BLAST ®

Basic Local Alignment Search Tool

NCBI/ BLAST/ Microbes/ **Formatting Results - 0V0XK1R5015**
Formatting options
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Blast report description

Protein Sequence (27 letters)

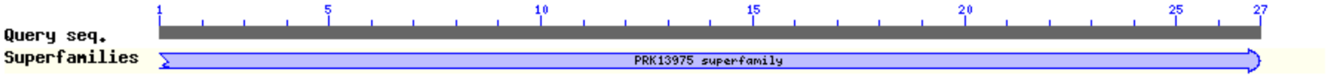
RID 0V0XK1R5015 (Expires on 09-09 18:23 pm)

Query ID lcl|71609
Description None
Molecule type amino acid
Query Length 27

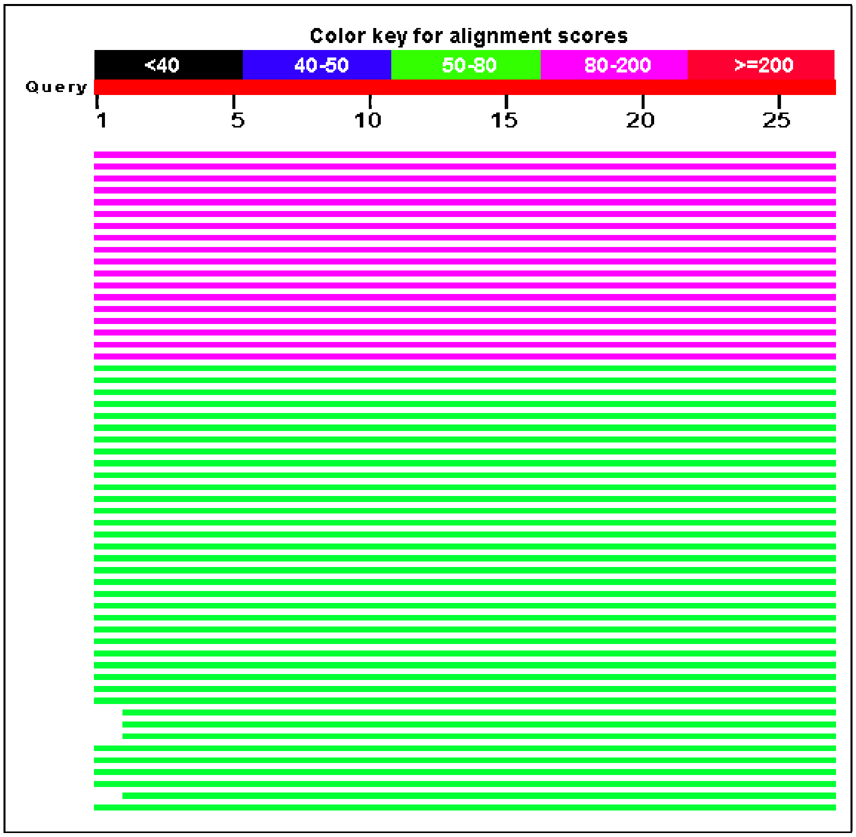
Database Name Microbial proteins
Description
ProgramBLASTP 2.2.29+

Graphic Summary

Putative conserved domains have been detected, click on the image below for detailed results.



