选择

TRINITY\_DN23320\_c1\_g5 AGP 1426bp

AGP DN23320-F: ATGGATGCCAGCAGTATGATGG

AGP DN23320-R: TCAAGTAGAAGAATGAAAGGTC

TRINITY\_DN7735\_c0\_g1 AGP 1791bp

ADP-glucose pyrophosphorylase 1 [Colocasia esculenta]

AGP DN7735-F:ATGGCGATGGCGATGGCGAC

AGP DN7735-R: CTAAAAGGAACATAGAAG

TRINITY\_DN1266\_c0\_g1 CSLA 1620bp

CSLA DN1266-F: ATGGAGCGCCTCTCGTCGACG

CSLA DN1266-R: CTAGTTGGGAACGAAGGTTCC

TRINITY\_DN21109\_c0\_g2 CSLD 1752bp

cellulose synthase-like protein D2 [Phoenix dactylifera]

CSLA DN21109-F: ATGTTGAAGCCTCCGAGTGATG

CSLA DN21109-R: TCATGGGAATGTGAAGGAGC

TRINITY\_DN23320\_c1\_g5

putative ADP-glucose pyrophosphorylase, partial [Amorphophallus konjac]

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| H\_0 |  | Petiole | Root | Tuber |
| 4.2567 |  | 8.0867 | 0.9033 | 39.0667 |

>Genome sequence TRINITY\_DN23320\_c1\_g5

CTTCCTCCTCCTCCTCCTCCTCCTCCTCTGCCCCTGTTTCTTCTCACTGCTGGAGAAACCTGCGGCAGAGACCTTTCTGGCTCTCAAGGGTCTGGACATCGGGTCCTCCTCGGCTTAGAGGTGGTCTCTCTCTCTCTGTATGTGTGTGTGGATCAGCACCAGAGAGCTGACTCTTCAGTAGGTTCTGGTGACTGGGCACTTATAACGCCTCTTCCGGACCTTAACAACAGAGGAAGCAAAAAGAAAGGGAGAAAAAGAAAGGAGACAGAGAGGGAGAGAGAGATTCTGATTCTGCAAACATGGATGCCAGCAGTATGATGGTCACAAGCTTCGGTGCCAACGCCCCGTTTGTGAACCGGTCACACCGCCAAGGGGGTGGCGGTGGCATCATGGGAGGGAGACCAATCTGGGGAGATGAAGTGCGTGGTGGCAGTTCAGAGAGCAGAGGAATATGGGGCACCACCAAGTTGCCAATGAGCTCTCTGGGCAACAGGGCTCCGGCTGCCAGAAGGCGCACAGGTCCCGCGGGCGCGACTGTCTCTGCCATCCTTACTCCAGAAATCAGCAAGGATACCTTGACCTTCCAGTCGCCATTCTTTGAGAAGGAGTGGGCAAACCCGAAGAACGTGGCTGCGATCATCCTCGGTGGAGGTGCCGGGACTAAATTGTTCCCTCTGACTGGCAGAAGAGCTGAGCCTGCTGTCCCCATTGGAGGTTCCTATCGGCTTATTGACATTCCAATGAGCAACTGCATCAACAGTGGGATAAACAAGATTTATGTGATGACCCAGTTCAATTCTTGGTCTCTTAACCGCCATCTCGCTCGCACGTACAACTTTGGGAATGGTGTTAATTTTGGGGATGGATTTGTTGAGGTACTGGCAGCCACCCAAACTTCTGGTGAAGCTGGAATGAACTGGTTTCAGGGAACGGCAGATGCTGTGAGACAATTCATCTGGGTCTTTGAGGATCCAAGGAACAAGAACATAGAGCACGTACTGATCTTGTCTGGTGATCAGCTTTACAGAATGGATTATATGGACTTGGTGCAGAGGCACATGGACACTCGGGCAGATATTACGGTTTCATGTGTACCCGTGGACGACAGCCGTGCATCTGACTTCGGATTGATGAAGATCGATAAGGTTGGCCGGATTGTCCATTTCTCTGAGAAACCTAAGGGTTCTGTTCTGGATGCCATGAAGGTTGACACCACAATTCCTGGGTTATCTCCTTATGAAGCCAAAAATTTTCCCTACATTGCATCGATGGGAGTATATGCCTTCAGAACAGAAATCCTTCTAAACCTCTTGAGGTGGAGGTACCCAACATCCAATGATTTTGGATCTGAAATCATTCCTTCTGCTGTGAATGAGTACAATGTACAGGCTTATCTCTTCAAGGACTACTGGGAGGACATTGGAACAATTAAGACATTCTTTGAGGCAAATTTGGCTCTCACAGATCAGTCCCCAAAATTTCAATTTTATGATCCTCAGACACCATTCTACACATCACCTCGTTATTTGCCGCCTACCAAAGTGGATAAATGCAGGATTGTGGACTCCATCATATCCCATGGGTGTTTCCTAGATCAATGCAGTATTGAACATTCAATTGTAGGTGATCGGTCACGCTTGGAGTACAACGTCGAACTGAAGGTGATCCTTTCAATTAAGCACATGCACTCTTACACATGCTTAAAGACCTTTCATTCTTCTACTTGAGACATATAGGTAAAAGGCATTTATTTCTGAATCAACCAATATTAAGCACCCCAAGCACTGAAACCAGAAAGGAGAAGATAGGGATAACCTTGTACACATGAGCAGTTGTTCAAAGGATCTTATTACCACCTTTAGGATCCCTGCCCCTAAGGTGCTTTGCTGATTAAGTTCTGATCTTCTGTGTAGGACCAAATGTCATGCTTTCTCAAATACATATACCACGGAAATACTATATCTTACATTTTACGAATAGCTTAGCCACTCAAAACCAAATGCAATGAGAGTGAATATTGAATTTTCTCAATATTTCTGAACATAGCAGGAAATTGTAATACATAAAACCTTCATCTGCTTTAGAAAAGGGTAAAAATTTAAAAGATATTTAGAGATAGAAATGTGGATTTTGGTACAAAAACCACATTGTTGATGATAAAAAGTACAGTGTACTCAGTATGGATTCAGTCAGAGATCAATTTTCTTAGTTGTAGTTGATGAACGGGAAAAACGATGACGTGCATTGAGAACAGGCTCAATGGATTATTTATTGCTATCTGTCAAGCAATAGAATATCACTGCATAAGTTATCAAGTTAATGTTGTATGGCGTGACTCAGGTTTTTGCATTTTCCATATCTCATTCCTGAGAGTTATAGCTAACGAGAAACCAAAATATTATTGGATTCAGAATACCCATTGCTCTTCCATTTTATATTTCATTTGGATCGGAATTTCCCTTTTTTTTCATGGTTTACATTTCTAATCGTGAACCGCCCTGTGAAATAGACTATTTACCTCATTTTGAGAACTAAGATGGTCCAACCTGATGTCTTAGTAAGATTTTATGTTAAAAAGAAACCAATGAGAAAACCAGAAATTCAAGGCAGG

>CDs

ATGGATGCCAGCAGTATGATGGTCACAAGCTTCGGTGCCAACGCCCCGTTTGTGAACCGGTCACACCGCCAAGGGGGTGGCGGTGGCATCATGGGAGGGAGACCAATCTGGGGAGATGAAGTGCGTGGTGGCAGTTCAGAGAGCAGAGGAATATGGGGCACCACCAAGTTGCCAATGAGCTCTCTGGGCAACAGGGCTCCGGCTGCCAGAAGGCGCACAGGTCCCGCGGGCGCGACTGTCTCTGCCATCCTTACTCCAGAAATCAGCAAGGATACCTTGACCTTCCAGTCGCCATTCTTTGAGAAGGAGTGGGCAAACCCGAAGAACGTGGCTGCGATCATCCTCGGTGGAGGTGCCGGGACTAAATTGTTCCCTCTGACTGGCAGAAGAGCTGAGCCTGCTGTCCCCATTGGAGGTTCCTATCGGCTTATTGACATTCCAATGAGCAACTGCATCAACAGTGGGATAAACAAGATTTATGTGATGACCCAGTTCAATTCTTGGTCTCTTAACCGCCATCTCGCTCGCACGTACAACTTTGGGAATGGTGTTAATTTTGGGGATGGATTTGTTGAGGTACTGGCAGCCACCCAAACTTCTGGTGAAGCTGGAATGAACTGGTTTCAGGGAACGGCAGATGCTGTGAGACAATTCATCTGGGTCTTTGAGGATCCAAGGAACAAGAACATAGAGCACGTACTGATCTTGTCTGGTGATCAGCTTTACAGAATGGATTATATGGACTTGGTGCAGAGGCACATGGACACTCGGGCAGATATTACGGTTTCATGTGTACCCGTGGACGACAGCCGTGCATCTGACTTCGGATTGATGAAGATCGATAAGGTTGGCCGGATTGTCCATTTCTCTGAGAAACCTAAGGGTTCTGTTCTGGATGCCATGAAGGTTGACACCACAATTCCTGGGTTATCTCCTTATGAAGCCAAAAATTTTCCCTACATTGCATCGATGGGAGTATATGCCTTCAGAACAGAAATCCTTCTAAACCTCTTGAGGTGGAGGTACCCAACATCCAATGATTTTGGATCTGAAATCATTCCTTCTGCTGTGAATGAGTACAATGTACAGGCTTATCTCTTCAAGGACTACTGGGAGGACATTGGAACAATTAAGACATTCTTTGAGGCAAATTTGGCTCTCACAGATCAGTCCCCAAAATTTCAATTTTATGATCCTCAGACACCATTCTACACATCACCTCGTTATTTGCCGCCTACCAAAGTGGATAAATGCAGGATTGTGGACTCCATCATATCCCATGGGTGTTTCCTAGATCAATGCAGTATTGAACATTCAATTGTAGGTGATCGGTCACGCTTGGAGTACAACGTCGAACTGAAGGTGATCCTTTCAATTAAGCACATGCACTCTTACACATGCTTAAAGACCTTTCATTCTTCTACTTGA

