

- Shirai, M., Hirakawa, H., Kimoto, M., Tabuchi, M., Kishi, F., Ouchi, K., Shiba, T., Ishii, K., Hattori, M. & other authors (2000).** Comparison of whole genome sequences of *Chlamydia pneumoniae* J138 from Japan and CWL029 from USA. *Nucleic Acids Res* 28, 2311–2314.
- Slepenkin, A., Motin, V., de la Maza, L. M. & Peterson, E. M. (2003).** Temporal expression of Type III secretion genes of *Chlamydia pneumoniae*. *Infect Immun* 71, 2555–2562.
- Stephens, R. S., Kalma, S., Lammel, C., Fan, J., Marathe, R., Aravind, L., Mitchell, W., Olinger, L., Tatusov, R. L. & other authors (1998).** Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia trachomatis*. *Science* 282, 754–759.
- Tachibana, M., Sugimoto, K., Fukushima, T. & Shinkai, Y. (2001).** SET-domain containing protein, G9a, is a novel lysine-preferring mammalian histone methyltransferase with hyperactivity and specific selectivity to lysines 9 and 27 of histone H3. *J Biol Chem* 276, 25309–25317.
- Tao, S., Kaul, R. & Wenman, W. M. (1991).** Identification and nucleotide sequence of a developmentally regulated gene encoding a eukaryotic histone H1-like protein from *Chlamydia trachomatis*. *J Bacteriol* 173, 2818–2822.
- Thomson, N. R., Yeats, C., Bell, K., Holden, M. T., Bentley, S. D., Livingstone, M., Cerdeno-Tarrago, A. M., Harris, B., Doggett, J. & other authors (2005).** The *Chlamydophila abortus* genome sequence reveals an array of variable proteins that contribute to interspecies variation. *Genome Res* 15, 629–640.
- Xiao, B., Wilson, J. R. & Gamblin, S. J. (2003).** SET domains and histone methylation. *Curr Opin Struct Biol* 13, 699–705.
- Zhang, X., Yang, Z., Khan, S. I., Horton, J. R., Tamari, H., Selker, E. U. & Cheng, X. (2003).** Structural basis for the product specificity of histone lysine methyltransferases. *Mol Cell* 12, 177–185.

---

Edited by: J. Parkhill