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BLAST® » [blastp suite](#) » results for RID-UWS0FG8P013

Job Title	Protein Sequence ...
RID	UWS0FG8P013 Search expires on 01-23 19:31 pm
Program	BLASTP
Database	nr
Query ID	lcl Query_6700805
Description	unnamed protein product ...
Molecule type	amino acid
Query Length	34

Compare these results against the new Clustered nr database



Descriptions

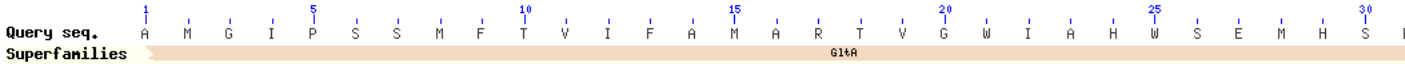
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Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
citrate/2-methylcitrate synthase [Klebsiella michiganensis]	Klebsiella michiganensis	76.6	76.6	100%	3e-16	97.06%	142	MDU4389148.1
TPA: citrate (Si)-synthase [Klebsiella oxytoca]	Klebsiella oxytoca	75.9	75.9	100%	4e-16	97.06%	121	HEC2128142.1
citrate/2-methylcitrate synthase [Klebsiella aerogenes]	Klebsiella aerogenes	76.6	76.6	100%	5e-16	97.06%	159	WP_323129656.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	9e-16	100.00%	96	MDY3720482.1
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	73.6	73.6	100%	9e-16	100.00%	76	WP_309301862.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	9e-16	100.00%	100	EIF4801338.1
citrate (Si)-synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	73.9	73.9	100%	9e-16	100.00%	78	MCL7660528.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.9	73.9	100%	9e-16	100.00%	86	WP_283571878.1
TPA: citrate (Si)-synthase [Escherichia coli]	Escherichia coli	73.9	73.9	100%	1e-15	100.00%	84	HBI9786764.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	1e-15	100.00%	94	MWR90423.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.9	73.9	100%	1e-15	100.00%	84	WP_286205966.1
citrate (Si)-synthase [Enterobacteriaceae bacterium TzEc052]	Enterobacteriaceae bacterium TzEc052	73.9	73.9	100%	1e-15	100.00%	86	KAE9897545.1
citrate (Si)-synthase [Salmonella enterica]	Salmonella enterica	75.5	75.5	100%	1e-15	94.12%	142	FAZ0641620.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	73.9	73.9	100%	1e-15	100.00%	83	MBA1933872.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	1e-15	100.00%	108	MSI35684.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	1e-15	100.00%	100	WP_322098633.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.9	73.9	100%	1e-15	100.00%	87	WP_302306452.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	1e-15	100.00%	95	WP_283570149.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	73.9	73.9	100%	1e-15	100.00%	83	MDN1366952.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	1e-15	100.00%	108	MBS8847612.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	73.6	73.6	100%	1e-15	100.00%	81	MBS8919746.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	1e-15	100.00%	101	WP_275511187.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	73.6	73.6	100%	1e-15	100.00%	78	MCO0173501.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	1e-15	100.00%	121	WP_284147049.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.6	73.6	100%	1e-15	100.00%	75	WP_284737001.1
TPA: citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	1e-15	100.00%	105	HBD5505378.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.9	73.9	100%	1e-15	100.00%	94	WP_272732384.1
citrate (Si)-synthase [Salmonella enterica subsp. enterica serovar Typhimurium]	Salmonella enterica subsp. enterica serovar Typhimurium	75.1	75.1	100%	1e-15	94.12%	138	MBZ4878239.1
citrate synthase family protein [Escherichia coli 3-105-05_S3_C2]	Escherichia coli 3-105-05_S3_C2	74.3	74.3	100%	1e-15	100.00%	109	KDT38988.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.6	73.6	100%	1e-15	100.00%	75	WP_284737003.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	1e-15	100.00%	110	EGJ6209831.1
TPA: citrate (Si)-synthase [Escherichia coli]	Escherichia coli	73.2	73.2	100%	1e-15	100.00%	72	HCN8565948.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.6	73.6	100%	1e-15	100.00%	86	WP_272881025.1
citrate (Si)-synthase [Escherichia coli O145:H28]	Escherichia coli O145:H28	73.9	73.9	100%	1e-15	100.00%	98	EJH5202848.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.2	73.2	100%	1e-15	100.00%	71	WP_284696415.1
citrate (Si)-synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	74.7	74.7	100%	1e-15	100.00%	116	TNA27598.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	1e-15	100.00%	114	WP_032236753.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.6	73.6	100%	1e-15	100.00%	77	WP_289709520.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	1e-15	100.00%	116	MBI0909235.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	73.2	73.2	100%	1e-15	100.00%	70	MDM1725847.1
citrate (Si)-synthase [Salmonella enterica subsp. enterica serovar Typhimurium]	Salmonella enterica subsp. enterica serovar Typhimurium	75.1	75.1	100%	1e-15	94.12%	135	EHR9564451.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.2	73.2	100%	1e-15	100.00%	67	WP_284693070.1
citrate (Si)-synthase [Salmonella enterica]	Salmonella enterica	75.1	75.1	100%	1e-15	94.12%	137	EAM9290843.1
TPA: citrate (Si)-synthase [Escherichia coli]	Escherichia coli	72.8	72.8	100%	2e-15	100.00%	66	HCN7185207.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	2e-15	100.00%	118	MDU7304414.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	2e-15	100.00%	114	PZT65910.1
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	72.8	72.8	100%	2e-15	100.00%	64	WP_301952173.1
citrate/2-methylcitrate synthase [uncultured Enterobacter sp.]	uncultured Enterobacter sp.	74.3	74.3	100%	2e-15	94.12%	121	WP_288462100.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	72.8	72.8	100%	2e-15	100.00%	70	MDM1725853.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	2e-15	100.00%	138	MCA8592376.1
TPA: citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	2e-15	100.00%	138	HDS4039354.1
citrate (Si)-synthase [Pseudomonas aeruginosa]	Pseudomonas aeruginosa	73.6	73.6	100%	2e-15	97.06%	95	MBN0903844.1
citrate (Si)-synthase [Bacteroides heparinolyticus]	Bacteroides heparinolyticus	72.4	72.4	100%	2e-15	100.00%	64	MCF0257894.1

