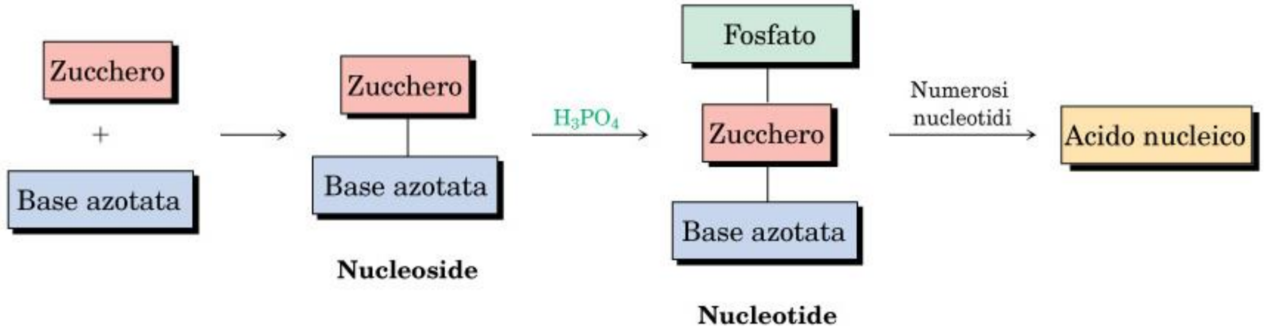
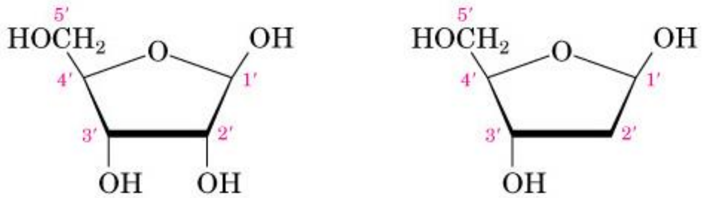
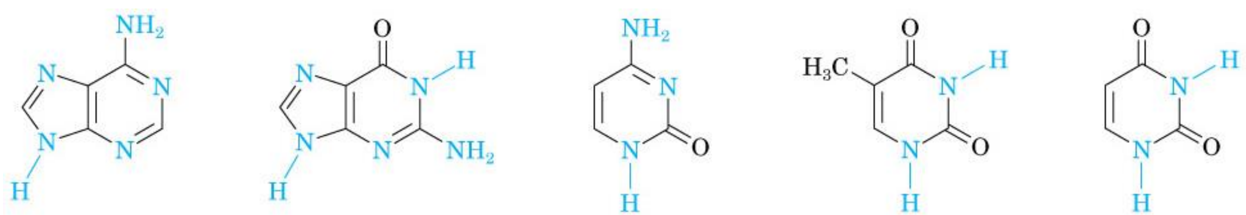
Acidi nucleici





Ribosio **2′-Deossiribosio**



Adenina (A) DNA RNA

Guanina (G) DNA RNA

Citosina (C) DNA RNA

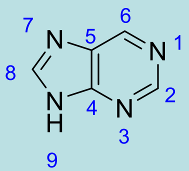
Timina (T) DNA

Uracile (U) RNA

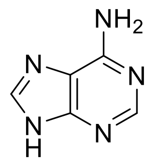
basi puriniche **basi pirimidiniche**

Basi puriniche e pirimidiche

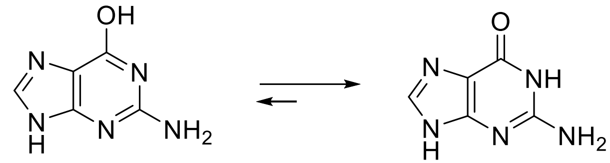
Basi puriniche



purina

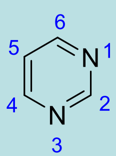


adenina
6-amminopurina

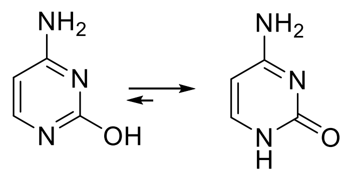


Guanina
2-ammino-6-idrossipurina
2-ammino-6-osso-1,6-diidropurina

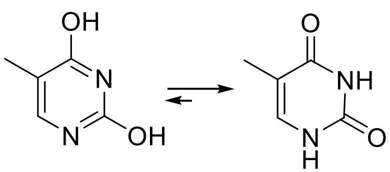
Basi pirimidiniche



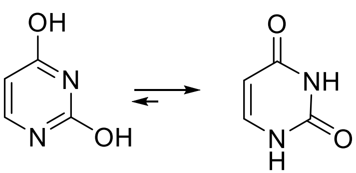
Pirimidina



Citosina
4-ammino-2-idrossipirimidina
4-ammino-2-osso-1,2-diidropirimidina



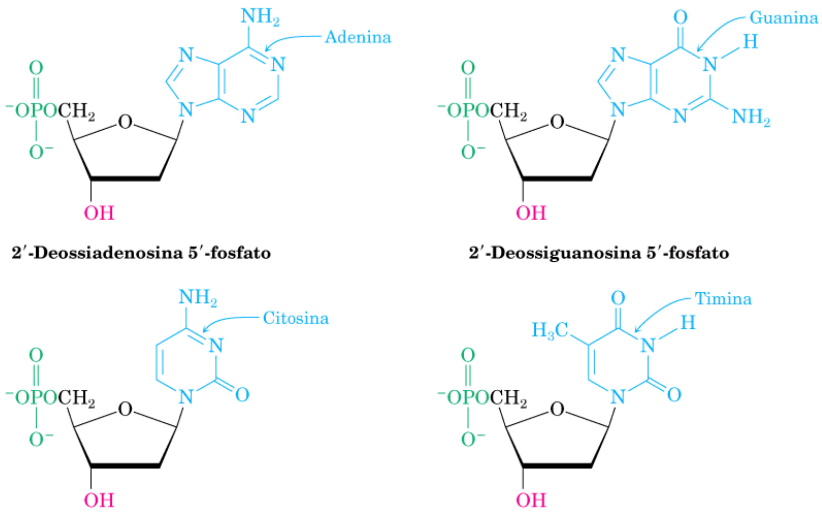
Timina
2,4-diidrossi-5-metilpirimidina
2,4-diosso-5-metil-1,2,3,4-tetraidropirimidina



Uracile
2,4-diidrossi-5-pirimidina
2,4-diosso-1,2,3,4-tetraidropirimidina

Acidi nucleici

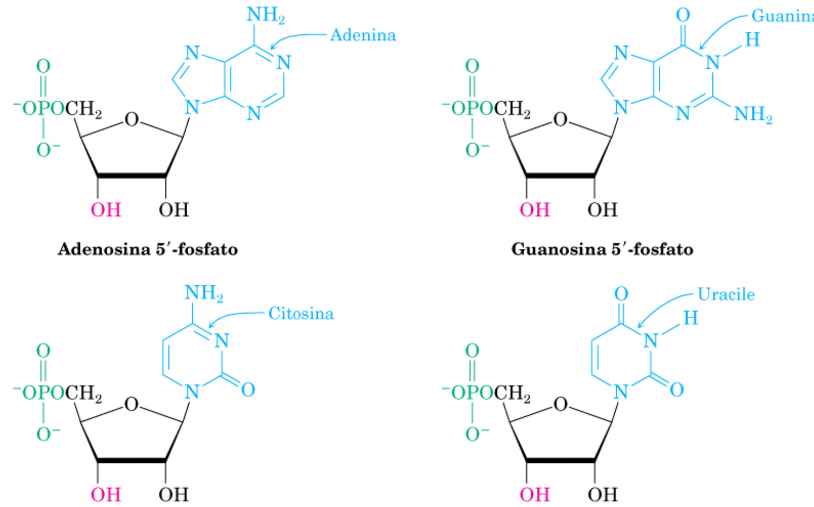
Deossiribonucleotidi



2′-Deossiadenosina 5′-fosfato · **2′-Deossiguanosina 5′-fosfato**

2′-Deossicitidina 5′-fosfato · **2′-Deossitimidina 5′-fosfato**

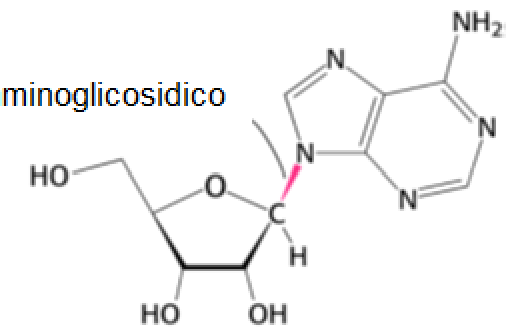
Ribonucleotidi



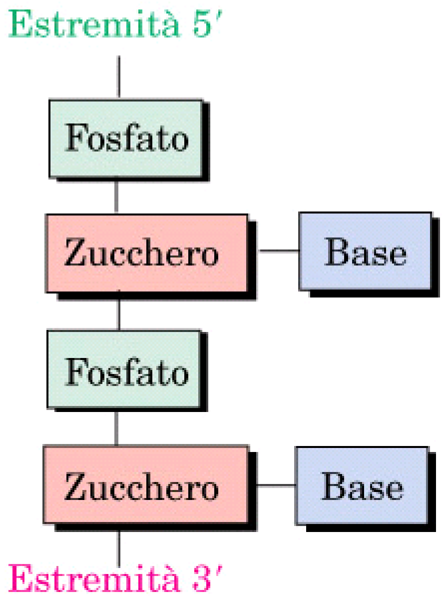
Adenosina 5′-fosfato · **Guanosina 5′-fosfato**