TRINITY\_DN23320\_c1\_g5 AGP

DN23320-F: ATGGATGCCAGCAGTATGATGG

DN23320-R: TCAAGTAGAAGAATGAAAGGTC

>peptide

MDASSMMVTSFGANAPFVNRSHRQGGGGGIMGGRPIWGDEVRGGSSESRGIWGTTKLPMSSLGNRAPAARRRTGPAGATVSAILTPEISKDTLTFQSPFFEKEWANPKNVAAIILGGGAGTKLFPLTGRRAEPAVPIGGSYRLIDIPMSNCINSGINKIYVMTQFNSWSLNRHLARTYNFGNGVNFGDGFVEVLAATQTSGEAGMNWFQGTADAVRQFIWVFEDPRNKNIEHVLILSGDQLYRMDYMDLVQRHMDTRADITVSCVPVDDSRASDFGLMKIDKVGRIVHFSEKPKGSVLDAMKVDTTIPGLSPYEAKNFPYIASMGVYAFRTEILLNLLRWRYPTSNDFGSEIIPSAVNEYNVQAYLFKDYWEDIGTIKTFFEANLALTDQSPKFQFYDPQTPFYTSPRYLPPTKVDKCRIVDSIISHGCFLDQCSIEHSIVGDRSRLEYNVELKVILSIKHMHSYTCLKTFHSST\*

TRINITY\_DN7735\_c0\_g1

ADP-glucose pyrophosphorylase 1 [Colocasia esculenta]

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| --- | --- | --- | --- |
| 186.5633 | 193.2833 | 72.7267 | 84.7567 |

>Genome sequence/ DN7735

GCCCATTTTGTTCATATTCAGATCAGAACGACTTACTTCCATCCAAAATGTCTGCCTAGGTCCACTCTGCCTCCGAACATCATGGCCAAAATTAGTACGATTGAACCTTCTGATAGTTTTGAAGGGCCATTACCTCATAATAATCAGCTCCCATCAGCAAGCTGTCTTCTATGACTGCACCTTCGGAAATATAGGAGCGTAGACCAACTACAGAATGGTGAATCTTGCAGTTCTGTAACGAAACAAGAAGCAAAGTTATCAGGTAATTAAAAGGATTGAATCATTAAACTCTAACTACGGACAGATATATACCAAGAGTAGAAAAACAACTACCAAGGAGGATTCTAAGAAATAGTGAGGCAAACATAAGAGTGCACTCTTTTGATGACAATGGAACAGGAAATAAGGTTTATAGGATGCCTTTGTACAAAAAATAAAATGAGAGGGAGACTATTATCCGCATAATAAAGTCTTGCATAACTTGGGTCGAGTCTTAAACCCTAATTAGGAATATAACATACGATAACCCTAAAAGGAACATAGAAGAAATAAAATTGAAGTACAAGGCAACATTATTGATGGCATTTGGGTAGCTATGGCTGATAGAAGAGAAAGCTGAGGATTAAAACAGAGCATAGGATGACACATTTTGATAATAAATAGCTTATCGCAGTTAAGTGATGCAATAAATAAGCATGCCAAGAAGTCAGCATAGCACCAAGCAGTTAATATACAGCTTACCTTGATAACACAACCTTCACCAATAACACTGTCCGTTATGTCAGCATCAAGCATTTTGGAAGGTGGTAAATATCGAGGTTGTGTATAAATTGGGGAGGAACGGTCATAGAAGCTGAAATCCGGAATAGGTTTCTTTGTGATCCCCAGATTTGCATTGTAGAATGCCTCAATGGTCCCAATATCTTCCCAGTAGCCATCATAAAGGTACGCTTGAACCTGTGATCCATCAAAATATTGATTCATGCAGAAAATTCTCTCTCACACACCATGCAAGTACAAAGAGCAGTTCAACCTATGTACCTTCTACATTACTCTCGAGATGGCATCATGCCACCAAGGCCCCATGCTATTCCAGGATCCTATTTTATATGAACTAATGAAGAATTTATGGGCCACAGTAACTCAAATGTTTAAAGCTTATAATGGAGTGCCTACCATATTGTATACTTATCTTACATTTTGTCTCCACTCAATGTGGGATTATTCTAACGTAATTTGCAAAGGAGAAGTTGCTAATAGGTACAGCAGGCATACCCTCATCCCAATGGAAGTGGCACCAGGTATGACCTCACTTCCAAAATCATTGGCCCCGGGGAACTTCTCACGAAGTAGCTCCAGCATGATATCTTTGCTCACTACATAAATGCCCATACTTGCTATATAAGGCATCTCTCTTGCCCTCTCGTCATCTAGGCCTAATATTGTTGTATCAACCTTCATTGCTTTCAGCTGCTCCCCTTTTGGCTTCTCAGCAAATTCAATGATGCGACCTTCCTCATCAATTTTCATCAAGCCAAAAGCAGTAGCCCTTTTCTCATCCATCGGAAGAGCTGCTACTGTAATATCAGCATCTGTTTCTCTGTGTGCTTGAATAAACCTCTCATAATCCATACGATATAAGTGATCTCCAGCAAGGACAAGGAACTCCATGACATTGTGCTCCTCAAAAAGCCATAGATACTGCCTCACAGCATCAGCAGTTCCCTGAAACCAGTTGGGGTTCTCGGGGCTCTGCTGTGCAGCAAGGACTTCAACGAAACCTTCATTCTTGTATCCACCAATGTTGTTGCCATATGCTCGTGAAAGGTGGCGGTTGAGAGATGCAGAGTTGAACTGGGTCAAGACGTATATTTTCGAAATGTTGCTGTTCAAGCAATTGCTGACAGGGATGTCAATCAACCGGTAGTTGGCTCCCAAAGGAACAGCGGGCTTTGCCCGCTTCTTAGTTAAAGGGTACAAGCGGGTCCCAGCTCCACCGCCCAATATAATTCCCAGGACACTCTTGCTGGCCTCGGGATCGAGGCAGGTCTGCGAGCTCTTGGAATCCGAAACGGCTTTCGGCGACACGAGGATCGGCAACCGCCCCCCCGATGCGAGCCTCGCCCGCCGGGAAGCCGCCTTGGGGAAGCACAGATCGCCGGAGACGTGGGAGGAAGACGAGGCGGCGAGGCCGTGGCCGGACGATCCGCCGAGGGCCAGGGTCACGGGGGCCGCGGGGCCGCCACTGGCGGGGCGGTTCTGGGAGGGGGGCGCGGTGGCGACGTACGTGGAAGCCACCGTCGCCATCGCCATCGCCATCGCCACCACTCGCAGCGCGCCTCCGGAAGAGAGTGTGCGGTCTGCTTCTGTGCGATCACCAGAGCCTGTGGAAGAGGACGCCGCGGGGGGGCTCCATATTTAATATAGCTCCAGATCTCACGGGAGCCTCATCAAGTGGACCTGAAAGTTATAAAATTACGACAAAAACCAGCCTCGGGACACCTGGGTTGCGGGCCGTGAAATGGTATTTCCGATATTTTAGCTGTCAACAATTAATTAAAAGTGGC

