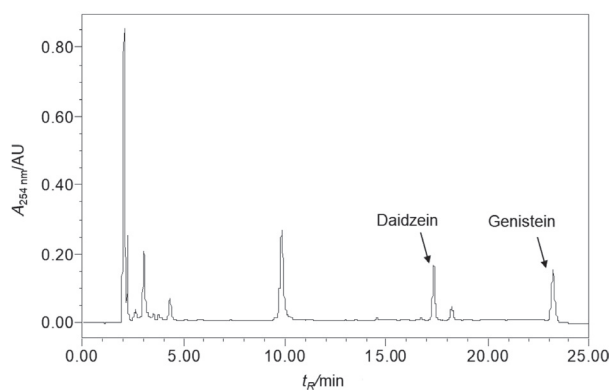
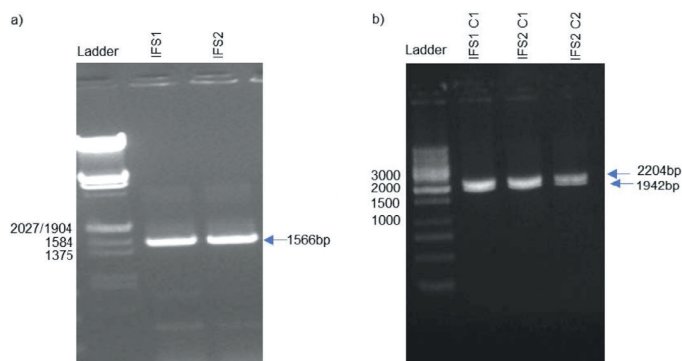


[Back to article](#)**Table S1.** Primer sequences used for quantitative-real time polymerase chain reaction (PCR) expression analysis and the cDNA cloning of isoflavone synthase IFS1 and IFS2 genes

Gene	Primer	Sequence
IFS1-qRT	F	AGAATTCGGTCCCGAGAGGTT
	R	TGCCATTCCTGAAGTAGCCAA
IFS2-qRT	F	AATGTGCCCTGGAGTCAATCTG
	R	GCGTCACCACCTTCAATAT
Actin 2/7-qRT	F	ACTTGCCCATCAGGAAGCTC
	R	TGTTACCACCTCTGCCAAG
IFS1	F	CACCATGTTGCTGGAACCTGCACTTGGT
	R	TTAAGAAAGGAGTTTAGATGCAACGCC
IFS2	F	CACCATGTTGCTGGAACCTGCACTTGGT
	R	TTAAGAAAGGAGTTTAGATGCAACGCC

[Back to article](#)**Fig. S1.** A representative chromatogram of soybean cultivar (PK1042) for isoflavone estimation. Peaks corresponding to major isoflavones, *i.e.* daidzein and genistein, are labelled[Back to article](#)**Fig. S2.** Polymerase chain reaction (PCR) amplification of isoflavone synthase isomers: a) IFS1 and IFS2 transcripts, b) PvuII restriction products (2204 and 1942 bp) of IFS1 and IFS2 cloned into the pEN-TR-D-TOPO vector

[Back to article](#)