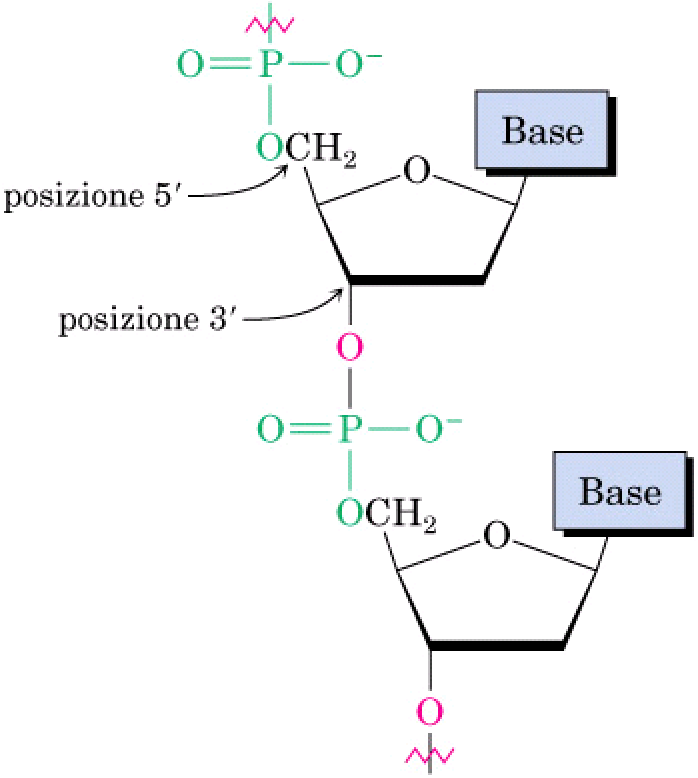
Citidina 5′-fosfato · **Uridina 5′-fosfato**

Legame β-amminoglicosidico



Acidi nucleici

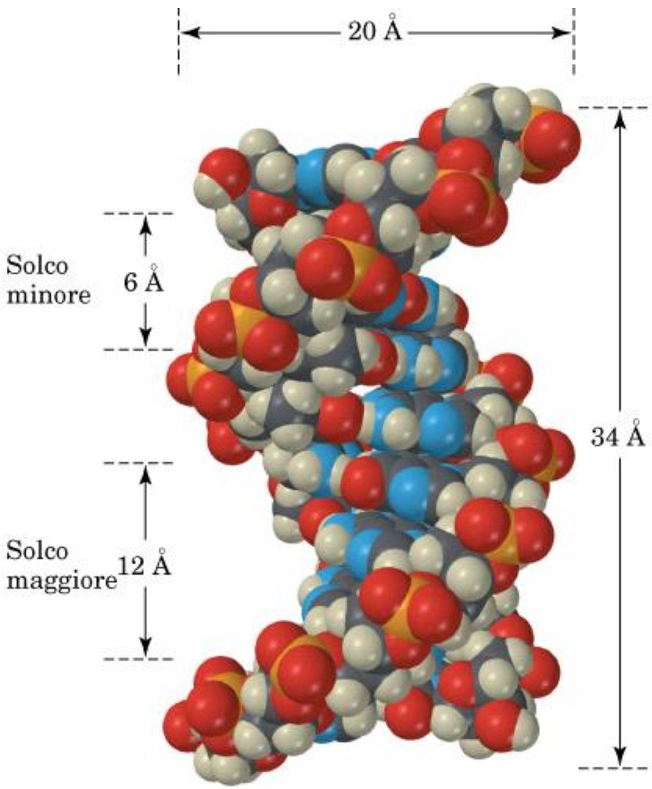


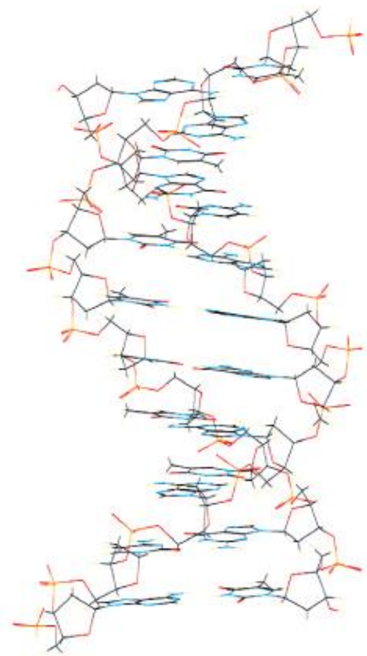


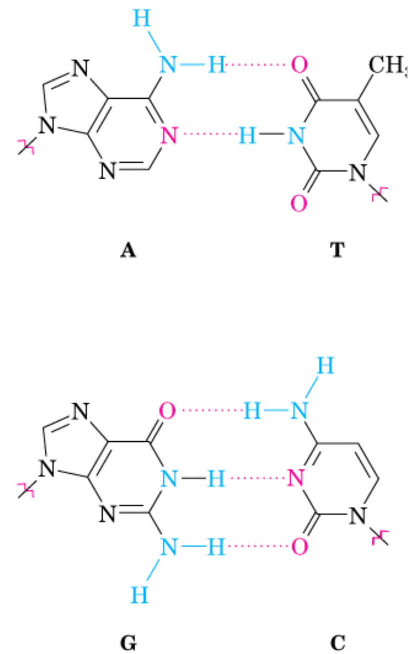
La sequenza dei nucleotidi in una catena di acido nucleico viene descritta partendo dall’estremità 5’ e identifica l’ordine di successione delle basi utilizzando le abbreviazioni A, G, C, T (o U nel RNA).

Acidi nucleici

Il contenuto in basi azotate del DNA dipende dalle specie considerate. Nell'uomo c'e' circa il 30% di A /T e il 20 % di G/C. Nel batterio *Clostridium perfringens* si ha 37% di A/T e 13% di G/C. In ogni caso le basi si presentano a coppie con la percentuale di A eguale a quella di T e quella di G a quella di C. Questo è dovuto al fatto che il DNA è costituito normalmente da una doppia elica costituita da due singoli filamenti complementari avvolti in senso opposto.

