

Orthogroup	seed ortholog	evalue	score	eggNOG OGs	max annot lvl	COG category	Description	Preferred name	GOs	EC
OG0000011	104355.XP_007865362.1	1.73E-66	238	KOG1339@1 root,KOG1339@2759	4751 Fungi	O	Belongs to the peptidase A1 family	-	-	3.4.23.25,3.4.23.5
OG0000011	104355.XP_007865362.1	1.73E-66	238	KOG1339@1 root,KOG1339@2759	4751 Fungi	O	Belongs to the peptidase A1 family	-	-	3.4.23.25,3.4.23.5
OG0000011	104355.XP_007865362.1	1.73E-66	238	KOG1339@1 root,KOG1339@2759	4751 Fungi	O	Belongs to the peptidase A1 family	-	-	3.4.23.25,3.4.23.5
OG0000011	104355.XP_007865362.1	1.73E-66	238	KOG1339@1 root,KOG1339@2759	4751 Fungi	O	Belongs to the peptidase A1 family	-	-	3.4.23.25,3.4.23.5
OG0000056	84751.XP_007879106.1	4.07E-126	390	COG2234@1 root,KOG2195@2759	4751 Fungi	O	Peptidase family M28	-	-	3.4.11.10
OG0000090	120017.I2FWJ6	0	1134	COG0308@1 root,KOG1046@2759	4751 Fungi	E	ERAP1-like C-terminal domain	APE2	GO:0000322,GO:0000323,GO:00	3.4.11.2
OG0000090	120017.I2FWJ6	0	1134	COG0308@1 root,KOG1046@2759	4751 Fungi	E	ERAP1-like C-terminal domain	APE2	GO:0000322,GO:0000323,GO:00	3.4.11.2
OG0000091	63405.XP_002850684.1	0	1813	COG2234@1 root,KOG2195@2759	4751 Fungi	OP	Transferrin receptor-like dimerisation domain	-	GO:0000322,GO:0000323,GO:00	3.4.17.21
OG0000091	63405.XP_002850684.1	0	1813	COG2234@1 root,KOG2195@2759	4751 Fungi	OP	Transferrin receptor-like dimerisation domain	-	GO:0000322,GO:0000323,GO:00	3.4.17.21
OG0000091	63405.XP_002850684.1	0	1813	COG2234@1 root,KOG2195@2759	4751 Fungi	OP	Transferrin receptor-like dimerisation domain	-	GO:0000322,GO:0000323,GO:00	3.4.17.21
OG0000130	63400.XP_003013138.1	0	2953	COG5560@1 root,KOG1870@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0000130	63400.XP_003013138.1	0	2953	COG5560@1 root,KOG1870@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0000130	63400.XP_003013138.1	0	2953	COG5560@1 root,KOG1870@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0000130	63400.XP_003013138.1	0	2953	COG5560@1 root,KOG1870@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0000135	430998.XP_007679405.1	0	1612	COG0466@1 root,KOG2004@2759	4751 Fungi	L	ATP-dependent serine protease that mediates the sel PIM1	-	GO:0000166,GO:0003674,GO:00	3.4.21.53
OG0000135	430998.XP_007679405.1	0	1612	COG0466@1 root,KOG2004@2759	4751 Fungi	L	ATP-dependent serine protease that mediates the sel PIM1	-	GO:0000166,GO:0003674,GO:00	3.4.21.53
OG0000135	430998.XP_007679405.1	0	1612	COG0466@1 root,KOG2004@2759	4751 Fungi	L	ATP-dependent serine protease that mediates the sel PIM1	-	GO:0000166,GO:0003674,GO:00	3.4.21.53
OG0000135	430998.XP_007679405.1	0	1612	COG0466@1 root,KOG2004@2759	4751 Fungi	L	ATP-dependent serine protease that mediates the sel PIM1	-	GO:0000166,GO:0003674,GO:00	3.4.21.53
OG0000135	430998.XP_007679405.1	0	1612	COG0466@1 root,KOG2004@2759	4751 Fungi	L	ATP-dependent serine protease that mediates the sel PIM1	-	GO:0000166,GO:0003674,GO:00	3.4.21.53
OG0000135	430998.XP_007679405.1	0	1612	COG0466@1 root,KOG2004@2759	4751 Fungi	L	ATP-dependent serine protease that mediates the sel PIM1	-	GO:0000166,GO:0003674,GO:00	3.4.21.53
OG0000135	430998.XP_007679405.1	0	1612	COG0466@1 root,KOG2004@2759	4751 Fungi	L	ATP-dependent serine protease that mediates the sel PIM1	-	GO:0000166,GO:0003674,GO:00	3.4.21.53
OG0000135	430998.XP_007679405.1	0	1612	COG0466@1 root,KOG2004@2759	4751 Fungi	L	ATP-dependent serine protease that mediates the sel PIM1	-	GO:0000166,GO:0003674,GO:00	3.4.21.53
OG0000171	1047171.Mycgr3P60951	2.53E-260	747	COG1362@1 root,KOG2596@2759	4751 Fungi	E	Belongs to the peptidase M18 family	-	GO:0000322,GO:0000323,GO:00	3.4.11.21
OG0000202	63418.F2PN26	6.36E-184	512	KOG1415@1 root,KOG1415@2759	4751 Fungi	O	ubiquitin	-	-	3.4.19.12
OG0000202	63418.F2PN26	6.36E-184	512	KOG1415@1 root,KOG1415@2759	4751 Fungi	O	ubiquitin	-	-	3.4.19.12
OG0000272	4909.A0A099NXQ2	0	1263	COG5560@1 root,KOG1870@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0000272	4909.A0A099NXQ2	0	1263	COG5560@1 root,KOG1870@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0000277	63405.XP_002845577.1	0	1212	COG4934@1 root,2QR6D@2759	Eu 4751 Fungi	O	Secreted tripeptidyl-peptidase which degrades protei SED4	-	-	3.4.14.9
OG0000277	63405.XP_002845577.1	0	1212	COG4934@1 root,2QR6D@2759	Eu 4751 Fungi	O	Secreted tripeptidyl-peptidase which degrades protei SED4	-	-	3.4.14.9
OG0000290	82508.K1WAW2	4.02E-256	733	KOG2605@1 root,KOG2605@2759	4751 Fungi	OT	OTU-like cysteine protease	-	-	3.4.19.12
OG0000290	82508.K1WAW2	4.02E-256	733	KOG2605@1 root,KOG2605@2759	4751 Fungi	OT	OTU-like cysteine protease	-	-	3.4.19.12
OG0000299	430998.XP_007675756.1	1.71E-235	679	COG0024@1 root,KOG2775@2759	4751 Fungi	J	Cotranslationally removes the N-terminal methionine MAP2	-	GO:0003674,GO:0003824,GO:00	3.4.11.18
OG0000299	430998.XP_007675756.1	1.71E-235	679	COG0024@1 root,KOG2775@2759	4751 Fungi	J	Cotranslationally removes the N-terminal methionine MAP2	-	GO:0003674,GO:0003824,GO:00	3.4.11.18
OG0000299	430998.XP_007675756.1	1.71E-235	679	COG0024@1 root,KOG2775@2759	4751 Fungi	J	Cotranslationally removes the N-terminal methionine MAP2	-	GO:0003674,GO:0003824,GO:00	3.4.11.18
OG0000299	430998.XP_007675756.1	1.71E-235	679	COG0024@1 root,KOG2775@2759	4751 Fungi	J	Cotranslationally removes the N-terminal methionine MAP2	-	GO:0003674,GO:0003824,GO:00	3.4.11.18
OG0000299	430998.XP_007675756.1	1.71E-235	679	COG0024@1 root,KOG2775@2759	4751 Fungi	J	Cotranslationally removes the N-terminal methionine MAP2	-	GO:0003674,GO:0003824,GO:00	3.4.11.18
OG0000361	4909.A0A099P560	0	1667	COG1404@1 root,COG3579@2759	4751 Fungi	O	Belongs to the peptidase S8 family	KEX2	GO:0000139,GO:0000322,GO:00	3.4.21.61
OG0000361	4909.A0A099P560	0	1667	COG1404@1 root,COG3579@2759	4751 Fungi	O	Belongs to the peptidase S8 family	KEX2	GO:0000139,GO:0000322,GO:00	3.4.21.61
OG0000378	5478.XP_446535.1	0	1513	COG0006@1 root,KOG2413@2759	4751 Fungi	E	Belongs to the peptidase M24B family	AMPP	GO:0000122,GO:0006355,GO:00	3.4.11.9
OG0000378	5478.XP_446535.1	0	1513	COG0006@1 root,KOG2413@2759	4751 Fungi	E	Belongs to the peptidase M24B family	AMPP	GO:0000122,GO:0006355,GO:00	3.4.11.9
OG0000378	5478.XP_446535.1	0	1513	COG0006@1 root,KOG2413@2759	4751 Fungi	E	Belongs to the peptidase M24B family	AMPP	GO:0000122,GO:0006355,GO:00	3.4.11.9
OG0000467	104355.XP_007860870.1	3.78E-147	490	KOG3691@1 root,KOG3691@2759	4751 Fungi	U	Sec8 exocyst complex component specific domain	SEC8	GO:0000003,GO:0000131,GO:00	3.4.11.9
OG0000485	5478.XP_445129.1	0	928	COG1404@1 root,KOG1153@2759	4751 Fungi	O	Belongs to the peptidase S8 family	SUB8	GO:0000003,GO:0000322,GO:00	3.4.21.48
OG0000485	5478.XP_445129.1	0	928	COG1404@1 root,KOG1153@2759	4751 Fungi	O	Belongs to the peptidase S8 family	SUB8	GO:0000003,GO:0000322,GO:00	3.4.21.48
OG0000571	82508.K1VFX1	0	1595	COG5077@1 root,KOG1863@2759	4751 Fungi	O	A repeated domain in UCH-protein	UBP2	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0000571	82508.K1VFX1	0	1595	COG5077@1 root,KOG1863@2759	4751 Fungi	O	A repeated domain in UCH-protein	UBP2	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0000587	5551.XP_003232985.1	0	4072	COG5155@1 root,KOG1849@2759	4751 Fungi	D	Peptidase family C50	ESP1	GO:0000003,GO:0000070,GO:00	3.4.22.49
