



- Audia, J.E., and Campbell, R.M. (2016). Histone modifications and cancer. Cold Spring Harb. Perspect. Biol. 8, a019521. https://doi.org/10.1101/cshperspect.a019521.
- Huen, M.S.Y., and Chen, J. (2008). The DNA damage response pathways: at the crossroad of protein modifications. Cell Res. 18, 8–16. https://doi.org/10.1038/cr.2007.109.
- Li, Y., Dou, Y., Da Veiga Leprevost, F., Geffen, Y., Calinawan, A.P., Aguet, F., Akiyama, Y., Anand, S., Birger, C., Cao, S., et al. (2023). Proteogenomic data and resources for pan-cancer analysis. Cancer Cell 41, 1397–1406.
- Archer, T.C., Ehrenberger, T., Mundt, F., Gold, M.P., Krug, K., Mah, C.K., Mahoney, E.L., Daniel, C.J., LeNail, A., Ramamoorthy, D., et al. (2018). Proteomics, post-translational modifications, and integrative analyses reveal molecular heterogeneity within medulloblastoma subgroups. Cancer Cell 34, 396–410.e8. https://doi.org/10.1016/j.ccell.2018.08.004.
- Karabulut, N.P., and Frishman, D. (2016). Sequence- and structurebased analysis of tissue-specific phosphorylation sites. PLoS One 11, e0157896. https://doi.org/10.1371/journal.pone.0157896.
- Garcia, B.A., Thomas, C.E., Kelleher, N.L., and Mizzen, C.A. (2008). Tissue-specific expression and post-translational modification of histone H3 variants. J. Proteome Res. 7, 4225–4236. https://doi.org/10.1021/pr800044q.
- Kim, J., Mouw, K.W., Polak, P., Braunstein, L.Z., Kamburov, A., Kwiat-kowski, D.J., Rosenberg, J.E., Van Allen, E.M., D'Andrea, A., and Getz, G. (2016). Somatic ERCC2 mutations are associated with a distinct genomic signature in urothelial tumors. Nat. Genet. 48, 600–606. https://doi.org/10.1038/ng.3557.
- Kasar, S., Kim, J., Improgo, R., Tiao, G., Polak, P., Haradhvala, N., Lawrence, M.S., Kiezun, A., Fernandes, S.M., Bahl, S., et al. (2015). Wholegenome sequencing reveals activation-induced cytidine deaminase signatures during indolent chronic lymphocytic leukaemia evolution. Nat. Commun. 6, 8866. https://doi.org/10.1038/ncomms9866.
- Taylor-Weiner, A., Aguet, F., Haradhvala, N.J., Gosai, S., Anand, S., Kim, J., Ardlie, K., Van Allen, E.M., and Getz, G. (2019). Scaling computational genomics to millions of individuals with GPUs. Genome Biol. 20, 228. https://doi.org/10.1186/s13059-019-1836-7.
- Johnson, J.L., Yaron, T.M., Huntsman, E.M., Kerelsky, A., Song, J., Regev, A., Lin, T.Y., Liberatore, K., Cizin, D.M., Cohen, B.M., et al. (2023). An atlas of substrate specificities for the human serine/threonine kinome. Nature 613, 759–766. https://doi.org/10.1038/s41586-022-05575-3.
- Babur, Ö., Luna, A., Korkut, A., Durupinar, F., Siper, M.C., Dogrusoz, U., Vaca Jacome, A.S., Peckner, R., Christianson, K.E., Jaffe, J.D., et al. (2021). Causal interactions from proteomic profiles: molecular data meet pathway knowledge. Patterns (N Y) 2, 100257. https://doi.org/10. 1016/j.patter.2021.100257.
- Krug, K., Mertins, P., Zhang, B., Hornbeck, P., Raju, R., Ahmad, R., Szucs, M., Mundt, F., Forestier, D., Jane-Valbuena, J., et al. (2019). A curated resource for phosphosite-specific signature analysis. Mol. Cell. Proteomics 18, 576–593. https://doi.org/10.1074/mcp.TIR118.000943.
- Dong, Y., Sun, Y., Huang, Y., Fang, X., Sun, P., Dwarakanath, B., Kong, L., and Lu, J.J. (2019). Depletion of MLKL inhibits invasion of radioresistant nasopharyngeal carcinoma cells by suppressing epithelial-mesenchymal transition. Ann. Transl. Med. 7, 741. https://doi.org/10.21037/ atm.2019.11.104.
- Edmond, V., Merdzhanova, G., Gout, S., Brambilla, E., Gazzeri, S., and Eymin, B. (2013). A new function of the splicing factor SRSF2 in the control of E2F1-mediated cell cycle progression in neuroendocrine lung tumors. Cell Cycle 12, 1267–1278. https://doi.org/10.4161/cc.24363.
- Kadoch, C., Hargreaves, D.C., Hodges, C., Elias, L., Ho, L., Ranish, J., and Crabtree, G.R. (2013). Proteomic and bioinformatic analysis of mammalian SWI/SNF complexes identifies extensive roles in human malignancy. Nat. Genet. 45, 592–601. https://doi.org/10.1038/ng.2628.

