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Education and Research Experience

Oct. 2011 – Present	Research Scientist, Riken, Japan
Apr. 2009 – Sep. 2011	Postdoctoral Visiting Fellow, NCBI, NIH, USA
Mar. 2009	Ph.D. Kyoto University, Japan
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. Fort, A., **Hashimoto, K.**, Yamada, D., Salimullah, M., Keya, C.A., Saxena, A., Bonetti, A., Voineagu, I., Bertin, N., Kratz, A., Noro, Y., Wong, C.H., de Hoon, M., Andersson, R., Sandelin, A., Suzuki, H., Wei, C.L., Koseki, H., FANTOM Consortium, Hasegawa, Y., Forrest, A.R., 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]
2. 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]
3. **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].
4. 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].

5. 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].
6. 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].
7. **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].
8. **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].
9. **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].
10. **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].
11. **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].
12. **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)
13. **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]
14. 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]
15. **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]
16. **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]
17. **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).

18. Binder, B., Ebenhoh, O., **Hashimoto, K.**, Heinrich, R.; Expansion of signal transduction networks. *IEE Proceedings-Systems Biology* 153, 364-368 (2006) [PMID: 16986318]
19. 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]
20. **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]
21. 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)

- 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., and Carninci, P.; Profiling of ncRNA transcriptome reveals aberrant activation of LTR retroviral promoters in human HCC. *MODHEP Annual Meeting 2014* Naples, Italy.
- Suzuki, A.M., **Hashimoto, K.**, and Carninci, P.; Transcriptome analysis of mouse and human HCC by CAGE. *MODHEP Annual Meeting 2012* Roma, Italy.
- Suzuki A.M., **Hashimoto, K.**, and Carninci, P.; Transcriptome of liver cancer using CAGE and RNA-seq. *MODHEP Annual Meeting 2012*, Paris, France.
- **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.