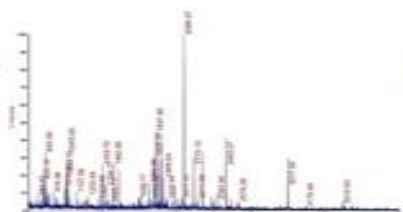


MALDI-TOF/TOF质谱鉴定结果说明

Peptide mixture



MS



MS/MS



Protein spot



Software



DNA/Protein
Database



Mascot Search Results

Search Results
Protein: **Protein**
Search criteria: **Protein**
Database: **Protein**
Protein: **Protein**
Protein: **Protein**

Mascot Score Histogram

Score is $-10 \log(P)$, where P is the probability that the observed match is a random event.
Individual score is > 20 indicates identity or extensive homology ($P < 0.05$).
Protein scores are derived from ion scores as a non-probabilistic basis for ranking protein hits.



Result



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案

我们的服务

Proteomics

2-DE
DIGE
MALDI-TOF/TOF
iTRAQ
SILAC

Bioinformatics

Cluster analysis
GO enrichment
Protein interaction
Pathway mapping
IPA analysis

Expression analysis

RT-PCR
Western-Blot
ELISA
IHC



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案

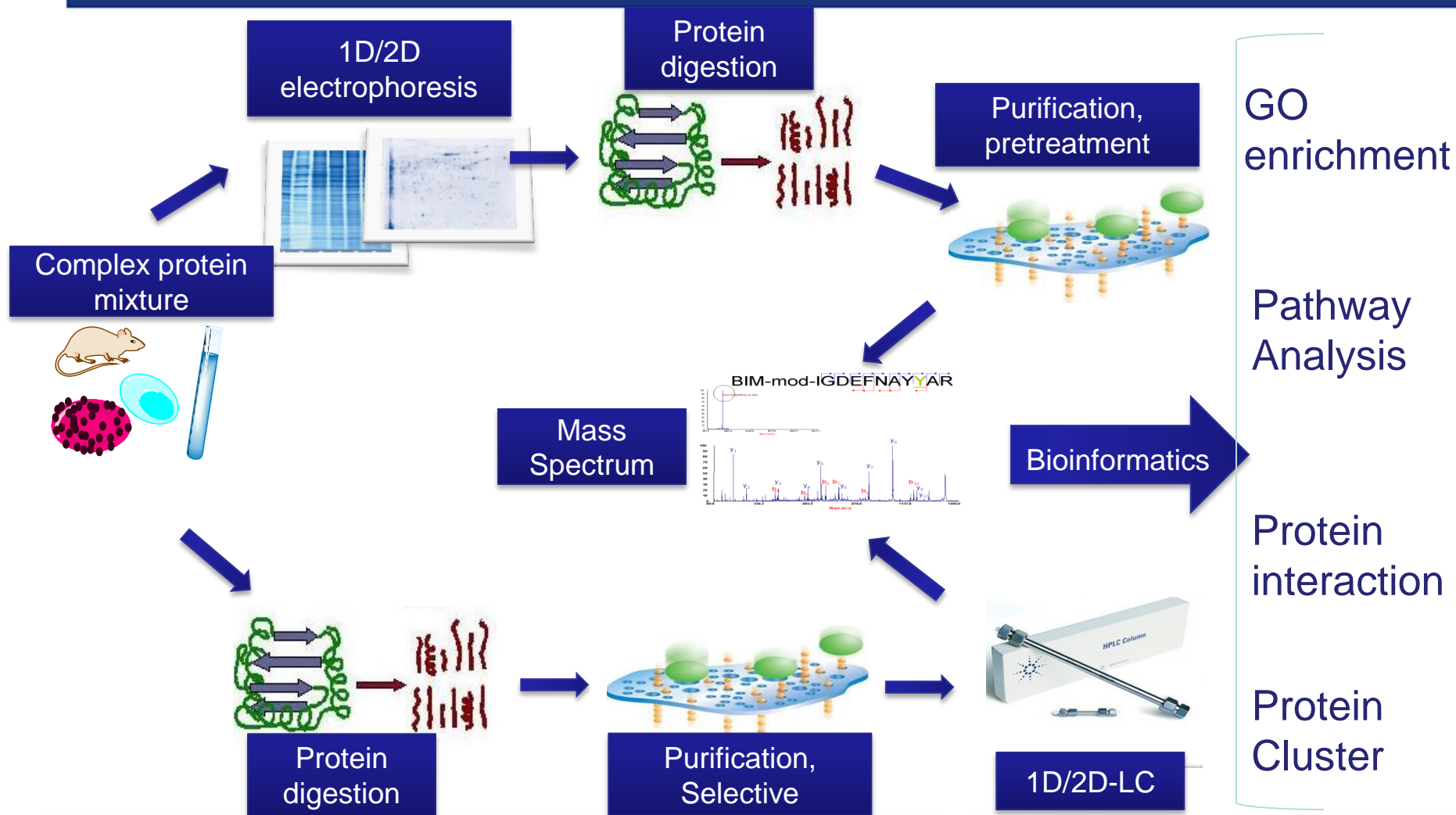
我们的试剂材料



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案

蛋白质组服务全景



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案

我们的合作伙伴



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案



发表的部分论文(2011)

Title: Effect of post-harvest heat treatment on proteome change of peach fruit during ripening, **J Proteomics.(IF:5.074)**

Title: Genetic, proteomic and metabolic analysis of the regulation of energy storage in rice seedlings in response to drought, **Proteomics.(IF:4.815)**

Title: Gamma-butyrolactone regulatory system of *Streptomyces chattanoogensis* links nutrient utilization, metabolism, and development, **Appl Environ Microbiol. (IF:3.778)**