OG0000599	430998.XP_007674026.1	1.05E-289	798	COG0612@1 root,KOG0960@2759	4751 Fungi	O	Belongs to the peptidase M16 family	MAS1	GO:0003674,GO:0003824,GO:00	3.4.24.64
OG0000599	430998.XP_007674026.1	1.05E-289	798	COG0612@1 root,KOG0960@2759	4751 Fungi	O	Belongs to the peptidase M16 family	MAS1	GO:0003674,GO:0003824,GO:00	3.4.24.64
OG0000599	430998.XP_007674026.1	1.05E-289	798	COG0612@1 root,KOG0960@2759	4751 Fungi	O	Belongs to the peptidase M16 family	MAS1	GO:0003674,GO:0003824,GO:00	3.4.24.64
OG0000643	5480.G8BJX7	0	2688	COG5077@1 root,KOG1863@2759	4751 Fungi	O	Belongs to the peptidase C19 family	UBP15	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0000643	5480.G8BJX7	0	2688	COG5077@1 root,KOG1863@2759	4751 Fungi	O	Belongs to the peptidase C19 family	UBP15	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0000714	4909.A0A099P410	0	2158	COG1025@1 root,KOG0959@2759	4751 Fungi	O	Belongs to the peptidase M16 family	STE23	GO:0003674,GO:0003824,GO:00	3.4.24.56
OG0000714	4909.A0A099P410	0	2158	COG1025@1 root,KOG0959@2759	4751 Fungi	O	Belongs to the peptidase M16 family	STE23	GO:0003674,GO:0003824,GO:00	3.4.24.56
OG0000714	4909.A0A099P410	0	2158	COG1025@1 root,KOG0959@2759	4751 Fungi	O	Belongs to the peptidase M16 family	STE23	GO:0003674,GO:0003824,GO:00	3.4.24.56
OG0000714	4909.A0A099P410	0	2158	COG1025@1 root,KOG0959@2759	4751 Fungi	O	Belongs to the peptidase M16 family	STE23	GO:0003674,GO:0003824,GO:00	3.4.24.56
OG0000714	4909.A0A099P410	0	2158	COG1025@1 root,KOG0959@2759	4751 Fungi	O	Belongs to the peptidase M16 family	STE23	GO:0003674,GO:0003824,GO:00	3.4.24.56
OG0000727	84751.XP_007880322.1	4.87E-164	489	COG0024@1 root,KOG2776@2759	4751 Fungi	J	Metallopeptidase family M24	-	GO:0003674,GO:0003676,GO:00	3.4.11.18
OG0000727	84751.XP_007880322.1	4.87E-164	489	COG0024@1 root,KOG2776@2759	4751 Fungi	J	Metallopeptidase family M24	-	GO:0003674,GO:0003676,GO:00	3.4.11.18

OG0000727	84751.XP_007880322.1	4.87E-164	489	COG0024@1 root,KOG2776@2759 4751 Fungi	J	Metallopeptidase family M24	-	GO:0003674,GO:0003676,GO:00 3.4.11.18
OG0000744	84751.XP_007879267.1	1.18E-136	441	COG0624@1 root,KOG2275@2759 4751 Fungi	E	Peptidase dimerisation domain	-	GO:0000322,GO:0000323,GO:00 3.4.17.4
OG0000744	84751.XP_007879267.1	1.18E-136	441	COG0624@1 root,KOG2275@2759 4751 Fungi	E	Peptidase dimerisation domain	-	GO:0000322,GO:0000323,GO:00 3.4.17.4
OG0000744	84751.XP_007879267.1	1.18E-136	441	COG0624@1 root,KOG2275@2759 4751 Fungi	E	Peptidase dimerisation domain	-	GO:0000322,GO:0000323,GO:00 3.4.17.4
OG0000770	430998.XP_007681750.1	1.56E-223	629	COG2355@1 root,KOG4127@2759 4751 Fungi	O	Belongs to the metallo-dependent hydrolases superfa	-	3.4.13.19
OG0000770	430998.XP_007681750.1	1.56E-223	629	COG2355@1 root,KOG4127@2759 4751 Fungi	O	Belongs to the metallo-dependent hydrolases superfa	-	3.4.13.19
OG0000875	208960.XP_007271200.1	3.62E-97	333	KOG1864@1 root,KOG1864@2759 4751 Fungi	O	Cysteine proteinase	creB	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0000875	208960.XP_007271200.1	3.62E-97	333	KOG1864@1 root,KOG1864@2759 4751 Fungi	O	Cysteine proteinase	creB	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0000952	82508.K1VPD7	0	1617	KOG1868@1 root,KOG1868@2759 4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	DOA4	GO:0000131,GO:0000502,GO:00 3.4.19.12
OG0000952	82508.K1VPD7	0	1617	KOG1868@1 root,KOG1868@2759 4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	DOA4	GO:0000131,GO:0000502,GO:00 3.4.19.12
OG0000952	82508.K1VPD7	0	1617	KOG1868@1 root,KOG1868@2759 4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	DOA4	GO:0000131,GO:0000502,GO:00 3.4.19.12
OG0000981	63402.XP_003177316.1	0	1024	KOG1872@1 root,KOG1872@2759 4751 Fungi	O	Belongs to the peptidase C19 family	UBP6	GO:0000502,GO:0003674,GO:00 3.4.19.12
OG0000981	63402.XP_003177316.1	0	1024	KOG1872@1 root,KOG1872@2759 4751 Fungi	O	Belongs to the peptidase C19 family	UBP6	GO:0000502,GO:0003674,GO:00 3.4.19.12
OG0000981	63402.XP_003177316.1	0	1024	KOG1872@1 root,KOG1872@2759 4751 Fungi	O	Belongs to the peptidase C19 family	UBP6	GO:0000502,GO:0003674,GO:00 3.4.19.12
OG0000981	63402.XP_003177316.1	0	1024	KOG1872@1 root,KOG1872@2759 4751 Fungi	O	Belongs to the peptidase C19 family	UBP6	GO:0000502,GO:0003674,GO:00 3.4.19.12
OG0000982	120017.I2FZJ5	1.7E-88	300	KOG1339@1 root,KOG1339@2759 4751 Fungi	O	Xylanase inhibitor N-terminal	-	3.4.23.5
OG0000982	120017.I2FZJ5	1.7E-88	300	KOG1339@1 root,KOG1339@2759 4751 Fungi	O	Xylanase inhibitor N-terminal	-	3.4.23.5
OG0000982	120017.I2FZJ5	1.7E-88	300	KOG1339@1 root,KOG1339@2759 4751 Fungi	O	Xylanase inhibitor N-terminal	-	3.4.23.5
OG0000982	120017.I2FZJ5	1.7E-88	300	KOG1339@1 root,KOG1339@2759 4751 Fungi	O	Xylanase inhibitor N-terminal	-	3.4.23.5
OG0001140	5270.UM00354P0	5.88E-89	312	COG5160@1 root,KOG0778@2759 4751 Fungi	O	Ulp1 protease family, C-terminal catalytic domain	-	GO:0000086,GO:0000278,GO:00 3.4.22.68
OG0001222	82508.K1VQG6	5.08E-168	471	COG0638@1 root,KOG0179@2759 4751 Fungi	O	Proteasome subunit beta type	PRE7	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0001222	82508.K1VQG6	5.08E-168	471	COG0638@1 root,KOG0179@2759 4751 Fungi	O	Proteasome subunit beta type	PRE7	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0001233	63405.XP_002843416.1	1.57E-140	402	COG0638@1 root,KOG0180@2759 4751 Fungi	O	Proteasome subunit beta	PUP3	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001233	63405.XP_002843416.1	1.57E-140	402	COG0638@1 root,KOG0180@2759 4751 Fungi	O	Proteasome subunit beta	PUP3	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001237	264951.V5G3Q3	0	1234	KOG1649@1 root,KOG2137@2759 4751 Fungi	O	Belongs to the peptidase M49 family	YOL057W	GO:0003674,GO:0003824,GO:00 3.4.14.4
OG0001260	327079.R9P279	6.7E-133	404	COG0638@1 root,KOG0173@2759 4751 Fungi	O	Proteasome beta subunits C terminal	PUP1	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001260	327079.R9P279	6.7E-133	404	COG0638@1 root,KOG0173@2759 4751 Fungi	O	Proteasome beta subunits C terminal	PUP1	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001260	327079.R9P279	6.7E-133	404	COG0638@1 root,KOG0173@2759 4751 Fungi	O	Proteasome beta subunits C terminal	PUP1	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001260	327079.R9P279	6.7E-133	404	COG0638@1 root,KOG0173@2759 4751 Fungi	O	Proteasome beta subunits C terminal	PUP1	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001260	327079.R9P279	6.7E-133	404	COG0638@1 root,KOG0173@2759 4751 Fungi	O	Proteasome beta subunits C terminal	PUP1	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001260	327079.R9P279	6.7E-133	404	COG0638@1 root,KOG0173@2759 4751 Fungi	O	Proteasome beta subunits C terminal	PUP1	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001272	5270.UM04116P0	6.51E-45	169	COG5539@1 root,KOG2606@2759 4751 Fungi	OT	OTU-like cysteine protease	OTU2	GO:0005575,GO:0005622,GO:00 3.4.19.12
OG0001272	5270.UM04116P0	6.51E-45	169	COG5539@1 root,KOG2606@2759 4751 Fungi	OT	OTU-like cysteine protease	OTU2	GO:0005575,GO:0005622,GO:00 3.4.19.12
