- 50. Celniker, S. E., Dillon, L. A., Gerstein, M. B., Gunsalus, K. C., Henikoff, S., Karpen, G. H., Kellis, M., Lai, E. C., Lieb, J. D., MacAlpine, D. M., Micklem, G., Piano, F., Snyder, M., Stein, L., White, K. P., Waterston, R. H., and mod, E. C. (2009) Unlocking the secrets of the genome. *Nature* **459**, 927-930
- 51. Fisher, W. W., Li, J. J., Hammonds, A. S., Brown, J. B., Pfeiffer, B. D., Weiszmann, R., MacArthur, S., Thomas, S., Stamatoyannopoulos, J. A., Eisen, M. B., Bickel, P. J., Biggin, M. D., and Celniker, S. E. (2012) DNA regions bound at low occupancy by transcription factors do not drive patterned reporter gene expression in Drosophila. *Proceedings of the National Academy of Sciences of the United States of America* **109**, 21330-21335
- 52. Walhout, A. J. (2011) What does biologically meaningful mean? A perspective on gene regulatory network validation. *Genome biology* **12**, 109
- 53. Muse, G. W., Gilchrist, D. A., Nechaev, S., Shah, R., Parker, J. S., Grissom, S. F., Zeitlinger, J., and Adelman, K. (2007) RNA polymerase is poised for activation across the genome. *Nat Genet* **39**, 1507-1511
- 54. Li, L. M., and Arnosti, D. N. (2011) Long- and short-range transcriptional repressors induce distinct chromatin states on repressed genes. *Current biology: CB* **21**, 406-412
- 55. Niefind, K., Guerra, B., Ermakowa, I., and Issinger, O. G. (2001) Crystal structure of human protein kinase CK2: insights into basic properties of the CK2 holoenzyme. *EMBO J* **20**, 5320-5331
- 56. Niefind, K., Raaf, J., and Issinger, O. G. (2009) Protein kinase CK2 in health and disease: Protein kinase CK2: from structures to insights. *Cell Mol Life Sci* **66**, 1800-1816
- 57. Meier, U. T., and Blobel, G. (1992) Nopp140 shuttles on tracks between nucleolus and cytoplasm. *Cell* **70**, 127-138
- 58. Fuller-Pace, F. V. (2006) DExD/H box RNA helicases: multifunctional proteins with important roles in transcriptional regulation. *Nucleic Acids Res* **34**, 4206-4215
- 59. Rossow, K. L., and Janknecht, R. (2003) Synergism between p68 RNA helicase and the transcriptional coactivators CBP and p300. *Oncogene* **22**, 151-156
- 60. Buszczak, M., and Spradling, A. C. (2006) The Drosophila P68 RNA helicase regulates transcriptional deactivation by promoting RNA release from chromatin. *Genes Dev* **20**, 977-989
- Wilson, B. J., Bates, G. J., Nicol, S. M., Gregory, D. J., Perkins, N. D., and Fuller-Pace, F. V. (2004) The p68 and p72 DEAD box RNA helicases interact with HDAC1 and repress transcription in a promoter-specific manner. *BMC molecular biology* 5, 11
- 62. Neubauer, G., King, A., Rappsilber, J., Calvio, C., Watson, M., Ajuh, P., Sleeman, J., Lamond, A., and Mann, M. (1998) Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex. *Nat Genet* **20**, 46-50
- 63. Liu, Z. R. (2002) p68 RNA helicase is an essential human splicing factor that acts at the U1 snRNA-5' splice site duplex. *Mol Cell Biol* **22**, 5443-5450
- 64. Reed, R. (2003) Coupling transcription, splicing and mRNA export. *Curr Opin Cell Biol* **15**, 326-331
- 65. Han, J., Xiong, J., Wang, D., and Fu, X. D. (2011) Pre-mRNA splicing: where and when in the nucleus. *Trends Cell Biol* **21**, 336-343
- 66. Bentley, D. L. (2005) Rules of engagement: co-transcriptional recruitment of pre-mRNA processing factors. *Curr Opin Cell Biol* 17, 251-256
- 67. Maniatis, T., and Reed, R. (2002) An extensive network of coupling among gene expression machines. *Nature* **416**, 499-506
- 68. Bentley, D. (2002) The mRNA assembly line: transcription and processing machines in the same factory. *Curr Opin Cell Biol* **14**, 336-342
- 69. Cramer, P., Caceres, J. F., Cazalla, D., Kadener, S., Muro, A. F., Baralle, F. E., and Kornblihtt, A. R. (1999) Coupling of transcription with alternative splicing: RNA pol II promoters modulate SF2/ASF and 9G8 effects on an exonic splicing enhancer. *Mol Cell* 4, 251-258