

Supplementary Material

Identification and expression analysis of *Stilbene synthase* genes in *Arachis hypogaea* in response to Methyl Jasmonate and Salicylic Acid induction

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1 Supplementary Figures and Tables

1.1 Supplementary Table

Table S1: Nucleotide sequence of the nine contigs found in <i>Arachis hypogaea</i>		
Sr. No.	Nucleotide Sequences	Contig Results
1	<i>Arachis hypogaea</i> mRNA for stilbene synthase, complete CDS	<ul style="list-style-type: none">• 20452 Conserved• 31055 Not conserved• 2394 Conserved• 26372 Not conserved• 19158 Not conserved
2	<i>Arachis hypogaea</i> clone JC2 putative stilbene synthase gene, complete cds	<ul style="list-style-type: none">• 20452 Conserved• 31055 Not conserved• 2394 Conserved• 19158 Not conserved
3	<i>Arachis hypogaea</i> cultivar Champyeong stilbene synthase (STS) mRNA, complete cds	<ul style="list-style-type: none">• 20452 Conserved• 31055 Not conserved• 2394 Conserved• 26372 Not conserved
4	<i>Arachis hypogaea</i> clone 05_08E putative stilbene synthase mRNA, partial cds	<ul style="list-style-type: none">• 20452 Conserved• 31055 Not conserved• 2394 Conserved• 26372 Not conserved
5	<i>Arachis hypogaea</i> clone 04_07D putative stilbene synthase mRNA, partial cds	<ul style="list-style-type: none">• 20452 Conserved• 31055 Not conserved• 2394 Conserved• 26372 Not conserved

6	<i>Arachis hypogaea</i> clone 03_11D putative stilbene synthase mRNA, partial cds	<ul style="list-style-type: none"> • 20452 Conserved • 31055 Not conserved • 2394 Conserved • 26372 Not conserved
7	<i>Arachis hypogaea</i> stilbene synthase mRNA, complete cds	<ul style="list-style-type: none"> • 20452 Conserved • 31055 Not conserved • 2394 Conserved • 26372 Not conserved
8	UNVERIFIED: <i>Arachis hypogaea</i> clone 04_06E putative stilbene synthase-like mRNA, partial sequence	<ul style="list-style-type: none"> • 20452 Conserved • 31055 Not conserved • 2394 Conserved • 26372 Not conserved
9	<i>A.hypogaea</i> gene for stilbene synthase	<ul style="list-style-type: none"> • 20452 Conserved • 31055 Not conserved • 2394 Conserved • 26372 Not conserved

Table S2. Attributes of five *Stilbene synthase* (*AhSTSs*) genes identified in peanut.

Genes	NCBI Accession No.	Nucleotide Sequence Length Bp	Length of coding sequence (position of CDS) Bp	Length of amino acid sequence Aa
<i>AhSTS1</i>	MT663407	1208 bp	1169 (7-1176)	389
<i>AhSTS2</i>	MT710308	1454 bp	1169 (82-1251)	389
<i>AhSTS3</i>	MT710309	1437 bp	1169 (50-1219)	389
<i>AhSTS4</i>	MT710310	1548 bp	869 (72-941)	289
<i>AhSTS6</i>	MT710312	1571 bp	1169 (81-1250)	389

Table S3. Physiochemical properties of *Stilbene synthase* (*AhSTSs*) genes identified in peanut.

Gene ID	^a aa	^b pI	^c Mw	^d II	^e AI	^f EC	^g GRAVY	Half life	Sub- cellular localization
<i>AhSTS1</i>	389	5.96	42952.7	35.03	91.23	33390	-0.088	>10 hours	cyto
<i>AhSTS2</i>	389	6.84	59343.75	40.66	93.70	54360	-0.070	>10 hours	cyto
<i>AhSTS3</i>	389	5.66	42840.39	35.17	91.98	33390	-0.078	>10 hours	cyto
<i>AhSTS4</i>	289	6.71	32125.13	33.36	90.42	19285	-0.107	>10 hours	cyto
<i>AhSTS6</i>	389	5.56	42817.30	32.02	92.01	34755	-0.084	>10 hours	cyto

^aAmino acid (protein length); ^bIsoelectric point; ^cMolecular weight (Da); ^dInstability index; ^eAliphatic Index; ^fExtinction co-efficient; ^gGrand average of hydrophobicity.

Table S4: Cis-acting elements in the promoter region of stilbene synthase (*AhSTSs*) genes

Gene ID	Name	Number	sequence	Function
<i>AhSTS1</i>	Box 4	3	ATTAAT	part of a conserved DNA module involved in light responsiveness
	CAAT-Box	26	CAAAT/CAAT	common cis-acting element in promoter and enhancer regions
	GATA-motif	1	AAGGATAAGG	part of a light responsive element
	LAMP-element	1	CTTTATCA	part of a light responsive element
	MRE	1	AACCTAA	MYB binding site involved in light responsiveness
	TATC-box	1	TATCCCA	cis-acting element involved in gibberellin-responsiveness
	TCA-element	1	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
	TGA-element	1	AACGAC	auxin-responsive element
	chs-			
	CMA1a	1	TTACTTAA	part of a light responsive element
<i>AhSTS2</i>	ABRE	3	ACGTG/CACGTG	cis-acting element involved in the abscisic acid responsiveness
	ARE	1	AAACCA	cis-acting regulatory element essential for the anaerobic induction
	Box 4	2	ATTAAT	part of a conserved DNA module involved in light responsiveness
	CAAT-box	30	CAAAT/CAAT/CCAAT	common cis-acting element in promoter and enhancer regions
	CGTCA-motif	3	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
	G-Box	2	CACGTT/CACGTG	cis-acting regulatory element involved in light responsiveness
	G-box	1	CACGTG	cis-acting regulatory element involved in light responsiveness
	TCT-motif	1	TCTTAC	part of a light responsive element
	TGA-element	1	AACGAC	auxin-responsive element