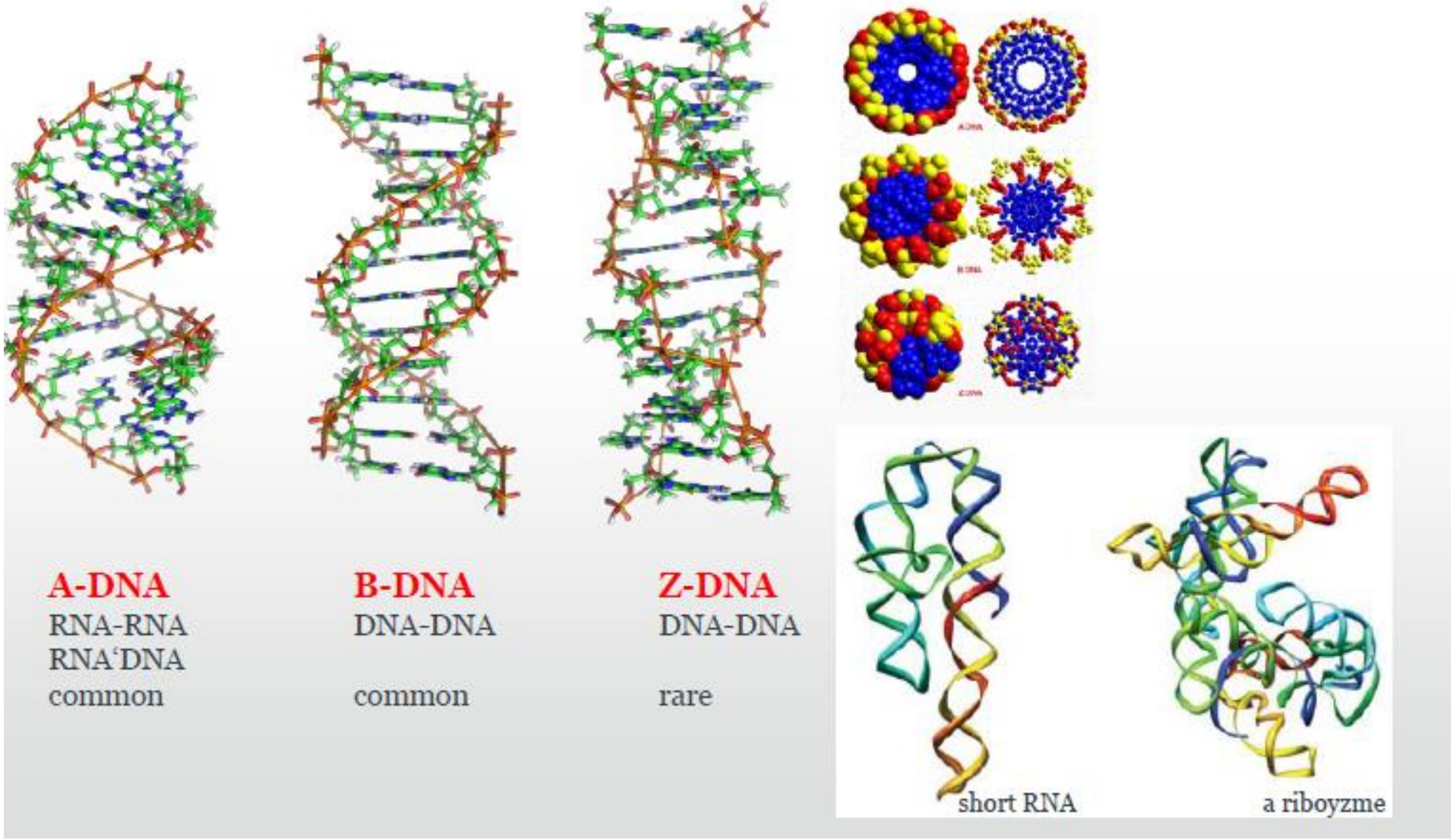






10 basi per giro d'elica

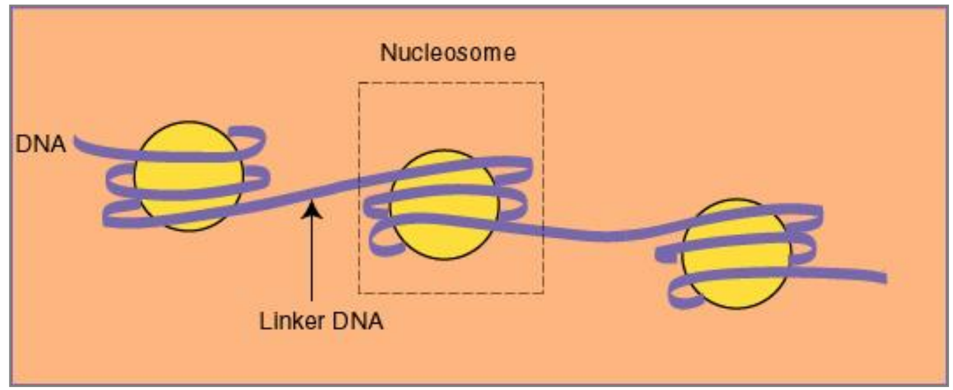
Acidi nucleici

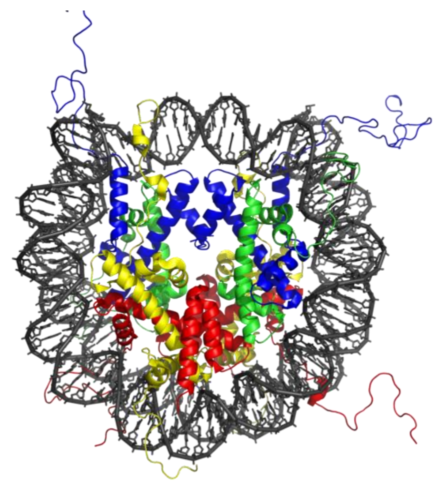


Acidi nucleici

Negli eucarioti, il DNA è solitamente presente all'interno di cromosomi che contengono un filamento lineare di DNA (circolari nei procarioti). La somma di tutti i cromosomi di una cellula ne costituisce il genoma; il genoma umano conta circa 3 miliardi di paia di basi contenute in 46 cromosomi. Nel caso del E. coli il DNA contiene 4.64 x 10^6 coppie di basi. Questo significa una lunghezza di filamento di 1.6 mm contro una lunghezza della cellula di soli 0.002 mm. Questo significa che il filamento di DNA deve essere densamente ripiegato. Nelle cellule eucariote il ripiegamento avviene attorno a proteine basiche (ricche di arginina e lisina) dette istoni. Il complesso DNA/istone è detto nucleosoma.

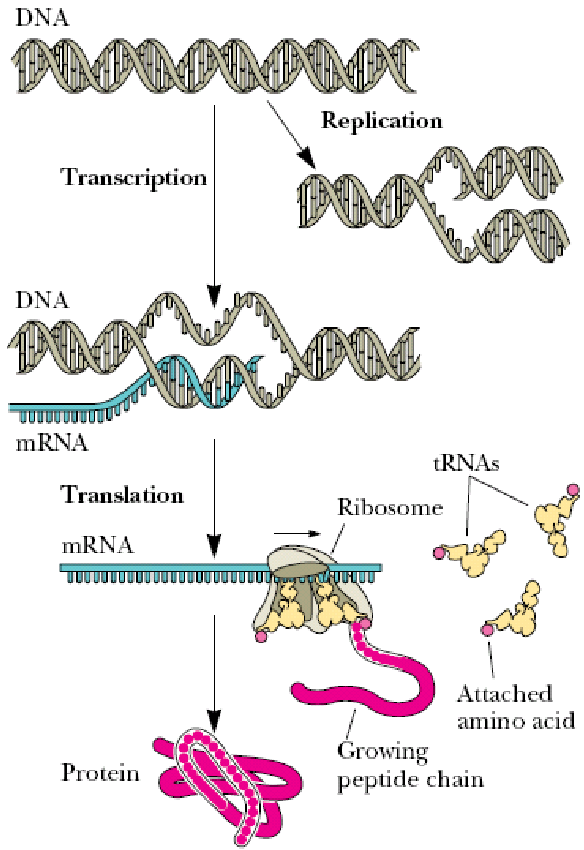
If the cell walls of bacteria such as *Escherichia coli* are partially digested and the cells are then osmotically shocked by dilution with water, the contents of the cells are extruded to the exterior. In electron micrographs, the most obvious extruded component is the bacterial chromosome, shown here surrounding the cell.





Acidi nucleici

Il DNA contiene l'informazione genetica che viene tramite trasmessa al RNA che ha il compito di decodificarla e tradurla nella sintesi proteica. Questi processi vanno sotto il nome di:



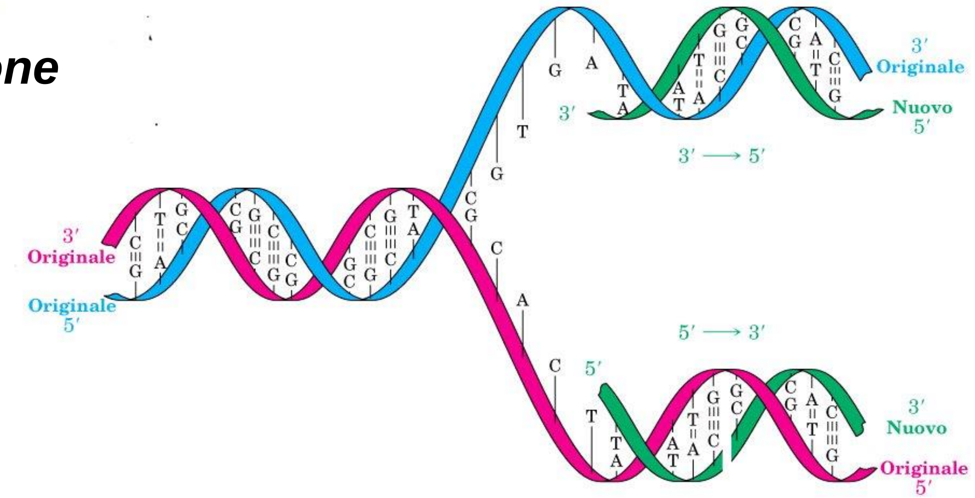
Replication
DNA replication yields two DNA molecules identical to the original one, ensuring transmission of genetic information to daughter cells with exceptional fidelity.

Transcription
The sequence of bases in DNA is recorded as a sequence of complementary bases in a single-stranded mRNA molecule.

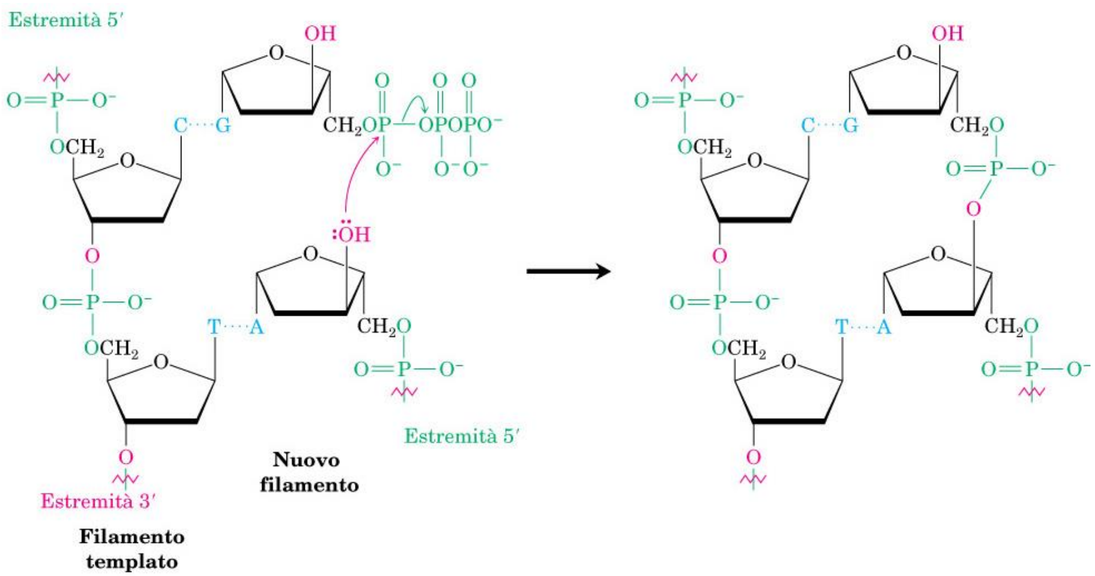
Translation
Three-base codons on the mRNA corresponding to specific amino acids direct the sequence of building a protein. These codons are recognized by tRNAs (transfer RNAs) carrying the appropriate amino acids. Ribosomes are the "machinery" for protein synthesis.

