

April 1st, 2016

Kosuke Hashimoto

Nationality: Japan
Year of Birth: 1978
Office Address: RIKEN Center for Life Science Technologies
Suehiro-cho 1-7-22, Tsurumi, Yokohama, Japan
Emails: (1) kosuke.hashimoto@riken.jp (2) khashimo1007@gmail.com

Education and Research Experience

Apr. 2016 – Present Senior Research Scientist, Riken, Japan
Oct. 2011 – Mar. 2016 Research Scientist, Riken, Japan
Apr. 2009 – Sep. 2011 Postdoctoral Visiting Fellow, NCBI, NIH, USA
Mar. 2009 Ph.D. Bioinformatics Center, Kyoto University, Japan
Adviser: Professor Minoru Kanehisa
Mar. 2006 M.Sc. Kyoto University, Japan
Aug. 2005 – Nov. Exchange Student, Humboldt University, Germany
Jun. 2004 – Sep. Exchange Student, Boston University, USA
Mar. 2001 Bachelor of Engineering. Osaka University, Japan

Fellowships

2010 – 2011 Research Fellow of the Japan Society for the Promotion of Science (NIH)
2006 – 2009 Research Fellow of the Japan Society for the Promotion of Science (DC1)

Publications (Refereed)

1. Tebbi A., Levillayer F., Jouvion G., Fiette L., Soubigou G., Varet H., Boudjadja N., Cairo S., **Hashimoto K.**, Suzuki AM., Carninci P., Carissimo A., di Bernado D., Wei Y.: Deficiency of multidrug resistance 2 contributes to cell transformation through oxidative stress. *Carcinogenesis*. 37, 39-48 (2016) [PMID: 26542370]
2. **Hashimoto K.**, Suzuki, AM., Santos, AD., Desterke, C., Collino, A., Ghisletti, S., Braun, E., Bonetti, A., Fort, A., Qin, XY., Radaelli, E., Kaczkowski, B., Forrest, AR., Kojima, S., Samuel, D., Natoli, G., Buendia, MA., Faivre, J., Carninci, P.; CAGE profiling of ncRNAs in hepatocellular carcinoma reveals widespread activation of retroviral LTR promoters in virus-induced tumors. *Genome Research*. 25, 1812-1824 (2015) [PMID: 26510915]
3. Konno, D., Kasukawa, T., **Hashimoto K.**, Itoh, T., Suetsugu, T., Miura, I., Wakana, S., Carninci, P., Matsuzaki, F.; STAP cells are derived from embryonic stem cells. *Nature*. 525, E4-5 (2015) [PMID: 26399834]

4. Fort A, Yamada D, **Hashimoto K**, Koseki H, Carninci P; Nuclear transcriptome profiling of induced pluripotent stem cells and embryonic stem cells identify non-coding loci resistant to reprogramming. *Cell Cycle*. 14, 1148-1155 (2015) [PMID: 25664506]
5. Taguchi, A., Nagasaka, K., Kawana, K., **Hashimoto, K.**, Kusumoto-Matsuo, R., Plessy, C, Thomas, M., Nakamura, H., Bonetti, A., Oda, K., Kukimoto, I., Carninci, P., Banks, L., Osuga, Y., Fujii, T.; Characterization of novel transcripts of human papillomavirus type 16 using CAGE technology. *J Virol*. 89, 2448-2452 (2015) [PMID: 25505068]
6. Fort, A., **Hashimoto, K.**, Yamada, D., Salimullah, M., Keya, CA., Saxena, A., Bonetti, A., Voineagu, I., Bertin, N., Kratz, A., Noro, Y., Wong, CH., de Hoon, M., Andersson, R., Sandelin, A., Suzuki, H., Wei, CL., Koseki, H., FANTOM Consortium, Hasegawa, Y., Forrest, AR., Carninci, P.; Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. *Nat Genet*. 46, 558-566 (2014) [PMID: 24777452]
7. Nishi, H., Tyagi, M., Teng, S., Shoemaker, B.A., **Hashimoto, K.**, Alexov, E., Wuchty, S., Panchenko, A.R.; Cancer missense mutations alter binding properties of proteins and their interaction networks. *PLoS One* e66273 (2013) [PMID: 23799087]
8. **Hashimoto, K.**, Rogozin, I.B., Panchenko, A.R.; Oncogenic potential is related to activating effect of cancer single and double somatic mutations in receptor tyrosine kinases. *Hum. Mutat*. 33, 1566-1575 (2012) [PMID: 22753356].
9. Izumi, Y., Li, J., Villers, C., **Hashimoto, K.**, Burg, M.B., Ferraris, J.D.; Mutations that reduce its specific DNA binding inhibit high NaCl-induced nuclear localization of the osmoprotective transcription factor NFAT5. *Am J Physiol Cell Physiol*. 303, C1061-C1069 (2012) [PMID: 22992674].
10. Tyagi, M., **Hashimoto, K.**, Shoemaker, B.A., Wuchty, S., and Panchenko, A.R.; Large-scale mapping of human protein interactome using structural complexes. *EMBO Rep*. 13, 266-271 (2012) [PMID: 22261719].
11. Nishi, H., **Hashimoto, K.**, and Panchenko, A.R.; Phosphorylation in protein-protein binding: effect on stability and function. *Structure* 19, 1807-1815 (2011) [PMID: 22153503].
12. **Hashimoto, K.**, Nishi, H., Bryant, S.H., and Panchenko, A.R.; Caught in self-interaction: evolutionary and functional mechanisms of protein homooligomerization. *Phys. Biol*. 8, 035007 (2011) [PMID: 21572178].
13. **Hashimoto, K.**, and Panchenko, A.R.; Mechanisms of protein oligomerization, the critical role of insertions and deletions in maintaining different oligomeric states. *Proc. Natl. Acad. Sci. USA* 107, 20352-20357 (2010) [PMID: 21048085].
14. **Hashimoto, K.**, Madej, T., Bryant, S.H., and Panchenko, A.R.; Functional States of Homooligomers: Insights from the Evolution of Glycosyltransferases. *J. Mol. Biol*. 399, 196-206 (2010) [PMID: 20381499].

