

assembled into pathways and subnetworks and can be used as modules to build larger-scale, well-constrained dynamical models that, when integrated with genomic and epigenomic information, will enable computer-based algorithms for precision medicine by coupling clinical phenotyping to cellular mechanisms. For long-term sustainability, it is paramount that this catalog use existing data repositories when possible.

The consensus at the workshop was that there are sufficient individual technologies to serve as a base for the Quantitative Encyclopedia of Human Cell Components for a selected set of human cell types. Model organisms, such as yeasts or worms, could serve as catalysts for the development of new technologies. The workshop involved a limited number of participants, and because a project of this scale may require a global endeavor, greater outreach and engagement of various research communities will be important.

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REFERENCES AND NOTES

- Human Quantitative Dynamics Workshop, www.sbcny.org/2015_workshop/index.htm.
- S. Yamanaka, Induced pluripotent stem cells: Past, present, and future. *Cell Stem Cell* **10**, 678–684 (2012).
- M. Melé, P. G. Ferreira, F. Reverter, D. S. DeLuca, J. Monlong, M. Sammeth, T. R. Young, J. M. Goldmann, D. D. Pervouchine, T. J. Sullivan, R. Johnson, A. V. Segrè, S. Djebali, A. Niarchou; GTEx Consortium, F. A. Wright, T. Lappalainen, M. Calvo, G. Getz, E. T. Dermizakis, K. G. Ardlie, R. Guigó, Human genomics. The human transcriptome across tissues and individuals. *Science* **348**, 660–665 (2015).
- ENCODE Project Consortium, An integrated encyclopedia of DNA elements in the human genome. *Nature* **489**, 57–74 (2012).
- T. W. Rhoads, A. Prasad, N. W. Kwiecien, A. E. Merrill, K. Zawack, M. S. Westphall, F. C. Schroeder, J. Kimble, J. J. Coon, NeuCode labeling in nematodes: Proteomic and phosphoproteomic impact of ascaroside treatment in *Caenorhabditis elegans*. *Mol. Cell. Proteomics* **14**, 2922–2935 (2015).
- T. Rolland, M. Taşan, B. Charlotiaux, S. J. Pevzner, Q. Zhong, N. Sahni, S. Yi, I. Lemmens, C. Fontanillo, R. Mosca, A. Kamburov, S. D. Ghiassian, X. Yang, L. Ghamsari, D. Balcha, B. E. Begg, P. Braun, M. Brehme, M. P. Broly, A.-R. Carvunis, D. Convery-Zupan, R. Corominas, J. Coulombe-Huntington, E. Dann, M. Dreze, A. Dricot, C. Fan, E. Franzosa, F. Gebreab, B. J. Gutierrez, M. F. Hardy, M. Jin, S. Kang, R. Kiro, G. N. Lin, K. Luck, A. MacWilliams, J. Menche, R. R. Murray, A. Palagi, M. M. Poulin, X. Rambout, J. Rasla, P. Reichert, V. Romero, E. Ruysinck, J. M. Sahalie, A. Scholz, A. A. Shah, A. Sharma, Y. Shen, K. Spirohn, S. Tam, A. O. Tejada, S. A. Trigg, J.-C. Twizere, K. Vega, J. Walsh, M. E. Cusick, Y. Xia, A.-L. Barabási, L. M. Iakoucheva, P. Aloy, J. De Las Rivas, J. Tavernier, M. A. Calderwood, D. E. Hill, T. Hao, F. P. Roth, M. Vidal, A proteome-scale map of the human interactome network. *Cell* **159**, 1212–1226 (2014).
- R. Vincentelli, K. Luck, J. Poirson, J. Polanowska, J. Abdat, M. Blémont, J. Turchetto, F. Iv, K. Ricquier, M.-L. Straub, A. Forster, P. Cassonnet, J.-P. Borg, Y. Jacob, M. Masson, Y. Nominé, J. Reboul, N. Wolff, S. Charbonnier, G. Travé, Quantifying domain-ligand affinities and specificities by high-throughput holdup assay. *Nat. Methods* **12**, 787–793 (2015).
- A.-C. Gingras, M. Gstaiger, B. Raught, R. Aebersold, Analysis of protein complexes using mass spectrometry. *Nat. Rev. Mol. Cell Biol.* **8**, 645–654 (2007).
- T. W.-M. Fan, P. K. Lorkiewicz, K. Sellers, H. N. B. Moseley, R. M. Higashi, A. N. Lane, Stable isotope-resolved metabolomics and applications for drug development. *Pharmacol. Ther.* **133**, 366–391 (2012).
- A.-E. Saliba, I. Vonkova, A.-C. Gavin, The systematic analysis of protein–lipid interactions comes of age. *Nat. Rev. Mol. Cell Biol.* **16**, 753–761 (2015).

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Quantitative human cell encyclopedia

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