

Figure S1. (A) Standard chromatogram mixture of daidzein (1), glycitin (2), genistin (3), daidzin (4), and genistein (5) (B), The chromatogram of SER and MEL treatments (E) in 100 μ M at 254 nm by HPLC method.

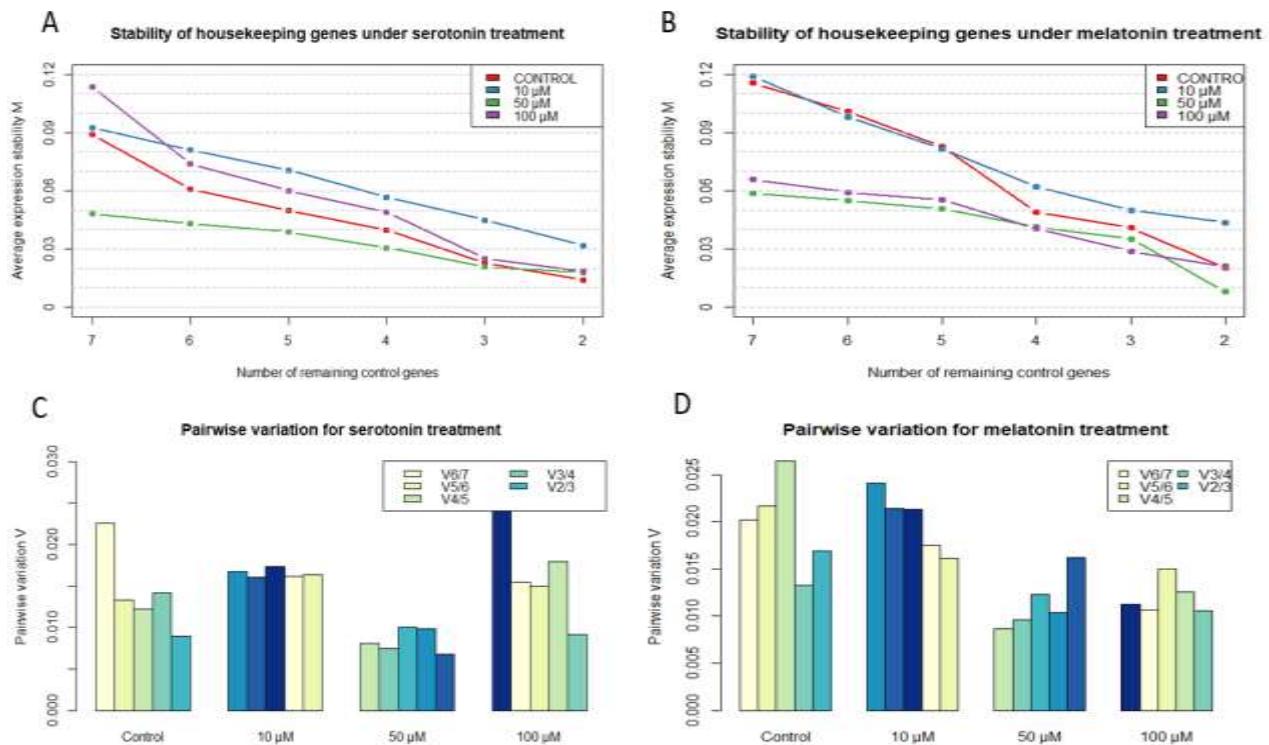


Figure S2. Expression stability of the seven reference genes in response of (A) SER and (B) MEL treatments of soybean suspension culture at different time intervals. Y-axis represents the average expression stability (M) values analysed by geNorm. Evaluation of optimal number of reference genes for effective normalization. Pairwise variation in (C) SER and (D) MEL treatments was performed by the geNorm program to determine the optimal number of reference genes, and carried out for qPCR data normalization in various sample

