

Genomic map showing domains β_1 through β_6 and α_1 through α_6 . Sequence alignment for *Haemophilus influenzae* Q2ERG0, *Escherichia coli* STP42972.1, *Wielierella bovis* ULJ69903.1, *Psychobacter* sp. WP_192991736.1, *Pasteurella bettyae* WP_005760985.1, and *Acinetobacter* sp. OAL82787.1. Consensus sequence is shown below.

Genomic map showing domains α_7 through α_{18} . Sequence alignment for *Haemophilus influenzae* Q2ERG0, *Escherichia coli* STP42972.1, *Wielierella bovis* ULJ69903.1, *Psychobacter* sp. WP_192991736.1, *Pasteurella bettyae* WP_005760985.1, and *Acinetobacter* sp. OAL82787.1. Consensus sequence is shown below.

Genomic map showing domains β_7 through β_{11} and α_9 through α_{17} . Sequence alignment for *Haemophilus influenzae* Q2ERG0, *Escherichia coli* STP42972.1, *Wielierella bovis* ULJ69903.1, *Psychobacter* sp. WP_192991736.1, *Pasteurella bettyae* WP_005760985.1, and *Acinetobacter* sp. OAL82787.1. Consensus sequence is shown below.

Genomic map showing domains β_{12} through β_{14} and α_{19} through α_{27} . Sequence alignment for *Haemophilus influenzae* Q2ERG0, *Escherichia coli* STP42972.1, *Wielierella bovis* ULJ69903.1, *Psychobacter* sp. WP_192991736.1, *Pasteurella bettyae* WP_005760985.1, and *Acinetobacter* sp. OAL82787.1. Consensus sequence is shown below.

Genomic map showing domains β_{15} through β_{19} and α_{28} through α_{36} . Sequence alignment for *Haemophilus influenzae* Q2ERG0, *Escherichia coli* STP42972.1, *Wielierella bovis* ULJ69903.1, *Psychobacter* sp. WP_192991736.1, *Pasteurella bettyae* WP_005760985.1, and *Acinetobacter* sp. OAL82787.1. Consensus sequence is shown below.

Genomic map showing domains β_{20} through β_{22} and α_{37} through α_{44} . Sequence alignment for *Haemophilus influenzae* Q2ERG0, *Escherichia coli* STP42972.1, *Wielierella bovis* ULJ69903.1, *Psychobacter* sp. WP_192991736.1, *Pasteurella bettyae* WP_005760985.1, and *Acinetobacter* sp. OAL82787.1. Consensus sequence is shown below.

Genomic map showing domains β_{23} through β_{26} and α_{45} through α_{50} . Sequence alignment for *Haemophilus influenzae* Q2ERG0, *Escherichia coli* STP42972.1, *Wielierella bovis* ULJ69903.1, *Psychobacter* sp. WP_192991736.1, *Pasteurella bettyae* WP_005760985.1, and *Acinetobacter* sp. OAL82787.1. Consensus sequence is shown below.

Genomic map showing domains α_{51} through α_{59} . Sequence alignment for *Haemophilus influenzae* Q2ERG0, *Escherichia coli* STP42972.1, *Wielierella bovis* ULJ69903.1, *Psychobacter* sp. WP_192991736.1, *Pasteurella bettyae* WP_005760985.1, and *Acinetobacter* sp. OAL82787.1. Consensus sequence is shown below.

Genomic map showing domains α_{56} through α_{59} . Sequence alignment for *Haemophilus influenzae* Q2ERG0, *Escherichia coli* STP42972.1, *Wielierella bovis* ULJ69903.1, *Psychobacter* sp. WP_192991736.1, *Pasteurella bettyae* WP_005760985.1, and *Acinetobacter* sp. OAL82787.1. Consensus sequence is shown below.