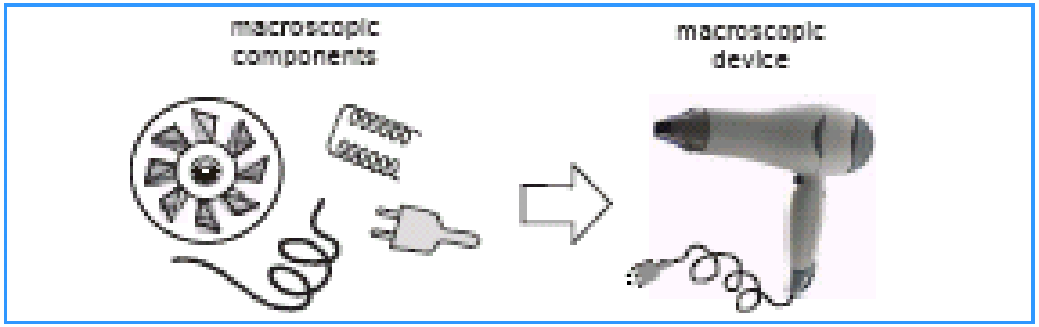
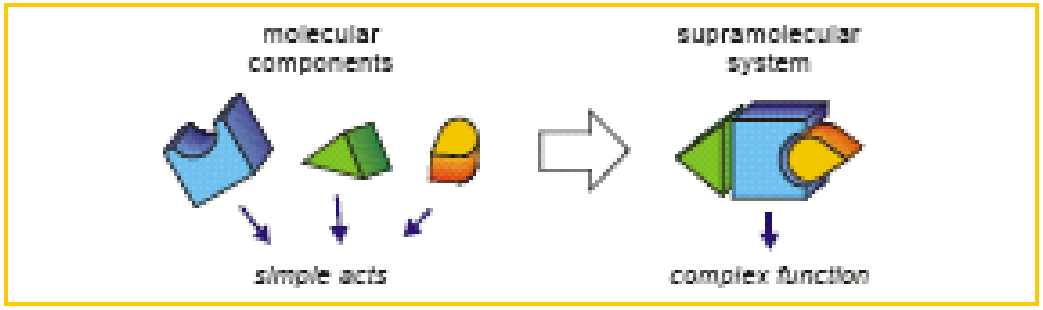
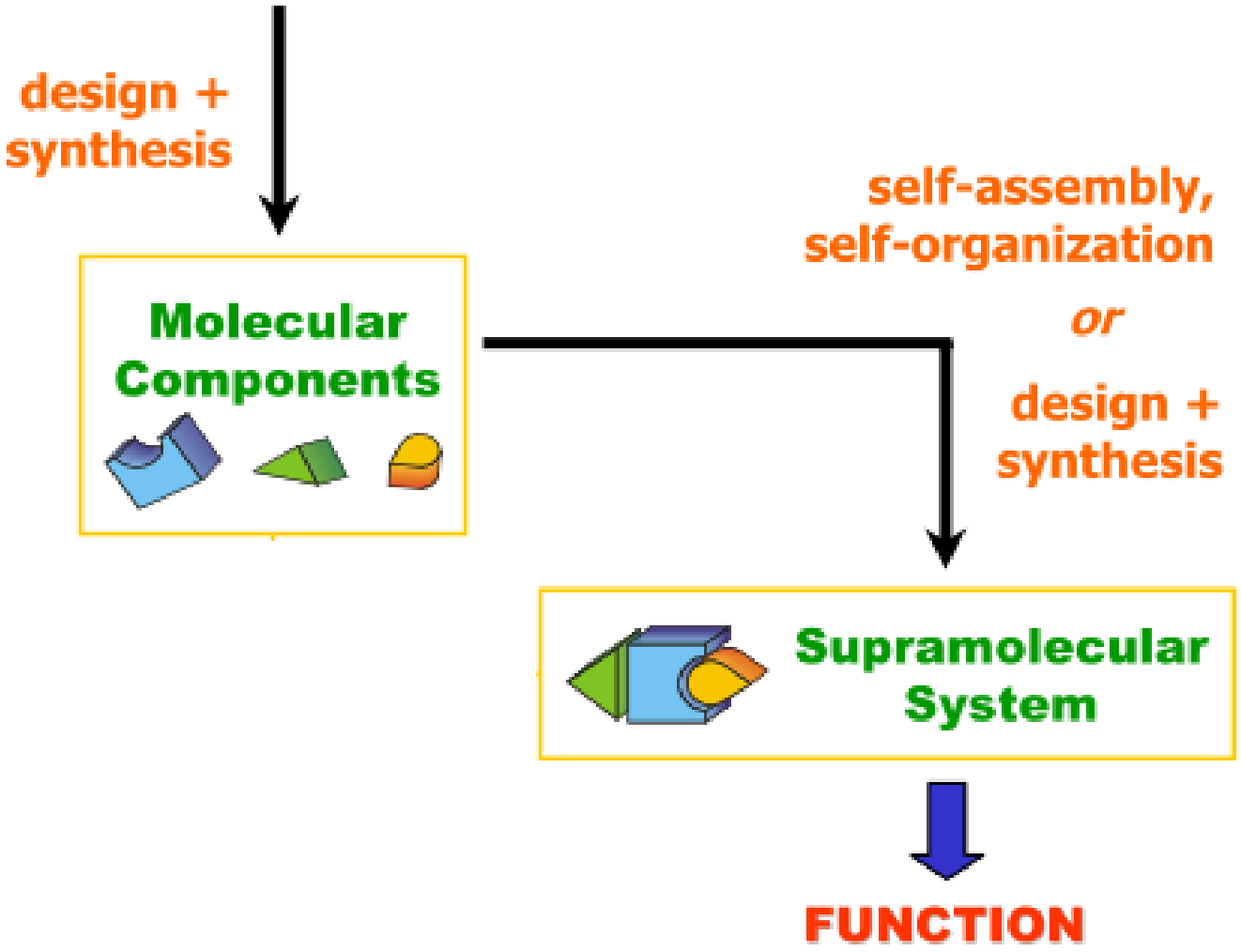
Devices and Machines

