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BLAST® > blastp suite > results for RID-UWSENZ5A013

Job Title	3rd Blast search ...
RID	UWSENZ5A013 Search expires on 01-23 19:38 pm
Program	BLASTP
Database	nr
Query ID	lclQuery_11474261
Description	unnamed protein product ...
Molecule type	amino acid
Query Length	34

**Descriptions**

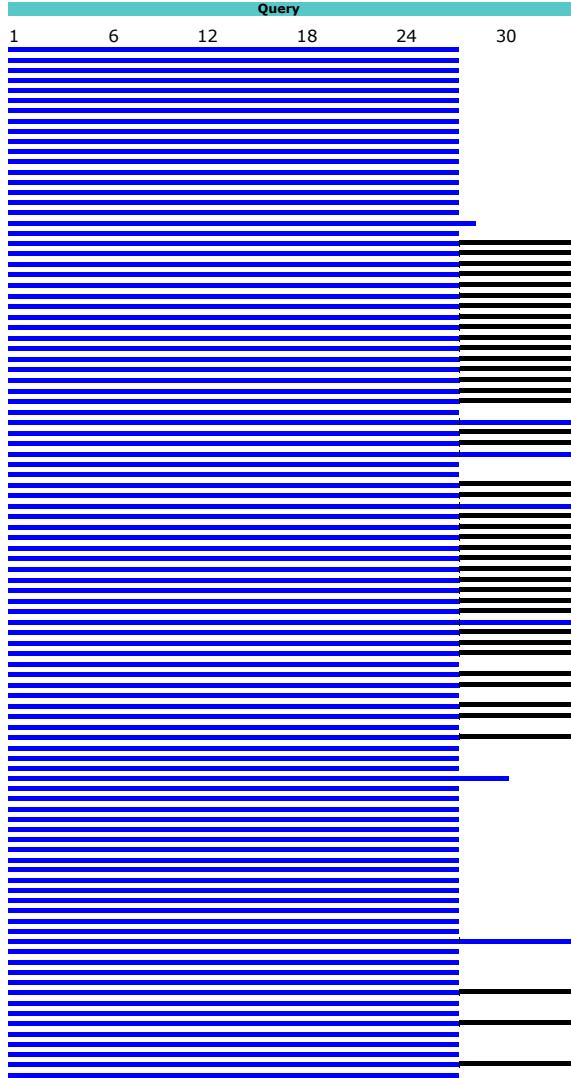
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
hypothetical protein [Escherichia coli]	Escherichia coli	43.5	43.5	79%	4e-04	70.37%	42	WP_244581302.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	43.5	43.5	79%	4e-04	70.37%	43	NAI03858.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.5	43.5	79%	4e-04	70.37%	44	WP_274536608.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	43.5	43.5	79%	5e-04	70.37%	47	MBF9180846.1