	TGACG-motif	3	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness
	chs-Unit 1 ml	1	ACCTAACCCGC	part of a light responsive element
AhSTS3	ABRE	2	CACGTG/ACGTG	cis-acting element involved in the abscisic acid responsiveness
	Box 4	6	ATTAAT	part of a conserved DNA module involved in light responsiveness
	CAAT-box	25	CAAAT/CAAT	common cis-acting element in promoter and enhancer regions
	CGTCA-motif	1	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
	G-Box	1	CACGTG	cis-acting regulatory element involved in light responsiveness
	G-box	1	CACGTG	cis-acting regulatory element involved in light responsiveness
	GATA-motif	1	AAGATAAGATT	part of a light responsive element
	I-box	1	atGATAAGGTC	part of a light responsive element
	RY-element	1	CATGCATG	cis-acting regulatory element involved in seed-specific regulation
	TCA-element	1	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
	TCT-motif	1	TCTTAC	part of a light responsive element
AhSTS4	TGACG-motif	1	TGACG	cis-acting regulatory element involved in the MeJA-responsiveness
	ABRE	2	CACGTG/ACGTG	is-acting element involved in the abscisic acid responsiveness
	Box 4	6	ATTAAT	part of a conserved DNA module involved in light responsiveness
	CAAT-box	26	CAAAT/CAAT	common cis-acting element in promoter and enhancer regions
	CGTCA-motif	1	CGTCA	cis-acting regulatory element involved in the MeJA-responsiveness
	G-Box	1	CACGTG	cis-acting regulatory element involved in light responsiveness
	G-box	1	CACGTG	cis-acting regulatory element involved in light responsiveness
	GATA-motif	1	AAGATAAGATT	part of a light responsive element

	I-box	1	atGATAAGGTC	part of a light responsive element cis-acting regulatory element
	RY- element	1	CATGCATG	involved in seed-specific regulation
	TCA- element	1	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
	TCT- motif	1	TCTTAC	part of a light responsive element cis-acting regulatory element
	TGACG- motif	1	TGACG	involved in the MeJA- responsiveness
AhSTS6	ABRE	2	CACGTG/ACGTG	cis-acting element involved in the abscisic acid responsiveness
	Box 4	6	ATTAAT	part of a conserved DNA module involved in light responsiveness
	CAAT- box	27	CAAAT/CAAT	common cis-acting element in promoter and enhancer regions
	CGTCA- motif	1	CGTCA	cis-acting regulatory element involved in the MeJA- responsiveness
	G-Box	1	CACGTG	cis-acting regulatory element involved in light responsiveness
	G-box	1	CACGTG	cis-acting regulatory element involved in light responsiveness
	GATA- motif	1	AAGATAAGATT	part of a light responsive element
	I-box	1	atGATAAGGTC	part of a light responsive element cis-acting regulatory element
	RY- element	1	CATGCATG	involved in seed-specific regulation
	TCA- element	1	CCATCTTTTT	cis-acting element involved in salicylic acid responsiveness
	TCT- motif	1	TCTTAC	part of a light responsive element cis-acting regulatory element
	TGACG- motif	1	TGACG	involved in the MeJA- responsiveness

Table S5. Primers identity and sequences used for Stilbene synthase (<i>AhSTSs</i>) gene amplification and RT-PCR analysis			
Primer Name	Purpose of primer	5'-Forward	3'-Reverse
<i>AhSTS</i> 1	Full length gene amplification	AGCGAAGCTTTACTCTCA	ATGGGCCAATCTAGACCT
	RT-PCR	ACCAGGTTGAACAGAAGGTG	ACCCCAATCAAATCCTTCTC
<i>AhSTS</i> 2	Full length gene amplification	TGATCTTCTGCACCACAA GC	CTCAGAACAAACCACCAGC A
	RT-PCR	CACGTGATGTTCTTAGCG AT	TTCAATAGTGAGGCCAGGTC
<i>AhSTS</i> 3	Full length gene amplification	TTTCAGCGCATTTGTGAA AG	CTTGGTTGCTGCCTCTTTTC
	RT-PCR	TCACACATTTGATCTTCT GC	TGTTATTTTCAGCCAAGTCC
<i>AhSTS</i> 4	Full length gene amplification	TTTCAGCGCATTTGTGAG AG	AGTTGCAGCCTCTTTTCCAA
	RT-PCR	AGCACATACGCAGATTAC TA	CAAGGACGGTGCTTTATATG
<i>AhSTS</i> 6	Full length gene amplification	TTTCAGCGCATTTGTGAG AG	AGTTGCAGCCTCTTTTCCAA
	RT-PCR	TGGTTCTGATCCTATTCC AG	AAAGCTTTAGTGAGTGCATC
Actin	Reference gene	CAGGCCGTTCTCTCCCTTT AT	CATCAAGGCATCGGTGAGAT

Table S6. Correlation between time and the expression of *Stilbene synthase* (*AhSTSs*) genes under the treatment of methyl jasmonate and salicylic acid in peanut.

Genes		Methyl Jasmonate	Salicylic Acid
		Bard-479	Bard-479
<i>AhSTS1</i>	<i>R</i>	0.8905	-0.4962
	<i>p</i> -value	0.0428	0.3952
<i>AhSTS 2</i>	<i>R</i>	0.7479	-0.5012
	<i>p</i> -value	0.1461	0.3897
<i>AhSTS 3</i>	<i>R</i>	0.2974	-0.4976
	<i>p</i> -value	0.6269	0.3936
<i>AhSTS 4</i>	<i>R</i>	0.9622	0.06101
	<i>p</i> -value	0.0088	0.9224
<i>AhSTS 6</i>	<i>R</i>	-0.3062	0.05057
	<i>p</i> -value	0.6163	0.9356

p-value (0.05) is considered to be significant; *r* is representing Pearson's correlation coefficient.

Table S7. Correlation among the expression of *Stilbene synthase* (*AhSTSs*) genes in peanut.

BARD-479		Methyl Jasmonate				Salicylic Acid			
		<i>AhSTS2</i>	<i>AhSTS3</i>	<i>AhSTS4</i>	<i>AhSTS6</i>	<i>AhSTS2</i>	<i>AhSTS3</i>	<i>AhSTS4</i>	<i>AhSTS6</i>
<i>AhSTS1</i>	<i>R</i>	0.6679	0.5668	0.7984	-0.2193	0.07160	0.2334	-0.5149	-0.5254
	<i>p</i> -value	0.2180	0.3191	0.1053	0.7231	0.9089	0.7056	0.3747	0.3632
<i>AhSTS2</i>	<i>R</i>	----	0.6804	0.7972	0.3949	----	0.9795	-0.3195	-0.3079
	<i>p</i> -value	---	0.2062	0.1062	0.5105	---	0.0035	0.6002	0.6142
<i>AhSTS3</i>	<i>R</i>	---	---	0.2755	0.6279	---	---	-0.3881	-0.3808
	<i>p</i> -value	----	----	0.6537	0.2567	----	---	0.5185	0.5271
<i>AhSTS4</i>	<i>R</i>	---	---	---	-0.1779	---	---	---	0.9997
	<i>p</i> -value	---	---	---	0.7747	---	---	---	< 0.0001

p-value (0.05) is considered to be significant; *r* is representing Pearson's correlation coefficient.