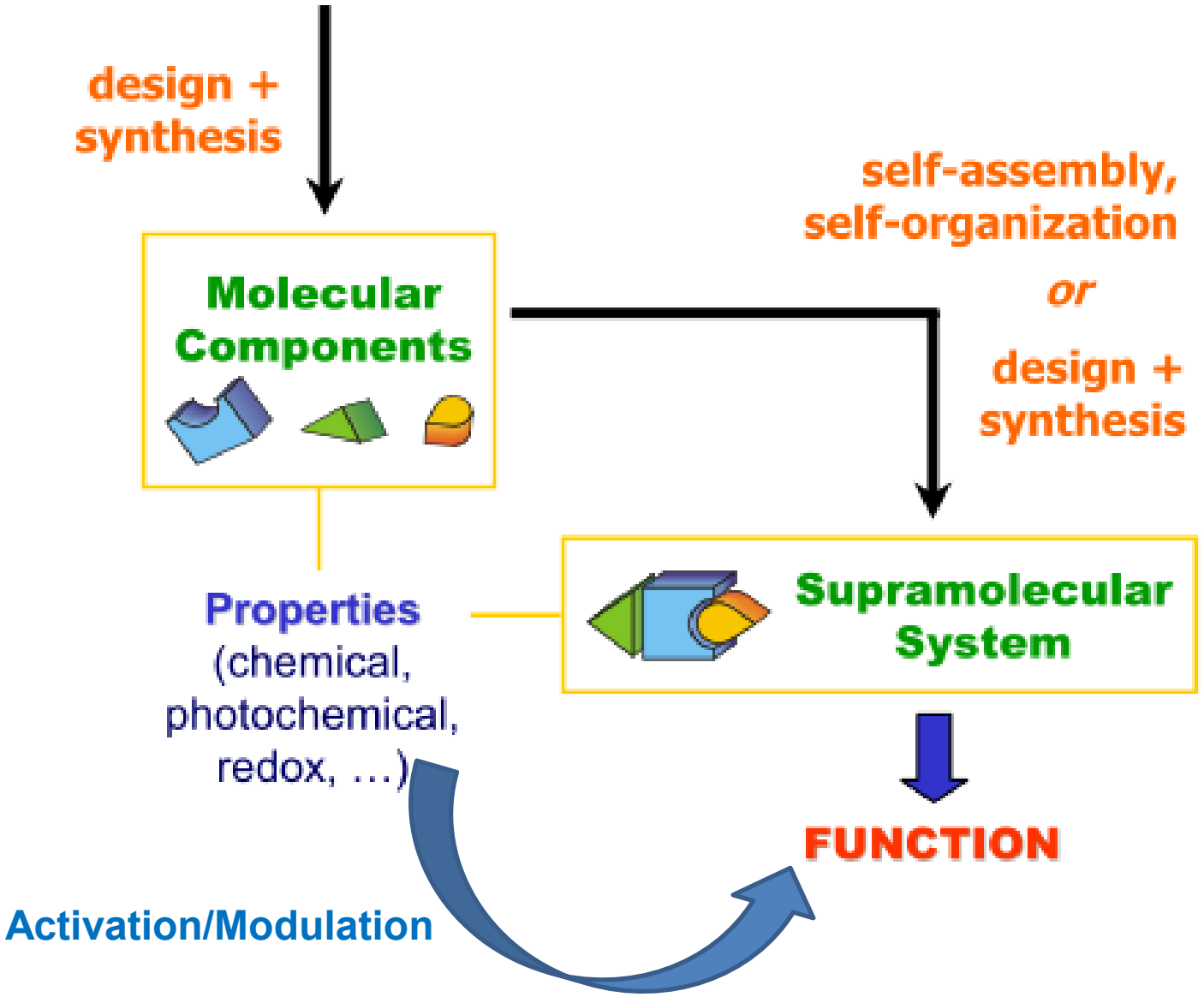
Macroscopic device



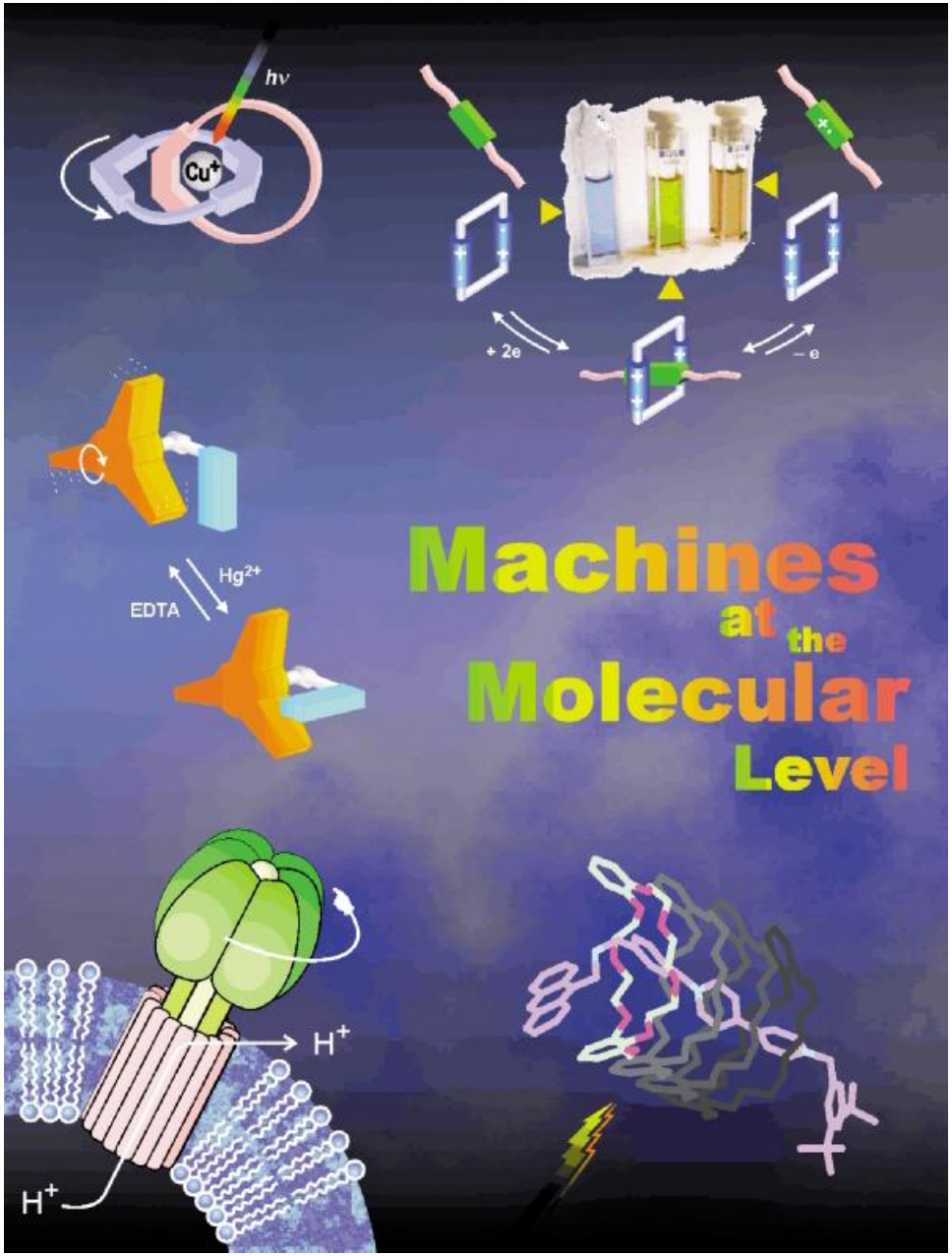
Molecular-level device




design +
synthesis
Molecular
Components
self-assembly,
self-organization
or
design +
synthesis
Supramolecular
System
FUNCTION


design +
synthesis
Molecular
Components
self-assembly,
self-organization
or
design +
synthesis
Supramolecular
System
Properties
(chemical,
photochemical,
redox, …)
FUNCTION
Activation/Modulation

