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BLAST Results

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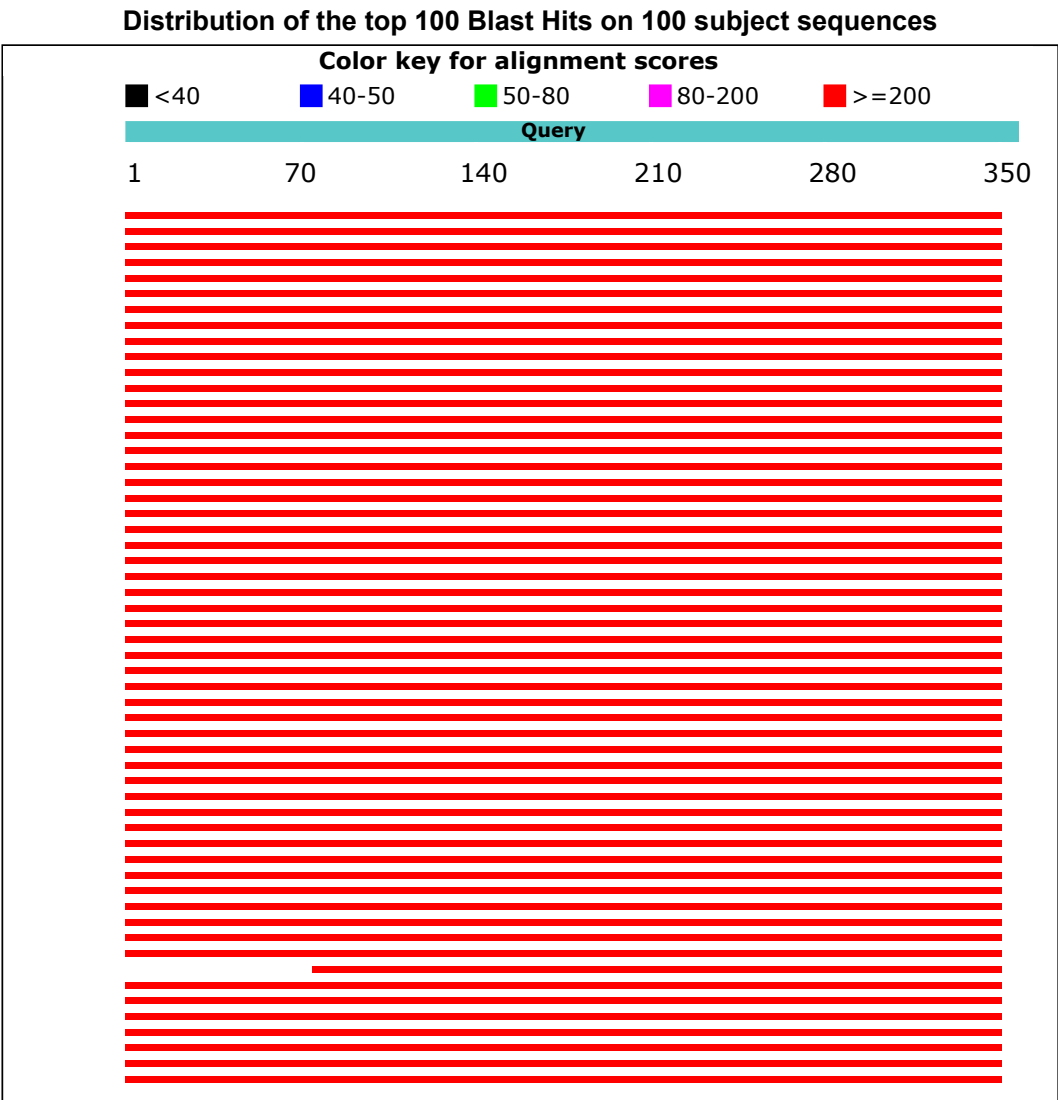
Job title: 2 sequences (Sequentie 1)

RID [DBFJ4AW6015](#) (Expires on 04-18 17:28 pm)

**Query ID** Icl|Query\_93343  
**Description** Sequentie 1  
**Molecule type** amino acid  
**Query Length** 350

**Database Name** nr  
**Description** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects  
**Program** BLASTP 2.8.0+

