Bulletin of Insectology Supplemental Material

Title: **Validation of reference genes for qRT-PCR analysis in *Megoura viciae* (Hemiptera Aphididae)**

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Table S1. All the possible ΔC_T combinations for all the samples and average standard deviation.

Figure S1. *Acyrthosiphon pisum* - *Megoura viciae* nucleotidic sequences alignments.

Figure S2. Google Scholar number of results from 2002 to 2014 using as searching words "Validation of reference genes".

Table S1. All the possible ΔC_T combinations for all the samples and average standard deviation.

Sample	Mean ΔC_T	Std dev	Mean Std dev
RPL32 VS NADH	4.879	0.494	
RPL32 VS SUCC	4.313	0.216	
RPL32 VS RPS9	0.139	0.268	
RPL32 VS TATA	5.920	0.434	
RPL32 VS ACT	0.440	0.843	
RPL32 VS TBU	6.001	0.959	
RPL32 VS UBIQ	3.366	0.274	0.499
NADH VS RPL32	4.879	0.494	
NADH VS SUCC	0.566	0.462	
NADH VS RPS9	4.740	0.526	
NADH VS TATA	1.041	0.667	
NADH VS ACT	4.439	1.165	
NADH VS TBU	1.122	0.736	
NADH VS UBIQ	1.513	0.378	0.632
SUCC VS RPL32	4.313	0.216	
SUCC VS NADH	0.566	0.462	
SUCC VS RPS9	4.174	0.363	
SUCC VS TATA	1.607	0.578	
SUCC VS ACT	3.873	0.798	
SUCC VS TBU	1.688	1.045	
SUCC VS UBIQ	0.948	0.301	0.538
RPS9 VS RPL32	0.139	0.268	
RPS9 VS NADH	4.740	0.526	
RPS9 VS SUCC	4.174	0.363	
RPS9 VS TATA	5.780	0.393	
RPS9 VS ACT	0.301	0.835	
RPS9 VS TBU	5.862	0.897	
RPS9 VS UBIQ	3.226	0.330	0.516
TATA VS RPL32	5.920	0.434	
TATA VS NADH	1.041	0.667	
TATA VS SUCC	1.607	0.578	
TATA VS RPS9	5.780	0.393	
TATA VS ACT	5.480	1.023	
TATA VS TBU	0.081	0.759	
TATA VS UBIQ	2.554	0.470	0.618
ACT VS RPL32	0.440	0.843	
ACT VS NADH	4.439	1.165	
ACT VS SUCC	3.873	0.798	
ACT VS RPS9	0.301	0.835	
ACT VS TATA	5.480	1.023	
ACT VS TBU	5.561	1.660	
ACT VS UBIQ	2.926	1.006	1.047
TBU VS RPL32	6.001	0.959	
TBU VS NADH	1.122	0.736	
TBU VS SUCC	1.688	1.045	
TBU VS RPS9	5.862	0.897	
TBU VS TATA	0.081	0.759	
TBU VS ACT	5.561	1.660	
TBU VS UBIQ	2.635	0.813	0.981
UBIQ VS RPL32	3.366	0.274	
UBIQ VS NADH	1.513	0.378	
UBIQ VS SUCC	0.948	0.301	
UBIQ VS RPS9	3.226	0.330	
UBIQ VS TATA	2.554	0.470	
UBIQ VS ACT	2.926	1.006	
UBIQ VS TBU	2.635	0.813	0.510

Figure S1. *Acyrthosiphon pisum* - *Megoura viciae* nucleotidic sequences alignments.

Ubiquitin-conjugating protein nucleotidic sequences alignments.

```
UBIQ_A.pisum      ATGTCAGAACTACAGTCGGCGCTATTATTAAAGAAACAACTGACTGAATTGCACAAGAAC 60
UBIQ_M.viciae     ATGTCAGAACTACAGTCGGCGCTATTATTAAAGAAACAACTCACTGAATTGCACAAGAAC 60
                  ************************************** *****************

UBIQ_A.pisum      CCAGTAGAAGGGTTCTCTGCTGGTCTCATAGATGATAATGATATTTACAAATGGGAAGTG 120
UBIQ_M.viciae     CCAGTCGAAGGGTTCTCTGCTGGTCTCATAGACGATAATGATATTTACAAATGGGAAGTG 120
                  ***** ************************* **************************

UBIQ_A.pisum      CTCATTATTGGACCTCCAGACACCTTGTATGAAGGAGGATTTTTCAAGGCTCATGTTAAT 180
UBIQ_M.viciae     CTCATTATTGGACCTCCGGACACCGTTTATGAAGGAGGGTTTTTCAAGGCTCATGTTAAT 180
                  **************** ****** * ********** ********************

UBIQ_A.pisum      TTTCCAAAGGAGTATCCATTAAGGCCACCAAAAATGAAATTTGTTACTGAAATTTGGCAC 240
UBIQ_M.viciae     TTTCCAAAAGAGTATCCATTAAGGCCACCAAAAATGAAATTTGTTACTGAAATTTGGCAC 240
                  ******* ************************************************

UBIQ_A.pisum      CCTAATATTGATAAAAGTGGTGATGTTTGTATATCAATACTTCATGAACCCGGTGATGAT 300
UBIQ_M.viciae     CCTAATATTGATAAAAGTGGTGATGTTTGTATATCAATACTTCATGAACCTGGTGATGAT 300
                  ************************************************ *********

UBIQ_A.pisum      AAGTGGGGTTATGAAAAAGCAAGTGAACGTTGGTTACCAGTGCATACTGTTGAAACTATA 360
UBIQ_M.viciae     AAGTGGGGTTATGAAAAAGCAAGTGAACGTTGGTTACCGGTGCATACTGTTGAGACTATA 360
                  ************************************** ************** ******

UBIQ_A.pisum      CTGATATCAGTTATTTCAATGTTGGCCGATCCAAATGATGAAAGTCCAGCTAATGTAGAT 420
UBIQ_M.viciae     TTGATATCAGTTATATCAATGTTGGCAGATCCAAATGATGAAAGTCCAGCTAATGTAGAT 420
                   ************* ********** ******************************

UBIQ_A.pisum      GCAGCTAAAGATTGGCGTGATAATTATCCAGAATTCAAACGCAAGGTTGCACGTTGTGTG 480
UBIQ_M.viciae     GCAGCTAAAGATTGGCGTGACAATTATCCAGAATTCAAACGCAAGGTTGCACGTTGCGTG 480
                  ******************* ********************************** ***

UBIQ_A.pisum      CGTAAGAGTCAAGAGGATATCTAA 504
UBIQ_M.viciae     CGTAAGAGTCAAGAGGATATCTAA 504
                  ************************
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Actin nucleotidic sequences alignments.

