

Figure S2. Structure-based multiple sequence alignment of the complete sequences of NApe, NExo, HAP1 and ExoIII sequences. Positions in the alignment are colour coded in darker blue according to the number of identical residues at that position. Residues involved in metal binding, catalysis and abasic ribose binding are coloured pink, green and yellow respectively, and the NExo sequence numbers are indicated under the sequence. The secondary structure is indicated in red for α -helices and red green for β -strands.