Graphic Summary



## Descriptions

Sequences producing significant alignments:

Description	Max score	Total score	Query cover	E value	Ident	Accession
acetate--CoA ligase [Lactococcus lactis]	735	735	100%	0.0	100%	<a href="#">WP_058213135.1</a>
acetate--CoA ligase [Lactococcus lactis]	735	735	100%	0.0	100%	<a href="#">WP_058218837.1</a>
long-chain acyl-CoA synthetase [Lactococcus lactis]	735	735	100%	0.0	100%	<a href="#">WP_010905493.1</a>
acetate--CoA ligase [Lactococcus lactis]	734	734	100%	0.0	100%	<a href="#">WP_081213417.1</a>
long-chain acyl-CoA synthetase [Lactococcus lactis subsp. lactis]	734	734	100%	0.0	99%	<a href="#">PCS18680.1</a>
acyl-coenzyme A synthetases/AMP- (fatty) acid ligases [Lactococcus lactis subsp. lactis]	733	733	100%	0.0	99%	<a href="#">GAM79651.1</a>
acetate--CoA ligase [Lactococcus lactis]	733	733	100%	0.0	99%	<a href="#">WP_033899641.1</a>
long-chain-fatty-acid--CoA ligase [Lactococcus lactis]	733	733	100%	0.0	99%	<a href="#">WP_023188928.1</a>
Acetate--CoA ligase [Lactococcus lactis subsp. lactis CNCM I-1631]	733	733	100%	0.0	99%	<a href="#">EHE94728.1</a>
acetate--CoA ligase [Lactococcus lactis]	733	733	100%	0.0	99%	<a href="#">WP_085624039.1</a>
acetate--CoA ligase [Lactococcus lactis]	733	733	100%	0.0	99%	<a href="#">WP_032398871.1</a>
long-chain acyl-CoA synthetase [Lactococcus lactis]	733	733	100%	0.0	99%	<a href="#">WP_021723121.1</a>
acetate--CoA ligase [Lactococcus lactis]	732	732	100%	0.0	99%	<a href="#">WP_098394061.1</a>
acetate--CoA ligase [Lactococcus lactis]	732	732	100%	0.0	99%	<a href="#">WP_058211161.1</a>
acetate--CoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	<a href="#">WP_098407787.1</a>
acetate--CoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	<a href="#">WP_060416383.1</a>
acetate--CoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	<a href="#">WP_058225361.1</a>
acetate--CoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	<a href="#">WP_058203219.1</a>
acetate--CoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	<a href="#">WP_014570399.1</a>
acetate--CoA ligase [Lactococcus lactis]	731	731	100%	0.0	99%	<a href="#">WP_058217542.1</a>
acetate--CoA ligase [Lactococcus lactis]	730	730	100%	0.0	99%	<a href="#">WP_104143433.1</a>
acetate--CoA ligase [Lactococcus lactis]	730	730	100%	0.0	99%	<a href="#">WP_038599620.1</a>
acetate--CoA ligase [Lactococcus lactis]	730	730	100%	0.0	99%	<a href="#">WP_029344950.1</a>
acetate--CoA ligase [Lactococcus lactis]	728	728	100%	0.0	99%	<a href="#">WP_058205270.1</a>
acetate--CoA ligase [Lactococcus lactis]	728	728	100%	0.0	99%	<a href="#">WP_058218957.1</a>