基因组序列和CDs对不上，换反向互补，比对上了



GCCACTTTTAATTAATTGTTGACAGCTAAAATATCGGAAATACCATTTCACGGCCCGCAACCCAGGTGTCCCGAGGCTGGTTTTTGTCGTAATTTTATAACTTTCAGGTCCACTTGATGAGGCTCCCGTGAGATCTGGAGCTATATTAAATATGGAGCCCCCCCGCGGCGTCCTCTTCCACAGGCTCTGGTGATCGCACAGAAGCAGACCGCACACTCTCTTCCGGAGGCGCGCTGCGAGTGGTGGCGATGGCGATGGCGATGGCGACGGTGGCTTCCACGTACGTCGCCACCGCGCCCCCCTCCCAGAACCGCCCCGCCAGTGGCGGCCCCGCGGCCCCCGTGACCCTGGCCCTCGGCGGATCGTCCGGCCACGGCCTCGCCGCCTCGTCTTCCTCCCACGTCTCCGGCGATCTGTGCTTCCCCAAGGCGGCTTCCCGGCGGGCGAGGCTCGCATCGGGGGGGCGGTTGCCGATCCTCGTGTCGCCGAAAGCCGTTTCGGATTCCAAGAGCTCGCAGACCTGCCTCGATCCCGAGGCCAGCAAGAGTGTCCTGGGAATTATATTGGGCGGTGGAGCTGGGACCCGCTTGTACCCTTTAACTAAGAAGCGGGCAAAGCCCGCTGTTCCTTTGGGAGCCAACTACCGGTTGATTGACATCCCTGTCAGCAATTGCTTGAACAGCAACATTTCGAAAATATACGTCTTGACCCAGTTCAACTCTGCATCTCTCAACCGCCACCTTTCACGAGCATATGGCAACAACATTGGTGGATACAAGAATGAAGGTTTCGTTGAAGTCCTTGCTGCACAGCAGAGCCCCGAGAACCCCAACTGGTTTCAGGGAACTGCTGATGCTGTGAGGCAGTATCTATGGCTTTTTGAGGAGCACAATGTCATGGAGTTCCTTGTCCTTGCTGGAGATCACTTATATCGTATGGATTATGAGAGGTTTATTCAAGCACACAGAGAAACAGATGCTGATATTACAGTAGCAGCTCTTCCGATGGATGAGAAAAGGGCTACTGCTTTTGGCTTGATGAAAATTGATGAGGAAGGTCGCATCATTGAATTTGCTGAGAAGCCAAAAGGGGAGCAGCTGAAAGCAATGAAGGTTGATACAACAATATTAGGCCTAGATGACGAGAGGGCAAGAGAGATGCCTTATATAGCAAGTATGGGCATTTATGTAGTGAGCAAAGATATCATGCTGGAGCTACTTCGTGAGAAGTTCCCCGGGGCCAATGATTTTGGAAGTGAGGTCATACCTGGTGCCACTTCCATTGGGATGAGGGTATGCCTGCTGTACCTATTAGCAACTTCTCCTTTGCAAATTACGTTAGAATAATCCCACATTGAGTGGAGACAAAATGTAAGATAAGTATACAATATGGTAGGCACTCCATTATAAGCTTTAAACATTTGAGTTACTGTGGCCCATAAATTCTTCATTAGTTCATATAAAATAGGATCCTGGAATAGCATGGGGCCTTGGTGGCATGATGCCATCTCGAGAGTAATGTAGAAGGTACATAGGTTGAACTGCTCTTTGTACTTGCATGGTGTGTGAGAGAGAATTTTCTGCATGAATCAATATTTTGATGGATCACAGGTTCAAGCGTACCTTTATGATGGCTACTGGGAAGATATTGGGACCATTGAGGCATTCTACAATGCAAATCTGGGGATCACAAAGAAACCTATTCCGGATTTCAGCTTCTATGACCGTTCCTCCCCAATTTATACACAACCTCGATATTTACCACCTTCCAAAATGCTTGATGCTGACATAACGGACAGTGTTATTGGTGAAGGTTGTGTTATCAAGGTAAGCTGTATATTAACTGCTTGGTGCTATGCTGACTTCTTGGCATGCTTATTTATTGCATCACTTAACTGCGATAAGCTATTTATTATCAAAATGTGTCATCCTATGCTCTGTTTTAATCCTCAGCTTTCTCTTCTATCAGCCATAGCTACCCAAATGCCATCAATAATGTTGCCTTGTACTTCAATTTTATTTCTTCTATGTTCCTTTTAGGGTTATCGTATGTTATATTCCTAATTAGGGTTTAAGACTCGACCCAAGTTATGCAAGACTTTATTATGCGGATAATAGTCTCCCTCTCATTTTATTTTTTGTACAAAGGCATCCTATAAACCTTATTTCCTGTTCCATTGTCATCAAAAGAGTGCACTCTTATGTTTGCCTCACTATTTCTTAGAATCCTCCTTGGTAGTTGTTTTTCTACTCTTGGTATATATCTGTCCGTAGTTAGAGTTTAATGATTCAATCCTTTTAATTACCTGATAACTTTGCTTCTTGTTTCGTTACAGAACTGCAAGATTCACCATTCTGTAGTTGGTCTACGCTCCTATATTTCCGAAGGTGCAGTCATAGAAGACAGCTTGCTGATGGGAGCTGATTATTATGAGGTAATGGCCCTTCAAAACTATCAGAAGGTTCAATCGTACTAATTTTGGCCATGATGTTCGGAGGCAGAGTGGACCTAGGCAGACATTTTGGATGGAAGTAAGTCGTTCTGATCTGAATATGAACAAAATGGGC

>CDs

ATGGCGATGGCGATGGCGACGGTGGCTTCCACGTACGTCGCCACCGCGCCCCCCTCCCAGAACCGCCCCGCCAGTGGCGGCCCCGCGGCCCCCGTGACCCTGGCCCTCGGCGGATCGTCCGGCCACGGCCTCGCCGCCTCGTCTTCCTCCCACGTCTCCGGCGATCTGTGCTTCCCCAAGGCGGCTTCCCGGCGGGCGAGGCTCGCATCGGGGGGGCGGTTGCCGATCCTCGTGTCGCCGAAAGCCGTTTCGGATTCCAAGAGCTCGCAGACCTGCCTCGATCCCGAGGCCAGCAAGAGTGTCCTGGGAATTATATTGGGCGGTGGAGCTGGGACCCGCTTGTACCCTTTAACTAAGAAGCGGGCAAAGCCCGCTGTTCCTTTGGGAGCCAACTACCGGTTGATTGACATCCCTGTCAGCAATTGCTTGAACAGCAACATTTCGAAAATATACGTCTTGACCCAGTTCAACTCTGCATCTCTCAACCGCCACCTTTCACGAGCATATGGCAACAACATTGGTGGATACAAGAATGAAGGTTTCGTTGAAGTCCTTGCTGCACAGCAGAGCCCCGAGAACCCCAACTGGTTTCAGGGAACTGCTGATGCTGTGAGGCAGTATCTATGGCTTTTTGAGGAGCACAATGTCATGGAGTTCCTTGTCCTTGCTGGAGATCACTTATATCGTATGGATTATGAGAGGTTTATTCAAGCACACAGAGAAACAGATGCTGATATTACAGTAGCAGCTCTTCCGATGGATGAGAAAAGGGCTACTGCTTTTGGCTTGATGAAAATTGATGAGGAAGGTCGCATCATTGAATTTGCTGAGAAGCCAAAAGGGGAGCAGCTGAAAGCAATGAAGGTTGATACAACAATATTAGGCCTAGATGACGAGAGGGCAAGAGAGATGCCTTATATAGCAAGTATGGGCATTTATGTAGTGAGCAAAGATATCATGCTGGAGCTACTTCGTGAGAAGTTCCCCGGGGCCAATGATTTTGGAAGTGAGGTCATACCTGGTGCCACTTCCATTGGGATGAGGGTATGCCTGCTGTACCTATTAGCAACTTCTCCTTTGCAAATTACGTTAGAATAATCCCACATTGAGTGGAGACAAAATGTAAGATAAGTATACAATATGGTAGGCACTCCATTATAAGCTTTAAACATTTGAGTTACTGTGGCCCATAAATTCTTCATTAGTTCATATAAAATAGGATCCTGGAATAGCATGGGGCCTTGGTGGCATGATGCCATCTCGAGAGTAATGTAGAAGGTACATAGGTTGAACTGCTCTTTGTACTTGCATGGTGTGTGAGAGAGAATTTTCTGCATGAATCAATATTTTGATGGATCACAGGTTCAAGCGTACCTTTATGATGGCTACTGGGAAGATATTGGGACCATTGAGGCATTCTACAATGCAAATCTGGGGATCACAAAGAAACCTATTCCGGATTTCAGCTTCTATGACCGTTCCTCCCCAATTTATACACAACCTCGATATTTACCACCTTCCAAAATGCTTGATGCTGACATAACGGACAGTGTTATTGGTGAAGGTTGTGTTATCAAGGTAAGCTGTATATTAACTGCTTGGTGCTATGCTGACTTCTTGGCATGCTTATTTATTGCATCACTTAACTGCGATAAGCTATTTATTATCAAAATGTGTCATCCTATGCTCTGTTTTAATCCTCAGCTTTCTCTTCTATCAGCCATAGCTACCCAAATGCCATCAATAATGTTGCCTTGTACTTCAATTTTATTTCTTCTATGTTCCTTTTAG

