

Supplementary table 18 A. <i>niger</i> genes involved in proteolytic degradation				
Gene	Description	Signal sequence (aa length)	PFAM (score> 15)	Class
An01g06080	strong similarity to energy-dependent regulator of proteolysis ClpX - <i>Mus musculus</i>		PF00004	
An02g01630	similarity to spastin protein Spast - <i>Homo sapiens</i>		PF00004	
An02g07190	26S protease regulatory subunit tbpA - <i>Aspergillus niger</i>		PF00004	
An02g12760	strong similarity to proteasome 19S regulatory particle subunit Rpt1 - <i>Saccharomyces cerevisiae</i>		PF00004	
An04g09180	strong similarity to valosin-containing protein like ATPase Cdc48 - <i>Saccharomyces cerevisiae</i> [deleted ORF]		PF00004	
An06g01740	strong similarity to SIN1-associated protein Sap1 - <i>Saccharomyces cerevisiae</i>		PF00004	
An11g03860	similarity to mitochondrial ATP-dependent protease ftsH2 - <i>Cyanidioschyzon merolae</i>		PF00004	
An14g00180	strong similarity to proteasome 19S regulatory particle subunit Rpt6 - <i>Saccharomyces cerevisiae</i>		PF00004	
An17g00270	strong similarity to 26S ATP/ubiquitin-dependent proteinase chain S4 - <i>Schizosaccharomyces pombe</i>		PF00004	
An18g05230	strong similarity to proteasome 19S regulatory particle subunit Rpt5 - <i>Saccharomyces cerevisiae</i>		PF00004	
An18g06230	strong similarity to proteasome 19S regulatory particle subunit Rpt4 - <i>Saccharomyces cerevisiae</i>		PF00004	
An04g09170	strong similarity to valosin-containing protein like AAA-ATPase Cdc48 - <i>Saccharomyces cerevisiae</i>		PF00004 PF02359	
An02g02850	similarity to intracellular microbial serine proteinase ISP-1 - <i>Bacillus subtilis</i>		PF00023	
An12g05680	similarity to erythrocyte splice form 1 of ankyrin ANK1 - <i>Homo sapiens</i>		PF00023	
An01g00370	strong similarity to aspergillopepsin apnS - <i>Aspergillus phoenicis</i>		PF00026	
An02g07210	aspartic protease pepE - <i>Aspergillus niger</i>	18	PF00026	secreted aspartyl protease
An04g01440	strong similarity to precursor of pepsin A3 - <i>Homo sapiens</i>	19	PF00026	secreted aspartyl protease

An12g03300	strong similarity to aspartic protease pr1 - <i>Phaffia rhodozyma</i>	20	PF00026	secreted aspartyl protease
An13g02130	strong similarity to aspartic proteinase Yps3 - <i>Saccharomyces cerevisiae</i>	18	PF00026	secreted aspartyl protease
An14g04710	aspartic proteinase aspergillopepsin I pepA - <i>Aspergillus niger</i>	20	PF00026	secreted aspartyl protease
An15g06280	strong similarity to aspartic proteinase aspergillopepsin I pepA - <i>Aspergillus niger</i> [truncated ORF]		PF00026	secreted aspartyl protease
An18g01320	strong similarity to extracellular protease precursor Bar1 - <i>Saccharomyces cerevisiae</i>	18	PF00026	secreted aspartyl protease
An04g03950	strong similarity to serine/threonine protein kinase Apg1 - <i>Saccharomyces cerevisiae</i>		PF00069	
An07g03880	serine proteinase pepC - <i>Aspergillus niger</i>	16	PF00082	
An09g03780	subtilisin-like serine protease pepD - <i>Aspergillus niger</i>	20	PF00082	
An09g00950	strong similarity to D-stereospecific aminopeptidase dap - <i>Ochrobactrum anthropi</i>		PF00144	intracellular aminopeptidase
