S2 Figure – continued on following page.
S2 Figure (continued from previous page). Multiple sequence alignment of RNase J from *M. tuberculosis* (Mtb), *M. smegmatis* (Msm), *Streptomyces coelicolor* (Sco), *Thermus thermophilus* (Tth), and *Deinococcus radiodurans* (Dra). Residues found to be mutated in INH-resistant Mtb clinical strains are highlighted in red. Sequences were aligned by Clustal Omega 1.2.4 (Madeira et al., 2022 [50]).