

Supplementary Material to “Mismatch uracil DNA glycosylase (Mug) is maintained in the *Corynebacterium pseudotuberculosis* genome and exhibits affinity for uracil but not other types of damage.”

Table S4 – Distance evaluation in Angstroms scale between Mug (*EcMug* or *CpMug*) and lesions.

Models	Lesion type	Catalytic residues ^a						Average
		Pro139	Asn140	Pro 141	Ser142	Gly143	Leu144	
<i>EcMug</i>	U	10.75	4.8	7.58	3.99	4.87	2.63	5.77
<i>EcMug</i>	8-oxo	10.32	4.48	6.84	3.34	4.87	5.18	5.84
<i>EcMug</i>	Tg	16.15	10.58	11.09	6.76	9.6	6.95	10.19
<i>EcMug</i>	THF	17.01	11.77	11.52	7.53	8.1	5.16	10.18
Models	Lesion type	Catalytic residues ^b						Average
		Pro 178	Gln179	Pro 180	Ser181	Gly182	Leu183	
<i>CpMug</i>	U	11.48	4.2	8.01	3.77	5.14	4.59	6.20
<i>CpMug</i>	8-oxo	10.58	5.44	7.55	3.16	4.97	4.87	6.10
<i>CpMug</i>	Tg	13.72	9.04	8.21	4.32	4.25	4.66	7.37
<i>CpMug</i>	THF	17.58	12.43	11.79	10.86	8.01	8.16	11.47

^aDistance measured in angstroms between the closest atom from the lesion and catalytic residues concerning the regions described by responsible for guanine interaction of the *E. coli* (139-145 residues).

^bDistance measured in angstroms between the closest atom from the lesion and catalytic residues concerning the regions responsible for guanine interaction of the *C. pseudotuberculosis* (178-184 residues).

*Residues closest to the lesion when compared to the uracil lesion.