- Kind of fuel (chemical/electrochemical/photons)
- Monitoring (NMR/photophysical techniques/electrochemical techniques)
- Cyclic porcess
- Time-scale (picoseconds-minuts)
- Function


hν
Cu+
+ 2e
– e
EDTA
Hg2+
H+
H+
Machines
at the
Molecular
Level

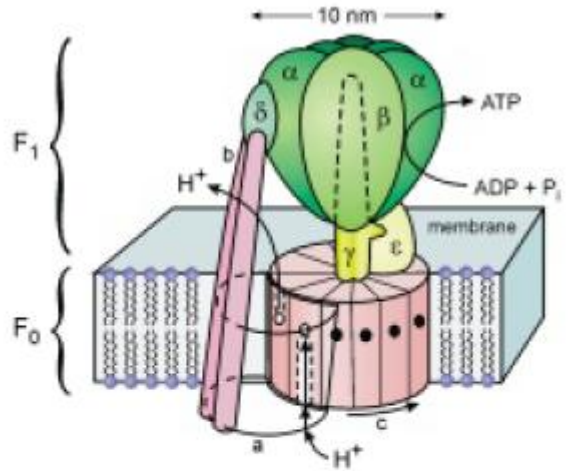


Figure 1. The structure of F_0F_1ATP synthase.[18] The catalytic region is composed of the subunits $\alpha-\varepsilon$. The proton channels lie at the interface between the subunits a and c (dashed lines indicate the putative inlet and outlet channels). Proton flow through the channels develops torque between the a and c subunits. This torque is transmitted to F_1 via the γ shaft and the ε subunit, where it is used to release ATP sequentially from the catalytic sites in F_1. The c subunit consists of 9–12 twin α-helices arranged in a central membrane-spanning array. The a subunit consists of 5–7 membrane-spanning α-helices and is connected to F_1 by the b and δ subunits. Reprinted by permission from ref. [16f] (Copyright© Macmillan Magazines Ltd 1998).

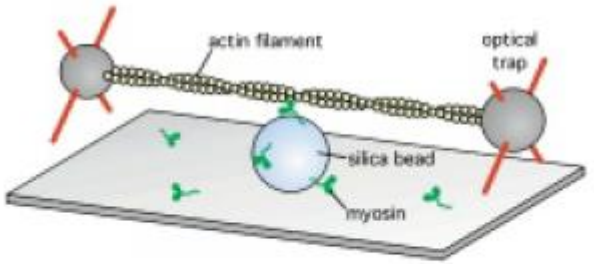
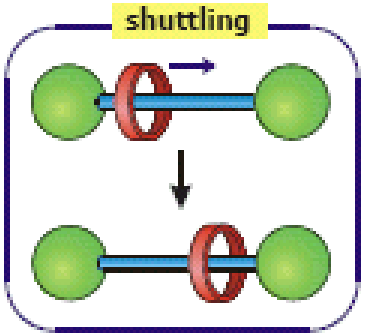
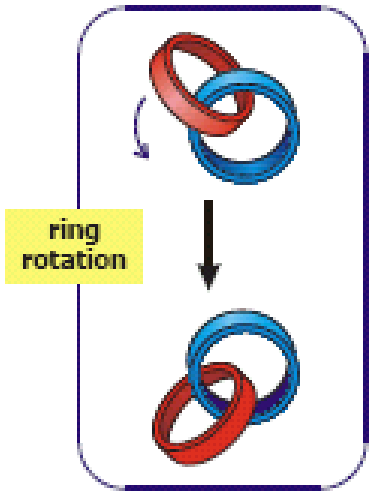
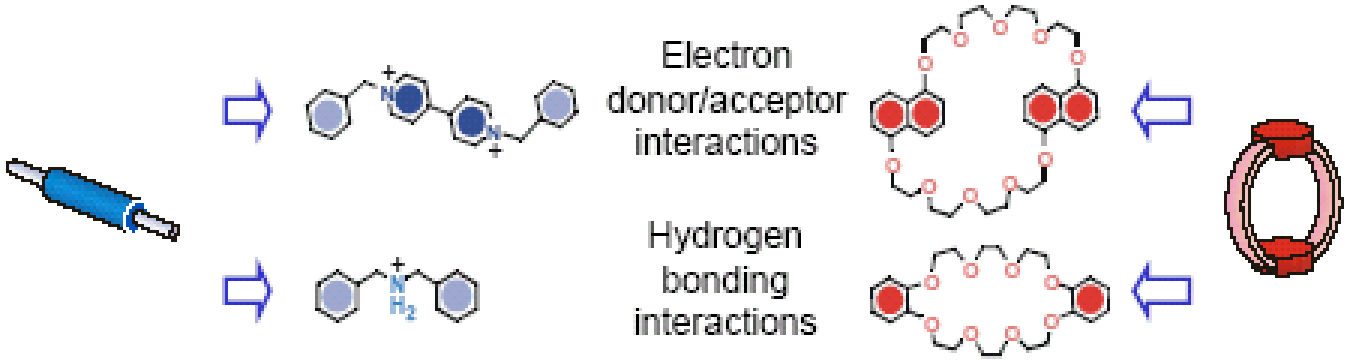


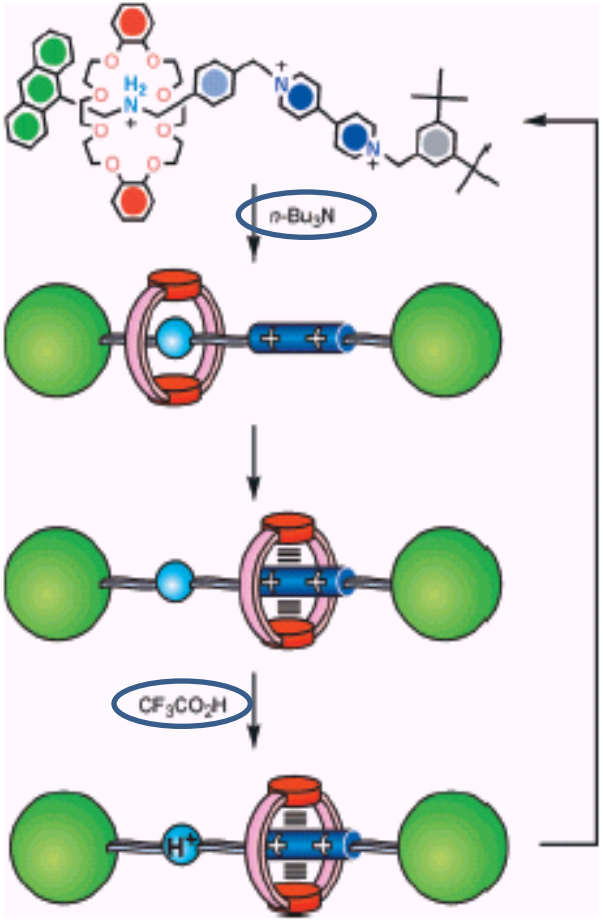
Figure 2. Experimental geometry used[19] to observe single myosin molecules binding and pulling an actin filament. The filament was attached at either end to a trapped bead. These beads were used to stretch the filament taut and move it near surface-bound silica beads that were decorated sparsely with myosin molecules. Adapted with permission from ref. [19] (Copyright© Macmillan Magazines Ltd 1994).

