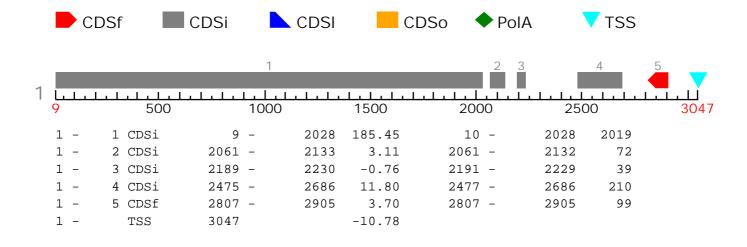
FGENESH 2.6 Prediction of potential genes in Ustilago genomic DNA

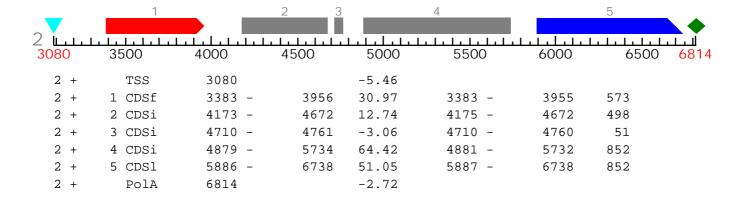
Seq name:

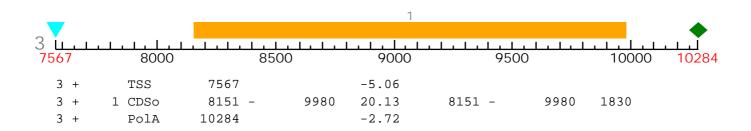
Length of sequence: 11735

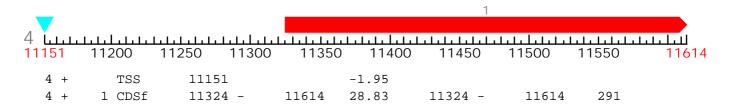
Number of predicted genes 4: in +chain 3, in -chain 1. Number of predicted exons 12: in +chain 7, in -chain 5.

Positions of predicted genes and exons: Variant 1 from 1, Score: 342.785937









Predicted protein(s):

