

Instructions to authors

Please read these instructions carefully and follow them strictly. In this way you will help ensure that the review and publication of your paper is as efficient and quick as possible. In particular ensure that your paper is within the length limit. The editors reserve the right to return manuscripts that are not in accordance with these instructions.

Papers must be clearly and concisely written in English. In the interests of speed, manuscripts are not extensively copy-edited, and authors are requested to check their texts carefully before submitting them.

Scope and policy of *Protein Engineering*

The field of protein engineering is a new but fast-moving area of biology characterized by the coordinate application of a number of specialized theoretical and experimental disciplines. The objectives of those engaged in this area of research are to investigate the principles by which particular structural features in proteins relate to the mechanisms through which the biological function is expressed, and to test these principles in an empirical fashion by introduction of specific changes followed by evaluation of any altered structural and/or functional properties. The specialized areas alluded to include determination and prediction of protein conformation (secondary, and tertiary), experimental studies of protein folding, chemical modification, mutagenesis (generalized and site-specific), and physical and/or biochemical methods for establishing structure-activity relationships.

Protein Engineering will provide for rapid publication of full-length papers describing original research of specific relevance to advancing our understanding of the structural and biochemical basis of protein function, employing some or all of the approaches described above. Preference will be given to those papers that both satisfy this criterion and report novel findings that significantly advance the field. While the editors encourage submission of papers that employ a multidisciplinary approach, papers describing the application of a single technique will be accepted if they are specifically relevant to the field. Papers should be as intelligible as possible to the broad audience likely to be interested in protein engineering and particular attention should be paid to indicating the general conclusions of the study and how it has advanced our understanding of protein structure and function. In this context, the Introduction and Discussion should be used to indicate the novel aspects of the research reported and how it has added to existing knowledge.

In addition to main papers, each issue of *Protein Engineering* will contain a Review article, a Commentary section, in which readers will be kept up to date with results and developments in techniques reported in other journals, and a Protocols section, which will contain short communications giving details of improvements in experimental methods in any field relevant to the study of protein structure and function.

Submission of manuscripts

The manuscript (the original and two copies) should be submitted to the appropriate executive editor and not to members of the editorial board.

For The Americas. Prof G A Petsko, Department of Chemistry, Building 2, Room 202, Massachusetts Institute of Technology, Cambridge, MA 02139, USA

For Japan. Dr T Imoto, Faculty of Pharmaceutical Sciences, Kyushu University 62, Maidashi, Higashi-ku, Fukuoka 812, Japan

For Europe and the Rest of the World. Dr A R Rees, Laboratory of Molecular Biophysics, Rex Richards Building, South Parks Road, Oxford OX1 3QU, UK

Submission of a paper implies that it reports unpublished work and that it is not under consideration for publication elsewhere. If previously published tables, illustrations or more than 200 words of text are to be included, then the copy-right holder's written permission must be obtained. Enclose copies of any such permission letters with your paper.

Review of manuscripts

The Editorial Board will subject every paper to independent review by appropriate referees and reject those that do not meet the journal's scientific standards or other requirements. For main papers decisions will be made within 3-4 weeks of receipt of the paper at the Editorial Office. Copies of manuscripts accepted for publication will not be returned to the authors. For contributions to Protocols a decision will be made by the executive editors within 1 week.

Speed of publication

We aim to publish main papers within 4 months of their receipt at the Editorial Office and protocols in the next available issue. At all stages, in order to avoid delays, maximum use will be made of the telephone and telex, followed by written confirmation. Help us by providing the telephone number(s), and/or telex number(s), at which author(s) can be contacted.

Page charges

Page charges will NOT be levied.

Proofs

Authors will be sent page proofs. To avoid delays in publication, proofs should be checked immediately for typographical errors and returned to the publishers by express (special delivery) post. Alternatively, to save time, corrections may be given by telephone to the Production Editor, *Protein Engineering*, IRL Press, telephone number +44 865 882283. Essential changes of an extensive nature may be made only by insertion of a Note Added in Proof. A charge will be made to authors who insist on amendment within the text at the page-proof stage.

Preparation of manuscripts

Manuscripts should be in their final form when they are submitted so that proofs will require only correction of typographical errors.

