

- Kim, J., Sitaraman, S., Hierro, A., Beach, B.M., Odorizzi, G., and Hurley, J.H. (2005). Structural basis for endosomal targeting by the Bro1 domain. *Dev. Cell* 8, 937-947.
- Kleywegt, G.J., and Jones, T.A. (1999). Software for handling macromolecular envelopes. *Acta Crystallogr. D Biol. Crystallogr.* 55, 941-944.
- Laskowski, R.A., MacArthur, M.W., Moss, D.S., and Thornton, J.M. (1993). PROCHECK: a program to check the stereochemical quality of protein structures. *J. Appl. Crystallogr.* 26, 283-291.
- McCoy, A.J., Grosse-Kunstleve, R.W., Storoni, L.C., and Read, R.J. (2005). Likelihood-enhanced fast translation functions. *Acta Crystallogr. D Biol. Crystallogr.* 61, 458-464.
- Merritt, E.A., and Painter, J. (2006). TLSMD web server for the generation of multi-group TLS models. *J. Appl. Crystallogr.* 39.
- Myszka, D.G. (1999). Improving biosensor analysis. *J. Mol. Recognit.* 12, 279-284.
- Olsen, J.C. (1998). Gene transfer vectors derived from equine infectious anemia virus. *Gene Ther.* 5, 1481-1487.
- Ory, D.S., Neugeboren, B.A., and Mulligan, R.C. (1996). A stable human-derived packaging cell line for production of high titer retrovirus/vesicular stomatitis virus G pseudotypes. *Proc. Natl. Acad. USA* 93, 11400-11406.
- Otwinowski, Z., and Minor, W. (1997). Processing of X-ray diffraction data collected in oscillation mode. *Methods in Enzymol.* 276, 307-326.
- Painter, J., and Merritt, E.A. (2006). Optimal description of a protein structure in terms of multiple groups undergoing TLS motion. *Acta Crystallogr. D Biol. Crystallogr.* 62, 439-450.
- Qin, X.F., An, D.S., Chen, I.S., and Baltimore, D. (2003). Inhibiting HIV-1 infection in human T cells by lentiviral-mediated delivery of small interfering RNA against CCR5. *Proc. Natl. Acad. USA* 100, 183-188.
- Read, R. (1986). Improved Fourier coefficients for maps using phases from partial structures with errors. *Acta Crystallogr. A* 42, 140-149.
- Schneider, T., and Pape, T. (2004). HKL2MAP: a graphical user interface for phasing with SHELX programs. *J. Appl. Crystallogr.* 37, 843-844.
- Sheldrick, G.M., and Schneider, T. (1997). SHELXL: High resolution refinement. *Methods Enzymol.* 277, 319-343.
- Studier, F.W. (2005). Protein production by auto-induction in high density shaking cultures. *Protein Expr. Purif.* 41, 207-234.