```
ACT_A.pisum      ATGTGTGACGATGATGTAGCAGCTTTGGTAGTCGACAATGGCTCCGGTATGTGCAAGGCC 60
ACT_M.viciae     ATGTGTGACGATGATGTAGCAGCTTTGGTAGTCGACAATGGCTCCGGTATGTGCAAGGCC 60
                 ************************************************************

ACT_A.pisum      GGTTTCGCTGGAGATGACGCACCCCGTGCCGTCTTCCCCTCCATCGTCGGCAGACCCCGT 120
ACT_M.viciae     GGTTTCGCTGGAGATGACGCACCCCGTGCCGTCTTCCCCTCCATCGTCGGCAGACCCCGT 120
                 ************************************************************

ACT_A.pisum      CATCAAGGAGTCATGGTCGGTATGGGACAAAAGGACAGCTACGTAGGCGATGAAGCCCAA 180
ACT_M.viciae     CATCAAGGAGTCATGGTCGGTATGGGACAAAAGGACAGCTACGTAGGCGATGAAGCCCAA 180
                 ************************************************************

ACT_A.pisum      AGCAAACGTGGTATCCTCACTTTGAAATACCCCATTGAACACGGAATCATCACCAACTGG 240
ACT_M.viciae     AGCAAACGTGGTATCCTTACTTTGAAATACCCCATTGAACACGGAATCATCACCAACTGG 240
                 **************** *********************************************

ACT_A.pisum      GATGATATGGAAAAAATCTGGCATCACACTTTCTACAACGAATTGCGTGTTGCCCCAGAA 300
ACT_M.viciae     GATGATATGGAAAAAATCTGGCATCACACTTTCTACAACGAATTGCGTGTCGCCCCAGAA 300
                 ************************************************* *********

ACT_A.pisum      GAGCACCCAATCCTGTTGACCGAAGCCCCATTGAACCCAAAGGCCAATCGTGAAAAGATG 360
ACT_M.viciae     GAGCACCCAATCCTGTTGACCGAAGCTCCATTGAACCCAAAGGCTAATCGTGAAAAGATG 360
                 ************************* **************** ***************

ACT_A.pisum      ACCCAAATCATGTTTGAAACCTTCAACACACCCGCCATGTATGTTGCCATCCAAGCCGTA 420
ACT_M.viciae     ACCCAAATCATGTTTGAAACCTTCAACACACCCGCCATGTATGTTGCCATCCAAGCTGTA 420
                 ******************************************************** ***

ACT_A.pisum      CTTTCCTTGTACGCTTCCGGTCGTACTACTGGTATCGTTTTGGACTCTGGTGACGGTGTC 480
ACT_M.viciae     CTCTCCTTGTACGCTTCCGGTCGTACCACTGGTATCGTTTTGGACTCTGGTGACGGTGTC 480
                 ** ********************** ********************************

ACT_A.pisum      TCACACACAGTACCCATCTATGAAGGTTATGCATTGCCCCATGCCATCCTCCGTTTGGAC 540
ACT_M.viciae     TCCCACACAGTACCCATCTATGAAGGTTATGCATTGCCCCATGCCATCCTCCGTTTGGAC 540
                 ** ********************************************************

ACT_A.pisum      TTGGCTGGTCGTGACTTGACCGACTACTTGATGAAGATCTTAACCGAGAGAGGTTACAGC 600
ACT_M.viciae     TTGGCTGGTCGTGACTTGACCGACTACTTGATGAAGATCTTAACCGAGAGAGGTTACAGC 600
                 ************************************************************

ACT_A.pisum      TTCACCACCACCGCTGAGCGAGAAATCGTCCGTGACATTAAGGAAAAATTGTGCTATGTC 660
ACT_M.viciae     TTCACCACCACCGCTGAGCGAGAAATCGTCCGTGACATCAAGGAAAAATTGTGCTATGTC 660
                 ************************************** *********************

ACT_A.pisum      GCTTTGGACTTCGAACAGGAAATGGCTACCGCCGCCGCTTCCACCTCATTGGAGAAATCC 720
ACT_M.viciae     GCTTTGGACTTCGAACAGGAAATGGCTACCGCTGCCGCTTCCACCTCATTGGAGAAATCC 720
                 ****************************** **************************

ACT_A.pisum      TATGAATTACCTGACGGACAGGTCATCACCATCGGAAACGAACGTTTCCGTTGCCCAGAA 780
ACT_M.viciae     TATGAATTACCTGACGGACAGGTCATCACCATCGGAAACGAACGTTTCCGTTGCCCAGAA 780
                 ************************************************************

ACT_A.pisum      GCCTTGTTCCAACCTTCATTCTTGGGAATGGAATCTTGCGGTATCCACGAAACCGTATAC 840
ACT_M.viciae     GCCTTGTTCCAACCTTCATTCTTGGGAATGGAATCTTGCGGAATCCACGAAACCGTATAC 840
                 ***************************************** ******************

ACT_A.pisum      AACTCCATCATGAAGTGCGATGTTGACATCAGGAAGGACTTGTACGCCAACACTGTACTT 900
ACT_M.viciae     AACTCCATCATGAAGTGCGATGTTGACATCAGAAAGGACTTGTACGCCAACACTGTACTT 900
                 ****************************** **************************

ACT_A.pisum      TCCGGAGGTACCACCATGTACCCAGGTATCGCCGACAGAATGCAAAAGGAAATCACCGCC 960
ACT_M.viciae     TCCGGAGGTACCACCATGTACCCAGGTATCGCCGACAGAATGCAAAAGGAAATCACCGCT 960
                 ************************************************************

ACT_A.pisum      TTGGCTCCAAGCACAATCAAGATCAAGATCATTGCCCCACCAGAACGTAAATACTCCGTA 1020
ACT_M.viciae     TTGGCTCCAAGCACAATCAAGATCAAGATCATTGCCCCACCAGAACGTAAATACTCCGTA 1020
                 ************************************************************
ACT_A.pisum      TGGATCGGTGGTTCCATCTTGGCTTCACTGTCCACCTTCCAACAGATGTGGATCTCCAAA 1080
ACT_M.viciae     TGGATCGGTGGTTCCATCTTGGCTTCTCTGTCCACCTTCCAACAGATGTGGATCTCCAAA 1080
                 ************************* ******************************

