

Distribution bias and biochemical characterization of *TOP1MT* single nucleotide variants

Hongliang Zhang¹, Yeonee Seol², Keli Agama¹, Keir C. Neuman², and Yves Pommier^{1*}

¹Laboratory of Molecular Pharmacology, Developmental Therapeutics Branch, Center for Cancer Research, NCI, National Institutes of Health, Bethesda, MD, 20892, USA

²Laboratory of Single Molecule Biophysics, NHLBI, National Institutes of Health, Bethesda, MD, 20892, USA

*For correspondence: pommier@nih.gov

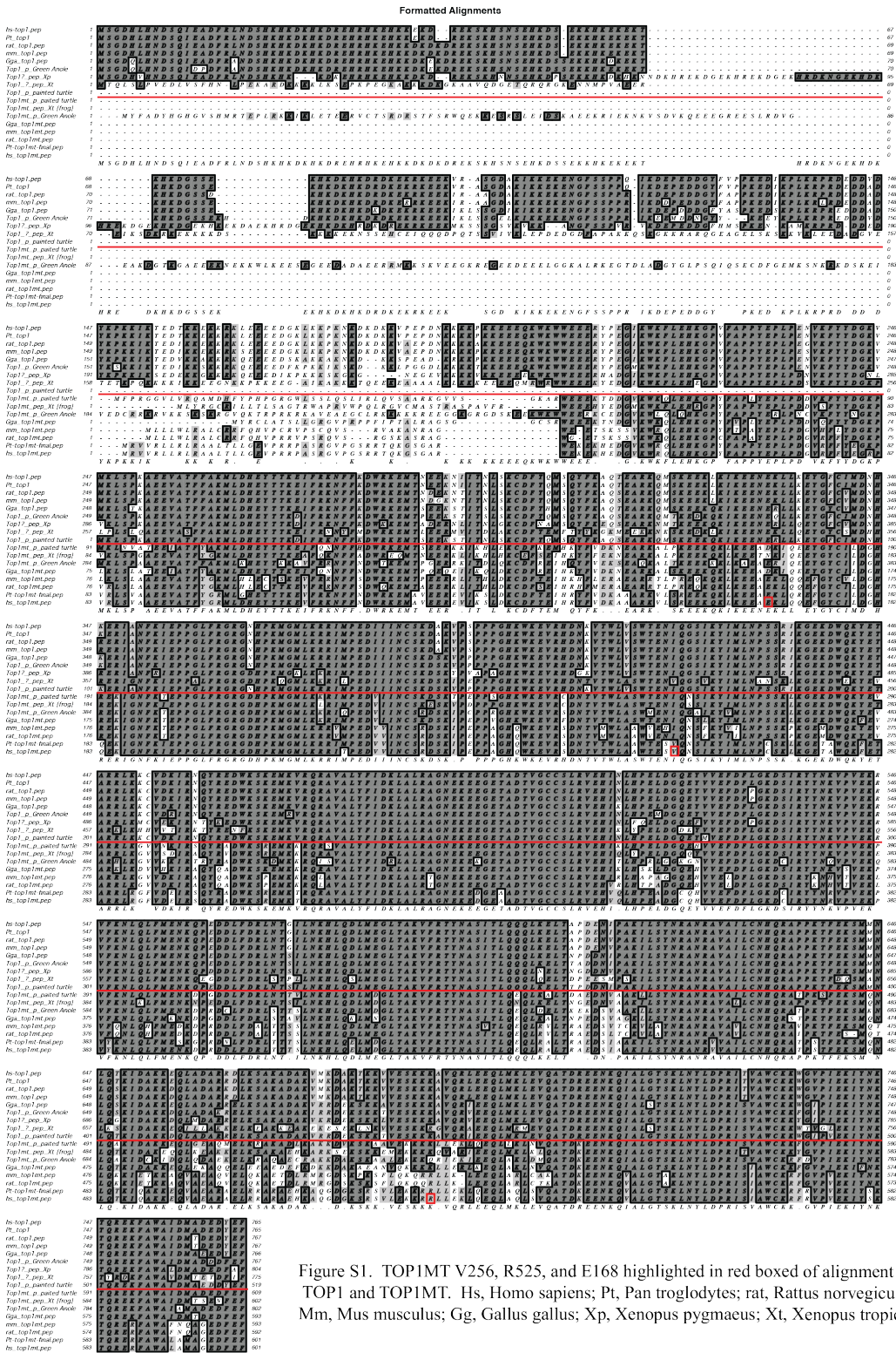


Figure S1. TOP1MT V256, R525, and E168 highlighted in red boxed of alignment of TOP1 and TOP1MT. Hs, Homo sapiens; Pt, Pan troglodytes; rat, Rattus norvegicus; Mm, Mus musculus; Gg, Gallus gallus; Xp, Xenopus pygmaeus; Xt, Xenopus tropicalis.