1.2 Supplementary Figures

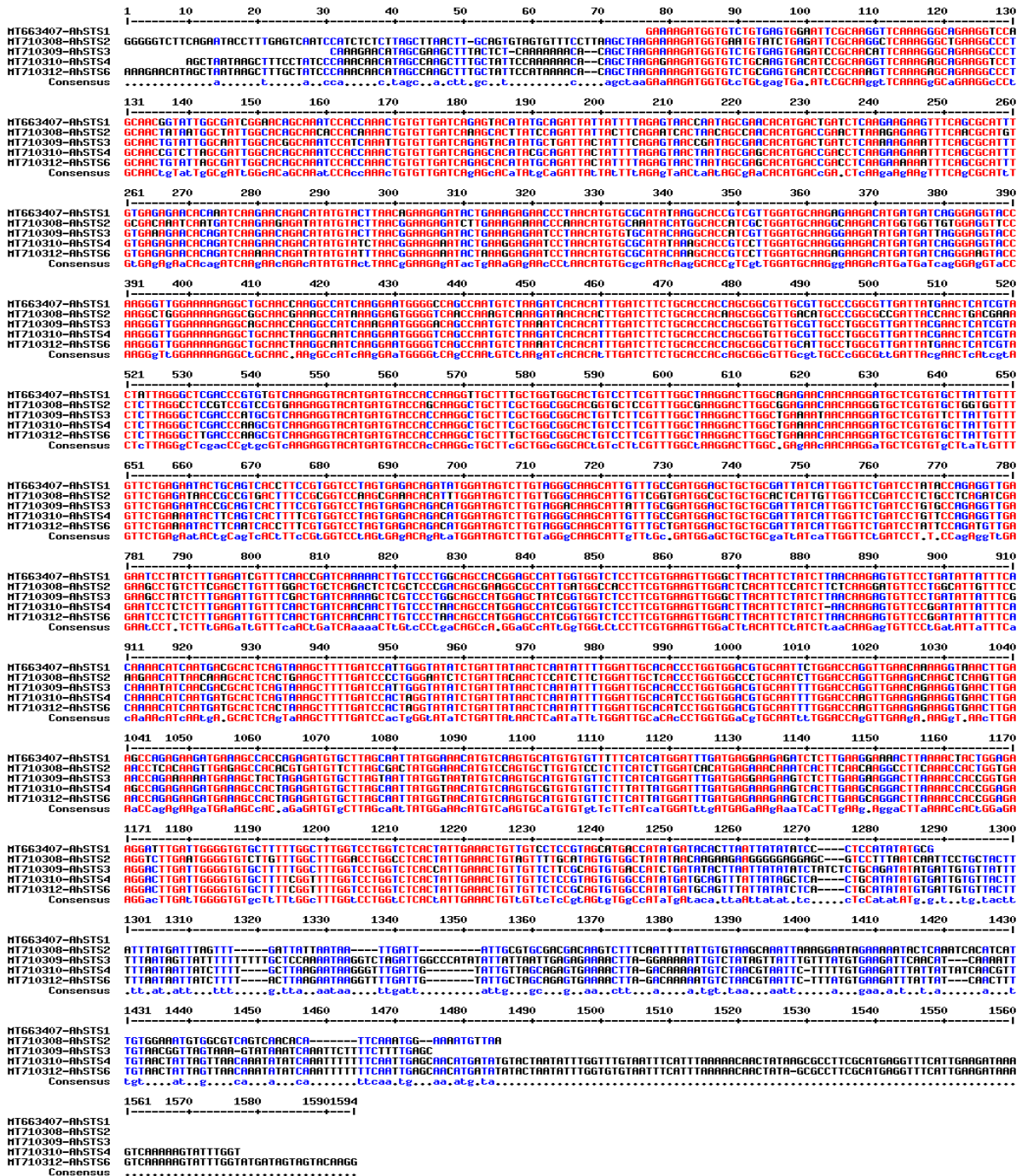


Figure S1. Multiple sequence alignment of nucleotide sequence of the *AhSTS1*, *AhSTS2*, *AhSTS3*, *AhSTS4*, *AhSTS6*. The sequences conserved across all genes are highlighted in red while non-conserved sequences are shown in black. The sequences highlighted in blue shows sequences conserved in some genes.

Multiple sequence alignment of amino acid sequences of *AhSTS1*, *AhSTS2*, *AhSTS3*, *AhSTS4*, and *AhSTS6*. The sequences conserved across all genes are highlighted in red while non-conserved sequences are shown in black. The sequences highlighted in blue shows sequences conserved in some genes.

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1      10      20      30      40      50      60      70      80      90      100     110     120     130
MT663407-AhSTS1  HVSVSGIIRKVQREGPATVLAIGTANPNCVDQSTYADYFRVTNSEHTDLKKFQRICERTQIKNRHMYLTEELKENPNHCAYKAPSLDAREDMHIREVPRVGKEARTKAKEWGQPSKITHLIFC
MT710309-AhSTS3  HVSVSSEIRNIQREGPATVLAIGTANPNCVDQSTYADYFRVTNSEHTDLKKFQRICERTQIKNRHMYLTEELKENPNHCAYKAPSLDAREDMHIREVPRVGKEARTKAKEWGQPSKITHLIFC
MT710312-AhSTS6  HVSSDIRKVQREGPATVLAIGTANPNCVDQSTYADYFRVTNSEHTDLKKFQRICERTQIKNRHMYLTEELKENPNHCAYKAPSLDAREDMHIREVPRVGKEARTKAKEWGQPSKITHLIFC
MT710308-AhSTS2  HVSSEIRKVQREGPATVLAIGTANPNCVDQSTYADYFRVTNSEHTDLKKFQRICERTQIKNRHMYLTEELKENPNHCAYKAPSLDAREDMHIREVPRVGKEARTKAKEWGQPSKITHLIFC
MT710310-AhSTS4  HVSSDIRKVQREGPATVLAIGTANPNCVDQSTYADYFRVTNSEHTDLKKFQRICERTQIKNRHMYLTEELKENPNHCAYKAPSLDAREDMHIREVPRVGKEARTKAKEWGQPSKITHLIFC
Consensus        HVSaSDIRkVQREGPATVLAIGTANPNCVDQSTYADYFRITTS#HT#LKKFQRIC#rtqIKnRhmYLTEELKENPNHCAYKAPSLDAR#DMH!rEVPRVGKEARTKAKEWGQPSKITHLIFC