FIGURE 11.1 • The fundamental process of information transfer in cells. Information encoded in the nucleotide sequence of DNA is transcribed through synthesis of an RNA molecule whose sequence is dictated by the DNA sequence. As the sequence of this RNA is read (as groups of three consecutive nucleotides) by the protein synthesis machinery, it is translated into the sequence of amino acids in a protein. This information transfer system is encapsulated in the dogma: DNA → RNA → protein.

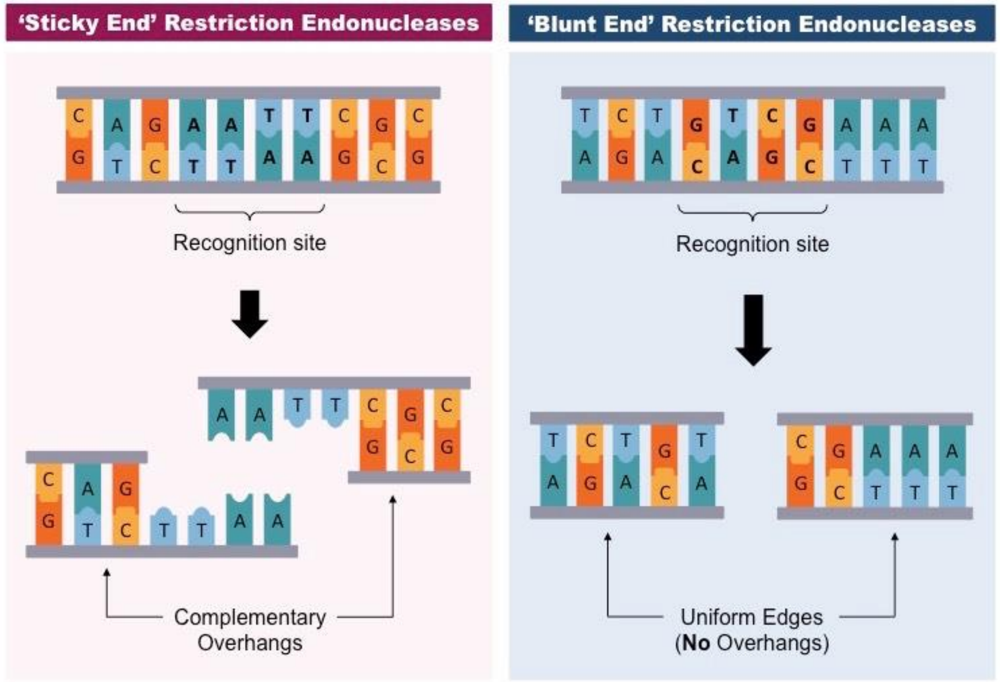
Replicazione

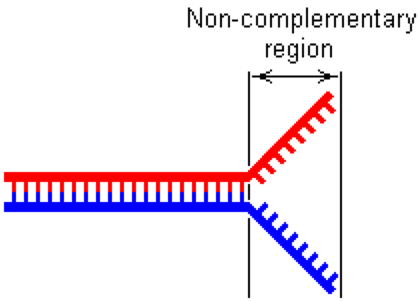


Il processo di sintesi del nuovo filamento di DNA è catalizzato da enzimi detti DNA-polimerasi e avviene nella direzione 5’ → 3’.



Acidi nucleici





Frayed ends

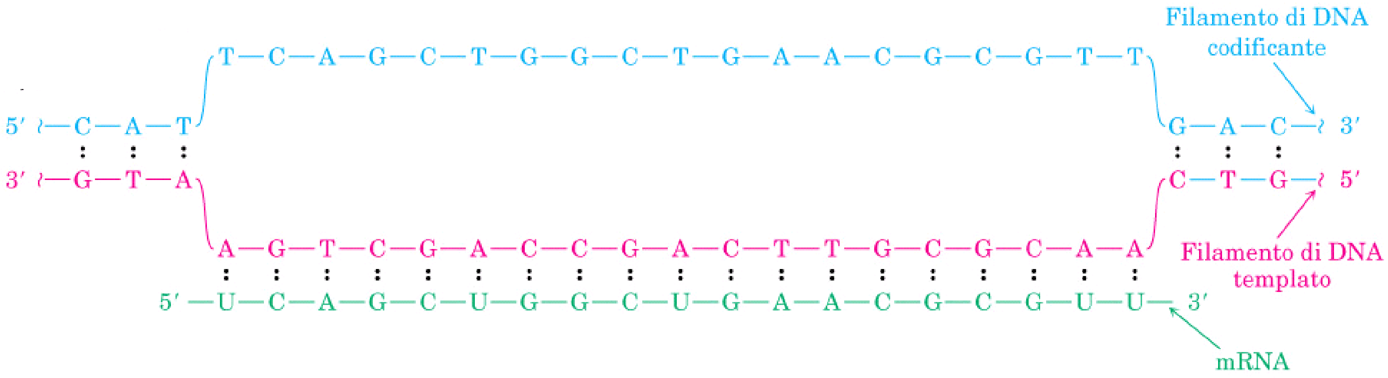
Acidi nucleici

• ***RNA messaggero (mRNA)***: porta le informazioni genetiche dal DNA ai ribosomi

• ***RNA ribosomiale (rRNA)***: complessato con materiale proteico costituisce i ribosomi e partecipa alla sintesi proteica.

• ***RNA di trasferimento (tRNA)***: trasporta gli amminoacidi ai ribosomi.

Il processo di trascrizione del DNA avviene con la sintesi del mRNA. Solo un filamento del DNA viene ricopiato. La sintesi del RNA avviene ad opera di enzimi detti RNA-polimerasi.



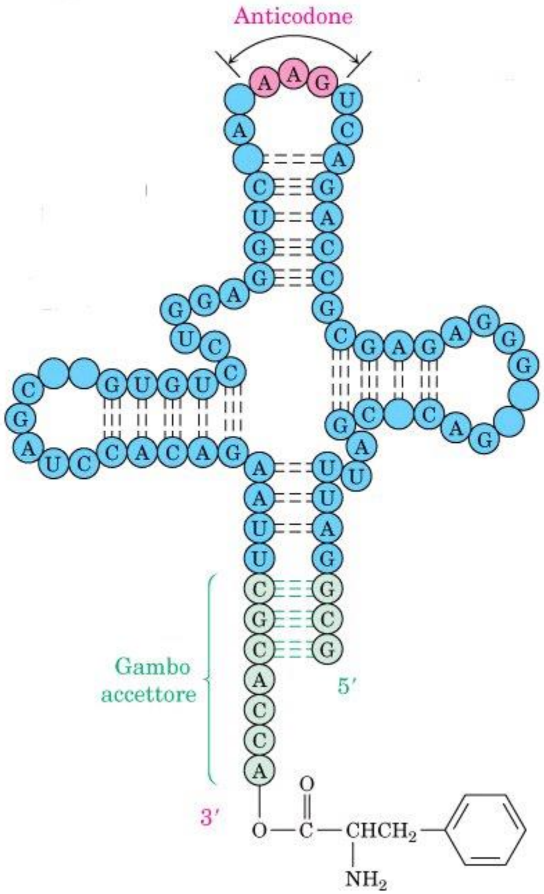
Acidi nucleici

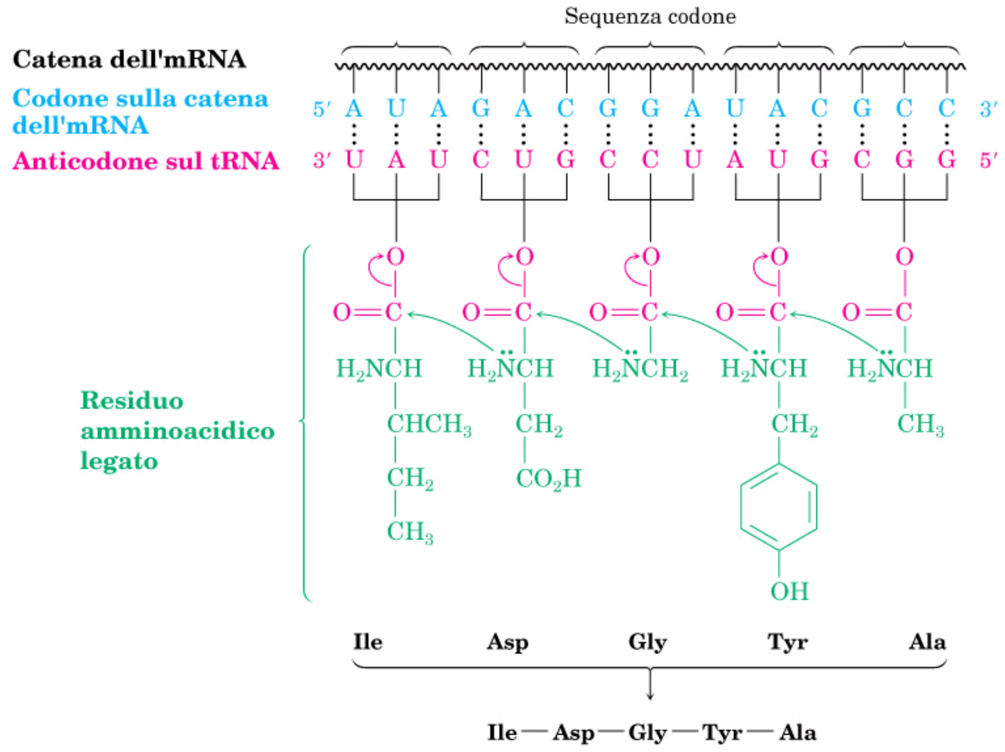
La traduzione del mRNA avviene a livello dei ribosomi, organelli presenti nel citoplasma e composti dal 60% di rRNA e dal 40% di proteine. La sequenza di basi nel mRNA costituisce l'informazione organizzata in codoni, sequenze di tre basi che identificano un amminoacido. Esistono 64 combinazioni possibili di cui 61 identificano un amminoacido e 3 identificano lo stop della sintesi. Ogni amminoacido è identificato da più di un codone.

