

Assessment of the Real-Time PCR Method Claiming to be Specific for Detection and Quantification of the First Commercialised Genome-Edited Plant

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Online Resource 1. *In silico* specificity analyses

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Primer-BLAST (SU-Forward and SU-Reverse primers) against NCBI non-redundant sequence database (nt)

Input PCR template

none

Specificity of primers

Target templates were found in selected database: Nucleotide collection (nt)

Search parameters and other details	
Number of Blast hits analyzed	6272
Entrez query	
Min total mismatches	2
Min 3' end mismatches	2
Defined 3' end region length	5
Mismatch threshold to ignore targets	6
Max target size	4000
Max number of Blast target sequences	50000
Blast E value	30000
Blast word size	7
Max candidate primer pairs	500
Min PCR product size	60
Max PCR product size	1000
Min Primer size	15
Opt Primer size	20
Max Primer size	25
Min Tm	57
Opt Tm	60
Max Tm	63
Max Tm difference	3
Repeat filter	AUTO
Low complexity filter	Yes

Primer pair 1

	Sequence (5'→3')	Length	Tm	GC%	Self complementarity
Forward primer	TCCTCGACGAGCTAACCG	18	58.51	61.11	7.00
Reverse primer	GCTTTGTAGAACCGATCTTCCA	22	58.40	45.45	5.00
Products on target templates					

>[AJ344991.1](#) *Raphanus raphanistrum* partial als gene for putative acetolactate synthase, specimen voucher 161825R2

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18

Template 1154G.1171

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22

Template 1487 1466

>[LR031878.1](#) *Brassica oleracea* HDEM genome, scaffold: C1

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18

Template 23644046 23644063

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22

Template 23644379C 23644358

>[XM_013793507.2](#) PREDICTED: Brassica napus acetolactate synthase 1, chloroplastic (LOC106353715), mRNA

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1406 1423

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1739C 1718

>[XM_013793508.2](#) PREDICTED: Brassica napus acetolactate synthase 1, chloroplastic (LOC106353716), mRNA

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1404 1421

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1737C 1716

>[XM_013806285.2](#) PREDICTED: Brassica napus acetolactate synthase 1, chloroplastic (LOC106366633), mRNA

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1406 1423

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1739C 1718

>[XM_013806286.2](#) PREDICTED: Brassica napus acetolactate synthase 1, chloroplastic (LOC106366634), mRNA

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1406 1423

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1739C 1718

>[KP985786.1](#) Brassica napus isolate K5 actohydroxyacid synthase 1 gene, complete cds

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 13641381

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1697C 1676

>[XM 013748148.1](#) PREDICTED: Brassica oleracea var. oleracea acetolactate synthase 1, chloroplastic (LOC106310919), mRNA

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1403 1420

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1736C 1715

>[KM816835.1](#) Brassica carinata cultivar Dodalla acetolactate synthetase (ALS1) gene, complete cds

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 13641381

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1697C 1676

>[KM816819.1](#) Brassica oleracea cultivar Texuan zhonggan No.11 acetolactate synthetase (ALS1) gene, complete cds

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1364 1381

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1697C 1676

>[KM816810.1](#) Brassica napus cultivar Zhongshuang No.9 acetolactate synthetase (ALS1) gene, complete cds

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 13641381

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1697C 1676

>[KM816807.1](#) Brassica napus cultivar SH11 SH11 acetohydroxyacid synthase (ALS1) gene, complete cds

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 13641381

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1697C 1676

>[GU192448.1](#) Brassica napus cultivar N415 acetohydroxyacid synthase (ALS1) gene, complete cds

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 13841401

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1717C 1696

>[M60068.1](#) B.napa acetolactate synthase mRNA, complete cds

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1234 1251

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1567C 1546

>[Z11524.1](#) B.napus gene for actohydroxyacid synthase I

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 38723889

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 4205C 4184

>[LR778314.1](#) Raphanus sativus genome assembly, chromosome: 5

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 22853721G.22853738

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
 Template 22854054C 22854033

>[XM_006404174.2](#) PREDICTED: Eutrema salsugineum acetolactate synthase 1, chloroplastic (LOC18021551), mRNA

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
 Template 1385A. 1402

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
 Template 1718C 1697

>[KM816834.1](#) Brassica rapa cultivar Rapido acetolactate synthetase (ALS3) gene, complete cds

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
 Template 1355C 1372

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
 Template 1688C 1667

>[KM816832.1](#) Brassica rapa cultivar Opava acetolactate synthetase (ALS3) gene, complete cds

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
 Template 1355C 1372

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
 Template 1688C 1667

>[KM816826.1](#) Brassica juncea cultivar Qianxiniuweiyoucai acetolactate synthetase (ALS3) gene, complete cds

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
 Template 1355C 1372

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
 Template 1688C 1667

>[AJ344995.1](#) Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161855R1

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18

Template 626G.643

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22

Template 959C 938

>[AJ344994.1](#) *Raphanus raphanistrum* partial als gene for putative acetolactate synthase, specimen voucher 161855R0

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18

Template 1154G.1171

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22

Template 1487C 1466

>[AJ344993.1](#) *Raphanus raphanistrum* partial als gene for putative acetolactate synthase, specimen voucher 161829R1

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18

Template 1154G.1171

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22

Template 1487C 1466

>[AJ344992.1](#) *Raphanus raphanistrum* partial als gene for putative acetolactate synthase, specimen voucher 161829R0

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18

Template 1154G.1171

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22

Template 1487C 1466

>[AJ344990.1](#) *Raphanus raphanistrum* partial als gene for putative acetolactate synthase, specimen voucher 161825R0

