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2 **Synergistic interaction of glyceraldehydes-3-phosphate dehydrogenase and ArsJ, a**
3 **novel organoarsenical efflux permease, confers arsenate resistance**

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10 **Legends to the Supplemental Figures:**

11

12 **Figure 1S. Multiple alignment of GAPDH sequences.** The protein sequence of GAPDH from
13 the *ars* operon of *P. aeruginosa* DK2 (WP_003109848.1) is compared with GAPDH sequences
14 of GapA (WP_003116409.1) and GapB (AFM64157.1) from the chromosome of *P. aeruginosa*
15 DK2, GapA from *E. coli* W3110 (BAA15576.1) and the European rabbit *Oryctolagus cuniculus*
16 (NP_001075722.1). Accession numbers are given in parentheses. The multiple alignment was
17 calculated with CLUSTAL W. Black or gray boxes indicate sequence identity or similarity,
18 respectively.

19

20 **Figure 2S. Multiple alignment of ArsJ sequences.** 2779 ArsJ entries in 2336 bacterial
21 species were identified in the NCBI database, and seven representative sequences were
22 analyzed. The protein sequence of ArsJ from *P. aeruginosa* DK2 (WP_003109849) is
23 compared with ArsJ sequences from *Shewanella putrefaciens* 200 (WP_014610147),
24 *Aeromonas media* (AHX62269), *Marinimicrobium agarilyticum* (WP_027330587), *Bermanella*
25 *marisrubri* (WP_040298205), *Oceanimonas sp.* GK1 (WP_014290953), *Marinobacter*
26 *daepoensis* (WP_029654587). Accession numbers are given in parentheses. The multiple

27 alignment was calculated with CLUSTAL W (Thompson *et al.*, 1994). Black or gray boxes
28 indicate sequence identity or similarity, respectively.

29
30 **Figure 3S. Arsenate and phosphate as substrates of GAPDH.** GAPDH activity was assayed
31 as described in *Experimental procedures* with 1 unit of commercial rabbit GAPDH, 0.6 mM
32 NAD^+ , 0.6 mM G3P, 10 mM DTT, with or without arsenate or phosphate, as indicated. Activity
33 was estimated from the absorbance at 340 nm resulting from reduction of NAD^+ to NADH. **A.**
34 Arsenate addition: (\square), no As(V); (o), 0.125 mM As(V); (∇), 0.25 mM As(V); GAPDH catalyzed
35 the phosphorolytic-arsenolytic reaction. **B.** Comparison of arsenate and phosphate: (o), no
36 addition; (∇), 50 μM As(V); (\square), 50 μM Na_2HPO_4 ; (\diamond), 1 mM Na_2HPO_4 . **C.** Activity with high
37 phosphate concentrations: (\square), no addition; (∇), 3 mM Pi; (o), 10 mM Pi; (\diamond), 25 mM Pi.

38
39 **Figure 4S. Substrate requirements for GAPDH activity.** GAPDH activity was assayed as
40 described in *Experimental procedures* with the indicated combinations of 1 unit of commercial
41 rabbit GAPDH, 0.6 mM NAD^+ , 0.6 mM G3P, 10 mM DTT, or with the indicated arsenicals at 0.1
42 mM, final concentration. **A:** Specificity for arsenicals: (Δ), none; (\blacktriangledown), As(V); (\square), As(III); (\diamond),
43 MAs(III); (∇), MAs(V); (o), DMAs(V). **B:** Requirement for the components of the GAPDH
44 reaction. (Δ), GAPDH, G3P, NAD^+ and As(V); (\diamond), G3P, NAD^+ and As(V); (∇), GAPDH, NAD^+
45 and As(V); (\square), GAPDH, G3P and NAD^+ ; (o), GAPDH, G3P and As(V).

46
47 **Figure 5S. Arsenate dependence of GAPDH activity.** GAPDH activity was assayed as
48 described in *Experimental procedures* with 1 unit of commercial rabbit GAPDH, 0.6 mM NAD^+ ,
49 0.6 mM G3P, 10 mM DTT and the indicated concentrations of As(V). A K_m of 0.46 mM As(V)
50 was calculated. Data are the mean \pm SE (n = 3).

