

## Structural analysis of the amino acid residues mutated in hOGG1 variants

Residue	Location	Primary contacts	Distance from oxoG <sup>1</sup>	Role
Arg46	Loop between $\alpha$ A and $\beta$ B (interior core)	Glu139 ( $\alpha$ E) His179 ( $\beta$ G)	14 Å	Structural
Ala85	Loop between $\beta$ E and $\alpha$ B (surface)	Solvent	38 Å	Unknown
Arg154	$\alpha$ F (invades DNA helix)	Estranged cytosine	11 Å	Specificity
Ser232	Loop between $\alpha$ J and $\alpha$ K (surface)	Solvent Glu235( $\alpha$ K)	22 Å	Unknown

<sup>1</sup>Measured from closest atom in residue to C1' of deoxyribose attached to 8oxoG base