Description	Max score	Total score	Query cover	E value	Ident	Accession
long-chain acyl-CoA synthetase [Lactococcus lactis subsp. lactis]	728	728	100%	0.0	99%	<a href="#">KRO23413.1</a>
acetate--CoA ligase [Lactococcus lactis]	727	727	100%	0.0	99%	<a href="#">WP_103054515.1</a>
acetate--CoA ligase [Lactococcus lactis]	727	727	100%	0.0	99%	<a href="#">WP_082272274.1</a>
acetate--CoA ligase [Lactococcus lactis]	727	727	100%	0.0	99%	<a href="#">WP_057720320.1</a>
long-chain acyl-CoA synthetase [Lactococcus lactis subsp. hordniae]	723	723	100%	0.0	98%	<a href="#">PCS10929.1</a>
acetate--CoA ligase [Lactococcus lactis]	723	723	100%	0.0	98%	<a href="#">WP_058209009.1</a>
long-chain acyl-CoA synthetase [Lactococcus lactis]	715	715	100%	0.0	97%	<a href="#">WP_015425959.1</a>
acetate--CoA ligase [Lactococcus lactis]	685	685	100%	0.0	92%	<a href="#">WP_061778018.1</a>
Acs family protein [Lactococcus lactis]	685	685	100%	0.0	92%	<a href="#">WP_021211606.1</a>
acetate--CoA ligase [Lactococcus lactis]	685	685	100%	0.0	92%	<a href="#">WP_014573007.1</a>
acetate--CoA ligase [Lactococcus lactis subsp. cremoris TIFN3]	684	684	100%	0.0	92%	<a href="#">EQC94180.1</a>
long-chain acyl-CoA synthetase [Lactococcus lactis]	684	684	100%	0.0	92%	<a href="#">WP_015082155.1</a>
amino acid adenylation domain protein [Lactococcus lactis subsp. cremoris]	684	684	100%	0.0	92%	<a href="#">KKW73985.1</a>
acetate--CoA ligase [Lactococcus lactis]	683	683	100%	0.0	92%	<a href="#">WP_063281423.1</a>
acetate--CoA ligase [Lactococcus lactis]	683	683	100%	0.0	92%	<a href="#">WP_011675629.1</a>
acetate--CoA ligase [Lactococcus lactis]	683	683	100%	0.0	92%	<a href="#">WP_011834637.1</a>
AMP-binding protein [Lactococcus lactis]	682	682	100%	0.0	92%	<a href="#">WP_021036845.1</a>
acetate--CoA ligase [Lactococcus lactis]	682	682	100%	0.0	92%	<a href="#">WP_081196842.1</a>
acetate--CoA ligase [Lactococcus lactis]	682	682	100%	0.0	92%	<a href="#">WP_101913658.1</a>
acetate--CoA ligase [Lactococcus lactis subsp. cremoris TIFN6]	681	681	100%	0.0	92%	<a href="#">EQC53627.1</a>
Acs family protein [Lactococcus lactis]	680	680	100%	0.0	92%	<a href="#">WP_021166362.1</a>
acetate--CoA ligase [Lactococcus lactis]	680	680	100%	0.0	92%	<a href="#">WP_043736020.1</a>
acetate--CoA ligase [Lactococcus lactis]	679	679	100%	0.0	91%	<a href="#">WP_046124848.1</a>
amino acid adenylation domain protein [Lactococcus lactis subsp. lactis]	576	576	78%	0.0	98%	<a href="#">KLK97297.1</a>
Acs family protein [Lactococcus petauri]	576	576	100%	0.0	76%	<a href="#">WP_086582890.1</a>
Acs family protein [Lactococcus garvieae]	574	574	100%	0.0	76%	<a href="#">WP_004256244.1</a>
acetate--CoA ligase [Lactococcus sp. DD01]	574	574	100%	0.0	76%	<a href="#">WP_061412802.1</a>
acetate--CoA ligase [Lactococcus garvieae]	574	574	100%	0.0	76%	<a href="#">WP_046400975.1</a>