15. **Hashimoto, K.**, Tokimatsu, T., Kawano, S., Yoshizawa, A.C., Okuda, S., Goto, S., and Kanehisa, M.; Comprehensive analysis of glycosyltransferases in eukaryotic genomes for structural and functional characterization of glycans. *Carbohydr. Res.* 344, 881-887 (2009) [PMID: 19327755].
16. **Hashimoto, K.**, Takigawa, I., Shiga, M., Kanehisa, M., and Mamitsuka, H.; Mining significant tree patterns in carbohydrate sugar chains. *Bioinformatics* 24, i167-i173 (2008) [PMID: 18689820].
17. **Hashimoto, K.**, Aoki-Kinoshita, K.F., Ueda, N., Kanehisa, M., and Mamitsuka, H.; A new efficient probabilistic model for mining labeled ordered trees applied to glycobiology. *ACM TKDD* 2(1), Article No.6 (2008)
18. **Hashimoto, K.**, Yoshizawa, A.C., Okuda, S., Kuma, K., Goto, S., and Kanehisa, M.; The repertoire of desaturases and elongases reveals fatty acid variations in 56 eukaryotic genomes. *J. Lipid Res.* 49, 183-191 (2008) [PMID: 17921532]
19. Suga, A., Yamanishi, Y., **Hashimoto, K.**, Goto, S., and Kanehisa, M.; An improved scoring scheme for predicting glycan structures from gene expression data. *Genome Informatics* 18, 237-246 (2007) [PMID: 18546491]
20. **Hashimoto, K.**, Yoshizawa, A.C., Saito, K., Yamada, T., and Kanehisa, M.; The repertoire of desaturases for unsaturated fatty acid synthesis in 397 genomes. *Genome Informatics* 17, 173-183 (2006) [PMID: 17503367]
21. **Hashimoto, K.**, Goto, S., Kawano, S., Aoki-Kinoshita, K.F., Ueda, N., Hamajima, M., Kawasaki, T., and Kanehisa, M.; KEGG as a glycome informatics resource. *Glycobiology* 16, 63R-70R (2006) [PMID: 16014746]
22. **Hashimoto, K.**, Aoki-Kinoshita, K., Ueda, N., Kanehisa, M., and Mamitsuka, H.; A new efficient probabilistic model for mining labeled ordered trees. *ACM SIGKDD* (2006).
23. Binder, B., Ebenhoh, O., **Hashimoto, K.**, Heinrich, R.; Expansion of signal transduction networks. *IEE Proceedings-Systems Biology* 153, 364-368 (2006) [PMID: 16986318]
24. Kawano, S., **Hashimoto, K.**, Miyama, T., Goto, S., and Kanehisa, M.; Prediction of glycan structures from gene expression data based on glycosyltransferase reactions. *Bioinformatics* 21, 3976-3982 (2005) [PMID: 16159923]
25. **Hashimoto, K.**, Kawano, S., Goto, S., Aoki-Kinoshita, K., Kawashima, M., and Kanehisa, M.; A global representation of the carbohydrate structures: a tool for the analysis of glycan. *Genome Informatics* 16, 214-222 (2005) [PMID: 16362924]
26. Hizukuri, Y., Yamanishi, Y., **Hashimoto, K.**, and Kanehisa, M.; Extraction of species-specific glycan substructures. *Genome Informatics* 15, 69-81 (2004) [PMID: 15712113]