ACT_A.pisum      CAAGAATACGACGAATCCGGCCCAGGCATTGTCCACCGTAAATGCTTCTAA 1131
ACT_M.viciae     CAAGAATACGACGAATCCGGCCCAGGCATTGTCCACCGTAAATGCTTCTAA 1131
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OBP4 nucleotidic sequences alignments.

```
obp4_A.pisum      ATGCGTGGAAATTATTCTTCGATGGTTTTCCTACTTTTTGCAATTGGATTTCAAGATATT 60
obp4_M.viciae     ATGCGTGGAAATTATTCTTTGATGGTTTTTCTACTTTTGGCAATCGGATCACAAGATATT 60
                  ****************** ******** ******* ***** ****  *********

obp4_A.pisum      TTCTGTCAAAAACAAGAACCATCAGGAAAATGTAGAGCTCCCGATAAGGCACCTTTAAAT 120
obp4_M.viciae     TACTGTCAAAAACAAGAACTATCAGGAAAATGTAAAGCTCCCGATAAGGCACCTTTAAAT 120
                  * ***************** ************* ************************

obp4_A.pisum      CTCGAAATAATAATTAATACATGCCAAGAAGAAATCAAATCCGCATTACTTCAAGAAGCC 180
obp4_M.viciae     CTCGAAATAATAATTAATATTTGTCAAGAAGAAATCAAATCCGCATTACTTCAAGAAGCC 180
                  ******************  ** ***********************************

obp4_A.pisum      TTAGATATTTTAAATGATGGCAATGTGGAACAAAATACGCCAAACTATAGCAGTAGATCA 240
obp4_M.viciae     TTAGATATTCTCAATGAGGGTAATTTGGAACAAAATACGCCAAGCTATAGCAGTAGATCA 240
                  ********* * ***** ** *** ***************** ***************

obp4_A.pisum      AAAAGAGAGGCCGAAGAAGATTTGACAAACGAAGAACGTAGAGTTGCAGGGTGTTTGCTC 300
obp4_M.viciae     AAAAGAGAGGCCGATGAAGATTTGACAAACGAAGAACGTAGAGTTGCAGGGTGTTTGCTC 300
                  ************* ******************************************

obp4_A.pisum      CAGTGCGTCTACAAGAAAGTGAAAGCAGTTGATGAAACTGGTTTTCCGGTAGTAGACGGC 360
obp4_M.viciae     CAGTGCGTCTACAAGAAAGTGAAAGCAGTTGATGAAACTGGTTTTCCAGTAGTCGACGGC 360
                  ********************************************* ***** ******

obp4_A.pisum      TTGATGAAACTGTACAACGAAGGTGTCCAGGACAGAAACTACTACATAGCTACGTTATCC 420
obp4_M.viciae     TTGATGAAACTGTACAATGAAGGTGTCCAGGACAGAAATTACTACATGGCTACGTTATCC 420
                  **************** ******************* ******** ************

obp4_A.pisum      GCAGTTAGGCATTGTATTTCTATCGCGCAACAGCTAAAGCAACAGCAGCCCTCCAAAAGT 480
obp4_M.viciae     GCCGTTAGGCATTGTATTTCCATCGCGCAACAGCTAAAGCAGCAACAGCCCTCTAAAAGT 480
                  ** **************** ******************* ** ******** ******

obp4_A.pisum      TTCGATGACGGACAAACGTGTGATCTTGCATATGAAATGTTCGAATGCGTCAGTGAAAAA 540
obp4_M.viciae     TTCGATGATGGACAAACGTGTGATCTTGCATATGAAATGTTTGAATGCGTCAGTGAAAAA 540
                  ******** ****************************** *****************

obp4_A.pisum      ATCGAAGAAAACTGCGGAGTCGAAAATAAGTCAAATAACTGA----------------- 582
obp4_M.viciae     ATCGAAGAAAACTGTGGAGTCGAAAATAAGTCAAATAACCTAAGCCAACGTCAAGTTTAA 600
                  ************* ************************  *
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NADH dehydrogenase (ubiquinone) flavoprotein 1 nucleotidic sequences alignments.

```
NADH_A.pisum      ATGAACGGCTCAGCTTTGGTGAGGTCAAACCTGGTGGTTAAAGGTCACGGAGGGGCTATT 60
NADH_M.viciae     ATGAACGGCTCAGCTTTGGTGAGGTCAAACCTAGTGGCTAAAGGTCACGGCGGGGCTATT 60
                  ******************************** **** ************ *********

NADH_A.pisum      GGGCTACCTAGTTTGGCGTTTAAAAATGTATTGCAGACACGCCAAAACACTACTGCAGCG 120
NADH_M.viciae     GGGCTACCCAGTTTGGCGTTTAAAAACGCGTTACAGACACGCCGAAACACTACTGCAGCG 120
                  ******* ***************** *  ** ********** ****************

NADH_A.pisum      GCCCCTCCACCAGAATTAAAGGCGTCGTACGGTAATCTTTCAGATTCTGATAGGATTTTC 180
NADH_M.viciae     GCTCCTCCGCCAGCATTAAAGGCGTCATATGGTAATCTGTCAGATTCAGACAGGATTTTC 180
                  ** ***** **** ************ ** ******** ******** ** *********

NADH_A.pisum      ACGAACCTGTATGGACGCCACGACTGGCAACTGAAGGGTGCGTTAAAACGCGGTGATTGG 240
NADH_M.viciae     ACGAATCTGTATGGACGCCACGACTGGCAACTGAAGGGTGCGTTAAAACGCGGTGATTGG 240
                  ***** ****************************************************

NADH_A.pisum      TACAAGACGAAAGAAATTTTGATAAAAGGTACGGATTACATTATTAATGAAGTTAAAACT 300
NADH_M.viciae     TACAAGACGAAAGAAATTTTGATAAAAGGTACCGATTACATTATTAATGAAATTAAGACT 300
                  ******************************** ****************** **** ***

NADH_A.pisum      TCCGGTTTGAGGGGACGTGGTGGTGCCGGTTTCCCGACTGGTATGAAATGGAGTTTTATG 360
NADH_M.viciae     TCGGGTTTGAGGGGACGCGGTGGTGCCGGTTTCCCAACTGGTATGAAATGGAGTTTTATG 360
                  ** ************** ***************** ************************

NADH_A.pisum      AACAAACCTTCTGATGGTCGCCCAAAGTACTTGGTCGTTAACGCTGACGAAGGTGAACCA 420
NADH_M.viciae     AACAAACCTTCAGATGGTCGCCCAAAATATTTGGTTGTTAACGCTGATGAAGGTGAACCA 420
                  *********** ************** ** ***** *********** ************

NADH_A.pisum      GGCACTTGCAAAGATCGTGAAATTATGAGACACGATCCACATAAATTGATTGAAGGATGT 480
NADH_M.viciae     GGCACTTGCAAAGATCGTGAAATTATGAGACACGATCCACATAAATTGATTGAAGGGTGT 480
                  ******************************************************** ***

NADH_A.pisum      TTGGTTGCTGGCCGAGCAATGGGAGCTTGTGCTGCTTATATTTACATCCGCGGAGAGTTT 540
NADH_M.viciae     TTGGTTGCTGGCCGAGCAATGGGAGCTTGTGCTGCTTATATTTACATCCGAGGAGAGTTT 540
                  ************************************************* *********

NADH_A.pisum      TACAATGAAGCTTCCAATCTGCAACAAGCTATTTGCGAGGCGTATCAAGCTGGTCTTATT 600
NADH_M.viciae     TACAATGAAGCTTCTAATCTGCAACAAGCTATTTGCGAGGCGTATCAAGCTGGTCTTATA 600
                  ************** ******************************************

NADH_A.pisum      GGAAAAAATGCATGCAACTCTGGTTATGACTTTGATGTATTTGTGCACAGGGGAGCTGGT 660
NADH_M.viciae     GGAAAAAATGCGTGCAACTCTGGATATGACTTTGATGTATTTGTGCACAGAGGAGCTGGT 660
                  *********** *********** ************************** *********

NADH_A.pisum      GCTTATATTTGTGGAGAAGAAACAGCTCTCATTGAATCACTTGAAGGCAAACAAGGCAAA 720
NADH_M.viciae     GCTTATATTTGTGGAGAAGAAACAGCACTTATTGAATCACTTGAAGGCAAACAAGGTAAA 720
                  ************************** ** ************************** ***

