Center for Genomic Epidemiology

Home Services Instructions Output

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 lenght
 322.0

atched	-,	_111	rtial=00;start_type=ATG;	rbs_motif=None;rbs_spacer=Nor	ne;gc_cont=0.6	555
tched	PROJECT ID ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTIT
amily	10690 CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	probably methylase/helicase	ABG61938	97.19
nput quence	PROJECT ID ACCESSION ID	013.1_117 # 121783 # 125055 # 1 # ID=53_1 10bp ORGANISMS Mesorhizobium sp. BNC1, complete	p;gc_cont=0.588	PROTEIN FUNCTION	PROTEIN ID	%IDENTIT
mily	10690 CP000390	genome.	Alphaproteobacteria	helicase-like	ABG61944	98.62
iput uence	_) # 84858 # 87296 # -1 # ID=53_80;partial=00				0.663
	PROJECT ID ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTIT
tched mily	10690 CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	ATPas	ABG61909	98.52
nput uence	1 421 010000		14;partial=00;start_type= p;gc_cont=0.663	ATG;rbs_motif=GGAG/GAGG;rb	s_spacer=5-	
•	PROJECT ID ACCESSION ID			ATG;rbs_motif=GGAG/GAGG;rb	PROTEIN ID	%IDENTIT
•			o;gc_cont=0.663	· -	_ ·	%IDENTIT 96.5
ched mily out ience	PROJECT ID ACCESSION ID 10690 CP000390	ORGANISMS Mesorhizobium sp. BNC1, complete	o;gc_cont=0.663 class Alphaproteobacteria	PROTEIN FUNCTION ParB family protein	PROTEIN ID ABG61941	
uence ched	PROJECT ID ACCESSION ID 10690 CP000390 FQZF01000037 PROJECT ID ACCESSION ID 10690 CP000390	ORGANISMS Mesorhizobium sp. BNC1, complete genome. 1_24 # 23695 # 25647 # -1 # ID=41_24;partions of the complete genome.	class Alphaproteobacteria al=00;start_type=ATG;rb class Alphaproteobacteria	PROTEIN FUNCTION ParB family protein s_motif=None;rbs_spacer=None PROTEIN FUNCTION heavy metal translocating P- type ATPase	PROTEIN ID ABG61941 ;gc_cont=0.64 PROTEIN ID ABG65243	96.5 1 %IDENTIT 89.85

ORGANISMS

Mesorhizobium sp. BNC1, complete

genome.

PROJECT ID

10690

Matched

Family

ACCESSION ID

CP000390

%IDENTITY

90.29

PROTEIN ID

ABG61919

PROTEIN FUNCTION

conserved hypothetical protein

Alphaproteobacteria

equence			# 82455 # 83804 # -1 # ID=53_77;partial=00					
	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENT	
Matched Family	<u>10690</u>	<u>CP000390</u>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	TrbL/VirB6 plasmid conjugal transfer protein	<u>ABG61906</u>	99.3	
Input sequence	FQ	ZF01000013.1_	85 # 89447 # 90715 # 1 # ID=53_85;partial	=00;start_type=ATG;rbs_	_motif=AGGAG;rbs_spacer=5-10b	p;gc_cont=0.6	654	
equence	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDEN	
Matched Family	10690	<u>CP000390</u>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	HipA-like	ABG61914	91.4	
Input	FO	7F01000013 1	74 # 79596 # 80795 # -1 # ID=53 74;partial	=00:start_type=ATG:rbs	motif=GGAGG:rbs_spacer=5-10b	on:ac cont=0.6	 682	
equence	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDEN	
Matched Family	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conjugation Trbl-like protein	ABG61903	99.	
Input equence	FQZF PROJECT ID	F01000013.1_11	10 # 110350 # 111414 # -1 # ID=53_110;par organisms	tial=00;start_type=ATG;rl	bs_motif=GGAGG;rbs_spacer=3-4	4bp;gc_cont=0).664 %IDEN	
Matched Family	10690	<u>CP000390</u>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABG61937	94.	
Input equence				p;gc_cont=0.648				
Matched Family	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	replication protein A	ABG61926	%IDEI	
Input equence	PROJECT ID	ACCESSION ID	1_83 # 87916 # 88857 # -1 # ID=53_83;part ORGANISMS Mesorhizobium sp. BNC1, complete	CLASS	os_motif=None;rbs_spacer=None; PROTEIN FUNCTION type II secretion system protein	PROTEIN ID	%IDEN	
Family	10690	<u>CP000390</u>	genome.	Alphaproteobacteria	, E, ,	ABG61912	97.	
Input equence			75 # 80792 # 81520 # -1 # ID=53_75;partial					
Matched Family	10690	CP000390	ORGANISMS Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	PROTEIN FUNCTION Conjugal transfer protein TrbG/VirB9/CagX	ABG61904	%IDEI	
Input equence	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							
latched Family	10690	CP000390	ORGANISMS Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	PROTEIN FUNCTION Domain of unknown function DUF1738	ABG61942	%IDE	
Input equence	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							
/latched	PROJECT ID	ACCESSION ID	ORGANISMS Mesorhizobium sp. BNC1, complete	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDEN	
Family	10690	<u>CP000390</u>	genome.	Alphaproteobacteria	conserved hypothetical protein	ABG61936	97.	
	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							
Input equence				<u> </u>				
Input equence	PROJECT ID	ACCESSION ID	ORGANISMS Rhodopseudomonas palustris BisA53,	CLASS	PROTEIN FUNCTION AAA ATPase, central domain	PROTEIN ID	%IDEN	

