Table SM1

Organism and GenBank Accession number	Fragment expressed	Primer sequence (5Õ3Õ)	Digestion	Expression vector construction
Synechocystis PCC 6803				
BAA17078	Full-length	F1: CCAATTTGTCCTTGAAGAGGAGTTGTC CATATGAATCCGGAAACGAAAGC F2: CCTTGAAGAGGAGTTGTCT CCATGGATCCGGAAACGAAAGCAAGAATTG R: CCCCACGGCGATCGCCAGCG GGATCCACCGAATGTGAAGCCCTAGGAAGC	NdeI-BamHI NcoI-BamHI	pET28-*SyGrx3* (His+) pET28-*SyGrx3* (His-)
Gloeobacter violaceus				
BAC91281	Full-length	F: GATGGCCAGGAGCTTGAA CATATGTCCCAGTCAACACACGAAAAAATCG R: GTTCCCTGATATCTGGGG GGATCCGCGGGAGAATTTAGGCTTTGGCCCC	NdeI-BamHI	pET28-*GvGrx3*
Thermosynechococcus elongatus				
BAC08426	Full-length	F: GCACAACGTCAGTGATTT CATATGCAATTTTGTAACTGGTC R: GAGTTTCAGTGAATG GGATCCAAAACTATGAAGCTAAGGCCACC	NdeI-BamHI	pET28-*TeGrx3*
Escherichia coli				
1YKAA	Full-length	F: CGTAAAGAAGTTTGAGGAAGCAAG CATATGAGCACCACTATCG R: CCGTCAGTAT GGATCCACGGATTATTCCGCGTCCGGCTCTTCAG	NdeI-BamHI	pET28-*EcGrx4*
Arabidopsis thaliana				
NP 191050	Amino acids 63 to 173	F: CCAACTAAATTCCGA CATATGGCGTCGGCTCTTACGCCGCAAC R: CACAAAAACCAAGGATCCAAATCAGGATCAAGAGCACATAGCTTTCTCC	NdeI-BamHI	pET28-*AtGrx5*
Homo sapiens				
Q86SX6	Amino acids 48 to 157	F: GGGGTCCGGGCGTGCGG CATATGGGCTCGGGCGCGGGCGGC R: CTCTGCTCAGCGAAGATCTGGCCGCCCTCACTTGGAGTCTTGGTCTTTC	NdeI-BglII	pET28-*HsGrx5*
Saccharomyces cerevisiae				
Q03835	Amino acids 180 to 285	F: CCACAACATATGGAGGAGCAAATAAACGCTAGATT R: CAATTTACACTAAAT AGATCTATTTATTTAAGATTGGAG	NdeI-BglII	pET28-*ScGrx3 GrxD*
P32642	Amino acids 130 to 244	F: CCACAACATATGGGGTCTTCCGATGATGAAGAG R: GAATATAGTTTTGGATCCAAAATAAGGCTTACTGTAGAGC	NdeI-BamHI	pET28-*ScGrx4 GrxD*
Q02784	Amino acids 31 to 150	F: CCAAAATCGGATGTATTTGCATATGGAGATAAGAAAAGCTATTG R: CCACCAGTTCCTATTTTGGATCCAGTGGTAACAAAATCAACGATCTTTGG	NdeI-BamHI	pET28-*ScGrx5*