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.5	43.5	79%	5e-04	70.37%	47	MBF9176786.1
Citrate synthase [Escherichia coli DORA_A_5_14_21]	Escherichia coli DORA_A_5_14_21	43.1	43.1	79%	5e-04	70.37%	42	ETJ26103.1
TPA: citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.5	43.5	79%	5e-04	70.37%	45	HAJ5512484.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.5	43.5	79%	5e-04	70.37%	48	WP_305766138.1
hypothetical protein [Escherichia coli]	Escherichia coli	43.1	43.1	79%	5e-04	70.37%	39	MDF0764298.1
hypothetical protein [Escherichia coli]	Escherichia coli	43.1	43.1	79%	5e-04	70.37%	39	MDM8620142.1
hypothetical protein MUTS16_31810 [Escherichia coli]	Escherichia coli	43.1	43.1	79%	6e-04	70.37%	49	BDZ02108.1
type II citrate synthase [Shigella sonnei]	Shigella sonnei	43.1	43.1	79%	6e-04	70.37%	49	CSF75830.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.1	43.1	79%	6e-04	70.37%	44	MCF2047846.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.1	43.1	79%	6e-04	70.37%	51	WP_289710214.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.1	43.1	79%	6e-04	70.37%	45	EJP4275022.1
citrate/2-methylcitrate synthase [Vibrio parahaemolyticus]	Vibrio parahaemolyticus	43.1	43.1	79%	7e-04	55.56%	46	WP_283957688.1
citrate/2-methylcitrate synthase [Shigella sonnei]	Shigella sonnei	43.1	43.1	79%	7e-04	70.37%	53	WP_289844962.1
hypothetical protein [Klebsiella oxytoca]	Klebsiella oxytoca	43.1	43.1	82%	7e-04	60.71%	53	WP_266097662.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.1	43.1	79%	8e-04	70.37%	50	MCM4299108.1
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	43.5	82.8	100%	8e-04	70.37%	76	WP_309301862.1
citrate (S)-synthase [Enterobacteriaceae bacterium TzEc052]	Enterobacteriaceae bacterium TzEc052	43.9	83.2	100%	8e-04	70.37%	86	KAE9897545.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	8e-04	70.37%	86	WP_283571878.1
TPA: citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.5	82.8	100%	8e-04	70.37%	84	HBI9786764.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	8e-04	70.37%	96	MDY3720482.1
citrate (S)-synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	43.5	82.8	100%	9e-04	70.37%	78	MCL7660528.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.5	82.8	100%	9e-04	70.37%	84	WP_286205966.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	9e-04	70.37%	94	MWR90423.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.5	82.8	100%	9e-04	70.37%	75	WP_284737003.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.5	82.8	100%	9e-04	70.37%	83	MBA1933872.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.5	82.8	100%	9e-04	70.37%	83	MDN1366952.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.5	82.8	100%	9e-04	70.37%	75	WP_284737001.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.5	82.8	100%	9e-04	70.37%	81	MBS8919746.1
TPA: citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.5	82.8	100%	9e-04	70.37%	72	HCN8565948.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.1	82.0	100%	9e-04	70.37%	71	WP_284696415.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.5	82.8	100%	0.001	70.37%	87	WP_302306452.1
Citrate synthase (S) [Klebsiella pneumoniae]	Klebsiella pneumoniae	42.7	42.7	79%	0.001	66.67%	42	SVN06291.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	44.3	84.3	100%	0.001	70.37%	121	WP_284147049.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	0.001	70.37%	100	EIF4801338.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.5	82.8	100%	0.001	70.37%	78	MC00173501.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.9	83.9	100%	0.001	70.37%	108	MSI35684.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	42.7	42.7	79%	0.001	70.37%	55	WP_302314285.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	42.7	42.7	79%	0.001	70.37%	55	MBA1846289.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.1	82.0	100%	0.001	70.37%	70	MDM1725847.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.1	82.0	100%	0.001	70.37%	67	WP_284693070.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.9	83.9	100%	0.001	70.37%	108	MBS8847612.1
TPA: citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.1	82.0	100%	0.001	70.37%	66	HCN7185207.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	0.001	70.37%	95	WP_283570149.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.1	82.4	100%	0.001	70.37%	77	WP_289709520.1
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	43.1	82.0	100%	0.001	70.37%	64	WP_301952173.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.5	83.2	100%	0.001	70.37%	86	WP_272881025.1
TPA: citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	0.001	70.37%	105	HBD5505378.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	0.001	70.37%	110	EGJ6209831.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	0.001	70.37%	100	WP_32098633.1
citrate synthase family protein [Escherichia coli 3-105-05_S3_C2]	Escherichia coli 3-105-05_S3_C2	43.9	83.6	100%	0.001	70.37%	109	KDT38988.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.5	83.2	100%	0.001	70.37%	94	WP_272732384.1
citrate (S)-synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	43.9	83.9	100%	0.001	70.37%	116	TNA27598.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	0.001	70.37%	114	WP_032236753.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	0.001	70.37%	116	MBI090235.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	0.001	70.37%	101	WP_275511187.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.5	43.5	79%	0.001	55.56%	87	MCV5836431.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	0.001	70.37%	118	MDU7304414.1
citrate (S)-synthase [Escherichia coli O145:H28]	Escherichia coli O145:H28	43.5	83.2	100%	0.001	70.37%	98	EJH5202848.1
citrate synthase family protein [Vibrio harveyi]	Vibrio harveyi	43.1	43.1	79%	0.001	55.56%	70	EKM1525.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.1	82.0	100%	0.001	70.37%	70	MDM1725853.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.9	83.6	100%	0.001	70.37%	114	PZT65910.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	44.3	44.3	79%	0.001	70.37%	138	MCA8592376.1
citrate (S)-synthase [Bacteroides heparinolyticus]	Bacteroides heparinolyticus	42.7	81.6	100%	0.001	70.37%	64	MCF0257894.1
citrate/2-methylcitrate synthase [Vibrio parahaemolyticus]	Vibrio parahaemolyticus	43.5	43.5	79%	0.001	55.56%	99	MDF4990707.1
TPA: citrate (S)-synthase [Escherichia coli]	Escherichia coli	44.3	44.3	79%	0.001	70.37%	138	HDS403954.1
citrate/2-methylcitrate synthase [Vibrio vulnificus]	Vibrio vulnificus	42.7	42.7	79%	0.001	55.56%	67	WP_309250606.1
citrate synthase [Escherichia coli]	Escherichia coli	45.1	45.1	88%	0.001	63.33%	420	WP_063103628.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	44.3	44.3	79%	0.001	70.37%	146	RIB41964.1
citrate/2-methylcitrate synthase [Vibrio sp. FNV 38]	Vibrio sp. FNV 38	44.3	44.3	79%	0.001	70.37%	138	MDR9824555.1
citrate (S)-synthase [Escherichia coli]	Escherichia coli	43.9	43.9	79%	0.001	70.37%	129	MBK1748728.1
citrate/2-methylcitrate synthase [Vibrio fluvialis]	Vibrio fluvialis	43.9	43.9	79%	0.001	70.37%	130	WP_275125840.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.9	43.9	79%	0.001	70.37%	130	WP_074522594.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.9	43.9	79%	0.001	70.37%	132	WP_07779533.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	43.9	43.9	79%	0.001	70.37%	132	WP_289508712.1

