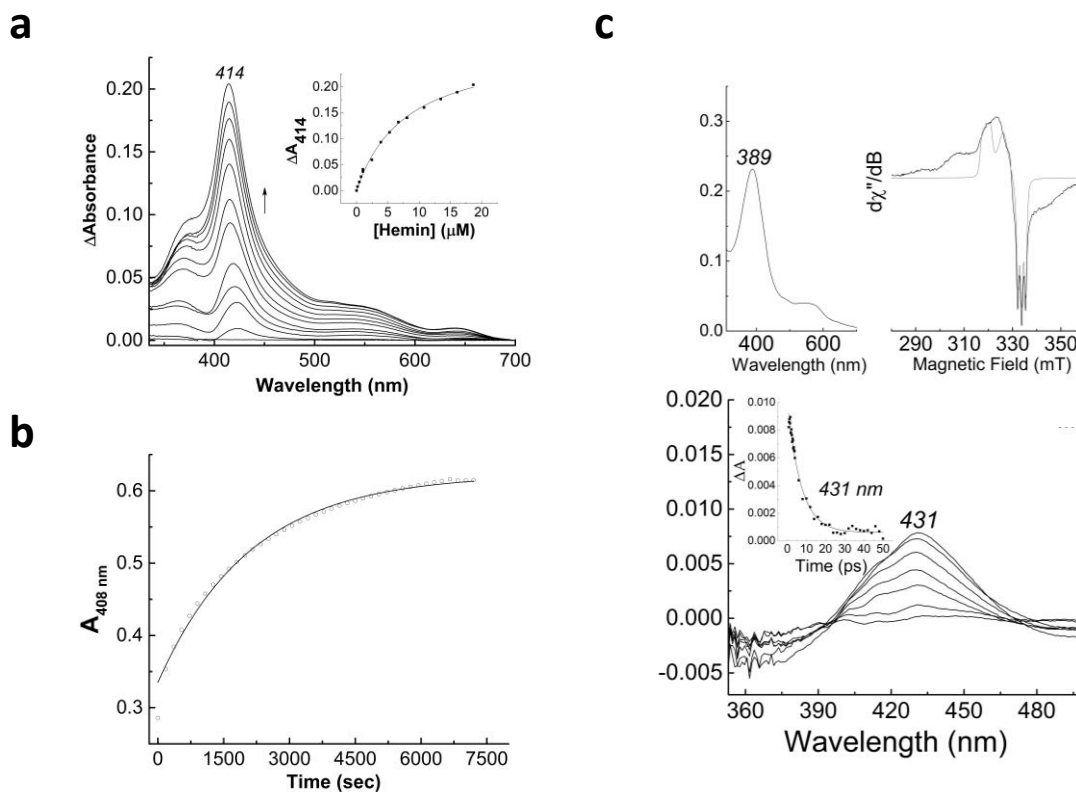


Supplementary Figure 1. Application of CO without the prior application of heme fails to increase K_{ATP} channel activity.

(a) Wild type channels were perfused with a control physiological buffer solution and under conditions where only CO was added without prior application of heme (or ATP), there was no increase in average Popen observed. This is in contrast to the increase in channel activity seen when CO was added in the presence of heme (compare **Fig. 1b (top)**). It is worth noting that a proportion of the cells (5/8) showed a decrease in Popen in response to application of CO alone while the other 3/8 cells showed no change and on average there was no significant difference ($P > 0.05$, paired T Test).

(b) K_{ATP} channels expressing the triple C628S/H631A/H648A mutant (in which the heme binding site is removed) showed no significant change in average K_{ATP} channel activity ($n=4$, $P > 0.05$, paired T Test). Without prior addition of heme, an increase in Popen was not observed upon addition of CO (compare **Fig. 1b (bottom)**). It is worth noting that there was no significant change in the average Popen, however half cells tested showed a large decrease in response to CO application whilst the other half of the cells tested showed no change in activity. In the absence of prior application of heme, any decrease in K_{ATP} activity observed with CO alone indicates that the effects of CO must be due to interaction with the channel at a site that is independent of the SUR2A heme-binding binding motif, which is consistent with the idea that there is more than one mechanism for CO regulation in cells.



Supplementary Figure 2.

Quantification of SUR2A interaction with heme and ligands.

(a) Difference spectra observed during titration of SUR2A⁶¹⁵⁻⁹³³ with ferric heme. Inset shows hyperbolic fitting to a 1:1 binding equation ($K_d = 8.0 \pm 0.6 \mu\text{M}$).

