

Supplementary Table 16 Components of the secretory pathway								
<i>Aspergillus niger</i>		Description of putative <i>Aspergillus niger</i> gene	Best homolog to putative <i>A.niger</i> gene					
<i>A.niger</i> orf	<i>A.niger</i> gene		<i>A.nidulans</i>	<i>A.fumigatus</i>	<i>A.oryzae</i>	<i>N.crassa</i>	<i>S.cerevisiae</i>	Mammal
<b>Entry into ER</b>								
<b>Signal recognition</b>								
An01g02800		strong similarity to signal recognition particle 68K protein SRP68 - <i>Canis lupus</i>	AN4043.2	Afu1g03940	AO090003000956	NCU10927.2	YKL122c YPL243w	
An04g06890		similarity to 72-kD protein of the signal recognition particle SRP72 <i>Canis lupus</i>	AN2014.2	Afu4g10180	AO090003001205	NCU01455.2	YPL210c	
An01g10070		strong similarity to signal recognition particle chain Sec65 - <i>Saccharomyces cerevisiae</i>	AN0643.2 AN0642.2	Afu1g16820		NCU03485.2	YML105c	
An15g06470		similarity to signal sequence receptor alpha chain - <i>Canis lupus familiaris</i>	AN2140.2	Afu2g16120	AO090012000186	NCU01146.2		
An07g05800		similarity to signal recognition particle protein srp14 - <i>Canis lupus</i>	AN4580.2	Afu2g01990	AO090011000469		YDL092w	
An09g06320		similarity to signal recognition particle 54K protein SRP54 - <i>Saccharomyces cerevisiae</i>	AN8246.2	Afu5g03880	AO090102000593	NCU09696.2	YPR088c	
<b>Signal peptidase</b>								
An01g00560		strong similarity to signal peptidase subunit Sec11 - <i>Saccharomyces cerevisiae</i>	AN3126.2	Afu3g12840	AO090012000838	NCU04519.2	YIR022w	
An17g02095		similarity to signal peptidase subunit Spc1 - <i>Saccharomyces cerevisiae</i>		Afu5g05800			YJR010c-a	
An16g07390		strong similarity to signal peptidase subunit Spc2 - <i>Saccharomyces cerevisiae</i>	AN1525.2	Afu8g05340	AO090005000615	NCU00965.2	YML055w	
An09g05420		similarity to signal peptidase subunit Spc3 - <i>Saccharomyces cerevisiae</i>	AN9460.2	Afu5g03220	AO090102000523	NCU06677.2	YLR066w	
<b>Translocation into ER</b>								
An03g04340		strong similarity to ER membrane translocation facilitator Sec61 - <i>Yarrowia lipolytica</i>	AN7721.2	Afu5g08130	AO090701000730	NCU08897.2	YLR378c	
An01g03820		strong similarity to ER protein-translocation complex subunit Sbh2 <i>Saccharomyces cerevisiae</i>	AN0417.2	Afu1g04890	AO090003000853	NCU08379.2	YER087c-b	
An01g11630		strong similarity to translocation complex component Sss1 - <i>Saccharomyces cerevisiae</i>	AN4589.2			NCU04127.2	YDR086c	
An01g03820		strong similarity to ER protein-translocation complex subunit Sbh2 <i>Saccharomyces cerevisiae</i>	AN0417.2	Afu1g04890	AO090003000853	NCU08379.2	YER019c-a	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
An02g01510		strong similarity to component of the endoplasmic reticulum protein translocation machinery Sec62 - <i>Saccharomyces cerevisiae</i>	AN6269.2	Afu2g12580	AO090026000361	NCU06333.2	YPL094c	

An01g13070		strong similarity to signal recognition particle receptor Sec63 - <i>Saccharomyces cerevisiae</i>	AN0834.2	Afu1g14940	AO090005001238	NCU00169.2	YOR254c	
An16g08830		strong similarity to component of ER protein-translocation subcomplex Sec71 from patent WO9949028-A1 - <i>Saccharomyces cerevisiae</i>	AN1442.2	Afu8g04260	AO090103000044	NCU02681.2	YBR171w	
An15g01670		strong similarity to signal sequence receptor alpha subunit SRP101 - <i>Yarrowia lipolytica</i>	AN6627.2	Afu6g03850	AO090701000163	NCU00625.2	YDR292c	
An05g00140		similarity to signal recognition particle receptor beta chain Srp102 - <i>Saccharomyces cerevisiae</i>	AN5819.2	Afu2g07600	AO090011000933	NCU08217.2	YKL154w	
<b>Processes in ER</b>								
<b>Protein folding</b>								
An02g14800	PdiA	protein disulfide isomerase A pdiA - <i>Aspergillus niger</i>	AN7436.2	Afu2g06150	AO090001000733	NCU09223.2	YCL043c	
An18g02020	TigA	disulfide isomerase tigA - <i>Aspergillus niger</i>	AN0075.2	Afu5g12260	AO090120000344	NCU03739.2	YCL043C	
An01g04600	PrpA	PDI related protein A prpA - <i>Aspergillus niger</i>	AN0248.2	Afu1g05320	AO090003000829	NCU00813.2	YOR288c	
An02g05890	EpsA	strong similarity to protein disulfide-isomerase pdi1 - <i>Caenorhabditis elegans</i>	AN5970.2	Afu2g10590	AO090011000579	NCU06344.2	YOR288C	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
An16g07620	EroA	strong similarity to endoplasmic reticulum oxidising protein Ero1 - <i>Saccharomyces cerevisiae</i>	AN1510.2	Afu8g05140	AO090005000630	NCU02074.2	YML130c	
An18g04260		similarity to secreted protein HNTME13 from patent WO9839446-A2 - <i>Homo sapiens</i>	AN4068.2	Afu1g05440	AO090009000400	NCU10721.2	YPL244c	
An08g07810		similarity to flavin adenine dinucleotide synthase Fad1 - <i>Saccharomyces cerevisiae</i>	AN0591.2	Afu6g11040	AO090023000516	NCU09233.2	YDL045c	
An08g06370		strong similarity to GTP-cyclohydrolase II RIB1 - <i>Pichia guilliermondii</i>	AN0670.2	Afu1g13300	AO090012000551	NCU07188.2	YBL033c	
An10g00350		similarity to GTP cyclohydrolase II ribA - <i>Actinobacillus pleuropneumoniae</i>	AN7660.2	Afu2g01220	AO090701000398	NCU01449.2		
An12g06490		similarity to N-oxide-forming dimethylaniline monooxygenase FMO1 - <i>Homo sapiens</i>	AN2629.2	Afu6g01900	AO090038000052	NCU06296.2		
An18g06470		strong similarity to DnaJ-like protein MTJ1 - <i>Mus musculus</i>	AN5770.2	Afu6g06610	AO090003000036	NCU02490.2		
An05g00880		strong similarity to dnaJ protein homolog Scj1 - <i>Saccharomyces cerevisiae</i>	AN6170.2	Afu2g08300	AO090011000874	NCU11102.2	YMR214w	
An01g08420	ClxA	strong similarity to calcium-binding protein precursor cnx1p - <i>Schizosaccharomyces pombe</i>	AN3592.2	Afu4g12850	AO090009000313	NCU09265.2	YAL058w	
An04g02020	CypB	strong similarity to cyclophilin cypB - <i>Aspergillus nidulans</i>	AN4467.2	Afu4g07650	AO090023000811	NCU01200.2	YDR155c	
An01g06670	CypB	strong similarity to peptidyl-prolyl isomerase FKBP-21 - <i>Neurospora crassa</i>	AN8343.2	Afu2g03870	AO090005001515	NCU04140.2	YDR519w	
An11g04180	BipA	dnaK-type molecular chaperone bipA - <i>Aspergillus niger</i>	AN2062.2	Afu2g04620	AO090003000257	NCU03982.2	YJL034w	
An01g13220	LhsA	strong similarity to 150 kDa oxygen regulated protein ORP150 - <i>Rattus norvegicus</i>	AN0847.2	Afu1g15050	AO090005001222	NCU09485.2	YKL073w	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	