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
TPA: citrate (Si)-synthase [Escherichia coli]	Escherichia coli	43.9	43.9	79%	0.001	70.37%	130	HDO5165782.1
citrate (Si)-synthase [Lutimaribacter sp. EGI FJ00015]	Lutimaribacter sp. EGI FJ00015	44.3	44.3	79%	0.001	70.37%	144	MCO0615641.1
citrate (Si)-synthase [Vibrio vulnificus]	Vibrio vulnificus	43.5	43.5	79%	0.001	55.56%	103	POF55226.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	44.3	44.3	79%	0.001	70.37%	157	EEZ0587125.1
citrate synthase [Escherichia coli]	Escherichia coli	43.9	43.9	79%	0.001	70.37%	126	GDS03942.1
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	42.4	42.4	79%	0.002	66.67%	53	WP_319937664.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	44.3	44.3	79%	0.002	70.37%	154	WP_324251799.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	44.3	44.3	79%	0.002	70.37%	151	WP_074466000.1
TPA: citrate (Si)-synthase [Klebsiella oxytoca]	Klebsiella oxytoca	43.9	84.7	100%	0.002	66.67%	121	HEC2128142.1
citrate synthase [Escherichia coli UCI S1]	Escherichia coli UCI S1	44.3	44.3	79%	0.002	70.37%	153	KDG76081.1
citrate synthase domain protein [Escherichia coli DECSE]	Escherichia coli DECSE	43.9	43.9	79%	0.002	70.37%	126	EHV50680.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	44.3	44.3	79%	0.002	70.37%	153	EEY6517482.1
citrate synthase [Vibrio sp. Of7-15]	Vibrio sp. Of7-15	44.7	44.7	79%	0.002	62.96%	429	WP_239182335.1
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	42.4	81.2	100%	0.002	66.67%	58	MDU2996401.1
citrate synthase [Escherichia coli]	Escherichia coli	44.3	44.3	79%	0.002	70.37%	155	STL43725.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	44.3	44.3	79%	0.002	70.37%	164	MSH86413.1
citrate (Si)-synthase [Pseudomonas aeruginosa]	Pseudomonas aeruginosa	43.1	82.8	100%	0.002	66.67%	95	MBN0903844.1
citrate (Si)-synthase [Mycobacterium tuberculosis]	Mycobacterium tuberculosis	42.0	42.0	79%	0.002	66.67%	54	MBX4322326.1
hypothetical protein [Klebsiella varicola subsp. varicola]	Klebsiella varicola subsp. varicola	42.0	42.0	79%	0.002	66.67%	55	MCS5946155.1
citrate/2-methylcitrate synthase [Shewanella xiamensis]	Shewanella xiamensis	44.3	44.3	79%	0.002	70.37%	165	WP_279255920.1
citrate (Si)-synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	42.7	82.4	100%	0.002	66.67%	81	PIN64336.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	43.5	43.5	79%	0.002	55.56%	120	MCV5940372.1

Graphic Summary

Distribution of the top 146 Blast Hits on 100 subject sequences

**Alignments**

Alignment view Pairwise CDS feature

hypothetical protein, partial [Escherichia coli]

Sequence ID: **WP_244581302.1** Length: 42 Number of Matches: 1

Range 1: 4 to 29

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(101)	4e-04()	Compositional matrix adjust.	19/27(70%)	22/27(81%)	1/27(3%)	
Query 1	TVGWIWSEMHSDGMKAMGIPSSMFT	27				
Sbjct 4	TVGWIWSEMHSDGMK-IARPRQLYT	29				

citrate (Si)-synthase [Escherichia coli]

Sequence ID: **NAI03858.1** Length: 43 Number of Matches: 1

Range 1: 5 to 30

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(101)	4e-04()	Compositional matrix adjust.	19/27(70%)	22/27(81%)	1/27(3%)	
Query 1	TVGWIWSEMHSDGMKAMGIPSSMFT	27				
Sbjct 5	TVGWIWSEMHSDGMK-IARPRQLYT	30				

citrate/2-methylcitrate synthase, partial [Escherichia coli]

Sequence ID: **WP_274536608.1** Length: 44 Number of Matches: 1

Range 1: 6 to 31

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(101)	4e-04()	Compositional matrix adjust.	19/27(70%)	22/27(81%)	1/27(3%)	
Query 1	TVGWIWSEMHSDGMKAMGIPSSMFT	27				
Sbjct 6	TVGWIWSEMHSDGMK-IARPRQLYT	31				

citrate (Si)-synthase [Escherichia coli]

Sequence ID: **MBF9180846.1** Length: 47 Number of Matches: 1

Range 1: 9 to 34

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(101)	5e-04()	Compositional matrix adjust.	19/27(70%)	22/27(81%)	1/27(3%)	
Query 1	TVGWIWSEMHSDGMKAMGIPSSMFT	27				
Sbjct 9	TVGWIWSEMHSDGMK-IARPRQLYT	34				

citrate (Si)-synthase [Escherichia coli]

Sequence ID: **MBF9176786.1** Length: 47 Number of Matches: 1

Range 1: 9 to 34

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(101)	5e-04()	Compositional matrix adjust.	19/27(70%)	22/27(81%)	1/27(3%)	
Query 1	TVGWIWSEMHSDGMKAMGIPSSMFT	27				
Sbjct 9	TVGWIWSEMHSDGMK-IARPRQLYT	34				

MAG: Citrate synthase, partial [Escherichia coli DORA_A_5_14_21]

Sequence ID: **ETJ26103.1** Length: 42 Number of Matches: 1

Range 1: 4 to 29

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(100)	5e-04()	Compositional matrix adjust.	19/27(70%)	22/27(81%)	1/27(3%)	
Query 1	TVGWIWSEMHSDGMKAMGIPSSMFT	27				
Sbjct 4	TVGWIWSEMHSDGMK-IARPRQLYT	29				

citrate (Si)-synthase [Escherichia coli]

Sequence ID: **HAJ5512484.1** Length: 45 Number of Matches: 1

Range 1: 7 to 32

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(101)	5e-04()	Compositional matrix adjust.	19/27(70%)	22/27(81%)	1/27(3%)	
Query 1	TVGWIWSEMHSDGMKAMGIPSSMFT	27				
Sbjct 7	TVGWIWSEMHSDGMK-IARPRQLYT	32				

citrate/2-methylcitrate synthase, partial [Escherichia coli]

Sequence ID: **WP_305766138.1** Length: 48 Number of Matches: 1

Range 1: 10 to 35

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.5 bits(101)	5e-04()	Compositional matrix adjust.	19/27(70%)	22/27(81%)	1/27(3%)	
Query 1	TVGWIWSEMHSDGMKAMGIPSSMFT	27				
Sbjct 10	TVGWIWSEMHSDGMK-IARPRQLYT	35				

hypothetical protein [Escherichia coli]

