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REFERENCE: PlantCARE: a database of plant cis-acting regulatory elements and a portal to tools for in silico analysis of promoter sequences.

Lescot, M., Déhais, P., Moreau, Y., De Moor, B., Rouzé, P., and Rombauts, S.

Nucleic Acids Res., Database issue(2002), 30(1):325-327.

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>PlantCARE 29331
+ GGGTTGGGGT TTCTACAGGA CGTAAACTAG TCAGATCTAC CATGGTGGAC TCCTCTTAGA ATTCCCGGGG
- CCCAACCCCA AAGATGTCTT GCATTTGATC AGTCTAGATG GTACCACCTG AGGAGAATCT TAAGGGCCCC

+ ATCCGTCGAC GCATCCAGCC CCAAAACTGT CAGAAAAATA CGCATGGGTA AGTGTGGCT ACGAGTTAGT
- TAGGCAGCTG CGTAGGTCGG GGTTTTGACA GTCTTTTAT GCGTACCCAT TCACAACCGA TGCTCAATCA

+ TGATATTTTT GTAGATATGG AACGTACCTT CATTTTCGTT CTGACACACG ATACTAGAGG AGAAAGTGAC
- ACTATAAAAA CATCTATACC TTGCATGGAA GTAAAAGCAA GACTGTGTGC TATGATCTCC TCTTTCAC TG

+ TTTTATAGAG AACCATGATT GCTTGAAAGC CCATGATATA GTAGTGAGTT AGTTCCTAAC AGTACCTAAA
- AAAATATCTC TTGGTACTFA CGAAGCTTCG GGTACTATAT CATCACTCAA TCAAGGATTG TCATGGATTT

+ GACTTTTAGG TTGATGACAG TGGAGACCAA CACCAAGAAA GCTACAAAAT TTTGGTTGGC CGTTCTCTTT
- CTGAAAATCC AACTACTGTC ACCTCTGTT GTGGTCTTT CGATGTTTTA AAACCAACCG GCAAGAGAAA

+ CAAGATCACA TCAAGAACAA GTTGGAGGCC CCTTACAAAC ATGAGGCTAC TGTGTGGTT ACATGACATG
- GTTCTAGTGT AGTTCCTGTT CAACCTCCGG GGAATGTTTG TACTCCGATG ACAACACCAA TGTACTGTAC

+ GAATTGGAGT AGCTATCCGT AATTACAATC ATCTATCATC TCAGGTATTA CAGTTTGATC TTGAATTGAG
- CTTAACCTCA TCGATAGGCA TTAATGTTAG TAGATAGTAG AGTCCATAAT GTCAAACTAG AACTTAACTC

+ TTTCTATATC ATAAAAAGTA GTGGATATTT TTGTGGCGTT CATGAGCCAT CGATATTATA TTAACGAGTC
- AAAGATATAG TATTTTTCAT CACCTATAAA AACACCGCAA GTACTCGGTA GCTATAATAT AATTGCTCAG

+ GTTTTGTTAA TAAATATCC ATAATAGTGG ATGCAAAATG AATATTTCTA TTGCTTTGTG TTGTGTAGCC
- CAAAACAATT ATTTTATAGG TATTATCACC TACGTTTTAC TTATAAAGAT AACGAAACAC AACACATCGG

+ TCTTGATTTT TAGAAATCTT TTCTGCTAG TTTTGATAAC ATAATCAAAC CATCTCATGT ACGCTTGAAG
- AGAACTAAAA ATCTTTAAGA AAGGACGATC AAACTATTG TATTAGTTTG GTAGAGTACA TGCGAACTTC

+ GGAGTATGCA CTCTGTTTGT AATTTAGATA CATAGCGAAC GTGACTGGAT GGTACAAACT ATTAGTTATA
- CCTCATACGT GAGACAAACA TTAAATCTAT GTATCGCTTG CACTGACCTA CCATGTTTGA TAATCAATAT

