

115. Yaffe, M.B., and Smerdon, S.J. (2004). The use of in vitro peptide-library screens in the analysis of phosphoserine/threonine-binding domain structure and function. *Annu. Rev. Biophys. Biomol. Struct.* 33, 225–244. <https://doi.org/10.1146/annurev.biophys.33.110502.133346>.
116. Turk, B.E., Huang, L.L., Piro, E.T., and Cantley, L.C. (2001). Determination of protease cleavage site motifs using mixture-based oriented peptide libraries. *Nat. Biotechnol.* 19, 661–667. <https://doi.org/10.1038/90273>.
117. Manning, G., Whyte, D.B., Martinez, R., Hunter, T., and Sudarsanam, S. (2002). The protein kinase complement of the human genome. *Science* 298, 1912–1934. <https://doi.org/10.1126/science.1075762>.
118. Agricola, E., Randall, R.A., Gaarenstroom, T., Dupont, S., and Hill, C.S. (2011). Recruitment of TIF1 γ to chromatin via its PHD finger-bromodomain activates its ubiquitin ligase and transcriptional repressor activities. *Mol. Cell* 43, 85–96. <https://doi.org/10.1016/j.molcel.2011.05.020>.
119. Yasui, Y., Urano, T., Kawajiri, A., Nagata, K.-I., Tatsuka, M., Saya, H., Furukawa, K., Takahashi, T., Izawa, I., and Inagaki, M. (2004). Autophosphorylation of a newly identified site of aurora-B is indispensable for cytokinesis. *J. Biol. Chem.* 279, 12997–13003. <https://doi.org/10.1074/jbc.M311128200>.
120. Goto, H., Tomono, Y., Ajiro, K., Kosako, H., Fujita, M., Sakurai, M., Okawa, K., Iwamatsu, A., Okigaki, T., Takahashi, T., et al. (1999). Identification of a novel phosphorylation site on histone H3 coupled with mitotic chromosome condensation. *J. Biol. Chem.* 274, 25543–25549. <https://doi.org/10.1074/jbc.274.36.25543>.
121. Cai, G., Yang, Q., and Sun, W. (2021). RSF1 in cancer: interactions and functions. *Cancer Cell Int.* 21, 315. <https://doi.org/10.1186/s12935-021-02012-9>.
122. Lee, H.-S., Park, Y.-Y., Cho, M.-Y., Chae, S., Yoo, Y.-S., Kwon, M.-H., Lee, C.-W., and Cho, H. (2015). The chromatin remodeler RSF1 is essential for PLK1 deposition and function at mitotic kinetochores. *Nat. Commun.* 6, 7904. <https://doi.org/10.1038/ncomms8904>.
123. Lee, H.-S., Lin, Z., Chae, S., Yoo, Y.-S., Kim, B.-G., Lee, Y., Johnson, J.L., Kim, Y.-S., Cantley, L.C., Lee, C.-W., et al. (2018). The chromatin remodeler RSF1 controls centromeric histone modifications to coordinate chromosome segregation. *Nat. Commun.* 9, 3848. <https://doi.org/10.1038/s41467-018-06377-w>.
124. Elia, A.E.H., Cantley, L.C., and Yaffe, M.B. (2003). Proteomic screen finds pSer/pThr-binding domain localizing Plk1 to mitotic substrates. *Science* 299, 1228–1231. <https://doi.org/10.1126/science.1079079>.
125. Yaron, T.M., Heaton, B.E., Levy, T.M., Johnson, J.L., Jordan, T.X., Cohen, B.M., Kerelsky, A., Lin, T.-Y., Liberatore, K.M., Bulaon, D.K., et al. (2020). The FDA-approved drug Alectinib compromises SARS-CoV-2 nucleocapsid phosphorylation and inhibits viral infection in vitro. <https://doi.org/10.1101/2020.08.14.251207>.
126. Zheng, Y., Ramsamooj, S., Li, Q., Johnson, J.L., Yaron, T.M., Sharra, K., and Cantley, L.C. (2019). Regulation of folate and methionine metabolism by multisite phosphorylation of human methylenetetrahydrofolate reductase. *Sci. Rep.* 9, 4190. <https://doi.org/10.1038/s41598-019-40950-7>.
127. Chang, Y.-C., Chiou, J., Yang, Y.-F., Su, C.-Y., Lin, Y.-F., Yang, C.-N., Lu, P.-J., Huang, M.-S., Yang, C.-J., and Hsiao, M. (2019). Therapeutic targeting of aldolase A interactions inhibits lung cancer metastasis and prolongs survival. *Cancer Res.* 79, 4754–4766. <https://doi.org/10.1158/0008-5472.CAN-18-4080>.
128. Luby, A., and Alves-Guerra, M.-C. (2021). Targeting metabolism to control immune responses in cancer and improve checkpoint blockade immunotherapy. *Cancers* 13, 5912. <https://doi.org/10.3390/cancers13235912>.
129. Stevens, B.M., Jones, C.L., Pollyea, D.A., Culp-Hill, R., D'Alessandro, A., Winters, A., Krug, A., Abbott, D., Goosman, M., Pei, S., et al. (2020). Fatty acid metabolism underlies venetoclax resistance in acute myeloid leukemia stem cells. *Nat. Cancer* 1, 1176–1187. <https://doi.org/10.1038/s43018-020-00126-z>.
