

Supplementary Materials:

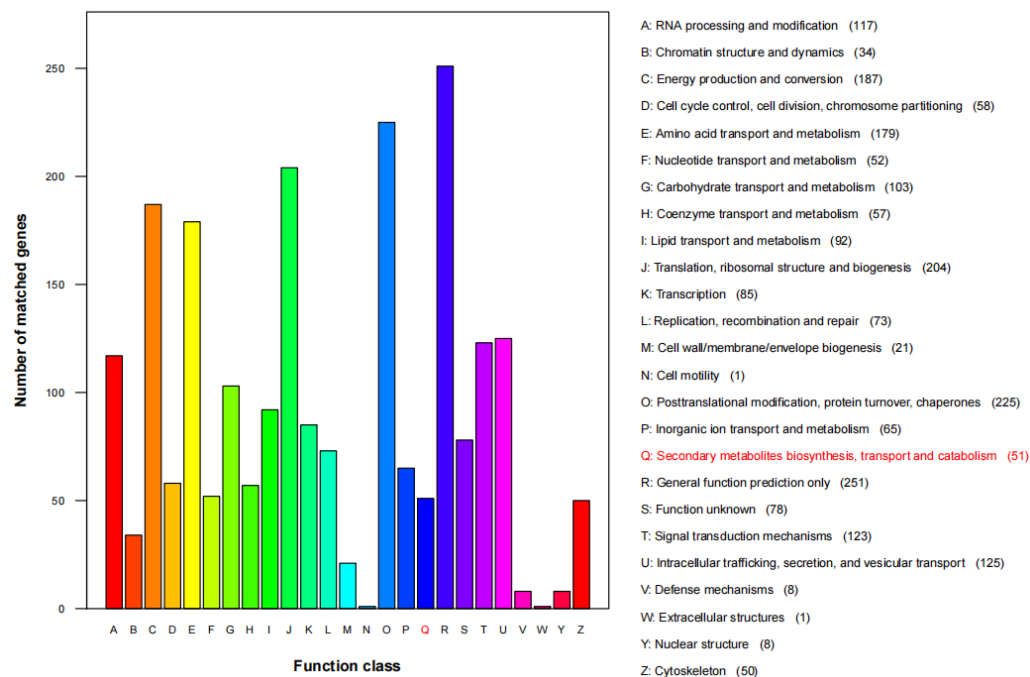


Figure S1. KOG distribution of predicted proteins from *Eurotium cristatum* E1 genome. KOG categories are as follows. M, O, T, U, V, W, Y and Z belong to cellular processes and signaling. A, B, J, K and L belong to information storage and processing. C, D, E, F, G, H, I, P and Q belong to metabolism. R and S belong to poorly characterized.