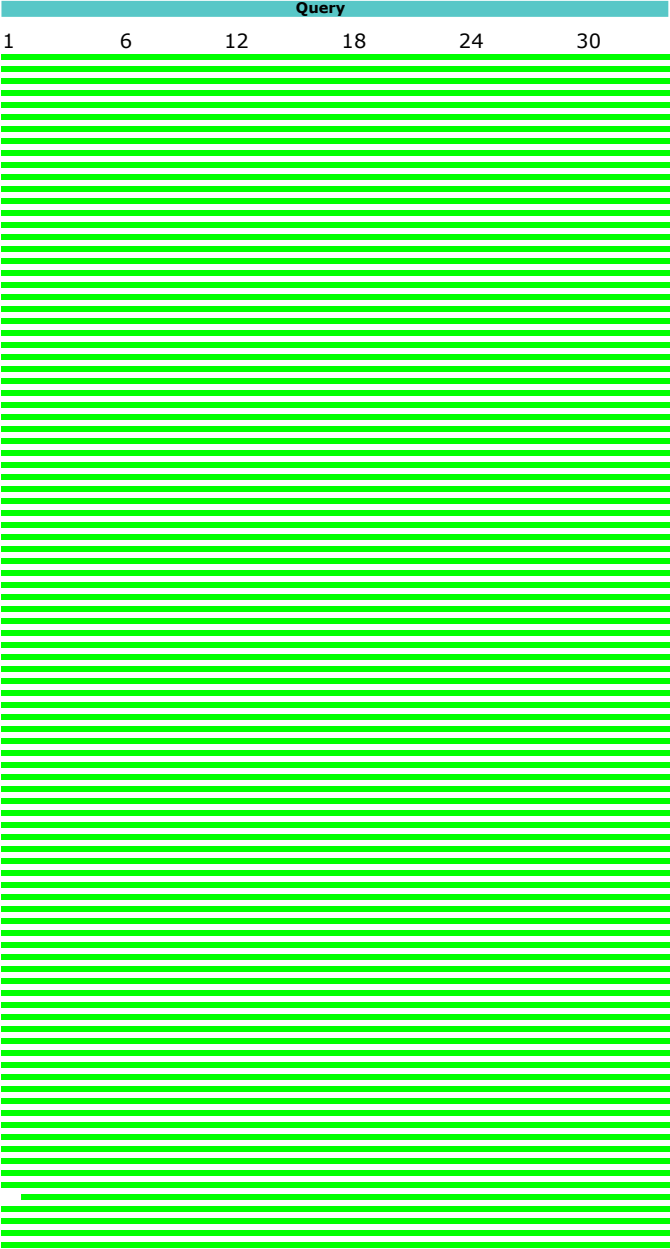
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	2e-15	100.00%	132	WP_077779533.1
TPA: citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	2e-15	100.00%	130	HDQ5165782.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	2e-15	100.00%	132	WP_289508712.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	2e-15	100.00%	130	WP_074522594.1
citrate synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	2e-15	100.00%	126	GDS03942.1
citrate/2-methylcitrate synthase [Vibrio sp. FNV 38]	Vibrio sp. FNV 38	74.7	74.7	100%	2e-15	100.00%	138	MDR9824555.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.3	74.3	100%	2e-15	100.00%	129	MBK1748728.1
citrate synthase domain protein [Escherichia coli DEC5E]	Escherichia coli DEC5E	74.3	74.3	100%	2e-15	100.00%	126	EHV50680.1
citrate (Si)-synthase [Lutimaribacter sp. EGI FJ00015]	Lutimaribacter sp. EGI FJ00015	74.7	74.7	100%	2e-15	100.00%	144	MCO0615641.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	2e-15	100.00%	146	RIB41964.1
citrate synthase [Escherichia coli UCI 51]	Escherichia coli UCI 51	74.7	74.7	100%	3e-15	100.00%	153	KDG76081.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	3e-15	100.00%	154	WP_324251799.1
citrate (Si)-synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	72.8	72.8	100%	3e-15	97.06%	81	PIN64336.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	3e-15	100.00%	157	EEZ0587125.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	3e-15	100.00%	151	WP_074466000.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	73.2	73.2	100%	3e-15	97.06%	94	WP_324251827.1
citrate/2-methylcitrate synthase [Klebsiella michiganensis]	Klebsiella michiganensis	72.4	72.4	100%	3e-15	97.06%	77	WP_308298152.1
citrate synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	3e-15	100.00%	155	STL43725.1
citrate (Si)-synthase [Pseudomonas aeruginosa]	Pseudomonas aeruginosa	73.2	73.2	100%	3e-15	97.06%	99	MBN0423480.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	3e-15	100.00%	153	EEY6517482.1
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	72.0	72.0	100%	3e-15	97.06%	58	MDU2996401.1
citrate/2-methylcitrate synthase [Pluralibacter sp.]	Pluralibacter sp.	73.2	73.2	100%	3e-15	97.06%	108	WP_293592788.1
hypothetical protein K26_27600 [Klebsiella pneumoniae]	Klebsiella pneumoniae	72.0	72.0	100%	3e-15	97.06%	63	KTG66061.1
citrate/2-methylcitrate synthase [Klebsiella quasipneumoniae]	Klebsiella quasipneumoniae	73.2	73.2	100%	3e-15	97.06%	108	WP_284025715.1
TPA: citrate (Si)-synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	73.2	73.2	100%	3e-15	97.06%	105	HBY5377556.1
citrate (Si)-synthase [Myxococcus sp. AM001]	Myxococcus sp. AM001	72.8	72.8	100%	3e-15	97.06%	89	NVJ12137.1
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	73.2	73.2	100%	3e-15	97.06%	112	WP_319792845.1
Citrate synthase (si) [Klebsiella pneumoniae]	Klebsiella pneumoniae	73.2	73.2	100%	3e-15	97.06%	109	VTM53379.1
citrate (Si)-synthase [Escherichia coli]	Escherichia coli	74.7	74.7	100%	3e-15	100.00%	164	MSH86413.1
Citrate synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	73.2	73.2	100%	4e-15	97.06%	110	VXZ87087.1
Citrate synthase (si) [Klebsiella pneumoniae subsp. rhinoscleromatis]	Klebsiella pneumoniae subsp. rhinoscleromatis	73.6	73.6	100%	4e-15	97.06%	121	STW02890.1
citrate/2-methylcitrate synthase [Shewanella xiamenensis]	Shewanella xiamenensis	74.7	74.7	100%	4e-15	100.00%	165	WP_279255920.1
Citrate synthase (si) [Klebsiella pneumoniae subsp. ozaenae]	Klebsiella pneumoniae subsp. ozaenae	73.6	73.6	100%	4e-15	97.06%	121	STV52690.1
citrate/2-methylcitrate synthase [Citrobacter sp.]	Citrobacter sp.	73.6	73.6	100%	4e-15	97.06%	122	MDU1753658.1
citrate (Si)-synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	73.2	73.2	100%	5e-15	97.06%	124	PLB95647.1
Citrate synthase (si) [Klebsiella variicola]	Klebsiella variicola	73.2	73.2	100%	5e-15	97.06%	126	STU80410.1
citrate/2-methylcitrate synthase [uncultured Citrobacter sp.]	uncultured Citrobacter sp.	72.4	72.4	100%	5e-15	94.12%	100	WP_288627250.1
Citrate synthase (si) [Klebsiella michiganensis]	Klebsiella michiganensis	73.6	73.6	100%	5e-15	97.06%	138	STR40740.1
hypothetical protein K16_05185 [Klebsiella pneumoniae]	Klebsiella pneumoniae	71.6	71.6	100%	5e-15	97.06%	74	KTG78194.1
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	Klebsiella pneumoniae	73.6	73.6	100%	5e-15	97.06%	142	WP_319951103.1
TPA: citrate (Si)-synthase [Salmonella enterica subsp. enterica serovar Infantis]	Salmonella enterica subsp. enterica serovar Infantis	71.6	71.6	100%	6e-15	94.12%	76	HCI9980600.1
citrate/2-methylcitrate synthase [Salmonella enterica]	Salmonella enterica	71.6	71.6	100%	6e-15	94.12%	73	WP_290367269.1
citrate/2-methylcitrate synthase [Escherichia coli]	Escherichia coli	71.2	71.2	97%	6e-15	100.00%	55	WP_302314285.1
hypothetical protein EIMP300_69540 [Escherichia coli]	Escherichia coli	73.9	73.9	100%	6e-15	100.00%	163	BBU85554.1
citrate (Si)-synthase [Salmonella enterica subsp. enterica serovar Enteritidis]	Salmonella enterica subsp. enterica serovar Enteritidis	72.0	72.0	100%	6e-15	94.12%	81	EDA8932280.1

