

1 **Revised Manuscript: AEM00286-21**

2 **Oxygen generation via water splitting by a novel biogenic metal ion binding**
3 **compound**

4 **Philip Dershwitz¹, Nathan L. Bandow^{1Ψ}, Junwon Yang², Jeremy D. Semrau², Marcus T.**
5 **McEllistrem³, Rafael A. Heinze³, Matheus Fonseca³, Joshua C. Ledesma¹, Jacob R. Jennett¹,**
6 **Ana M. DiSpirito¹, Navjot S. Athwal^{1Υ}, Mark S. Hargrove¹, Thomas A. Bobik¹, Hans Zischka⁴,**
7 **and Alan A. DiSpirito^{1*}**

8 ¹Roy J. Carver Department of Biochemistry, Biophysics and Molecular Biology. Iowa State
9 University, Ames, IA 50011-3260, USA

10 ²Department of Civil and Environmental Engineering, University of Michigan, Ann Arbor, MI,
11 48109-2125, USA

12 ³Materials Science and Biomedical Engineering, University of Wisconsin-Eau Claire, WI, 54602,
13 USA

14 ⁴Institute of Molecular Toxicology and Pharmacology, Helmholtz Center Munich, German
15 Research Center for Environmental Health, Ingolstaedter Landstrasse 1, D-85764 Neuherberg,
16 Germany. and Technical University Munich, School of Medicine, Institute of Toxicology and
17 Environmental Hygiene, Biedersteiner Strasse 29, D-80802 Munich, Germany.

18 ^Ψ Current address: Allogene Therapeutics, Inc., South San Francisco, CA 94080, USA

19 ^Υ Current address: Stemcell Technologies, Vancouver, BC Canada

20 *To whom correspondence should be addressed: Email: aland@iastate.edu; Phone: 1-515-294-
21 2944; Fax: 1-515-294-0453

22 Running title: Oxidation of water by methanobactin

- 23 **Keywords:** Methanobactin • chalkophore • water oxidation • methanotroph • aerobic methane
24 oxidation • gold nanoparticle.

25 **ABSTRACT**

26 Methanobactins (MBs) are small (<1,300 Da) post-translationally modified copper-binding
27 peptides and represent the extracellular component of a copper acquisition system in some
28 methanotrophs. Interestingly, MBs can bind a range of metal ions, with some reduced after
29 binding, e.g., Cu^{2+} reduced to Cu^+ . Other metal ions, however, are bound but not reduced, e.g.,
30 K^+ . The source of electrons for selective metal ion reduction has been speculated to be water
31 but never empirically shown. Here, using H_2^{18}O , we show that when MB from *Methylocystis sp.*
32 strain SB2 (MB-SB2) and *Methylosinus trichosporium* OB3b (MB-OB3) were incubated in the
33 presence of either Au^{3+} , Cu^{2+} , and Ag^+ , $^{18,18}\text{O}_2$ and free protons were released. No $^{18,18}\text{O}_2$
34 production was observed either in presence of MB-SB2 or MB-OB3b alone, gold alone, copper
35 alone, silver alone or when K^+ or Mo^{2+} was incubated with MB-SB2.

36 In contrast to MB-OB3b, MB-SB2 binds Fe^{3+} with an N_2S_2 coordination and will also
37 reduce Fe^{3+} to Fe^{2+} . Iron reduction was also found to be coupled to oxidation of $2\text{H}_2\text{O}$ and
38 generation of O_2 . MB-SB2 will also couple Hg^{2+} , Ni^{2+} and Co^{2+} reduction to the oxidation of $2\text{H}_2\text{O}$
39 and generation of O_2 , but MB-OB3b will not, ostensibly as MB-OB3b binds but does not reduce
40 these metal ions.

41 To determine if the O_2 generated during metal ion reduction by MB could be coupled to
42 methane oxidation, $^{13}\text{CH}_4$ oxidation by *Methylosinus trichosporium* OB3b was monitored under
43 anoxic conditions. The results demonstrate O_2 generation from metal ion reduction by MB-
44 OB3b can support methane oxidation.

45

46

47 **IMPORTANCE**

48 The discovery that MB will couple the oxidation of H₂O to metal ion reduction and the release
49 of O₂ suggests that methanotrophs expressing MB may be able to maintain their activity in
50 hypoxic/anoxic conditions through “self-generation” of dioxygen required for the initial
51 oxidation of methane to methanol. Such an ability may be an important factor in enabling
52 methanotrophs to not only colonize the oxic-anoxic interface where methane concentrations
53 are highest, but also tolerate significant temporal fluctuations of this interface. Given that
54 genomic surveys often show evidence of aerobic methanotrophs within anoxic zones, the
55 ability to express MB (and thereby generate dioxygen) may be an important parameter in
56 facilitating their ability to remove methane, a potent greenhouse gas, before it enters the
57 atmosphere.

58

59 **INTRODUCTION**

60 Aerobic methane oxidizing bacteria (methanotrophs) oxidize methane to carbon dioxide via a
61 series of two electron steps with methanol, formaldehyde and formate as intermediates (1).
62 The initial oxidation of methane to methanol is an oxygen and energy dependent reaction and
63 is catalyzed by either a soluble cytoplasmic methane monooxygenase (sMMO) or a particulate
64 or membrane-associated methane monooxygenase (pMMO) (1-8). The reductant for the initial
65 oxidation of methane is supplied by NADH for the sMMO and by quinols for the pMMO (2, 3, 9-
66 11). Methanol is oxidized to formaldehyde by a calcium or rare earth dependent methanol
67 dehydrogenase using a *c*-type cytochrome as an electron acceptor (12-17) Formaldehyde is
68 either assimilated or oxidized using either NAD⁺ or quinone as the electron acceptor (10, 18-

69 20). The final two electron oxidation of formate to carbon dioxide is catalyzed by the NAD⁺-
70 linked formate dehydrogenase (21-23). Electrons from NADH, quinol or cytochrome *c* are
71 either utilized in biosynthetic reactions or oxidized for energy using either dioxygen (11), nitrate
72 (24) or ferric iron (25) as the terminal electron acceptor.

73 In methanotrophs capable of expressing both forms of the MMO, expression is
74 regulated by copper (1, 9, 26-28). In addition to the MMOs, a number of genes are regulated by
75 copper (1) and some methanotrophs of the *Alphaproteobacteria* have a novel copper
76 acquisition systems based on the extracellular copper binding peptide methanobactin (MB) (29-
77 31). Methanobactins (MBs) are low molecular mass (<1,300Da), high potential (E_m 483 – 745
78 mV) ribosomally synthesized post-translationally modified peptides (RiPPs) and were the first
79 examples of a chalkophore, i.e., a compound excreted by bacteria for the purpose of
80 scavenging copper from the surrounding environment (30, 32). Structurally MBs are divided
81 into two groups. Both Group I and II MBs are characterized by an internal oxazolone group with
82 an associated thioamide and a second N-terminal 5 or 6 membered ring which in Group I MBs is
83 either an oxazolone or pyrazinedione group with an associated thioamide while Group II MBs
84 has either an imidazoline or pyrazinedione group with an associated thioamide (30, 32-36). The
85 ring and associated thioamide are derived from an X-Cys dipeptide via a series of partially
86 characterized post-translational modifications (29, 31, 37). Group I MBs are characterized by an
87 internal disulfide bridge and the copper bound form a dicyclic structure (33, 34, 38). Group II
88 MBs lack this disulfide bridge and the copper bound form has a hairpin-like structure and is
89 characterized by a central sulfonated threonine (30, 36).

90 In addition to copper ions, MBs will bind many metal ions (39-42) and reduce some, but
91 not all metal ions that are bound (39, 43). In MB from *Methylosinus trichosporium* OB3b, MB-
92 OB3b, metal ions such as copper, silver and gold are coordinated via an N₂S₂ ligand set utilizing
93 a N from each ring and the two thioamides and these metals are reduced after binding (30, 34,
94 39, 44). Other metal ions such as iron, nickel and cobalt are coordinated via an N₁S₁ ligand set
95 using one ring and its associated thioamide and are not reduced (39). Based on coordination
96 metals were classified as either Group A metals coordinated by a N₂S₂ ligand set, or Group B
97 metals coordinated by a N₁S₁ ligand set. In contrast, all of the metals bound by MB from
98 *Methylocystis* strain SB2 (MB-SB2) are coordinated by a N₂S₂ ligand set ((40, 41, 43, 45) and this
99 report).

100 Since metal ion reduction assays are often carried out in unbuffered reaction mixtures in
101 the absence of an external reductant, water has been proposed, but not shown to be the
102 electron donor (36). Here, we examine the binding and reduction of oxidized forms of gold (as
103 HAuCl₄), copper (as CuCl₂), silver (as AgF), iron (as FeCl₃), nickel (as NiCl₂), mercury (HgCl₂),
104 cobalt (as CoCl₂) and potassium (as KCl) in the presence and absence of H₂¹⁸O by MB-SB2 as
105 well as the binding and reduction of gold, copper and silver in the presence of H₂¹⁸O by MB-
106 OB3b.

107

108 RESULTS

109 Spectral and Thermodynamic Properties of AuCl₄⁻ binding by MB-SB2

110 UV-visible absorption, fluorescence and circular dichroism spectra (Figs. S1-S3) and
111 thermodynamic measurements (Fig. S4; Table S1) demonstrate changes following the addition

112 of H₂AuCl₄ to MB-SB2 were complex with transitions apparent at 0.25, 0.5, 0.75, 1.0 and 2.0 Au
113 per MB-SB2. As MB-SB2 has only one identified metal binding motif (i.e. an N₂S₂ ligand set), we
114 therefore interpret these data to indicate changes in Au coordination, when MB-SB2
115 transitions from an oligomeric state(s) to a monomer.

116 The increased fluorescence emission intensity following H₂AuCl₄ addition may be due to
117 disruption of internal quenching between the imidazolone and oxazolone groups and is
118 consistent with the intramolecular exciton transfer previously demonstrated following
119 hydrolysis of the oxazolone group (43)(Fig. S2). The decreased fluorescence at H₂AuCl₄ to MB-
120 SB2 ratios greater than 1.0 suggests direct metal quenching or intra-/ inter-exciton transfer
121 between the oxazolone and imidazolone groups, or may be associated with nanoparticle
122 formation which occurs at Au to MB-SB2 ratios greater than 1:1.

123 As Au nanoparticle formation requires Au³⁺ reduction (46), nanoparticle formation (Fig.
124 S5; Table 2S) by MB-SB2 indicated that MB-SB2 binds and reduces multiple Au³⁺ to Au⁰. Such
125 findings accentuated the need to determine the electron source for metal reduction by MBs. To
126 extend these preliminary studies, we examined reduction of H₂AuCl₄ via MB-SB2 when dissolved
127 in either H₂¹⁶O or H₂¹⁸O.

128

129 **X-Ray Photoelectric Spectroscopy (XPS), Kinetics and Chloride Determination**

130 In reaction mixtures containing H₂AuCl₄ and MB-SB2 dissolved in H₂¹⁶O, MB-SB2 was observed to
131 reduce AuCl₄⁻ to Au⁰ + 4Cl⁻, as determined by XPS and argentometric titrations, respectively (Fig.
132 1; Table 1). MB-SB2 reduced up to 19 Au³⁺ to 19Au⁰ with a time-dependent average Au³⁺ to Au⁰
133 reduction rate of 0.3 ± 0.06 min⁻¹ for those assays where rates could be determined. This time-

134 dependent reduction was the reason samples were frozen in liquid nitrogen and lyophilized
135 overnight to stop the reaction and dry the samples for analysis. As observed with MB-OB3b
136 (39), Au³⁺ and Au⁰ were the only oxidation states detected, indicating a direct three-electron
137 reduction of HAuCl₄ (Fig. 1).