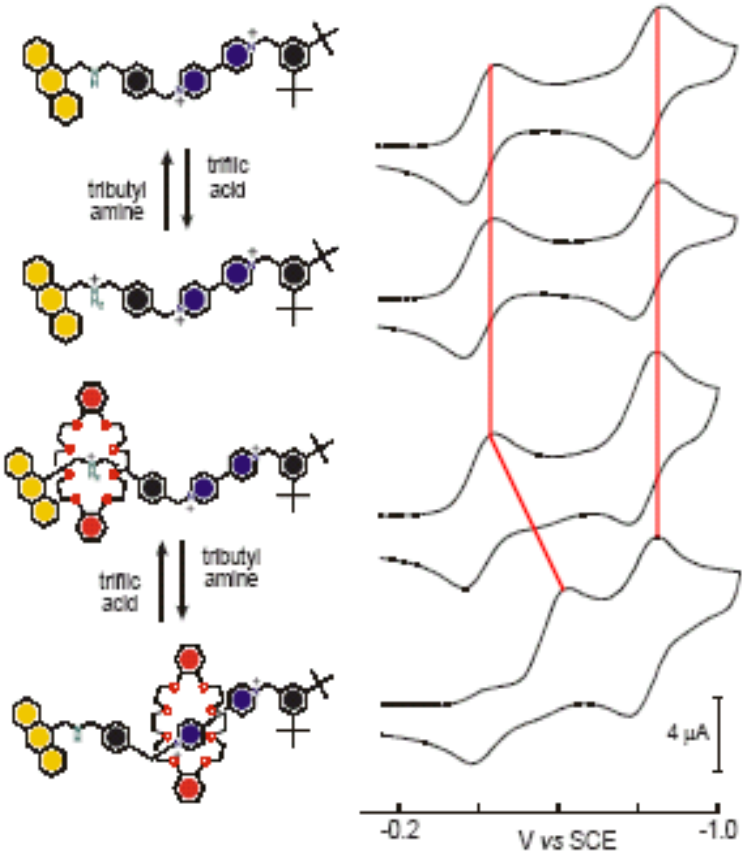

shuttling


ring
rotation

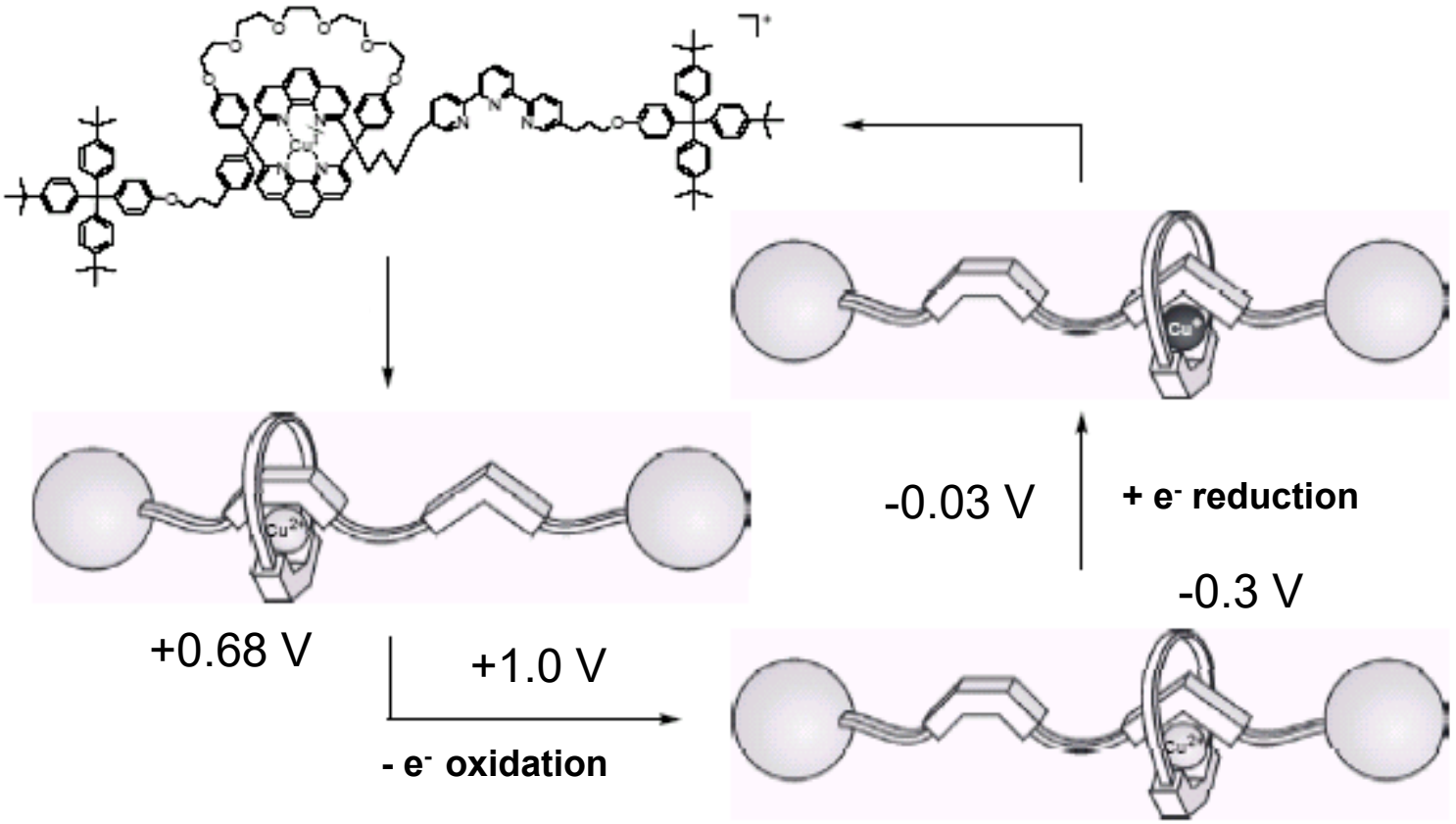

Electron
donor/acceptor
interactions
Hydrogen
bonding
interactions

Chemical Input

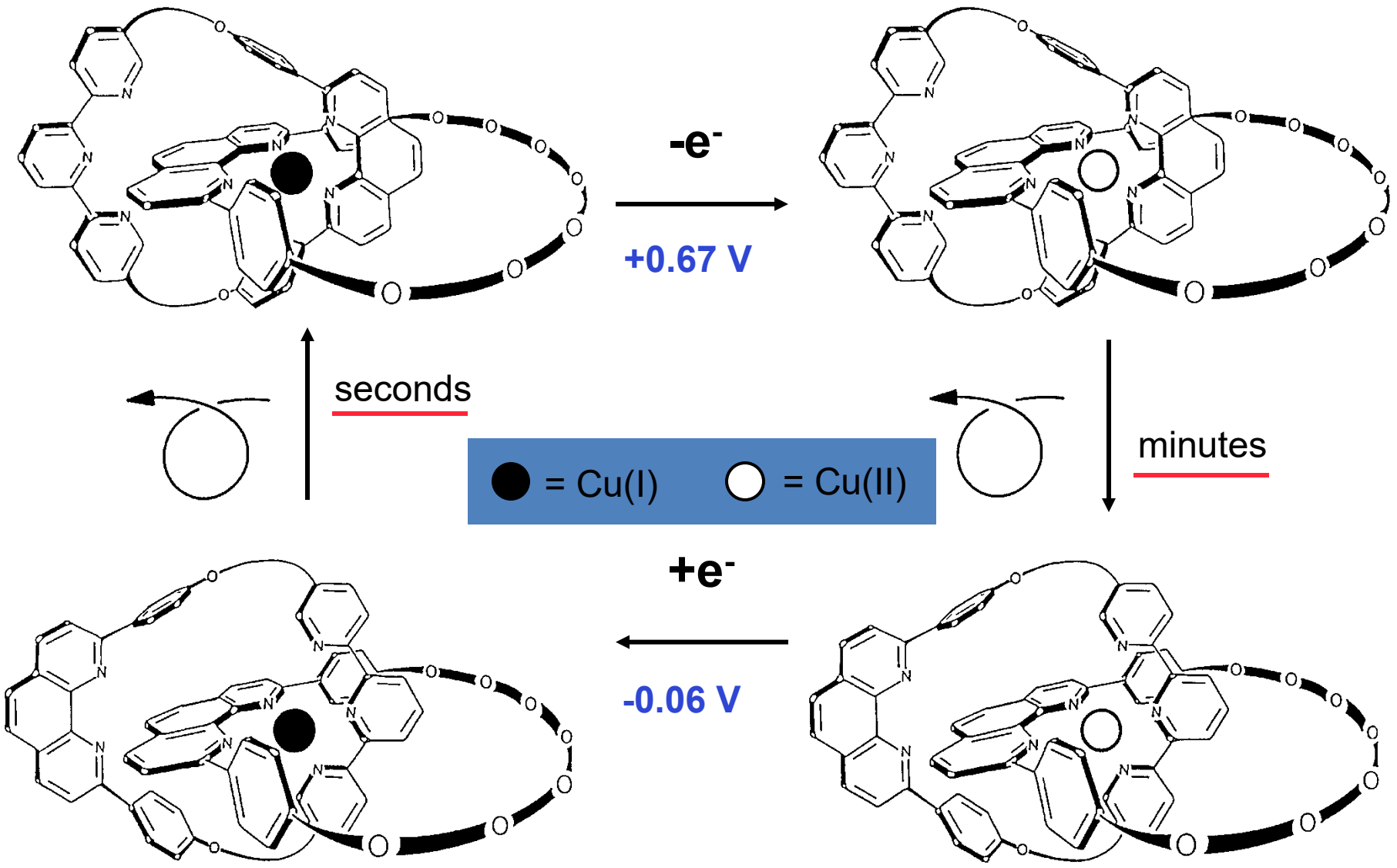


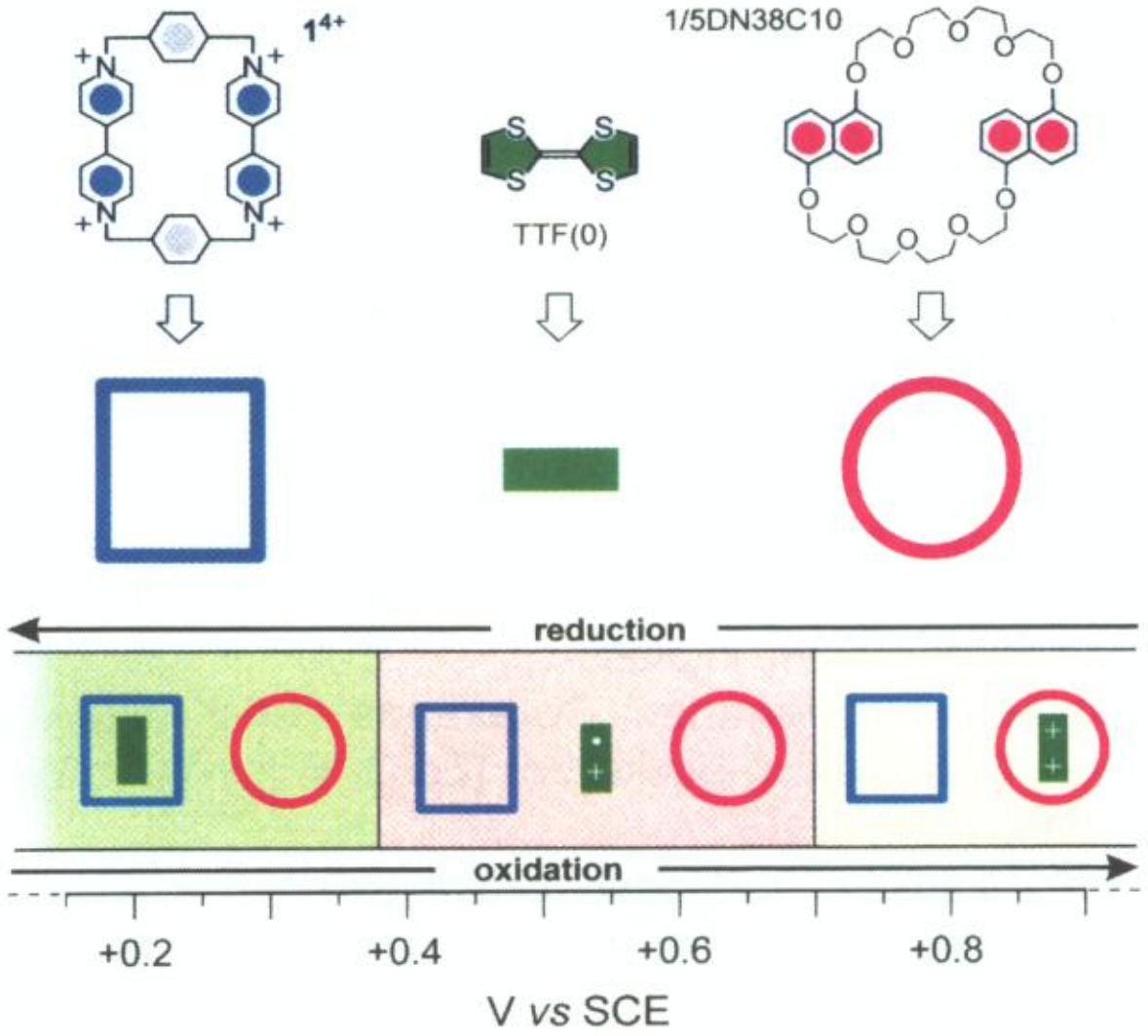


Electrochemical Input

