

DNA-Polymerasen

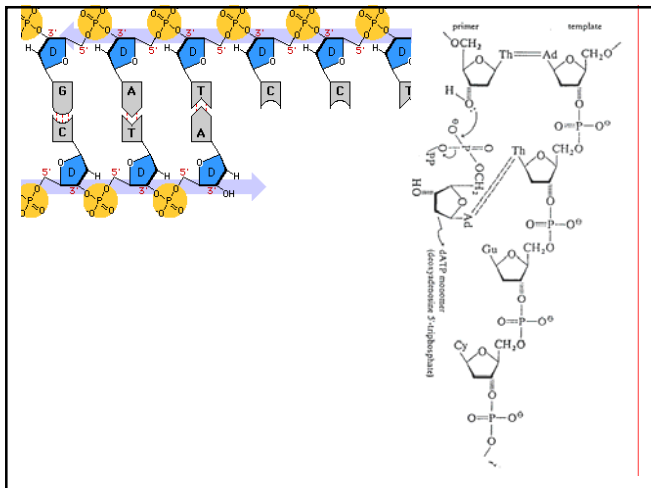
Funktionen
 Replikation, Transkription
 Reparatur von DNA

Voraussetzungen
 Startstrang (PRIMER)
 Matrize (TEMPLATE)
 Substrate (Desoxynucleosid-Triphosphate)
 Magnesiumionen

Richtung 5' - 3'
 Pyrophosphorolyse

Template-primer	Product
(i) Intact duplexes	No change
(ii) Nicked duplexes	No change
(iii) Gapped duplex	
(iv) Single strands	
(v) Primed single strand	

Labels in diagram: Sliding clamp, DNA polymerase on leading strand, DNA primase, Okazaki fragment, Parental DNA, New Okazaki fragment, Single-strand DNA-binding protein, New primer, Lagging-strand template, Clamp loader, DNA polymerase on lagging strand (just finishing an Okazaki fragment).



DNA-Polymerase I

Escherichia coli
 M: 103 kD, 928 Aminosäuren
 400 Moleküle/Zelle
 Aktivität: 670 Nucleotide / min
 Funktion: Reparatur und Präzision der Basenpaarung
 (Fehlerrate 1: 1.000.000)

(DNA-Polymerase III Replikationsenzym: 1000 Nucleotide / s)
 Bindungsstellen für Matrize, Starter und Substrate
 Zusätzlich Exonuklease-aktivität in 3'-5' und 5'-3' Richtung

Spaltung mit Subtilisin

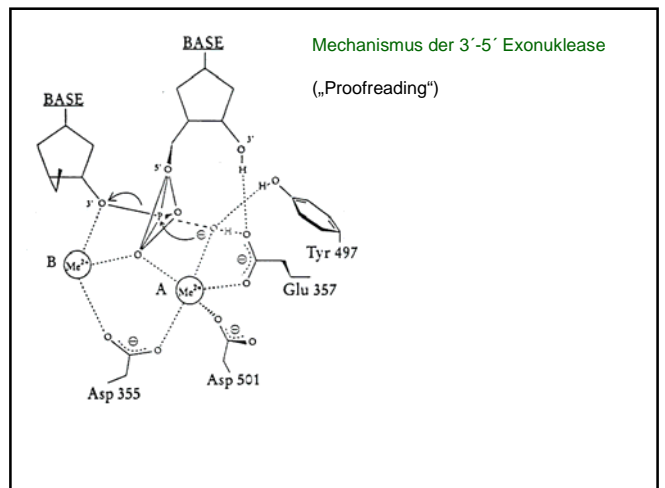
Abbau zu Einzelstrang (Startstrang)

Klenow-Fragment

Röntgenstruktur des Klenow-Fragments

605 Aminosäuren, PDB: 2KZM

Labels: 3'→5'-Exonucleasenzentrum, 5'-Matrizenstrang, Polymerasezentrum.