51

52 **Figure 6S. GAPDH is not an arsenate reductase.** Reduction of As(V) to As(III) was assayed
53 both *in vivo* and *in vitro*. **A:** Arsenate is not reduced in cells of *E. coli* W3110 (parental strain),
54 AW3110 ($\Delta arsRBC$) or WC3110 ($\Delta arsC$) expressing the *Pseudomonas aeruginosa* DK2 *ars*
55 operon *gapdh* gene (pGAPDH). **B:** Purified rabbit GAPDH reduced almost no As(V) to As(III)
56 after 20 or 40 min of reaction with 1 unit of commercial rabbit GAPDH, 1.2 mM NAD⁺, 1.2 mM
57 G3P, 10 mM DTT and 10 μ M As(V). Samples were speciated by HPLC using a C18 reverse
58 phase column, and the amount of arsenic in relative counts per second (cps) was estimated by
59 ICP-MS.

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arsGAPDH      1  -----MAIKVGINGFGRIGRLALRAAWN---WPE----FEFVQINDPAGDAATHAH
PaGapA         1  -----MTIRLAINGFGRIGRNVLRALYTGHYREQ----LQVVAIND-LGDAAVNAH
PaGapB        121  VGKQNGDAREGTDVVLVYGFGRIGRLLARILIEKTGGGDGLRLRAIVVRKGAENDLVKRAS
EcGapA         1  -----MTIKVGINGFGRIGRIVFRAAQK---RSD----IEIVAIND-LLDADY MAY
O.cuniculus  1  -----MVKVGVNGFGRIGRLVTRAAFN---SGK----VDVVAINDPFIDLHYMVY

arsGAPDH      45  LINFDSVHGRWHHEASSD--GDSVVIGGKRIKKTANKAIADTDWS--GCD--LVIEASGK
PaGapA         47  LFQYDSVHGRFPGEVEHD--AESLRVMGDRIAVSAIRNPAELPWKSLGVD--IVLECTGL
PaGapB        181  LLRRDSVHGPF DGTITIDEENNTLTANGNLIQVIYSNDPASIDYTQYGIKNALLVDNTGK
EcGapA         44  MLKYDSTHGRFDGTVEVK--DGHLIVNGKKIRVTAERDPANLKWDEVGVD--VVAEATGL
O.cuniculus  44  MFQYDSTHGKFFHGTVKAE--NGKLVINGKAITIFQERDPANIKWGDAGAE--YVVESTGV

arsGAPDH      99  MKTVAVLQTYLD-QGVKRVVVSAPVKEKGALNVVMGVNQHLFDPAQHRIVTAASCTTNCL
PaGapA        103  FTSRDKAAAHLQ-AGAGKVLISAPGKDVDA-TVVYGVNHEVLR-ASHRIVSNASCTTNCL
PaGapB        241  WRDAEGLGQHLKCPGIDRVVLTAPGKGALK-NIVHGINHTDIG-ADDKIISAASCTTNAI
EcGapA        100  FLTDETARKHIT-AGAKKVVMTGPSKDNTP-MFVKGANFDKYA-G-QDIVSNASCTTNCL
O.cuniculus  100  FTTMEKAGAHLK-GGAKRVIIISAPSX-DAP-MFVMGVNHEKYD-NSLKIIVSNASCTTNCL

arsGAPDH      158  APVVKVIHENLGI RHGSIITTIHDLTNTQSILDQPHKD-LRRARASGMSLIPTTTGSATAI
PaGapA        160  APVAQVLHRELGI EHGMLTTIHAYTNDQNLSDVYHPD-LYRARSATQSMIPTKTGAAEAV
PaGapB        299  VPVLKAVNDQYGI VNGHVETVHSYTNDQNLI DN FHKG-SRRGRSAPLNMVITETGAATAA
EcGapA        156  APLAKVINDNFGIIEGLMTTVHATTATQKTVDGPSHKDWRGGRGASQNIIPSSTGAAKAV
O.cuniculus  156  APLAKVIHDHFGI VEGMLTTVHAITATQKTVDGPSGKLWRDGRGAAQNIIPASTGAAKAV

