

Underexpression of *PpDXS1* gene decreased plant height and resulted in altered accumulation of phytohormones

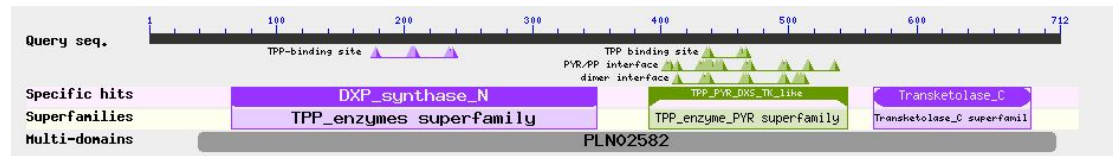
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a

Query: 1-deoxy-D-xylulose-5-phosphate synthase [Poa pratensis] Query ID: AXS78096.1 Length: 712

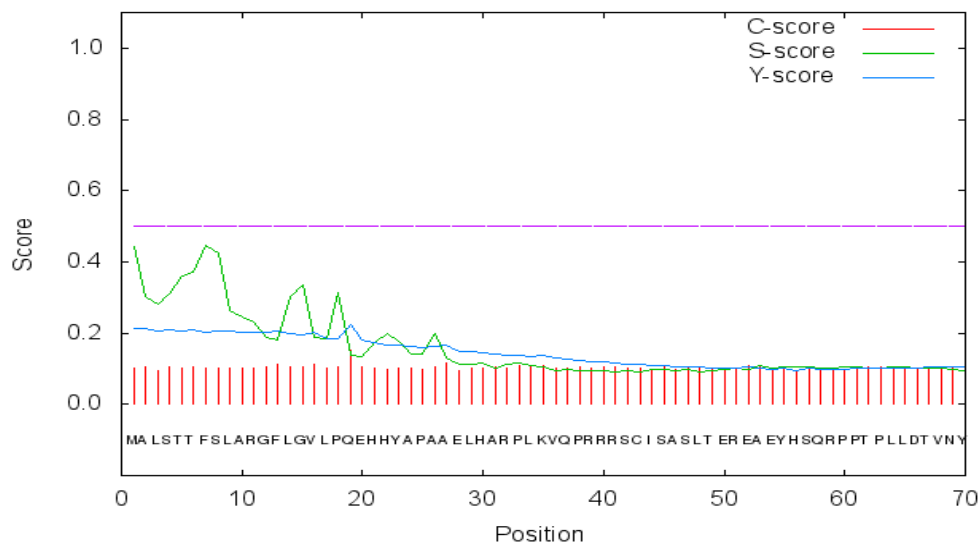
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AXS78096.1	1	MALSTTFLARGFLGVLPOEHHYAPAA-----ELHA-----RPLKVPQRRR-S-CISASL-T-EREA-EYHSQRPPPTLLDTVNYPIHMKNSLKEQLQSDLRSDVIFHVSKTGGHLSGLGVVELVALHYVFNTPQDKLLWDWG	133
EAE8772512.1	1	MALSTTFLARGFLGVLPOEHHYAPAA-----ELQA-----RPLKTPRRS-S-CISASL-S-EREA-EYHSQRPPPTLLDTVNYPIHMKNSLKEQLQSDLRSDVIFHVSKTGGHLSGLGVVELVALHYVFNTPQDKLLWDWG	133
XP_020161542.1	1	MALSTTFLARGFLGVLPOEHHYAPAA-----ELHA-----RPLKTPRRS-Y-CISASL-S-EREA-EYHSQRPPPTLLDTVNYPIHMKNSLKEQLQSDLRSDVIFHVSKTGGHLSGLGVVELVALHYVFNTPQDKLLWDWG	133
XP_003568467.1	1	MALSTT-----QPLGVLPOEHHYAPAL-----ELQT-----RSLK--PRKR-S-CISASL-S-EREA-EYHSQRPPPTLLDTVNYPIHMKNSLKEQLQSDLRSDVIFHVSKTGGHLSGLGVVELVALHYVFNTPQDKLLWDWG	127
XP_004962111.1	1	MALSTTFLARGFLGVLPOEHHYAPAA-----ELHAHQLOARPIK--PRRPA-CVSASL-S-EREA-EYHSQRPPPTLLDTVNYPIHMKNSLKEQLQSDLRSDVIFHVSKTGGHLSGLGVVELVALHYVFNTPQDKLLWDWG	138
XP_006654395.2	1	MAL-TAFSPFPGVGLPQEGHFAAAELCLHLLQT-----RPPK-QPRRR--SSCISASLST-EREAAYHSQRPPPTLLDTVNYPIHMKNSLKEQLQSDLRSDVIFHVSKTGGHLSGLGVVELVALHYVFNTPQDKLLWDWG	140
Query	134	HQSYPHKILTGRDKMPTMRQTNLSCFVKRSESEYDFSGTGHSSSTIIAALGMAVGRDLGAKNNVAVIGDAGANTAGQAYEAMNAGYLDSDMIIVLNDNKGVSPLATLDGPAAPPVAGLSCALSKLQSSRPLRELREAVKVTQIQG	283
AXS78096.1	134	HQSYPHKILTGRDKMPTMRQTNLSCFVKRSESEYDFSGTGHSSSTIIAALGMAVGRDLGAKNNVAVIGDAGANTAGQAYEAMNAGYLDSDMIIVLNDNKGVSPLATLDGPAAPPVAGLSCALSKLQSSRPLRELREAVKVTQIQG	283
EAE8772512.1	134	HQSYPHKILTGRDKMPTMRQTNLSCFVKRSESEYDFSGTGHSSSTIIAALGMAVGRDLGAKNNVAVIGDAGANTAGQAYEAMNAGYLDSDMIIVLNDNKGVSPLATLDGPAAPPVAGLSCALSKLQSSRPLRELREAVKVTQIQG	283
XP_020161542.1	134	HQSYPHKILTGRDKMPTMRQTNLSCFVKRSESEYDFSGTGHSSSTIIAALGMAVGRDLGAKNNVAVIGDAGANTAGQAYEAMNAGYLDSDMIIVLNDNKGVSPLATLDGPAAPPVAGLSCALSKLQSSRPLRELREAVKVTQIQG	283
XP_003568467.1	128	HQSYPHKILTGRDKMPTMRQTNLSCFVKRSESEYDFSGTGHSSSTIIAALGMAVGRDLGAKNNVAVIGDAGANTAGQAYEAMNAGYLDSDMIIVLNDNKGVSPLATLDGPAAPPVAGLSCALSKLQSSRPLRELREAVKVTQIQG	277
XP_004962111.1	139	HQSYPHKILTGRDKMPTMRQTNLSCFVKRSESEYDFSGTGHSSSTIIAALGMAVGRDLGAKNNVAVIGDAGANTAGQAYEAMNAGYLDSDMIIVLNDNKGVSPLATLDGPAAPPVAGLSCALSKLQSSRPLRELREAVKVTQIQG	288
XP_006654395.2	141	HQSYPHKILTGRDKMPTMRQTNLSCFVKRSESEYDFSGTGHSSSTIIAALGMAVGRDLGAKNNVAVIGDAGANTAGQAYEAMNAGYLDSDMIIVLNDNKGVSPLATLDGPAAPPVAGLSCALSKLQSSRPLRELREAVKVTQIQG	290
Query	284	GSVHEIAAKVDYARGMISGSGSSLFEELGLYYIGPVDGHNIDDLITILREVKGTKITGPVLIHVITEKRGYPPAERASDKYHGVAKFPDPTGKQKSPAKTLYTNVFAEALIAEABQDSKIVAIHAANGGCTGLNPLRFRPNRCFD	433
AXS78096.1	284	GSVHEIAAKVDYARGMISGSGSSLFEELGLYYIGPVDGHNIDDLITILREVKGTKITGPVLIHVITEKRGYPPAERASDKYHGVAKFPDPTGKQKSPAKTLYTNVFAEALIAEABQDSKIVAIHAANGGCTGLNPLRFRPNRCFD	433
EAE8772512.1	284	GSVHEIAAKVDYARGMISGSGSSLFEELGLYYIGPVDGHNIDDLITILREVKGTKITGPVLIHVITEKRGYPPAERASDKYHGVAKFPDPTGKQKSPAKTLYTNVFAEALIAEABQDSKIVAIHAANGGCTGLNPLRFRPNRCFD	433
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XP_004962111.1	289	GSVHEIAAKVDYARGMISGSGSSLFEELGLYYIGPVDGHNIDDLITILREVKGTKITGPVLIHVITEKRGYPPAERASDKYHGVAKFPDPTGKQKSPAKTLYTNVFAEALIAEABQDSKIVAIHAANGGCTGLNPLRFRPNRCFD	438
XP_006654395.2	291	GSVHEIAAKVDYARGMISGSGSSLFEELGLYYIGPVDGHNIDDLITILREVKGTKITGPVLIHVITEKRGYPPAERASDKYHGVAKFPDPTGKQKSPAKTLYTNVFAEALIAEABQDSKIVAIHAANGGCTGLNPLRFRPNRCFD	440
Query	434	VGIAEQHAYTFAAGLACEGLKFPFCAYSSFLQRYDQVVDLQKLPVRFANDRAGLVGADGPTGCGAFDVTFMACLNPNVVMAPSDAEALNNVATAAIDDRPSCFRTPRNGIGVPLPENYKGTPIEVGGRIMIEGERVALLGCG	583
AXS78096.1	434	VGIAEQHAYTFAAGLACEGLKFPFCAYSSFLQRYDQVVDLQKLPVRFANDRAGLVGADGPTGCGAFDVTFMACLNPNVVMAPSDAEALNNVATAAIDDRPSCFRTPRNGIGVPLPENYKGTPIEVGGRIMIEGERVALLGCG	583
EAE8772512.1	434	VGIAEQHAYTFAAGLACEGLKFPFCAYSSFLQRYDQVVDLQKLPVRFANDRAGLVGADGPTGCGAFDVTFMACLNPNVVMAPSDAEALNNVATAAIDDRPSCFRTPRNGIGVPLPENYKGTPIEVGGRIMIEGERVALLGCG	583
XP_020161542.1	434	VGIAEQHAYTFAAGLACEGLKFPFCAYSSFLQRYDQVVDLQKLPVRFANDRAGLVGADGPTGCGAFDVTFMACLNPNVVMAPSDAEALNNVATAAIDDRPSCFRTPRNGIGVPLPENYKGTPIEVGGRIMIEGERVALLGCG	583
XP_003568467.1	428	VGIAEQHAYTFAAGLACEGLKFPFCAYSSFLQRYDQVVDLQKLPVRFANDRAGLVGADGPTGCGAFDVTFMACLNPNVVMAPSDAEALNNVATAAIDDRPSCFRTPRNGIGVPLPENYKGTPIEVGGRIMIEGERVALLGCG	577
XP_004962111.1	439	VGIAEQHAYTFAAGLACEGLKFPFCAYSSFLQRYDQVVDLQKLPVRFANDRAGLVGADGPTGCGAFDVTFMACLNPNVVMAPSDAEALNNVATAAIDDRPSCFRTPRNGIGVPLPENYKGTPIEVGGRIMIEGERVALLGCG	588
XP_006654395.2	441	VGIAEQHAYTFAAGLACEGLKFPFCAYSSFLQRYDQVVDLQKLPVRFANDRAGLVGADGPTGCGAFDVTFMACLNPNVVMAPSDAEALNNVATAAIDDRPSCFRTPRNGIGVPLPENYKGTPIEVGGRIMIEGERVALLGCG	590
Query	584	SAVQYCAAASIVAGHGLRVTVADARFCFKPLDHALIRSLAKSHEVITVBEESIGGGSHVAQFMALDGLLDGKLRPVPVLPDKYIDHGPSADQLSEAGLTPSHIAATVFNILGQAREALAINTPVN	712
AXS78096.1	584	SAVQYCAAASIVAGHGLRVTVADARFCFKPLDHALIRSLAKSHEVITVBEESIGGGSHVAQFMALDGLLDGKLRPVPVLPDKYIDHGPSADQLSEAGLTPSHIAATVFNILGQAREALAINTPVN	712
EAE8772512.1	584	SAVQYCAAASIVAGHGLRVTVADARFCFKPLDHALIRSLAKSHEVITVBEESIGGGSHVAQFMALDGLLDGKLRPVPVLPDKYIDHGPSADQLSEAGLTPSHIAATVFNILGQAREALAINTPVN	711
XP_020161542.1	584	SAVQYCAAASIVAGHGLRVTVADARFCFKPLDHALIRSLAKSHEVITVBEESIGGGSHVAQFMALDGLLDGKLRPVPVLPDKYIDHGPSADQLSEAGLTPSHIAATVFNILGQAREALAINTPVN	711
XP_003568467.1	578	SAVQYCAAASIVAGHGLRVTVADARFCFKPLDHALIRSLAKSHEVITVBEESIGGGSHVAQFMALDGLLDGKLRPVPVLPDKYIDHGPSADQLSEAGLTPSHIAATVFNILGQAREALAINTPVN	705
XP_004962111.1	589	SAVQYCAAATLVERHGLRVTVADARFCFKPLDHALIRSLAKSHEVITVBEESIGGGSHVAQFMALDGLLDGKLRPVPVLPDKYIDHGPSADQLSEAGLTPSHIAATVFNILGQAREALAINTPVN	716
XP_006654395.2	591	SAVQYCAAASIVAGHGLRVTVADARFCFKPLDGLLIRLANSEHVITVBEESIGGGSHVAQFMALDGLLDGKLRPVPVLPDKYIDHGPSADQLSEAGLTPSHIAATVFNILGQAREALAINTPVN	718

b



c

SignalP-4.1 prediction (euk networks): Poa



d

CENTER FOR
BIOLOGICAL
SEQUENCE
ANALYSIS
CBS

TargetP 1.1 Server - prediction results

Technical University of Denmark

targetp v1.1 prediction results #####
 Number of query sequences: 6
 Cleavage site predictions not included.
 Using PLANT networks.

Name	Len	cTP	mTP	SP	other	Loc	RC

Poa	712	0.410	0.375	0.009	0.074	C	5
Hordeum	712	0.749	0.164	0.012	0.053	C	3
Aegilops	712	0.437	0.277	0.015	0.147	C	5
Brachypodium	706	0.473	0.161	0.052	0.252	C	4
Setaria	717	0.376	0.235	0.007	0.228	C	5
Oryza	719	0.532	0.115	0.010	0.165	C	4

cutoff		0.000	0.000	0.000	0.000		

e

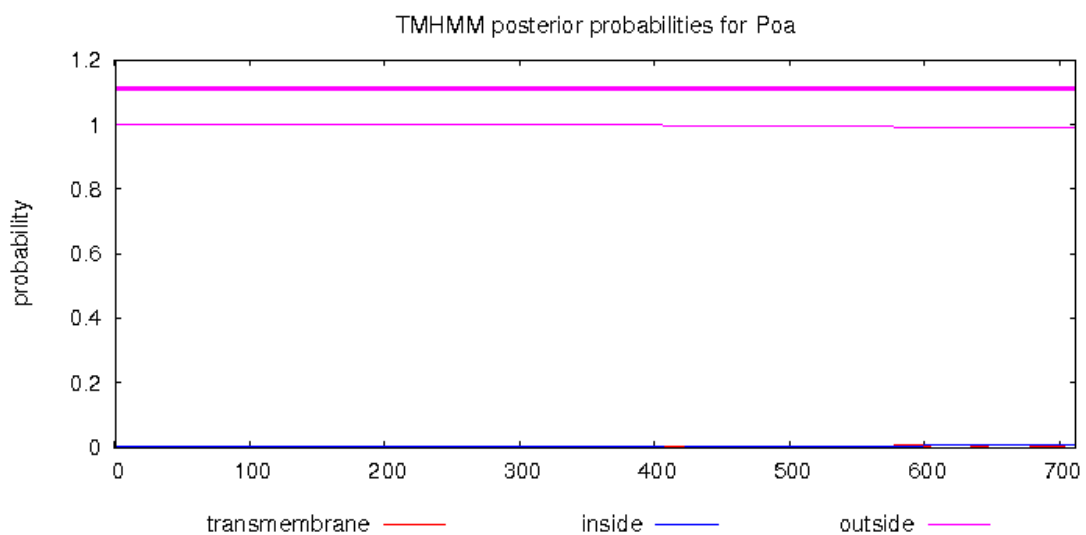


Figure S1. Bioinformative analysis for PpDXS1 protein. (a) Amino acid sequence alignment of DXS1. (b) Prediction of function domain. (c) Prediction of signal peptide. (d) Prediction of subcellular localization. (e) Prediction of transmembrane topological structures.