Sequence ID: **MDF0764298.1** Length: 39 Number of Matches: 1

Range 1: 1 to 26

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(100)	5e-04()	Compositional matrix adjust.	19/27(70%)	22/27(81%)	1/27(3%)	

```
Query 1 TVGWIWSEMHSDGMKAMGIPSSMFT 27
          TVGWIWSEMHSDGMK + P ++T
Sbjct  1 TVGWIWSEMHSDGMK-IARPRQLYT 26
```

hypothetical protein [Escherichia coli]

Sequence ID: MDM8620142.1 Length: 39 Number of Matches: 1
Range 1: 1 to 26

Score	Expect	Method	Identities	Positives	Gaps	Frame
43.1 bits(100)	5e-04()	Compositional matrix adjust.	19/27(70%)	22/27(81%)	1/27(3%)	
Query 1	TVGWIWSEMHSDGMKAMGIPSSMFT	27				
Sbjct 1	TVGWIWSEMHSDGMK-IARPRQLYT	26				

Taxonomy

Reports

Lineage

Organism	Blast Name	Score	Number of Hits	Description
Bacteria	bacteria	153		
.Pseudomonadota	proteobacteria	151		
.Gammaproteobacteria	g-proteobacteria	150		
...Enterobacteriaceae	enterobacteria	134		
...Escherichia	enterobacteria	114		
...Escherichia coli	enterobacteria	43.5	108	Escherichia coli hits
...Escherichia coli DORA_A_5_14_21	enterobacteria	43.1	1	Escherichia coli DORA_A_5_14_21 hits
...Escherichia coli 3-105-05_S3_C2	enterobacteria	43.9	1	Escherichia coli 3-105-05_S3_C2 hits
...Escherichia coli 3-475-03_S4_C1	enterobacteria	43.9	1	Escherichia coli 3-475-03_S4_C1 hits
...Escherichia coli O145:H28	enterobacteria	43.5	1	Escherichia coli O145:H28 hits
...Escherichia coli UCI_51	enterobacteria	44.3	1	Escherichia coli UCI_51 hits
...Escherichia coli DECSE	enterobacteria	43.9	1	Escherichia coli DECSE hits
...Shigella sonnei	enterobacteria	43.1	3	Shigella sonnei hits
...Klebsiella oxytoca	enterobacteria	43.1	2	Klebsiella oxytoca hits
...Klebsiella pneumoniae	enterobacteria	43.5	11	Klebsiella pneumoniae hits
...Enterobacteriaceae bacterium TzEc052	enterobacteria	43.9	2	Enterobacteriaceae bacterium TzEc052 hits
...Shigella flexneri	enterobacteria	44.3	1	Shigella flexneri hits
...Klebsiella variicola subsp. varicola	enterobacteria	42.0	1	Klebsiella variicola subsp. varicola hits
...Vibrio parahaemolyticus	g-proteobacteria	43.1	4	Vibrio parahaemolyticus hits
...Vibrio harveyi	g-proteobacteria	43.1	1	Vibrio harveyi hits
...Vibrio vulnificus	g-proteobacteria	42.7	3	Vibrio vulnificus hits
...Vibrio sp. FNV_38	g-proteobacteria	44.3	1	Vibrio sp. FNV_38 hits
...Vibrio fluvialis	g-proteobacteria	43.9	2	Vibrio fluvialis hits
...Vibrio sp. Of7-15	g-proteobacteria	44.7	2	Vibrio sp. Of7-15 hits
...Pseudomonas aeruginosa	g-proteobacteria	43.1	1	Pseudomonas aeruginosa hits
...Shewanella xiamensis	g-proteobacteria	44.3	2	Shewanella xiamensis hits
...Lutimaribacter sp. EGI_FJ00015	a-proteobacteria	44.3	1	Lutimaribacter sp. EGI_FJ00015 hits
.Bacteroides heparinolyticus	CFB group bacteria	42.7	1	Bacteroides heparinolyticus hits
.Mycobacterium tuberculosis	high G+C Gram-positive bacteria	42.0	1	Mycobacterium tuberculosis hits

Organism

Description	Score	E value	Accession
Escherichia coli [enterobacteria]			
hypothetical protein, partial [Escherichia coli]	43.5	4e-04	WP_244581302
citrate (Si)-synthase [Escherichia coli]	43.5	4e-04	NAI03858
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.5	4e-04	WP_274536608
citrate (Si)-synthase [Escherichia coli]	43.5	5e-04	MBF9180846
citrate (Si)-synthase [Escherichia coli]	43.5	5e-04	MBF9176786
hypothetical protein [Escherichia coli]	43.1	5e-04	MCM2771263
hypothetical protein [Escherichia coli]	43.1	5e-04	MCM2773728
hypothetical protein [Escherichia coli]	43.1	5e-04	MCV5090616
citrate (Si)-synthase [Escherichia coli]	43.5	5e-04	HAJ5512484
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.5	5e-04	WP_305766138
citrate (Si)-synthase [Escherichia coli]	43.5	5e-04	MDP4446547
citrate (Si)-synthase [Escherichia coli]	43.5	5e-04	MDW4800201
hypothetical protein [Escherichia coli]	43.1	5e-04	MDF0764298
hypothetical protein [Escherichia coli]	43.1	5e-04	MDM8617484
hypothetical protein [Escherichia coli]	43.1	5e-04	MDM8620142
hypothetical protein MUTS16_31810 [Escherichia coli]	43.1	6e-04	BDZ02108
citrate (Si)-synthase [Escherichia coli]	43.1	6e-04	MCF2047846
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.1	6e-04	WP_289710214
citrate (Si)-synthase [Escherichia coli]	43.1	6e-04	MBC9681936
citrate (Si)-synthase [Escherichia coli]	43.1	6e-04	EJP4275022

