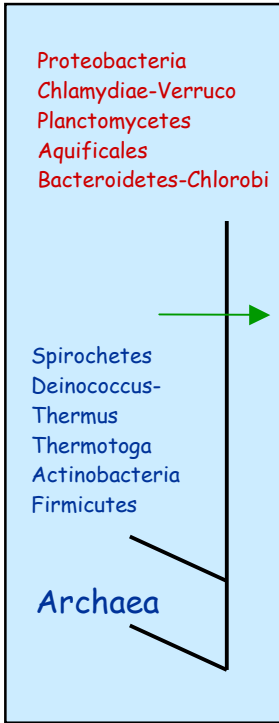


Main Line Signature in RNA Polymerase β Subunit (RpoB)

Gupta, R.S.(2003) Photosynthesis Res.76:173-183; Griffiths and Gupta (2004) Int. Microbiol. 7, 41-52

	919	919	1058	
Proteobacteria	E. coli	RVPNGVSGTVIDVQVFTRD	GVE (91aa) KRRKIT QGDD LAPGVLKIVKVYLAVKR	
	Pas. multocida	-----S-----	---(91aa) Q-G--I-----V-----	
	Pse. aeruginosa	---T-TK-----	---(103aa) -K--LQ-----I-----	
	V. cholerae	---A-----	---(92aa)-----	
	Ral. solanaceum	---S-M-----E	--T (104aa) --K-L---E P---I-M-----	
	Nei. meningitidis	-M-T-M-----E	-IQ (104aa) -KK-L---E -Q---Q-M---FI-I--	
	Ca. crescentus	-L-P--A--IV--R--N-H	---D (103aa) -VD--Q R--E -P---M-MV--FV---	
	A. tumefaciens	-M-P-TF--IVE-R--N-H	---(104aa) -VE-VQ R--E MP---M-M---FV---	
	Geo. sulfurreducens	---P--E---GAKI-S-K	-AD (111aa) -VQ-LK R--- -P---I-M---I-I--	
	Bde. bacteriovorus	-A-S--Y-----A--YS-E	-AD (110aa) -IDRLR K--E -P---I-M---V-I--	
Aquificales	Hel. pylori	YC-PSLE-----K--KK	-Y- (108aa) EKLS-L EK--I-PN--I-K--L-I-T--	
	Camp. jejuni	YATASLE-V-V--KI--KK	-Y- (108aa) EKLE-L EK--I-PS--I-L---I-T--	
	Aqu. aeolicus	-C-P--E-I-----K	-TG (110aa) EKKETL LKRRD-P---ITL--FI-N--	
	Sul. azorensis	---I--E-V-V---I-AKK	RKD (114aa) -KEVLE E-A- -K---IEL---I-Q--	
	Per. marina	---A--E-I-----A-K	KTG (113aa) QKAAVQ K-S- -K---NEL---I-Q--	
	Hydro. marinus	---T--E-I-V---A-K	-I- (125aa) -IKEVE K-A- -K---NEL---I-Q--	
	Cal. hydrogenophilum	-C-P--E-V-V---A-K	VG- (110aa) -EES-G KRSE -PA--IAL---I-Q--	
	Proto. amoebophila	IA-P-TE-V-M--K--S-R	DRL (113aa) LEFMRK GDT- -D---IRQ---V-S--	
	Sim. negevensis	IA-P-TE-V-M--K--S-R	DRL (113aa) VEYMRK GDTE -D---IRQ---V-T--	
	Chlamydiales and Verrucomicrobium	Chl. trachomatis	T--P-TE-V-M--K--S-K	DRL (113aa) EAEH-K E--AD-DH--IRQ---V-S--
Chl. muridarum		T--P-TE-V-M--K--S-K	DRL (113aa) EAAHIKE GDA- -DH--IRQ---V-S--	
Chlam. felis		T--P-TE-V-M--K--S-K	DRL (113aa) VEHIRE GDA- -DH--IRQ---V-S--	
Chlam. pneumoniae		T--P-TE-V-M--K--S-K	DRL (113aa) EVEH-R E--AD-DH--IRQ---V-S--	
Chlam. caviae		T--P-TE-V-M--K--S-K	DRL (113aa) VEHIRE GDA- -DH--IRQ---V-S--	
Chlam. abortus		T--P-TE-V-M--K--S-K	DRL (113aa) VEHIRE GDA- -DH--IRQ---V-S--	
Ver. spinosum		---S-CT-I-M--R--SS-N	-AD (110aa) GLDRLE --EE MES--I-Q---FI-S--	
Gem. obscuriglobus		--QS-TE-I---AAHR-S-R	AHM (104aa) -LNSLN R--E -PS--QQM---V-T--	
Rho. baltica		---S-IE-I---T-K-S-R	MSL (104aa) -LNSMK R--E -RS---QM---I-I-T--	