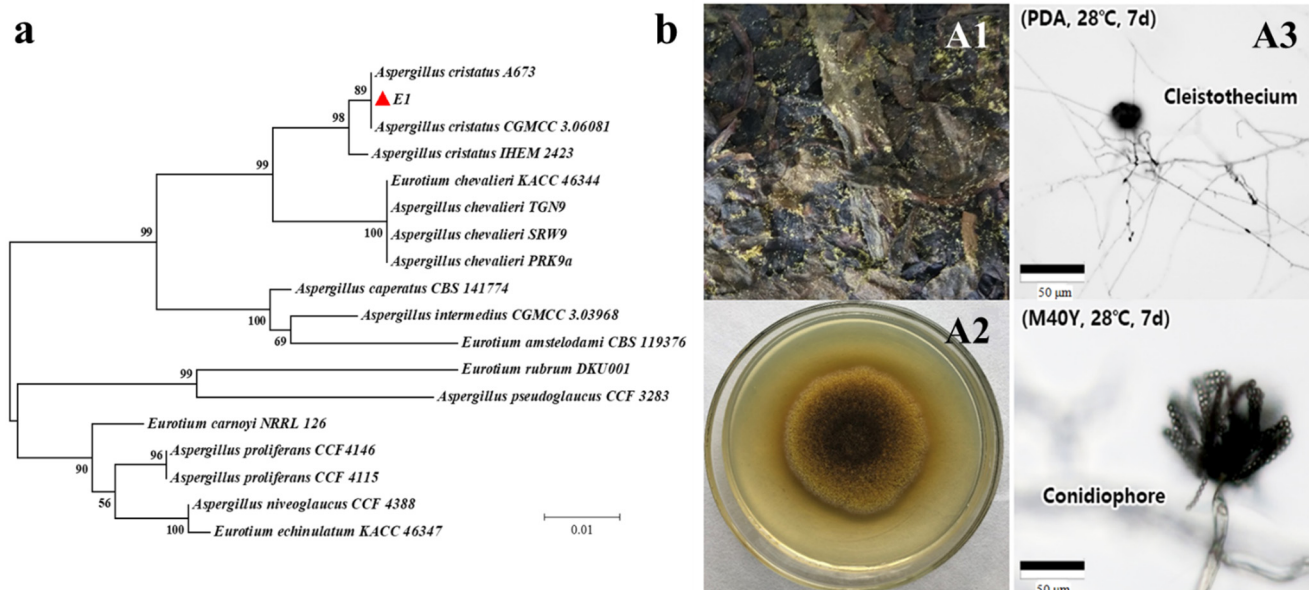


Figure S2. Confirmation of the taxonomic classification of *Eurotium cristatum* E1. (a) Phylogenetic tree. *E. cristatum* E1 sequence was compared with fragments of the partial β -tubulin (*BenA*), calmodulin (*CaM*) and RNA polymerase II second largest subunit (*RPB2*) genes of 18 *Aspergillus* species and *Eurotium* species retrieved from GenBank. [The phylogenetic tree was constructed by MEGA 5.05 based on Neighbor-Joining method.](#) Detail information of the sequences used in phylogenetic tree can be found in Supplementary Table S1. (b) Morphological characteristics of *E. cristatum* E1 isolated from Fuzhuan brick tea. (A1) A piece of Fuzhuan brick-tea with "Jinhua" (yellow dots) visible to the naked eye; (A2) Single colony grown on PDA agar in a 7 cm petri dish at 28 °C for 9 days; (A3) Microscopic image of cleistothecium and conidiophore (×200).

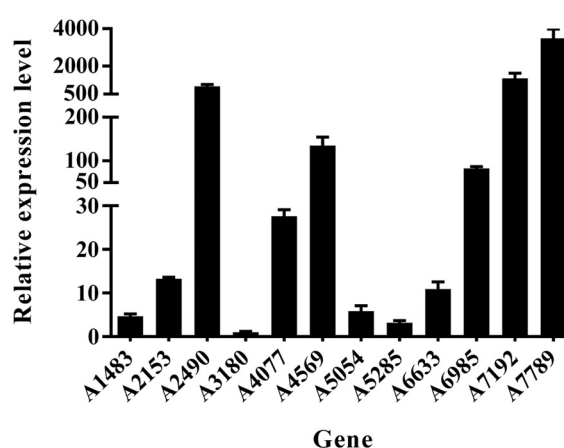


Figure S3. Real-time RT-PCR analysis of the PKS genes in *Eurotium cristatum* E1. Relative expression of the PKS genes in *E. cristatum* E1 was incubated in PDA medium for 5 days at 28 °C. β -actin was used as the reference gene. The error bars indicate the standard deviations of three independent repetitions.

