

# Mascot Search

## 1. Search website :

[http://www.matrixscience.com/search\\_form\\_select.html](http://www.matrixscience.com/search_form_select.html)



## Mascot Search

*MS search*

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2008

- **Peptide Mass Fingerprint:** The experimental data are a list of peptide mass values from an enzymatic digest of a protein.

- [Example of results report](#)
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- **Sequence Query:** One or more peptide mass values associated with information such as partial or ambiguous sequence strings, amino acid composition information, MS/MS fragment ion masses, etc. A super-set of a sequence tag query.

- [Example of results report](#)
- [More information](#)

- **MS/MS Ion Search:** Identification based on raw MS/MS data from one or more peptides.

- [Example of results report](#)
- [More information](#)

**Search Form Defaults:** Follow this link to save your preferred search form defaults as a browser cookie.

## 2. Set search parameter

### MASCOT Peptide Mass Fingerprint

The screenshot shows the MASCOT Peptide Mass Fingerprint search interface. The form includes the following fields and annotations:

- Your name:** yichen
- Email:** yichen@dragon.nchu.edu.tw
- Search title:** (empty)
- Database:** NCBIInr (Annotation: 選擇蛋白質資料庫)
- Taxonomy:** All entries (Annotation: 選擇水解酵素及相關選項)
- Enzyme:** Trypsin (Annotation: 選擇物種)
- Allow up to:** 1 missed cleavages (Annotation: 按住 Ctrl 可同時選擇 2 種以上選項)
- Fixed modifications:** Acetyl (K), Acetyl (N-term), Acetyl (Protein N-term), Amidated (C-term), Amidated (Protein C-term)
- Variable modifications:** mTRAQ:13C(3)15N(1) (N-term), mTRAQ:13C(3)15N(1) (Y), NIPCAM (C), Oxidation (HW), Oxidation (M) (Annotation: 選擇可能產生之修飾反應)
- Protein mass:** (empty) kDa
- Peptide tol. ±:** 0.3 Da (Annotation: 調整誤差範圍(可先設定 200-300 ppm, 再依結果調整))
- Mass values:**  MH<sup>+</sup>  M<sub>r</sub>  M-H<sup>-</sup>
- Monoisotopic:**  Monoisotopic  Average
- Data file:** (empty) 瀏覽...
- Query:** (empty) (Annotation: 輸入 mass list 或 txt file)
- Decoy:**
- Report top:** AUTO hits (Annotation: 選擇輸出資料之筆數)
- Buttons:** Start Search ..., Reset Form

**Carbamidomethylation**  
於 in-gel digestion 中利用 DTT 破壞雙硫鍵，再用 iodoacetamide block -SH group