(b) Plot of absorbance at 408 nm (reporting on formation of heme-bound myoglobin) on reaction of apo-myoglobin (36 μM) with heme-SUR2A⁶¹⁵⁻⁹³³ complex (6.4 μM). The observed first-order rate constant for heme dissociation, $K_{\text{off}}(\text{heme})$, is $4.8 \pm 0.1 \times 10^{-4} \text{ s}^{-1}$.

(c) (Top) Left: Absorption spectrum of ferrous heme-SUR2A⁶¹⁵⁻⁹³³ in complex with NO; the spectrum is consistent with a 5-coordinate NO-bound species, as observed in other heme systems^{21,107-109}. **Right:** X-band EPR spectrum of ferrous heme-SUR2A⁶¹⁵⁻⁹³³ in complex with NO and the best-fit simulation (g values 2.100 ± 0.010 , 2.033 ± 0.010 and 2.008 ± 0.005 ; ^{14}NO nitrogen hyperfine coupling 50 ± 5 , 67 ± 10 and 45 ± 5 MHz). These g -values and hyperfine coupling constants are consistent with other five-coordinate ligand-bound complexes in other heme proteins^{106,110}. **(Bottom)** Transient absorption spectra observed on exposure of the heme-NO-SUR2A⁶¹⁵⁻⁹³³ to a femtosecond laser pulse, at various delay times (1.8, 3, 4, 6, 8, 18 and 50 ps). The ligand dissociates and the figure shows transients at 431 nm for recombination of the ligand. The spectra are dominated by an increased absorption at 431 nm and bleaching of the ground state 380 nm transition. Global analysis reveals a very fast component assigned to excited state photophysics^{111,112} and a 7-ps component assigned to geminate ligand recombination. Fitting of the kinetic trace at 431 nm reveals that only a very small fraction (~6%) of the NO does not rebind within 50 ps. The remainder of the NO (94%) rebinds in a single exponential phase. These features are similar to other 5-coordinate heme-NO complexes (Supplementary Table S6).

Supplementary Table 1: Association (k_{on}) and dissociation (k_{off}) rate constants, and equilibrium constants (K_d), for heme binding to SUR2A and other heme proteins

Protein	k_{on} ($M^{-1}s^{-1}$)	k_{off} (s^{-1})	K_d (M)	References
SUR2A ⁶¹⁵⁻⁹³³	0.6×10^2 *	4.8×10^{-4}	8×10^{-6}	This work
SOUL	2.5×10^5	1.2×10^{-3}	4.8×10^{-9}	1
p22HBP	2.1×10^8	4.4×10^{-3}	2.1×10^{-11}	1
Sperm whale Mb	7.0×10^7	8.4×10^{-7}	1.2×10^{-14}	2,3
Sperm whale Mb H93G	7.0×10^7	1.2×10^{-2}	1.6×10^{-10}	2,3
Hb	2.9×10^7	7.1×10^{-6} (α)	2.5×10^{-13}	2-4
		9.4×10^{-4} (β)	3.2×10^{-11}	2,3
BSA	5.7×10^7	1.1×10^{-2}	2.2×10^{-10}	2
mPer2-PAS-A	3.5×10^7	6.3×10^{-4}	1.8×10^{-11}	5
NPAS2-bHLH-PAS-A	3.3×10^7	5.3×10^{-3}	1.6×10^{-10}	6
HRI	1.1×10^7	1.5×10^{-3}	1.4×10^{-10}	7

* Calculated from $K_d = k_{off}/k_{on}$.

IV. Supplementary Table 2. Comparison of absorption maxima for various heme proteins^a

Protein	Fe(II)	Fe(II)-CO	References
SUR2A ⁶¹⁵⁻⁹³³	385, 425, 531, 559, 577	420, 540, 569	This work
heme	383, 550, 574	407, 537, 567	This work
BK channel, HBD	426, 530, 560	419, 535, 568	8
<i>O₂ binding proteins</i>			
Sperm whale myoglobin	434, 556	423, 542, 579	9
<i>E. coli</i> DOS	427, 532, 563	423, 540, 570	10,11
FixL*	433.5, 565	425, 545, 576	12,13
SOUL	422, 527, 558	418, 536, 563	1
P22HBP	422, 530, 560	416, 537, 567	1
<i>Catalytic enzymes</i>			
Nitric oxide synthase	412, 560	444	14
P450 _{cam}	409, 542	448, 550	15
Chloroperoxidase	408, 552	445, 550	15
<i>Regulatory proteins</i>			
E75	425, 530, 558	421, 540, 569	16
Rev-erb β	428,533,558	421, 540, 568	16
RcoM-2	425, 532, 562	423, 540, 570	17
CooA	425, 530, 559	422, 540, 569	18,19
Cystathione β synthase	450	422	20
Heme-regulated eIF2 α	428, 530, 560	423, 540, 570	21
<i>PAS domain proteins</i>			
Clock PAS-A	423, 527, 559	420, 540, 570	22
NPAS2-PAS-A	423, 530, 558	420, 530, 568	6
NPAS2-PAS-B	424, 529, 557	420, 536, 571	23
		426, 530, 561	24
mPer2-PAS-A	425, 529, 558	420, 539, 565	5

