表 2 蛋白质谱鉴定结果

Table 2 Results of protein mass spectrometry

	差异点	登陆号	功能	基因	蛋白量比值	分子量(kD)	等电点	检索分	覆盖率(%)	信号肽
	Spot	Accession	Identification	Gene	Protein ratio	MW-t/g (kD)	pI-t/g	Protein Score	Coverage (%)	Signal peptide
代谢	8	gi|145602874	Serine carboxypeptidase S28	MGG_13765	11.2[a]	61.2/73.8	4.9/4.7	838	61	Y
Metabolism	9	gi|145602874		MGG_13765	S	61.2/71.8	4.9/4.7	997	67	Y
	12	gi|145610386	Glycosyl hydrolase family 7	MGG_02532	2.2[a]	46.6/55.7	5.1/4.9	511	38	Y
	20	gi|39971981	mixed-linked glucanase	MGG_07306	3.7[a]	77.4/88.6	5.3/5.0	285	51	Y
	27	gi|39974523	Glycosyl hydrolases family 16	MGG_00592	S	38.5/37.5	6.3/5.4	413	38	Y
	28	gi|39976459	β-mannase	MGG_05844	0.5[b]	44.7/44.3	5.4/5.3	400	39	Y
催化/信号传导	13	gi|39971041	Carboxylesterase	MGG_02987	0.3[b]	57.3/58.8	4.8/4.8	523	45	N
Catalysis/Signal transduction										
代谢/应激	5	gi|39970863	Eukaryotic aspartyl protease	MGG_02898	2.3[a]	42.5/39.2	6.7/4.7	1020	46	Y
Metabolism/Stress	7	gi|39964139	hypothetical protein	MGG_09818	0.2[b]	48.7/63.7	4.9/4.7	494	55	Y
	14	gi|39973165	Prolyl oligopeptidase family	MGG_07877	2.6[a]	78.6/116.5	4.9/4.8	402	32	Y
	15	gi|39973165		MGG_07877	3.2[a]	78.6/115.1	4.9/4.9	853	24	Y
	21	gi|39973165		MGG_07877	2.5[a]	78.6/116.1	4.9/5.0	638	18	Y
定位	16	gi|145613536	ML domain	MGG_01557	12.4[a]	19.7/17.5	5.1/5.0	351	53	Y
Location										
发育/代谢	30	gi|39968551	Kelch motif	MGG_02368	10.1[a]	70.2/70.5	5.7/6.3	223	55	Y
Development/Metabolism										
防御抗胁迫	26	gi|145610394	PA domain	MGG_02531	2.6[a]	87.4/75.1	5.3/5.3	500	45	Y
Defense of stress										
细胞器官形成/代谢	29	gi|39940016	Hypothetical protein	MGG_05232	12.3[a]	30/26	6.3/6.4	402	42	Y
Cells organ formation/Meta-	10	gi|39946606	Aldose 1-epimerase	MGG_08597	S	35.1/42.5	4.9/4.8	443	72	N
bolism	11	gi|1456101281	Peptidase family	MGG_08758	3.0[a]	53.5/55.6	5.2/4.8	583	48	Y
	22	gi|39952025	WSC domain	MGG_01655	0.3[b]	108.6/124.9	5.1/5.0	734	56	Y
细胞器官形成/代谢/细胞分裂	19	gi|39974697	Beta-glucosidase	MGG_00505	2.2a	44.2/31.3	5.7/5.1	94	36	Y
Cells organ formation/Meta-										
bolism/Cell division										
功能未知	1	gi|39970423	Hypothetical protein	MGG_15022	19.2[a]	14.5/16.4	5.1/4.4	184	61	Y
Unknown	2	gi|145605481	Hypothetical protein	MGG_11750	0.2[b]	35.2/27.2	6.2/4.6	443	45	Y
	3	gi|145611892	Hypothetical protein	MGG_00052	0.5[b]	24.2/31.9	4.9/4.6	625	35	Y

续表 2

Continuing table 2

	差异点	登陆号	功能	基因	蛋白量比值	分子量(kD)	等电点	检索分	覆盖率(%)	信号肽
功能未知	23	gi|39975141	Hypothetical protein	MGG_00283	0.2[b]	16.2/16.9	5.5/5.2	534	28	Y
Unknown	18	gi|39975479	Hypothetical protein	MGG_00114	S	21.4/25.0	5.1/5.1	325	26	N
	24	gi|39969693	Hypothetical protein	MGG_10456	0.5[b]	16.5/18.9	5.8/5.2	384	42	Y

注: 1: 蛋白量比值指 Y98−16 菌株在氮饥饿诱导下分泌蛋白表达量除以全氮培养下分泌蛋白表达量的比值; a 表示比值大于 2 倍且上调的蛋白; b 表示比值小于 0.5 且下调的蛋白; 2: S 表示氮饥饿诱导下特异表达的蛋白; 3: MW-t 是该蛋白质的分子量是通过质谱鉴定后得到的序列由 Mascot 程序计算而得到; MW-g 是该点在电泳后的凝胶上检测到实际分子量值; 4: pI-t 是该蛋白质的等电点是通过质谱鉴定后得到的序列由 Mascot 程序计算而得到; pI-g 是该点在电泳后的凝胶上检测到实际等电点值; 5: 覆盖率是指该蛋白质的通过质谱鉴定后匹配上的氨基酸数量占该蛋白质所有氨基酸数量的比例

Note: 1: Protein quantity ratio: secreted protein expressing level of nitrogen starvation medium/secreted protein expressing level of complete medium; a: Expression quantity ratio greater than 2 is up-regulated expression; b: Expression quantity ratio less than 0.5 is down-regulated expression; 2: S indicates specific proteins expressed ar nitrogen starvation; 3: MW-p: Calculated value with Mascot; MW-g: Calculated value with gel; 4: pI-p: Calculated value with Mascot; pI-g: Calculated value with gel; 5: Coverage: percentage of the number of matched Amino acid: whole number of Amino in a protein sequence