

# CURRICULUM VITAE

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## **Education:**

- 1992/4-1994/3 Stream Natural Science I, College of Arts and Sciences (Junior Division), The University of Tokyo
- 1994/4-1996/3 Department of Biophysics and Biochemistry, Faculty of Science, The University of Tokyo  
Awarded the degree of BS in Biophysics and Biochemistry
- 1996/4-1998/3 Department of Biophysics and Biochemistry, Graduate School of Science, The University of Tokyo  
Awarded the degree of MS in Biophysics and Biochemistry  
Work supervised by Lecturer Dr. Yutaka Muto
- 1998/4-2001/3 Department of Biophysics and Biochemistry, Graduate School of Science, The University of Tokyo  
Awarded the degree of Ph.D. in Biophysics and Biochemistry for a thesis entitled “Structural Biological Studies of RNA-binding domains of human U2AF<sup>65</sup>”.  
Work supervised by Professor Dr. Shigeyuki Yokoyama

## **Research experience:**

- 1998/4-2001/3 Research Fellow of the Japan Society for the Promotion of Science (DC1)
- 2001/4-2004/8 Postdoctoral research fellow at Department of Biological Chemistry and Molecular Pharmacology, Harvard Medical School, supervised by Professor Dr. Gerhard Wagner

2004/9-2005/3	Research associate at Genomic Science Center, RIKEN
2005/3-2010/6	Research associate at Department of Biophysics and Biochemistry, Graduate School of Science, The University of Tokyo
2010/7-2012/3	Project research associate at Laboratory of Structural Biology, Graduate School of Science, The University of Tokyo
2012/4-2013/3	Research scientist at Systems and Structural Biology Research Team, RIKEN Systems and Structural Biology Center
2013/4-present	Unit Leader at Translation Factors Structural Biology Unit, RIKEN Center for Life Science Technologies

### **Publication:**

#### **Original Papers**

1. Kuwasako, K., Nameki, N., Tsuda, K., Takahashi, M., Sato, A., Tochio, N., Inoue, M., Terada, T., Kigawa, T., Kobayashi, N., Shirouzu, M., **Ito, T.**, Sakamoto, T., Wakamatsu, K., Güntert, P., Takahashi, S., Yokoyama, S. and Muto, Y. (2017) Solution structure of the first RNA recognition motif domain of human spliceosomal protein SF3b49 and its mode of interaction with a SF3b145 fragment. *Protein Sci.*, **26**, 280-291. DOI: 10.1002/pro.3080.
2. Christian, T., Sakaguchi, R., Perlinska, A.P., Lahoud, G., **Ito, T.**, Taylor, E.A., Yokoyama, S., Sulkowska, J.I. and Hou, Y.-M. (2016) Methyl transfer by substrate signaling from a knotted protein fold. *Nat Struct Mol Biol.*, **23**, 941-948. DOI:10.1038/nsmb.3282. (Epub 2016 Aug 29)
3. Kashiwagi, K., Shigeta, T., Imatake, H., **Ito, T.**\* and Yokoyama, S.\* (2016) Expression, purification, and crystallization of *Schizosaccharomyces pombe* eIF2B. *J Struct Funct Genomics*, **17**, 33-38. DOI: 10.1007/s10969-016-9203-3. (Epub 2016 Mar 29) (\* co-corresponding authors)
4. Kashiwagi, K., Takahashi, M., Nishimoto, M., Hiyama, T.B., Higo, T., Umehara, T., Sakamoto, K., **Ito, T.**\* and Yokoyama, S.\* (2016) Crystal structure of eukaryotic translation initiation factor 2B. *Nature*, **531**, 122-125. DOI: 10.1038/nature16991. (Epub 2016 Feb 22) (\* co-corresponding authors)
5. **Ito, T.**, Masuda, I., Yoshida, K., Goto-Ito, S., Sekine, S., Suh, S.W., Hou, Y.-M. and Yokoyama, S. (2015) Structural Basis for methyl-donor-dependent and sequence-specific binding to tRNA substrates by knotted methyltransferase TrmD. *Proc Natl Acad Sci U S A*, **112**, E4197-E4205. DOI: 10.1073/pnas.1422981112. (Epub 2015 Jul 16)
6. Ehara, H., Makino, M., Kodama, K., **Ito, T.**, Sekine, S., Fukuzawa, S., Yokoyama,