OG0001273	42374.XP_002419484.1	0	1321	KOG1867@1 root,KOG1867@2759 4751 Fungi	O	Belongs to the peptidase C19 family	UBP1	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0001273	42374.XP_002419484.1	0	1321	KOG1867@1 root,KOG1867@2759 4751 Fungi	O	Belongs to the peptidase C19 family	UBP1	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0001379	82508.K1WLE3	0	987	COG2939@1 root,KOG1282@2759 4751 Fungi	EO	Serine carboxypeptidase	KEX1	GO:0000322,GO:0000323,GO:00 3.4.16.6
OG0001379	82508.K1WLE3	0	987	COG2939@1 root,KOG1282@2759 4751 Fungi	EO	Serine carboxypeptidase	KEX1	GO:0000322,GO:0000323,GO:00 3.4.16.6
OG0001506	63418.F2PQ96	0	1954	COG5160@1 root,KOG0779@2759 4751 Fungi	O	Ulp1 protease family, C-terminal catalytic domain	-	GO:0000075,GO:0000278,GO:00 3.4.22.68
OG0001506	63418.F2PQ96	0	1954	COG5160@1 root,KOG0779@2759 4751 Fungi	O	Ulp1 protease family, C-terminal catalytic domain	-	GO:0000075,GO:0000278,GO:00 3.4.22.68
OG0001506	63418.F2PQ96	0	1954	COG5160@1 root,KOG0779@2759 4751 Fungi	O	Ulp1 protease family, C-terminal catalytic domain	-	GO:0000075,GO:0000278,GO:00 3.4.22.68
OG0001654	552467.XP_003194809.1	2.56E-161	456	COG0638@1 root,KOG0178@2759 4751 Fungi	O	Proteasome subunit	PRE9	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0001654	552467.XP_003194809.1	2.56E-161	456	COG0638@1 root,KOG0178@2759 4751 Fungi	O	Proteasome subunit	PRE9	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0001656	5270.UM03777P0	1.64E-120	400	KOG1871@1 root,KOG1871@2759 4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003676,GO:00 3.4.19.12
OG0001656	5270.UM03777P0	1.64E-120	400	KOG1871@1 root,KOG1871@2759 4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003676,GO:00 3.4.19.12
OG0001656	5270.UM03777P0	1.64E-120	400	KOG1871@1 root,KOG1871@2759 4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003676,GO:00 3.4.19.12
OG0001656	5270.UM03777P0	1.64E-120	400	KOG1871@1 root,KOG1871@2759 4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003676,GO:00 3.4.19.12
OG0001656	5270.UM03777P0	1.64E-120	400	KOG1871@1 root,KOG1871@2759 4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003676,GO:00 3.4.19.12
OG0001705	63400.XP_003017381.1	0	1877	COG5406@1 root,KOG1189@2759 4751 Fungi	E	FACT complex subunit spt16	SPT16	GO:0000228,GO:0000785,GO:00 3.4.11.9
OG0001705	63400.XP_003017381.1	0	1877	COG5406@1 root,KOG1189@2759 4751 Fungi	E	FACT complex subunit spt16	SPT16	GO:0000228,GO:0000785,GO:00 3.4.11.9
OG0001711	64363.EME39502	8.17E-178	501	COG0638@1 root,KOG0184@2759 4751 Fungi	O	Proteasome subunit alpha type	PRE10	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001711	64363.EME39502	8.17E-178	501	COG0638@1 root,KOG0184@2759 4751 Fungi	O	Proteasome subunit alpha type	PRE10	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001813	120017.I2FPF6	1.8E-123	361	COG0638@1 root,KOG0182@2759 4751 Fungi	O	Proteasome subunit A N-terminal signature	Add an a SCL1	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0001813	120017.I2FPF6	1.8E-123	361	COG0638@1 root,KOG0182@2759 4751 Fungi	O	Proteasome subunit A N-terminal signature	Add an a SCL1	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0001838	1392244.V5GVJ0	2E-230	680	COG5207@1 root,KOG0944@2759 4751 Fungi	O	Ubiquitin Carboxyl-terminal Hydrolase-like zinc finger ubp14	-	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0001838	1392244.V5GVJ0	2E-230	680	COG5207@1 root,KOG0944@2759 4751 Fungi	O	Ubiquitin Carboxyl-terminal Hydrolase-like zinc finger ubp14	-	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0001838	1392244.V5GVJ0	2E-230	680	COG5207@1 root,KOG0944@2759 4751 Fungi	O	Ubiquitin Carboxyl-terminal Hydrolase-like zinc finger ubp14	-	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0001838	1392244.V5GVJ0	2E-230	680	COG5207@1 root,KOG0944@2759 4751 Fungi	O	Ubiquitin Carboxyl-terminal Hydrolase-like zinc finger ubp14	-	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0001901	84751.XP_007880004.1	2.65E-148	428	COG0638@1 root,KOG0175@2759 4751 Fungi	O	Proteasome subunit	PRE2	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0001901	84751.XP_007880004.1	2.65E-148	428	COG0638@1 root,KOG0175@2759 4751 Fungi	O	Proteasome subunit	PRE2	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0002044	1047171.Mycgr3P66573	3.19E-181	506	KOG0181@1 root,KOG0181@2759 4751 Fungi	O	Proteasome subunit alpha type	PRE8	GO:0000502,GO:0005575,GO:00 3.4.25.1

OG0002044	1047171.Mycgr3P66573	3.19E-181	506	KOG0181@1 root,KOG0181@2759	4751 Fungi	O	Proteasome subunit alpha type	PRE8	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0002079	5478.XP_447358.1	2.67E-178	497	COG0638@1 root,KOG0176@2759	4751 Fungi	O	Belongs to the peptidase T1A family	PUP2	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0002079	5478.XP_447358.1	2.67E-178	497	COG0638@1 root,KOG0176@2759	4751 Fungi	O	Belongs to the peptidase T1A family	PUP2	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0002098	264951.V5FNK1	7.62E-199	570	KOG0185@1 root,KOG0185@2759	4751 Fungi	O	Proteasome subunit beta	PRE4	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0002098	264951.V5FNK1	7.62E-199	570	KOG0185@1 root,KOG0185@2759	4751 Fungi	O	Proteasome subunit beta	PRE4	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0002143	120017.I2FMB5	4.94E-230	680	COG0339@1 root,KOG2090@2759	4751 Fungi	O	Mitochondrial intermediate peptidase	OCT1	GO:0003674,GO:0003824,GO:00 3.4.24.59
OG0002143	120017.I2FMB5	4.94E-230	680	COG0339@1 root,KOG2090@2759	4751 Fungi	O	Mitochondrial intermediate peptidase	OCT1	GO:0003674,GO:0003824,GO:00 3.4.24.59
OG0002152	5480.G8BHE2	4.84E-291	805	KOG1339@1 root,KOG1339@2759	4751 Fungi	O	Belongs to the peptidase A1 family	BAR1	GO:0000322,GO:0000323,GO:00 3.4.23.24,3.4.23.35,3.4.
OG0002152	5480.G8BHE2	4.84E-291	805	KOG1339@1 root,KOG1339@2759	4751 Fungi	O	Belongs to the peptidase A1 family	BAR1	GO:0000322,GO:0000323,GO:00 3.4.23.24,3.4.23.35,3.4.
OG0002188	63402.XP_003171688.1	0	1112	COG0612@1 root,KOG2067@2759	4751 Fungi	O	Belongs to the peptidase M16 family	MAS2	GO:0003674,GO:0003824,GO:00 3.4.24.64
OG0002188	63402.XP_003171688.1	0	1112	COG0612@1 root,KOG2067@2759	4751 Fungi	O	Belongs to the peptidase M16 family	MAS2	GO:0003674,GO:0003824,GO:00 3.4.24.64
OG0002188	63402.XP_003171688.1	0	1112	COG0612@1 root,KOG2067@2759	4751 Fungi	O	Belongs to the peptidase M16 family	MAS2	GO:0003674,GO:0003824,GO:00 3.4.24.64
OG0002188	63402.XP_003171688.1	0	1112	COG0612@1 root,KOG2067@2759	4751 Fungi	O	Belongs to the peptidase M16 family	MAS2	GO:0003674,GO:0003824,GO:00 3.4.24.64
OG0002197	82508.K1VRV8	8.59E-159	447	COG0638@1 root,KOG0177@2759	4751 Fungi	O	Proteasome subunit beta	PRE1	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0002197	82508.K1VRV8	8.59E-159	447	COG0638@1 root,KOG0177@2759	4751 Fungi	O	Proteasome subunit beta	PRE1	GO:0000502,GO:0003674,GO:00 3.4.25.1
OG0002231	84751.XP_007880909.1	3.55E-136	399	COG0638@1 root,KOG0183@2759	4751 Fungi	O	Proteasome subunit A N-terminal signature Add an a	PRE6	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0002231	84751.XP_007880909.1	3.55E-136	399	COG0638@1 root,KOG0183@2759	4751 Fungi	O	Proteasome subunit A N-terminal signature Add an a	PRE6	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0002398	82508.K1VJ77	4.33E-70	218	COG0681@1 root,KOG3342@2759	4751 Fungi	U	Catalytic component of the signal peptidase complex	SEC11	GO:0003674,GO:0003824,GO:00 3.4.21.89
