

Table S1. Oligonucleotide Primers

Application	S/AS*	Sequence (5'-3') [†]	Notes
RT-PCR to define 5' ends of <i>Tg</i> PBGS3 ORF	S	1 ATGCGTCCTCTCTCGCTTTTCTTCC 25	5' UTR
	AS1	4233 GAGGGCGTCTTGAATGGGAAGCC 4210	conserved PBGS sequence (in exon 3)
	AS2	4913 ATCGAGGGAATCGGCACACTCG 4892	conserved PBGS sequence (in exon 4)
RT-PCR to define 5' end of <i>Tg</i> SPP ORF	S	1 ATGCGTCCTCTCTCGCTTTTCTTCC 25	5' UTR
	AS1	11088 AGCGACCCTGGAGGGTACGCATGGGG 11063	conserved SPP sequence (in exon 8)
	AS2	11148 ATGCCGCGCTCGTCTCTCCCTCGCTGG 11121	conserved SPP sequence (in exon 8)
	AS3	11208 CGAATCAAGGCCTCTCGCTTTCGACTGC 11181	conserved SPP sequence (in exon 8)
<i>Tg</i> PBGS3 Q-PCR (Fig. 1B)	S	6246 CTGTGCAAACAGGCGATTACGCTT 6687	spans splice junction of exons 5 and 6 conserved PBGS sequence (in exon 6)
	AS	6780 TGTGCAACCTTCCATGTCGAGAGA 6757	
<i>Tg</i> SPP Q-PCR (Fig. 1B)	S	11148 TCGCCCATCTCTGCGAACATATCA 11171	conserved SPP sequence (in exon 8)
	AS	11236 TGTGTACGCGTTGGTTTCTGCTTG 11213	conserved SPP sequence (in exon 8)
RACE to define 5' ends of <i>Tg</i> PBGS1/2/3 transcripts	S	<u>AAGCAGTGGTATCAACGCAGAGT</u>	upstream vector primer (Clontech)
	AS1	5037 AGCATGAACGCCTTGATGCCGTAGCTTCGGGC 4966	conserved PBGS sequence (in exon 4)
	AS2	4964 TCGCCACCTCCTTCAACAGATCTTCC 4938	nested, just upstream of AS1
RT-PCR to assess <i>Tg</i> PBGS transcription (Fig. 1D)	S	6797 CCTACTCTGCAAATACGCCTCCTCGTTC 6825	in exon 6
	AS	7937 TAGCAGGGTCTGTAAACTTCTGCGTTC 7909	in exon 7
wild-type <i>Tg</i> PBGS3 for enzymatic studies (Fig. 1F)	S	4165 <u>TATACATATGACGCCACGGGGCCCTCGAC</u> 4187	<i>Nde</i> I & <i>Bam</i> HI sites introduced for bacterial expression vector
	AS	7941 <u>GATGGATCCTT</u> AGTAGCAGGGTTCTGTAAACTTCTGC 7914	
<i>Tg</i> PBGS3 C-terminal deletion for enzyme studies (Fig. 1F)	S	4165 <u>TATACATATGACGCCACGGGGCCCTCGAC</u> 4187	<i>Nde</i> I & <i>Bam</i> HI sites introduced for bacterial expression vector
	AS	7899 <u>GATGGATCCTT</u> ACTCGACCATCCATTTGGCCGCC 7878	
<i>Tg</i> PBGS _{L394} -eGFP for localization (Fig. 1E)	S	-105 <u>CGAGATCTAAAATG</u> AGCTTCTTCCTCCTGTTCTTTCTCC -78	from upstream ATG through exon 4; <i>Bgl</i> II & <i>Avr</i> II for pTub Toxo vector
	AS	4998 <u>GGCTAGGGAG</u> CATGAACGCCTTGATGCCGTAGCTTCGG 4968	
<i>Tg</i> PBGS-GST-HA to map N-ter processing (Fig. 1F)	S	-105 <u>CGGGATCCAAAATG</u> AGCTTCTTCCTCCTGTTCTTTCTCC -78	from upstream ATG through exon 4; <i>Bam</i> HI & <i>Spe</i> I for GST-HA vector
	AS	4998 <u>GGACTAGT</u> GAGCATGAACGCCTTGATGCCGTAGCTTCGG 4968	
<i>Tg</i> PBGS-His6 for antibody production	S	4912 <u>GGATCCATG</u> CCTGGCCAAAGTCGTC 4930	conserved region from exons 4-7; <i>Bam</i> HI sites for His6 vector
	AS	7938 <u>GGATCCG</u> TAGCAGGGTTCTGTAAACTTCTGC 7914	