^a Reviewed also in reference ²⁶.

V. Supplementary Table 3: Association (k_{CO}) and dissociation (k_2) rate constants, and equilibrium constants (K_d), for CO binding to SUR2A and other heme proteins

Protein	k_{CO} ($M^{-1}s^{-1}$) ^a	k_2 (s^{-1}) ^a	K_d (μM)	k_1 (s^{-1}) ^a	References
SUR2A ⁶¹⁵⁻⁹³³	0.17-0.37 x 10 ⁶	0.05	0.6	20-30	This work
<i>A. thaliana</i> Hbs ^d	0.55-50 x 10 ⁶	0.0012-0.0013		34/43	26-28
<i>A. thaliana</i> GLB3	0.014 x 10 ⁶	0.001			27
Tomato SOLy GLB1	1 x 10 ⁶	0.02	0.02	200	29
<i>Oryza sativa</i> Hb1	7.2/6.8 x 10 ⁶	0.001	0.00014	40	30-32
<i>Oryza sativa</i> Hb2	1.8 x 10 ⁶			15	31
<i>Synechocystis</i> Hb	90 x 10 ⁶			14	31,33
Human Ngb	50/65 x 10 ⁶	0.014	0.00021	0.6/4.5	28,34
Murine Ngb	55/72 x 10 ⁶	0.013	0.00018	0.5-0.6/1.2	28,34-36
Human Cgb	5.6 x 10 ⁶	0.003	0.0217	~0.5/0.09	31,37
Barley Hb	0.57 x 10 ⁶	0.0011	0.00193		38
Drosophila Hb	13 x 10 ⁶			30/40	28,39
Hb α -chain R/ β -chain R	2.9/7.1 x 10 ⁶	0.0046/0.0072			40
Sperm whale Mb	0.51 x 10 ⁶	0.019	0.037		40, 40
<i>A. xylosoxidans</i> cytc	101 x 10 ⁶	0.028	280		41
cytc mutants				70	42
<i>E. coli</i> DOS, full-length	0.00081/4 x 10 ⁶	0.0025/0.007	3.1	2/9	43,44
<i>E. coli</i> DOS, PAS domain	0.0078/5/0.0011 x 10 ⁶	0.0045/0.011	0.58/10	400	44-46
<i>B. japonicum</i> FixLH	0.005 x 10 ⁶	0.045	9		47
<i>R. meliloti</i> FixLH	1.7x10 ⁻⁴	0.083			47
sGC	3.6 x 10 ⁴	3.5	98		48
AxPDEA1	0.21 x 10 ⁶	0.058	0.28		49
Fe(PPIX)(2-Melm)(CO)	1.6 x 10 ⁶				45

^a k_{CO} , k_1 and k_2 are defined or derived from Scheme 1 in the main text. k_1 is the first-order rate constant for dissociation of a distal protein ligand in a 6-coordinate heme species (also defined Eq 1), which can be extracted from kinetic data for CO binding.

^b There are two types of *A. thaliana* Hb (*A. thaliana* Hb1 and *A. thaliana* Hb2), so we report a range of reported values in the table.

VI. Supplementary Table 4. Comparison of high frequency vibrational modes of CO-bound complexes of heme proteins.

Protein	ν_4	ν_3	ν_2	References
SUR2A ⁶¹⁵⁻⁹³³	1370	1498	1584	This work
Heme	1372	1501	1589	This work
horseMb	1373	1501	1585	50
<i>E. coli</i> DOS	1370	1496	1581	51
SOUL	1371	1499	1582	1
p22HBP	1372	1499	1583	1
E75(LBD)	1367	1493	1579	16
Reverb β (LBD)	1368	1493	1581	16
CooA	1371	1493	1579	52,53
HemAT-Bs	1368	1495	1578	54
sGC	1370	1499	1584	55
NPAS PASA	1372	1497/1468	1583/1556	56
NPAS2-PASB	1372	1498/1467	1583/1558	23
mPer2 PASA	1370	1465/1497	1554/1586	5

VII. Supplementary Table 5. Comparison of $\nu(\text{Fe-CO})$ and $\nu(\text{C-O})$ stretching frequencies of various heme proteins.

