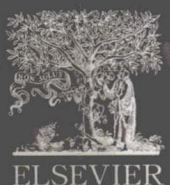


# The Desk Encyclopedia of Microbiology

## 微生物学案头百科

Editor : Moselio Schaechter



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Moselio Schaechter

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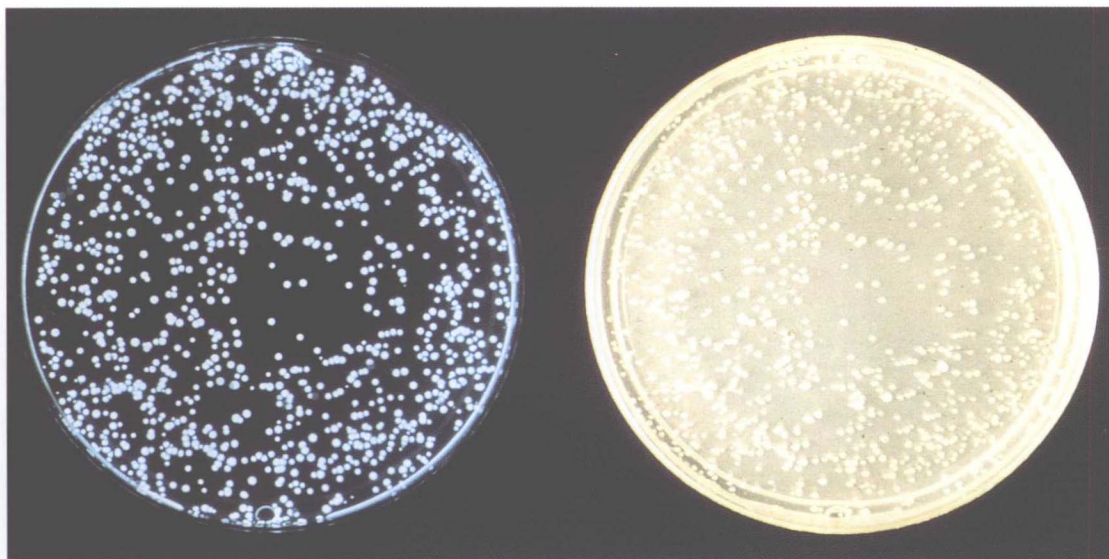
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**PLATE 1** The attachment of uropathogenic *Escherichia coli* to the luminal surface of the bladder epithelium by type 1 pili as visualized by high-resolution freeze-fracture, deep-etch electron microscopy. See Fig. 1.1.

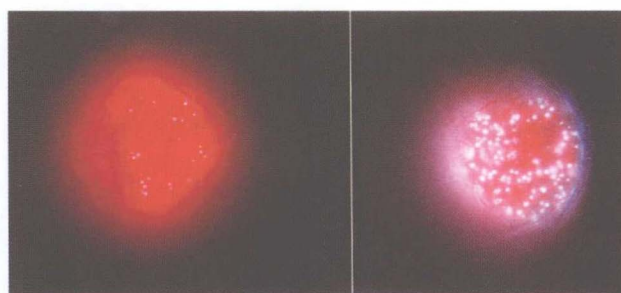




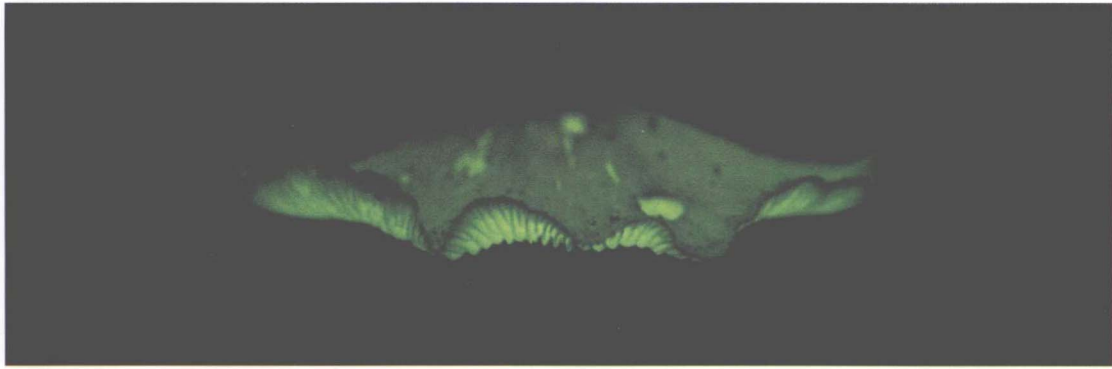
**PLATE 2** Colonies of luminous bacteria photographed by their own light (left) and in room light (right). Light is emitted continuously but is controlled by a quorum-sensing mechanism (autoinducer) and is thus not proportional to growth or cell density. See Fig. 14.2.