An16g06750	similarity to D-stereospecific aminopeptidase - <i>Ochrobactrum anthropi</i>		PF00144	intracellular aminopeptidase
An06g01040	strong similarity to ubiquitin conjugation enzyme Ubc7 - <i>Saccharomyces cerevisiae</i>		PF00179	
An07g03890	strong similarity to ubiquitin conjugating enzyme Cdc34 - <i>Saccharomyces cerevisiae</i>		PF00179	
An08g03520	similarity to ubiquitin conjugating enzyme UBE2 - <i>Homo sapiens</i> [putative frameshift]		PF00179	
An08g10310	strong similarity to ubiquitin conjugating enzyme Ubc11 - <i>Saccharomyces cerevisiae</i>		PF00179	
An09g04000	strong similarity to ubiquitin conjugating enzyme hUbc12 - <i>Homo sapiens</i>		PF00179	
An11g06900	strong similarity to ubiquitin conjugating enzyme TaUBC4 - <i>Triticum aestivum</i>		PF00179	
An11g10490	strong similarity to ubiquitin conjugating enzyme Ubc4 - <i>Saccharomyces cerevisiae</i>	22	PF00179	
An12g07810	strong similarity to ubiquitin-conjugating enzyme 2 UCE2 from patent CN1268564-A - <i>Homo sapiens</i>		PF00179	
An14g00230	strong similarity to ubiquitin conjugating enzyme Ubc6 - <i>Saccharomyces cerevisiae</i>		PF00179	
An15g06900	strong similarity to non-canonical ubiquitin conjugating enzyme 1 ncube1 - <i>Mus musculus</i> [truncated ORF]		PF00179	

An17g00260	strong similarity to ubiquitin conjugating enzyme Ubc1 - <i>Saccharomyces cerevisiae</i>		PF00179	
An04g05530	similarity to disintegrin and metalloproteinase ADAM19 - <i>Homo sapiens</i>	24	PF00200	
An01g13070	strong similarity to signal recognition particle receptor Sec63 - <i>Saccharomyces cerevisiae</i>		PF00226	
An02g03400	strong similarity to proteasome 20S subunit Pup2 - <i>Saccharomyces cerevisiae</i>		PF00227	
An02g07040	strong similarity to proteasome 20S subunit Scl1 - <i>Saccharomyces cerevisiae</i>		PF00227	
An02g10790	strong similarity to proteasome 20S subunit Pre6 - <i>Saccharomyces cerevisiae</i>		PF00227	
An04g01800	strong similarity to proteasome 20S subunit Pup3 - <i>Saccharomyces cerevisiae</i>		PF00227	
An04g01870	strong similarity to proteasome 20S subunit Pre1 - <i>Saccharomyces cerevisiae</i> [putative sequencing error]		PF00227	
An07g02010	strong similarity to proteasome 20S subunit Pre8 - <i>Saccharomyces cerevisiae</i>		PF00227	
An11g01760	strong similarity to proteasome 20S subunit Pre2 - <i>Saccharomyces cerevisiae</i>		PF00227	
An11g04620	strong similarity to proteasome 20S subunit Pup1 - <i>Saccharomyces cerevisiae</i>		PF00227	
An11g06720	strong similarity to proteasome 20S subunit Pre9 - <i>Saccharomyces cerevisiae</i>		PF00227	
An13g01210	strong similarity to proteasome 20S subunit Pre3 - <i>Saccharomyces cerevisiae</i>		PF00227	
An15g00510	strong similarity to proteasome 20S subunit C2 - <i>Rattus norvegicus</i>		PF00227	
An18g06680	strong similarity to proteasome 20S subunit Pre4 - <i>Saccharomyces cerevisiae</i>		PF00227	
An18g06700	strong similarity to proteasome 20S subunit Pre7 - <i>Saccharomyces cerevisiae</i>		PF00227	
An18g06800	strong similarity to proteasome 20S subunit Pre10 - <i>Saccharomyces cerevisiae</i>		PF00227	
An04g06510	strong similarity to polyubiquitin 5 Ubi4 - <i>Saccharomyces cerevisiae</i>		PF00240	