OG0002418	327079.R9P0B8	1.94E-128	376	COG0638@1 root,KOG0863@2759	4751 Fungi	O	Proteasome subunit A N-terminal signature Add an a	PRE5	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0002418	327079.R9P0B8	1.94E-128	376	COG0638@1 root,KOG0863@2759	4751 Fungi	O	Proteasome subunit A N-terminal signature Add an a	PRE5	GO:0000502,GO:0005575,GO:00 3.4.25.1
OG0002489	83344.XP_007923374.1	4.88E-174	510	COG0006@1 root,KOG2737@2759	4751 Fungi	E	Aminopeptidase P, N-terminal domain	PEPP	- 3.4.13.9
OG0002489	83344.XP_007923374.1	4.88E-174	510	COG0006@1 root,KOG2737@2759	4751 Fungi	E	Aminopeptidase P, N-terminal domain	PEPP	- 3.4.13.9
OG0002489	83344.XP_007923374.1	4.88E-174	510	COG0006@1 root,KOG2737@2759	4751 Fungi	E	Aminopeptidase P, N-terminal domain	PEPP	- 3.4.13.9
OG0002489	83344.XP_007923374.1	4.88E-174	510	COG0006@1 root,KOG2737@2759	4751 Fungi	E	Aminopeptidase P, N-terminal domain	PEPP	- 3.4.13.9
OG0002815	63400.XP_003012504.1	0	1469	COG0339@1 root,KOG2089@2759	4751 Fungi	O	Peptidase family M3	PRD1	GO:0000322,GO:0000323,GO:00 3.4.24.37
OG0002815	63400.XP_003012504.1	0	1469	COG0339@1 root,KOG2089@2759	4751 Fungi	O	Peptidase family M3	PRD1	GO:0000322,GO:0000323,GO:00 3.4.24.37
OG0002815	63400.XP_003012504.1	0	1469	COG0339@1 root,KOG2089@2759	4751 Fungi	O	Peptidase family M3	PRD1	GO:0000322,GO:0000323,GO:00 3.4.24.37
OG0002888	5551.XP_003233502.1	0	1044	KOG1865@1 root,KOG1865@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	- 3.4.19.12
OG0002888	5551.XP_003233502.1	0	1044	KOG1865@1 root,KOG1865@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	- 3.4.19.12
OG0002902	4909.A0A099P060	0	1947	COG0258@1 root,COG5207@1 roo	4751 Fungi	O	Ubiquitinyl hydrolase 1	ubp14	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0002902	4909.A0A099P060	0	1947	COG0258@1 root,COG5207@1 roo	4751 Fungi	O	Ubiquitinyl hydrolase 1	ubp14	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0002975	5551.XP_003237755.1	0	950	KOG3991@1 root,KOG3991@2759	4751 Fungi	O	Peptidase C65 Otubain	-	- 3.4.19.12
OG0003081	5551.XP_003235559.1	0	1532	KOG3675@1 root,KOG3675@2759	4751 Fungi	O	Belongs to the peptidase M49 family	YOL057W	GO:0003674,GO:0003824,GO:00 3.4.14.4
OG0003126	84751.XP_007880520.1	4.22E-49	194	COG1310@1 root,KOG2880@2759	4751 Fungi	T	Mov34-domain-containing protein	-	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0003307	82508.K1WG46	8.59E-113	340	COG0024@1 root,KOG2738@2759	4751 Fungi	O	Removes the N-terminal methionine from nascent pri	-	- 3.4.11.18
OG0003307	82508.K1WG46	8.59E-113	340	COG0024@1 root,KOG2738@2759	4751 Fungi	O	Removes the N-terminal methionine from nascent pri	-	- 3.4.11.18
OG0003307	82508.K1WG46	8.59E-113	340	COG0024@1 root,KOG2738@2759	4751 Fungi	O	Removes the N-terminal methionine from nascent pri	-	- 3.4.11.18
OG0003307	82508.K1WG46	8.59E-113	340	COG0024@1 root,KOG2738@2759	4751 Fungi	O	Removes the N-terminal methionine from nascent pri	-	- 3.4.11.18
OG0003369	109871.XP_006681033.1	2.95E-24	112	KOG3059@1 root,KOG3059@2759	4751 Fungi	I	phosphatidylinositol	GPI2	GO:0000506,GO:0003674,GO:00 3.4.11.19
OG0003369	109871.XP_006681033.1	2.95E-24	112	KOG3059@1 root,KOG3059@2759	4751 Fungi	I	phosphatidylinositol	GPI2	GO:0000506,GO:0003674,GO:00 3.4.11.19
OG0003475	5551.XP_003231292.1	2.41E-228	642	KOG2778@1 root,KOG2778@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	GO:0000338,GO:0003674,GO:00 3.4.19.12
OG0003475	5551.XP_003231292.1	2.41E-228	642	KOG2778@1 root,KOG2778@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	GO:0000338,GO:0003674,GO:00 3.4.19.12
OG0003493	42374.XP_002418670.1	0	938	COG0596@1 root,2QSNW@2759 Ei	4751 Fungi	S	alpha/beta hydrolase fold	-	- 3.4.11.5
OG0003493	42374.XP_002418670.1	0	938	COG0596@1 root,2QSNW@2759 Ei	4751 Fungi	S	alpha/beta hydrolase fold	-	- 3.4.11.5
OG0003569	82508.K1VCT3	3.7E-148	431	COG0596@1 root,2QPPY@2759 Eui	4751 Fungi	I	Alpha/beta hydrolase family	-	- 3.4.11.5
OG0003569	82508.K1VCT3	3.7E-148	431	COG0596@1 root,2QPPY@2759 Eui	4751 Fungi	I	Alpha/beta hydrolase family	-	- 3.4.11.5
OG0003585	5480.G8B8J6	0	1613	28K46@1 root,2QSIQ@2759 Eukary	4751 Fungi	U	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0003585	5480.G8B8J6	0	1613	28K46@1 root,2QSIQ@2759 Eukary	4751 Fungi	U	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00 3.4.19.12
OG0003679	5551.XP_003235838.1	0	1040	COG0705@1 root,KOG2980@2759	4751 Fungi	U	Rhomboid family	-	GO:0003674,GO:0003824,GO:00 3.4.21.105
OG0003679	5551.XP_003235838.1	0	1040	COG0705@1 root,KOG2980@2759	4751 Fungi	U	Rhomboid family	-	GO:0003674,GO:0003824,GO:00 3.4.21.105
OG0003715	63402.XP_003175727.1	0	863	KOG2605@1 root,KOG2605@2759	4751 Fungi	OT	OTU-like cysteine protease	-	- 3.4.19.12
OG0003715	63402.XP_003175727.1	0	863	KOG2605@1 root,KOG2605@2759	4751 Fungi	OT	OTU-like cysteine protease	-	- 3.4.19.12
OG0003729	63418.F2Q2W8	3.19E-245	690	COG2828@1 root,KOG3246@2759	4751 Fungi	S	Ulp1 protease family, C-terminal catalytic domain	-	GO:0000338,GO:0003674,GO:00 3.4.22.68
OG0003729	63418.F2Q2W8	3.19E-245	690	COG2828@1 root,KOG3246@2759	4751 Fungi	S	Ulp1 protease family, C-terminal catalytic domain	-	GO:0000338,GO:0003674,GO:00 3.4.22.68
OG0003747	63402.XP_003173289.1	0	997	COG3579@1 root,KOG4128@2759	4751 Fungi	E	Papain family cysteine protease	LAP3	GO:0000096,GO:0000098,GO:00 3.4.22.40
OG0003747	63402.XP_003173289.1	0	997	COG3579@1 root,KOG4128@2759	4751 Fungi	E	Papain family cysteine protease	LAP3	GO:0000096,GO:0000098,GO:00 3.4.22.40
OG0003814	83344.XP_007929348.1	0	1025	COG4934@1 root,2QTN1@2759 Eu	4751 Fungi	E	Pro-kumamolisin, activation domain	-	- 3.4.14.9
OG0003814	83344.XP_007929348.1	0	1025	COG4934@1 root,2QTN1@2759 Eu	4751 Fungi	E	Pro-kumamolisin, activation domain	-	- 3.4.14.9
OG0004026	63405.XP_002846715.1	0	4907	COG5077@1 root,KOG1866@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	- 3.4.19.12
OG0004026	63405.XP_002846715.1	0	4907	COG5077@1 root,KOG1866@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	- 3.4.19.12
OG0004156	430998.XP_007672752.1	3.88E-149	446	KOG2778@1 root,KOG2778@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	- 3.4.19.12

OG0004156	430998.XP_007672752.1	3.88E-149	446	KOG2778@1 root,KOG2778@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	-	3.4.19.12
OG0004156	430998.XP_007672752.1	3.88E-149	446	KOG2778@1 root,KOG2778@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	-	3.4.19.12
OG0004588	63400.XP_003017015.1	2.59E-295	806	COG1446@1 root,KOG1592@2759	4751 Fungi	E	Asparaginase	-	-	3.4.19.5,3.5.1.1
OG0004588	63400.XP_003017015.1	2.59E-295	806	COG1446@1 root,KOG1592@2759	4751 Fungi	E	Asparaginase	-	-	3.4.19.5,3.5.1.1
OG0004976	83344.XP_007923374.1	3.34E-169	498	COG0006@1 root,KOG2737@2759	4751 Fungi	E	Aminopeptidase P, N-terminal domain	PEPP	-	3.4.13.9
OG0004976	83344.XP_007923374.1	3.34E-169	498	COG0006@1 root,KOG2737@2759	4751 Fungi	E	Aminopeptidase P, N-terminal domain	PEPP	-	3.4.13.9
OG0004976	83344.XP_007923374.1	3.34E-169	498	COG0006@1 root,KOG2737@2759	4751 Fungi	E	Aminopeptidase P, N-terminal domain	PEPP	-	3.4.13.9
OG0005002	63402.XP_003174780.1	0	1211	COG2939@1 root,KOG1282@2759	4751 Fungi	EO	Belongs to the peptidase S10 family	-	-	3.4.16.6
OG0005002	63402.XP_003174780.1	0	1211	COG2939@1 root,KOG1282@2759	4751 Fungi	EO	Belongs to the peptidase S10 family	-	-	3.4.16.6