Sections of the manuscript

Main papers. Please subdivide manuscripts into the following sequence of sections: Title page, Abstract, Introduction, Materials and methods, Results, Discussion, Acknowledgements, References, Tables, Legends to Figures. In the journal the Materials and methods, Acknowledgements and References will be printed in smaller type to accommodate more text (nevertheless, double-spaced typing please).

Protocols. Each submitted manuscript should contain a brief Introduction to a major section consisting of Materials and methods. Where possible, any applications of the methodology described should be indicated. References should only be included where essential.

Length of the manuscript

Main papers should ideally be six printed pages in total. Publication of longer manuscripts is at the discretion of the editors. To estimate the length of a paper or protocol in typescript, allow 1400 words for each full page of printed text, remembering to allow sufficient space for tables/illustrations within the six-page limit.

General format

Manuscripts should be legibly typed on A4 or American quarto paper. All sections of the manuscript must be double-spaced (space between the lines of type not less than 6 mm). Margins of 25 mm (1 inch) should be left at the sides, top and bottom of each page. Number each page top right (Title page is 1). Please avoid footnotes, use instead, and as sparingly as possible, parenthesis within brackets. Underline only words or letters to appear in italics. Clearly identify unusual or handwritten symbols and Greek letters. Differentiate between the letter O and zero, and the letters I and l and number 1. Mark the position of each figure and table in the margin.

Title page

The title should be short, specific and informative. The surname and initials of each author should be followed by his or her department, institution, city with postal code and country. Any changes of address may be given in numbered footnotes. The author(s) to whom proofs are to be addressed should be indicated. Please provide a running title of not more than 50 characters.

Key words

Up to five key words, which may or may not appear in the title, should be given in alphabetical order, below the title, each separated by a slash (/). In addition to being printed in the article, these key words, together with the title, will be the sole basis of the annual Subject Index. Thus, please give them careful consideration.

Abstract (main papers only)

The second page of every manuscript must contain only the Abstract, which should be a single paragraph not exceeding 200 words. Please abide strictly by this limitation of length. The Abstract should be comprehensible to readers *before* they have read the paper, and abbreviations and reference citations should be avoided.

Acknowledgements

These should be included at the end of the text and not in footnotes. Personal acknowledgements should precede those of institutions or agencies.

References

Authors are responsible for the accuracy of the References. Published articles and those in the press (state the journal which has accepted them) and enclose

Continued overleaf

a copy of the manuscript) may be included. In the text a reference should be cited by author and date, not more than two authors may be cited per reference; if there are more than two authors use *et al*. At the end of the manuscript the citations should be typed in alphabetical order, with the authors' surnames and initials inverted. References should include, in the following order: authors' names, year, journal title, volume number, inclusive page numbers, and name and address of publisher (for books only). The name of the journal should be abbreviated according to the *International List of Periodical Title Word Abbreviations* and underlined to indicate italics. References should therefore be listed (and will subsequently appear in type) as follows:

Hamming, J., Arnberg, A. and Gruber, M. (1981) *Nucleic Acids Res.*, **9**, 1339–1350

Köster, H. (ed.) (1980) *Nucleic Acids Synthesis: Applications to Molecular Biology and Genetic Engineering*. IRL Press, London

Norris, K. E., Norris, F. and Brunfeldt, K. (1980) In Köster, H. (ed.), *Nucleic Acids Synthesis: Applications to Molecular Biology and Genetic Engineering*. IRL Press, London, pp. 233–241

Personal communications (J. Smith, personal communication) should be authorized in writing by those involved, and unpublished data should be cited as (unpublished data). Both should be used as sparingly as possible and only when the unpublished data referred to is peripheral rather than central to the discussion. References to manuscripts in preparation, or submitted, but not yet accepted, should be cited in the text as (B. Smith and N. Jones, in preparation) and should NOT be included in the list of references.

Tables

Tables should be typed on separate sheets and numbered consecutively with Roman numerals. Tables should be self-explanatory and include a brief descriptive title. Footnotes to tables indicated by lower case letters are acceptable, but they should not include extensive experimental detail. An arrow in the text margin should be used to indicate where a table should be inserted in the text.

Illustrations

All illustrations (line drawings and photographs) should be referred to in the text as Figure 1 etc., which should be abbreviated to 'Fig. 1' only in the figure legend. Write the title of your paper, the name of the first author and the figure number lightly in blue pencil on the back of each figure. On the back also indicate clearly the top margin of each figure. On the manuscript indicate with an arrow in the margin the most appropriate position for the figure.