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
citrate/2-methylcitrate synthase [Salmonella enterica]	Salmonella enterica	72.0	72.0	100%	6e-15	94.12%	86	WP_315942705.1
citrate synthase [Salmonella enterica subsp. enterica] [Salmonella enterica subsp. enterica serovar Menston]	Salmonella enterica subsp. enterica serovar Menston	72.4	72.4	100%	6e-15	94.12%	102	SQJ25585.1

Graphic Summary



Distribution of the top 100 Blast Hits on 100 subject sequences



Alignments

Alignment view Pairwise ☐ CDS feature Restore defaults

citrate/2-methylcitrate synthase [Klebsiella michiganensis]
Sequence ID: **MDU4389148.1** Length: 142 Number of Matches: 1
Range 1: 87 to 120

Score	Expect	Method	Identities	Positives	Gaps	Frame
76.6 bits(187)	3e-16()	Composition-based stats.	33/34(97%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	34				
Sbjct 87	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	120				

citrate (Si)-synthase [Klebsiella oxytoca]
Sequence ID: **HEC2128142.1** Length: 121 Number of Matches: 1

Range 1: 66 to 99

Score	Expect	Method	Identities	Positives	Gaps	Frame
75.9 bits(185)	4e-16()	Composition-based stats.	33/34(97%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	34			
Sbjct 66	AMGIPSSMFTVIFAMARTVGWIAHW+EMHS	SDGMK	99			

citrate/2-methylcitrate synthase, partial [Klebsiella aerogenes]
Sequence ID: **WP_323129656.1** Length: 159 Number of Matches: 1
Range 1: 104 to 137

Score	Expect	Method	Identities	Positives	Gaps	Frame
76.6 bits(187)	5e-16()	Composition-based stats.	33/34(97%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	34			
Sbjct 104	AMGIPSSMFTVIFAMARTVGWIAHW+EMHS	SDGMK	137			

citrate/2-methylcitrate synthase [Escherichia coli]
Sequence ID: **MDY3720482.1** Length: 96 Number of Matches: 1
Range 1: 41 to 74

Score	Expect	Method	Identities	Positives	Gaps	Frame
74.3 bits(181)	9e-16()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	34			
Sbjct 41	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	74			

citrate/2-methylcitrate synthase, partial [Klebsiella pneumoniae]
Sequence ID: **WP_309301862.1** Length: 76 Number of Matches: 1
Range 1: 20 to 53

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.6 bits(179)	9e-16()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	34			
Sbjct 20	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	53			

citrate (Si)-synthase [Escherichia coli]
Sequence ID: **EIF4801338.1** Length: 100 Number of Matches: 1
Range 1: 45 to 78

Score	Expect	Method	Identities	Positives	Gaps	Frame
74.3 bits(181)	9e-16()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	34			
Sbjct 45	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	78			

citrate (Si)-synthase [Klebsiella pneumoniae]
Sequence ID: **MCL7660528.1** Length: 78 Number of Matches: 1
Range 1: 36 to 69

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.9 bits(180)	9e-16()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	34			
Sbjct 36	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	69			

citrate/2-methylcitrate synthase, partial [Escherichia coli]
Sequence ID: **WP_283571878.1** Length: 86 Number of Matches: 1
Range 1: 31 to 64

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.9 bits(180)	9e-16()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	34			
Sbjct 31	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	SDGMK	64			

citrate (Si)-synthase [Escherichia coli]
Sequence ID: **HBI9786764.1** Length: 84 Number of Matches: 1
Range 1: 29 to 62

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.9 bits(180)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	

Query 1 AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK 34
Sbjct 29 AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK 62

citrate (Si)-synthase [Escherichia coli]
Sequence ID: **MWR90423.1** Length: 94 Number of Matches: 1
Range 1: 39 to 72

Score	Expect	Method	Identities	Positives	Gaps	Frame
74.3 bits(181)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	34				
Sbjct 39	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	72				

citrate/2-methylcitrate synthase, partial [Escherichia coli]
Sequence ID: **WP_286205966.1** Length: 84 Number of Matches: 1
Range 1: 29 to 62

