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The title must be clearly intelligible to a non-specialist. The use of jargon and non-standard abbreviations in the title is not permitted.

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The abstract should be a single paragraph, not exceeding 200 words. URLs and references to figures or schemes should NOT be included. However, note that URLs **MUST** be included in the abstract of manuscripts submitted to the Database and Web Server issues. References should not normally be included in the abstract.

Funding

Details of all funding sources for the work in question should be given in a separate section entitled 'Funding'. This should appear before the 'Acknowledgements' section.

The following rules should be followed:

- The sentence should begin: 'This work was supported by ...'
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- Multiple grant numbers should be separated by a comma as follows: '[grant numbers xxxx, yyyy]'
- Agencies should be separated by a semi-colon (plus 'and' before the last funding agency)
- Where individuals need to be specified for certain sources of funding the following text should be added after the relevant agency or grant number 'to [author initials]'.

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References

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Citations should conform to the following examples. Journal names should be abbreviated in the style of *Chemical Abstracts*. Where the list of authors is extensive it is acceptable to list the first 10 authors followed by *et al*. **NOTE THAT FULL TITLES OF JOURNAL ARTICLES MUST BE PROVIDED.**

1. Schmitt,E., Panvert,M., Blanquet,S. and Mechulam,Y. (1995) Transition state stabilisation by the 'high' motif of class I aminoacyl-tRNA synthetases: the case of *Escherichia coli* methionyl-tRNA synthetase. *Nucleic Acids Res.*, **23**, 4793-4798.
2. Huynh,T.V., Young,R.A. and Davies,R.W. (1988) Constructing and screening cDNA libraries in lambda_{bd}gt10 and lambda_{bd}gt11. In Glover,D.M. (ed.), *DNA Cloning - A Practical Approach*. IRL Press, Oxford, Vol. I, pp. 49-78.
3. Maniatis,T., Fritsch,E.F. and Sambrook,J. (1982) Molecular Cloning: A Laboratory Manual. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.
4. Burnett,R.C. (1993) EMBL accession no. X52486.
5. Capaldi,S., Getts,R.C. and Jayasena,S.D. (2000) Signal amplification through nucleotide extension and excision on a dendritic DNA platform. *Nucleic Acids Res.*, **28**, e21.
6. Qiao,D., Chen,W., Stratagoulis,E. and Martinez,J. (March 10, 2000) Bile acid-induced activation of activator protein-1 requires both extracellular signal-regulated kinase and protein kinase C signaling. *J. Biol. Chem.*, 10.1074/jbc.M908890199
7. Qiao,D., Chen,W., Stratagoulis,E. and Martinez,J. (2000) Bile acid-induced activation of activator protein-1 requires both extracellular signal-regulated kinase and protein kinase C signaling. *J. Biol. Chem.*, **275**, 15090-15098. First published on

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May 19, 2000, 10.1074/jbc.M908890199

8. Bernhagen J., Elkin, B., Geiger, G., Tovar, G. and Vitzthum, F. (1999) Patent DE-198198889.2-44; PCT/WO/EP/99/03047.

Nomenclature conventions

Restriction enzymes, DNA methyltransferases and homing endonucleases should be named or referred to using the conventions described in Roberts R.J. *et al.* (2003) *Nucleic Acids Res.*, **31**, 1805-1812. Note that restriction enzyme names should NOT be italicized.

Computer programs

For Computational Biology papers that describe a computer program, the authors should either make the program accessible as a web server with no login requirements or be prepared to make available to the reviewers an executable version of the program and instructions for use. Any costs associated with a reader acquiring the program must be specified in the text. Note that in general any complicated mathematics needed to explain an algorithm should be included as supplementary material.

NMR papers

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Supplementary references which have not already been cited in the manuscript must appear in the main reference list, as the last references in the list, as well as in the relevant supplementary files. A statement must be added at the end of the manuscript, listing all supplementary references. An example is shown below:

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Deposition of sequence and structural data

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2. Authors should be encouraged to upload, as unpublished supplementary material, the output of the an appropriate structural validation server corresponding to deposited structure file structures described in the manuscript (see <http://deposit.pdb.org/validate/>). This material will be available to reviewers .

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4. Databases:

The Cambridge Crystallographic Data Centre (CCDC) is appropriate for deposition of data on nucleosides, nucleotides and other small molecules.

A member site of the [Worldwide Protein Data Bank: RCSB PDB](#), [Protein Databank in Europe \(PDBe\)](#), [Protein Databank in Japan \(PDBj\)](#), or [BMRB](#) is appropriate for deposition of data on proteins determined by X-ray crystallography and for all macromolecules determined by NMR methods.

The Nucleic Acid Database (NDB) is appropriate for atomic co-ordinate and structure factor data for crystal structures of nucleic acids. This can generally be handled by the Worldwide Protein Data Bank or RCSB Protein Data Bank described above.

5. NMR papers: Resonance assignments should be reported relative to DSS and not to HOD.

For papers reporting novel protein sequences

Protein sequences, which have been determined by direct sequencing of the protein, must be submitted to [UniProt](#) using the interactive submission tool SPIN. Please note that they do not provide accession numbers, IN ADVANCE, for protein sequences that are the result of translation of nucleic acid sequences. These translations will be forwarded automatically from the nucleotide sequence databases (EMBL/GenBank/DBJ) and assigned UniProt accession numbers on incorporation into UniProt. Results from characterization experiments should also be submitted to UniProt: for novel sequences, these should be included with the sequence submission. Existing UniProt entries should also be updated. This can include information such as function, subcellular location, subunit, etc.

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