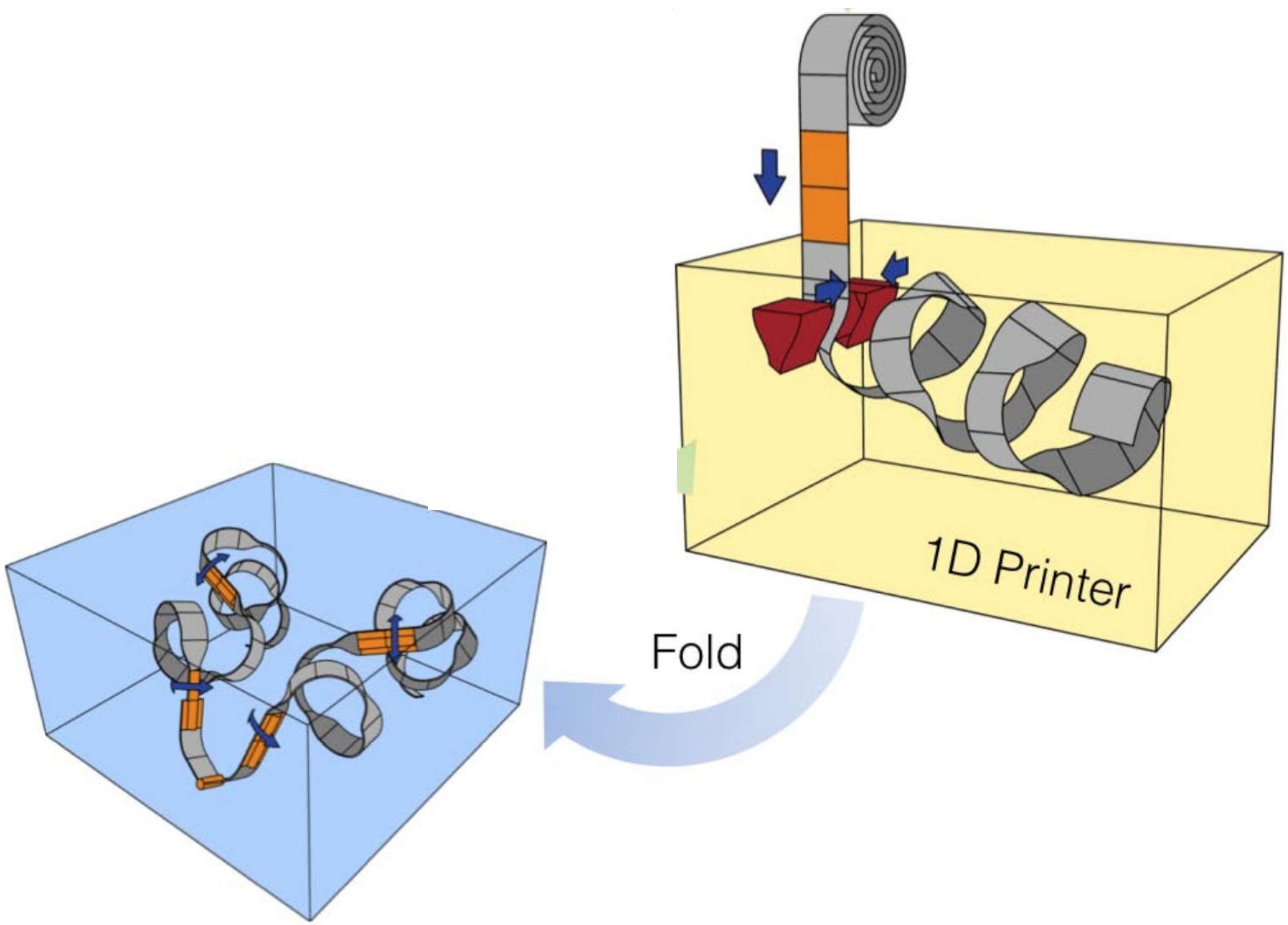
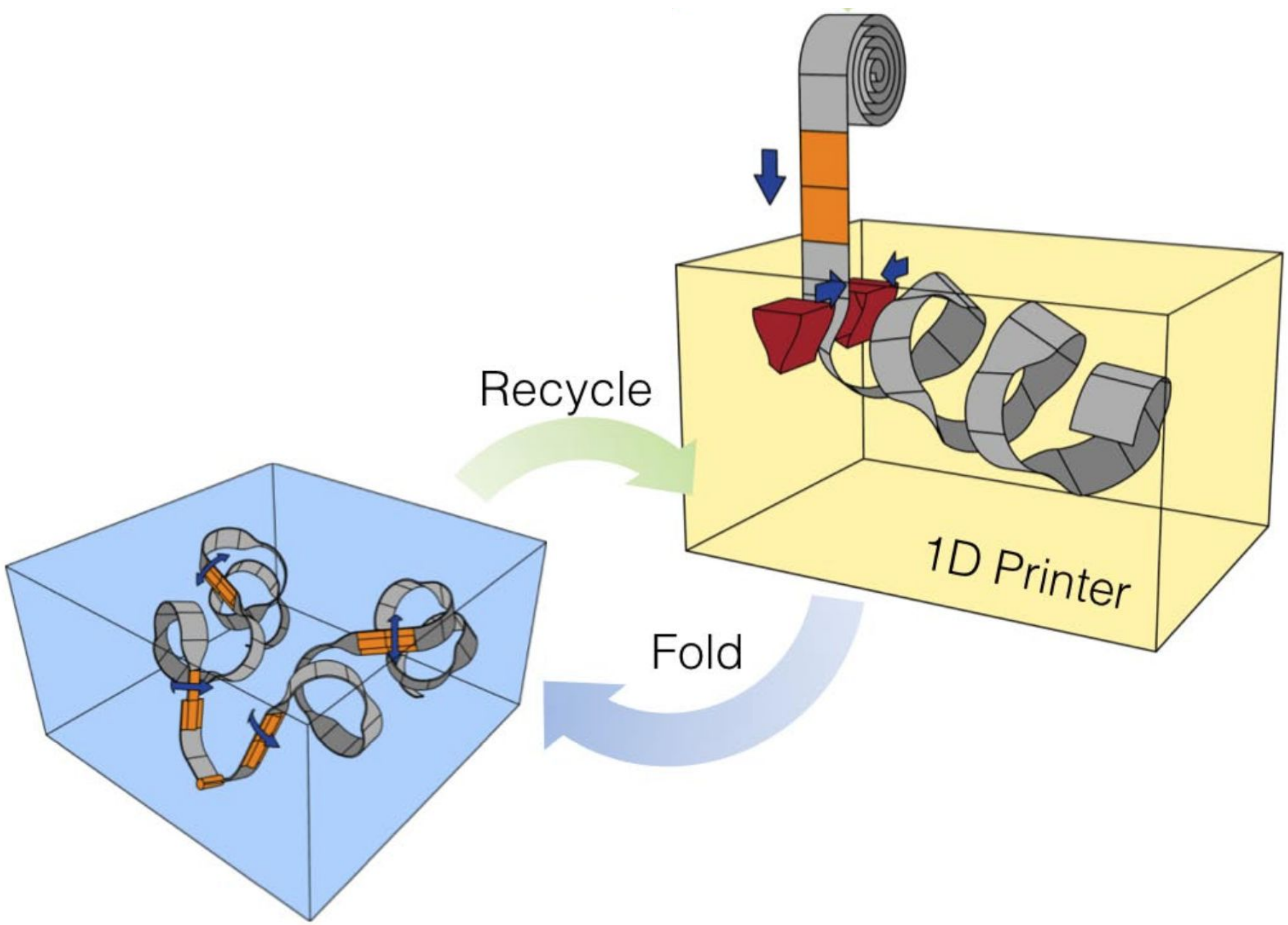