Publications (Non-Refereed)

- Nishi, H., **Hashimoto, K.**, Madej, T., Panchenko, A.R.; Evolutionary, physicochemical, and

functional mechanisms of protein homooligomerization. In "Progress in Molecular Biology and Translational Science", pp.3–24, ELSEVIER (2013).

- Takigawa, I., **Hashimoto, K.**, Shiga, M., Kanehisa, M., and Mamitsuka, H.; Mining patterns from glycan structures. In "Proceedings of the International Beilstein Symposium on Glyco-Bioinformatics" (Hicks, M.G and Kettner, C.), pp. 13-24, Beilstein-Institut (2010).
- **Hashimoto, K.** and Kanehisa, M.; KEGG GLYCAN for integrated analysis of pathways, genes, and glycan structures. In "Handbook of Glycomics" (Cummings, R.D. and Pierce, J.M., eds.), pp. 197-210, Academic Press (2009).
- **Hashimoto, K.**, and Kanehisa, M.; KEGG GLYCAN for integrated analysis of pathways, genes, and structures. In "Experimental Glycoscience" (Taniguchi, N., Suzuki, A., Ito, Y., Narimatsu, H., Kawasaki, T., and Hase, S., eds.), pp. 441-444, Springer (2008).
- **Hashimoto, K.**, Goto, S., and Kanehisa, M.; KEGG GLYCAN and glycome informatics. (in Japanese) In "Tanpakushitsu Kakusan Koso", Vol.53(12) pp. 1698-1702, Kyoritsu, (2008). [PMID: 21089391]

Publications (Japanese)

- 「トランスクリプトーム解析の変遷と国際 ncRNA プロジェクトの現在」, 実験医学 33(20), pp.106-107 (2015) 羊土社
- 橋本浩介「肝臓がんで発現するキメラ non-coding RNA」, 実験医学 32(9), pp.1378-1379 (2014) 羊土社
- 橋本浩介, 五斗 進, 金久 實 「KEGG GLYCAN データベースと糖鎖インフォマティクス」, 蛋白質 核酸 酵素 53(12), pp.1698-1702 (2008) 共立出版
- 橋本浩介, 五斗 進, 金久 實「KEGG: 生命システム情報統合データベース」実験医学 26(7), pp.1142-1147 (2008) 羊土社

Presentations at International Conferences (Talk)

- **Hashimoto, K.**, Suzuki, A.M., Carninci, P.; Activation of retroviral LTR promoters in hepatocellular carcinoma. *Systems Biology of Liver Cancer* 2015 Yokohama, Japan
- **Hashimoto, K.**, Carninci, P.; Activation of LTR derived non-coding RNAs in liver cancer. *International Symposium on Bioinformatics and its Application* 2014 Tokyo, Japan
- **Hashimoto, K.**, and Panchenko, A.R.; Mechanisms of protein oligomerization, the critical role of insertions and deletions in maintaining different oligomeric states. *Albany 2011: The 17th Conversation* 2011, Albany, USA.
- **Hashimoto, K.**, Takigawa, I., Shiga, M., Kanehisa, M., and Mamitsuka, H.; Mining significant tree patterns in carbohydrate sugar chains. *European Conference on Computational Biology* 2008,

Cagliari, Italy.

- **Hashimoto, K.**, Yoshizawa, A.C., Saito, K., Yamada, T., and Kanehisa, M.; The repertoire of desaturases for unsaturated fatty acid synthesis in 397 genomes. *International Workshop on Bioinformatics and Systems Biology 2006*, Boston, USA.
- **Hashimoto, K.**, Kawano, S., Goto, S., Aoki-Kinoshita, K., Kawashima, M., and Kanehisa, M.; A global representation of the carbohydrate structures: a tool for the analysis of glycan. *International Workshop on Bioinformatics and Systems Biology 2005*, Berlin, Germany.