Distribution of 100 Blast Hits on the Query Sequence



Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
thymidylate kinase Tmk [Mycobacterium tuberculosis UT0124]	90.1	90.1	100%	5e-20	100%	KBM28427.1
thymidylate kinase [Mycobacterium tuberculosis]	90.1	90.1	100%	3e-19	100%	AIH62975.1
thymidylate kinase [Mycobacterium tuberculosis]	90.1	90.1	100%	3e-19	100%	AIH98343.1
thymidylate kinase [Mycobacterium bovis]	90.1	90.1	100%	3e-19	100%	WP_024459054.1
thymidylate kinase [Mycobacterium tuberculosis]	90.1	90.1	100%	4e-19	100%	AIH23782.1
thymidylate kinase [Mycobacterium tuberculosis]	90.1	90.1	100%	4e-19	100%	WP_003904223.1
thymidylate kinase Tmk [Mycobacterium tuberculosis BTB11-133]	90.1	90.1	100%	4e-19	100%	KCQ37814.1
thymidylate kinase Tmk [Mycobacterium tuberculosis BTB07-206]	90.1	90.1	100%	4e-19	100%	KCN91622.1
thymidylate kinase Tmk [Mycobacterium tuberculosis M1520]	90.1	90.1	100%	4e-19	100%	KBA42335.1
thymidylate kinase Tmk [Mycobacterium tuberculosis M1461]	90.1	90.1	100%	4e-19	100%	KBA29358.1
thymidylate kinase Tmk [Mycobacterium tuberculosis M1417]	90.1	90.1	100%	4e-19	100%	KAZ51277.1
MULTISPECIES: thymidylate kinase [Mycobacterium tuberculosis complex]	90.1	90.1	100%	4e-19	100%	WP_003417036.1
Putative thymidylate kinase TmK (dTMP kinase) (thymidylic acid kinase) (TMPK) [Mycobacterium canettii]	90.1	90.1	100%	4e-19	100%	WP_015294285.1
Putative thymidylate kinase TmK (dTMP kinase) (thymidylic acid kinase) (TMPK) [Mycobacterium canettii]	90.1	90.1	100%	4e-19	100%	WP_015291311.1
Putative thymidylate kinase TmK (dTMP kinase) (thymidylic acid kinase) (TMPK) [Mycobacterium canettii]	90.1	90.1	100%	4e-19	100%	WP_015303784.1
thymidylate kinase [Mycobacterium tuberculosis]	90.1	90.1	100%	4e-19	100%	WP_015456493.1
thymidylate kinase [Mycobacterium canettii]	90.1	90.1	100%	4e-19	100%	WP_014001640.1
thymidylate kinase [Mycobacterium tuberculosis]	87.6	87.6	100%	3e-18	96%	WP_024748275.1
hypothetical protein [Mycobacterium avium]	64.3	64.3	100%	7e-11	74%	WP_023877133.1
Thymidylate kinase [Mycobacterium marinum]	65.5	65.5	100%	1e-10	78%	WP_020727270.1
Thymidylate kinase [Mycobacterium sp. 012931]	65.5	65.5	100%	1e-10	78%	WP_020788368.1
thymidylate kinase Tmk [Mycobacterium liflandii]	65.5	65.5	100%	1e-10	78%	WP_015354855.1
thymidylate kinase [Mycobacterium marinum]	65.5	65.5	100%	1e-10	78%	WP_012393166.1
thymidylate kinase [Mycobacterium ulcerans]	65.5	65.5	100%	1e-10	78%	WP_011740536.1
thymidylate kinase [Mycobacterium kansasii 732]	64.7	64.7	100%	2e-10	74%	EUA14516.1
thymidylate kinase [Mycobacterium sp. TKK-01-0059]	64.3	64.3	100%	3e-10	74%	KEF99753.1
thymidylate kinase [Mycobacterium avium subsp. hominissuis 3388]	64.3	64.3	100%	3e-10	74%	KDO94907.1
thymidylate kinase [Mycobacterium avium]	64.3	64.3	100%	3e-10	74%	WP_003874565.1
thymidylate kinase [Mycobacterium avium]	64.3	64.3	100%	3e-10	74%	WP_023864921.1
thymidylate kinase [Mycobacterium avium]	64.3	64.3	100%	3e-10	74%	WP_023883946.1
thymidylate kinase [Mycobacterium avium subsp. hominissuis TH135]	64.3	64.3	100%	3e-10	74%	BAN32696.1
thymidylate kinase [Mycobacterium indicus pranii]	64.3	64.3	100%	3e-10	74%	WP_014942809.1
thymidylate kinase [Mycobacterium intracellulare]	64.3	64.3	100%	3e-10	74%	WP_009957361.1
thymidylate kinase [Mycobacterium avium]	64.3	64.3	100%	3e-10	74%	WP_009978739.1
thimidylate kinase [Mycobacterium avium subsp. paratuberculosis]	64.3	64.3	100%	3e-10	74%	AAL10206.1
thymidylate kinase [Mycobacterium genavense]	61.7	61.7	100%	2e-09	74%	WP_025737680.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
thymidylate kinase [Segniliparus rotundus]	61.3	61.3	100%	3e-09	74%	WP_013139117.1
thymidylate kinase [Mycobacterium gastri 'Wayne']	61.3	61.3	100%	3e-09	70%	ETW22207.1
