

Discovery of a Novel Dibromoquinoline Compound Exhibiting Potent Antifungal and Antivirulence Activity that Targets Metal ion Homeostasis

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Supplementary Table 1: *S. cerevisiae* heterozygous diploid deletion strains identified as sensitive to compound 4b via chemogenomic profiling.

Gene Name	Gene Function ^a
<i>ssa1</i>	ATPase subunit of the chaperonin-containing T-complex (CCT, TriC)
<i>nup60</i>	FG-nucleoporin component of central core of the nuclear pore complex
<i>kin3</i>	Serine/threonine protein kinase
<i>cox17</i>	Copper metallochaperone that transfers copper to Sco1p and Cox11p
<i>snf7</i>	One of four subunits of the ESCRT-III complex; involved in the sorting of transmembrane proteins into the multivesicular body (MVB) pathway
<i>ypl251w</i>	Dubious open reading frame; unlikely to encode a functional protein
<i>yah1</i>	Ferredoxin of the mitochondrial matrix; required for formation of cellular iron-sulfur proteins; involved in heme A biosynthesis;
<i>ns11</i>	Essential component of the MIND kinetochore complex; joins kinetochore subunits contacting DNA to those contacting microtubules; required for accurate chromosome segregation
<i>aft2</i>	Iron-regulated transcriptional activator; activates genes involved in intracellular iron use and required for iron homeostasis and resistance to oxidative stress
<i>isu1</i>	Conserved protein of the mitochondrial matrix; performs a scaffolding function during assembly of iron-sulfur clusters
<i>grx3</i>	Glutathione-dependent oxidoreductase
<i>rli1</i>	Essential Fe-S protein; required for ribosome biogenesis, translation initiation/termination
<i>rim101</i>	Cys2His2 zinc-finger transcriptional repressor; involved in alkaline responsive gene repression as part of adaptation to alkaline conditions; involved in cell wall assembly
<i>sbe22</i>	Protein involved in bud growth; involved in the transport of cell wall components from the Golgi to the cell surface
<i>spc97</i>	Component of the microtubule-nucleating Tub4p (gamma-tubulin) complex
<i>nfs1</i>	Cysteine desulfurase; involved in iron-sulfur cluster (Fe/S) biogenesis and in thio-modification of mitochondrial and cytoplasmic tRNAs
<i>kdx1</i>	Protein kinase; implicated in Slt2p mitogen-activated (MAP) kinase signaling pathway
<i>isu2</i>	Mitochondrial protein required for iron-sulfur protein synthesis
<i>nej1</i>	Protein involved in regulation of nonhomologous end joining
<i>fks1</i>	Catalytic subunit of 1,3-beta-D-glucan synthase; involved in cell wall synthesis and maintenance
<i>htb1</i>	Histone H2B; core histone protein required for chromatin assembly and chromosome function
<i>mig2</i>	Zinc finger transcriptional repressor
<i>git1</i>	Plasma membrane permease; mediates uptake of glycerophosphoinositol and glycerophosphocholine as sources of the nutrients inositol and phosphate

<i>mrs4</i>	Iron transporter of the mitochondrial carrier family; mediates Fe ²⁺ transport across the inner mitochondrial membrane
<i>sec28</i>	Epsilon-COP subunit of the coatamer; regulates retrograde Golgi-to-ER protein traffic
<i>fet4</i>	Low-affinity Fe(II) transporter of the plasma membrane
<i>sec31</i>	Component of the Sec13p-Sec31p complex of the COPII vesicle coat; COPII coat is required for vesicle formation in ER to Golgi transport
<i>sok1</i>	Protein of unknown function
<i>mrh1</i>	Protein that localizes primarily to the plasma membrane; also found at the nuclear envelope
<i>spc98</i>	Component of the microtubule-nucleating Tub4p (gamma-tubulin) complex
<i>gcd10</i>	Subunit of tRNA (1-methyladenosine) methyltransferase with Gcd14p; required for the modification of the adenine at position 58 in tRNAs, especially tRNA ⁱ -Met
<i>ecm33</i>	GPI-anchored protein of unknown function; possible role in apical bud growth and hyphae formation (in <i>Candida</i>)
<i>spt15</i>	TATA-binding protein (TBP); general transcription factor that interacts with other factors to form the preinitiation complex at promoters
<i>yjr039w</i>	Putative protein of unknown function

^aInformation obtained from the *Saccharomyces* Genome Database

Supplementary Table 2: Minimum inhibitory concentration (MIC) of compound **4b**, in the presence of CuSO₄ or FeSO₄, screened against *S. cerevisiae* BY4743 and *C. albicans* P60002.