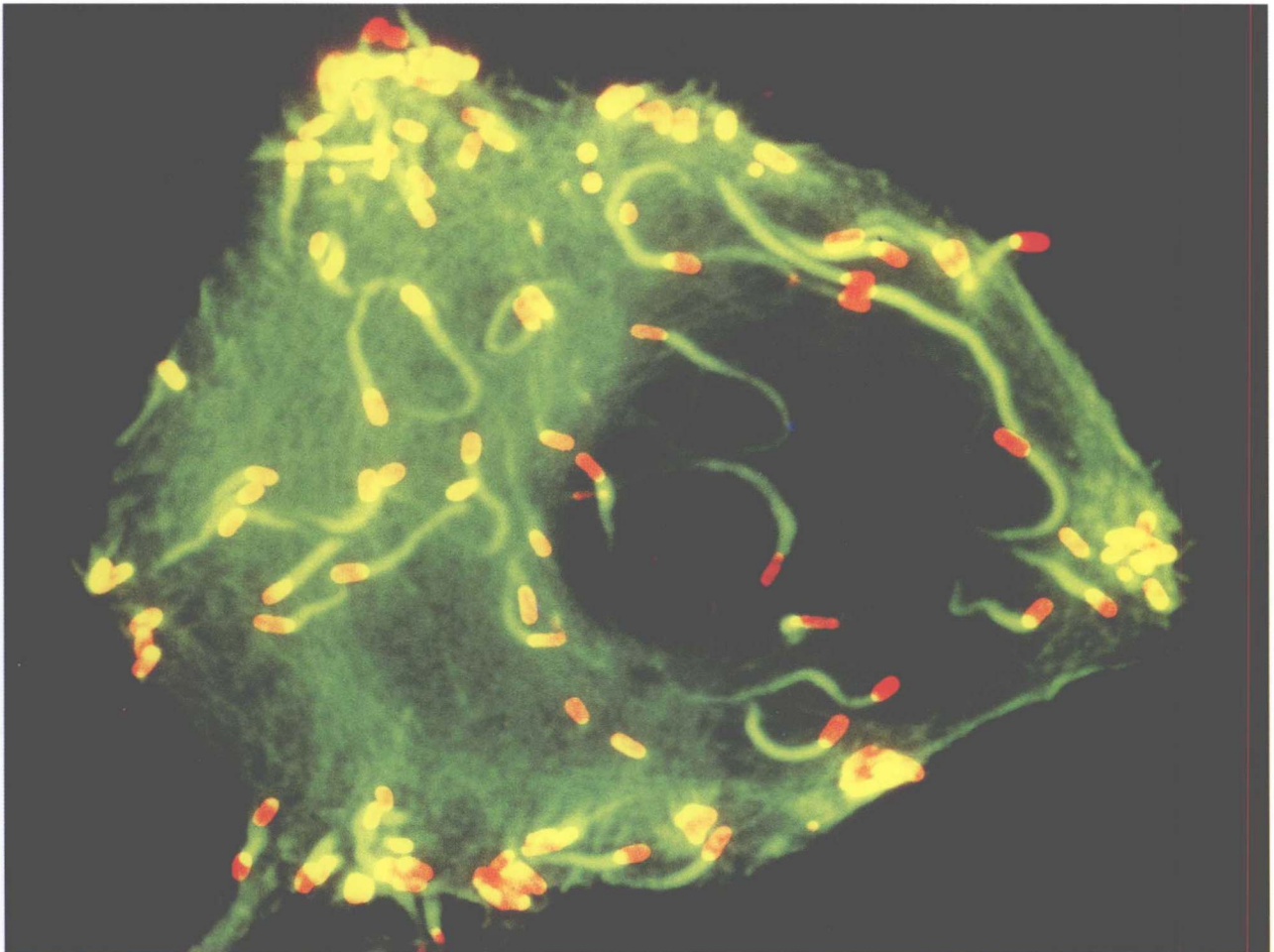
**PLATE 3** The flashlight fish (photoblepharon) showing the exposed light organ, which harbors luminous bacteria and is located just below the eye. A special lid allows the fish to turn the light on and off. See Fig. 14.3.



