Phytochemistry is a leading international journal publishing studies of plant chemistry, biochemistry, molecular biology and genetics, structure and bioactivities of phytochemicals, including '-omics' and bioinformatics/computational biology approaches. Phytochemistry is a primary source for papers dealing with phytochemicals, especially reports concerning their biosynthesis, regulation, and biological properties both in planta and as bioactive principles. Articles are published online as soon as possible as Articles-in-Press and in 12 volumes per year. Occasional topic-focussed special issues are published composed of papers from invited authors.

Article types

Full papers are original research papers reporting new discoveries that lead to a deeper understanding of any aspect of plants covered by the journal. Full papers are invited in the following sections, but these are not exclusive.

Molecular Genetics and Genomics contains papers which demonstrate novelty and/or biological significance in relation to all aspects of gene structure and expression, and their role in plant function, regulation, comparative genomics, and reconstitution of biochemical pathways. This section may also contain studies of genetically modified plants that have been analysed for changes in their profiles of phytochemical production.

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Ecological Biochemistry and Chemistry contains papers on how plants interact with their environment, including adaptation to environmental stress, symbiosis, interactions with other
organisms, phytoalexins, phytotoxins, pollination (bio)chemistry, and the use of phytochemicals by other organisms.

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GUIDE FOR AUTHORS

INTRODUCTION

*Phytochemistry* invites research articles on all aspects of pure and applied plant chemistry, plant biochemistry, plant molecular biology and chemical ecology. The Journal is currently divided up into the following sections:

Editorial Comment, Molecules of Interest, Review Articles, Structural Elucidation and Full Papers.

*Editorial Comment* will be an occasional series where Regional Editors, Board Members or other scientists will be invited to comment on phytochemistry topics of global interest and debate.

*Molecules of Interest* will consist of invited short reviews (3-4) printed pages of individual compounds or macromolecules of plant, fungal or algal origin. These can be novel compounds or newly discovered properties of familiar compounds. Please contact Dr Richard J Robins if you wish to prepare a Molecules of Interest paper.

*Review Articles* are published at regular intervals, ranging in scope from primary metabolism and regulation of plant growth, through plant enzymology to natural product chemistry and the biological activity of plant products. They deal with significant new areas of research and are intended to command the interest of the general reader. Authors should consult their Regional Editors with an outline of their proposed Review before preparing such articles. Published Reviews include a biography and picture of each author.

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- Bioactive Products
- Chemotaxonomy
- Chemistry
- Ecological Biochemistry
- Metabolism
- Molecular Genetics & Genomics
- Protein Biochemistry & Proteomics
- Update in Bioinformatics

They are comprehensive papers, typically 6-8 printed pages in length (a minimum of 20 pages of double-spaced manuscript). Papers on plant chemistry must be substantial and contain convincing justification for undertaking the study, as well as having conclusions (e.g. on the biology, chemotaxonomy, new biosynthetic pathways etc.). Papers submitted under the Bioactive Products area are unlikely to be accepted if the bioactivity is measured on a mixture of compounds without further resolution.

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Paper chromatography: PC
Precipitate: ppt.
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Saturated: satd.
Solution: soln.
Solvent mixtures including chromatographic solvents: abbreviate as follows $n$-BuOH–HOAc–H2O (4:1:5)
Statistics: LSD (least significant difference), s.d. (standard deviation), s.e. (standard error)
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Temperature: temp.
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In Table headings and legends on graph axes numerical data should be identified in the form data name/units.
For **Presentation of Data** please see the full instructions to authors, including all special characters, available for download as a pdf file. [pdf link](#)

Mass spectral data should be presented in full as Supplementary Information for all newly identified compounds. If the data are already published elsewhere then relevant references should be quoted. Presentation of mass spectral data should in general follow the recommendations given in Int. J. Mass Spectrom. Ion Processes, 142, 211-240 (1995), and must indicate the method used (EIMS, CIMS, GC-MS, TOFMS, FABMS, SIMS, APCI etc.) and the relevant experimental details (ionizing energy, voltages etc.). The data should give only diagnostically important ions, the character of the fragmentation ions in relation to the molecular ion and the intensity relative to the major ion. For example-EIMS (probe) 70 eV, m/z (rel. int.): 386 [M]+ (36), 368 [M - H2O]+ (100), 353 [M - H2O - Me] + (23), 275 [M - 111] + (35), etc. CIMS (iso-butane, probe), 200 eV, m/z (rel. int.): 387 [M + H] + (100), 369 [(M + H) - H2O] + (23), etc. High-resolution spectra can be given in more detail if necessary for [M] + and the more important fragment ions.