0/24, 11.55	AIVI			alliogeni indei - Nesui				
Input Sequence								
ocquence	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENT	
Matched Family	<u>15751</u>	CP000463	Rhodopseudomonas palustris BisA53, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABJ06405	93.9	
Input		FQZF01000	013.1_95 # 100409 # 101173 # -1 # ID=53_95		.TG;rbs_motif=GGA/GAG/AGG;rbs	s_spacer=5-		
Sequence	PROJECT ID	ACCESSION ID	1UDD ORGANISMS	cLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENT	
Matched Family	10690	<u>CP000390</u>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	Lytic transglycosylase, catalytic	ABG61920	94.8	
Input	FQZF	01000013.1 7	'9 # 84100 # 84861 # -1 # ID=53_79;partial=00);start_type=ATG;rbs_m	otif=GGAG/GAGG;rbs spacer=5-	10bp;gc cont=	=0.647	
Sequence	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENT	
Matched Family	10690	<u>CP000390</u>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conjugal transfer protein trbJ	ABG61908	98.8	
Input		FQZF01000	013.1_123 # 134437 # 135162 # -1 # ID=53_1		=ATG;rbs_motif=GGAG/GAGG;rb	s_spacer=5-		
Sequence	PROJECT ID	ACCESSION ID	ORGANISMS	cLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENT	
Matched Family	<u>15751</u>	<u>CP000463</u>	Rhodopseudomonas palustris BisA53, complete genome.	Alphaproteobacteria	conserved hypothetical protein	<u>ABJ06404</u>	92.9	
Input Sequence	FQ PROJECT ID	ZF01000013.1	1_76 # 81769 # 82458 # -1 # ID=53_76;partial=	=00;start_type=ATG;rbs_	_motif=GGAGG;rbs_spacer=5-10b protein function	pp;gc_cont=0.6	670 %IDEN	
Matched Family	<u>10690</u>	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	Conjugal transfer protein	ABG61905	98.6	
Input Sequence			20 # 20113 # 20775 # -1 # ID=41_20;partial=00					
Matahad	PROJECT ID	ACCESSION ID	ORGANISMS Vanthabactar autotraphique Dv2 plannid	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENT	
Matched Family	<u>15756</u>	CP000782	Xanthobacter autotrophicus Py2 plasmid pXAUT01, complete sequence.	Alphaproteobacteria	Isoprenylcysteine carboxyl methyltransferase	ABS70095	92.7	
Input Sequence	FQZF	F01000013.1_	112 # 115864 # 116508 # -1 # ID=53_112;partia	al=00;start_type=ATG;rb	os_motif=GGAGG;rbs_spacer=5-1	0bp;gc_cont=	0.633	
•	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDEN	
Matched Family	<u>10690</u>	<u>CP000390</u>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABG61939	95.3	
Input		FQZF010000	13.1_129 # 138804 # 139325 # 1 # ID=53_129	9;partial=00;start_type=0	GTG;rbs_motif=GGA/GAG/AGG;rl	os_spacer=5-		
Sequence	DDO IFOT ID	100500101110	10bp organisms	p;gc_cont=0.567	PROTEIN FUNCTION	PROTEINUR	e/ IDEN	
Matched Family	15751	CP000463	Rhodopseudomonas palustris BisA53, complete genome.	Alphaproteobacteria	PROTEIN FUNCTION protein of unknown function DUF955	ABJ06411	93.0	
Input	FQZF0	1000013 1 98	# 102105 # 102620 # -1 # ID=53_98;partial=0	00:start_type=ATG:rbs_r		-10bp:gc_con	t=0.66	
Sequence	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDEN	
Matched Family	10690	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABG61923	98.2	
	FQZF01000013.1_125 # 136091 # 136591 # -1 # ID=53_125;partial=00;start_type=ATG;rbs_motif=GGA/GAG/AGG;rbs_spacer=11-12bp;gc_cont=0.585							
Input Sequence			12bp	7,gc_con=0.565				
•	PROJECT ID	ACCESSION ID	0RGANISMS Rhodopseudomonas palustris BisA53,	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENT	