>FGENESH:[mRNA] 1 5 exon (s) 9 - 2905 2445 bp, chain -ATGGGAAGCGTGTTTTCGTGCCTCGCATCTACGTTTGTGTACGTGGGCGAGTTGCTCGAA AACGTGTTCCTAGCGATTGGAGAGATTGGCGCGGTGTTGACCAACACGGCGGCGATAACC AGCACGACGCTTGCAACGGTGGGCGGAAAGCAGGTTTTGTCGAGCGTGTTTTCCAAGGAG GGGAGAGCACAGCGAAAGGATCAAGGCTGCGAGGAGGAAGGGTGCGGCGCTCAAGGCG GAGGAAGAAGGAGAAGGAGAAGGAGAATACAGCGAAAGGAGATCAAGGCTGC GACGTTGTGTGTGAATCCAATCGGACCGTGCCTCCGTGGCAGCGTGTGGCGCGCGAGCAG AGCACACAGCAATACACCAATACAGCATACGATCCAACCGCCAACGCGGCTATCGAGGCG CTTCCAACCCACCTGCTCTTGCGCACCTTCCTTCTCCCACCATCCCTGTCCGACGCGACC TCCTCCGTTCCTCGTCCCCCGTGCTCGTATCGCACTCGCAGCTGGCGTTGCCTCGTCCC CGCATGTTGGCGAGTCGTTCTGTGCTTCTCGCCGTGACGCTTGCCGGTGGTGCTGCCGCT AGCTACACGCTTGTCAAGCCGAGTCTGTACGCCGATGCTCCCGATGCTGTGCCTGGCGAT ACTCGTCCACATCCTCTCGGTCGCCCCCCACGCGTGCGCAGATGCTCGACGCACTCAGG CAGTCTTCCGCCAACAGTCTCCGCCCCAATGCTTCGCGTGACAACTCCCTCAACTCGAGT GGTGTCGACGACCAAGACGCAGACGCTTCGACATCCTTGTGGTTGGAGGCGGTGCGACT GGCTCTGGGGTTGCGGTGGATGCGGCCACGCGTGGGCTTAGTGTAGCCATGGTCGAGCGC GATGATTTCGGCGCTGGAACTTCGTCCAAGTCCACTAAGCTTGTGCATGGAGGCGTTCGA TATCTTCAGAAGGCGGTGTTTGAGCTCGACTACGAACAGTACAAGATGGTGCGCGAGGCG TTGCACGAGCGAAAGACTTTCCTCCACATTGCTCCTTATCTTTCGGATCATCTGCCCATC ATGCTGCCCGTGTACAAGTGGTGGCACATCCCCTACTACTGGGCGGCACCAAGATGTAC GACATGCTCGCCGGTTCCGAGAACATGGAGAGCTCGTACGTTCTCGGCAAGGGCAAGGCG CTCGAGGCGTTTCCCATGCTCAAGTCTGCCGGTCTCGCTGGTGCCGTCGTGTACTACGAC GGTCAGCACACGACGCGCATGAACGTCGCTCTCGCCATGACTGCAGTCCACCACGGC GCGGTTGTAGCCAACCACCGAGGTGGTTGCCATTCACAAGAAGCGTGTTCCGGGCAGG CCCGATCAGATCTGCGGTGCTCGTGTGCGTGATGTGCTCACGGGAGACGAGTGGGATGTC AAGTGCAAGTGTCTTATCAATGCAACCGGTCCGTTTTCCGACACGCTGCGAAAGCTCGAT GCGCCCACGGCTCACGAGATCGTCGCCGCGTCGTCCGGCGTGCACATTACGCTTCCGGGC TACTTTTCGCCGCGGGATATGGGTCTCATCGACCCGCACACCTCGGATGGCCGAGTGATT TTCTTCCTGCCTGGCAGGGAAACACGATTGCCGGCACCACCGACACTGCGGCGCGCGTC GAGGCGCATCCGCGGCCCAAGGAGGAGGAGATCGAGTGGATTCTGGACGAGGTGCGCAAC CGACCGTTGGTCAAGGATCCTGCCGCCACAGACACGCAGTCGCTCGTGCGCAACCACATG ATCAACGTGTCGCAATCGGGTCTGCTCACCATCGCGGGGGGTAAGTGGACGACGTACCGT GAGATGGCGGAGCAGACGGTGGACCGCCCATCCAAGAGTTTGAGCTGAAGCCGCAGCGT GGATGCGTGACCAAGAACACACGACTGCTCGGCAGCCACGGGTGGACCAAGACCATGTAC GTCAAGCTTCTGCAGCGTTTTGGTCTGGAGACCGACGTCGCGCGTCACCTCTCCAACACG TACGGCGACCGAGCGTGGAGCGTGTTTCCATCGCCGAGCCCACG

>FGENESH: 1 5 exon (s) 9 - 2905 815 aa, chain - MGSVFSCLASTFVYVGELLENVFLAIGEIGAVLTNTAAITSTTLATVGGKQVLSSVFSKE GRAQRKEIKAARRKGAALKAEEEKEKEKEKEKEKENTAKGDQGCEEEGSSNVRYRSAFRQTHCG DVVCESNRTVPPWQRVAREQSFPVANSSKQQQQTAAAHSSSTQQYTNTAYDPTANAAIEA LPTHLLLRTFLLPPSLSDATSSVPRPPVLVSHSQLALPRPSIMFRRPLAIAPRARVRLAS TSSTSSSSSSSSSSSSSAGORRMLASRSVLLAVTLAGGAAASYTLVKPSLYADAPDAVPGD