+ GAATAACAGT AGACTTTGTT GTACACTGTG CTGCTTTCCA GAGTGATTTA TTTAGTTTTT ATTTGAAAGA
- CTTATTTGCA TCTGAAACAA CATGTGACAC GACGAAAGGT CTCCTAAAT AAATCAAAA TAACTTTCT

+ AGAATCAATG CTGGCTCCTT TGTTCACTTA GAGTGATTGA AACTGCATTA TGTTGAAATA GTTCCAGTG
- TCTTAGTTAC GACCGAGGAA ACAAGTGAAT CTCCTAACT TTGACGTAAT ACACTTTAT CAAAGGTCAC

+ AAAATAAGTA CTGTTTCGTT CTGCTTTTGT AGTCTTGGCC GTCTCTGACA AGAAGAAAAG GCATATATAT
- TTTTATTCAT GACAAAGCAA GACGAAAACA TCAGAACCGG CAGAGACTGT TCTTCTTTTC CGTATATATA

+ ATGACTTCTG TTGTGCAGAA AAGTAAAGAA AGAGTGCTTT TTCCAGGAAG CCTATGGGAA GCTCTGTGAC
- TACTGAAGAC AACACGCTTT TTCATTCTTT TCTCACGAAA AAGGTCCTTC GGATACCCTT CGAGACACTG

+ AAAACAACAA CGACTGCTTT TGGTACTAGT TGATTTAGAC AAGTGAAGCC GTCCACGACA TCAGGTACTG
- TTTTGTTGTT GCTGACGAAA ACCATGATCA ACTAAATCTG TTCACTTCGG CAGGTGCTGT AGTCCATGAC

+ TATTTCTGCA GCAATGTTTT GTTTGCGTTG TAATATTACT ATTGGTAATG TAATGGGATT TTTGCGCTTT
- ATAAAGACGT CGTTACAAAA CAAACGCAAC ATTATAATGA TAACCATTAC ATTACCCTAA AAAGCGGAAA

+ ATTAATATATA TCCTATACCC GGTTCCTTAG CCGTAGAAGC ACATTGTTTT GGTAGATGCA AGTAGAAACT
- TAATTTATAT AGGATATGGG CCAAGGAATC GGCATCTTCG TGTAACAAAA CCATCTACGT TCATCTTTGA

+ GAACCGTAAA CACTTAGGCG TCTGTGTGAA AACACCATAG ACAGTGAAGC AGATTAGATT AGATTATAAT
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+ TGATCTGATT TGATTAGATT AGCGGGAACA AAGACAAGGA TGAGGGAACA AAATAAAAAAT GAGAAAGAAA
- ACTAGACTAA ACTAATCTAA TCGCCCTTGT TTCTGTTCCT ACTCCCTTGT TTTATTTTTA CTCTTCTTTT

+ AAGGGTGGTT AAGTAGGATT AAAAGAGGAA AGAAGCATCT GGGGGTTGAA AGATAGGAAC AAACAGAAAT
- TTCCCACCAA TTCATCTTAA TTTTCTCCTT TCTTCGTAGA CCCCACACTT TCTATCCTTG TTTGTCTTCA

+ AGTTAGTTAT GAGGTATGGG ACCAAGAGGG AAGCAGTACA CTTTGTGTTCC AGAATTAAAC AAACTTACAA
- TCAATCAATA TCCTATACCC TGGTTCTCCC TTCGTATGT GAAACAAGG TCTTAATTTG TTTGAATGTT