Planctomycetes		Bla. marina	---S-IE-I---HTDK-A-R	MSL (104aa) VINSMK R--E -RS---QI---I-T--
	Bact. fragilis	KASPSPK-V---KKL-S-V	IKN (103aa) -KFA-- IG-E -PA-I IQMA---I-K--	
	Ch. tepidum	H--A-MK-I---KTKL-S-K	KKI (110aa) EKY--N V--E -P--IEELA---I-Q--	
	Por. gingivalis	KATPSLR-V---TKL-SKA	AKK (108aa) RKLDE- IG-E -PA-IVQMA---I-K--	
	Bacteroidetes-Chlorobi Group	Bor. burgdorferi	K--H-TE-----RI-KE	DVGN -S---EE-L---V-K--
		Tre. pallidum	---H--E-----RLR-S	E----N---SEV---LI-T--
		Nostoc sp. PCC 7120	---P-EG-I-VRT -RL-R	---E -P--ANMV-R--V-Q--
		Gloe. violaceus	---E-K-R-V--R---E	---E -P--ANMV-R---Q--
		D. radiodurans	--QS-QG-I-VKTVR-R-G	DEGVD-K---REM-R--V-Q--
		The. thermophilus	---P-EG-I-VRT -RL-R	GDPGVE-K---REV-RG-V-Q--
T. maritima		-L-H--E-R--R-D-YDQN	DIAE -GA---L-R--V-SRK	
Cor. glutamicum		K--H-ET-K--G-RH-S-E	DD-- -----NEMIRI-V-Q--	
Myc. tuberculosis		K--H-E--K--GIR--SHE	DD-E -PA--NEL-R--V-Q--	
Actinobacteria		Str. coelicolor	K--H-EI-K--G-R--D-E	E--E -P---NQL-R--V-Q--
	Bac. subtilis	---H-GG-IH--K--N-E	D--E -P---NQL-R--IVQ--	
	Clo. acetobutylicum	---H-EA-IIV--K---E	N--- -S---NEL-RC-I-Q--	
	Sta. aureus	---H-AG-I-L--K--N-E	E---T-S---NQL-R--IVQ--	
	Strep. pneumoniae	---H-AD-V-R--KI---V	N--E -QS--NML-R--I-Q--	
	Firmicutes	Halo. sp. NCR-1	TMRS-ED-VVDT-TLMEG-	DGSK-AK-SVRDE-
		Meth. barkeri	TMRSNET-I-DT-ILTESI	NGTRLA--KVRDE-
		Pyr. aerophilum	A-RR-EK-I-DK-IITESP	EGN-L---R-REL-

No exceptions to the indicated pattern observed in sequences for >600 species.



A large insert (~100 aa) in RpoB homologs (boxed) in various species belonging to Proteobacteria, Bacteroidetes-Chlorobi, Chlamydiales, Planctomycetes, V. spinosum and Aquificales phyla. The absence of this insert in various other phyla as well as archaeal homologs indicates that the groups lacking this insert are ancestral. The genetic change (RGC) responsible for this insert likely occurred at the evolutionary stage indicated in interpretive diagram on the right. Dashes in the alignment show identity with the amino acid on the top line. Sequence information for only representative species from is presented. However, all other available sequences from these groups behaved in the indicated manner. Sequences for a few of the species (marked TIGR) were obtained by Blast searches at The Institute for Genomic Research website at <http://www.tigr.org>.