

44. Dreveny, I., Kondo, H., Uchiyama, K., Shaw, A., Zhang, X. & Freemont, P. S. (2004). Structural basis of the interaction between the AAA ATPase p97/VCP and its adaptor protein p47. *Embo J* **23**, 1030-9.
45. Guo, F., Maurizi, M. R., Esser, L. & Xia, D. (2002). Crystal structure of ClpA, an Hsp100 chaperone and regulator of ClpAP protease. *J Biol Chem* **277**, 46743-52.
46. Lee, S., Sowa, M. E., Watanabe, Y. H., Sigler, P. B., Chiu, W., Yoshida, M. & Tsai, F. T. (2003). The structure of ClpB: a molecular chaperone that rescues proteins from an aggregated state. *Cell* **115**, 229-40.
47. Zhang, X., Shaw, A., Bates, P. A., Newman, R. H., Gowen, B., Orlova, E., Gorman, M. A., Kondo, H., Dokurno, P., Lally, J., Leonard, G., Meyer, H., van Heel, M. & Freemont, P. S. (2000). Structure of the AAA ATPase p97. *Mol Cell* **6**, 1473-84.
48. Wang, J., Song, J. J., Franklin, M. C., Kamtekar, S., Im, Y. J., Rho, S. H., Seong, I. S., Lee, C. S., Chung, C. H. & Eom, S. H. (2001). Crystal structures of the HslVU peptidase-ATPase complex reveal an ATP-dependent proteolysis mechanism. *Structure* **9**, 177-84.
49. Yamada-Inagawa, T., Okuno, T., Karata, K., Yamanaka, K. & Ogura, T. (2003). Conserved pore residues in the AAA protease FtsH are important for proteolysis and its coupling to ATP hydrolysis. *J Biol Chem* **278**, 50182-7.
50. Weibezahn, J., Tessarz, P., Schlieker, C., Zahn, R., Maglica, Z., Lee, S., Zentgraf, H., Weber-Ban, E. U., Dougan, D. A., Tsai, F. T., Mogk, A. & Bukau, B. (2004). Thermotolerance requires refolding of aggregated proteins by substrate translocation through the central pore of ClpB. *Cell* **119**, 653-65.
51. DeLaBarre, B., Christianson, J. C., Kopito, R. R. & Brunger, A. T. (2006). Central pore residues mediate the p97/VCP activity required for ERAD. *Mol Cell* **22**, 451-62.
52. Roll-Mecak, A. & Vale, R. D. (2008). Structural basis of microtubule severing by the hereditary spastic paraplegia protein spastin. *Nature* **451**, 363-7.
53. White, S. R., Evans, K. J., Lary, J., Cole, J. L. & Lauring, B. (2007). Recognition of C-terminal amino acids in tubulin by pore loops in Spastin is important for microtubule severing. *J Cell Biol* **176**, 995-1005.
54. DeLaBarre, B. & Brunger, A. T. (2005). Nucleotide dependent motion and mechanism of action of p97/VCP. *J Mol Biol* **347**, 437-52.
55. DeLaBarre, B. & Brunger, A. T. (2003). Complete structure of p97/valosin-containing protein reveals communication between nucleotide domains. *Nat Struct Biol*.
56. Lee, S. Y., De La Torre, A., Yan, D., Kustu, S., Nixon, B. T. & Wemmer, D. E. (2003). Regulation of the transcriptional activator NtrC1: structural studies of the regulatory and AAA+ ATPase domains. *Genes Dev* **17**, 2552-63.
57. De Carlo, S., Chen, B., Hoover, T. R., Kondrashkina, E., Nogales, E. & Nixon, B. T. (2006). The structural basis for regulated assembly and function of the transcriptional activator NtrC. *Genes Dev* **20**, 1485-95.
58. Laue, T., Shah, B., Ridgeway, T. & Pelletier, S. (1992). Computer-aided interpretation of analytical sedimentation data for proteins. In