

# Center for Genomic Epidemiology

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## The input organism was predicted as non human pathogen

Probability of being a human pathogen 0.34

Input proteome coverage (%) 0.88

Matched Pathogenic Families 0

Matched Not Pathogenic Families 44

Sequences 4993  
 Total bpp 1608150  
 Longest seq 2483  
 Shortest seq 30  
 Avg seq length 322.0

### Input Sequence

FQZF01000013.1\_111 # 111411 # 115676 # -1 # ID=53\_111;partial=00;start\_type=ATG;rbs\_motif=None;rbs\_spacer=None;gc\_cont=0.655

### Matched Family

PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY
<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	probably methylase/helicase	<a href="#">ABG61938</a>	97.19

### Input Sequence

FQZF01000013.1\_117 # 121783 # 125055 # 1 # ID=53\_117;partial=00;start\_type=ATG;rbs\_motif=GGAG/GAGG;rbs\_spacer=5-10bp;gc\_cont=0.588

### Matched Family

PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY
<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	helicase-like	<a href="#">ABG61944</a>	98.62

### Input Sequence

FQZF01000013.1\_80 # 84858 # 87296 # -1 # ID=53\_80;partial=00;start\_type=ATG;rbs\_motif=GGAG/GAGG;rbs\_spacer=5-10bp;gc\_cont=0.663

### Matched Family

PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY
<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	ATPas	<a href="#">ABG61909</a>	98.52

### Input Sequence

FQZF01000013.1\_114 # 117023 # 119167 # -1 # ID=53\_114;partial=00;start\_type=ATG;rbs\_motif=GGAG/GAGG;rbs\_spacer=5-10bp;gc\_cont=0.663

### Matched Family

PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY
<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	ParB family protein	<a href="#">ABG61941</a>	96.5

### Input Sequence

FQZF01000037.1\_24 # 23695 # 25647 # -1 # ID=41\_24;partial=00;start\_type=ATG;rbs\_motif=None;rbs\_spacer=None;gc\_cont=0.641

### Matched Family

PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY
<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	heavy metal translocating P-type ATPase	<a href="#">ABG65243</a>	89.85

### Input Sequence

FQZF01000013.1\_89 # 93043 # 95031 # -1 # ID=53\_89;partial=00;start\_type=TTG;rbs\_motif=GGAG/GAGG;rbs\_spacer=5-10bp;gc\_cont=0.649

### Matched Family

PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY
<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	TRAG protein	<a href="#">ABG61918</a>	96.68

### Input Sequence

FQZF01000013.1\_94 # 98398 # 100161 # -1 # ID=53\_94;partial=00;start\_type=ATG;rbs\_motif=GGAGG;rbs\_spacer=5-10bp;gc\_cont=0.683

### Matched Family

PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY
<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	<a href="#">ABG61919</a>	90.29

<b>Input Sequence</b>	FQZF01000013.1_77 # 82455 # 83804 # -1 # ID=53_77;partial=00;start_type=ATG;rbs_motif=GGA/GAG/AGG;rbs_spacer=5-10bp;gc_cont=0.679					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	TrbL/VirB6 plasmid conjugal transfer protein	ABG61906 99.33
<b>Input Sequence</b>	FQZF01000013.1_85 # 89447 # 90715 # 1 # ID=53_85;partial=00;start_type=ATG;rbs_motif=AGGAG;rbs_spacer=5-10bp;gc_cont=0.654					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	HipA-like	ABG61914 91.47
<b>Input Sequence</b>	FQZF01000013.1_74 # 79596 # 80795 # -1 # ID=53_74;partial=00;start_type=ATG;rbs_motif=GGAGG;rbs_spacer=5-10bp;gc_cont=0.682					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conjugation TrbL-like protein	ABG61903 99.0
<b>Input Sequence</b>	FQZF01000013.1_110 # 110350 # 111414 # -1 # ID=53_110;partial=00;start_type=ATG;rbs_motif=GGAGG;rbs_spacer=3-4bp;gc_cont=0.664					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABG61937 94.63
<b>Input Sequence</b>	FQZF01000013.1_101 # 103488 # 104549 # -1 # ID=53_101;partial=00;start_type=ATG;rbs_motif=GGA/GAG/AGG;rbs_spacer=5-10bp;gc_cont=0.648					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	replication protein A	ABG61926 98.58
<b>Input Sequence</b>	FQZF01000013.1_83 # 87916 # 88857 # -1 # ID=53_83;partial=00;start_type=ATG;rbs_motif=None;rbs_spacer=None;gc_cont=0.696					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	type II secretion system protein E	ABG61912 97.76
<b>Input Sequence</b>	FQZF01000013.1_75 # 80792 # 81520 # -1 # ID=53_75;partial=00;start_type=GTG;rbs_motif=GGxGG;rbs_spacer=5-10bp;gc_cont=0.675					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	Conjugal transfer protein TrbG/VirB9/CagX	ABG61904 98.76
<b>Input Sequence</b>	FQZF01000013.1_115 # 119328 # 120296 # -1 # ID=53_115;partial=00;start_type=ATG;rbs_motif=GGAG/GAGG;rbs_spacer=5-10bp;gc_cont=0.682					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	Domain of unknown function DUF1738	ABG61942 99.07
<b>Input Sequence</b>	FQZF01000013.1_109 # 109072 # 109995 # -1 # ID=53_109;partial=00;start_type=ATG;rbs_motif=GGAG/GAGG;rbs_spacer=5-10bp;gc_cont=0.646					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABG61936 97.72
<b>Input Sequence</b>	FQZF01000013.1_127 # 137061 # 137984 # -1 # ID=53_127;partial=00;start_type=ATG;rbs_motif=GGAG/GAGG;rbs_spacer=5-10bp;gc_cont=0.640					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	15751	CP000463	Rhodopseudomonas palustris BisA53, complete genome.	Alphaproteobacteria	AAA ATPase, central domain protein	ABJ06408 94.46