Description	Max score	Total score	Query cover	E value	Ident	Accession
acetate--CoA ligase [Lactococcus garvieae]	572	572	100%	0.0	76%	<a href="#">WP_096369325.1</a>
acetate--CoA ligase [Lactococcus garvieae]	572	572	100%	0.0	76%	<a href="#">WP_019293837.1</a>
acetate--CoA ligase [Lactococcus garvieae]	570	570	100%	0.0	75%	<a href="#">WP_081166459.1</a>
acetate--CoA ligase [Lactococcus garvieae]	570	570	100%	0.0	76%	<a href="#">WP_017369201.1</a>
Acs family protein [Lactococcus garvieae]	570	570	100%	0.0	75%	<a href="#">WP_003135509.1</a>
acetate--CoA ligase [Lactococcus garvieae]	568	568	100%	0.0	75%	<a href="#">WP_042219301.1</a>
acetate--CoA ligase [Lactococcus garvieae]	568	568	100%	0.0	75%	<a href="#">WP_017371191.1</a>
acetate--CoA ligase [Lactococcus garvieae TRF1]	568	568	100%	0.0	75%	<a href="#">ETD05431.1</a>
acetate--CoA ligase [Lactococcus garvieae]	567	567	100%	0.0	75%	<a href="#">WP_074750230.1</a>
acetate--CoA ligase [Lactococcus garvieae]	566	566	100%	0.0	75%	<a href="#">WP_014024564.1</a>
acetate--CoA ligase [Enterococcus quebecensis]	446	446	100%	9e-152	59%	<a href="#">WP_069635203.1</a>
acetate--CoA ligase [Carnobacterium gallinarum]	445	445	100%	1e-151	60%	<a href="#">WP_034561934.1</a>
acetate--CoA ligase [Enterococcus aquimarinus]	444	444	100%	2e-151	61%	<a href="#">WP_071874412.1</a>
AMP-binding protein [Enterococcus haemoperoxidus]	443	443	100%	1e-150	59%	<a href="#">WP_010762120.1</a>
AMP-binding enzyme [Listeria grayi DSM 20601]	443	443	100%	1e-150	62%	<a href="#">EFI84138.1</a>
acetate--CoA ligase [Listeria grayi]	442	442	100%	1e-150	62%	<a href="#">WP_040486682.1</a>
acetate--CoA ligase [Enterococcus sp. TR]	442	442	100%	3e-150	59%	<a href="#">WP_025870565.1</a>
acetate--CoA ligase [Enterococcus termitis]	442	442	100%	3e-150	59%	<a href="#">WP_086345729.1</a>
acetate--CoA ligase [Listeria grayi]	441	441	100%	6e-150	62%	<a href="#">WP_036103250.1</a>
acetate--CoA ligase [Enterococcus ureasiticus]	440	440	100%	1e-149	59%	<a href="#">WP_069647056.1</a>
acetate--CoA ligase [Enterococcus sp. 9D6_DIV0238]	440	440	100%	1e-149	59%	<a href="#">WP_087641642.1</a>
AMP-binding protein [Enterococcus cecorum]	440	440	100%	2e-149	61%	<a href="#">WP_016250857.1</a>
AMP-binding protein [Enterococcus cecorum DSM 20682 = ATCC 43198]	440	440	100%	2e-149	61%	<a href="#">OJG33678.1</a>
AMP-binding protein [Enterococcus moraviensis]	439	439	100%	2e-149	59%	<a href="#">WP_010766613.1</a>
acetate--CoA ligase [Enterococcus rotai]	438	438	100%	6e-149	59%	<a href="#">ALS36562.1</a>
acetate--CoA ligase [Enterococcus sp. 7F3_DIV0205]	438	438	100%	7e-149	59%	<a href="#">WP_086314805.1</a>
acetate--CoA ligase [Enterococcus cecorum]	438	438	100%	7e-149	61%	<a href="#">WP_087213839.1</a>
AMP-binding protein [Enterococcus faecalis]	438	438	100%	1e-148	58%	<a href="#">WP_016624877.1</a>