An02g07010	strong similarity to ubiquitin ubi1 - <i>Aspergillus nidulans</i>		PF00240 PF01599	

An04g02850	similarity to X-Pro dipeptidyl-peptidase IV - Xanthomonas maltophilia		PF00326	intracellular dipeptidylaminopeptidase
An03g04600	strong similarity to WD-repeat protein required for ubiquitin-mediated proteolysis Doa1 - Saccharomyces cerevisiae		PF00400	
An01g08470	strong similarity to ubiquitin carboxyl-terminal hydrolase UBP1 - Pichia anomala		PF00443	
An06g01380	strong similarity to ubiquitin specific protease Ubp2 - Saccharomyces cerevisiae		PF00443	
An07g09730	strong similarity to ubiquitin specific protease Ubp3 - Saccharomyces cerevisiae		PF00443	
An12g08370	strong similarity to ubiquitin specific protease Ubp6 - Saccharomyces cerevisiae		PF00443 PF00240	
An11g04380	strong similarity to ubiquitin specific protease Ubp5 - Saccharomyces cerevisiae		PF00443 PF00581	
An02g04690	strong similarity to serine-type carboxypeptidase I cdpS - Aspergillus saitoi	18	PF00450	secreted serine carboxypeptidase
An03g05200	strong similarity to carboxypeptidase S1 - Penicillium janthinellum	19	PF00450	secreted serine carboxypeptidase
An05g01870	strong similarity to carboxypeptidase y CPY - Candida albicans	19	PF00450	secreted serine carboxypeptidase
An05g02170	strong similarity to serine-type carboxypeptidase F CPD-II - Aspergillus niger	22	PF00450	secreted serine carboxypeptidase
An06g00310	similarity to carboxypeptidase D - Penicillium janthinellum	16	PF00450	secreted serine carboxypeptidase
An07g08030	serine carboxypeptidase pepF - Aspergillus niger	23	PF00450	secreted serine carboxypeptidase
An08g08750	carboxypeptidase Y cpy from patent WO9609397-A1 - Aspergillus niger	15	PF00450	secreted serine carboxypeptidase
An11g06350	strong similarity to carboxypeptidase C cpy1p - Schizosaccharomyces pombe	15	PF00450	secreted serine carboxypeptidase
An14g02150	strong similarity to serine-type carboxypeptidase precursor cpdS - Aspergillus phoenicis	18	PF00450	secreted serine carboxypeptidase
An16g09010	strong similarity to carboxypeptidase I protein from patent WO9814599-A1 - Aspergillus oryzae [putative frameshift]	18	PF00450	secreted serine carboxypeptidase
An01g14920	similarity to aminopeptidase P pepP - Lactococcus lactis		PF00557	intracellular aminopeptidase

An01g13040	strong similarity to prolidase PEPD from patent JP02104286-A - Homo sapiens		PF00557 PF05195	intracellular aminopeptidase
An05g00050	strong similarity to prolidase - Suberites domuncula		PF00557 PF05195	intracellular aminopeptidase
An11g06960	strong similarity to aminopeptidase II pepP - Escherichia coli		PF00557 PF05195	intracellular aminopeptidase
An09g02370	similarity to proteinase SlpE - Streptomyces lividans	23	PF00561	secreted tripeptidylaminopeptidase
An12g08560	strong similarity to proteinase SlpE - Streptomyces lividans		PF00561	secreted tripeptidylaminopeptidase
An13g02620	strong similarity to proteinase P5-6 from patent WO9517512-A - Streptomyces lividans	23	PF00561	secreted tripeptidylaminopeptidase
An13g02790	strong similarity to tripeptidylaminopeptidase Tap - Streptomyces lividans		PF00561	intracellular tripeptidylaminopeptidase