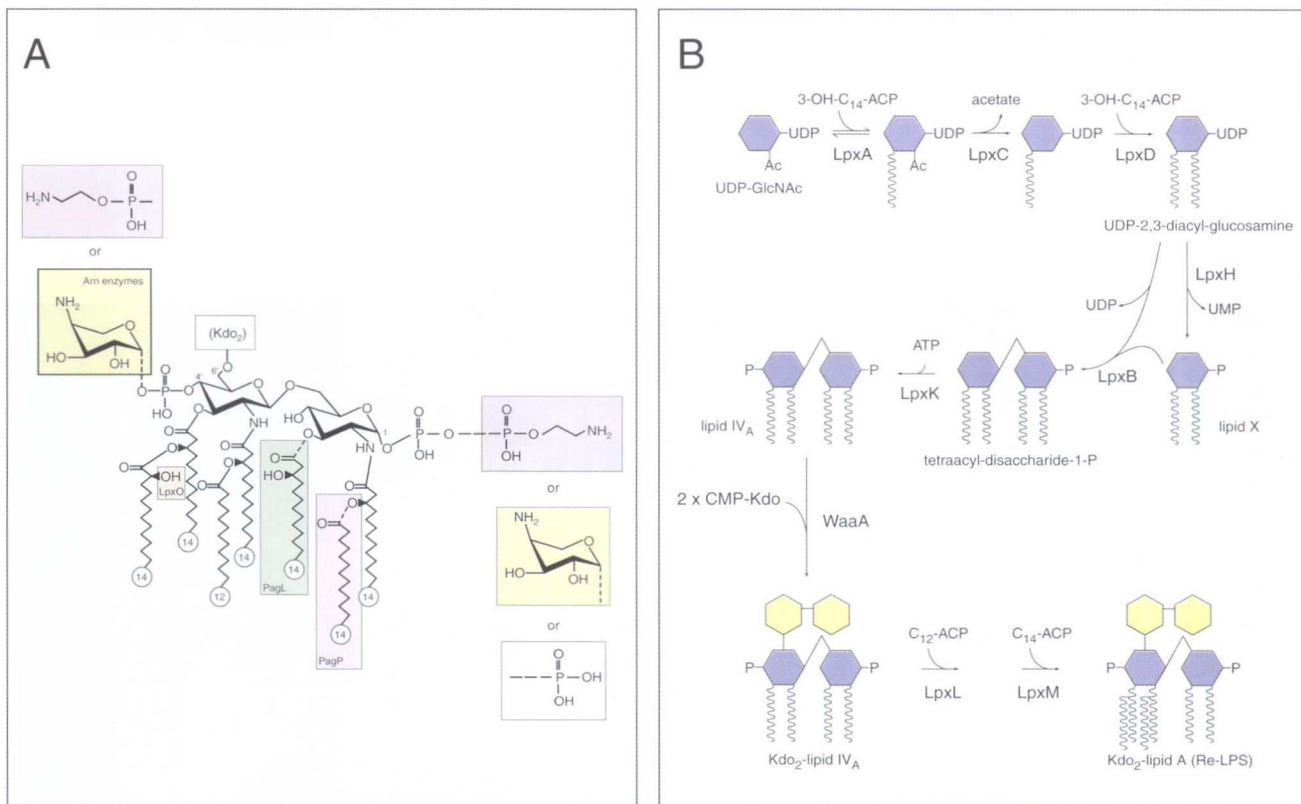
**PLATE 4** *Gonyaulax* cells viewed by fluorescence microscopy showing scintillons (bioluminescent organelles) visualized by the fluorescence of dinoflagellate luciferin ( $\lambda_{\text{max}}$  of emission, 475 nm), with chlorophyll fluorescence as the red background. Scintillons are structurally formed and destroyed on a daily basis, controlled by the circadian clock. (Right) Night phase cell with many scintillons; (left) day phase cell with few scintillons. See Fig. 14.7.