Photographs These must be submitted in the desired final size so that reduction can be avoided. The type area of a page is 244 (height) × 183 mm (width) and photographs, including their legends, must not exceed this area. A single column is 88 mm wide, a double column is 183 mm wide. Ideally, photographs should fit either a single or a double column. Photographs should be of sufficiently high quality with respect to detail, contrast and fineness of grain to withstand the inevitable loss of contrast and detail inherent in the printing process. Please indicate the magnification by a rule on the photograph. When several prints of varying quality of the same figure are provided, please indicate which print should be used for reproduction in the journal.

Colour plates The inclusion of colour plates is encouraged, particularly for the reproduction of computer graphics displays or protein structures. Authors are asked to consult the editors for details of charges and of the special arrangements available to keep the cost to a minimum.

Line drawings Please provide these as clear, sharp prints, suitable for reproduction as submitted. No additional artwork, redrawing or typesetting will be done. Therefore, all labelling should preferably be made with a lettering set. Ensure that the size of lettering is in proportion with the overall dimensions of the drawing. Ideally, line drawings should be submitted in the desired final size to avoid reduction (maximum dimensions 244 × 183 mm including legends) and should fit either a single (88 mm) or a double column width (183 mm). If submitting line drawings which require reduction, please check that the lettering will be clearly legible after the drawing has been reduced to the size at which it will be printed. After reduction, letters should not be smaller than 1.5 mm in height.

Figure legends These should be on a separate, numbered manuscript sheet. Define all symbols and abbreviations used in the figure. Common abbreviations and others in the preceding text should not be redefined in the legend.

Conventions

In general, the journal follows the conventions of the *Committee of Biological Editors Style Manual* (5th edn, 1983).

Follow *Chemical Abstracts* and its indexes for chemical names. For guidance in the use of biochemical terminology follow the recommendations issued by the IUPAC-IUB Commission on Biochemical Nomenclature, as given in *Biochemical Nomenclature and Related Documents*, published by the Biochemical Society, UK. For enzymes, use the recommended name assigned by the IUPAC-IUB Commission on Biochemical Nomenclature, 1978, as given in *Enzyme Nomenclature*, published by Academic Press, New York, 1980. Where possible, use the recommended SI (Système International) units.

For bacterial genetics nomenclature follow Demerec *et al.* (1966) *Genetics*, **54**, 61–76. For details of the nomenclature to be used for mutant proteins see Vol. 1, No. 1 of this journal.

Abbreviations

Try to restrict the use of abbreviations to SI symbols and those recommended by the IUPAC, with the exception that Angström units (Å) may be employed in place of nanometers (nm). Abbreviations should be defined in brackets after their first mention in the text. Standard units of measurements and chemical symbols of elements may be used without definition in the body of the paper.

Reprints

The publishers supply 30 reprints free of charge. Reprint order forms are sent out with the proofs, and must be returned with the proofs to IRL Press if extra reprints are required. Late orders submitted after the journal is printed are subject to increased prices.

Policy concerning availability of materials

It is understood that by publishing a paper in *Protein Engineering* the authors agree, where feasible, to make freely available to colleagues in academic research any of the cells, nucleic acids, proteins, etc. that were used in the research reported and that are not available from commercial suppliers.

PROTEIN ENGINEERING

Protein Engineering offers accelerated publication for full-length papers describing original research that will advance our understanding of the structural and biochemical basis of protein function. The journal gives priority to papers reporting novel results which significantly advance the field. While the editors encourage the submission of papers which employ a multi-disciplinary approach, papers describing the application of a single technique will be accepted, if they are specifically relevant to the field.

Regular contents

- Full-length, refereed papers reporting original research
- Review articles
- Commentaries – news of results and novel techniques published elsewhere
- Protocols – short communications for improvements to experimental methods in all relevant fields

Personal subscribers qualify for a large reduction in the price. Recommend the journal to your librarian or use the form below to make sure you get to read *Protein Engineering* in 1987.

SUBSCRIPTION ORDER FORM (North and South America)

To order a subscription to volume 1, check the appropriate boxes below, complete the name and address section overleaf in block capitals and mail to IRL Press. Individuals with access to the journal subscribed locally at the full rate should complete section 3 to obtain a personal subscription.