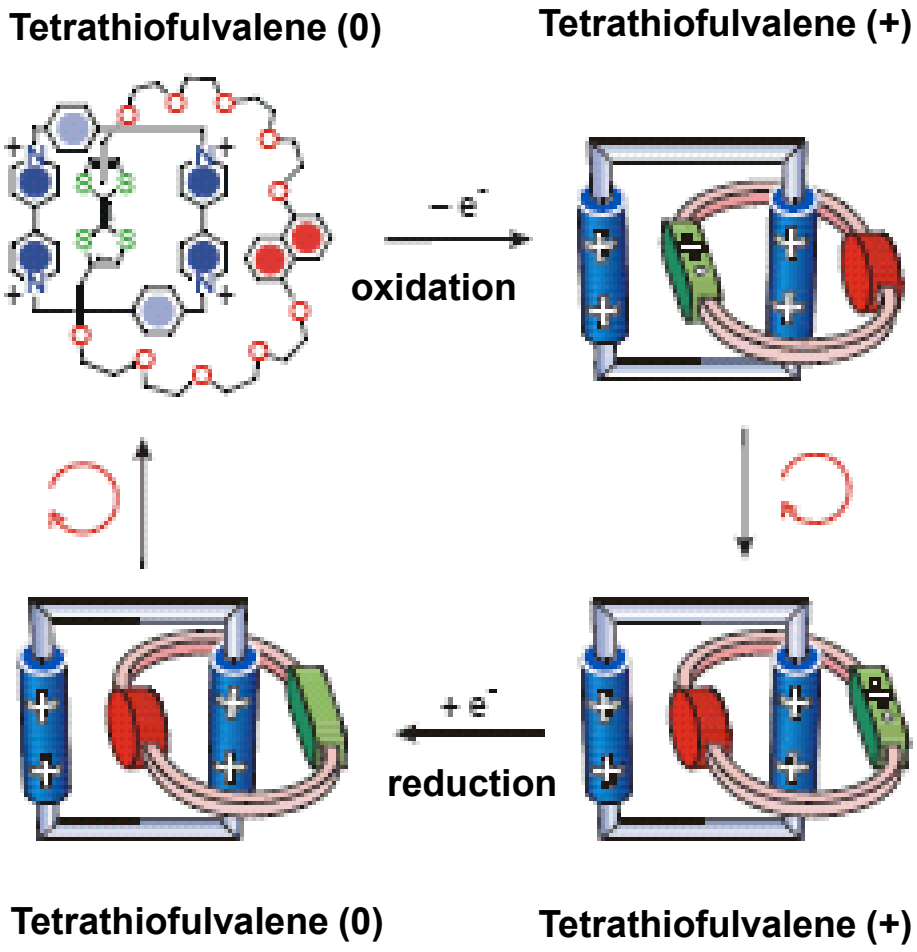


Electrochemical Input




1/5DN38C10
TTF(0)
reduction
oxidation
+0.2
+0.4
+0.6
+0.8
V vs SCE

Electrochemical Input



Photochemical Input

Unidirectional rotation in a mechanically interlocked molecular rotor