138

139 **Kinetics of AuCl₄⁻ Binding and Reduction**

140 The time course for the binding of Au³⁺ to the oxazolone and imidazolone rings in MB-SB2 was
141 measured as the decrease in absorbance at 341 and 389 nm, respectively, following stopped-
142 flow mixing of MB-SB2 with Au³⁺ at 4°C (Fig. 2A). Unfortunately, even at 4°C, initial binding
143 rates could only be determined for the oxazolone ring, since the binding to the imidazolone ring
144 was complete before mixing of the sample was complete (1.4 msec). In contrast, the binding
145 rates to the oxazolone ring were low, 12 - 57 s⁻¹, at Au³⁺ to MB-SB2 ratios below 0.3, increased
146 at Au³⁺ to MB-SB2 ratios between 0.3 and 1.5 Au³⁺ per MB-SB2 up to a maximum rate of ~1600
147 s⁻¹, followed by a decline in rate at molar ratios >1.5 Au³⁺ per MB-SB2 (Fig. 2A).

148 Au³⁺ reduction rates (0.3 ± 0.06 min⁻¹; Table 1) were much slower to the initial binding
149 rates (greater than 2,000 s⁻¹; Fig. 2A). The difference may be due to the different binding rates
150 between the imidazolone and oxazolone groups. Monitoring the florescent changes over time
151 at HAuCl₄ to MB-SB2 below 1:1, suggest final Au coordination required several minutes to
152 complete (Fig. 2B). At gold to MB-SB2 concentrations greater than 1.0 an initial disruption of
153 exciton coupling resulting in increased florescent intensity followed by quenching (Fig. 2B).
154 What is pertinent to this discussion is that Au initially binds primarily if not exclusively to the

155 imidazolone group followed by binding to the oxazolone group and a final reorientation. The
156 time scale for these changes are in keeping with gold reduction rates.

157

158 **Oxidation of H₂O coupled to Au³⁺ reduction by MB-SB2**

159 As four Cl⁻ were generated in reaction mixtures for every HAuCl₄ reduced to Au⁰, chlorine was
160 ruled out as a potential electron donor. To determine if H₂O was the electron donor, H⁺
161 concentrations were monitored during HAuCl₄ titrations of MB-SB2. Unfortunately, pH changes
162 associated with the addition of HAuCl₄ to unbuffered reaction mixtures made pH changes
163 associated with binding of AuCl₄⁻ difficult to determine (Fig. 3A). To examine if H₂O could serve
164 as an electron source for Au³⁺ reduction, ^{18,18}O₂ production was monitored in reaction mixtures
165 containing 97% H₂¹⁸O. No ^{18,18}O₂ production was observed in reaction mixtures containing
166 either MB-SB2 alone (Fig. 4A) or HAuCl₄ alone (result not shown). However, following HAuCl₄
167 addition to MB-SB2, ^{18,18}O₂ was observed demonstrating the coupling of water oxidation with
168 metal reduction (Figs. 4B and 5).

169 It should be noted that there is seemingly an electron imbalance, with three electrons
170 required for Au³⁺ to Au⁰ while four electrons are released for every two molecules of water
171 oxidized. There are two possibilities to resolve this issue (47) the reduction of four atoms of
172 Au³⁺ are coupled to the oxidation of six molecules of water and (2) the reduction of one atom of
173 Au³⁺ is coupled to the oxidation of two molecules of water with the fourth electron used to
174 reduce dioxygen to superoxide. Assays show that reduced MB-SB2 will reduce dioxygen to
175 superoxide (Table S3). Under the low pH conditions following HAuCl₄ addition to MB-SB2 (Fig.
176 3) superoxide would be expected to undergo dismutation reactions generating H₂O₂ (48). In

177 addition, as observed in MB-OB3b (49), Au-MB-SB2 complexes show superoxide dismutase
178 activity (Table S3). Thus, H₂O₂ should appear in reaction mixtures if the fourth electron was
179 used to reduce dioxygen. The rate of ^{18,18}O₂ production increased by approximately 18%
180 following the addition of catalase, suggesting the production of H₂O₂ (Fig. 5).

181

182 **Oxidation of H₂O coupled to Cu²⁺ reduction by MB-SB2**

183 Although the oxidation of water to dioxygen coupled to Au³⁺ reduction is chemically interesting
184 it is not likely biologically relevant. To determine if the oxidation of H₂O was specific to Au³⁺
185 reduction or a more general property of metal ion reduction by MB-SB2, similar experiments in
186 H₂¹⁸O were carried out with CuCl₂ as it is believed the primary purpose of MB is the collection of
187 copper critical for methanotrophic activity. Previous spectral and thermodynamic studies have
188 shown MB-SB2 will reduce multiple Cu²⁺ to Cu⁺ in the absence of an external reductant,
189 suggesting that water served as the reductant (43). ^{18,18}O₂ evolution was observed following
190 the addition of CuCl₂ to a H₂¹⁸O solution of MB-SB2 (Fig 4C). Further, such evolution followed a
191 similar trend to that for HAuCl₄ and a substantial pH drop was observed (Fig. 3B - 5). Perhaps of
192 greater environmental relevance is the finding of substantial (>100 μM) evolution of dioxygen
193 from water oxidation when MB-SB2 bound and reduced copper (Fig. 5).

194 The ratio of AuCl₄⁻ and Cu²⁺ to MB-SB2 in the experiments described above, as well as
195 other metals showing ^{18,18}O₂ production (Fig. 4) described below was 10:1. To determine the
196 number of electrons needed to be extracted from MB-SB2 before water oxidation occurs,
197 reaction mixtures containing 0.5, 1, 2, 3, 4, and 5 Cu²⁺ per MB-SB2 in 97% H₂¹⁸O were examined.
198 No ^{18,18}O₂ was observed in samples containing 0.5, 1, 2, 3, or 4 Cu²⁺ per MB-SB2 (results not

199 shown). $^{18,18}\text{O}_2$ was observed in samples containing 5 Cu^{2+} per MB-SB2 indicating for the initial
200 water oxidation to occur five electrons must be extracted from MB-SB2 (Fig.4D).

201 K^+ was also examined as a metal ion bound by MB-SB2 (Fig. S6A), but not reduced, as no
202 evidence of the formation of metallic K^0 was observed (50). No $^{18,18}\text{O}_2$ was observed following
203 the addition of KCl (Fig.4E) and comparatively minor changes in pH (Fig. 3C) were observed
204 demonstrating water oxidation by MB-SB2 after binding a metal ion is contingent upon that
205 metal being reduced. MB-SB2 does not bind Mo^{2+} (Fig. S6B) and was used as a negative control.
206 As expected, no $^{18,18}\text{O}_2$ was observed in reaction mixtures containing NaMoO_4 and MB-SB2
207 (results not shown).

208

209 **Oxidation of H_2O coupled to Ag^+ , Hg^{2+} , Fe^{3+} , Ni^{2+} and Co^{2+} reduction by MB-SB2**

210 As described above Group A metal ions bound by MB-OB3b are reduced following binding. Ag^+
211 and Hg^{2+} are Group A metals, MB-SB2 bound both metals via an N_2S_2 coordination (Figs. S6C
212 and S6D) and $^{18,18}\text{O}_2$ was observed in reaction mixtures containing MB-SB2 and AgF (Fig. 4F) or
213 HgCl_2 (Fig. 4G) at levels similar to that observed with gold and copper .

214 In contrast to MB-OB3b (39), MB-SB2 binds all metal ions tested via an N_2S_2
215 coordination (40, 41, 43) (Fig. S6). Also in contrast to MB-OB3b, MB-SB2 will reduce Fe^{3+} to Fe^{2+}
216 at a rate of $1.02 \pm 0.09 \text{ min}^{-1}$ as measured via the ferrozine assay (51, 52)(Fig. 6A). In fact, MB-
217 SB2 will dissolve insoluble Fe^{3+} hydroxides in the light (Fig. S6E insert) or dark (Fig. 6C). The one
218 electron ferric iron reduction rate was approximately three times faster than the three electron
219 gold reduction rate. In reaction mixtures containing MB-SB2 and FeCl_3 (Fig. 4H) $^{18,18}\text{O}_2$ was
220 observed at concentrations 1.3 ± 0.1 fold higher than those observed with Au^{3+} and Cu^{2+} .

221 $^{18,18}\text{O}_2$ was also observed in reaction mixtures containing NiCl_2 (Figs. 4I and S6F) or CoCl_2 (Figs.
222 4H and S6G) and MB-SB2, although the concentration of $^{18,18}\text{O}_2$ was consistently low with CoCl_2 .

223

224 **Oxidation of H_2O coupled to Au^{3+} , Cu^{2+} , and Ag^+ reduction by MB-OB3b**

225 To determine if water oxidation coupled to metal ion reduction was specific to MB-SB2, a
226 Group II MB, or a more general property of MBs, water oxidation was examined in the Group I
227 MB from *M. trichosporium* OB3b (MB-OB3b) (53). Previous studies have shown MB-OB3b binds
228 and reduces Au^{3+} , Cu^{2+} and Ag^+ to Au^0 , Cu^+ and Ag^0 , respectively, and bound but did not reduce
229 Fe^{3+} (Fig. 6B; (39, 44)). Thus, $^{18,18}\text{O}_2$ production was monitored in reaction mixtures containing
230 HAuCl_4 , CuCl_2 , AgF and FeCl_3 with or without MB-OB3b prepared in 97% H_2^{18}O . Again, no $^{18,18}\text{O}_2$
231 production was observed in reaction mixtures containing either MB-OB3b alone (Fig. 7A) or
232 with HAuCl_4 , CuCl_2 or AgF alone (result not shown). However, following HAuCl_4 (Fig. 7B), CuCl_2
233 (Fig. 7C) or AgF (Fig. 7D) addition to reaction mixtures containing MB-OB3b, $^{18,18}\text{O}_2$ was
234 observed although the concentrations of $^{18,18}\text{O}_2$ were less than 25% of the $^{18,18}\text{O}_2$ produced in
235 similar reactions with MB-SB2. No $^{18,18}\text{O}_2$ was observed following FeCl_3 addition to a reaction
236 mixture containing MB-OB3b.

237

238 **Methane oxidation coupled to O_2 generated from Cu^{2+} reduction by MB-OB3b**

239 To determine if dioxygen generated during metal ion reduction could support methane
240 oxidation by *M. trichosporium* OB3b, incubations with $^{13}\text{CH}_4$ in the presence and absence of
241 MB-OB3b and Cu^{2+} were performed under anoxic conditions in an anaerobic glove box. In cell
242 suspensions with no additional amendments of either copper or MB-OB3b, $0.72 \pm 0.17 \mu\text{mol}$

243 $^{13}\text{CO}_2$ was observed after three days (assumed to be driven by the presence of residual
244 dioxygen in the reaction mixtures (Fig. 8)). In cell suspensions amended with $25\ \mu\text{M}\ \text{Cu}^{2+}$, $0.97 \pm$
245 $0.03\ \mu\text{mol}\ ^{13}\text{CO}_2$ was observed (a 34% increase, not significantly different from the amount of
246 $^{13}\text{CO}_2$ measured with no amendment, $p = 0.06$). If $5\ \mu\text{M}\ \text{MB-OB3b}$ were added instead, $1.47 \pm$
247 $0.08\ \mu\text{mol}\ ^{13}\text{CO}_2$ was measured (an increase of $\sim 104\%$, significantly greater from no
248 amendment, $p = 2.2 \times 10^{-3}$, presumably to MB-OB3b binding and reducing metals part of the
249 growth medium). If both $25\ \mu\text{M}\ \text{Cu}$ and $5\ \mu\text{M}\ \text{MB-OB3b}$ were added, $2.5 \pm 0.37\ \mu\text{mol}\ ^{13}\text{CO}_2$ was
250 observed, an increase of $\sim 250\%$ from that in no amendment (again significantly different, $p =$
251 1.5×10^{-3}), indicating that metal ion reduction by MB can support methane oxidation in anoxic
252 conditions (Fig.8).