+ ATGCTAAGTT TTGCAATCTC GAGTCACTTC CACTGCTCCC ACTCCATTAT ATATATATCT CTTTGAGAAAT
- TACGATTCAA AACGTTAGAG CTCAGTGAAG GTGACGAGGG TGAGGTAATA TATATATAGA GAACTCTTTA
TACGATTCAA AACGTTAGAG CTCAGTGAAG GTGACGAGGG TGAGGTAATA TATATATAGA GAACTCTTTA
+ GTGATGGACT TGTGTCAAAA TTCACGTGGA CACTTGATAA GCCGATTCTC TTCTTTGTCA GTTTCCCAA
- CACTACCTGA ACACAGTTTT AAGTGCACCT GTGAACATTT CGGCTAAGAG AAGAAACAGT CAAAGGGGTT
- CACTACCTGA ACACAGTTTT AAGTGCACCT GTGAACATTT CGGCTAAGAG AAGAAACAGT CAAAGGGGTT
+ TCATATCTTC TTTTGGTATA ATATCCAACA GTTTCACCTT CTTTGTGTTCC CATGTTGATG ATATACATAA
- AGTATAGAAG AAAACCATAT TATAGTTTGT CAAAGTGAAA GAAACAAGG GTACAACCTAC TATATGTATT
- AGTATAGAAG AAAACCATAT TATAGTTTGT CAAAGTGAAA GAAACAAGG GTACAACCTAC TATATGTATT
+ TAGAAAGATC AACAATAAAA AAAATAATCG TCTTTTCTAT TATTTTCTC TACTGTCTTC ATCTGTAGTG
- ATCTTTCTAG TTGTTATTTT TTTTATTAGC AGAAAAGATA ATAAAAAGAG ATGACAGAAG TAGACATCAC
- ATCTTTCTAG TTGTTATTTT TTTTATTAGC AGAAAAGATA ATAAAAAGAG ATGACAGAAG TAGACATCAC
+ GGTCTAGACT CAAAAGATTT GATTCTGATA GTGACTGCTA GGGAGAGAGC TTCCTAATCC GGTTTAACCG
- CCAGTACTGA GTTTTCTAAA CTAAGACTAT CACTGACGAT CCCTCTCTCG AAGAATTAGG CCAATTGGC
- CCAGTACTGA GTTTTCTAAA CTAAGACTAT CACTGACGAT CCCTCTCTCG AAGAATTAGG CCAATTGGC
+ GCCCACCCAA GTTTGTCATT CCTACCGAGT AAACAAGTAA AACTTCTCCC TGTAATTAC ACTTTACCGA
- CCGGTGGGTT CAAACAGTAA GGATGGCTCA TTTGTTCTATT TTGAAGAGGG ACATTAAATG TGAAATGGCT
- CCGGTGGGTT CAAACAGTAA GGATGGCTCA TTTGTTCTATT TTGAAGAGGG ACATTAAATG TGAAATGGCT
+ TTTTATCTT ATACTAGATT TTGATCTCGG CGCCGCGCGG GATGTTATTT TAATTGCAA TGTCATTTTT
- AAAATTAGAA TATGATCTAA AACTAGACGC GCGGCGCGCG CTACAATAAA ATTAACGTT ACAGTAAAAA
- AAAATTAGAA TATGATCTAA AACTAGACGC GCGGCGCGCG CTACAATAAA ATTAACGTT ACAGTAAAAA
+ TAAACAATTT TCTTGATATA ATTGATATA TGTAACCATG TCAGTTAGGG ATAGTTTTTT TGGTTTAATT
- ATTTGTTAAA AGAATATAT TAACATATAT ACATTGGTAC AGTCAATCCC TATCAAAAAA ACCAAATTAA
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+ACTGAATCGGAGTTGGTTTATTTGGATCTATAGAAAAGCCTTAAACCAAAGTCATACCGAAATTAAGTTTAgTTTG
- GACTTAAGCC GAACCAAATA AACCTAGATA CTTTGGAAAT TGGTTTCAGT TGGGTTTAAT CAAATCAAAC

+ GTATGTGCTT GTTTAGTTCA CTTGAAGGTT GCGCGGGGG GCGCAACATG GTGGAGCAGG AGACTCTGGT
- CATACACGAA CAAATCAAGT GAACCTCGAA CCGCGCGGCC CGGGTTGTAC CACCTCGTGC TGTGAGAGCA