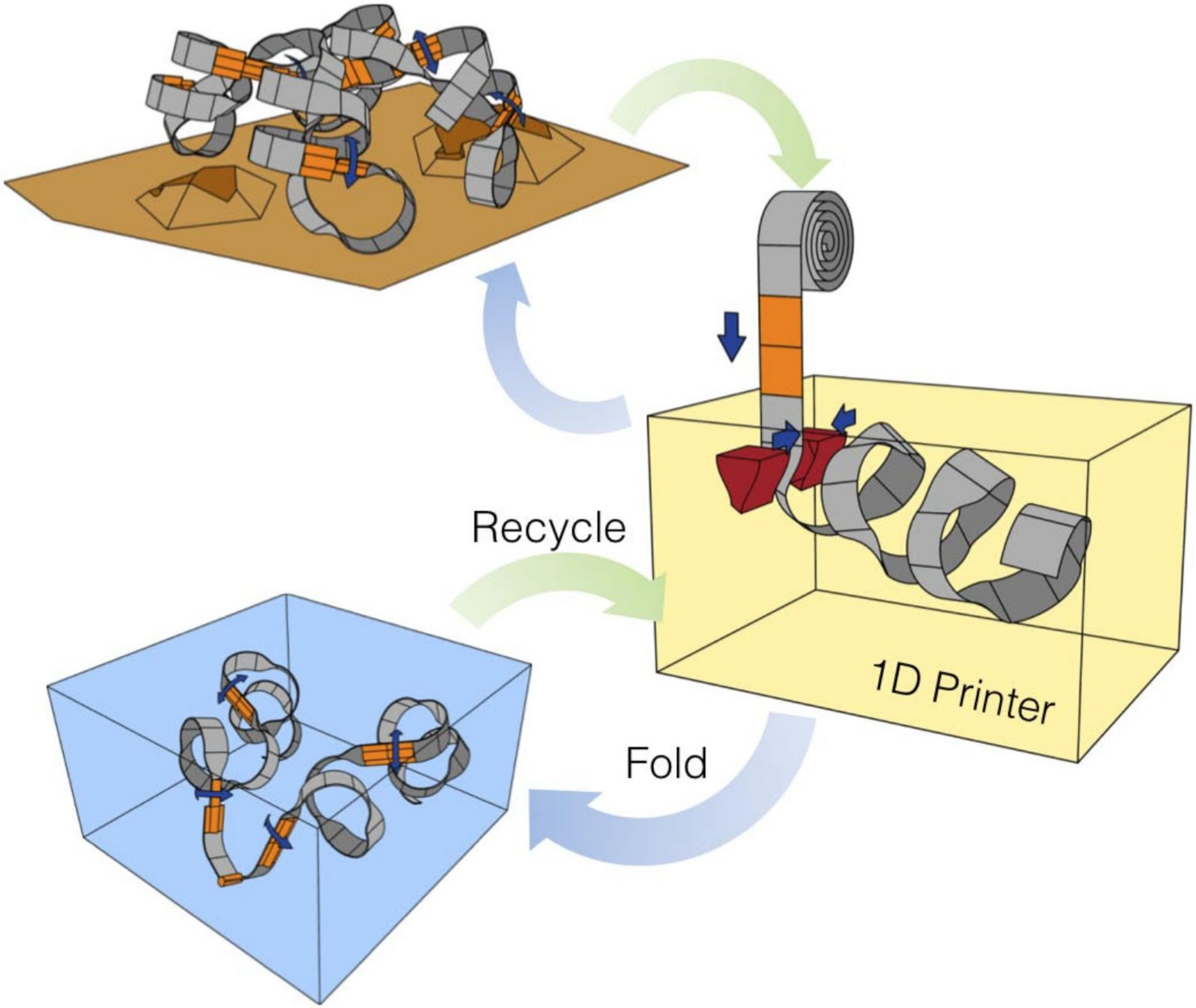
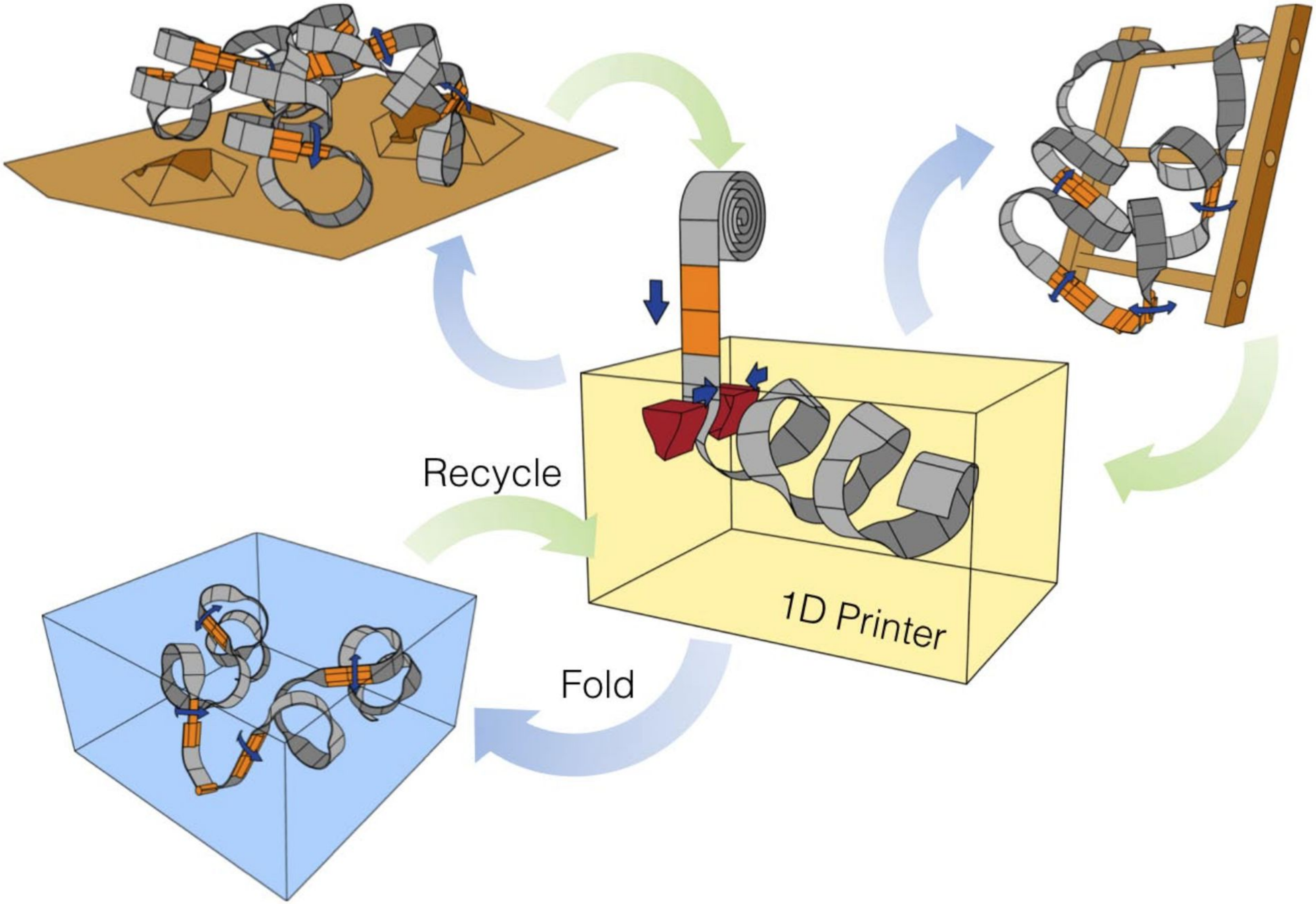