Glycosylation							
<b>Synthesis of sugar donors</b>							
1. UDP-Glc							
An12g08610	GlkA	strong similarity to glucose kinase GLK1/hexokinase HXK1 - Saccharomyces cerevisiae	AN8689.2	Afu6g02230	AO090120000109	NCU00575.2	YCL040w
An15g05940		strong similarity to glucose kinase GLK1/hexokinase HXK1 - Saccharomyces cerevisiae	AN2180.2	Afu2g15700	AO090012000259	NCU06996.2	YFR053c
An16g01620		strong similarity to glucose kinase GLK1/hexokinase HXK1 - Saccharomyces cerevisiae	AN2180.2	Afu2g08110	AO090003001508	NCU06996.2	YFR053c
An02g14380	hvk	strong similarity to glucose kinase GLK1/hexokinase HXK1 - Saccharomyces cerevisiae	AN7459.2	Afu2g05910	AO090001000710	NCU02542.2	YFR053c
An06g00380		strong similarity to glucose kinase GLK1/hexokinase HXK1 - Saccharomyces cerevisiae	AN2638.2	Afu2g05910	AO090001000710	NCU02542.2	YFR053c
An13g00510		strong similarity to glucose kinase GLK1/hexokinase HXK1 - Saccharomyces cerevisiae	AN4255.2	Afu7g04040	AO090005000083	NCU04728.2	YFR053c
An02g07650		strong similarity to phosphoglucomutase PGM2, less to PGM1 - Saccharomyces cerevisiae	AN2867.2	Afu3g11830	AO090003000746	NCU10058.2	YMR105c
An07g06780		strong similarity to phosphoglucomutase PGM2, less to PGM1 - Saccharomyces cerevisiae	AN4591.2	Afu2g02120	AO090011000487		YMR278w
An12g00820		strong similarity to UDP-glucose pyrophosphorylase	AN9148.2	Afu7g01830	AO090038000558	NCU02797.2	YKL035w
An16g05420		strong similarity to glucose-6-phosphate isomerase	AN6037.2	Afu2g09790	AO090011000659	NCU07281.2	YBR196c
2. UDP-GlcNAc							
An18g06820		strong similarity to fructose-6-phosphate transaminase	AN5794.2	Afu6g06340	AO090003000003	NCU10234.2	YKL104c
An03g05940		strong similarity to fructose-6-phosphate transaminase	AN5794.2	Afu6g06340	AO090003000003	NCU10234.2	YKL104c
An12g07840		strong similarity to glucosamine-6-phosphate N-acetyltransferase	AN8706.2	Afu6g02460	AO090120000132	NCU01902.2	YFL017c
An18g05160		strong similarity to phosphoacetylglucosamine mutase	AN4234.2	Afu1g06210	AO090001000429	NCU07458.2	YEL058w
An18g05170		strong similarity to phosphoacetylglucosamine mutase	AN4234.2	Afu1g06210	AO090001000429	NCU07458.2	YEL058w
An12g00480		strong similarity to UDP-N-acetylglucosamine diphosphorylase	AN9094.2	Afu7g02180	AO090038000595	NCU02109.2	YDL103c
3. GDP-Man							
An04g03200		strong similarity to mannose-6-phosphate isomerase	AN1715.2	Afu4g08410	AO090023000719	NCU02322.2	YER003c
An08g06350		strong similarity to mannose-6-phosphate isomerase	AN0667.2	Afu1g13280	AO090012000554	NCU07165.2	YER003c
An18g06500		strong similarity to phosphomannomutase	AN5772.2	Afu6g06580	AO090003000030	NCU02829.2	YFL045c
An07g06780		strong similarity to phosphomannomutase	AN4591.2	Afu2g02120	AO090011000487		YMR278w
An04g04990		strong similarity to mannose-1-phosphate guanylyltransferase	AN5586.2	Afu4g11510	AO090003001069	NCU10584.2	YDL055c
An11g02380		strong similarity to mannose-1-phosphate guanylyltransferase	AN1911.2	Afu6g07620	AO090003000189	NCU05937.2	YDL055c
4. UDP-Gal							
An16g04160		strong similarity to galactokinase	AN4957.2	Afu3g10300	AO090003000570	NCU08687.2	YBR020w
An02g03590		strong similarity to UTP--hexose-1-phosphate uridyltransferase	AN6182.2	Afu2g11560	AO090026000490	NCU04460.2	YBR018c
An11g10890		strong similarity to UDP-glucose 4-epimerase	AN3432.2	Afu3g05740	AO090020000042	NCU09705.2	YBR019c
An12g10410		strong similarity to UDP-glucose 4-epimerase	AN2951.2	Afu4g14090	AO090005001490	NCU05133.2	YBR019c

An16g00180		strong similarity to UDP-glucose 4-epimerase	AN2951.2	Afu3g07910	AO090011000701	NCU00403.2	YBR019c	
An01g11440		strong similarity to UDP-glucose 4-epimerase	AN6398.2	Afu7g00360	AO090003001495	NCU08549.2		
An02g11320		strong similarity to UDP-glucose 4-epimerase	AN2951.2	Afu3g07910	AO090005001490	NCU05133.2	YBR019c	
An02g09090		strong similarity to UDP-glucose 4-epimerase	AN3184.2	Afu3g13240	AO090012000809	NCU08516.2	YHR210c	
An02g08660	GlfA	strong similarity to UDP-galactopyranose mutase	AN3112.2	Afu3g12690	AO090012000855	NCU01824.2		
An16g02380	GlfA	strong similarity to UDP-galactopyranose mutase	AN3112.2	Afu3g12690	AO090012000855	NCU01824.2		
<b>Transporters of sugar nucleotide donors</b>								
1. GDP-Man								
An17g02140		strong similarity to GDP-Man transporter	AN8848.2	Afu5g05740	AO090009000688	NCU06198.2	YGL225w	
An11g02020		strong similarity to GDP-Man transporter	AN3948.2	Afu6g08100	AO090003000119	NCU03097.2	YML038c	
2. UDP-GlcNAc								
An03g06940		strong similarity to UDP-GlcNAc transporter	AN8875.2	Afu8g02830	AO090010000775	NCU02980.2	YEL004w	
3. UDP-Gal								
An08g10400		strong similarity to UDP-Gal transporter	AN5515.2	Afu6g13070	AO090003000432	NCU09792.2		
An18g04260		strong similarity to UDP-Gal transporter	AN4068.2	Afu1g05440	AO090009000400	NCU10721.2	YPL244c	
<b>Oligosaccharyltransferase subunits</b>								
An02g14560		strong similarity to subunit of oligosaccharyltransferase complex	AN7472.2	Afu2g05790	AO090001000698	NCU02541.2	YJL002c	
An04g03495		strong similarity to subunit of oligosaccharyltransferase complex	AN1683.2	Afu4g08660	AO090023000690	NCU03224.2	YMR149w	
An07g04190		strong similarity to subunit of oligosaccharyltransferase complex	AN4683.2	Afu5g08970	AO090020000468	NCU00669.2	YEL002c	
An18g03920		strong similarity to subunit of oligosaccharyltransferase complex	AN4031.2	Afu1g03810		NCU09216.2	YOR103c	
An02g14930		strong similarity to subunit of oligosaccharyltransferase complex	AN7426.2	Afu2g06280	AO090001000747	NCU03995.2	YOR085w	
An16g08570		strong similarity to subunit of oligosaccharyltransferase complex	AN1455.2	Afu8g04430	AO090103000069	NCU10497.2	YGL022w	
An08g07485		strong similarity to subunit of oligosaccharyltransferase complex						
<b>Synthesis of the dolichol phosphate linked ER-precursor Glc3Man9GlcNAc2</b>								
An04g03960		strong similarity to dolichol kinase	AN1653.2	Afu4g09060	AO090023000648	NCU03771.2	YMR013c	
An16g04330		strong similarity to dolichyl-phosphate mannosyltransferase (polypeptide 1)	AN4947.2	Afu3g10400	AO090003000589	NCU07965.2	YPR183w	DPM1
An01g05200		strong similarity to dolichyl-phosphate mannosyltransferase (polypeptide 2) strong similarity to DPM2 - Mus musculus		Afu1g03020		NCU00067.2		DPM2
An14g00270		strong similarity to dolichyl-phosphate mannosyltransferase (polypeptide 3) weak similarity to dolichol-phosphate-mannose synthase DPM3 - Homo sapiens	AN6992.2			NCU05544.2		DPM3
An03g04410		strong similarity to UDP-glucose:dolichyl-phosphate glucosyltransferase	AN7715.2	Afu5g08210	AO090701000739	NCU06386.2	YPL227c	
An02g03240		strong similarity to UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase Alg7	AN5888.2	Afu2g11240	AO090026000526	NCU10762.2	YBR243c	

