## **Supporting information**

## Novel antitrypanosomal agents based on palladium nitrofurylthiosemicarbazone complexes: DNA and redox metabolism as potential therapeutic targets

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Empirical formula	$C_{22}H_{32}N_8O_9PdS_5$		
Formula weight	819.26		
Temperature (K)	293(2)		
Wavelength	0.71073 Å		
Crystal system	triclinic		
Space group	P-1		
	$a=9.5720(5)$ Å $\alpha=78.497(4)^{\circ}$		
Unit cell dimensions <sup>a)</sup>	b=12.0590(9) Å β=77.746(4)°		
	c=16.613(1) Å $\gamma$ =66.717(4)°		
Volume(Å <sup>3</sup> )	1707.0(2)		
Z	2		
Calculated density (Mg/m <sup>3</sup> )	1.594		
Absorption coefficient $\mu$ (mm <sup>-1</sup> )	0.907		
F(000)	836		
Crystal size (mm)	0.20 x 0.11 x 0.06		
Crystal color/shape	red/prismatic		
Diffractometer/scan	KappaCCD/ $\phi$ and $\omega$		
Radiation / graphite monochromator	$MoK_{\alpha}  /  \lambda {=} 0.71073 \ \text{\AA}$		
$\vartheta$ range for data collection	2.94 to 25.00° deg.		
Limiting indices	-11≤h≤10, -14≤k≤14, -19≤l≤19		
Reflections collected/unique	17315 / 5974 [R(int)=0.0533]		
Completeness to $\vartheta$ =25.00°	99.3%		
Reflections observed [I> $2\sigma(I)$ ]	4227		
Absorption correction	PLATON <sup>1</sup>		
Max. and min. transm.	0.945 and 0.840		
Data reduction and correction <sup>b)</sup>	DENZO and SCALEPACK <sup>2</sup>		
and structure solution <sup>c)</sup> and	SHELXS-97 <sup>3</sup>		
refinement <sup>d)</sup> programs	SHELXL-97 <sup>4</sup>		
Refinement method	Full-matrix least-squares on F <sup>2</sup>		
Weights, w	$[\sigma^{2}(F_{o}^{2})+(0.1465P)^{2}+4.10P]^{-1}$ P= $[Max(F_{o}^{2},0)+2F_{c}^{2}]/3$		
Data/restraints/param.	5974 / 0 / 398		
Goodness-of-fit on F <sup>2</sup>	1.040		
Final R indices [I> $2\sigma(I)$ ]	R1=0.0779, wR2=0.2151		
R indices (all data) <sup>e)</sup>	R1=0.1081, wR2=0.2472		
Largest diff. peak and hole (e.Å <sup>-3</sup> )	1.998 and -1.504		

Table S1. Crystal data and structure solution methods and refinement results for  $[Pd(L5)_2]$ ·3DMSO

<sup>a</sup> Least-squares refinement of the angular settings for 16315 reflections in the  $2.94 < \vartheta < 25.00^{\circ}$  range.

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<sup>b</sup> Corrections: Lorentz, polarization and absorption.

<sup>c</sup> Neutral scattering factors and anomalous dispersion corrections.

<sup>d</sup> Structure solved by Patterson and Fourier methods. The final molecular model obtained by anisotropic full-matrix least-squares refinement of the non-hydrogen atoms.

<sup>e</sup> R indices defined as:  $RI = \Sigma ||F_o| - |F_c||/\Sigma |F_o|$ ,  $wR_2 = [\Sigma w (F_o^2 - F_c^2)^2 / \Sigma w (F_o^2)^2]^{1/2}$ .

(1) Spek, A. L. Acta Cryst. 1990, , A46-C34.

(2) Otwinowski, Z. & Minor, W. in *Methods in Enzymology* (eds. Carter, C. W. & Sweet, R. M.) 307-326 (Academic Press, New York, 1997).

- (3) Sheldrick, G. M. (Univ. of Göttingen, Göttingen, Germany, 1997).
- (4) Sheldrick, G. M. (Univ. of Göttingen, Göttingen, Germany, 1997).

Compound	% C found (calcd.)	% H found (calcd.)	% N found (calcd.)	% S found (calcd.)
9	18.8(18.4)	1.48(1.54)	14.5(14.3)	7.91(8.19)
10	21.0(20.7)	2.05(1.97)	14.0(13.8)	7.81(7.89)
11	23.0(22.9)	2.60(2.38)	13.7(13.4)	7.77(7.63)
12	31.2(30.8)	1.95(2.14)	12.0(12.0)	6.82(6.85)
13	23.2(23.0)	1.74(1.92)	13.6(13.4)	7.53(7.67)
14	24.7(25.0)	2.27(2.31)	12.7(13.0)	7.66(7.42)
15	26.9(26.9)	2.79(2.69)	12.3(12.6)	7.44(7.18)
16	35.1(34.8)	2.66(2.43)	11.6(11.3)	6.29(6.49)
17 <sup>·</sup> DMSO	27.3(27.5)	2.48(2.62)	18.5(18.3)	15.4(15.7)
18	30.5(30.0)	2.16(2.50)	19.7(20.0)	11.2(11.4)
19	31.2(31.2)	2.95(3.06)	18.9(19.0)	10.7(10.9)
20	42.2(42.1)	2.66(2.63)	16.1(16.4)	9.00(9.35)
21 <sup>·</sup> 3DMSO	32.5(32.3)	3.58(3.91)	13.7(13.7)	19.3(19.6)
22	35.6(35.3)	2.94(2.93)	18.5(18.3)	10.3(10.4)
23	37.0(37.5)	3.39(3.44)	17.5(17.5)	9.66(9.99)
24 <sup>.</sup> 2DMSO	42.8(43.0)	4.00(3.81)	12.7(12.6)	13.9(14.3)

Table S2. Microanalytical results