+ CTACTCCBAG AATATCAABG ATACAGTCTE AGAAGAGCAA AGGGCTATTG AGACTTTTGA ACBAAGGGTA
- GATGAGGTTT TTATAGTTTC TATGTCAGAG TCTTCTGGTT TCCCGATAAC TCTGAAAAGT TGTTCCTCAT

+ ATATGGGCAA ACCTCTCTCG ATTGCATTGC CCAGCTATCT GTCAGTTCAT CAAAAGGAGA GTAGAAAAGG
- TATAGCCCTT TGGAGGAGCC TAAGGTAACG GGTGATAGA CAGTGAAGTA GTTTTCCTGT CATCTTTTCC

+ AAGGTGGCAC CTAGAAATGC CATGATGCG ATAAAGGAAA GGCTATGCTT CAAGATGCC CTGCCCACAG
- TTCCACCGTG GATGTTTACG GTAGTAACGC TATTTCTTT CCGATAGCAA GTTCTACGGA GACGGCTGTC

+ TGCCACCGTG GATGTTTACG GTAGTAACGC TATTTCTTT CCGATAGCAA GTTCTACGGA GACGGCTGTC
- AC

- Acifs Found

+

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
	organism	35	+	4	motif_sequence	short_function
	organism	1685	+	4	motif_sequence	short_function
	organism	1229	-	4	motif_sequence	short_function
	organism	2173	+	4	motif_sequence	short_function
	organism	687	+	4	motif_sequence	short_function
	organism	1862	-	4	motif_sequence	short_function
	organism	1309	-	4	motif_sequence	short_function
	organism	2439	+	4	motif_sequence	short_function
	organism	151	-	4	motif_sequence	short_function
	organism	1798	+	4	motif_sequence	short_function
	organism	1242	-	4	motif_sequence	short_function
	organism	2366	-	4	motif_sequence	short_function
	organism	796	+	4	motif_sequence	short_function
	organism	1984	+	4	motif_sequence	short_function
	organism	1658	+	4	motif_sequence	short_function

+

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
3-AF1 binding site	Solanum tuberosum	1420	+	10	TAAGAGAGGAA	light responsive element

+

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
A-box	Petroselinum crispum	1099	+	6	CCGTCC	cis-acting regulatory element

+

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
AAGAA-motif	Avena sativa	647	-	7	GAAAGAA	
AAGAA-motif	Avena sativa	1002	+	9	gGTAAAGAAA	
AAGAA-motif	Avena sativa	1428	+	7	GAAAGAA	
AAGAA-motif	Avena sativa	835	+	7	GAAAGAA	
AAGAA-motif	Avena sativa	1393	+	7	GAAAGAA	

+

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
ABRE	Arabidopsis thaliana	739	+	5	ACGTG	cis-acting element involved in the abscisic acid responsiveness
ABRE	Arabidopsis thaliana	1634	+	5	ACGTG	cis-acting element involved in the abscisic acid responsiveness
ABRE	Arabidopsis thaliana	1633	-	6	CACGTG	cis-acting element involved in the abscisic acid responsiveness

+

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
AP-1	Arabidopsis thaliana	255	+	8	TGAGTTAG	

+

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
ARE	Zea mays	677	+	6	AAACCA	cis-acting regulatory element essential for the anaerobic induction
ARE	Zea mays	2113	-	6	AAACCA	cis-acting regulatory element essential for the anaerobic induction
ARE	Zea mays	2091	-	6	AAACCA	cis-acting regulatory element essential for the anaerobic induction

+

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
ATCT-motif	Pisum sativum	1311	-	9	AATCTAATCC	part of a conserved DNA module involved in light responsiveness
ATCT-motif	Pisum sativum	1341	-	9	AATCTAATCC	part of a conserved DNA module involved in light responsiveness
ATCT-motif	Pisum sativum	1316	-	9	AATCTAATCC	part of a conserved DNA module involved in light responsiveness