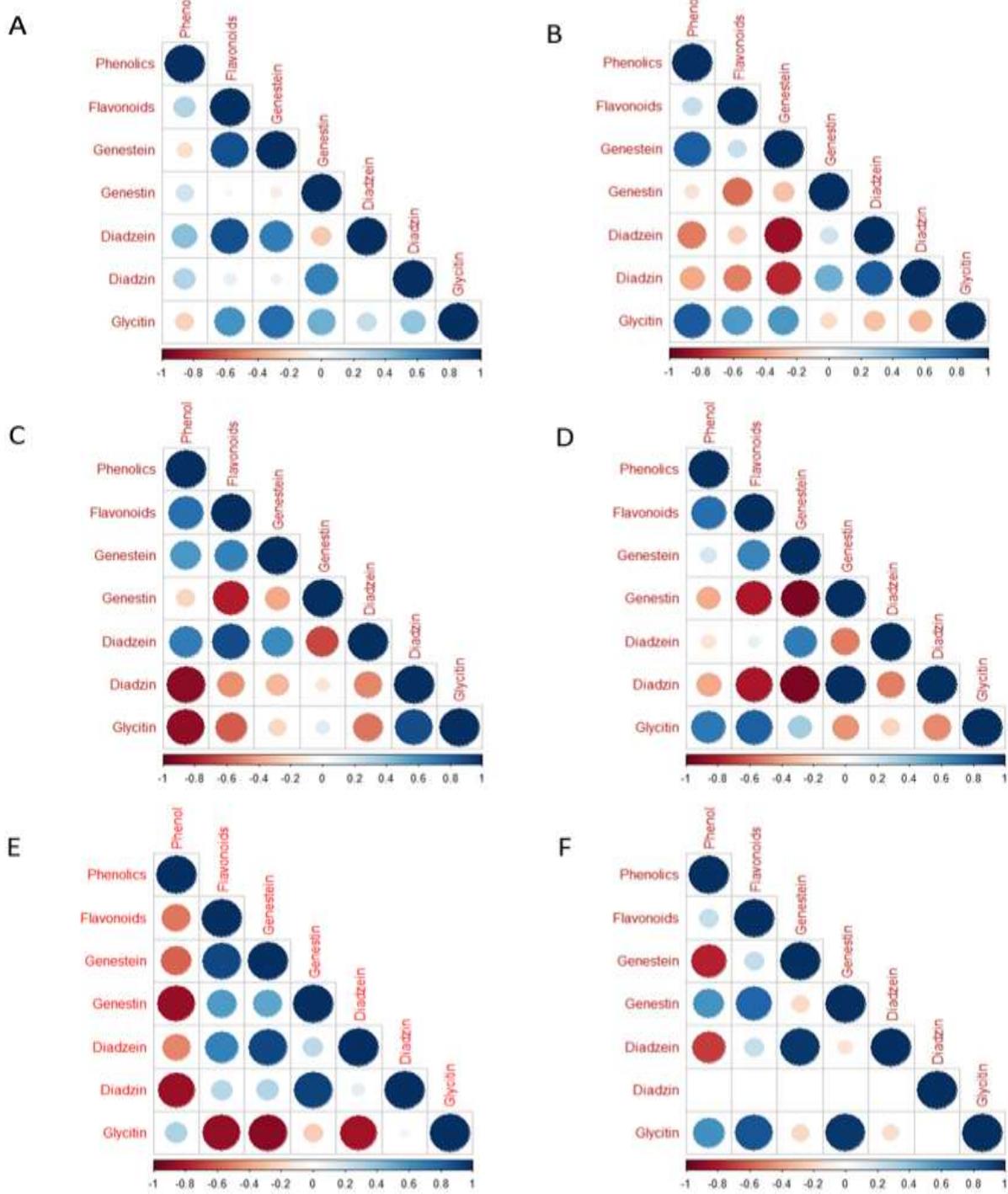


Figure S3. Correlation matrix of total phenolic, total flavonoid and isoflavones under SER treatment at (A) 24 h, (C) 48 h and (E) 72 h, and MEL treatment at (B) 24 h, (D) 48 h and (F) 72 h. The color and the shape of each dot in the triangular matrix show the strength of Pearson correlation (positive or negative) between metabolites. Positive strong correlations are in dark blue. Lighter colors indicate the weaker relations between the metabolites.

Table. S1 List of reference and biosynthesis genes used in qPCR.