Title: Identification of proteins associated with water-deficit tolerance in C(4) perennial grass species, *Cynodon dactylon* × *Cynodon transvaalensis* and *Cynodon dactylon*, **Physiol Plant. (IF:3.067)**

Title: Proteomic identification of differentially expressed proteins in *Arabidopsis* in response to methyl jasmonat, **J Plant Physiol. (IF:2.677)**





发表的部分论文(2012)

Title: Proteomic analysis of the nucleus accumbens in rhesus monkeys of morphine dependence and withdrawal intervention , **J**

Proteomics.(IF:5.074)

Title: Comparative proteomic analysis of seedling leaves of different salt tolerant soybean genotypes, **J Proteomics.(IF:5.074)**

Title: Secretome of Aspergillus oryzae in Shaoxing rice wine koji, **Int J Food Microbiol. (IF:3.143)**

Title: Proteomic analysis of the effects of exogenous calcium on hypoxic-responsive proteins in cucumber roots, **Proteome Sci.(IF:2.488)**

Title: A proteomic approach to analyze nitrogen- and cytokinin-responsive proteins in rice root, **Mol Biol Rep. (IF:1.875)**



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案



发表的部分论文(2013)

Title: Comparative proteomic analysis of the sun- and freeze-dried earthworm *Eisenia fetida* with differentially thrombolytic activities, *J Proteomics*.(IF:5.074)

Title: Neonate-to-adult transition of snake venomomics in the short-tailed pit viper, *Gloydus brevicaudus*, *J Proteomics*.(IF:5.074)

Title: An integrated proteomic and metabolomic study on the chronic effects of mercury in *Suaeda salsa* under an environmentally, *PLoS One*.(IF:4.441)

Title: Differential expression of proteins associated with seasonal bud dormancy at four critical stages in Japanese apricot , *Plant Biol*. (IF:2.409)

Title: Proteomics reveal cucumber Spd-responses under normal condition and salt stress, *Plant Physiol Biochem*. (2.402)