+

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
AT-TATA-box	Arabidopsis thaliana	974	+	6	TATATA	
AT-TATA-box	Arabidopsis thaliana	1592	-	6	TATATA	
AT-TATA-box	Arabidopsis thaliana	1588	-	6	TATATA	
AT-TATA-box	Arabidopsis thaliana	2055	-	6	TATATA	
AT-TATA-box	Arabidopsis thaliana	976	+	6	TATATA	
AT-TATA-box	Arabidopsis thaliana	1590	-	6	TATATA	

+

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CAAT-box						

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CAAT-box	Nicotiana glutinosa	228	-	4	CAAT	
CAAT-box	Arabidopsis thaliana	423	-	5	CCAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	446	+	4	CAAT	
CAAT-box	Nicotiana glutinosa	485	-	4	CAAT	
CAAT-box	Nicotiana glutinosa	610	-	4	CAAT	
CAAT-box	Pisum sativum	831	-	5	CAAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	846	+	4	CAAT	
CAAT-box	Nicotiana glutinosa	876	-	4	CAAT	
CAAT-box	Nicotiana glutinosa	1132	+	4	CAAT	
CAAT-box	Arabidopsis thaliana	1161	-	5	CCAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	1233	-	4	CAAT	
CAAT-box	Nicotiana glutinosa	1329	-	4	CAAT	
CAAT-box	Pisum sativum	1338	-	5	CAAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Pisum sativum	1538	+	5	CAAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	1554	+	4	CAAT	
CAAT-box	Arabidopsis thaliana	1677	+	5	CCAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	1678	+	4	CAAT	
CAAT-box	Nicotiana glutinosa	1763	+	4	CAAT	
CAAT-box	Pisum sativum	1837	-	5	CAAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Pisum sativum	2013	-	5	CAAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	2018	+	4	CAAT	
CAAT-box	Nicotiana glutinosa	2035	+	4	CAAT	
CAAT-box	Nicotiana glutinosa	2051	-	4	CAAT	
CAAT-box	Pisum sativum	2119	-	5	CAAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Pisum sativum	2154	+	5	CAAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	2287	-	4	CAAT	
CAAT-box	Nicotiana glutinosa	2336	-	4	CAAT	
CAAT-box	Pisum sativum	2394	+	5	CAAAAT	common cis-acting element in promoter and enhancer regions
CAAT-box	Nicotiana glutinosa	2405	-	4	CAAT	

+ CCGTCC motif

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CCGTCC motif	Nicotiana tabacum	1099	+	6	CCGTCC	

+ CCGTCC-box

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CCGTCC-box	Petroselinum hortense	1099	+	6	CCGTCC	

+ CTAG-motif

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
CTAG-motif	Avena sativa	652	-	9	ACTAGCAGAA	
CTAG-motif	Avena sativa	1843	-	9	ACTAGCAGAA	

+ DRE core

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
DRE core	Arabidopsis thaliana	2443	+	6	GCCGAC	

+ G-Box

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
G-Box	Pisum sativum	738	-	6	CACGTT	cis-acting regulatory element involved in light responsiveness
G-Box	Pisum sativum	1633	-	6	CACGTG	cis-acting regulatory element involved in light responsiveness

+ G-box

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
G-box	Brassica oleracea	129	-	9	TAACACGTAG	cis-acting regulatory element involved in light responsiveness
G-box	Arabidopsis thaliana	1633	-	6	CACGTG	cis-acting regulatory element involved in light responsiveness
G-box	Zea mays	1104	+	6	CACGAC	cis-acting regulatory element involved in light responsiveness
G-box	Zea mays	2227	+	6	CACGAC	cis-acting regulatory element involved in light responsiveness

+ GARE-motif

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
GARE-motif	Brassica oleracea	987	+	7	TCGTGTG	gibberellin-responsive element