253

254 **DISCUSSION**

255 Metal ion binding by MBs has focused on MB-OB3b, a Group I MB (34, 39, 44). MB-OB3b
256 bound Group A metal ions such as Cu^{2+} , Au^{3+} , Ag^+ , Hg^{2+} via an N_2S_2 ligand set. Other metal ions
257 such as Fe^{3+} , Co^{2+} , Cd^{2+} , Mn^{2+} , Ni^{2+} and Zn^{2+} showed an N_1S_1 coordination and were placed in
258 Group B. Of the metal ions examined Group A metals were reduced following binding whereas
259 Group B metal ions were not. In this and previous reports (40, 41, 43, 45), MB-SB2, a Group II
260 MB, coordinates all metals bound via N_2S_2 coordination and reduced metals previously place
261 Group A and B. With the exception of K^+ , metal ions bound via an N_2S_2 coordination are
262 reduced and here we show that H_2O can serve as an electron donor driving metal ion reduction.

263 The finding that MB, after binding specific metal ions can split water to form dioxygen
264 and that this reaction can drive methane oxidation under anoxic conditions suggests that this

265 may be another strategy whereby aerobic methanotrophy can occur in an anoxic environment.
266 That is, it has been shown that methane oxidation via aerobic methanotrophy occurs in anoxic
267 zones of shallow lakes (i.e., at a depth of ~10 m), with such activity driven by oxygenic
268 photosynthesis as sunlight could penetrate to this depth (54, 55). In these studies, it was found
269 that methane oxidation rates increased in the light vs. dark, and such activity was abolished
270 when a selective inhibitor of photosynthesis was added. Thus, it appears that methanotrophs
271 can form very effective relationships with oxygenic photosynthetic microbes to scavenge trace
272 amounts of dioxygen, and by so doing, enhance methane removal from these environments.

273 More germane to the findings here, however, is the discovery that aerobic
274 methanotrophs were also active in deep lake water (~160 m) where oxygenic photosynthesis is
275 highly unlikely as sunlight cannot penetrate to this depth (56). Such activity, however, could be
276 stimulated by the addition of dioxygen and oxidized metals. Here it was concluded that
277 methanotrophs may survive anoxic environments by utilizing alternative electron acceptors.
278 Others have shown that aerobic methanotrophs of the *Methylobacter* genus can be stimulated
279 in anoxic lake waters through the addition of either nitrate or sulfate (57). Indeed, it has been
280 shown that some aerobic methanotrophs can respire nitrate (24) or ferric iron (25). Such a
281 strategy could conserve trace amounts of dioxygen to enable methane oxidation by the MMOs.
282 Alternatively, it has been shown that some methanotrophs will couple methane oxidation to
283 fermentation to putatively conserve dioxygen (58), and such a strategy has been speculated to
284 be responsible for methanotrophic activity in dioxygen-limited lakes (57). Finally, it has been
285 speculated that alternatively or in conjunction, methanotrophs may form syntrophic
286 partnerships with other microbes to facilitate methane oxidation (57) when dioxygen is limiting.

287 It should be noted, however, that in studies of methane oxidation in anoxic lake water
288 samples, great care was taken to exclude any oxygen intrusion and any trace amounts of
289 oxygen present were quite small and could not explain the extent of methane oxidation
290 observed. How these microbes then are able to oxidize methane in the absence of dioxygen is
291 still unclear. That is, for the identified methanotrophs to oxidize methane, dioxygen is required
292 for either form of MMO regardless if alternative terminal electron acceptors can be used or if
293 effective microbial partnership(s) can be formed. Thus, either unknown sources of dioxygen
294 exist in these environments and/or these microbes possess some novel, as yet undescribed
295 mechanism of anaerobic methane oxidation, i.e., novel forms of MMO that can utilize oxidized
296 sulfur and nitrogen species in place of dioxygen.

297 Here we present an alternative explanation for the presence and activity of aerobic
298 methanotrophs in anoxic environments, particularly alphaproteobacterial methanotrophs. That
299 is, genes for MB biosynthesis have only been found in the genomes of various *Methylosinus* and
300 *Methylocystis* species of the *Alphaproteobacteria* (53). It has been repeatedly shown that these
301 genera prefer high methane/low oxygen conditions found at the oxic-anoxic interface *in situ*
302 (59, 60). Further, they are the predominant methanotrophic genera present in completely
303 anoxic zones of rice paddy soils (61). Thus, it is tempting to speculate that the ability to produce
304 MB enables methanotrophs to colonize methane-rich environments by self-producing dioxygen
305 to ensure that methane oxidation can continue even when ambient concentrations of dioxygen
306 are quite low. Such a strategy is particularly important for methanotrophs that colonize the
307 oxic-anoxic interface in soils, for not only are these locations dark (thus excluding the possibility
308 of methanotrophy/phototrophy synergy), this interface shifts quickly in response to episodic

309 precipitation and drying periods. As such, methanotrophs that colonize this interface must be
310 prepared to tolerate periodic and possibly quite extended anoxic conditions. The ability to
311 produce dioxygen from water would thus enable these microbes to continue to oxidize
312 methane under anoxia, thereby generating ATP, as well as providing intermediates required for
313 carbon assimilation (i.e., formaldehyde). Doing so would enable them to survive extended
314 periods in the absence of oxygen, if not allow for some continued growth in anoxic conditions.

315 It should be noted, however, is that in aforementioned lake studies concluding aerobic
316 methanotrophy occurs in anoxic environments, gammaproteobacterial methanotrophs
317 appeared to be predominantly responsible for methane oxidation and to date, no
318 representatives of this group have been shown to have the genes required for MB biosynthesis,
319 although it is clear that at least some can and do secrete a copper-binding compound (62). It
320 may be that these methanotrophs utilize dioxygen created by others via MB production (i.e.,
321 some sort of collaboration between gamma- and alpha-proteobacteria as concluded between
322 methanotrophs and oxygenic photosynthetic microbes) and/or also can generate dioxygen via
323 some unknown mechanism.

324 Finally, prior to discovery of dioxygen production via splitting of water by metal-MB
325 complexes reported here, dioxygen production by biological systems has been observed in only
326 four known pathways: oxygenic photosynthesis (63, 64), detoxification of oxygen radicals (65,
327 66), (per)chlorate respiration (67) and nitric oxide dismutation by *Candidatus Methyloirabilis*
328 oxyferans of the NC10 phylum (68). The latter two mechanisms may provide some explanation
329 as to the significance of MB-mediated water oxidation. That is, it has been shown that dioxygen
330 evolution from (per)chlorate respiration occurs when the intermediate chlorite is dismutated to

331 chloride and dioxygen, and it is speculated that the dioxygen is then used for an antibiotic-
332 producing monooxygenase in *Haloferaxvol- volcanii* (69). Further, *Ca. M. oxyferans* is a
333 methanotroph, but respire nitrite rather than dioxygen. Interestingly, dioxygen is critical for its
334 growth as this microbe utilizes the membrane-associated methane monooxygenase for
335 methane oxidation to methanol (68). Stable isotope studies showed that *Ca. M. oxyferans*
336 dismutates nitric oxide to dinitrogen and dioxygen, the latter which is used for methane
337 oxidation (the mechanism(s) by which this occurs, however, is still unknown). It may be that
338 MB-expressing aerobic methanotrophs perform a similar feat to ensure that there is adequate
339 dioxygen for continued MMO activity in hypoxic/anoxic conditions.

340 In conclusion, the discovery of water oxidation by specific metal-methanobactin
341 complexes is not only unusual, it also implies a strategy whereby aerobic methanotrophs can
342 survive, if not thrive in anoxic conditions. As such, MB-driven dioxygen generation may be an
343 important but hitherto unrecognized process whereby methane emissions are regulated.

344

345 MATERIALS AND METHODS

346 Materials

347 Anhydrous CuCl_2 (Acros Organics, Geel, Belgium), HAuCl_4 (Acros Organics), HgCl_2 (Acros
348 Organics, Geel, Belgium), AgF (Acros Organics, Geel, Belgium), FeCl_3 (Acros Organics, Geel,
349 Belgium), NiCl_2 (Acros Organics, Geel, Belgium), CoCl_2 (Acros Organics, Geel, Belgium), NaMoO_4
350 (Sigma-Aldrich) and KCl (Sigma-Aldrich) were stored in a desiccator under Ar_2 . H_2^{18}O was
351 obtained from Cambridge Isotope Laboratories, Inc. (Andover, MA, USA) and $^{18,18}\text{O}_2$ from Sigma
352 Aldrich. Ar_2 , $^{16,16}\text{O}_2$ and CP grade CH_4 were obtained from Airgas USA LLC. HPLC grade

353 acetonitrile, methanol and other reagents/chemicals were purchased from Fisher Scientific and
354 used without additional purification. Dianion HP-20 was purchased from Sigma-Aldrich C. LLC.

355

356 **Organism, Culture Conditions and Isolation of Methanobactin**

357 *Methylocystis* strain SB2 and *M. trichosporium* OB3b were cultured in nitrate mineral salts
358 media (70) amended with either 0.2 or 1.0 μM CuSO_4 to optimize production of its
359 methanobactin (MB-SB2). MB-SB2 was purified from the spent media as previously described
360 with the following exception (71). The freeze-dried sample from the Dianion HP20 column was
361 resuspended in deionized H_2O and loaded onto a 250mm x 20mm Targa C18 column (Higgins
362 Analytical Inc., Mountain View, Ca, USA) on an Azurk HPLC system (Knauer, Berlin, Germany).
363 MB-SB2 eluted in the 12-25% methanol fraction in a methanol: H_2O gradient. The purified
364 methanobactin was then freeze-dried as described above.

365

366 **X-Ray Photoelectric Spectroscopy (XPS)**

367 XPS was performed as previously described (39, 44) with the following modifications. HAuCl_4
368 and HAuCl_4 plus MB-SB2 samples were dried onto highly oriented pyrolytic graphite by freeze-
369 drying. The 1 cm square graphite substrates were immersed in either HAuCl_4 or HAuCl_4 plus MB-
370 SB2 solutions, frozen in liquid nitrogen and lyophilized overnight. The graphite was then
371 mounted onto an XPS puck and analyzed. Other drying methods were employed such as drying
372 in air under a stream of He gas with a drying time of 30 min or filtered through a porous
373 alumina filter followed by a 2 min drying time. However, samples produced by these methods
374 showed additional reduction.

375 As previously observed (39), XPS analysis of Au was complicated by X-ray induced
376 reduction during the measurement process. Au 4f peak areas were therefore measured as a
377 function of X-ray exposure, the peak areas for a given X-ray dose determined using the CASA
378 XPS fitting program, and the areas plotted as a function of time. An exponential fit to the data
379 using Igor Pro fitting program allowed a determination of the unirradiated sample's Au³⁺ and
380 Au⁰ peak areas.

381 XPS measurements were carried out on a custom-designed system that incorporated a
382 SPECS hemispherical analyzer (SPECS Scientific Instruments, Sarasota, FL, USA), Al X-ray source,
383 and load-lock to allow for rapid sample exchanges.

384

385 **Kinetics of Au³⁺ Binding.** The rates of Au³⁺ binding to mb-SB2 were determined by measuring
386 absorption changes at 338 nm and 387 nm using a four-syringe Biologic SFM/4000/S stopped
387 flow reactor coupled to a MOS-500 spectrophotometer (Bio-Logic (40). Science Instrument SA,
388 Claix, France) at 4°C as previous described (40). In contrast to the absorbance maxima using
389 Cary 50 spectrometer, the absorbance maximum for the oxazolone was 338 nm and for the
390 imidazolone ring 387 nm on with this system. Stock solutions of HAuCl₄ were prepared in
391 >18MΩ•cm H₂O. The stock solutions for MB-SB2 were prepared by dissolving freeze-dried MB-
392 SB2 in > 18MΩ•cm H₂O. Final concentration of the stock solutions of MB-SB2 were determined
393 after filtration by UV-visible absorption spectroscopy as previously described (40). Path length
394 for the cuvette used in the Biologic SFM/4000/S stopped flow reactor was 1.5 mm and dead
395 time of the system was 1.4 ms. The system was cooled and maintained at 4°C. Reaction
396 mixtures contained 400 μM of MB-SB2 and either 40, 100, 200, 240, 280, 320, 360, 400, 600,

397 700, or 800 μM of HAuCl_4 . Rates obtained for each concentration were an average of either 5 or
398 7 traces. The rates were determined by fitting the traces to the exponential function in Biokine
399 operational software (Bio-Logic Science Instrument SA). Binding rates were calculated in mol Au
400 bound per sec per mol MB-SB2 and reported as the binding number (s^{-1}).