Media supplemented with	MIC (μg/mL) for 4b	
	<i>S. cerevisiae</i> BY4743	<i>C. albicans</i> P60002
50 μM CuSO ₄	128	128
100 μM CuSO ₄	>128	>128
50 μM FeSO ₄	64	128
100 μM FeSO ₄	128	128
500 μM FeSO ₄	>128	128
1 mM FeSO ₄	>128	>128

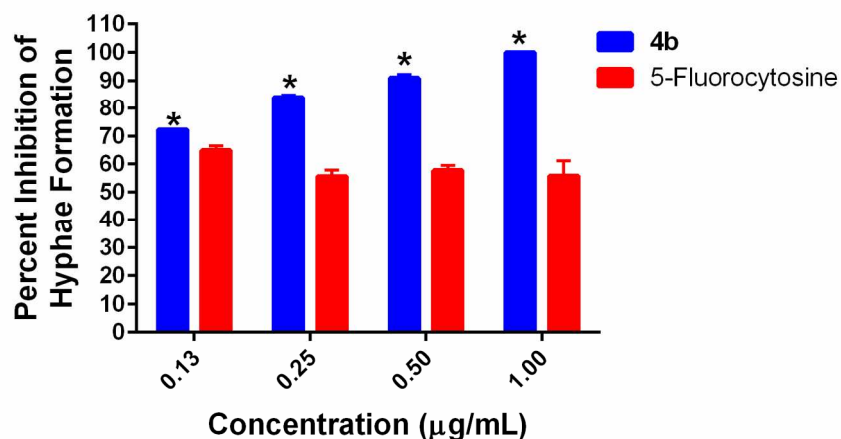
Supplementary Table 3: Aqueous turbidometric solubility assessment of compound **4b** and control drugs.

Compound/Drug	Aqueous solubility limit ^a (μg/mL)	NOTES
4b	>218	High solubility
Tamoxifen	6	Low solubility control
Verapamil	>227	High solubility control

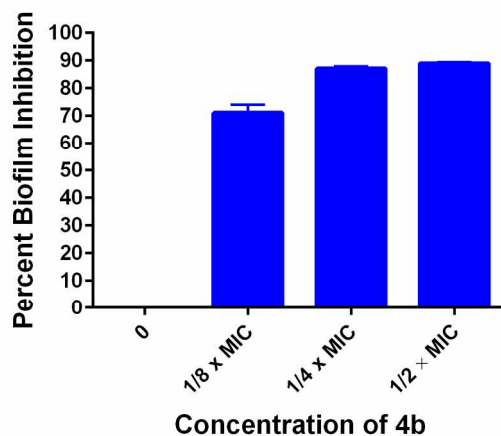
^aSolubility limit corresponds to the highest concentration of test compound where no precipitate was detected (OD₅₄₀)

Supplementary Table 4: Fungal strains used in this study.