First base	Second base: U	Second base: C	Second base: A	Second base: G	Third base
U	UUU Phenyl-alanine F	UCU Serine S	UAU Tyrosine Y	UGU Cysteine C	U
U	UUC Phenyl-alanine F	UCC Serine S	UAC Tyrosine Y	UGC Cysteine C	C
U	UUA Leucine L	UCA Serine S	UAA Stop codon	UGA Stop codon	A
U	UUG Leucine L	UCG Serine S	UAG Stop codon	UGG Tryptophan W	G
C	CUU Leucine L	CCU Proline P	CAU Histidine H	CGU Arginine R	U
C	CUC Leucine L	CCC Proline P	CAC Histidine H	CGC Arginine R	C
C	CUA Leucine L	CCA Proline P	CAA Glutamine Q	CGA Arginine R	A
C	CUG Leucine L	CCG Proline P	CAG Glutamine Q	CGG Arginine R	G
A	AUU Isoleucine I	ACU Threonine T	AAU Asparagine N	AGU Serine S	U
A	AUC Isoleucine I	ACC Threonine T	AAC Asparagine N	AGC Serine S	C
A	AUA Isoleucine I	ACA Threonine T	AAA Lysine K	AGA Arginine R	A
A	AUG M Methionine start codon	ACG Threonine T	AAG Lysine K	AGG Arginine R	G
G	GUU Valine V	GCU Alanine A	GAU Aspartic acid D	GGU Glycine G	U
G	GUC Valine V	GCC Alanine A	GAC Aspartic acid D	GGC Glycine G	C
G	GUA Valine V	GCA Alanine A	GAA Glutamic acid E	GGA Glycine G	A
G	GUG Valine V	GCG Alanine A	GAG Glutamic acid E	GGG Glycine G	G

Acidi nucleici

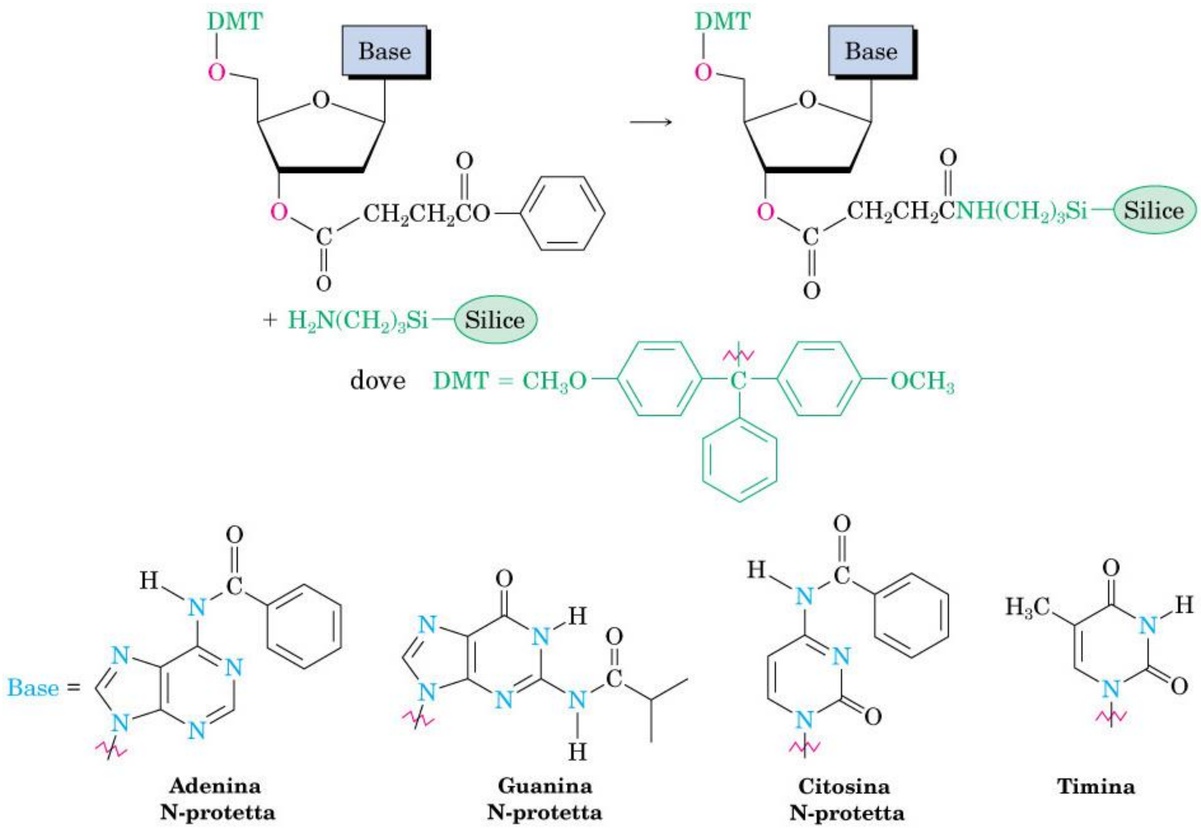
Il messaggio scritto nei codoni viene letto dal tRNA. Esistono 61 tRNA, uno per ogni codone. Sono costituti da un singolo filamento di RNA lungo circa 70-100 nucleobasi.



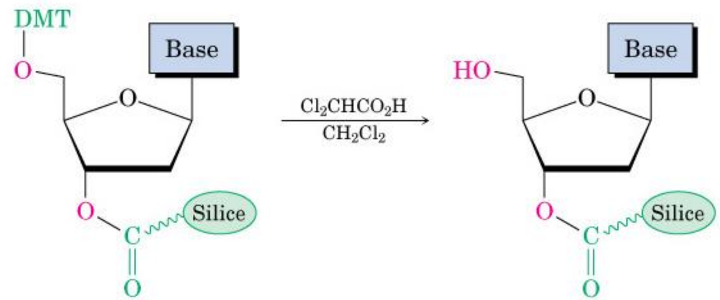


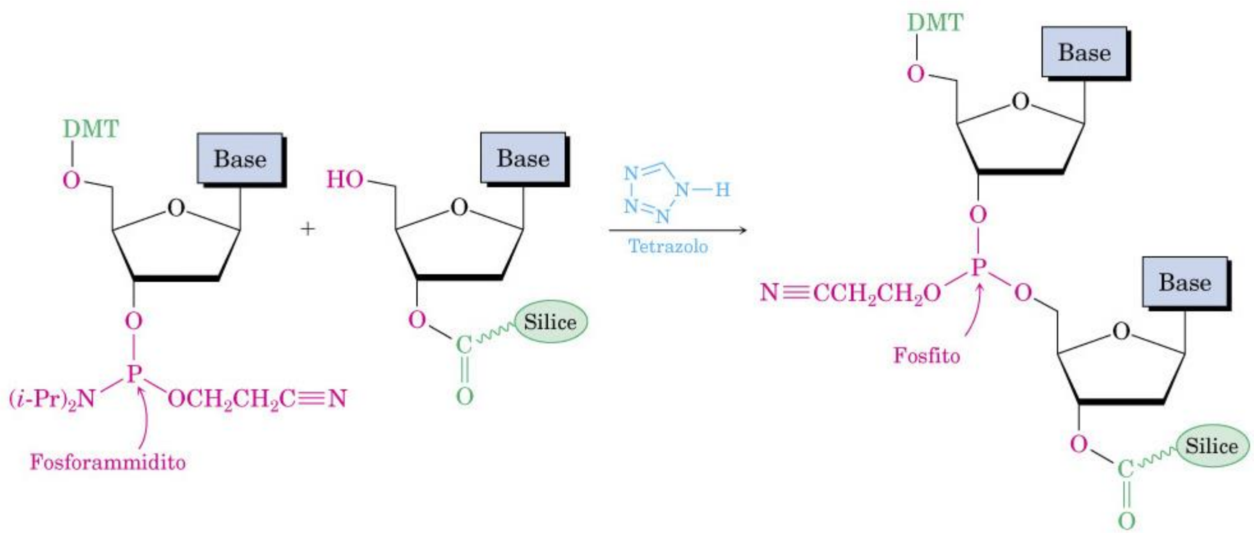
Acidi nucleici

La sintesi chimica di oligonucleotidi è stata automatizzata analogamente a quella peptidica. Si riescono a preparare oligonucleotidi fino a 200 basi.