401 Fluorescence changes overtime were monitored at 429 nm on a Cary Eclipse (Agilent
402 Technologies Inc. Santa Clara, CA, USA following excitation at 341nm.

403

404 **Water Oxidation**

405 Saturated solutions of anhydrous CuCl_2 , HAuCl_4 , HgCl_2 , AgF , FeCl_3 , NiCl_2 , CoCl_2 , NaMoO_4 and KCl
406 were prepared in a Coy anaerobic chamber (atmosphere 95% Ar 5% H_2)(Coy Laboratory
407 Products, Ann Arbor, MI, USA). Oxidation of $2\text{H}_2\text{O}$ to $\text{O}_2 + 4\text{H}^+$ in reaction mixtures containing a
408 metal ion and either MB-SB2 or MB-OB3b was determined by monitoring production of $^{18,18}\text{O}_2$
409 and H^+ and in the case of HAuCl_4 , production of Cl^- . In oxygen evolution experiments, freeze-
410 dried MB-SB2, MB-OB3b, catalase, as well as anhydrous metal stock solution were prepared in
411 97% H_2^{18}O (Sigma Aldrich, St. Louis, Mo, USA) in 0.8 ml brown airtight vials (DWK Life Sciences,
412 Millville, NJ, USA). Reaction mixtures contained 0 or 2mM MB-SB2 or MB-OB3b and 0 – 20mM
413 metal ion in a final volume of 100 μl H_2^{18}O . Reaction mixtures were prepared in 2 ml brown
414 serum vials, sealed with Teflon lined silicon septa. Initial experiments were determined with
415 aluminum foil wrapped vials, but that practice was discontinued once it was clear that identical
416 results were produced regardless if vials were wrapped or not. Generation of $^{18,18}\text{O}_2$ from H_2^{18}O
417 was monitored by direct injection (1 μl or 2 μl) of head space.

418 Gas samples were manually injected into an Agilent 7890B GC system (Santa Clara, CA,
419 USA with a 7250 Accurate-Mass Q-TOF GC/MS and a DB5-ms column. Except for the $^{18,18}\text{O}_2$
420 injections for standard curves, all injections were $1\mu\text{l}$ using gas tight Hamilton syringes.
421 Standard curves were generated with $1\mu\text{l}$, $1.5\mu\text{L}$ and $2\mu\text{l}$ injections of 97% $^{18,18}\text{O}_2$ (Sigma
422 Aldrich, St. Louis, Mo, USA). The head space in the vials was sampled before and after the
423 addition of the metals, as was the outside air in the mass spectroscopy as controls. After the
424 standards and controls were injected, the samples were mixed and head space samples were
425 immediately collected, with subsequent samples taken every 30-60 seconds. After several
426 minutes, collection slowed to 1 sample every 2-3 minutes. The quantization of generated $^{18,18}\text{O}_2$
427 came from an extracted-ion chromatogram set to 35.9978 Da. A small shift in the MS location
428 of the $^{18,18}\text{O}_2$ was observed on some dates. If a drift in the MS of $^{18,18}\text{O}_2$ was observed, identity
429 of the peak was verified with 97% $^{18,18}\text{O}_2$ standard.

430

431 **Oxidase, Superoxide Dismutase, Hydrogen Peroxide Reductase and Iron reductase Activity**
432 **and pH Measurements**

433 Oxidase, superoxide dismutase and hydrogen peroxide reductase activity were determined as
434 previously described by Choi *et al.* (49). Ferrozine assay was used to determine iron reductase
435 activity (51, 52).

436 pH changes during metal titrations were monitored on either a Radiometer PHM 220
437 meter with a pH2005-7 combined pH electrode (Radiometer Analytical, Villeurbanne Cerdex,
438 France) or on an Oakion Ion 700 pH meter (Cole-Parmer, Vermon Hills, IL, USA).

439 Free chloride produced from the binding and deduction of HAuCl_4 to Au^0 was measured
440 via argentometric titration (72). HAuCl_4 :MB-SB2 solutions were prepared at a molar ratio of 9:1
441 and incubated for at least 72 h. Following the incubation period, the solution was titrated with
442 a standardized AgNO_3 solution, delivered with a Ramé-hart 2.0 ml microsyringe. The titration
443 processes were monitored with a custom-made Ag wire working electrode and Ag/AgCl
444 reference electrode.

445

446 **Methane oxidation coupled to O_2 generated from Cu^{2+} reduction by MB-OB3b**

447 **Sample preparation.** *M. trichosporium* OB3b was grown on nitrate mineral salts medium (NMS)
448 (70) at 30°C in 250-ml side-arm flask sealed with rubber stoppers. Cultures were shaken at 200
449 rpm under a methane-to-air ratio of 1:2, until the mid-exponential phase ($\text{OD}_{600} \sim 0.3$). 2 ml of
450 the cell culture was then transferred to 8.5 ml serum vials containing a Teflon-coated magnetic
451 stir bar. Four separate conditions were prepared: (1) *M. trichosporium* OB3b with no
452 amendments; (2) *M. trichosporium* OB3b + 25 μM copper (5 μl added from a filter sterilized
453 (0.22 μm) 10 mM stock solution of CuCl_2); (3) *M. trichosporium* OB3b + 5 μM MB-OB3b (10 μl
454 added from a filter sterilized (0.22 μm) 1 mM stock solution of MB-OB3b), and (4) *M.*
455 *trichosporium* OB3b + 25 μM copper + 5 μM MB-OB3b. Biological triplicate samples were
456 prepared for all conditions. The vials were then crimp-sealed and degassed using pre-purified
457 grade filter-sterilized (0.22 μm) nitrogen gas (N_2 , 99.998%) for 20 minutes at a flow rate of 3.42
458 ml/s using 22- and 25-gauge needles for N_2 gas flow in and out. After degassing, the needles
459 were removed and the samples immediately placed in an anaerobic chamber filled with a H_2/N_2
460 gas mixture (1:9 mixing ratio). Once in the anaerobic chamber, 1 ml of ^{13}C -labeled methane

461 ($^{13}\text{CH}_4$, 99%) (Sigma-Aldrich, St. Louis, MO) was added using a 10 ml gas-tight syringe (Hamilton
462 Company, Reno, NV). Vacuum-grease was then spread on the top of the sealed septa. The vials
463 were finally covered by aluminum foil and incubated inverted (septum side down) on a
464 magnetic stir plate in the anaerobic chamber for 3 days at 25°C.

465 **Gas chromatography/mass spectrometry analysis.** Gas chromatography/mass
466 spectrometry (GC/MS) analyses was performed using an Agilent 7890B gas chromatograph
467 system coupled with Agilent 5977B single quadrupole mass spectrometer (Agilent
468 Technologies, Santa Clara, CA, USA). A Carboxen[®]-1010 PLOT capillary column with 30 m \times 0.32
469 mm was used for separation (Supelco, Bellefonte, PA). 10 μL of headspace gas of each sample
470 was injected manually using a 25 μL gas-tight syringe (Hamilton Company, Reno, NV). GC
471 system conditions were as follows: carrier gas and flow rate, He 10 ml/min; split injection with
472 split ratio of 5:1; inlet temperature 170°C; oven temperature maintained at 145°C throughout
473 the analysis. The mass spectrometry ion source and quadrupole temperatures were 250°C and
474 200°C, respectively. Under these conditions $^{13}\text{CH}_4$ and $^{13}\text{CO}_2$ were detected at 2.16 min and
475 2.86 min, respectively. Data were acquired in selected ion monitoring (SIM) mode, monitoring
476 m/z 17 for $^{13}\text{CH}_4$ and m/z 45 for $^{13}\text{CO}_2$.

477

478 **ACKNOWLEDGEMENTS**

479 **Funding:** This research was supported by the U.S. Department of Energy Office of Science
480 (Grants #DE-SC0018059; JDS and ADS), the National Science Foundation (Grant #1912482; JDS),
481 the Materials Science and Engineering Center at UW-Eau Claire (MTM), and the ISU Bailey
482 Research and Career Development (TAB). Use of ITC and Biologic SFM/4000 stopped flow

483 reactor coupled to a MOS-500 spectrophotometer was made possible through a generous gift
484 from the Roy J. Carver Charitable Trust (Muscatine, Iowa).
485 **Competing interests:** Authors declare they have no competing interests.

486 REFERENCES

- 487 1. Semrau JD, DiSpirito AA, Yoon S. 2010. Methanotrophs and copper. *FEMS Microbiol*
488 *Rev* 34:496-531.
- 489 2. Basu P, Katterle B, Andersson KK, Dalton H. 2003. The membrane-associated form of
490 methane mono-oxygenase from *Methylococcus capsulatus* (Bath) is a copper/iron
491 protein. *Biochem J* 369:417-427.
- 492 3. Choi DW, Kunz RC, Boyd ES, Semrau JD, Antholine WE, Han JI, Zahn JA, Boyd JM, de
493 la Mora AM, DiSpirito AA. 2003. The membrane-associated methane
494 monooxygenase (pMMO) and pMMO-NADH:quinone oxidoreductase complex from
495 *Methylococcus capsulatus* Bath. *J Bacteriol* 185:5755-64.
- 496 4. Elango N, Radhakrishnan R, Froland WA, Wallar BJ, Earhart CA, Lipscomb JD,
497 Ohlendorf DH. 1997. Crystal structure of the hydroxylase component of methane
498 monooxygenase from *Methylosinus trichosporium* OB3b. *Protein Sc* 6:556 - 568.
- 499 5. Fox BG, Hendrich MP, Surerus KK, Andersson KK, Froland WA, Lipscomb JD, Münck
500 E. 1993. Mössbauer, EPR, and ENDOR studies of the hydroxylase and reductase
501 components of methane monooxygenase from *Methylosinus trichosporium* Ob3b. *J*
502 *Am Chem Soc* 115:3688-3701.
- 503 6. Lipscomb JD. 1994. Biochemistry of the soluble methane monooxygenase. *Ann Rev*
504 *Microbiol* 48:371-399.
- 505 7. Colby J, Dalton H. 1978. Resolution of the methane monooxygenase of *Methylococcus*
506 *capsulatus* (Bath) into three components. Purification and properties of component
507 C, a flavoprotein. *Biochem J* 171:461 - 468.

- 508 8. Lieberman RL, Rosenzweig AC. 2005. Crystal structure of a membrane-bound
509 metalloenzyme that catalyses the biological oxidation of methane. *Nature* 434:177-
510 182.
- 511 9. Dalton H, Prior SD, Leak DJ, Stanley SH. 1984. Regulation and Control of Methane
512 Monooxygenase. *In* Crawford RL, Hanson RS (ed), *Microbial Growth in C1*
513 *Compounds*. American Society for Microbiology, Washington, D.C.
- 514 10. Zahn JA, Bergmann DJ, Boyd JM, Kunz RC, DiSpirito AA. 2001. Membrane-associated
515 quinoprotein formaldehyde dehydrogenase from *Methylococcus capsulatus* Bath. *J*
516 *Bacteriol* 183:6832-6840.
- 517 11. DiSpirito AA, Kunz RC, Choi DW, Zahn JA. 2004. Electron flow during methane
518 oxidation in methanotrophs., p 141-169. *In* Zannoni D (ed), *Respiration in Archaea*
519 *and Bacteria* Kluwer Scientific, The Netherlands.
- 520 12. Picone N, Camp HJMOd. 2019. Role of rare earth elements in methanol oxidation.
521 *Curr Opin Chem Biol* 49:39-44.
- 522 13. Anthony C. 1982. *The Biochemistry of Methylotrophs*. Academic Press, London.
- 523 14. Anthony C. 1992. The structure of bacterial quinoprotein dehydrogenases. *Int J*
524 *Biochem* 24:29 - 30.
- 525 15. Williams PA, Coates L, Mohammed F, Gill R, Erskine PT, Coker A, Wood SP, Anthony
526 C, Cooper JB. 2004. The atomic structure of methanol dehydrogenase from
527 *Methylobacterium extorquens*. *Biol Crystall* D61:75-79.
- 528 16. Read J, Gill R, Dales SL, Cooper JB, Wood SP, Anthony C. 1999. The molecular
529 structure of an unusual cytochrome c_2 determined at 2.0Å; the cytochrome c_H from
530 *Methylobacterium extorques*. *Protein Sc* 8:1232-1240.

