

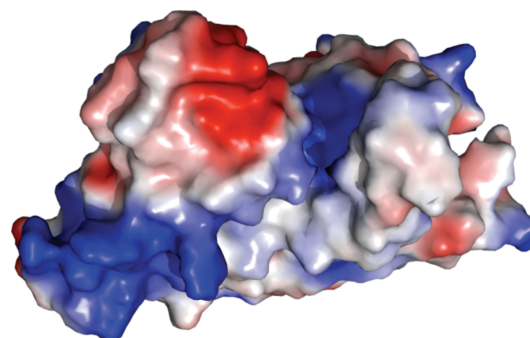
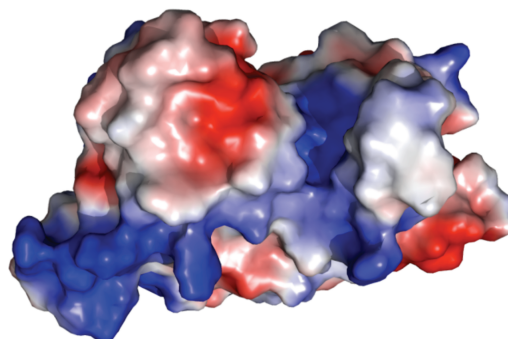
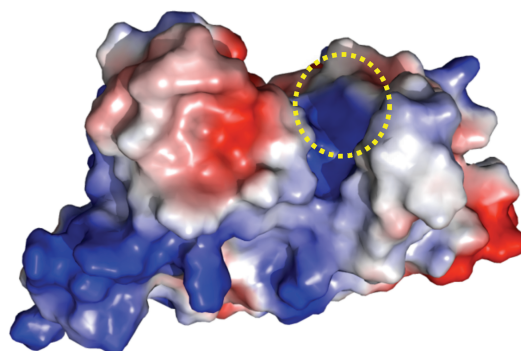
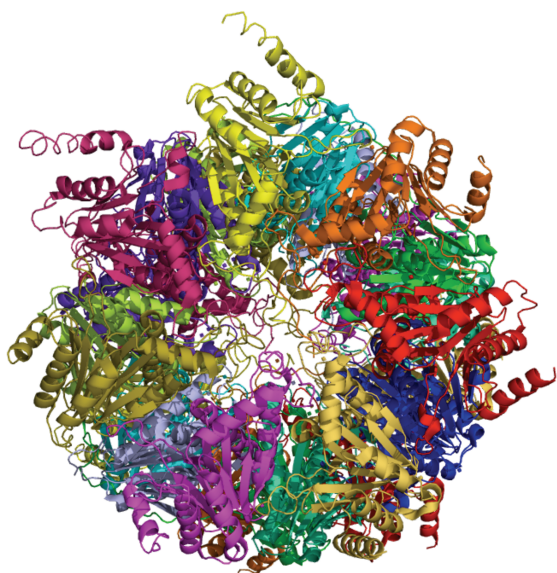
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- Protein Synthesis
- DNA-Protein Interaction
- RNA Processing
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- Genetic Diseases
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Cell Cycle
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COVER:

Discovery in Japan

Structural features of mammalian 20S proteasomes (courtesy of Dr. Tsunehiro Mizushima, Nagoya City University, Japan). Left panel: tertiary structure (ribbon diagram) of standard 20S proteasomes from the bovine liver (top and side views, upper and lower, respectively). Right panel: diagrams of electrostatic surface potential of S1 pockets for the chymotryptic active sites of the standard proteasome (upper), immunoproteasome (middle) and thymoproteasome (lower). The surface is colored according to the electrostatic potential (*blue*, positive; *red*, negative). The catalytic threonine residue is surrounded by a dotted circle (right-top panel). The models of the immunoproteasome and thymoproteasome were predicted from the standard structure.

The proteasome system in vertebrates has acquired considerable diversity among the catalytic subunits, which have evolved during the acquisition of adaptive immunity; i.e., the standard proteasome (1), immunoproteasome (2, 3), and thymoproteasome (4, 5). Whereas the standard proteasome is ubiquitously distributed in many cells and tissues, the immunoproteasome and the thymoproteasome are specifically in the immune tissues, such as the liver and the spleen, and the thymus, respectively (for details, see a review 6).

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