OG0005246	63402.XP_003169234.1	3.11E-161	455	COG2039@1 root,KOG4755@2759	4751 Fungi	O	Pyroglutamyl peptidase	-	-	3.4.19.3
OG0005246	63402.XP_003169234.1	3.11E-161	455	COG2039@1 root,KOG4755@2759	4751 Fungi	O	Pyroglutamyl peptidase	-	-	3.4.19.3
OG0006055	63418.F2Q0Z3	0	1516	COG5077@1 root,KOG1863@2759	4751 Fungi	O	ICP0-binding domain of Ubiquitin-specific protease 7	UBP15	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0006055	63418.F2Q0Z3	0	1516	COG5077@1 root,KOG1863@2759	4751 Fungi	O	ICP0-binding domain of Ubiquitin-specific protease 7	UBP15	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0006173	82508.K1VCQ7	0	1335	COG3590@1 root,KOG3624@2759	4751 Fungi	E	Endothelin-converting enzyme 1	-	-	3.4.24.71
OG0006366	5480.G8BIL3	0	884	COG0385@1 root,KOG4821@2759	4751 Fungi	S	SBF-like CPA transporter family (DUF4137)	RCH1	GO:0003674,GO:0005215,GO:00	3.4.25.1
OG0006513	82508.K1WDX7	7.07E-266	748	COG0260@1 root,KOG2597@2759	4751 Fungi	E	leucine aminopeptidase	-	-	GO:0003674,GO:0003824,GO:00 3.4.11.1,3.4.11.5
OG0006513	82508.K1WDX7	7.07E-266	748	COG0260@1 root,KOG2597@2759	4751 Fungi	E	leucine aminopeptidase	-	-	GO:0003674,GO:0003824,GO:00 3.4.11.1,3.4.11.5
OG0006513	82508.K1WDX7	7.07E-266	748	COG0260@1 root,KOG2597@2759	4751 Fungi	E	leucine aminopeptidase	-	-	GO:0003674,GO:0003824,GO:00 3.4.11.1,3.4.11.5
OG0006693	1392244.V5GME1	0	918	COG1505@1 root,KOG2237@2759	4751 Fungi	O	Prolyl oligopeptidase, N-terminal beta-propeller dom	-	-	3.4.21.26
OG0006693	1392244.V5GME1	0	918	COG1505@1 root,KOG2237@2759	4751 Fungi	O	Prolyl oligopeptidase, N-terminal beta-propeller dom	-	-	3.4.21.26
OG0006827	63400.XP_003010393.1	2.41E-304	831	COG2355@1 root,KOG4127@2759	4751 Fungi	O	Belongs to the metallo-dependent hydrolases superfa	-	GO:0008150,GO:0008152,GO:00	3.4.13.19
OG0006827	63400.XP_003010393.1	2.41E-304	831	COG2355@1 root,KOG4127@2759	4751 Fungi	O	Belongs to the metallo-dependent hydrolases superfa	-	GO:0008150,GO:0008152,GO:00	3.4.13.19
OG0006980	5478.XP_447088.1	0	2093	KOG1868@1 root,KOG1868@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0006980	5478.XP_447088.1	0	2093	KOG1868@1 root,KOG1868@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0006980	5478.XP_447088.1	0	2093	KOG1868@1 root,KOG1868@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0007061	82508.K1W9S1	0	875	COG0750@1 root,KOG2921@2759	4751 Fungi	O	Peptidase family M50	-	-	3.4.24.85
OG0007313	72558.CBQ67928	0	1197	COG1404@1 root,KOG1114@2759	4751 Fungi	O	Tripeptidyl peptidase II	-	GO:0003674,GO:0003824,GO:00	3.4.14.10
OG0007313	72558.CBQ67928	0	1197	COG1404@1 root,KOG1114@2759	4751 Fungi	O	Tripeptidyl peptidase II	-	GO:0003674,GO:0003824,GO:00	3.4.14.10
OG0007443	82508.K1VN39	2.26E-82	258	COG0705@1 root,KOG2980@2759	4751 Fungi	T	Rhomboid family	-	-	3.4.21.105
OG0007443	82508.K1VN39	2.26E-82	258	COG0705@1 root,KOG2980@2759	4751 Fungi	T	Rhomboid family	-	-	3.4.21.105
OG0007503	101852.XP_008082346.1	9.5E-118	355	COG3191@1 root,2QRNQ@2759	El 4751 Fungi	EQ	peptidase family	-	-	3.4.11.19
OG0007503	101852.XP_008082346.1	9.5E-118	355	COG3191@1 root,2QRNQ@2759	El 4751 Fungi	EQ	peptidase family	-	-	3.4.11.19
OG0007559	63418.F2PYE7	3.56E-138	403	COG3579@1 root,KOG4128@2759	4751 Fungi	E	Papain family cysteine protease	LAP3	GO:0000096,GO:0000098,GO:00	3.4.22.40
OG0007559	63418.F2PYE7	3.56E-138	403	COG3579@1 root,KOG4128@2759	4751 Fungi	E	Papain family cysteine protease	LAP3	GO:0000096,GO:0000098,GO:00	3.4.22.40
OG0007942	82508.K1VNS3	5.69E-148	426	COG0705@1 root,KOG2980@2759	4751 Fungi	T	Rhomboid family	-	-	3.4.21.105
OG0007942	82508.K1VNS3	5.69E-148	426	COG0705@1 root,KOG2980@2759	4751 Fungi	T	Rhomboid family	-	-	3.4.21.105
OG0008677	63405.XP_002848625.1	0	1355	28SEW@1 root,2QZ4I@2759	Eukar 4751 Fungi	G	Pro-kumamolisin, activation domain	-	-	3.4.14.9
OG0008677	63405.XP_002848625.1	0	1355	28SEW@1 root,2QZ4I@2759	Eukar 4751 Fungi	G	Pro-kumamolisin, activation domain	-	-	3.4.14.9
OG0008996	5482.XP_002547785.1	8.81E-166	501	COG5077@1 root,KOG1863@2759	4751 Fungi	O	Belongs to the peptidase C19 family	UBP15	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0009388	5480.G8B7S5	0	1795	COG2234@1 root,KOG2195@2759	4751 Fungi	OP	Belongs to the peptidase M28 family	-	GO:0005575,GO:0005622,GO:00	3.4.17.21
OG0009388	5480.G8B7S5	0	1795	COG2234@1 root,KOG2195@2759	4751 Fungi	OP	Belongs to the peptidase M28 family	-	GO:0005575,GO:0005622,GO:00	3.4.17.21
OG0009688	42374.XP_002419203.1	2.1E-277	763	KOG1674@1 root,KOG1674@2759	4751 Fungi	S	Cyclin	-	-	3.4.13.9
OG0009969	5478.XP_448611.1	0	1569	COG2234@1 root,KOG2195@2759	4751 Fungi	OP	to Saccharomyces cerevisiae TRE2 (YOR256C) and TRI	-	GO:0000322,GO:0000323,GO:00	3.4.17.21
OG0009969	5478.XP_448611.1	0	1569	COG2234@1 root,KOG2195@2759	4751 Fungi	OP	to Saccharomyces cerevisiae TRE2 (YOR256C) and TRI	-	GO:0000322,GO:0000323,GO:00	3.4.17.21
OG0009969	5478.XP_448611.1	0	1569	COG2234@1 root,KOG2195@2759	4751 Fungi	OP	to Saccharomyces cerevisiae TRE2 (YOR256C) and TRI	-	GO:0000322,GO:0000323,GO:00	3.4.17.21
OG0010107	82508.K1WIS9	0	935	COG5077@1 root,KOG1863@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	-	3.4.19.12
OG0010107	82508.K1WIS9	0	935	COG5077@1 root,KOG1863@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	-	3.4.19.12
OG0010107	82508.K1WIS9	0	935	COG5077@1 root,KOG1863@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	-	3.4.19.12
OG0010594	430998.XP_007676575.1	3.12E-45	174	KOG1865@1 root,KOG1865@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	-	3.4.19.12
OG0010594	430998.XP_007676575.1	3.12E-45	174	KOG1865@1 root,KOG1865@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	-	3.4.19.12
OG0011049	160860.XP_007353564.1	4.02E-25	116	COG0501@1 root,KOG2719@2759	4751 Fungi	O	CAAX prenyl protease N-terminal, five membrane hel	STE24	GO:0003674,GO:0003824,GO:00	3.4.24.84
OG0011099	63405.XP_002846325.1	3.65E-147	455	COG5560@1 root,KOG1870@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0011248	82508.K1VCS3	0	882	COG0006@1 root,KOG2413@2759	4751 Fungi	E	Creatinase/Prolidase N-terminal domain	-	-	3.4.11.9
OG0011248	82508.K1VCS3	0	882	COG0006@1 root,KOG2413@2759	4751 Fungi	E	Creatinase/Prolidase N-terminal domain	-	-	3.4.11.9
OG0011248	82508.K1VCS3	0	882	COG0006@1 root,KOG2413@2759	4751 Fungi	E	Creatinase/Prolidase N-terminal domain	-	-	3.4.11.9
OG0011248	82508.K1VCS3	0	882	COG0006@1 root,KOG2413@2759	4751 Fungi	E	Creatinase/Prolidase N-terminal domain	-	-	3.4.11.9
OG0012337	84751.XP_007881177.1	4.26E-28	117	KOG1868@1 root,KOG1868@2759	4751 Fungi	O	USP8 dimerisation domain	DOA4	GO:0000131,GO:0000502,GO:00	3.4.19.12
OG0012985	82508.K1WDN2	0	897	2CXKC@1 root,2RY6I@2759	Eukary 4751 Fungi	-	-	-	-	3.4.25.1
OG0013519	82508.K1VKP1	4.5E-166	498	COG5560@1 root,KOG1873@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	-	3.4.19.12

OG0013519	82508.K1VKP1	4.5E-166	498	COG5560@1 root,KOG1873@2759	4751 Fungi	O	Ubiquitin carboxyl-terminal hydrolase	-	-	3.4.19.12
OG0014075	28564.XP_002481148.1	2.33E-75	255	COG0339@1 root,KOG2089@2759	4751 Fungi	O	Peptidase family M3	PRD1	GO:0000322,GO:0000323,GO:00	3.4.24.37
OG0014244	83344.XP_007920930.1	3.93E-34	132	COG1404@1 root,KOG1153@2759	4751 Fungi	O	Belongs to the peptidase S8 family	-	-	3.4.21.48
OG0014244	83344.XP_007920930.1	3.93E-34	132	COG1404@1 root,KOG1153@2759	4751 Fungi	O	Belongs to the peptidase S8 family	-	-	3.4.21.48
