## Table S1: Comparison of sequence and structure similarities for the Neisseria AP endonuclease/ Exonuclease proteins.

The percentage sequence identities obtained from the structure based alignments in figure S2 are shown in the upper right quadrant of the table. The root mean square deviations between the structures (with the number of C-alpha atoms included in the calculations in parentheses) are shown in the lower left quadrant of the table.

| | | % Sequence identity observed between proteins | | | |
|---|---|---|---|---|---|
| | | HAP1 | ExoIII | NExo | NApe |
| Rmsd Between protein structures (Å) | HAP1 | | 27 | 30 | 33 |
| | ExoIII | 1.57 (235) | | 34 | 23 |
| | NExo | 1.45 (236) | 1.38 (239) | | 27 |
| | NApe | 1.47 (230) | 1.57 (210) | 1.62 (222) | |