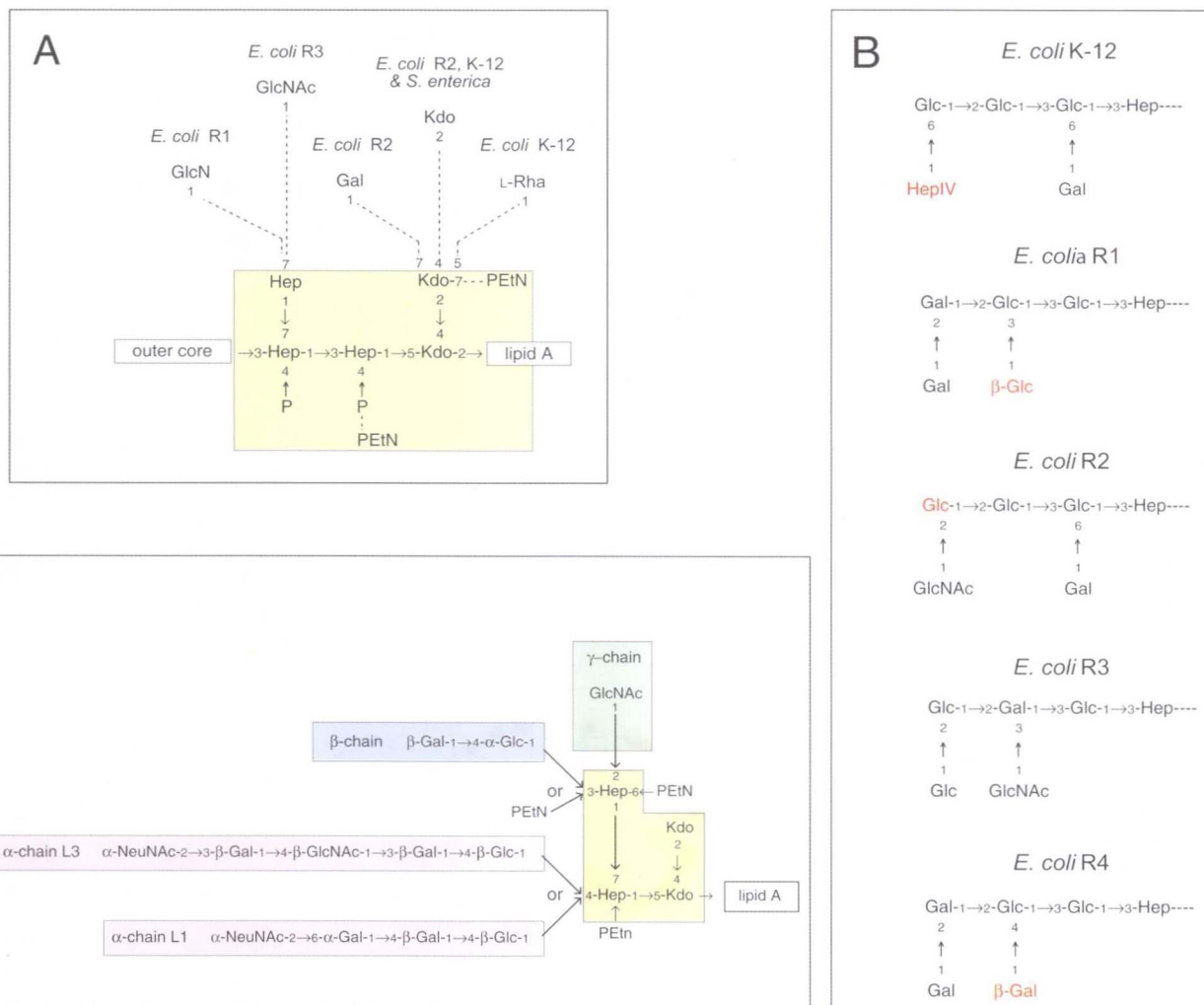
**PLATE 5** Bioluminescent mushroom photographed by its own light. See Fig. 14.10.