* Sense (same strand) or antisense (opposite strand) relative to mRNA.

[†] Underlining indicates vector/linker sequences; nucleotide positions refer to genomic DNA, relative to the presumed translational initiation site of *Tg*PBGS3; restriction sites shown in italics, start and stop codons in bold.

Table S2. Purification of recombinant *TgPBGS* and *TgPBGSDC*

Protein	Column	Volume (ml)	Protein (mg)	Specific Activity ($\mu\text{mol/hr/mg}$)	Yield ($\mu\text{mol/hr}$)
<i>TgPBGS</i>	phenyl sepharose	90	90	15.0 [*]	1350
	Q-sepharose	40	50	20.9 [*]	1045
<i>TgPBGS</i> Δ C	phenyl sepharose	40	100	0.22 [†]	22
	Q-sepharose	40	16.4	0.84 [†]	14

* Assays run 20 min with 5 μg protein from individual fractions; data represent the average of pooled fractions.

[†] Assays run 8 min with 50 μg protein from pooled fractions.

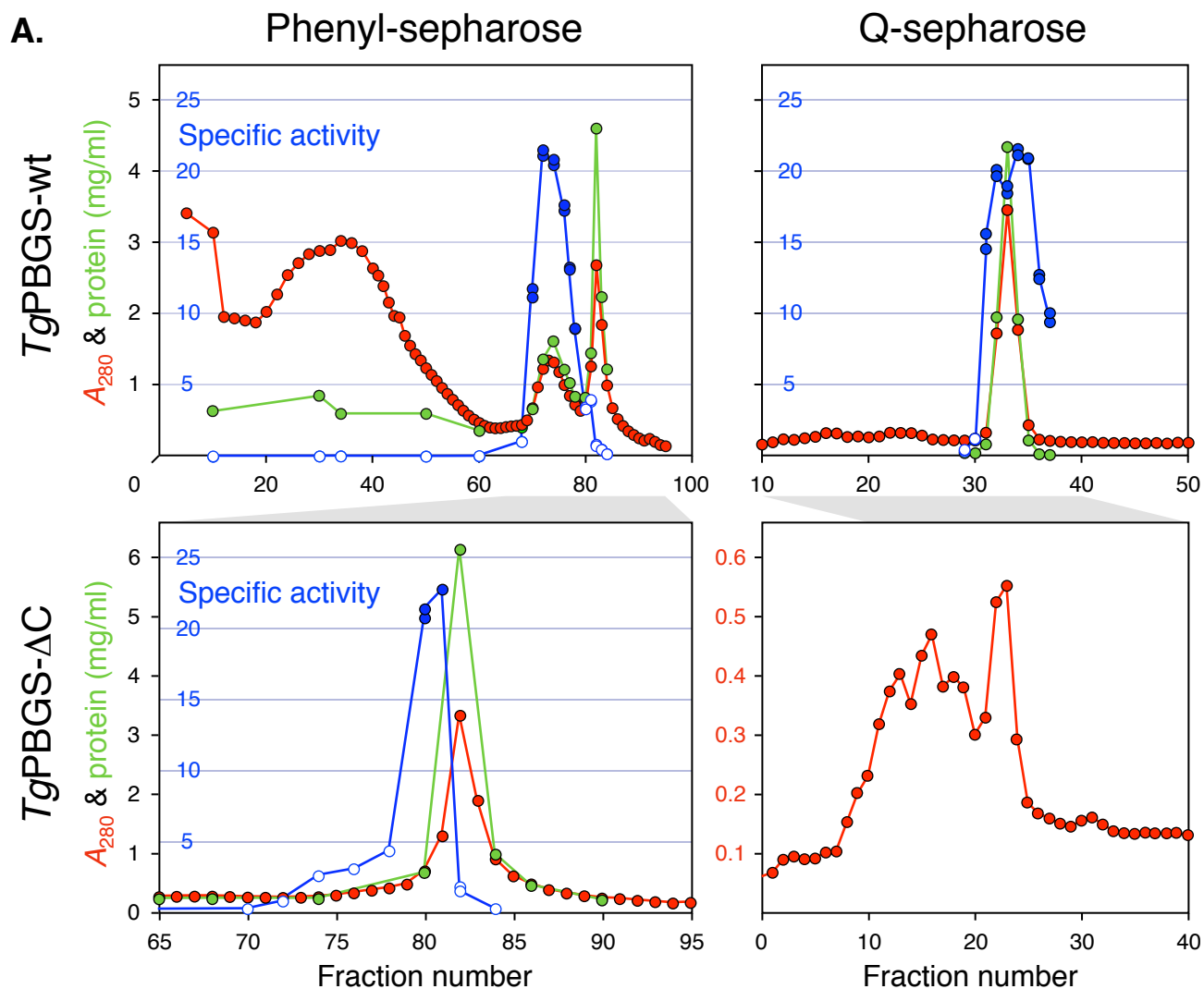
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Bacteria	<i>Escherichia coli</i>	<i>Eco</i> ...	GADLIFS	YFALDLA	EKKILR*
	<i>Mycobacterium tuberculosis</i>	<i>Mtu</i> ...	GADIVLT	YWAVDA	AAGWLT*
	<i>Vibrio cholerae</i>	<i>Vch</i> ...	GADGILTY	FAKEVA	EWLAEDSAKAAQFLPKK*
Archaea	<i>Sulfolobus solfataricus</i>	<i>Sso</i> ...	GADLIITY	YANDIAR	WIKDGVPF*
Eukaryota	Fungi	<i>Klebsiella lactis</i>	<i>Kla</i> ...	GARLIISY	FTEPFLEWLDEN*
		<i>Neurospora crassa</i>	<i>Ncr</i> ...	GATIIISY	FVPEFLDWLST*