arsGAPDH      217  AEIFPELRGRLNGH A VRVPLANASLTDCVFEVERQTSADENVQLLKRAAENE-L-KDILG
PaGapA        219  GLVLPPELAGKLTGL AVRPVINVSLVDLTVQVARDTSVDEVNRLREASEGS----PVLG
PaGapB        358  AKALPVLKKGKLTGN AIRVPTPNVSMAILNLNLEKATTREETNEYLRQMAMHSDLQKQIDF
EcGapA        216  GKVLPELNGKLTGM AFRVPTPNVSVVDLTVRLEKAATYEQIKA AVKAAAEGE-M-KGVLG
O.cuniculus  216  GKVIPELNGKLTGM AFRVPTPNVSVVDLTCRLEKAAKYDDIKKVVKQASEGP-L-KGILG

arsGAPDH      275  YEERPLVSIIDYRTDPRSSIIDALSTMV VNGTQVKLYAWYDNEWGYANRTVELAKLVGLAG
PaGapA        275  YNTQPLVSVDFNHDPRSSIFDANHT-KVSGRLVKAMAWYDNERGFSNRMLDSALALAAAR
PaGapB        418  VSSQEVVSTDFV GSRHAGVVDAEAT-ICNDNRVVLVWYDNEFGYSCQVVRVMEDMAGVN
EcGapA        274  YTEDDVVSTDFN GEVCTSVDKAGIALNDNFVKLVSWYDNETGYSNKVLDLIAHISK--
O.cuniculus  274  YTEDQVVSCDFNSATHSSTFDAGAGIALNDHFVKLISWYDNEFGYSNRVVDLMVHMASKE

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Pseudomonas 1 ----MKALSSLSPEVROYLLVTGNYWAFTLTDGALRMLVVLHFHSLGYSPLQIAALFLFY
Shewanella 1 MAKLTGFLSNISPEIROYLVTGNYWAFTLTDGALRMLVVLHFHSLGYSPLQIAMLFLFY
Marinobacter 1 -----MNSAIRQYLVI TGNywaftLTDGALRMLVVLHFHSLGYSPLAIALLFLFY
Bermanella 1 -----MALANLSTEIROYLIVTGNywaftLTDGALRMLVVLHFHSLGYSPESIAMLFLFY
Aeromonas 1 -----MALTRLSPETROYLLVTGNYWAFTLTDGALRMLVVLVYFHLGYSPLAIASLFLFY
Oceanimonas 1 -----MLNRLSPGIROYLVVTGNYWAFTLTDGALRMLVVLHFHSLGYSPLAIALLFLFY
Marinimicrobium 1 -----MLAQLSPAIRQYLLITGNYWAFTLTDGALRMLVVLHFHSLGYSPLAIALLFLFY

Pseudomonas 57 EFGVVTNLVGGYLGARVGLNRTMNI GLAMQVVALMLTVP SALLTPVVMGAQALSgia
Shewanella 61 EFGVVTNLVGGWLGARLGLNKTMMNVGLFMQIVALSMLLVP SGM LTVAVWMAAQALSgia
Marinobacter 51 EFGVVTNLVGGYLGARLGLNRTMNI GLELQIVALLMLAVPAAALTVPVWMAAQALSgia
Bermanella 56 EFGVITNLVGGWLGARLGLNRTMNI GLLLOIVALLMMLVPLEWLTVPVWMAAQALSgia
Aeromonas 56 EFGVVTNLVGGWLGARLGLNRTMNI GLALQVVALGMLLAPSLWLTVPVVMGAQALSgia
Oceanimonas 55 EFGVITNLVGGWLGARLGLNRTMNI GLALQVVALGMLLVPAAWLTVPVWMAAQALSgia
Marinimicrobium 55 EFGVITNLVGGWLGARLGLNRTMNI GLLLOVVALSMLLVPAAMLTVPVWMAAQALSgia

Pseudomonas 117 KDLNKMSAKSSIKLLVPEAQGKLYKQWVAITLTSKNALKGVGFFLGGALLALLCFKKAVAL
Shewanella 121 KDLNKMSAKSSIKLLVPEAQGELYKQWVAMITGSKNALKGAGFFLGGALLTLFGFQLAVAL
Marinobacter 111 KDLNKMSAKSGIKLLVPEAQGRLYKQWVAITLTSKNALTKGVGFFLGGVLLMSAGFRGAVV
Bermanella 116 KDLNKMSAKSAIKLLVPEAQGQLYKQVSIITGSKNALKGAGFFMGGVLLTALCFKKAVAL
Aeromonas 116 KDLNKMSAKSSIKLLVPEAQGQLYQWVAITLTSKNALKGMGFFLGGALLTLIGFOGAVL
Oceanimonas 115 KDLNKMSAKSSIKLLVPEAQGTLYQWVAITLTSKNALKGVGFFMGGALLMGLGFAGAVA
Marinimicrobium 115 KDLNKMSAKSSIKLLVPEAQGALYKQWVAITLTSKNALKAGFFLGGALLMALGFAGAVG