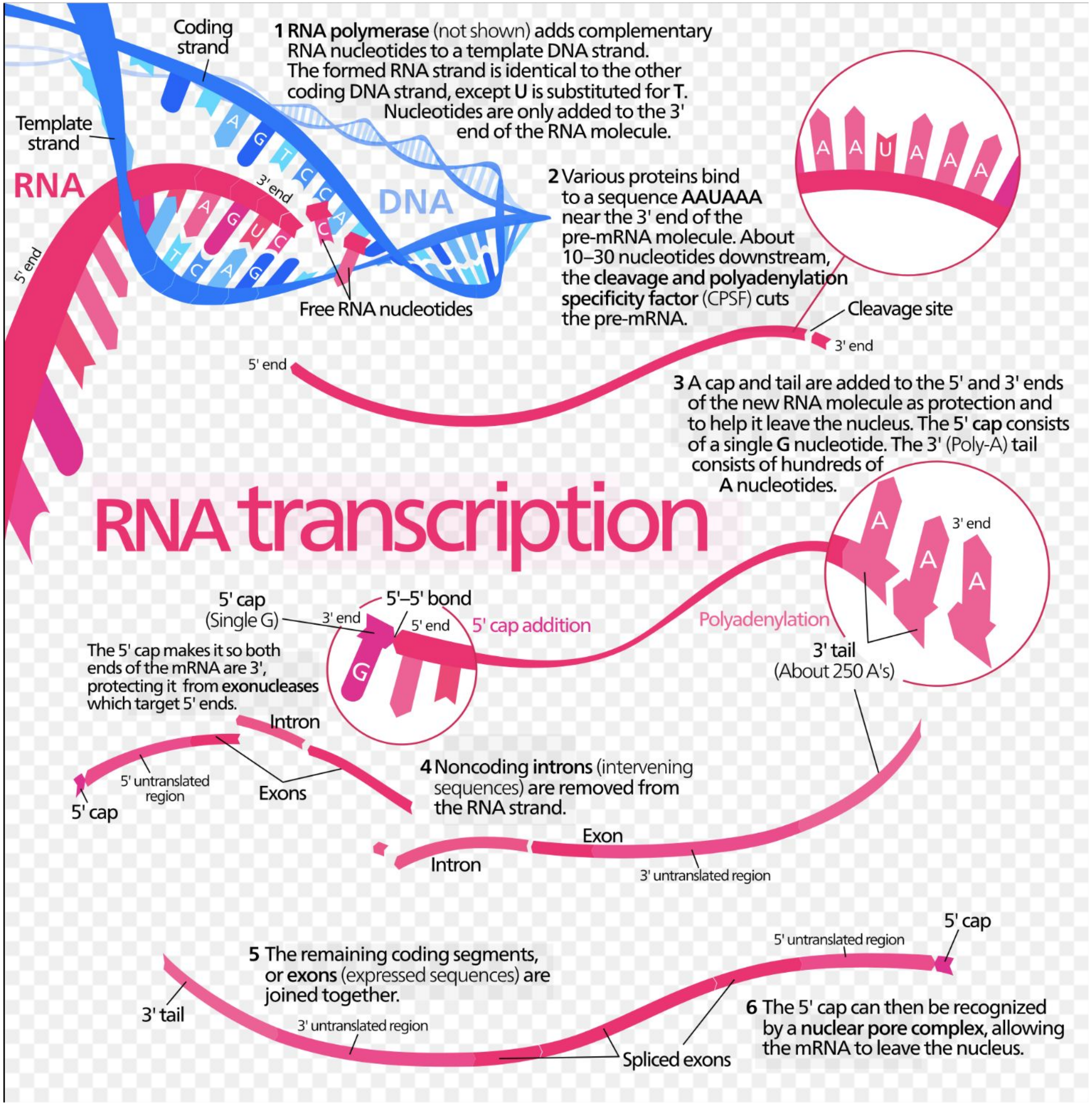
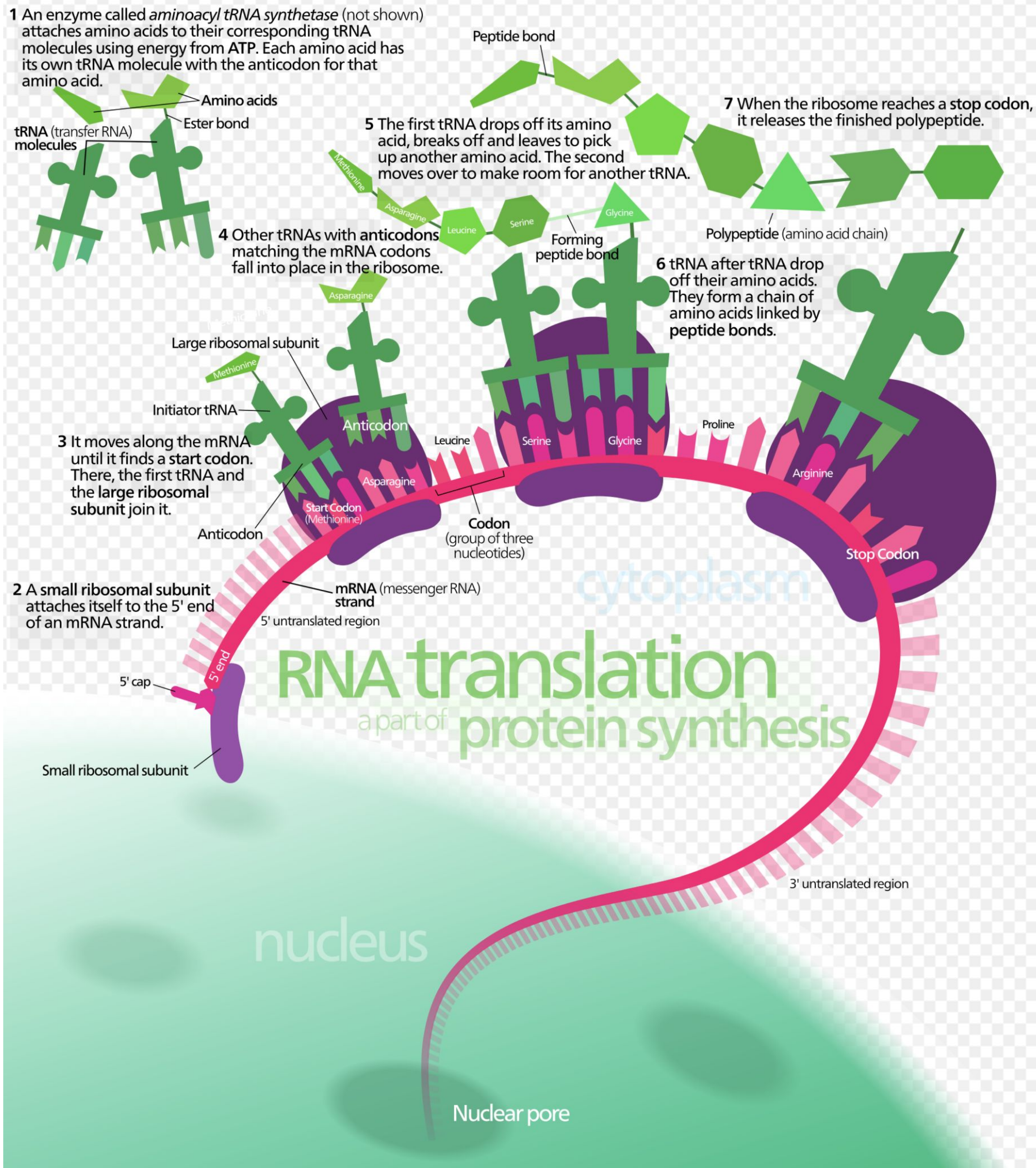