thymidylate kinase [Mycobacterium parascrofulaceum]	60.9	60.9	100%	4e-09	70%	WP_007168096.1
thymidylate kinase [Mycobacterium kansasii]	60.4	60.4	100%	5e-09	70%	WP_023371563.1
thymidylate kinase [Mycobacterium intracellulare MIN_061107_1834]	59.2	59.2	100%	1e-08	70%	ETZ31677.1
thymidylate kinase [Mycobacterium intracellulare MIN_052511_1280]	59.2	59.2	100%	1e-08	70%	ETZ27386.1
thymidylate kinase [Mycobacterium avium MAV_120809_2495]	59.2	59.2	100%	1e-08	70%	ETZ47660.1
thymidylate kinase [Mycobacterium sp. H4Y]	59.2	59.2	100%	1e-08	70%	WP_008259770.1
thymidylate kinase [Mycobacterium sp. MOTT36Y]	59.2	59.2	100%	1e-08	70%	WP_014712266.1
thymidylate kinase [Mycobacterium intracellulare]	59.2	59.2	100%	1e-08	70%	WP_014385672.1
thymidylate kinase [Mycobacterium intracellulare]	59.2	59.2	100%	1e-08	70%	WP_014380959.1
thymidylate kinase [Mycobacterium tuberculosis TKK-01-0051]	59.2	59.2	96%	1e-08	73%	KBZ68881.1
thymidylate kinase [Mycobacterium colombiense]	59.2	59.2	96%	1e-08	73%	WP_007773133.1
thymidylate kinase [Mycobacterium yongonense]	57.5	57.5	96%	5e-08	69%	WP_020823379.1
thymidylate kinase [Mycobacterium intracellulare]	55.8	55.8	100%	2e-07	67%	WP_014383184.1
thymidylate kinase [Mycobacterium triplex]	54.1	54.1	100%	7e-07	67%	CDO87354.1
thymidylate kinase [Gordonia otitidis]	52.4	52.4	100%	2e-06	67%	WP_007238888.1
thymidylate kinase [Segniliparus rugosus]	52.0	52.0	100%	3e-06	70%	WP_007470136.1
thymidylate kinase [Turicella otitidis]	51.5	51.5	96%	4e-06	65%	WP_004601034.1
thymidylate kinase [Mycobacterium abscessus]	51.5	51.5	100%	4e-06	59%	WP_005117148.1
thymidylate kinase [Mycobacterium abscessus]	51.5	51.5	100%	4e-06	59%	WP_005102107.1
thymidylate kinase [Mycobacterium abscessus]	51.5	51.5	100%	5e-06	59%	WP_025239600.1
thymidylate kinase [Mycobacterium abscessus]	51.5	51.5	100%	5e-06	59%	WP_005088442.1
thymidylate kinase [Mycobacterium abscessus]	51.5	51.5	100%	5e-06	59%	WP_005080864.1
thymidylate kinase [Mycobacterium abscessus]	51.5	51.5	100%	5e-06	59%	WP_005070201.1
thymidylate kinase [Mycobacterium abscessus]	51.5	51.5	100%	5e-06	59%	WP_005056276.1
thymidylate kinase [Mycobacterium abscessus]	51.5	51.5	100%	5e-06	59%	WP_005111910.1
thymidylate kinase [Rhodococcus sp. UNC23MFCrub1.1]	51.1	51.1	96%	6e-06	69%	WP_027506870.1
MULTISPECIES: thymidylate kinase [Mycobacterium]	50.7	50.7	100%	9e-06	59%	WP_025088603.1
thymidylate kinase [Gordonia sputi]	49.8	49.8	100%	2e-05	63%	WP_005208003.1
thymidylate kinase [Mycobacterium abscessus]	49.0	49.0	100%	3e-05	59%	WP_016892938.1
thymidylate kinase [Gordonia paraffinivorans]	48.6	48.6	100%	4e-05	63%	WP_006899672.1
thymidylate kinase [Corynebacterium halotolerans]	48.1	48.1	100%	6e-05	59%	WP_015400173.1
thymidylate kinase [Mycobacterium sp. JDM601]	47.7	47.7	100%	8e-05	59%	WP_013829916.1
hypothetical protein [Gordonia kroppenstedtii]	47.7	47.7	81%	8e-05	62%	WP_018180987.1
thymidylate kinase [Mycobacterium abscessus]	47.3	47.3	100%	1e-04	56%	WP_005077366.1
thymidylate kinase [Mycobacterium leprae]	46.9	46.9	96%	1e-04	69%	WP_010907920.1
thymidylate kinase [Gordonia effusa]	46.9	46.9	100%	1e-04	63%	WP_007315852.1
thymidylate kinase [Gordonia polyisoprenivorans]	46.9	46.9	81%	1e-04	65%	WP_026919949.1
thymidylate kinase [Gordonia polyisoprenivorans]	46.9	46.9	81%	1e-04	65%	WP_006370363.1
thymidylate kinase [Dietzia cinnamea]	46.9	46.9	59%	1e-04	88%	WP_007630481.1
thymidylate kinase [Tomitella biformata]	46.4	46.4	100%	2e-04	64%	WP_024793529.1
thymidylate kinase [Gordonia terrae]	46.4	46.4	81%	2e-04	68%	WP_004023514.1
thymidylate kinase [Mycobacterium xenopi 3993]	46.0	46.0	100%	2e-04	59%	EUA32800.1
hypothetical protein [Corynebacterium capitovis]	46.0	46.0	96%	3e-04	57%	WP_018017662.1
thymidylate kinase [Mycobacterium avium]	46.0	46.0	100%	3e-04	59%	WP_019737853.1

