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The trypanosome alternative oxidase

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<u>Summary</u>

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New drugs against Trypanosoma brucei, the causative agent of Human African 28 Trypanosomiasis, are urgently needed to replace the highly toxic and largely 29 ineffective therapies currently used. The trypanosome alternative oxidase (TAO) is an 30 essential and unique mitochondrial protein in these parasites and is absent from 31 mammalian mitochondria, making it an attractive drug target. The structure and 32 function of the protein are now well characterized, with several inhibitors reported in 33 34 the literature which show potential as clinical drug candidates. In this review we provide an update on the functional activity and structural aspects of TAO. We then 35 discuss TAO inhibitors reported to date, problems encountered with *in vivo* testing of 36 these compounds, and discuss the future of TAO as a therapeutic target. 37

Key Words: Trypanosome Alternative Oxidase, Drug Discovery, Chemotherapy,
Human African Trypanosomiasis, Sleeping Sickness, Trypanosoma brucei
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48 THE TRYPANOSOME ALTERNATIVE OXIDASE: A POTENTIAL DRUG TARGET?

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50 INTRODUCTION

51 Up to 70 million people in sub-Saharan Africa are at risk of contracting Human African Trypanosomiasis (HAT) (Simarro et al. 2012), also known as African 52 53 Sleeping Sickness, caused by the kinetoplastid parasite *Trypanosoma brucei*. Two subspecies of the parasite cause disease in humans; T. brucei gambiense in West 54 Africa and T. brucei rhodesiense in East Africa, both of which are spread by the 55 56 tsetse fly. Both forms are fatal if untreated and are estimated to cause up to 20,000 57 cases of HAT per year (World Health Organization 2013). T. brucei evades the 58 mammalian host immune system by changing their major surface coat proteins, 59 known as variant surface glycoproteins (VSG), prior to each wave of host antibodies raised against the previous VSG type. Due to this sophisticated immune evasion 60 technique known as antigenic variation, a vaccine against the disease is unlikely in 61 62 the near future. Drugs currently in clinical use are associated with severe adverse effects, difficult administration, and increasing concerns regarding drug resistance. 63 Therefore, new drugs are urgently required (Lüscher et al. 2007). The drugs 64 indicated for treatment of the disease (Figure 1) depend upon the subspecies of 65 66 parasite and stage of the disease.

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Early stage *T. b. gambiense* is treated with pentamidine, a diamidine hypothesized to act as a trypanocidal agent through several mechanisms, including disruption of the nucleus, kinetoplast and mitochondrial membrane potential (Baker *et al.* 2013). Late stage *T. b. gambiense* is treated with a combinational therapy of nifurtimox and effornithine. Effornithine is the only drug for HAT with a defined target, the ornithine

73 decarboxylase, but the drug has poor potency against *T. brucei* and combination 74 therapy is required to prevent drug resistance acquired by loss of the drug uptake transporter (Barrett & Croft 2012). Suramin is recommended only for early stage T. 75 76 b. rhodesiense due to its inability to penetrate the blood brain barrier. Although the mechanism of uptake by the parasites is known, the trypanocidal mode of action still 77 78 remains to be determined (Barrett & Croft 2012, Zoltner et al. 2016). The arsenicalbased drug melarsoprol is recommended for late stage T. b. rhodesiense due to its 79 80 ability to cross the blood brain barrier, however this property creates the often fatal 81 adverse effect of encephalopathy in up to 10% of patients treated with the drug 82 (Kuepfer et al. 2012).

Differences in the biochemical processes between mammalian and trypanosomatid mitochondria make the mitochondrion an attractive drug target. One main difference between *T. brucei* and mammalian mitochondrial respiration is the presence of the trypanosome alternative oxidase (TAO), an essential non-cytochrome terminal oxidase which has been extensively characterized as a drug target. This review will summarize the structure and function of TAO and discuss the current progress towards the development of inhibitors against this protein.

