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Manuscripts of the following types will be declined without full review because they do not satisfy the guidelines for publication in the Journal.

Insufficient Novelty, Importance or Biochemical Contribution

Manuscripts that report contributions that are judged to be of insufficient importance or novelty or that fail to provide mechanistic insights into biological processes at the biochemical or molecular level. In the absence of novelty and biochemical importance, medical relevance or pharmacological potential alone will not be considered sufficient to justify publication.

Methodology

Manuscripts that report development of a new technique without also reporting novel and significant biochemical insights.

Sequencing and Cloning

Manuscripts reporting an amino acid or nucleotide sequence, or the cloning and expression of a gene, if the same protein or gene from another tissue or organism has already been described.

Manuscripts reporting the cloning and sequencing of a novel gene without providing experimental evidence for its biological function.

Enzymology

Manuscripts describing just the purification and/or characterization of an enzyme or protein if the same enzyme or protein has been described from another tissue or organism.

Macromolecular Interactions

Manuscripts that describe biochemical analyses of interactions between macromolecules or between macromolecules and small ligands OR results of two-hybrid screens, co-immunoprecipitation, gel mobility shift, or related assays without providing information about the functional consequences of the interactions.

Manuscripts that rely solely on the use of protein over-expression in transfected cells or the use of recombinant proteins to demonstrate protein-protein interactions, without providing evidence that such interactions occur between protein partners expressed from the endogenous genes in relevant cell lines or tissues.

Transcription and RNA Processing

Manuscripts that focus on identifying regulatory elements and the proteins that bind them without providing new insights into molecular mechanisms of gene expression or regulatory protein function. Manuscripts that simply identify methylated sites in a gene or promoter, or demonstrate that the methylation status of a gene correlates with gene expression, without providing novel information about how methylation is controlled or how methylation controls gene expression.

Regulation of Metabolism and Gene Expression

Manuscripts that merely describe the effects of agents such as drugs, hormones, cytokines, or the effects of the state of differentiation on an "end point" (enzyme activity, protein level, mRNA abundance, or descriptive aspect of a cellular response). Manuscripts in which reagents are assumed to act specifically without a suitable demonstration or reference documenting their specificity. Manuscripts that rely solely on the use of pharmacological agents to define a biochemical process.

Post-translational Modification

Manuscripts describing modification of a protein by a well-established process such as glycosylation, phosphorylation, fatty acylation, or prenylation without showing the biological or biochemical significance of the modification or providing novel insights into the mechanism of the modification process.

Glycobiology

Manuscripts that report the structure of an oligosaccharide not differing substantially from an oligosaccharide that was described earlier for another glycoconjugate.

Mutational Analysis of Proteins

Manuscripts reporting that mutation of a protein alters its function without providing clear evidence about the mechanism by which the function is altered.

Transgenics and Knockouts

Manuscripts that use transgenes or knockouts to confirm results reported previously in model systems without adding new mechanistic insight into the processes involved. Manuscripts that report generation of transgenic or knockout mutants that lack demonstrated phenotypes and/or that fail to provide new insights into biochemical processes.

Functional Genomic, Metabolomic, and Proteomic Analysis

Manuscripts that describe genome-, metabolome-, or proteome-scale functional analysis by differential display, microarray, mass spectrometry, or other methods without providing novel insight into a biochemical process or its regulation.

Computational Biochemistry and Biomolecular Networks

Manuscripts describing computational analyses in structural biology, enzyme kinetics, systems biology and bioinformatics that do not provide significant new insights into biochemical processes.

Studies on Cell Cycle and Apoptosis with Flow Cytometry

Manuscripts describing studies of either cell cycle or apoptosis that use inadequate FACS analysis procedures (e.g., single parameter DNA histograms of a single time point) to establish biological states.

RNAi

Manuscripts that report experiments using RNA interference (RNAi) without appropriate controls as described in Nature Cell Biology 5, 489-490 (2003). Such controls may include use of siRNAs with one or two nucleotide changes from the target sequence, multiple siRNAs for the same target, and rescue by expression of target sequences refractory to siRNA.

Experimental Uncertainty and Reproducibility

Manuscripts that report results that are not accompanied by explicit analyses of experimental uncertainty and reproducibility. Acceptable analyses of experimental uncertainty of numerical data include the standard deviation, the standard error, or the mean and range of values obtained from replicate experiments, as appropriate. Bar graphs and scatter plots (X,Y plots) should include error bars and the meaning of the error bars should be defined in the text. Plots that include lines that represent computed fits of experimental data to equations must be accompanied by the equation used to calculate the fit, the values of the fit parameters, and statistics that characterize the quality of the fit.

Last Updated: **23 April 2008**