TRINITY\_DN7735\_c0\_g1 AGP

ADP-glucose pyrophosphorylase 1 [Colocasia esculenta]

DN7735-F:ATGGCGATGGCGATGGCGAC

DN7735-R: CTAAAAGGAACATAGAAG

>Pep

MAMAMATVASTYVATAPPSQNRPASGGPAAPVTLALGGSSGHGLAASSSSHVSGDLCFPKAASRRARLASGGRLPILVSPKAVSDSKSSQTCLDPEASKSVLGIILGGGAGTRLYPLTKKRAKPAVPLGANYRLIDIPVSNCLNSNISKIYVLTQFNSASLNRHLSRAYGNNIGGYKNEGFVEVLAAQQSPENPNWFQGTADAVRQYLWLFEEHNVMEFLVLAGDHLYRMDYERFIQAHRETDADITVAALPMDEKRATAFGLMKIDEEGRIIEFAEKPKGEQLKAMKVDTTILGLDDERAREMPYIASMGIYVVSKDIMLELLREKFPGANDFGSEVIPGATSIGMRVCLLYLLATSPLQITLE\*SHIEWRQNVR\*VYNMVGTPL\*ALNI\*VTVAHKFFISSYKIGSWNSMGPWWHDAISRVM\*KVHRLNCSLYLHGV\*ERIFCMNQYFDGSQVQAYLYDGYWEDIGTIEAFYNANLGITKKPIPDFSFYDRSSPIYTQPRYLPPSKMLDADITDSVIGEGCVIKVSCILTAWCYADFLACLFIASLNCDKLFIIKMCHPMLCFNPQLSLLSAIATQMPSIMLPCTSILFLLCSF\*

CSL

TRINITY\_DN25492\_c0\_g1 CSLA

putative mannan synthase [Amorphophallus konjac]

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| --- | --- | --- | --- |
| 0.45 | 0.18 | 0.05 | 595.2167 |

CDs序列不对

>Genome sequence/ DN25492

CCTAGCTGGAGAGAGAGCCTCAGCCCCCCTTGGAGGTGGGCTTCTTCCCCTCACTAACGTACCAGGGGGAGCCAAAGAAAATGGAGGGCCTAATGAAGGTCGCCTACCTGCCTCGCTCCCTCATGTACTCGATCATGGGGGGCCGGGAATTGTCGTTTTGGCCGGAGATGGCCATCGACTGGGCGAGAATCCTCTACATTTGGGGTCAGGTGAGAACCATGGTGCTTATTCCGGCAATGAGGATCGCCGTGTTGCTGTGCCTCATCATGTCGGTGATGCTGCTAATGGAGAAGCTCCTCATGGGTGGTGTGAGCCTGTACGTGAAGGTCTTCCGCCGGCGGCCCAAGAAGGTCTACAGGTGGGAGCCCGTGGGAGGGGACGAGGAGTTGGGCACTGCAGCCTACCCAATGGTCCTCGTCCAAATACCCATGTACAATGAGAGAGAGGTTTACCACCTGTCGATCAAAGCTGCATGCTGCCTCCAATGGCCGTCGGATCGGCTGATCGTCCAAGTTCTTGATGATTCCACAGACCCAATGATTAAGGTGATATATTCTACGACTGATCTCAGAAAAGAGTTCTAACCAGATAAAATTCACCTGAATTCGTGTGCAGATTCTAGAAGTTGGCAAGGGGAAGTTGATGTACTGGTTTCTTAGCAAATCGACGGCCACGTTGAAAGAGCCAGCAATGTCGAGCAATATTTAATTTGCTGCTGAACTTTCAATGAATATATATATATATATGCCTAGAGCACACCAAGGAATTATGTACGTACATATATAGGAGAGTCTGGCAGGGTTCTCTCTCTCTATATATATGATCAGGGCCAAGTGGCCCTTATGGCCCTTGAATCACCCAAGAATACTTTTACAACCTCCACATGCTATATATCTAACCATTCTTCTTCCTCCGAGACCATGCATTTGATTCTCAAAGATTATATATGAACAAAATTGTTTTTAAGTATCTTTTAATAAAATATCTTTTAATAAAATAACTTCATATATATCCCAGCTTGCTAGCTAGCTAGCTGGTGGCCAACGTAATCAGCAATATTGGGACCATTTGATATTAATGTCATGATATATATATAAATTCGTTATAATTCCTTCCCCCCCGCCCCTTAATTGGGGGGATCATGATCTCCAGGATCTCGTGTACAAGGAATGCCAGAAATGGGCTTTGGATGGGGTGAACATAAAATATGAGACCAGGGCCAACAGAAATGGGTACAAGGCGGGTGCCCTCAAGGAAGGAATGAAGTACAGTTACGTGGAGGAGTGCGACTACGTCGCCATCTTTGATGCCGACTTCCAAGCAGACCCCGACTACCTTGTGCAGATGGTACCTTTTCTCATCCACAACCCGGAGATCGGTCTCGCTCAGGCTCGCTGGAACTTTGTAAATGCTGAGGAGTGCTTGATGACAAGACTACAAGAGATGTCAATGGACTACCACTTCAAGGTGGAGCAGGAGTCAGGCTCATCCATTCATGCATTCTTCGGCTTCAATGGAACTGCTGGGGTTTGGAGAATCCGGGCCCTTAATGAAGCCGGAGGTTGGAAGGACCGCACCACTGTGGAGGACATGGACTTGGCCATTAGGGCGACTCTTGAAGGTTGGAAGTTTGTCTACGTGGGAGACGTCAAGGTTAAAAGTGAATTACCAAGCACTTTCAAGGCTTTTCGCTACCAACAGCATCGATGGTCATGCGGGCCCGCAAATCTGGTGAGGAAGATGGCAATAGAAATCCTGATGACTAAGAAAGTGCCACTGTGGAAGAAATTCTACTTACTCTACAATTTCTTCCTCACTCGAAAGATCGTAGCTCATTTCGTCACCTTCTTCTTCTATTGTGTCGTGTTTCCAACAGCCGTGTTCTTTCCTGAAATCAGTATTCCATTATGGGCAGTAGTGCATCTCCCGACAACCATCACGATCCTTAATGCTTGTGGAACGCCAAGGTTTGAGATCTTCATGAAATCTTAATTAGCATCATCACCTTTCTACGCTATCGTACGTACGTTTCAAATTTCATTTTAGGATCATATGTAGCTCATTACGCGCGCCAAGGTTTTTCAAATAGATTTAGCACTAAATCTGCTAGTACTCTTGCTACGCACGCACTTTCCCTTGTTAGTTAGTTAGGGAACTAGGAAAATTAATTAGTTAATAATCCATGAAGGACTACATGCATGTATATATTAATTTAAGGGCTTGAGTAATTTAATGATCATGTAGCACTTACGAAGATCTCATTAGCATTCCCTATATATTATTATATATGTTCTGACGCCTTGCATGTATAATAGGTCTATTCATCTGATAGTGTTCTGGACCCTATTTGAGAATGTCATGGCACTCCACCGTTGCAAAGGTGTAATCATCGGTTTGTTGGAGATCGGGAGGGTCAACGAGTGGGTCGTCACAGAGAAGTTGGGTGATGCACTCAAACTCAAACCGAATGGTAATCAAAACTTTGCAAGGAAAGCTCGTACCAAGTACTTCCAGAGGTGATCGATCTCCCACTCTAATTACGTGTGCTTTCGACAATCCTATTTAATTTGTGTTATATCCACACCGCTATCTAGTACTCTTGCTACGCACTTTCCCTTGTTAGTTAGTTAGAGTCGAACATGAGCAGTCAAGGTCGATTGACCCACATATCTCACTCAATCTTTGCTAGCGTAGGCTCGATACAAATTGAATTGAAAGACTTTGAGTTTGGCTGCGCACAAGCACCAATTGCAATAACATAAGAAGAACACATCCTTTATAGGATAGAAATGGGGTTTGATTTGATTGGGCTGAGTAATTACTTGGGCTAGTTAGGTTAGTCCCATCTGGGTTATTTTAAGTTCGGAGAAAAGCTTGCTGCAGCACACATGTGATGCACATCCTGGTTGTGCAGAGCTTTTATTTTTAAAAAATAAATAAAAGTAATCCCCAAGGTACTCTAGTTTGGGGTATAAGTCACGTAACTATTTGATTATCCGAAAAAAATTTAATATAAAATGAATCAATTTTTAAAAGAATGGATCCAACACTATTTATTTGATTTATTTTTTATATTTTTTAAATAATTCAATGGTGGCATGATTTGCATCTCAAATTAGGATACTTTGAGATCCACTTCAAAAAAAATTCAAAAAAAATAACTGATCTTTCTCTTCAAGTTGGGGCAAGCGATAGAATCTTATCAAAACTTCAGCCGAAGATTGGCTTTGGCTATGAGCTAGCCCACCACTAGCTGAAAACTTAATTAGTTAACGTTACATTAAATGTGAATATTAGGTTGCTAACAATGATTTCCTCATTAAAGTATTACAAACTAAACTTTATATGAGCATTGGGTTTCATATTGTAAGCAGCCTAACATTGTTTTTTTTTTCTGCCGTCATCACCAGATTCCACTTCTTGGAGATTGGGCTTGCACTATACCTCATCATCTGTGCATCCTATAATTACATGCATGCAAACAACTATTGCTACATTTACATCTATCTACAATCTCTCGCATTTTTGGTGATGGGACTTGGTTATGTTGGCACCTTTGTTCCTAGTGAAAAGTAGAGGATGAAAGGAGATGAAGCCACCATTGTTCCAATGTTTCCTTGTGGTGGATGCCATTGATGGCGGAGAAAATCTACCTTTGGTGCTTTTGTTTGTAATGGTTGACCAAATATGGCCACCAATATTTTATTCCTATATATGTGAAGTGGATGTATTCTATTGAAAGAGC

