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INTRODUCTION

Cytokine is devoted exclusively to the study of the molecular biology, biochemistry, immunology, diagnostic and clinical applications of all known interleukins, hematopoietic factors, growth factors, cytotoxins, interferons, and new cytokines. Cytokine provides comprehensive coverage of cytokines and their receptors, 12 times a year, by publishing original high quality refereed scientific papers from prominent investigators in both the academic and industrial sectors.

New requirements
Authors must provide the name, position, institution, and e-mail contacts of at least 5 potential reviewers, who are not the collaborators, friends and relatives, and are working at the authors' organization/institution.

Authors cannot use broad terminologies, such as Cytokines, Chicken, Human, etc., at the time of submission of their manuscripts. Such terms are not useful for identifying potential reviewers. They should provide at least 6 keywords based on the content of the study. For example, if an author is submitting a paper, "Interleukin-6 effects on arthritis and the study describes therapy with a new drug and the discovery of biomarkers for the action of the said drug" they must provide some keywords like the following: IL-6, arthritis, transcriptome, signal transduction, inhibition, B-cells, macrophage, therapeutics.

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To accelerate the speed of review and publication of data, we limit the reviews to a maximum of 3 rounds per manuscript (original submission+ 2 rounds of revision). The first revision must address all major concerns (e.g., new data and experiments are needed). After that we will allow only one more revision, that addresses any minor concerns (e.g., display of graphs, tables, missing statements and grammatical mistakes). Please revise thoroughly and check the manuscript for any mistakes before submitting the revised version.

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To ensure the authenticity and reproducibility of the data, we require the authors to include the following in their papers as applicable.
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Mycoplasma contamination of cell lines produces spurious data. Authors should certify in the Material and Methods section in written statement that cell lines in their study have been tested and found free of Mycoplasma.

A significant concern worldwide is the contamination of cell lines with other cell types or cancer types. Authors should certify that the cell lines' authenticity was verified using STTR markers, whole-genome sequencing, or an equivalent method. Disclose details of analysis in the Material and Methods section.

Several antibodies for the same protein for different applications are commercially available, e.g., Western blot, Immunoprecipitation, Immunohistochemistry, ELISA, and Chromatin Immunoprecipitation analyses. Many are not suitable for all/some of the applications. In light of these, authors should mention the Source of the antibody, Catalog number, the intent (e.g. Western) and dilutions used in their study.

All primers, their sequence and the expected PCR product sizes must be presented in a tabular format. The application for which a primer set was used (for example RT-PCR, or ChIP assay, mutational analyses) should be indicated in the table legend.

Unless there are large data sets that cannot fit into a standard figure or table, all relevant supplementary data should be part of the main paper for an easier understanding.

The importance of a protein involved in a given biological process must be validated using RNAi technology. shRNA expression vectors for many genes are commercially available. A control shRNA and a gene-specific shRNA must be included when validating the data. Exogenous add-back of knocked-down gene product could be used for better validation controls of phenotypes as well. Authors must evaluate quantitatively the efficiency of knockdown in their experimental system.

Studies using animal models should include both equal/comparable numbers of females and males to establish a global relevance to both genders. Some exceptions to this requirement are: 1) the disease is gender-specific (e.g., breast cancer in females and prostate cancer in males); and 2) the genetic model produces the disease only in a gender-specific manner. The authors should make explicit statements in case only one gender was mainly used for experimental read out. Power calculations for choosing the numbers of animals per each experimental group, Statistical methods used, the exact significance of the differences must be indicated for each experiment.

**Types of paper**

**Review Articles** are comprehensive appraisals of research and clinical outcomes in a field of current interest related to cytokine biology. All reviews are subject to the normal peer review process. Reviews are mostly invited by the *Editor-in-Chief*. Interested authors may contact our Support Center to present an outline.

**Research Articles** are full-length descriptions of original research. The scope may include basic science, clinical results, or applications. These manuscripts will undergo standard review.

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**CYTOKINE policy on papers using cell lines** In light of increasing evidence that many cell lines grown in some labs previously (Bian et al, A Combination of Species Identification and STR Profiling Identifies Cross-contaminated Cells from 482 Human Tumor Cell Lines. Sci
Rep. 2017 Aug 29;7(1):9774; Ye et al, Genetic profiling reveals an alarming rate of cross-contamination among human cell lines used in China. FASEB J. 2015 Oct;29(10):4268-72 may have been cross-contaminated (https://iclac.org/databases/cross-contaminations/). Cytokine is concerned about the validity of the data obtained using such cell lines. Therefore, all studies that report cell line-based data should authenticate the cell lines used. Some recommended methods for authenticating cell lines can be found here: https://www.atcc.org/en/Services/Testing_Services/Cell_Authentication_Testing_Service/Cell_Line_Authentication_Test_Recommendations.aspx https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4907466/ The authors should make an explicit statement in the Materials and Methods section that their specific cell lines have been verified using one of the above methods.

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1) All genetic polymorphism (such as Single Nucleotide Polymorphism) analyses must include at least 400 individual samples.

2) SNP data must be accompanied with the measurement of specific immunological parameters such as cytokine measurement, flow cytometry, cellular responses, etc., demonstrating a comparison of biological data between subjects with the genetic variant and those who lack the genetic variant being studied. Expression of cell surface receptors by flow coupled with the genetics of that receptor, or looking at TH1/TH2 skewing or cellular maturation in the setting of particular variants are recommended.

3) Papers lacking such data will not be considered for review.

**New policies following an editorial meeting at Vienna, Oct 20, 2019:**

Since many manuscripts are taking longer than the usual time to publish from the date of first submission and it is becoming increasingly difficult to recruit reviewers, the editorial board in consultation with the Editor-in-Chief, and the publisher, made the following recommendations. These guidelines will be updated at the submission website too.

Manuscripts will be reviewed to a maximum of 3 rounds (i.e., original+2 rounds of revision). A revision of manuscript is indicated by the letter R. After the original review is completed, reviewer comments will be provided to authors. The authors must complete all major revisions in the R1 version. Major revisions include providing data from additional experiments, data presentation and analyses, and quality of the images and the correct use of scientific English. Only minor revisions such as modification of an interpretation, missing references, reploting the data or order of figure presentation (if necessary), and inclusion of a missing control will be allowed in the R2 version. If a manuscript is not suitably modified by the R2 stage, editors can reject a further review.

Author response (rebuttal) to review comments must be complete. Responses such as, "Done", "Completed", "Changed", "Modified as suggested" are no longer acceptable. The rebuttal must indicate the details of all modifications made in response to each question/concern raised in the review. Such details must include the exact page numbers, paragraphs, figure or table numbers, subsection of a manuscript. They also must detail all data changes (deleted or added) to the revised manuscript and references (added or deleted), the subpanels of a figure, or the columns and rows of the revised manuscript where the new data are presented. Manuscripts not adhering to these instructions will not be considered.

Authors must provide the name, position, institution, and e-mail contacts of at least 5 potential reviewers, who are not the collaborators, friends and relatives, and are working at the authors' organization/institution.

Authors cannot use broad terminologies, such as Cytokines, Chicken, Human, etc., at the time of submission of their manuscripts. Such terms are not useful for identifying potential reviewers. They should provide at least 6 keywords based on the content of the study. For example, if an author is submitting a paper, "Interleukin-6 effects on arthritis and the study describes therapy with a new drug and the discovery of biomarkers for the action of the said drug" they must provide some keywords like the following: IL-6, arthritis, transcriptome, signal transduction, inhibition, B-cells, macrophage, therapeutics.
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