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91 <u>STRUCTURE AND FUNCTION OF THE TRYPANOSOME ALTERNATIVE</u> 92 OXIDASE

93 Function

In 1960, Grant and Sargent first described the glycerol-3-phosphate oxidase (GPO)
 system as a cyanide-insensitive, oxygen-dependent mechanism of respiration in
 Trypanosoma brucei rhodesiense (Grant & Sargent 1960). The GPO system
 consists of two enzymes; a mitochondrial FAD⁺-dependent glycerol-3-phosphate

98 dehydrogenase (mG3PDH) and a terminal oxidase they termed the glycerol-3-99 phosphate oxidase. Clarkson et al (Clarkson et al. 1989) proved that ubiquinol links 100 the dehydrogenase and oxidase of the GPO system by acting as an electron carrier, 101 and proposed that glycerol-3-phosphate oxidase was similar to the plant alternative oxidase (AOX) and therefore should be renamed the trypanosome alternative 102 103 oxidase (TAO). The GPO system is responsible for the cyanide-insensitive oxygen-104 dependent respiration in bloodstream form T. brucei, where the GPO shuttle facilitates the reoxidation of NADH to NAD⁺ required for glycolysis. As shown in 105 106 Figure 2, the mG3PDH oxidizes glycerol-3-phosphate (Gly-3-P) to dihydroxyacetone 107 phosphate (DHAP), during which four electrons are transferred to ubiquinol. The 108 electrons from ubiquinol are subsequently oxidized by TAO to convert dioxygen into 109 water. Alternative oxidases are found across a broad range of organisms, including plants, nematodes, algae, yeast and T. brucei, but, curiously, are not known to be 110 111 present in the other human-infective trypanosomatids such as T. cruzi or Leishmania 112 spp.

113 TAO was first identified in *Trypanosoma brucei* by Chaudhuri et al (Chaudhuri et al. 114 1995) using antibodies against the alternative oxidase from Sauromatum guttatum, 115 which detected a 33 kDa protein in the parasite's mitochondria. This 33 kDa protein 116 was subsequently purified from bloodstream form T. brucei mitochondria and confirmed to have ubiquinol oxidase activity. Chaudhuri et al (Chaudhuri et al. 117 118 1998) found that bloodstream form T. brucei express TAO 100-fold more than procyclic form, which is believed to be due to the ability of procyclic forms to express 119 Complexes III and IV for ATP production via oxidative phosphorylation. Using areas 120 121 of high conservation in plant alternative oxidases, primers were designed to amplify 122 TAO from *T. brucei* gDNA (Chaudhuri & Hill 1996). This enabled the identification of

123 the single copy TAO gene (Tb927.10.7090) and subsequent cloning of TAO for recombinant expression in Escherichia coli (Chaudhuri & Hill 1996). Recombinant 124 TAO (rTAO) was subsequently used to determine the functional activity, kinetics and 125 126 inhibitors of the enzyme. Due to the endogenous ubiquinol oxidase activity of E. coli by the cytochrome bo and bd complexes, it was necessary to perform these 127 128 investigations using hemA mutant E. coli, which are unable to synthesize the heme necessary for cytochrome assembly. The ability of rTAO to restore respiration in 129 130 these cells showed the ability of TAO to function as a cyanide-insensitive terminal 131 oxidase. Research of rTAO by the Kita group established protocols for the 132 overproduction, solubilization and purification of rTAO for use in kinetic, structural 133 and inhibitor studies (Fukai et al. 1999; Fukai et al. 2003; Nihei et al. 2003; Yabu et 134 al. 2003).