Pseudomonas 177 AMAVVLALIVWGSMLSLKKDLGKAKAKPKFERDMLSKSRAINILSAARMLFGARDVWFVV
Shewanella 181 GMAIGLLLVWIFSLLSLQDLGKAKNPKPFEIIFSKSSSVNTLSAARMLFGARDVWFVV
Marinobacter 171 AMAVVLGLVWLASLFLGODLGKSKAKPKFSIDLKSRAINVLSAARMLFGARDVWFVV
Bermanella 176 AMASMLILVWLFSLIAKLELGGKAKNPKPFSOLF SKSTAINVLSAARMLFASRDVWLVV
Aeromonas 176 VMALALALVWCISMLTLKRDLGKAKNPKPFEIIFSKSRAINVLSAARMLFGARDVWFVV
Oceanimonas 175 AMAVALTLVWLLSLMLLTDLGGKAKQPKPFERDMLSKSRAINLLSAARMLFGARDVWFVV
Marinimicrobium 175 SMAALLFVWIASLIFLRKDLGRAKSKPKPSEIIFSKSTAVNVLSAARMLFGARDVWFVV

Pseudomonas 237 ALPVYLSETLSWDFWL VGGFLAAWVIGYGI VQSFAPALTGKKR---GHVPDGRAAFI WAL
Shewanella 241 ALPVYLASAFGWDHWYVGGFLALWVIGYGI VQGFAPRLTGTKSASQNKVPDGRSALGWAA
Marinobacter 231 ALPVYMATVFGWDHWQVGGFLACWVIGYGEVQTVAPRITGLASGK-----AGAVFWAA
Bermanella 236 ALPVYLASQFNWDHWT VGGFLALWVIGYGEVQTOAPNITGAKR---GKHPDGKTAALWAL
Aeromonas 236 ALPVYLASSLGDWNGYVGSFLALWV IAYGVVQTOAPRFTGKRE---GRVPDGKVAMGWAL
Oceanimonas 235 ALPVFLSQSLGWHHGQTGGFMALWVIGYGLVQALAPRVTKGAA---GNVPDGRVATGWAL
Marinimicrobium 235 ALPVFLASQFDWDHWK VGGFLALWVIGYGA VQSVAPRITGRNT---GTPDGRATFGWAL

Pseudomonas 294 ILAVLPAATIALGLDMNLSAQIVLLGGLMIFGALFAVNSSLHSYLIVSYAKEDGVSLDVGF
Shewanella 301 ILSIVPAGIALAISYDFHAANILIWGLMIFGALFAINSSLHSYLIVSYADEEDGVSLDVGF
Marinobacter 284 LLAGVPAAMAGALVVGWPEWVIGGLLFGILFAINSSLHSYLIVRYARGDGVSLDVGF
Bermanella 293 VMAGLPALIALALSNDSYTLISIVFGLLIFGFVFAINSSVHSYLIVSYASNDGVSLDVGF
Aeromonas 293 VLALTPALIALALHFDLHPAISLVGGLMVFALFAINSSLHSYLIVSYAGSDGVSLDVGF
Oceanimonas 292 GLTLVPGLIALGLMTGLNPAMVLI GGLLIFGALFAVNSSLHSYLIVSHAGRDGVSLDVGF
Marinimicrobium 292 GLTLVPALIALALLGDVAPQWSLLGGLMVFGLFAVNSSLHSYLIVSYAKEDGVSLDVGF

