

# A Isolate query aligned to *C. kamaaina* subject

Range 1: 12 to 692 [GenBank](#) [Graphics](#) [Next Match](#) [Previous](#)

Score	Expect	Identities	Gaps	Strand
815 bits(441)	0.0	619/698(89%)	42/698(6%)	Plus/Minus
Query 1	AATCGTAAGGACTTCGGACATACGACATCACTGGAAGACTACACCTATACGCCACATGTC	60		
Sbjct 692	AATCGTAAGGACTTCGGACATACGACATCACTGGAAGACTACACCTATACGCCACATGTC	633		
Query 61	GTAGCAGCCAATGACTGAACGATTTCGGCGCTGGGCTCTTCCCGTTTCACTCGCGTTACT	120		
Sbjct 632	GTAGCAGCCAATGACTGAACGATTTCGGCGCTGGGCTCTTCCCGTTTCACTCGCGTTACT	573		
Query 121	AAGGGAATCCTTTTCTAGTTTCTTTCTCCGCTAAATGATATGCTTAAGTTCAAGCGGTA	180		
Sbjct 572	AAGGGAATCCTTTTCTAGTTTCTTTCTCCGCTAAATGATATGCTTAAGTTCAAGCGGTA	513		
Query 181	ATCACGACTGAGTTTCAGGTTGGAATAGCAAGACGCACACTCTTAGGTCAACGTCATCA	240		
Sbjct 512	ATCACGACTGAGTTTCAGGTTGGAATAGCAAGACGCACACTCTTAGGTCAACGTCATCA	459		
Query 241	ATGACGATCGTCGTCGACCAACGAATCTCTTTATATGTTTG--CAATCGAGCGGCATA	299		
Sbjct 458	A--GACGA--CGA--CTTCAACGAATCTCTTTAAACGTTAGGCAATCGAGCGGCATA	407		
Query 300	CCGGTCTGACTTCACA--TAAGCAGCAACATCCGATTTCGA---GCACAATCAAAGACAGT	355		
Sbjct 4	CCGGTCTGACTTCAAAATAGGCAGCAACATTCTCCGCCAGCCGACCAATCAGAGACAGT	347		
Query 356	TATGATACACGCTCTTGATGCACAACAAAGTGAACATCAGAAAGTCAAGTTGGTCGCC--T	414		
Sbjct 346	TATGATACACGCTCTTGATGCACAACGAGGTGAACATCAGAAAGTCAAGTTGGTCGCCAT	287		
Query 415	TTAGCAGCCCTA--TCGCTCAACAAAGCAAAGAGAAGCGCGTCCCATTACGAATGACTCCT	473		
Sbjct 286	TTGGCAGCCCAAATTGCTAACACAAGCAAAGAGAAGCGCGTCCCATTACGGATGACTCGT	227		
Query 474	TGGAGAGAGGAGCCACCCGACTTGAGATGCTTTCTTACTGGAATAAGATCAGACGACGC--	532		
Sbjct 226	TAGAGAGAC--AG--AGCCGACTTGAGATGCTTTCTGACTGGAATAAGATCGGGCGACAC	170		
Query 533	CG--A--AA--CGT--C--T---CCCAATGTACTCGACAAGCCGAAACGAA--AA--AAC--	577		
Sbjct 169	CGTATGAAAACGCGCGTGCACCAATGTGTACTCGACAAGCCGAAACGCAATGAACG	110		
Query 578	--GAATTCGACAGTAGGTTAAACAACCTGAACACAGCTACCGACTGGNGACCCAGTCG	635		
Sbjct 109	AAGAAATTCGACAGTAAGTTAAACAACCTGAACACAGCTACCGACTGGAGACCCAGTCG	50		
Query 636	GTGCTATGCGTTTCGAAATTTTACCACCTCTAAGCGTCTG	673		
Sbjct 49	GTGCTATGCGTTTCGAAATTTTACCACCTCTAAGCGTCTG	12		

# B Isolate query aligned to *C. oiwi* subject

Range 1: 76 to 706 [GenBank](#) [Graphics](#) [Next Match](#) [Previous](#)

Score	Expect	Identities	Gaps	Strand
1157 bits(626)	0.0	630/632(99%)	1/632(0%)	Plus/Minus
Query 1	GCACCCCTCTCTGGTTTATGGCCCTCAATCGTAAGGACTTCGGACATACGACATCACTGGAA	60		
Sbjct 706	GCACCCCTCTCTGGTTTATGGCCCTCAATCGTAAGGACTTCGGACATACGACATCACTGGAA	647		
Query 61	GACTACACCTATACGCCACATGTCGTAGCAGCAATGACTGAACGATTTCGGCGCTGGGCT	120		
Sbjct 646	GACTACACCTATACGCCACATGTCGTAGCAGCAATGACTGAACGATTTCGGCGCTGGGCT	587		
Query 121	CTTCCCGTTTCACTCGCCGTTACTAAGGGAATCCTTTTCTAGTTTCTTTCTCCGCTAAA	180		
Sbjct 586	CTTCCCGTTTCACTCGCCGTTACTAAGGGAATCCTTTTCTAGTTTCTTTCTCCGCTAAA	527		
Query 181	TGATATGCTTAAAGTTACAGCGGTAATCACGACTGAGTTCAAGTTGAGAATAGCAAGACGC	240		
Sbjct 526	TGATATGCTTAAAGTTACAGCGGTAATCACGACTGAGTTCAAGTTGAGAATAGCAAGACGC	467		
Query 241	ACACTGTTAGGTCAACGTCATCAATGACGATCGTCGTCGACCAACAACGAATCTCTTTA	300		
Sbjct 466	ACACTGTTAGGTCAACGTCATCAATGACGATCGTCGTCGACCAACAACGAATCTCTTTA	407		
Query 301	TATGTTTGCAATCGAGCGGCACACCGGCTGACTTCACATAAGCAGCAACATCCGATTTCG	360		
Sbjct 6	TATGTTTGCAATCGAGCGGCACACCGGCTGACTTCACATAAGCAGCAACATCCGATTTCG	347		
Query 361	AGCACAATCAAAGACAGCTTATGATACACGTCCTTGATGCACCTCAAAGTGAACATCACAG	420		
Sbjct 346	AGCACAATCAAAGACAGCTTATGATACACGTCCTTGATGCACCTCAAAGTGAACATCACAG	287		
Query 421	AAGTCAAGTTGGTCGCTTTAGCAGCCCTATCGCTCACAAAAGCAAAGAGAAGCGCGTCC	480		
Sbjct 286	AAGTCAAGTTGGTCGCTTTAGCAGCCCTATCGCTCACAAAAGCAAAGAGAAGCGCGTCC	227		
Query 481	CATTACGAATGACTCCTAGGAGAGAGGAGCCACCCGACTTGAGATGCTTCTTTACTGGAA	540		
Sbjct 226	CATTACGAATGACTCCTAGGAGAGAGGAGCCACCCGACTTGAGATGCTTCTTTACTGGAA	167		
Query 541	ATAAGATCAGACGACGCCGAAACGCTCTCCAATGTTACTCGACAAGCCGAAACGAANAA	600		
Sbjct 166	--TAAGATCAGACGACGCCGAAACGCTCTCCAATGTTACTCGACAAGCCGAAACGAAGAA	108		
Query 601	ACGAATTCGACAGTAGGTTAAACAACCTGAA	632		
Sbjct 107	ACGAATTCGACAGTAGGTTAAACAACCTGAA	76		