TAO has been implicated in several other cellular activities, such as protection 135 136 against reactive oxygen species and regulation of surface protein expression. A role 137 of AOX in photosynthetic plants is the rapid turnover of NADPH to protect the photosynthetic machinery from radicals. It is possible that TAO has a related 138 139 function in *T. brucei*, to protect the rapidly metabolizing cells from damaging radicals. 140 The inhibition of TAO has been shown to induce oxidative damage to proteins and 141 increase production of reactive oxygen species (Fang & Beattie 2003). Similarly, 142 inhibition of the electron transport chain and exposure to hydrogen peroxide causes 143 an upregulation in the expression of TAO (Fang & Beattie 2003). This protection against oxidative damage may explain the ability of TAO to inhibit drug-induced 144 programmed cell death-like phenomena in T. brucei (Tsuda et al. 2006). Vassella et 145 al (Vassella et al. 2004) reported the effects of TAO inhibition on the expression 146 levels of the procyclin GPEET, a cell surface protein found in procyclic form T. 147

brucei. In the presence of the TAO inhibitor salicylhydroxamic acid (SHAM), GPEET levels were heavily reduced, leading the authors to hypothesize that the level of GPEET expression may be linked to the activity levels of TAO. Later studies showed that the expression of TAO influences the expression of GPEET, where a downregulation of both proteins may be important in the adaptation of the parasite to survive within the tsetse fly midgut (Walker *et al.* 2005).

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155 Structure

156 Several structures of the alternative oxidase were proposed (Andersson & Nordlund 157 1999; Berthold et al. 2000) prior to the publication of the crystal structure. Initially, 158 hydropathy plots suggested the alternative oxidases contain two conserved 159 transmembrane regions, however later studies by Andersson and Nordlund 160 (Andersson & Nordlund 1999) suggested alternative oxidases are not 161 transmembrane proteins, but rather interfacial inner membrane proteins. This was 162 confirmed with the solving of the crystal structure of TAO (Shiba et al. 2013) which is devoid of any transmembrane domains, and instead has a hydrophobic face to 163 partially bury the protein into the membrane (Figure 3). The recent publication of 164 165 the crystal structure (Shiba et al. 2013) should help in the design of improved TAO inhibitors. Sequence analysis of T. b. brucei, T. b. gambiense and T. b. rhodesiense 166 showed that the amino acid sequence of TAO is identical in all three species, and 167 168 therefore studies on TAO inhibitors and its co-structures can be directly applied from the common laboratory model *T. b. brucei* to the human disease-causing subspecies 169 (Nakamura *et al.* 2010). 170

Early studies on plant alternative oxidases revealed that they were inhibited by metal chelators (Schonbaum *et al.* 1971), and subsequent investigations using electron

173 paramagnetic resonance (EPR) (Berthold et al. 2002; Moore et al. 2008) and inductively coupled plasma-mass spectrometry (ICP-MS) (Kido et al. 2010) showed 174 175 that the alternative oxidases contained a non-heme diiron catalytic core that was 176 essential for catalytic activity and released during enzyme inactivation. In the crystal structure in its oxidized state, the two Fe (III) ions are coordinated in a distorted 177 178 square pyramidal geometry to four glutamate residues and a hydroxo-bridge (Figure 4). Two conserved histidines located nearby are also likely to be involved in Fe-179 180 coordination in the reduced state, as determined through Fourier transform infrared 181 spectroscopy (FTIR) investigations (Marechal et al. 2009). Together, the two 182 histidines and two glutamates form part of the two ExxH iron-binding motifs which 183 are common to all AOX proteins and are required for activity (Chaudhuri et al. 1998; 184 Ajayi et al. 2002).

185

186 Mechanism of Catalysis

187 The structure of TAO in complex with ubiquinol has not yet been solved so hypotheses regarding ubiquinol-binding have been made based upon the structure 188 189 of TAO complexed with ascofuranone analog AF2779OH. Superposition of ubiquinol 190 over AF2779OH indicates that during catalysis a ubiquinol molecule is highly likely to 191 occupy the same position. The molecules gain entry to the diiron active site through a relatively short (~10 Å) hydrophobic channel from the membrane-bound side of 192 193 In this position the aromatic head of ubiquinol is less then 4.4 Å TAO (Figure 4). 194 from the diiron core and is capable of forming hydrogen bonds with Arg118, Cys119 and Tyr220, all of which may be involved directly in catalysis rather than purely 195 196 substrate binding.