Protein	$\nu(\text{Fe-C})$	$\nu(\text{C-O})$	References
SUR2A ⁶¹⁵⁻⁹³³	494	1965	This work
Sperm whale Mb	512	1944	57
Human HbA	507	1951	57
HRP form II	537	1904	58,59
form III	516	1934	60
CCP form II	530	1922	61
form II'	503	1948	61
CCPMI (alk)	503	1922	62
Mtb. KatG-WT form I	522	1926	63
Mtb. KatG-WT pH=7.2	525	1923	64
pH=10	520	1928	64
HemAT	494	1964	54
<i>E. coli</i> DOS	486	1973	51,65
FixL	498	1962	66
DosS	490	1971	67
NPAS2-PAS-A	491	1962	56
GAF _{All4978}	514	1957	68
CBS	497	1961	20
CooA	487	1982	69
	487	1969	70,71
sGC ₁	497	1959	72,73
sGC ₂	473	1987	74,75
HRI	492	1967	21
HRI-NTD	494	1963	21,76
HRI-NTD	493	1960	77
NP4	499	1962	78
	513	1950	
Rev-erb β (LBD)	500	1948	79
	515	1948	79
E75(LBD)	494	1958	79
cytochrome c'	491	1966	80
PPDMe(ImH)	495	1960	58
nNOS, substrate-free	487	1949	81
nNOS, substrate-free	501	1930	81
nNOS + Arg	503	1929	81
iNOS _{FL} , substrate-free	487	1945	82
iNOS _{FL} + Arg	512	1906	82
iNOS _{oxy} , substrate-free	491	1946	83
iNOS _{oxy} + Arg	512	1907	83
iNOS _{oxy} + H ₄ B	490	1944	83
iNOS _{oxy} + Arg/H ₄ B	512	1905	83

CYP101, substrate-free	464	1963	84-87
CYP101 + norcamphor	473	1947	87
CYP101 + adamantanone	474	1942	87,88
CYP101 + camphoroquinone	476	1941	87
CYP101 + fenchone	480	1945	87
CYP101 + camphor	481	1940	84-87,89,90
CYP101 + tetramethylcyclohexanone	485	1934	87
CYP17, substrate-free	472	1957	91
CYP17, substrate-free	485	1946	91
CYP17 + 17-OH pregnenolone	491	1938	91
CYP17 + 17-OH pregnenolone	505	1928	91
CYP17 + 17-OH progesterone	491	1938	91
CYP17 + progesterone	498	1932	91
CYP17 + pregnenolone	498	1940	91
TPP(OH)DMF	527	1947	92
TPP(NH ₂)/DMF	527	1948	92
TPP(OCH ₃)/DMF	526	1949	92
TPP/DMF	525	1951	92
TSMP/H ₂ O	527	1957	93
TPivP/THF	526	1957	94
TPP(CN)/DMF	521	1957	92
TPP(2,6-difluoro)/DMF	521	1963	92
TPP(2,6-dichloro)/DMF	516	1966	92
TPP/Bz	524	1973	95
BSA	526	1962	1
HSA	524	1960	96
heme in PBS, pH 6.9	525	1962	96
Heme (80% glycerol)	530	1955	97
heme in Hepes, pH 7.5	525	1948	This work

VIII. Supplementary Table 6: Parameters of ligand recombination in heme proteins.

Protein	Recombination time constants / ps (rebinding fraction)	Non-decaying phase	References
SUR2A ⁶¹⁵⁻⁹³³	22 (14%), 150 (26%), 2500 (50%)	10%	This work
DNR	100 (30%), 900(35%)	35%	98
CooA	78(60%), 386(30%)	10%	99,100
<i>E. coli</i> DOS	1500(60%)	40%	101
R220H FixL	280(25%), 2400(35%)	40%	102
RcoM-2	170(65%), 500(35%)	0%	103
NO Binding			
SUR2A ⁶¹⁵⁻⁹³³	7(94%)	6%	This work
sGC	7.5 (97%)	3%	104
<i>A.xylosoxidans</i> cyt c'	7.0 (100%)	0%	105
cytc/CL	7.0 (89%)	11%	106

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