OG0014589	1047171.Mycgr3P104550	2.37E-101	306	KOG1674@1 root,KOG1674@2759	4751 Fungi	S	Cyclin	-	-	3.4.13.9
OG0014589	1047171.Mycgr3P104550	2.37E-101	306	KOG1674@1 root,KOG1674@2759	4751 Fungi	S	Cyclin	-	-	3.4.13.9
OG0014646	120017.I2G000	7.63E-11	71.6	COG5077@1 root,KOG1863@2759	4751 Fungi	O	A repeated domain in UCH-protein	UBP2	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0015950	82508.K1WG46	1.9E-114	337	COG0024@1 root,KOG2738@2759	4751 Fungi	O	Removes the N-terminal methionine from nascent pri	-	-	3.4.11.18
OG0016220	83344.XP_007928201.1	1.18E-22	107	KOG1339@1 root,KOG1339@2759	4751 Fungi	O	Belongs to the peptidase A1 family	APR1	GO:0000322,GO:0000323,GO:00	3.4.23.25
OG0016220	83344.XP_007928201.1	1.18E-22	107	KOG1339@1 root,KOG1339@2759	4751 Fungi	O	Belongs to the peptidase A1 family	APR1	GO:0000322,GO:0000323,GO:00	3.4.23.25
OG0016397	82508.K1VCS3	0	869	COG0006@1 root,KOG2413@2759	4751 Fungi	E	Creatinase/Prolidase N-terminal domain	-	-	3.4.11.9
OG0016397	82508.K1VCS3	0	869	COG0006@1 root,KOG2413@2759	4751 Fungi	E	Creatinase/Prolidase N-terminal domain	-	-	3.4.11.9
OG0016397	82508.K1VCS3	0	869	COG0006@1 root,KOG2413@2759	4751 Fungi	E	Creatinase/Prolidase N-terminal domain	-	-	3.4.11.9
OG0017431	430998.XP_007677788.1	7.62E-32	126	COG1404@1 root,KOG3525@2759	4751 Fungi	O	Belongs to the peptidase S8 family	KEX2	GO:0000139,GO:0000322,GO:00	3.4.21.61
OG0017831	84751.XP_007877016.1	8.51E-06	53.5	COG5077@1 root,KOG1863@2759	4751 Fungi	O	A repeated domain in UCH-protein	UBP2	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0017839	84751.XP_007882239.1	0.000198	54.3	COG5155@1 root,KOG1849@2759	4751 Fungi	D	Peptidase family C50	ESP1	GO:0000003,GO:0000070,GO:00	3.4.22.49
OG0017906	51453.EGR47517	3.06E-12	72.4	KOG1868@1 root,KOG1868@2759	4751 Fungi	O	Rhodanese Homology Domain	DOA4	GO:0000131,GO:0000502,GO:00	3.4.19.12
OG0018281	4909.A0A099NW18	5.81E-288	821	COG0339@1 root,KOG2090@2759	4751 Fungi	O	Cleaves proteins, imported into the mitochondrion, tr	OCT1	GO:0003674,GO:0003824,GO:00	3.4.24.59
OG0018293	4909.A0A099P1Q3	1.2E-199	586	KOG0126@1 root,KOG1868@1 root	4751 Fungi	O	Belongs to the peptidase C19 family	DOA4	GO:0000131,GO:0000502,GO:00	3.4.19.12
OG0018369	4909.A0A099P8Z7	6.52E-93	290	KOG1868@1 root,KOG1868@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0018369	4909.A0A099P8Z7	6.52E-93	290	KOG1868@1 root,KOG1868@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0018818	4909.A0A099P8Z7	7.83E-110	342	KOG1868@1 root,KOG1868@2759	4751 Fungi	O	Belongs to the peptidase C19 family	-	GO:0003674,GO:0003824,GO:00	3.4.19.12
OG0018860	4909.A0A099P550	2.31E-99	308	COG2260@1 root,KOG3675@1 root	4751 Fungi	O	Belongs to the peptidase M49 family	YOL057W	GO:0003674,GO:0003824,GO:00	3.4.14.4
OG0018965	4909.A0A099NY23	4.34E-85	275	COG0466@1 root,KOG2004@2759	4751 Fungi	O	ATP-dependent serine protease that mediates the sel	-	GO:0005575,GO:0005622,GO:00	3.4.21.53
OG0019284	263815.XP_007874215.1	0.000201	47.8	COG0501@1 root,KOG2719@2759	4751 Fungi	O	CAAX prenyl protease N-terminal, five membrane hel	STE24	GO:0003674,GO:0003824,GO:00	3.4.24.84
OG0019406	5551.XP_003235282.1	2.38E-27	108	COG1404@1 root,KOG1153@2759	4751 Fungi	O	Secreted subtilisin-like serine protease with keratinol	PRB1	GO:0000003,GO:0000322,GO:00	3.4.21.48

KEGG ko	KEGG Pathway	KEGG Module	KEGG Reaction	KEGG rclass	BRITE	KEGG TC	CAZy	BiGG Reaction
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ko:K01415	-	-	-	-	ko00000,ko01000,ko01002,ko04147	-	-	-
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ko:K01381	ko04138,map04138	-	-	-	ko00000,ko00001,ko01000,ko01002	-	-	-
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PFAMs	IPR term	IPR description	Blastocladiella emersonii 22665	Candida dubliniensis 11945	Candida dubliniensis 2747
Asp	IPR001461	Aspartic peptidase A1	1	6	6
Asp	IPR021109	Aspartic peptidase domain superfamily	1	6	6
Asp	IPR021109	Aspartic peptidase domain superfamily	1	6	6
Asp	IPR035427	Tim10-like domain superfamily	1	6	6
Peptidase_M28	IPR037737	Regulator of phospholipase D Srf1	0	1	1
ERAP1_C,Peptidase_M1	IPR050344	Peptidase M1 family aminopeptidases	4	1	1
ERAP1_C,Peptidase_M1	IPR042097	Aminopeptidase N-like , N-terminal domain superfam	4	1	1
PA,Peptidase_M28,TFR_dimer	IPR039373	Transferrin receptor protein 1/Glutamate carboxypep	0	2	2
PA,Peptidase_M28,TFR_dimer	IPR036757	Transferrin receptor-like, dimerisation domain superf	0	2	2
PA,Peptidase_M28,TFR_dimer	IPR046450	PA domain superfamily	0	2	2
DUSP,UCH	IPR036871	PX domain superfamily	2	3	2
DUSP,UCH	IPR038765	Papain-like cysteine peptidase superfamily	2	3	2
DUSP,UCH	IPR035927	DUSP-like superfamily	2	3	2
DUSP,UCH	IPR051079	Sorting Nexin Autophagy-related	2	3	2
AAA,LON_substr_bdg,Lon_C	IPR036291	NAD(P)-binding domain superfamily	2	2	2
AAA,LON_substr_bdg,Lon_C	IPR027065	Lon protease	2	2	2
AAA,LON_substr_bdg,Lon_C	IPR027417	P-loop containing nucleoside triphosphate hydrolase	2	2	2
AAA,LON_substr_bdg,Lon_C	IPR027503	Lon protease homologue, chloroplastic/mitochondria	2	2	2
AAA,LON_substr_bdg,Lon_C	IPR029069	HotDog domain superfamily	2	2	2
AAA,LON_substr_bdg,Lon_C	IPR029069	HotDog domain superfamily	2	2	2
AAA,LON_substr_bdg,Lon_C	IPR020568	Ribosomal protein uS5 domain 2-type superfamily	2	2	2
AAA,LON_substr_bdg,Lon_C	IPR015947	PUA-like superfamily	2	2	2
Peptidase_M18	IPR001948	Peptidase M18	1	3	3
Peptidase_C12	IPR038765	Papain-like cysteine peptidase superfamily	2	1	1
Peptidase_C12	IPR001578	Peptidase C12, ubiquitin carboxyl-terminal hydrolase	2	1	1
UCH	IPR038765	Papain-like cysteine peptidase superfamily	2	2	2
UCH	IPR050164	Ubiquitin carboxyl-terminal hydrolases	2	2	2
Peptidase_S8,Pro-kuma_activ	IPR036852	Peptidase S8/S53 domain superfamily	0	0	0
Peptidase_S8,Pro-kuma_activ	IPR050819	Tripeptidyl-peptidase I and related peptidases	0	0	0
OTU	IPR052786	Outer_spore_wall_assembly	1	1	1
OTU	IPR038765	Papain-like cysteine peptidase superfamily	1	1	1
Peptidase_M24	IPR036005	Creatinase/aminopeptidase-like	1	1	1
Peptidase_M24	IPR036390	Winged helix DNA-binding domain superfamily	1	1	1
Peptidase_M24	IPR036188	FAD/NAD(P)-binding domain superfamily	1	1	1
Peptidase_M24	IPR050247	Methionine Aminopeptidase Type 2	1	1	1
Peptidase_M24	IPR002468	Peptidase M24A, methionine aminopeptidase, subfar	1	1	1
P_proprotein,Peptidase_S8	IPR008979	Galactose-binding-like domain superfamily	2	1	1
P_proprotein,Peptidase_S8	IPR036852	Peptidase S8/S53 domain superfamily	2	1	1
Creatinase_N,Creatinase_N_2,Peptid:	IPR050422	Xaa-Pro aminopeptidase P	1	2	1
Creatinase_N,Creatinase_N_2,Peptid:	IPR029149	Creatinase/Aminopeptidase P/Spt16, N-terminal	1	2	1
Creatinase_N,Creatinase_N_2,Peptid:	IPR036005	Creatinase/aminopeptidase-like	1	2	1
Sec8_exocyst	IPR039682	Exocyst complex component Sec8/EXOC4	1	1	1
Inhibitor_I9,Peptidase_S8	IPR050131	Subtilisin-like serine protease	2	2	2
Inhibitor_I9,Peptidase_S8	IPR036852	Peptidase S8/S53 domain superfamily	2	2	2
RPT,UCH	IPR038765	Papain-like cysteine peptidase superfamily	0	1	1
RPT,UCH	IPR044635	Ubiquitin carboxyl-terminal hydrolase 14-like	0	1	1
Peptidase_C50	IPR005314	Peptidase C50, separate	3	1	2
Peptidase_M16,Peptidase_M16_C	IPR050361	Mitochondrial Processing Peptidase/Ubiquinol-cytoch	1	2	1