- 531 17. DiSpirito AA, Lipscomb JD, Lidstrom ME. 1990. Soluble cytochromes from the
532 marine methanotroph *Methylomonas* sp. strain A4. J Bacteriol 172:5360-7.
- 533 18. Vorholt JA. 2002. Cofactor-dependent pathways of formaldehyde oxidation in
534 methylotrophic bacteria. Arch Microbiol 178:239-49.
- 535 19. Vorholt JA, Chistoserdova L, Lidstrom ME, Thauer RK. 1998. Distribution of
536 tetrahydromethanopterin-dependent enzyme in methylotrophic bacteria and
537 phylogeny of methenyl tetrahydromethopterin cyclohydrolases. J Bacteriol
538 180:5351 - 5756.
- 539 20. Vorholt JA, Chistoserdova L, Stolyar SM, Thauer RK, Lidstrom ME. 1999. Distribution
540 of tetrahydromethanopterin-dependent enzymes in methylotrophic bacteria and
541 phylogeny of methenyl tetrahydromethanopterin cyclohydrolases. J Bacteriol
542 181:5750-5757.
- 543 21. Jollie DR, Lipscomb JD. 1990. Formate dehydrogenase from *Methylosinus*
544 *trichosporium* OB3b. Meth Enzymol 188:331 - 334.
- 545 22. Jollie DR, Lipscomb JD. 1991. Formate dehydrogenase from *Methylosinus*
546 *trichosporium* OB3b. J Biol Chem 266:21853 - 21863.
- 547 23. Yoch DC, Chen CL, Hardt MG. 1990. Formate dehydrogenase from the methane
548 oxidizer *Methylosinus trichosporium* OB3b. J Bacteriol 172:4456 - 4463.
- 549 24. Kits KD, Klotz MG, Stein LY. 2015. Methane oxidation coupled to nitrate reductio
550 under hypoxia by gammaproteobacterium *Methylomonas denitrificans*, sp. nov. type
551 strain FJG1. Environ Microbiol 17:3219-3232.

- 552 25. Sheng Y, Wang H, Liu Y, Zhu B, Li J, Yang Y, Qin W, Chen L, Wu X, Chistoserdova L,
553 Zhao F. 2020. Methane-dependent mineral reduction by aerobic methanotrophs
554 under hypoxia. *Environ Sc Technol Lett* doi:doi.org/10.1021/acs.estlett.0c00436.
- 555 26. Csaki R, Bodrossy L, Klem J, Murrell JC, Kovacs KL. 2003. Genes involved in the
556 copper-dependent regulation of soluble methane monooxygenase of *Methylococcus*
557 *capsulatus* (Bath): cloning, sequencing and mutational analysis. *Microbiology*
558 149:1785-1795.
- 559 27. Murrell JC, McDonald IR, Gilbert B. 2000. Regulation of expression of methane
560 monooxygenases by copper ions. *Trend Microbiol* 8:221-225.
- 561 28. Prior SD, Dalton H. 1985. Copper stress underlines the fundamental change in
562 intracellular location of the membrane monooxygenase in methane oxidizing
563 organisms: studies in batch and ontinuous culture. *J Gen Microbiol* 131:155 - 163.
- 564 29. DiSpirito AA, Semaru JD, Murrell JC, Gallagher WH, Dennison C, Vuilleumier S. 2016.
565 Methanobactin and the link between copper and bacterial methane oxidation.
566 *Microbiol Mol Biol Rev* 80:387-409.
- 567 30. El Ghazouani A, Basle A, Gray J, Graham DW, Firbank SJ, Dennison C. 2012.
568 Variations in methanobactin structure influences copper utilization by methane-
569 oxidizing bacteria. *Proc Natl Acad Sci U S A* 109:8400-4.
- 570 31. Semrau JD, DiSpirito AA, Obulisamy PK, Kang-Yun CS. 2020. Methanobactin from
571 methanotrophs: genetics, structure, function and potential applications. *FEMS*
572 *Microbiol Lett* 367:fnaa045.

- 573 32. Kim HJ, Graham DW, DiSpirito AA, Alterman MA, Galeva N, Larive CK, Asunskis D,
574 Sherwood PMA. 2004. Methanobactin, a copper-acquisition compound from
575 methane-oxidizing bacteria. *Science* 305:1612-1615.
- 576 33. Behling LA, Hartsel SC, Lewis DE, DiSpirito AA, Choi DW, Masterson LR, Veglia G,
577 Gallagher WH. 2008. NMR, mass spectrometry and chemical evidence reveal a
578 different chemical structure for methanobactin that contains oxazolone rings. *J Am*
579 *Chem Soc* 130:12604-5.
- 580 34. El Ghazouani A, Basle A, Firbank SJ, Knapp CW, Gray J, Graham DW, Dennison C.
581 2011. Copper-binding properties and structures of methanobactins from
582 *Methylosinus trichosporium* OB3b. *Inorg Chem* 50:1378-91.
- 583 35. Kenney GE, Goering AW, Ross MO, DeHart CJ, Thomas PM, Hoffman BM, Kelleher NL,
584 Rosenzweig AC. 2016. Characterization of methanobactin from *Methylosinus* sp.
585 SW4. *J Am Chem Soc* 138:11124 - 11127.
- 586 36. Krentz BD, Mulheron HJ, Semrau JD, DiSpirito AA, Bandow NL, Haft DH, Vuilleumier
587 S, Murrell JC, McEllistrem MT, Hartsel SC, Gallagher WH. 2010. A comparison of
588 methanobactins from *Methylosinus trichosporium* OB3b and *Methylocystis* strain SB2
589 predicts methanobactins are synthesized from diverse peptide precursors modified
590 to create a common core for binding and reducing copper ions. *Biochemistry*
591 49:10117-10130.
- 592 37. Gu W, Baral BS, DiSpirito AA, Semrau JD. 2017. An aminotransferase is responsible
593 for the deamination of the N-terminal leucine and required for formation of
594 oxazolone ring A in Methanobactin of *Methylosinus trichosporium* OB3b. *Appl*
595 *Environ Microbiol* 82:e01619-16.

- 596 38. Kim HJ, Graham DW, DiSpirito AA, Alterman MA, Galeva N, Larive CK, Asunskis D,
597 Sherwood PM. 2004. Methanobactin, a copper-acquisition compound from methane-
598 oxidizing bacteria. *Science* 305:1612-5.
- 599 39. Choi DW, Do YS, Zea CJ, McEllistrem MT, Lee SW, Semrau JD, Pohl NL, Kisting CJ,
600 Scardino LL, Hartsel SC, Boyd ES, Geesey GG, Riedel TP, Shafe PH, Kranski KA,
601 Tritsch JR, Antholine WE, DiSpirito AA. 2006. Spectral and thermodynamic
602 properties of Ag(I), Au(III), Cd(II), Co(II), Fe(III), Hg(II), Mn(II), Ni(II), Pb(II), U(IV),
603 and Zn(II) binding by methanobactin from *Methylosinus trichosporium* OB3b. *J Inorg*
604 *Biochem* 100:2150-61.
- 605 40. Baral BS, Bandow NL, Vorobev A, Freemeier BC, Bergman BH, Herdendorf T, Fuentes
606 N, Ellias L, Turpin E, Semrau JD, Di Spirito AA. 2014. Mercury binding by
607 methanobactin from *Methylocystis* strain SB2. *J Inorgan Biochem* 141:161 - 169.
- 608 41. Bandow NL. 2014. Isolation and binding properties of methanobactin from the
609 facultative methanotroph *Methylocystis* strain SB2. Ph.D. Iowa State University,
610 Ames, IA.
- 611 42. Lu X, Gu W, Zhao L, Fagan UHM, DiSpirito AA, Semrau JD, Gu B. 2017. Methylmercury
612 uptake and degradation by methanotrophs. *Science Adv* 3:e1700041.
- 613 43. Bandow N, Gilles VS, Freesmeier B, Semrau JD, Krentz B, Gallaghe W, McEllistrem
614 MT, Hartse SC, Cho DW, Hargrove MS, Heard TM, Chesner LM, Braunreiter KM, Cao
615 BV, Gavitt MM, Hoopes JZ, Johnson JM, Polster EM, Schoenick BD, A.M. U, DiSpirito
616 AA. 2012. Spectral and copper binding properties of methanobactin from the
617 facultative methanotroph *Methylocystis* strain SB2. *J Inorgan Biochem* 110:72 - 82.

- 618 44. Choi DW, Zea CJ, Do YS, Semrau JD, Antholine WE, Hargrove MS, Pohl NL, Boyd ES,
619 Geesey GG, Hartsel SC, Shafe PH, McEllistrem MT, Kisting CJ, Campbell D, Rao V, de la
620 Mora AM, Dispirito AA. 2006. Spectral, kinetic, and thermodynamic properties of
621 Cu(I) and Cu(II) binding by methanobactin from *Methylosinus trichosporium* OB3b.
622 *Biochemistry* 45:1442-53.
- 623 45. Baral BS. 2017. Methanobactin: Metal binding properties, physiological function and
624 biosynthesis. Ph.D. Iowa State University.
- 625 46. Zahao P, Astruc NLD. 2013. State of the art in gold nanoparticle synthesis. *Coord*
626 *Chem Rev* 257:638-665.
- 627 47. Chatwood LL, Müller J, Gross JD, Wagner G, S.J. L. 2004. NMR structure of the flavin
628 domain from soluble methane monooxygenase reductase from *Methylococcus*
629 *capsulatus* (Bath). *Biochemistry* 43:11983 - 11991.
- 630 48. Hayyan M, Hashim MA, AlNashef IM. 2016. Superoxide ion: generation and chemical
631 implications. *Chem Rev* 116:3029 - 3065.
- 632 49. Choi DW, Semrau JD, Antholine WE, Hartsel SC, Anderson RC, Carey JN, Dreis AM,
633 Kenseth EM, Renstrom JM, Scardino LL, Van Gorden GS, Volkert AA, Wingad AD,
634 Yanzer PJ, McEllistrem MT, de la Mora AM, DiSpirito AA. 2008. Oxidase, superoxide
635 dismutase, and hydrogen peroxide reductase activities of methanobactin from types
636 I and II methanotrophs. *J Inorg Biochem* 102:1571-80.
- 637 50. Latimer WM, Hildebrand JH. 1940. Reference Book of Inorganic Chemistry. The
638 Macmillan Co. , New York, NY, USA.
- 639 51. Carter P. 1971. Spectrometric determination of serum iron at the submicrogram
640 level with a new reagent (ferrozine). *Anal Biochem* 40:450-458.

