

Welcome

This site features **Mascot**, a powerful search engine that uses mass spectrometry data to identify proteins from primary sequence databases. To assist you, the [help text](#) for Mascot forms a substantial knowledge base concerning protein identification by MS.

If this is your first visit, please check for [browser compatibility](#) and read the [small print](#). If you include results from Mascot in a publication, please cite either www.matrixscience.com or Electrophoresis, **20(18)** 3551-67 (1999) ([abstract](#)).

Security

Mascot incorporates a role based security model, which allows the system administrator to control which functionality is available to individual users. If security has been enabled, you may be prompted to log in if you attempt to access a page or perform a task that requires authorisation. If security is not enabled, which is the default, the following links will simply confirm this.

- [Log in](#)
- [Log out](#)
- [Change password](#)
- [Edit settings](#)
- [Current session information](#)

Whether or not Mascot security is enabled, in order to comply with the licensing conditions, access to this Mascot server must be restricted to authorised users. We strongly recommend that your server is protected by a secure firewall. For more information, start from the [WWW Security FAQ](#).

蛋白質資料庫搜尋引擎

應用: 最常用的功能包含Peptide Mass Fingerprint :及MS/MS Ion Search。其中Peptide Mass Fingerprint的方式是比對蛋白質經酵素水解成peptides後其分子量的分布，來計算資料庫中之發生隨機比對符合(random matches)的機率。其給分方式使用以下公式: $-10 \cdot \text{LOG}_{10}(P)$ ，其中P代表發生隨機比對符合的機率。因此高分代表資料庫中隨機比對符合的可能性低。MS/MS Ion Search則是將所得到之胜肽母離子及其碎片分子的質量的資訊統合，在與蛋白質序列(模擬經蛋白酵素水解後)之資料庫進進行比對，搜尋隨機比對符合機率最低的的胜肽及其所屬的蛋白質，以共後續實驗參照。