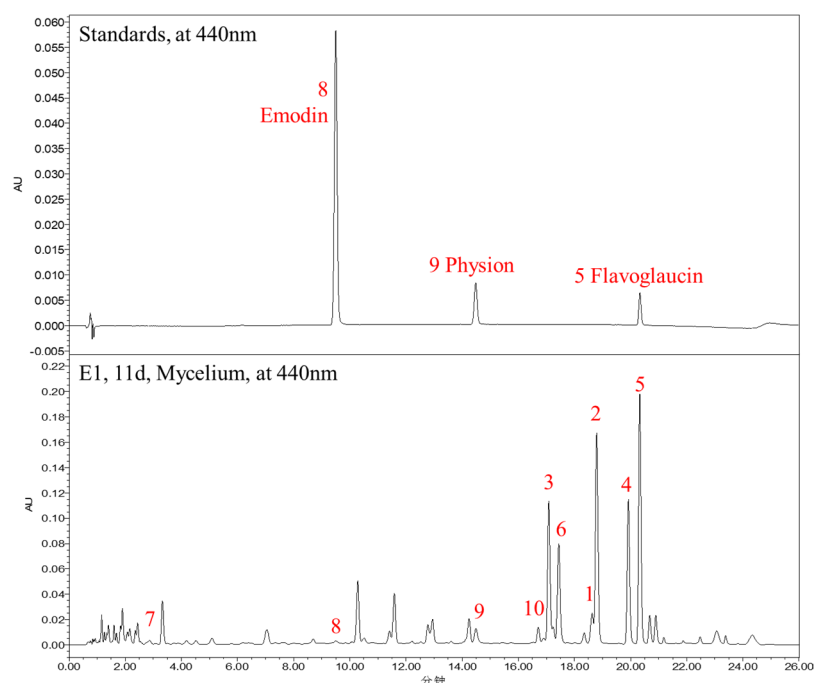


Figure S4. UPLC analysis of *Eurotium cristatum* E1 extracts. The strains were cultivated in PDA medium for 11 days at 28 °C.

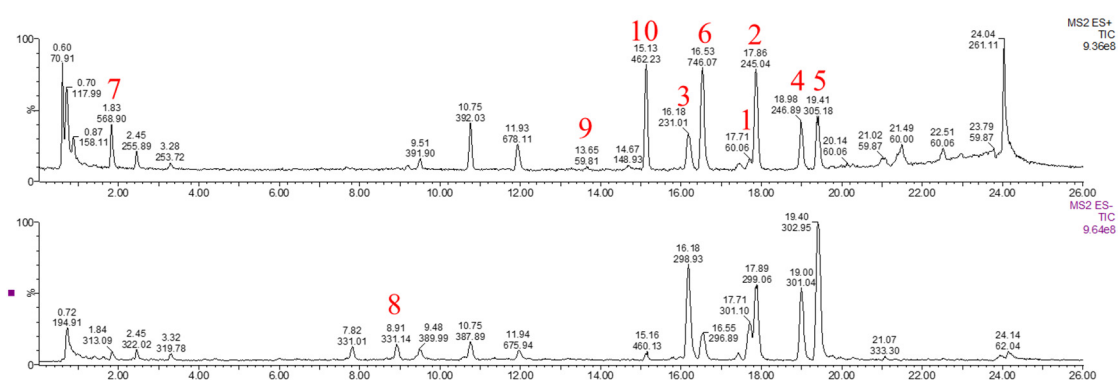


Figure S5. UPLC-MS analysis of *Eurotium cristatum* E1 extracts. The strains were cultivated in PDA medium for 11 days at 28 °C.