		<i>Saccharomyces cerevisiae</i>	<i>Sce</i> ...	GARLIITY	LAPEFLDWLDEEN*
	Metazoa	<i>Drosophila melanogaster</i>	<i>Dme</i> ...	GADCIITY	YTPFLLDIIGKVK*
		<i>Homo sapiens</i>	<i>Hsa</i> ...	GADIIITY	YTPQLLQWLKEE*
	Plants/Algae	<i>Arabidopsis thaliana</i>	<i>Ath</i> ...	GADIILTY	FALQAATCLCGEKR*
		<i>Chlamydomonas reinhardtii</i>	<i>Cre</i> ...	GADLILTY	YGIEASKWLAGEK*
		<i>Oryza sativa</i>	<i>Osa</i> ...	GADIILTY	FARQAANVLCGMRSN*
		<i>Pisum sativum</i>	<i>Psa</i> ...	GADIILTY	FALQAARTLCGEKR*
	Amoebazoa	<i>Dictyostelium discoideum</i>	<i>Ddi</i> ...	GCDIFITY	FTPQLLDWLKL*
	Ciliates	<i>Tetrahymena thermophila</i>	<i>Tth</i> ...	GIDIITY	FTEPELLDWVKEEF*
	Apicomplexa	<i>Plasmodium berghei</i>	<i>Pbe</i> ...	GANIIITY	FAKQYGLYIKNLYEKKIHIEDNNSNPNFV*
	(Haemosporidia)	<i>Plasmodium falciparum</i>	<i>Pfa</i> ...	GANIIITY	FAKQYGLYMKKLYDKNIIIDDNSNPNFNI*
		<i>Plasmodium knowlesi</i>	<i>Pkn</i> ...	GANIIISY	FAKQFGLYLKLNLYNRNVDKEDDLNSPNFNI*
		<i>Plasmodium vivax</i>	<i>Pvi</i> ...	GANIIISY	FAKQYGLYLKDLDRNVDVDDDLNSPNFNV*
		<i>Plasmodium yoelii</i>	<i>Pyo</i> ...	GANIIITY	FAKQYGLYIKNLYEKKINIEDNNSNPNFNI*
	Apicomplexa	<i>Eimeria tenella</i>	<i>Etn</i> ...	GADAIATY	YAKDVAKWMEDDCRSSRSFTEPCY*
	(Coccidia)	<i>Neospora caninum</i>	<i>Ncn</i> ...	GADAIATY	YAKEAAKWMVAEDMKGAQKFTEPCY*
		<i>Toxoplasma gondii</i>	<i>Tgo</i> ...	GADAVATY	YAKEAAKWMVE <u>DMKGTOKFTEPCY</u> *