Einsatz der DNA-Polymerasen zur Sequenzbestimmung

Taq-Polymerase (*Thermophilus aquaticus*)

a DNA polymerase

5'-TGGGCTAAACAAGCAAATGATCTGTAG
3'-ACCCGATTTTTCGTTACTAGACATCAAATGCTCTA

b

TGGGCTAAACAAGCAAATGATCTGTAGT
TGGGCTAAACAAGCAAATGATCTGTAG
TGGGCTAAACAAGCAAATGATCTGTAG
TGGGCTAAACAAGCAAATGATCTGT
TGGGCTAAACAAGCAAATGATCTGT
TGGGCTAAACAAGCAAATGATCTGT
TGGGCTAAACAAGCAAATGATCTGT
TGGGCTAAACAAGCAAATGATCTGT
TGGGCTAAACAAGCAAATGATCTGT
TGGGCTAAACAAGCAAATGATCTGT

c

d

Chemische Oligonukleotidsynthesen

Aufklärung des genetischen Codes
Synthese von Startsequenzen
Modifikation von DNA und RNA
Linker, Adapter für Klonierungsexperimente
„Antisense“ Oligonukleotide, Hybridisierungsproben für mRNA und cDNA
Gensynthesen

Voraussetzungen:
Bildung des 3'-5' Phosphodiesters, Schutz aller anderen nukleophilen Zentren (Phosphat, Basen, Pentose)
Aktivierung zur Phosphodiesterbildung – Hohe Ausbeuten notwendig

Schutzgruppen: Möglichst quantitative Einführung und Abspaltung
Stabilität unter Synthesebedingungen
Festphasensynthese an polymeren Trägern

Schutzgruppen

Aminogruppen der N-Basen:

Isobutyryl: CC(C)C(=O)N
Benzoyl: c1ccccc1C(=O)N
Methoxybenzoyl (Anisoyl): COc1ccc(cc1)C(=O)N

Other groups shown: Cc1c[nH]c2c1c[nH]2, Cc1c[nH]c2c1c[nH]2, Cc1c[nH]c2c1c[nH]2, Cc1c[nH]c2c1c[nH]2

Schutzgruppen

OH-Gruppen der Pentosen

Triphenylmethyl-(Trityl) Methoxytrityl-: COC1=CC=C(C=C1)C2=CC=C(C=C2)C3=CC=C(C=C3)C4OC5OC(O)C(O)C5O4

tert-Butyldimethylsilyl (tBDMSI): CC(C)(C)Si(C)C1OC2OC(O)C(O)C2O1

Methoxytetrahydropyranyl: COC1OC2OC(O)C(O)C2O1

OH-Gruppen der Phosphate

2-Chlorphenyl-: Clc1ccccc1

2-Cyanoethyl-: N#CCO

Trichlorethyl-: CCl(Cl)CCl

Reaction: N#CCO + F- -> N#CC=C + HOR

Kopplung

Dicyclohexylcarbodiimid (DCC): C1CCN1C#NC2CCCC2

Mesitylsulfochlorid: CC1=CC(=C(C=C1)S(=O)(=O)Cl)C

Aktivierung als Phosphoramidit

Chloro-N,N-Diisopropylphosphoramidit: CC(C)N(C(C)C)P(=O)(Cl)OR

Reaction: ROH + Chloro-N,N-Diisopropylphosphoramidit -> RO-P(=O)(N(C(C)C)2)OH

Phosphotriestermethode

Umkehr der enzymatischen Reaktion: 5'-OH als Nukleophil

a) DMTO-O-P(=O)(OR')OH + HO-O-B -> DMTO-O-P(=O)(OR')(OR)O-B (condensing agent)

b) DMTO-O-P(=O)(OR')OH + HO-O-B -> DMTO-O-P(=O)(OR')(OR)O-B (1. coupling, 2. oxidation)

Phosphoramiditmethode

c) DMTO-O-P(=O)(OR')OH + HO-O-B -> DMTO-O-P(=O)(OR')(OR)O-B (1. coupling, 2. oxidation)

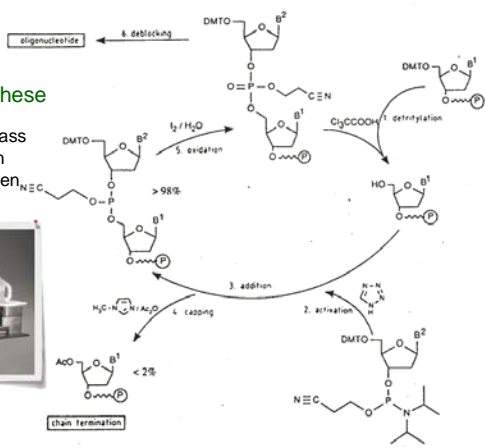
H-Phosphonatmethode

Festphasensynthese

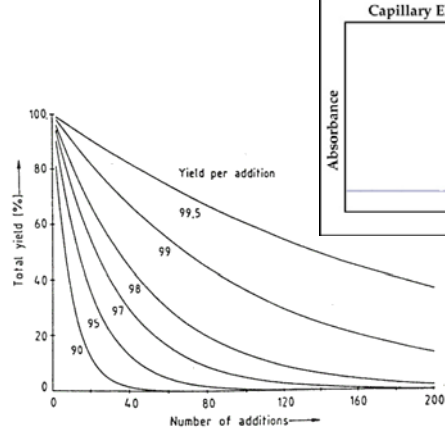
Controlled pore glass
500 Å: ~ 80 Basen
1000 Å: ~200 Basen