Pseudomonas 354 YYMSNAMGRLLGTVLSGWVFOAY----GLVACLWISAAFLVLLAALISIALPRHAEVVT
Shewanella 361 YYMANAMGRLLGTVLSGWVYQVY----GMAACLWISAAFLAALALISIKLPRHRAI---
Marinobacter 344 YYMSNAAGRLMGTLLSGWVYQAW----GLEACLWISAAFLVAMAALLSLGLPDRRDAIIG
Bermanella 353 YYMANAMGRLLGTVLSGWLYQAY----GLEACLWVSSAFLILTFIISLALPKEGTAKPS
Aeromonas 353 YYMANALGRLLGTVLSGLVFOQLH----GLEACLWVSTLFIILLAALISLGLPRHQPPVSS
Oceanimonas 352 YYMANAMGRLLGTVLSGGLFQWAGQGSAGMQACLWVSMFLLLTTLISLRLPRSVVN---
Marinimicrobium 352 YYMANAMGRLLGTVLSGWVYQVA----GLVACLWISAAFLALATVIALALPRRD-----

Pseudomonas 409 PN-----
Shewanella -----
Marinobacter 399 EQRFV-
Bermanella 408 -----
Aeromonas 408 QSHGVS
Oceanimonas -----
Marinimicrobium -----