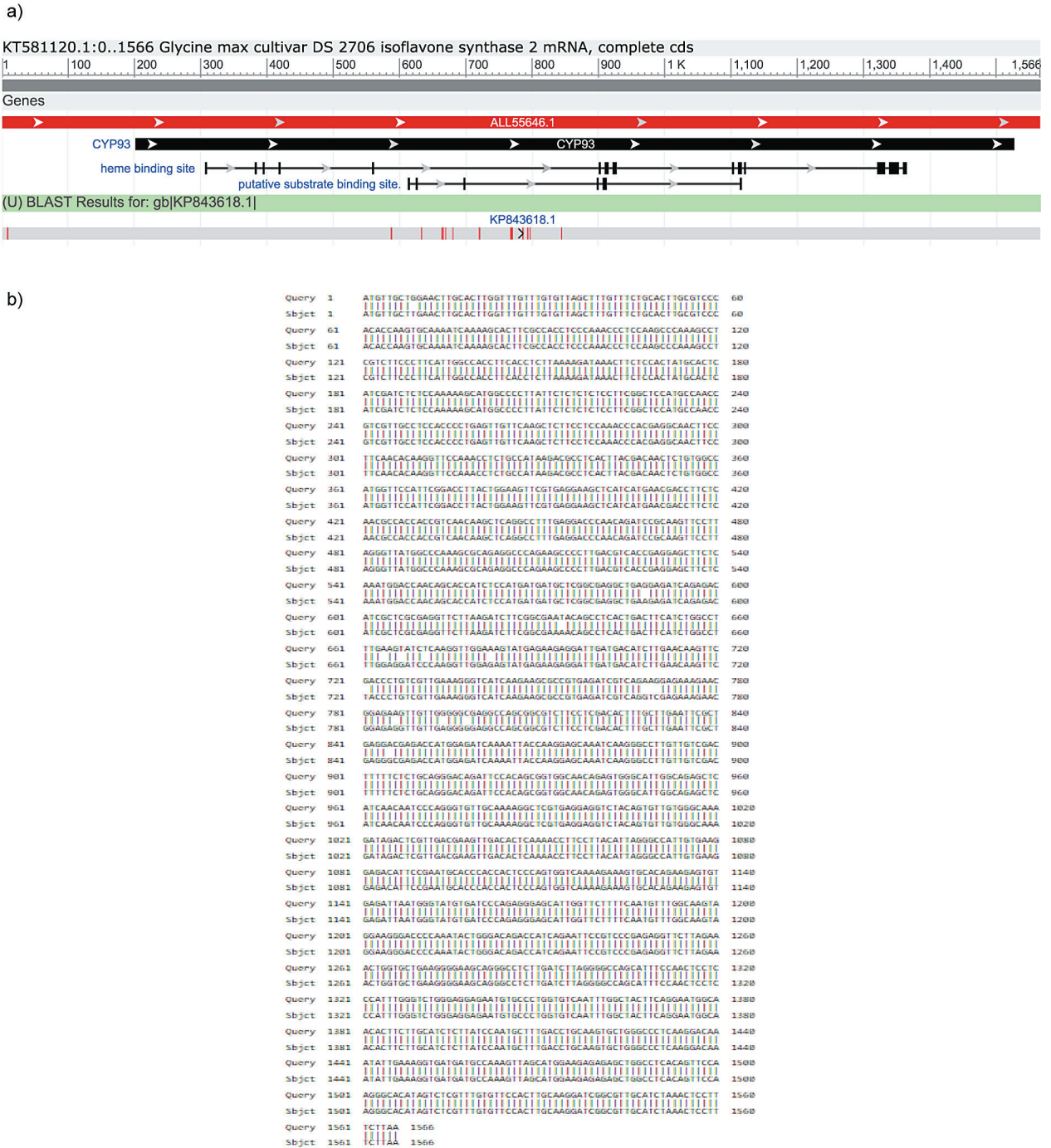


Fig. S3. Nucleotide sequence alignment of IFS1 and IFS2 coding sequences showing 99.04 % identity: a) graphical summary of the alignment, and b) sequence alignment with IFS1 as query sequence and IFS2 as subject sequence

[Back to article](#)