197 A mechanism of catalytic activity has been proposed (Moore et al. 2013 and Figure 198 5), which begins with the diiron core in a reduced state (i.e. as Fe(II/II) bridged by a 199 hydroxide). Upon binding of molecular oxygen to the Fe(II/II) diiron core (Figure 5A), 200 one iron passes an electron to an oxygen atom, forming a superoxo intermediate 201 comprising an oxygen radical joined to an Fe(II/III) core. The oxygen radical 202 immediately abstracts a hydrogen atom (proton plus electron) from ubiquinol, 203 yielding a ubisemiquinone and a hydroperoxo intermediate (Figure 5B). The unstable 204 intermediate then undergoes a rearrangement whereby the hydroperoxo loses its 205 proton and electron to the hydroperoxide bridge, which is then released as water 206 (Figure 5C). The Fe(II/III) core then gains an interaction with one of the histidines as 207 determined in FTIR experiments (Marechal et al. 2009) and the second atom of the 208 dioxygen forming a peroxodiiron. Homolytic cleavage of the O-O bond (Figure 5D) 209 yields an oxodiiron core, and one of the oxygens abstracts a hydrogen atom (proton 210 plus electron) from Tyr220 generating a tyrosyl radical, as observed by Marechal et 211 al (Marechal et al. 2009). The tyrosyl can then pick up an electron and proton from 212 the ubisemiquinone, either directly or via Cys119, releasing ubiquinone and returning 213 Tyr220 to its resting state. Moore's model suggests that ubiquinol in a second 214 channel can then provide two electrons and protons to release a second water and 215 reduce the diiron core back to its original Fe(II/II) state bridged by a hydroxide ion 216 through an unknown mechanism (Figure 5E). However, the second ubiquinol 217 channel may not be needed as the release of ubiquinone creates the space for the 218 binding of a second ubiquinol in the same channel in a ping-pong binding fashion. 219 Furthermore, the mechanism of electron and proton transfer could proceed through a 220 similar route as for the first ubiquinol.

221

222 INHIBITORS OF THE TRYPANOSOME ALTERNATIVE OXIDASE

The effectiveness of TAO inhibition to kill T. brucei has been well debated, with 223 224 conflicting historical reports in the literature as to whether the inhibition of the GPO 225 system alone is sufficient to kill the cells. As shown in Figure 2, bloodstream form T. *brucei* rely solely on glycolysis for ATP production, as opposed to the ATP-producing 226 227 oxidative phosphorylation used by procyclic forms. In the presence of TAO inhibitors the oxidation of Gly-3-P to DHAP is blocked, causing an accumulation of Gly-3-P in 228 229 the alycosome, which is converted to alycerol by the ATP-producing alycerol kinase 230 (Yabu *et al.* 2006). This allows the recycling of glycosomal NAD⁺/NADH necessary 231 to continue glycolysis anaerobically.

232 Early reports of in vivo testing of TAO inhibitors suggested that although the 233 compounds were able to inhibit the protein in vitro, this action alone was not sufficient to clear an infection when tested in animal models, due to anaerobic ATP 234 235 production by the trypanosomes (Clarkson & Brohn 1976; Grady et al. 1993; Yabu et 236 al. 1998). It was believed that in order to cause cell death the anaerobic production 237 of ATP also needed to inhibited with the co-administration of glycerol. However, later investigations showed that bloodstream T. brucei exposed to TAO inhibitors 238 239 alone are unable to survive for more than 24 hours using only anaerobic respiration (Helfert et al. 2001). Furthermore, subsequent studies of a TAO inhibitor with an 240 241 optimized dosing regimen but in the absence of glycerol, showed that TAO inhibition 242 alone is sufficient to clear an infection in vivo (Yabu et al. 2003), indicating that inhibition of TAO is indeed a valid drug target. 243

There are few compounds that have been shown to be inhibitors of TAO. These compounds (Figure 6) all show structural similarity to the TAO substrate ubiquinol and are thought to act as competitive inhibitors, by binding to the ubiquinol binding

247 site.