Primer name	Sequence (5'-3')	Accession ID
Elongation factor1B	TGA GAT GCC TGG TTT ATT GTG G CTC AAC TGT CAA GCG TTC CT	Glyma.02g276600
Ubiquitin family (UBQ-F)	CAT TGG CGA TGA GCG TTT C ATC CAG ACA CTG TAT TTT CTC TCC	Glyma07g32020
18s	CCA GAC ATA GTA AGG TTG ACA GAC ATC GCT CCA CCA ACT AAG AAC	X02623.1
60s Ribosomal protein	AAA GTG GAC CAA GGC ATA TCG TCG TCA GGA CAT TCT CCG CAA GAT TCC	Glyma17g05270
Glucose-6-phosphate dehydrogenase	ACT CCT TGA TAC CGT TGT CCA T GTT TGT TAT CCG CCT ACA GCC T	Glyma19g24250
elongationfactor1A	GAC CTT CTT CGT TTC TCG CA GA ACC TCT CAA TCA CAC G	Glyma19g07240
Actin	ATC TTG ACT GAG CGT GGT TAT TCC GCT GGT CCT GGC TGT CTC C	Glyma18g52780
Ubiquitin-conjugating enzyme E2	GAG CGA GCA GTT TCA GAC CAT AGG AGG GAC GAT ACG	Glyma18g44850
Transcription factor MYBJ3	GAC GAC AAC AAC AAT GGA GAC CAA GGA GTC AAG GGC ATA CT	Glyma.06G193600
Phenylalanine ammonia- lyase	TGC CTT CAA ATC TCA CTG CTA CAT CCT GGT TGT GTT GCT C	Glyma.03g181600
Isoflavone synthase	ACT GTT CCA AGG GCA CAT AG GAA TGA GAC CTT ATT GAA ATG ATG	Glyma.13G173500
Chalcone synthase	GAA TGG GGT GTG TTG TTC G AAG CAA GTT TGA AAA GTG GTA CAC	Glyma.13G173500
Chalcone reductase	TTG ACT GGG CAT TGA CTG AA GCG AGT TGT GGT TTG GTG	Glyma.02G307300
SNAT-2	GCT CAA GGC TGG ATT TTG G GGC AGA GGT TCT TCG TCT TC	Glyma.18G216900
SNAT-1	GAA GAC GAA GAA CCT CTG CC ATC ATA AAC ATC AAC ATC TCC ACC TG	Glyma.09G272400
ASMT-2	TGA CAC TAC ACC ATT TGA AAC GG AAT GAC TCC AAT CCC ATG AAC ATT C	Glyma.14G201100

ASMT-1	GTC TCT TCA ATG AGG CTA TGG C TTC CAC CAC CAA CAT CCA C	Glyma.10G176600
S-adenosylmethionine synthetase	GAG TGG TGC CTA CAT TGT GAG ATC TTC CCA GTG CCA TAA GTG	Glyma15g21890
S-adenosylmethionine synthetase-1	GAT GCT GGT CTC ACT GGA AG CAT TTG CCA CGA CAC TCT TTG	Glyma03g38190
Nonexpresser of PR genes	TGC TGT TAG TAT TTG TAG GAG G TGG GAA GAC ATA CAG GCA TC	Glyma.09g020800
Abscisic aldehyde oxidase2	TAA CCT ATT GAT TGG CAG TCC T GCT CCC CAG ATG ACA GTA AG	Glyma.02g272200
abscisic aldehyde oxidase-14	AAC CCA CTT CTT GAC GCT TC GCT CAC CAA CAG GAT GAT AGT C	Glyma.14g045100
Aminocyclopropane carboxylate oxidase1	ATC TCC ATT GCC ACC TTC TA GAG CCT TTT CAC CGA ACT TG	Glyma05g36310
Allene Oxide Synthase-2	CGG AAA AGA CTT CGT CAC CTT AAG TAA TAG TAA CGG AAG AAC CC	Glyma.17g246500
Melatonin 2-hydroxylase	ATC ACC AAA GTC CCA GAA CG ACG CAT GAT CCA GCT TCT CT	Glyma.02G124700
1-Aminocyclopropane-1-Carboxylic Acid Oxidase	ATC TCC ATT GCC ACC TTC TA GAG CCT TTT CAC CGA ACT TG	Glyma.05G222400

Table. S2 Ranking of candidate reference genes by geNorm analysis using comparative Ct method, and overall rank under SER treatment