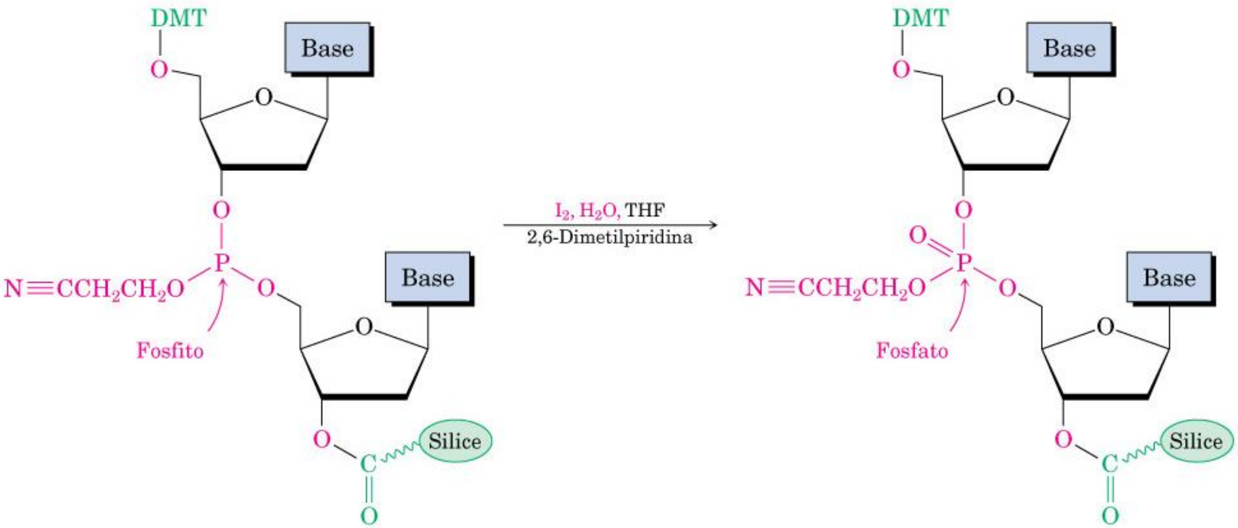


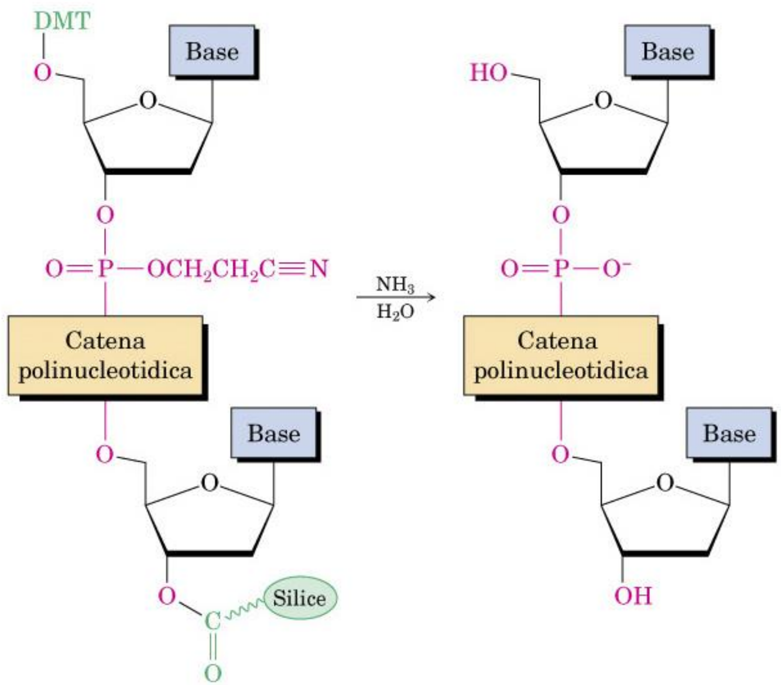
Acidi nucleici





Acidi nucleici

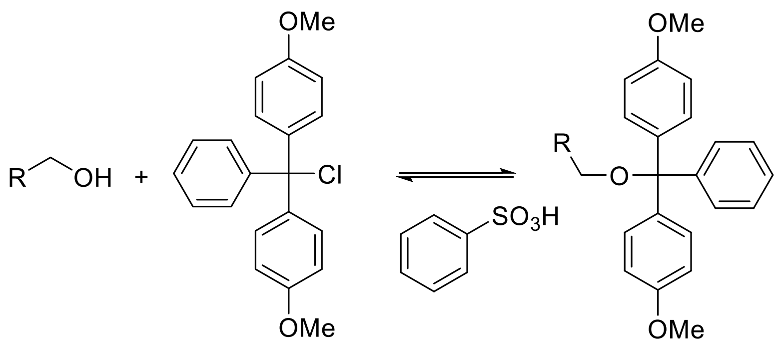




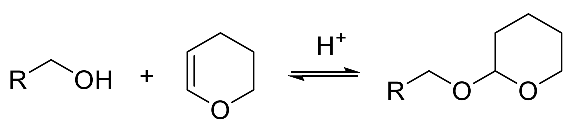
Acidi nucleici

Gruppi proteggenti

per il 5'-OH	Dmtr (4,4'-dimetossitritile)	per la deprotezione	AcOH 80%, 100 °C (BSA 2%, CH_2Cl_2)
3'-OH	Ac (acetile)		NaOH 2M, 0 °C (NH_3, CH_3OH, t.a.)
2'-OH	Thpr (tetraidropiranile)		HCl 0,01M, t.a.
NH_2 [A, C e G]	Ac(acetile), Bz(benzoile)		NaOH 1M, t.a.



DMTCl DMT

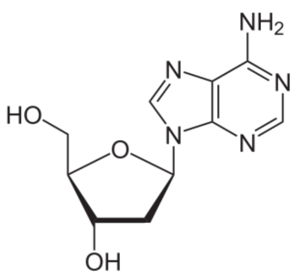


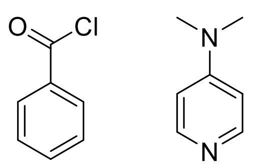
THP

Gruppi proteggenti

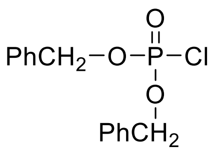
per il 5'-OH	Dmtr (4,4'-dimetossitritile)	per la deprotezione	AcOH 80%, 100 °C (BSA 2%, CH_2Cl_2)
3'-OH	Ac (acetile)		NaOH 2M, 0 °C (NH_3, CH_3OH, t.a.)
2'-OH	Thpr (tetraidropiranile)		HCl 0,01M, t.a.
NH_2 [A, C e G]	Ac(acetile), Bz(benzoile)		NaOH 1M, t.a.