Input			<u> </u>							
Sequence	lence FQZF01000013.1_126 # 136366 # 137064 # -1 # ID=53_126;partial=00;start_type=A1G;rbs_motil=GGAGG;rbs_spacel=5-10bp									
Matched Family	15751	CP000463	Rhodopseudomonas palustris BisA53, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABJ06407	92.41			
			complete general.				I			
Input Sequence			107 # 107634 # 108074 # -1 # ID=53_107;parti	al=00;start_type=ATG;rl			0.646			
Matched Family	10690	CP000390	Mesorhizobium sp. BNC1, complete	Alphaproteobacteria	conserved hypothetical protein	ABG61933	95.89			
			genome.							
Input Sequence	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									
	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY			
Matched Family	<u>10690</u>	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	helix-turn-helix protein, CopG	ABG61917	92.09			
		F07F04000		10	ATO all a 112 alif 00 A 0 (0 A 0 0 al					
Input Sequence	PROJECT ID	ACCESSION ID	0013.1_113 # 116501 # 116917 # -1 # ID=53_17 10bp organisms	o;gc_cont=0.635	PROTEIN FUNCTION	S_SPACET=5-	%IDENTITY			
Matched Family	<u>10690</u>	<u>CP000390</u>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	<u>ABG61940</u>	96.38			
Input Sequence	FQZ PROJECT ID	F01000013.1_	_96 # 101177 # 101515 # -1 # ID=53_96;partia	I=00;start_type=ATG;rbs	s_motif=AGGAG;rbs_spacer=5-10	bp;gc_cont=0	.664 %IDENTITY			
Matched Family	<u>10690</u>	<u>CP000390</u>	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	protein of unknown function DUF736	ABG61921	98.21			
Input Sequence	FQ	ZF01000013.	1_82 # 87587 # 87919 # -1 # ID=53_82;partial=	=00;start_type=ATG;rbs	_motif=AGGAG;rbs_spacer=5-10b	p;gc_cont=0.6	664			
Madalaad	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY			
Matched Family	<u>10690</u>	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	Conjugal transfer protein TrbC	ABG61911	97.27			
Input	E07E	01000012.1		al=00:start_type=ATC:r	hs motif=ACCAC:rhs spacer=5.1	Ohn:go_cont=	0 661			
Sequence			106 # 106697 # 107023 # -1 # ID=53_106;parti							
Matched Family	10690	CP000390	ORGANISMS Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	PROTEIN FUNCTION protein of unknown function DUF736	ABG61932	100.0			
Input Sequence	FQZF	01000013.1_7	78 # 83808 # 84089 # -1 # ID=53_78;partial=00	;start_type=ATG;rbs_m	otif=GGAG/GAGG;rbs_spacer=5-	10bp;gc_cont=	0.702			
Matchad	PROJECT ID	ACCESSION ID	ORGANISMS Mosorbizabium on PNC1 complete	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY			
Matched Family	<u>10690</u>	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	conserved hypothetical protein	ABG61907	95.7			
		I.								
Input										
Input Sequence	F PROJECT ID	FQZF0100001	3.1_81 # 87306 # 87587 # -1 # ID=53_81;parti: 	al=00;start_type=ATG;rt	os_motif=None;rbs_spacer=None;	gc_cont=0.64				
-										
Sequence Matched Family	PROJECT ID 10690	CP000390	ORGANISMS Mesorhizobium sp. BNC1, complete genome.	CLASS Alphaproteobacteria	PROTEIN FUNCTION conjugal transfer protein trbB	ABG61910	%IDENTITY 96.77			
Sequence Matched	PROJECT ID 10690	CP000390	ORGANISMS Mesorhizobium sp. BNC1, complete genome. 102 # 104560 # 104841 # -1 # ID=53_102;particles	CLASS Alphaproteobacteria al=00;start_type=ATG;rl	PROTEIN FUNCTION conjugal transfer protein trbB conjugal transfer protein trbB	ABG61910	%IDENTITY 96.77			
Sequence Matched Family Input	PROJECT ID 10690	CP000390	ORGANISMS Mesorhizobium sp. BNC1, complete genome.	CLASS Alphaproteobacteria	PROTEIN FUNCTION conjugal transfer protein trbB	ABG61910	%IDENTITY 96.77			

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>	CP000390	Mesorhizobium sp. BNC1, complete genome.	Alphaproteobacteria	transcriptional regulator, XRE family	ABG61913	94.38		
Input Sequence	F	QZF01000013	3.1_104 # 105857 # 106123 # -1 # ID=53_104;p 10bp;g	artial=00;start_type=G gc_cont=0.644	TG;rbs_motif=AGxAGG/AGGxGG	;rbs_spacer=5	i-		
	PROJECT ID	ACCESSION ID	ORGANISMS	CLASS	PROTEIN FUNCTION	PROTEIN ID	%IDENTITY		