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.9 bits(180)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	34				
Sbjct 29	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	62				

citrate (Si)-synthase, partial [Enterobacteriaceae bacterium TzEc052]
Sequence ID: **KAE9897545.1** Length: 86 Number of Matches: 1
Range 1: 31 to 64

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.9 bits(180)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	34				
Sbjct 31	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	64				

citrate (Si)-synthase [Salmonella enterica]
Sequence ID: **EAZ0641620.1** Length: 142 Number of Matches: 1
Range 1: 87 to 120

Score	Expect	Method	Identities	Positives	Gaps	Frame
75.5 bits(184)	1e-15()	Composition-based stats.	32/34(94%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	34				
Sbjct 87	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	120				

citrate (Si)-synthase [Escherichia coli]
Sequence ID: **MBA1933872.1** Length: 83 Number of Matches: 1
Range 1: 28 to 61

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.9 bits(180)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	34				
Sbjct 28	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	61				

citrate (Si)-synthase [Escherichia coli]
Sequence ID: **MSI35684.1** Length: 108 Number of Matches: 1
Range 1: 53 to 86

Score	Expect	Method	Identities	Positives	Gaps	Frame
74.7 bits(182)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	34				
Sbjct 53	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	86				

citrate/2-methylcitrate synthase, partial [Escherichia coli]
Sequence ID: **WP_322098633.1** Length: 100 Number of Matches: 1
Range 1: 45 to 78

Score	Expect	Method	Identities	Positives	Gaps	Frame
74.3 bits(181)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	34				
Sbjct 45	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS DGMK	78				

citrate/2-methylcitrate synthase, partial [Escherichia coli]
Sequence ID: **WP_302306452.1** Length: 87 Number of Matches: 1
Range 1: 32 to 65

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.9 bits(180)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	DKMK	34			
Sbjct 32	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	DKMK	65			

citrate/2-methylcitrate synthase, partial [Escherichia coli]
Sequence ID: **WP_283570149.1** Length: 95 Number of Matches: 1
Range 1: 40 to 73

Score	Expect	Method	Identities	Positives	Gaps	Frame
74.3 bits(181)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	DKMK	34			
Sbjct 40	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	DKMK	73			

citrate (Si)-synthase [Escherichia coli]
Sequence ID: **MDN1366952.1** Length: 83 Number of Matches: 1
Range 1: 28 to 61

Score	Expect	Method	Identities	Positives	Gaps	Frame
73.9 bits(180)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	DKMK	34			
Sbjct 28	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	DKMK	61			

citrate (Si)-synthase [Escherichia coli]
Sequence ID: **MBS8847612.1** Length: 108 Number of Matches: 1
Range 1: 53 to 86

Score	Expect	Method	Identities	Positives	Gaps	Frame
74.3 bits(181)	1e-15()	Compositional matrix adjust.	34/34(100%)	34/34(100%)	0/34(0%)	
Query 1	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	DKMK	34			
Sbjct 53	AMGIPSSMFTVIFAMARTVGWIAHWSEMHS	DKMK	86			

Taxonomy

Reports

◦ Lineage

Organism	Blast Name	Score	Number of Hits	Description
Bacteria	bacteria		143	
.Pseudomonadota	proteobacteria		141	
..Gammaproteobacteria	g-proteobacteria		140	
...Enterobacteriaceae	enterobacteria		135	
....Klebsiella	enterobacteria		28	
.....Klebsiella michiganensis	enterobacteria	76.6	4	Klebsiella michiganensis hits
.....Klebsiella oxytoca	enterobacteria	75.9	1	Klebsiella oxytoca hits
.....Klebsiella aerogenes	enterobacteria	76.6	1	Klebsiella aerogenes hits
.....Klebsiella pneumoniae	enterobacteria	73.6	17	Klebsiella pneumoniae hits
.....Klebsiella quasipneumoniae	enterobacteria	73.2	2	Klebsiella quasipneumoniae hits
.....Klebsiella pneumoniae subsp. rhinoscleromatis	enterobacteria	73.6	1	Klebsiella pneumoniae subsp. rhinoscleromatis hits
.....Klebsiella pneumoniae subsp. ozaenae	enterobacteria	73.6	1	Klebsiella pneumoniae subsp. ozaenae hits
.....Klebsiella varicola	enterobacteria	73.2	1	Klebsiella varicola hits
....Escherichia coli	enterobacteria	74.3	84	Escherichia coli hits
...Enterobacteriaceae bacterium TzEc052	enterobacteria	73.9	2	Enterobacteriaceae bacterium TzEc052 hits
...Salmonella enterica	enterobacteria	75.5	4	Salmonella enterica hits
...Salmonella enterica subsp. enterica serovar Typhimurium	enterobacteria	75.1	2	Salmonella enterica subsp. enterica serovar Typhimurium hits
...Escherichia coli 3-105-05_S3_C2	enterobacteria	74.3	1	Escherichia coli 3-105-05_S3_C2 hits
...Escherichia coli 3-475-03_S4_C1	enterobacteria	74.3	1	Escherichia coli 3-475-03_S4_C1 hits
...Escherichia coli O145:H28	enterobacteria	73.9	1	Escherichia coli O145:H28 hits
...uncultured Enterobacter sp.	enterobacteria	74.3	1	uncultured Enterobacter sp. hits
...Escherichia coli DEC5E	enterobacteria	74.3	1	Escherichia coli DEC5E hits
...Shigella flexneri	enterobacteria	74.7	1	Shigella flexneri hits
...Escherichia coli UCI 51	enterobacteria	74.7	1	Escherichia coli UCI 51 hits