Mascot MS/MS在线检索

MASCOT MS/MS Ions Search

Your name bioanalysis		Email bioanalysis@163.com	
Search title			
Database(s) Human_EST Fungi_EST Environmental_EST SwissProt NCBInr		Enzyme Trypsin	
		Allow up to 1 missed cleavages	
		Quantitation None	
Taxonomy . . . Metazoa (Animals)			
Fixed modifications --- none selected --- Display all modifications <input type="checkbox"/>		Species Acetyl (K) Acetyl (N-term) Acetyl (Protein N-term) Amidated (C-term) Amidated (Protein C-term) Ammonia-loss (N-term C) Biotin (K) Biotin (N-term) Carbamyl (K) Carbamyl (N-term) Carboxymethyl (C)	
Variable modifications Carbamidomethyl (C) Oxidation (M)			
Peptide tol. ± 50 ppm		MS/MS tol. ± 0.3 Da	
Peptide charge 1+		Monoisotopic <input checked="" type="radio"/> Average <input type="radio"/>	
Data file 浏览...		Precursor m/z	
Data format Mascot generic		Error tolerant <input checked="" type="checkbox"/>	
Instrument MALDI-TOF-TOF		Report top AUTO hits	
Decoy <input type="checkbox"/>			
Start Search ...		Reset Form	

最大酶漏切位点数

数据库

物种

固定修饰, 做了明确的化学修饰反应则选

可变修饰

母离子质量容差

碎片离子质量容差

导入的搜库文件

电荷数

单同位素峰



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案

Mascot MS/MS 检索实例-检索结果

{MATRIX} Mascot Search Results

数据检索及数据库信息

使用者
蛋白点编号
数据来源
检索数据库
物种
检索时间

```
User       : boyuan_tech
Email      : boyuan_tech@163.com
Search title : Project: training, Spot Set: training\20110112, Label: G2, Spot Id: 200836, Peak List Id: 466623, MS Job Run Id: 16365
MS data file : ppw_G2_129958410001.txt
Database    : NCBItr 20121208 (21985448 sequences; 7548358033 residues)
Taxonomy    : Mus musculus (house mouse) (146339 sequences)
Timestamp   : 10 Dec 2012 at 08:54:02 GMT
Protein hits : gi|12697592 MNCb-1930 protein [Mus musculus]
```

Mascot Score Histogram

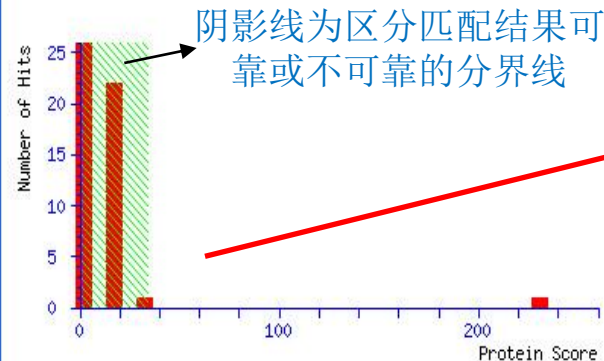
鉴定到的蛋白的GI号、蛋白名称（物种）

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.

Individual ions scores > 34 indicate identity or extensive homology ($p < 0.05$).

蛋白鉴定评价标准，大于34分即为鉴定成功

Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



纵坐标为比对的蛋白数目；横坐标为蛋白质总得分，超过阴影部分的hits表示鉴定结果的可靠性超过显著水平，这里34分为阈值分数。



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案

Mascot MS/MS 检索实例-检索结果

Select All Select None Search Selected ☐ Error tolerant 可以进入该蛋白质鉴定的详细信息，包括覆盖率，等电点等，见蛋白信息页面

1. [gi|12697592](#) Mass: 53170 Score: 230 Matches: 3(3) Sequences: 3(3) emPAI: 0.33
MNCb-1930 protein [Mus musculus]

☐ Check to include this hit in error tolerant search

鉴定成功的蛋白肽段信息及可靠性评价

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 24	1126.5885	1125.5812	1125.6142	-0.0330	0	49	0.0035	1	U	K.TGQEIPVNL.R
<input checked="" type="checkbox"/> 35	1220.5432	1219.5359	1219.5689	-0.0330	0	80	2.4e-06	1	U	R.MMEVAAADVQR.L
<input checked="" type="checkbox"/> 50	1497.6595	1496.6522	1496.6896	-0.0373	0	103	9.2e-09	1	U	K.AVFQYIDENQDR.Y