- 641 52. Moody MD, Dailey HA. 1983. Aerobic ferrisiderophore reductase assay and activity
642 stain for native polyacrylamide gels. *Anal Biochem* 134:235-239.
- 643 53. Semau JD, DiSpirito AA, Obulisamy PK, Kang CS. 2020. Methanobactin from
644 methanotrophs: genetics, structure, function and potential applications. *FEMS*
645 *Microbiol Lett* 367:feaa045.
- 646 54. Milucka J, Kirf M, Lu L, Krupke A, Lam P, Littmann S, Kuypers MMM, Schubert CJ.
647 2015. Methane oxidation coupled to oxygenic photosynthesis in anoxic waters. *ISME*
648 *J* 9:1991-2002.
- 649 55. Oswald K, Milucka J, Brand A, Littmann S, Wehrll B, Kuypers MMM, Schubert CJ.
650 2015. Light-dependent aerobic methane oxidation reduces methane emissions from
651 seasonally stratified lakes. *PLOS One* 10.1371/journal.pone.0132574.
- 652 56. Oswald K, Jegge C, Tischer J, Berg J, Brand A, Miracle MR, Soria X, Vicente E,
653 Lehmann M, Zopfi J, Schubert CJ. 2016. Methanotrophy under versatile conditions in
654 water column of the ferruginous meromictic lake La Cruz (Spain). *Front Microbiol*
655 7:7:1762. doi: 10.3389/fmicb.2016.01762.
- 656 57. van Grinsven S, Damste JSS, Harrison J, Villanueva L. 2020. Impact of electron
657 acceptor availability on methane-influenced microorganisms in an enrichment
658 culture obtained from a stratified lake. *Front Microbiol* 10:3389/micb.2020.00715.
- 659 58. Gilman A, Fu Y, Hendershott M, Chu F, Puri AW, Smith AL, Pesecky M, Lieberman R,
660 Beck DAC. 2017. Oxygen-limited metabolism in the methanotroph
661 *Methylomicrobium buryatense* 5GB1C. *PeerJ* 5:e3945.
- 662 59. Amaral JA, Knowles R. 1995. Growth of methanotrophs in methane and oxygen
663 counter gradients. *FEMS Microbiol Lett* 216:215-220.

- 664 60. Henckel T, Roslev P, Conrad R. 2000. Effects of O₂ and CH₄ on presence and activity
665 of the indigenous methanotrophic community in rice field soil *Microbiology* 2:666-
666 679.
- 667 61. Lee HJ, Jeong SE, Kim PJ, Madsen EL, Jeon CO. 2015. High resolution depth
668 distribution of Bacteria, Archaea, methanotrophs, and methanogens in the bulk and
669 rhizosphere soils of a flooded rice paddy. *Front, Microbiol*
670 6:doi.org/10.3389/fmicb.2015.00639.
- 671 62. Choi DW, Bandow NL, McEllistrem MT, Semrau JD, Antholine WE, Hartsel SC,
672 Gallagher W, Zea CJ, Pohl NL, Zahn JA, DiSpirito AA. 2010. Spectral and
673 thermodynamic properties of methanobactin from gamma-proteobacterial methane
674 oxidizing bacteria: a case for copper competition on a molecular level. *J Inorg*
675 *Biochem* 104:1240-7.
- 676 63. Mandal M, Kawashima K, Saito K, Ishikita H. 2020. Redox Potential of the Oxygen-
677 Evolving Complex in Electron Transfer Cascade of Photosystem II. *J Phys Chem Lett*
678 11:249-255.
- 679 64. Vass I, Styring S. 1991. pH-Dependent Charge Equilibria between Tyrosine-D and
680 the S States in Photosystem II. Estimation of Relative Midpoint Redox Potentials.
681 *Biochemistry* 30:830-839.
- 682 65. Nicholls P, Fita I, Loewen PC. 2001. Enzymology and structure of catalases. *Adv*
683 *Inorg Chem* 51:51-106.
- 684 66. Apel K, Hurt H. 2004. Reactive oxygen species: metabolism, oxidative stress, and
685 signal transduction. *Annu Rev Plant Biol* 55:373-399.

- 686 67. Youngblut MD, Tsai C-L, Clark IC, Carlson HK, Magiaqui AP, Gau-Pan PS, Redford SA,
687 Wong A, Tainer JA, Coates JD. 2016. Perchlorate reductase is distinguished by active
688 site aromatic gate residues. *J Biol Chem*, 291:9190-9202.
- 689 68. Ettwig KF, Butler MK, Le Paslier D, Pelletier E, Mangenot S, Kuypers MM, Schreiber
690 F, Dutilh BE, Zedelius J, de Beer D, Gloerich J, Wessels HJ, van Alen T, Luesken F, Wu
691 ML, van de Pas-Schoonen KT, Op den Camp HJ, Janssen-Megens EM, Francoijs KJ,
692 Stunnenberg H, Weissenbach J, Jetten MS, Strous M. 2010. Nitrite-driven anaerobic
693 methane oxidation by oxygenic bacteria. *Nature* 464:543 - 548.
- 694 69. Bab-Dinitz E, Shmueli H, Maupin-Fulow J, Eichler J, Shaanan B. 2006. *Haloferax*
695 *volcanii* PitA: an example of functional interaction between Pfam chlorite dismutase
696 and antibiotic biosynthesis monooxygenase families? *Bioinformatics* 22:671-675.
- 697 70. Whittenbury R, Phillips KC, Wilkinson JF. 1970. Enrichment, isolation and some
698 properties of methane-utilizing bacteria. *J Gen Microbiol* 61:205-18.
- 699 71. Bandow NL, Gallagher WH, Behling L, Choi DW, Semrau JD, Hartsel SC, Gilles VS,
700 Dispirito AA. 2011. Isolation of methanobactin from the spent media of methane-
701 oxidizing bacteria. *Meth Enzymol* 495:259-69.
- 702 72. Harris DC. 2007. *Quantitative Chemical Analysis*, 7th Ed. W.H. Freeman and
703 Company.
704
705

706

707

Table 1

708 Distribution of Au as Au³⁺ and Au⁰ following incubation of MB-SB2 and HAuCl₄. Reduction rate

709 where determined from samples where less than 100 percent reduction was observed.

HAuCl ₄ : MB-SB2 Ratio	Time (min)	Percent		Reduction Rate (Au ³⁺ reduced min ⁻¹)
		Au ³⁺	Au ⁰	
0.9	30	0	100	-
2.25	30	0	100	-
9	30	8	92	0.27
14	30	11	89	0.41
19	30	59	41	0.26
9	60	0	100	-
14	60	0	100	-
19	60	10	90	0.28
19	360	0	100	-

710

711

712 **Figure Legends**

713 **Fig. 1.** Gold X-ray photoelectric spectra of MS-SB2 **(A)** at gold to MB-SB2 molar ratio of 14 to 1
714 after 30 min incubation (**○**) and **(B)** at gold to MB-SB2 molar ratio of 19 to 1 after
715 30 min incubation. Experimental results (circles) fit with CASA XPS software to four
716 Gaussian/Lorentzian curves, using two peaks for Au³⁺ (orange curves) and two
717 peaks for Au⁰ (blue curves). Gold 4f core electrons are spin-orbit split as 4f_{7/2} and
718 4f_{5/2}, with a splitting of 3.7 eV and area ratio of 4:3, so that only two peaks are
719 independently fit: the 4f_{7/2} peaks for Au³⁺ and Au⁰. The 4f_{5/2} peaks' position and
720 area are determined by the spin-orbit splitting; those parameters and the peak
721 widths are fixed in the fitting program. Background used was a Shirley type.

722
723 **Fig. 2. A. A.** Kinetics of Au binding by MB-SB2 at 4°C. **(A)** Rate of HAuCl₄ binding to the
724 imidazolone (**△**) and oxazolone (**○**) rings of mb-SB2 at 4°C as measured from the
725 absorbance change at 386 nm and 341 nm, respectively. The rates for Au binding
726 >2000 sec⁻¹, and were set at 2000 sec⁻¹ in the figure. **B.** Emission at 429nm from
727 SB2-MB following excitation at 341nm after the addition of 0 (**—**), 0.25 (**—**), 0.5
728 (**—**), 0.75 (**—**), or 2.25 (**—**) HAuCl₄ per MB-SB2.

729
730 **Fig. 3. A.** pH changes following the addition of HAuCl₄ to aqueous solutions (**△**) or aqueous
731 solution of 40 μM MB-SB2 (**△**). **B.** pH changes following the addition of CuCl₂ to
732 aqueous solutions (**△**) or aqueous solution of 40 μM MB-SB2 (**○**). **C.** pH changes

733 following the addition of KCl to aqueous solutions (Δ) or aqueous solution of 40
734 μM MB-SB2 (\circ).

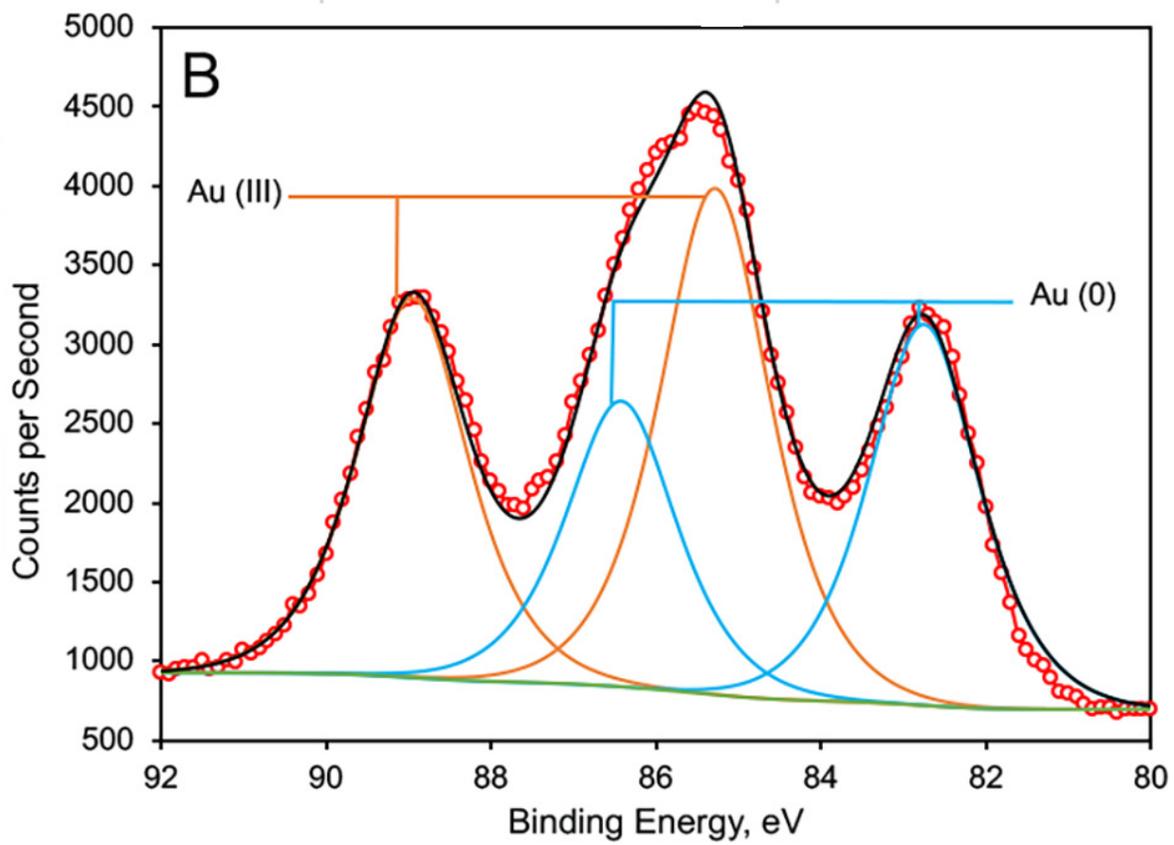
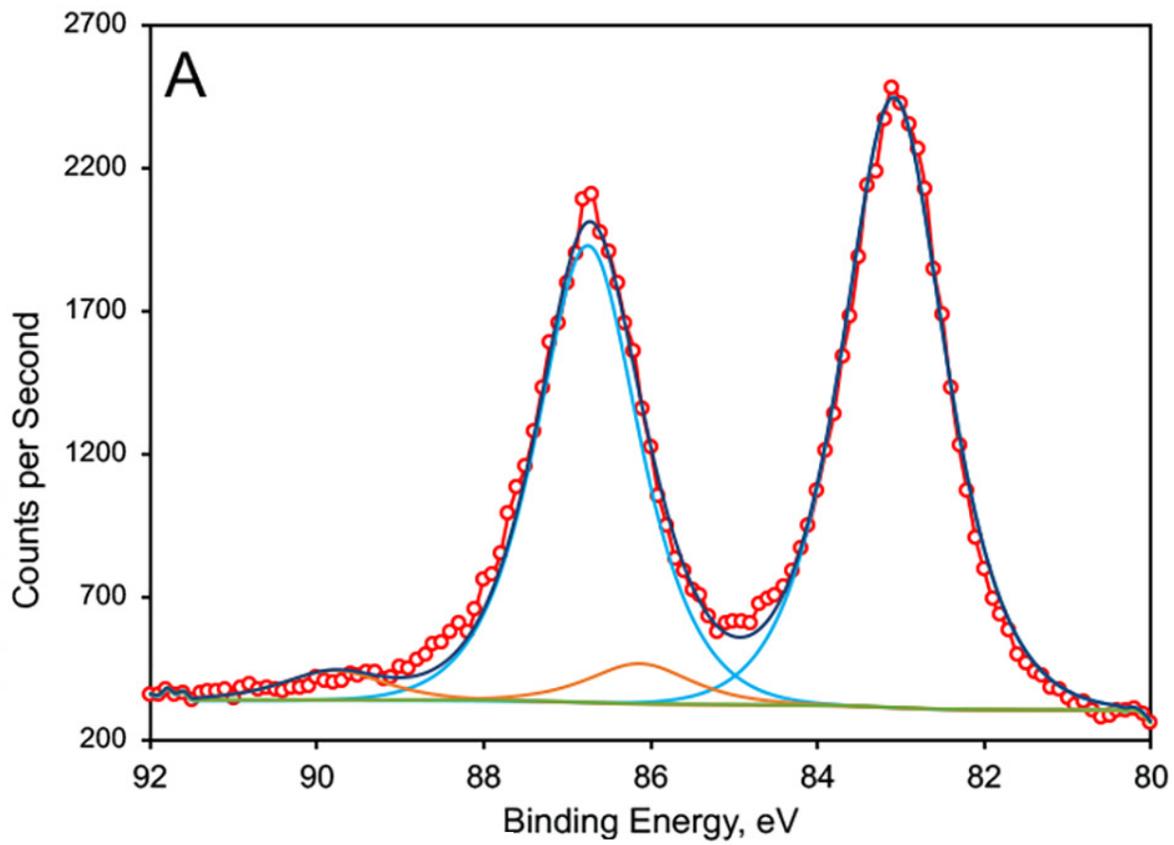
735 **Fig.4.** Mass spectra of head space gas of a reaction mixture containing 2mM MB-SB2 in 97%
736 H_2^{18}O (A) and following the addition of 20mM HAuCl_4 (B), 20mM CuCl_2 (C), , 10mM
737 CuCl_2 (D), 20mM KCl (E), , 20mM AgF (F), 20mM FeCl_3 (G), , 20mM HgCl_2 (H), ,
738 20mM NiCl_2 (I), 20mM CoCl_2 (J).