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18

Template 1154G.1171

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1487M 1466

>[AJ344989.1](#) *Raphanus raphanistrum* partial als gene for putative acetolactate synthase, specimen voucher 161654R1

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1154G.1171

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1487C 1466

>[AJ344988.1](#) *Raphanus raphanistrum* partial als gene for putative acetolactate synthase, specimen voucher 161654R0

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1154G.1171

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1487C 1466

>[AJ344986.1](#) *Raphanus raphanistrum* partial als gene for putative acetolactate synthase, specimen voucher 161789S1

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1154G.1171

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1487C 1466

>[AJ344985.1](#) *Raphanus raphanistrum* partial als gene for putative acetolactate synthase, specimen voucher 161653S2

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18
Template 1154G.1171

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22
Template 1487C 1466

>[AJ344984.1](#) *Raphanus raphanistrum* partial als gene for putative acetolactate synthase, specimen voucher 161653S1

product length = 334

Forward primer 1 TCCTCGACGAGCTAACCG 18

Template 1154G.1171

Reverse primer 1 GCTTTGTAGAACCGATCTTCCA 22

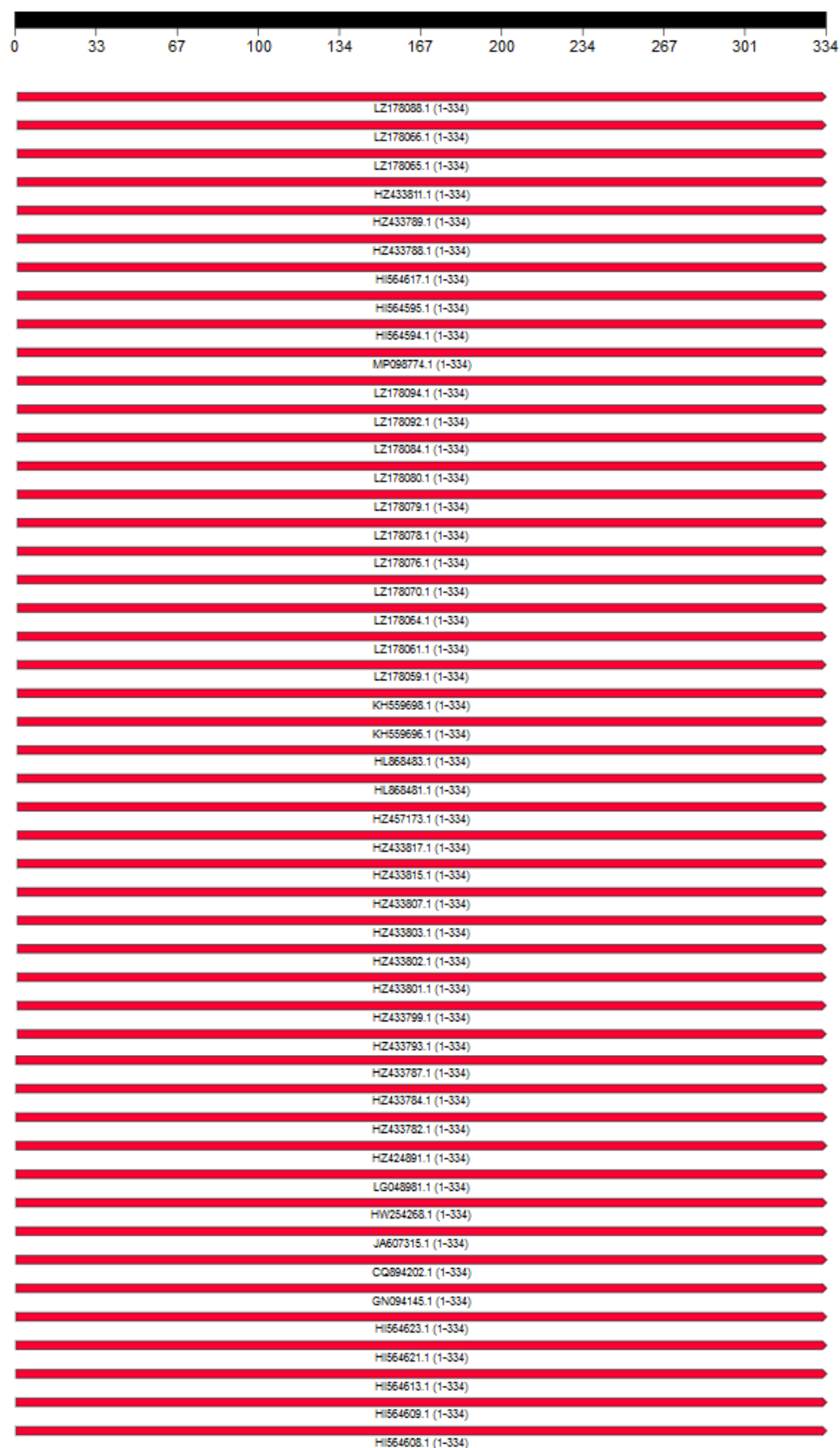
Template 1487C 1466

Amplicon BLAST against Patent nt database maintained at JRC

NOTE: 452 additional hits found and not shown

queryId	subjectId	percIdentity	alnLength	mismatchCount	gapOpenCount	queryStart	queryEnd	subjectStart	subjectEnd	eVal	bitScore
amplicon	LZ178088.1	99.70	334	1	0	1	334	1364	1697	3e-172	612
amplicon	LZ178066.1	99.70	334	1	0	1	334	1364	1697	3e-172	612
amplicon	LZ178065.1	99.70	334	1	0	1	334	1364	1697	3e-172	612
amplicon	HZ433811.1	99.70	334	1	0	1	334	1364	1697	3e-172	612
amplicon	HZ433789.1	99.70	334	1	0	1	334	1364	1697	3e-172	612
amplicon	HZ433788.1	99.70	334	1	0	1	334	1364	1697	3e-172	612
amplicon	HI564617.1	99.70	334	1	0	1	334	1364	1697	3e-172	612
amplicon	HI564595.1	99.70	334	1	0	1	334	1364	1697	3e-172	612
amplicon	HI564594.1	99.70	334	1	0	1	334	1364	1697	3e-172	612
amplicon	MP098774.1	99.40	334	2	0	1	334	1378	1711	1e-170	606
amplicon	LZ178094.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	LZ178092.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	LZ178084.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	LZ178080.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	LZ178079.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	LZ178078.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	LZ178076.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	LZ178070.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	LZ178064.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	LZ178061.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	LZ178059.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	KH559698.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	KH559696.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HL868483.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HL868481.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ457173.1	99.40	334	2	0	1	334	1378	1711	1e-170	606
amplicon	HZ433817.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ433815.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ433807.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ433803.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ433802.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ433801.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ433799.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ433793.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ433787.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ433784.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ433782.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HZ424891.1	99.40	334	2	0	1	334	1405	1738	1e-170	606
amplicon	LG048981.1	99.40	334	2	0	1	334	1405	1738	1e-170	606
amplicon	HW254268.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	JA607315.1	99.40	334	2	0	1	334	1154	1487	1e-170	606
amplicon	CQ894202.1	99.40	334	2	0	1	334	722	1055	1e-170	606
amplicon	GN094145.1	99.40	334	2	0	1	334	1405	1738	1e-170	606
amplicon	HI564623.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HI564621.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HI564613.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HI564609.1	99.40	334	2	0	1	334	1364	1697	1e-170	606
amplicon	HI564608.1	99.40	334	2	0	1	334	1364	1697	1e-170	606

Color key for alignment scores



Amplicon-BLAST against NCBI non-redundant sequence database (nt)

Search Parameters	
Program	blastn