Esempio di sintesi di un nucleotide

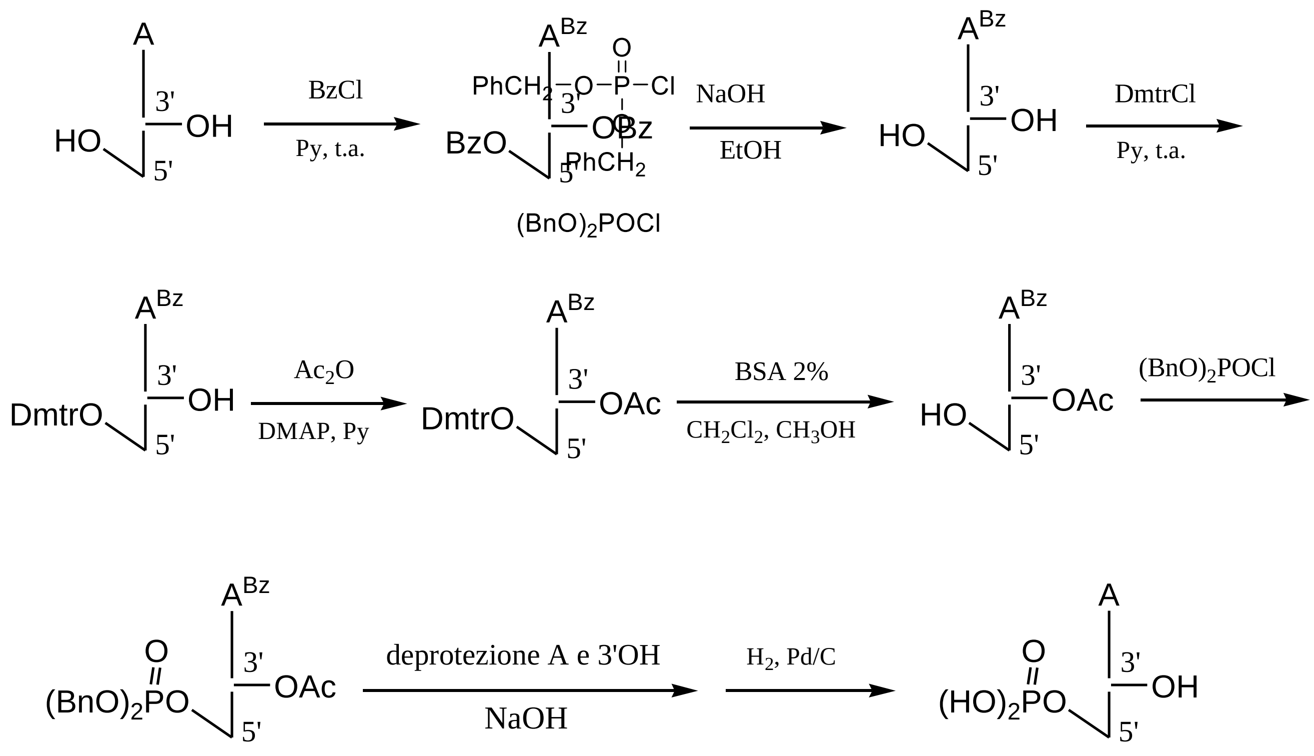




BzCl DMAP

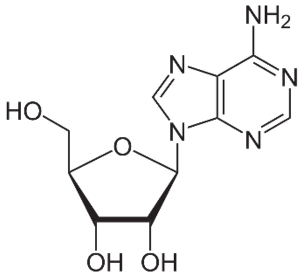


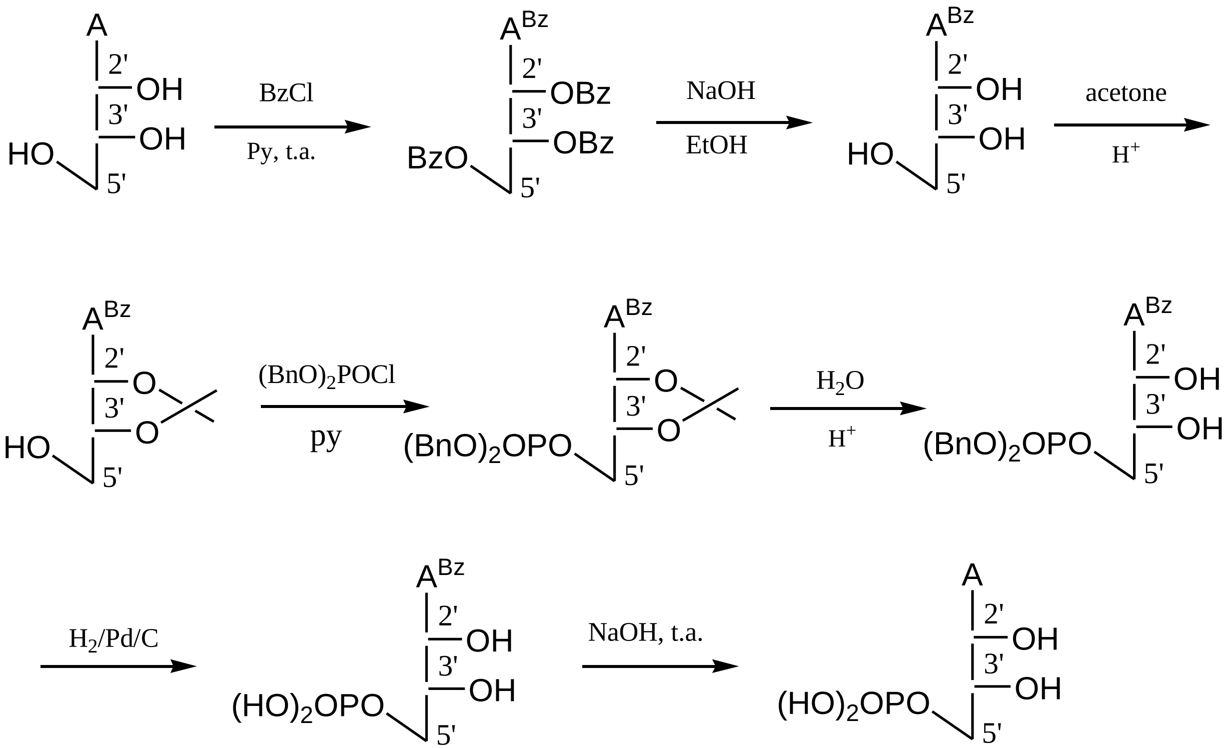
$(BnO)_2POCl$



ac. 5'-deossiadenilico

Sintesi di Adenosina 5'-monofosfato o acido 5'-adenilico





DNA Origami

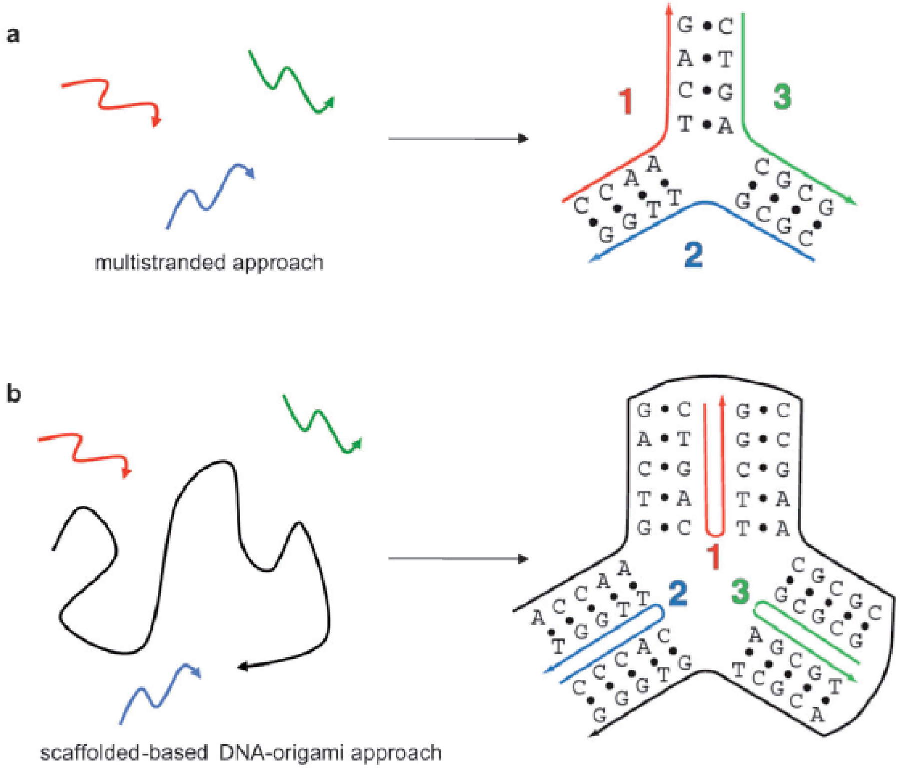
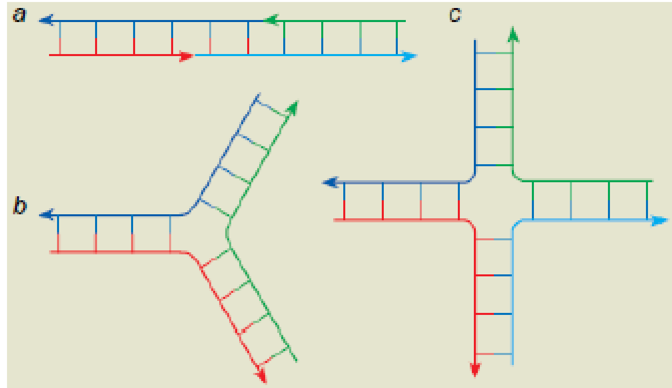
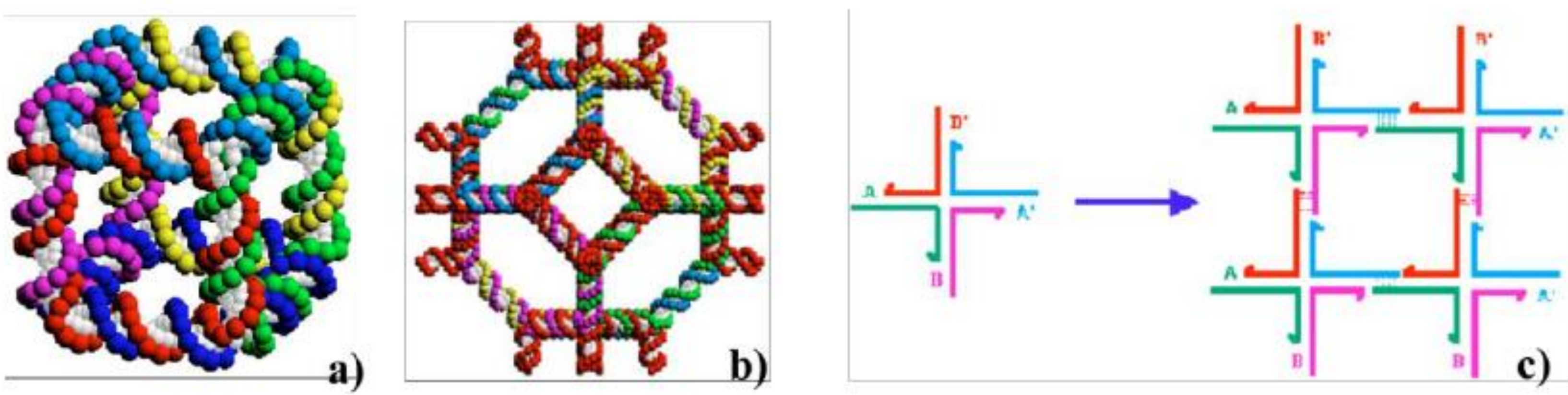


Figure 1. Schematic representation of the two main approaches used for the construction of DNA-based architectures. a) In the multistranded approach oligonucleotides are designed to self-assemble with each other to form a well-defined branched DNA motif, also called a tile. Hierarchical assembly of such motifs into larger (finite or infinite) structures is achieved through the cohesion of sticky ends. b) In the DNA origami technique, a long single-stranded scaffold is folded into a desired finite-sized shape by means of hundreds of shorter staple strands. This so-called scaffold-based assembly is highly efficient.