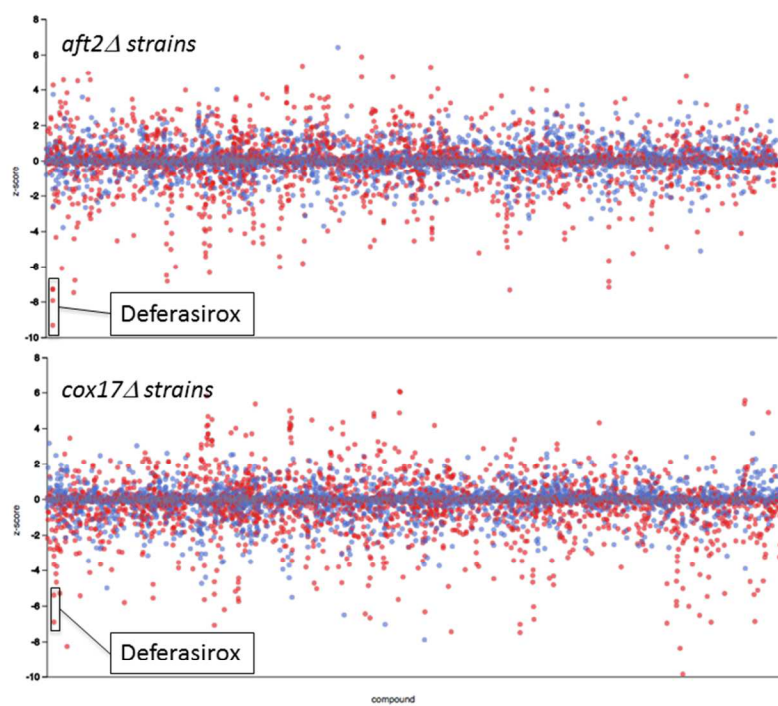
Strain Name	Alternative Strain Designation	Description
<i>Candida albicans</i> NR-29448	P60002	Isolated from a bloodstream infection, collected in Arizona, USA.
<i>Candida albicans</i> NR-29351	18M	Isolated from patient in China.
<i>Candida albicans</i> NR-29365	23F	Isolated from patient in China.
<i>Candida albicans</i> NR-29368	28C	Isolated from patient in China.
<i>Candida albicans</i> NR-29446	P94015	Isolated from a bloodstream infection collected in Utah, USA.
<i>Candida albicans</i> ATCC MYA-573	M4	Isolated from patient with AIDS in Germany. Resistant to fluconazole.
<i>Candida albicans</i> ATCC 64124	Darlington	Isolated from a mouth swab. Resistant to ketoconazole.
<i>Candida krusei</i> ATCC 14243		None.
<i>Candida krusei</i> ATCC 34135	ST-112	Clinical specimen isolated from Minnesota, USA.
<i>Candida parapsilosis</i> ATCC 22019	CBS 604	Isolated from a case of sprue in Puerto Rico
<i>Candida glabrata</i> ATCC MYA-2950	303542	None.
<i>Candida glabrata</i> ATCC 66032	AmMS 231	None.
<i>Candida tropicalis</i> ATCC 1369	CCY 29-7-7	None.
<i>Candida tropicalis</i> ATCC 13803	FDA PCI M-59	None.
<i>Cryptococcus gattii</i> NR-43208	R265	Isolated from a patient on Vancouver Island, Canada in late 1990s.
<i>Cryptococcus gattii</i> NR-43209	CBS1930	Isolated from a goat in Aruba prior to an outbreak in Vancouver, Canada.
<i>Cryptococcus neoformans</i> NR-41292	Isolate 2	Isolated from human cerebrospinal fluid in China in February 2012.
<i>Aspergillus brasiliensis</i> ATCC 16404	WLRI 034(120)	Isolated from North Carolina, USA.
<i>Aspergillus niger</i> ATCC 6275	4247	None.
<i>Aspergillus niger</i> ATCC 16888	WB 326	None.
<i>Aspergillus fumigatus</i> NR-35302	B5854	Isolated from human peritoneal fluid in California, USA in 1998.
<i>Aspergillus fumigatus</i> NR-35301	B5852	Isolated from human abdominal tissue in California, USA in 1998.



Supplementary Figure 1. Percent inhibition *C. albicans* P60002 hyphae formation. *C. albicans* ($\sim 6 \times 10^5$ CFU/mL) in RPMI-1640 medium supplemented with MOPS was exposed to **4b** (0.13 µg/ml up to 1 µg/mL), 5-Fluorocytosine (0.13 µg/ml up to 1 µg/mL), or left untreated for three hours at 35 °C to induce yeast-to-hyphae transition. Morphological changes were observed via a Nikon TiS inverted microscope (40× objective lens) in at least two different fields of view and the number of yeast and filamentous cells were counted to determine the percent inhibition of hyphae formation. Data were analyzed via a two-way ANOVA with post-hoc Dunnet's test for multiple comparisons. Asterisks (*) indicate significant difference ($P < 0.05$) between values obtained for yeast treated with **4b** compared to 5-Fluorocytosine.