**PLATE 6** Actin tail formation by *Shigella flexneri*. Actin microfilaments are polymerized at one end of the bacterium and help it to move within the host cell cytoplasm. Bacteria are stained in red and actin in green. The areas where bacteria and actin colocalize appear in yellow. See Fig. 34.1.

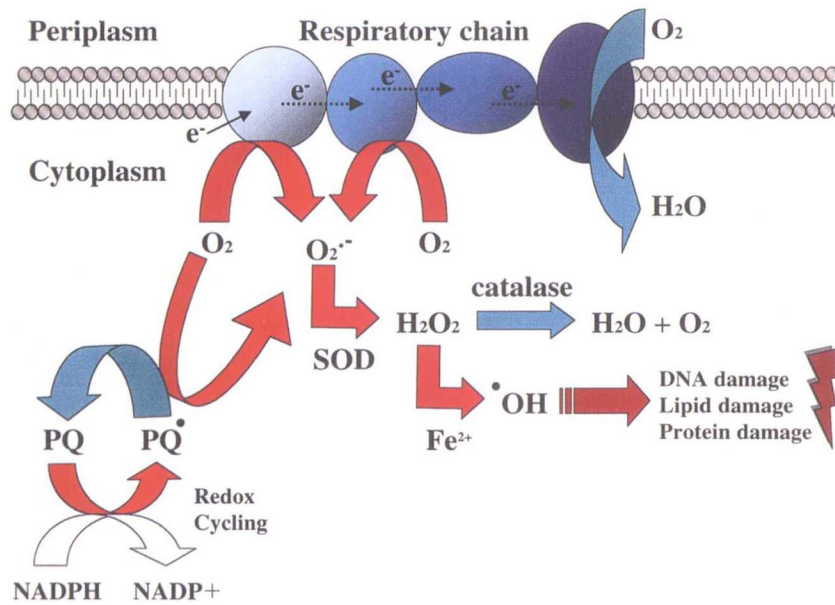


**PLATE 7** Structure and biosynthesis of lipid A. Panel A shows the structure of the lipid A from *E. coli* and *Salmonella*. The basic structure is given in *black* and regulated modifications and, where known, the enzymes responsible are indicated in the *colored* boxes. 4-amino-*L*-arabinose (*yellow* box) is found mainly on the 4' phosphate, whereas phosphorylethanolamine (*blue* box) is mainly located at position 1. Under some growth conditions a pyrophosphate group is found at position 1. PagP (*pink* box) is a PhoP/PhoQ-regulated palmitoyl transferase located in the outer membrane. PagL (*green* box) selectively removes a  $\beta$ -hydroxymyristoyl residue. LpxO (*brown* box) hydroxylates the 3' secondary acyl chain and the process is oxygen-dependent. Panel B shows the pathway for biosynthesis of lipid A from *E. coli* K-12. The enzymes responsible for each step in the pathway are indicated. The completed Re-LPS provides an acceptor for sequential assembly of the core oligosaccharide at the cytoplasmic face of the inner membrane. The completed molecule is then exported across the inner membrane by the ABC-transporter, MsbA (not shown). See Fig. 56.2.