Description	Score	E value	Accession
citrate (S)-synthase [Escherichia coli]	43.1	8e-04	MCM4299108
citrate (S)-synthase [Escherichia coli]	43.9	8e-04	MWQ98706
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.9	8e-04	WP_283571878
citrate (S)-synthase [Escherichia coli]	43.5	8e-04	HBI9786764
citrate/2-methylcitrate synthase [Escherichia coli]	43.9	8e-04	MDY3720482
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.5	9e-04	WP_286205966
citrate (S)-synthase [Escherichia coli]	43.9	9e-04	MWR90423
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.5	9e-04	WP_284737003
citrate (S)-synthase [Escherichia coli]	43.5	9e-04	MBA2041438
citrate (S)-synthase [Escherichia coli]	43.5	9e-04	MBA1933872
citrate (S)-synthase [Escherichia coli]	43.5	9e-04	MDN1366952
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.5	9e-04	WP_284737001
citrate (S)-synthase [Escherichia coli]	43.5	9e-04	MBA2037725
citrate (S)-synthase [Escherichia coli]	43.5	9e-04	MBS8919746
citrate (S)-synthase [Escherichia coli]	43.5	9e-04	HCN8565948
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.1	9e-04	WP_284696415
citrate (S)-synthase [Escherichia coli]	43.1	9e-04	MBF7986016
citrate (S)-synthase [Escherichia coli]	43.1	9e-04	MWM20870
citrate (S)-synthase [Escherichia coli]	43.1	9e-04	MWR75286
citrate (S)-synthase [Escherichia coli]	43.1	9e-04	MWT26135
citrate (S)-synthase [Escherichia coli]	43.1	9e-04	MXJ13823
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.5	0.001	WP_302306452
citrate/2-methylcitrate synthase [Escherichia coli]	43.5	0.001	MDO2792760
citrate synthase [Escherichia coli]	43.5	0.001	VED36794
citrate/2-methylcitrate synthase, partial [Escherichia coli]	44.3	0.001	WP_284147049
citrate (S)-synthase [Escherichia coli]	43.9	0.001	EIF4801338
citrate (S)-synthase [Escherichia coli]	43.9	0.001	EIO7639400
citrate (S)-synthase [Escherichia coli]	43.9	0.001	HDI5885905
citrate (S)-synthase [Escherichia coli]	43.5	0.001	MC00173501
citrate (S)-synthase [Escherichia coli]	43.9	0.001	MSI35684
citrate/2-methylcitrate synthase, partial [Escherichia coli]	42.7	0.001	WP_302314285
citrate/2-methylcitrate synthase [Escherichia coli]	42.7	0.001	MDO2838954
hypothetical protein MUTS15_21620 [Escherichia coli]	42.7	0.001	BDY93505
citrate (S)-synthase [Escherichia coli]	42.7	0.001	MBA1846289
hypothetical protein [Escherichia coli]	42.7	0.001	MCZ5847718
citrate synthase [Escherichia coli]	42.7	0.001	STP21204
citrate (S)-synthase [Escherichia coli]	43.1	0.001	MDM1725847
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.1	0.001	WP_284693070
citrate (S)-synthase, partial [Escherichia coli]	43.1	0.001	KAE9718461
citrate (S)-synthase [Escherichia coli]	43.9	0.001	MBS8847612
citrate (S)-synthase [Escherichia coli]	43.1	0.001	HCN7185207
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.9	0.001	WP_283570149
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.1	0.001	WP_289709520
citrate (S)-synthase [Escherichia coli]	43.1	0.001	MBA1884166
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.5	0.001	WP_272881025
citrate (S)-synthase [Escherichia coli]	43.5	0.001	MCF6615264
citrate (S)-synthase [Escherichia coli]	43.5	0.001	MWQ97432
citrate (S)-synthase [Escherichia coli]	43.9	0.001	HBD5505378
citrate (S)-synthase [Escherichia coli]	43.9	0.001	EGJ6209831
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.9	0.001	WP_322098633
citrate (S)-synthase [Escherichia coli]	43.9	0.001	MCF4025416
citrate synthase [Escherichia coli]	43.9	0.001	VED13032
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.5	0.001	WP_272732384
citrate (S)-synthase [Escherichia coli]	43.5	0.001	HCY92746
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.9	0.001	WP_032236753
citrate (S)-synthase [Escherichia coli]	43.9	0.001	MBI0909235
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.9	0.001	WP_275511187
citrate (S)-synthase [Escherichia coli]	43.5	0.001	MCV5836431
citrate/2-methylcitrate synthase [Escherichia coli]	43.9	0.001	MDU7304414
citrate (S)-synthase [Escherichia coli]	43.1	0.001	MDM1725853
citrate (S)-synthase, partial [Escherichia coli]	43.9	0.001	PZT65910
citrate (S)-synthase [Escherichia coli]	44.3	0.001	MCA8592376
citrate (S)-synthase [Escherichia coli]	44.3	0.001	HDS4039354
citrate synthase, partial [Escherichia coli]	45.1	0.001	WP_063103628
citrate (S)-synthase, partial [Escherichia coli]	44.3	0.001	RIB41964
citrate (S)-synthase [Escherichia coli]	44.3	0.001	HDK0967306
citrate (S)-synthase [Escherichia coli]	43.9	0.001	MBK1748728
citrate (S)-synthase [Escherichia coli]	43.9	0.001	MBL1016225
citrate (S)-synthase [Escherichia coli]	43.9	0.001	MBL1036152
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.9	0.001	WP_074522594