- 1 Enter my subscription to volume 1 (12 issues Sept 1986–Dec 1987) of *Protein Engineering* at the following rate.

Full (library/institution) US\$255
Personal US\$110

Note Orders must be accompanied by payment. The price includes handling and postage by air. Subscriptions are entered on a per-volume basis only and despatch will commence only after receipt of correct payment.





SUBSCRIPTION ORDER FORM (Rest of the world*)

To order a subscription to volume 1, check the appropriate boxes below, complete the name and address section overleaf in block capitals and mail to IRL Press. Individuals with access to the journal subscribed locally at the full rate should complete section 3 to obtain a personal subscription.

- 1 Enter my subscription to volume 1 (12 issues Sept 1986–Dec 1987) of *Protein Engineering* at the following rate.

Full (library/institution) £144
Personal £60





Note Orders must be accompanied by payment. The price includes handling and postage (by air beyond Europe). Subscriptions are entered on a per-volume basis only and despatch will commence only after receipt of correct payment.

2 Charge my     Expiry date _____

Card no

Signature _____
(All credit card orders must be signed)

- Payment enclosed
Cheque/bank draft/postal or money order/UNESCO coupons made payable to IRL Press for US\$ _____
- Payment sent separately
- National or international giro to account no 597 8351
- Bank transfer to Midland Bank plc, 220 High Holborn, London WC1V 7BZ, UK, bank sorting code 40-03-27; account no 68587170 (US\$). If paying by bank transfer, sufficient funds must be remitted to pay all bank handling charges, including those of any forwarding bank in the UK.

2 Charge my     Expiry date _____
(Except France)

Card no

Signature _____
(All credit card orders must be signed)

- Payment enclosed
Cheque/bank draft/postal or money order/UNESCO coupons made payable to IRL Press for £ _____
- Payment sent separately
- National or international giro to account no 597 8351
- Bank transfer to Midland Bank plc, 220 High Holborn, London WC1V 7BZ, UK; bank sorting code 40-03-27; account no 91084143 (£). If paying by bank transfer, sufficient funds must be remitted to pay all bank handling charges, including those of any forwarding bank in the UK.

3 Personal subscribers must complete this section
'In accepting this personal subscription, I acknowledge that use of the journal will be restricted to me, that the copyright restrictions printed in the journal will be honoured and that the issues will not be donated to a library.'

Signature _____

Date _____

Name and address of full-rate subscriber within local access:

4 NAME _____

ADDRESS _____

_____ Code _____

Return to:
IRL Press Inc,
PO Box Q,
McLean, VA 22101,
USA

 **IRL PRESS**

3 Personal subscribers must complete this section:
'In accepting this personal subscription, I acknowledge that the use of the journal will be restricted to me, that the copyright restrictions printed in the journal will be honoured and that the issues will not be donated to a library.'

Signature _____

Date _____

Name and address of full-rate subscriber within local access:

4 NAME _____

ADDRESS _____

_____ Code _____

Return to:
IRL Press Ltd,
PO Box 1, Eynsham,
Oxford OX8 1JJ, UK

 **IRL PRESS**

IBI/PUSTELL DNA/PROTEIN SEQUENCE ANALYSIS PACKAGE

J. Pustell, Harvard University

User-friendly and competitively priced, this software contains one of the most extensive sequence analysis facilities available to molecular biologists. The latest version of this successful package will provide you with both a screen-orientated DNA-sequence database manager, offering a uniquely-tailored work environment, and powerful and comprehensive programs to manipulate and analyse data. The package includes a digitiser interface which, in conjunction with an IBI Gel Reader, enables you to enter data directly from autoradiograms of DNA sequencing gels.

DNA Sequence Database Manager in Cyborg Environment

The database manager presents compacted databases like *Nucleotide Sequences* (see below) as if they were large directories of normal sequence files. In seconds you can select sets and subsets of entries by name, accession number, author or one of over 750 keywords. Then you can apply to the extracted sequence any of the comprehensive range of programs in the DNA/Protein Sequence Analysis System.