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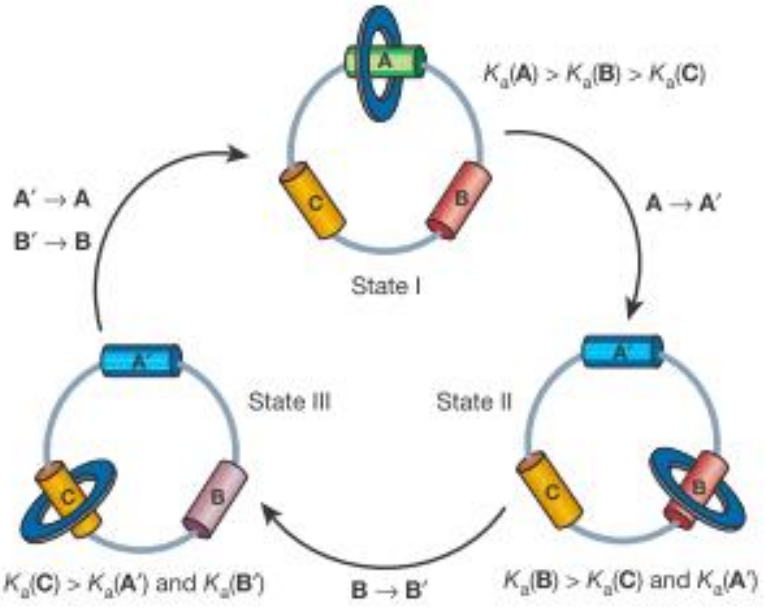
** School of Chemistry, University of Edinburgh, The King's Buildings, West Mains Road, Edinburgh EH9 3JJ, UK*
† Dipartimento di Chimica 'G. Ciamician', Universita degli Studi di Bologna, via F. Selmi 2, 40126 Bologna, Italy