An01g09110		strong similarity to atalytic component of UDP-GlcNAc transferase, required for the second step of dolichyl-linked oligosaccharide synthesis		Afu4g13400	AO090009000234		YGL047w	
An06g01100		strong similarity to mannosyltransferase	AN5346.2	Afu6g14180	AO090103000403	NCU07261.2	YBR110w	
An14g05910		strong similarity to mannosyltransferase	AN6874.2	Afu5g13210	AO090120000461	NCU03503.2	YGL065c	
An18g05910		strong similarity to alpha-1,2-mannosyltransferase	AN5725.2	Afu1g06890	AO090001000490	NCU06779.2	YNL048w	
An02g14940		strong similarity to flippase = flipping of the precursor oligosaccharide	AN7425.2	Afu2g06300	AO090001000748	NCU05783.2	YBL020w	
An04g03130		strong similarity to putative flipping of Dol-P-Man/Glc	AN1721.2	Afu4g08350	AO090023000724	NCU10517.2		
An18g02360		strong similarity to Dol-P-Man dependent alpha(1-3) mannosyltransferase Alg3	AN0104.2	Afu5g11990	AO090120000319	NCU06552.2	YBL082c	
An08g07020		strong similarity to mannosyltransferase	AN0729.2	Afu1g13870	AO090012000489	NCU04454.2	YNL219c	
An01g08460		strong similarity to mannosyltransferase	AN3588.2	Afu4g12900	AO090009000318	NCU07472.2	YNR030w	
An02g12630		strong similarity to glucosyltransferase	AN4864.2	Afu3g07700	AO090020000410	NCU03317.2	YOR002w	
An04g08820		strong similarity to glucosyltransferase	AN7301.2	Afu2g16790	AO090102000146	NCU00163.2	YOR067c	
An02g02980		strong similarity to glucosyltransferase	AN5902.2	Afu2g11080	AO090026000548	NCU07328.2	YGR227w	
<b>Processing of the ER-precursor Glc3Man9GlcNAc2 after transfer to a polypeptide</b>								
1. ER								
An15g01420		strong similarity to glucosidase I	AN6606.2	Afu6g04210	AO090701000141	NCU03657.2	YGL027c	
An18g05620		strong similarity to glucosidase II alpha subunit	AN3504.2	Afu1g06560	AO090023000288	NCU04203.2	YBR229c	
An01g04880		strong similarity to glucosidase II alpha subunit	AN0280.2	Afu1g03140	AO090005000767	NCU04203.2	YBR229c	
An01g10930		strong similarity to glucosidase II alpha subunit	AN0941.2	Afu1g16250	AO090005001084	NCU04674.2	YBR229c	
An04g06920		strong similarity to glucosidase II alpha subunit	AN2017.2	Afu4g10150	AO090003001209	NCU02583.2	YBR229c	
An09g03300		strong similarity to glucosidase II alpha subunit	AN7120.2	Afu1g03140	AO090701000639	NCU04203.2	YBR229c	
An09g05880		strong similarity to glucosidase II alpha subunit	AN8217.2	Afu5g03500	AO090102000559	NCU04203.2	YBR229c	
An13g00620		strong similarity to glucosidase II beta subunit from <i>S. pombe</i> (D89245)	AN5697.2	Afu7g04110	AO090005000093	NCU05606.2	YDR221w	
An07g06430		strong similarity to UDP-glucose glycoprotein glucosyltransferase (gpt1 from <i>S. pombe</i> )	AN4623.2	Afu2g02360	AO090011000515	NCU02349.2	YOR336w	
An18g06220		strong similarity to ER-alpha-1,2-mannosidase	AN5748.2	Afu6g06790	AO090003000057	NCU02778.2	YJR131w	
An01g12550		strong similarity to ER-alpha-1,2-mannosidase	AN0787.2	Afu1g14560	AO090003000476	NCU07067.2	YJR131w	
An04g06990		strong similarity to ER-alpha-1,2-mannosidase	AN2045.2	Afu4g10070	AO090003001225	NCU01059.2	YJR131w	
An06g01510		strong similarity to ER-alpha-1,2-mannosidase	AN3733.2	Afu6g12360	AO090009000178	NCU02235.2	YLR057w	
An12g00340		strong similarity to alpha mannosidase-like protein of the endoplasmic reticulum required for degradation of glycoproteins MNL1- <i>Saccharomyces cerevisiae</i>	AN9084.2	Afu7g02290	AO090038000608	NCU02091.2	YHR204w	
2. Golgi								
An03g01090		strong similarity to alpha1,6-mannosyltransferase	AN2626.2	Afu8g02040	AO090010000615	NCU00609.2	YJR075w	
An05g01750		strong similarity to alpha1,6-mannosyltransferase	AN7534.2	Afu6g14040	AO090003001503	NCU07338.2	YJR075w	
An05g02320		alpha1,6-mannosyltransferase	AN2626.2	Afu8g02040	AO090010000615	NCU00609.2	YJR075w	
An07g04940		strong similarity to alpha1,6-mannosyltransferase	AN4716.2	Afu5g08580	AO090120000208	NCU00609.2	YJR075w	
An11g07490		strong similarity to alpha1,6-mannosyltransferase	AN7534.2	Afu6g14040	AO090003001503	NCU08232.2		
An12g07020		strong similarity to alpha1,6-mannosyltransferase	AN7534.2	Afu6g14040	AO090003001503	NCU08232.2	YJR075w	
An14g07140		strong similarity to alpha1,6-mannosyltransferase	AN4716.2	Afu1g01380	AO090120000208	NCU00609.2	YJR075w	