Query	1	MLLELALGLFVLALFLHLRPTPSAKSKALRHLNPPSPKRLPFIGHLHLKDKLLHYAL	60
Sbjct	1	MLLELALGLFVLALFLHLRPTPSAKSKALRHLNPPSPKRLPFIGHLHLKDKLLHYAL	60
Query	61	IDLSKKHGPLFSLSFGSMPTVVASTPELFLQTHEATSFNTRFQTSAIRRLTYDNSVA	120
Sbjct	61	IDLSKKHGPLFSLSFGSMPTVVASTPELFLQTHEATSFNTRFQTSAIRRLTYDNSVA	120
Query	121	MVPFGPYWKFVRKLIIMNDLLNATTVNKLRPLRTOQIRKFLRVMAQSAEAQKPLDVTEELL	180
Sbjct	121	MVPFGPYWKFVRKLIIMNDLLNATTVNKLRPLRTOQIRKFLRVMAQSAEAQKPLDVTEELL	180
Query	181	KWTNSTISMMMLGEAEIIRDIAREVLKIFGEYSLTDFIWLKYLKVGKYEKRIDDILNKF	240
Sbjct	181	KWTNSTISMMMLGEAEIIRDIAREVLKIFGENSLTDFIWLPLEDPKVGEYKRIIDDILNKF	240
Query	241	DPVVERVIKKRREIVRRKNGEVVGEASGVFLDTLLEFAEETMEIKITKEQIKGLVVD	300
Sbjct	241	YPVVERVIKKRREIVRSRKNGEVVEGEASGVFLDTLLEFAEGETMEIKITKEQIKGLVVD	300
Query	301	FFSAGTDSAVATEWALAEINNPRVLQKAREEVSVVGGKDRLVDEVDTQNLPIYIRAIVK	360
Sbjct	301	FFSAGTDSAVATEWALAEINNPRVLQKAREEVSVVGGKDRLVDEVDTQNLPIYIRAIVK	360
Query	361	ETFRMHPLPVVKRKCTEECEINGYVIEGALVLFNVWQVGRDPKYWDRPSEFRPERFLE	420
Sbjct	361	ETFRMHPLPVVKRKCTEECEINGYVIEGALVLFNVWQVGRDPKYWDRPSEFRPERFLE	420
Query	421	TGAEGEAGPLDLRGQHFQLLPFGSRRMCPGVNLATSGMATLLASLIQCFDLQVLGPQGQ	480
Sbjct	421	TGAEGEAGPLDLRGQHFQLLPFGSRRMCPGVNLATSGMATLLASLIQCFDLQVLGPQGQ	480
Query	481	ILKGDDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS	521
Sbjct	481	ILKGDDAKVSMEERAGLTVPRAHSLVCVPLARIGVASKLLS	521

Fig. S4. Sequence alignment of isoflavone synthase IFS1 and IFS2 proteins showing 98.27 % identity

[Back to article](#)

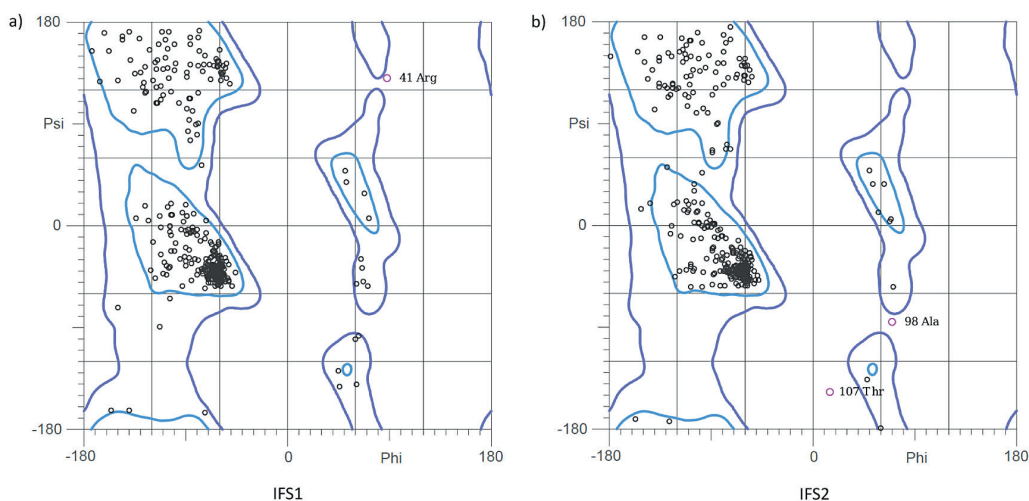


Fig. S5. Ramachandran plot generated on the RoseTTAFold (25) for isoflavone synthase: a) IFS1 and b) IFS2 3D models