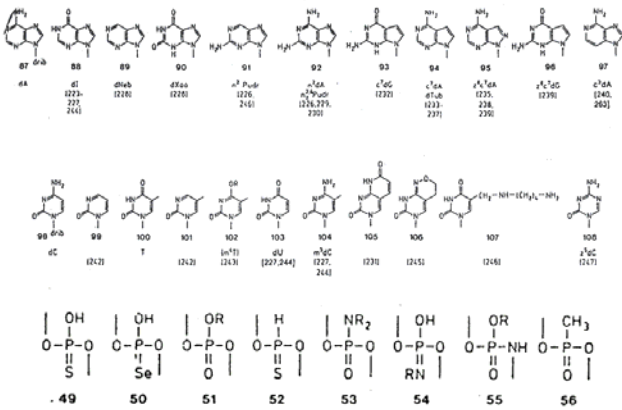
PolyPlex



Gesamtausbeute und Reinheit bei vielstufigen Synthesen

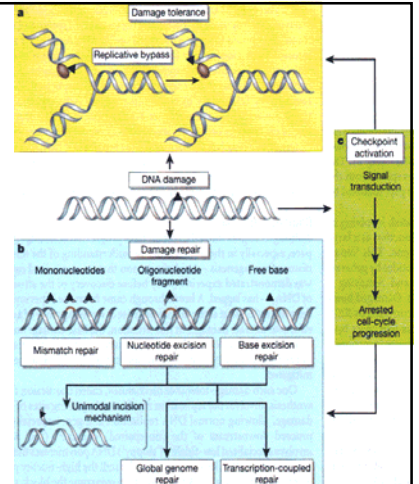


Modifizierte Nucleotide

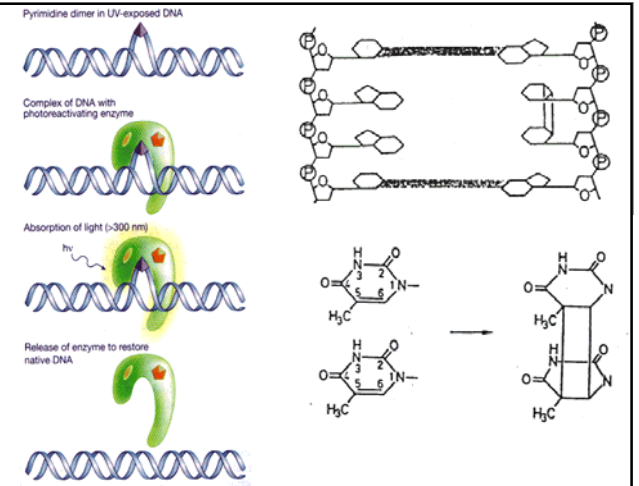
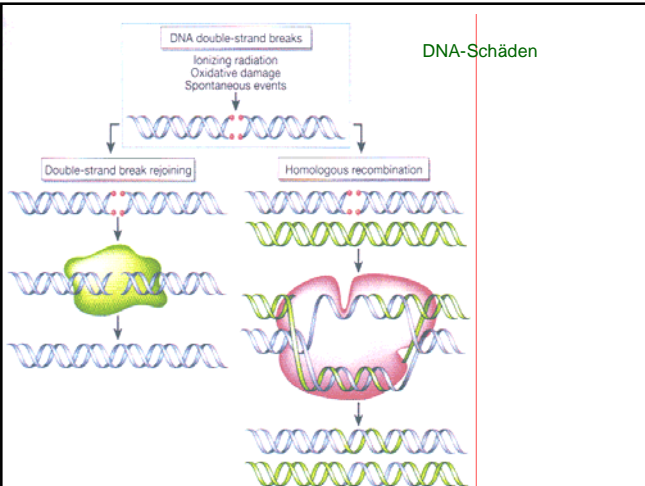