An03g05010		strong similarity to alpha1,6-mannosyltransferase	AN7672.2	Afu2g01450	AO090701000814	NCU02635.2	YPL050c	
An04g01260		strong similarity to alpha1,6-mannosyltransferase	AN4395.2	Afu4g06870	AO090023000901	NCU08939.2	YEL036c	
An15g06230		strong similarity to alpha1,6-mannosyltransferase	AN2159.2	Afu2g15910	AO090012000213	NCU08024.2	YEL036c	
An15g03330		strong similarity to alpha1,6-mannosyltransferase	AN7562.2	Afu2g14910	AO090012000403	NCU03055.2	YDR245w	
An04g05940		strong similarity to alpha1,6-mannosyltransferase	AN1969.2	Afu4g10750	AO090003001140	NCU06762.2	YJL183w	
An04g06730		strong similarity to alpha1,2-mannosyltransferase	AN6571.2	Afu6g04450	AO090003000707	NCU04887.2	YBR015c	
An14g06060		strong similarity to alpha1,2-mannosyltransferase	AN6857.2	Afu5g13090	AO090120000434	NCU04887.2	YBR015c	
An15g00920		strong similarity to alpha1,2-mannosyltransferase	AN6571.2	Afu6g04450	AO090701000099	NCU04887.2	YBR015c	
<b>O-Glycosylation in ER</b>								
An11g09890		strong similarity to protein O-mannosyltransferase	AN4761.2	Afu3g06450	AO090020000105	NCU01912.2	YDL095w	
An07g10350		strong similarity to protein O-mannosyltransferase	AN5105.2	Afu1g07690	AO090012001021	NCU01648.2	YAL023c YOR321w	
An16g08490		strong similarity to protein O-mannosyltransferase	AN1459.2	Afu8g04500	AO090023000336	NCU09332.2	YJR143c	
<b>O- and/or N-Glycosylation in Golgi</b>								
An14g03910		strong similarity to alpha-1,2-mannosyltransferase	AN2752.2	Afu5g10760	AO090010000465	NCU06541.2	YOR099w	
An02g09940		strong similarity to alpha-1,2-mannosyltransferase	AN8119.2	Afu5g02740	AO090102000391	NCU01388.2	YOR099w	
An18g02170		strong similarity to mannosyltransferase	AN0086.2	Afu5g12160	AO090120000333	NCU05680.2	YIL085c	
An18g03940		strong similarity to gene involved in phospho-mannosylation	AN4030.2	Afu1g03790	AO090113000130	NCU03213.2	YKL201c	
An08g05380		strong similarity to gene involved in phospho-mannosylation	AN1048.2	Afu1g12630	AO090113000130	NCU06792.2	YKL201c	
An15g04810		strong similarity to alpha 1,3-mannosyltransferase		Afu6g14480	AO090038000177		YIL014w	
<b>Other genes possibly involved in glycosylation events</b>								
GlcNAc transferases								
An03g02990		strong similarity to a-1,2-GlcNAc-transferase	AN8887.2	Afu8g02690	AO090010000760		YOR320c	
An11g10260		strong similarity to a-1,2-GlcNAc-transferase	AN8887.2	Afu8g02690	AO090010000760		YOR320c	
S. pombe galactosyltransferase								
An07g01780			AN0222.2	Afu7g01100		NCU09888.2		
Other putative alpha-1,2-mannosidase (no homology to the MNS1/ER-alpha-1,2-mannosidase family; highest homology to an Alpha-1,2-mannosidase family protein from Aspergillus fumigatus)								
An08g03060			AN1197.2	Afu1g10790	AO090038000337	NCU07269.2		
An08g08370			AN5392.2	Afu6g13760	AO090103000376	NCU04798.2 NCU07269.2		
An13g01260			AN5392.2	Afu7g04720	AO090005000167	NCU07269.2		
An14g04240			AN2325.2	Afu5g10520	AO090010000486	NCU04798.2		
An16g02910			AN3054.2	Afu5g10520	AO090005001308	NCU04798.2		
Aspecific alpha-mannosidase (vacuolar alpha-mannosidase Ams1p S. cerevisiae/Homo sapiens alpha-mannosidases from classes 2A - including mannosidase II, 2B, 2C)								
An02g11720			AN2936.2	Afu3g08200	AO090005001458	NCU07404.2	YGL156w	
Other putative GPI-anchored mannosidases required for cell wall biogenesis in bud formation (homologous to S. cerevisiae DCW1 or DFG5) or filamentous growth (homologous to S. cerevisiae)								
An03g00740			AN2825.2	Afu3g00700	AO090003001408	NCU02032.2	YKL046c	
An18g01410			AN2825.2	Afu4g00620	AO090003001408	NCU02032.2	YKL046c	
An14g03520			AN8421.2	Afu3g02040	AO090103000109	NCU04262.2	YKL046c	
An16g08090			AN8421.2	Afu3g02040	AO090005000561	NCU02032.2	YKL046c	
An06g00360			AN8421.2	Afu1g01730	AO090005000561	NCU02032.2	YKL046c	
An01g06500			AN8421.2	Afu1g01730	AO090005000927	NCU04262.2	YKL046c	
An02g02660			AN0393.2	Afu3g00340	AO090010000622	NCU04262.2	YKL046c	
An11g01240			AN3049.2	Afu1g01730	AO090010000096	NCU08127.2	YKL046c	

An12g05930			AN3049.2	Afu1g01730	AO090102000171	NCU04262.2	YKL046c	
An04g09650			AN6472.2	Afu2g00680	AO090102000035	NCU07005.2	YKL046c	
An07g07700			AN4504.2	Afu2g03270	AO090120000260	NCU03215.2		
<b>Protein misfolding</b>								
<b>Unfolded Protein Response (UPR)</b>								
An01g00160	HacA	similarity to regulator of unfolded protein response (UPR) Hac1 - <i>Saccharomyces cerevisiae</i>	AN9397.2	Afu3g04070	AO090124000074	NCU01856.2		
An01g06550	IreA	strong similarity to protein kinase Ire1 - <i>Saccharomyces cerevisiae</i>	AN0235.2	Afu1g01720	AO090005000934	NCU02202.2	YHR079c	
An14g04770	PtcA	strong similarity to phosphoprotein phosphatase 2C ptc1p - <i>Schizosaccharomyces pombe</i>	AN6892.2	Afu5g13340	AO090120000479	NCU00434.2	YDL006w	
An08g00830	PtcB	strong similarity to protein phosphatase type 2C Ptc2 - <i>Saccharomyces cerevisiae</i>	AN1358.2	Afu1g09280	AO090005001595	NCU04600.2	YER089c	
An08g01480		strong similarity to tRNA ligase Trl1 - <i>Saccharomyces cerevisiae</i>	AN1296.2	Afu1g09690	AO090012000873	NCU04410.2	YJL087c	
An01g07900	CpcA	similarity to GCN4 - <i>Saccharomyces cerevisiae</i>	AN3675.2	Afu4g12470	AO090009000459	NCU04050.2	YEL009c	
An11g11250		similarity to XDJ1 - <i>Saccharomyces cerevisiae</i>	AN3463.2	Afu3g05400	AO090020000010	NCU02424.2	YLR090w	P58
An01g08980		strong similarity to membrane protein NHMP1 from patent WO9833817-A1 - <i>Homo sapiens</i>	AN1933.2	Afu4g13270	AO090009000257	NCU11109.2	YGR038w	
<b>ERAD</b>								
An04g09170		strong similarity to valosin-containing protein like AAA-ATPase Cdc48 - <i>Saccharomyces cerevisiae</i>	AN7254.2	Afu2g17110	AO090102000107	NCU00018.2	YDL126c	
An01g05330		strong similarity to nuclear transport regulator Npl4 - <i>Saccharomyces cerevisiae</i>	AN0295.2	Afu1g02830	AO090005000811	NCU02680.2	YBR170c	
An01g05760		strong similarity to ubiquitin fusion degradation protein Ufd1 - <i>Saccharomyces cerevisiae</i>	AN0329.2	Afu1g02430	AO090005000853	NCU06856.2	YGR048w	
An15g00640		strong similarity to hypothetical protein GABA-A receptor epsilon subunit - <i>Caenorhabditis elegans</i>		Afu6g04670	AO090701000076	NCU00146.2		
An03g04600		strong similarity to WD-repeat protein required for ubiquitin-mediated proteolysis Doa1 - <i>Saccharomyces cerevisiae</i>	AN7704.2	Afu5g08370	AO090701000756	NCU00880.2	YKL213c	
An08g09000		strong similarity to ubiquitin like protein Dsk2 - <i>Saccharomyces cerevisiae</i>	AN5451.2	Afu6g13420	AO090003000467	NCU03028.2	YMR276w	
An16g07970		similarity to autocrine motility factor receptor Amfr - <i>Mus musculus</i>	AN1488.2	Afu8g04840	AO090005000658	NCU04633.2	YOL013c	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
An03g04340		strong similarity to ER membrane translocation facilitator Sec61 - <i>Yarrowia lipolytica</i>	AN7721.2	Afu5g08130	AO090701000730	NCU08897.2	YLR378c	
An17g00260		Ubiquitin-conjugating enzyme that mediates selective degradation of short-lived and abnormal proteins; plays a role in vesicle biogenesis and ER-associated protein degradation (ERAD); component of the cellular stress response	AN2212.2	Afu5g07040	AO090701000280	NCU01225.2	YDR177w	