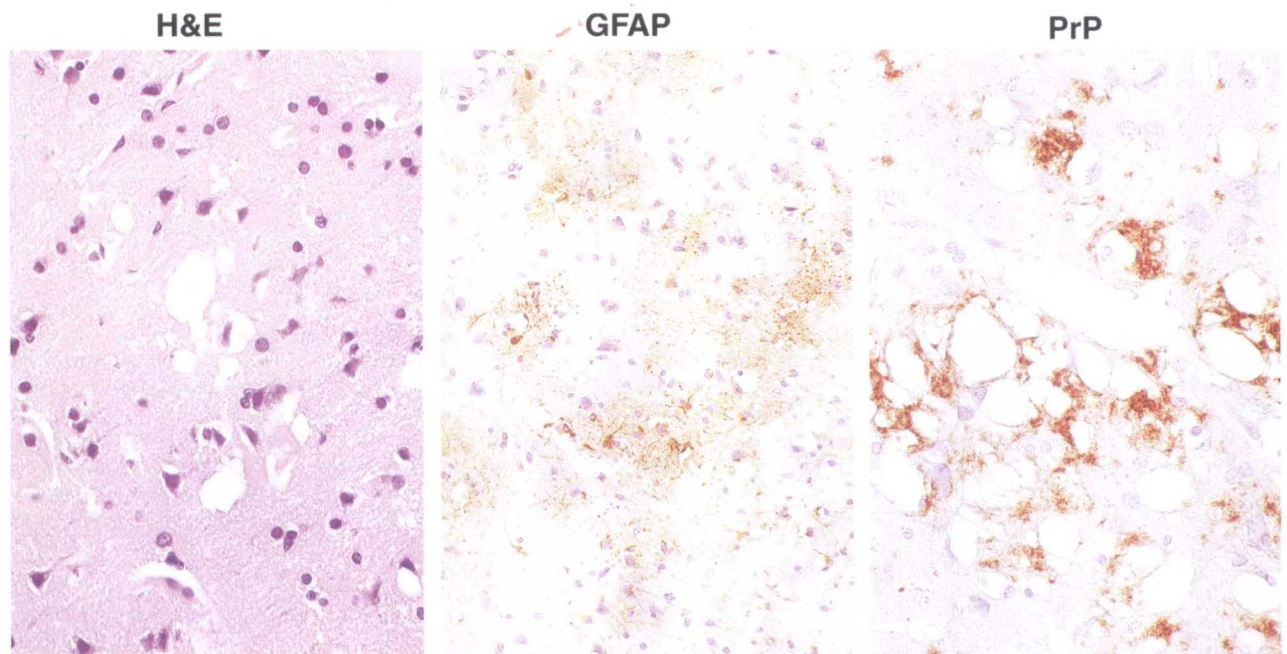


**PLATE 8** Structure of the core OS region of LPS and LOS. Panel A shows the inner core region of the core OSs from *E. coli* K-12. The backbone structure (yellow box) is conserved but nonstoichiometric glycosyl modifications (dotted lines) vary in different core types. Panel B shows the known outer core structures from the five core OSs of *E. coli*. They share a common overall structure, consisting of five glycosyls linked to Hep II, but they differ in glycosyl content, glycosyl sequence, and side branch position. The site of O-PS ligation is not known for all of the core OS types but, where it has been determined, the residue providing the attachment site is indicated in red. Panel C shows a representative LOS structure from *N. gonorrhoeae*. The LOS core (yellow box) is conserved among different strains but there are strain-specific differences in the attached oligosaccharide chains. Shown are 2 possible variants (L1 and L3) of  $\alpha$ -chain (pink boxes) and the  $\beta$ - and  $\gamma$ -chains. Unless otherwise indicated, all residues in the various structures are linked in the  $\alpha$ -configuration. See Fig. 56.3.





**PLATE 9** Reactive oxygen species, oxidative stress, and cellular damage. The majority of the oxygen that enters the cell is reduced to water by the respiratory chain, a reaction that consumes four electrons. However, a small proportion of the oxygen molecules can be reduced in a series of one-electron reactions. Molecular oxygen forms superoxide ( $O_2^{\cdot-}$ ) by reaction with reduced components of the respiratory chain. Superoxide can also be formed by reaction with redox-cycling drugs such as paraquat (PQ), which is enzymatically re-reduced at the expense of NADPH. Superoxide is eliminated by superoxide dismutase (SOD) to form hydrogen peroxide ( $H_2O_2$ ). Hydrogen peroxide can either be detoxified by conversion into water and oxygen by catalase, or react with reduced transition metals such as iron and copper to form a hydroxyl radical ( $\cdot OH$ ). The hydroxyl radical is a highly reactive molecule that can damage virtually all the fundamental cellular components. Solid arrows indicate reactions that yield oxidants. Open arrows indicate reactions that yield innocuous products. See Fig. 66.1.



**PLATE 10** Characteristic features of Creutzfeldt-Jakob disease. Hematoxylin-eosin stain (left) shows the typical vacuoles in the brain of a CJD patient, which leads to the spongiform appearance. Proliferation of reactive astrocytes is visualized by staining with antibodies against glial fibrillary acidic protein (GFAP, middle). PrP protein deposits are shown with anti-PrP immunostaining. See Fig. 71.7.

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