Supplementary Materials: Cloning, Expression and Characterization of a Novel Fructosyltransferase from *Aspergillus oryzae* ZZ-01 for the Synthesis of Sucrose 6-Acetate

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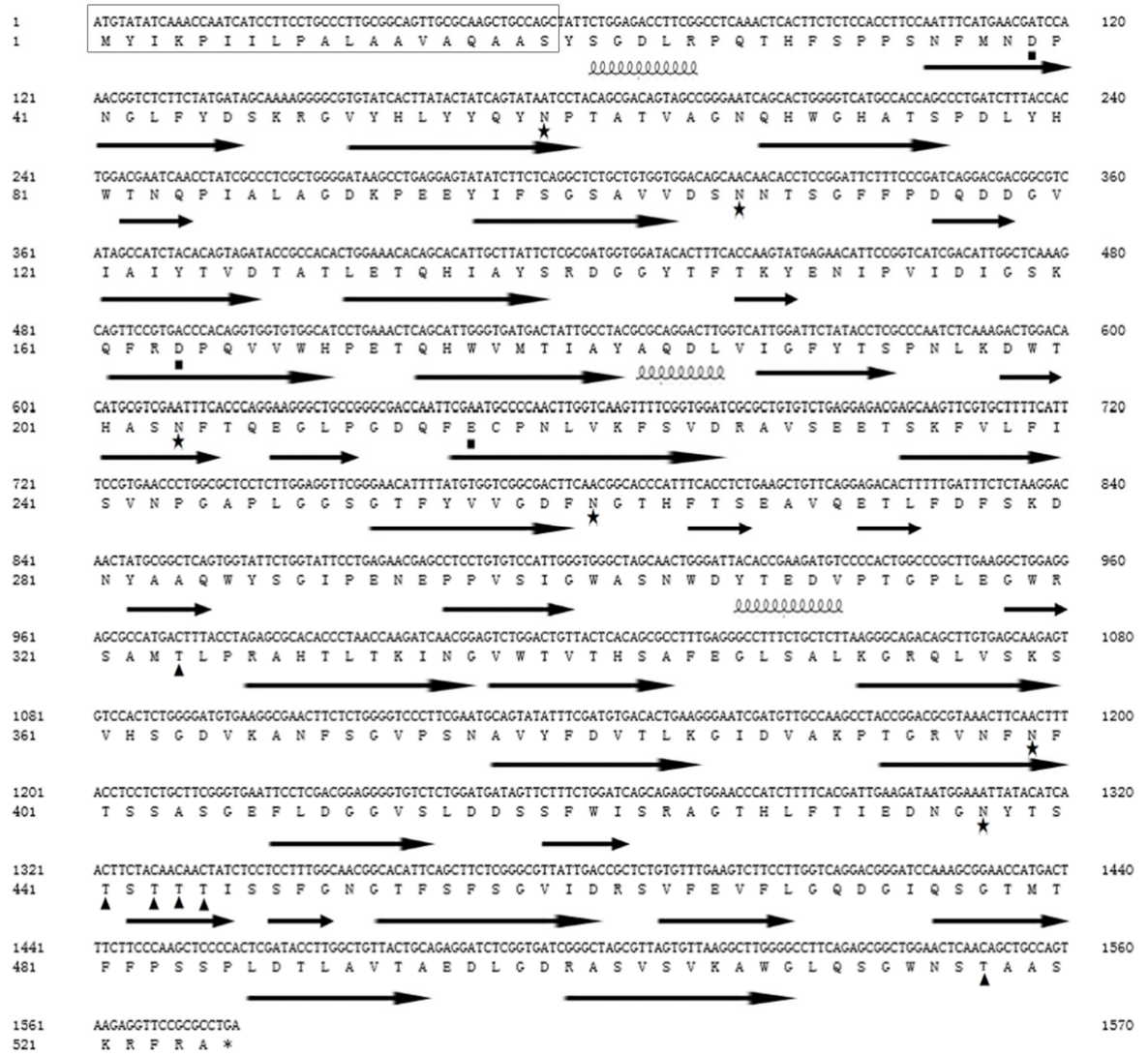