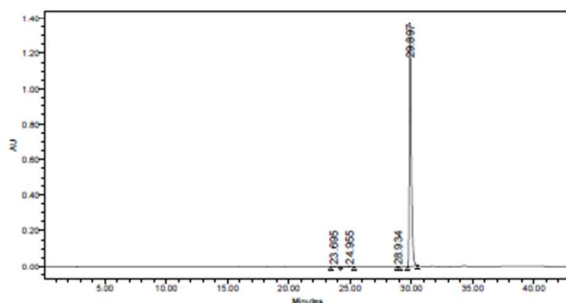


Supplementary Figure 2. Percent inhibition *C. albicans* P60002 biofilm formation. An overnight suspension of *C. albicans* was diluted in RPMI-1640 medium supplemented with MOPS (to achieve a starting inoculum $\sim 5 \times 10^5$ CFU/mL) and exposed to **4b** (at subinhibitory concentrations) or left untreated for 24 hours at 37 °C to permit biofilm formation. The biofilm was stained with 0.1% crystal violet, de-stained with ethanol, and biofilm mass quantified at OD₅₉₅. Data are presented as percent biofilm inhibition by **4b** in relation to the untreated control wells.



Supplementary Figure 3. Yeast chemogenomic profiling results for *aft2Δ* and *cox17Δ* deletion strains showing relative sensitivity of each strain against 1800 compounds. The graph depicts data for heterozygous (Red dots) and homozygous deletion strains (Blue dots) as plotted by z-score and compound. Negative z-score indicates increased sensitivity. The *aft2Δ* heterozygous strain (labeled black box) is most sensitive to deferasirox compared to 1800 compounds. The *cox17Δ* strain is also relatively sensitive to deferasirox.

SAMPLE INFORMATION			
Sample Name:	NO_10_2.F.DI	Acquired By:	System
Sample Type:	Unknown	Sample Set Name:	
Vial:	20	Acq. Method Set:	Trial 1
Injection #:	1	Processing Method:	Reem
Injection Volume:	50.00 μ l	Channel Name:	239.0nm
Run Time:	43.0 Minutes	Proc. Chnl. Descr.:	POA 239.0 nm
Date Acquired:	12/16/2017 12:27:10 PM EET		
Date Processed:	12/16/2017 1:37:53 PM EET		

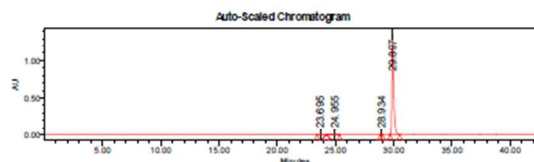


Reported by User: System
 Report Method: Advanced Individual Report
 Report Method ID: 1035
 Page: 1 of 6

Project Name: Reem Zewail
 Date Printed: 12/16/2017
 1:44:01 PM Africa/Cairo

RT	Area	% Area	Height	Resolution	USP Plate Count
1 23.695	70224	0.48	2520		1.446166e+004
2 24.955	89040	0.61	4359	2.086517e+000	4.965714e+004
3 28.934	5668	0.04	754	1.241572e+001	3.149117e+005
4 29.897	14500479	98.88	1365322	4.202743e+000	2.027713e+005

USP Tailing	Purity1 Threshold	Purity1 Angle	USP Resolution
1	3.315	3.596	
2	2.709	8.900	1.929899e+000
3 9.417961e-001	11.000	8.393	1.190986e+001
4 1.542232e+000	0.336	0.112	3.939511e+000



Instrument Method: Trial 1

Stored: 12/16/2017 11:38:01 AM EET

Method Information

Comments
 Modified User: System
 Locked: No
 Method ID: 1015
 Method Version: 1
 Edit User:
 Source S/W Info: Empower 2 Software Build 2154 DB ID: 736065124