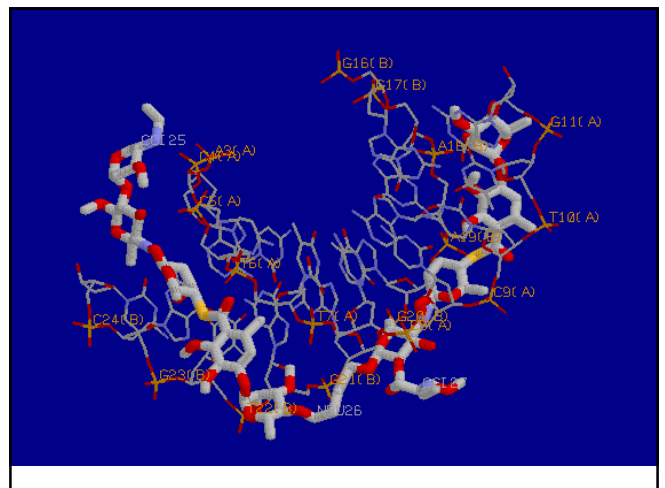
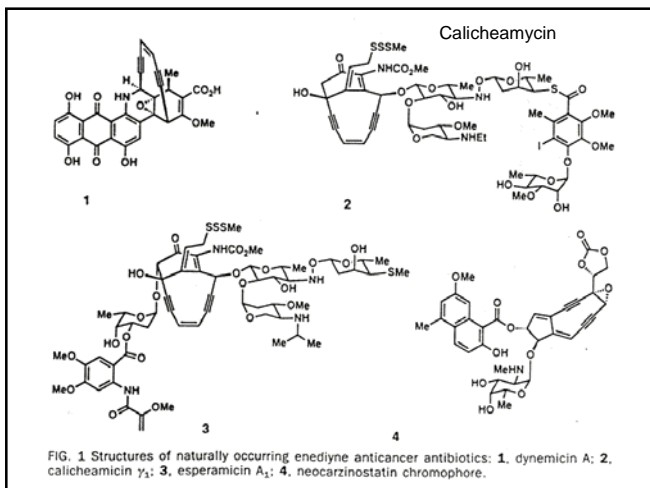
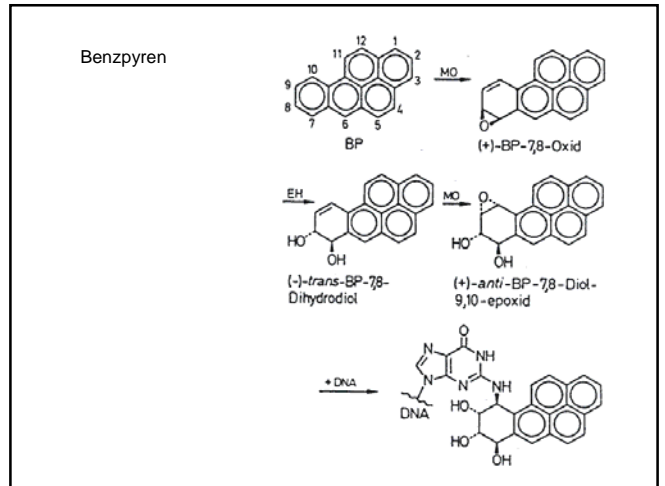
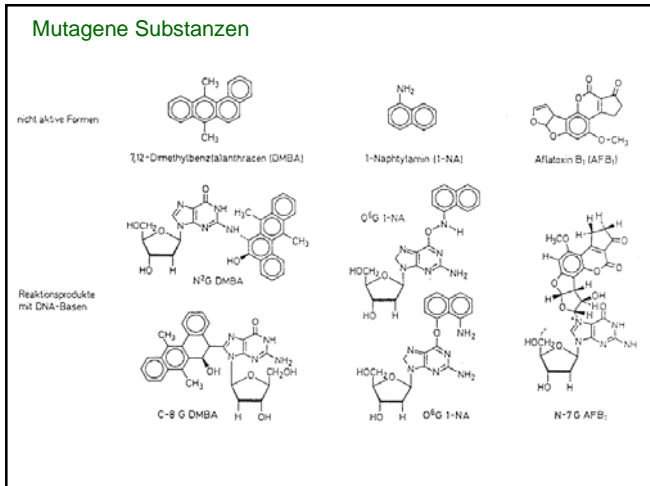
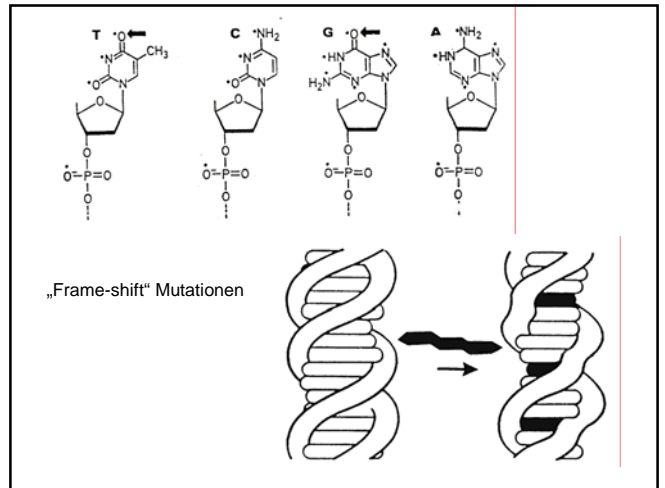
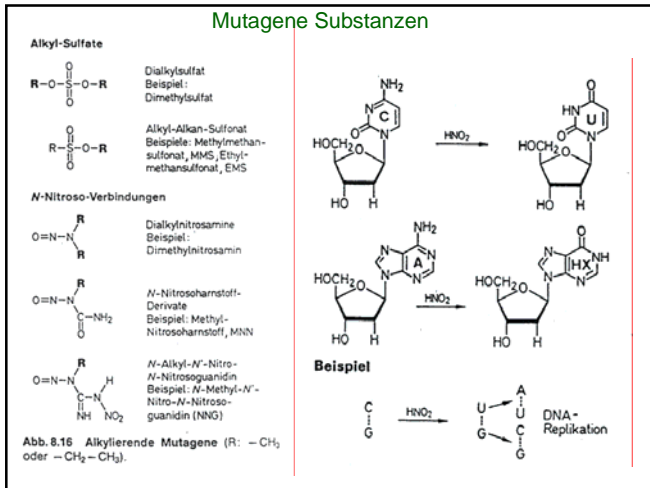
DNA-Schäden