Figure 3S

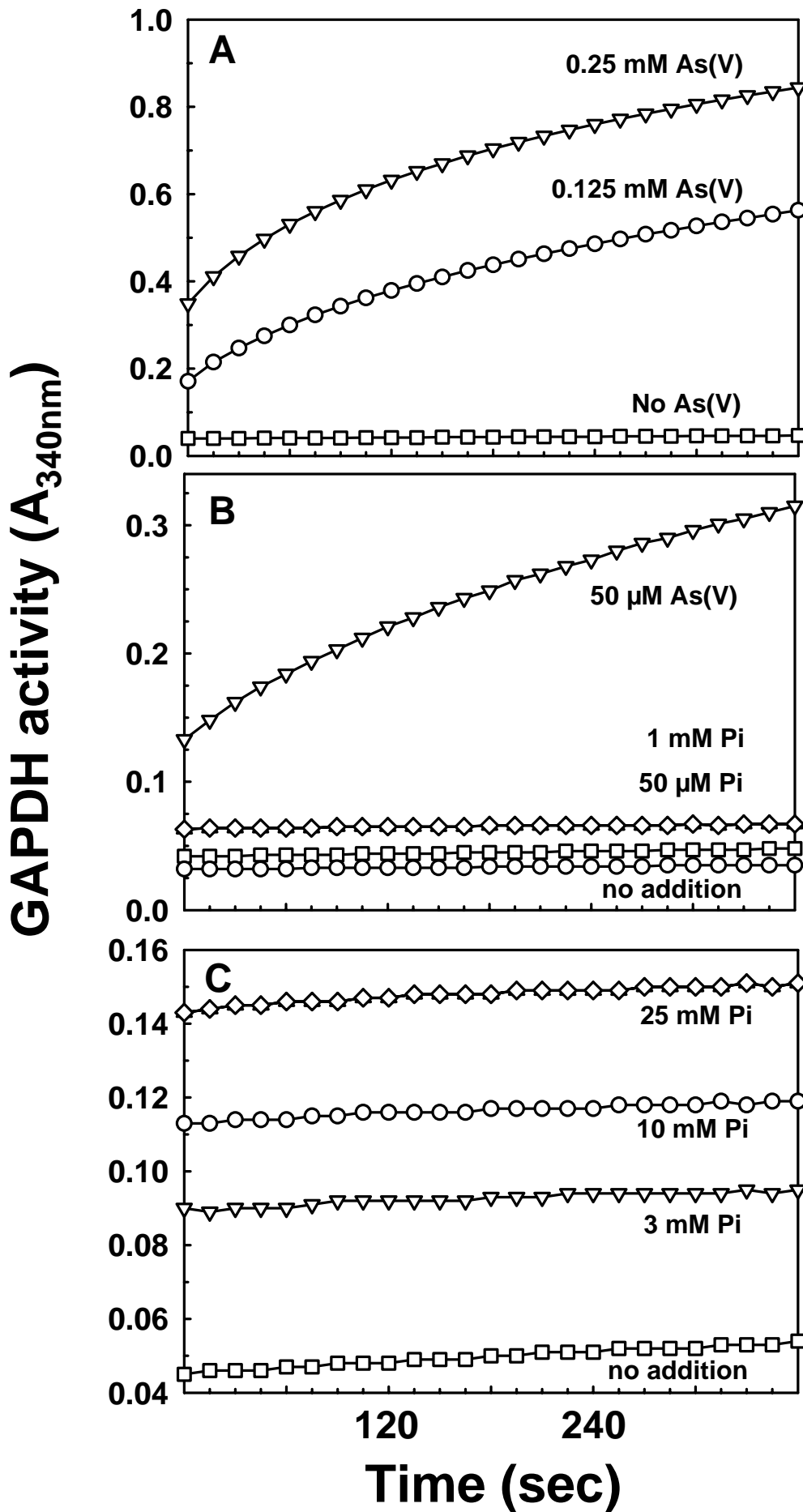


Figure 4S

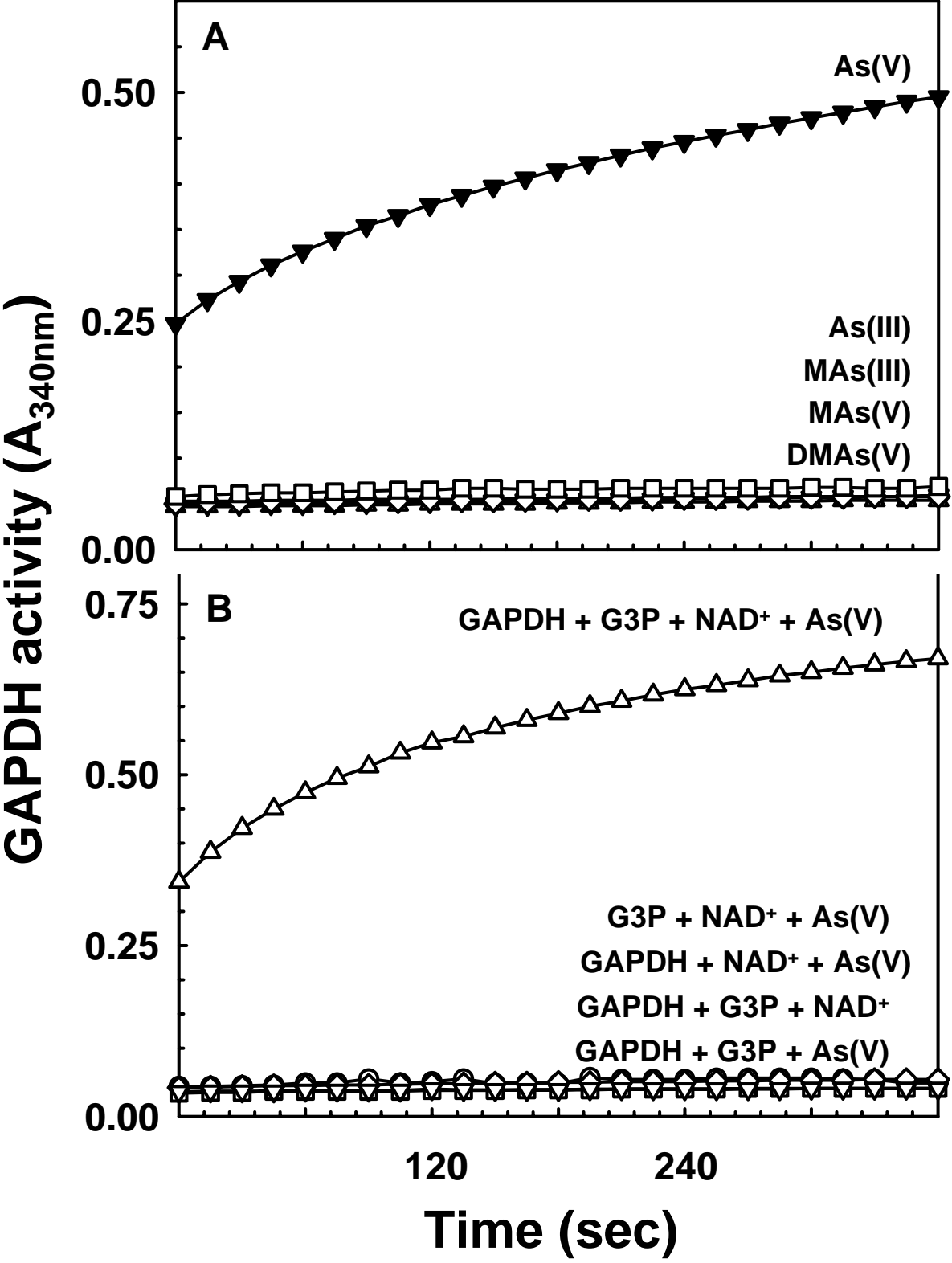


