So far no crystal structures have been reported of the two other oxidation damage repair glycosylases (MutY and MutM; Table 2) from *D. radiodurans*, however some biochemical characterisation of these enzymes has been performed. The A/G specific adenine DNA glycosylase, MutY, of *D. radiodurans* (drMutY) has been cloned, expressed and characterised, and was found to possess adenine glycosylase activity towards classical MutY substrates with A:G, A:C and A:8oxoG (7,8-dihydro-8-oxoguanine) base pairs like its homologue from *E. coli* [50]. *D. radiodurans* MutM/Fpg (drMutM) has also been characterised and similarly to *E. coli* MutM/Fpg (ecMutM) was found to excise both 2,6-diamino-4-hydroxy-5*N*-methylformamidopyrimidine (Fapy) from DNA paired with both guanine and adenine and to a lesser extent 8oxoG paired with guanine [51]. However, while ecMutM excises these three substrates with similar efficiencies, drMutM was found to prefer Fapy as a substrate [51].

Also, no structural information is available for the downstream end processing, base incorporation and ligation enzymes of *D. radiodurans*, however several of these have been produced and characterised [52, 53]. The unique AP endonuclease (Exonuclease III) of *D. radiodurans* (drExoIII) has been produced recombinantly and preliminary data indicate that the enzyme possesses classical Exonuclease III activity (Moe's laboratory, unpublished data). Originally only one DNA ligase (NAD dependent drLigA) was identified in the genome of *D. radiodurans* (DR_2069) [9], and only later a second gene encoding a divergent ATP-dependent DNA ligase (drLigB/DR_B0100) was discovered [52]. Characterisation of these enzymes revealed that drLigA is a functional DNA ligase on its own [52], while drLigB is only active as a ligase in complex with a hypothetical protein (DR_B0098) encoded by the LigB operon and a pleitropic protein promoting DNA repair enzyme (PprA) [53]. It was also shown that deleting the *ligB* gene makes the LigB operon non-functional and results in loss of DNA damage tolerance [53]. No studies of the DNA polymerase from *D. radiodurans* have so far been reported.

These various studies of *D. radiodurans* BER enzymes have contributed to a better understanding of the fundamental processes leading to repair of damaged bases *via* the BER pathway, but have also revealed that most *D. radiodurans* DNA glycosylases either exhibit increased enzymatic efficiency (*e.g.* drUNG) and/or broader substrate specificity

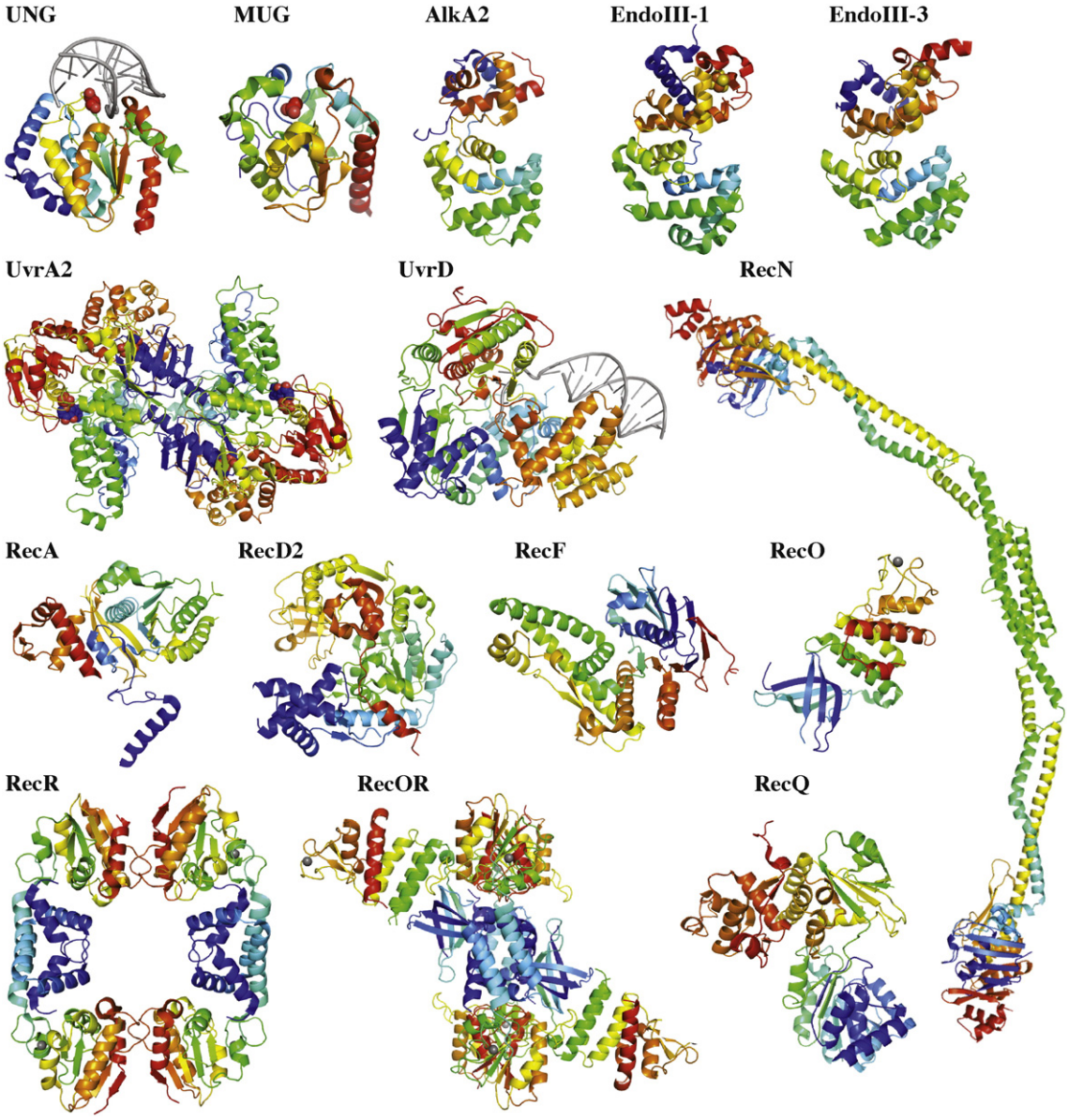

Fig. 1. Illustration of the structures of *D. radiodurans* proteins involved in DNA repair processes. All structures are presented in rainbow colours (N-termini in blue and C-termini in red). The following PDB codes were used to prepare the figures using Pymol [126]: UNG (4uqm), MUG (2c2p), AlkA2 (2yg8), EndoIII-1 (4unf), EndoIII-3 (4uob), UvrA2 (2vf7), UvrD (4c2v), RecN (4aby; 4abx; 4ad8), RecA (1xp8), RecD2 (3e1s), RecF (2o5v), RecO (1w3s), RecR (1vdd), RecOR (4jcv) and RecQ (4q47).