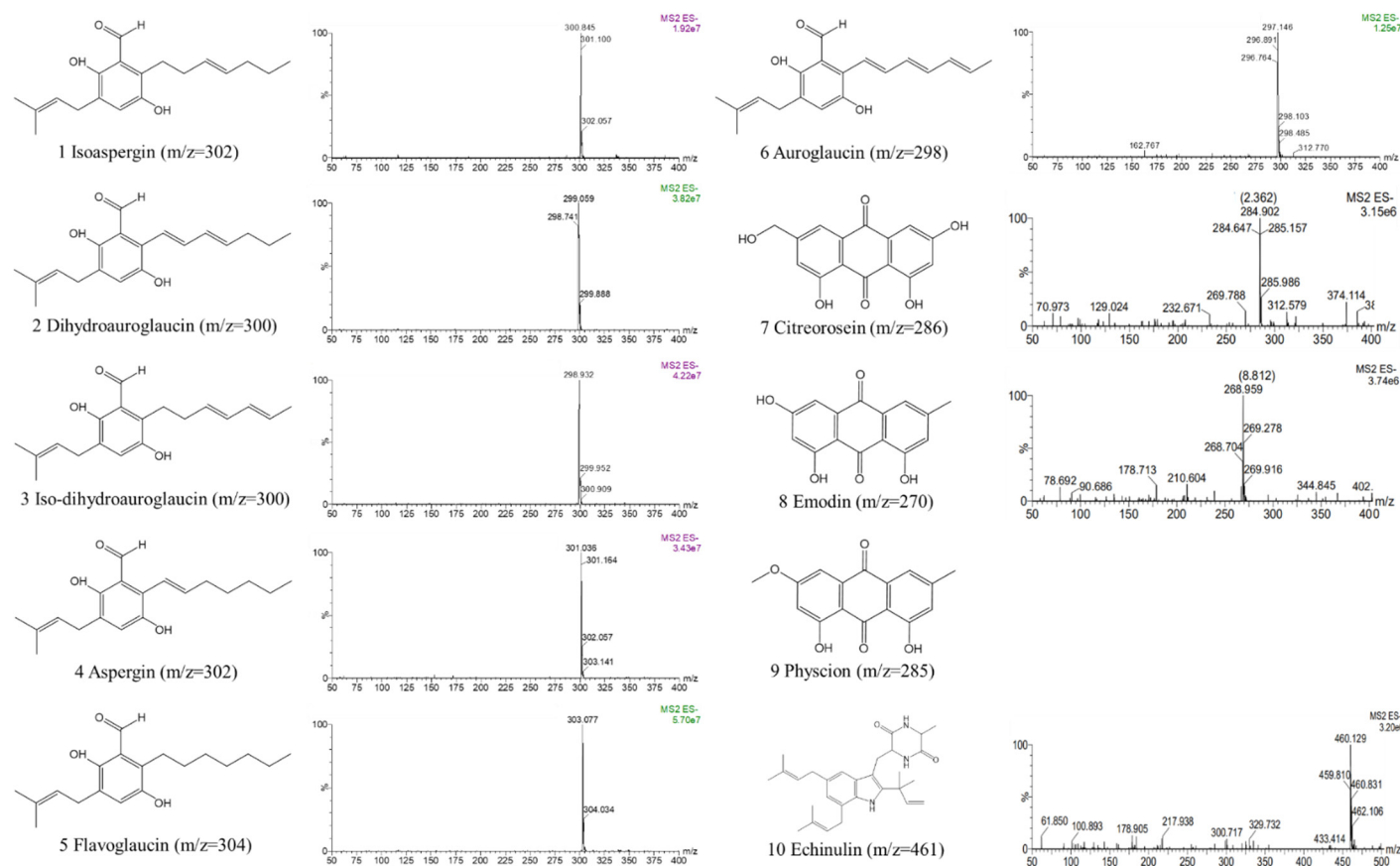


Figure S6. ESIMS spectra in negative mode of flavoglaucin and its derivatives (1-6), citreorosein (7), emodin (8), physcion (9) and echinulin (10).

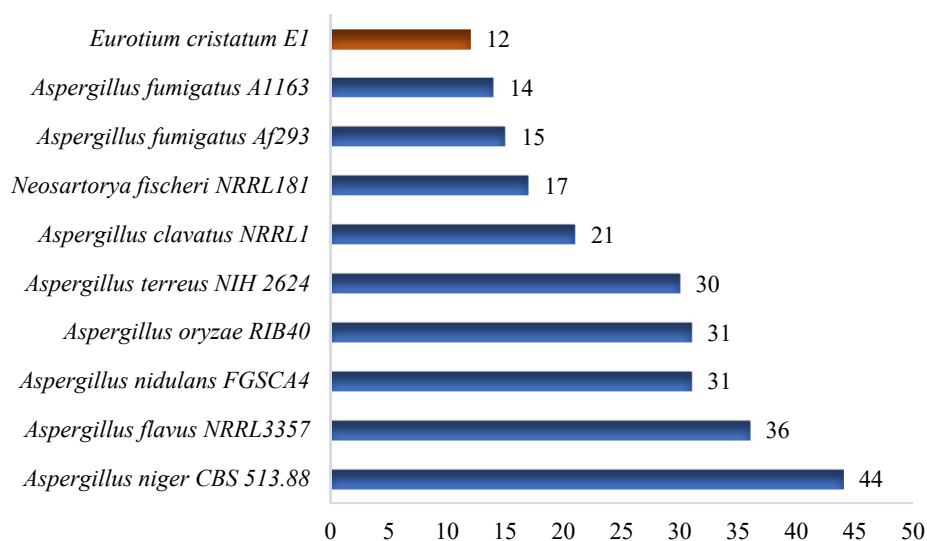


Figure S7. The number of PKS genes in some sequenced *Aspergillus* species.

Table S1. Strains and accession information of genes used for phylogenetic tree construction.