<b>Input Sequence</b>	FQZF01000013.1_124 # 135195 # 136091 # -1 # ID=53_124;partial=00;start_type=ATG;rhs_motif=AGGAG;rhs_spacer=5-10bp;gc_cont=0.561					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	<a href="#">15751</a>	<a href="#">CP000463</a>	Rhodopseudomonas palustris BisA53, complete genome.	Alphaproteobacteria	conserved hypothetical protein	<a href="#">ABJ06405</a> 93.96
<b>Input Sequence</b>	FQZF01000013.1_95 # 100409 # 101173 # -1 # ID=53_95;partial=00;start_type=ATG;rhs_motif=GGA/GAG/AGG;rhs_spacer=5-10bp;gc_cont=0.703					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	Lytic transglycosylase, catalytic	<a href="#">ABG61920</a> 94.88
<b>Input Sequence</b>	FQZF01000013.1_79 # 84100 # 84861 # -1 # ID=53_79;partial=00;start_type=ATG;rhs_motif=GGAG/GAGG;rhs_spacer=5-10bp;gc_cont=0.647					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conjugal transfer protein trbJ	<a href="#">ABG61908</a> 98.81
<b>Input Sequence</b>	FQZF01000013.1_123 # 134437 # 135162 # -1 # ID=53_123;partial=00;start_type=ATG;rhs_motif=GGAG/GAGG;rhs_spacer=5-10bp;gc_cont=0.551					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	<a href="#">15751</a>	<a href="#">CP000463</a>	Rhodopseudomonas palustris BisA53, complete genome.	Alphaproteobacteria	conserved hypothetical protein	<a href="#">ABJ06404</a> 92.95
<b>Input Sequence</b>	FQZF01000013.1_76 # 81769 # 82458 # -1 # ID=53_76;partial=00;start_type=ATG;rhs_motif=GGAGG;rhs_spacer=5-10bp;gc_cont=0.670					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	Conjugal transfer protein	<a href="#">ABG61905</a> 98.69
<b>Input Sequence</b>	FQZF01000037.1_20 # 20113 # 20775 # -1 # ID=41_20;partial=00;start_type=ATG;rhs_motif=GGAG/GAGG;rhs_spacer=5-10bp;gc_cont=0.582					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	<a href="#">15756</a>	<a href="#">CP000782</a>	Xanthobacter autotrophicus Py2 plasmid pXAUT01, complete sequence.	Alphaproteobacteria	Isoprenylcysteine carboxyl methyltransferase	<a href="#">ABS70095</a> 92.73
<b>Input Sequence</b>	FQZF01000013.1_112 # 115864 # 116508 # -1 # ID=53_112;partial=00;start_type=ATG;rhs_motif=GGAGG;rhs_spacer=5-10bp;gc_cont=0.633					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	<a href="#">ABG61939</a> 95.33
<b>Input Sequence</b>	FQZF01000013.1_129 # 138804 # 139325 # 1 # ID=53_129;partial=00;start_type=GTG;rhs_motif=GGA/GAG/AGG;rhs_spacer=5-10bp;gc_cont=0.567					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	<a href="#">15751</a>	<a href="#">CP000463</a>	Rhodopseudomonas palustris BisA53, complete genome.	Alphaproteobacteria	protein of unknown function DUF955	<a href="#">ABJ06411</a> 93.06
<b>Input Sequence</b>	FQZF01000013.1_98 # 102105 # 102620 # -1 # ID=53_98;partial=00;start_type=ATG;rhs_motif=GGAG/GAGG;rhs_spacer=5-10bp;gc_cont=0.669					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	<a href="#">10690</a>	<a href="#">CP000390</a>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	<a href="#">ABG61923</a> 98.25
<b>Input Sequence</b>	FQZF01000013.1_125 # 136091 # 136591 # -1 # ID=53_125;partial=00;start_type=ATG;rhs_motif=GGA/GAG/AGG;rhs_spacer=11-12bp;gc_cont=0.585					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	<a href="#">15751</a>	<a href="#">CP000463</a>	Rhodopseudomonas palustris BisA53, complete genome.	Alphaproteobacteria	conserved hypothetical protein	<a href="#">ABJ06406</a> 95.78