Word size	11
Expect value	10
Hitlist size	100
Match/Mismatch scores	2,-3
Gapcosts	5,2
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Database	
Posted date	Sep 8, 2020 2:59 PM
Number of letters	322,365,415,490
Number of sequences	60,407,830
Entrez query	None

Karlin-Altschul statistics		
Lambda	0.633731	0.625
K	0.408146	0.41
H	0.912438	0.78

Results Statistics	
Length adjustment	38
Effective length of query	296

Effective length of database	320069917950
Effective search space	94740695713200
Effective search space used	94740695713200

Brassica oleracea HDEM genome, scaffold: C1

Sequence ID: [LR031878.1](#)Length: 52030199Number of Matches: 1

Range 1: 23644046 to 23644379[GenBankGraphics](#)Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus

Features:

[unnamed protein product](#)

Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60
Sbjct 23644046		
23644105		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120
Sbjct 23644106		
23644165		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCTGATG	180
Sbjct 23644166		
23644225		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240
Sbjct 23644226		
23644285		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGA	300
Sbjct 23644286		
23644345		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334
Sbjct 23644346	 G	23644379

PREDICTED: Brassica napus acetolactate synthase 1, chloroplastic (LOC106353715), mRNA

Sequence ID: [XM_013793507.2](#)Length: 2244Number of Matches: 1

Related Information

[Gene-associated gene details](#)

[Genome Data Viewer](#)-aligned genomic context

Range 1: 1406 to 1739[GenBankGraphics](#)Next MatchPrevious Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1406		1465		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		

```

Sbjct  1466  ..... 1525
Query  121  TCGGAGCTATGGGTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCCTGATG 180
Sbjct  1526  ..... 1585
Query  181  CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240
Sbjct  1586  ..... 1645
Query  241  CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300
Sbjct  1646  ..... 1705
Query  301  TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
Sbjct  1706  .....G ..... 1739

```

PREDICTED: Brassica napus acetolactate synthase 1, chloroplastic (LOC106353716), mRNA

Sequence ID: [XM_013793508.2](#) Length: 2242 Number of Matches: 1

Related Information

[Gene](#)-associated gene details

[Genome Data Viewer](#)-aligned genomic context

Range 1: 1404 to 1737 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

	Score	Expect	Identities	Gaps	Strand	
	599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus	
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA					60
Sbjct 1404						1463
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCTCGTCATCAGGCC					120
Sbjct 1464						1523
Query 121	TCGGAGCTATGGGTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCCTGATG					180
Sbjct 1524						1583
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA					240
Sbjct 1584						1643
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA					300
Sbjct 1644						1703
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334					
Sbjct 1704	G 1737					

PREDICTED: Brassica napus acetolactate synthase 1, chloroplastic (LOC106366633), mRNA

Sequence ID: [XM_013806285.2](#) Length: 2244 Number of Matches: 1

Related Information

[Gene](#)-associated gene details

[Genome Data Viewer](#)-aligned genomic context

Range 1: 1406 to 1739 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

	Score	Expect	Identities	Gaps	Strand	
	599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus	

Query	1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60
Sbjct	1406		1465
Query	61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120
Sbjct	1466		1525
Query	121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180
Sbjct	1526		1585
Query	181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240
Sbjct	1586		1645
Query	241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300
Sbjct	1646		1705
Query	301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334
Sbjct	1706	 G	1739

PREDICTED: Brassica napus acetolactate synthase 1, chloroplastic (LOC106366634), mRNA

Sequence ID: [XM_013806286.2](#) Length: 2244 Number of Matches: 1

Related Information

[Gene](#)-associated gene details

[Genome Data Viewer](#)-aligned genomic context

Range 1: 1406 to 1739 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1406		1465		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1466		1525		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1526		1585		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1586		1645		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1646		1705		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 1706	 G	1739		