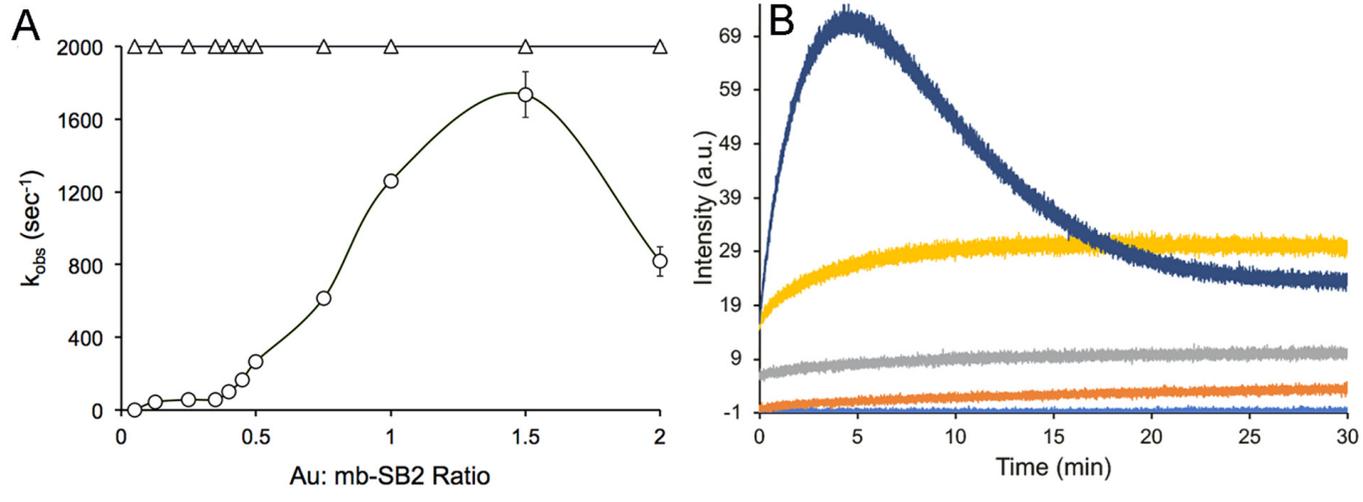
739 **Fig. 5.** $^{18,18}\text{O}_2$ concentration in the head space of a reaction mixture containing 2 mM MB-SB2
740 plus 20mM HAuCl_4 (Δ) or 20mM CuCl_2 (\circ) in 97% H_2^{18}O and following the addition
741 of 7.3 mM of catalase.

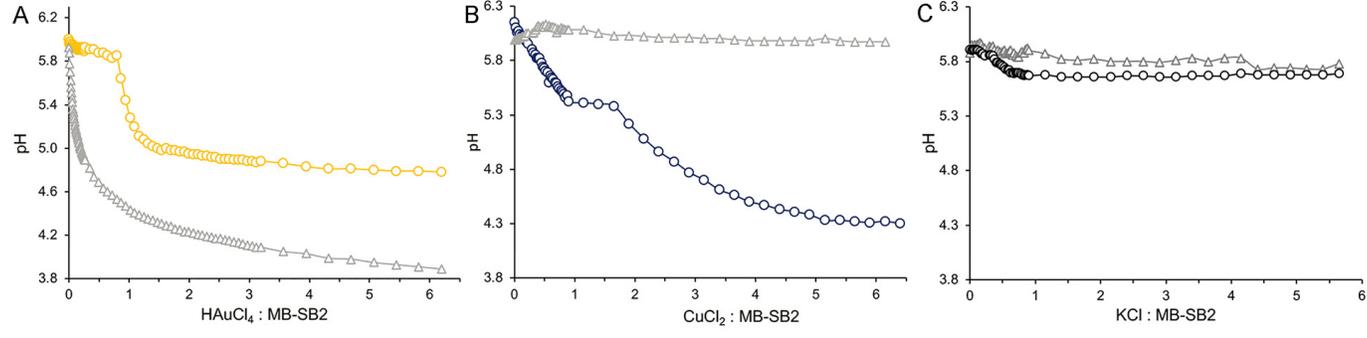
742 **Fig. 6.** Iron reductase activity of MB-SB2 (A) and MB-OB3b (B). Absorption change at 562 nm of
743 reaction mixtures containing 1mM ferrozine plus 10mM FeCl_3 (—), 1mM ferrozine plus
744 23.4 μM MB-SB (—), 1mM ferrozine plus 10mM FeCl_3 and either 5.8 (—), 11.6 (—),
745 17.4 (—) or 23.4 (—) μM MB-SB2 (A) or MB-OB3b (B). C. Aqueous 4M FeCl_3 solution
746 (a) and a 4M FeCl_3 solution plus 20 mM MB-SB2 4 hours after the addition of MB-SB2.

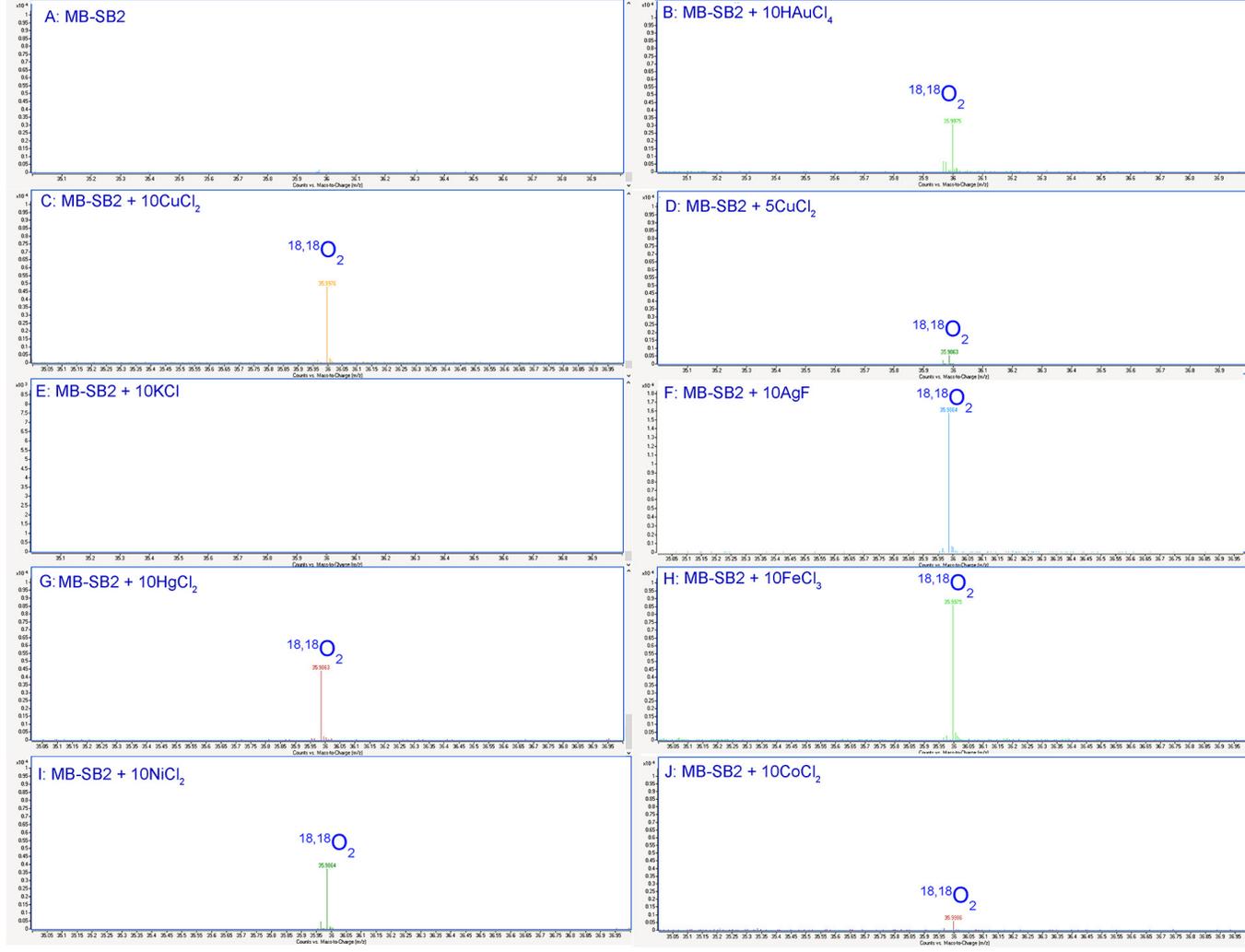
747 **Fig.7.** Mass spectra of head space gas of a reaction mixture containing 2mM MB-OB3b in 97%
748 H_2^{18}O (A) and following the addition of 20mM HAuCl_4 (B), 20mM CuCl_2 (C), and
749 20mM AgF (D).