1D Printer
Fold


Recycle
1D Printer
Fold


Recycle
1D Printer
Fold

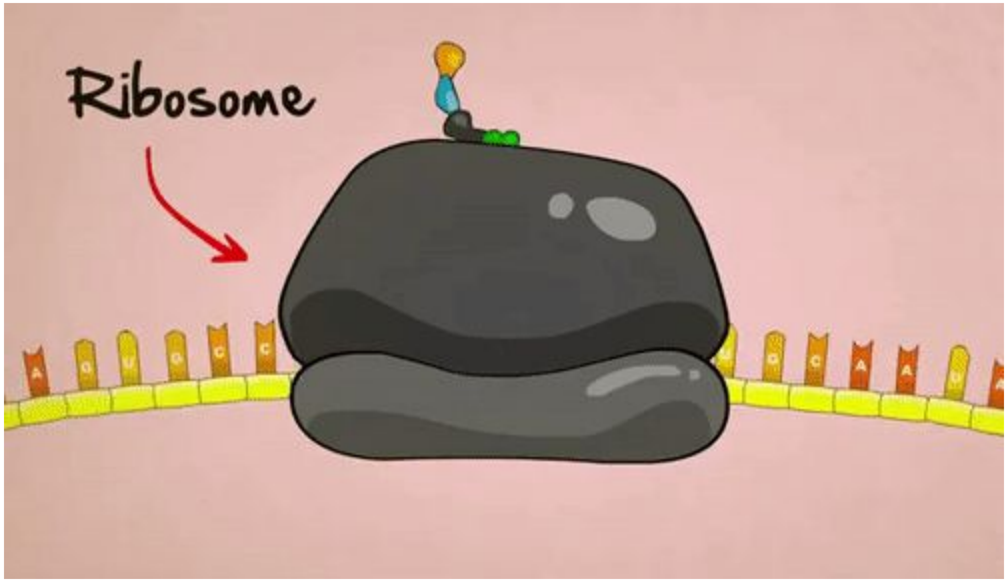

Recycle
1D Printer
Fold

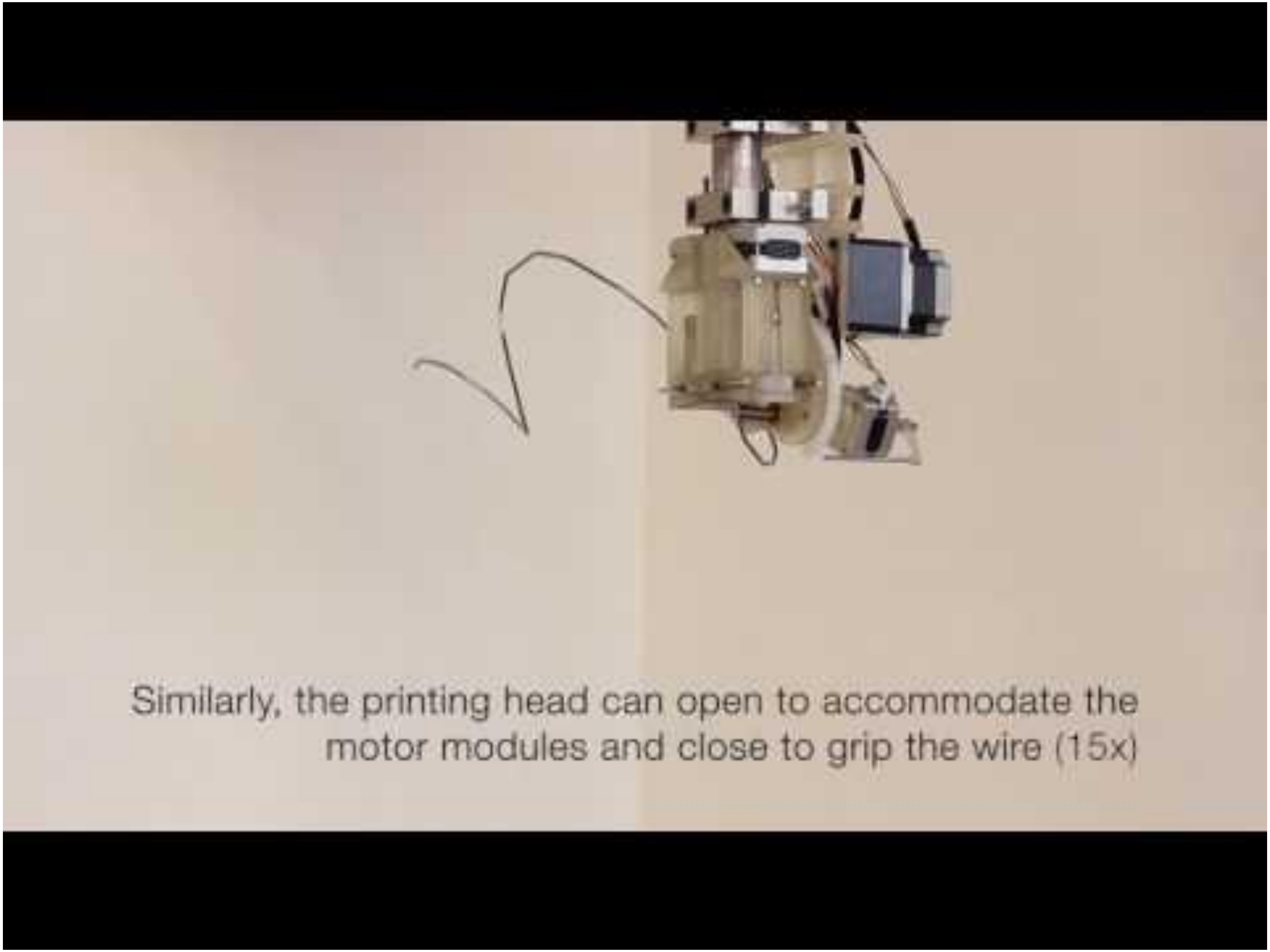

RNA transcription
Coding strand
Template strand
RNA
DNA
3' end
5' end
Free RNA nucleotides
1 RNA polymerase (not shown) adds complementary RNA nucleotides to a template DNA strand. The formed RNA strand is identical to the other coding DNA strand, except U is substituted for T. Nucleotides are only added to the 3' end of the RNA molecule.
2 Various proteins bind to a sequence AAUAAA near the 3' end of the pre-mRNA molecule. About 10–30 nucleotides downstream, the cleavage and polyadenylation specificity factor (CPSF) cuts the pre-mRNA.
Cleavage site
3' end
5' end
3 A cap and tail are added to the 5' and 3' ends of the new RNA molecule as protection and to help it leave the nucleus. The 5' cap consists of a single G nucleotide. The 3' (Poly-A) tail consists of hundreds of A nucleotides.
5' cap (Single G)
5'–5' bond
5' cap addition
Polyadenylation
3' tail (About 250 A's)
The 5' cap makes it so both ends of the mRNA are 3', protecting it from exonucleases which target 5' ends.
Intron
Exons
5' untranslated region
5' cap
4 Noncoding introns (intervening sequences) are removed from the RNA strand.
Exon
Intron
3' untranslated region
5 The remaining coding segments, or exons (expressed sequences) are joined together.
3' tail
3' untranslated region
Spliced exons
5' untranslated region
5' cap
6 The 5' cap can then be recognized by a nuclear pore complex, allowing the mRNA to leave the nucleus.