An06g01120		strong similarity to ubiquitin conjugating enzyme Ubc1 - <i>Saccharomyces cerevisiae</i>	AN5344.2	Afu6g14210	AO090103000407	NCU09731.2	YGL058w	
An09g06110		strong similarity to ubiquitin conjugating enzyme ubcp3p - <i>Schizosaccharomyces pombe</i>	AN8258.2	Afu5g04060	AO090102000609	NCU03623.2	YMR022w	
An04g01730		strong similarity to ubiquitin fusion degradation protein Ufd2 - <i>Saccharomyces cerevisiae</i>	AN4442.2	Afu4g07340	AO090023000839	NCU03357.2	YDL190c	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
An04g01720		similarity to DnaJ protein SIS1 - <i>Cryptococcus curvatus</i>	AN4441.2	Afu4g07330	AO090023000840	NCU03335.2	YMR161w	
An12g00340		similarity to alpha 1,2-mannosidase IB - <i>Homo sapiens</i>	AN9084.2	Afu7g02290	AO090038000608	NCU02091.2	YHR204w	
An18g06220		strong similarity to alpha-mannosidase Mns1 - <i>Saccharomyces cerevisiae</i>	AN5748.2	Afu6g06790	AO090003000057	NCU02778.2	YJR131w	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
An04g00360		strong similarity to transport vesicle formation protein Sec13 - <i>Saccharomyces cerevisiae</i>	AN4317.2	Afu4g06090	AO090023000986	NCU04063.2	YLR208w	
An12g04000		similarity to mrna stability protein Ssm4 - <i>Saccharomyces cerevisiae</i>	AN6136.2	Afu2g08650	AO090011000840	NCU07516.2	YIL030c	
An14g00230		strong similarity to ubiquitin conjugating enzyme Ubc6 - <i>Saccharomyces cerevisiae</i>	AN6990.2	Afu4g04600	AO090206000028	NCU05592.2	YER100w	
An01g04280		strong similarity to dnaJ protein homolog Ydj1 - <i>Saccharomyces cerevisiae</i>	AN2731.2	Afu1g05040	AO090003000801	NCU07414.2	YNL064c	
An15g01420		strong similarity to glucosidase I Cwh41 - <i>Saccharomyces cerevisiae</i>	AN6606.2	Afu6g04210	AO090701000141	NCU03657.2	YGL027c	
<b>Proteasome</b>								
An18g06520		strong similarity to protein involved in cell wall biogenesis and architecture Ecm29 - <i>Saccharomyces cerevisiae</i>	AN5774.2	Afu6g06540	AO090003000026	NCU00770.2	YHL030w	
An18g03010		strong similarity to 26S proteasome regulatory subunit S2 - <i>Homo sapiens</i>	AN0125.2	Afu5g11720	AO090120000290	NCU07721.2	YHR027c	
An04g03270		strong similarity to proteasome 19S regulatory particle subunit Rpn2 - <i>Saccharomyces cerevisiae</i>	AN1700.2	Afu4g08480	AO090023000714	NCU09450.2	YIL075c	
An11g10380		strong similarity to 26S proteasome regulatory subunit rpn3p - <i>Schizosaccharomyces pombe</i>	AN2767.2	Afu3g06110	AO090020000084	NCU02224.2	YER021w	
An08g06850		similarity to hypothetical C2H2 zinc-finger protein SPBC1105.14 - <i>Schizosaccharomyces pombe</i>	AN0709.2	Afu1g13750	AO090012000498	NCU01640.2	YDL020c	
An11g09690		strong similarity to proteasome 19S regulatory particle subunit Rpn5 - <i>Saccharomyces cerevisiae</i>	AN4775.2	Afu3g06610	AO090020000338	NCU02650.2	YDL147w	
An18g05070		strong similarity to 26S proteasome subunit 9 - <i>Homo sapiens</i>	AN4225.2	Afu1g06300	AO090001000417	NCU01596.2	YDL097c	
An11g02610		strong similarity to proteasome 19S regulatory particle subunit Rpn7 - <i>Saccharomyces cerevisiae</i>	AN1922.2	Afu6g07760	AO090003000166	NCU03972.2	YPR108w	
An07g10110		strong similarity to 26S proteasome regulatory chain 12 rpn12 - <i>Homo sapiens</i>	AN5121.2	Afu1g07540	AO090012001005	NCU01547.2	YOR261c	
An08g10710		strong similarity to proteasome 19S regulatory particle subunit Rpn9 - <i>Saccharomyces cerevisiae</i>	AN3716.2	Afu6g12770	AO090003000397	NCU02374.2	YDR427w	

An15g03020		strong similarity to proteasome 19S regulatory particle multiubiquitin chain binding subunit RPN10 - <i>Physcomitrella patens</i>	AN7579.2	Afu2g15070	AO090012000427	NCU02982.2	YHR200w	
An07g07860		strong similarity to 26S proteasomal subunit ad1p - <i>Schizosaccharomyces pombe</i>	AN4492.2	Afu2g03400	AO090120000247	NCU00823.2	YFR004w	
An16g02210		strong similarity to proteasome 19S regulatory particle subunit Rpn12 - <i>Saccharomyces cerevisiae</i>	AN3019.2	Afu3g08940	AO090005001381	NCU10067.2	YFR052w	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
An02g12760		strong similarity to proteasome 19S regulatory particle subunit Rpt1 - <i>Saccharomyces cerevisiae</i>	AN2917.2	Afu3g07820	AO090020000414	NCU02840.2	YKL145w	
An17g00270		strong similarity to 26S ATP/ubiquitin-dependent proteinase chain S4 - <i>Schizosaccharomyces pombe</i>	AN2213.2	Afu5g07050	AO090701000279	NCU01224.2	YDL007w	
An02g07190		strong similarity to RPT3 - <i>Saccharomyces cerevisiae</i>	AN2904.2	Afu3g11390	AO090003000692	NCU02260.2	YDR394w	
An18g06230		strong similarity to proteasome 19S regulatory particle subunit Rpt4 - <i>Saccharomyces cerevisiae</i>	AN5747.2	Afu6g06780	AO090003000056	NCU07367.2	YOR259c	
An18g05230		strong similarity to proteasome 19S regulatory particle subunit Rpt5 - <i>Saccharomyces cerevisiae</i>	AN4236.2	Afu1g06170	AO090001000434	NCU04414.2	YOR117w	
An14g00180		strong similarity to proteasome 19S regulatory particle subunit Rpt6 - <i>Saccharomyces cerevisiae</i>	AN6988.2	Afu4g04660	AO090206000022	NCU05363.2	YGL048c	
<b>Protein complex involved in protein transport</b>								
<b>Exocyst</b>								
An01g03190		strong similarity to subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p)-	AN0462.2	Afu1g04360	AO090003000913	NCU09869.2	YER008c	
An08g05570		strong similarity to subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p)-	AN1002.2	Afu1g12790	AO090012000630	NCU07698.2	YDR166c	
An04g06180		strong similarity to subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p)-	AN1988.2	Afu4g10490	AO090003001162	NCU03341.2	YIL068c	
An03g04210		strong similarity to subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p)-	AN7730.2	Afu5g08040	AO090701000719	NCU04190.2	YPR055w	
An03g06900		strong similarity to subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p)-	AN8879.2	Afu8g02790	AO090010000771	NCU09313.2	YLR166c	
An15g00010		strong similarity to subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p)-	AN6493.2	Afu6g05290	AO090701000006	NCU00117.2	YGL233w	
An02g04030		strong similarity to subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p)-	AN6210.2	Afu2g11960	AO090026000449	NCU08012.2	YJL085w	
An08g07370		strong similarity to subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p)-	AN0560.2	Afu6g11370	AO090023000477	NCU06631.2	YBR102c	
An14g00010		strong similarity to subunit of the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, Exo84p)-	AN6974.2	Afu4g04810	AO090206000003	NCU06404.2	YFL005w	