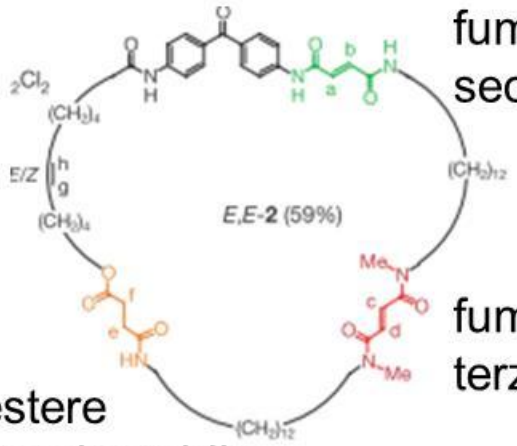


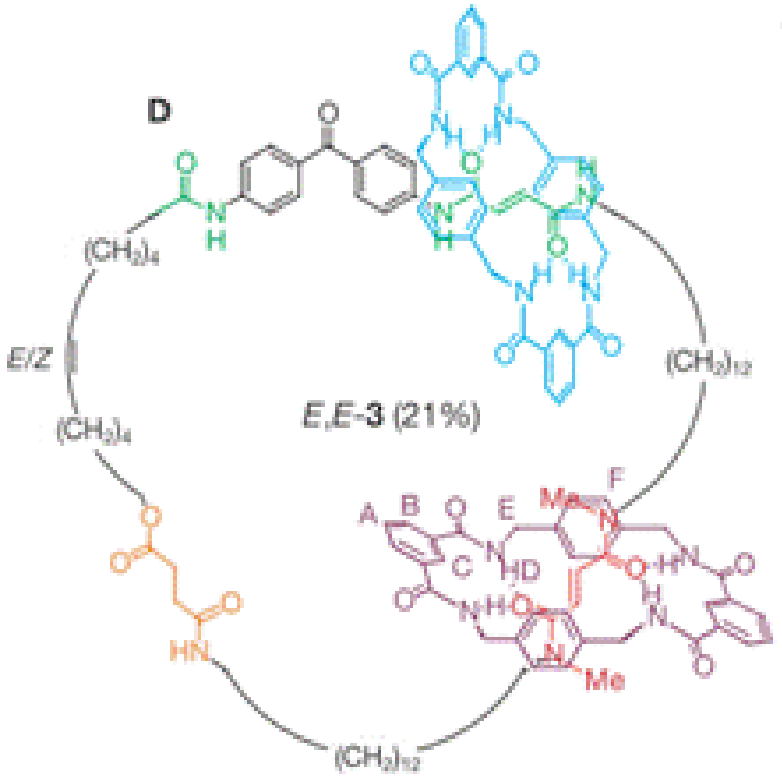
benzofenone

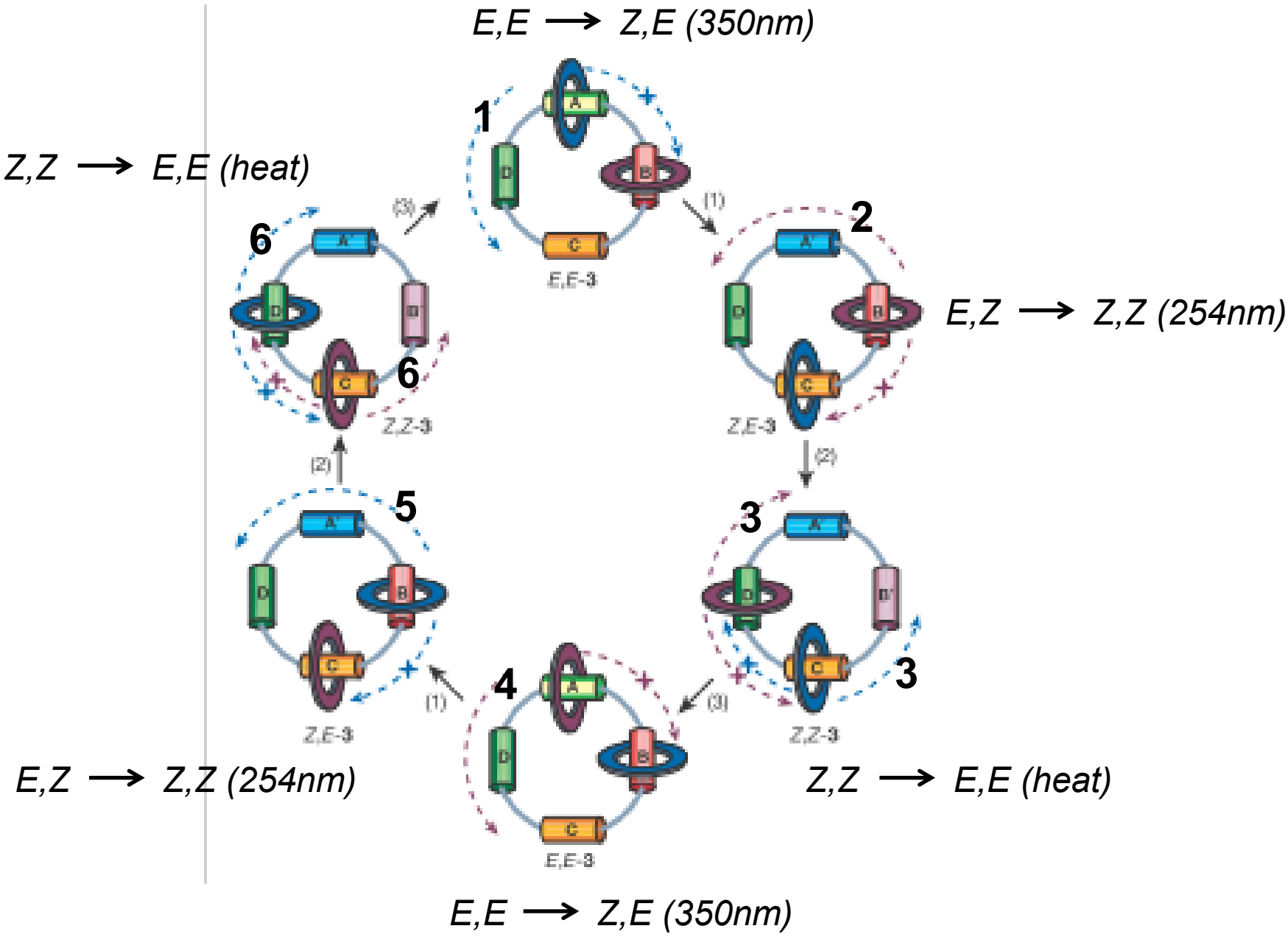
fumaramide
secondaria *E*

fumaramide
terziaria *E*

estere
succinamidico

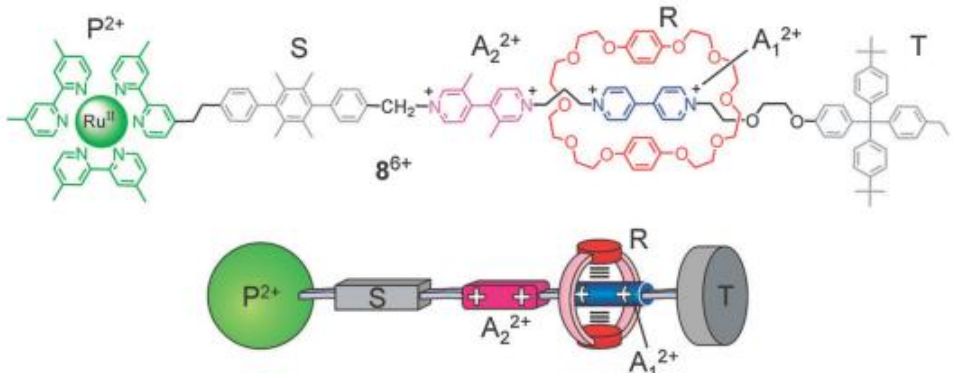




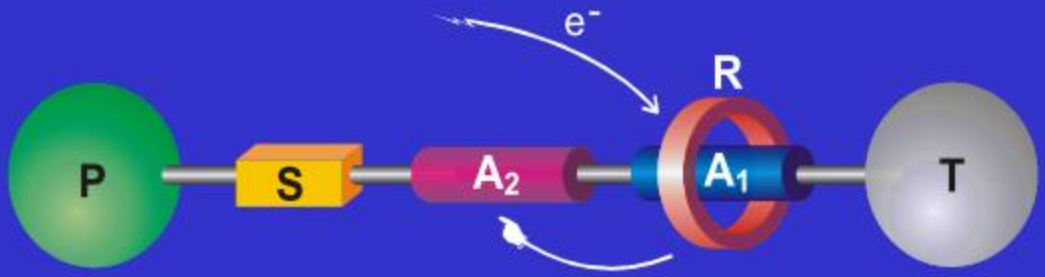

E,E ⟶ Z,E (350nm)
Z,Z ⟶ E,E (heat)
E,Z ⟶ Z,Z (254nm)
E,Z ⟶ Z,Z (254nm)
Z,Z ⟶ E,E (heat)
E,E ⟶ Z,E (350nm)
1
2
3
4
5
6
E,E-3
Z,E-3
Z,Z-3
(1)
(2)
(3)

