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Hierarchy Browser - Start

[\[help \]](#)

Strain:	<input type="radio"/> Type	<input type="radio"/> Non Type	<input checked="" type="radio"/> Both
Source:	<input type="radio"/> Uncultured	<input checked="" type="radio"/> Isolates	<input type="radio"/> Both
Size:	<input checked="" type="radio"/> ≥ 1200	<input type="radio"/> < 1200	<input type="radio"/> Both
Quality:	<input checked="" type="radio"/> Good	<input type="radio"/> Suspect	<input type="radio"/> Both
Taxonomy:	<input checked="" type="radio"/> Nomenclatural	<input type="radio"/> NCBI	

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Note: Javascript must be enabled on your browser to use most RDP tools

Options

Strain: Type strain information is provided by [bacterial taxonomy](#). *Hint:* Type strains link taxonomy with phylogeny. Include type strain sequences in your analysis to provide documented landmarks.

Source: View only environmental (uncultured) sequences, only sequences from individual isolates, or both. Source classification is based on sequence annotation and the [NCBI taxonomy](#).

Size: View only near-full-length sequences (≥ 1200 bases), short partials, or both.

Quality: View only good quality sequences, suspect quality sequences, or both. Sequences were flagged (*) as suspect quality. [\[more quality detail\]](#)

Taxonomy: View sequences placed into a new phylogenetically consistent higher-order [bacterial taxonomy](#) overlaid on the 16S rRNA classification. For the nomenclatural taxonomy, a set of well characterized (vetted) sequences was provided by these workers. Other sequences were placed into this scheme using the [RDP Naïve Bayesian classifier](#).

Note: You must start a new Hierarchy Browser session to change your taxonomy choice.