.... Pluralibacter sp.	enterobacteria	73.2	2	Pluralibacter sp. hits
.... Citrobacter sp.	enterobacteria	73.6	1	Citrobacter sp. hits
.... uncultured Citrobacter sp.	enterobacteria	72.4	1	uncultured Citrobacter sp. hits
.... Salmonella enterica subsp. enterica serovar Infantis	enterobacteria	71.6	1	Salmonella enterica subsp. enterica serovar Infantis hits
.... Salmonella enterica subsp. enterica serovar 4,[5],12:i:-	enterobacteria	71.6	1	Salmonella enterica subsp. enterica serovar 4,[5],12:i:- hits
.... Salmonella enterica subsp. enterica serovar Enteritidis	enterobacteria	72.0	1	Salmonella enterica subsp. enterica serovar Enteritidis hits
.... Salmonella enterica subsp. enterica serovar Menston	enterobacteria	72.4	1	Salmonella enterica subsp. enterica serovar Menston hits
... Pseudomonas aeruginosa	g-proteobacteria	73.6	2	Pseudomonas aeruginosa hits
... Vibrio sp. FNV 38	g-proteobacteria	74.7	1	Vibrio sp. FNV 38 hits
... Shewanella xiamenensis	g-proteobacteria	74.7	2	Shewanella xiamenensis hits
.. Lutimaribacter sp. EGI FJ00015	a-proteobacteria	74.7	1	Lutimaribacter sp. EGI FJ00015 hits
.. Bacteroides heparinolyticus	CFB group bacteria	72.4	1	Bacteroides heparinolyticus hits
.. Myxococcus sp. AM001	bacteria	72.8	1	Myxococcus sp. AM001 hits

o Organism

Description	Score	E value	Accession
Klebsiella michiganensis [enterobacteria]			
citrate/2-methylcitrate synthase [Klebsiella michiganensis]	76.6	3e-16	MDU4389148
citrate/2-methylcitrate synthase, partial [Klebsiella michiganensis]	72.4	3e-15	WP_308298152
citrate (Si)-synthase, partial [Klebsiella michiganensis]	72.4	3e-15	PLN97258
Citrate synthase (si) [Klebsiella michiganensis]	73.6	5e-15	STR40740
Klebsiella oxytoca [enterobacteria]			
citrate (Si)-synthase [Klebsiella oxytoca]	75.9	4e-16	HEC2128142
Klebsiella aerogenes [enterobacteria]			
citrate/2-methylcitrate synthase, partial [Klebsiella aerogenes]	76.6	5e-16	WP_323129656
Escherichia coli [enterobacteria]			
citrate/2-methylcitrate synthase [Escherichia coli]	74.3	9e-16	MDY3720482
citrate (Si)-synthase [Escherichia coli]	74.3	9e-16	EIF4801338
citrate (Si)-synthase [Escherichia coli]	74.3	9e-16	EIO7639400
citrate (Si)-synthase [Escherichia coli]	74.3	9e-16	HDI5885905
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.9	9e-16	WP_283571878
citrate (Si)-synthase [Escherichia coli]	73.9	1e-15	HBI9786764
citrate (Si)-synthase [Escherichia coli]	74.3	1e-15	MWR90423
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.9	1e-15	WP_286205966
citrate (Si)-synthase [Escherichia coli]	73.9	1e-15	MWQ98706
citrate (Si)-synthase [Escherichia coli]	73.9	1e-15	MBA1933872
citrate (Si)-synthase [Escherichia coli]	74.7	1e-15	MSI35684
citrate/2-methylcitrate synthase, partial [Escherichia coli]	74.3	1e-15	WP_322098633
citrate (Si)-synthase [Escherichia coli]	74.3	1e-15	MCF4025416
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.9	1e-15	WP_302306452
citrate/2-methylcitrate synthase [Escherichia coli]	73.9	1e-15	MDO2792760
citrate synthase [Escherichia coli]	73.9	1e-15	VED36794
citrate/2-methylcitrate synthase, partial [Escherichia coli]	74.3	1e-15	WP_283570149
citrate (Si)-synthase [Escherichia coli]	73.9	1e-15	MDN1366952
citrate (Si)-synthase [Escherichia coli]	74.3	1e-15	MBS8847612
citrate (Si)-synthase [Escherichia coli]	73.6	1e-15	MBS8919746
citrate/2-methylcitrate synthase, partial [Escherichia coli]	74.3	1e-15	WP_275511187
citrate (Si)-synthase [Escherichia coli]	73.6	1e-15	MCO0173501
citrate/2-methylcitrate synthase, partial [Escherichia coli]	74.7	1e-15	WP_284147049
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.6	1e-15	WP_284737001
citrate (Si)-synthase [Escherichia coli]	73.6	1e-15	MBA2037725
citrate (Si)-synthase [Escherichia coli]	74.3	1e-15	HBD5505378
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.9	1e-15	WP_272732384
citrate (Si)-synthase [Escherichia coli]	73.9	1e-15	HCY92746
citrate synthase [Escherichia coli]	74.3	1e-15	VED13032
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.6	1e-15	WP_284737003
citrate (Si)-synthase [Escherichia coli]	73.6	1e-15	MBA2041438
citrate (Si)-synthase [Escherichia coli]	74.3	1e-15	EGJ6209831
citrate (Si)-synthase [Escherichia coli]	73.2	1e-15	HCN8565948
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.6	1e-15	WP_272881025
citrate (Si)-synthase [Escherichia coli]	73.6	1e-15	MCF6615264
citrate (Si)-synthase [Escherichia coli]	73.6	1e-15	MWQ97432
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.2	1e-15	WP_284696415