An18g05980		GTP-binding protein of the rho subfamily of Ras-like proteins, involved in establishment of cell polarity; regulates protein kinase C (Pkc1p) and the cell wall synthesizing enzyme 1,3-beta-glucan synthase (Fks1p and Gsc2p)	AN5740.2	Afu6g06900	AO090003000071	NCU01484.2	YPR165w	
An02g14200		strong similarity to RHO1 - <i>Saccharomyces cerevisiae</i>	AN7487.2	Afu2g05740	AO090001000693	NCU06454.2	YLR229c	
An11g09620		strong similarity to GTPase Rho3 - <i>Saccharomyces cerevisiae</i>	AN4782.2	Afu3g06690	AO090020000329	NCU00600.2	YIL118w	
<b>SEC34/SEC35 COMPLEX</b>								
An02g06840		strong similarity to component of the conserved oligomeric Golgi complex (COG1 through COG8) - <i>Saccharomyces cerevisiae</i>	AN4886.2	Afu3g11090	AO090003000663	NCU02268.2	YER157w	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
An02g14400		strong similarity to component of the conserved oligomeric Golgi complex (COG1 through COG8) - <i>Saccharomyces cerevisiae</i>	AN7462.2	Afu2g05890	AO090001000708		YPR105c	
An16g03450		strong similarity to component of the conserved oligomeric Golgi complex (COG1 through COG8) - <i>Saccharomyces cerevisiae</i>	AN5001.2	Afu3g09810	AO090005001269	NCU05067.2	YNL051w	
An06g01630		strong similarity to component of the conserved oligomeric Golgi complex (COG1 through COG8) - <i>Saccharomyces cerevisiae</i>	AN3723.2	Afu6g12470	AO090009000163	NCU02421.2	YNL041c	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
<b>TRAPP complex</b>								
An12g00380		Hydrophilic protein that acts in conjunction with SNARE proteins in targeting and fusion of ER to Golgi transport vesicles; component of the TRAPP (transport protein particle) complex	AN9086.2	Afu7g02270	AO090038000605	NCU05796.2	YKR068c	
An17g01875		Component of the TRAPP (transport protein particle) complex, which plays an essential role in the vesicular transport from endoplasmic reticulum to Golgi	AN8828.2	Afu5g05970	AO090009000664	NCU06176.2	YML077w	
An04g08690		similarity to polynucleotide sequence SEQ ID NO:3913 from patent WO200058473-A2 - <i>Homo sapiens</i>	AN7311.2	Afu2g16670	AO090102000156	NCU05213.2	YDR108w	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
An15g00470		strong similarity to hypercellular protein hypA - <i>Aspergillus nidulans</i>	AN6533.2	Afu6g04840	AO090701000055	NCU06715.2	YDR407c	
An08g05190		similarity to unknown protein	AN1038.2	Afu1g12540	AO090001000223	NCU02225.2	YMR218c	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
An15g03010		strong similarity to hypothetical protein B7F18.180 - <i>Neurospora crassa</i>		Afu2g15080		NCU11085.2	YDR246w	
An14g06440		strong similarity to protein of sequence 1 from patent WO0075305 - <i>Candida albicans</i>	AN6825.2	Afu5g12880	AO090120000403	NCU08874.2	YDR472w	

An15g00060		strong similarity to TRAPP complex subunit involved in targeting and fusion of ER transport vesicles to golgi Trs33 - <i>Saccharomyces cerevisiae</i>	AN6498.2	Afu6g05220	AO090701000012	NCU06212.2	YOR115c	
<b>COPI SUBUNITS</b>								
An16g05370		similarity to zinc-finger protein Glo3 - <i>Saccharomyces cerevisiae</i>	AN6033.2	Afu2g09830	AO090011000652	NCU08811.2	YER122c	
An16g02460		strong similarity to alpha subunit of COPI vesicle coatomer complex - <i>Saccharomyces cerevisiae</i>	AN3026.2	Afu3g08840	AO090005001354	NCU10066.2	YDL145c	
An01g14260		strong similarity to alpha subunit of COPI vesicle coatomer complex - <i>Saccharomyces cerevisiae</i>	AN0922.2	Afu1g15860	AO090005001114	NCU00493.2	YFR051c	
An12g04830		strong similarity to alpha subunit of COPI vesicle coatomer complex - <i>Saccharomyces cerevisiae</i>	AN6080.2	Afu2g09180	AO090011000777	NCU02538.2	YPL010w	
An07g06030		strong similarity to alpha subunit of COPI vesicle coatomer complex - <i>Saccharomyces cerevisiae</i>	AN4547.2	Afu2g02560	AO090026000599	NCU01992.2	YNL287w	
An02g05870		strong similarity to essential beta'-coat protein of the COPI coatomer - <i>Saccharomyces cerevisiae</i>	AN5972.2	Afu2g10610	AO090011000577	NCU07319.2	YGL137w	
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10					YBR283c	
An08g03690		strong similarity to ADP-ribosylation factor, GTPase of the Ras superfamily, functionally interchangeable with Arf2p - <i>Saccharomyces cerevisiae</i>	AN1126.2	Afu1g11730	AO090038000254	NCU08340.2	YDL137w	
<b>COPII SUBUNITS</b>								
An01g04040		strong similarity to GTPase, GTP-binding protein of the ARF family - <i>Saccharomyces cerevisiae</i>	AN0411.2	Afu1g04940	AO090003000842	NCU00381.2	YPL218w	
An08g03270		strong similarity to essential subunit of the COP II vesicle coat - <i>Saccharomyces cerevisiae</i>	AN1177.2	Afu1g10970	AO090038000308	NCU04404.2	YDR238c	
An04g00360		strong similarity to component of both the Nup84 nuclear pore sub-complex and of the COPII complex (Sar1p, Sec13p, Sec16p, Sec23p, Sec24p, Sec31p, Sfb2p, and Sfb3p) - <i>Saccharomyces cerevisiae</i>	AN4317.2	Afu4g06090	AO090023000986	NCU04063.2	YLR208w	
An02g01690		strong similarity to essential phosphoprotein component (p150) of the COPII coat of secretory pathway vesicles, in complex with Sec13p - <i>Saccharomyces cerevisiae</i>	AN6257.2	Afu2g12980	AO090026000337	NCU06738.2	YDL195w	
An01g04730		strong similarity to GTPase-activating protein; component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat - <i>Saccharomyces cerevisiae</i>	AN0261.2	Afu1g03400	AO090005000760	NCU01318.2	YPR181c	
An08g10650		strong similarity to component of the Sec23p-Sec24p heterodimeric complex of the COPII vesicle coat - <i>Saccharomyces cerevisiae</i>	AN3720.2	Afu6g12830	AO090003000403	NCU02391.2	YIL109c	
An16g03320		strong similarity to member of the Sec24p family; forms a complex, with Sec23p, that is involved in sorting of Pma1p into COPII vesicles - <i>Saccharomyces cerevisiae</i>	AN3080.2	Afu3g09700	AO090005001279	NCU06868.2	YHR098c	
An15g01520		strong similarity to COPII vesicle coat protein required for ER	AN6615.2	Afu6g03960	AO090701000149	NCU03819.2	YPL085w	
<b>Proteins involved in vesicle formation and docking</b>								

