

Supplemental Table 2. Proteins of the secretome of 7-day-old xylose grown sandwiched colonies of the $\Delta flbA$ strain of *A. niger* that are predicted to be released into the culture medium via the non-classical secretion pathway by the SecretomeP prediction tool. The abundance (expressed as the $^2\log$ fold change) of these proteins in zones 1, 2, 4 and 5 is related to zone 3. Green and red shading indicate increased and decreased abundance, respectively, when compared to zone 3.

Accession	related to non-classical secreted proteins	zone 1/3	zone 2/3	zone 4/3	zone 5/3
An02g07020	Chitinase chiB - Aspergillus niger	0.1	0.2	-3.9	-5.4
An12g00240	strong similarity to translational inhibitor uk14 - Homo sapiens [truncated ORF]	-0.5	0.0	-0.5	-2.2
An01g00370	aspergillopepsin apnS - Aspergillus niger	0.0	0.0	0.0	0.0
An09g00270	alpha-galactosidase aglC - Aspergillus niger [truncated ORF]	0.2	0.3	-1.0	-3.1
An02g01830	cytochrome c cyc - Aspergillus niger	0.0	0.0	-0.7	-2.3
An09g02830	strong similarity to acylaminoacyl-peptidase DPP V - Aspergillus fumigatus	0.7	0.7	-3.9	0.0
An15g05960	strong similarity to hypothetical protein Afu2g15710 - Aspergillus fumigatus	-1.3	-0.4	-0.9	-3.4
An11g01120	strong similarity to NADPH-dependent aldehyde reductase - Sporobolomyces salmonicolor	-1.5	-0.1	0.7	1.1
An12g08570	similarity to type 2 peroxiredoxin PrxII - Brassica napus	-2.6	-0.3	1.0	0.5
An04g06510	strong similarity to polyubiquitin 5 Ubi4 - Saccharomyces cerevisiae	-3.3	-1.1	-0.1	-1.2
An01g02500	strong similarity to thioredoxin - Aspergillus nidulans	-2.3	-0.8	0.0	-1.1
An02g08660	strong similarity to hypothetical protein H04M03.4 - Caenorhabditis elegans	-0.8	-0.5	0.2	-1.5
An16g08760	similarity to zinc metalloprotease ZmpB from patent WO9964610-A1 - Streptococcus pneumoniae	0.0	0.0	-0.4	-2.4
An07g05830	strong similarity to formamidase fmdS - Aspergillus nidulans	-0.8	0.0	0.0	0.0
An03g06870	strong similarity to cytidine deaminase - Homo sapiens	-1.9	-1.0	-1.0	-4.7
An14g02250	strong similarity to flavocytochrome b2 L-lactate dehydrogenase CYB2 - Pichia anomala	0.0	0.0	0.1	0.0
An18g04590	strong similarity to rho GDP dissociation inhibitor Rdi1 - Saccharomyces cerevisiae	0.0	0.0	1.0	1.0
An07g01100	similarity to glutathione S-transferase omega - Sus scrofa	0.0	0.0	-0.4	0.0