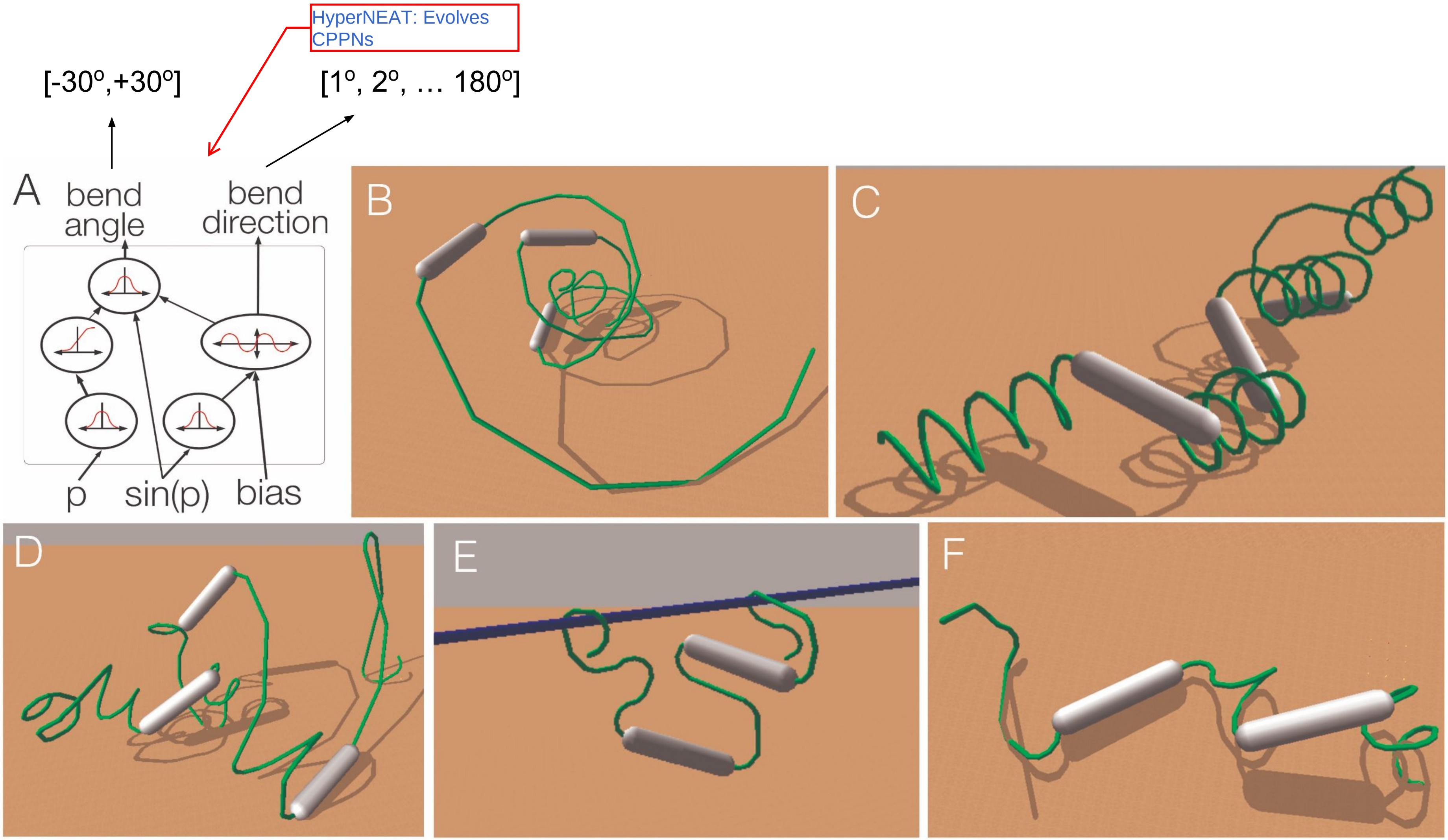


1 An enzyme called aminoacyl tRNA synthetase (not shown) attaches amino acids to their corresponding tRNA molecules using energy from ATP. Each amino acid has its own tRNA molecule with the anticodon for that amino acid.
Amino acids
Ester bond
tRNA (transfer RNA) molecules
Peptide bond
5 The first tRNA drops off its amino acid, breaks off and leaves to pick up another amino acid. The second moves over to make room for another tRNA.
7 When the ribosome reaches a stop codon, it releases the finished polypeptide.
Methionine
Asparagine
Leucine
Serine
Glycine
Forming peptide bond
Polypeptide (amino acid chain)
4 Other tRNAs with anticodons matching the mRNA codons fall into place in the ribosome.
6 tRNA after tRNA drop off their amino acids. They form a chain of amino acids linked by peptide bonds.
Asparagine
Large ribosomal subunit
Methionine
Initiator tRNA
Anticodon
3 It moves along the mRNA until it finds a start codon. There, the first tRNA and the large ribosomal subunit join it.
Leucine
Serine
Glycine
Proline
Arginine
Asparagine
Start Codon (Methionine)
Anticodon
Codon (group of three nucleotides)
Stop Codon
cytoplasm
2 A small ribosomal subunit attaches itself to the 5' end of an mRNA strand.
mRNA (messenger RNA) strand
5' untranslated region
5' end
RNA translation
a part of protein synthesis
5' cap
Small ribosomal subunit
3' untranslated region
nucleus
Nuclear pore

translation:




Similarly, the printing head can open to accommodate the
motor modules and close to grip the wire (15x)

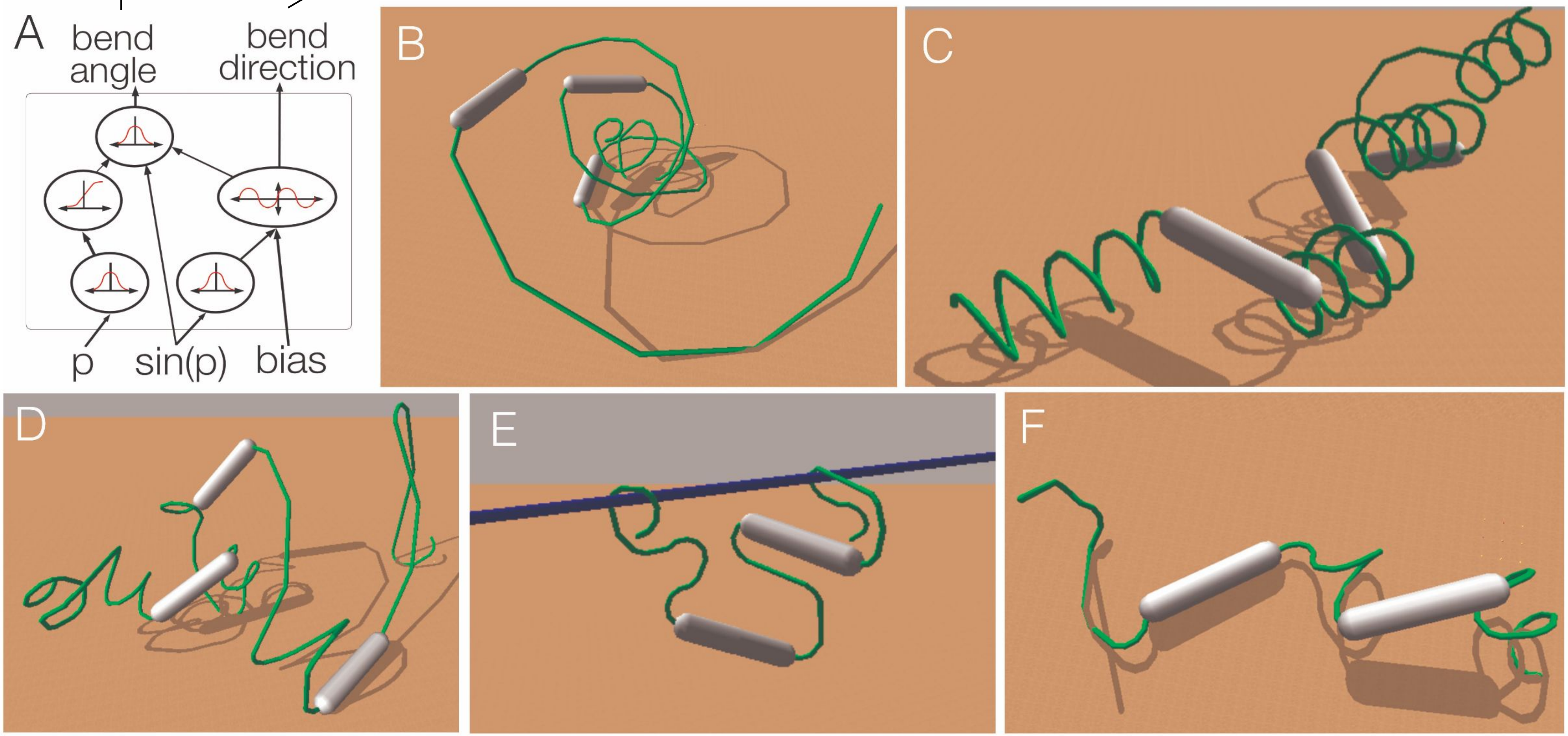


p stands for peptide

Number of segments N between ~50 and 100:
Number of folds = N-1

$2^{N-1}\ 180^{N-1} \rightarrow 2^{49}\ 180^{49} \rightarrow 1.81 \times 10^{125}$

[-30°,+30°]   [1°, 2°, … 180°]

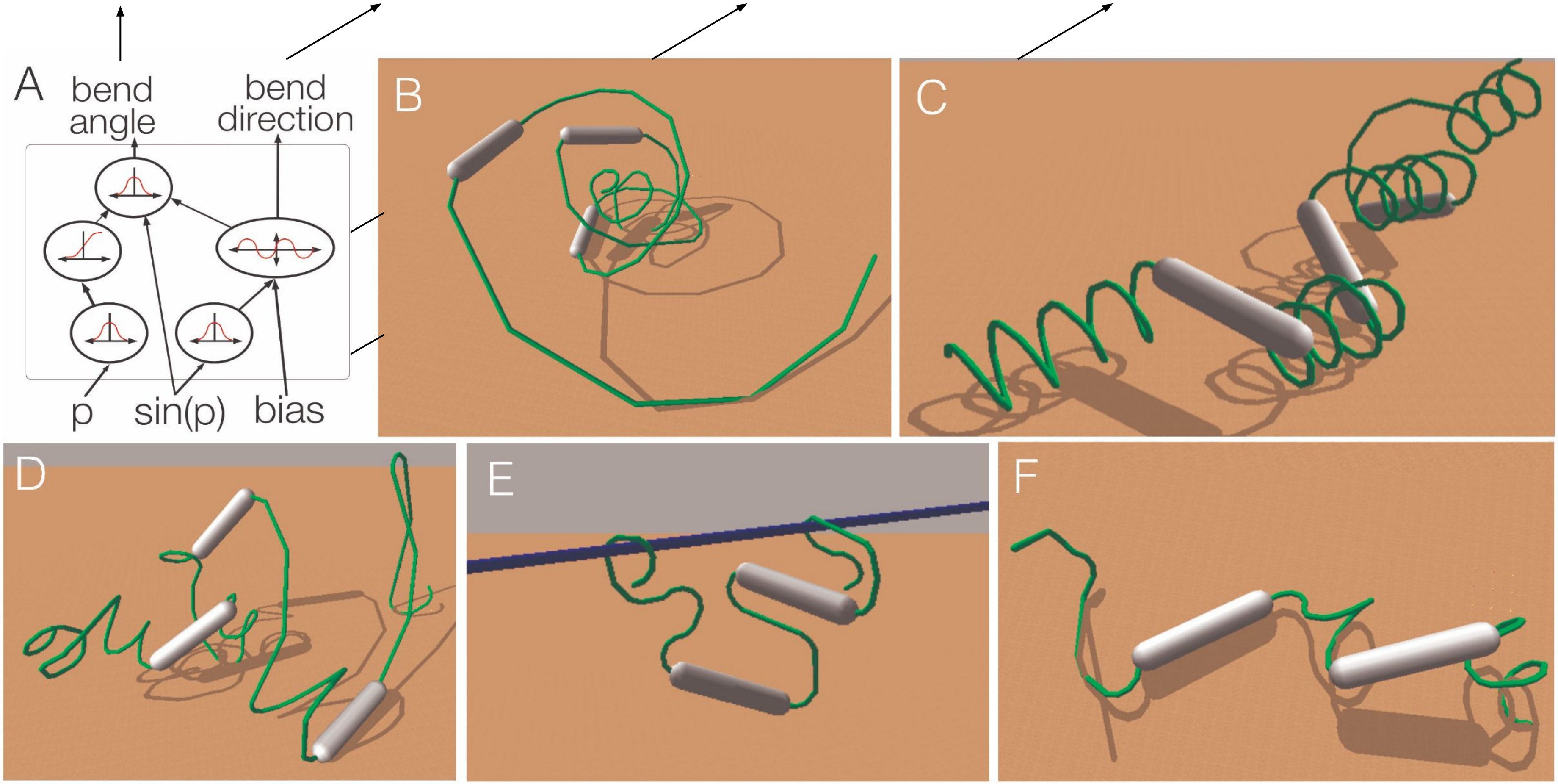


[-30º,+30º]

[1º, 2º, … 180º]

Amplitude A = [0.0,1.0]

Phase offset φ = [−π/2, +π/2]



$$F_1 = |p_s - p_e|$$

p_s = [s]tarting [p]osition
p_e = [e]nding [p]osition

$$F_1 = |p_s - p_e| \ (1.0 - tq)$$

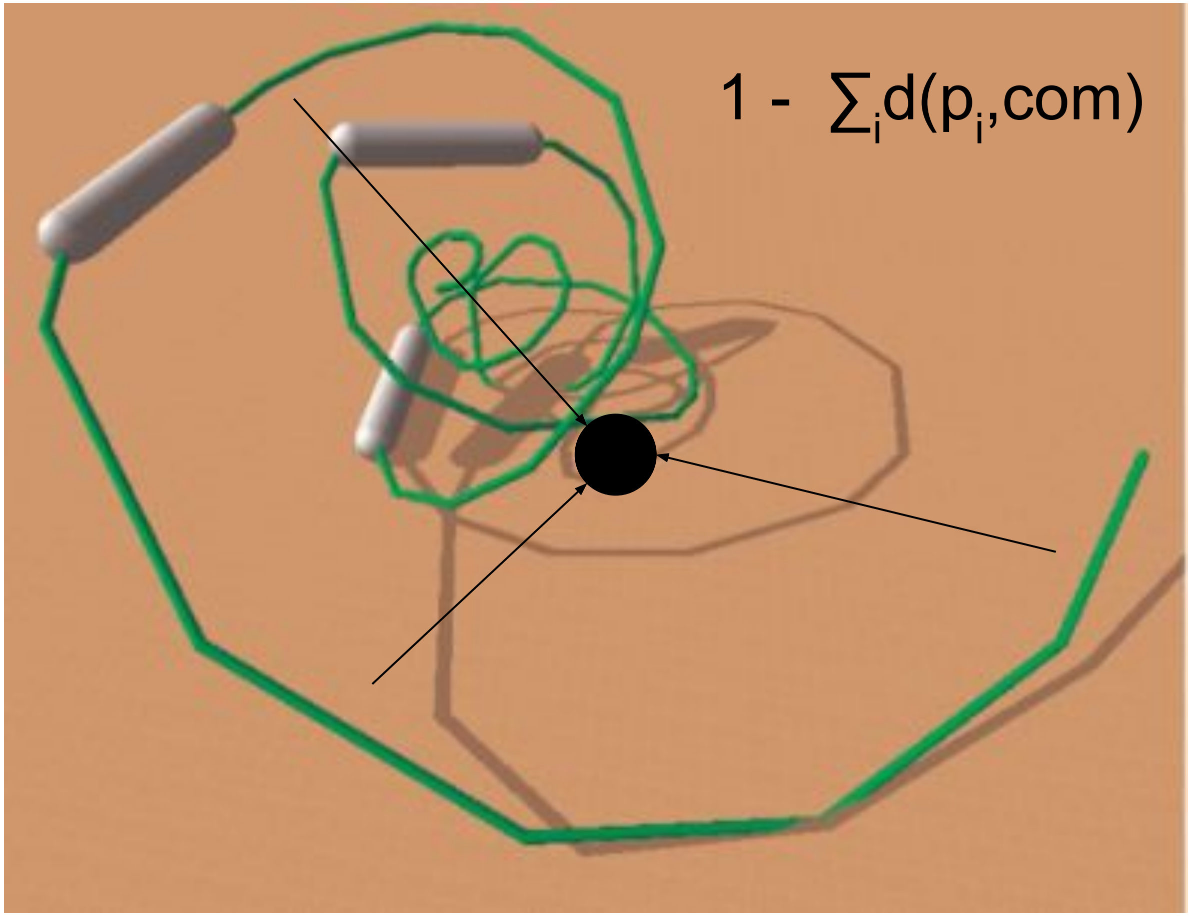
Incentive for conservation of energy. If reaches maximum distance but using all the motors are max the F = 0, if it does not move F = 0.

p_s = [s]tarting [p]osition
p_e = [e]nding [p]osition
tq = maximum [t]or[q]ue

$$F_1 = |p_s - p_e| \; (1.0 - tq) \; c$$

p_s = [s]tarting [p]osition
p_e = [e]nding [p]osition
tq = maximum [t]or[q]ue
c = [c]ompactness

Weighted sum of the positions of all the segments to compute the center of mass of the robot.



$$F_1 = \frac{|p_s - p_e| \ (1.0 - tq) \ c}{1 + cl}$$

p_s = [s]tarting [p]osition
p_e = [e]nding [p]osition
tq = maximum [t]or[q]ue
c = [c]ompactness
cl = [c]o[l]lisions

