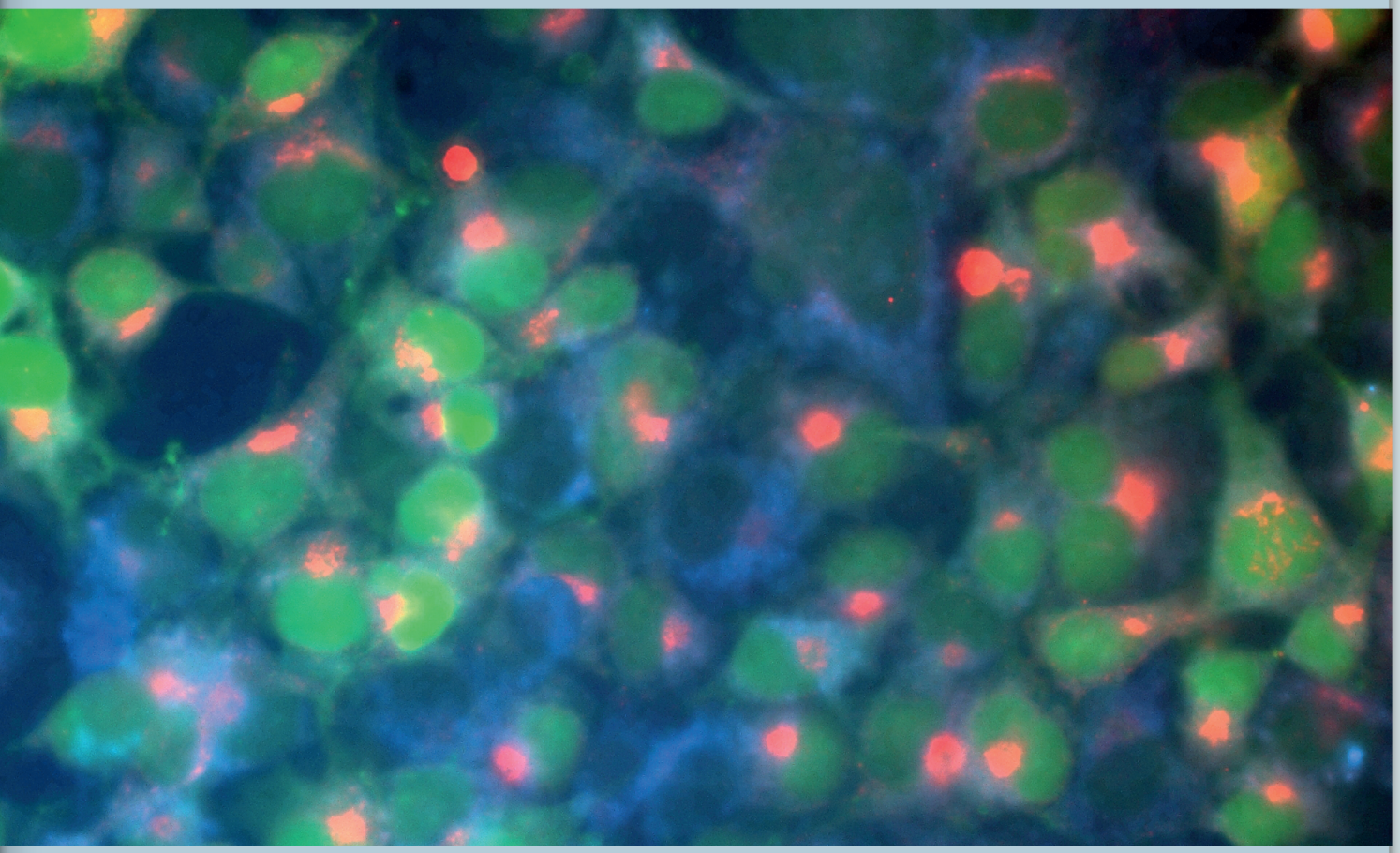
DE GRUYTER

2018 · VOLUME 399 · ISSUE 6
ISSN 1431-6730 · e-ISSN 1437-4315

BIOLOGICAL CHEMISTRY



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BIOLOGICAL CHEMISTRY

Founded in 1877 by Felix Hoppe-Seyler as
Zeitschrift für Physiologische Chemie

Felix Hoppe-Seyler (1825–1895) was a pioneer of biochemistry, remembered not only for his discovery of hemoglobin and his contributions to the chemical characterization of many other biological compounds and processes but also for having been the mentor of Friedrich Miescher and Albrecht Kossel. In his preface to the first issue of ***Zeitschrift für Physiologische Chemie,*** Felix Hoppe-Seyler coined the term ***Biochemistry*** ('Biochemie') for the then newly emerging discipline.

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ABSTRACTED/INDEXED IN Academic OneFile (Gale/Cengage Learning), ASFA1: Biological Sciences & Living Resources, Biochemistry & Biophysics Citation Index, Biological Abstracts, BIOSIS Previews, CAB Abstracts, Calcium and Calcified Tissue Abstracts, Chemical Abstracts and the CAS databases, CSA Illustrata - Natural Sciences, CSA Neurosciences Abstracts, Current Contents/Life Sciences, Elsevier BIOBASE/Current Awareness in Biological Sciences (CABS), EMBASE - the Excerpta Medica database, EMBiology, Index Medicus/MEDLINE, Journal Citation Reports/Science Edition, Reaction Citation Index, Reference Update, Science Citation Index, Science Citation Index Expanded (SciSearch), Scopus, SIIC Data Bases, Zoological Record.

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ISSN 1431-6730 · e-ISSN 1437-4315 · CODEN BICHF3

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TYPESETTING Compuscript Ltd., Shannon, Ireland

PRINTING Franz X. Stückle Druck und Verlag e.K., Ettenheim

COVER ILLUSTRATION
On the front cover, immunofluorescence analysis of COS-7 African green monkey kidney cells expressing the mouse Serpina1 paralog DOM-7 is depicted (red: DOM-7; blue: endoplasmic reticulum marker Grp78/BiP; green: eGFP). The murine *Serpina1* genes are the orthologues to human α1-antitrypsin (*SERPINA1*) and they are important targets for the creation of authentic mouse models recapitulating human severe α1-antitrypsin deficiency. The mouse *Serpina1* cluster consists of three to five genes which are arranged on a ~250 kb stretch on chromosome 12 and the number of paralogs as well as their exact arrangement is strain-dependent. So far, seven paralogs have been identified in different mouse strains (DOM-1 to -7) and it is known that DOM-1 and DOM-2 are efficient inhibitors of neutrophil elastase, whereas DOM-3, -4, -5 and -6 mostly inhibit chymotrypsin. So far, DOM-7 has not been functionally characterized. In their study presented on pp. 577–582 in this issue, Jülicher et al. isolated DOM-7 cDNA from BALB/cAnnCrl mice and confirmed the presence of a DOM-7-specific sequence in the BALB/c genome. DOM-7 was then overexpressed in COS-7 cells, and cell supernatants were used for functional analyses. In specialized assays DOM-7 inhibited both, neutrophil elastase and chymotrypsin. These results suggest that DOM-7 needs to be considered when aiming at the generation of authentic α1-antitrypsin deficiency models from DOM-7-positive mouse strains. Moreover, the complexity of the mouse Serpina1 gene locus may be larger than previously anticipated, and therefore needs to be properly analyzed before and after genome engineering by state-of-the-art methods, such as CRISPR.
Image courtesy of Reto Eggenschwiler, Hannover Medical School, Hannover, Germany.

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