- S. and Tachibana, K. (2015) Crystal Structure of okadaic acid binding protein 2.1: a sponge protein implicated in cytotoxin accumulation. *Chembiochem*, **16**, 1435-1439. DOI: 10.1002/cbic.201500141. (Epub 2015 May 12)
7. Kanamori, T., Ohzeki, H., Masaki, Y., Ohkubo, A., Takahashi, M., Tsuda, K., Ito, T., Shirouzu, M., Kuwasako, K., Muto, Y., Sekine, M. and Seio, K. (2015) Controlling the fluorescence of benzofuran-modified uracil residues in oligonucleotides by triple-helix formation. *Chembiochem*, **16**, 167-76. DOI: 10.1002/cbic.201402346. (Epub 2014 Dec 2)
8. Kuwasako, K.<sup>#</sup>, Takahashi, M.<sup>#</sup>, Unzai, S., Tsuda, K., Yoshikawa, S., He, F., Kobayashi, N., Guntert, P., Shirouzu, M., Ito, T., Tanaka, A., Yokoyama, S., Hagiwara, M., Kuroyanagi, H. and Muto, Y. (2014) RBFOX and SUP-12 sandwich a G base to cooperatively regulate tissue-specific splicing. *Nat Struct Mol Biol*, **21**, 778-86. DOI: 10.1038/nsmb.2870. (Epub 2014 Aug 17) (# equally contributed)
9. Kashiwagi, K., Ito, T. and Yokoyama, S. (2014) Crystal structure of the eukaryotic translation initiation factor 2A from *Schizosaccharomyces pombe*. *J Struct Funct Genomics*, **15**, 125-130. DOI: 10.1007/s10969-014-9177-y. (Epub 2014 Feb 26)
10. Nakagawa, H., Kuratani, M., Goto-Ito, S., Ito, T., Katsura, K., Terada, T., Shirouzu, M., Sekine, S., Shigi, N. and Yokoyama, S. (2013) Crystallographic and mutational studies on the tRNA thiouridine synthetase TtuA. *Proteins*, **81**, 1232-44. DOI: 10.1002/prot.24273. (Epub 2013 Apr 10)
11. Hanawa-Suetsugu, K., Kukimoto-Niino, M., Mishima-Tsumagari, C., Akasaka, R., Ohsawa, N., Sekine, S.-I., Ito, T., Tochio, N., Koshiba, S., Kigawa, T., Terada, T., Shirouzu, M., Nishikimi, A., Urano, T., Katakai, T., Kinashi, T., Kohda, D., Fukui, Y. and Yokoyama, S. (2012) Structural basis for mutual relief of the Rac guanine nucleotide exchange factor DOCK2 and its partner ELMO1 from their autoinhibited forms. *Proc Natl Acad Sci U S A*, **109**, 3305-10. DOI: 10.1073/pnas.1113512109. (Epub 2012 Feb 13)
12. Georges, L., Goto-Ito, S., Yoshida, K., Ito, T., Yokoyama, S. and Hou, Y.-M. (2011) Differentiating analogous tRNA methyltransferases by fragments of the methyl donor. *RNA*, **17**, 1236-1246. DOI: 10.1261/rna.2706011. (Epub 2011 May 20)
13. Ito, T.\*, Ito, T.\* and Yokoyama, S. (2011) Plasma-assisted biological macromolecular crystallization. *Applied Physics Express*, **4**, 026201. DOI: 10.1143/APEX.4.026201. (Epub 2011 Feb 8) (\* equally contributed)
14. Ito, T. and Yokoyama, S. (2010) Two enzymes bound to one transfer RNA assume