- Sun, X., Wang, S.C., Wei, Y., Luo, X., Jia, Y., Li, L., Gopal, P., Zhu, M., Nassour, I., Chuang, J.-C., et al. (2017). Arid1a has context-dependent oncogenic and tumor suppressor functions in liver cancer. Cancer Cell 32, 574–589.e6. https://doi.org/10.1016/j.ccell.2017.10.007.
- Xu, S., and Tang, C. (2021). The role of ARID1A in tumors: tumor initiation or tumor suppression? Front. Oncol. 11, 745187. https://doi.org/10. 3389/fonc.2021.745187.
- Akimov, V., Barrio-Hernandez, I., Hansen, S.V.F., Hallenborg, P., Pedersen, A.-K., Bekker-Jensen, D.B., Puglia, M., Christensen, S.D.K., Vanselow, J.T., Nielsen, M.M., et al. (2018). UbiSite approach for comprehensive mapping of lysine and N-terminal ubiquitination sites. Nat. Struct. Mol. Biol. 25, 631–640. https://doi.org/10.1038/s41594-018-0084-y.
- Haradhvala, N.J., Polak, P., Stojanov, P., Covington, K.R., Shinbrot, E., Hess, J.M., Rheinbay, E., Kim, J., Maruvka, Y.E., Braunstein, L.Z., et al. (2016). Mutational strand asymmetries in cancer genomes reveal mechanisms of DNA damage and repair. Cell 164, 538–549. https://doi.org/10. 1016/j.cell.2015.12.050.
- 44. Alexandrov, L.B., Kim, J., Haradhvala, N.J., Huang, M.N., Tian Ng, A.W., Wu, Y., Boot, A., Covington, K.R., Gordenin, D.A., Bergstrom, E.N., et al. (2020). The repertoire of mutational signatures in human cancer. Nature 578, 94–101. https://doi.org/10.1038/s41586-020-1943-3.
- Polak, P., Kim, J., Braunstein, L.Z., Karlic, R., Haradhavala, N.J., Tiao, G., Rosebrock, D., Livitz, D., Kübler, K., Mouw, K.W., et al. (2017). A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. Nat. Genet. 49, 1476–1486. https://doi.org/10.1038/ng.3934.
- Degasperi, A., Zou, X., Amarante, T.D., Martinez-Martinez, A., Koh, G.C.C., Dias, J.M.L., Heskin, L., Chmelova, L., Rinaldi, G., Wang, V.Y.W., et al. (2022). Substitution mutational signatures in wholegenome-sequenced cancers in the UK population. Science 376, abl9283. https://doi.org/10.1126/science.abl9283.
- Polo, S.E., and Jackson, S.P. (2011). Dynamics of DNA damage response proteins at DNA breaks: a focus on protein modifications. Genes Dev. 25, 409–433. https://doi.org/10.1101/gad.2021311.
- Wang, H., and Xu, X. (2017). Microhomology-mediated end joining: new players join the team. Cell Biosci. 7, 6. https://doi.org/10.1186/s13578-017-0136-8.
- Sfeir, A., and Symington, L.S. (2015). Microhomology-mediated end joining: A back-up survival mechanism or dedicated pathway? Trends Biochem. Sci. 40, 701–714. https://doi.org/10.1016/j.tibs.2015.08.006.
- Li, Z., Wang-Heaton, H., Cartwright, B.M., Makinwa, Y., Hilton, B.A., Musich, P.R., Shkriabai, N., Kvaratskhelia, M., Guan, S., Chen, Q., et al. (2021). ATR prevents Ca2+ overload-induced necrotic cell death through phosphorylation-mediated inactivation of PARP1 without DNA damage signaling. FASEB J. 35, e21373. https://doi.org/10.1096/fj.202001636RRR.
- Gupte, R., Liu, Z., and Kraus, W.L. (2017). PARPs and ADP-ribosylation: recent advances linking molecular functions to biological outcomes. Genes Dev. 31, 101–126. https://doi.org/10.1101/gad.291518.116.
- Brunyanszki, A., Olah, G., Coletta, C., Szczesny, B., and Szabo, C. (2014). Regulation of mitochondrial poly(ADP-ribose) polymerase activation by the β-adrenoceptor/cAMP/protein kinase A axis during oxidative stress. Mol. Pharmacol. 86, 450–462. https://doi.org/10.1124/mol.114. 094318.
- 53. Zatreanu, D., Robinson, H.M.R., Alkhatib, O., Boursier, M., Finch, H., Geo, L., Grande, D., Grinkevich, V., Heald, R.A., Langdon, S., et al. (2021). Pol@ inhibitors elicit BRCA-gene synthetic lethality and target PARP inhibitor resistance. Nat. Commun. 12, 3636. https://doi.org/10.1038/s41467-021-23463-8.
- 54. Ceccaldi, R., Liu, J.C., Amunugama, R., Hajdu, I., Primack, B., Petalcorin, M.I.R., O'Connor, K.W., Konstantinopoulos, P.A., Elledge, S.J., Boulton, S.J., et al. (2015). Homologous-recombination-deficient tumours are dependent on Polθ-mediated repair. Nature 518, 258–262. https://doi.org/10.1038/nature14184.