Back to article

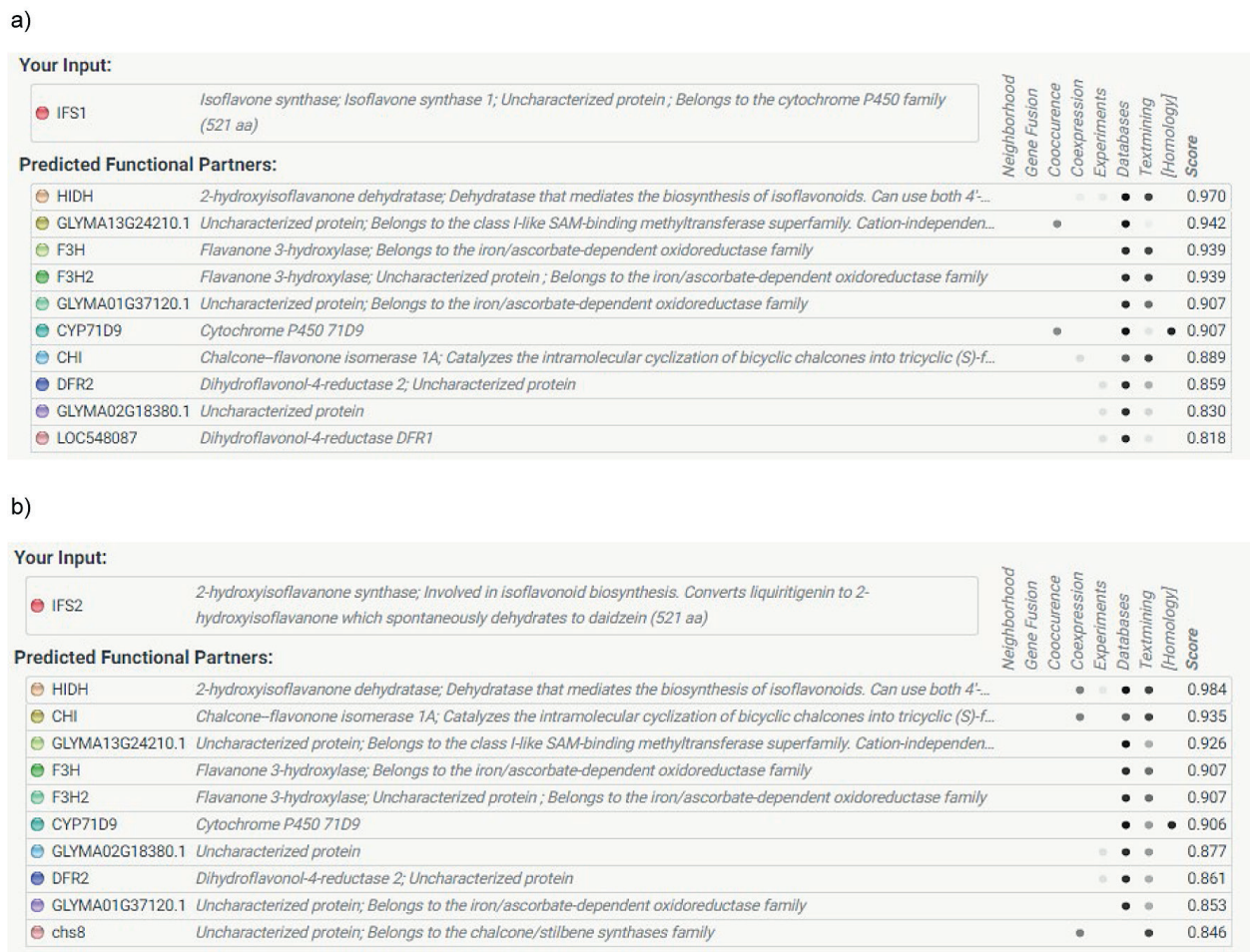


Fig. S6. STRING scores for isoflavone synthase isomers: a) IFS1 and b) IFS2 with different proteins