Strain	Accession		
	β -tubulin	CaM	RPB2
<i>Aspergillus caperatus</i> CBS 141774	LT671008.1	LT671009.1	LT671010.1
<i>Aspergillus chevalieri</i> NRRL 78	EF651911.1	EF652002.1	EF651954.1
<i>Aspergillus chevalieri</i> NRRL 4755	EF651913.1	EF652004.1	EF651956.1
<i>Aspergillus cristatus</i> CGMCC 3.06081	LT671061.1	LT671062.1	LT671063.1
<i>Aspergillus cristatus</i> IHEM 2423	LT671058.1	LT671059.1	LT671060.1
<i>Eurotium cristatum</i> NRRL 4222	EF651914.1	EF652001.1	EF651957.1
<i>Eurotium echinulatum</i> NRRL 131	EF651907.1	EF651998.1	EF651939.1
<i>Eurotium herbariorum</i> NRRL 116	EF651887.1	EF651989.1	EF651934.1
<i>Eurotium repens</i> NRRL 13	EF651915.1	EF652005.1	EF651950.1
<i>Eurotium rubrum</i> NRRL 52	EF651920.1	EF652009.1	EF651947.1
<i>Eurotium tonophilum</i> NRRL 5124	EF651919.1	EF652000.1	EF651969.1
<i>Aspergillus intermedius</i> CGMCC 3.03968	LT671082.1	LT671083.1	LT671084.1
<i>Aspergillus proliferans</i> CCF 4146	HE578076.1	HE650909.1	HE801304.1
<i>Aspergillus proliferans</i> CCF 4115	FR851855.1	HE578090.1	HE578107.1
<i>Aspergillus pseudoglaucus</i> CCF 3283	FR775360.2	HE974439.1	HE578110.2
<i>Eurotium amstelodami</i> NRRL 90	EF651897.1	EF652017.1	EF651963.1
<i>Eurotium amstelodami</i> NRRL 4716	EF651899.1	EF652018.1	EF651965.1
<i>Eurotium carnoyi</i> NRRL 126	EF651903.1	EF651985.1	EF651942.1

Table S2. Primers used for qRT-PCR.

Primers	Sequences (5'→3')	Functions
A1483-qPCR-f	AGGTGGATGGTTGAGAAGGG	For real time RT-PCR analysis of <i>A1483</i>
A1483-qPCR-r	TTCCTCCTACCGGCTTTCTG	
A2153-qPCR-f	GTCGTGGAGAAGGAGTTGGA	For real time RT-PCR analysis of <i>A2153</i>
A2153-qPCR-r	CGAGCGGATGAGAGATTCCCT	
A2490-qPCR-f	TCATTGATGACCCGGCTCTT	For real time RT-PCR analysis of <i>A2490</i>
A2490-qPCR-r	TTGCCTGGCCATAGAAGACA	
A3180-qPCR-f	CCTAGCAGTTGTGTCCAGAGA	For real time RT-PCR analysis of <i>A3180</i>
A3180-qPCR-r	TCAAAATCAACAGCTGCCCC	
A4077-qPCR-f	ATGAGGGCGTTAGGTTCCAA	For real time RT-PCR analysis of <i>A4077</i>
A4077-qPCR-r	ATGAGGACCCATTTCTGCCA	
A4569-qPCR-f	TGGAGGCCAAGCGATATCAT	For real time RT-PCR analysis of <i>A4569</i>
A4569-qPCR-r	TAGACCGACAATACTCCCGC	
A5054-qPCR-f	ACCGTGAGATCAACAGTGGT	For real time RT-PCR analysis of <i>A5054</i>
A5054-qPCR-r	GTGAATAGCGGCAAGACTGG	
A5285-qPCR-f	GGAAGAAACATTGCGTGGGT	For real time RT-PCR analysis of <i>A5285</i>
A5285-qPCR-r	AAGCCTGGAAAGTCGATGGA	
A6633-qPCR-f	CCAGTGGTGAAATTGCTGCT	For real time RT-PCR analysis of <i>A6633</i>
A6633-qPCR-r	GATTGTCGTGCTGGATGGAC	
A6985-qPCR-f	GGAAGGCCAATTGACGATCC	For real time RT-PCR analysis of <i>A6985</i>
A6985-qPCR-r	CTTCGTGCCAGTTAATCCGG	
A7192-qPCR-f	CTTGGGTTTCGAGCTATCAC	For real time RT-PCR analysis of <i>A7192</i>
A7192-qPCR-r	GTTGAGCACTACGTCGACAC	
A7789-qPCR-f	TACGATCCTCATCAACGGGG	For real time RT-PCR analysis of <i>A7789</i>
A7789-qPCR-r	GAAATCATCCACGTCGCGAA	
β -actin-qPCR-f	TCTGGCACCACACATTCTACA	For real time RT-PCR analysis of β -actin
β -actin-qPCR-r	CGAAGACGATCTGGGTCATCT	

