

1. Craig, L., Volkmann, N., Arvai, A.S., Pique, M.E., Yeager, M., Egelman, E.H. and Tainer, J.A. (2006) Type IV pilus structure by cryo-electron microscopy and crystallography: implications for pilus assembly and functions. *Mol Cell*, **23**, 651-662.
2. Fethiere, J., Eggimann, B. and Cygler, M. (1999) Crystal structure of chondroitin AC lyase, a representative of a family of glycosaminoglycan degrading enzymes. *J Mol Biol*, **288**, 635-647.
3. Forest, K.T., Dunham, S.A., Koomey, M. and Tainer, J.A. (1999) Crystallographic structure reveals phosphorylated pilin from *Neisseria*: phosphoserine sites modify type IV pilus surface chemistry and fibre morphology. *Mol Microbiol*, **31**, 743-752.
4. Graycar, T., Knapp, M., Ganshaw, G., Dauberman, J. and Bott, R. (1999) Engineered *Bacillus lentus* subtilisins having altered flexibility. *J Mol Biol*, **292**, 97-109.
5. Hahn, M., Keitel, T. and Heinemann, U. (1995) Crystal and molecular structure at 0.16-nm resolution of the hybrid *Bacillus endo*-1,3-1,4-beta-D-glucan 4-glucanohydrolase H(A16-M). *Eur J Biochem*, **232**, 849-858.
6. Hahn, M., Piotukh, K., Borriss, R. and Heinemann, U. (1994) Native-like in vivo folding of a circularly permuted jellyroll protein shown by crystal structure analysis. *Proc Natl Acad Sci U S A*, **91**, 10417-10421.
7. Huang, W., Boju, L., Tkalec, L., Su, H., Yang, H.O., Gunay, N.S., Linhardt, R.J., Kim, Y.S., Matte, A. and Cygler, M. (2001) Active site of chondroitin AC lyase revealed by the structure of enzyme-oligosaccharide complexes and mutagenesis. *Biochemistry*, **40**, 2359-2372.
8. Huang, W., Lunin, V.V., Li, Y., Suzuki, S., Sugiura, N., Miyazono, H. and Cygler, M. (2003) Crystal structure of *Proteus vulgaris* chondroitin sulfate ABC lyase I at 1.9A resolution. *J Mol Biol*, **328**, 623-634.
9. Huang, W., Matte, A., Li, Y., Kim, Y.S., Linhardt, R.J., Su, H. and Cygler, M. (1999) Crystal structure of chondroitinase B from *Flavobacterium heparinum* and its complex with a disaccharide product at 1.7 A resolution. *J Mol Biol*, **294**, 1257-1269.
10. Igura, M., Maita, N., Kamishikiryo, J., Yamada, M., Obita, T., Maenaka, K. and Kohda, D. (2008) Structure-guided identification of a new catalytic motif of oligosaccharyltransferase. *EMBO J*, **27**, 234-243.
11. Keitel, T., Meldgaard, M. and Heinemann, U. (1994) Cation binding to a *Bacillus* (1,3-1,4)-beta-glucanase. Geometry, affinity and effect on protein stability. *Eur J Biochem*, **222**, 203-214.
12. Maita, N., Nyirenda, J., Igura, M., Kamishikiryo, J. and Kohda, D. Comparative structural biology of eubacterial and archaeal oligosaccharyltransferases. *J Biol Chem*, **285**, 4941-4950.
13. Michel, G., Pojasek, K., Li, Y., Sulea, T., Linhardt, R.J., Raman, R., Prabhakar, V., Sasisekharan, R. and Cygler, M. (2004) The structure of chondroitin B lyase complexed with glycosaminoglycan oligosaccharides unravels a calcium-dependent catalytic machinery. *J Biol Chem*, **279**, 32882-32896.
14. Ozbek, S., Muller, J.F., Figgemeier, E. and Stetefeld, J. (2005) Favourable mediation of crystal contacts by cocoamidopropylbetaine (CAPB). *Acta Crystallogr D Biol Crystallogr*, **61**, 477-480.

15. Parge, H.E., Forest, K.T., Hickey, M.J., Christensen, D.A., Getzoff, E.D. and Tainer, J.A. (1995) Structure of the fibre-forming protein pilin at 2.6 Å resolution. *Nature*, **378**, 32-38.
16. Rangarajan, E.S., Bhatia, S., Watson, D.C., Munger, C., Cygler, M., Matte, A. and Young, N.M. (2007) Structural context for protein N-glycosylation in bacteria: The structure of PEB3, an adhesin from *Campylobacter jejuni*. *Protein Sci*, **16**, 990-995.
17. Shaya, D., Tocilj, A., Li, Y., Myette, J., Venkataraman, G., Sasisekharan, R. and Cygler, M. (2006) Crystal structure of heparinase II from *Pedobacter heparinus* and its complex with a disaccharide product. *J Biol Chem*, **281**, 15525-15535.
18. Spagnolo, L., Toro, I., D'Orazio, M., O'Neill, P., Pedersen, J.Z., Carugo, O., Rotilio, G., Battistoni, A. and Djinojic-Carugo, K. (2004) Unique features of the sodC-encoded superoxide dismutase from *Mycobacterium tuberculosis*, a fully functional copper-containing enzyme lacking zinc in the active site. *J Biol Chem*, **279**, 33447-33455.
19. Stetefeld, J., Jenny, M., Schulthess, T., Landwehr, R., Engel, J. and Kammerer, R.A. (2000) Crystal structure of a naturally occurring parallel right-handed coiled coil tetramer. *Nat Struct Biol*, **7**, 772-776.
20. Sugiyama, S., Matsuo, Y., Maenaka, K., Vassylyev, D.G., Matsushima, M., Kashiwagi, K., Igarashi, K. and Morikawa, K. (1996) The 1.8-Å X-ray structure of the *Escherichia coli* PotD protein complexed with spermidine and the mechanism of polyamine binding. *Protein Sci*, **5**, 1984-1990.
21. Sugiyama, S., Vassylyev, D.G., Matsushima, M., Kashiwagi, K., Igarashi, K. and Morikawa, K. (1996) Crystal structure of PotD, the primary receptor of the polyamine transport system in *Escherichia coli*. *J Biol Chem*, **271**, 9519-9525.
22. Waddling, C.A., Plummer, T.H., Jr., Tarentino, A.L. and Van Roey, P. (2000) Structural basis for the substrate specificity of endo-beta-N-acetylglucosaminidase F(3). *Biochemistry*, **39**, 7878-7885.
23. Yeo, H.J., Yokoyama, T., Walkiewicz, K., Kim, Y., Grass, S. and Geme, J.W., 3rd. (2007) The structure of the *Haemophilus influenzae* HMW1 pro-piece reveals a structural domain essential for bacterial two-partner secretion. *J Biol Chem*, **282**, 31076-31084.