NADH_A.pisum      CCAAGGTTGAAGCCCCCTTTCCCAGCTGATGTTGGAGTTTTTGGCTGTCCCACTACAGTA 780
NADH_M.viciae     CCAAGGTTGAAACCCCCTTTTCCAGCTGATGTTGGAGTTTTTGGCTGTCCCACTACTGTA 780
                  *********** ******** ********************************** ***

NADH_A.pisum      TCAAATGTTGAAACAGTAGCCGTTGCACCTACCATTTGTCGTCGTGGTGGTGCATGGTTC 840
NADH_M.viciae     TCTAATGTTGAAACAGTAGCCGTTGCACCTACCATTTGCCGCCGTGGTGGTGCATGGTTC 840
                  ** ********************************** ** ******************

NADH_A.pisum      TTGGGTCTTGGAAGACCTAGGAATTCCGGAACTAAGCTCTTCAATATATCTGGTCATGTA 900
NADH_M.viciae     TTGGGCCTTGGAAGACCTCGAAATTCCGGAACTAAGCTCTTCAATATATCTGGTCATGTT 900
                  ***** ************ * ************************************

NADH_A.pisum      AACAATCCGTGTACTGTTGAAGAAGAAATGTCAATTCCATTGAAAGAGTTGATTGAGCGA 960
NADH_M.viciae     AACAACCCGTGTACTGTTGAAGAAGAAATGTCAATTCCGTTGAAAGAGTTGATTGAGCGA 960
                  ***** ******************************** *********************

NADH_A.pisum      CATGCTGGTGGTATAATTGGTGGTTGGGATAATTTGTTGGCCGTAATTCCTGGAGGCTCA 1020
NADH_M.viciae     CATGCTGGTGGTATAATTGGTGGTTGGGATAATTTGTTGGCTGTAATTCCTGGAGGTTCA 1020
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NADH_A.pisum      TCGACACCACTTATACCAAAACACGTTTGTGAAACAGCAATTATGGACTTTGATGGTTTG 1080
NADH_M.viciae     TCAACACCACTTATACCAAAACATGTTTGTGAAACGGCAATTATGGACTTTGACGGTTTA 1080
                  ** ******************* *********** **************** *****

NADH_A.pisum      GTAGCAGCTCAAACTAGTTTAGGAACAGCAGCTCTGATTGTAATGAACAAGCAAACTGAT 1140
NADH_M.viciae     GTAGCAGCTCAAACTAGTTTAGGAACAGCAGCTCTGATTGTAATGAACAAGCAAACTGAT 1140
                  ************************************************************

NADH_A.pisum      ATTGTAAAAGCTATTGCTCGTTTGATTATGTTCTATAAACATGAATCATGCGGACAATGT 1200
NADH_M.viciae     ATCGTAAAAGCTATTGCTCGTTTGATTATGTTTTATAAACATGAATCATGCGGGCAATGT 1200
                  ** ***************************** ******************* ******

NADH_A.pisum      ACACCTTGTCGTGAGGGCATTAATTGGATGAACAAAATTATGTATAGGTTTGTTGACGGA 1260
NADH_M.viciae     ACACCTTGTCGGGAGGGCATTAATTGGATGAACAAAATTATGTATAGGTTTGTTGATGGG 1260
                  *********** ****************************************** **

NADH_A.pisum      CAAGCTCAATCTTCAGAAATTGACATGTTGTGGGAGATTAGTAAGCAAATTGAAGGGCAC 1320
NADH_M.viciae     CAAGCTCAATCTTCAGAAATTGACATGTTGTGGGAAATTAGTAAGCAAATTGAAGGGCAC 1320
                  ********************************** ************************

NADH_A.pisum      ACGATTTGTGCACTTGGAGATGGTGCCGCATGGCCTGTACAGGGGCTGATTAGACATTTT 1380
NADH_M.viciae     ACAATTTGTGCACTTGGAGATGGTGCCGCATGGCCTGTACAAGGGCTGATTAGACATTTT 1380
                  ** ************************************** *****************

NADH_A.pisum      AGACCTGAACTCGAATGCAGAATGAAAAAGTACCAAGAGCAGAATGAAAAACAAGCTTTA 1440
NADH_M.viciae     AGACCTGAACTTGAAGGCAGAATGAAAAAGTACCAAGAGCAAAATGAAAAACAAGCTTTA 1440
                  *********** *** ************************ *****************

NADH_A.pisum      TCCAACTAA 1449
NADH_M.viciae     TCCAACTAA 1449
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Ribosomal protein L32 nucleotidic sequences alignments.

```
RPL32_A.pisum      ATGTCGATCAAGCCGAAGTATCGCCCAACAATTATCAAAAAACGTACCAAGAAATTCATC 60
RPL32_M.viciae     ATGTCGATCAAGCCGAAGTATCGCCCACAAATTATCAAAAAACGTACCAAGAAGTTCATC 60
                   **************************  ************************ ******

RPL32_A.pisum      AGACATCAAAGTGATCGTTATGACAAACTCAAGCCCAACTGGCGTAAACCAAAGGGTATT 120
RPL32_M.viciae     AGACATCAAAGTGATCGTTATGACAAACTCAAGCCCAACTGGCGTAAACCGAAGGGTATT 120
                   ************************************************ *********

RPL32_A.pisum      GACAACAGAGTCCGAAGACGATTCAAGGGACAGTATTTGATGCCCAATGTTGGTTATGGT 180
RPL32_M.viciae     GACAACAGAGTCCGAAGACGATTCAAGGGACAGTATTTGATGCCCAATGTTGGTTATGGT 180
                   ************************************************************

RPL32_A.pisum      AGTGACAAGAGAACCAGACACATGCTGCCTTCCAAATTCCGTAAAGTCCTTGTACACAAC 240
RPL32_M.viciae     AGTGACAAGAGAACCAGACATATGTTGCCTTCCAAATTCCGTAAAGTCCTTGTACACAAT 240
                   ******************** *** ********************************

RPL32_A.pisum      GTAAGAGAATTGGAAATGTTGATGATGCAGAACAGGAAATACTGTGGAGAGATCGCTCAT 300
RPL32_M.viciae     GTTAGGGAATTGGAAATGTTGATGATGCAGAACAGGAAATACTGTGGAGAGATTGCTCAT 300
                   ** ** ********************************************** ******

RPL32_A.pisum      GGGGTTTCATCCAAAAATCGTAAAACCATTGTTTCTAGAGCCCAAGAGTTATCTATCAGA 360
RPL32_M.viciae     GGGGTTTCATCCAAAAATCGTAAAACGATTGTTTCTAGAGCCCAAGAGTTATCTATCAGA 360
                   ************************* ******************************

RPL32_A.pisum      TTGACCAATGGAAATGCACGTATTCGTACACAAGAGGGTTAA 402
RPL32_M.viciae     TTGACCAATGGAAATGCACGTATTCGTACACAAGAGGGTTAA 402
                   ****************************************
```