Description	Score	E value	Accession
citrate (Si)-synthase [Escherichia coli]	73.2	1e-15	MBF7986016
citrate (Si)-synthase [Escherichia coli]	73.2	1e-15	MWM20870
citrate (Si)-synthase [Escherichia coli]	73.2	1e-15	MWR75286
citrate (Si)-synthase [Escherichia coli]	73.2	1e-15	MWT26135
citrate (Si)-synthase [Escherichia coli]	73.2	1e-15	MXJ13823
citrate/2-methylcitrate synthase, partial [Escherichia coli]	74.3	1e-15	WP_032236753
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.6	1e-15	WP_289709520
citrate (Si)-synthase [Escherichia coli]	73.6	1e-15	MBA1884166
citrate (Si)-synthase [Escherichia coli]	74.3	1e-15	MBI0909235
citrate (Si)-synthase [Escherichia coli]	73.2	1e-15	MDM1725847
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.2	1e-15	WP_284693070
citrate (Si)-synthase, partial [Escherichia coli]	73.2	1e-15	KAE9718461
citrate (Si)-synthase [Escherichia coli]	72.8	2e-15	HCN7185207
citrate/2-methylcitrate synthase [Escherichia coli]	74.3	2e-15	MDU7304414
citrate (Si)-synthase, partial [Escherichia coli]	74.3	2e-15	PZT65910
citrate (Si)-synthase [Escherichia coli]	72.8	2e-15	MDM1725853
citrate (Si)-synthase [Escherichia coli]	74.7	2e-15	MCA8592376
citrate (Si)-synthase [Escherichia coli]	74.7	2e-15	HDS4039354
citrate/2-methylcitrate synthase, partial [Escherichia coli]	74.3	2e-15	WP_077779533
citrate (Si)-synthase [Escherichia coli]	74.3	2e-15	HDQ5165782
citrate/2-methylcitrate synthase, partial [Escherichia coli]	74.3	2e-15	WP_289508712
citrate/2-methylcitrate synthase, partial [Escherichia coli]	74.3	2e-15	WP_074522594
citrate (Si)-synthase [Escherichia coli]	74.3	2e-15	MCJ8623990
citrate synthase, partial [Escherichia coli]	74.3	2e-15	OKU52881
citrate (Si)-synthase [Escherichia coli]	74.3	2e-15	HBB7874832
citrate synthase [Escherichia coli]	74.3	2e-15	GDS03942
citrate synthase [Escherichia coli]	74.3	2e-15	STJ45176
citrate (Si)-synthase [Escherichia coli]	74.3	2e-15	MBK1748728
citrate (Si)-synthase [Escherichia coli]	74.3	2e-15	MBL1016225
citrate (Si)-synthase [Escherichia coli]	74.3	2e-15	MBL1036152
citrate synthase [Escherichia coli]	74.3	2e-15	VDZ04469
citrate (Si)-synthase [Escherichia coli]	74.7	2e-15	MCU8644358
citrate (Si)-synthase, partial [Escherichia coli]	74.7	2e-15	RIB41964
citrate (Si)-synthase [Escherichia coli]	74.7	2e-15	HDK0967306
citrate/2-methylcitrate synthase, partial [Escherichia coli]	74.7	3e-15	WP_324251799
citrate (Si)-synthase [Escherichia coli]	74.7	3e-15	MCC7986975
citrate (Si)-synthase [Escherichia coli]	74.7	3e-15	EEZ0587125
citrate/2-methylcitrate synthase, partial [Escherichia coli]	74.7	3e-15	WP_074466000
citrate/2-methylcitrate synthase, partial [Escherichia coli]	73.2	3e-15	WP_324251827
citrate (Si)-synthase [Escherichia coli]	73.2	3e-15	MCC7989130
citrate synthase [Escherichia coli]	74.7	3e-15	STL43725
citrate (Si)-synthase [Escherichia coli]	74.7	3e-15	EEY6517482
citrate (Si)-synthase [Escherichia coli]	74.7	3e-15	MSH86413
citrate/2-methylcitrate synthase, partial [Escherichia coli]	71.2	6e-15	WP_302314285
citrate/2-methylcitrate synthase [Escherichia coli]	71.2	6e-15	MDO2838954
hypothetical protein MUTS15_21620 [Escherichia coli]	71.2	6e-15	BDY93505
hypothetical protein EIMP300_69540 [Escherichia coli]	73.9	6e-15	BBU85554
Klebsiella pneumoniae [enterobacteria]			
citrate/2-methylcitrate synthase, partial [Klebsiella pneumoniae]	73.6	9e-16	WP_309301862
citrate (Si)-synthase, partial [Klebsiella pneumoniae]	73.6	9e-16	RBN11767
citrate (Si)-synthase [Klebsiella pneumoniae]	73.9	9e-16	MCL7660528
citrate (Si)-synthase, partial [Klebsiella pneumoniae]	74.7	1e-15	TNA27598
citrate/2-methylcitrate synthase, partial [Klebsiella pneumoniae]	72.8	2e-15	WP_301952173
citrate (Si)-synthase [Klebsiella pneumoniae]	72.8	2e-15	NDR82707
citrate (Si)-synthase, partial [Klebsiella pneumoniae]	72.8	3e-15	PIN64336
citrate/2-methylcitrate synthase [Klebsiella pneumoniae]	72.0	3e-15	MDU2996401
hypothetical protein K26_27600, partial [Klebsiella pneumoniae]	72.0	3e-15	KTG66061
citrate (Si)-synthase [Klebsiella pneumoniae]	73.2	3e-15	HBY5377556
citrate/2-methylcitrate synthase, partial [Klebsiella pneumoniae]	73.2	3e-15	WP_319792845
citrate (Si)-synthase, partial [Klebsiella pneumoniae]	73.2	3e-15	KAB7893513
Citrate synthase (si) [Klebsiella pneumoniae]	73.2	3e-15	VTM53379
Citrate synthase [Klebsiella pneumoniae]	73.2	4e-15	VXZ87087