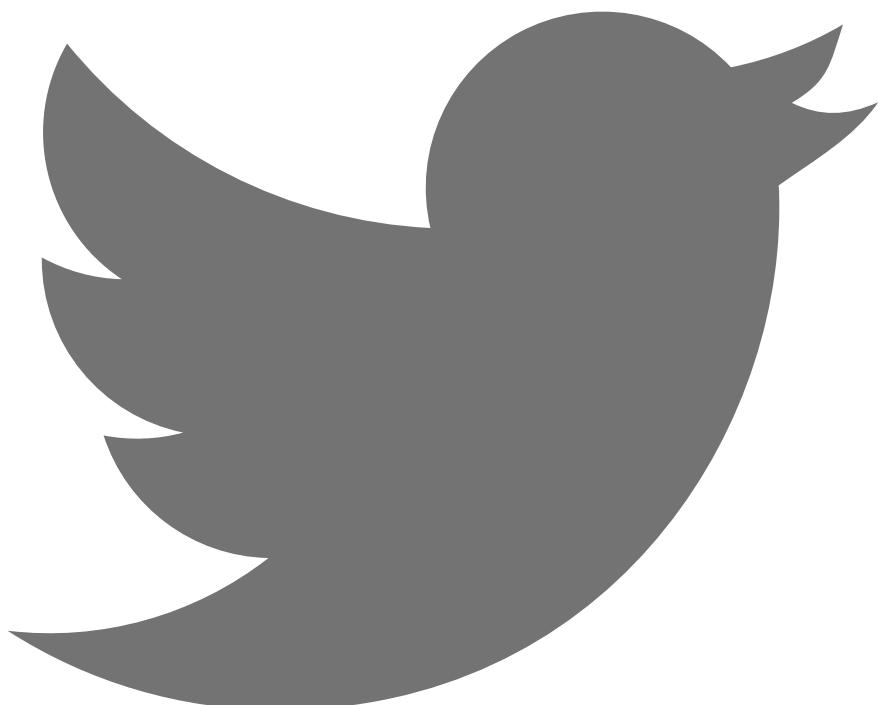
Description	Score	E value	Accession
citrate (S)-synthase [Escherichia coli]	43.9	0.001	MCJ8623990
citrate synthase, partial [Escherichia coli]	43.9	0.001	OKU52881
citrate (S)-synthase [Escherichia coli]	43.9	0.001	HBB7874832
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.9	0.001	WP_077779533
citrate/2-methylcitrate synthase, partial [Escherichia coli]	43.9	0.001	WP_289508712
citrate (S)-synthase [Escherichia coli]	43.9	0.001	HDQ5165782
citrate (S)-synthase [Escherichia coli]	44.3	0.001	MCU8644358
citrate (S)-synthase [Escherichia coli]	44.3	0.001	EZ0587125
citrate synthase [Escherichia coli]	43.9	0.001	GDS03942
citrate synthase [Escherichia coli]	43.9	0.001	STJ45176
citrate/2-methylcitrate synthase, partial [Escherichia coli]	44.3	0.002	WP_324251799
citrate (S)-synthase [Escherichia coli]	44.3	0.002	MCC7986975
citrate/2-methylcitrate synthase, partial [Escherichia coli]	44.3	0.002	WP_074466000
citrate synthase [Escherichia coli]	43.9	0.002	VDZ04469
citrate (S)-synthase [Escherichia coli]	44.3	0.002	EEY6517482
citrate synthase [Escherichia coli]	44.3	0.002	STL43725
citrate (S)-synthase [Escherichia coli]	44.3	0.002	MSH86413
citrate (S)-synthase [Escherichia coli]	43.5	0.002	MCV5940372
Escherichia coli DORA_A_5_14_21 [enterobacteria]			
MAG: Citrate synthase, partial [Escherichia coli DORA_A_5_14_21]	43.1	5e-04	ETJ26103
Shigella sonnei [enterobacteria]			
type II citrate synthase [Shigella sonnei]	43.1	6e-04	CSF75830
citrate/2-methylcitrate synthase, partial [Shigella sonnei]	43.1	7e-04	WP_289844962
type II citrate synthase [Shigella sonnei]	42.7	0.001	CSG51799
Vibrio parahaemolyticus [g-proteobacteria]			
citrate/2-methylcitrate synthase, partial [Vibrio parahaemolyticus]	43.1	7e-04	WP_283957688
citrate/2-methylcitrate synthase [Vibrio parahaemolyticus]	43.1	7e-04	MDF5393982
citrate (S)-synthase [Vibrio parahaemolyticus]	43.1	7e-04	NMV11735
citrate/2-methylcitrate synthase [Vibrio parahaemolyticus]	43.5	0.001	MDF4990707
Klebsiella oxytoca [enterobacteria]			
hypothetical protein [Klebsiella oxytoca]	43.1	7e-04	WP_266097662
citrate (S)-synthase [Klebsiella oxytoca]	43.9	0.002	HEC2128142
Klebsiella pneumoniae [enterobacteria]			
citrate/2-methylcitrate synthase, partial [Klebsiella pneumoniae]	43.5	8e-04	WP_309301862
citrate (S)-synthase, partial [Klebsiella pneumoniae]	43.5	8e-04	RBN11767
citrate (S)-synthase [Klebsiella pneumoniae]	43.5	9e-04	MCL7660528
Citrate synthase (S) [Klebsiella pneumoniae]	42.7	0.001	SVN06291
citrate/2-methylcitrate synthase, partial [Klebsiella pneumoniae]	43.1	0.001	WP_301952173
citrate (S)-synthase [Klebsiella pneumoniae]	43.1	0.001	NDR82707
citrate (S)-synthase, partial [Klebsiella pneumoniae]	43.9	0.001	TNA27598
citrate/2-methylcitrate synthase, partial [Klebsiella pneumoniae]	42.4	0.002	WP_319937664
citrate (S)-synthase [Klebsiella pneumoniae]	42.4	0.002	MRD57650
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	42.4	0.002	MDU2996401
citrate (S)-synthase, partial [Klebsiella pneumoniae]	42.7	0.002	PIN64336
Enterobacteriaceae bacterium TzEc052 [enterobacteria]			
citrate (S)-synthase, partial [Enterobacteriaceae bacterium TzEc052]	43.9	8e-04	KAE9897545
citrate (S)-synthase, partial [Enterobacteriaceae bacterium TzEc052]	43.5	0.001	KAE9897179
Escherichia coli 3-105-05_S3_C2 [enterobacteria]			
citrate synthase family protein [Escherichia coli 3-105-05_S3_C2]	43.9	0.001	KDT38988
Escherichia coli 3-475-03_S4_C1 [enterobacteria]			
citrate synthase family protein [Escherichia coli 3-475-03_S4_C1]	43.9	0.001	KDT77254
Escherichia coli O145:H28 [enterobacteria]			
citrate (S)-synthase [Escherichia coli O145:H28]	43.5	0.001	EJH5202848
Vibrio harveyi [g-proteobacteria]			
citrate synthase family protein, partial [Vibrio harveyi]	43.1	0.001	EKM31525
Bacteroides heparinolyticus [CFB group bacteria]			
citrate (S)-synthase [Bacteroides heparinolyticus]	42.7	0.001	MCF0257894
Vibrio vulnificus [g-proteobacteria]			
citrate/2-methylcitrate synthase, partial [Vibrio vulnificus]	42.7	0.001	WP_309250606
citrate (S)-synthase, partial [Vibrio vulnificus]	42.7	0.001	RAH29523
citrate (S)-synthase, partial [Vibrio vulnificus]	43.5	0.001	POF55226
Vibrio sp. FNV 38 [g-proteobacteria]			
citrate/2-methylcitrate synthase [Vibrio sp. FNV 38]	44.3	0.001	MDR9824555
Vibrio fluvialis [g-proteobacteria]			
citrate/2-methylcitrate synthase, partial [Vibrio fluvialis]	43.9	0.001	WP_275125840
citrate (S)-synthase [Vibrio fluvialis]	43.9	0.001	MCG6406930
Lutimicrobacter sp. EGI FJ00015 [a-proteobacteria]			
citrate (S)-synthase [Lutimicrobacter sp. EGI FJ00015]	44.3	0.001	MC00615641
Shigella flexneri [enterobacteria]			
citrate (S)-synthase [Shigella flexneri]	44.3	0.001	HCR7336522