X-ray crystallography
Only essential data (e.g. a three-dimensional structural drawing with bond distances) should be included in manuscripts. A complete list of data in CIF (Crystallographic Information File) format should be prepared separately and deposited with the Cambridge Crystallographic Data Centre (see [http://www.ccdc.cam.ac.uk](http://www.ccdc.cam.ac.uk) for further information) before the paper is submitted. A footnote indicating this fact is to be included in the manuscript. "CCDC...contains the supplementary crystallographic data for this paper. These data can be obtained free of charge via [http://www.ccdc.cam.ac.uk/conts/retrieving.html](http://www.ccdc.cam.ac.uk/conts/retrieving.html) (or from the CCDC, 12 Union Road, Cambridge CB2 1EZ, UK; fax: +44 1223 336033; e-mail: deposit@ccdc.cam.ac.uk)". Crystal structures of proteins should be submitted to the Protein Data Bank (see [http://www.rcsb.org/pdb](http://www.rcsb.org/pdb); e-mail: info@rcsb.org). Please submit a copy of the CIF data when you submit your manuscript.

Elemental analysis results for compounds which have been adequately described in the literature must be given in the form: (Found: C, 62.9; H, 5.4. Calc. for C13H13O4N: C, 63.2; H, 5.3%.) New compounds must be indicated by giving analytical results in the form: (Found: C, 62.9; H, 5.4. C13H13O4N requires: C, 63.2; H, 5.3%).

Thin-layer chromatography
(a) For analytical TLC, dimensions of the plates can be deleted if layer thickness is 0.25 mm.
(b) Abbreviate common adsorbents: (but use silica gel, not SiO2 as this does not describe the material accurately), Al2O3 (alumina).
(c) Preparative forms of the technique should include details of (i) layer thickness (preparative TLC only), (ii) amount of sample applied to the layer, (iii) method of detection used to locate the bands and (iv) the solvent used to recover the compounds from the adsorbent after development.
(d) Special forms of TLC on impregnated adsorbents can be abbreviated, e.g. AgNO3-silica gel (1:9), by wt can be assumed.
(e) Solvent mixtures should be specified as under **Abbreviations** above.

Gas chromatography
(a) Detector used should be specified, e.g. dual FID, EC, etc.
(b) Carrier gas and flow rate or inlet pressure should be given, e.g. N2 at 3 ml min-1/10 psi.
(c) Operating conditions, such as injector and detector heater temperatures, oven temperature programme, should be included.
(d) Packed columns, e.g. 6 m x 3 mm (i.d. measurement only) packed with 1% SE-30 (support material and mesh size can be omitted unless unusual).
(e) Capillary columns the type (e.g. WCOT, SCOT), manufacturer's designation (e.g. DB5) and dimensions (length, internal/external diameter, film thickness) should be specified.

High performance liquid chromatography
(a) Solvent or solvent gradients used together with flow rate should be given.
(b) Column dimensions (length x i.d. only) and packing used.
(c) Method of detection employed, e.g. UV or refractive index.

Biochemical conventions
Unless a common biochemical term (e.g. ATP, NADH), biochemicals that are abbreviated should be spelled out in full (in brackets) immediately following their first usage in the text.
Enzyme names are typically not abbreviated, unless there are accepted abbreviations, such as ATPase. Where possible, E.C. numbers should be used for enzymes, and the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB) should be used (see below).

Enzyme characterization
(a) Enzyme activity is expressed in units of katals (symbol kat), the conversion of one mol of substrate per sec. It should be made clear that the measurements were made under specified optimum conditions and were not seriously affected by losses during extraction and analysis.
(b) pH optima should be given together with pH values for half maximal activity.
(c) Kinetic parameters should be expressed as $V_{\text{max}}$, $K_m$ etc.
(d) Enzyme inhibitors-effectiveness should be expressed as $K_i$ or concentration for half-maximal activity.
(e) Optimal temperature of enzymes should not be given. This should be expressed in terms of "Energy of Activation" and "Energy of Activation for Denaturation".
(g) Labeling of proteins and nucleic acids-use of labeled precursors in assessing the rate of synthesis of macromolecules must be validated by evidence of real, direct incorporation. The possibility of occlusion or adsorption of isotopic material should be noted and it should be shown that the labeled precursor is incorporated without prior catabolism.

Protein and nucleotide sequences
The Experimental must contain explicit documentation of the ends of nucleotide probes used in the study if previously unpublished, or by appropriate reference to published nucleotide numbers and/or restriction map. In manuscripts to be published in Phytochemistry, any new protein and/or nucleotide sequence must have been submitted to EMBL, GenBank™ or DNA Data Bank of Japan databases, with designated accession number(s) obtained prior to paper acceptance by the Regional Editor. The Author(s) must ensure access to this database information by timely release of data prior to publication, as well as providing necessary documentation to those already in the databases.

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EMBL Nucleotide Sequence Submissions, European Bioinformatics Institute, Hinxton Hall, Hinxton, Cambridge CB10 1SD, UK. Tel.: +44 (0) 1223-494401; fax: +44 (0) 1223-494472; e-mail: datasubs@ebi.ac.uk; world wide web: http://www.ebi.ac.uk/embl
DNA Data Bank of Japan, Center for Information Biology, National Institute of Genetics, Mishima, Shizuoka 411-8540, Japan. Tel.: (+81) 559-81-6853; fax: (+81) 559-81-6849; e-mail: ddbsub@ddbj.nig.ac.jp (for data submissions); world wide web: http://www.ddbj.nig.ac.jp.
Contributors must obtain the designated accession number, which will be incorporated into the paper, prior to printing.

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