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249 Salicylhydroxamic Acid

The first compounds to be investigated as TAO inhibitors were the aromatic 250 hydroxamates, such a salicylhydroxamic acid (SHAM) (Figure 6). SHAM was known 251 252 to be a potent inhibitor of the alternative oxidase in plants prior to the discovery of the GPO system in trypanosomes, hence the compound was investigated as a 253 254 potential inhibitor of TAO. It is thought that hydroxamic acids compete with ubiquinol 255 for binding to TAO, and thus the compounds prevent the translocation of electrons 256 from ubiquinol to oxygen (Pollakis et al. 1995). SHAM was found to have moderate 257 $(EC_{50} = 15 \mu M)$ activity against *T. brucei in vitro* and was shown to specifically inhibit 258 all TAO activity at 1 mM (Opperdoes et al. 1976), although only a little effect was seen on ATP production. However, when the trypanocidal effect of SHAM was 259 260 investigated in vivo, the compound was unable to clear an infection and was only shown to be trypanocidal when co-administered with glycerol (Clarkson & Brohn 261 262 1976).

SHAM is a poor clinical candidate, due to its low solubility in water (Nihei et al. 263 264 2002), which impairs the compounds from crossing the blood brain barrier, a critical 265 characteristic required for drugs to effectively treat HAT. Numerous attempts were made to improve the potency of hydroxamic acids against TAO, but were unable to 266 match the potency of SHAM when tested in vivo (Grady et al. 1993). Recently this 267 268 issue has been revisited, Ott et al (Ott et al. 2006) developed novel SHAM analogs 269 to improve its potency and solubility. SHAM analogs such as ACD16 (Figure 6) were 270 designed to include a prenyl side chain, as found in the TAO substrate ubiquinol, and 271 a carbohydrate group to improve solubility, whilst keeping the 2-hydroxybenzoic acid

found in SHAM which is essential for TAO inhibition. These modifications lead to the development of three compounds with up to five-fold greater potency than SHAM against rTAO, however *in vitro* testing against *T. b. brucei* growth and respiration revealed none of the modified compounds were more potent than SHAM. There have been no subsequent reports on SHAM as a TAO inhibitor, although recent reports on the efficacy of TAO inhibitors without glycerol (Yabu et al. 2003) may renew interest in attempts to improve upon this compound.

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280 3,4-Dihydroxybenzoic Acid

281 3,4-dihydroxybenzoic acids (Figure 6) were synthesized and tested as alternative 282 inhibitors of TAO, and displayed higher inhibitory activity than SHAM when tested in 283 vitro, but this high potency was lost when the compounds were tested in vivo (Grady et al. 1993). To improve the bioavailability of the compounds, a series of N-n-alkyl-284 285 3,4-dihydroxybenzamides were synthesized to increase solubility and decrease 286 hydrolysis by serum esterases (Grady et al. 1993). Structure activity relationships of this series of compounds showed increasing potency and decreasing solubility as 287 288 the length of the alkyl substituent increases. From this, N-n-butyl-3,4-289 dihydroxybenzamide progressed to in vivo studies, and was found to effectively cure mice, but only when administered in conjunction with high doses of glycerol (450 290 291 mg/kg drug with 15 g/kg glycerol). Similar to SHAM, the high amount of glycerol 292 necessary for a trypanocidal effect of N-n-butyl-3,4-dihydroxybenzamide rendered 293 the compound unfavourable as a clinical drug candidate, and no work has been 294 undertaken to identify if an optimized dosing regimen might clear infection in vivo 295 without glycerol.