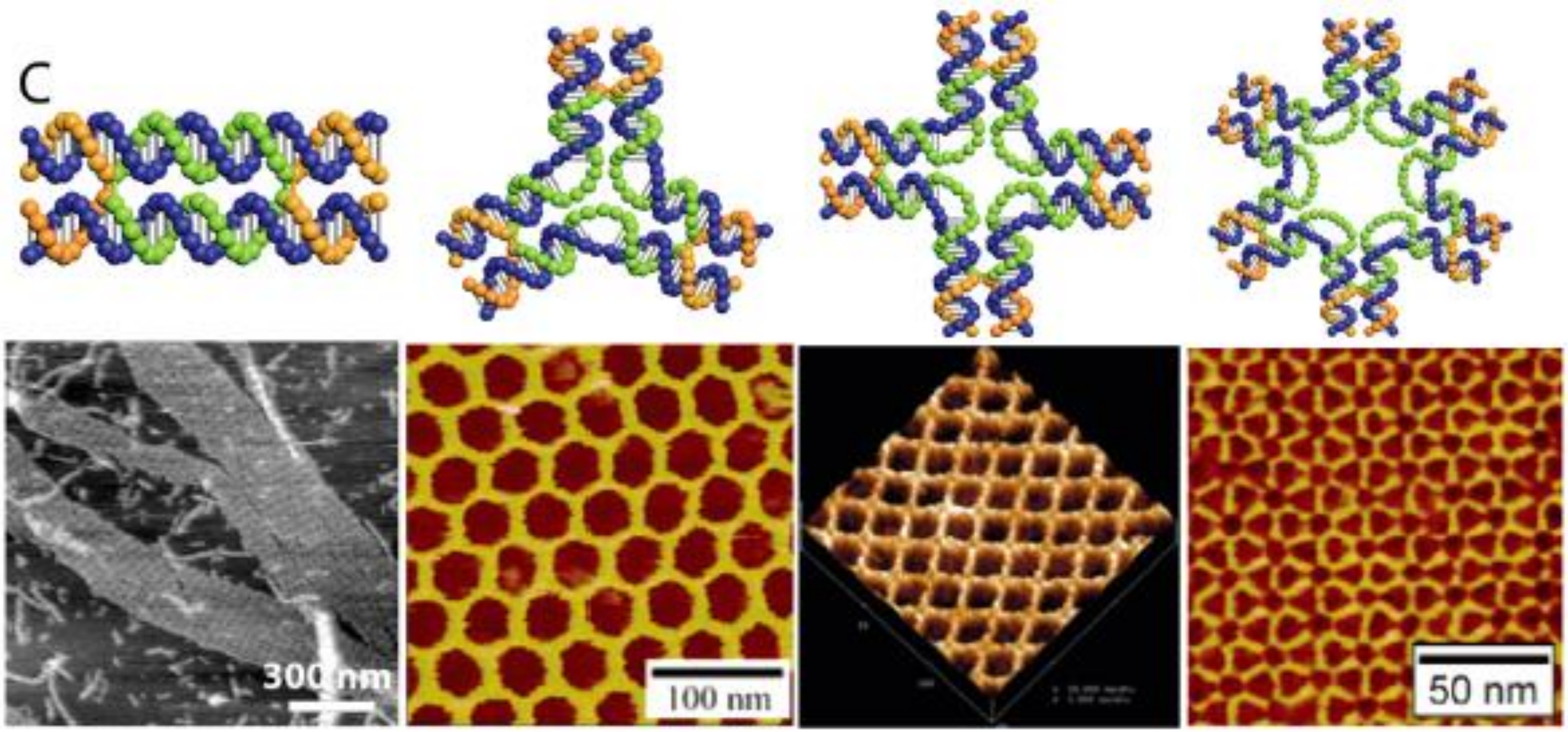
DNA Origami



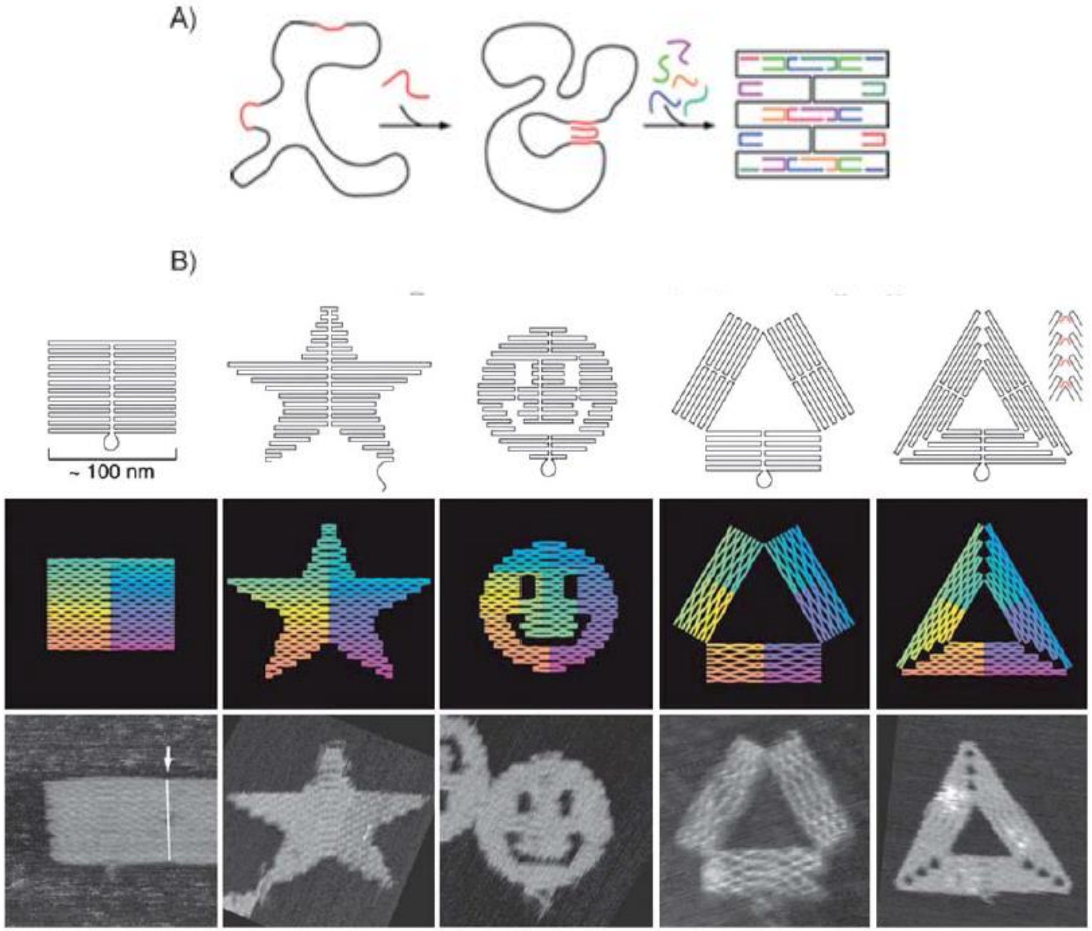
Two-, three- and four-arm junctions can be fabricated from DNA, which along with stiff DNA rods are the basic building blocks of DNA nanostructures. The two-arm junction (a) joins two helices by the overlap of complementary sticky ends on each adjacent helix. The three-arm (b) and four-arm "Holliday" junctions (c) are formed in a similar way. The Holliday junction also occurs biologically, as an intermediate stage in genetic recombination.



DNA Origami



DNA Origami



DNA Nanotecnologie

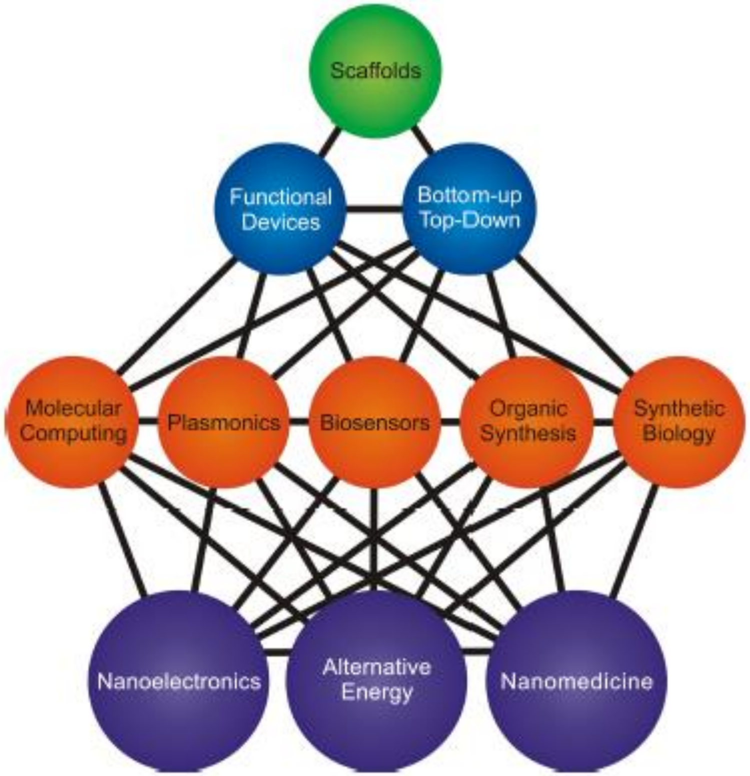


Figure 5.
Hierarchy of areas impacted by DNA origami technology. The foundational DNA scaffolds (green) are used to create devices (blue) for a broad variety of applications (orange) that can be combined to enhance numerous emerging interdisciplinary fields (purple). Disclaimer: the nucleic acid nanotechnology field will not be limited by our current vision.