131     140     150     160     170     180     190     200     210     220     230     240     250     260
MT663407-AhSTS1  TTSGVALPGVDYELIVLLGLDPCVKRYMYHQGCFAGGTVLRLAKDLAENNKDARVLYVCSENTAVTFRGPSETDMSLVGQALFAGGAARIIGSDPIPEVENPIFEIVSTDOQLVPGSHGAIGGLRE
MT710309-AhSTS3  TTSGVALPGVDYELIVLLGLDPCVKRYMYHQGCFAGGTVLRLAKDLAENNKDARVLYVCSENTAVTFRGPSETDMSLVGQALFAGGAARIIGSDPIPEVEKPIFEIVSTDOQLVPGSHGAIGGLRE
MT710312-AhSTS6  TTSGVALPGVDYELIVLLGLDPCVKRYMYHQGCFAGGTVLRLAKDLAENNKDARVLYVCSENTAVTFRGPSETDMSLVGQALFAGGAARIIGSDPIPEVENPIFEIVSTDOQLVPGSHGAIGGLRE
MT710308-AhSTS2  TTSGVDHPGADYQLTKLLGLRPSVKRYMYHQGCFAGGTVLRLAKDLAENNKDARVLYVCSENTAVTFRGPSETHLDSLVGQALFAGGAARIIGSDPLPIQIEKPVFELVMTAQTLPDSEGAIDGHLRE
MT710310-AhSTS4  TTSGVDHPGADYQLTKLLGLRPSVKRYMYHQGCFAGGTVLRLAKDLAENNKDARVLYVCSENTAVTFRGPSETHLDSLVGQALFAGGAARIIGSDPLPIQIEKPVFELVMTAQTLPDSEGAIDGHLRE
Consensus        TTSGVaPGVDY#LiVLLGLDPSVKRYMYHQGCFAGGTVLRLAKDLAENNKDARVLYVCSENTAVTFRGPSETDMSLVGQALFAGGAARIIGSDPV#EnPIFEIVSTDOQLVPGSHGAIGGLRE

261     270     280     290     300     310     320     330     340     350     360     370     380     389
MT663407-AhSTS1  VGLTFYLNKSVPDLIISQNINDALSKAFDPLGISDYNSIFAIHAPGGRAILDQVEKVNLKPEKHKATRDVLSNYGNHSSACVFFIMDLARKSLEGKLKTIGEGFDHGVLFFGPGPLTIETVVLRSMTI
MT710309-AhSTS3  VGLTFYLNKSVPDLIISQNINDALSKAFDPLGISDYNSIFAIHAPGGRAILDQVEKVNLKPEKHKATRDVLSNYGNHSSACVFFIMDLARKSLEGKLKTIGEGFDHGVLFFGPGPLTIETVVLRSVTI
MT710312-AhSTS6  VGLTFYLNKSVPDLIISQNINDALSKAFDPLGISDYNSIFAIHAPGGRAILDQVEKVNLKPEKHKATRDVLSNYGNHSSACVFFIMDLARKSLEGKLKTIGEGFDHGVLFFGPGPLTIETVVLRSVAI
MT710308-AhSTS2  VGLTFHLLKDVPGLIYSKNINKLTAFDPLGISDYNSIFAIHAPGGRAILDQVEKLKLKPKHLKATRDVLSNYGNHSSACVFFIMDLARKSLQGLQLTIGEGLEHGVLFFGPGPLTIETVVLRSVAI
MT710310-AhSTS4  VGLTFYLTWFRILFAHTSNHMSKLLTH
Consensus        VGLTFYL.k.vp.i.sknin.al.kafdplgisdynsifaihappg.aildqve.k..lkp.k..atrdvls.ygnhssacv.fid.mr..sl...l.ttgeg...ugvlfgpggllietvvl.s...i

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Figure S2. Multiple sequence alignment of amino acid sequences of *AhSTS1*, *AhSTS2*, *AhSTS3*, *AhSTS4*, and *AhSTS6*. The sequences conserved across all genes are highlighted in red while non-conserved sequences are shown in black. The sequences highlighted in blue shows sequences conserved in some genes.

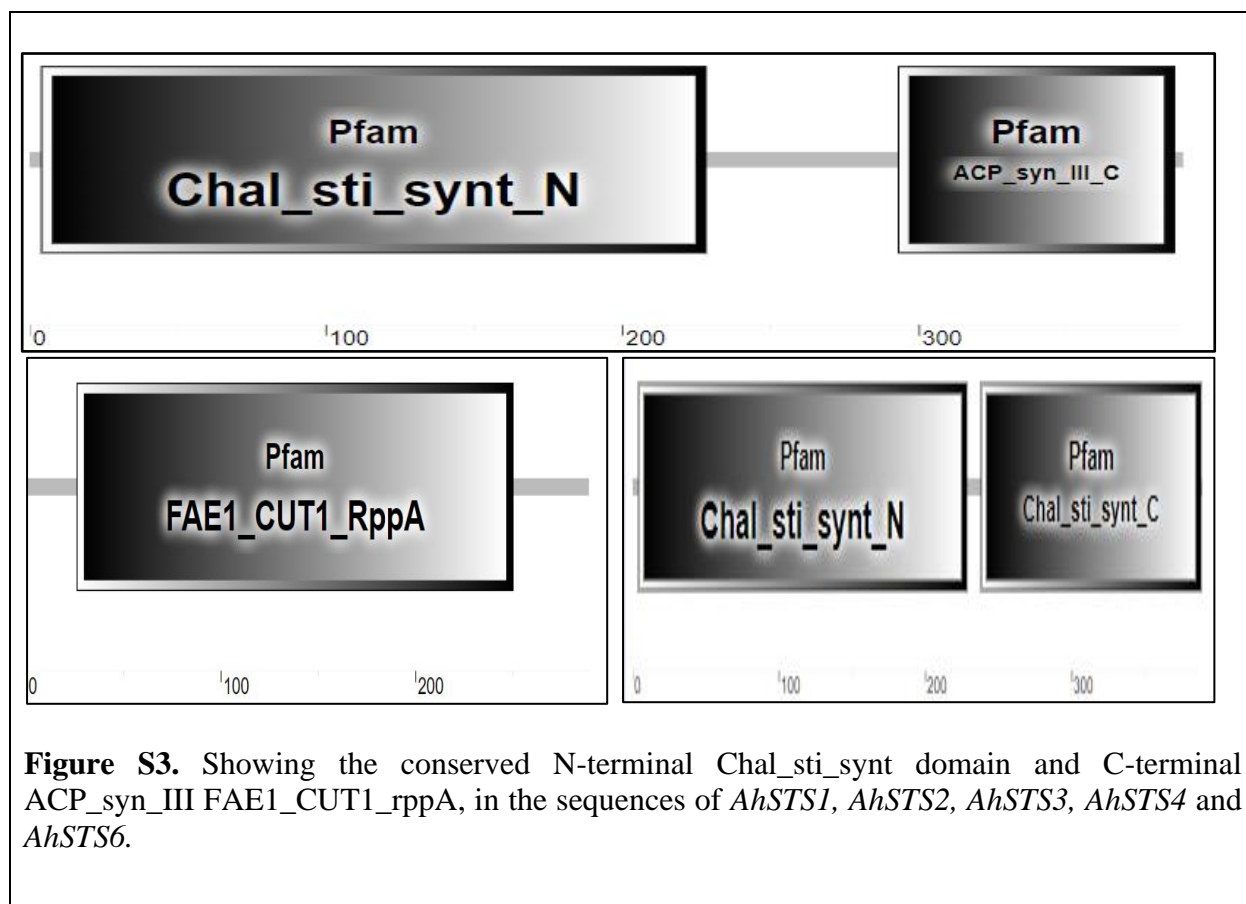


Figure S3. Showing the conserved N-terminal Chal_sti_synt domain and C-terminal ACP_syn_III FAE1_CUT1_rppA, in the sequences of *AhSTS1*, *AhSTS2*, *AhSTS3*, *AhSTS4* and *AhSTS6*.