Brassica napus isolate K5 actohydroxyacid synthase 1 gene, complete cds

Sequence ID: [KP985786.1](#) Length: 1968 Number of Matches: 1

Range 1: 1364 to 1697 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		

```

Sbjct  1364  ..... 1423

Query  61    TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120
Sbjct  1424  ..... 1483

Query  121   TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCCTGATG 180
Sbjct  1484  ..... 1543

Query  181   CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240
Sbjct  1544  ..... 1603

Query  241   CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300
Sbjct  1604  ..... 1663

Query  301   TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
Sbjct  1664  .....G ..... 1697

```

PREDICTED: Brassica oleracea var. oleracea acetolactate synthase 1, chloroplastic (LOC106310919), mRNA

Sequence ID: [XM_013748148.1](#) Length: 2187 Number of Matches: 1

Related Information

[Gene](#)-associated gene details

[Genome Data Viewer](#)-aligned genomic context

Range 1: 1403 to 1736 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1403 1462				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1463 1522				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCCTGATG 180				
Sbjct 1523 1582				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240				
Sbjct 1583 1642				
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300				
Sbjct 1643 1702				
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 1703G 1736				

Brassica carinata cultivar Dodalla acetolactate synthetase (ALS1) gene, complete cds

Sequence ID: [KM816835.1](#) Length: 1968 Number of Matches: 1

- [See 1 more title\(s\)](#) [See all Identical Proteins \(IPG\)](#)

Range 1: 1364 to 1697 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus

Query	1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60
Sbjct	1364		1423
Query	61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120
Sbjct	1424		1483
Query	121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180
Sbjct	1484		1543
Query	181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240
Sbjct	1544		1603
Query	241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300
Sbjct	1604		1663
Query	301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334
Sbjct	1664	 G	1697

Brassica oleracea cultivar Texuan zhonggan No.11 acetolactate synthetase (ALS1) gene, complete cds

Sequence ID: [KM816819.1](#) Length: 1968 Number of Matches: 1

Related Information

[Gene](#)-associated gene details

Range 1: 1364 to 1697 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1364		1423		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1424		1483		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1484		1543		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1544		1603		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1604		1663		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 1664	 G	1697		

Brassica napus cultivar Zhongshuang No.9 acetolactate synthetase (ALS1) gene, complete cds

Sequence ID: [KM816810.1](#) Length: 1968 Number of Matches: 1

- [See 4 more title\(s\)](#) [See all Identical Proteins \(IPG\)](#)

Range 1: 1364 to 1697 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		

```

Sbjct  1364  ..... 1423

Query  61    TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120
Sbjct  1424  ..... 1483

Query  121   TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180
Sbjct  1484  ..... 1543

Query  181   CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240
Sbjct  1544  ..... 1603

Query  241   CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300
Sbjct  1604  ..... 1663

Query  301   TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
Sbjct  1664  .....G ..... 1697

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Brassica napus cultivar SH11 SH11 acetohydroxyacid synthase (ALS1) gene, complete cds

Sequence ID: [KM816807.1](#) Length: 1968 Number of Matches: 1

- [See 1 more title\(s\)](#) [See all Identical Proteins \(IPG\)](#)

Related Information

[Gene](#)-associated gene details

Range 1: 1364 to 1697 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA			60	
Sbjct 1364			1423	
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC			120	
Sbjct 1424			1483	
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG			180	
Sbjct 1484			1543	
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA			240	
Sbjct 1544			1603	
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA			300	
Sbjct 1604			1663	
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 1664G 1697				

Brassica napus cultivar N415 acetohydroxyacid synthase (ALS1) gene, complete cds

Sequence ID: [GU192448.1](#) Length: 2006 Number of Matches: 1

Range 1: 1384 to 1717 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA			60	
Sbjct 1384			1443	

Query	61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120
Sbjct	1444		1503
Query	121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180
Sbjct	1504		1563
Query	181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240
Sbjct	1564		1623
Query	241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300
Sbjct	1624		1683
Query	301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334
Sbjct	1684	 G	1717

B.napus gene for actohydroxyacid synthase I

Sequence ID: [Z11524.1](#)**Length:** 4724**Number of Matches:** 1

Related Information

[Gene](#)-associated gene details

Range 1: 3872 to 4205[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 3872		3931		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 3932		3991		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 3992		4051		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 4052		4111		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 4112		4171		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 4172	 G	4205		

B.napa acetolactate synthase mRNA, complete cds

Sequence ID: [M60068.1](#)**Length:** 2019**Number of Matches:** 1

Range 1: 1234 to 1567[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
599 bits (663)	8e-167	333/334 (99%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1234		1293		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1294		1353		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		

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Sbjct  1354  ..... 1413

Query  181  CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240
Sbjct  1414  ..... 1473

Query  241  CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300
Sbjct  1474  ..... 1533

Query  301  TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
Sbjct  1534  .....G .....1567

```

Brassica napus cultivar SH11 SH11 acetohydroxyacid synthase (ALS3) gene, complete cds

Sequence ID: [KM816809.1](#) Length: 1959 Number of Matches: 1

Related Information

[Gene](#)-associated gene details

Range 1: 1355 to 1688 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
590 bits (653)	4e-164	331/334 (99%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1355A.....C..... 1414				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1415 1474				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCCTGATG 180				
Sbjct 1475 1534				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240				
Sbjct 1535 1594				
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300				
Sbjct 1595 1654				
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 1655G 1688				