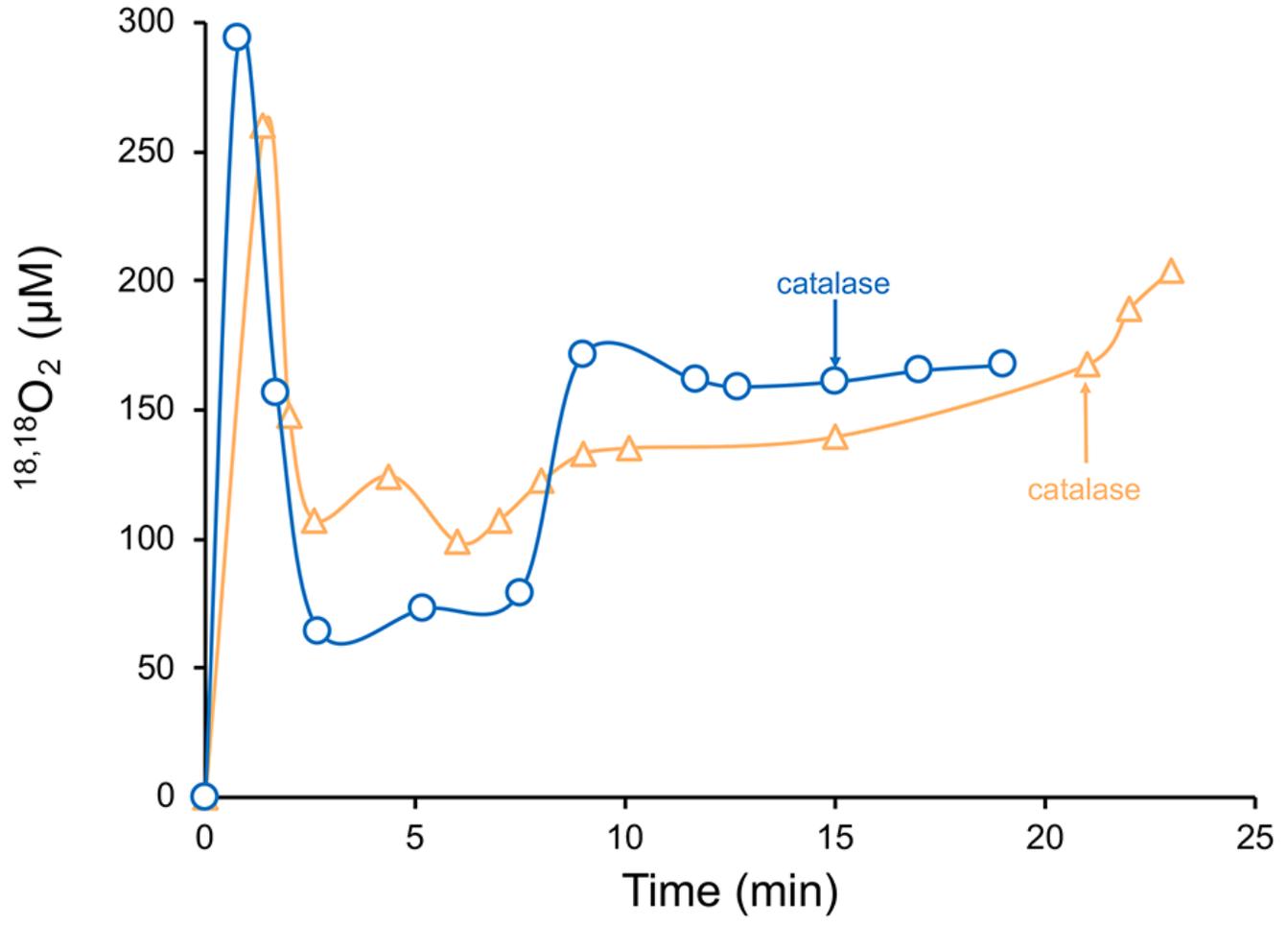
750 **Fig. 8.** $^{13}\text{CO}_2$ production by *M. trichosporium* OB3b wild type (WT), WT plus 25 μM CuCl_2 , WT
751 plus 5 μM MB-OB3b, and WT plus 25 μM CuCl_2 and 5 μM MB-OB3b incubated in an
752 Anaerobic glove box for 3 days.

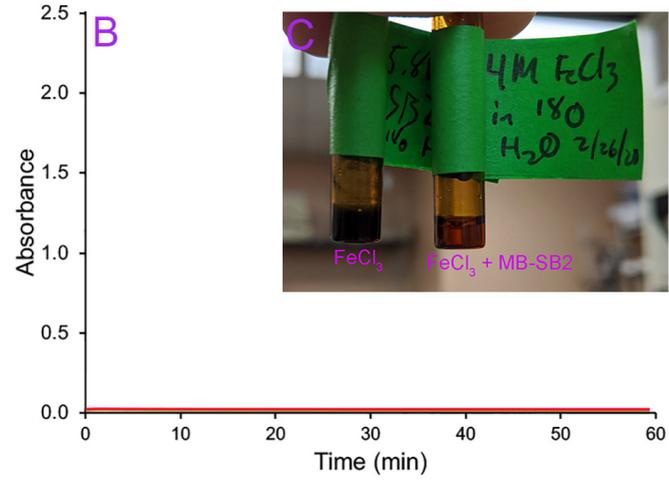
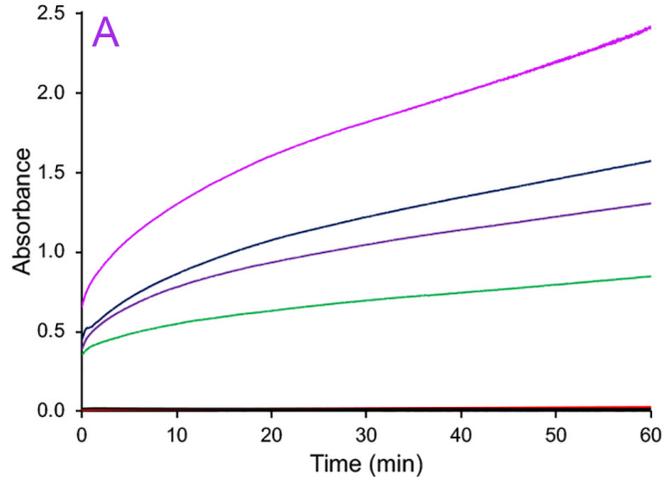


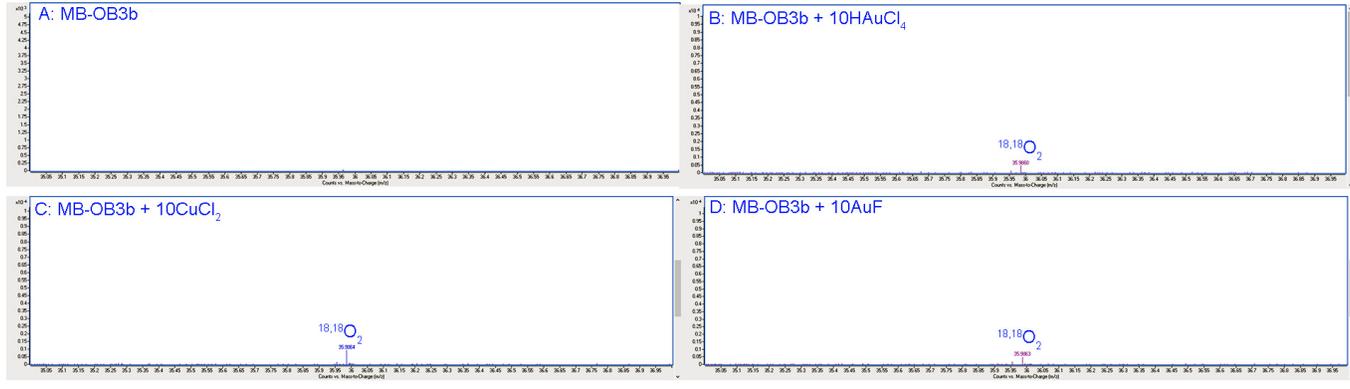












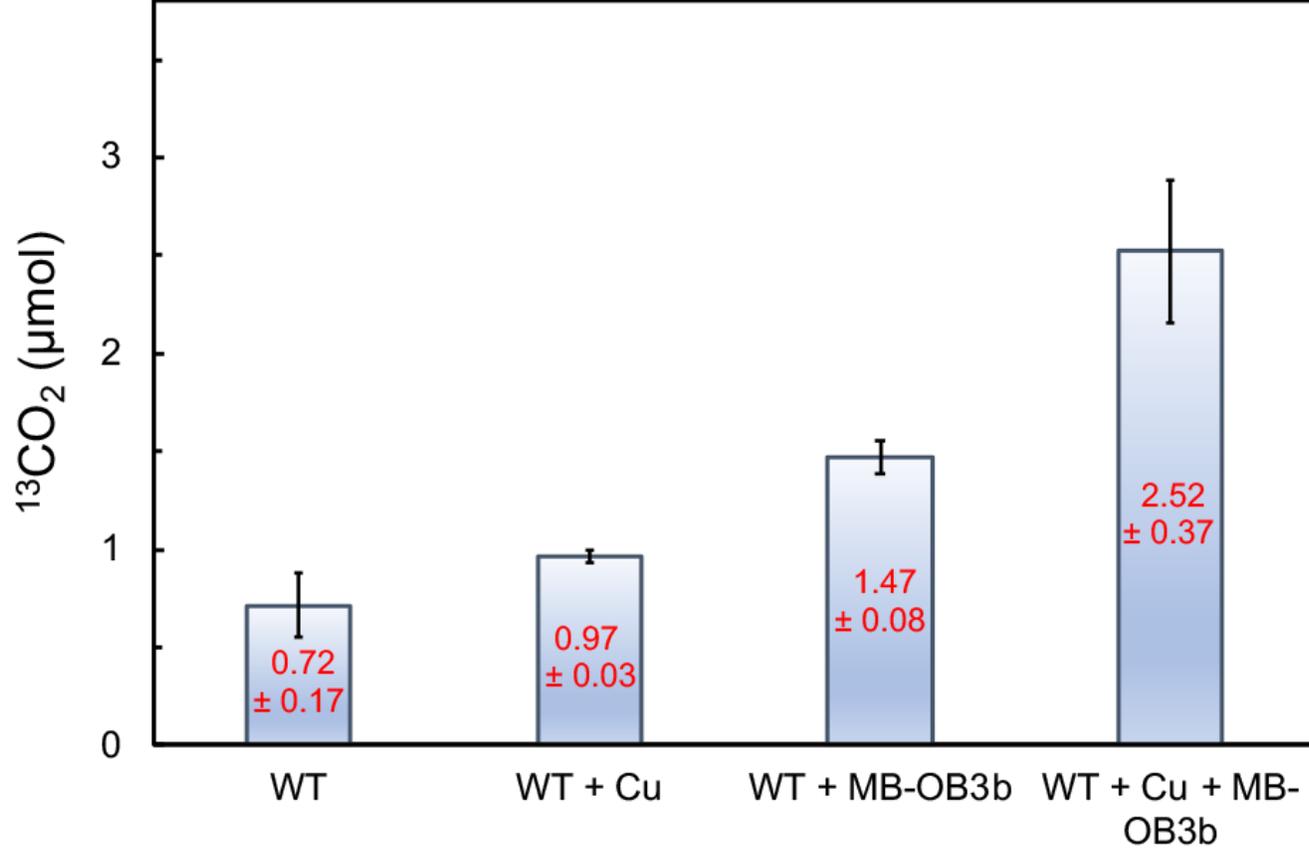


Table 1

Distribution of Au as Au³⁺ and Au⁰ following incubation of MB-SB2 and HAuCl₄. Reduction rate where determined from samples were less than 100 percent reduction was observed.

HAuCl ₄ : MB-SB2 Ratio	Time (min)	Percent		Reduction Rate (Au ³⁺ reduced min ⁻¹)
		Au ³⁺	Au ⁰	
0.9	30	0	100	-
2.25	30	0	100	-
9	30	8	92	0.27
14	30	11	89	0.41
19	30	59	41	0.26
9	60	0	100	-
14	60	0	100	-
19	60	10	90	0.28
19	360	0	100	-