+ GATA-motif

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
GATA-motif	Solanum tuberosum	1366	+	9	AAGGATAAGG	part of a light responsive element
GATA-motif	Arabidopsis thaliana	1679	-	10	AAGATAAGATT	part of a light responsive element
GATA-motif	Arabidopsis thaliana	1452	+	7	GATAGGA	part of a light responsive element

+ GCN4_motif

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
GCN4_motif	Oryza sativa	1826	-	7	TGAGTCA	cis-regulatory element involved in endosperm expression

+ GT1-motif

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
GT1-motif	Arabidopsis thaliana	1407	+	6	GGTTAA	light responsive element
GT1-motif	Arabidopsis thaliana	2138	-	6	GGTTAA	light responsive element
GT1-motif	Arabidopsis thaliana	1884	-	6	GGTTAA	light responsive element

+ MRE

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
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MRE	Petroselinum crispum	286	-	7	AACCTAA	MYB binding site involved in light responsiveness
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MYB

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
MYB	Arabidopsis thaliana	333	-	6	CAACCA	
MYB	Arabidopsis thaliana	1406	-	6	TAACCA	
MYB	Arabidopsis thaliana	406	-	6	TAACCA	
MYB	Arabidopsis thaliana	2063	+	6	TAACCA	
MYB	Arabidopsis thaliana	400	-	6	CAACAG	
MYB	Arabidopsis thaliana	1706	+	6	CAACAG	
MYB	Arabidopsis thaliana	988	-	6	CAACAG	
MYB	Arabidopsis thaliana	2139	+	6	TAACCA	

+

MYB-like sequence

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
MYB-like sequence	Arabidopsis thaliana	406	-	6	TAACCA	
MYB-like sequence	Arabidopsis thaliana	2063	+	6	TAACCA	
MYB-like sequence	Arabidopsis thaliana	1406	-	6	TAACCA	
MYB-like sequence	Arabidopsis thaliana	2139	+	6	TAACCA	

+

MYC

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
MYC	Arabidopsis thaliana	1538	-	6	CATTGT	
MYC	Arabidopsis thaliana	2394	-	6	CATTGT	

+

Myb

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Myb	Arabidopsis thaliana	2072	-	6	TAACGT	

+

Myb-binding site

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Myb-binding site	Nicotiana tabacum	400	-	6	CAACAG	
Myb-binding site	Nicotiana tabacum	1706	+	6	CAACAG	
Myb-binding site	Nicotiana tabacum	988	-	6	CAACAG	

+

O2-site

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
O2-site	Zea mays	412	+	9	GATGACATGG	cis-acting regulatory element involved in zein metabolism regulation
O2-site	Zea mays	2352	-	8	GATGA (C/T) (A/G) TG (A/G)	cis-acting regulatory element involved in zein metabolism regulation

+

P-box

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
P-box	Oryza sativa	2361	-	7	CCTTTTG	gibberellin-responsive element

+

STRE

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
STRE	Arabidopsis thaliana	379	-	5	AGGGG	

+

TATA-box

Site Name	Organism	Position	Strand	Matrix score.	sequence	function
TATA-box	Oryza sativa	147	-	7	TACAAAA	core promoter element around -30 of transcription start
TATA-box	Pisum sativum	211	-	7	TATAAAA	core promoter element around -30 of transcription start
TATA-box	Helianthus annuus	212	-	6	TATAAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	213	-	5	TATAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	214	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	247	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Oryza sativa	323	+	7	TACAAAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	495	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	545	+	6	ATTATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	546	-	5	TATAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	547	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	766	-	5	TATAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	767	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	815	-	9	taTATAAAtc	core promoter element around -30 of transcription start
TATA-box	Oryza sativa	935	-	7	TACAAAA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	973	+	6	ATATAT	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	974	+	6	TATATA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	975	+	6	ATATAT	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	976	+	6	TATATA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	977	+	6	ATATAT	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	978	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	1196	+	6	ATATAT	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1197	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1204	+	4	TATA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	1323	+	6	ATTATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1324	-	5	TATAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1325	-	4	TATA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	1586	+	6	ATTATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1587	-	7	TATATAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1588	-	6	TATATA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	1589	-	6	ATATAT	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1590	-	6	TATATA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	1591	-	6	ATATAT	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1592	-	6	TATATA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	1593	-	6	ATATAT	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1594	-	4	TATA	core promoter element around -30 of transcription start

