/v) acetonitrile with 0.1% (v/v) formic acid. The digested peptides were subjected to 70 min reversed phase chromatography (RPC) gradient, followed by acquisition of the data on linear trap quadropole (LTQ)-Orbitrap-Mass spectroscopy (Thermo Scientific, USA). The generated peptide fragments data were searched against Uniprot Swiss-Prot database, UniprotTrEMBL and yeast RefSeq database (from NCBI). Mass spectroscopic analysis of the purified protein was performed at the Centre for Cellular and Molecular Platforms (C-CAMP), Department of Biotechnology, Government of India.