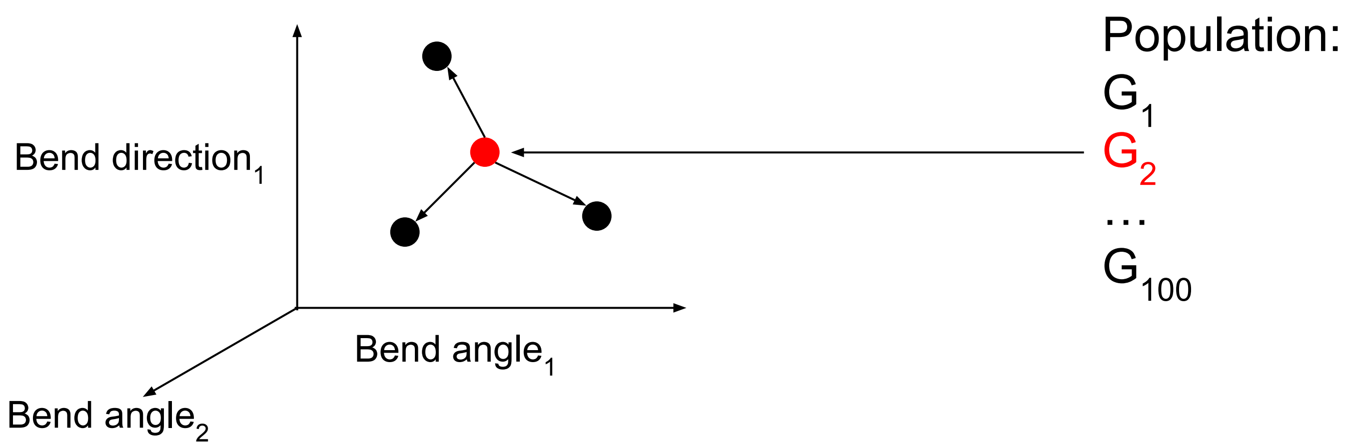
$$F_1 = \frac{|p_s - p_e| \ (1.0 - tq) \ c}{1 + cl} \quad F_2 = p,$$

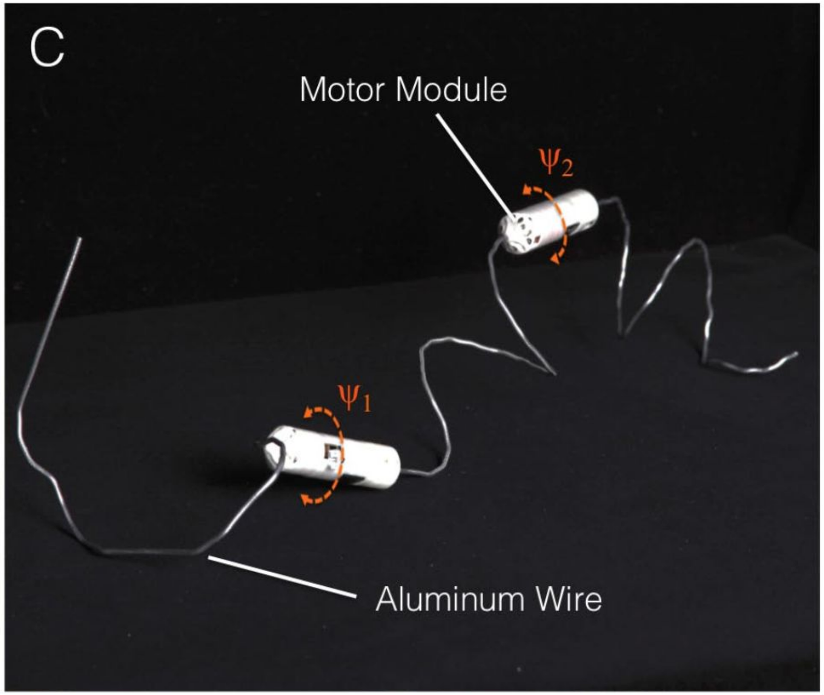
p_s = [s]tarting [p]osition
p_e = [e]nding [p]osition
tq = maximum [t]or[q]ue
c = [c]ompactness
cl = [c]o[l]lisions
p = [p]henotypic novelty

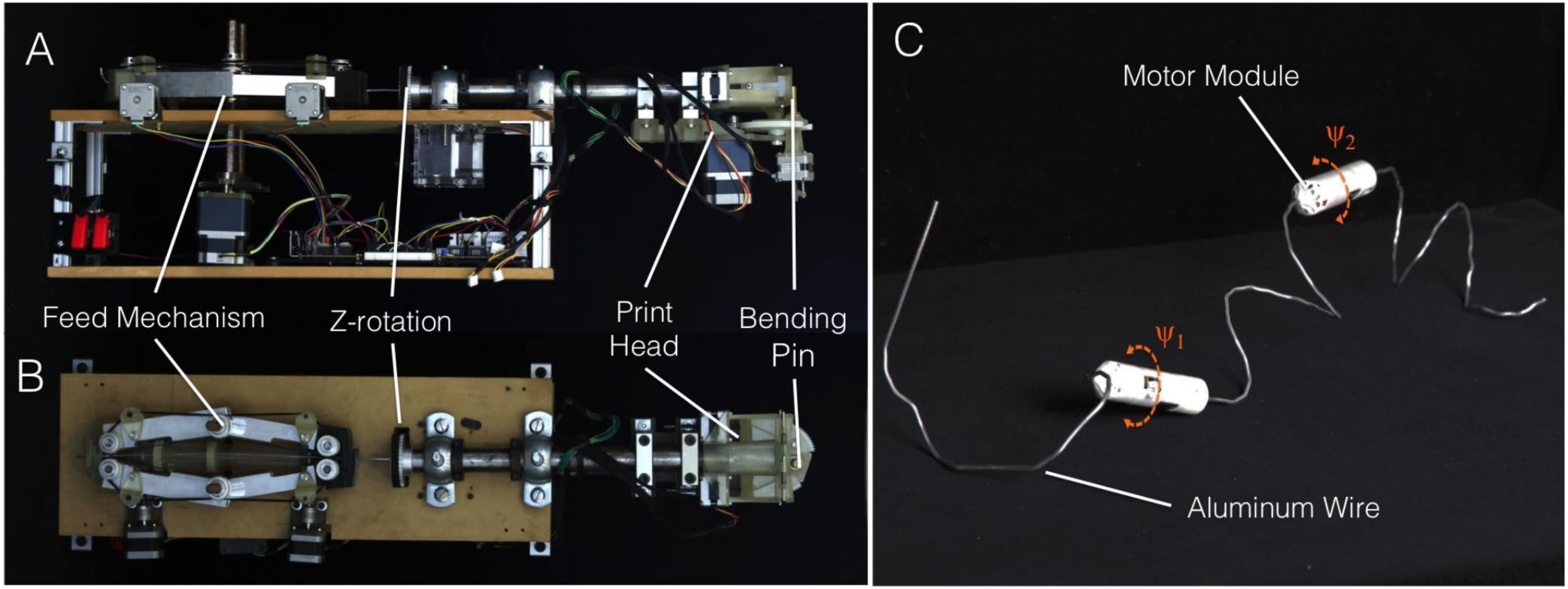
$$F_1 = \frac{|p_s - p_e| \ (1.0 - tq) \ c}{1 + cl} \qquad F_2 = p,$$

