Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88

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Supplementary Table 3 Panorthologous proteins used for phylogenetic analysis

Protein	**Description** ***Saccharomyces cerevisiae* protein**
SDH1	Succinate dehydrogenase flavoprotein precursor
UBA3	Ubiquitin-like protein activating enzyme
IMP4	Component of the U3 small nucleolar ribonucleoprotein
RPN10	26S proteasome regulatory subunit
POL12	DNA-directed DNA polymerase alpha, 70 kDa subunit
NMD2	Nonsense-mediated mRNA decay protein 2
YND1	Yeast nucleoside diphosphatase
NPA3	Cytoplasmic protein required for cell viability, identified by association with pre-ribosomal particles
CSE1	Importin-beta-like protein
RPN9	Subunit of the regulatory particle of the proteasome
RAD3	DNA helicase/ATPase
ARH1	Mitochondrial protein putative ferredoxin-NADP+ reductase
CAM1	Translation elongation factor eEF1 gamma homolog
RPA135	DNA-directed RNA polymerase I, 135 kDa subunit
SEC62	ER protein-translocation complex subunit
TAF2	Component of TFIID complex
TAH18	Protein with a potential role in DNA replication
FYV10	Protein involved in proteasome-dependent catabolite inactivation of fructose-1,6-bisphosphatase
PRI2	DNA-directed DNA polymerase alpha , 58 kDa subunit (DNA primase)
HSH155	Multi-protein splicing factor