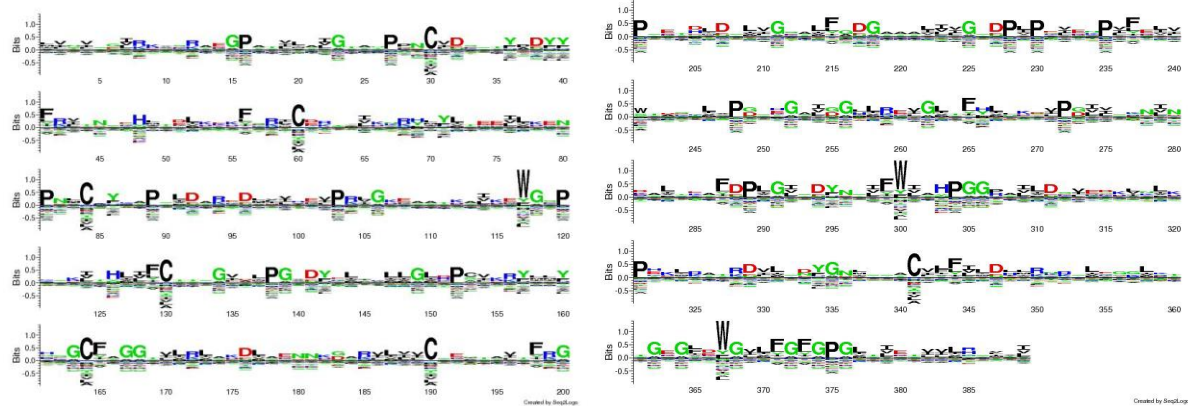


Figure S4. Sequence logo of *AhSTSs*. X-axis showing the position of position of amino acid whereas stack of symbols representing the amino acids (big stacks represent conserved positions and small stacks represents variable position).

Predicted Secondary Structure of *Arachis hypogaea*

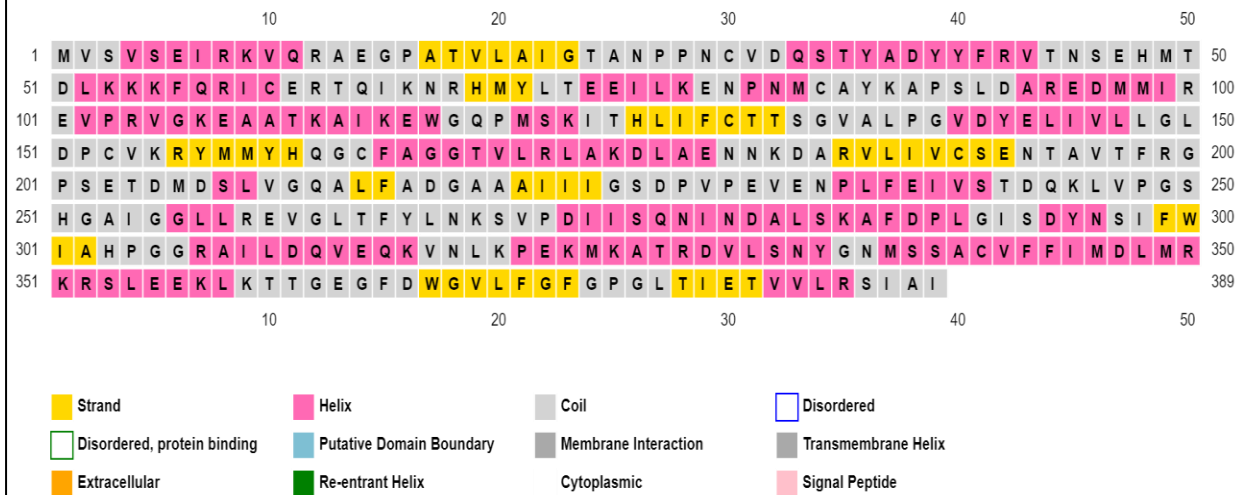


Figure S5: secondary structure of *Arachis hypogaea STS1* showing alpha helices and beta sheets. Loops are also observed in the structure.



Figure S6: Predicted secondary structure of *Arachis hypogaea* STS2 showing alpha helices and beta sheets. Loops are also observed in the structure.

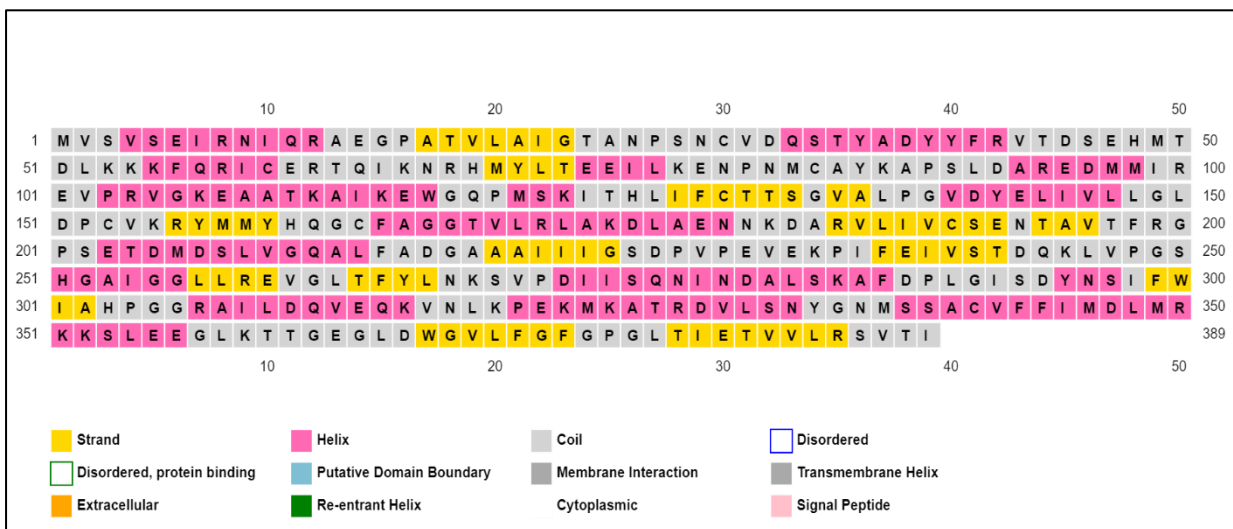


Figure S7: Predicted secondary structure of *Arachis hypogaea* STS3 showing alpha helices and beta sheets. Loops are also observed in the structure.