An16g06070	strong similarity to prolyl aminopeptidase PIP - Bacillus coagulans		PF00561	intracellular aminopeptidase
An02g11960	strong similarity to endopeptidase Clp chain P clpP - Escherichia coli		PF00574	
An08g01060	strong similarity to ubiquitin protein ligase ub1p - Schizosaccharomyces pombe		PF00632 PF00168 PF00397	
An11g02950	similarity to calpain nCL-3 from patent DE19650142-A1 - Mus musculus		PF00648	
An07g06490	strong similarity to insulin-degrading enzyme IDE - Rattus norvegicus		PF00675 PF05193	
An16g01860	strong similarity to protease involved in a-factor processing Ste23 - Saccharomyces cerevisiae		PF00675 PF05193	
An07g03020	strong similarity to O-sialoglycoprotein endopeptidase A1 - Pasteurella haemolytica	39	PF00814	
An15g00900	strong similarity to O-sialoglycoprotein endopeptidase - Pasteurella haemolytica		PF00814	
An08g05870	strong similarity to cullin 1 - Homo sapiens		PF00888	
An14g06520	strong similarity to ubiquitin protein ligase CUL4A - Homo sapiens		PF00888	

An15g06020	strong similarity to ubiquitin activating protein Uba1 - <i>Saccharomyces cerevisiae</i>		PF00899 PF02134	
An02g11420	dipeptidyl aminopeptidase type IV dapB - <i>Aspergillus niger</i>		PF00930 PF00326	intracellular dipeptidylaminopeptidase
An02g13920	strong similarity to ubiquitin thiolesterase Yuh1 - <i>Saccharomyces cerevisiae</i>		PF01088	
An12g01820	similarity to ubiquitin thiolesterase L3 - <i>Homo sapiens</i>		PF01088	
An12g04750	strong similarity to prohibitin Phb2 - <i>Saccharomyces cerevisiae</i>		PF01145	
An01g11740	strong similarity to hypothetical membrane dipeptidase - <i>Schizosaccharomyces pombe</i>		PF01244	intracellular dipeptidylaminopeptidase
An07g07860	strong similarity to 26S proteasomal subunit ad1p - <i>Schizosaccharomyces pombe</i>		PF01398	
An07g10110	strong similarity to 26S proteasome regulatory chain 12 rpn12 - <i>Homo sapiens</i>	27	PF01398	
An08g10710	strong similarity to proteasome 19S regulatory particle subunit Rpn9 - <i>Saccharomyces cerevisiae</i>		PF01399	
An11g02610	strong similarity to proteasome 19S regulatory particle subunit Rpn7 - <i>Saccharomyces cerevisiae</i>		PF01399	
An11g09690	strong similarity to proteasome 19S regulatory particle subunit Rpn5 - <i>Saccharomyces cerevisiae</i>		PF01399	
An11g10380	strong similarity to 26S proteasome regulatory subunit rpn3p - <i>Schizosaccharomyces pombe</i>		PF01399	
An16g07210	strong similarity to COP9 signalosome chain COP8 - <i>Arabidopsis thaliana</i>		PF01399	
An18g05070	strong similarity to 26S proteasome subunit 9 - <i>Homo sapiens</i>		PF01399	
An07g00470	strong similarity to cytoplasmic metalloproteinase mepB - <i>Aspergillus fumigatus</i>		PF01432	
An07g01970	strong similarity to cytoplasmic metalloproteinase mepB - <i>Aspergillus fumigatus</i>		PF01432	
An15g02290	strong similarity to cytoplasmic metalloproteinase mepB - <i>Aspergillus fumigatus</i>		PF01432	
An04g03930	lysine aminopeptidase apsA - <i>Aspergillus niger</i>		PF01433	intracellular aminopeptidase
An05g00070	strong similarity to leukotriene-A4 hydrolase - <i>Mus musculus</i>		PF01433	