Description	Max score	Total score	Query cover	E value	Ident	Accession
acetate--CoA ligase [Enterococcus cecorum]	437	437	100%	3e-148	60%	<a href="#">WP_047341861.1</a>
acetate--CoA ligase [Enterococcus wangshanyuanii]	436	436	100%	4e-148	59%	<a href="#">WP_088270465.1</a>
acetate--CoA ligase [Enterococcus sp. 12C11_DIV0727]	436	436	100%	4e-148	59%	<a href="#">WP_086445388.1</a>
MULTISPECIES: acetate--CoA ligase [Enterococcus]	436	436	100%	4e-148	59%	<a href="#">WP_086277663.1</a>
acetate--CoA ligase [Enterococcus ureilyticus]	436	436	100%	5e-148	58%	<a href="#">WP_069640119.1</a>
AMP-binding protein [Enterococcus cacciae]	436	436	100%	6e-148	59%	<a href="#">WP_010770289.1</a>
acetate--CoA ligase [Enterococcus cecorum]	436	436	100%	8e-148	60%	<a href="#">WP_047242231.1</a>
acetate--CoA ligase [Enterococcus cecorum]	436	436	100%	8e-148	60%	<a href="#">WP_047340890.1</a>
acetate--CoA ligase [Enterococcus sp. 4G2_DIV0659]	435	435	100%	1e-147	58%	<a href="#">WP_086330426.1</a>
acetate--CoA ligase [Enterococcus rivorum]	434	434	100%	3e-147	57%	<a href="#">WP_069697264.1</a>
AMP-binding protein [Enterococcus termitis]	434	434	100%	3e-147	58%	<a href="#">OJG99592.1</a>
acetate--CoA ligase [Enterococcus thailandicus]	434	434	100%	4e-147	59%	<a href="#">WP_067482067.1</a>
acetate--CoA ligase [Enterococcus cecorum]	434	434	100%	5e-147	60%	<a href="#">WP_087662663.1</a>
acetate--CoA ligase [Enterococcus termitis]	434	434	100%	5e-147	58%	<a href="#">WP_069663271.1</a>
acetate--CoA ligase [Enterococcus cecorum]	433	433	100%	6e-147	60%	<a href="#">WP_087402632.1</a>
acetate--CoA ligase [Enterococcus plantarum]	433	433	100%	8e-147	59%	<a href="#">WP_069653501.1</a>
acetate--CoA ligase [Enterococcus cecorum]	433	433	100%	9e-147	60%	<a href="#">WP_047334704.1</a>
acetate--CoA ligase [Enterococcus sp. 5B7_DIV0075]	433	433	100%	9e-147	59%	<a href="#">WP_086270931.1</a>
acetate--CoA ligase [Enterococcus silesiacus]	433	433	100%	1e-146	58%	<a href="#">WP_071878110.1</a>

## Alignments

acetate--CoA ligase [Lactococcus lactis]

Sequence ID: **WP\_058213135.1** Length: 507 Number of Matches: 1

**See 1 more title(s)**

Range 1: 71 to 420

Score	Expect	Method	Identities	Positives	Gaps	Frame
735 bits(1897)	0.0()	Compositional matrix adjust.	350/350(100%)	350/350(100%)	0/350(0%)	
Features:						
Query	1	IFKSSAFDITYLLAVAVSYLGAVPAMISYHLP	AE	TMDILAGRLGNPWLIYDQVTDKTVNEM	60	
Sbjct	71	IFKSSAFDITYLLAVAVSYLGAVPAMISYHLP	AE	TMDILAGRLGNPWLIYDQVTDKTVNEM	130	
Query	61	KNLEDSKKLSVSKFALEKPTQIADSQOLASDEIAYL	190	THTSGTTGVPKLI	120	
Sbjct	131	KNLEDSKKLSVSKFALEKPTQIADSQOLASDEIAYL	190	THTSGTTGVPKLI	190	

```

Query 121 VLQRTVMDWMPDKEEILAFHISPVHSRFNIGVSSAMTFGFGMLPLNDLSKDNLVNLFAXH 180
Sbjct 191 VLQRTVMDWMPDKEEILAFHISPVHSRFNIGVSSAMTFGFGMLPLNDLSKDNLVNLFAXH 250

Query 181 QPYAFETHPNDFVRLANLAKQEPFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ 240
Sbjct 251 QPYAFETHPNDFVRLANLAKQEPFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ 310

Query 241 IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADEGDGNECPAGTPGRIHFLS 300
Sbjct 311 IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADEGDGNECPAGTPGRIHFLS 370

Query 301 KGRALTYKKEERFNKEVYGDWWDGWDGWMNEDGILFLHDRQVDLIDKI 350
Sbjct 371 KGRALTYKKEERFNKEVYGDWWDGWDGWMNEDGILFLHDRQVDLIDKI 420

```

acetate--CoA ligase [*Lactococcus lactis*]Sequence ID: **WP\_058218837.1** Length: 507 Number of Matches: 1**See 1 more title(s)**

