Bioin | Mot-5b | Mot-6a | Mot-6b | Mot-7 | Var 6 | Var 7
--- | --- | --- | --- | --- | --- | ---
Ident | - | - | - | - | - | -
Chem | - | - | - | - | - | -
Funct | - | - | - | - | - | -
Major | - | - | - | - | - | -

Major are the 187 residues conserved above a 70% majority threshold (210 sequences) with invariant residues shown in uppercase. The numbering of the alignment is based upon the E. coli RecA protein sequence.

Escherichia coli
Mycobacterium tuberculosis
Aquifex pyrophilus
Bacteroides fragilis
Chlamydia trachomatis
Deinococcus radiodurans
Neisseria gonorrhoeae
Rhodobacter capsulatus
Gemmata obscuriglobus
Fusobacterium nucleatum
Anabaena variabilis
Chlamydia trachomatis
Bacteroides fragilis
Mycobacterium tuberculosis

Additional File 1. Multiple sequence alignment of bacterial RecA homologs. A subset of the 300 sequences is shown representing each of the major bacterial phyla. In the alignment, a dash (-) indicates a gap and a period (.) indicates an amino acid identical to the E. coli RecA protein. NCBI Protein database accession numbers are listed at the end representing each of the major bacterial phyla. In the alignment, a dash (-) indicates a gap and a period (.) indicates an amino acid identical to the E. coli RecA protein. NCBI Protein database accession numbers are listed at the end.