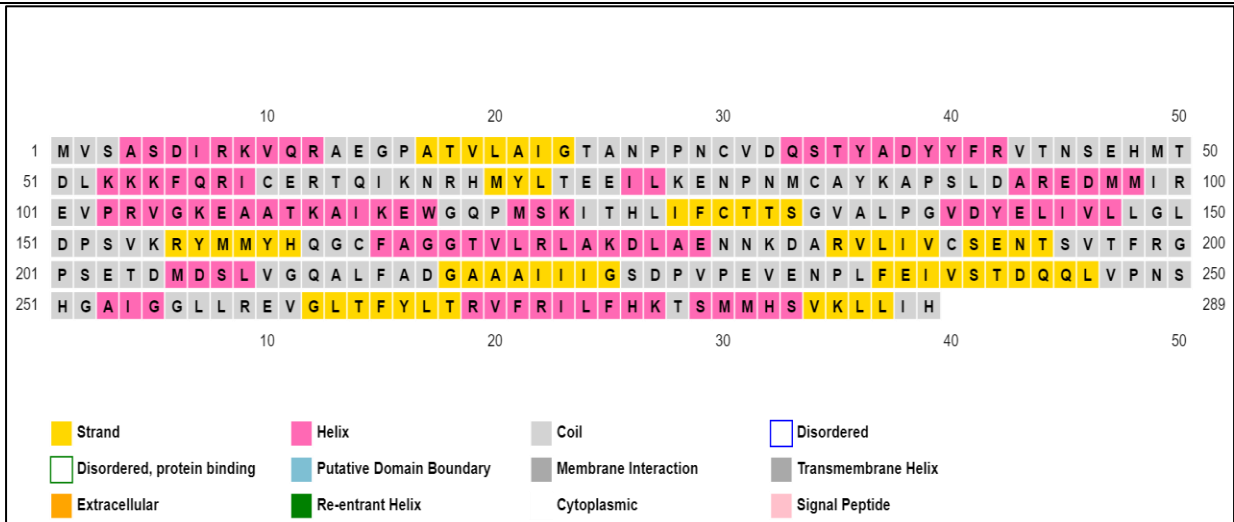


Figure S8: Predicted secondary structure of *Arachis hypogaea* STS4 showing alpha helices and beta sheets. Loops are also observed in the structure.

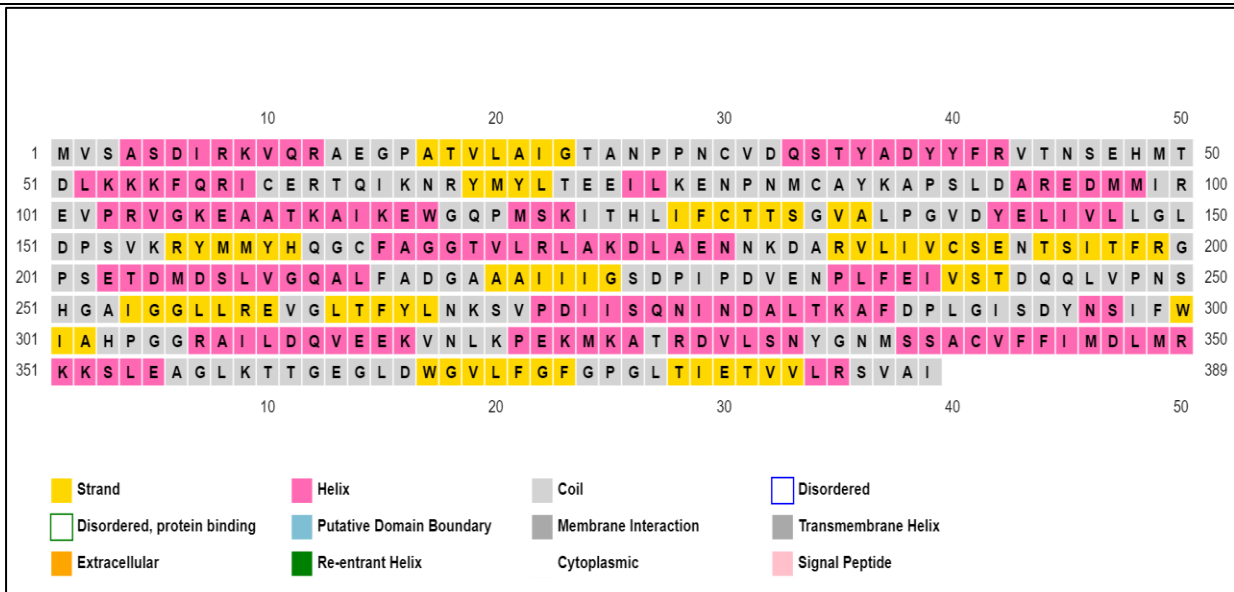


Figure S9: Predicted secondary structure of *Arachis hypogaea* STS6 showing alpha helices and beta sheets. Loops are also observed in the structure.



Figure S10. 3D structure of *AhSTS1* predicted from the SWISS-MODEL. The red colour indicates helices, green colour represents loops and cyan colour represent β -sheets.

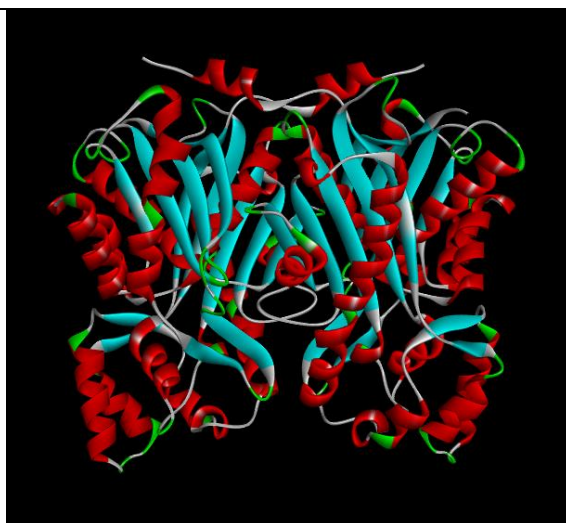


Figure S11. 3D structure of *AhSTS2* predicted from the SWISS-MODEL. The red colour indicates helices, green colour represents loops and cyan colour represent β -sheets.