Ribosomal protein S9 nucleotidic sequences alignments.

```
RPS9_A.pisum      ATGGTTAACGGACGCATCCCGTCCGTGTACAGTAAGACGTACGTGACGCCCCGTCGTCCG 60
RPS9_M.viciae     ATGGTTAACGGACGCATCCCGTCCGTGTACAGTAAAACGTACGTGACGCCCCGTCGTCCG 60
                  ********************************* ************************

RPS9_A.pisum      TATGAGAAAGCACGTTTGGACCAGGAGTTGAAGATCATCGGAGAATATGGTCTGAGGAAC 120
RPS9_M.viciae     TATGAGAAAGCACGTTTGGACCAAGAATTGAAGATCATCGGAGAATATGGTCTGAGAAAC 120
                  ********************** ** **************************** ***

RPS9_A.pisum      AAGCGCGAAGTATGGCGTGTGAAATACACATTGGCCAAGATCCGTAAAGCCGCTCGTGAA 180
RPS9_M.viciae     AAGCGTGAAGTATGGCGTGTGAAATACACATTGGCCAAGATCCGTAAAGCCGCTCGTGAA 180
                  ***** ***************************************************

RPS9_A.pisum      CTGTTGACCCTCGAAGAGAAAGATCAAAAGCGACTTTTCGAAGGTAACGCTTTGTTGCGT 240
RPS9_M.viciae     CTGTTGACCCTCGAAGAGAAGGATCAAAAACGACTTTTCGAAGGTAACGCTTTGTTGCGT 240
                  ******************** ******** ****************************

RPS9_A.pisum      AGGTTGGTTCGTATTGGAGTACTAGATGAAGGCCGCATGAAGCTTGATTACGTTTTGGGT 300
RPS9_M.viciae     AGGTTGGTTCGTATTGGAGTATTAGATGAAGGCCGCATGAAGCTTGATTACGTTTTGGGT 300
                  ******************** ************************************

RPS9_A.pisum      TTGAAAATTGAAGATTTCTTGGAACGCAGACTTCAAACTCAGGTATTCAAATTGGGATTA 360
RPS9_M.viciae     TTGAAAATTGAAGATTTCTTGGAACGCAGACTTCAAACTCAGGTATTCAAATTGGGATTA 360
                  ************************************************************

RPS9_A.pisum      GCCAAATCCATTCATCATGCACGAGTTTTGATCCGTCAAAGACACATTCGTGTGCGCAAA 420
RPS9_M.viciae     GCCAAATCCATTCATCATGCACGAGTTTTGATCCGTCAAAGACACATTCGTGTGCGCAAA 420
                  ************************************************************

RPS9_A.pisum      CAGGTAGTAAATGTACCATCATTCATTGTTCGTCTGGACTCCCAGAAACACATTGACTTC 480
RPS9_M.viciae     CAGGTAGTAAATGTTCCATCATTCATTGTTCGTTTGGACTCCCAGAAACACATTGACTTC 480
                  ************** ***************** *************************

RPS9_A.pisum      TCCCTGAAATCGCCATTCGGTGGTGGCCGTCCAGGACGTGTAAAGAGGAAGAACTTGAGA 540
RPS9_M.viciae     TCCCTGAAATCACCATTCGGTGGTGGTCGTCCAGGACGTGTAAAGAGGAAGAACTTGAGA 540
                  *********** ************** ********************************

RPS9_A.pisum      AAGGCCAAGACTGCCAAGGACGATGGCAATGCTGCTGAAGAAGAAGAAGATTAA 594
RPS9_M.viciae     AAGGCCAAGACTGCCAAGGACGATGGCAATGCTGCCGAAGAAGAAGAAGATTAA 594
                  ********************************** ******************
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Succinate dehydrogenase complex subunit A nucleotidic sequences alignments.

```
SUCC_A.pisum            ATGAGTGGCTTATTAAAAATTGTCAATCCAATATCACGAAGTACTTATTC 50
SUCC_M.viciae_partial   --------------------------------------------------

SUCC_A.pisum            AAAAATTAATAATTGGAACCGTCCATTAATTTGCACAAGAAACTTACATC 100
SUCC_M.viciae_partial   --------------------------------------------------

SUCC_A.pisum            AATCTCAATATTATTCAGCTAAACAGAGTTCAGCAGGAACAAATGCATAT 150
SUCC_M.viciae_partial   --------------------------------GCAGGAACAAATGCATAT 18
                                                        ******************

SUCC_A.pisum            TCAGTAATTGATCATGAATATGATGCTGTCGTAGTCGGTGCTGGAGGAGC 200
SUCC_M.viciae_partial   TCGGTAATTGATCATGAATATGATGCTGTTGTAGTTGGTGCTGGAGGAGC 68
                        ** ************************* ***** **************

SUCC_A.pisum            TGGTCTCCGTGCCGCTTTTGGCCTAGTACAAGAAGGATTTAAAACAGCAG 250
SUCC_M.viciae_partial   TGGTCTCCGTGCAGCATTTGGCCTGGTACAAGAAGGATTTAAAACAGCAG 118
                        ************ ** ******** ************************

SUCC_A.pisum            TTATTACTAAACTATTTCCAACAAGATCTCATACGGTTGCTGCACAGGGC 300
SUCC_M.viciae_partial   TTATTACTAAACTATTTCCAACAAGATCTCATACGGTTGCTGCTCAAGGA 168
                        ****************************************** ** **

SUCC_A.pisum            GGAATTAATGCTGCGTTAGGGAATATGGAAGATGATGATTGGCGATGGCA 350
SUCC_M.viciae_partial   GGAATTAATGCTGCGTTAGGGAATATGGAAGATGATGATTGGCGATGGCA 218
                        ************************************************

SUCC_A.pisum            TATGTTTGATACTGTTAAAGGTTCAGATTGGTTAGGGGATCAAGATGCTA 400
SUCC_M.viciae_partial   TATGTTTGATACTGTCAAAGGTTCAGATTGGTTAGGAGATCAGGATGCTA 268
                        *************** ******************** ***** *******

SUCC_A.pisum            TACATTATTTAACTAGAGAGGCACCTGCAGCTGTCATTGAGTTAGAAAAT 450
SUCC_M.viciae_partial   TACATTATTTAACTAGAGAGGCACCTGCAGCTGTCATTGAGTTAGAAAAT 318
                        ************************************************

SUCC_A.pisum            TATGGTATGCCTTTTAGTCGTACTGATGAAGGTAAAATATATCAACGTGC 500
SUCC_M.viciae_partial   TATGGTATGCCTTTTAGTCGTACTGATGAAGGTAAAATCTATCAACGTGC 368
                        ************************************* ***********

SUCC_A.pisum            ATTTGGTGGTCAGAGCTTACAATATGGAAAAGGTGGTCAGGCTCATCGTA 550
SUCC_M.viciae_partial   ATTTGGCGGTCAGAGCTTACAGTATGGAAAAGGTGGTCAGGCTCATCGTA 418
                        ****** ************** ***************************

SUCC_A.pisum            CTTGTTGTGTAGCTGATAGAACGGGTCATTCCCTCTTACATACTTTATAT 600
SUCC_M.viciae_partial   CTTGTTGTGTAGCTGACAGAACGGGTCACTCCCTCTTACATACTTTATAT 468
                        *************** *********** *********************

