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CURRICULUM VITAE

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Education:

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| 1997 | Ph. D. University of Tokyo |
| 1992-1997 | Graduate School of Science, University of Tokyo |
| 1988-1992 | Faculty of Science, Tohoku University |

Academic Experience:

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| 2013-present | Team Leader, Supramolecular Structural Biology Team,
RIKEN Center for Life Science Technologies (CLST) |
| 2012-2013 | Senior Research Scientist,
RIKEN Systems and Structural Biology Center (SSBC) |
| 2010-2012 | Associate professor, Laboratory of Structural Biology,
Graduate School of Science, University of Tokyo |
| 2004-2010 | Lecturer, Department of Biophysics and Biochemistry,
Graduate School of Science, University of Tokyo |
| 2001-2004 | Researcher, RIKEN Cellular Signaling Lab. |
| 1999-2001 | Special Postdoctoral Researcher, RIKEN Cellular Signaling Lab. |
| 1998-1999 | Contract Researcher, RIKEN Cellular Signaling Lab. |
| 1997-1998 | JSPS PD Research Fellow, University of Tokyo |

Field of research:

Structural Biology, Biochemistry, Molecular Biology

Publications

Journal Articles:

- Sekine, S., *† Murayama, Y., * Svetlov, V., Nudler, E. and Yokoyama, S. † (2015) The ratcheted and ratchetable structural states of RNA polymerase underlie multiple transcriptional functions. *Mol. Cell* 57, 408-21. (*Co-first authors, †correspondence)
- Sekine, S., † Murayama, Y., Svetlov, V., Nudler, E. and Yokoyama, S. † (2015) Ratcheting of RNA polymerase toward structural principles of RNA polymerase operations. *Transcription* 6: 56-60. (†correspondence)
- Tomabechi, Y., Hosoya, T., Ehara, H., Sekine, S., Shirouzu, M. and Inouye, S. (2015) *Biochem. Biophys. Res. Commun.* 470, 88-93.
- 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, E4197-205.
- Ehara, H., Makino, M., Kodama, K., Konoki, 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.
- Itoh, Y., Sekine, S. and Yokoyama, S. (2015) Crystal structure of the full-length bacterial selenocysteine-specific elongation factor SelB. *Nucleic Acids Res.* 43, 9028-9038.
- Antonopoulos, I.H., Murayama, Y., Warner, B.A., Sekine, S., Yokoyama, S., Carey, P.R. (2015) Time-resolved Raman and polyacrylamide gel electrophoresis observations of nucleotide incorporation and misincorporation in RNA within a bacterial RNA polymerase crystal. *Biochemistry* 54, 652-665.
- Yanagisawa, T., Ishii, R., Hikida, Y., Fukunaga, R., Sengoku, T., Sekine, S. and Yokoyama, S. (2015) A SelB/EF-Tu/aIF2 γ -like protein from *Methanosarcina mazei* in the GTP-bound form binds cysteinyl-tRNA^{Cys}. *J. Struct. Funct. Genomics.* 16, 25-41.
- Higo, T., Suka, N., Ehara, H., Wakamori, M., Sato, S., Maeda, H., Sekine, S., Umehara, T. and Yokoyama, S. (2014) Development of a hexahistidine-3×FLAG-tandem affinity purification method for endogenous protein complexes in *Pichia*

pastoris. *J. Struct. Funct. Genomics.* 15, 191-199.

Severinov, K., Minakhin, L., Sekine, S., Lopatina, A. and Yokoyama, S. (2014) Molecular basis of RNA polymerase promoter specificity switch revealed through studies of *Thermus* bacteriophage transcription regulator. *Bacteriophage* 4, e29399

Naganuma, M., Sekine, S., Chong, Y.E., Guo, M., Yang, X.L., Gamper, H., Hou, Y.M., Schimmel, P. and Yokoyama, S. (2014) The selective tRNA aminoacylation mechanism based on a single G•U pair. *Nature* 510, 507-511.