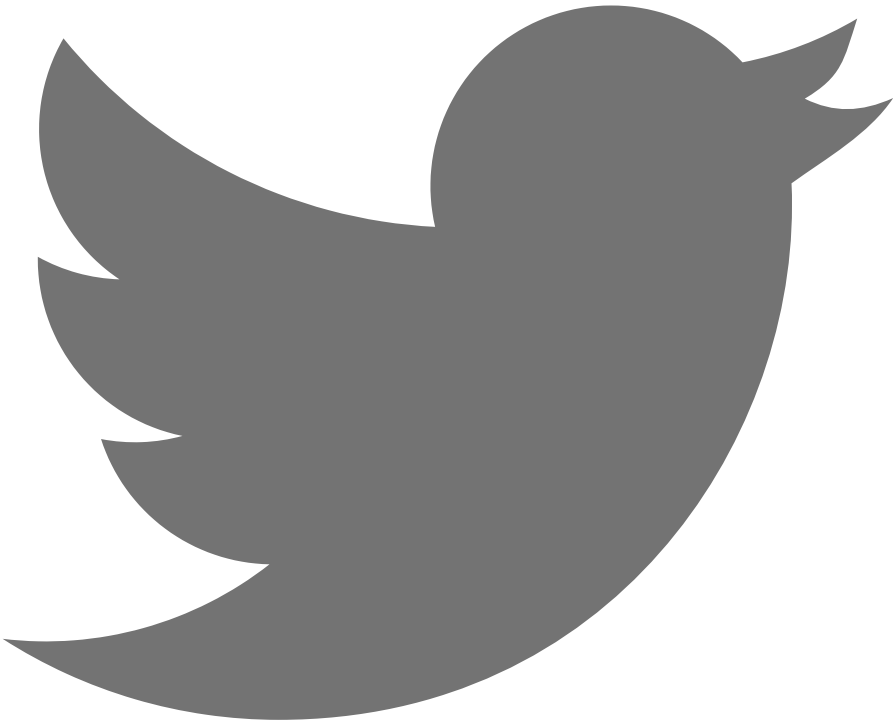
Description	Score	E value	Accession
citrate (Si)-synthase,partial [Klebsiella pneumoniae]	73.2	5e-15	PLB95647
hypothetical protein K16_05185,partial [Klebsiella pneumoniae]	71.6	5e-15	KTG78194
citrate/2-methylcitrate synthase,partial [Klebsiella pneumoniae]	73.6	5e-15	WP_319951103
Enterobacteriaceae bacterium TzEc052 [enterobacteria]			
citrate (Si)-synthase,partial [Enterobacteriaceae bacterium TzEc052]	73.9	1e-15	KAE9897545
citrate (Si)-synthase,partial [Enterobacteriaceae bacterium TzEc052]	73.6	1e-15	KAE9897179
Salmonella enterica [enterobacteria]			
citrate (Si)-synthase [Salmonella enterica]	75.5	1e-15	FAZ0641620
citrate (Si)-synthase [Salmonella enterica]	75.1	1e-15	FAM9290843
citrate/2-methylcitrate synthase,partial [Salmonella enterica]	71.6	6e-15	WP_290367269
citrate/2-methylcitrate synthase,partial [Salmonella enterica]	72.0	6e-15	WP_315942705
Salmonella enterica subsp. enterica serovar Typhimurium [enterobacteria]			
citrate (Si)-synthase [Salmonella enterica subsp. enterica serovar Typhimurium]	75.1	1e-15	MBZ4878239
citrate (Si)-synthase [Salmonella enterica subsp. enterica serovar Typhimurium]	75.1	1e-15	EHR9564451
Escherichia coli 3-105-05_S3_C2 [enterobacteria]			
citrate synthase family,protein [Escherichia coli 3-105-05_S3_C2]	74.3	1e-15	KDT38988
Escherichia coli 3-475-03_S4_C1 [enterobacteria]			
citrate synthase family,protein [Escherichia coli 3-475-03_S4_C1]	74.3	1e-15	KDT77254
Escherichia coli O145:H28 [enterobacteria]			
citrate (Si)-synthase [Escherichia coli O145:H28]	73.9	1e-15	EJH5202848
uncultured Enterobacter sp. [enterobacteria]			
citrate/2-methylcitrate synthase,partial [uncultured Enterobacter sp.]	74.3	2e-15	WP_288462100
Pseudomonas aeruginosa [g-proteobacteria]			
citrate (Si)-synthase [Pseudomonas aeruginosa]	73.6	2e-15	MBN0903844
citrate (Si)-synthase [Pseudomonas aeruginosa]	73.2	3e-15	MBN0423480
Bacteroides heparinolyticus [CFB group bacteria]			
citrate (Si)-synthase [Bacteroides heparinolyticus]	72.4	2e-15	MCF0257894
Vibrio sp. FNV 38 [g-proteobacteria]			
citrate/2-methylcitrate synthase [Vibrio sp. FNV 38]	74.7	2e-15	MDR9824555
Escherichia coli DEC5E [enterobacteria]			
citrate synthase domain protein [Escherichia coli DEC5E]	74.3	2e-15	EHV50680
Lutimaribacter sp. EGI FJ00015 [a-proteobacteria]			
citrate (Si)-synthase [Lutimaribacter sp. EGI FJ00015]	74.7	2e-15	MCO0615641
Shigella flexneri [enterobacteria]			
citrate (Si)-synthase [Shigella flexneri]	74.7	2e-15	HCR7336522
Escherichia coli UCI 51 [enterobacteria]			
citrate synthase [Escherichia coli UCI 51]	74.7	3e-15	KDG76081
Pluralibacter sp. [enterobacteria]			
citrate/2-methylcitrate synthase,partial [Pluralibacter sp.]	73.2	3e-15	WP_293592788
citrate (Si)-synthase [Pluralibacter sp.]	73.2	3e-15	MBV8043537
Klebsiella quasipneumoniae [enterobacteria]			
citrate/2-methylcitrate synthase,partial [Klebsiella quasipneumoniae]	73.2	3e-15	WP_284025715
citrate/2-methylcitrate synthase [Klebsiella quasipneumoniae]	73.2	3e-15	MDK1365021
Myxococcus sp. AM001 [bacteria]			
citrate (Si)-synthase [Myxococcus sp. AM001]	72.8	3e-15	NVJ12137
Klebsiella pneumoniae subsp. rhinoscleromatis [enterobacteria]			
Citrate synthase (si) [Klebsiella pneumoniae subsp. rhinoscleromatis]	73.6	4e-15	STW02890
Shewanella xiamenensis [g-proteobacteria]			
citrate/2-methylcitrate synthase,partial [Shewanella xiamenensis]	74.7	4e-15	WP_279255920
citrate (Si)-synthase [Shewanella xiamenensis]	74.7	4e-15	MDG5902435
Klebsiella pneumoniae subsp. ozaenae [enterobacteria]			
Citrate synthase (si) [Klebsiella pneumoniae subsp. ozaenae]	73.6	4e-15	STV52690
Citrobacter sp. [enterobacteria]			
citrate/2-methylcitrate synthase [Citrobacter sp.]	73.6	4e-15	MDU1753658
Klebsiella variicola [enterobacteria]			
Citrate synthase (si) [Klebsiella variicola]	73.2	5e-15	STU80410
uncultured Citrobacter sp. [enterobacteria]			
citrate/2-methylcitrate synthase,partial [uncultured Citrobacter sp.]	72.4	5e-15	WP_288627250
Salmonella enterica subsp. enterica serovar Infantis [enterobacteria]			
citrate (Si)-synthase [Salmonella enterica subsp. enterica serovar Infantis]	71.6	6e-15	HCI9980600
Salmonella enterica subsp. enterica serovar 4,[5],12:i:- [enterobacteria]			
type II citrate synthase,partial [Salmonella enterica subsp. enterica serovar 4,[5],12:i:-]	71.6	6e-15	KUA64007