SUCC_A.pisum            GGATATTCATTAAAATTTAATTGCAATTACTTTGTGGAATATTTTGCTTT 650
SUCC_M.viciae_partial   GGATATTCATTAAAATTTAATTGCAATTACTTTGTGGAATATTTTGCTTT 518
                        ************************************************

SUCC_A.pisum            GGATTTAATTATGGATAAAGGACAATGTGTTGGAGTAATTGCTTTATGCT 700
SUCC_M.viciae_partial   GGATTTAATTATGGATAATGGACAATGTGTTGGAGTTATTGCCTTATGCT 568
                        ***************** **************** ***** *******

SUCC_A.pisum            TGGAAGATGGTACTATTCATCGCTTTAGAGCTAAGAATACAGTTTTAGCT 750
SUCC_M.viciae_partial   TGGAAGATGGTACTATTCATCGCTTTAGAGCTAAGAATACAGTTTTAGCT 618
                        ************************************************

SUCC_A.pisum            ACTGGTGGTTATGCTAGAGCTTACTTTTCGTGTACAGCTGCTCATACTTG 800
SUCC_M.viciae_partial   ACCGGAGGTTATGCTAGAGCTTACTTTTCATGTACAGCTGCTCATACTTG 668
                        ** ** ********************** ******************

SUCC_A.pisum            TACAGGCGATGGTCAAGCTCTAGCATCAAGGGCTGGTATTCCAATGCAAG 850
SUCC_M.viciae_partial   TACAGGCGATGGTCAAGCTTTAGCATCAAGAGCTGGTATTCCAATGCAAG 718
                        ****************** ********** ******************
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SUCC_A.pisum            ATATGGAATTTGTACAATTCCACCCTACTGGTATATATGGCGCTGGCTGT 900
SUCC_M.viciae_partial   ATATGGAATTTGTACAATTCCACCCTACTGGTATATATGGTGCTGGTTGT 768
                        ************************************** ***** ***

SUCC_A.pisum            TTAATGACAGAGGGTTGTCGCGGTGAAGGAGGATATTTAATCAATGGTTT 950
SUCC_M.viciae_partial   TTAATGACAGAGGGTTGTCGTGGTGAAGGAGGATATTTAATCAATGGTTT 818
                        ******************* ****************************

SUCC_A.pisum            AGGTGAAAGATTTATGGAGAAATATGCACCTAATGCTAAAGAACTTGCAT 1000
SUCC_M.viciae_partial   AGGTGAAAGATTTATGGAGAAGTATGCACCTAATGCTAAAGAACTTGCAT 868
                        ******************** ****************************

SUCC_A.pisum            CTAGAGATGTTGTATCTAGGTCAATGACTATGGAAATCATGGAAGGAAGA 1050
SUCC_M.viciae_partial   CCAGAGATGTTGTATCTAGGTCAATGACTGTTGAAATCATGGAAGGAAGA 918
                        * *************************** * ******************

SUCC_A.pisum            GGATGTGGTCCAGAAAAAGATCATGTTTATCTTCAACTATATCATTTGCC 1100
SUCC_M.viciae_partial   GGATGTGGTCCAGAAAAAGATCATGTTTATCTTCAACTATATCATTTGCC 968
                        ************************************************

SUCC_A.pisum            GGCTGAACAGCTTCACGCTAGATTACCGGGTATTTCAGAAACTGCTTTGA 1150
SUCC_M.viciae_partial   AGCCGAACAACTCCATGCTAGGTTACCAGGTATTTCAGAAACCGCCATGA 1018
                         ** ***** ** ** ***** ***** ************** **  ***

SUCC_A.pisum            TATTTGCTGGAGTTGATGTTACTAAAGAACCTATACCTGTGTTGCCAACA 1200
SUCC_M.viciae_partial   TATTTGCTGGAGTTGATGTTACTAAAGAACCTATACCTGTATTGCCAACG 1068
                        ************************************** ********

SUCC_A.pisum            GTCCATTATAACATGGGTGGAATACCAACAAACTATAGAGGACAGGTTAT 1250
SUCC_M.viciae_partial   GTTCATTATAACATGGGTGGAATACCAACAAACTATAGAGGACAGGTAAT 1118
                        ** ****************************************** **

SUCC_A.pisum            TAATCCTGAAAATGGAGAAGATAAAGTAGTACCTGGATTGTATGCTTGTG 1300
SUCC_M.viciae_partial   CAATCCTGAAAATGGAGAAGATAAAGTAGTACCTGGATTGTATGCTTGTG 1168
                         ***********************************************

SUCC_A.pisum            GTGAAGCTGCATGTACTTCTGTTCATGGAGCTAACCGTCTTGGTGCTAAT 1350
SUCC_M.viciae_partial   GTGAAGCTGCATGTACTTCTGTTCATGGAGCCAATCGTCTTGGTGCTAAT 1218
                        ****************************** ** ***************

SUCC_A.pisum            TCATTACTCGAGTTGGTGGTATTTGGACGTTCTTGCGCTTTAGACATTGC 1400
SUCC_M.viciae_partial   TCGTTACTCGAGTTAGTGGTATTTGGACGTTCTTGTGCTTTAGACATTGC 1268
                        ** *********** ******************* **************

SUCC_A.pisum            TAAATGTAACAAACCTGGAGATAAAATACCACAAATTAGTGATAATGCTG 1450
SUCC_M.viciae_partial   TAAATATAACAAACCTGGAGATAAAATACCACAAATTAGTGATAATGCTG 1318
                        ***** ******************************************

SUCC_A.pisum            GCGAAGAATCCATTAATAACATTGACAAATTACGTTTTAATAGTGGAACA 1500
SUCC_M.viciae_partial   GCGAAGAATCCATTACTAATATTGACAAATTGCGTTTCAATAATGGAACA 1368
                        ************** *** *********** ***** **** *******

SUCC_A.pisum            ATACCTACAGCAGACTTACGTTTAGACATGCAAAAAACTATGCAACTTTA 1550
SUCC_M.viciae_partial   ATACCTACAGCAGACTTACGTTTAGACATGCAAAAAACTATGCAACTTTA 1418
                        ************************************************

SUCC_A.pisum            TGCCGCTGTGTTTAGAACTGGATCTACACTTGATGAGGGCCGCAATAAAA 1600
SUCC_M.viciae_partial   TGCTGCTGTTTTTAGAACTGGATCTACACTGGATGAAGGCCGTCATAAAA 1468
                        *** ***** ******************* ***** *****  ******

SUCC_A.pisum            TGCAATCCATTTATTCAAAGCTTAAGGATATTAAGATAAATGATCGATCA 1650
SUCC_M.viciae_partial   TGCAAGCCATTTATTCAAAGCTTAAGGATATTAAGATAAACGATAGTTCA 1518
                        ***** ********************************** *** * ***

SUCC_A.pisum            ATGGTTTGGAATTCAGATTTAGTGGAATCATTAGAATTACAAAACTTAAT 1700
SUCC_M.viciae_partial   ATGGTTTGGAATTCAGATTTAGTGGAAACATTAGAATTACAAAATTTAAT 1568
                        *************************** **************** *****
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SUCC_A.pisum              GACTACTGCACAACAAACAATTGTATCTGCTGCTGAACGAAAAGAATCCA 1750
SUCC_M.viciae_partial     GACCACTGCACAGCAAACAATCGTATCTGCTGCCGAACGAAAAGAATCCA 1618
                          *** ******** ******** *********** ***************

