

Volume 1843, Issue 1, January 2014



Cover image: Conformational transition of the proteasome from a substrate-free to an actively degrading state. The structures of the 265 proteasome in its substrate-free (left) and substrate-engaged state (right) (identically orientate-free (left) and substrate-engaged state (right) (identically orientate-lessed on their 250 peptidase (grey), with a dashed line indicating the central axis of the peptidase pore. Substrate engagement induces a conformational rearrangement of the regulatory particle, including a rotation of Rpn2 (dark blue), Rpn13 (light ronge), and the lid subcomplex (yeldw), the formation of contacts between the ubiquitin receptor Rpn10 (pupple) and the Rpd4-Rpt5 colled coil, and a coasial alignment of the A-ring and the AAA-ring (both cyan) with the peptidase. Furthermore, the DUB Rpn11 (green) shifts to a certaral location, occluding the processing pore. (The extra density (red) observed in the reconstruction of the degrading proteasome is attributed to a globular domain of the substrate) (from A Arthrity, see M.E. Matyskela, G.C. Lander, A. Martin (2013) Nat. Struct. Mol. Biol. 20, 781–788.).

Publication information: Biochimica et Biophysica Acta (Molecular Cell Research) (ISSN 0167-4889). For 2013, volume 1833 (12 issues) is scheduled for publication. Subscription prices are available upon request from the Publisher or from the Elsevier Customer Service Department nearest you or from this journal's website (http://www.elsevier.com/locate/bbamcr). Further information is available on this journal and other Elsevier products through Elsevier's website (http://www.elsevier.com/locate/bbamcr). Further information is available on this journal and other Elsevier products through Elsevier's website (http://www.elsevier.com/. Subscriptions are accepted on a prepaid basis only and are entered on a calendar year basis. Issues are sent by standard mail (surface within Europe, air delivery outside Europe). Priority rates are available upon request. Claims for missing issues should be made within isx months of the date of dispatch. Orders, claims, and journal inquiries: please contact the Elsevier Customer Service Department nearest you. St. Louis: Elsevier Customer Service Department, 3251 Riverport Lane, Maryland Heights, MO 63043, USA; phone: (http://www.esvier.com/oxford: Elsevier Customer Service Department, 1251 Riverport Lane, Maryland Heights, MO 63043, USA; phone: (http://st.) (1865) 843424; fax: (http://st.) (1865) 843424; fax: (http://st.) (1865) 843424; fax: (http://st.) (1865) 843424; fax: (http.) (1865) 843970; e-mail: JournalsCustomerService Usatmer Service Department, 1865) (1865) 843424; fax: (http.) (1865) 843970; e-mail: journalsCustomerService(papam@elsevier.com/oxford. 1865) 8430222; fax: (http.) (1865) 8430227; fax: (htt

Printed by Polestar Wheatons Ltd., Exeter, United Kingdom

The paper used in this publication meets the requirements of ANSI/NISO Z39.48-1992 (Permanence of Paper)

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