Figure S1. Gene and amino acid sequences of the r-*Ao*FT. Six Potential *N*-glycosilation sites (N59, N107, N204, N261, N399 and N437) and six potential *O*-glycosylation sites (T324, T441, T443, T444, T445 and T516) are represented by asterisks and triangles, respectively. The signal peptide is showed in the white box. The closed black squares represent the amino acids of the catalytic residues Asp39, Asp164, and Glu 216. Symbols above blocks of sequence represent the predicted secondary structure, springs represent helices, and arrows represent β-strands.

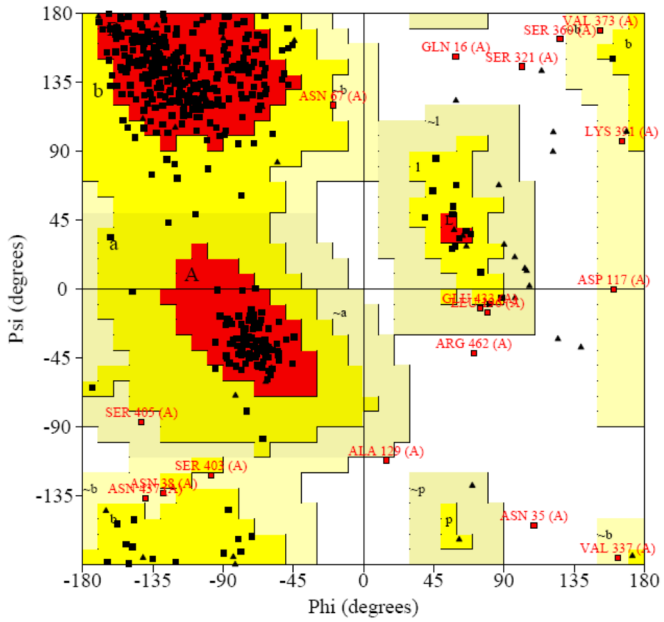

Figure S2. Ramacchandran plots of the r-*Ao*FT models by PROCHECK analysis.

Table S1. Comparision of transfructosylation activity of the mutants N38L, Ser99A, N38V, N38I and Ser99V.

Mutants	Specific Activities (μmol/min/mg)	K_m (mg/mL)	V_{max} (μmol/min/mg)
r-*Ao*FT	38.0	21.0	75.0
N38L	42.1	24.3	89.2
Ser99A	40.1	22.2	81.2
N38V	32.0	16.1	54.2
N38I	33.6	17.9	58.3
Ser99V	25.9	13.7	42.0

Table S2. Synthetic oligonucleotide primers used for the construction of the site-directed mutants mutants.

Vectors	Upper Primers [a]	Lower Primers [b]
N38L	5′-TTCCAATTTCATGCTCGATCCAAACGGTCTCT-3′	5′-ATCGTTCATGAAATGAGAAGGTGGAGAGAAGT-3′
Ser99A	5′-GAGTATATCTTCTCGCGCTCTGCTGTGGTGG-3′	5′-CAGCAGAGCCTGAGCGGATATACTCCTCAGGC-3′
Y282A	5′-TCTAAGGACAACTACGGGGCTCAGTGGTATTC-3′	5′-CTCAGCCGCAGCCTTGTCCTTAGAGAAA-3′
D39A	5′-CAATTTCATGAACGGCCCAAACGGTCTCTTCTA-3′	5′-CGTTTGGATGGCCCATGAAATTGGAAGGTG-3′
D164A	5′-GAACATTCCGGCATCGACATTGGCTCAAA-3′	5′-AATGTCGATGCCCGGAATGTTCTCATACTTG-3′
E216A	5′-AATTCGAGGCCCCCAACTTGGTCAAGTTTT-3'	5′-ATCGAATGGGCCATTCGAATTGGTCGCCCGG-3′

[a,b] The sites of mutations are underlined.