TATA-box	Arabidopsis thaliana	1697	-	4	TATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1742	-	4	TATA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1969	-	5	TATAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	1970	-	4	TATA	core promoter element around -30 of transcription start
TATA-box	Brassica oleracea	2046	+	6	ATATAA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	2047	-	4	TATA	core promoter element around -30 of transcription start
TATA-box	Helianthus annuus	2053	-	6	TATACA	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	2055	-	6	TATATA	core promoter element around -30 of transcription start
TATA-box	Brassica napus	2056	-	6	ATATAT	core promoter element around -30 of transcription start
TATA-box	Arabidopsis thaliana	2057	-	4	TATA	core promoter element around -30 of transcription start

+	TC-rich repeats					
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
TC-rich repeats	Nicotiana tabacum	765	-	9	ATTCTCTAAC	cis-acting element involved in defense and stress responsiveness

+	TCCC-motif					
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
TCCC-motif	Spinacia oleracea	1860	-	7	TCTCCCT	part of a light responsive element
TCCC-motif	Spinacia oleracea	1935	+	7	TCTCCCT	part of a light responsive element

+	TGA-element					
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
TGA-element	Brassica oleracea	558	-	6	AACGAC	auxin-responsive element
TGA-element	Brassica oleracea	1059	+	6	AACGAC	auxin-responsive element

+	Unnamed__1					
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Unnamed__1	Zea mays	1103	-	5	CGTGG	
Unnamed__1	Zea mays	1635	+	5	CGTGG	

+	Unnamed__2					
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Unnamed__2	Zea mays	65	-	6	CCCCGG	

+	Unnamed__4					
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Unnamed__4	Petroselinum hortense	50	+	4	CTCC	
Unnamed__4	Petroselinum hortense	1582	+	4	CTCC	
Unnamed__4	Petroselinum hortense	426	-	4	CTCC	
Unnamed__4	Petroselinum hortense	2244	+	4	CTCC	
Unnamed__4	Petroselinum hortense	302	-	4	CTCC	
Unnamed__4	Petroselinum hortense	1936	+	4	CTCC	
Unnamed__4	Petroselinum hortense	855	+	4	CTCC	
Unnamed__4	Petroselinum hortense	2323	+	4	CTCC	
Unnamed__4	Petroselinum hortense	199	-	4	CTCC	
Unnamed__4	Petroselinum hortense	1862	-	4	CTCC	
Unnamed__4	Petroselinum hortense	701	-	4	CTCC	
Unnamed__4	Petroselinum hortense	2223	-	4	CTCC	
Unnamed__4	Petroselinum hortense	374	-	4	CTCC	
Unnamed__4	Petroselinum hortense	1576	+	4	CTCC	

+	Unnamed__6					
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
Unnamed__6	Zea mays	1590	+	10	taTAAATATct	

+	WRE3					
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
WRE3	Pisum sativum	2382	-	6	CCACCT	

+	chs-CMA2a					
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
chs-CMA2a	Petroselinum crispum	2188	+	8	TCACTTGA	part of a light responsive element

+	circadian					
Site Name	Organism	Position	Strand	Matrix score.	sequence	function
circadian	Lycopersicon esculentum	142	-	9	CAAAGATATC	cis-acting regulatory element involved in circadian control
circadian	Lycopersicon esculentum	514	-	9	CAAAGATATC	cis-acting regulatory element involved in circadian control