Figure 55

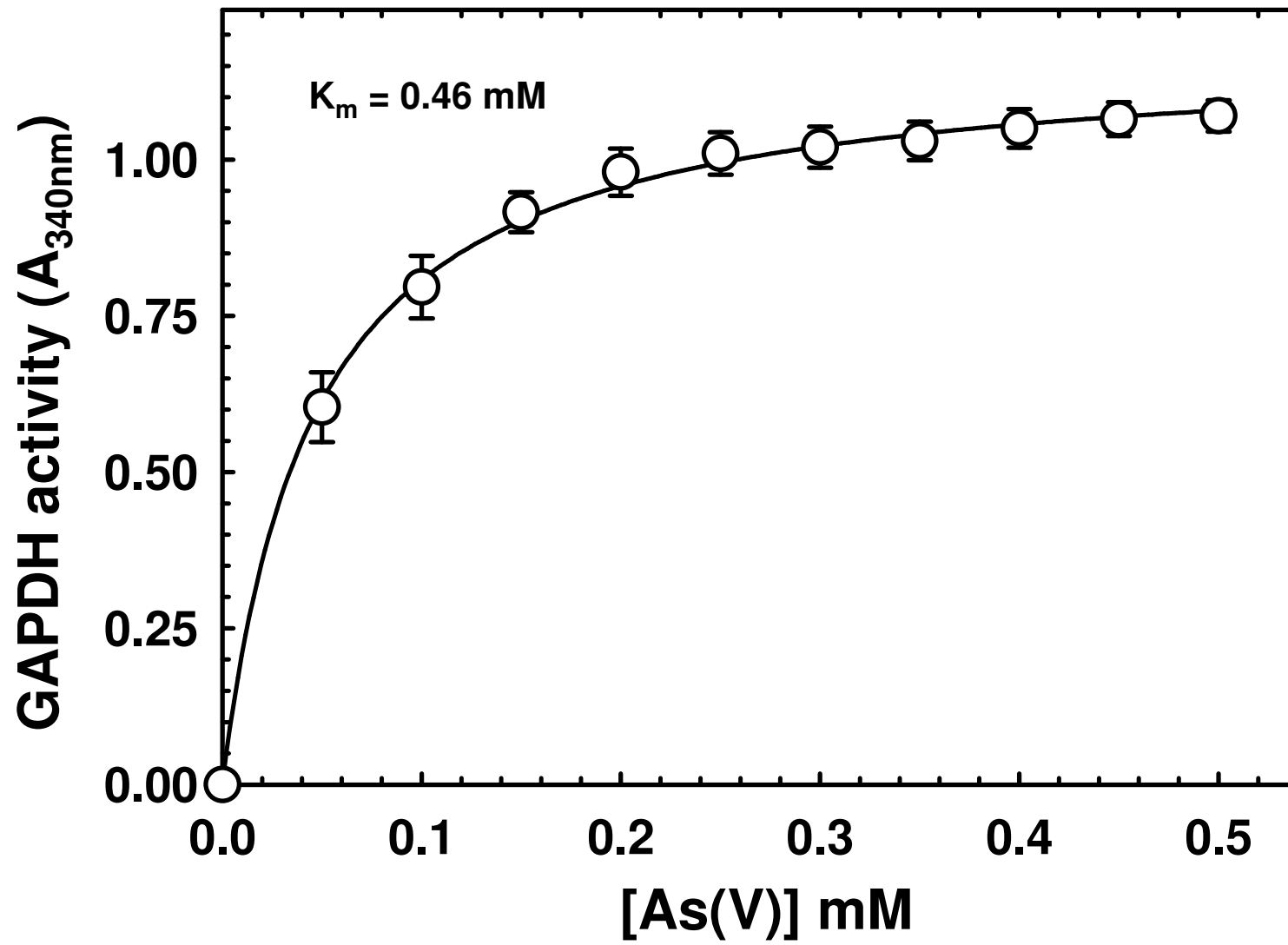


Figure 6S