Rank	Control	10 µM	50 µM	100 µM
1	<i>60s</i>	<i>ELF</i>	<i>ELF</i>	<i>ACT</i>
1	<i>UBQ.E</i>	<i>UBQ.E</i>	<i>UBQ.F</i>	<i>UBQ.F</i>
2	<i>G6PD</i>	<i>UBQ.F</i>	<i>18s</i>	<i>UBQ.E</i>
3	<i>UBQ.F</i>	<i>60s</i>	<i>G6PD</i>	<i>G6PD</i>
4	<i>ELF</i>	<i>ACT</i>	<i>ACT</i>	<i>18s</i>
5	<i>ACT</i>	<i>G6PD</i>	<i>UBQ.E</i>	<i>ELF</i>
6	<i>18s</i>	<i>18s</i>	<i>60s</i>	<i>60s</i>
M-value				
	0.013976099	0.017950858	0.031763079	0.018682658

Table. S3 Ranking of candidate reference genes by geNorm analysis using comparative Ct method, and overall rank under MEL treatment.

Rank	Control	10 µM	50 µM	100 µM
1	<i>60s</i>	<i>60s S4</i>	<i>60s</i>	<i>18s</i>
1	<i>UBQ.F</i>	<i>UBQ.E</i>	<i>UBQ.E</i>	<i>ACT</i>
2	<i>G6PD</i>	<i>ACT</i>	<i>ACT</i>	<i>60s</i>
3	<i>ELF</i>	<i>G6PD</i>	<i>G6PD</i>	<i>G6PD</i>
4	<i>ACT</i>	<i>18S</i>	<i>ELF</i>	<i>ELF</i>
5	<i>UBQ.E</i>	<i>UBQ.F</i>	<i>UBQ.F</i>	<i>UBQ.E</i>
6	<i>18s</i>	<i>ELF</i>	<i>18s</i>	<i>UBQ.F</i>
M-value				
	0.02030994	0.008124994	0.0436865	0.020979381

Table. S4 The expression raw data of sample, concentration, condition, gene, fold-change, p-value, false discovery rate (fdr), and log2FC used for volcano plot in [Figure 6](#)

sample	concentration	condition	Gene	fold.change	p.value	fdr	log2FC
1a	10 μM	SER	PAL	0.46	1.75E-02	0.0249933	- 1.1202942
1b	10 μM	SER	IFS	7.92	4.79E-03	0.0087923	2.9855004
1c	10 μM	SER	CHS	0.01	9.99E-05	0.0020551	- 6.6438562
1d	10 μM	SER	CHR	4.31	3.69E-03	0.0072789	2.1076879
1e	10 μM	SER	MYBJ	4.33	1.41E-03	0.0043476	2.114367
1f	10 μM	SER	SNAT-2	0.46	4.01E-02	0.0511136	- 1.1202942
1g	10 μM	SER	SNAT-1	0.5	5.58E-03	0.0098043	-1
1h	10 μM	SER	ASMT-2	0.63	8.11E-02	0.0965633	- 0.6665763
1i	10 μM	SER	ASMT-1	0.65	1.05E-02	0.0160941	- 0.6214884
1j	10 μM	SER	SAMS	23.85	7.81E-04	0.0030403	4.5759174
1k	10 μM	SER	SAMS-1	8.97	1.34E-03	0.0042504	3.165108
1l	10 μM	SER	NPR	3.28	1.85E-03	0.0046762	1.7136958
1m	10 μM	SER	AAO-2	0.65	4.61E-03	0.0085015	- 0.6214884
1n	10 μM	SER	AAO-14	0.4	1.36E-02	0.0200718	- 1.3219281
1o	10 μM	SER	AOS	0.33	4.96E-03	0.0090447	- 1.5994621
1p	10 μM	SER	M2H	0.61	6.57E-01	0.6756686	- 0.7131189
2a	50 μM	SER	PAL	0.1	2.20E-03	0.0051864	- 3.3219281
2b	50 μM	SER	IFS	5.23	2.85E-03	0.0060123	2.386811
2c	50 μM	SER	CHS	0.05	2.00E-03	0.0049206	- 4.3219281
2d	50 μM	SER	CHR	0.29	1.88E-02	0.0264117	- 1.7858752
2e	50 μM	SER	MYBJ	0.37	2.46E-02	0.0336686	- 1.4344028
2f	50 μM	SER	SNAT-2	0.11	2.30E-04	0.0023637	- 3.1844246
2g	50 μM	SER	SNAT-1	0.19	4.18E-04	0.0024384	- 2.3959287
2h	50 μM	SER	ASMT-2	0.06	7.50E-04	0.0030403	- 4.0588937
2i	50 μM	SER	ASMT-1	0.15	5.63E-03	0.0098234	- 2.7369656
2j	50 μM	SER	SAMS	1.62	3.59E-02	0.0466999	0.6959938
2k	50 μM	SER	SAMS-1	1.01	9.74E-01	0.9843537	0.0143553
2l	50 μM	SER	NPR	0.37	1.80E-03	0.0046762	- 1.4344028
2m	50 μM	SER	AAO-2	0.31	1.92E-03	0.0048109	- 1.6896599