Peptidase_M16,Peptidase_M16_C	IPR011249	Metalloenzyme, LuxS/M16 peptidase-like	1	2	1
Peptidase_M16,Peptidase_M16_C	IPR011249	Metalloenzyme, LuxS/M16 peptidase-like	1	2	1
MATH,UCH,USP7_C2,USP7_ICP0_bdg	IPR038765	Papain-like cysteine peptidase superfamily	1	1	1
MATH,UCH,USP7_C2,USP7_ICP0_bdg	IPR050164	Ubiquitin carboxyl-terminal hydrolases	1	1	1
Peptidase_M16,Peptidase_M16_C,Pe	IPR050626	Peptidase M16	3	1	1
Peptidase_M16,Peptidase_M16_C,Pe	IPR011249	Metalloenzyme, LuxS/M16 peptidase-like	3	1	1
Peptidase_M16,Peptidase_M16_C,Pe	IPR011249	Metalloenzyme, LuxS/M16 peptidase-like	3	1	1
Peptidase_M16,Peptidase_M16_C,Pe	IPR011249	Metalloenzyme, LuxS/M16 peptidase-like	3	1	1
Peptidase_M16,Peptidase_M16_C,Pe	IPR011249	Metalloenzyme, LuxS/M16 peptidase-like	3	1	1
Peptidase_M24	IPR036390	Winged helix DNA-binding domain superfamily	1	2	1
Peptidase_M24	IPR036005	Creatinase/aminopeptidase-like	1	2	1

Peptidase_M24	IPR047113	Proliferation-associated protein 2G4/ARX1	1	2	1
M20_dimer,Peptidase_M20,Peptidase_M20	IPR036264	Bacterial exopeptidase dimerisation domain	1	2	2
M20_dimer,Peptidase_M20,Peptidase_M20	IPR036264	Bacterial exopeptidase dimerisation domain	1	2	2
M20_dimer,Peptidase_M20,Peptidase_M20	IPR047177	Peptidase M20A	1	2	2
Peptidase_M19	IPR008257	Peptidase M19	0	0	0
Peptidase_M19	IPR032466	Metal-dependent hydrolase	0	0	0
UCH	IPR038765	Papain-like cysteine peptidase superfamily	1	1	1
UCH	IPR050164	Ubiquitin carboxyl-terminal hydrolases	1	1	1
Rhodanese,UCH,USP8_dimer	IPR050185	Ubiquitin carboxyl-terminal hydrolase	2	1	1
Rhodanese,UCH,USP8_dimer	IPR038765	Papain-like cysteine peptidase superfamily	2	1	1
Rhodanese,UCH,USP8_dimer	IPR036873	Rhodanese-like domain superfamily	2	1	1
UCH,ubiquitin	IPR038765	Papain-like cysteine peptidase superfamily	1	1	1
UCH,ubiquitin	IPR044635	Ubiquitin carboxyl-terminal hydrolase 14-like	1	1	1
UCH,ubiquitin	IPR029071	Ubiquitin-like domain superfamily	1	1	1
UCH,ubiquitin	IPR029069	HotDog domain superfamily	1	1	1
Asp	IPR021109	Aspartic peptidase domain superfamily	1	2	2
Asp	IPR021109	Aspartic peptidase domain superfamily	1	2	2
Asp	IPR035427	Tim10-like domain superfamily	1	2	2
Asp	IPR001461	Aspartic peptidase A1	1	2	2
Peptidase_C48	IPR038765	Papain-like cysteine peptidase superfamily	2	1	0
Proteasome	IPR023333	Proteasome B-type subunit	1	1	1
Proteasome	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
Proteasome	IPR023333	Proteasome B-type subunit	1	1	1
Proteasome	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
Peptidase_M49	IPR011333	SKP1/BTB/POZ domain superfamily	1	1	1
Pr_beta_C,Proteasome	IPR050446	FAD-dependent Oxidoreductases and Apoptosis Regu	1	1	1
Pr_beta_C,Proteasome	IPR036188	FAD/NAD(P)-binding domain superfamily	1	1	1
Pr_beta_C,Proteasome	IPR036922	Rieske [2Fe-2S] iron-sulphur domain superfamily	1	1	1
Pr_beta_C,Proteasome	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
Pr_beta_C,Proteasome	IPR016156	FAD/NAD-linked reductase, dimerisation domain superfamily	1	1	1
Pr_beta_C,Proteasome	IPR036188	FAD/NAD(P)-binding domain superfamily	1	1	1
OTU	IPR050704	Peptidase C85-like	2	1	1
OTU	IPR038765	Papain-like cysteine peptidase superfamily	2	1	1
UCH	IPR038765	Papain-like cysteine peptidase superfamily	1	1	1
UCH	IPR050164	Ubiquitin carboxyl-terminal hydrolases	1	1	1
Peptidase_S10	IPR029058	Alpha/Beta hydrolase fold	2	1	1
Peptidase_S10	IPR001563	Peptidase S10, serine carboxypeptidase	2	1	1
Peptidase_C48	IPR038765	Papain-like cysteine peptidase superfamily	1	1	1
Peptidase_C48	IPR023398	Translation Initiation factor eIF- 4e-like	1	1	1
Peptidase_C48	IPR051947	Sentrin-specific protease	1	1	1
Proteasome,Proteasome_A_N	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
Proteasome,Proteasome_A_N	IPR050115	Proteasome subunit alpha	1	1	1
UCH	IPR050164	Ubiquitin carboxyl-terminal hydrolases	1	1	1
UCH	IPR038765	Papain-like cysteine peptidase superfamily	1	1	1
UCH	IPR035979	RNA-binding domain superfamily	1	1	1
UCH	IPR036867	R3H domain superfamily	1	1	1
FACT-Spt16_Nlob,Peptidase_M24,Rtt	IPR036005	Creatinase/aminopeptidase-like	1	1	1
FACT-Spt16_Nlob,Peptidase_M24,Rtt	IPR040258	FACT complex subunit Spt16	1	1	1
Proteasome,Proteasome_A_N	IPR050115	Proteasome subunit alpha	1	1	1
Proteasome,Proteasome_A_N	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
Proteasome,Proteasome_A_N	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
Proteasome,Proteasome_A_N	IPR050115	Proteasome subunit alpha	1	1	1
UBA,UCH,UCH_1,zf-UBP	IPR038765	Papain-like cysteine peptidase superfamily	1	1	1
UBA,UCH,UCH_1,zf-UBP	IPR009060	UBA-like superfamily	1	1	1
UBA,UCH,UCH_1,zf-UBP	IPR001837	Adenylate cyclase-associated CAP	1	1	1
UBA,UCH,UCH_1,zf-UBP	IPR036223	Adenylate cyclase-associated CAP, C-terminal superfamily	1	1	1
Proteasome	IPR023333	Proteasome B-type subunit	1	1	1
Proteasome	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
Proteasome,Proteasome_A_N	IPR050115	Proteasome subunit alpha	1	1	0

Proteasome,Proteasome_A_N	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	0
Proteasome,Proteasome_A_N	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
Proteasome,Proteasome_A_N	IPR050115	Proteasome subunit alpha	1	1	1
Proteasome	IPR023333	Proteasome B-type subunit	1	1	1
Proteasome	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
Peptidase_M3	IPR036249	Thioredoxin-like superfamily	1	1	1
Peptidase_M3	IPR045090	Peptidase M3A/M3B	1	1	1
Asp	IPR021109	Aspartic peptidase domain superfamily	1	1	1
Asp	IPR001461	Aspartic peptidase A1	1	1	1
Peptidase_M16,Peptidase_M16_C	IPR011249	Metalloenzyme, LuxS/M16 peptidase-like	0	0	0
Peptidase_M16,Peptidase_M16_C	IPR050361	Mitochondrial Processing Peptidase/Ubiquinol-cytof	0	0	0
Peptidase_M16,Peptidase_M16_C	IPR011249	Metalloenzyme, LuxS/M16 peptidase-like	0	0	0
Proteasome	IPR050115	Proteasome subunit alpha	1	1	1
Proteasome	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
Proteasome,Proteasome_A_N	IPR050115	Proteasome subunit alpha	1	1	0
Proteasome,Proteasome_A_N	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	0
Peptidase_S24	IPR001733	Peptidase S26B	1	1	1
Proteasome,Proteasome_A_N	IPR050115	Proteasome subunit alpha	1	1	1
Proteasome,Proteasome_A_N	IPR029055	Nucleophile aminohydrolases, N-terminal	1	1	1
AMP_N,Peptidase_M24	IPR029149	Creatinase/Aminopeptidase P/Spt16, N-terminal	1	1	0
AMP_N,Peptidase_M24	IPR052433	Xaa-Pro dipeptidase-like	1	1	0
AMP_N,Peptidase_M24	IPR036005	Creatinase/aminopeptidase-like	1	1	0
AMP_N,Peptidase_M24	IPR036005	Creatinase/aminopeptidase-like	1	1	0
Peptidase_M3	IPR027417	P-loop containing nucleoside triphosphate hydrolase	4	1	1
Peptidase_M3	IPR045090	Peptidase M3A/M3B	4	1	1
Peptidase_M3	IPR036770	Ankyrin repeat-containing domain superfamily	4	1	1
UCH	IPR050164	Ubiquitin carboxyl-terminal hydrolases	1	0	0
UCH	IPR038765	Papain-like cysteine peptidase superfamily	1	0	0
UBA,UCH,UCH_1,zf-UBP	IPR006084	XPG/Rad2 endonuclease	0	1	1
UBA,UCH,UCH_1,zf-UBP	IPR029060	PIN-like domain superfamily	0	1	1
Peptidase_C65	IPR038765	Papain-like cysteine peptidase superfamily	1	0	0
Peptidase_M49	IPR039461	Peptidase family M49	0	1	0
JAB,USP8_dimer			1	0	0
Peptidase_M24	IPR036005	Creatinase/aminopeptidase-like	1	0	0
Peptidase_M24	IPR029052	Metallo-dependent phosphatase-like	1	0	0
Peptidase_M24	IPR000979	Phosphodiesterase MJ0936/Vps29	1	0	0
GPI2	IPR029058	Alpha/Beta hydrolase fold	3	0	1