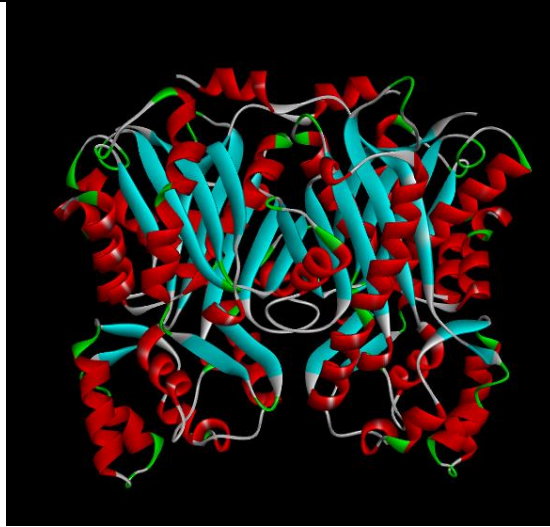


Figure S12. 3D structure of *AhSTS3* predicted from the SWISS-MODEL. The red colour indicates helices, green colour represents loops and cyan colour represent β -sheets.

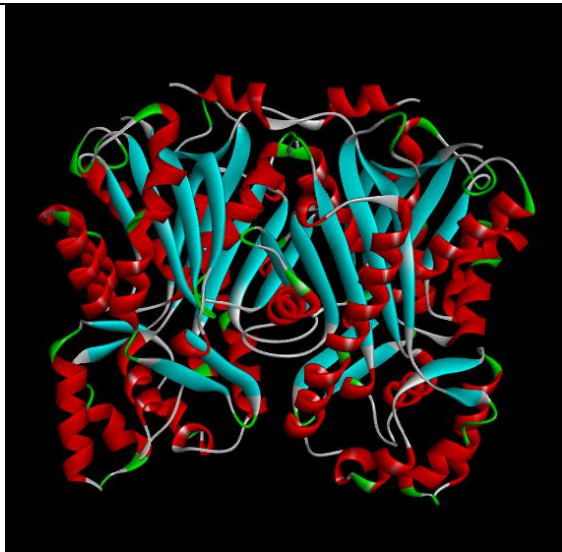


Figure S13. 3D structure of *AhSTS4* predicted from the SWISS-MODEL. The red colour indicates helices, green colour represents loops and cyan colour represent β -sheets.



Figure S14. 3D structure of *AhSTS6* predicted from the SWISS-MODEL. The red colour indicates helices, green colour represents loops and cyan colour represent β -sheets.

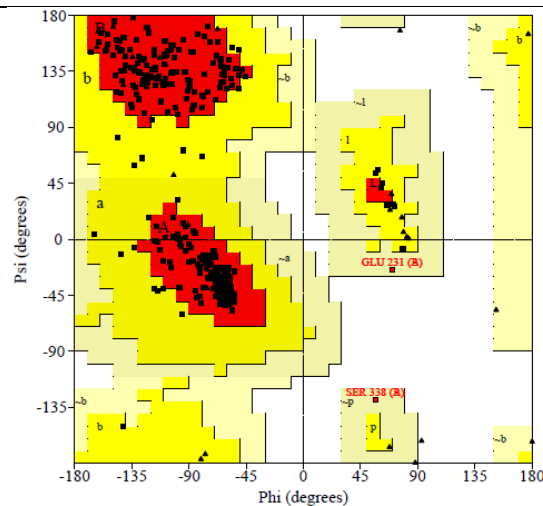


Figure S15. Ramachandran Plot of *stilbene synthase* protein in *Arachis hypogaea*. The graph shows the location of amino acid residues in the favored region of protein. For *AhSTS1*, the location of amino acids in the favored region 92.9% forming a stable protein.

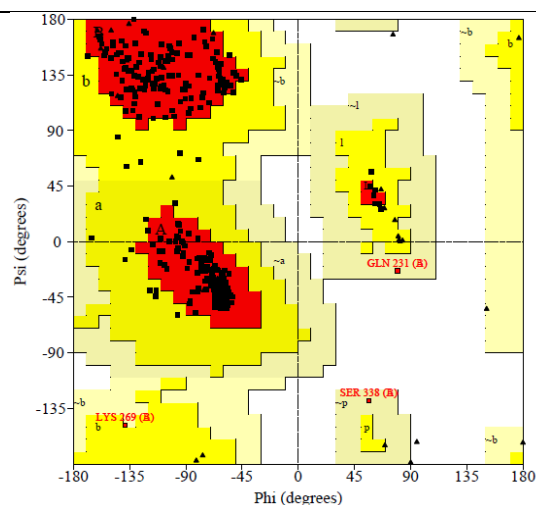


Figure S16. Ramachandran Plot of *stilbene synthase* protein in *Arachis hypogaea*. The graph shows the location of amino acid residues in the favored region of protein. For *AhSTS2*, the location of amino acids in the favored region 93.8% forming a stable protein.

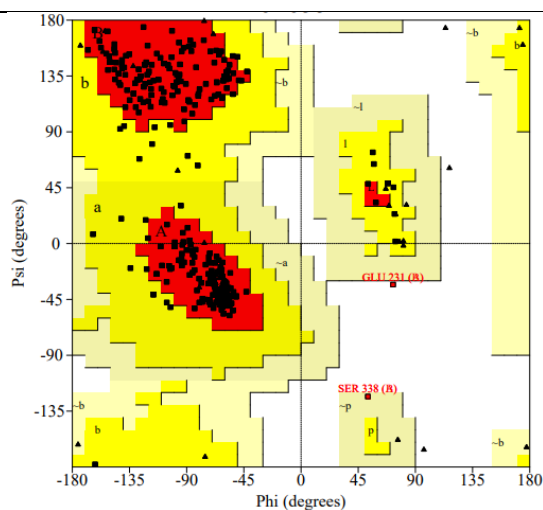


Figure S17. Ramachandran Plot of *stilbene synthase* protein in *Arachis hypogaea*. The graph shows the location of amino acid residues in the favored region of protein. For *AhSTS3*, the location of amino acids in the favored region 92 % forming a stable protein.