Range 1: 71 to 420

Score	Expect	Method	Identities	Positives	Gaps	Frame
735 bits(1897)	0.0()	Compositional matrix adjust.	350/350(100%)	350/350(100%)	0/350(0%)	

Features:

```

Query 1 IFKSSAFDITYLLAVAVSYLGAVPAMISYHLP AETMDILAGRLGNPWLIYDQVTDKTVNEM 60
Sbjct 71 IFKSSAFDITYLLAVAVSYLGAVPAMISYHLP AETMDILAGRLGNPWLIYDQVTDKTVNEM 130

Query 61 KNLEDSKKLSVSKFALEKPTQIADSQQLASDEIAYLTHTSGTTGVPKLI AHSANS MGWRW 120
Sbjct 131 KNLEDSKKLSVSKFALEKPTQIADSQQLASDEIAYLTHTSGTTGVPKLI AHSANS MGWRW 190

Query 121 VLQRTVMDWMPDKEEILAFHISPVHSRFNIGVSSAMTFGFGMLPLNDLSKDNLVNLFAXH 180
Sbjct 191 VLQRTVMDWMPDKEEILAFHISPVHSRFNIGVSSAMTFGFGMLPLNDLSKDNLVNLFAXH 250

Query 181 QPYAFETHPNDFVRLANLAKQEPFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ 240
Sbjct 251 QPYAFETHPNDFVRLANLAKQEPFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ 310

Query 241 IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADEGDGNECPAGTPGRIHFLS 300
Sbjct 311 IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADEGDGNECPAGTPGRIHFLS 370

Query 301 KGRALTYKKEERFNKEVYGDWWDGWDGWMNEDGILFLHDRQVDLIDKI 350
Sbjct 371 KGRALTYKKEERFNKEVYGDWWDGWDGWMNEDGILFLHDRQVDLIDKI 420

```

long-chain acyl-CoA synthetase [*Lactococcus lactis*]Sequence ID: **WP\_010905493.1** Length: 507 Number of Matches: 1**See 39 more title(s)**

Range 1: 71 to 420

Score	Expect	Method	Identities	Positives	Gaps	Frame
735 bits(1897)	0.0()	Compositional matrix adjust.	350/350(100%)	350/350(100%)	0/350(0%)	

Features:

```

Query 1 IFKSSAFDITYLLAVAVSYLGAVPAMISYHLP AETMDILAGRLGNPWLIYDQVTDKTVNEM 60
Sbjct 71 IFKSSAFDITYLLAVAVSYLGAVPAMISYHLP AETMDILAGRLGNPWLIYDQVTDKTVNEM 130

Query 61 KNLEDSKKLSVSKFALEKPTQIADSQQLASDEIAYLTHTSGTTGVPKLI AHSANS MGWRW 120
Sbjct 131 KNLEDSKKLSVSKFALEKPTQIADSQQLASDEIAYLTHTSGTTGVPKLI AHSANS MGWRW 190

Query 121 VLQRTVMDWMPDKEEILAFHISPVHSRFNIGVSSAMTFGFGMLPLNDLSKDNLVNLFAXH 180
Sbjct 191 VLQRTVMDWMPDKEEILAFHISPVHSRFNIGVSSAMTFGFGMLPLNDLSKDNLVNLFAXH 250

Query 181 QPYAFETHPNDFVRLANLAKQEPFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ 240
Sbjct 251 QPYAFETHPNDFVRLANLAKQEPFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ 310

Query 241 IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADEGDGNECPAGTPGRIHFLS 300
Sbjct 311 IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADEGDGNECPAGTPGRIHFLS 370

Query 301 KGRALTYKKEERFNKEVYGDWWDGWDGWMNEDGILFLHDRQVDLIDKI 350
Sbjct 371 KGRALTYKKEERFNKEVYGDWWDGWDGWMNEDGILFLHDRQVDLIDKI 420

```

acetate--CoA ligase [*Lactococcus lactis*]Sequence ID: **WP\_081213417.1** Length: 507 Number of Matches: 1**See 1 more title(s)**