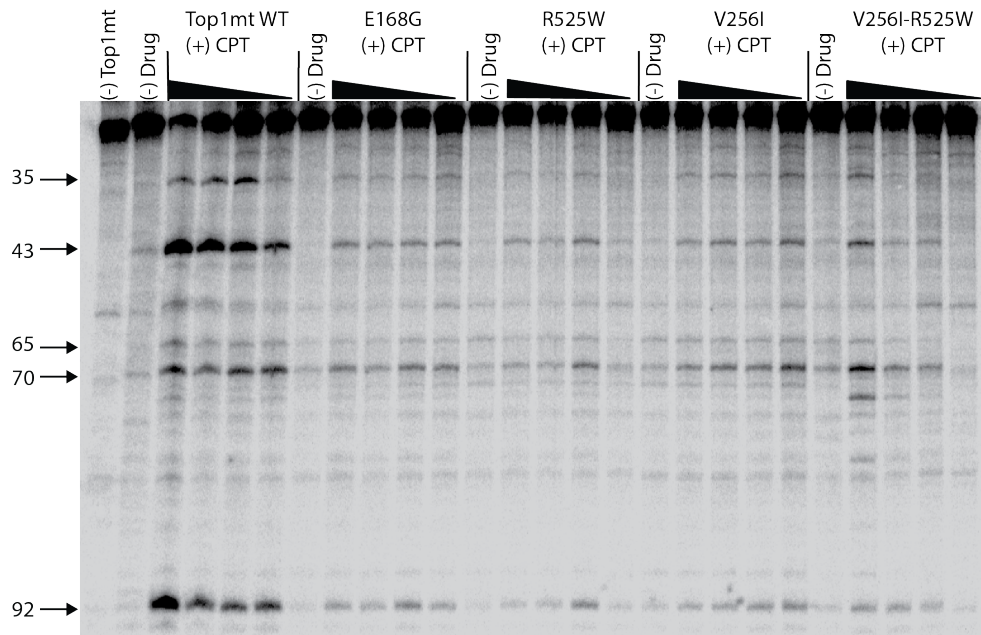


Figure S2. Cleavage assay of purified Top1mt mutant proteins: (lane 1) DNA alone; (lane 2) Top1mt alone; (lane 3-6) 1:3 fold serial dilution of Top1mt incubated with 1 μ M camptothecin; (lane 7) E168G Top1mt alone; (lanes 8-11) 1:3 fold serial dilution of E168G Top1mt incubated with 1 μ M camptothecin; (lane 12) R525W Top1mt alone; (lane 13-16) 1:3 fold serial dilution of R525W Top1mt incubated with 1 μ M camptothecin; (lane 17) V256I Top1mt alone; (lane 18-21) 1:3 fold serial dilution of V256I Top1mt incubated with 1 μ M camptothecin; (lane 22) R525W-V256I Top1mt alone; (lane 23-26) 1:3 fold serial dilution of R525W-V256I Top1mt incubated with 1 μ M camptothecin.