

## Specimen Details Current

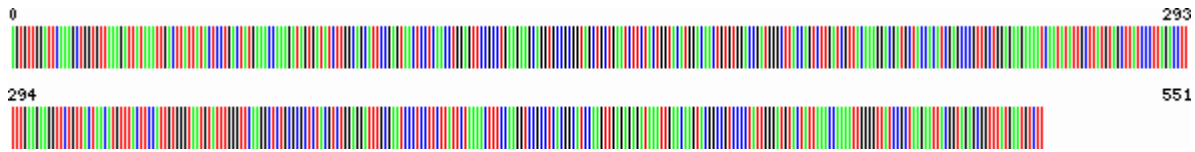
**Sample ID:** GCUL-FDGK-469  
**Process ID:** GCUDG469-13  
**Project:** GCUDG  
**Tax Names:** Magnoliophyta, Magnoliopsida, Fabales, Fabaceae, Acacia, Acacia brownii  
**Taxon:** Acacia brownii  
**Rank Name:** species  
**Sampling Protocol:** N/A  
**BIN URI:** N/A  
**Kingdom:** Plantae

## Marker Summary

Marker Code	Sequence Length	GC	Ambiguous	Trace Count
rbcLa	552	43.5%	0%	2
matK	810	32.8%	0%	2

## rbcLa

### Illustrative Barcode



### Nucleotide Sequence

AGTGTGGATTCAAAGCTGGTGTAAAGATTATAAATTGACTTATTATACTCCTGACTATGAAACAAA  
 GATAGTGATATCTTGGCAGCATTCAGTAACCTCAACCTGGAGTTCCGCCTGAAGAAGCAGGTGCC  
 GCGGTAGCTGCTGAATCTTCTACTGGTACATGGACAACCTGTGTGGACCGATGGGTTACCAAGTCTTGAT  
 CGTTACAAGGACGATGCTACCACATCGAGCCGGTTGCTGGAGAAGAAAATCAATATATGGCTTATGTA  
 GCTTATCCCTTAGACCTTTTGAAGAAGTTCTGTTACTAACATGTTTACTTCCATTGTGGGTAATGTA  
 TTTGGGTTCAAGGCTCTGCGCGCTCTACGCTGGAGGATTTGCGAATCCCTCCTTCTTATTCTAAAAC  
 TTCCAAGGTCGGCCTCACGGCATCCAAGTTGAGAGAGATAAATGGAACAAGTACGGCCGTCCTTATG  
 GGATGTACTATTAAACCAAATGGGGTTATCCGCTAAGAATTACGGTAGAGCGGTTTATGAATGTCTT

### Sequence Metadata

**Genbank Accession:** N/A  
**Translation Matrix:** Standard Code  
**Last Updated:** 2013-07-11 13:17:23.580319  
**Sequence Runsite:** Biodiversity Institute of Ontario

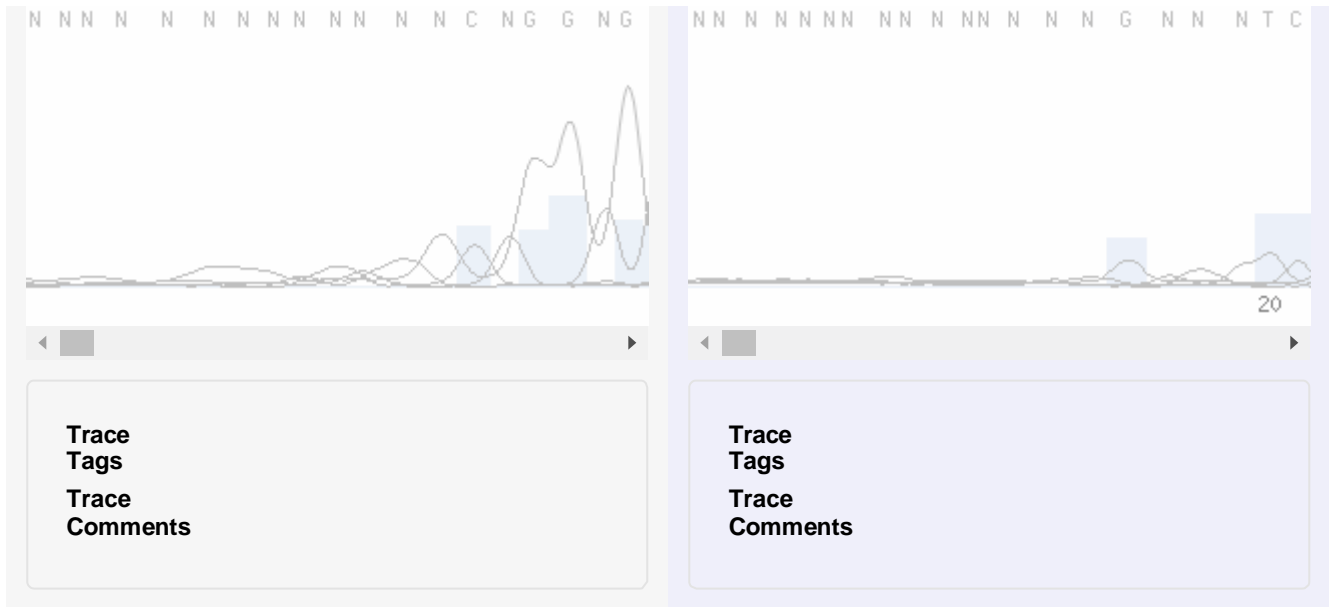
### Amino Acid Sequence

SVFGKAGVKDYKLYTTPDYETKDSIDLAAFRVTPQPGVPPPEAGAAVAEESSTGTWTVTWDGLTSLD  
 RYKGRYHIIEPVAGEENQYIAYVAYPLDLFEEGSVNMFMTSIVGNVFGFKALRALRLEDLRIPPSYSKT  
 FQGPPIHQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECL

## rbcLa Tags & Comments

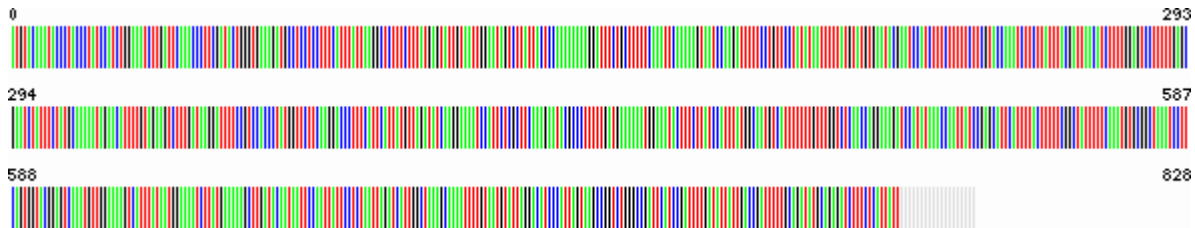
**Sequencing Date** 2013-06-12 13:32:31  
**Trace Direction** F  
**Forward Primer** rbcLa-F  
**Reverse Primer** rbcLa-R  
**Sequence Primer** rbcLa-F  
**Status** high qual  
**Trace Runsite** Biodiversity Institute of Ontario

**Sequencing Date** 2013-06-12 19:44:51  
**Trace Direction** R  
**Forward Primer** rbcLa-F  
**Reverse Primer** rbcLa-R  
**Sequence Primer** rbcLa-R  
**Status** high qual  
**Trace Runsite** Biodiversity Institute of Ontario



## matK

### Illustrative Barcode



### Nucleotide Sequence

```

ATGTACAATACCCATCCCTATCCaTCTGGAAATCTTGATTCAAACCTTCGATACTGGGTGAAAGATG
CCTCCTCCTTTCATTTATTAAGGCTCTTCTTTATGAGTATTGTAATTGGAATAGTCTTATTACTCCA
AAAAAAGGATTTCTGCTTTTCAAATTCAAAAAGTAATCCAAGATTTTCTGTTCCTATATAATTTTT
ATGTATGTGAATACGAATCCATCTTCTTTTTCTTCGTACCAAAATCTCTTATTACGATTAACATCTT
TTGGAGTCTTTTGGAGCGAATCATTCTTATGCAAAAATAGAACATTTGTAGAAGTCTTTGATAAGG
ATTTCCGTCACCCCTATGGTTCTCAAGGACCTTTTCATTATTGTTAGATATCAAGGAAAAATCCA
TTCTCGCTCAAAGAATACGCCCTTTTGTGAAAAAATGGAAATACTTCTTATCCATTTATGGCAAT
GTCATTTTTTGTGGTCTCAACCAGGAAAGATCCATATAAACCAATTATCCGAGCATTCATTTTACT
TTTTCGGCTATTTTCAAATGTGCGGCTAAATCTTCAGTGGTACGGAGTCAAATGTTGAAAAAGTCAT
TTATAATGAAAAATCTTATGAAAAAGCTTGATACAATAATCCAATTATTCCTCAATTAGATCATTGG
CTAAAGCAAAATTTTGAATGTATAGGACATCCCATTAGTAAGCCGGTCTGGCCGATTTCATCCGATT
TTGATATTATGACCGATTTTGCAGATATGCAGAGaTCTTTCTCATTATT-----
-

```

### Sequence Metadata

**Genbank Accession:** N/A  
**Translation Matrix:** Standard Code  
**Last Updated:** 2013-08-09 10:57:30.703329  
**Sequence Runsite:** Biodiversity Institute of Ontario

### Amino Acid Sequence

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VQIPYPIHLEILIQTLRYWVKDASSFHLLRFLYEYCNWNSLITPKKRISAFSNSKSNPRFFLLYNYF
VCEYESIFLFLRTKSSYLRLTSFGVLFERIFYAKIEHFVEVFDKDFPSTLWFFKDPFIHYVRYQGKSI
LASKNTPFLMKKWKYFLIHLWQCHFFVNSQPGKIHINQLSEHSFYFFGYFSNVRNPSVVRSQLKESF
IMENLMKLDITIIPIPLIRSLAKAKFCNVLGHPISKVPWADSSDFDIIDRFLQICRDLSHYX-----

```

### matK Tags & Comments

**Sequencing Date** 2013-07-19 15:02:44  
**Trace Direction** R  
**Forward Primer** matK\_xF  
**Reverse Primer** matK-MALPR1  
**Sequence Primer** matK-MALPR1  
**Status** med qual  
**Trace Runsite** Biodiversity Institute of Ontario

**Sequencing Date** 2013-07-19 18:10:43  
**Trace Direction** F  
**Forward Primer** matK\_xF  
**Reverse Primer** matK-MALPR1  
**Sequence Primer** matK\_xF  
**Status** med qual  
**Trace Runsite** Biodiversity Institute of Ontario