GPI2	IPR009450	Phosphatidylinositol N-acetylglucosaminyltransferase	3	0	1
Peptidase_C12	IPR038765	Papain-like cysteine peptidase superfamily	1	1	1
Peptidase_C12	IPR001578	Peptidase C12, ubiquitin carboxyl-terminal hydrolase	1	1	1
Abhydrolase_1	IPR051601	Serine protease/Carboxylesterase S33	0	1	1
Abhydrolase_1	IPR029058	Alpha/Beta hydrolase fold	0	1	1
Abhydrolase_1,Abhydrolase_4	IPR029058	Alpha/Beta hydrolase fold	1	0	0
Abhydrolase_1,Abhydrolase_4	IPR005944	Proline iminopeptidase	1	0	0
UCH	IPR050164	Ubiquitin carboxyl-terminal hydrolases	0	1	1
UCH	IPR038765	Papain-like cysteine peptidase superfamily	0	1	1
Rhomboid	IPR050925	Rhomboid protease S54	0	1	1
Rhomboid	IPR035952	Rhomboid-like superfamily	0	1	1
OTU	IPR038765	Papain-like cysteine peptidase superfamily	0	0	0
OTU	IPR050704	Peptidase C85-like	0	0	0
Peptidase_C48	IPR007400	PrpF-like	1	1	1
Peptidase_C48	IPR038765	Papain-like cysteine peptidase superfamily	1	1	1
Peptidase_C1_2	IPR038765	Papain-like cysteine peptidase superfamily	0	1	1
Peptidase_C1_2	IPR004134	Peptidase C1B, bleomycin hydrolase	0	1	1
Pro-kuma_activ	IPR050819	Tripeptidyl-peptidase I and related peptidases	1	0	0
Pro-kuma_activ	IPR036852	Peptidase S8/S53 domain superfamily	1	0	0
DUF3517,UCH	IPR051143	TrkH Potassium Transport	0	0	0
DUF3517,UCH	IPR038765	Papain-like cysteine peptidase superfamily	0	0	0
Peptidase_C12	IPR038765	Papain-like cysteine peptidase superfamily	0	0	0

Peptidase_C12	IPR001578	Peptidase C12, ubiquitin carboxyl-terminal hydrolase	0	0	0
Peptidase_C12	IPR038765	Papain-like cysteine peptidase superfamily	0	0	0
Asparaginase_2	IPR029055	Nucleophile aminohydrolases, N-terminal	1	0	0
Asparaginase_2	IPR000246	Peptidase T2, asparaginase 2	1	0	0
AMP_N,Peptidase_M24	IPR036005	Creatinase/aminopeptidase-like	0	0	0
AMP_N,Peptidase_M24	IPR052433	Xaa-Pro dipeptidase-like	0	0	0
AMP_N,Peptidase_M24	IPR029149	Creatinase/Aminopeptidase P/Spt16, N-terminal	0	0	0
Peptidase_S10	IPR029058	Alpha/Beta hydrolase fold	0	0	0
Peptidase_S10	IPR001563	Peptidase S10, serine carboxypeptidase	0	0	0
Peptidase_C15	IPR036440	Peptidase C15, pyroglutamyl peptidase I-like superfar	1	0	0
Peptidase_C15	IPR016125	Peptidase C15, pyroglutamyl peptidase I-like	1	0	0
MATH,UCH,USP7_C2,USP7_ICP0_bdg	IPR038765	Papain-like cysteine peptidase superfamily	0	0	0
MATH,UCH,USP7_C2,USP7_ICP0_bdg	IPR050164	Ubiquitin carboxyl-terminal hydrolases	0	0	0
Peptidase_M13,Peptidase_M13_N	IPR000718	Peptidase M13	2	0	0
SBF_like	IPR016833	Putative sodium bile acid cotransporter	1	1	1
Peptidase_M17,Peptidase_M17_N	IPR023042	Peptidase M17, leucine aminopeptidase	2	0	0
Peptidase_M17,Peptidase_M17_N	IPR043472	Macro domain-like	2	0	0
Peptidase_M17,Peptidase_M17_N	IPR011356	Peptidase M17, leucine aminopeptidase/peptidase B	2	0	0
Peptidase_S9,Peptidase_S9_N	IPR051167	Prolyl oligopeptidase and macrocyclase	6	0	0
Peptidase_S9,Peptidase_S9_N	IPR029058	Alpha/Beta hydrolase fold	6	0	0
Peptidase_M19	IPR008257	Peptidase M19	0	0	0
Peptidase_M19	IPR032466	Metal-dependent hydrolase	0	0	0
UCH	IPR036873	Rhodanese-like domain superfamily	0	1	1
UCH	IPR050185	Ubiquitin carboxyl-terminal hydrolase	0	1	1
UCH	IPR038765	Papain-like cysteine peptidase superfamily	0	1	1
Peptidase_M50	IPR001193	Membrane-bound transcription factor site-2 protease	1	0	0
Peptidase_S8,TPPII	IPR036852	Peptidase S8/S53 domain superfamily	1	0	0
Peptidase_S8,TPPII	IPR050131	Subtilisin-like serine protease	1	0	0
Rhomboid	IPR035952	Rhomboid-like superfamily	1	0	0
Rhomboid	IPR050925	Rhomboid protease S54	1	0	0
Peptidase_S58	IPR016117	ArgI-like domain superfamily	0	0	0
Peptidase_S58	IPR005321	Peptidase S58, DmpA	0	0	0
Peptidase_C1_2	IPR004134	Peptidase C1B, bleomycin hydrolase	0	0	0
Peptidase_C1_2	IPR038765	Papain-like cysteine peptidase superfamily	0	0	0
Rhomboid	IPR050925	Rhomboid protease S54	1	0	0
Rhomboid	IPR035952	Rhomboid-like superfamily	1	0	0
Pro-kuma_activ	IPR036852	Peptidase S8/S53 domain superfamily	0	0	0
Pro-kuma_activ	IPR050819	Tripeptidyl-peptidase I and related peptidases	0	0	0
MATH,UCH,USP7_C2,USP7_ICP0_bdg	IPR050804	MATH and coiled-coil domain-containing protein	0	0	0
PA,Peptidase_M28,TFR_dimer	IPR046450	PA domain superfamily	0	1	1
PA,Peptidase_M28,TFR_dimer	IPR039373	Transferrin receptor protein 1/Glutamate carboxypep	0	1	1
Cyclin			0	1	1
PA,Peptidase_M28,TFR_dimer	IPR036757	Transferrin receptor-like, dimerisation domain superf	0	0	0
PA,Peptidase_M28,TFR_dimer	IPR046450	PA domain superfamily	0	0	0
PA,Peptidase_M28,TFR_dimer	IPR039373	Transferrin receptor protein 1/Glutamate carboxypep	0	0	0
UCH,ubiquitin	IPR050164	Ubiquitin carboxyl-terminal hydrolases	1	0	0
UCH,ubiquitin	IPR038765	Papain-like cysteine peptidase superfamily	1	0	0
UCH,ubiquitin	IPR029071	Ubiquitin-like domain superfamily	1	0	0
UCH	IPR050164	Ubiquitin carboxyl-terminal hydrolases	0	0	0
UCH	IPR038765	Papain-like cysteine peptidase superfamily	0	0	0
Peptidase_M48,Peptidase_M48_N			0	0	0
DUSP,UCH			0	0	0
Creatinase_N,Creatinase_N_2,Peptid: IPR029149		Creatinase/Aminopeptidase P/Spt16, N-terminal	0	0	0
Creatinase_N,Creatinase_N_2,Peptid: IPR050422		Xaa-Pro aminopeptidase P	0	0	0
Creatinase_N,Creatinase_N_2,Peptid: IPR036005		Creatinase/aminopeptidase-like	0	0	0
Creatinase_N,Creatinase_N_2,Peptid: IPR036259		MFS transporter superfamily	0	0	0
Rhodanese,UCH,USP8_dimer			0	0	0
-			0	0	0
UCH,zf-UBP	IPR038765	Papain-like cysteine peptidase superfamily	0	0	0

UCH,zf-UBP	IPR050164	Ubiquitin carboxyl-terminal hydrolases	0	0	0
Peptidase_M3	IPR045090	Peptidase M3A/M3B	0	0	0
Peptidase_S8	IPR050131	Subtilisin-like serine protease	0	0	0
Peptidase_S8	IPR036852	Peptidase S8/S53 domain superfamily	0	0	0
Cyclin	IPR013922	Cyclin PHO80-like	0	0	0
Cyclin	IPR036915	Cyclin-like superfamily	0	0	0
RPT,UCH			0	0	0
Peptidase_M24	IPR036005	Creatinase/aminopeptidase-like	0	0	0
Asp	IPR001461	Aspartic peptidase A1	0	0	0
Asp	IPR021109	Aspartic peptidase domain superfamily	0	0	0
Creatinase_N,Creatinase_N_2,Peptid: IPR036005		Creatinase/aminopeptidase-like	0	0	0
Creatinase_N,Creatinase_N_2,Peptid: IPR029149		Creatinase/Aminopeptidase P/Spt16, N-terminal	0	0	0
Creatinase_N,Creatinase_N_2,Peptid: IPR050422		Xaa-Pro aminopeptidase P	0	0	0
P_proprotein,Peptidase_S8			0	0	0
RPT,UCH	IPR038765	Papain-like cysteine peptidase superfamily	0	0	0
Peptidase_C50			0	0	0
Rhodanese,UCH,USP8_dimer	IPR036873	Rhodanese-like domain superfamily	0	0	0
Peptidase_M3			0	0	0
Rhodanese,UCH,USP8_dimer			0	0	0
UCH	IPR038765	Papain-like cysteine peptidase superfamily	0	0	0
UCH	IPR050164	Ubiquitin carboxyl-terminal hydrolases	0	0	0
UCH			0	0	0
Peptidase_M49	IPR039461	Peptidase family M49	0	0	0
AAA,LON_substr_bdg,Lon_C			0	0	0
Peptidase_M48,Peptidase_M48_N			0	0	0
Inhibitor_I9,Peptidase_S8			0	0	0

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1	0	2	1	2
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1	1	2	1	2
1	1	3	1	2
1	1	3	1	2
1	1	2	1	2

[illegible]

[illegible]

Malassezia furfur 14140-1	Malassezia furfur 14140-2	Malassezia furfur 1878	Malassezia furfur 6000	Malassezia globosa 7705
4	4	9	10	2
4	4	9	10	2
4	4	9	10	2
4	4	9	10	2
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3	3	2	5	1
3	3	2	5	1
3	3	2	5	1
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1	1	2	2	1
2	2	4	5	2
2	2	4	5	2
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