Table S3. Analysis of A2490 gene cluster in *Eurotium cristatum* E1.

ORF	Size (bp/aa)	Homologs and related description	Sequence identity
A2499	4608/1535	hypothetical protein (GenBank: XP_040633901.1)	75%
A2498	1028/266	TATA-box-binding protein (GenBank: XP_043134035.1)	99%
A2497	1452/436	fructosyl amino acid oxidasesarcosine oxidase (GenBank: XP_040641941.1)	95%
A2495	1110/351	ubiquinone/menaquinone biosynthesis-related protein (GenBank: XP_040641942.1)	87%
A2494	1397/402	hypothetical protein (GenBank: XP_022402423.1)	92%
A2493	2139/694	fungal-specific transcription factor (GenBank: KAE8149832.1)	46%
A2492	993/295	NADH-cytochrome b5 reductase-like protein (GenBank: XP_040641945.1)	88%
A2491	669/222	Methyltransferase (GenBank: XP_040641946.1)	91%
A2490	5496/1778	polyketide synthase (GenBank: Q5BH30.1)	53%
A2489	982/308	metallo-beta-lactamase (GenBank: XP_040641948.1)	91%
A2488	1777/513	pisatin demethylase (GenBank: XP_040641950.1)	92%
A2487	1749/484	cytochrome P450 (GenBank: XP_040641951.1)	91%
A2486	1202/359	NAD(P)-binding protein (GenBank: XP_040641952.1)	91%
A2484	1349/409	hypothetical protein (GenBank: XP_043134047.1)	94%
A2483	956/207	hypothetical protein (GenBank: RJE24327.1)	64%
A2482	1555/494	hypothetical protein (GenBank: XP_043134049.1)	97%
A2481	2804/878	C6 transcription factor (GenBank: XP_025574120.1)	60%

Table S4. Analysis of A7192 gene cluster in *Eurotium cristatum* E1.

ORF	Size (bp/aa)	Homologs and related description	Sequence identity
A7187	1689/562	hypothetical protein (GenBank: XP_002375531.1)	48.21%
A7189	4983/1660	Mitogen-Activated Protein (MAP) kinase (GenBank: EYE95333.1)	95.54%
A7190	1437/478	ammonium transporter (GenBank: EYE95334.1)	97.06%
A7191	1158/385	nuclear mRNA splicing factor-associated protein (GenBank: XP_025499988.1)	81.41%
A7192	7389/2462	polyketide synthase (GenBank: EYE95336.1)	92.26%
A7193	822/273	short chain dehydrogenase (GenBank: EYE95337.1)	91.54%
A7194	612/203	short chain dehydrogenase (GenBank: EYE95337.1)	94.03%
A7195	861/286	short chain dehydrogenase (GenBank: EYE95338.1)	93.01%
A7196	1497/498	cytochrome P450 (GenBank: EYE95339.1)	86.80%
A7197	1497/498	FAD-binding oxidoreductase (GenBank: EYE95340.1)	91.77%
A7198	1047/348	short chain dehydrogenase (GenBank: EYE95341.1)	91.95%
A7200	1308/435	DMATS superfamily prenyltransferase (GenBank: ATP76208.1)	90.57%
A7201	1245/414	Transcription factor (GenBank: EYE95343.1)	86.06%
A7202	1389/462	tubulin beta chain (GenBank: EYE95344.1)	99.32%
A7203	1233/410	hypothetical protein (GenBank: XP_001269171.1)	70.75%
A7204	750/249	hypothetical protein (GenBank: XP_022400343.1)	74.77%
A7205	2619/872	protein kinase domain family protein (GenBank: TPR03492.1)	32.93%