An09g06800	strong similarity to leucyl aminopeptidase Ape2 - <i>Saccharomyces cerevisiae</i>		PF01433	intracellular aminopeptidase
An07g07000	strong similarity to mitochondrial m-AAA protease subunit Yta12 - <i>Saccharomyces cerevisiae</i>		PF01434 PF00004	
An02g00990	strong similarity to amidohydrolase from patent WO0100843-A - <i>Corynebacterium glutamicum</i>		PF01546	
An02g13740	strong similarity to Gly-X carboxypeptidase precursor Yscs - <i>Saccharomyces cerevisiae</i>	20	PF01546	
An15g06440	strong similarity to karyopherin alpha Srp1 - <i>Saccharomyces cerevisiae</i> [truncated ORF]		PF01749 PF00514 PF03130	
An01g00530	proteinase aspergillopepsin II - <i>Aspergillus niger</i>	18	PF01828	
An07g00320	strong similarity to non-aspartyl acid protease acp1 - <i>Sclerotinia sclerotiorum</i>		PF01828	
An14g03250	strong similarity to aspergillopepsin II - <i>Aspergillus niger</i>	19	PF01828	
An15g07700	strong similarity to aspergillopepsin II precursor (acid proteinase A) - <i>Aspergillus niger</i>	18	PF01828	
An18g03010	strong similarity to 26S proteasome regulatory subunit S2 - <i>Homo sapiens</i>		PF01851	
An16g00930	similarity to hypothetical protein of the nonactin biosynthesis cluster nonF - <i>Streptomyces griseus</i>		PF01965	
An02g00090	strong similarity to prolidase - <i>Aureobacterium esteraromaticum</i>		PF01979	
An11g05920	strong similarity to prolidase - <i>Aureobacterium esteraromaticum</i>		PF01979	
An14g02080	strong similarity to prolidase - <i>Aureobacterium esteraromaticum</i>		PF01979	
An14g03560	strong similarity to prolidase - <i>Aureobacterium esteraromaticum</i>		PF01979	
An15g04370	similarity to proline dipeptidase from patent JP11318454-A - <i>Microbacterium esteraromaticum</i>		PF01979	
An02g11940	strong similarity to aminopeptidase METPRO02 from patent EP939131-A2 - <i>Homo sapiens</i>		PF02127	intracellular aminopeptidase
An09g06250	strong similarity to vacuolar aminopeptidase Ysci - <i>Saccharomyces cerevisiae</i>		PF02127	intracellular aminopeptidase
An01g02070	strong similarity to metalloprotease mep - <i>Aspergillus fumigatus</i>	30	PF02128	
An11g01610	similarity to ubiquitin protein ligase Ubr1 - <i>Saccharomyces cerevisiae</i>		PF02207	

An14g03420	strong similarity to CAAX prenyl protein protease RCE1 - Homo sapiens		PF02517	
An15g03020	strong similarity to proteasome 19S regulatory particle multiubiquitin chain binding subunit RPN10 - Physcomitrella patens		PF02809	
An12g05900	strong similarity to extracellular metalloproteinase precursor Prt1 - Erwinia carotovora		PF02868 PF01447	
An09g05400	strong similarity to SUMO-1-specific protease SSP1 - Homo sapiens		PF02902	
An13g01190	similarity to cysteine-type peptidase Ulp1 - Saccharomyces cerevisiae		PF02902	
An07g10020	strong similarity to microtubule-associated protein Aut7 - Saccharomyces cerevisiae		PF02991	
An01g01720	strong similarity to bleomycin hydrolase Blh1 - Saccharomyces cerevisiae		PF03051	
An04g03270	strong similarity to proteasome 19S regulatory particle subunit Rpn2 - Saccharomyces cerevisiae	17	PF03130 PF01851	
An01g05760	strong similarity to ubiquitin fusion degradation protein Ufd1 - Saccharomyces cerevisiae		PF03152	
