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.

Biological Chemistry is associated with the Gesellschaft für Biochemie und Molekularbiologie e.V. (GBM)

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COVER ILLUSTRATION
Since 2005, the DFG Graduiertenkolleg (Research Training Group) 1026 'Conformational transitions in macromolecular interactions' in Halle/Saale, Germany, has focused on the relationship between protein folding transitions and their interactions with biological macromolecules using a wide range of methodologies, examples of which are depicted on the front cover. Top left image: Munc13 proteins play an important role in the control of neuronal short term synaptic plasticity. Crosslinks between Munc13-3 (blue) and calmodulin (grey) are indicated by dotted lines with their distances (in Å) between covalently linked amino acids (green sticks), together with photo-affinity labelling constraints (connected residues as purple sticks). See the article by Herbst et al. on pp. 763–768 in this issue. Top right: single molecule fluorescence techniques yield information concerning the heterogeneous conformational ensembles of unfolded proteins and their journeys to the folded state. By monitoring Förster resonance energy transfer (FRET) between donor and acceptor fluorophores of a doubly labelled polypeptide in a confocal setup, the subpopulation of unfolded chains can be identified, even in the presence of an excess of folded proteins. See the article by Hofmann on pp. 791–799. Bottom left: the murine polyomavirus encodes three structural proteins, VP1-VP3, which together form the viral capsid. The outer shell is composed of 72 VP1 pentamers arranged in an icosahedral manner (illustrated), whereas the minor coat proteins VP2 and VP3 form an inner shell with each VP1 pentamer binding either VP2 or VP3 in its inner central cavity. Whereas the structure and functions of VP1 are well understood, the propensity of the minor coat proteins to aggregate has precluded further characterization until now. The refolding as well as initial biophysical and functional analyses of these proteins are presented by Burkert et al. on pp. 871–881 in this issue. Bottom right: a high-resolution crystallographic structure determination of a protein-ligand complex is generally accepted as the 'gold standard' for structure-based drug design. Yet how much does a crystal structure actually reveal about ligand affinity? A model system, in which the ligand binding pocket of coagulation factor Xa has been grafted on to the homologous digestive enzyme trypsin, has been developed in order to investigate issues of affinity and selectivity. Unexpectedly, the chimeric factor Xa-like trypsin variants demonstrate significant differences in structure (shades of blue) both in the presence (grey sticks) and absence of ligands. Moreover, the variants exhibit a range of dynamic properties that allow interrogation of the influence of protein flexibility on ligand interactions. See the articles by Tziridis et al. on pp. 891–903 and Menzel et al. on pp. 905–911.

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