可以进入该肽段的详细信息，
见肽段信息页面

Proteins matching the same set of peptides:

[gi|31981273](#) Mass: 53198 Score: 230 Matches: 3(3) Sequences: 3(3)

cytosolic non-specific dipeptidase [Mus musculus]

[gi|47847404](#) Mass: 44987 Score: 230 Matches: 3(3) Sequences: 3(3)

mFLJ000064 protein [Mus musculus]

[gi|74182267](#) Mass: 53228 Score: 230 Matches: 3(3) Sequences: 3(3)

unnamed protein product [Mus musculus]

[gi|190016263](#) Mass: 53583 Score: 230 Matches: 3(3) Sequences: 3(3)

Chain A, Crystal Structure Of Mouse Carnosinase Cn2 Complexed With Mn Bestatin



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案



Select All

Select None

Search Selected

☐ Error tolerant

1. [gi|12697592](#) Mass: 53170 Score: 230 Matches: 3(3) Sequences: 3(3) emPAI: 0.33

MNCb-1930 protein [Mus musculus]

蛋白名称及物种

分子量

蛋白得分

蛋白匹配到的肽段数（匹配到Expect值小于0.05的肽段数）

蛋白匹配到的非冗余肽段数（匹配到Expect值小于0.05的肽段数）

代表该蛋白的丰度值

Query	测量值 Observed	理论值 Mr(expt)	计算值 Mr(calc)	Delta	Miss	Score	P值 Expect	Rank	Unique	肽段序列 Peptide	酶切位点
<input checked="" type="checkbox"/> <u>24</u>	1126.5885	1125.5812	1125.6142	-0.0330	0	49	0.0035	1	U	K.TGQEIPVNL.R	
<input checked="" type="checkbox"/> <u>35</u>	1220.5432	1219.5359	1219.5689	-0.0330	0	80	2.4e-06	1	U	R.MMEVAAADVQR.L	
<input checked="" type="checkbox"/> <u>50</u>	1497.6595	1496.6522	1496.6896	-0.0373	0	103	9.2e-09	1	U	K.AVFQYIDENQDR.Y	





Mascot MS/MS 检索实例-检索结果

✓	108	2503.0620	2502.0777
✓	110	2519.0920	2518.0847
✓	111	2565.1125	2564.1052
✓	112	2681.2163	2680.2090
✓	113	2807.2227	2806.2154
✓	114	2808.2605	2807.2532
✓	115	2839.2322	2838.2249
✓	116	2914.4197	2913.4124
✓	117	3077.5151	3076.5078
✓	118	3094.5601	3093.5528
✓	119	3331.5254	3330.5181
✓	120	3337.6697	3336.6624
✓	121	3346.6331	3345.6258
✓	122	3353.6372	3352.6299
✓	123	3364.5027	3363.4954

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : [Carboxymethyl \(C\)](#)
Variable modifications : [Acetyl \(Protein N-term\)](#), [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 0.15 Da
Fragment Mass Tolerance: ± 0.25 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 123

搜库参数信息

Mascot: <http://www.matrixscience.com/>



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案

Mascot MS/MS 检索实例-蛋白信息

MASCOT Search Results

Protein View: gi|12697592 → 登录号
MNCb-1930 protein [Mus musculus] → 蛋白名称 (物种)

Database: NCBI nr
Score: 230
Nominal mass (M_r): 53170 分子量
Calculated pI: 5.43 等电点
Taxonomy: [Mus musculus](#)

Sequence similarity is available as [an NCBI BLAST search of gi|12697592 against nr](#).

