

- Hoeller, D., Crosetto, N., Blagoev, B., Raiborg, C., Tikkanen, R., Wagner, S., Kowanzet, K., Breitling, R., Mann, M., Stenmark, H., and Dikic, I. (2006). Regulation of ubiquitin-binding proteins by monoubiquitination. *Nat. Cell Biol.* **8**, 163–169.
- Howe, L., Auston, D., Grant, P., John, S., Cook, R.G., Workman, J.L., and Pillus, L. (2001). Histone H3 specific acetyltransferases are essential for cell cycle progression. *Genes Dev.* **15**, 3144–3154.
- Hudson, B.P., Martinez-Yamout, M.A., Dyson, H.J., and Wright, P.E. (2000). Solution structure and acetyl-lysine binding activity of the GCN5 bromodomain. *J. Mol. Biol.* **304**, 355–370.
- Jacobson, R.H., Ladurner, A.G., King, D.S., and Tjian, R. (2000). Structure and function of a human TAFII250 double bromodomain module. *Science* **288**, 1422–1425.
- Kasten, M., Szerlong, H., Erdjument-Bromage, H., Tempst, P., Werner, M., and Cairns, B.R. (2004). Tandem bromodomains in the chromatin remodeler RSC recognize acetylated histone H3 Lys14. *EMBO J.* **23**, 1348–1359.
- Kornberg, R.D., and Lorch, Y. (1999). Twenty-five years of the nucleosome, fundamental particle of the eukaryote chromosome. *Cell* **98**, 285–294.
- Kouzarides, T. (2000). Acetylation: a regulatory modification to rival phosphorylation? *EMBO J.* **19**, 1176–1179.
- Kuriyan, J., and Cowburn, D. (1997). Modular peptide recognition domains in eukaryotic signaling. *Annu. Rev. Biophys. Biomol. Struct.* **26**, 259–288.
- Lo, W.S., Trievel, R.C., Rojas, J.R., Duggan, L., Hsu, J.Y., Allis, C.D., Marmorstein, R., and Berger, S.L. (2000). Phosphorylation of serine 10 in histone H3 is functionally linked in vitro and in vivo to Gcn5-mediated acetylation at lysine 14. *Mol. Cell* **5**, 917–926.
- Mujtaba, S., He, Y., Zeng, L., Farooq, A., Carlson, J.E., Ott, M., Verdine, E., and Zhou, M.M. (2002). Structural basis of lysine-acetylated HIV-1 Tat recognition by PCAF bromodomain. *Mol. Cell* **9**, 575–586.
- Owen, D.J., Ornaghi, P., Yang, J.C., Lowe, N., Evans, P.R., Ballario, P., Neuhaus, D., Filetici, P., and Travers, A.A. (2000). The structural basis for the recognition of acetylated histone H4 by the bromodomain of histone acetyltransferase gcn5p. *EMBO J.* **19**, 6141–6149.
- Roberts, D.N., Stewart, A.J., Huff, J.T., and Cairns, B.R. (2003). The RNA polymerase III transcriptome revealed by genome-wide localization and activity-occupancy relationships. *Proc. Natl. Acad. Sci. USA* **100**, 14695–14700.
- Rojas, J.R., Trievel, R.C., Zhou, J., Mo, Y., Li, X., Berger, S.L., Allis, C.D., and Marmorstein, R. (1999). Structure of Tetrahymena GCN5 bound to coenzyme A and a histone H3 peptide. *Nature* **401**, 93–98.
- Saha, A., Wittmeyer, J., and Cairns, B.R. (2002). Chromatin remodeling by RSC involves ATP-dependent DNA translocation. *Genes Dev.* **16**, 2120–2134.
- Saha, A., Wittmeyer, J., and Cairns, B.R. (2005). Chromatin remodeling through directional DNA translocation from an internal nucleosomal site. *Nat. Struct. Mol. Biol.* **12**, 747–755.
- Shen, W., Xu, C., Huang, W., Zhang, J., Carlson, J.E., Tu, X., Wu, J., and Shi, Y. (2007). Solution structure of human Brg1 bromodomain and its specific binding to acetylated histone tails. *Biochemistry* **46**, 2100–2110.
- Soutourina, J., Bordas-Le Floch, V., Gendrel, G., Flores, A., Ducrot, C., Dumay-Odelot, H., Soularue, P., Navarro, F., Cairns, B.R., Lefebvre, O., and Werner, M. (2006). Rsc4 connects the chromatin remodeler RSC to RNA polymerases. *Mol. Cell. Biol.* **26**, 4920–4933.
- Strahl, B.D., and Allis, C.D. (2000). The language of covalent histone modifications. *Nature* **403**, 41–45.
- Sun, H., Liu, J., Zhang, J., Shen, W., Huang, H., Xu, C., Dai, H., Wu, J., and Shi, Y. (2007). Solution structure of BRD7 bromodomain and its interaction with acetylated peptides from histone H3 and H4. *Biochem. Biophys. Res. Commun.* **358**, 435–441. Published online May 2, 2007. 10.1016/j.bbrc.2007.04.139.
- Syntichaki, P., Topalidou, I., and Thireos, G. (2000). The Gcn5 bromodomain co-ordinates nucleosome remodelling. *Nature* **404**, 414–417.
- Thatcher, J.W., Shaw, J.M., and Dickinson, W.J. (1998). Marginal fitness contributions of nonessential genes in yeast. *Proc. Natl. Acad. Sci. USA* **95**, 253–257.
- Trievel, R.C., Rojas, J.R., Sterner, D.E., Venkataramani, R.N., Wang, L., Zhou, J., Allis, C.D., Berger, S.L., and Marmorstein, R. (1999). Crystal structure and mechanism of histone acetylation of the yeast GCN5 transcriptional coactivator. *Proc. Natl. Acad. Sci. USA* **96**, 8931–8936.
- Yu, J., Li, Y., Ishizuka, T., Guenther, M.G., and Lazar, M.A. (2003). A SANT motif in the SMRT corepressor interprets the histone code and promotes histone deacetylation. *EMBO J.* **22**, 3403–3410.
- Yukawa, M., Katoh, S., Miyakawa, T., and Tsuchiya, E. (1999). Nps1/Sth1p, a component of an essential chromatin-remodeling complex of *Saccharomyces cerevisiae*, is required for the maximal expression of early meiotic genes. *Genes Cells* **4**, 99–110.

Accession Numbers

Protein Data Bank entry codes are 2R0S for Rsc4(36–340), 2R0Y for Rsc4(36–340) peptide soak, 2R0V for acetylated Rsc4(1–340), and 2R1O for acetylated histone-Rsc4(1–321) chimera.