

Nucleotide sequence of rye chloroplast DNA fragment, comprising *psbD*, *psbC* and *trnS* genes

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Here we present the nucleotide sequence of rye chloroplast DNA fragment, comprising two genes *psbD* and *psbC* that code for 34 kD D2 and 43 kD Chl *a*-binding polypeptides of Photosystem II, respectively, and *trnS*(UGA) gene. The first two genes have 50 bp region of overlap, their start and stop codons and potential ribosome-binding sites are underlined. The *trnS* gene resides on the opposite strand, its first and last nucleotides are underlined.

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GAATTCAAAGGTTATTCT TTCTATAGTATAAGAAAGAA CAAAATTTATTCTATTTC TATAGTATAAGAAAAACAAA TAGTATAAGAAAAACAATC 100
GAATCAAAATTCATG6ATTTA CCACGACCTCG6ATGTGACT CCATAGATAAAAAATAG6AAA TTTCTCTCTCGAGACCATT GAAAAAGGGCATTGAACGAG 200
AAAGAAATCGTCCACAGATA ATAAACTATCATATGCCTT G6AAAGTGATATGAGGTGCT CG6AAATG6TTGAAGTAAAT GAATAGGAGGATCACTATGA 300
CTATAGCCCTT6GTAGAAAT CCTAAAGAAGAAAATGATCT ATTTGATACTATGGATGACT G6TTACGAAGGGACCGTTTC GTTTTGTAG6ATG6TCTG6 400
CCTATTGCTCTTTCCCTT6TG CTTATTTCCGCTTAA66666T T6GTTTACAG66ACAACCTT T6TAACCTCTT6GTATACC AT66ATG6CTAGTCCCTAT 500
TT66AAG6TTGTAATTTCTT AACCGCAGCAGTTTCTACCC CTGCCAAATAGTTAGCACAC TC1TT6TGTCTACTAT6666 GCCCGAAGCACAAGGAGATT 600
TTACTCGTTG6GTCAATTA G6C66TCTAT6GACTTTTGT AGCTCTCCACG666CCTTTG CACTAATAGGTTTCACTGTA CG6CAATTTGAACTT6CTG 700
ATCTGTTCAATG6C66CCTT ATAATGCAATCTCACTTCTCT G6TCCAAATGCTGTTTTTGT TTCTGTATCCCTATTATTC CACTG666CAATCT66TTG6 800
TTCTTTG6CCG6AGTTTTG6 C6TAGCAGCAGATATTTG6AT TCATCCTTTTCTCCAAG6A TTTCAATAATG6ACGTT6AA CCCATTTTCATATGAT666AG 900
TT6CCG6AGTATAG6T6CA GCTCTGCTAT6CGCTATTTCA T6GAGCGACCGTAGAAAAACA CTCTATTTGAGGACG6T6AT G6TGCAAAATACCTTCC6T6C 1000
TTTTAACCCAACTCAAGCTG AAGAACAATTTCAAT66TC ACTGCTAACCGCTTTTGTGTC CCAAACTTTG6TGTGCTT TTTCCAAATAACGTT66TGA 1100
CATTTCTTTTGTCTATTG6T ACCCGTCAACCG6TTTATG6A TGAGTCTATTG6CGTAGTT G6CCTTGGCTCTGAACTTAGC T6GCTATGACTT6TTTCC 1200
A66AAATCCGTCAGC666AA GATCCT6AATTTGAGACTTT CTACACCAAAAAATTTCTTT TAAACGAG66TATTCTG6TG T66AT66CAGCTCAG6ATCA 1300
G6CTCATGAAAATCTTATAT TCCCTGAG6AG6TCTTACCA C6T66AAACGCTCTTTAATG GAACTTTCTGTTTATGCT6GT C6TGACCAAGAAACCCAG6 1400
CTTTG6TTG6T666CT666A ATG6CAGACTATCAAAATTTG TCC66TAAACTACTT66AGC TCATGTAGCCCATG6CCG6AT TAATCGTATTTCT666C66A 1500
GCAATGAACCTATTTGAAGT G66CCCATTTGCTACCAGAAA AGCCCATGATGAACAAG66G TTGATTTACTTCCACACT AGCTACTCTAG6TT6666AG 1600
TAG66CCAG666666AAGTT CTAGACTATTTCCATACTT T6TATCT66C6TACTTACC TAAATTCCTCCG6AGTCTTA G6CTT66T66CATTATTA 1700
CG6CCTCTT666ACCC6GAGA CTCTTGAG6AATC6TTTCCA TTTCTTGGTTATGCTG6AA AGATCGAAATAAAATGACTA CAATTTGG6TATTTACTTA 1800
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TCTAG6ATCTTCCCTTTTGT T666CCATTTT66CATGCA G6AAGAGCCCGAGCTGCTG6 AGCAG6TTTGAAGAAAG6AA G6CATGCTGATTTG6AAGC 2700
GTTCTTTACATGAACCTCT TAACTAAGATTTTCTATTT ATACCTGTTCTACTTTTTT CTGTTCT66CTG6TTATTC CATCTAGCCAGCCATTTCAT 2800
TCCTTTTTATGAAGAAAGA TAAG66CAGAAAAAAGAAA AAAAAAATGAAAGAAACA AACGTATTAACAAGCAAAA G6AGAGAGAG666ATTCG6AA 2900
CCCTCGATAGTCTTAGAAC TATACG66TTTTCAAGACCG GAGCTATCAACCACTAGCC ATCTCTCCACG6CTAATCC TTATTTACTCC 2992

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