<b>Input Sequence</b>	FQZF01000013.1_126 # 136588 # 137064 # -1 # ID=53_126;partial=00;start_type=ATG;rbs_motif=GGAGG;rbs_spacer=5-10bp;gc_cont=0.608					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	15751	CP000463	Rhodopseudomonas palustris BisA53, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABJ06407 92.41
<b>Input Sequence</b>	FQZF01000013.1_107 # 107634 # 108074 # -1 # ID=53_107;partial=00;start_type=ATG;rbs_motif=GGAGG;rbs_spacer=5-10bp;gc_cont=0.646					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABG61933 95.89
<b>Input Sequence</b>	FQZF01000013.1_88 # 92616 # 93035 # -1 # ID=53_88;partial=00;start_type=ATG;rbs_motif=GGAG/GAGG;rbs_spacer=5-10bp;gc_cont=0.652					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	helix-turn-helix protein, CopG	ABG61917 92.09
<b>Input Sequence</b>	FQZF01000013.1_113 # 116501 # 116917 # -1 # ID=53_113;partial=00;start_type=ATG;rbs_motif=GGAG/GAGG;rbs_spacer=5-10bp;gc_cont=0.635					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABG61940 96.38
<b>Input Sequence</b>	FQZF01000013.1_96 # 101177 # 101515 # -1 # ID=53_96;partial=00;start_type=ATG;rbs_motif=AGGAG;rbs_spacer=5-10bp;gc_cont=0.664					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	protein of unknown function DUF736	ABG61921 98.21
<b>Input Sequence</b>	FQZF01000013.1_82 # 87587 # 87919 # -1 # ID=53_82;partial=00;start_type=ATG;rbs_motif=AGGAG;rbs_spacer=5-10bp;gc_cont=0.664					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	Conjugal transfer protein TrbC	ABG61911 97.27
<b>Input Sequence</b>	FQZF01000013.1_106 # 106697 # 107023 # -1 # ID=53_106;partial=00;start_type=ATG;rbs_motif=AGGAG;rbs_spacer=5-10bp;gc_cont=0.661					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	protein of unknown function DUF736	ABG61932 100.0
<b>Input Sequence</b>	FQZF01000013.1_78 # 83808 # 84089 # -1 # ID=53_78;partial=00;start_type=ATG;rbs_motif=GGAG/GAGG;rbs_spacer=5-10bp;gc_cont=0.702					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABG61907 95.7
<b>Input Sequence</b>	FQZF01000013.1_81 # 87306 # 87587 # -1 # ID=53_81;partial=00;start_type=ATG;rbs_motif=None;rbs_spacer=None;gc_cont=0.645					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conjugal transfer protein trbB	ABG61910 96.77
<b>Input Sequence</b>	FQZF01000013.1_102 # 104560 # 104841 # -1 # ID=53_102;partial=00;start_type=ATG;rbs_motif=GGAGG;rbs_spacer=5-10bp;gc_cont=0.688					
<b>Matched Family</b>	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID %IDENTITY
	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	phage transcriptional regulator, AlpA	ABG61927 100.0

Input Sequence	FQZF01000013.1_84 # 89181 # 89450 # 1 # ID=53_84;partial=00;start_type=ATG;rbs_motif=GGA/GAG/AGG;rbs_spacer=5-10bp;gc_cont=0.626						
	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY
Matched Family	<u>10690</u>	<u>CP000390</u>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	transcriptional regulator, XRE family	<u>ABG61913</u>	94.38
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Input Sequence	FQZF01000013.1_104 # 105857 # 106123 # -1 # ID=53_104;partial=00;start_type=GTG;rbs_motif=AGxAGG/AGGxGG;rbs_spacer=5-10bp;gc_cont=0.644						
	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY