

>1-4

AATCACTACTGTGATGATAACGAAGACAATTCCAAGGAGCTGAAAATCATCATCATCATCATCAT
CAATCAGCTAAGATTAAGAATTATGATAAACCTAAACCGTTCGGTTTCGATTTGGATCGTATTATCAT
TATTTCTCTCACTCTTCCTTTCTCAAGCTGAAGTTATAACCCTAACTCCTGAAACATTCTCTGACAAGG
TGAAGGAGAAAGACACGGCATGGTTTGTCAAATTTTGTGTGCCATGGTGTAAAGCATTGTAAGAATTTG
GGGACCTTGTGGGAAGAGGTTGGGAAGGCAATGGAGGGGGAAGATGAAATAGAGGTTGGAGAAGTT
GACTGCGGCGCCAGCAAATCTGTCTGTTCTAAAGCTGATATCCACTCTTACCCTACTTTTAAGCTCTTT
TTTGATGGAGAAGAAGTTGCTAAATATCAAGGGCCAAGAGATGTTGAATCTCTTAAAGCATTTCGTTTT
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AGGcAAATCTCCTTTTCaATATTTCCATCTGTTTGTCAATAGTGATTTATCCAGAGACGTTGTGGACATCC
CCATTGGGGCAGTGGAGCCTCACAATGGAATAAATTTGATTTTGCAAACGCCCCAGTTCAGATTACCT
TGTGCGTTGTAGCAGATAATATTTGACAATATGCCCATTTTGGTTGTCATCTTGTAGGAGGAGGTCTG
CAACAATGGATGGAAACCCAGTCAGGAATATAACAAAACTTGTAGGCACTGATAATGGATCCATT
GCGAAGTTATATCATCCTTACACAGGAATTTCAACATAATGTCTTGAACAGTTTAATTATATTAGCGA
GTGTAATTGGTAACATATTTTCTCTTCTAAACAAGCGAAGTTAGTGAAAAAAAAAAAAAAAAAAAAAA
AA

PREDICTED: Populus alba protein disulfide-isomerase 5-1 (LOC118034619), transcript variant X1, mRNA.
XM_035039958.1

Descriptions											
Sequences producing significant alignments											
<input type="checkbox"/> select all 0 sequences selected											
GenBank Graphics Distance tree of results New MSA Viewer											
	Description	Scientific Name	Common Name	Taxid	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input type="checkbox"/>	PREDICTED: Populus alba protein disulfide-isomerase 5-1 (LOC118034619), transcript va...	Populus...	white po...	43335	1711	1711	97%	0.0	99.89%	992	XM_035039958.1
<input type="checkbox"/>	PREDICTED: Populus trichocarpa protein disulfide-isomerase 5-1 (LOC7491175), transcri...	Populus...	black co...	3694	1437	1437	94%	0.0	95.70%	978	XM_002313510.3
<input type="checkbox"/>	PREDICTED: Populus euphratica protein disulfide-isomerase 5-1 (LOC105114437), transc...	Populus...	Euphrat...	75702	1399	1399	97%	0.0	94.04%	995	XM_011010982.1
<input type="checkbox"/>	PREDICTED: Populus alba protein disulfide-isomerase 5-1 (LOC118034619), transcript va...	Populus...	white po...	43335	1000	1363	77%	0.0	99.82%	801	XM_035039959.1
<input type="checkbox"/>	PREDICTED: Populus euphratica protein disulfide-isomerase 5-1 (LOC105114437), transc...	Populus...	Euphrat...	75702	850	1346	94%	0.0	95.40%	957	XM_011010983.1
<input type="checkbox"/>	PREDICTED: Populus trichocarpa protein disulfide-isomerase 5-1 (LOC7491175), transcri...	Populus...	black co...	3694	699	699	45%	0.0	95.89%	867	XM_024608065.1
<input type="checkbox"/>	PREDICTED: Populus euphratica protein disulfide-isomerase 5-1 (LOC105114437), transc...	Populus...	Euphrat...	75702	662	662	45%	0.0	94.52%	827	XM_011010981.1
<input type="checkbox"/>	PREDICTED: Jatropha curcas protein disulfide-isomerase 5-1 (LOC105628125), mRNA	Jatroph...	NA	180498	431	431	39%	7e-116	87.43%	1000	XM_012209472.3

>2-1

GGAGACAATCACTCCGACCTGACTATATCAAGATGTTTGTATTGGATGAAGCAGATGAAATGCTCTCA
AGAGGATTCAAGGATCAGATATATGATATTTTCCAATTACTGCCCCAAAGATTTCAGGTTGGGGTCTT
CTCTGCTACTATGCCACCTGAGGCCCTAGAAATTACGAGGAAGTTCATGAATAAACCTGTGAGGATTT
TAGTGAAGCGTGATGAGCTTACCCTTGAGGGTATCAAGCAATTCTATGTTAATGTTGACAAGGAGGA
ATGGAAGCTTGAGACACTTTGTGATCTATATGAGACCTTGGCAATAACCCAAAGTGTTATCTTTGTGA
ACACCAGGCGCAAGGTGGATTGGCTCACAGACAAGATGCGCAGTCGTGATCACACAGTCTCTGCCAC
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ATCTCCCTACCCAGCCAGAGAACTACCTCCATCGTATTGGTCGTAGTGGACGTTTTGGAAGGAAGGGT
GTTGCTATAAACTTTGTTACCAGGGACGATGAAAGAATGCTTCTGACATCCAGAGATTCTATAATGT

AACGGTTGAGGAGCTGCCATCAAATGTTGCTGATCTTCTTTGAAGCAATTTTGGTTCTCCAAGGTAAA
TGGCTGAGCTTGGAAGTTAAACTATTATGCTGTTTGCAGTTTTGGGGCCTCTATTTAGCATGGATTG
GACTAGCCCTGCAGGTTTGGTTCTGAGCATTTGAGATTGGGGTCAATCCCATTTTCGGGTGCAGGAGTC
CCTTGTGTAAATTTTGTGCAAGTTTGTTTTTGCTTTTTCTTTTTGTGTGCGGAGTAAAATTTGCAGAA
TTATGGTAGTGTCCATCATAATATTTTACTCTCTGCGTGGTTTTTCATTTTATGCAAGGGAATTTTCATG
TAGGTAAAAAACATATGATAAAGTCATTATGTTATAATATTGGGCTCTCCGTTGCTGTTCTCTTGAGC
AATAAAAAAAAAAAAAAAAAAAAAAAAAA

PREDICTED: *Populus alba* eukaryotic initiation factor 4A-9-like (LOC118030765), transcript variant X2, mRNA.
XM_035035016.1

Descriptions	Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments								
Download ▼ New Select columns ▼ Show 100 ▼ ?								
<input checked="" type="checkbox"/> select all 100 sequences selected								
GenBank Graphics Distance tree of results New MSA Viewer								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> PREDICTED: Populus alba eukaryotic initiation factor 4A-9-like (LOC118030765), transcript variant X2, ...	Populus alba	2004	2004	97%	0.0	99.73%	1823	XM_035035016.1
<input checked="" type="checkbox"/> PREDICTED: Populus alba eukaryotic initiation factor 4A-9-like (LOC118030765), transcript variant X1, ...	Populus alba	2004	2004	97%	0.0	99.73%	1832	XM_035035015.1
<input checked="" type="checkbox"/> Populus trichocarpa clone WS0111_L18 unknown mRNA	Populus trichoc...	1969	1969	99%	0.0	98.83%	1779	EF145043.1
<input checked="" type="checkbox"/> PREDICTED: Populus trichocarpa eukaryotic initiation factor 4A-9 (LOC7470684), transcript variant X3, ...	Populus trichoc...	1956	1956	97%	0.0	98.99%	1822	XM_024604079.1
<input checked="" type="checkbox"/> PREDICTED: Populus trichocarpa eukaryotic initiation factor 4A-9 (LOC7470684), transcript variant X2, ...	Populus trichoc...	1956	1956	97%	0.0	98.99%	1822	XM_024604078.1
<input checked="" type="checkbox"/> PREDICTED: Populus trichocarpa eukaryotic initiation factor 4A-9 (LOC7470684), transcript variant X1, ...	Populus trichoc...	1956	1956	97%	0.0	98.99%	1823	XM_002308509.3
<input checked="" type="checkbox"/> PREDICTED: Populus euphratica eukaryotic initiation factor 4A-9-like (LOC105122170), transcript varia...	Populus euphra...	1912	1912	97%	0.0	98.35%	1812	XM_011021112.1
<input checked="" type="checkbox"/> PREDICTED: Populus euphratica eukaryotic initiation factor 4A-9-like (LOC105122170), transcript varia...	Populus euphra...	1912	1912	97%	0.0	98.35%	1814	XM_011021111.1
<input checked="" type="checkbox"/> PREDICTED: Populus trichocarpa eukaryotic initiation factor 4A-15 (LOC112325060), transcript variant, ...	Populus trichoc...	1428	1428	96%	0.0	90.53%	1808	XM_024590479.1

>2-3

AGAGCTACATAGACAAGCAGATGCAATCTTCCACCTCTATGGAACGGTCACTGCTCTTCTCTCTTTCT
TGCTCTTCTCAATATCCATCGTTGCCCAATCTACTGTCCCTTCAAATTCCACATTTAAGAAAGTCAATA
CTGGAGAGTGGGCGGAAGCCATTTACAGAGTACCGTTCAGATTTTCGTGCCCTGGACATCTCTACCTCC
GTTTTCCAAGTTTGCTTTTATAACACCACCCCTAATGCATTCACTCTCGCAATACGTATGGGTACGAGG
AGGTCACCGGCAGTGAGGCGGTTTGTGTTGGGAAGCCAACCGAGGCAACCCAGTTGGTGAAGATGCCA
CTCTCACTTTTGGTGAGGACGGAACCTTATCTTGGCCGATGCTGATGGCAGGGTTGCTTGGCAAACC
AACACTGCCGACAAAGGTGTTGTAGGGTTGCAAATGCTACCGAATGGTAACATGGTGCTTCATGACT
CTAAGGGCAATTTTCATCTGGCAAAGTTTGTATTATCCCACTGATACTCTTTTGGTGGGTCAATCTCTTC
GTGTTGGAGCCGTAACCAGGCTTGTGAGTCGAGCCTCTGACAAAATGAACACAAACGGAGCCTATAG
TCTGGTATTAGAACCCAAAAGAATAGCCATGTACTATAAGAGTCCAACTCTCCCAAGCCATACGTCT
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AATGACCTGAGTCTTCAGTTCTCTACCGGTGGTGGACCCTTGCTCTCTAAGCCCGATTTCAACAGCAC
GTTGTCATTTCTCCGGCTTGGGGTAGATGGCAATCTTAGAGTCTACAGTTTCAACAACCAGGAACTT
CAGCTTCTTGGGACGTGACTTTCACTCTTTTCTCCAAAGATGTAGGTGTTTGGGAAAGTGAGTGTCAA
TTACCAGAGAAATGTGGCAAGTTTGGGCTCTGTGAGGACAGCCAATGCGTTGGTTGCCCGTTACCAA
ATGGGCTCGGGAAGTGGACCGAGAGCTGTGAACCTGTGAAGGTGACTGTATGTAACAAGAACTTCCA
TTACTATAAACTAGAAGGGGTTGATCATTCCATGAGCAAGTATGGAAAAGGAAATGGACCCTTGAAG
GAGAACGATTGTGAGAAGGAATGTTCCAGTGACTGCAAGTGTTTCAGGTACTTTTACAACACAAAGA
CATCTATGTGTTGGATTGCTTATGATCTGCAAACCTCTGACGAGGGTTGCAAATTCTACACATGTGGGT

TACATAAAAGTGCCGAATCACCAGTGAAGCTGGCCTGCTTGTTCACCAAGGCATGTAGTAGAATAC
 TGAGATCGTTTACTTGGCGAGGCTAGTTTATCGCTTGCTGACATTTCTGGAGCAGTGTTCGTTGCAAG
 TGCCTGATCTCTCTGCTTACTGTTTCCTTCTGTAGCAAAATAAAAGTGGTAATAAAAAACATTTGAGC
 ATTTCAAAAAAAAAAAAAAAAAAAAA

PREDICTED: Populus alba epidermis-specific secreted glycoprotein EP1-like (LOC118043395), mRNA.
 XM_035051360.1

Descriptions									
Sequences producing significant alignments									
Download Select columns Show 100									
select all 27 sequences selected									
GenBank Graphics Distance tree of results New MSA Viewer									
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	PREDICTED: Populus alba epidermis-specific secreted glycoprotein EP1-like (LOC118043395), mRNA	Populus alba	2760	2760	98%	0.0	99.87%	1542	XM_035051360.1
<input checked="" type="checkbox"/>	PREDICTED: Populus trichocarpa epidermis-specific secreted glycoprotein EP1 (LOC18095492), mRNA	Populus trichoc...	2398	2398	98%	0.0	95.46%	1660	XM_006370091.2
<input checked="" type="checkbox"/>	PREDICTED: Populus euphratica epidermis-specific secreted glycoprotein EP1-like (LOC105117520),...	Populus euphra...	2337	2337	98%	0.0	94.57%	1561	XM_011015205.1
<input checked="" type="checkbox"/>	PREDICTED: Populus euphratica epidermis-specific secreted glycoprotein EP1-like (LOC10511758),...	Populus euphra...	2320	2320	98%	0.0	94.38%	1553	XM_011007210.1
<input checked="" type="checkbox"/>	PREDICTED: Populus trichocarpa epidermis-specific secreted glycoprotein EP1 (LOC18103363), mRNA	Populus trichoc...	1458	1458	88%	0.0	86.30%	1545	XM_024581031.1
<input checked="" type="checkbox"/>	Populus trichocarpa clone POP038-L21, complete sequence	Populus trichoc...	1458	2681	88%	0.0	86.30%	106705	AC214468.1
<input checked="" type="checkbox"/>	PREDICTED: Populus euphratica epidermis-specific secreted glycoprotein EP1-like (LOC105129278),...	Populus euphra...	1413	1413	88%	0.0	85.75%	1553	XM_011031270.1
<input checked="" type="checkbox"/>	PREDICTED: Populus alba epidermis-specific secreted glycoprotein EP1-like (LOC118038309), mRNA	Populus alba	1408	1408	88%	0.0	85.67%	1560	XM_035044633.1
<input checked="" type="checkbox"/>	PREDICTED: Populus trichocarpa epidermis-specific secreted glycoprotein EP1 (LOC7455947), mRNA	Populus trichoc...	636	636	82%	2e-177	76.20%	1532	XM_002316823.3
<input checked="" type="checkbox"/>	PREDICTED: Populus alba epidermis-specific secreted glycoprotein EP1-like (LOC118038308), mRNA	Populus alba	621	621	81%	6e-173	76.03%	1645	XM_035044632.1
<input checked="" type="checkbox"/>	PREDICTED: Populus trichocarpa epidermis-specific secreted glycoprotein EP1 (LOC7472351), mRNA	Populus trichoc...	586	586	81%	2e-162	75.55%	1413	XM_024580973.1
<input checked="" type="checkbox"/>	PREDICTED: Populus alba epidermis-specific secreted glycoprotein EP1-like (LOC118038307), mRNA	Populus alba	564	564	81%	1e-155	75.22%	1478	XM_035044631.1
<input checked="" type="checkbox"/>	PREDICTED: Populus euphratica epidermis-specific secreted glycoprotein EP1-like (LOC105129277),...	Populus euphra...	536	536	71%	2e-147	75.92%	1503	XM_011031269.1

>2-5

ACTTTGAAATCCGAAACAATTGTCCTTACACTGTGTGGGCCGCAGCCTCACCTGGCGGTGGGCGCCGT
 CTAGACCGTGGCCAAACTTGAATCTTAACGTGCCTGCTGGCACGTCCATGGCTCGTATATGGGGCCG
 GACAAATTGTAACTTTGATGGTAGCGGTACGGGTCTGTTGCCAAACCGGGGATTGCACCGGTGGCCTA
 CAGTGCAAGGGCTGGGGTGTCCCTCCCAACACTCTAGCAGAATATGCGTTAAATCAGTTTGGTGACTT
 GGATTTTTATGATATATCGCTTGTTGATGGATTTAATATCCCTATGGAATTTAGTCCAACATCAAGCGG
 TGGCTCAGGGAAGTGTCAAGCGCTTCTGTGCACAGCAGATATTAATGGGCAATGTCCTAATGAATTG
 AGGGCTCCTGGGGGGTGTAAATAACCCATGCACTGTGTTCAAAACTAACGAATACTGCTGCACTAATG
 GGCAGGGGAGCTGTGGCCCTACCTATTTCTCAAGGTTTTTTAAGGATAGGTGCCCTACTTCTTACAGC
 TATCCCCAGGATGACCCTTCGAGCACATTTACATGCCCTGGCGGGACCAACTATAGGGTTGTCTTTTG
 CCCTCGGGGGTCTCCTCATTTCCCTTGGAGATGGTTGAAGAACAGCGTGCAGAGTAAGCAAGAAGC
 TAAGAACATAGCTGACGACTTGATTTATAATAAATATTATGTGCTGCCTTGAAAACCTTGGTGAGTTGA
 GGTCCGTGTGTTATGTACGTATGGCTGTGTGTATCTTTTTTCTTTTCTTTTCTTTTCTGCTAAAAGAACAAA
 AAACGAGTCTGTGTTTTGTTCTTGCCTGTTTCCATGCTGGGATGTAATAAAAATTCCAGTGAAATAAA
 GAAATGTTTAATCACAAAAAAAAAAAAAAAAAAAAAAAAAAAA

PREDICTED: Populus alba osmotin-like protein OSM34 (LOC118033711), mRNA. XM_035038801.1

Descriptions	Graphic Summary	Alignments	Taxonomy
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Sequences producing significant alignments

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	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	PREDICTED: Populus alba osmotin-like protein OSM34 (LOC118033711). mRNA	Populus alba	1489	1489	97%	0.0	96.39%	1108	XM_035038801.1
<input checked="" type="checkbox"/>	PREDICTED: Populus trichocarpa osmotin-like protein OSM34 (LOC7472761). mRNA	Populus trichocarpa	1445	1445	97%	0.0	95.77%	1024	XM_002299485.3
<input checked="" type="checkbox"/>	PREDICTED: Populus alba osmotin-like protein OSM34 (LOC118033665). mRNA	Populus alba	1151	1151	91%	0.0	91.51%	1024	XM_035038738.1
<input checked="" type="checkbox"/>	PREDICTED: Populus euphratica osmotin-like protein OSM34 (LOC105129023). mRNA	Populus euphratica	1136	1136	96%	0.0	90.08%	1039	XM_011030919.1
<input checked="" type="checkbox"/>	PREDICTED: Populus euphratica osmotin-like protein OSM34 (LOC105120343). parti...	Populus euphratica	1120	1311	90%	0.0	96.20%	899	XM_011018508.1
<input checked="" type="checkbox"/>	PREDICTED: Populus euphratica osmotin-like protein OSM34 (LOC105129073). mRNA	Populus euphratica	1114	1305	90%	0.0	96.05%	973	XM_011031003.1
<input checked="" type="checkbox"/>	Populus deltoides pathogenesis-related thaumatin (PR52-1). gene .partial cds	Populus deltoides	1083	1083	70%	0.0	96.61%	723	GU129189.1
<input checked="" type="checkbox"/>	PREDICTED: Populus trichocarpa osmotin-like protein OSM34 (LOC7479328). mRNA	Populus trichocarpa	1053	1053	91%	0.0	89.70%	1017	XM_002299511.3
<input checked="" type="checkbox"/>	Populus trichocarpa x Populus deltoides clone WS0132_Q22 unknown mRNA	Populus trichocarpa x Populus de...	998	998	69%	0.0	94.90%	641	EF148520.1
<input checked="" type="checkbox"/>	Populus balsamifera pathogenesis-related thaumatin (PR52-1). gene .partial cds	Populus balsamifera	627	627	41%	8e-175	95.87%	461	GU129190.1
<input checked="" type="checkbox"/>	Populus nigra pathogenesis-related thaumatin (PR52-1). gene .partial cds	Populus nigra	616	616	41%	2e-171	94.57%	461	GU129188.1
<input checked="" type="checkbox"/>	Hevea brasiliensis cultivar RR11-105 osmotin 2 gene .complete cds	Hevea brasiliensis	477	477	69%	9e-130	80.34%	813	MN683521.1

>3-1

AGGCAAGACCATTACACTTGAGGTGGAGAGTTCTGACACCATTGATAATGTGAAAGCTAAGATCCAA
GACAAGGAGGGTATCCCGCCAGACCAGCAGAGACTCATCTTTGCCGGCAAGCAGCTTGAGGATGGCC
GTACCCTTGCGGATTATAACATCCAGAAGGAGTCCACCCTCCATTTGGTCCTTCGCTTTCGTGGTGGT
ATGCAGATCTTTGTGAAGACCCTCACAGGAAAGACCATCACCTTGGAGGTGGAGAGCTCTGATACCA
TTGACAATGTGAAAGCCAAGATCCAAGACAAGGAAGGCATCCCCCAGACCAGCAGAGGTTGATTTT
TGCTGGGAAGCAGCTTGAAGATGGGAGGACTCTTGCTGACTACAACATTCAGAAGGAGTCAACCCTT
CACCTGGTGCTGCGTCTCCGTGGAGGAATGCAGATTTTTGTCAAGACTTTGACCGGAAAGACCATCAC
CCTGGAGGTCGAGAGCTCGGACACCATTGACAACGTGAAGGCCAAGATCCAGGACAAGGAAGGTAT
TCCCCAGACCAACAAAGGTTGATCTTCGCTGGAAAGCAGTTGGAAGATGGGCGCACCTTGGCTGACT
ACAATATCCAGAAGGAATCCACACTTCACCTTGTCCTTCGTCTCCGTGGTGGTTTTTAAGATGTGCTGT
TCATGTTGTCCAAGATAATGTCTTGGTTTATATGCTATTACTCTGGATTATGGTTCTCTTGTGTGTTCA
GTGGCCATCTTTGAATGGTTGCTTTTAATAATCTGTTGAACTCTTTTTAAAAAAAAAAAAAAAAAAAA
AA

PREDICTED: Populus alba polyubiquitin-like (LOC118062990), mRNA. XM_035076890.1

Descriptions	Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments								
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<input checked="" type="checkbox"/> select all 100 sequences selected								
GenBank Graphics Distance tree of results New MSA Viewer								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> PREDICTED: Populus alba polyubiquitin-like (LOC118062990).mRNA	Populus alba	1380	1380	97%	0.0	98.11%	1532	XM_035076890.1
<input checked="" type="checkbox"/> Populus trichocarpa clone WS0125_N24 unknown mRNA	Populus trichocarpa	1341	1950	97%	0.0	97.23%	1438	EF147905.1
<input checked="" type="checkbox"/> PREDICTED: Populus trichocarpa polyubiquitin (LOC18095912).mRNA	Populus trichocarpa	1336	1950	97%	0.0	97.10%	1544	XM_006370571.2
<input checked="" type="checkbox"/> Populus trichocarpa ubiquitin mRNA, complete cds	Populus trichocarpa	1336	1944	97%	0.0	97.10%	1411	FJ438462.1
<input checked="" type="checkbox"/> Populus trichocarpa clone WS0127_P02 unknown mRNA	Populus trichocarpa	1336	1950	97%	0.0	97.10%	1435	EF148144.1
<input checked="" type="checkbox"/> Populus trichocarpa clone PX0011_N13 unknown mRNA	Populus trichocarpa	1336	1950	97%	0.0	97.10%	1448	EF144248.1
<input checked="" type="checkbox"/> PREDICTED: Populus euphratica polyubiquitin (LOC105142396).mRNA	Populus euphratica	1301	1701	97%	0.0	96.34%	1484	XM_011049998.1
<input checked="" type="checkbox"/> Populus EST from leave	Populus tremula x Popul...	1243	1243	97%	0.0	94.87%	1003	CU224824.1
<input checked="" type="checkbox"/> Populus EST from leave	Populus tremula x Popul...	1131	1131	84%	0.0	96.37%	1246	CU222992.1
<input checked="" type="checkbox"/> Poplar cDNA sequences	Populus trichocarpa x Po...	1118	1118	81%	0.0	97.27%	712	CT029634.1
<input checked="" type="checkbox"/> Poplar cDNA sequences	Populus trichocarpa x Po...	1118	1118	81%	0.0	97.27%	712	CT029633.1
<input checked="" type="checkbox"/> Poplar cDNA sequences	Populus trichocarpa x Po...	1118	1118	81%	0.0	97.27%	713	CT029613.1
<input checked="" type="checkbox"/> Poplar cDNA sequences	Populus trichocarpa x Po...	1083	1083	77%	0.0	97.77%	677	CT029614.1

>4-2

ATTGGGATCAAAAAGATCATCATCACAATCATCATTAATGTCATTATCACAATCATCATCACTTCCCAT
CAATCCATGCCCACCTTCCAAATTCCCTATTTTGGTTTCTTGATCATTTCTCTGCTGTCTCAGTATGGTCA
ATGGGAGCTGAAAGTGGGGTTCTTGAGACAACTAGTAGCTGAAAGTGGAGAAGAACACAAGCCC
TTGTCTGCTGAAATATTGGGTTGCTCGGATTCCTTTTCTTCAGGCTTTTGAAGTGTGTTGAACCTTGT
TTCTTGTAATAACGCAAGTGAGTTCGGTGAGTCGGACGTGGGTGTGTGTGATCGCCTGTGTAGCTA
ACAATAAACATGTTTGGATCTGTGTTGCTCCTCTCCACTTGCTTTCTTGCTGCACACCTTTTGAGCTG
CTGCATCTGTAGTAGTTTCTGTACAAGAAAAAGAATCGAATTTTAGCCATGTTTAGTGAGAAGAATCA
AGATATTTTAAAGAAAAGAAGGAAAAA

PREDICTED: Populus alba probable WRKY transcription factor 27 (LOC118037092), mRNA. XM_035042975.1

Descriptions	Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments								
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<input checked="" type="checkbox"/> select all 14 sequences selected								
GenBank Graphics Distance tree of results New MSA Viewer								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> PREDICTED: Populus alba probable WRKY transcription factor 27 (LOC118037092). mRNA	Populus alba	778	778	84%	0.0	99.30%	1740	XM_035042975.1
<input checked="" type="checkbox"/> PREDICTED: Populus trichocarpa probable WRKY transcription factor 27 (LOC18106446). mR...	Populus trichocarpa	778	778	84%	0.0	99.30%	1724	XM_006372308.2
<input checked="" type="checkbox"/> PREDICTED: Populus euphratica probable WRKY transcription factor 27 (LOC105140777). m...	Populus euphratica	736	736	84%	0.0	97.67%	2003	XM_011047753.1
<input checked="" type="checkbox"/> PREDICTED: Populus trichocarpa probable WRKY transcription factor 27 (LOC7468350). mRNA	Populus trichocarpa	479	479	84%	1e-130	86.70%	1727	XM_002305235.3
<input checked="" type="checkbox"/> PREDICTED: Populus alba probable WRKY transcription factor 27 (LOC118030321). mRNA	Populus alba	455	455	74%	2e-123	88.45%	1547	XM_035034378.1
<input checked="" type="checkbox"/> PREDICTED: Populus euphratica uncharacterized LOC105120336 (LOC105120336). ncRNA	Populus euphratica	388	388	74%	2e-103	85.30%	1348	XR_841307.1
<input checked="" type="checkbox"/> Malus domestica genome assembly, chromosome: 7	Malus domestica	132	132	33%	4e-26	80.70%	35442570	OU744997.1
<input checked="" type="checkbox"/> Malus domestica genome assembly, chromosome: 7	Malus domestica	132	132	33%	4e-26	80.70%	35756407	OU744959.1
<input checked="" type="checkbox"/> Malus domestica genome assembly, chromosome: 7	Malus domestica	132	132	33%	4e-26	80.70%	36203908	OU744548.1
<input checked="" type="checkbox"/> Malus sylvestris genome assembly, chromosome: 7	Malus sylvestris	132	132	33%	4e-26	80.70%	35530347	OU696509.1
<input checked="" type="checkbox"/> Malus domestica genome assembly, chromosome: 7	Malus domestica	132	132	33%	4e-26	80.70%	35293072	OU696683.1
<input checked="" type="checkbox"/> PREDICTED: Malus domestica probable WRKY transcription factor 27 (LOC108173713). mRNA	Malus domestica	128	128	31%	5e-25	80.86%	1813	XM_017333280.2
<input checked="" type="checkbox"/> PREDICTED: Tarenaya hassleriana probable WRKY transcription factor 27 (LOC104811943). ...	Tarenaya hassleriana	126	126	28%	2e-24	82.19%	1495	XM_010538831.1

>4-5

AGTAAGGAACTGGAGAAGGAGCCCAAGTTCCTGAAGAACGGTGATGCTGGTATGATTAAGATGATTC
CCACCAAGCCCATGGTGGTGGAGACTTTCTCAGCGTATCCTCCACTCGGTCGTTTTGCTGTGAGGGAC
ATGCGCCAGACCGTTGCTGTGGGAGTTATCAAGAACGTGGAGAAGAAGGATCCCCTCTGGTGCTAAGG
TGACCAAATCTGCTGCCAAGAAGGGTGCCAAGTGAACCGTGCAGGTTGATGCACTAAGAAGCTTTAA
TAAAAATCAAGAGTGGGTTCTTGTTACTGGTCCATTTCTTGATGTCCATCTGTTCATTATGAGAACTG
TAGTCTTAAGTCATCACCTTCATTGCAAGGCTTTTGTTCACAGAACTGGGTTCTTGATAGGCGGTGGC
GGGGTTTTGGTCTTGATGTTTTTCCGAGTCATTGTTGTGTCTCCCATGTTGAGAATTTTAATCTGTTTT
AATTTTCACTTGCTCTGCTGAGAGTTTAGTATTTTGCTGTGATGTTAAGTACCCATGAATACTGTTTAC
AATTTTACTTGTCTAGTTTTTGTTCGTCTACTTAGTTTCTACCTATGCCTTTGTAGAAGAGTGATATTCT
GAATGTTTTTTCAAAAAAAAAAAAAAAAAAAAAA

PREDICTED: Populus alba elongation factor 1-alpha (LOC118059947), mRNA. XM_035072992.1

Descriptions		Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments									
Download		New	Select columns	Show 100					
<input checked="" type="checkbox"/> select all 100 sequences selected		GenBank	Graphics	Distance tree of results					
		New MSA Viewer							
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	PREDICTED: Populus alba elongation factor 1-alpha (LOC118059947), mRNA	Populus alba	1107	1107	96%	0.0	98.56%	1988	XM_035072992.1
<input checked="" type="checkbox"/>	PREDICTED: Populus trichocarpa elongation factor 1-alpha-like (LOC112328984), transcript variant X2...	Populus trichoc...	1035	1035	96%	0.0	96.49%	1859	XM_024610823.1
<input checked="" type="checkbox"/>	PREDICTED: Populus trichocarpa elongation factor 1-alpha-like (LOC112328984), transcript variant X1...	Populus trichoc...	1035	1035	96%	0.0	96.49%	1916	XM_024610822.1
<input checked="" type="checkbox"/>	PREDICTED: Populus trichocarpa elongation factor 1-alpha (LOC7489636), mRNA	Populus trichoc...	1029	1029	96%	0.0	96.33%	1915	XM_002316315.3
<input checked="" type="checkbox"/>	Populus trichocarpa clone JGIACSB1089-D10, complete sequence	Populus trichoc...	989	1827	96%	0.0	95.37%	39340	AC208942.1
<input checked="" type="checkbox"/>	PREDICTED: Populus euphratica elongation factor 1-alpha (LOC105137070), mRNA	Populus euphra...	915	915	90%	0.0	94.87%	1825	XM_011042649.1
<input checked="" type="checkbox"/>	Populus trichocarpa x Populus deltoides translation elongation factor 1 alpha mRNA, partial cds	Populus trichoc...	575	575	58%	2e-159	92.86%	481	GQ253565.1
<input checked="" type="checkbox"/>	PREDICTED: Populus euphratica elongation factor 1-alpha-like (LOC105130805), mRNA	Populus euphra...	521	521	71%	3e-143	86.97%	1404	XM_011033484.1
<input checked="" type="checkbox"/>	PREDICTED: Populus trichocarpa elongation factor 1-alpha (LOC7457880), mRNA	Populus trichoc...	516	516	71%	1e-141	86.75%	1825	XM_002311071.3
<input checked="" type="checkbox"/>	Populus trichocarpa clone WS01122_Q05 unknown mRNA	Populus trichoc...	516	516	71%	1e-141	86.75%	1742	EF145289.1
<input checked="" type="checkbox"/>	PREDICTED: Populus alba elongation factor 1-alpha-like (LOC118052437), mRNA	Populus alba	499	499	72%	1e-136	85.77%	1805	XM_035063421.1
<input checked="" type="checkbox"/>	PREDICTED: Populus alba elongation factor 1-alpha (LOC118059944), mRNA	Populus alba	475	475	67%	2e-129	87.05%	1864	XM_035072988.1
<input checked="" type="checkbox"/>	PREDICTED: Populus euphratica elongation factor 1-alpha-like (LOC105137066), transcript variant X1...	Populus euphra...	473	473	67%	8e-129	86.36%	1856	XM_011042642.1