Features

- *Autotranslation* – software utilises the information in the sites/features table to translate nucleic acid sequences correctly
- *Data output* – allows you to manipulate, display and print out data from every operation in a multitude of formats
- *Measure fragment sizes* – in conjunction with the IBI Gel Reader, calculates mobility of restriction fragments or proteins using cubic spline and least squares methods
- *User-friendly work environment* – variables and commands are entered by pointing to the desired option, function keys perform complicated tasks with a single key stroke, and on-screen help is always available

FREE DEMONSTRATION DISC

NUCLEOTIDE SEQUENCES DATABASE

GenBank® Genetic Sequence Data Bank

This vast reference work is the result of a unique international collaboration between the EMBL Nucleotide Sequence Data Library staff, the staff of GenBank at Los Alamos National Laboratory and Bolt Beranek and Newman, Inc.

Based on GenBank release 40.0, the database comprises almost 6 000 000 bases from over 6 600 reported sequences – including the human β -globin genome and the AIDS virus – with selected annotation indicating the locations of coding regions and other experimentally determined sites of biological significance. Full bibliographic information is included, plus brief summaries of experimental results and observations made about the sequences when published originally.

The sequences are organised in 12 major groups and logically ordered within them. There are keyword phrase, taxonomy, author and library location indexes to assist you in consulting the database. Four BASIC programs are provided to help you write software to access the database, but to maximise its potential, database management software like the IBI/Pustell *DNA/Protein Sequence Analysis Package* ABOVE is recommended. A 56-page user manual is included with the set of 20 floppy discs.

DNA/Protein Sequence Analysis System

The analysis programs represent one of the most comprehensive DNA/protein data-handling systems available in a single package.

Features

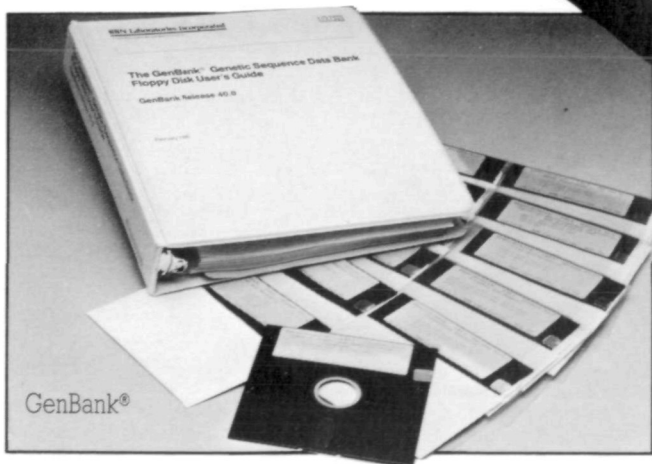
- *Restriction file editor* – over 100 restriction enzyme entries, which you can modify
- *Codon bias file* – for locating protein coding regions
- *Translation* – translates nucleic acid sequences into peptides.
- *Reverse translation* – predicts possible nucleic acid sequences of peptides etc
- *Restriction analysis* – lists all cut sites (not recognition sites) in alphabetical order
- *Calculate base composition*
- *Plot base composition* – as ratio or percentage
- *Calculate amino acid composition*
- *Plot amino acid composition*
- *Homology searches*
- *Subsequence match* – rapid search with match percentage and user-defined bases
- *Forward and reverse matrices* – high-speed 'dot matrix' comparisons to locate similarities, tandem repeats, inverted repeats, potential stem loops and palindromes
- *Automatic matched sequences* – for examining homologies in detail
- *Manually align sequences* – to produce consensus sequences by flexible criteria for slides or publication
- *Locate protein coding regions*

SPECIAL INTRODUCTORY OFFER

This package is available at the introductory price of US\$980/£520

IBM PC/XT/AT: March 1986, £520 (Europe, plus 15% VAT in UK), US\$980 (rest of world), published by International Biotechnologies' Inc., distributed worldwide by IRL Press. Full documentation and after-sales back-up is included in the basic price. Requires 256K RAM, PC-DOS 2.1 or higher and two 360K floppy disc drives.

PLUS



IBM PC/XT/AT: April 1986, US\$125.00/£90.00 (+ VAT in UK), published by GenBank (registered trademark of the US Department of Health and Human Sciences), distributed worldwide by IRL Press.

Orders to

IRL Press Ltd, PO Box 1, Eynsham, Oxford OX8 1JJ, UK
IRL Press Inc., PO Box Q, McLean, VA 22101-0880, USA

PROTEIN ENGINEERING