W2690/5 Instrument Setup

Type: W2690/5
 Instrument Status: On
 Channel Name: 2690/5
 Description:
 Use Channel Monitor: On
 Monitor Parameter: System Pressure
 Stroke Volume: 130 μ L (flow rates <= 10.000 mL/min)
 Chart Out: %A
 Syringe Draw Rate: Normal

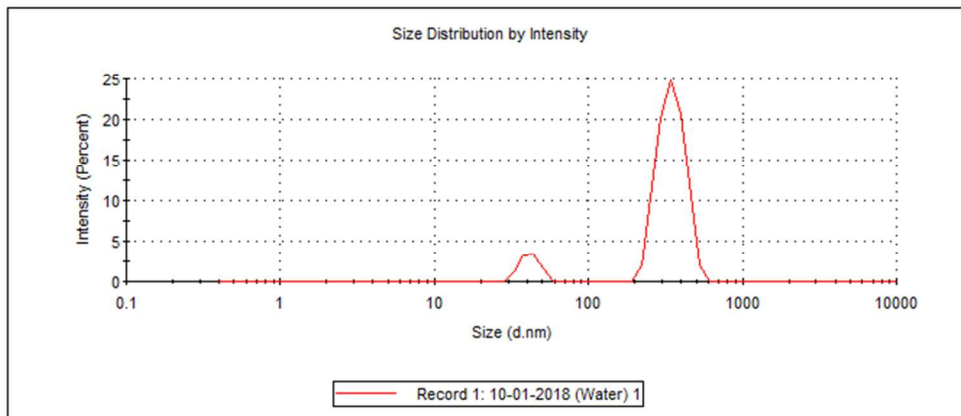
Reported by User: System
 Report Method: Advanced Individual Report
 Report Method ID: 1035
 Page: 2 of 6

Project Name: Reem Zewail
 Date Printed: 12/16/2017
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Supplementary Figure 4. HPLC trace of compound **4b** appearing at 29.897 min.

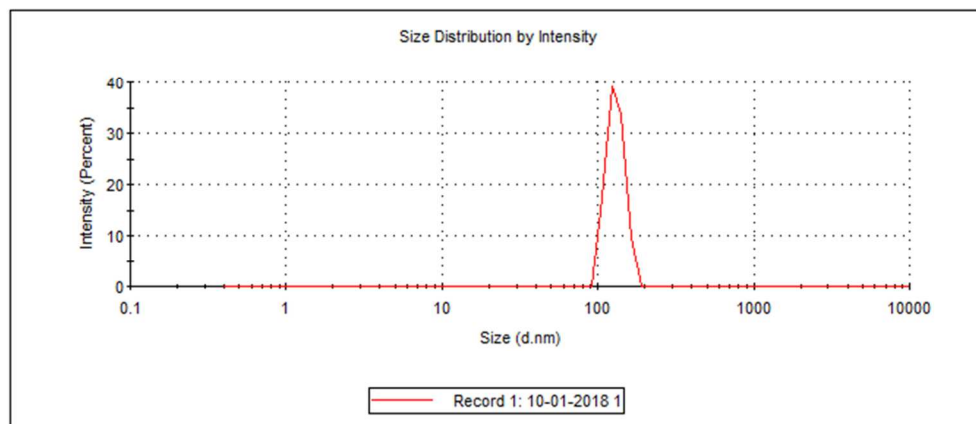
	Size (d.nm):	% Intensity:	St Dev (d.nm):
Z-Average (d.nm): 485.3	Peak 1: 349.1	90.7	68.26
Pdl: 0.506	Peak 2: 41.42	9.3	5.605
Intercept: 0.666	Peak 3: 0.000	0.0	0.000

Result quality : Refer to quality report



	Size (d.nm):	% Intensity:	St Dev (d.nm):
Z-Average (d.nm): 350.1	Peak 1: 130.0	100.0	16.86
Pdl: 0.661	Peak 2: 0.000	0.0	0.000
Intercept: 0.601	Peak 3: 0.000	0.0	0.000

Result quality : Refer to quality report



Supplementary Figure 5. Dynamic Light Scattering result for compound **4b** in water (top panel) and DMSO (bottom panel).