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GCTCTTTCAATAGAATACATCCACTTCACATATATAGGAATAAAATATTGGTGGCCATATTTGGTCAACCATTACAAACAAAAGCACCAAAGGTAGATTTTCTCCGCCATCAATGGCATCCACCACAAGGAAACATTGGAACAATGGTGGCTTCATCTCCTTTCATCCTCTACTTTTCACTAGGAACAAAGGTGCCAACATAACCAAGTCCCATCACCAAAAATGCGAGAGATTGTAGATAGATGTAAATGTAGCAATAGTTGTTTGCATGCATGTAATTATAGGATGCACAGATGATGAGGTATAGTGCAAGCCCAATCTCCAAGAAGTGGAATCTGGTGATGACGGCAGAAAAAAAAAACAATGTTAGGCTGCTTACAATATGAAACCCAATGCTCATATAAAGTTTAGTTTGTAATACTTTAATGAGGAAATCATTGTTAGCAACCTAATATTCACATTTAATGTAACGTTAACTAATTAAGTTTTCAGCTAGTGGTGGGCTAGCTCATAGCCAAAGCCAATCTTCGGCTGAAGTTTTGATAAGATTCTATCGCTTGCCCCAACTTGAAGAGAAAGATCAGTTATTTTTTTTGAATTTTTTTTGAAGTGGATCTCAAAGTATCCTAATTTGAGATGCAAATCATGCCACCATTGAATTATTTAAAAAATATAAAAAATAAATCAAATAAATAGTGTTGGATCCATTCTTTTAAAAATTGATTCATTTTATATTAAATTTTTTTCGGATAATCAAATAGTTACGTGACTTATACCCCAAACTAGAGTACCTTGGGGATTACTTTTATTTATTTTTTAAAAATAAAAGCTCTGCACAACCAGGATGTGCATCACATGTGTGCTGCAGCAAGCTTTTCTCCGAACTTAAAATAACCCAGATGGGACTAACCTAACTAGCCCAAGTAATTACTCAGCCCAATCAAATCAAACCCCATTTCTATCCTATAAAGGATGTGTTCTTCTTATGTTATTGCAATTGGTGCTTGTGCGCAGCCAAACTCAAAGTCTTTCAATTCAATTTGTATCGAGCCTACGCTAGCAAAGATTGAGTGAGATATGTGGGTCAATCGACCTTGACTGCTCATGTTCGACTCTAACTAACTAACAAGGGAAAGTGCGTAGCAAGAGTACTAGATAGCGGTGTGGATATAACACAAATTAAATAGGATTGTCGAAAGCACACGTAATTAGAGTGGGAGATCGATCACCTCTGGAAGTACTTGGTACGAGCTTTCCTTGCAAAGTTTTGATTACCATTCGGTTTGAGTTTGAGTGCATCACCCAACTTCTCTGTGACGACCCACTCGTTGACCCTCCCGATCTCCAACAAACCGATGATTACACCTTTGCAACGGTGGAGTGCCATGACATTCTCAAATAGGGTCCAGAACACTATCAGATGAATAGACCTATTATACATGCAAGGCGTCAGAACATATATAATAATATATAGGGAATGCTAATGAGATCTTCGTAAGTGCTACATGATCATTAAATTACTCAAGCCCTTAAATTAATATATACATGCATGTAGTCCTTCATGGATTATTAACTAATTAATTTTCCTAGTTCCCTAACTAACTAACAAGGGAAAGTGCGTGCGTAGCAAGAGTACTAGCAGATTTAGTGCTAAATCTATTTGAAAAACCTTGGCGCGCGTAATGAGCTACATATGATCCTAAAATGAAATTTGAAACGTACGTACGATAGCGTAGAAAGGTGATGATGCTAATTAAGATTTCATGAAGATCTCAAACCTTGGCGTTCCACAAGCATTAAGGATCGTGATGGTTGTCGGGAGATGCACTACTGCCCATAATGGAATACTGATTTCAGGAAAGAACACGGCTGTTGGAAACACGACACAATAGAAGAAGAAGGTGACGAAATGAGCTACGATCTTTCGAGTGAGGAAGAAATTGTAGAGTAAGTAGAATTTCTTCCACAGTGGCACTTTCTTAGTCATCAGGATTTCTATTGCCATCTTCCTCACCAGATTTGCGGGCCCGCATGACCATCGATGCTGTTGGTAGCGAAAAGCCTTGAAAGTGCTTGGTAATTCACTTTTAACCTTGACGTCTCCCACGTAGACAAACTTCCAACCTTCAAGAGTCGCCCTAATGGCCAAGTCCATGTCCTCCACAGTGGTGCGGTCCTTCCAACCTCCGGCTTCATTAAGGGCCCGGATTCTCCAAACCCCAGCAGTTCCATTGAAGCCGAAGAATGCATGAATGGATGAGCCTGACTCCTGCTCCACCTTGAAGTGGTAGTCCATTGACATCTCTTGTAGTCTTGTCATCAAGCACTCCTCAGCATTTACAAAGTTCCAGCGAGCCTGAGCGAGACCGATCTCCGGGTTGTGGATGAGAAAAGGTACCATCTGCACAAGGTAGTCGGGGTCTGCTTGGAAGTCGGCATCAAAGATGGCGACGTAGTCGCACTCCTCCACGTAACTGTACTTCATTCCTTCCTTGAGGGCACCCGCCTTGTACCCATTTCTGTTGGCCCTGGTCTCATATTTTATGTTCACCCCATCCAAAGCCCATTTCTGGCATTCCTTGTACACGAGATCCTGGAGATCATGATCCCCCCAATTAAGGGGCGGGGGGGAAGGAATTATAACGAATTTATATATATATCATGACATTAATATCAAATGGTCCCAATATTGCTGATTACGTTGGCCACCAGCTAGCTAGCTAGCAAGCTGGGATATATATGAAGTTATTTTATTAAAAGATATTTTATTAAAAGATACTTAAAAACAATTTTGTTCATATATAATCTTTGAGAATCAAATGCATGGTCTCGGAGGAAGAAGAATGGTTAGATATATAGCATGTGGAGGTTGTAAAAGTATTCTTGGGTGATTCAAGGGCCATAAGGGCCACTTGGCCCTGATCATATATATAGAGAGAGAGAACCCTGCCAGACTCTCCTATATATGTACGTACATAATTCCTTGGTGTGCTCTAGGCATATATATATATATATTCATTGAAAGTTCAGCAGCAAATTAAATATTGCTCGACATTGCTGGCTCTTTCAACGTGGCCGTCGATTTGCTAAGAAACCAGTACATCAACTTCCCCTTGCCAACTTCTAGAATCTGCACACGAATTCAGGTGAATTTTATCTGGTTAGAACTCTTTTCTGAGATCAGTCGTAGAATATATCACCTTAATCATTGGGTCTGTGGAATCATCAAGAACTTGGACGATCAGCCGATCCGACGGCCATTGGAGGCAGCATGCAGCTTTGATCGACAGGTGGTAAACCTCTCTCTCATTGTACATGGGTATTTGGACGAGGACCATTGGGTAGGCTGCAGTGCCCAACTCCTCGTCCCCTCCCACGGGCTCCCACCTGTAGACCTTCTTGGGCCGCCGGCGGAAGACCTTCACGTACAGGCTCACACCACCCATGAGGAGCTTCTCCATTAGCAGCATCACCGACATGATGAGGCACAGCAACACGGCGATCCTCATTGCCGGAATAAGCACCATGGTTCTCACCTGACCCCAAATGTAGAGGATTCTCGCCCAGTCGATGGCCATCTCCGGCCAAAACGACAATTCCCGGCCCCCCATGATCGAGTACATGAGGGAGCGAGGCAGGTAGGCGACCTTCATTAGGCCCTCCATTTTCTTTGGCTCCCCCTGGTACGTTAGTGAGGGGAAGAAGCCCACCTCCAAGGGGGGCTGAGGCTCTCTCTCCAGCTAGG