296

297 Ascofuranone

298 Ascofuranone (Figure 6), is a biologically active natural product isolated from the fungus Ascochyta viciae. Minagawa et al first showed that ascofuranone is a potent 299 300 inhibitor of mitochondrial respiration of T. b. brucei, specifically the glucose- and glycerol-3-phosphate-dependent respiration (Minagawa et al. 1997). Despite its high 301 302 potency against TAO, ascofuranone was initially found to only be trypanocidal in the presence of glycerol, similar to the other TAO inhibitors. The minimum inhibitory 303 304 concentration of ascofuranone alone was 250 µM, whereas in the presence of 4 mM 305 glycerol potency was improved several thousand-fold to 30 nM (Minagawa et al. 306 1997). Initially *in vivo* testing using mouse models found that ascofuranone was only 307 curative when co-administered with a large amount (3 g/kg) of glycerol (Yabu et al. 308 1998). Despite these less than favourable initial results, the dosage of ascofuranone 309 was improved to once again render it a promising clinical drug candidate. Yabu et al 310 (Yabu et al. 2003) trialled the optimal dosage to cure T. b. brucei mice without glycerol and determined that 100 mg/kg intraperitoneally for 4 days and 400 mg/kg 311 312 orally for 8 days completely cleared an infection, with a 50% lethal dose (LD₅₀) of 313 >1.2 g/kg over 8 days. This study also provided evidence of the effects of 314 ascofuranone treatment on TAO, finding that ascofuranone decreased TAO activity 315 by 30% and increased the level of TAO expression within the cells (Yabu et al. 316 2003).

Ascofuranone was also shown to inhibit the TAO of *T. vivax*, which causes animal trypanosomiasis (Nagana) in cattle. The *T. vivax* TAO has 76% identical amino acid residues to *T. brucei* TAO (Suzuki *et al.* 2004) and the recombinant protein was shown to be three-fold more sensitive to ascofuranone. Subsequent *in vivo* testing of ascofuranone in *T. vivax* infected mice found that a single intramuscular dose of

322 50 mg/kg ascofuranone without glycerol was sufficient to clear an infection, which 323 could be reduced still further to 6 mg/kg over 4 days whilst retaining 100% cure rate 324 within 48 hours. The high efficacy of ascofuranone against *T. vivax* may make this 325 compound a suitable drug for use against animal trypanosomiasis.

Kinetic analysis of ascofuranone inhibition of rTAO indicated a competitive 326 327 mechanism of inhibition against ubiquinol (Nihei et al. 2003). Recent studies of ascofuranone have revealed the mechanism of inhibition, interaction with TAO and 328 329 the pharmacophore responsible for the inhibitory activity of ascofuranone (Saimoto 330 et al. 2013). The length of the linker chain between the aromatic ring and furanone 331 ring was shown to be important for its inhibitory activity, where the potency of 332 inhibitor with a propyl linker was a thousand-fold lower compared to nonyl and decyl 333 linkers. This is likely due to the interactions between the prenyl tail and membrane lipid bilayers, where hydrophobicity of the inhibitor is influenced by the length of the 334 335 prenyl tail, which is important to access the membrane-associated TAO (Mogi et al. 336 2009; Saimoto et al. 2013). Attempts to improve the potency and selectivity of 337 ascofuranone-like analogs have been reported, such as the prenylphenol LL-Z1272 series by Mogi et al (Mogi et al. 2009) (Figure 6), although no results from in vivo 338 339 testing have been reported to date.