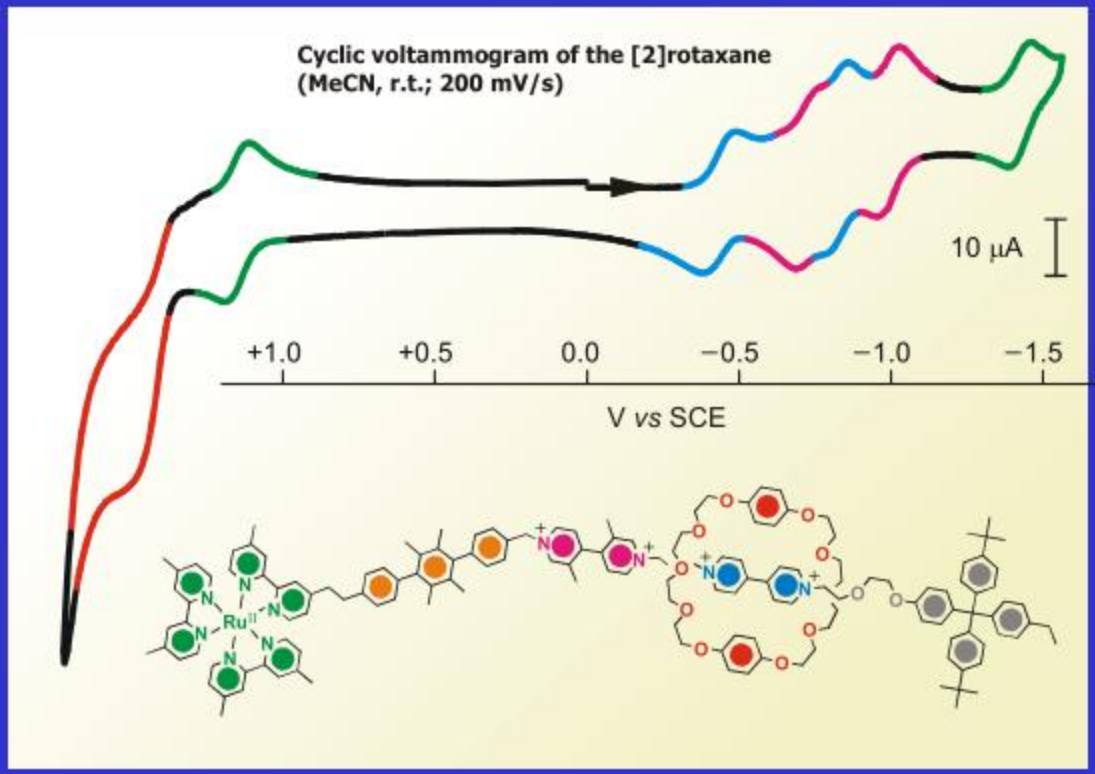
Photochemical Input

Ru(II)polypyridine complex (P^{2+})
p-terphenyl-type rigid spacer (S)
4,4'-bipyridinium (A_1^{2+})
3,3'-dimethyl-4,4'-bipyridinium (A_2^{2+})
Tetraarylmethane group (T)
Six PF_6^- counterions



a) Redox-induced ring motion





Photochemical Input

Ru(II)polypyridine complex (P^{2+})
p-terphenyl-type rigid spacer (S)
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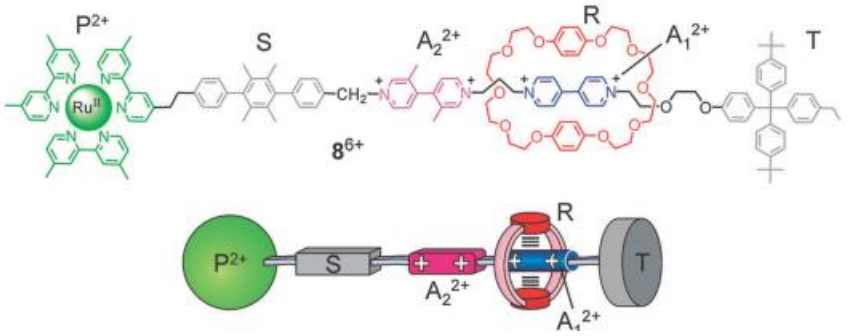
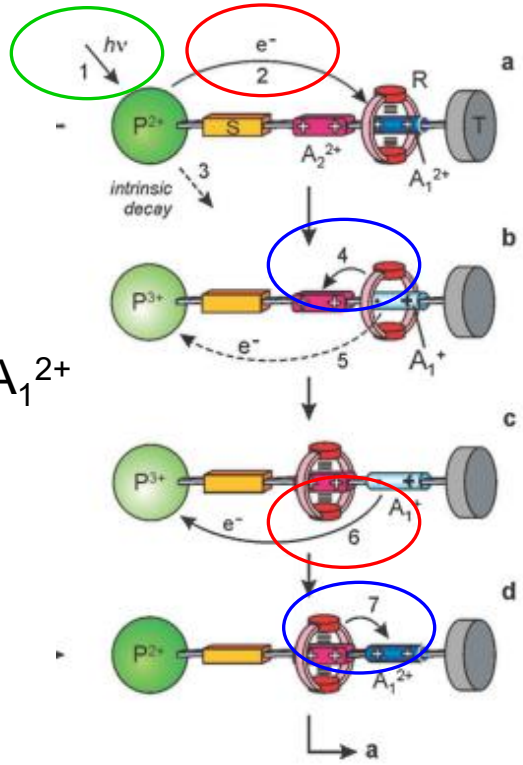
3,3'-dimethyl-4,4'-bipyridinium (A_2^{2+})
Tetraarylmethane group (T)
Six PF_6^- counterions





1 $P^{2+} \longrightarrow {}^*P^{2+}$

2 ${}^*P^{2+} + A_1^{2+} \longrightarrow P^{3+} + A_1^{1+}$
-0.8 V -0.44 V

3 ${}^*P^{2+} \longrightarrow P^{2+}$

4 Shuttling (5 nm)

5 $P^{3+} + A_1^{1+} \longrightarrow {}^*P^{2+} + A_1^{2+}$

6 $P^{3+} + A_1^{1+} \longrightarrow P^{2+} + A_1^{2+}$

7 Shuttling (5 nm)

Photochemical + Chemical Inputs (sacrificial agents: TEA and O_2