

Supporting Information

Computational De Novo Design and Characterization of a Protein that Selectively Binds a Highly Hyperpolarizable Abiological Chromophore

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Chart S1. Sequence alignment between the monomeric single chain protein *PA_{SC}* and *SCR_{PZ}-1*. The highlighted regions represent segments of helical overlap that were used to guide the alignment.

Figure S1. Backbone alignment of models of *PA_{sc}* (blue) and the template tertiary structure (red) of *SCR_{PZ}-1* and *SCR_{PZ}-2*.

Figure S2. Model structures illustrating acidic and basic residues of *SCR_{PZ}-1* (top), *SCR_{PZ}-2* (middle) and *PA_{SC}* (Bottom) rendered in a spacefilling format from four different viewpoints. Lysine and arginine residues (blue) and aspartic and glutamic acid (red) and glutamine (purple) are highlighted to detail the differences between *SCR_{PZ}-1* (Top) and *SCR_{PZ}-2* (Bottom).

Gene Sequences for *SCR_{PZ} 1-3*

Synthesis of [RuPZn](PF₆)₂

Scheme S1. Synthesis of the *RuPZn* chromophore.

Chart S1. Sequence alignment between the monomeric single chain protein PA_{sc} and $SCR\text{PZ-}I$. The highlighted regions represent segments of helical overlap that were used to guide the alignment.

			N15---	--N6	N C	C6---	-----C15
PA (SC)	1	SPEEAMQEAQ	QTAREAEQAM	QKHR	QAYDKG	DQKAL	OTAK EFQQAMQKHK
SCR PZ	1	ELEKLR	QTGEQILQIA	KQVN	EIMLKG	DDDSLEQLLK	LAYELIQQHT
				N15-----N6	NC	C6-----	
PA (SC)	51	QYMN---QA	ISESVQKTAR	YFEQAMQKHR	QAYDKGDQK	AL	OTAKEAQQ
SCR PZ	47	QLAYNRQEA	DTE-IMKQGQ	QILEIAQQVN	EVLKGDKDS	LE	QLIKLAYQ
							-C15
PA (SC)	98	AMQKHSQALR	G				
SCR PZ	96	LIQQLQELFE	KKN-----	--			

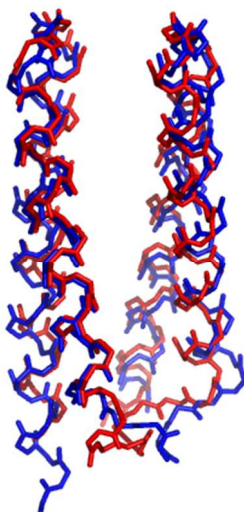


Figure S1. Backbone alignment of models of PA_{sc} (blue) and the template tertiary structure (red) of $SCR\text{PZ-}1$ and $SCR\text{PZ-}2$.