Brassica rapa cultivar Rapido acetolactate synthetase (ALS3) gene, complete cds

Sequence ID: [KM816834.1](#) Length: 1959 Number of Matches: 1

Related Information

[Gene](#)-associated gene details

Range 1: 1355 to 1688 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
572 bits (633)	1e-158	327/334 (98%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1355C..... 1414				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1415A.....G.....A..... 1474				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCCTGATG 180				

Sbjct 1475C..... 1534

Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240

Sbjct 1535C..... 1594

Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300

Sbjct 1595 1654

Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334

Sbjct 1655G.....1688

Brassica rapa cultivar Opava acetolactate synthetase (ALS3) gene, complete cds

Sequence ID: [KM816832.1](#)Length: 1959Number of Matches: 1

Related Information

[Gene](#)-associated gene details

Range 1: 1355 to 1688[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
572 bits (633)	1e-158	327/334 (98%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1355C..... 1414				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1415A.....G.....A..... 1474				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180				
Sbjct 1475C..... 1534				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240				
Sbjct 1535C..... 1594				
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300				
Sbjct 1595 1654				
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 1655G..... 1688				

Brassica juncea cultivar Qianxiniuweiyoucai acetolactate synthetase (ALS3) gene, complete cds

Sequence ID: [KM816826.1](#)Length: 1959Number of Matches: 1

Range 1: 1355 to 1688[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
572 bits (633)	1e-158	327/334 (98%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1355C..... 1414				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1415G.....A..... 1474				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180				
Sbjct 1475C..... 1534				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240				

Sbjct 1535C.....C1594

Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300

Sbjct 15951654

Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334

Sbjct 1655G1688

PREDICTED: Brassica rapa acetolactate synthase 3, chloroplastic (LOC103874743), mRNA

Sequence ID: [XM_009153182.3](#)**Length:** 2211**Number of Matches:** 1

Range 1: 1405 to 1738[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
567 bits (628)	1e-157	326/334 (98%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1405A.....C1464				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1465G.....C....A. 1524				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180				
Sbjct 1525C1584				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240				
Sbjct 1585C1644				
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300				
Sbjct 16451704				
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 1705G1738				

Brassica rapa genome, scaffold: A01

Sequence ID: [LR031571.1](#)**Length:** 37915545**Number of Matches:** 1

Range 1: 14097918 to 14098251[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
567 bits (628)	1e-157	326/334 (98%)	0/334 (0%)	Plus/Plus

Features:

[unnamed protein product](#)

Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60	
Sbjct 14097918A.....C14097977	
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120	
Sbjct 14097978G.....C....A. 14098037	
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180	
Sbjct 14098038C14098097	
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240	

Sbjct 14098098C.....
14098157

Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300
Sbjct 14098158
14098217

Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
Sbjct 14098218G14098251

Brassica napus isolate K1 actohydroxyacid synthase 3 gene, complete cds

Sequence ID: [KP985783.1](#) Length: 1959 Number of Matches: 1

- [See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Related Information

[Gene](#)-associated gene details

Range 1: 1355 to 1688 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
567 bits (628)	1e-157	326/334 (98%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1355A.....C..... 1414				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1415G.....C....A. 1474				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCTGATG 180				
Sbjct 1475C..... 1534				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240				
Sbjct 1535C..... 1594				
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300				
Sbjct 1595 1654				
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 1655G..... 1688				

Brassica rapa cultivar Binxianyimenyoucai acetolactate synthetase (ALS3) gene, complete cds

Sequence ID: [KM816830.1](#) Length: 1959 Number of Matches: 1

Related Information

[Gene](#)-associated gene details

Range 1: 1355 to 1688 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
567 bits (628)	1e-157	326/334 (98%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1355A.....C..... 1414				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1415G.....C....A. 1474				

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Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCTGATG 180
Sbjct 1475 .....C..... 1534

Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240
Sbjct 1535 .....C..... 1594

Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300
Sbjct 1595 ..... 1654

Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
Sbjct 1655 .....G..... 1688

```

Brassica juncea cultivar Weiyuandahuangjie acetolactate synthetase (ALS3) gene, complete cds

Sequence ID: [KM816822.1](#) Length: 1959 Number of Matches: 1

- [See 2 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Related Information

[Gene](#)-associated gene details

Range 1: 1355 to 1688 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

	Score	Expect	Identities	Gaps	Strand
	567 bits (628)	1e-157	326/334 (98%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA			60	
Sbjct 1355	A.....C.....			1414	
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC			120	
Sbjct 1415	G.....C....A.			1474	
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCTGATG			180	
Sbjct 1475	C.....			1534	
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA			240	
Sbjct 1535	C.....			1594	
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA			300	
Sbjct 1595				1654	
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 1655	G..... 1688				

Brassica napus cultivar Zhongshuang No.9 acetolactate synthetase (ALS3) gene, complete cds

Sequence ID: [KM816812.1](#) Length: 1959 Number of Matches: 1

- [See 3 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Related Information

[Gene](#)-associated gene details

Range 1: 1355 to 1688 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

	Score	Expect	Identities	Gaps	Strand
	567 bits (628)	1e-157	326/334 (98%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA			60	
Sbjct 1355	A.....C.....			1414	

```

Query 61      TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120
Sbjct 1415    .....G.....C....A. 1474

Query 121     TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180
Sbjct 1475    .....C..... 1534

Query 181     CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240
Sbjct 1535    .....C..... 1594

Query 241     CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300
Sbjct 1595    ..... 1654

Query 301     TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
Sbjct 1655    .....G.....1688

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Brassica rapa subsp. pekinensis BrALS3 gene for acetolactate synthase, complete cds