>CDs

TATATATATAAATTCGTTATAATTCCTTCCCCCCCGCCCCTTAATTGGGGGGATCATGATCTCCAGGATCTCGTGTACAAGGAATGCCAGAAATGGGCTTTGGATGGGGTGAACATAAAATATGAGACCAGGGCCAACAGAAATGGGTACAAGGCGGGTGCCCTCAAGGAAGGAATGAAGTACAGTTACGTGGAGGAGTGCGACTACGTCGCCATCTTTGATGCCGACTTCCAAGCAGACCCCGACTACCTTGTGCAGATGGTACCTTTTCTCATCCACAACCCGGAGATCGGTCTCGCTCAGGCTCGCTGGAACTTTGTAAATGCTGAGGAGTGCTTGATGACAAGACTACAAGAGATGTCAATGGACTACCACTTCAAGGTGGAGCAGGAGTCAGGCTCATCCATTCATGCATTCTTCGGCTTCAATGGAACTGCTGGGGTTTGGAGAATCCGGGCCCTTAATGAAGCCGGAGGTTGGAAGGACCGCACCACTGTGGAGGACATGGACTTGGCCATTAGGGCGACTCTTGAAGGTTGGAAGTTTGTCTACGTGGGAGACGTCAAGGTTAAAAGTGAATTACCAAGCACTTTCAAGGCTTTTCGCTACCAACAGCATCGATGGTCATGCGGGCCCGCAAATCTGGTGAGGAAGATGGCAATAGAAATCCTGATGACTAAGAAAGTGCCACTGTGGAAGAAATTCTACTTACTCTACAATTTCTTCCTCACTCGAAAGATCGTAGCTCATTTCGTCACCTTCTTCTTCTATTGTGTCGTGTTTCCAACAGCCGTGTTCTTTCCTGAAATCAGTATTCCATTATGGGCAGTAGTGCATCTCCCGACAACCATCACGATCCTTAATGCTTGTGGAACGCCAAGGTTTGAGATCTTCATGAAATCTTAATTAGCATCATCACCTTTCTACGCTATCGTACGTACGTTTCAAATTTCATTTTAGGATCATATGTAGCTCATTACGCGCGCCAAGGTTTTTCAAATAGATTTAGCACTAAATCTGCTAGTACTCTTGCTACGCACGCACTTTCCCTTGTTAGTTAGTTAGGGAACTAGGAAAATTAATTAGTTAATAATCCATGAAGGACTACATGCATGTATATATTAATTTAAGGGCTTGAGTAATTTAATGATCATGTAGCACTTACGAAGATCTCATTAGCATTCCCTATATATTATTATATATGTTCTGACGCCTTGCATGTATAATAGGTCTATTCATCTGATAGTGTTCTGGACCCTATTTGAGAATGTCATGGCACTCCACCGTTGCAAAGGTGTAATCATCGGTTTGTTGGAGATCGGGAGGGTCAACGAGTGGGTCGTCACAGAGAAGTTGGGTGATGCACTCAAACTCAAACCGAATGGTAATCAAAACTTTGCAAGGAAAGCTCGTACCAAGTACTTCCAGAGGTGA

>Pep

YIYKFVIIPSPPPLNWGDHDLQDLVYKECQKWALDGVNIKYETRANRNGYKAGALKEGMKYSYVEECDYVAIFDADFQADPDYLVQMVPFLIHNPEIGLAQARWNFVNAEECLMTRLQEMSMDYHFKVEQESGSSIHAFFGFNGTAGVWRIRALNEAGGWKDRTTVEDMDLAIRATLEGWKFVYVGDVKVKSELPSTFKAFRYQQHRWSCGPANLVRKMAIEILMTKKVPLWKKFYLLYNFFLTRKIVAHFVTFFFYCVVFPTAVFFPEISIPLWAVVHLPTTITILNACGTPRFEIFMKS\*LASSPFYAIVRTFQISF\*DHM\*LITRAKVFQIDLALNLLVLLLRTHFPLLVS\*GTRKIN\*LIIHEGLHACIY\*FKGLSNLMIM\*HLRRSH\*HSLYIIIYVLTPCMYNRSIHLIVFWTLFENVMALHRCKGVIIGLLEIGRVNEWVVTEKLGDALKLKPNGNQNFARKARTKYFQR\*

TRINITY\_DN1266\_c0\_g1 CSLA

glucomannan 4-beta-mannosyltransferase 9 isoform X1 [Syzygium oleosum]

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| --- | --- | --- | --- |
| 1.4267 | 1.66 | 8.6467 | 30.7833 |