2n	50 µM	SER	AAO-14	0.32	2.67E-03	0.0058211	-	1.6438562
2o	50 µM	SER	AOS	0.08	1.46E-03	0.00442	-	3.6438562
2p	50 µM	SER	M2H	0.28	1.78E-01	0.1968369	-	1.8365013
3a	100 µM	SER	PAL	0.87	7.57E-01	0.7698657	-	0.2009127
3b	100 µM	SER	IFS	23.59	9.50E-04	0.0032967	4.5601035	
3c	100 µM	SER	CHS	0.11	2.81E-03	0.0060123	-	3.1844246
3d	100 µM	SER	CHR	0.21	2.92E-03	0.006013	-	2.2515388
3e	100 µM	SER	MYBJ	6.43	2.41E-03	0.0054405	2.6848187	
3f	100 µM	SER	SNAT-2	2.82	9.39E-03	0.0146226	1.4956952	
3g	100 µM	SER	SNAT-1	5.05	3.85E-03	0.0074977	2.3362834	
3h	100 µM	SER	ASMT-2	1.26	1.71E-01	0.1903691	0.3334237	
3i	100 µM	SER	ASMT-1	3.55	1.75E-02	0.0249933	1.827819	
3j	100 µM	SER	SAMS	12.74	1.60E-03	0.0045538	3.6712934	
3k	100 µM	SER	SAMS-1	3.22	1.06E-02	0.0162383	1.6870607	
3l	100 µM	SER	NPR	2.84	6.54E-03	0.0107696	1.5058909	
3m	100 µM	SER	AAO-2	3.67	4.57E-04	0.0024384	1.8757801	
3n	100 µM	SER	AAO-14	2.31	3.77E-03	0.0073822	1.2078929	
3o	100 µM	SER	AOS	4.87	2.13E-03	0.0051031	2.2839218	
3p	100 µM	SER	M2H	2.39	1.21E-01	0.1375115	1.2570106	
4a	10 µM	SER	PAL	0.84	2.24E-02	0.0310708	-	0.2515388
4b	10 µM	SER	IFS	6.52	4.37E-04	0.0024384	2.704872	
4c	10 µM	SER	CHS	7.36	4.24E-04	0.0024384	2.8797058	
4d	10 µM	SER	CHR	9.67	1.77E-03	0.0046762	3.2735159	
4e	10 µM	SER	MYBJ	0.25	7.99E-03	0.0127952	-2	
4f	10 µM	SER	SNAT-2	0.44	1.24E-02	0.0187275	-	1.1844246
4g	10 µM	SER	SNAT-1	0.5	5.91E-03	0.0100681	-1	
4h	10 µM	SER	ASMT-2	0.25	4.51E-04	0.0024384	-2	
4i	10 µM	SER	ASMT-1	0.49	5.10E-04	0.0026239	-	1.0291464
4j	10 µM	SER	SAMS	16.26	1.34E-04	0.0021536	4.0232554	
4k	10 µM	SER	SAMS-1	4.21	1.57E-03	0.0045538	2.0738202	
4l	10 µM	SER	NPR	2.52	2.67E-02	0.0362717	1.3334237	
4m	10 µM	SER	AAO-2	0.65	3.62E-02	0.0466999	-	0.6214884
4n	10 µM	SER	AAO-14	0.65	1.53E-01	0.1709023	-	0.6214884
4o	10 µM	SER	AOS	0.09	1.42E-03	0.0043476	-	3.4739312
4p	10 µM	SER	M2H	0.53	9.99E-01	1	-	0.9159357
5a	50 µM	SER	PAL	0.21	6.50E-04	0.0029264	-	2.2515388
5b	50 µM	SER	IFS	88.13	1.25E-04	0.0021536	6.4615613	