Tagami, S., * Sekine, S., * Minakhin, L., * Esyunina, D., Akasaka, R., Shirouzu, M., Kulbachinskiy, A., Severinov, K. and Yokoyama, S. (2014) Structural basis for promoter specificity switching of RNA polymerase by a phage factor. *Genes Dev.* 28, 521-531. (*Co-first authors)

Itoh, Y., Bröcker, M.J., Sekine, S., Söll, D. and Yokoyama, S. (2014) Dimer-dimer interaction of the bacterial selenocysteine synthase SelA promotes functional active-site formation and catalytic specificity. *J. Mol. Biol.* 426, 1723-1735.

Itoh, Y., Sekine, S., Suetsugu, S. and Yokoyama, S. (2013) Tertiary structure of bacterial selenocysteine tRNA. *Nucleic Acids Res.* 41, 6729-6738.

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, 1232-1244.

Itoh, Y., Bröcker, M.J., Sekine, S., Hammond, G., Suetsugu, S., Söll, D. and Yokoyama, S. (2013) The decameric SelA tRNA^{Sec} ring structure reveals the mechanism of bacterial selenocysteine formation. *Science* 340, 75-78.

Murayama, Y., Sekine, S.[†] and Yokoyama, S.[†] (2013) Crystallization and preliminary X-ray crystallographic analyses of *Thermus thermophilus* backtracked RNA polymerase. *Acta Cryst. F*69, 174–177. ([†]correspondence)

Itoh, Y., Sekine, S. and Yokoyama, S. (2012) Crystallization and preliminary X-ray crystallographic analysis of *Aquifex aeolicus* SelA, a bacterial selenocysteine synthase. *Acta Crystallogr. F*68, 1128-1133.

Itoh, Y., Sekine, S. and Yokoyama, S. (2012) Crystallization and preliminary X-ray crystallographic analysis of bacterial tRNA^{Sec} in complex with seryl-tRNA

synthetase. *Acta Crystallogr. F* 68, 678-682.

Sekine, S., Tagami, S. and Yokoyama, S. (2012) Structural basis of transcription by bacterial and eukaryotic RNA polymerases. *Curr. Opin. Struct. Biol.* 22, 110-118.

Hanawa-Suetsugu, K., Kukimoto-Niino, M., Mishima-Tsumagari, C., Akasaka, R., Ohsawa, N., Sekine, S., 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, 3305-3310.

Ehara, H., Sekine, S. and Yokoyama, S., (2011) Crystal structure of the C17/25 subcomplex from *Schizosaccharomyces pombe* RNA Polymerase III. *Protein Sci.* 20, 1558-1565.

Tagami, S., Sekine, S. and Yokoyama, S. (2011) A novel conformation of RNA polymerase sheds light on the mechanism of transcription. *Transcription* 2, 162-167.

Tagami, S., Sekine, S.,[†] Kumarevel, T., Hino, N., Murayama, Y., Kamegamori, S., Yamamoto, M., Sakamoto, K. and Yokoyama, S.[†] (2010) Crystal structure of bacterial RNA polymerase bound with a transcription inhibitor protein. *Nature* 468, 978-982. ([†]correspondence)

Chiba, S., Itoh, Y., Sekine, S. and Yokoyama, S. (2010) Structural basis for the major role of *O*-phosphoseryl-tRNA kinase in the UGA-specific encoding of selenocysteine. *Mol. Cell* 39, 410-420.

Hikida, Y., Kuratani, M., Bessho, Y., Sekine, S. and Yokoyama, S. (2010) Crystal structure of an archaeal homologue of the bacterial Fmu/RsmB/RrmB rRNA cytosine 5-methyltransferase. *Acta Crystallogr. D* 66, 1301-1307.

Kuratani, M., Hirano, M., Goto-Ito, S., Itoh, Y., Hikida, Y., Nishimoto, M., Sekine, S., 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.

Tagami, S., Sekine, S.,[†] Kumarevel, T., Yamamoto, M. and Yokoyama, S.[†] (2010) Crystallization and preliminary X-ray crystallographic analysis of *Thermus*

thermophilus transcription elongation complex bound to Gfh1. *Acta Crystallogr. F*66, 64-68. ([†]correspondence)

Itoh, Y., Chiba, S., Sekine, S. and Yokoyama S. (2009) Crystal structure of human selenocysteine tRNA. *Nucleic Acids Res.* 37, 6259-6268.