>Genome/ DN1266

GGCGGGGAGAGGAAGAGAGAGAGCGAGCGCGAGAAGCAGAGGAGGAAGCCAAGCCAAGGATACCCTTCTCTTCTTCCTTCCTCCGCTCCCCCCGATATATCTCTCCCTCGTTGTTGGCTTGGCATTTCTTTCCCAATCCTCTGCGCCGACTGCTGGCCTTACGCTTCTGCTGTTTCTCCTCTGCTGCTAAAAACGTGCAAAAGGGCGGGCTGGTTTGCTATCATTCGCCTTCCTCTCTCTCTCTCTCTCGATCTGCCCCACACACACTCTGCGTTCAGCCCACCACCATTGTCCATTGCTTCGGTTCCCATCCTGCGTTGGCTTTGCTGGTTGTCAACTAAAAGCGAGCAGGTCGGCTGGTGAGGAGTGATGAGAAATCTGCAGAGGTCATAATTCCCTCTCTCCCACCATTCCATCCCTTCGTCCCAACCCATTTCCCTCCACCATCTGCAAGCCCCGTTTGGCAGCTCCATCTTACTAGCTCTCCCTTTCCAGGGTCTTGCTGATCTTTTGCCTCTCGCTGACGGGTGTGGGAGCCGGGACTTCCAGCCATTCAACCGACACTACAGCTCCACTGCATTGTCCTTTGCGTAGCGCCCCAGCAAGCCAACCCCTCCTGCAATATATACCTACATATAGATATATAGCCAAAGACAGAGGGGGGGGGGGGACATCACACGCGCGCACACACAGACACGCACGCACGCACGCAGAGAGAAAGAGAGAGAAGCAAAGAAAGGAAAGGGGGGGATGCATGATACTTTGATCGCAAGGAAAGGAAAGCCCTTGAAGGCCCATGCAGATCTAACGGGCTCCGTTGGCGGGCATCGTCGTCCATAAGGACCGCAACATACCCCGTCCTCCCTCCCACTGCAGCTGCAGCATGGCCGCGTAGAATCCCAGCCATCCGCCCGATCTGATCCAATCCCTCCATCTCCGGTAAATATCCCTCCTCCCTCTCCCCCAAGCCCATTTTCCGGACATAAAAGGAGAGGTGAAGAACAGAAGAGAACCGAACCAAAATCAGAAACAGGGGAGGGGGGCGAAAACGAACACAGGATAAACAGAGGAGGCGGAGGCCCGCGGGTTCGGGACCGGTGGTGGGTCGGCGACGGGCGTGGGGAGCGGTGCAGGATGGAGCGCCTCTCGTCGACGAGCCTGCTGCCGGAGGCATTCCAGGGGGGACGGGACGACCTGGCCGGGCAGATTGGGCTTGTGTGGCAGCAGGTGCGTGCGCCGGTCATCGTGCCCCTGCTCCGGGTGGCCGTGGTGCTGTGCCTGGCCATGTCGCTGATGCTGTTCGTGGAGCGTGTGTACATGGGCGTCGTCATCCTCCTCGTCAAGCTCTTTGGCCGGCGGCCGGAGAGGCGGTACAAGTGGGAGCCCATCAAGGACGATGTGGAGATGGGTAATTCGGCGTATCCCATGGTCCTCGTCCAAATCCCCATGTACAACGAGAAGGAGGTGTACCAGCTCTCCATTGGCGCTGCATGTGGGCTGTCCTGGCCTTCCGATCGCATCATAATTCAGGTCCTTGATGACTCCACCGACCCCATTATCAAGAACCTGGTGGAGGTGGAGTGCCAGCGGTGGGCGAGCAAGGGGATCAACATCAAGTACGAGATCCGGGACAACAGGAAGGGGTACAAGGCGGGCGCCCTCAAGGAGGGGATGAAGCGCGGCTACGTCCGGGACTGCGACTACGTGGCCATCTTCGACGCCGACTTCCAGCCGGAGCCCGACTTCCTCTGGCGCACCATCCCCTTCCTCACCCTCAACCCCGACGTCGCCCTCGTCCAGGCCCGCTGGAGGTTCGTGAACTCGGACGAGTGCCTGATGACTCGGATACAGGAAATGTCCCTGGACTACCACTTCACCGTGGAGCAGGAAGTAGGCTCCTCCACCTACGCCTTCTTTGGCTTCAACGGAACGGCCGGAGTGTGGAGGATCGCGGCGCTGAATGAGGCGGGAGGGTGGAAGGATCGGACCACCGTGGAGGACATGGATTTGGCCGTCCGAGCCAGCCTCAAGGGCTGGAAGTTCATCTACGTCGGTGACCTCCAGGTTAAAAATGAGTTGCCAAGCACGTACAAAGCATATCGCTATCAACAGCATCGGTGGTCCTGCGGGCCTGCAAACCTGTTCAGGAAGATGGTGATGGAAATAGTGAGGAACAAGAAAGTGTCGCTGTGGAAGAAGGTCTATGTCATCTACAGCTTCTTCTTCGTTCGGAAGATCATCGCCCACATCGTGACCTTCATATTTTACTGCGTGGTGATTCCGATCACCGTGTTTGTCCCGGAGGTGGAGATCCCAAAGTGGGGCGCCATCTACATCCCTTCCGTCATCACCCTCCTCAACGCCGTCGGAACTCCAAGGTCGATACATCTGCTGGTATTCTGGATCCTCTTCGAGAACGTGATGTCCGTTCACAGAACCAAGGCGACCTTCATCGGGTTGCTGGAGGCAGGGCGGGTGAACGAGTGGGTGGTCACCGAGAAGTTGGGGGACGCCCTCAAGGCCAAGGCGGCGGCATCAGTCAACAACAACAAAGCCTCCAAGAAGCCTCCGCCTCGTTTCAGGATAGGCGACAGGCTGCACGTTCTGGAACTGGGTGTGGGAGCCTTCCTCTTCTTCTGCGCGTGCTACGATGTTGCCTTCGGGAAGAACCACTTCTTCATCTACCTCTTTCTCCAGGCAGTTGCTTTCTTCGTTATGGGGTTTGGATATGTTGGAACCTTCGTTCCCAACTAGCTAGGTCTTATAATTAGCTAGTGAACAAATCAACATAATTATAATTAGTTGCCCCAAGCTCGATCATGCACGCATGCCTCATAATTATATATATATTTATATATATATGCCTCCAGTACGTACTGTGCTGCATGCATGCATGCTCTCTTTGATCTTCATGATCACACATGTACGTGACGGTACTTGTCCGTGGCTCTTTAATTAATCTTGTCATCGATGTATAAGGGATCGATATATCCACGTACCCACATTTTTTTCTCTTTTTTTCTTTTCCTTTTGTTTGGTGAGTCGAGAATTAGAAGCATTAATTACTTGCCAGGAATAGATATTGTCCCGTCCCGTTGAGGGACTTGTTCCTCTCACACATATGTGATCACGTACAGCTTCTTCAAGTATTGTACTATACATACTGCGCGGGTGGTTGGTAATTGTCGATCTGCAGAGAAAATTAATGAGAGACAAGAGGCGTACGTAGGTAGACAAGTTTTGGATATATACATATATATTCCCCTCTTCGCCCAGCAGCAGCAGCAGCAGCGGGAGCAACGTACAATAGCAGCAGCAGCAGCAGAAGAACATATATAGAAAGCAGCTTCTGTTCATAATTAAGTTGGTGTTTGTAAAACAAAGACGTTTAACTATATATATATGTGTGTAGAGGTGACATGATCACAATATCATCTTTCTTTTTTTTGGGTCTCTGCAGTCGG

>CDs

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DN1266-F: ATGGAGCGCCTCTCGTCGACG

DN1266-R: CTAGTTGGGAACGAAGGTTCC

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MERLSSTSLLPEAFQGGRDDLAGQIGLVWQQVRAPVIVPLLRVAVVLCLAMSLMLFVERVYMGVVILLVKLFGRRPERRYKWEPIKDDVEMGNSAYPMVLVQIPMYNEKEVYQLSIGAACGLSWPSDRIIIQVLDDSTDPIIKNLVEVECQRWASKGINIKYEIRDNRKGYKAGALKEGMKRGYVRDCDYVAIFDADFQPEPDFLWRTIPFLTLNPDVALVQARWRFVNSDECLMTRIQEMSLDYHFTVEQEVGSSTYAFFGFNGTAGVWRIAALNEAGGWKDRTTVEDMDLAVRASLKGWKFIYVGDLQVKNELPSTYKAYRYQQHRWSCGPANLFRKMVMEIVRNKKVSLWKKVYVIYSFFFVRKIIAHIVTFIFYCVVIPITVFVPEVEIPKWGAIYIPSVITLLNAVGTPRSIHLLVFWILFENVMSVHRTKATFIGLLEAGRVNEWVVTEKLGDALKAKAAASVNNNKASKKPPPRFRIGDRLHVLELGVGAFLFFCACYDVAFGKNHFFIYLFLQAVAFFVMGFGYVGTFVPN\*

TRINITY\_DN21109\_c0\_g2 CSLD

cellulose synthase-like protein D2 [Phoenix dactylifera]

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| --- | --- | --- | --- | --- |
| 0.8967 | 1.49 | 14.57 |  | 15.9867 |

