

## RDP: Release 11

### SeqMatch :: Summary


[\[ new match | summary | help \]](#)


 Display depth: 

#### Lineage

#### Hierarchy View:

rootrank Root (6) (query sequences)


[\[ options \]](#)

domain Bacteria (6)

phylum "Proteobacteria" (6)

class Gammaproteobacteria (6)

order Pseudomonadales (6)

family Pseudomonadaceae (6)

genus Pseudomonas (6)

 NODE\_23\_length\_103367\_cov\_10.081286:35530-37075 [\[view selectable matches\]](#)

 NODE\_2\_length\_378948\_cov\_10.006665:348499-350044 [\[view selectable matches\]](#)

 NODE\_6\_length\_298784\_cov\_8.918606:13925-15470 [\[view selectable matches\]](#)

 NODE\_5\_length\_327223\_cov\_9.241629:46285-47830 [\[view selectable matches\]](#)

 NODE\_4\_length\_332509\_cov\_9.114046:137011-138556 [\[view selectable matches\]](#)

 NODE\_18\_length\_154232\_cov\_9.584186:124541-126086 [\[view selectable matches\]](#)

#### Data Set Options:

<b>Strain:</b>	<input type="radio"/> Type	<input type="radio"/> Non Type	<input checked="" type="radio"/> Both
<b>Source:</b>	<input type="radio"/> Uncultured	<input type="radio"/> Isolates	<input checked="" type="radio"/> Both
<b>Size:</b>	<input checked="" type="radio"/> ≥1200	<input type="radio"/> <1200	<input type="radio"/> Both
<b>Quality:</b>	<input checked="" type="radio"/> Good	<input type="radio"/> Suspect	<input type="radio"/> Both
<b>KNN matches:</b>	20 ▼		

**Strain:** View only sequences from species type strains, non-type strain sequences or both. Type strain information is provided by [Bergey's Trust](#). *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. [\[more quality detail\]](#)

**KNN matches:** Number of matches displayed per sequence, also number used to classify queries by unanimous vote.

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