Crystallographic Studies of *Homo sapiens* A-sites Complexed with Aminoglycosides

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Toxicity resulting from the clinical use of aminoglycoside antibiotic drugs is known to originate from the binding of these drugs to the *Homo sapiens* A-sites. In order to design antibiotics with higher selectivity for bacterial ribosomes and less toxicity to eukaryotes, further structural investigations have been carried out with a number of A-site complexes. In all cases, the structure solution by molecular replacement was not straightforward and required simultaneous applications of several programs and various approaches.

In the case of the cytoplasmic A-site with paromomycin, a $P2_12_12$ crystal with one RNA duplex in the asymmetric unit was obtained. The same solution was found with *AMoRe* using the bulk-solvent correction technique and with *PHASER*. After applying normal-mode refinement for only the central stem region in the 10-5.0 Å resolution range, R_{free} and CC_{free} values are 30.5% and 32.3%, respectively.

The crystal of the mitochondrial A-site with tobramycin (space group *P1*) contains two RNA duplexes in the asymmetric unit. Orientation of the duplexes has been found by combination of information from *PHASER*, the self-rotation function from *GLRF* and other sources. Position of the duplexes was obtained essentially from the packing analysis.

The solution of other similar complexes (1 or 2 strands in the A.U., trigonal unit cells) also required specific approaches.

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