Search parameters

MS data file: ppw_G2_129958410001.txt
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: [Carboxymethyl \(C\)](#)
Variable modifications: [Acetyl \(Protein N-term\)](#), [Oxidation \(M\)](#)

Protein sequence coverage: 6% 覆盖率, 红色区域
Matched peptides shown in **bold red**. 为匹配上的肽段

```
1 MSALKAVFQY IDENQDRYVK KLAENVAIQS VSAWPEKRG E IRRMMEVAAA
51 DVQR LGGSVE LVDIGKQKLP DGSEIPLPPI LLGKLGS DPQ KKTVC IYGH L
101 DVQPAALEDG WDSEPF TLVE REGKLYGRGS TDDKGPVAGW MNALEAYQKT
151 GQEIPVNLRF CLEGMEESGS EGLDELIFAQ KDKFFKDV D VCISDN YWLG
201 KKNPCITYGL RGICYFFIEV ECSDKDLHSG VYGGSVHEAM TDLISLMGCL
```

对于注释为unknown或者hypothetical蛋白质可以通过点击此进行blast同源比对, 找出相关的基因注释信息



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案

Mascot MS/MS 检索实例-肽段信息

{MATRIX} *{SCIENCE}* Mascot Search Results

Peptide View

肽段详细信息说明

MS/MS Fragmentation of **TGQEIPVNL**R

Found in **gi|12697592** in **NCBI**nr, MNCb-1930 protein [Mus musculus]

Match to Query 24: 1125.581224 from(1126.588500,1+) intensity(0.0000) index(1)

Title: Label: G2, Spot_Id: 200836, Peak_List_Id: 466667, MSMS Job_Run_Id: 16366, Comment:

Data file ppw_G2_129958410001.txt

Click mouse within plot area to zoom in by factor of two about that point

Or, to Da

Label all possible matches ☐ Label matches used for scoring ☒

Show Y-axis ☐



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案

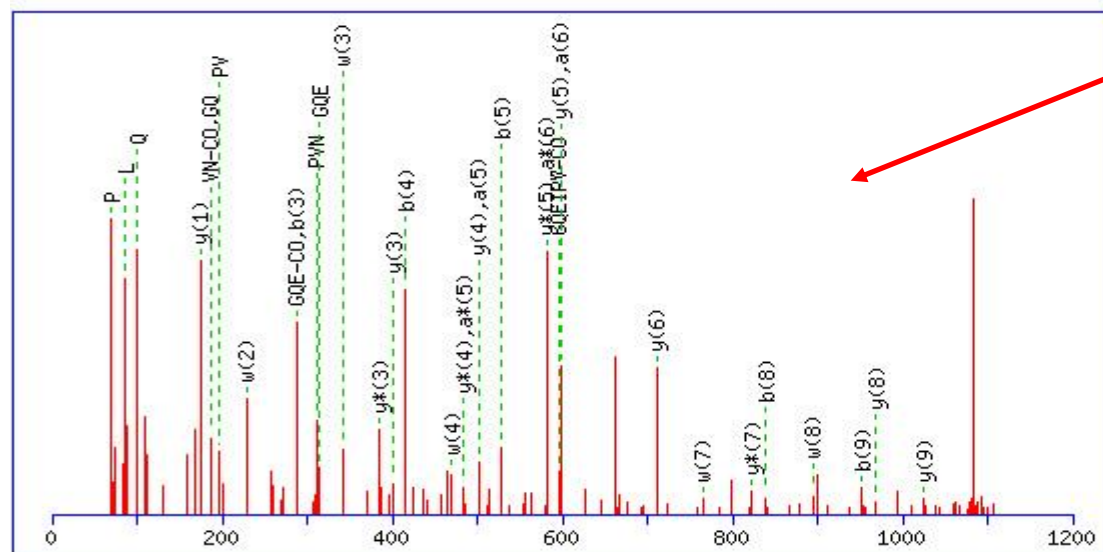
Mascot MS/MS 检索实例-肽段信息

Click mouse within plot area to zoom in by factor of two about that point

Or, Plot from 0 to 1200 Da Full range

Label all possible matches ☐ Label matches used for scoring ☒

Show Y-axis ☐



拟合的二级质谱图

Monoisotopic mass of neutral peptide Mr(calc): 1125.6142

Fixed modifications: Carboxymethyl (C) (apply to specified residues or termini only)

Ions Score: 49 Expect: 0.0035

Matches : 36/157 fragment ions using 44 most intense peaks ([help](#))



博苑科技 www.boyuanbio.com

BIO-TECH 蛋白质组完整解决方案