Konno, M., Sumida, T., Uchikawa, E., Mori, Y., Yanagisawa, T., Sekine, S. and Yokoyama, S. (2009) Modeling of tRNA-assisted mechanism of Arg activation based on a structure of Arg-tRNA synthetase, tRNA, and an ATP analog (ANP). *FEBS J.* 276, 4763-4779.

Naganuma, M., Sekine, S., Fukunaga, R. and Yokoyama, S. (2009) Unique protein architecture of alanyl-tRNA synthetase for aminoacylation, editing, and dimerization. *Proc. Natl. Acad. Sci. U.S.A.* 106, 8489-8494.

Itoh, Y., * Sekine, S., * Matsumoto, E., Akasaka, R., Takemoto, C., Shirouzu, M. and Yokoyama, S. (2009). Structure of selenophosphate synthetase essential for selenium incorporation into proteins and RNAs. *J. Mol. Biol.* 385, 1456-1469. (*Co-first authors)

Itoh, Y., Sekine, S., Kuroishi, C., Terada, T., Shirouzu, M., Kuramitsu, S. and Yokoyama, S. (2008). Crystallographic and mutational studies of seryl-tRNA synthetase from the archaeon *Pyrococcus horikoshii*. *RNA Biol.* 5, 169-177.

Matsumoto, E., * Sekine, S., * Akasaka, R., Otta, Y., Katsura, K., Inoue, M., Kaminishi, T., Terada, T., Shirouzu, M. and Yokoyama, S. (2008). Structure of an N-terminally truncated selenophosphate synthetase from *Aquifex aeolicus*. *Acta Crystallogr. F*64, 453-458. (*Co-first authors)

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*63, 1059-1068.

Shinkai, A., * Sekine, S., * Urushibata, A., Terada, T., Shirouzu, M. and Yokoyama, S. (2007). The putative DNA-binding protein Sto12a from the thermoacidophilic archaeon *Sulfolobus tokodaii* contains intrachain and interchain disulfide bonds. *J. Mol. Biol.* 372, 1293-1304. (*Co-first authors)

Bessho, Y., Shibata, R., Sekine, S., Murayama, K., Higashijima, K., Hori-Takemoto, C., Shirouzu, M., Kuramitsu, S. and Yokoyama, S. (2007). Structural basis for functional mimicry of long-variable-arm tRNA by transfer-messenger