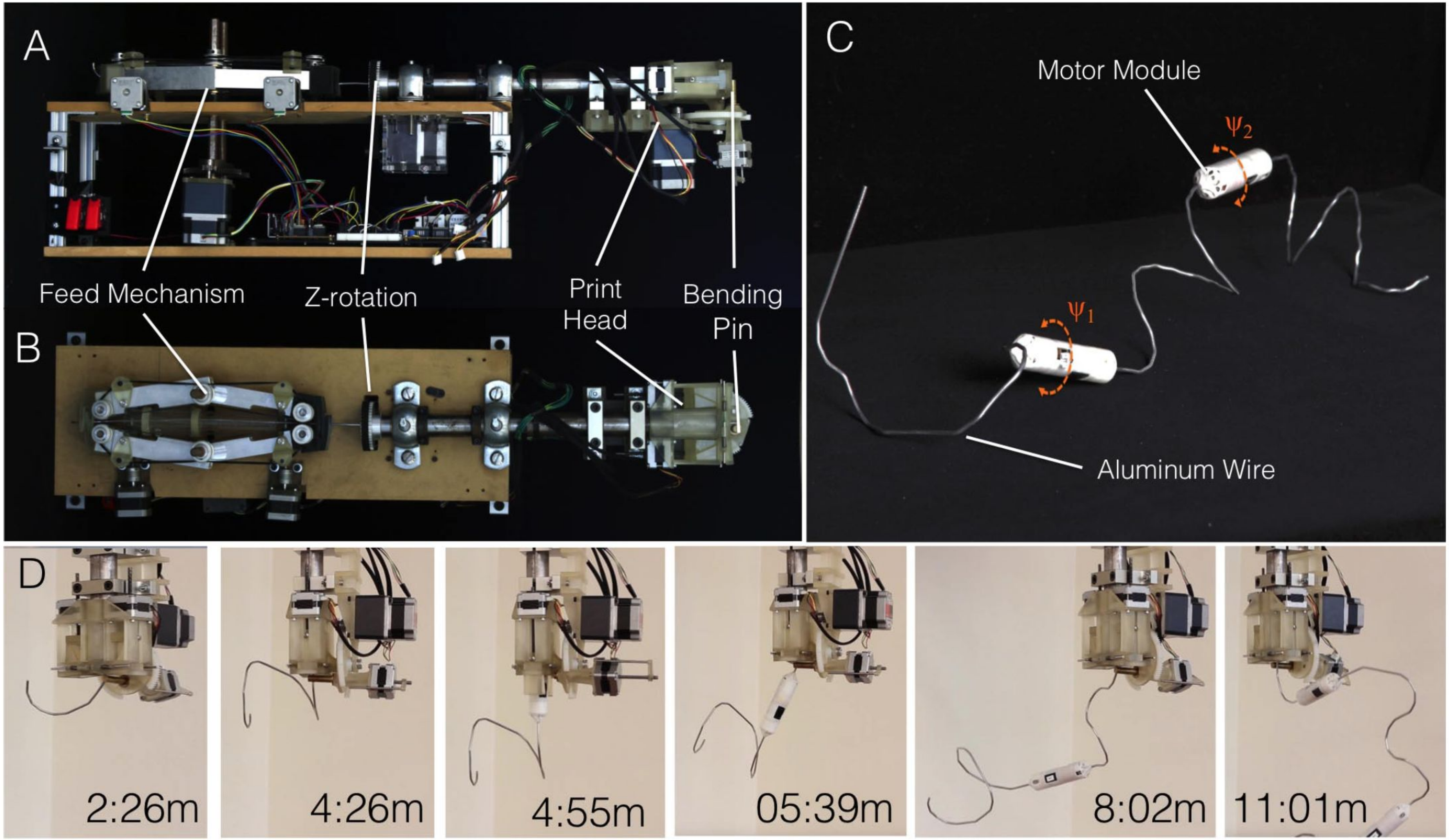
- p_s = [s]tarting [p]osition
- p_e = [e]nding [p]osition
- tq = maximum [t]or[q]ue
- c = [c]ompactness
- cl = [c]o[l]lisions
- p = [p]henotypic novelty

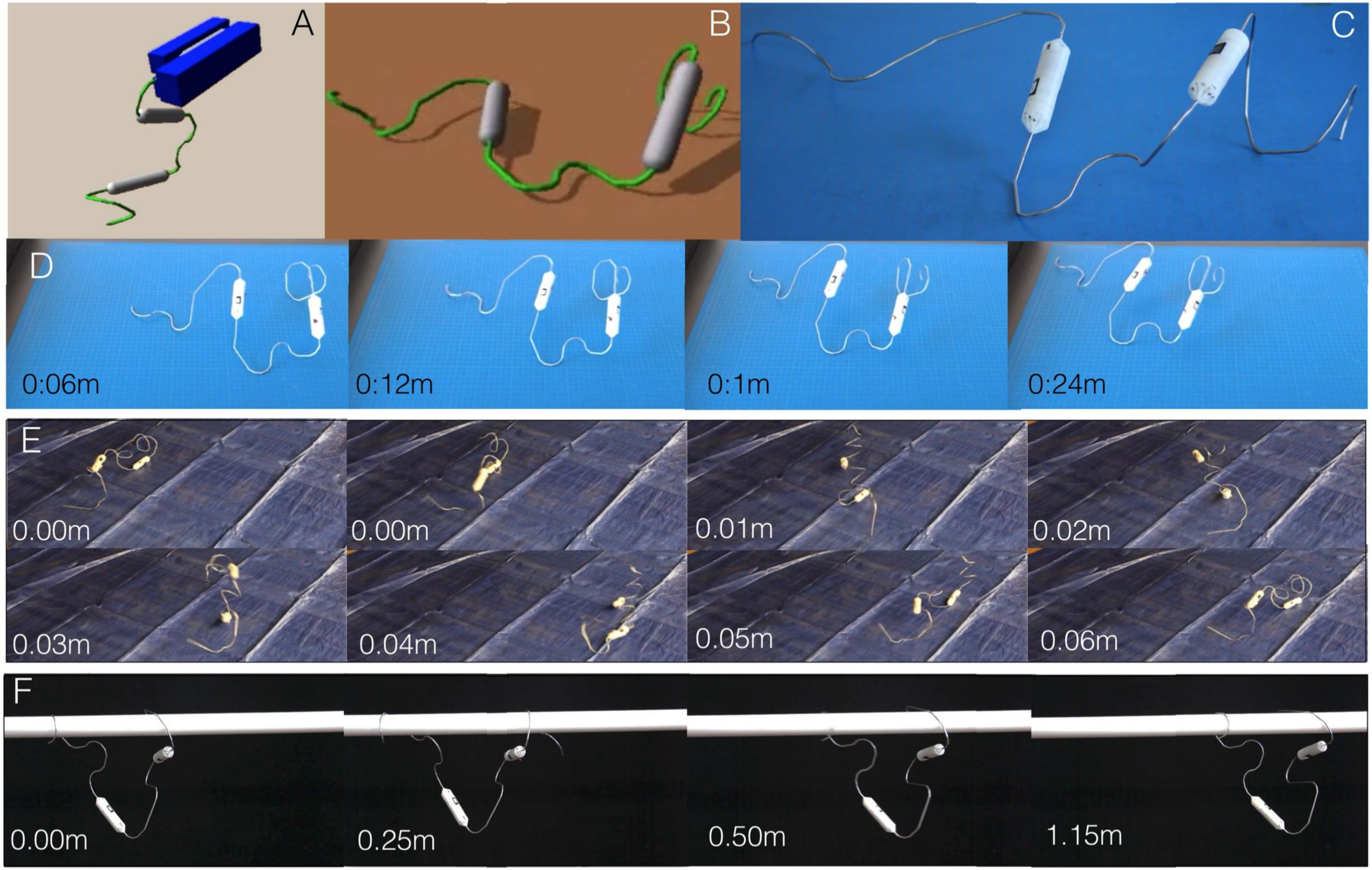
$$\rho(x) = \frac{1}{k} \sum_{i=1}^{k} \mathrm{dist}(x, \mu_i)$$




C
Motor Module
ψ_2
ψ_1
Aluminum Wire


A
B
C
Feed Mechanism
Z-rotation
Print
Head
Bending
Pin
Motor Module
ψ_2
ψ_1
Aluminum Wire


A
B
C
D
Feed Mechanism
Z-rotation
Print Head
Bending Pin
Motor Module
ψ_2
ψ_1
Aluminum Wire
2:26m
4:26m
4:55m
05:39m
8:02m
11:01m



A
B
C
D
0:06m
0:12m
0:1m
0:24m
E
0.00m
0.00m
0.01m
0.02m
0.03m
0.04m
0.05m
0.06m
F
0.00m
0.25m
0.50m
1.15m