

Supporting Information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Table S1 Primer sequences used in CDS cloning

Primer name	Primer sequences (5' - 3')	Primer use
FoMnSOD2-F	ATCCTCTAAAATGCTGTCCCTTC	cDNA cloning
FoMnSOD2-R	TCCGAGAAACGCTTGGAGAC	
3'FoMnSOD2 Outer	GATTACGCCAAGCTTCTGGCAGAACCTTACTCCTGA	Amplification of 3'end cDNA(3'-RACE)
3'FoMnSOD2 Inner	GATTACGCCAAGCTTCCTCATCCCATTGCTGGGTA	
c FoMnSOD2-F	TTTGTTTCGTTGTTTTGACCA	Verification of full-length cDNA
cFoMnSOD2-R	ACAAGTCTCGTTGAGTACAA	
FoCCS1-F	CGCAATTTGACGCAACTGGG	cDNA cloning
FoCCS1-R	ATCACCTTGTGTGGAATCGGT	
3'FoCCS1-Outer	GATTACGCCAAGCTTCACAGGCTGGCTTGTGGTAT	Amplification of 3'end cDNA(3'-RACE)
3'FoCCS1-Inner	GATTACGCCAAGCTTGGCTTGGGTGCAAGTGAAAA	
c FoCCS1-F	CAAGTTTGGTGGTGGTGTCAT	Verification of full-length cDNA
c FoCCS1-R	TCACCTTGTGTGGAATCGGTAT	

Table S2 Primer sequences used in quantitative reverse transcription PCR (RT-qPCR) and double-stranded (ds) RNA synthesis

Gene	Primer use	Sequence (5'-3')	Product length
<i>FoCCS1</i>	qPCR	F: GGTTTAGTGCTGTTGGCGTC R: CATGCAGCCCATGTTTACCAG	114 bp
<i>FoMnSOD2</i>	qPCR	F: TGCAAGGAACTACTGGCCTC R: CCGAGAAACGCTTGGAGACA	147 bp
<i>FoCCS1</i>	dsRNA synthesis	F: TAATACGACTCACTATAGGG GATGCAATTCTCCGAGGTGT R: TAATACGACTCACTATAGGG CAATACGAAAAACAGCCCGT	358 bp
	qPCR	F: GTGTGGGATATTATTGGCCG R: ATTATACCACAAGCCAGCCT	122 bp
<i>eGFP</i>	dsRNA synthesis	F: TAATACGACTCACTATAGGG CCCTGAAGTTCATCTGCACC R: TAATACGACTCACTATAGGG GTGCTCAGGTAGTGGTTGTC	481 bp
<i>EF-1</i>	qPCR	F: TCAAGGAACTGCGTCGTGGAT R: ACAGGGGTGTAGCCGTTAGAG	130 bp

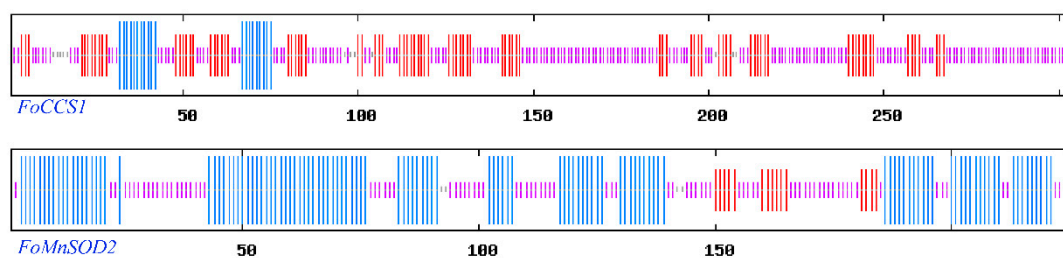


Figure S1: Secondary structure of the protein sequence of FoCCS1 and FoMnSOD2. Violet represents α -helices, blue represents random coils, and red represents extended strands.

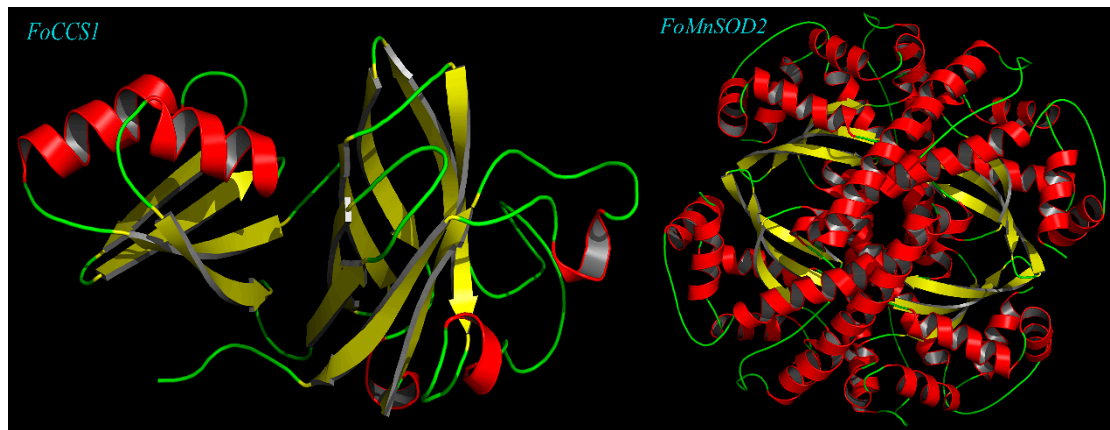


Figure S2 Predicted tertiary structure of FoCCS1 and FoMnSOD2 protein sequences. Red represents α -helices, yellow represents β -sheets, and green represents random coils.