Sequence ID: [AB618066.1](#) Length: 4988 Number of Matches: 1

Range 1: 3672 to 4005 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
567 bits (628)	1e-157	326/334 (98%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA			60	
Sbjct 3672A.....C.....			3731	
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC			120	
Sbjct 3732G.....C....A. 3791				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG			180	
Sbjct 3792C..... 3851				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA			240	
Sbjct 3852C..... 3911				
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA			300	
Sbjct 3912 3971				
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 3972G..... 4005				

B.napus gene for acetohydroxyacid synthase III

Sequence ID: [Z11526.1](#) Length: 3386 Number of Matches: 1

Related Information

[Gene](#)-associated gene details

Range 1: 1612 to 1945 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
567 bits (628)	1e-157	326/334 (98%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA			60	
Sbjct 1612A.....C.....1671				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC			120	
Sbjct 1672G.....C....A. 1731				

Query	121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180
Sbjct	1732	 C	1791
Query	181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240
Sbjct	1792	 C	1851
Query	241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300
Sbjct	1852		1911
Query	301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334
Sbjct	1912	 G	1945

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161825R2

Sequence ID: [AJ344991.1](#)**Length:** 1758**Number of Matches:** 1

Range 1: 1154 to 1487[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
524 bits (580)	1e-144	316/334 (95%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1154	 G T T .. C	1213		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1214	 A .. A G T .. N	1273		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1274	.. T C T C	1333		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1334	 C C N C	1393		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1394	 G	1453		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 1454		1487		

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161825R0

Sequence ID: [AJ344990.1](#)**Length:** 1758**Number of Matches:** 1

Range 1: 1154 to 1487[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
520 bits (576)	2e-143	315/334 (94%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1154	 G T T .. C	1213		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1214	 A .. A G T .. A	1273		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1274	.. T C T C	1333		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1334	 N C A C	1393		

Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300
Sbjct 1394**G**1453

Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
Sbjct 1454**K**1487

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161855R1

Sequence ID: [AJ344995.1](#) Length: 1230 Number of Matches: 1

Range 1: 626 to 959 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
519 bits (575)	6e-143	315/334 (94%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 626 G T T .. C N 685				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 686 A .. A G T .. N 745				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180				
Sbjct 746 .. T C C C 805				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240				
Sbjct 806 C A C 865				
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300				
Sbjct 866 G 925				
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 926 G 959				

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161653S2

Sequence ID: [AJ344985.1](#) Length: 1758 Number of Matches: 1

Range 1: 1154 to 1487 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
518 bits (574)	6e-143	315/334 (94%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1154 G T T .. C N 1213				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1214 A .. A G T .. A 1273				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180				
Sbjct 1274 .. T C C C 1333				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240				
Sbjct 1334 C A C 1393				
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300				
Sbjct 1394 G 1453				
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				

Sbjct 1454G1487

PREDICTED: Raphanus sativus acetolactate synthase 3, chloroplastic (LOC108842604), mRNA

Sequence ID: [XM_018615577.1](#)**Length:** 2205**Number of Matches:** 1

Related Information

[Gene](#)-associated gene details

[Genome Data Viewer](#)-aligned genomic context

Range 1: 1416 to 1749[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
517 bits (573)	2e-142	315/334 (94%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1416	T.....T..C.....	1475		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1476	A..A.....G.....T...A.....	1535		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1536	.T.....C.....T.....C.....	1595		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1596	C.....C.....A.....C.....	1655		
Query 241	CAATCCGTGTAGAGAATCTTCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1656	G.....	1715		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 1716	G...G.....	1749		

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161829R1

Sequence ID: [AJ344993.1](#)**Length:** 1758**Number of Matches:** 1

Range 1: 1154 to 1487[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
517 bits (573)	2e-142	315/334 (94%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1154	G.....T.....T..C.....A.....	1213		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1214	A..A.....G.....T...A.....	1273		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1274	.T.....C.....C.....C.....	1333		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1334	C.....A.....C.....	1393		
Query 241	CAATCCGTGTAGAGAATCTTCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1394	G.....	1453		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		

Sbjct 1454G1487

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161829R0

Sequence ID: [AJ344992.1](#)**Length:** 1758**Number of Matches:** 1

Range 1: 1154 to 1487[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
517 bits (573)	2e-142	315/334 (94%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1154	G.....T.....T..C.....A.....	1213		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1214	A..A.....G.....T...A.....	1273		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1274	.T.....C.....C.....C.....	1333		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1334	C.....A.....C.....	1393		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1394	G.....	1453		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 1454	G.....	1487		

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161789S1

Sequence ID: [AJ344986.1](#)**Length:** 1758**Number of Matches:** 1

- [See 1 more title\(s\)](#) [See all Identical Proteins\(IPG\)](#)

Related Information

[Gene](#)-associated gene details

Range 1: 1154 to 1487[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
517 bits (573)	2e-142	315/334 (94%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1154	G.....T.....T..C.....A.....	1213		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1214	A..A.....G.....T...A.....	1273		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1274	.T.....C.....C.....C.....	1333		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1334	C.....A.....C.....	1393		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1394	G.....	1453		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 1454	G.....	1487		

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161855R0

Sequence ID: [AJ344994.1](#)**Length:** 1758**Number of Matches:** 1

Range 1: 1154 to 1487[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
515 bits (570)	7e-142	314/334 (94%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA			60	
Sbjct 1154G.....T.....T..C.....C.....N.....			1213	
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC			120	
Sbjct 1214A..A.....G.....T...A.....			1273	
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCTGATG			180	
Sbjct 1274 .T.....C.....N.....C.....			1333	
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA			240	
Sbjct 1334C.....A.....C.....			1393	
Query 241 CAATCCGTGTAGAGAATCTTCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA			300	
Sbjct 1394G.....			1453	
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334			
Sbjct 1454G..... 1487				