<b>SNAREs</b>								
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10						YBR283c
An12g01190		strong similarity to plasma membrane t-SNARE involved in fusion of secretory vesicles at the plasma membrane - <i>Saccharomyces cerevisiae</i>	AN3416.2	Afu7g01510	AO090010000311	NCU10398.2		YPL232w
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10						YBR283c
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10						YBR283c
An07g02170		strong similarity to v-SNARE (vesicle specific SNAP receptor), localized to the endoplasmic reticulum membrane - <i>Saccharomyces cerevisiae</i>			AO090005000437	NCU04943.2		YLR078c
An08g02460		strong similarity to SNARE protein of Golgi compartment - <i>Saccharomyces cerevisiae</i>	AN1229.2	Afu1g10500	AO090038000376	NCU02706.2		YHL031c
An02g05390		strong similarity to t-SNARE Sec9 - <i>Saccharomyces cerevisiae</i>	AN2419.2	Afu2g13760		NCU09243.2		YGR009c
An07g09960		strong similarity to v-SNARE with similarity to synaptobrevins required for vesicular transport between the endoplasmic reticulum and Golgi complex - <i>Saccharomyces cerevisiae</i>	AN5127.2	Afu1g07420	AO090012000993	NCU01741.2		YIL004c
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10						YBR283c
An15g01380		strong similarity to Synaptobrevin homolog v-SNARE - <i>Saccharomyces cerevisiae</i>		Afu6g04150	AO090701000139	NCU06708.2		YLR268w
An04g07020		strong similarity to syntaxin Tlg2 - <i>Saccharomyces cerevisiae</i>	AN2048.2	Afu4g10040	AO090003001228	NCU04119.2		YOL018c
An04g01530		strong similarity to transport vesicle docking protei	AN4416.2	Afu4g07110	AO090023000864	NCU06777.2		YOR036w
An04g05980		strong similarity to v-SNARE Vti1 - <i>Saccharomyces cerevisiae</i>	AN1973.2	Afu4g10710	AO090003001144	NCU05959.2		YMR197c
An09g04890		similarity to syntaxin 6 - <i>Homo sapiens</i>	AN8171.2	Afu5g02900	AO090102000487	NCU01199.2		YDR468c
An04g08480		strong similarity to cell division control protein - <i>Saccharomyces cerevisiae</i>	AN8488.2	Afu4g09520	AO090023000584	NCU08973.2		YKL196c
An08g07470		v-SNARE component of the vacuolar SNARE complex involved in vesicle fusion - <i>Saccharomyces cerevisiae</i>	AN0571.2	Afu6g11270	AO090023000485	NCU06370.2		YLR093c
An12g07570		Vesicle membrane receptor protein (v-SNARE) involved in the fusion between Golgi-derived secretory vesicles with the plasma membrane; proposed to be involved in endocytosis - <i>Saccharomyces cerevisiae</i>	AN8769.2	Afu6g02920	AO090012000430	NCU00566.2		YAL030w
		no <i>A.niger</i> homolog found with an E-value smaller than 1e-10						YBR283c
An07g05990		similarity to endosomal t-SNARE yup1 - <i>Ustilago maydi</i>	AN4551.2	Afu2g02610	AO090026000605	NCU00242.2		YGL212w
An02g12980		strong similarity to cis-Golgi t-SNARE syntaxin required for vesicular transport between the ER and the Golgi complex - <i>Saccharomyces cerevisiae</i>	AN9526.2	Afu3g07590	AO090020000134	NCU01907.2		YLR026c
An04g01530		strong similarity to transport vesicle docking protein - <i>Saccharomyces cerevisiae</i>	AN4416.2	Afu4g07110	AO090023000864	NCU06777.2		YOR106w
An02g06780		strong similarity to suppressor of rho3 Sro7 - <i>Saccharomyces cerevisiae</i>	AN4890.2	Afu3g11040	AO090003000659	NCU09432.2		YPR032w
<b>Secretion related GTPases and interacting proteins</b>								
An14g00010	SrgA	strong similarity to protein Sec4 - <i>Saccharomyces cerevisiae</i>	AN6974.2	Afu4g04810	AO090206000003	NCU06404.2		YFL005w

An09g06790	SrgB	strong similarity to protein Ypt1 - <i>Saccharomyces cerevisiae</i>	AN4281.2	Afu5g04320	AO090102000638	NCU08477.2	YFL038c	
An01g06060		strong similarity to protein Rab11 - Mammalian	AN0347.2	Afu1g02190	AO090005000880	NCU01523.2	YER031c	Rab11
An15g05740	SrgC	strong similarity to protein Rab6 - Mammalian	AN7602.2	Afu2g15570	AO090012000273	NCU05234.2	YLR262c	Rab6
An04g02470		strong similarity to protein Ypt52 - <i>Saccharomyces cerevisiae</i>	AN3842.2	Afu4g08040	AO090023000765	NCU06410.2	YOR089c	
An12g00040		strong similarity to protein Rab4 - Mammalian	AN9072.2	Afu7g02540	AO090038000630	NCU00889.2	YER031c	Rab4
An18g02210		strong similarity to protein Ypt7 - <i>Saccharomyces cerevisiae</i>	AN0089.2	Afu5g12130	AO090120000329	NCU03711.2	YML001w	
An02g06400		strong similarity to protein Ypt53 - <i>Saccharomyces cerevisiae</i>	AN4915.2	Afu3g10740	AO090003000619	NCU06410.2	YOR089c	
An07g10340	SrgD	strong similarity to protein Ypt31/32 - <i>Saccharomyces cerevisiae</i>	AN5106.2	Afu1g07680	AO090012001020	NCU01647.2	YER031c	
An14g02260		strong similarity to protein Rab24 - Mammalian	AN2474.2	Afu4g03100	AO090102000257	NCU08271.2	YKR014c	Rab24
An02g10450	vps1	strong similarity to GTP-binding protein Vps1 - <i>Saccharomyces cerevisiae</i>	AN8023.2	Afu5g02360	AO090102000348	NCU04100.2	YKR001c	
An11g09910	sec2	strong similarity to protein Sec2 - <i>Saccharomyces cerevisiae</i>	AN4759.2	Afu3g06430	AO090020000107	NCU01911.2	YNL272c	
An02g03120	gdi1	strong similarity to GDP dissociation inhibitor in the secretory pathway Gdi1 - <i>Saccharomyces cerevisiae</i>	AN5895.2	Afu2g11150	AO090026000537	NCU05288.2	YER136w	
An01g04040		secretion-associated GTP-binding protein sarA - <i>Aspergillus niger</i>	AN0411.2	Afu1g04940	AO090003000842	NCU00381.2	YPL218w	
An02g07780		strong similarity to ADP-ribosylation factor 6 ARF6 - <i>Homo sapiens</i>	AN5020.2	Afu3g12080	AO090003000769	NCU07173.2	YOR094w	
An08g03690		strong similarity to ADP-ribosylation factor arf1 - <i>Ajellomyces capsulatus</i>	AN1126.2	Afu1g11730	AO090038000254	NCU08340.2	YDL137w	
An11g01790		strong similarity to ADP ribosylation factor 1 ARF1 - <i>Toxoplasma gondii</i>	AN3934.2	Afu6g08290	AO090003000097	NCU08618.2	YDL192w	
An17g00400		strong similarity to ARF GAP zinc finger protein Gcs1 - <i>Saccharomyces cerevisiae</i>	AN2222.2	Afu5g07130	AO090701000265	NCU07734.2	YDL226c	
An18g02490		strong similarity to ARF guanine-nucleotide exchange factor 2 Gea2 - <i>Saccharomyces cerevisiae</i>	AN0112.2	Afu5g11900	AO090120000299	NCU08023.2	YEL022w	
<b>ER to Golgi and Intra-Golgi transport</b>								
An11g02650	age2	strong similarity to hypothetical gtpase activating protein SPAC824.09c - <i>Schizosaccharomyces pombe</i>	AN1931.2	Afu6g07830	AO090003000156	NCU03890.2	YIL044c	
An08g04350	chs7	similarity to chitin synthase III like Chs7 - <i>Saccharomyces cerevisiae</i>	AN1069.2	Afu1g12040	AO090001000344	NCU05720.2	YHR142w	
An08g03590	emp24	strong similarity to precursor of protein Emp24 - <i>Saccharomyces cerevisiae</i>	AN1154.2	Afu1g11470	AO090038000276	NCU08339.2	YGL200c	
An09g05490	erp2	strong similarity to COP-coated vesicle membrane protein P24 homolog lbrA - <i>Polysphondylium pallidum</i>	AN8194.2	Afu5g03260	AO090102000528	NCU03800.2	YDL018c	
An07g09160	erv14	strong similarity to pattern formation protein cni - <i>Drosophila melanogaster</i>	AN5195.2	Afu6g07290	AO090005001572	NCU06922.2	YGL054c	
An01g08870	erv25	strong similarity to component of COPII-coated vesicles Erv25 - <i>Saccharomyces cerevisiae</i>	AN4165.2	Afu4g13190	AO090009000262	NCU01342.2	YML012w	