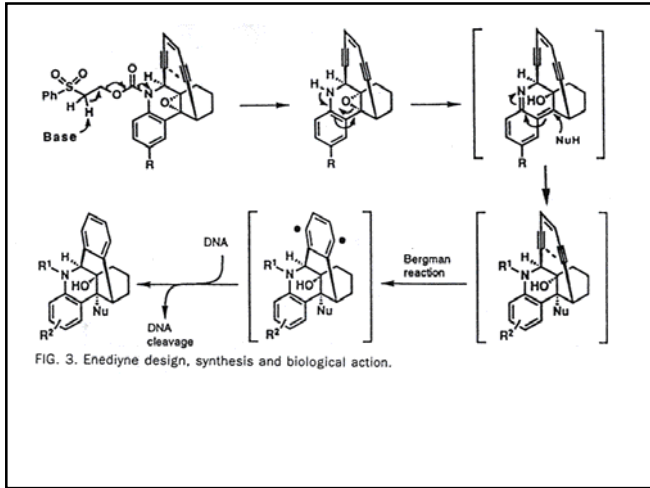
Reparaturmechanismen



DNA-Schäden







CYTOTOXICITIES OF DESIGNED ENEDIYNE 7 AGAINST 19 TUMOUR CELL LINES (TOP) AND FOUR NORMAL CELL LINES (BOTTOM)

Cell type	Cell line	IC ₅₀ (M)	Cell type	Cell line	IC ₅₀ (M)
Melanoma	SK-Mel-28	3.1×10^{-6}	Lung carcinoma	UCLA P-3	9.8×10^{-8}
Melanoma	M-14	1.6×10^{-6}	Pancreatic carcinoma	Capan-1	3.1×10^{-9}
Melanoma	M-21	1.6×10^{-6}	T-cell leukaemia	TCAF	1.1×10^{-9}
Colon carcinoma	HT-29	1.6×10^{-6}	Multidrug resistant T-cell leukaemia	TCAF-DAX	1.7×10^{-9}
Ovarian carcinoma	Ovar-3	7.8×10^{-7}	Myeloma	RPMI-8226	7.7×10^{-9}
Astrocytoma	U-87 UG	7.8×10^{-7}	Mouse leukaemia	P-388	4.6×10^{-9}
Glioblastoma	U-251 MG	3.9×10^{-7}	Mouse leukaemia	L-1210	1.3×10^{-8}
Breast carcinoma	MCF-7	7.8×10^{-7}	Promyelocytic leukaemia	HL-60	3.6×10^{-11}
Lung carcinoma	H-358	2.0×10^{-7}	T-cell leukaemia	Molt-4	2.0×10^{-14}
Lung carcinoma	H-522	9.8×10^{-8}			
Bone marrow	HNBM	5.0×10^{-5}	Normal human dermal fibroblast	NHDF	5.0×10^{-6}
Human mammary epithelial cells	HMEC	6.3×10^{-6}	Chinese hamster ovary	CHO	3.1×10^{-6}