- alternative conformations for consecutive reactions. *Nature*, **467**, 612-616. DOI: 10.1038/nature09411. (Epub 2010 Sep 29)
15. Kuratani, M., Hirano, M., Goto-Ito, S., Itoh, Y., Hikida, Y., Nishimoto, M., Sekine, SI., Bessho, Y., **Ito, T.**, Grosjean, H. and Yokoyama, S. (2010) Crystal Structure of *Methanocaldococcus jannaschii* Trm4 complexed with sinefungin. *J Mol Biol*, **401**, 323-333. DOI: 10.1016/j.jmb.2010.06.046. (Epub 2010 Jun 30)
  16. **Ito, T.**, Kiyasu, N., Matsunaga, R., Takahashi, S. and Yokoyama, S. (2010) Crystal structure of nondiscriminating glutamyl-tRNA synthetase from *Thermotoga maritima*. *Acta Crystallogr D Biol Crystallogr*, **66**, 813-820. DOI: 10.1107/S0907444910019086. (Epub 2010 Jun 19)
  17. Goto-Ito, S., **Ito, T.**, Kuratani, M., Bessho, Y. and Yokoyama, S. (2009) Tertiary structure checkpoint at anticodon loop modification in tRNA functional maturation. *Nat Struct Mol Biol*, **16**, 1109-1115. DOI: 10.1038/nsmb.1653. (Epub 2009 Sep 13)
  18. Hiyama, T.B., **Ito, T.**, Imataka, H. and Yokoyama, S. (2009) Crystal Structure of the alpha subunit of human translation initiation factor 2B. *J Mol Biol*, **392**, 937-951. DOI: 10.1016/j.jmb.2009.07.054. (Epub 2009 Jul 22)
  19. Goto-Ito, S., **Ito, T.**, Ishii, R., Muto, Y., Bessho, Y. and Yokoyama, S. (2008) Crystal Structure of Archaeal tRNA (m1G37) methyltransferase aTRM5. *Proteins*, **72**, 1274-1289. DOI: 10.1002/prot.22019. (Epub 2008 Apr 2)
  20. Goto-Ito, S., Ishii, R., **Ito, T.**, Shibata, R., Fusatomi E., Sekine, S., Bessho, Y. and Yokoyama, S. (2007) Structure of an archaeal TYW1, the enzyme catalyzing the second step of wye-base biosynthesis. *Acta Crystallogr D Biol Crystallogr*, **63**, 1059-1068. DOI: 10.1107/S0907444907040668. (Epub 2007 Sep 19)
  21. **Ito, T.** and Wagner, G. (2007) Resonance assignments of the  $\alpha$  subunit of human eukaryotic initiation factor 2 (eIF2 $\alpha$ ). *J Biomol NMR*, **38**, 173. DOI: 10.1007/s10858-006-9099-5. (Epub 2006 Nov 23)
  22. Gelev, V., Aktas, H., Marintchev, A., **Ito, T.**, Frueh, D., Hemond, M., Rovnyak, D., Debus, M., Hyberts, S., Usheva, A., Halperin, J. and Wagner, G. (2006) Mapping of the Auto-Inhibitory Interactions of Protein Kinase R by Nuclear Magnetic Resonance. *J Mol Biol*, **364**, 352-363. DOI: 10.1016/j.jmb.2006.08.077. (Epub 2006 Sep 1)
  23. Frueh, D.P., **Ito, T.**, Li, J.-S., Wagner, G., Glaser, S.J., and Khaneja, N. (2005) Sensitivity enhancement in NMR of macromolecules by application of optimal control theory. *J Biomol NMR*, **32**, 23-30. DOI: 10.1007/s10858-005-3592-0.
  24. **Ito, T.**, Marintchev, A. and Wagner, G. (2004) Solution structure of human