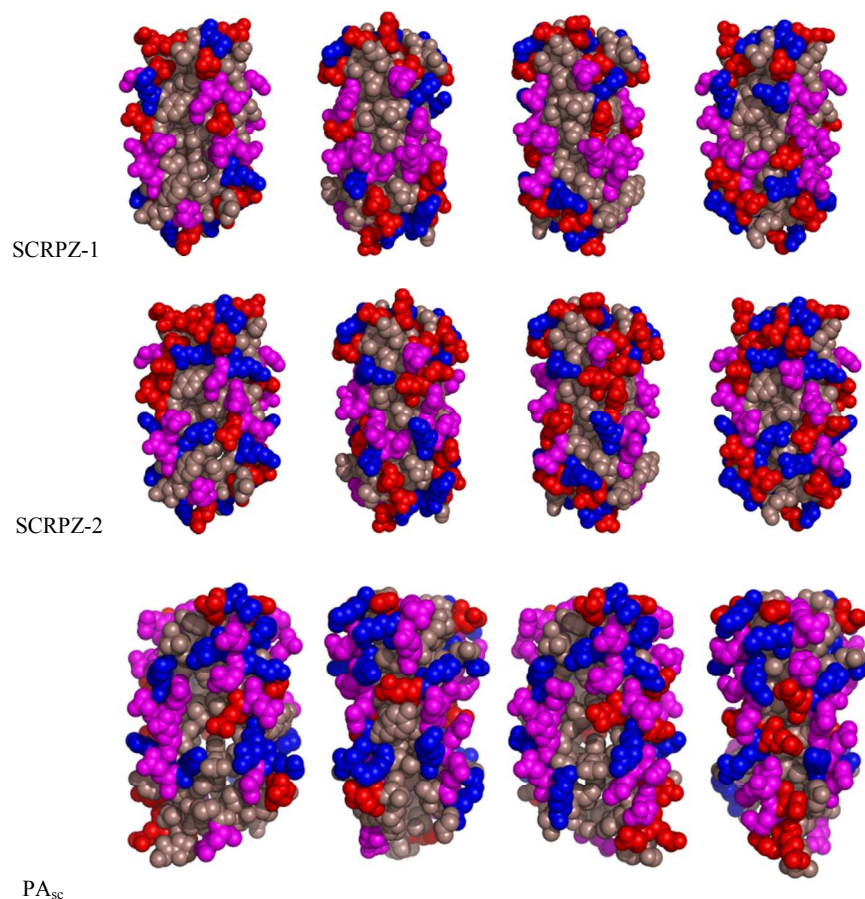


Figure S2. Model structures illustrating acidic and basic residues of *SCRYPZ-1* (top), *SCRYPZ-2* (middle) and PA_{sc} (Bottom) rendered in a spacefilling format from four different viewpoints. Lysine and arginine residues (blue) and aspartic and glutamic acid (red) and glutamine (purple) are highlighted to detail the differences between *SCRYPZ-1* (Top) and *SCRYPZ-2* (Bottom).

Gene Sequences for *SCRPZ 1-3*.

SCRPZ-1:

5' *CATATGGA*ACTGGAAAACTGCGTCAGACTGGTGAACAGATCCTGCAAATTGCGA
AACAGGTTAACGAGATTATGCTGAAGGGTGATGACGACTCTCTGGAGCAGCTGATT
AAACTGGCGTACGAACTGATCCAACAACACACCCAGCTGGCGTACAATCGTCAGGA
AGCTGCGGATACGGAGATCATGAAACAGGGTCAGCAGATTCTGGAAATTGCCCAGC
AGGTGAACGAAGTGCTGCTGAAAGGCGACAAAGACTCTCTGGAACAGCTGTAAAG
CTGGCGTATCAGCTGATTCAGCAACTGCAGGAGCTGTTCGAAAAGAAAACTAAAA
GCTT 3'

SCRPZ-2:

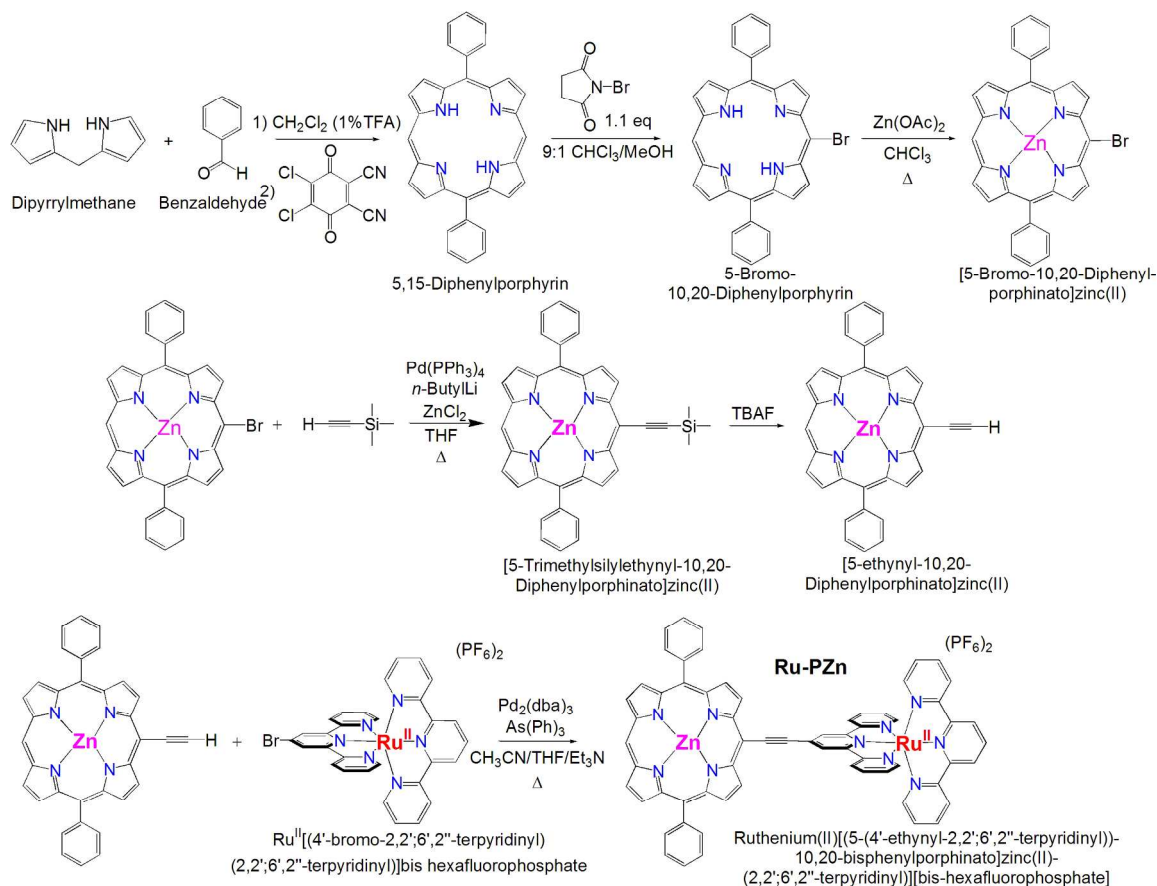
5' *CATATGGA*ACTGGAAAAGCTGCGTCAAACCTGGTGAACAGATCCTGCAAATTGCCCA
GCGCGTGCCTGAGATTATGGACAAAGGTGACGACGATAGCCTGGAGCAACTGTTGG
AGGAAGCCTATGAGCTGATCCAAAAGCACCGCCAACTGGCCTACAACCGTCAGGAG
GCCGCGGACACCGAAATTATGAAACAAGGTGACCAGATTCTGCAAATCGCACAGCG
TGTGCGCGAGGTTCTGGACAAGGGCGACAAGGACTCCCTGGAGCAGTTGATTGAGG
AGGCGTACCAGCTGATTCAAAGTTGCGCGAGCTGTTCGAGAAAAGAACTAAGCTT
3'

SCRPZ-3:

5' *CATATGGA*ACTGGAAAACTGCGTCAGACTGGTGAACAGATCCTGCAAATTGCGA
AACAGGTTAACGAGATTATGCTGAAGGGTGATGACGACTCTCTGGAGCAGCTGATT
AAACTGGCGTACGAACTGATCCAACAACACACCCAGCTGGCGTACAATCGTCAGGA
AGCTGCGGATACGGAGATCATGAAACAGGGTCAGCAGATTCTGGAAATTGCCCAGC
AGGTGAACGAAGTGCTGCTGAAAGGCGACAAAGACTCTCTGGAACAGCTGTTAAAG
CTGGCGTATCAGCTGATTCAGCAACTGCAGGAGCTGTTCGAAAAGAAAACTAAAA
GCTT 3'

Synthesis of [RuPZn](PF₆)₂

The synthesis of the compound followed previous literature methods¹³ but used the unsubstituted 5,15-diphenylporphyrin. For clarity, the reaction scheme is provided in the supporting information. ¹H-NMR (d₆-DMSO, 500 MHz) 10.2 (s, 1), 10.01 (d, 2), 9.35 (d, 2), 9.30 (d, 2), 9.04 (d, 2), 8.89 (d, 2), 8.77 (d, 2), 8.73 (d, 2), 8.51 (d, 2), 8.45 (t, 1), 8.25 (d, 4), 7.97 (t, 2), 7.93 (t, 2), 7.85 (m, 6), 7.56 (d, 2), 7.41 (d, 2), 7.22 (t, 4). UV/Visible (THF): λ_{max} = 428, 506, 637 nm MALDI-TOF MS: *m/z* = 1258.46 (M⁺, -PF₆) (calculated *m/z* for C₆₄H₄₀F₆N₁₀PRuZn: 1259.14) and 1114.40 (M⁺, -2PF₆) (calculated *m/z* for C₆₄H₄₀N₁₀RuZn: 1114.18).



Scheme S1. Synthesis of the **RuPZn** chromophore.