- RNA. *Proc. Natl. Acad. Sci. U.S.A.* 104, 8293-8298.
- Hiyama, T.B., Zhao, M., Kitago, Y., Yao, M., Sekine, S., Terada, T., Kuroishi, C., Liu, Z.J., Rose, J.P., Kuramitsu, S., Shirouzu, M., Watanabe, N., Yokoyama, S., Tanaka, I. and Wang, B.C. (2007). Structural basis of CoA recognition by the *Pyrococcus* single-domain CoA-binding proteins. *J. Struct. Funct. Genomics* 7, 119-129.
- Sekine, S., Shichiri, M., Bernier, S., Chênevert, R., Lapointe, J. and Yokoyama, S. (2006) Structural bases of transfer RNA-dependent amino acid recognition and activation by glutamyl-tRNA synthetase. *Structure* 14, 1791-1799.
- Sasaki, H.M., Sekine, S., Sengoku, T., Fukunaga, R., Hattori, M., Utsunomiya, Y., Kuroishi, C., Kuramitsu, S., Shirouzu, M. and Yokoyama, S. (2006) Structural and mutational studies of the amino acid-editing domain from archaeal/eukaryal phenylalanyl-tRNA synthetase. *Proc. Natl. Acad. Sci. U.S.A.* 103, 14744-14749.
- Iwasaki, W., Sekine, S., Kuroishi, C., Kuramitsu, S., Shirouzu, M. and Yokoyama, S. (2006) Structural basis of the water-assisted asparagine recognition by asparaginyl-tRNA synthetase. *J. Mol. Biol.* 360, 329-342.
- Kuratani, M., Sakai, H., Takahashi, M., Yanagisawa, T., Kobayashi, T., Murayama, K., Chen, L., Liu, Z.J., Wang, B.C., Kuroishi, C., Kuramitsu, S., Terada, T., Bessho, Y., Shirouzu, M., Sekine, S. and Yokoyama, S. (2006) Crystal structures of tyrosyl-tRNA synthetases from Archaea. *J. Mol. Biol.* 355, 395-408.
- Kuratani, M., Ishii, R., Bessho, Y., Fukunaga, R., Sengoku, T., Shirouzu, M., Sekine, S. and Yokoyama, S. (2005) Crystal structure of tRNA adenosine deaminase (TadA) from *Aquifex aeolicus*. *J. Biol. Chem.* 280, 16002-16008.
- Hanawa-Suetsugu, K., Sekine, S., Sakai, H., Hori-Takemoto, C., Terada, T., Unzai, S., Tame, J.R., Kuramitsu, S., Shirouzu, M. and Yokoyama, S. (2004) Crystal structure of elongation factor P from *Thermus thermophilus* HB8. *Proc. Natl. Acad. Sci. U.S.A.* 101, 9595-9600.
- Artsimovitch, I., Patlan, V., Sekine, S., Vassylyeva, M.N., Hosaka, T., Ochi, K., Yokoyama, S. and Vassylyev, D.G. (2004) Structural basis for transcription regulation by alarmone ppGpp. *Cell* 117, 299-310.
- Randau, L., Schauer, S., Ambrogelly, A., Salazar, J.C., Moser, J., Sekine, S.,

- Yokoyama, S., Söll, D. and Jahn, D. (2004) tRNA recognition by glutamyl-tRNA reductase. *J. Biol. Chem.* 279, 34931-34937.
- Sekine, S., Nureki, O., Dubois, D.Y., Bernier, S., Chenevert, R., Lapointe, J., Vassylyev, D.G. and Yokoyama, S. (2003) ATP binding by glutamyl-tRNA synthetase is switched to the productive mode by tRNA binding. *EMBO J.* 22, 676-688.
- Fukai, S., Nureki, O., Sekine, S., Shimada, A., Vassylyev, D.G. and Yokoyama, S. (2003) Mechanism of molecular interactions for tRNA^{Val} recognition by valyl-tRNA synthetase. *RNA* 9, 100-111.
- Sakai, H., Vassylyeva, M.N., Matsuura, T., Sekine, S., Gotoh, K., Nishiyama, M., Terada, T., Shirouzu, M., Kuramitsu, S., Vassylyev, D.G. and Yokoyama, S. (2003) Crystal structure of a lysine biosynthesis enzyme, LysX, from *Thermus thermophilus* HB8. *J. Mol. Biol.* 332, 729-740.
- Vassylyeva, M.N., Sakai, H., Matsuura, T., Sekine, S., Nishiyama, M., Terada, T., Shirouzu, M., Kuramitsu, S., Vassylyev, D.G. and Yokoyama, S. (2003) Cloning, expression, purification, crystallization and initial crystallographic analysis of the lysine-biosynthesis LysX protein from *Thermus thermophilus* HB8. *Acta Crystallogr. D59*, 1651-1652.
- Vassylyev, D.G., Sekine, S., Laptenko, O., Lee, J., Vassylyeva, M.N., Borukhov, S. and Yokoyama, S. (2002) Crystal structure of a bacterial RNA polymerase holoenzyme at 2.6 Å resolution. *Nature* 417, 712-719.
- Vassylyeva, M.N., Lee, J., Sekine, S., Laptenko, O., Kuramitsu, S., Shibata, T., Inoue, Y., Borukhov, S., Vassylyev, D.G. and Yokoyama, S. (2002) Purification, crystallization and initial crystallographic analysis of RNA polymerase holoenzyme from *Thermus thermophilus*. *Acta Crystallogr D58*, 1497-1500.
- Sekine, S., Nureki, O., Shimada, A., Vassylyev, D.G. and Yokoyama, S. (2001). Structural basis for anticodon recognition by discriminating glutamyl-tRNA synthetase. *Nature Struct. Biol.* 8, 203-206.
- Sekine, S., Shimada, A., Nureki, O., Cavarelli, J., Moras, D., Vassylyev, D.G. and Yokoyama, S. (2001). Crucial role of the HIGH-loop lysine for the catalytic activity of arginyl-tRNA synthetase. *J. Biol. Chem.* 276, 3723-3726.
- Fukai, S., Nureki, O., Sekine, S., Shimada, A., Tao, J., Vassylyev, D.G. and