- initiation factor eIF2 $\alpha$  reveals homology to the elongation factor eEF1B. *Structure*, **12**, 1693-1704. DOI: 10.1016/j.str.2004.07.010.
25. Kato, M., **Ito, T.**, Wagner, G. and Ellenberger, T. (2004) A molecular handoff between bacteriophage T7 DNA primase and T7 DNA polymerase initiates DNA synthesis. *J Biol Chem*, **279**, 30554-62. DOI: 10.1074/jbc.M403485200. (Epub 2004 May 8)
  26. **Ito, T.** and Wagner, G. (2004) Using codon optimization, chaperone co-expression, and rational mutagenesis for production and NMR assignments of human eIF2 $\alpha$ . *J Biomol NMR*, **28**, 357-367. DOI: 10.1023/B:JNMR.0000015405.62261.cb.
  27. Kato, M., **Ito, T.**, Wagner, G., Richardson, C.C. and Ellenberger, T. (2003) Modular architecture of the bacteriophage T7 primase couples RNA primer synthesis to DNA synthesis. *Mol Cell*, **11**, 1349-1360. DOI: 10.1016/S1097-2765(03)00195-3.
  28. Kitamura, A., Muto, Y., Watanabe, S., Kim, I., **Ito, T.**, Nishiya, Y., Sakamoto, K., Ohtsuki, T., Kawai, G., Watanabe, K., Hosono, K., Takaku, H., Katoh, E., Yamazaki, T., Inoue, T. and Yokoyama, S. (2002) Solution structure of an RNA fragment with the P7/P9.0 region and the 3'-terminal guanosine of the tetrahymena group I intron. *RNA*, **8**, 440-451. DOI: 10.1017.S1355838202026043.
  29. **Ito, T.**, Muto, Y., Green, M.R. and Yokoyama, S. (1999) Solution structures of the first and second RNA-binding domains of human U2 small nuclear ribonucleoprotein particle auxiliary factor (U2AF<sup>65</sup>). *EMBO J*, **18**, 4523-4534. DOI: 10.1093/emboj/18.16.4523. (Epub 1999 Aug 16)

## Proceedings

1. Kitamura, A., Muto, Y., Watanabe, S., Kim, I., **Ito, T.**, Nishiya, Y., Ohtsuki, T., Kawai, G., Watanabe, K., Hosono, K., Takaku, H., Katoh, E., Yamazaki, T., Inoue, T. and Yokoyama, S. (1999) The guanosine binding mechanism of the Tetrahymena group I intron. *Nucleic Acids Symp Ser*, **42**, 191-192.

## Review in English

1. Goto-Ito, S., **Ito, T.**\* and Yokoyama, S.\* (2017) Trm5 and TrmD: two enzymes from distinct origins catalyze the identical tRNA modification, m<sup>1</sup>G37. *Biomolecules*, **7**, E32. DOI:10.3390/biom7010032. (Epub 2017 Mar 21) (\* co-corresponding authors)
2. Kashiwagi, K., **Ito, T.**\* and Yokoyama, S.\* (2017) Crystal structure of eIF2B and insights into eIF2-eIF2B interactions. *FEBS J*, **284**, 868-874

DOI:10.1111/febs.13896. (Epub 2016 Sep 14) (\* co-corresponding authors)

3. **Ito, T.** and Yokoyama, S. (2011) Crystal structure of glutamine transamidosome: two enzymes bond to one transfer RNA function cooperatively for consecutive reactions. *Photon Factory Activity Report 2010*, **28**, 48-49.
4. **Ito, T.** and Yokoyama, S. (2011) Crystal structure of glutamine transamidosome reveals how two enzymes bound to one tRNA assume alternative conformations for consecutive reactions. *Spring-8 Research Frontiers 2010*, 20-21.