TRPHPLWSPPTRAQMLDALRQSSANSLRPNASRDNSLNSSLLPLANHAPSSTPTPPASRG
GVDDQDADGFDILVVGGGATGSGVAVDAATRGLSVAMVERDDFGAGTSSKSTKLVHGGVR
YLQKAVFELDYEQYKMVREALHERKTFLHIAPYLSDHLPIMLPVYKWWHIPYYWAGTKMY
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APTAHEIVAASSGVHITLPGYFSPRDMGLIDPHTSDGRVIFFLPWQGNTIAGTTDTAARV
EAHPRPKEEEIEWILDEVRNYLSPDIKVRRGDVLSAWSGLRPLVKDPAATDTQSLVRNHM
INVSQSGLLTIAGGKWTTYREMAEQTVDRAIQEFELKPQRGCVTKNTRLLGSHGWTKTMY
VKLLQRFGLETDVARHLSNTYGDRAWSVCSIAEPT

>FGENESH: [mRNA] 2 5 exon (s) 3383 - 6738 2835 bp, chain + ATGGCGCACACCGAGTATCCACCACACACCACAACCACAAGCTGCCAAGCAGCCGGA AATGAGTTCTTCCGCAACAACTATGGCCCGAGGCCATCGGCGCGTATACTGCGGCGCAC ATGGCCGATCCCACCGAGCCAACATACCCGCTCAACCGTGCCATGGCCTACATCAAGTTG GTCAAGGCGCTCTACCGTAGAGCATCCGCCAGATTGTGCGCCACCAGCCTTCCGAACAAC CTTGCTTTGCGATTCACGATTTAGAGGCCGTCTTGCGCTTGGATCCAACTAACCCAGAC GATCCGATCCACCTGCAACATCTCACCAATCCACCCGATAGCGTCCCTCGGAAGTCAACC ACTCAAGTCGACCTTCCAGCATCCAAAGTGAACACCGCTTCAACCGAGTCAAGCAGCTGC GTCGAGCCAGCAGAAACTTCCTGCAACACGTTGTACTCAACAAGACAGTGTGTGCATCA ACTCGCTCGATTCGCACCAGCGTGGAAAACACAGCATCCGCGCTCAATTTCGGCGCATCA AGAACGCACAAGGCACCACAAAATCACAGCTATTGAATTCCACCGCAGATGGAAGAAC AAGCGCGAGCGTCTGGCGCTGCTATCATCGCTCGATCCCGAGTCAATACCTCGCATGATG GATGCGATGCTTGAGCCCCAACTCGTTGCTGAGATCTTGCAAACACTAGCGCAAGCCAAG CGCTGTTCGCCCCAACATGGTCATCTCACAAGCCTAGTTGCAGCCATTCTGGCGGCACTT GCTCGATGCAAGCGCTTCGGCATGACGGTGTCCATGCTCGACGCCTCTGAAAAGCAAGAT GCAGCGTATCTCATTGATGCCATCCGCAGCCACGACTTGAAACGCGTTTGGGAGCGTTGT GTTCCAAATGCACCCAAAGTGATGCTGTGCGTGTGCGTGTGCCCGTCCAAGTCGCC GTCGTGTTCGTGTCTTGCCCGCCACCAACACCATCTGGGCTCATGCGAACCACTCCCACC ACATTGGTTTATCCTCGATTCAGCACAAAACCCTCCCGCACTCCCGCCATGTCTCTGCCA TCCGCGCCCGACTACGACTTTAACCCCAACCTCGACGTGCATACCATCGACCCGCCGGTG CAGATAGGCGCCAAATGGGCGCAGTCGTATCCCTCGAGCTCGTCTCCCCTCGCAGCTGCT GACGTGTTGCCTCATTTCCCGTTGCTCAATCTTGCACAGGGTGTTCCCGCTCACCCGCCC ACAGCAGCGCTGCTTCACAGGATCCAGTTCGAGTCTCGCCCCCAAAACCTATCGTCCCCC GCCGCCCACACGCATGGCTACGGCCCCGTGTTTGGAGATCCCAAGCTGCGTCACGCCGTC GCAAGCGACATCAACCGAGTCTACCGATCCTCTGCAAACGGCGTCAAAAATCAAGTCACC CACCACAATGTCGCCATCACTGCTGGCGCCAATCTTGCGTTTAGCGCAGTGGCTACCTCC ATCGCCGCTCCAGGAGATGCGCTCATCGTCTGCCACCCCTGGTATTTCAACCATCACATG ACGCTCACCGCGTTCGGCATCCAAGTTGCCGCCGTGCACACCAAGCCGCCCGAATACTTT CCCGATGTACACATGATCCGTGCGCTGCTCGCGAGCGACGCCAAAGCTTCCACCAAGACC ATCAAAGGTGTTGTTCTCGTGACGCCCAACAACCCTACTGGTGCCATCTATCCGCCACAA CTCATCCGACACTTGCCGCACTCTGCAAAAACCATCGAGTCGCCCTCATCCTTGATGAA ACCTATCGCGACTTTCTCTTGACGGGCAGCGACCTCGACCATGCTTCTCAGCCCGCTGCT ${\tt TCTGCCTCACCCCGCTCGCTTGCTTACAACTTTGCTCGTCCACACGACCTGTTCGAAGAC}$ GCCCCGCCGGTCTAGCAGACGCATGCTGGGATCCAGACTGGGACTGGCGCAACACCCTC ATTCAGCTCTTCAGCTTCTCCAAGAGCTTTGCCATCCCCGGACATCGCTTAGGAGGCTTC GTCGCGCATGCTGCCTCCAGCAAACCATCACCGACGACGCTGGATCTGAAAAGCTC

>FGENESH: 2 5 exon (s) 3383 - 6738 944 aa, chain + MAHTEYPPHNHNAQAAKQAGNEFFRNKLWPEAIGAYTAAHMADPTEPTYPLNRAMAYIKL GKFVDAERDCTTALLLSPNNVKALYRRASARLCATSLPNNLALAIHDLEAVLRLDPTNPD AKAALTKARQAVDAAKPNTTDPIHLQHLTNPPDSVPRKSTTQVDLPASKVNTASTESSSC VEAARNFLQHVVLNKTVCASTRSIRTSVENTASALNFGASAAQTTAAQTTAASFAHQPTP RTHKAPHKITAIEFHRRWKNKRERLALLSSLDPESIPRMMDAMLEPQLVAEILQTLAQAK RCSPQHGHLTSLVAAILAALARCKRFGMTVSMLDASEKQDAAYLIDAIRSHDLKRVWERC VPNAPKVMLCVCVRVPVQVAVVFVSCPPPTPSGLMRTTPTTLVYPRFSTKPSRTPAMSLP SAPDYDFNPNLDVHTIDPPVQIGAKWAQSYPSSSSPLAAADVLPHFPLLNLAQGVPAHPP TAALLHRIQFESRPONLSSPAAHTHGYGPVFGDPKLRHAVASDINRVYRSSANGVKNQVT HHNVAITAGANLAFSAVATSIAAPGDALIVCHPWYFNHHMTLTAFGIOVAAVHTKPPEYF PDVHMIRALLASDAKASTKTIKGVVLVTPNNPTGAIYPPQLIRHIAALCKNHRVALILDE TYRDFLLTGSDLDHASQPAASASPRSLAYNFARPHDLFEDAPAGLADACWDPDWDWRNTL IOLFSFSKSFAIPGHRLGGFVAHAALLOOTITDDAGSEKLVFGPTAKALDNFOVAPPRID TORAVAWAIODAOOLEWRSOIANOLRIRRRAFIOALSRPVAPFLNOHASALVAPASEPSL AKSPSEWGWHVESAGAYYVFLRHPFASTRSEKVAQALAELVGVVVLPGAFFMPTDAESTG GSAGSRLRVSVANVSTOMLANLAERLAILSELWHKKGAGWGIAT