An01g14120	similarity to proteasome alpha subunit ProsMA5 - Drosophila melanogaster		PF03256	
An04g05670	similarity to vacuolar sorting protein Snf7 - Saccharomyces cerevisiae		PF03357	
An18g05430	strong similarity to endosomal protein Snf7 - Saccharomyces cerevisiae		PF03357	
An11g11320	strong similarity to protein involved in autophagy Aut2 - Saccharomyces cerevisiae		PF03416	
An04g00410	strong similarity to dipeptidyl peptidase III - Rattus norvegicus		PF03571	intracellular dipeptidylaminopeptidase
An03g04380	strong similarity to autophagocytosis protein Aut1 - Saccharomyces cerevisiae		PF03987 PF03986	
An11g06920	strong similarity to autophagy modulator Agp12 - Saccharomyces cerevisiae		PF04110	
An02g01770	strong similarity to arginyl-tRNA-protein transferase Ate1 - Saccharomyces cerevisiae		PF04377 PF04376	
An14g00620	strong similarity to aminopeptidase from patent WO9628542-A1 - Aspergillus oryzae	19	PF04389	secreted aminopeptidase

An17g00390	strong similarity to aminopeptidase from patent WO9628542-A1 - <i>Aspergillus oryzae</i>	18	PF04389	secreted aminopeptidase
An03g01660	strong similarity to vacuolar aminopeptidase Y Ape3 - <i>Saccharomyces cerevisiae</i>	20	PF04389 PF02225	vacuolar aminopeptidase
An18g03980	strong similarity to glutamate carboxypeptidase II - <i>Rattus norvegicus</i>		PF04389 PF02225	
An02g06300	similarity to naaladase II - <i>Homo sapiens</i>		PF04389 PF02225 PF04253	intracellular aminopeptidase
An04g01730	strong similarity to ubiquitin fusion degradation protein Ufd2 - <i>Saccharomyces cerevisiae</i>		PF04564	
An16g02210	strong similarity to proteasome 19S regulatory particle subunit Rpn12 - <i>Saccharomyces cerevisiae</i>		PF04653	
An04g02320	strong similarity to metalloprotease 1 MP1 - <i>Homo sapiens</i>		PF05193	
An18g02980	strong similarity to endopeptidase La 2 IonD - <i>Myxococcus xanthus</i>		PF05362 PF00004	
An02g03760	strong similarity to precursor of endopeptidase La-like enzyme Pim1 - <i>Saccharomyces cerevisiae</i>		PF05362 PF02190 PF00004	
An01g01750	similarity to lysosomal protease CLN2 - <i>Rattus norvegicus</i>	18		secreted tripeptidylaminopeptidase
An01g03590	strong similarity to peptidase HPEP-6 from patent WO200042201-A2 - <i>Homo sapiens</i>			
An02g01550	strong similarity to secreted serine protease 19 kDa CS antigen CS-Ag - <i>Coccidioides immitis</i>	19		
An02g04820	similarity to cytokeratin-like protein Apg17 - <i>Saccharomyces cerevisiae</i>			
An03g01010	strong similarity to lysosomal pepstatin insensitive protease CLN2 - <i>Homo sapiens</i>	18		secreted tripeptidylaminopeptidase
An03g04140	strong similarity to N-terminal amidase Nta1 - <i>Saccharomyces cerevisiae</i>			
An04g08320	strong similarity to protease Mch5 - <i>Saccharomyces cerevisiae</i>	35		
An04g09960	similarity to serine protease SP1 YUXL from patent WO9903984-A2 - <i>Bacillus subtilis</i>			
An06g00190	strong similarity to lysosomal pepstatin insensitive protease CLN2 - <i>Homo sapiens</i>	20		secreted tripeptidylaminopeptidase

An06g00780	weak similarity to aminopeptidase N - <i>Felis catus</i>	20		secreted aminopeptidase
An07g00580	similarity to serine protease SP1 from patent WO9903984-A2 - <i>Bacillus subtilis</i>	18		