>Genome/ DN21109

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CTCTTCTGAGCTCCTCCTCTCTCCATCTTCCCTGCCCGTCCTCTCTCCATCTTCCCTGCCCGTCTTCAACCCCGCCGGCGCAATCGGTGGTCGGAGCCGGAAGAACGTTTGGGCGGCGGAGGATCTCAATCGCTGATCTTGCCATTGCCAGAGACGAGTAGCTAGCTTCTCCCGAAGCTCGCCGCCGGGGCCCTGCTCCCGGAGCTCTTCTGCTGTTGCTTGCATCAGGTCTGGGGATTCCACCGAACCTGGTCTTCTGCCGCTGCTTCCGTTTCTGCACAGTCCCCGGGGGGTCGCAGTCGGGGGCGACATCACCAAGTCTGCTCGTGCACCTTTTCCTTGGTTTGAACACTTCTCCTGTTCGGCCATTGCCACCGTCTCACCTGCTGTCGCTTTCGTCACTGCCGTGTGGGCCGTCACCCCGCTGCCGTCACTGGTGGGGGAAGGCGGGGTCCCAATTCCTCTCTGCAACAATGTTGTGATCGGCCAACCTCACTTGTTCTTCGCCTGAGCCCGACGAGGTAATCGCCACCTGCATCAGCCTTCTCCGATCACTTGACCACTCCATATGTTTCATGTTTTGCGTGAGATTTGGATCGATCGCGTTCTTATGTCTTCTTGCTTTCTACGATTTCTCGGCTTTTCTTGTGATCTTGGTCTATTTTTCTTTTCATAAGTAGAGAATTTCCAAGCCCCTCGATCTCTCTGCTCTATGAGCTCAGAATCTTTCTATACGGAAGGAGATGTTAAAATTGATAGGTACACCAAACAGTCCTTGTTTTGAAGGAAGCCCTTCCATATGGAGGAGAAGTGATTTATTAGAAGTACTTCTAAGGGCTTACCAAACGCATCCTTCGTGTTCAAGTATGTTCGATTTTGATTTCAAAGTGGAGCTTGTTAGCTGGCGGATTTCCAGTTTTTTGGAATTTTTCCTGGCCCTCTTCATGAGACTTTCCGATTTTTGCTCGTCTCAATCCGTATTTTTCTCGGTTTCCTTCTCTGTGTCCATTAAGCTCTGCTGATTCTTCTCTGTCGCAGAGCTTTGTTTCCAACCAAGACCACCATTGTTGGATCCACCACAGCACGATGGCCACTAACAGTGCCCTCAAGGGCAGCCGGCTGGCAGCCTCGGAGTCTTCGCTCTCCGCTGCCGAAGGCGGGAAGCCTCCGGTGCCACCGCCGCCGGTCGTCACCTTCGGCCGGCGGACATTGTCCGGGCGCTACATCAGTTACTCCCGGGACGACCTGGACTCGGAGCTCGGCAGCGGCGAGTTCGCCAATTACCATGTCCACATCCCGCCGACGCCGGACAACCAGCCCATGGACGACGAGGCTGCCCCCGTCGACCCGGCCATCTCCGCCCGCGTCGAGGAGCAGTACGTCTCCAGCTCCCTCTTCACGGGCGGCTTCAACAGCGTCACCCGCGCCCACCTCATGGACAAGGTGATCGAGTCGGACGCCAGCGGACACCCGCAGATGGCCGGCGCCAAAGGTTCCTCCACCTGCGCCATCCCCGGCTGCGACTCCAAGGTCATGAGGGACGAGCGTGGCAACGACATCCTCCCCTGCGAGTGCGACTTCAAGATCTGCACCGAGTGCTTCTCGGACGCCGTCAAGACGGGCGGCGGAGTCTGCCCGGGCTGCAAGGAACCCTACAAGACGACGGACATGGAGGAGGTGGTGAAGAACACCAACGGCGGCCGGCCGCCTCTGTCGCTGCCGCCGCCGCCCGCGGGGGTGACGAAGATGGAACGGAGGCTGTCGCTGATGAAGTCGACGAAGCTGACCAGGAGCCAGACGGGGGACTTCGACCACAACAGGTGGCTGTTTGAGACCAAGGGGACGTACGGCTATGGCAACGCCTTCTGGCCCAAGGAGGGTGGCAGTGGGAGTGACGCTGGGAGCAGCACTGGGAGCGGGCAGCCGTCTGAATTCATGAGCAAGCCATGGCGGCCGCTCACGCGGAAGCTGAAGATCCCGGCGGCCGTTCTAAGCCCTTACAGGCTTCTAATCCTCATTCGGATGGCTGCACTAGGGATGTTTCTTGCATGGAGGATCAAACACCAGAATCAGGATGCAATTTGGCTTTGGGGCATGTCCGTTGTCTGCGAAATATGGTTTGCTTTCTCTTGGCTTTTGGACCAGCTCCCTAAATTATGCCCCGTCAACCGGGCAACTGATCTTTCAGTCTTGAAAGAGAAATTTGAGACGCCTGGTCCTCACAACCCAACTGGAAAATCCGACCTTCCAGGCGTTGATGTCTTTGTTTCCACTGCTGATCCAGAAAAGGAACCTGTCTTGGTCACTGCCAACACAATTCTTTCCATTCTTGCTGCTGATTACCCCGTCGAGAAGCTTGCTTGCTATGTCTCAGATGATGGAGGTGCACTTCTAACTTTTGAAGCAATGGCTGAGGCCGCAAGTTTTGCCGACATCTGGGTTCCTTTTTGTCGGAAGCATGACATAGAACCCAGAAACCCTGAAAGCTATTTCAGTTTGAAAAGGGATCCCTACAAGAACAAGGTTCGTCCGGACTTTGTCAGGGACAGGAGACGGGCAAAGCGTGAATATGATGAGTTTAAGGTCCGTATCAATGGCCTGCCCGATTCAATTCGACGACGATCTGATGCATATAATGCTCGAGAGGAGATCAAGGCCATGAAACTCCAGAGAGAAACCGCTGGCGATGAAGTCGTTGAAGCTGTAAAGATCCCAAAGGCCACTTGGATGGCCGATGGTACTCACTGGCCTGGCACTTGGATGACTCCCTTGCGAGAGCATTCCAAGGGCGATCATGCTGGAATCATACAGGTAATTCTTTTGATAGGTTTTCTACTAATCCTATTGCCGCCATATCTTTAGATAAGTTTCCCTTTGTTGTTCTTTCAGAAGGCAAAGCATAGTTTCTCATGCACAAATCTGATGATCAATGAACTTGAGTGTTTATCCCTGCCATTCCTTTTGACGAATTAAGGGCATAGAAGCTTCAAAATTTGAAGTCCCCTTCTGGATGGCATTTTGTTCCAGTTGGTTGGTGAATGGCGAGTGCATCATGACTCATGAGGAAGGGGGGAGGCTCCGGCAGTGGGGAAATTTCTTCCTTCTGTTTTTAGACACTACGCTTGGACTCGGGAGTTTTCAAACACACAAACTATGACATTGGGTGTATAATTGATTACCATGGGGGCAACATTACTTGATTATGAGTGGAAAAATCAACTAACATGCCAAAACCGAGTTTTTTTTTTTCATTTGTTTGCCTCATATGCTTGTTATGCCCACCTCCTCTTAATGTTGCTATTGTTGACATATTGTATATGTATGGCTTTCTGATTTGACGAAAGCTAACTTGTTTGAATTCTACATTTTCCCCTGATCTGCTTTCATGCACGTTATTAATCCAGAAGAAATTTCGAATTAGGGAACGGAAACGTCACGATGCGGATGCTAGATGTTTCACTCTCCTCCTGATTTTGCAGGTCATGTTGAAGCCTCCGAGTGATGTACCATTGCAAGGAGACGGTGATGAGGGAAGGCCCCTTGACCTCACAGATGTTGACATCCGTCTGCCAATGCTCGTCTACGTTTCGCGTGAGAAGCGCCCTGGTTACGACCACAACAAGAAGGCAGGCGCCATGAACGCCCTGGTTCGTGCCTCTGCAGTCATGTCCAATGGGCCATTTATCCTGAATCTCGACTGTGATCACTACGTGTATAACTCGAAGGCTCTCCGCGAAGGTATGTGCTTCATGATGGACAGGGGCGGTGACCGTCTCTGTTACGTCCAGTTCCCACAGCGGTTTGAGGGCATTGATCCCTCTGATCGGTATGCCAACCACAACACTGTCTTCTTCGACGTCAACATGCGTGCACTGGATGGCCTCCAGGGACCAGTTTATGTAGGCACGGGCTGTCTCTTCCGTCGCATTGCCCTCTATGGGTTTGACCCTCCCCGTTCCAAGGATCACTCTCCCGGGTGTTGCAGCTGCTGTTTCCCTCGCCCCCGCAAGAGCCGTGCGGCTGTTGCCTCCGAAGAGAGCCGGGCTCTCCGGATGGGAGATTCCGATGATGAAGACATGAACTTGTCGTCGTTTCCGAAGAAATTTGGCAATTCCAACATGCTCATCGAATCGATACCAGTTGCAGAGTATCAAGGACGCCCACTTGCAGACCACCCTGCGGTTAAGAATGGACGCCCACCCGGTGCTCTCACCATCGCCCGGGACCTGCTCGATGCGCCAACGGTGGCTGAGGCCATCAGTGTCATCTCCTGCTGGTATGAAGACAAGACCGAGTGGGGGCAGCGGGTTGGGTGGATCTACGGATCCGTGACTGAAGACGTGGTCACTGGCTACAGAATGCACAACAGGGGATGGAAGTCTGTCTACTGTGTGACAAAGCCCGATGCGTTCCGTGGCACTGCTCCTATAAACCTCACCGATCGGCTCCACCAGGTGCTCCGGTGGGCTACAGGTTCTGTGGAGATCTTCTTCTCCCGCAACAATGCAATTCTTGCCAGCCCCAAGATGAAGGTCCTACAGAGGATTGCATACCTCAACGTGGGGATCTATCCATTCACTTCCATCTTCCTCATCGTGTACTGCTTCCTACCGGCTCTGTCGCTCTTCTCCGGCCAGTTCATCGTCCAGACACTGAACGTGGCCTTCCTCACTTACCTCCTCGTCATCACCTTGACCCTCTGCATGCTTGCTGTGCTTGAGATCCGCTGGTCTGGCATCGAGCTGGAAGAATGGTGGAGAAACGAGCAGTTCTGGCTGATCGGAGGCACTAGTTCACATCTTGCTGCTGTGCTGCAGGGGCTACTGAAGGTAATTGCCGGGATTGAGATCTCATTCACCCTCACTTCCAAATCAGCCGGAGATGACGTCGACGACGAGTTTGCGGACCTGTACGCTGTGAAGTGGACTTCTCTGATGATTCCTCCGCTTACCATCATCATGGTGAACCTGATAGCCATTGCTGTGGGCATCAGCCGGACA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>CDs

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TRINITY\_DN21109\_c0\_g2 CSLD

cellulose synthase-like protein D2 [Phoenix dactylifera]

DN21109-F: ATGTTGAAGCCTCCGAGTGATG

DN21109-R: TCATGGGAATGTGAAGGAGC

>Pep

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