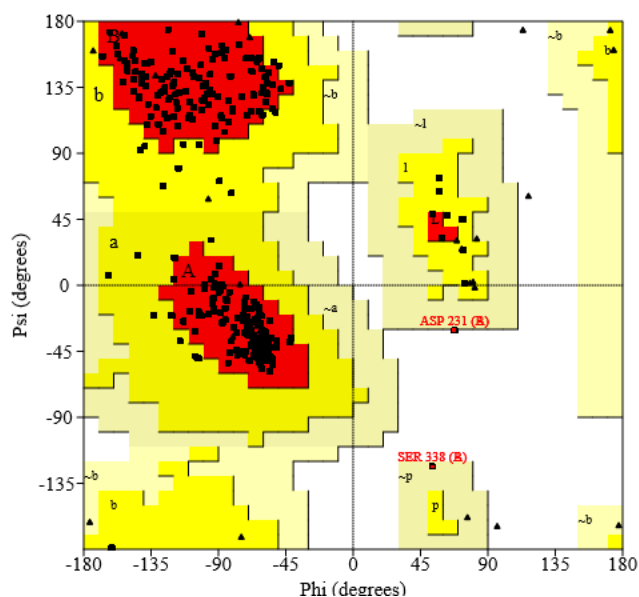


Figure S18. Ramachandran Plot of *stilbene synthase* protein in *Arachis hypogaea*. The graph shows the location of amino acid residues in the favored region of protein. For *AhSTS4*, the location of amino acids in the favored region 92.3 % forming a stable protein.

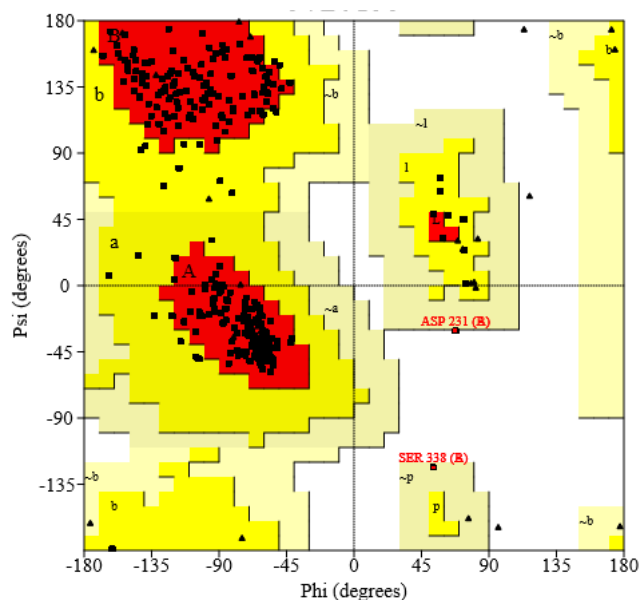


Figure S19. Ramachandran Plot of *stilbene synthase* protein in *Arachis hypogaea*. The graph shows the location of amino acid residues in the favored region of protein. For *AhSTS6*, the location of amino acids in the favored region 92.3 % forming a stable protein.

2. Hormonal Stock Solution 100 μ M MeJA

Density of MeJA = 1.03g/cm³

To find molarity of solution

MeJA in solution = 1.03 x 1000

$$= 1030\text{g/l}$$

Molarity = given mass / Molar mass

$$= 1030/244.3$$

$$= 4.5\text{M}$$

To prepare 150ml stock solution of 100 μ M MeJA

$$M_1V_1 = M_2V_2$$

$$4.5 \times 10^6 \times V_1 = 100 \times 150$$

$$V_1 = 15000/4500000$$

$$V_1 = 0.0033 \text{ ml} \times 1000$$

$$V_1 = 3.3 \mu\text{l MeJA}$$

Procedure:

1. Take 100 ml of distilled water in a sterilized beaker.
2. Place the beaker on hot plate. Pre-warm the distilled water. Add 3.3 μ l of MeJA to the water and stir the solution. Add absolute ethanol dropwise to dissolve MeJA. Keep on stirring the solution.
3. As soon as MeJA dissolves in dH₂O an insoluble transparent layer disappears. Make the volume up to 150 ml by adding warm distilled water. Place the stock solution in transparent bottle wrapped in aluminum foil in refrigerator.
4. Do not add too much alcohol as it will disturb the volume concentration.

Hormonal Stock Solution 1mM SA

1M SA is prepared by adding 138.121 g powdered SA in 1 litre water.

1mM SA is prepared by adding 138.1 mg powdered SA in 1 litre water.

To prepare 200 ml 1mM SA, 27.62mg of SA is dissolved in 200ml dH₂O.

Procedure:

- Take a clean beaker and fill it with 150 ml distilled water.
- Place the beaker on hot plate and put magnetic stirrer in the beaker.
- Pre-warm dH₂O and add SA pinch by pinch.

- Keep the magnetic stirrer on.
- A white foam is formed.
- Start adding absolute ethanol drop wise in the solution.
- SA starts dissolving. Keep the solution stirred to get smooth consistency.
- When a clear SA solution is formed add dH₂O to make up the volume to 200.

Arachis hypogaea Stilbene synthase (AhSTS1) complete CDS

ATGGTGTCTGTGAGTGAGATTCGCAAGGTTCAAAGGGCAGAAGGTCCAGCAACTGTATTGGCGATTGG
AACAGCAAATCCACCAAAGTGTGTTGATCAGAGTACATATGCAGATTATTATTTTAGAGTAACTAACAGC
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Putative promoter region *AhSTS1*

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Arachis hypogaea Stilbene synthase (AhSTS2) complete CDS

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 GCCATAAAGGAGTGGGGTCAACCAAAGTCAAAGATAACACACTTGATCTTCTGCAC
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5. Putative promoter region *AhSTS2*

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6. *Arachis hypogaea* Stilbene synthase (*AhSTS3*) complete CDS

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7. Putative promoter region *AhSTS3*

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TCC

C

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8. *Arachis hypogaea* Stilbene synthase (*AhSTS4*) complete CDS

ATGGTGTCTGCAAGTGACATCCGCAAGGTTCAAAGAGCAGAAGGTCCTGCAACCGT
CTTAGCGATTGGCACAGCAAATCCACCAAACCTGTGTTGATCAGAGCACATACGCAG
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AGCGCATTTGTGAGAGAACACAGATCAAGAACAGACATATGTATCTAACGGAAGAA
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CTTGTCCTAACAGCCATGGAGCCATCGGTGGTCTCCTTCGTGAAGTTGGACTTACA
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9. Putative promoter region *AhSTS4*

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CATA

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10. *Arachis hypogaea* Stilbene synthase (*AhSTS6*) complete CDS

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ATTAGCGATTGGCACAGCAAATCCACCAAACCTGTGTTGATCAGAGCACATATGCAG
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AGCGCATTTGTGAGAGAACACAGATCAAAAACAGATATATGTATTTAACGGAAGAA
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GCAATCAAGGAATGGGGTCAGCCAATGTCTAAAATCACACATTTGATCTTCTGCACC
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11. Putative promoter region *AhSTS6*

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