An07g00950	similarity to aspartyl proteinase candidapepsin - <i>Candida albicans</i>	18		secreted aspartyl protease
An07g02110	similarity to vacuolar carboxypeptidase Y Cpy - <i>Saccharomyces cerevisiae</i>			
An07g03830	similarity to DEEBY103 rescued locus from patent WO9811203-A1 - <i>Aspergillus oryzae</i>			
An07g10060	strong similarity to proteinase B inhibitor 2 Pbi2 - <i>Saccharomyces cerevisiae</i>	18		
An07g10130	weak similarity to ubiquitin specific processing protease DUB1 - <i>Mus musculus</i>			
An07g10410	strong similarity to metalloprotease Mep1 - <i>Metarhizium anisopliae</i>	25		
An08g04640	strong similarity to hypothetical lysosomal pepstatin insensitive protease CLN2 - <i>Canis lupus</i>	19		secreted tripeptidylaminopeptidase
An08g05390	strong similarity to hypothetical zinc-metalloprotease SPCC1442.07c - <i>Schizosaccharomyces pombe</i>			
An08g05890	similarity to cell cycle control protein Cdc53 - <i>Saccharomyces cerevisiae</i>			
An09g00700	similarity to X-Pro dipeptidase pepQ - <i>Lactobacillus lactis</i>			
An09g00700.1	strong similarity to cytoplasmic form of aminopeptidase P - <i>Homo sapiens</i>			intracellular aminopeptidase
An09g02830	strong similarity to acylaminoacyl-peptidase DPP V - <i>Aspergillus fumigatus</i>			
An09g03630	strong similarity to hypothetical protein Aut4 - <i>Saccharomyces cerevisiae</i>			
An09g03800	strong similarity to hydrolase protein YQJL from patent WO9927081-A2 - <i>Bacillus subtilis</i>	30		
An11g00310	similarity to aspartyl proteinase candidapepsin - <i>Candida albicans</i>	25		secreted aspartyl protease
An11g00748	weak similarity to ubiquitin protein ligase Asi3 - <i>Saccharomyces cerevisiae</i> [truncated ORF]			

An11g01110	strong similarity to lysosomal pepstatin insensitive protease CLN2 - Homo sapiens	15		secreted tripeptidylaminopeptidase
An11g01970	similarity to pyroglutamyl-peptidase I PGPI - Pyrococcus furiosus			
An11g04730	prolyl aminopeptidase papA - Aspergillus niger			intracellular aminopeptidase
An11g04890	similarity to multicatalytic endopeptidase regulator Rpn5 - Drosophila melanogaster			
An11g07120	strong similarity to glutamyl endoprotease polypeptide from patent WO200268623-A2 - Aspergillus niger	18		
An12g05960	strong similarity to dipeptidyl peptidase II DPPII - Rattus norvegicus	17		secreted dipeptidylaminopeptidase
An14g01120	strong similarity to thymus specific serine peptidase TSSP - Homo sapiens			intracellular dipeptidylaminopeptidase
An14g01530	similarity to intracellular serine proteinase isp - Bacillus polymyxa			
An15g03750	similarity to adhesion protease from patent WO0109293-A - Homo sapiens			
An16g02250	strong similarity to lysosomal pepstatin insensitive protease CLN2 - Homo sapiens	19		secreted tripeptidylaminopeptidase
An16g02960	strong similarity to prenylcysteine lyase PCL1 - Homo sapiens	33		
An16g06260	weak similarity to alkaline serine protease ispQ - Bacillus sp.			
An16g08150	strong similarity to dipeptidyl-peptidase V DPP V - Aspergillus fumigatus			intracellular dipeptidylaminopeptidase
An18g04970	weak similarity to subtilisin E precursor aprE - Bacillus subtilis			