Range 1: 71 to 420

Score	Expect	Method	Identities	Positives	Gaps	Frame
734 bits(1896)	0.0()	Compositional matrix adjust.	350/350(100%)	350/350(100%)	0/350(0%)	
Features:						
Query 1	IFKSSAFD	TYLLAVAVSYLGAVPAMISYHLP	PAETMDILAGRLGNPWLIYDQVTDKTVNEM	60		
Sbjct 71	IFKSSAFD	TYLLAVAVSYLGAVPAMISYHLP	PAETMDILAGRLGNPWLIYDQVTDKTVNEM	130		
Query 61	KNLEDSKKLSVSKFALEKPTQIADSQQLASDEIAYLTHTSGTTGVPKLI	IAHSANS	MGWRW	120		
Sbjct 131	KNLEDSKKLSVSKFALEKPTQIADSQQLASDEIAYLTHTSGTTGVPKLI	IAHSANS	MGWRW	190		
Query 121	VLQRTVMDWMPDKEEILAFHISPVHSRNFNIGVSSAMTFGFGMLPLNDLSKDNLVNLF	FAKH	180			
Sbjct 191	VLQRTVMDWMPDKEEILAFHISPVHSRNFNIGVSSAMTFGFGMLPLNDLSKDNLVNLF	FAKH	250			
Query 181	QPYAFETHPNDFVRLANLAKQEP	EIFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ	240			
Sbjct 251	QPYAFETHPNDFVRLANLAKQEP	EIFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ	310			
Query 241	IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADE	DGNECPAGTPGRIHFLS	300			
Sbjct 311	IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADE	DGNECPAGTPGRIHFLS	370			
Query 301	KGRALTYKKEEERFNKEVYGDWWD	TGDWGLMNE	DGILFLHDRQVDLIDKI	350		
Sbjct 371	KGRALTYKKEEERFNKEVYGDWWD	TGDWGLMNE	DGILFLHDRQVDLIDKI	420		

long-chain acyl-CoA synthetase [*Lactococcus lactis* subsp. *lactis*]Sequence ID: **PCS18680.1** Length: 498 Number of Matches: 1

Range 1: 62 to 411

Score	Expect	Method	Identities	Positives	Gaps	Frame
734 bits(1894)	0.0()	Compositional matrix adjust.	349/350(99%)	350/350(100%)	0/350(0%)	
Features:						
Query 1	IFKSSAFD	TYLLAVAVSYLGAVPAMISYHLP	PAETMDILAGRLGNPWLIYDQVTDKTVNEM	60		
Sbjct 62	IFKSSAFD	TYLLAVAVSYLGAVPAMISYHLP	PAETMDILAGRLGNPWLIYDQVTDKTVNEM	121		
Query 61	KNLEDSKKLSVSKFALEKPTQIADSQQLASDEIAYLTHTSGTTGVPKLI	IAHSANS	MGWRW	120		
Sbjct 122	KNLEDSKKLSVSKFALEKPTQIADSQQLASDEIAYLTHTSGTTGVPKLI	IAHSANS	MGWRW	181		
Query 121	VLQRTVMDWMPDKEEILAFHISPVHSRNFNIGVSSAMTFGFGMLPLNDLSKDNLVNLF	FAKH	180			
Sbjct 182	VLQRTVMDWMPDKEEILAFHISPVHSRNFNIGVSSAMTFGFGMLPLNDLSKDNLVNLF	FAKH	241			
Query 181	QPYAFETHPNDFVRLANLAKQEP	EIFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ	240			
Sbjct 242	QPYAFETHPNDFVRLANLAKQEP	EIFASIRYLHSTFDAINKETMHTFLSASKQKDPVFLQ	301			
Query 241	IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADE	DGNECPAGTPGRIHFLS	300			
Sbjct 302	IYGQSECGPMIWKKHRLSTLADTNAREMGIGMPGLSKARIADE	DGNECPAGTPGRIHFLS	361			
Query 301	KGRALTYKKEEERFNKEVYGDWWD	TGDWGLMNE	DGILFLHDRQVDLIDKI	350		
Sbjct 362	KGRALTYKKEEERFNKEVYGDWWD	TGDWGLMNE	DGILFLHDRQVDLIDKI	411		

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