

## Sequence Alignment of RecA Protein Showing a Conserved Insert Shared by all Epsilon Proteobacteria and Desulfovibrio Species

Gupta, R.S. (2000) FEMS Microbiol. Rev. 24: 367-402 and BMC Genomics (2006), 7, 167

		189	224
Epsilon Proteobacteria	Helicobacter pylori	634052	LIFINQIRMKIGMM G YGSPETTGGNALKFYASVR
	Helicobacter acinonychis	30961735	-----
	Helicobacter hepaticus	32262181	-----T-----
	Wolinella succinogenes	34483548	V-----
	Campylobacter lari	28971929	V-----T-----
	T. denitrificans	78498736	V-----
	Campylobacter jejuni	57167488	V-----A-----T-----
	Campylobacter upsaliensis	57505301	V-----A-----T-----
	Campylobacter coli	57504667	V-----A-----T-----
	Campylobacter fetus	2642184	VV-----A-----T-----
d-Proteobacteria (Desulfovibrio)	Desulfo. desulfuricans	78219821	V-----T-----C---
	Desulfo. vulgaris	46448917	V-----T-----S---
	Lawsonia intracellularis	94731873	V-----VV-----S---
Other d-Proteo	Geobacter metallireducens	78192677	V-----V-----F-----
	Geobacter sulfurreducens	39982018	V-----V-----F-N-----
	Bdellovibrio bacteriovorus	39574648	V-----V-----F-N-----S---
	Escherichia coli	12517139	-----V-----F-N-----
	Yersinia pestis	406794	-----V-----F-N-----
	Chromobacterium violaceum	61097707	V-----V-----F-N-----
	Neisseria meningitidis	45176	VV-----V-----F-----S---
	Bordetella pertussis	1350558	V-----V-----F-N-----S---
	Caulobacter crescentus	13422391	V-----H--V-----
	Rhodopseudomonas palustris	39936912	V-----V-----
Other Bacteria	Mesorhizobium sp. BNC1	68191462	V-----V-----F-----
	Rickettsia prowazekii	730486	TV-----V-----F-----
	Porphyromonas gingivalis	2500092	C----L-E--VL F-N-----I-
	Chlorobium tepidum	2760912	CL---L-D--V- -----K----S---
	Treponema pallidum	3322995	-----L-----I- F-N-----I----S---
	Borrelia burgdorferi	2500084	IM-----R--V- F-N-----S-L-
	Chlamydomonas pneumoniae	4377070	AV-----E--VS F-N-----R----S-I-
	Chlamydia trachomatis	1350559	A-----E--VS F-N-----R----S-I-
	Aquifex aeolicus	2984348	-----E--V- F-N----P--R---FSDM-
	Deinococcus radiodurans	2251089	A----V-E--V- --N-----R-----
	Thermus thermophilus	1072968	A----V-E-V-VT --N----P--R-----
	Streptomyces coelicolor	2687334	A----L-E--V- F-----R-----
	Mycobacterium tuberculosis	132229	A----L-D--V- F-----K-----
	Staphylococcus aureus	1172890	A-----E-V-V- F-N----P--R----S---
	Clostridium perfringens	3219851	V----L-E-V-I- F-N----P--R-----
	Lactococcus lactis	266894	A----L-E-V-V- F-----P--R-----
	Mycoplasma pulmonis	730485	V----V-E--VV F-N----P--R----I-
	Streptococcus pneumoniae	400970	A----L-E-V-V- F-N----P--R-----
	Bacillus subtilis	132222	A-----E-V-V- F-N----P--R----S---

Note: Epsilon proteobacteria branch very close to the delta proteobacteria in different phylogenetic trees. The shared presence of this signature could be due to either LGT or a shared ancestry of these species.