340

341 Aurachin D

Recently the natural product Aurachin D (Figure 6), a ubiquinol oxidase inhibitor isolated from the bacterium *Stigmatella aurantiaca* strain Sg a15, was shown to have inhibitory activity against *T. b. gambiense* (Li *et al.* 2013). Aurachin D is a mimic of ubiquinol, with a quinolone core and prenyl chain. Li et al (Li *et al.* 2013) found that Aurachin D inhibited *T. b. gambiense* with an IC₅₀ of 1 μ M, with a selectivity index

347 greater than 35. Various analogs of Aurachin D were synthesized and tested for
348 trypanocidal activity, but none were improved compared to the natural product and
349 hence the compound has not been taken forward into animal models.

350

351 CONCLUSIONS AND FUTURE PERSPECTIVES

352 Although drugs against TAO have been studied for over 40 years, there are still no drug candidates approaching clinical trials. The search for an effective TAO inhibitor 353 354 has been hampered until recently by the difficulty in obtaining a crystal structure of 355 the relatively unstable purified protein, and the historical conflicting reports on 356 whether inhibition of TAO alone is sufficient to kill T. brucei in vivo. However, recent 357 evidence renews the idea of TAO as a valid drug target. Although there are few 358 inhibitors of TAO reported in the literature, it is hoped that the publication of the crystal structure of TAO will significantly improve the design of novel, potent 359 inhibitors against the enzyme. Further work is also still required to confirm the 360 361 mechanism of electron transfer by TAO and that ubiquinol is the true native cofactor. 362

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Figure 1. Distribution of countries endemic for Trypanosoma brucei according to WHO and the currently used clinical drugs





BSF T. brucei metabolise glucose to 1,3-BPGA in the glycosome and 1,3-BPGA to pyruvate in the cytosol. A high rate of glycolysis means that sufficient ATP is produced through this rout alone and the parasite can secrete the pyruvate produced as waste rather than spend energy consuming it further. The GPO system (mGPDH and TAO) is required to maintain glycolytic NAD(H) redox. If the GPO system is inhibited BSF T. brucei will convert Gly-3-P to the secreted end product glycerol to maintain glycolytic NAD(H) redox.

Proline is converted to acetate and alanine in a TCA-like, non-cyclical fashion. ATP is generated through oxidative phosphorylation and TAO, present at PFT. brucei are able to metabolise glucose, however, in the insect midgut glucose is so low in abundance that the main carbon source is proline. low levels, is hardly used.

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Figure 3. The TAO dimer in complex with diiron/hydroxo core (shown as spheres) and inhibitor AF2779OH (shown in yellow carbon stick). For surface representation, hydrophobic areas are grey and hydrophilic areas are blue/red. The upper face of the dimer is highly hydrophobic allowing TAO to burry itself within a single layer of the inner mitochondrial membrane. The approximate position of the membrane/matrix interface is represented by a dashed line. The diiron catalytic core is burried deep within the protein structure and a channel from the membrane to the core allows access of ubiquinol substrate (or analogous inhibitor AF2779OH).



Figure 4. The TAO active site with ubiquinol (green) superposed in the place of inhibitor AF2779OH. The diiron core is in theFe(III/III) oxodiiron state (see mechanism part in the main body text), coordinated by four glutamates, two histidines, an oxygen and a hydroxyl (yellow dashed lines).

For the first ubiquinol oxidation, the coordinated OH would abstract a hydrogen atom (proton plus electron) from ubiquinol (blue dashed line) and leave as water, reducing the core to Fe(II/III) and oxidising ubiquinol to semiubiquinol. The oxygen bridge will take a hydrogen from Tyr220 to form a hydroxo bridge and the resulting tyrosyl radical will take a hydrogen from semiubiquinol either directly or via Cys119 and return to its native state, leaving the core in a reduced diferrous Fe(II/II) state bridged by a sinle hydroxyl. With the reaction complete, ubiquinone will leave allowing molecular oxygen and a second ubiquinol to enter.

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Figure 5. Chemical structures of TAO substrate ubiquinol and the TAO inhibitors salicylhydroxamic acid (SHAM), ascofuranone, 3,4-dihydroxybenzoic acid and Aurachin D.