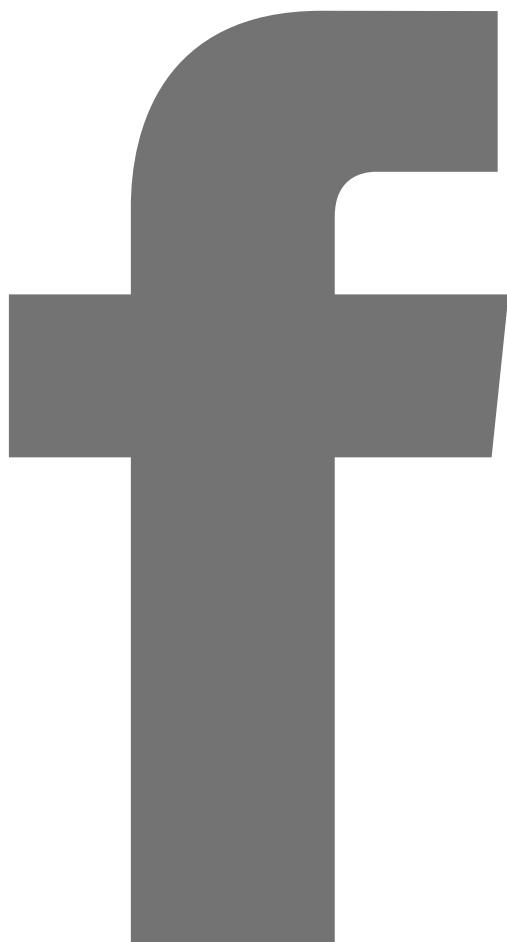
Description		Score	E value	Accession
Escherichia coli UCI 51 [enterobacteria]				
citrate synthase [Escherichia coli UCI 51]		44.3	0.002	KDG76081
Escherichia coli DEC5E [enterobacteria]				
citrate synthase domain protein [Escherichia coli DEC5E]		43.9	0.002	EHV50680
Vibrio sp. Of7-15 [g-proteobacteria]				
citrate synthase [Vibrio sp. Of7-15]		44.7	0.002	WP_239182335
citrate synthase [Vibrio sp. Of7-15]		44.7	0.002	MCG7495781
Pseudomonas aeruginosa [g-proteobacteria]				
citrate (Si)-synthase [Pseudomonas aeruginosa]		43.1	0.002	MBN0903844
Mycobacterium tuberculosis [high G+C Gram-positive bacteria]				
citrate (Si)-synthase [Mycobacterium tuberculosis]		42.0	0.002	MBX4322326
Klebsiella varicola subsp. varicola [enterobacteria]				
hypothetical protein [Klebsiella varicola subsp. varicola]		42.0	0.002	MCS5946155
Shewanella xiamensis [g-proteobacteria]				
citrate/2-methylcitrate synthase, partial [Shewanella xiamensis]		44.3	0.002	WP_279255920
citrate (Si)-synthase [Shewanella xiamensis]		44.3	0.002	MDG5902435