Description	Max score	Total score	Query cover	E value	Ident	Accession
thymidylate kinase [Mycobacterium xenopi 4042]	46.0	46.0	100%	3e-04	59%	EUA06831.1
thymidylate kinase [Mycobacterium xenopi]	46.0	46.0	100%	3e-04	59%	WP_003920064.1
thymidylate kinase [Corynebacterium genitalium]	45.6	45.6	88%	4e-04	67%	WP_005286098.1
hypothetical protein [Corynebacterium doosanense]	45.2	45.2	100%	5e-04	63%	WP_018021130.1
thymidylate kinase [Corynebacterium tuberculostearicum]	45.2	45.2	100%	5e-04	59%	WP_005326584.1
thymidylate kinase [Corynebacterium pseudogenitalium]	45.2	45.2	100%	5e-04	59%	WP_005322408.1
thymidylate kinase [Rhodococcus pyridinivorans]	45.2	45.2	100%	5e-04	59%	WP_006550215.1
hypothetical protein [Corynebacterium lubricantis]	44.8	44.8	92%	7e-04	62%	WP_018296139.1
MULTISPECIES: thymidylate kinase [Corynebacterium]	44.8	44.8	100%	7e-04	59%	WP_023020774.1
thymidylate kinase [Mycobacterium neoaurum]	44.8	44.8	100%	7e-04	59%	WP_030134849.1
thymidylate kinase [Gordonia bronchialis]	44.8	44.8	92%	7e-04	60%	WP_012835337.1
hypothetical protein [Smaragdicoccus niigatensis]	44.8	44.8	96%	7e-04	58%	WP_018163288.1
thymidylate kinase [Gordonia soli]	44.3	44.3	85%	0.001	59%	WP_007617234.1
thymidylate kinase [Corynebacterium urealyticum]	44.3	44.3	100%	0.001	56%	WP_015381340.1
thymidylate kinase [Corynebacterium urealyticum]	44.3	44.3	100%	0.001	56%	WP_012359732.1
thymidylate kinase [Mycobacterium aromaticivorans JS19b1]	43.9	43.9	100%	0.001	59%	KDE98580.1
hypothetical protein [Corynebacterium pyruviciproducens]	43.5	43.5	100%	0.002	59%	WP_016458814.1
thymidylate kinase [Dietzia sp. UCD-THP]	43.5	43.5	92%	0.002	67%	WP_017836632.1

