

DAFTAR PUSTAKA

- Adjo Aka, J., Lin, S.X., 2012. Comparison of functional proteomic analyses of human breast cancer cell lines T47D and MCF7. *PLoS One* 7: e31532.
- Alfira, E.N., 2018. Identifikasi peptida spesifik pada gelatin babi menggunakan liquid chromatography-high resolution mass spectrometry (lc-hrms). Universitas Gadjah Mada.
- Cao, X.X., Xu, J. Da, Xu, J.W., Liu, X.L., Cheng, Y.Y., Li, Q.Q., Xu, Z. De, Liu, X.P., 2011. RACK1 promotes breast carcinoma migration/metastasis via activation of the RhoA/Rho kinase pathway. *Breast Cancer Res. Treat.* 126: 555–563.
- Cazzalini, O., Sommati, S., Tillhon, M., Dutto, I., Bachi, A., Rapp, A., Nardo, T., Scovassi, A.I., Necchi, D., Cardoso, M.C., Stivala, L.A., Prospero, E., 2014. CBP and p300 acetylate PCNA to link its degradation with nucleotide excision repair synthesis. *Nucleic Acids Res.* 42: 8433–8448.
- Chen, E.I., Cociorva, D., Norris, J.L., Yates, J.R., III, 2007. Optimization of mass spectrometry-compatible surfactants for shotgun proteomics. *J. Proteome Res.* 6: 2529–2538.
- Di Luca, A., Henry, M., Meleady, P., O'Connor, R., 2015. Label-free LC-MS analysis of HER2+ breast cancer cell line response to HER2 inhibitor treatment. *DARU, J. Pharm. Sci.* 23.
- Feist, P., Hummon, A.B., 2015. Proteomic challenges: Sample preparation techniques for microgram-quantity protein analysis from biological samples. *Int. J. Mol. Sci.* 16: 3537–3563.
- Friedrich, C.A., Ferrell, R.E., Siciliano, M.J., Kitto, G.B., 1988. Biochemical and genetic identity of alpha-keto acid reductase and cytoplasmic malate dehydrogenase from human erythrocytes. *Ann. Hum. Genet.* 52: 25–37.
- Gundry, R.L., White, M.Y., Murray, C.I., Kane, L.A., Fu, Q., Stanley, B.A., Van Eyk, J.E., 2009. Preparation of proteins and peptides for mass spectrometry analysis in a bottom-up proteomics workflow. *Curr Protoc Mol Biol Chapter* 10: Unit10.25.
- He, Y., Smith, R., 2009. Nuclear functions of heterogeneous nuclear ribonucleoproteins A/B. *Cell. Mol. Life Sci.* 66: 1239–1256.
- Hird, S.J., Lau, B.P.Y., Schuhmacher, R., Krska, R., 2014. Liquid chromatography-mass spectrometry for the determination of chemical contaminants in food. *TrAC - Trends Anal. Chem.* 59: 59–72.
- Holliday, D.L., Speirs, V., 2011. Choosing the right cell line for breast cancer research. *Breast Cancer Res.* 13: 215.
- Hustoft, H.K., Reubsaet, L., Greibrokk, T., Lundanes, E., Malerod, H., 2011. Critical assessment of accelerating trypsination methods. *J Pharm Biomed Anal* 56: 1069–1078.
- Karpievitch, Y.V., Polpitiya, A.D., Anderson, G.A., Smith, R.D., Dabney, A.R., 2011. Liquid Chromatography Mass Spectrometry-Based Proteomics: Biological and Technological Aspects. *Ann Appl Stat* 4: 1797–1823.

- Keydar, I., Chen, L., Karby, S., Weiss, F.R., Delarea, J., Radu, M., Chaitcik, S., Brenner, H.J., 1979. Establishment and characterization of a cell line of human breast carcinoma origin. *Eur J Cancer* 15: 659–670.
- Kohler, B.A., Sherman, R.L., Howlader, N., Jemal, A., Ryerson, A.B., Henry, K.A., Boscoe, F.P., Cronin, K.A., Lake, A., Noone, A., Henley, S.J., Ehemann, C.R., Anderson, R.N., Penberthy, L., 2015. Annual report to the nation on the status of cancer, 1975 – 2011, featuring incidence of breast cancer subtypes by race / ethnicity, poverty, and state. *Natl Cancer Inst* 107: 1–25.
- Kraut, A., Marcellin, M., Adrait, A., Kuhn, L., Louwagie, M., Kieffer-Jaquinod, S., Lebert, D., Masselon, C.D., Dupuis, A., Bruley, C., Jaquinod, M., Garin, J., Gallagher-Gambarelli, M., 2009. Peptide storage: Are you getting the best return on your investment? Defining optimal storage conditions for proteomics samples. *J Proteome Res.* 8: 3778–3785.
- Kwan, M.L., Kushi, L.H., Weltzien, E., Maring, B., Kutner, S.E., Fulton, R.S., Lee, M.M., Ambrosone, C.B., Caan, B.J., 2009. Epidemiology of breast cancer subtypes in two prospective cohort studies of breast cancer survivors. *Breast Cancer Res.* 11: 1–13.
- Lawrence, R.T., Perez, E.M., Hernández, D., Miller, C.P., Haas, K.M., Irie, H.Y., Lee, S.I., Blau, A.C., Villén, J., 2015. The proteomic landscape of triple-negative breast cancer. *Cell Rep.* 11: 630–644.
- Read, J.A., Winter, V.J., Eszes, C.M., Sessions, R.B., Brady, R.L., 2001. Structural basis for altered activity of M- and H-isozyme forms of human lactate dehydrogenase. *Proteins* 43: 175–85.
- Smith, L., Qutob, O., Watson, M.B., Beavis, A.W., Potts, D., Welham, K.J., Garimella, V., Lind, M.J., Drew, P.J., Cawkwell, L., 2009. Proteomic identification of putative biomarkers of radiotherapy resistance: a possible role for the 26S proteasome? *Neoplasia* 11: 1194–1207.
- Sotoca, A.M., Sollewijn Gelpke, M.D., Boeren, S., Ström, A., Gustafsson, J.-Å., Murk, A.J., Rietjens, I.M.C.M., Vervoort, J., 2011. Quantitative proteomics and transcriptomics addressing the estrogen receptor subtype-mediated effects in t47d breast cancer cells exposed to the phytoestrogen genistein. *Mol Cell Proteomics* 10: M110.002170.
- Tyanova, S., Albrechtsen, R., Kronqvist, P., Cox, J., Mann, M., Geiger, T., 2016. Proteomic maps of breast cancer subtypes. *Nat Commun* 7: 1–11.
- Yates, J.R., 1997. Protein and peptide analysis by mass spectrometry, *Analytica Chimica Acta*.
- Yu, S., Kim, T., Yoo, K.H., Kang, K., 2017. The T47D cell line is an ideal experimental model to elucidate the progesterone-specific effects of a luminal A subtype of breast cancer. *Biochem. Biophys. Res. Commun.* 486: 752–758.
- Zhang, X., 2015. Less is more: membrane protein digestion beyond urea–trypsin solution for next-level proteomics. *Mol Cell Proteomics* 14: 2441–2453.