SUCC_A.pisum              GAGGGGCACATGCACGAGATGATTTCAAAGATCGTATTGATGAATTTGAT 1800
SUCC_M.viciae_partial     GAGGGGCACATGCACGAGATGATTTTAAAGATCGCGTTGATGAATTTGAT 1668
                          ************************ ********  **************

SUCC_A.pisum              TATAAAAAACCGTTGGAAGGACAAACTCAAGTACCAATTGAAAAGCACTG 1850
SUCC_M.viciae_partial     TATAAAAAACCACTGGAAGGACAAACCCAAGTTCCTATTGAAAAACATTG 1718
                          ***********  ************* ***** ** ******** ** **

SUCC_A.pisum              GAGGAAGCATACACTTGCATGTATCAATCCAGACACTGGAGAGATTAAAT 1900
SUCC_M.viciae_partial     GAGAAAGCACACACTCGCACATATTAATCCAGATTCCGGAGAGATTAAAT 1768
                          *** ***** ***** ***  *** ********  * *************

SUCC_A.pisum              TAACTTATAGACCTGTAATTGATCACACATTGGATGATAAAGAAGTGAAA 1950
SUCC_M.viciae_partial     TAACTTATAGACCTGTAATTGATCACACATTGGATGATAAAGAAGTGAAA 1818
                          ************************************************

SUCC_A.pisum              TCAGTGCCACCTATGATTAGATCTTATTAA 1980
SUCC_M.viciae_partial     TCAGTTCCACCTATGATCAGATCTTATTAA 1848
                          ***** *********** ************
```

TATA-box binding protein nucleotidic sequences alignments.

```
TATA_A.pisum      ATGGATTTAAGTGATGATGAAGAATTTTATGATTCTGATCAGAGTGATGTGGACGAACAA 60
TATA_M.viciae     ATGGATTTGAGTGATGATGA---ATTTTATGATTCTGATCAGAGTGATGTTGGTGAACAA 57
                  ******* ***********   *************************** *  ******

TATA_A.pisum      AGCTTACATACTATGCTCAGTAAAACTCTTTACGATAAAGACCATGAGTATGAAGAATAT 120
TATA_M.viciae     AGTTTACATGCTCTGCTCAGTAAAACTCTTTACGATAAAGACAATGAGTATGAAGAATAT 117
                  ** ****** ** ***************************** ****************

TATA_A.pisum      GGAGAACAAATTGCTGGTGAAGAAGAAGCATTAGGTAGTGTGCAAGAGGAAGTACTTGGT 180
TATA_M.viciae     GGAGAACACATTGCTGGCGAAGAAGAAGAATTAGGTAGTGTGCAAGAGGAAGTACTTGGT 177
                  ******* ******* ********* ******************************

TATA_A.pisum      AAAGTCACCGATGATGTTGTTCAACAAGAAGTTGTCCTAGGTCCAGTGTATAGTGA---- 236
TATA_M.viciae     AAAGTCACCGATGATACTGGTCAAGAAGAAGTTGTCCTAGGTCCAGTATATAGTGATATA 237
                  ***************  ** **** ********************** *******

TATA_A.pisum      --------GAATGA------------GCCAGATTTAACAC------AAAAATTAGAAGAT 270
TATA_M.viciae     GAAGAAACAAATGAAAAATCAATAGGGCCAGATTCAAAATTTGTTAAAAAATTAGAAGAT 297
                           *****            ******* ** *       **************

TATA_A.pisum      GCTGAAAAAGTAGTTTTAACACCAGAAGTTATAGGGGAGTTAGAAAACAAACATTTTTTT 330
TATA_M.viciae     GCTGAAGAAGTAGTTTTAACACCAGAAGTTATAGGCGAATTAGAAAACAAACATTTTTTT 357
                  ****** **************************** ** ********************

TATA_A.pisum      GATGGACTTGATGATGATAATTTTGAACCATTAAAAAAAAAACAAAAAACAAGCAATGAA 390
TATA_M.viciae     GATGGACTTGATGACGATAACTTTGAACCAGTAAAAAAAAAACAAAAACTAAACAATGAA 417
                  ************** ***** ******** ****************  ** *******

TATA_A.pisum      GATA------ATGCAAATCCTCATAAAACTATTATTATGCATATACCTCGATTCATTCGG 444
TATA_M.viciae     GATAGTAGCAATGTAAATCCTCATAAAACTATTATTATGCACATACCTCAATTCATTCGG 477
                  ****      *** *************************** ******* **********

TATA_A.pisum      TGTAACAAAATTAGTCAATCTATTCAAGTTCAAAACATTGTATGTGGTGCAAACATGGGA 504
TATA_M.viciae     TGTAACAAAGGGGGTCAATCTATTCAAGTCCAAAACATTGTATGTGGTGCAAACATGGGA 537
                  *********    *************** ******************************

TATA_A.pisum      TGTCCTTTGGACTTGGTAAGAATTGTCATGTGGACTAGTAACTCAGAGTATAATCCACTG 564
TATA_M.viciae     TGTCCTTTGGACTTGGTAAGAATCGTCATGTGGACTAGTAACTCTGAGTATAATCCACAG 597
                  ********************** ******************* ************* *

TATA_A.pisum      CGATTTAATGGACTAATTATGCGTCTTCGTACACCTAATGTCACCAGCCTATTATTTCCA 624
TATA_M.viciae     CGGTTTAATGGACTAATTATGCGTCTTCGTACACCTAATGTCACCAGCCTATTATTTCCA 657
                  ** ************************************************************

TATA_A.pisum      TCAGGTAAAATGATCATGCAAGGTGCTAAGGATGACCGAACGGGAAATTTAGGATGTCGA 684
TATA_M.viciae     TCAGGTAAAATGATCATGCAAGGTGCCAAGGATGACCGAACTGGAAATTTAGGATGTCGA 717
                  ************************* ************* *****************

TATA_A.pisum      AAAGTAGCAAAAATCTTAGAACGCCTTGGACACAATGTAAAATTTTCTGATTATACAGTG 744
TATA_M.viciae     AAAGTAGCAAAAATTTTAGAACGACTTGGACACAATGTACAATTTTGTGATTATGCAGTG 777
                  ************** ******* ************** ****** ******* *****

TATA_A.pisum      CATAATATTGTATGCACATGGGATGTTGGTTTCCCAATAATGTTGGAAGAATTAAATACT 804
TATA_M.viciae     CATAATATTGTATGCACATGGGATGTTGGTTTCCCAATAATGTTGGAAGAATTAAATACT 837
                  ************************************************************

TATA_A.pisum      GCTCACTCACAATTTACCAGCTTTGAGCCTGAAGTATTTCCTGCGTTAATTTATCGGATG 864
TATA_M.viciae     GCTCACTCACAGTTTACCAGCTTTGAGCCAGAAGTATTTCCTGCGTTAATTTATCGGATG 897
                  *********** **************** ******************************