5c	50 µM	SER	CHS	1.95	5.32E-03	0.0095778	0.9634741
5d	50 µM	SER	CHR	134.78	2.90E-04	0.0023637	7.0744626
5e	50 µM	SER	MYBJ	0.95	5.35E-01	0.5602909	- 0.0740006
5f	50 µM	SER	SNAT-2	0.23	1.25E-03	0.0040644	- 2.1202942
5g	50 µM	SER	SNAT-1	0.37	1.78E-03	0.0046762	- 1.4344028
5h	50 µM	SER	ASMT-2	0.17	8.34E-04	0.0031231	- 2.5563934
5i	50 µM	SER	ASMT-1	0.35	9.41E-04	0.0032967	- 1.5145732
5j	50 µM	SER	SAMS	34.79	3.36E-04	0.0023637	5.1206008
5k	50 µM	SER	SAMS-1	10.45	9.40E-05	0.0020551	3.385431
5l	50 µM	SER	NPR	1.57	1.57E-02	0.022765	0.6507646
5m	50 µM	SER	AAO-2	0.27	4.11E-03	0.0078893	- 1.8889687
5n	50 µM	SER	AAO-14	0.17	1.74E-03	0.0046762	- 2.5563934
5o	50 µM	SER	AOS	0.03	6.91E-04	0.003014	- 5.0588937
5p	50 µM	SER	M2H	0.12	2.42E-03	0.0054405	- 3.0588937
6a	100 µM	SER	PAL	7.31	2.10E-04	0.0023637	2.8698714
6b	100 µM	SER	IFS	842.84	4.51E-05	0.0020551	9.719115
6c	100 µM	SER	CHS	85.97	1.09E-04	0.002087	6.4257614
6d	100 µM	SER	CHR	2516.3	1.69E-04	0.0023637	11.297088
6e	100 µM	SER	MYBJ	6.79	9.75E-05	0.0020551	2.7634116
6f	100 µM	SER	SNAT-2	4.92	6.16E-03	0.0102531	2.2986583
6g	100 µM	SER	SNAT-1	5.01	1.75E-03	0.0046762	2.3248106
6h	100 µM	SER	ASMT-2	1.42	4.19E-02	0.0531341	0.5058909
6i	100 µM	SER	ASMT-1	3.24	8.54E-02	0.1008236	1.6959938
6j	100 µM	SER	SAMS	43.03	3.89E-04	0.0024384	5.4272709
6k	100 µM	SER	SAMS-1	232.81	6.04E-04	0.0028174	7.8630092
6l	100 µM	SER	NPR	15.02	3.88E-04	0.0024384	3.9088129
6m	100 µM	SER	AAO-2	4.83	1.03E-03	0.0034865	2.2720232
6n	100 µM	SER	AAO-14	7.36	7.80E-04	0.0030403	2.8797058
6o	100 µM	SER	AOS	3.15	3.06E-04	0.0023637	1.6553518
6p	100 µM	SER	M2H	1.77	4.00E-02	0.0511136	0.8237494
7a	10 µM	SER	PAL	0.24	1.23E-03	0.0040644	- 2.0588937
7b	10 µM	SER	IFS	7.39	2.06E-03	0.0050122	2.8855744
7c	10 µM	SER	CHS	10.15	3.32E-04	0.0023637	3.3434078
7d	10 µM	SER	CHR	12.97	2.73E-04	0.0023637	3.6971066
7e	10 µM	SER	MYBJ	0.38	2.92E-03	0.006013	- 1.3959287
7f	10 µM	SER	SNAT-2	0.79	1.79E-01	0.1970759	- 0.3400754
7g	10 µM	SER	SNAT-1	0.61	5.45E-02	0.0673154	- 0.7131189