Yokoyama, S. (2000). Structural basis for double-sieve discrimination of L-valine from L-isoleucine and L-threonine by the complex of tRNA^{Val} and valyl-tRNA synthetase. *Cell* 103, 793-803.

Madore, E., Florentz, C., Giegé, R., Sekine, S., Yokoyama, S. and Lapointe, J. (1999). Effect of modified nucleotides on *Escherichia coli* tRNA^{Glu} structure and on its aminoacylation by glutamyl-tRNA synthetase. Predominant and distinct roles of the mnm⁵ and s² modifications of U34. *Eur. J. Biochem.* 266, 1128-1135.

Sekine, S., Nureki, O., Tateno, M. and Yokoyama, S. (1999). The identity determinants required for the discrimination between tRNA^{Glu} and tRNA^{Asp} by glutamyl-tRNA synthetase from *Escherichia coli*. *Eur. J. Biochem.* 261, 354-360.

Sekine, S., Nureki, O., Sakamoto, K., Niimi, T., Tateno, M., Go, M., Kohno, T., Brisson, A., Lapointe, J. and Yokoyama, S. (1996). Major identity determinants in the “augmented D helix” of tRNA^{Glu} from *Escherichia coli*. *J. Mol. Biol.* 256, 685-700.

Tateno, M., Nureki, O., Sekine, S., Kaneda, K., Go, M. and Yokoyama, S. (1995). A three-dimensional structure model of the complex of glutamyl-tRNA synthetase and its cognate tRNA. *FEBS Letters* 377, 77-81.

Nureki, O., Vassylyev, D.G., Katayanagi, K., Shimizu, T., Sekine, S., Kigawa, T., Miyazawa, T., Yokoyama, S. and Morikawa, K. (1995). Architectures of class-defining and specific domains of glutamyl-tRNA synthetase. *Science* 267, 1958-1965.

Reviews & Book chapters:

関根俊一、田上俊輔、横山茂之 (2011) 転写因子による RNA ポリメラーゼの制御のメカニズム- 細菌の転写を阻害する新たな仕組みの解明 化学と生物 49, 732-734.

関根俊一、横山茂之 (2011) セレンをタンパク質に正確に取り込む:セレノシスティン tRNA 認識の構造基盤 生物物理 51, 272-273.

関根俊一 数万もの生命の設計図を間違いなく書き写せるのはなぜ? ブルーバックス 放射光が解き明かす驚異のナノ世界 -魔法の光が拓く物質世界の可能性- 日本放射光学会編

伊藤拓宏, 関根俊一, 横山茂之 (2004) RNA の構造生物学：転写から翻訳まで
躍進する RNA 研究（実験医学 22 増刊）中村義一・塩見春彦編, 28-34 (2378-
2384).

Dubois, D.Y., Lapointe, J. and Sekine, S. (2004) Glutamyl-tRNA synthetase *in*
Aminoacyl-tRNA synthetases, eds. Ibba, M., Francklyn, C. and Cusack, S. (*Landes Bioscience*).

関根俊一, Vassilyev, D.G., 横山茂之 (2003) RNA ポリメラーゼホロ酵素の結晶
構造が示す転写開始のメカニズム 蛋白質核酸酵素 48, 1-8.

関根俊一 (2002) Structural basis for anticodon discrimination revealed by crystal
structure of glutamyl-tRNA synthetase•tRNA^{Glu} complex. 日本結晶学会誌 44, 375-
379.