TATA_A.pisum      GTCAAACCTCGAGCAGTGTTTTTAATGTTCGTAAATGGAAAAGTAGTTTTAACAGGTCTT 924
TATA_M.viciae     GTCAAACCACGAGCCGTGTTTTTAATGTTTGTAAATGGAAAAGTAGTTTTGACAGGTCTT 957
                  ******** ***** ************** ******************** *********

TATA_A.pisum      AAAACAAAATCAGATATAAAAGAATCTGTATTTTTGATGCAAGATGTATTAAACAGTTTC 984
TATA_M.viciae     AAAACAAAAGCAGATATAAAAGAATCTATTTTTTTGATGCAAGATGTATTAAACAATTTC 1017
                  ********* **************** * ************************* ****

TATA_A.pisum      AAAAAAACTTGA 996
TATA_M.viciae     AGAAAAACTTAA 1029
                  * ******** *
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β –tubulin nucleotidic sequences alignments.

```
TUB_A.pisum      ATGAGGGAAATCGTACACTTGCAAGCCGGACAATGCGGAAACCAGATCGGCGCCAAGTTC 60
TUB_M.viciae     ATGAGGGAAATCGTACACTTGCAAGCTGGACAATGCGGAAACCAAATCGGTGCCAAGTTC 60
                 ************************* **************** ***** *********

TUB_A.pisum      TGGCAAGTCATATCCGAAGAGCACGGAATCGACTATACAGGATTCTACAAGGGCACATCC 120
TUB_M.viciae     TGGCAAGTCATATCCGAAGAGCACGGAATCGACTACACGGGATTCTACAAGGGCACGTCC 120
                 ********************************** ** **************** ***

TUB_A.pisum      GATCTACAGCTGGAACGCATTAACGTTTACTATAACGAAGGGTCTGCCGCCAACCGTTCG 180
TUB_M.viciae     GATCTACAGCTGGAACGCATTAACGTTTACTACAACGAAGGGTCTGCCGCCAACCGTTCG 180
                 ****************************** *************************

TUB_A.pisum      GAAGGTGGAAAATATGTGCCACGAGCCGTCTTACTCGACCTGGAACCCGGTACCATGGAG 240
TUB_M.viciae     GAAGGTGGAAAATATGTGCCACGAGCCGTCTTACTCGACCTGGAACCCGGTACCATGGAA 240
                 ************************************************************

TUB_A.pisum      TCCATCCGGTCCGGACCTTACGGCGCGCTTTTCCGGCCGGACAACTTCGTGTTCGGTCAG 300
TUB_M.viciae     TCCATCCGATCCGGACCTTACGGCGCGCTCTTCCGGCCGGACAACTTCGTGTTCGGTCAG 300
                 ******* ******************* ****************************

TUB_A.pisum      TCGGGCGCTGGAAACAACTGGGCCAAGGGTCATTACACTGAGGGTGCCGAACTCGTGGAC 360
TUB_M.viciae     TCGGGCGCCGGAAACAACTGGGCCAAGGGCCATTACACGGAGGGCGCCGAACTTGTGGAC 360
                 ******* ******************* ******** ***** ******** ******

TUB_A.pisum      GCCGTGTTGGACGTGGTTCGCAAAGAGAGCGAGAACTGTGACTGTTTGCAGGGATTCCAG 420
TUB_M.viciae     GCCGTGTTGGACGTGGTGCGCAAAGAGAGCGAGAACTGCGACTGTCTGCAGGGATTCCAG 420
                 **************** ******************* ****** **************

TUB_A.pisum      TTGGCGCACTCGTTGGGCGGTGGCACCGGTTCCGGACTGGGTACACTTCTGATATCGAAG 480
TUB_M.viciae     TTGGCGCACTCGTTGGGCGGCGGCACCGGTTCCGGGCTGGGCACACTTTTGATATCGAAG 480
                 ******************* ************** ***** ****** ***********

TUB_A.pisum      ATCCGCGAGGAGTACCCTGACCGCATAATGAATACGTACTCAGTGATGCCATCTCCAAAG 540
TUB_M.viciae     ATCCGCGAGGAGTATCCCGACCGGATAATGAACACGTACTCGGTTATGCCATCGCCGAAG 540
                 ************** ** ***** ******** ******** ** ******** ** ***

TUB_A.pisum      GTGTCGGACACGGTGGTGGAGCCGTACAACGCGACCTTGTCCGTGCACCAGCTGGTGGAG 600
TUB_M.viciae     GTGTCGGACACGGTCGTGGAGCCGTACAACGCGACGTTGTCCGTGCACCAGCTGGTGGAG 600
                 ************** ******************* ************************

TUB_A.pisum      AATACCGACGAGTCGTACCTGATCGACAACGAGGCGCTGTACGACATTTGCTTCCGGACG 660
TUB_M.viciae     AACACCGACGAGTCGTACCTGATCGATAACGAGGCGCTGTACGACATTTGCTTCCGGACA 660
                 ** ********************** ******************************

TUB_A.pisum      CTGAAGCTGACCAACCCGACGTACGGCGACCTCAACCACCTTGTGTCGCTGACAATGTCC 720
TUB_M.viciae     TTGAAGCTGACCAACCCGACGTACGGCGACCTCAACCACCTGGTGTCGCTGACCATGTCC 720
                  ************************************** *********** ******

TUB_A.pisum      GGCGTGACCACGTGCCTCCGGTTCCCCGGTCAGCTGAACGCCGACCTCCGCAAGCTGGCG 780
TUB_M.viciae     GGCGTAACCACGTGCCTCCGGTTCCCCGGTCAGCTGAACGCCGACCTCCGCAAGCTGGCG 780
                 ***** ******************************************************

TUB_A.pisum      GTCAACATGGTCCCGTTCCCCAGGCTCCACTTCTTCATGCCGGGATTCGCGCCTCTTACG 840
TUB_M.viciae     GTTAACATGGTCCCGTTCCCCCGGCTCCACTTCTTCATGCCGGGATTCGCACCGCTCACG 840
                 ** ***************** ************************** ** ** ***

TUB_A.pisum      GCCCGCGGAAGTCAGTCTTACCGGGCCATGAGCGTGCCCGAGCTCACTCAGCAAATGTTC 900
TUB_M.viciae     GCCCGCGGCAGTCAGTCTTACCGGGCCATGAGCGTGCCCGAGCTCACTCAGCAAATGTTC 900
                 ******* ****************************************************

TUB_A.pisum      GACGCCAAGAACATGATGGTCGCCTGCGACCCACGACACGGCCGCTACCTCACCGTCGCC 960
TUB_M.viciae     GACGCCAAGAACATGATGGTCGCCTGCGACCCACGACACGGCCGCTACCTCACCGTCGCC 960
                 ************************************************************

TUB_A.pisum      GCCATATTCAGGGGTCGCATGTCCATGAAAGAGGTGGACGAGCAGATGTTGAACGTGCAA 1020
TUB_M.viciae     GCCATATTCAGGGGTCGCATGTCCATGAAAGAGGTGGACGAGCAGATGTTGAACGTGCAA 1020
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Figure S2. Google Scholar number of results from 2002 to 2014 using as searching words "Validation of reference genes".