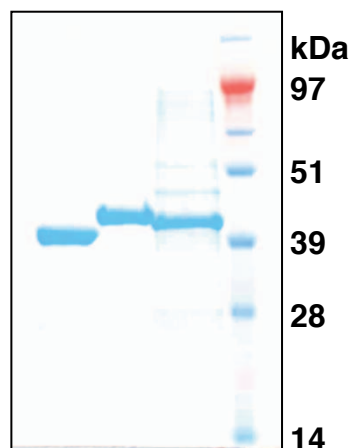
Identifiers: *Eco*, NP_414903.4; *Mtu*, NP_215026.1; *Vch*, NP_229764.1; *Sso*, NP_341737.1; *Kla*, KLLA0F09273g; *Ncr*, NCU01013; *Sce*, YGL040C; *Dme*, CG10335-PA; *Hsa*, ENSP00000363288; *Ath*, At1g69740.1; *Cre*, 186639; *Osa*, 12006.m09435; *Psa*, P30124; *Ddi*, DDB0231415; *Tth*, 91.m00108; *Pbe*, PB000542.01.0; *Pkn*, PF14_0381; *Pyo*, PKH_126610-1; *Pvi*, Pv118480; *Pyo*, PY04302; *Etn*, SNAP00000006525; *Ncn*, NC_LIV_04110; *Tgo*, 52.m01619

SUPPLEMENTAL FIGURE S1. Multiple sequence alignment of the PBGS C-terminal region. Alignment of PBGS proteins from various species with the C-terminal 32 amino acids of *Tg*PBGS (from Gly⁶²⁷, which is the last universally conserved amino acid). Sequences and alignments from OrthoMCL.org, except: *P. sativum*, from ncbi.nlm.nih.gov/protein; *N. caninum*, ToxoDB.org; *E. tenella*, GeneDB.org. Note the C-terminal extension found in *Toxoplasma* (underlined) and other apicomplexan parasites (box).

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B.



Hs Tgwt TgΔC

SUPPLEMENTAL FIGURE S2. Protein purification profiles. *A*, Elution of *TgPBGS-wt* (top) and *TgPBGS-DC* from phenyl-Sepharose (left) and Q-Sepharose (right). Protein concentration was determined by Bradford assay; see Methods for further details. Concentrations of *TgPBGS-DC* in individual Q-Sepharose column fractions were too low to assess specific activity. Pooled fractions are indicated by closed blue symbols (except bottom right). *B*, SDS PAGE analysis of Q sepharose eluates. *Hs*, human (for comparison); *Tgwt*, *TgPBGS-wt*; *TgDC*, *TgPBGS-DC*.