

1. [Pooled RNAi screen identifies ubiquitin ligase Itch as crucial for influenza A virus release from the endosome during virus entry.](#) [RNAiCore library, 82,000 shRNAs/16,000 genes]
Su WC *et al* and Lai MM (中國醫、中研院 與 RNAi 核心).
Proc Natl Acad Sci U S A. 2013; 110:17516.
2. [Functional genomic screen of human stem cell differentiation reveals pathways involved in neurodevelopment and neurodegeneration.](#) [TRC/Sigma library, 8,488 shRNAs/1,801 genes]
Zhang Y *et al* and Szekely AM (Stanford University).
Proc Natl Acad Sci U S A. 2013; 110:12361.
3. [RNAi screen identifies MAPK14 as a druggable suppressor of human hematopoietic stem cell expansion.](#) [TRC-Sigma library, 1000 druggable genes]
Baudet A *et al* and Larsson J (Lund University, Lund, Sweden).
Blood. 2012; 119:6255.
4. [High-throughput RNA interference screening using pooled shRNA libraries and next generation sequencing.](#) [GIPZ library, 61,416 shRNAs/15,739 genes]
Sims D *et al* and Lord CJ (The Institute of Cancer Research, UK).
Genome Biol. 2011; 12:R104.
5. [A whole-genome RNAi screen identifies an 8q22 gene cluster that inhibits death receptor-mediated apoptosis.](#) [70,000 shRNAs, miR30-based shRNA]
Dompe N *et al* and Davis DP (Genentech).
Proc Natl Acad Sci U S A. 2011; 108:E943.
6. [CD133 protein N-glycosylation processing contributes to cell surface recognition of the primitive cell marker AC133 epitope.](#) [54,000 shRNAs/11,248 genes]
Mak AB, *et al* and Moffat J (University of Toronto).
J Biol Chem. 2011; 286:41046.
7. [A genome-wide RNAi screen identifies novel targets of neratinib resistance leading to identification of potential drug resistant genetic markers.](#) Attila A *et al* (Pfizer Inc).
Mol. BioSyst., 2012; 8: 1553.
8. [A genome-wide RNAi screen identifies novel targets of neratinib sensitivity leading to neratinib and paclitaxel combination drug treatments.](#) [Open Biosystems library, 74,000 shRNAs/18,000 genes]
Seyhan AA *et al* (Pfizer Inc).
Mol Biosyst. 2011; 7: 1974.
9. [A genome-wide RNAi screen identifies multiple RSK-dependent regulators of cell migration.](#) [Open Biosystems library, 74,000 shRNAs/18,000 genes]
Smolen GA *et al.* and Haber DA (Harvard Medical School).
Genes Dev. 2010; 24:2654.
10. [Highly parallel identification of essential genes in cancer cells.](#) [TRC, 54,000 shRNAs/11,000 genes]
Luo B *et al* and Root DE (TRC/Broad).
Proc Natl Acad Sci U S A. 2008; 105:20380.
11. **[Protocol]** [Pooled shRNA screenings: experimental approach.](#) Rodriguez-Barrueco R, Marshall N, Silva JM. Methods Mol Biol. 2013; 980:353.
12. **[Protocol]** [Optimized PCR conditions and increased shRNA fold representation improve reproducibility of pooled shRNA screens.](#) Strezoska Ž *et al.* PLoS One. 2012; 7:e42341.
13. **[Protocol]** [A comprehensive platform for highly multiplexed mammalian functional genetic screens.](#) Ketela Tet al, Root DE, Moffat J, Nislow C. BMC Genomics. 2011; 12: 213.