Alignments

thymidylate kinase Tmk, partial [Mycobacterium tuberculosis UT0124]

Sequence ID: **gb|KBM28427.1|** Length: 90 Number of Matches: 1
Range 1: 24 to 50

Score	Expect	Method	Identities	Positives	Gaps	Frame
90.1 bits(205)	5e-20()		27/27(100%)	27/27(100%)	0/27(0%)	

Features:

```
Query  1    ERSRGRAQRDPGRARDNYERDAELQQR  27
            ERSRGRAQRDPGRARDNYERDAELQQR
Sbjct  24   ERSRGRAQRDPGRARDNYERDAELQQR  50
```

thymidylate kinase, partial [Mycobacterium tuberculosis]

Sequence ID: **gb|AIH62975.1|** Length: 171 Number of Matches: 1
Range 1: 105 to 131

Score	Expect	Method	Identities	Positives	Gaps	Frame
90.1 bits(205)	3e-19()		27/27(100%)	27/27(100%)	0/27(0%)	

Features:

```
Query  1    ERSRGRAQRDPGRARDNYERDAELQQR  27
            ERSRGRAQRDPGRARDNYERDAELQQR
Sbjct  105  ERSRGRAQRDPGRARDNYERDAELQQR  131
```

thymidylate kinase, partial [Mycobacterium tuberculosis]

Sequence ID: **gb|AIH98343.1|** Length: 175 Number of Matches: 1
Range 1: 109 to 135

Score	Expect	Method	Identities	Positives	Gaps	Frame
90.1 bits(205)	3e-19()		27/27(100%)	27/27(100%)	0/27(0%)	

Features:

```
Query  1    ERSRGRAQRDPGRARDNYERDAELQQR  27
```

```
                 ERSRGRAQRDPGRARDNYERDAELQQR
Sbjct  109   ERSRGRAQRDPGRARDNYERDAELQQR  135
```

thymidylate kinase, partial [Mycobacterium bovis]

Sequence ID: **ref|WP_024459054.1|** Length: 210 Number of Matches: 1

Range 1: 144 to 170

Score	Expect	Method	Identities	Positives	Gaps	Frame
90.1 bits(205)	3e-19()		27/27(100%)	27/27(100%)	0/27(0%)	

Features:

```
Query  1     ERSRGRAQRDPGRARDNYERDAELQQR  27
             ERSRGRAQRDPGRARDNYERDAELQQR
Sbjct  144   ERSRGRAQRDPGRARDNYERDAELQQR  170
```

thymidylate kinase [Mycobacterium tuberculosis]

Sequence ID: **gb|AIH23782.1|** Length: 214 Number of Matches: 1

Range 1: 148 to 174

Score	Expect	Method	Identities	Positives	Gaps	Frame
90.1 bits(205)	4e-19()		27/27(100%)	27/27(100%)	0/27(0%)	

Features:

```
Query  1     ERSRGRAQRDPGRARDNYERDAELQQR  27
             ERSRGRAQRDPGRARDNYERDAELQQR
Sbjct  148   ERSRGRAQRDPGRARDNYERDAELQQR  174
```