7h	10 µM	SER	ASMT-2	0.1	1.59E-03	0.0045538	-	3.3219281
7i	10 µM	SER	ASMT-1	2.74	5.75E-03	0.0099645	1.4541759	
7j	10 µM	SER	SAMS	3.34	1.79E-03	0.0046762	1.7398481	
7k	10 µM	SER	SAMS-1	2.95	9.12E-03	0.0143449	1.560715	
7l	10 µM	SER	NPR	2.02	2.73E-02	0.0367133	1.0143553	
7m	10 µM	SER	AAO-2	0.43	3.89E-03	0.0075247	-	1.2175914
7n	10 µM	SER	AAO-14	1.14	3.07E-01	0.3322827	0.1890338	
7o	10 µM	SER	AOS	0.76	2.30E-02	0.0316387	-	0.3959287
7p	10 µM	SER	M2H	0.54	1.00E+00	1	-	0.8889687
8a	50µM	SER	PAL	0.13	3.48E-03	0.0069021	-	2.9434165
8b	50 µM	SER	IFS	2.4	2.86E-03	0.0060123	1.2630344	
8c	50 µM	SER	CHS	2.06	5.78E-03	0.0099645	1.0426443	
8d	50 µM	SER	CHR	4.24	2.80E-03	0.0060123	2.0840643	
8e	50 µM	SER	MYBJ	0.19	4.60E-03	0.0085015	-	2.3959287
8f	50 µM	SER	SNAT-2	0.3	4.42E-03	0.0083256	-	1.7369656
8g	50 µM	SER	SNAT-1	0.23	9.10E-04	0.0032965	-	2.1202942
8h	50 µM	SER	ASMT-2	0.07	1.57E-03	0.0045538	-	3.8365013
8i	50 µM	SER	ASMT-1	0.75	1.53E-01	0.1709023	-	0.4150375
8j	50 µM	SER	SAMS	7.02	2.60E-03	0.0057072	2.811471	
8k	50 µM	SER	SAMS-1	8.59	1.84E-03	0.0046762	3.1026581	
8l	50 µM	SER	NPR	2.59	5.41E-03	0.0096686	1.3729521	
8m	50 µM	SER	AAO-2	0.23	1.96E-02	0.0274439	-	2.1202942
8n	50 µM	SER	AAO-14	0.37	1.84E-03	0.0046762	-	1.4344028
8o	50 µM	SER	AOS	0.21	1.35E-04	0.0021536	-	2.2515388
8p	50 µM	SER	M2H	0.15	8.30E-02	0.0983111	-	2.7369656
9a	100 µM	SER	PAL	1.15	4.24E-01	0.4517333	0.2016339	
9b	100 µM	SER	IFS	58.42	9.16E-04	0.0032965	5.8683905	
9c	100 µM	SER	CHS	36.93	9.37E-04	0.0032967	5.2067214	
9d	100 µM	SER	CHR	72.9	3.18E-04	0.0023637	6.1878469	
9e	100 µM	SER	MYBJ	2.71	2.39E-03	0.0054405	1.4382929	
9f	100 µM	SER	SNAT-2	5.25	7.58E-04	0.0030403	2.3923174	
9g	100 µM	SER	SNAT-1	2.66	5.97E-03	0.0100766	1.4114263	
9h	100 µM	SER	ASMT-2	2.36	9.56E-03	0.0147995	1.2387869	
9i	100 µM	SER	ASMT-1	7.61	2.46E-04	0.0023637	2.9278965	
9j	100 µM	SER	SAMS	21.26	5.48E-04	0.0026725	4.4100697	
9k	100 µM	SER	SAMS-1	18.93	5.42E-04	0.0026725	4.2426025	
9l	100 µM	SER	NPR	11.14	6.44E-06	0.0018547	3.4776773	

9m	100 µM	SER	AAO-2	3.32	8.12E-03	0.0129186	1.7311832
9n	100 µM	SER	AAO-14	5.09	4.44E-04	0.0024384	2.3476657
9o	100 µM	SER	AOS	4.9	1.55E-04	0.002351	2.2927818
9p	100 µM	SER	M2H	2.7	1.12E-01	0.1289689	1.4329594