

| PublisherInfo        |   |                |
|----------------------|---|----------------|
| PublisherName        | : | BioMed Central |
| PublisherLocation    | : | London         |
| PublisherImprintName | : | BioMed Central |

Articles selected by Faculty of **1000**: sugar arrays; *C. elegans* ORFeome v1.1; identifying tRNA genes; method to analyze human serum proteome; rates of molecular divergence

| ArticleInfo           |   |  |
|-----------------------|---|--|
| ArticleID             | : | 3464   |
| ArticleDOI            | : | 10.1186/gb-2003-4-6-325                              |
| ArticleCitationID     | : | 325  |
| ArticleSequenceNumber | : | 17   |
| ArticleCategory       | : | Paper report   |
| ArticleFirstPage      | : | 1  |
| ArticleLastPage       | : | 3  |
| ArticleHistory        | : | RegistrationDate : 2003-5-9<br>OnlineDate : 2003-5-9 |
| ArticleCopyright      | : | BioMed Central Ltd2003                               |

|                |   |           |
|----------------|---|-----------|
| ArticleGrants  | : |           |
| ArticleContext | : | 130594466 |

## The Author(s)

### Summary

A selection of evaluations from Faculty of **1000** covering the synthesis of sugar arrays, *C. elegans* ORFeome v1.1, a novel method for identifying tRNA genes, a step towards analysis of the human serum proteome and rates of molecular divergence in rearranged chromosomes.

## Sugar arrays

**Synthesis of sugar arrays in microtiter plate.** Fazio F, Bryan MC, Blixt O, Paulson JC, Wong CH. *J Am Chem Soc* 2002, **124**:14397-14402.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-6-325.asp#Fazio>

## *C. elegans* ORFeome v1.1

***C. elegans* ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression.** Reboul J, Vaglio P, Rual JF, Lamesch P, Martinez M, Armstrong CM, Li S, Jacotot L, Bertin N, Janky R, *et al.* *Nat Genet* 2003, **34**:35-41.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-6-325.asp#Reboul>

## Identifying tRNA genes

**A novel method for finding tRNA genes.** Tsui V, Macke T, Case DA. *RNA* 2003, **9**:507-517.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-6-325.asp#Tsui>

# Method to analyze human serum proteome

**Multi-component immunoaffinity subtraction chromatography: An innovative step towards a comprehensive survey of the human plasma proteome.** Pieper R, Su Q, Gatlin CL, Huang ST, Anderson NL, Steiner S. *Proteomics* 2003, **3**:422-432.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-6-325.asp#Pieper>

# Rates of molecular divergence

**Chromosomal speciation and molecular divergence--accelerated evolution in rearranged chromosomes.** Navarro A, Barton NH. *Science* 2003, **300**:321-324.

For the Faculty of 1000 evaluation of this article please see: <http://genomebiology.com/reports/F1000/gb-2003-4-6-325.asp#Navarro>