

- 1) Nucleotide sequence of the putative xylose reductase gene from *Chaetomium thermophilum* DSM 1495 (GenBank accession number XM\_006695955.1):

ATGGCTCCCCAGATCCCCAACATTAAGCTCAGCAGCGGCTATGACATGCC  
AGGTGGGCTTGGACTGTGGAAGGTCGACCGCTCGATCTGCGCCGACGTC  
CTACAACGCAATTAAAGATTGGCTACCGCCTGTTGACGGCGCTGCGACTATG  
GCAACGAAGTCGAGGCCGGCAGGGCATTGCCCAGGCCATCAAGGAGGGCA  
TCGTGAAGCGTGAGGAGCTTCCATCGTGTCCAAGCTCTGGAACACCTCAC  
GACGGCGACAAGGTCGAGCCCATCGTCCGCAAGCAGCTCGCCGACTGGGC  
ATTGACTACTTCGACCTCTACCTCGTCCACTCCCTGTCGCCCTGAGTACGTC  
GACCCCTCGGTCCGCTACCCGCCGGCTGGTCTACGATGGCGAGAAGGAGA  
TCCGCCAGCAAGGCCACCATCCAGGAGACCTGGACCGCCATGGAGTCC  
TCGTTGAGAAGGGTCTGGCCCGCAGCATTGGTGTCTCCAACCTCCAGGCC  
GCTCCTTACGACCTGCTGCGTACGCCAAGATCCGCCGCCACCCCTCAG  
ATCGAGCATCACCCCTCCTCGTCCAGCAGGAGCTGCTAACCTGGCCAAGG  
CCGAGGGCATTGCCGTGACTGCCTACAGCTCATTGGCCCTCAGAGCTCCTC  
GAGTTCAACATGAAGCACGCCGTGAGCTCACCCCGCTTCGAGGACGAGA  
CCATCAAGAAGATGCCGCCAAGTACAACCGTCTGCTCGCAGGTTCTCCT  
GCGCTGGGCCACTCAGCGCGTCTGCCATTATCCCCAAGAGCACCGGCC  
GAGATCATGAAGTCCAACCTCGAGAGCATCGAGTTGACCTCAGCGAGGAA  
GATATTGCCACCATCTGGCCTCGACCGCGGCTGCGCTCAACCAGCCA  
CAAACACTTCCCCACCGAGCACCTCTGGATCTTGGCTAA

- 2) Nucleotide sequence of the expressed xylose reductase gene from *Chaetomium thermophilum* (after codon optimization):

ATGGCTCCTCAAATACCTAATATTAAGTTATCAAGTGGTTATGATATGCC  
AGTTGGTTTGGTTATGGAAAGTAGATAGAAGTATTGTGCTGATGTAGTT  
ATAATGCAATTAAAGATAGGATATAGATTATTGATGGAGCTGTGATTATGG  
AATGAAGTAGAAGCAGGACAAGGTATAGCTAGAGCAATAAAAGAAGGTATT  
GTAAAGAGAGAAGAATTATTGTTCTAAGTTATGGAATACTTTCATGA  
TGGAGATAAGGTAGAACCAATTGTTAGAAAGCAATTAGCTGATTGGGTATT  
GATTATTGATTATTTAGTACATTCCAGTGCATTAGAATATGTAGAT  
CCTCAGTTAGATATCCACCTGGATGGTTATGATGGTAAAAGGAAATAA  
GACCTAGTAAGGCTACAATACAAGAAACTTGGACAGCAATGGAATCTTAGT  
AGAAAAGGATTAGCTAGAAGTATAAGTGTCTAATTTCAGCACAAATT  
TTATATGATTATTAAGATATGCTAAGATAAGACCAGCAACTTACAAATAG  
AACATCATCCATTAGTACAACAAGAATTATTAATTTAGCTAAAGCAGA  
AGGAATAGCTGTTACAGCATATTCTCATTGGTCCACAATCATTAGAAT  
TTAATATGAAGCATGCTGTACAATTAACTCCTTATTGAAGATGAAACAATA  
AAGAAAATAGCTGCAAAGTATAATAGACCAGCTTCACAAGTTATTAAGAT  
GGGCTACTCAAAGAGGATTAGCAATAATTCAAAGAGTACAAGACCTGAAA  
TAATGAAGTCAAATTAGAAAGTATAAGAATTGATTATCTGAAGAAGATAT  
TGCTACTATATCAGCATTGATAGAGGTTAAGATTAAATCAACCTACTAATT

ATTTCCCTACAGAACATTATGGATATTGGACTCGAGCACCACCAC  
CACTGA

3) Amino acid sequence of the expressed xylose reductase gene from *Chaetomium thermophilum*:

Met A P Q I P N I K L S S G Y D Met P Q V G F G L W K V D R S I C A D V V Y N A I  
K I G Y R L F D G A C D Y G N E V E A G Q G I A R A I K E G I V K R E E L F I V S  
K L W N T F H D G D K V E P I V R K Q L A D W G I D Y F D L Y L V H F P V A L E  
Y V D P S V R Y P P G W F Y D G E K E I R P S K A T I Q E T W T A Met E S L V E K  
G L A R S I G V S N F Q A Q L L Y D L L R Y A K I R P A T L Q I E H H P F L V Q Q  
E L L N L A K A E G I A V T A Y S S F G P Q S F L E F N Met K H A V Q L T P L F E  
D E T I K K I A A K Y N R P A S Q V L L R W A T Q R G L A I I P K S T R P E I Met K  
S N L E S I E F D L S E E D I A T I S A F D R G L R F N Q P T N Y F P T E H L W I F G  
L E H H H H H H Stop

4) pH optimum in alternative buffer systems

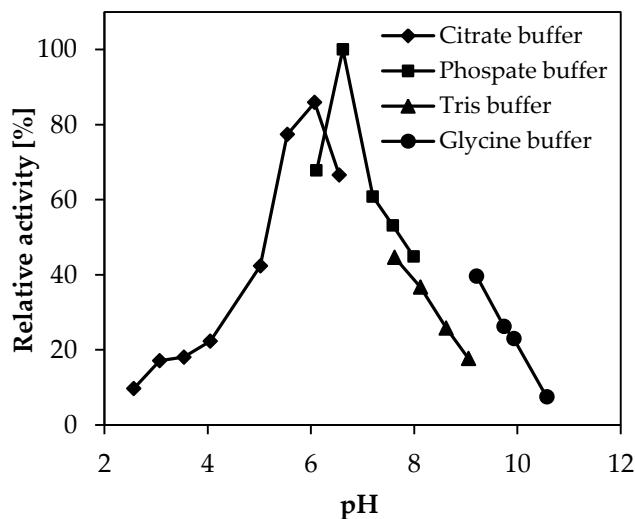


Figure S1: Xylose reductase activity at different pH values in alternative buffer systems. Measurements were taken at 30 °C in a set of different 50 mM buffers covering a pH range from 2.5 to 10.5 in steps of 0.5 pH units: ♦ citrate (2.5 – 6.5), ■ phosphate (6.0 – 8.0), ▲ tris (7.5 – 9.0) and ● glycine (9.0 – 10.5). NADPH was used as cofactor and D-xylose as substrate.