Raphanus raphanistrum isolate WARR30Leu574 acetohydroxyacid synthase gene, partial cds

Sequence ID: [JQ982498.1](#)**Length:** 1818**Number of Matches:** 1

Range 1: 1219 to 1552[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
514 bits (569)	3e-141	311/334 (93%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA			60	
Sbjct 1219Y.....G..M..T.....T..C.....R.....			1278	
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC			120	
Sbjct 1279A..A.....G.....T...A.....			1338	
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCTGATG			180	
Sbjct 1339 .T.....C.....Y.....K.....C.....			1398	
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA			240	
Sbjct 1399 .R.....Y.....C.....W.....Y.....			1458	
Query 241 CAATCCGTGTAGAGAATCTTCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA			300	
Sbjct 1459G.....			1518	
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334			
Sbjct 1519 1552				

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161653S1

Sequence ID: [AJ344984.1](#)**Length:** 1758**Number of Matches:** 1

Range 1: 1154 to 1487[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
514 bits (569)	3e-141	314/334 (94%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1154	G.....T.....T..C.....C.....N.....	1213		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1214	A..A.....G.....T...A.....	1273		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1274	.T.....C.....C.....C.....	1333		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1334	C.....A.....C.....	1393		
Query 241	CAATCCGTGTAGAGAATCTTCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1394	G.....	1453		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 1454	G.....	1487		

Raphanus sativus genome assembly, chromosome: 5

Sequence ID: [LR778314.1](#)**Length:** 43617977**Number of Matches:** 1

Range 1: 22853721 to 22854054[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
513 bits (568)	3e-141	314/334 (94%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 22853721	G.....T.....T..C.....C.....A.....			
22853780				
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 22853781	A..A.....G.....T...A.....			
22853840				
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 22853841	.T.....C.....C.....C.....			
22853900				
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 22853901	C.....A.....C.....			
22853960				
Query 241	CAATCCGTGTAGAGAATCTTCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 22853961	G.....			
22854020				
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 22854021	G.....	22854054		

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161654R1

Sequence ID: [AJ344989.1](#)**Length:** 1758**Number of Matches:** 1

Range 1: 1154 to 1487[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
513 bits (568)	3e-141	314/334 (94%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		

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Sbjct 1154 .....G.....T.....T..C.....A..... 1213
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120
Sbjct 1214 .....A..A.....G.....T...A.....A. 1273
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCCTGATG 180
Sbjct 1274 .T.....C.....T.....C..... 1333
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240
Sbjct 1334 .....C.....A.....C..... 1393
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300
Sbjct 1394 .....G..... 1453
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
Sbjct 1454 .....G..... 1487

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Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161654R0

Sequence ID: [AJ344988.1](#)**Length:** 1758**Number of Matches:** 1

Range 1: 1154 to 1487[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
513 bits (568)	3e-141	314/334 (94%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1154G.....T.....T..C.....A..... 1213				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1214A..A.....G.....T...A.....A. 1273				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCCTGATG 180				
Sbjct 1274 .T.....C.....T.....C..... 1333				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240				
Sbjct 1334C.....A.....C..... 1393				
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA 300				
Sbjct 1394G..... 1453				
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 1454G..... 1487				

Raphanus raphanistrum isolate WARR30Asp122 acetohydroxyacid synthase gene, partial cds

Sequence ID: [JQ982497.1](#)**Length:** 1818**Number of Matches:** 1

Range 1: 1219 to 1552[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
509 bits (564)	3e-140	310/334 (93%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1219	 Y G .. M .. T T .. C R	1278		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1279	 A .. A G T .. A	1338		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCCTGATG	180		
Sbjct 1339	.. T C Y K C	1398		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1399	.. R Y C W Y	1458		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1459	 G	1518		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 1519	 G	1552		

Raphanus raphanistrum isolate WARR30Tyr122 acetohydroxyacid synthase gene, partial cds

Sequence ID: [JQ982496.1](#)**Length:** 1818**Number of Matches:** 1

Range 1: 1219 to 1552[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
509 bits (564)	3e-140	310/334 (93%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1219	 Y G .. M .. T T .. C R	1278		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1279	 A .. A G T .. A	1338		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCCTGATG	180		
Sbjct 1339	.. T C Y K C	1398		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1399	.. R Y C W Y	1458		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1459	 G	1518		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC	334		
Sbjct 1519	 G	1552		

Raphanus raphanistrum partial als gene for putative acetolactate synthase, specimen voucher 161789S2

Sequence ID: [AJ344987.1](#)**Length:** 1758**Number of Matches:** 1

Range 1: 1154 to 1487[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
509 bits (564)	3e-140	313/334 (94%)	0/334 (0%)	Plus/Plus

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Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60
Sbjct 1154 .....G..A..T.....T..C.....A..... 1213

Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120
Sbjct 1214 .....A..A.....G.....T....A..... 1273

Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180
Sbjct 1274 .T.....C.....C.....C..... 1333

Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240
Sbjct 1334 .....N.....C.....A.....C..... 1393

Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGA 300
Sbjct 1394 .....G..... 1453

Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
Sbjct 1454 .....G ..... 1487

```

Sinapis arvensis Theodore_1 putative acetolactate synthase (ALS) gene, partial cds

Sequence ID: [AY964663.1](#) Length: 1730 Number of Matches: 1

Range 1: 1139 to 1472 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
504 bits (558)	1e-138	312/334 (93%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1139GC.T.....C.....G..AA. 1198				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1199A.....G.....T....A..... 1258				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180				
Sbjct 1259 .T.....C..C.....C.....C..... 1318				
Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240				
Sbjct 1319 .C.....C.....C..... 1378				
Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGA 300				
Sbjct 1379GC. 1438				
Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334				
Sbjct 1439T 1472				

Sinapis arvensis Theodore_2 putative acetolactate synthase (ALS) gene, partial cds

Sequence ID: [AY964664.1](#) Length: 1726 Number of Matches: 1

Range 1: 1139 to 1472 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
501 bits (555)	2e-137	311/334 (93%)	0/334 (0%)	Plus/Plus
Query 1 TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA 60				
Sbjct 1139GC.T.....C.....G..AA. 1198				
Query 61 TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC 120				
Sbjct 1199A.....G.....T....A..... 1258				
Query 121 TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG 180				

Sbjct 1259 ..T.....C..C.....C.....C..... 1318

Query 181 CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA 240

Sbjct 1319 ..C.....C.....C.....C..... 1378

Query 241 CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTGTGTTAAACAACCAGCATCTTGGGA 300

Sbjct 1379GC. 1438

Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334

Sbjct 1439T.....K 1472

Sinapis arvensis biotype MHS3 acetolactate synthase gene, partial cds

Sequence ID: [KP661600.1](#) Length: 1572 Number of Matches: 1

Range 1: 1053 to 1386 [GenBankGraphics](#) Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
499 bits(553)	6e-137	311/334 (93%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1053	GC.T.....C.....G..AA.	1112		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1113	A.....G.....T....A.....	1172		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1173	..T.....C..C.....C.....C.....	1232		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1233	..C.....C.....C.....C.....	1292		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTGTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1293	GC.	1352		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334			
Sbjct 1353	T.....G 1386			

Sinapis arvensis biotype RHR4 acetolactate synthase gene, partial cds

Sequence ID: [KP661599.1](#) Length: 1601 Number of Matches: 1

Range 1: 1037 to 1370 [GenBankGraphics](#) Next Match Previous Match

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
499 bits(553)	6e-137	311/334 (93%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1037	GC.T.....C.....G..AA.	1096		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1097	A.....G.....T....A.....	1156		
Query 121	TCGGAGCTATGGGTTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1157	..T.....C..C.....C.....C.....	1216		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1217	..C.....C.....C.....C.....	1276		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTGTGTTAAACAACCAGCATCTTGGGA	300		
Sbjct 1277	GC.	1336		

Query 301 TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334
 Sbjct 1337T.....G1370

Sinapis arvensis biotype MRS acetolactate synthase (ALS) gene, partial cds

Sequence ID: [FJ655877.1](#) Length: 1670 Number of Matches: 1

Range 1: 1075 to 1408 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
499 bits(553)	6e-137	311/334 (93%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1075	GC.T.....C.....G..A....A.	1134		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1135	A.....G.....T....A.....	1194		
Query 121	TCGGAGCTATGGGTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1195	.T.....C..C.....C.....C.....	1254		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1255	.C.....C.....C.....	1314		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTGTAAACAACCAGCATCTTGGGA	300		
Sbjct 1315	G.....C.	1374		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334			
Sbjct 1375	T.....G1408			

Sinapis arvensis biotype KNF2 acetolactate synthase (ALS) gene, partial cds

Sequence ID: [FJ655875.1](#) Length: 1672 Number of Matches: 1

Range 1: 1077 to 1410 [GenBankGraphics](#) [Next Match](#) [Previous Match](#)

Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
499 bits(553)	6e-137	311/334 (93%)	0/334 (0%)	Plus/Plus
Query 1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	60		
Sbjct 1077	GC.T.....C.....G..A....A.	1136		
Query 61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC	120		
Sbjct 1137	A.....G.....T....A.....	1196		
Query 121	TCGGAGCTATGGGTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG	180		
Sbjct 1197	.T.....C..C.....C.....C.....	1256		
Query 181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA	240		
Sbjct 1257	.C.....C.....C.....	1316		
Query 241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTGTAAACAACCAGCATCTTGGGA	300		
Sbjct 1317	G.....C.	1376		
Query 301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC 334			
Sbjct 1377	T.....G1410			

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**Sinapis arvensis Wetaskiwin_6 putative acetolactate synthase
(ALS) gene, partial cds**

Sequence ID: [AY964662.1](#)**Length:** 1730**Number**

of Matches: 1 Range 1: 1139 to

1472[GenBankGraphics](#)[Next Match](#)[Previous Match](#)

Alignment statistics for match #1

	Score		Expect	Identities	
			Gaps	Strand 499 bits(553)	
Query	1	TCCTCGACGAGCTAACCGAAGGGAAGGCAATTATCAGTACTGGTGTGGACAGCATCAGA	6e-137	311/334 (93%)	60
Sbjct	1139	GC.T.....C.....G..A....A.			1198
			0/334 (0%) Plus/Plus		
Query	61	TGTGGGCGGCGCAGTTTTACAAGTACAGGAAGCCGAGACAGTGGCTGTCGTCATCAGGCC			120
Sbjct	1199	A.....G.....T....A.....			1258
Query	121	TCGGAGCTATGGGTTTGGACTTCCTGCTGCGATTGGAGCGTCTGTGGCGAACCCTGATG			180
Sbjct	1259	.T.....C..C.....C.....C.....			1318
Query	181	CGATTGTTGTGGATATTGACGGTGATGGAAGCTTCATAATGAACGTTCAAGAGCTGGCCA			240
Sbjct	1319	.C.....C.....C.....			1378
Query	241	CAATCCGTGTAGAGAATCTTCCTGTGAAGATACTCTTGTTAAACAACCAGCATCTTGGGA			300
Sbjct	1379	G.....C.			1438
Query	301	TGGTCATGCAATTGGAAGATCGGTTCTACAAAGC		334	
Sbjct	1439	T.....G.....		1472	