130. van Galen, P., Hovestadt, V., Wadsworth, M.H., Hughes, T.K., Griffin, G.K., Battaglia, S., Verga, J.A., Stephansky, J., Pastika, T.J., Lombardi Story, J., et al. (2019). Single-cell RNA-Seq reveals AML hierarchies relevant to disease progression and immunity. *Cell* 176, 1265–1281.e24. <https://doi.org/10.1016/j.cell.2019.01.031>.
131. Sade-Feldman, M., Yizhak, K., Bjorgaard, S.L., Ray, J.P., de Boer, C.G., Jenkins, R.W., Lieb, D.J., Chen, J.H., Frederick, D.T., Barzily-Rokni, M., et al. (2018). Defining T cell states associated with response to checkpoint immunotherapy in melanoma. *Cell* 175, 998–1013.e20. <https://doi.org/10.1016/j.cell.2018.10.038>.
132. Pelka, K., Hofree, M., Chen, J.H., Sarkizova, S., Pirl, J.D., Jorgji, V., Bejnood, A., Dionne, D., Ge, W.H., Xu, K.H., et al. (2021). Spatially organized multicellular immune hubs in human colorectal cancer. *Cell* 184, 4734–4752.e20. <https://doi.org/10.1016/j.cell.2021.08.003>.
133. Ji, A.L., Rubin, A.J., Thrane, K., Jiang, S., Reynolds, D.L., Meyers, R.M., Guo, M.G., George, B.M., Mollbrink, A., Bergenstr hle, J., et al. (2020). Multimodal analysis of composition and spatial architecture in human squamous cell carcinoma. *Cell* 182, 497–514.e22. <https://doi.org/10.1016/j.cell.2020.05.039>.
134. Minakshi, P., Kumar, R., Ghosh, M., Saini, H.M., Ranjan, K., Brar, B., and Prasad, G. (2019). Chapter 14 - Single-cell proteomics: technology and applications. In *Single-Cell Omics*, D. Barh and V. Azevedo, eds. (Academic Press), pp. 283–318. <https://doi.org/10.1016/B978-0-12-814919-5.00014-2>.
135. Elyada, E., Bolisetty, M., Laise, P., Flynn, W.F., Courtois, E.T., Burkhart, R.A., Teinor, J.A., Belleau, P., Biffi, G., Lucito, M.S., et al. (2019). Cross-species single-cell analysis of pancreatic ductal adenocarcinoma reveals antigen-presenting cancer-associated fibroblasts. *Cancer Discov.* 9, 1102–1123. <https://doi.org/10.1158/2159-8290.CD-19-0094>.
136. Le Large, T.Y., Mantini, G., Meijer, L.L., Pham, T.V., Funel, N., van Grieken, N.C., Kok, B., Knol, J., van Laarhoven, H.W., Piersma, S.R., et al. (2020). Microdissected pancreatic cancer proteomes reveal tumor heterogeneity and therapeutic targets. *JCI Insight* 5, e138290. <https://doi.org/10.1172/jci.insight.138290>.
137. Chen, X., Schulz-Trieglaff, O., Shaw, R., Barnes, B., Schlesinger, F., K llberg, M., Cox, A.J., Kruglyak, S., and Saunders, C.T. (2016). Manta: rapid detection of structural variants and indels for germline and cancer sequencing applications. *Bioinformatics* 32, 1220–1222. <https://doi.org/10.1093/bioinformatics/btv710>.
138. Kim, S., Scheffler, K., Halpern, A.L., Bekritsky, M.A., Noh, E., K llberg, M., Chen, X., Kim, Y., Beyter, D., Krusche, P., et al. (2018). Strelka2: fast and accurate calling of germline and somatic variants. *Nat. Methods* 15, 591–594. <https://doi.org/10.1038/s41592-018-0051-x>.
139. Cibulskis, K., Lawrence, M.S., Carter, S.L., Sivachenko, A., Jaffe, D., Sougnez, C., Gabriel, S., Meyerson, M., Lander, E.S., and Getz, G. (2013). Sensitive detection of somatic point mutations in impure and heterogeneous cancer samples. *Nat. Biotechnol.* 31, 213–219. <https://doi.org/10.1038/nbt.2514>.
140. Taylor-Weiner, A., Stewart, C., Giordano, T., Miller, M., Rosenberg, M., Macbeth, A., Lennon, N., Rheinbay, E., Landau, D.-A., Wu, C.J., et al. (2018). DeTiN: overcoming tumor-in-normal contamination. *Nat. Methods* 15, 531–534. <https://doi.org/10.1038/s41592-018-0036-9>.
141. Koboldt, D.C., Zhang, Q., Larson, D.E., Shen, D., McLellan, M.D., Lin, L., Miller, C.A., Mardis, E.R., Ding, L., and Wilson, R.K. (2012). VarScan 2: somatic mutation and copy number alteration discovery in cancer by exome sequencing. *Genome Res.* 22, 568–576. <https://doi.org/10.1101/gr.129684.111>.
142. Ye, K., Schulz, M.H., Long, Q., Apweiler, R., and Ning, Z. (2009). Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. *Bioinformatics* 25, 2865–2871. <https://doi.org/10.1093/bioinformatics/btp394>.
143. Mermel, C.H., Schumacher, S.E., Hill, B., Meyerson, M.L., Beroukhi, R., and Getz, G. (2011). GISTIC2.0 facilitates sensitive and confident localization of the targets of focal somatic copy-number alteration in human