

X-ray crystallography of aminoacyl-tRNA synthetases complexed with tRNAs

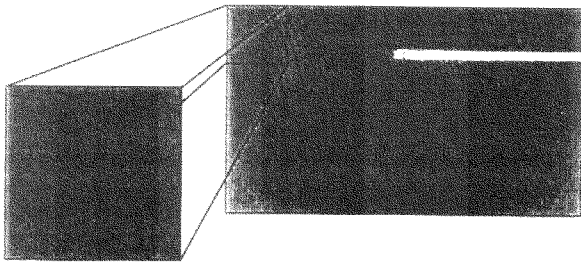
*Osamu Nureki (0003440), Shun-ichi Sekine (0001382), Noriko Tamura (0003525), Atsushi Shimada (0003538), Takashi Nakama (0003518), Shuya Fukai (0003519), Kazuki Kurimoto (0003520)

Department of Biophysics and Biochemistry, School of Science, University of Tokyo

T. thermophilus valyl-tRNA synthetase complexed with tRNA

Valyl-tRNA synthetase (ValRS) specifically attaches L-valine to tRNA^{Val}. ValRS misacylates minimally-distinct L-Thr, but hydrolytically edits its own misproducts upon binding with tRNA^{Val}. To elucidate the mechanism of editing activation by tRNA, we have crystallized ternary complex of *T.*

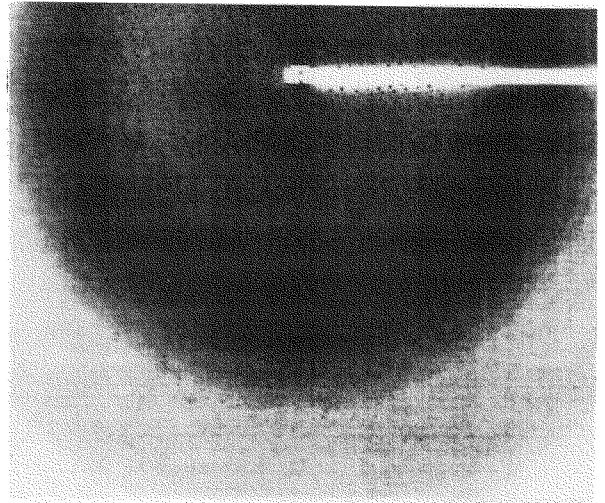
thermophilus ValRS, tRNA^{Val}, and Val-AMP analogue. The crystals belong to spacegroup $P4_2$ with extremely-large cell constants of $a=b=410\text{\AA}$ and $c=82.8\text{\AA}$. In this beam time, we have collected the diffraction data upto 2.8\AA resolution for 180° with oscillation angle of 4° ($\lambda=1.0\text{\AA}$, camera distance=500 mm, and Temp.=100K) (shown as below). However, the oscillation angle was so large that we had difficulty in the data processing.



T. thermophilus arginyl-tRNA synthetase

Arginyl-tRNA synthetase (ArgRS) specifically attaches L-arginine to tRNA^{Arg}. ArgRS catalyses the first step of aminoacylation (Arg-AMP synthesis) depending on the binding with tRNA^{Arg}. To elucidate the mechanism of aminoacylation activation by tRNA, we first crystallized *T. thermophilus* ArgRS. The crystals belong to space group $P6_5$ with cell constants of $a=b=156\text{\AA}$ and

$c=87.3\text{\AA}$. In this beam time, we have collected the diffraction data upto 2.4\AA resolution for 60° with oscillation angle of 3° ($\lambda=1.0\text{\AA}$, camera distance=500 mm, and Temp.=100K) (shown as below).



Drosophila Sxl protein complexed with *tra* pre-mRNA

Drosophila Sxl protein regulates alternative splicing of *tra* pre-mRNA to determine the sex of fly. Sxl protein binds to intron polyuridine tract at the specific splice site on *ra* pre-mRNA, in order to interfere the splicing formation. To elucidate how Sxl protein specifically bind to the polyuridine sequence, we have crystallized Sxl protein complexed with 17 mer target RNA. The crystals belong to spacegroup $I222$ with extremely-large cell constants of $a=77.7\text{\AA}$, $b=86.7\text{\AA}$ and $c=160.1\text{\AA}$. In this beam time, we have collected the diffraction data upto 2.4\AA resolution for 90° with oscillation angle of 6° ($\lambda=1.0\text{\AA}$, camera distance=500 mm, and Temp.=100K).