Description	Score	E value	Accession
Salmonella enterica subsp. enterica serovar Enteritidis [enterobacteria]			
citrate (Si)-synthase [Salmonella enterica subsp. enterica serovar Enteritidis]	72.0	6e-15	EDA8932280
Salmonella enterica subsp. enterica serovar Menston [enterobacteria]			
citrate synthase [Salmonella enterica subsp. enterica] [Salmonella enterica subsp. enterica serovar Menston]	72.4	6e-15	SQJ25585

o **Taxonomy**

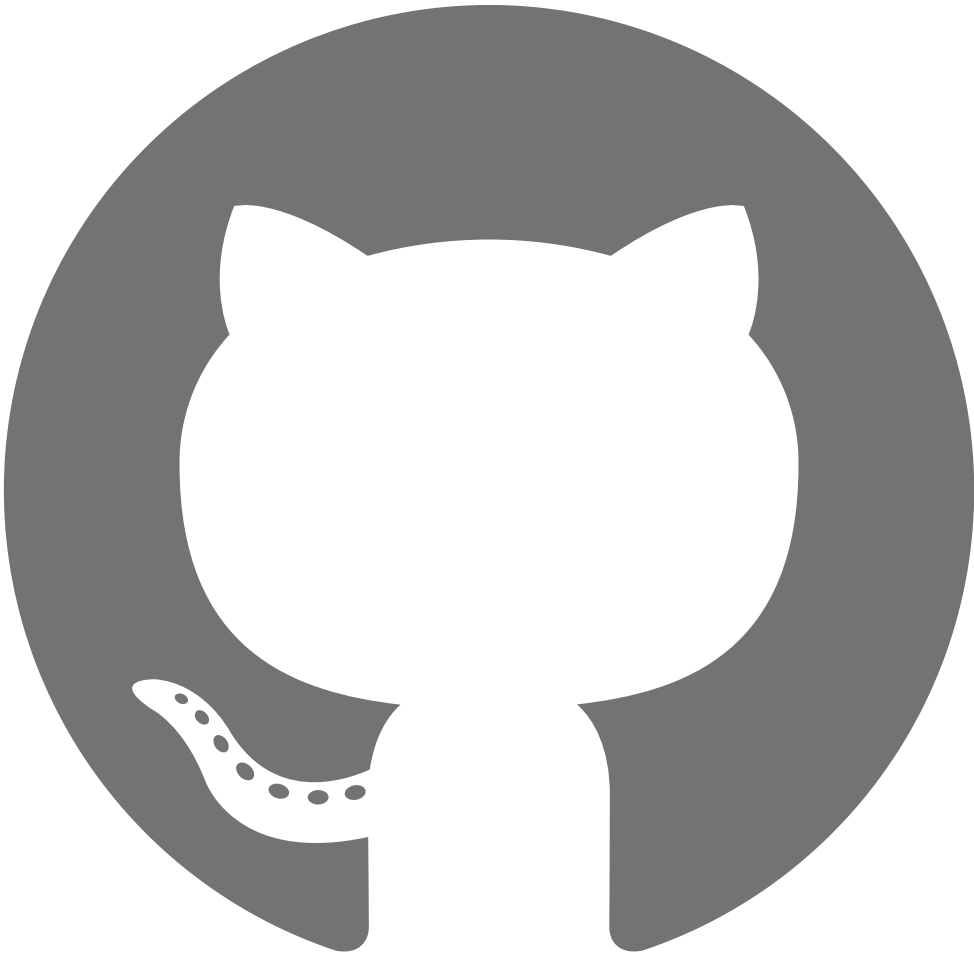
Taxonomy	Number of hits	Number of Organisms	Description
Bacteria	143	32	
. Pseudomonadota	141	30	
.. Gammaproteobacteria	140	29	
... Enterobacteriaceae	135	26	
.... Klebsiella	28	8	
..... Klebsiella michiganensis	4	1	Klebsiella michiganensis hits
..... Klebsiella oxytoca	1	1	Klebsiella oxytoca hits
..... Klebsiella aerogenes	1	1	Klebsiella aerogenes hits
..... Klebsiella pneumoniae	17	3	Klebsiella pneumoniae hits
..... Klebsiella pneumoniae subsp. rhinoscleromatis	1	1	Klebsiella pneumoniae subsp. rhinoscleromatis hits
..... Klebsiella pneumoniae subsp. ozaenae	1	1	Klebsiella pneumoniae subsp. ozaenae hits
..... Klebsiella quasipneumoniae	2	1	Klebsiella quasipneumoniae hits
..... Klebsiella variicola	1	1	Klebsiella variicola hits
.... Escherichia	89	6	
..... Escherichia coli	84	6	Escherichia coli 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 DEC5E	1	1	Escherichia coli DEC5E hits
..... Escherichia coli UCI 51	1	1	Escherichia coli UCI 51 hits
.... Enterobacteriaceae bacterium TzEc052	2	1	Enterobacteriaceae bacterium TzEc052 hits
... Salmonella	10	6	
..... Salmonella enterica	4	6	Salmonella enterica hits
..... Salmonella enterica subsp. enterica	6	5	
..... Salmonella enterica subsp. enterica serovar Typhimurium	2	1	Salmonella enterica subsp. enterica serovar Typhimurium hits
..... Salmonella enterica subsp. enterica serovar Infantis	1	1	Salmonella enterica subsp. enterica serovar Infantis hits
..... Salmonella enterica subsp. enterica serovar 4,[5],12:i:-	1	1	Salmonella enterica subsp. enterica serovar 4,[5],12:i:- hits
..... Salmonella enterica subsp. enterica serovar Enteritidis	1	1	Salmonella enterica subsp. enterica serovar Enteritidis hits
..... Salmonella enterica subsp. enterica serovar Menston	1	1	Salmonella enterica subsp. enterica serovar Menston hits
.... uncultured Enterobacter sp.	1	1	uncultured Enterobacter sp. hits
.... Shigella flexneri	1	1	Shigella flexneri hits
.... Pluralibacter sp.	2	1	Pluralibacter sp. hits
.... Citrobacter	2	2	
..... Citrobacter sp.	1	1	Citrobacter sp. hits
..... uncultured Citrobacter sp.	1	1	uncultured Citrobacter sp. hits
... Pseudomonas aeruginosa	2	1	Pseudomonas aeruginosa hits
.. Vibrio sp. FNV 38	1	1	Vibrio sp. FNV 38 hits
.. Shewanella xiamenensis	2	1	Shewanella xiamenensis hits
.. Lutimaribacter sp. EGI FJ00015	1	1	Lutimaribacter sp. EGI FJ00015 hits
. Bacteroides heparinolyticus	1	1	Bacteroides heparinolyticus hits
. Myxococcus sp. AM001	1	1	Myxococcus sp. AM001 hits

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