An08g03960	erv29	strong similarity to hypothetical edoplasmic reticulum associated protein - <i>Schizosaccharomyces pombe</i>	AN1117.2	Afu1g11770	AO090038000244	NCU03319.2	YGR284c	
An03g04940	erv41	strong similarity to <i>Erv41</i> - <i>Saccharomyces cerevisiae</i>	AN7679.2	Afu2g01530	AO090701000797	NCU04293.2	YML067c	
An01g04320	erv46	strong similarity to COPII vesicle coat component protein <i>Erv46</i> - <i>Saccharomyces cerevisiae</i>	AN2738.2	Afu1g05120	AO090003000808	NCU08607.2	YAL042w	
An18g05740	gga1	similarity to ARF binding protein <i>GGA2</i> - <i>Homo sapiens</i>	AN5710.2	Afu1g06680	AO090001000466	NCU10676.2	YHR108w	
An02g02830	rer1	strong similarity to protein <i>RER1</i> - <i>Homo sapiens</i>	AN5915.2	Afu2g10930	AO090011000535	NCU06447.2	YCL001w	
An07g02190	sec7	strong similarity to protein <i>Sec7</i> - <i>Saccharomyces cerevisiae</i>	AN6709.2	Afu7g05700	AO090005000435	NCU07658.2	YDR170c	
An02g01580	sec17	strong similarity to vesicular transport protein <i>SEC17</i> - <i>Pichia pastoris</i>	AN6267.2	Afu2g12870	AO090026000347	NCU01674.2	YBL050w	
An09g06840	sly41	strong similarity to protein involved in ER to Golgi transport <i>Sly41</i> - <i>Saccharomyces cerevisiae</i>	AN4287.2	Afu5g04360	AO090102000644	NCU05453.2	YOR307c	
An15g00060	trs33	strong similarity to TRAPP complex subunit involved in targeting and fusion of ER transport vesicles to golgi <i>Trs33</i> - <i>Saccharomyces cerevisiae</i>	AN6498.2	Afu6g05220	AO090701000012	NCU06212.2	YOR115c	
An08g06780	uso1	strong similarity to transport protein <i>Uso1</i> - <i>Saccharomyces cerevisiae</i>	AN0706.2	Afu1g13720	AO090012000504	NCU01644.2	YDL058w	
An04g04950	vps13	strong similarity to vacuolar protein sorting-associated protein <i>Vps13</i> - <i>Saccharomyces cerevisiae</i>	AN5579.2	Afu4g11560	AO090003001064	NCU05837.2	YLL040c	
An14g00210	yip1	similarity to Golgi membrane protein <i>Yip1</i> - <i>Saccharomyces cerevisiae</i>	AN6989.2	Afu4g04630	AO090206000026	NCU05514.2	YGR172c	
An18g06440	yip3	strong similarity to COPII vesicle component <i>Yip3</i> - <i>Saccharomyces cerevisiae</i>	AN5769.2	Afu6g06620	AO090003000038	NCU02518.2	YNL044w	
An01g08465	yos1	strong similarity to hypothetical protein <i>SPAC19A8.09</i> - <i>Schizosaccharomyces pombe</i>					YER074w-a	
An17g01875	bet5	similarity to protein <i>Synbindin</i> - <i>Mus musculus</i>	AN8828.2	Afu5g05970	AO090009000664	NCU06176.2	YML077w	
<b>Golgi and post-Golgi protein sorting</b>								
<b>Golgi to endosome transport</b>								
An08g01410	sft2	strong similarity to ER-Golgi transport protein <i>Sft2</i> - <i>Saccharomyces cerevisiae</i>	AN1297.2	Afu1g09680		NCU02723.2	YBL102w	
An07g08220	ent3	strong similarity to clathrin associated epsin 2A - <i>Homo sapiens</i>	AN3821.2	Afu2g03650	AO090120000220	NCU00725.2	YJR125c	
An16g03420	sys1	similarity to multicopy suppressor <i>Sys1</i> - <i>Saccharomyces cerevisiae</i>		Afu3g09790	AO090005001271	NCU02294.2	YJL004c	
<b>Vacuolar protein sorting</b>								
An02g06960	vps41	strong similarity to vacuolar assembly protein <i>VPS41</i> - <i>Lycopersicon esculentum</i>	AN4876.2	Afu3g11200	AO090003000675	NCU05902.2	YDR080w	
An15g00460	vps45	strong similarity to vacuolar protein sorting protein <i>hVps45</i> - <i>Homo sapiens</i>	AN6531.2	Afu6g04870	AO090701000053	NCU06192.2	YGL095c	
An14g03790	sec1	strong similarity to <i>sec1</i> -like protein - <i>Loligo pealei</i>	AN4724.2	Afu5g10810	AO090010000460	NCU08312.2	YDR164c	
An16g03010	vps4	strong similarity to vacuolar protein sorting-associated protein <i>Vps4</i> - <i>Saccharomyces cerevisiae</i>	AN3061.2	Afu3g09360	AO090005001298	NCU06942.2	YPR173c	

An02g01390	snx41	strong similarity to hypothetical protein SPBC14F5.11c - <i>Schizosaccharomyces pombe</i>	AN6351.2	Afu2g14160	AO090023000164	NCU06259.2	YDR425w	
An02g05380	vps33	strong similarity to vacuolar protein sorting-associated protein Vps33 - <i>Saccharomyces cerevisiae</i>	AN2418.2	Afu2g13750	AO090026000225	NCU09121.2	YLR396c	
An11g04400	vps27	strong similarity to vacuolar protein sorting-associated protein Vps27 - <i>Saccharomyces cerevisiae</i>	AN2071.2	Afu2g04740	AO090003000273	NCU04015.2	YNR006w	
An14g05130	vps16	strong similarity to vacuolar protein sorting-associated protein Vps16 - <i>Saccharomyces cerevisiae</i>	AN6911.2	Afu5g13600	AO090113000006	NCU06268.2	YPL045w	
An15g00540	vps68	strong similarity to hypothetical protein B13O20.120 - <i>Neurospora crassa</i>	AN6544.2	Afu6g04760	AO090701000062	NCU04188.2	YOL129w	
An01g08400	vps5	strong similarity to sorting nexin-1-like protein Vps5 - <i>Saccharomyces cerevisiae</i>	AN3594.2	Afu4g12830	AO090009000311	NCU04137.2	YOR069w	
An01g04080	vt1	similarity to hypothetical protein YOR359w - <i>Saccharomyces cerevisiae</i>	AN0406.2	Afu1g04990	AO090003000834	NCU00311.2	YOR359w	
An01g10830	vps28	strong similarity to hypothetical protein YPL065w - <i>Saccharomyces cerevisiae</i>	AN0945.2	Afu1g16320	AO090005001073		YPL065w	
An01g04550	vps8	strong similarity to vacuolar protein sorting-associated protein Vps8 - <i>Saccharomyces cerevisiae</i>	AN0244.2	Afu1g05280	AO090003000824	NCU02554.2	YAL002w	
An02g09460	pep7	strong similarity to vacuolar segregation protein Pep7 - <i>Saccharomyces cerevisiae</i>	AN3144.2	Afu3g13770	AO090012000772	NCU07584.2	YDR323c	
An08g01030	vps29	strong similarity to vacuolar protein sorting protein Vps29 - <i>Saccharomyces cerevisiae</i>	AN1341.2	Afu1g09480	AO090012000925	NCU01822.2	YHR012w	
An01g07920	vps9	strong similarity to vacuolar protein sorting-associated protein Vps9 - <i>Saccharomyces cerevisiae</i>	AN3678.2	Afu4g12490	AO090009000462	NCU07301.2	YML097c	
<b>Cellular export and secretion</b>								
An02g08450	sec18	strong similarity to secretory gene SEC18 - <i>Saccharomyces cerevisiae</i>	AN3098.2	Afu3g12510	AO090005000718	NCU03387.2	YBR080c	
An02g14450	pmr1	strong similarity to secretory pathway Ca <sup>2+</sup> -ATPase PMR1 - <i>Saccharomyces cerevisiae</i>	AN7464.2	Afu2g05860	AO090001000706	NCU03292.2	YGL167c	
An18g03100	ssp120	strong similarity to hypothetical precursor of secretory protein Ssp120 - <i>Saccharomyces cerevisiae</i>	AN0131.2	Afu5g11640	AO090026000662	NCU03423.2	YLR250w	