>FGENESH:[mRNA] 3 1 exon (s) 8151 - 9980 1830 bp, chain + ATGAGTGAAAAATCCAACAACGTCGCGCTCGTCATCGACACGAATCGCCAAAGACCGCCT CGACATTTGGAACCCACGCACCGCCTCGGAACAGCAGAACACTCGCCAGACACCTCGTGC TCCAGCACACCACCTCTGGTCATCCAGCATATCCCAAACCCCCTCAACCAGCACCACC ATCGCTTCGGCCCAAACACCCCACTCGGGCACGCCGATCCAGCATGGCTCATCTCCAAG ATCGACGAATACCTCGCCGAACTCGACATCCCGCTCGCGCCCATGTCGAAACCGATGCGC CCCACGTTGCGGATCGATGTGAATCCAGACGTGTTGGCGTCGGCGGAACGCGCATTGCCA TCGTCGCCCGAGGCGATCCGGGTGTCGAGGCGGATTTCATCGACCATGTTGCCCGTGGAG CGCAAGGTGCGGATGGCGATGGCGACGTCGCCGTTGGATTCGGACGCGGTGTTTTTG TCGCCGTTGTTTTATCGTTCGTTTCAGAGACCCGAGGTGGGGAGTATGGGCGATGACGCC GCACCGTTCCCGTACAGTCCGGGCAGAGAATGCGTGTTTCTCGATTCAGGCTTTTGCACC ACTGCGTTGAGCACGGCGACAGCATTCAGCACAGACAGAGGAGCAACTCGAACGACGCT TGGCAGCCGGAACACACACATGCGAAGCTAGCGAGGCTTGCGAAGCTTGCGAAGCTAGC GAGAAGACGCGGTCGCCGATCAAGCACAGACGAGAAGCAGACGCAAACCATGTTCCAAGC ATTCGACTGGAAACACCCGACGACGGCGAAGCATCAAGCTGCAACGCTAGCGACGCCCGC GGCGAAACGCCACTCGGTGGCTCATCACCAAGCAAGATGGCGTCGATTTTGGAGTGCGAG TCGGGGGCGAGCAGCGTGTGGATCGGAAGAGTGTGTTGTCGATCTCATTTGACTCG AGCTTGTCGGCTGCTATGAGCGATGGGTCAGTTGCAAAAAGCAACAATGGTGGCGGGAGC AAGTGCACGATCCAATCACCCACCATGGCAGCATCCAACTGTGCTGCATCGTTG TGCGTTCCAACGCCACTGCGCTCGCAGACCAACCCACACGGCGCACCCACTCAGCGAAGA ACGCTTGGACTATGCCGCTCGGCGTCGGCGGCAACCTGGTGCAACGCTTCCAACACCCA

>FGENESH: 3 1 exon (s) 8151 - 9980 609 aa, chain +
MSEKSNNVALVIDTNRQRPPRHLEPTHRLGTAEHSPDTSCSSTTTLWSSSISQTPSTSTT
IASAQTPHSGTADPAWLISKIDEYLAELDIPLAPMSKPMRPTLRIDVNPDVLASAERALP
SSPEAIRVSRRISSTMLPVERKVRMASMATSPLDSDAVFLSPLFYRSFQRPEVGSMGDDA
APFPYSPGRECVFLDSGFCTTALSTGDSIQHRQRSNSNDAWQPEHNTCEASEACEACEAS
EKTRSPIKHRREADANHVPSIRLETPDDGEASSCNASDARGETPLGGSSPSKMASILECE
SGASSKRVDRKSVLSISFDSSLSAAMSDGSVAKSNNGGGSKCTMQIESPTMAASNCAASL
CVPTPLRSQTNPHGAPTQRRTLGLCRSASAGNLVQRFQHPHVLHRTAPQKLAPTISDLCT
TNRTKQPTRTNQRSPTLLKPNAPNTSPTSTQIVEGVRKMNKLKKLLGDEVSTHISKQSCA
LGVTPATNVRGDVMKPLPYLPPLGSLQRSNTAGIQMGKKTMLGSHKPREKKHCIASASTS
GTGRPSTASETRCTCSNCDATQRVLGSALAGAGMRLGASHTLRRPNTSASVRARSIRSGG
GFVEMDEYI

HIAHMVGAVKAGKLPSQSQLNSFIESLMSSPVLDERS

预测到完整基因个数:2个

第三段基因起始密码子:8151-8153,终止密码子:9978-9980

其中外显子个数:1个,内含子个数0个