Taxonomy

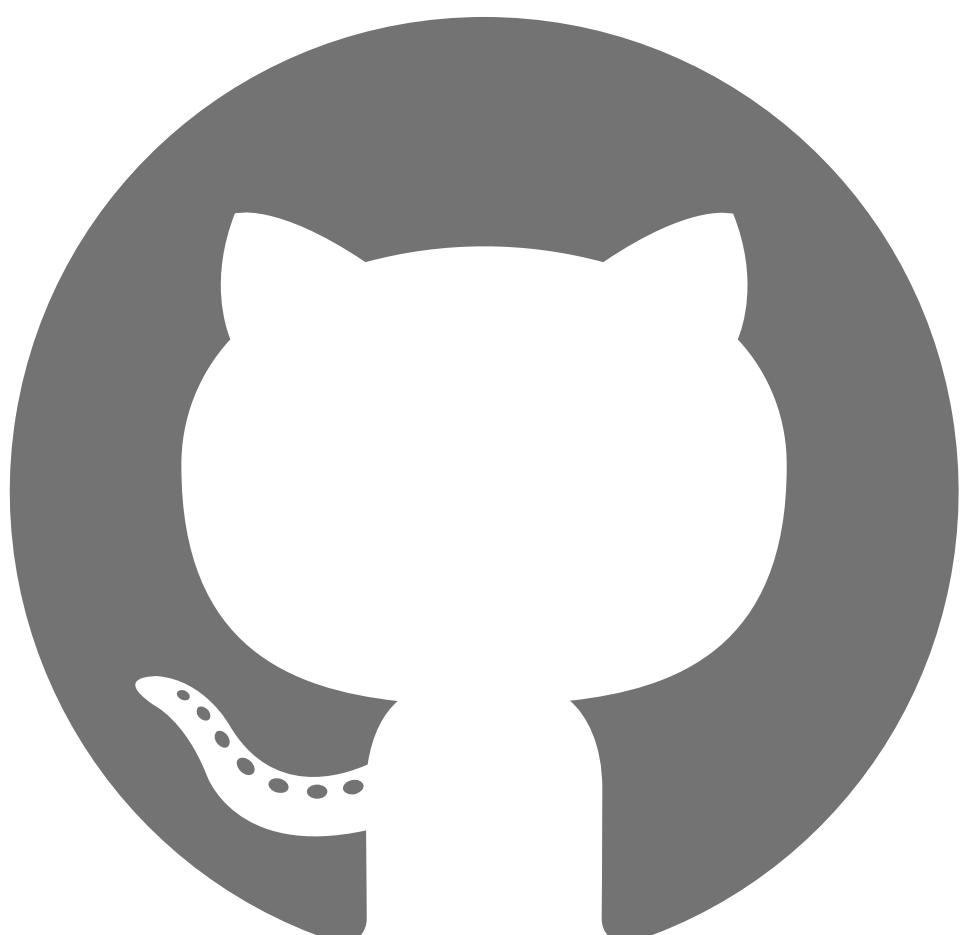
Taxonomy	Number of hits	Number of Organisms	Description
Bacteria	153	24	
. Pseudomonadota	151	22	
.. Gammaproteobacteria	150	21	
... Enterobacteriaceae	134	13	
.... Escherichia	114	7	
..... Escherichia coli	108	7	Escherichia coli hits
..... Escherichia coli DORA_A-5_14_21	1	1	Escherichia coli DORA_A-5_14_21 hits
..... Escherichia coli 3-105-05_S3_C2	1	1	Escherichia coli 3-105-05_S3_C2 hits
..... Escherichia coli 3-475-03_S4_C1	1	1	Escherichia coli 3-475-03_S4_C1 hits
..... Escherichia coli O145:H28	1	1	Escherichia coli O145:H28 hits
..... Escherichia coli UCI 51	1	1	Escherichia coli UCI 51 hits
..... Escherichia coli DEC5E	1	1	Escherichia coli DEC5E hits
.... Shigella	4	2	
.... Shigella sonnei	3	1	Shigella sonnei hits
.... Shigella flexneri	1	1	Shigella flexneri hits
.... Klebsiella	14	3	
.... Klebsiella oxytoca	2	1	Klebsiella oxytoca hits
.... Klebsiella pneumoniae	11	1	Klebsiella pneumoniae hits
.... Klebsiella variicola subsp. variicola	1	1	Klebsiella variicola subsp. variicola hits
.... Enterobacteriaceae bacterium TzEc052	2	1	Enterobacteriaceae bacterium TzEc052 hits
... Vibrio	13	6	
... Vibrio harveyi group	5	2	
.... Vibrio parahaemolyticus	4	1	Vibrio parahaemolyticus hits
.... Vibrio harveyi	1	1	Vibrio harveyi hits
.... Vibrio vulnificus	3	1	Vibrio vulnificus hits
.... unclassified Vibrio	3	2	
.... Vibrio sp. FNV 38	1	1	Vibrio sp. FNV 38 hits
.... Vibrio sp. Of7-15	2	1	Vibrio sp. Of7-15 hits
.... Vibrio fluvialis	2	1	Vibrio fluvialis hits
... Pseudomonas aeruginosa	1	1	Pseudomonas aeruginosa hits
... Shewanella xiamensis	2	1	Shewanella xiamensis hits
.. Lutimaribacter sp. EGI FJ00015	1	1	Lutimaribacter sp. EGI FJ00015 hits
. Bacteroides heparinolyticus	1	1	Bacteroides heparinolyticus hits
. Mycobacterium tuberculosis	1	1	Mycobacterium tuberculosis hits

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