

Degenerate Oligonucleotides

Wobble Bases

Description

Defined mixture of oligonucleotides with different bases at specific positions in the sequence (wobbles).

Advantages

Wobble bases are used when re-translating an amino acid sequence into DNA. Due to the degeneracy of the genetic code different nucleotide sequences code for the same amino acid. These coding differences are constricted to one or at maximum two positions in one triplet codon. Instead of ordering a number of different oligonucleotides to cover all possible DNA differences, we recommend wobble bases.

Please refer to the IUB Code for the correct denomination for equimolar wobble base mixtures and to the Codon-sun for the Universal Genetic Code.

Applications

- degenerate PCR
- cDNA synthesis
- functional genomics
- mutation analysis

Product offering

Standard wobbles

Standard wobble synthesis is performed automatically on our machines. Due to synthesis and instrument reasons, a slight overrepresentation of A > G > C > T can be observed. Thus, these standard wobbles are not recommended for synthesis of long stretches of random sequences or experiments requiring high batch-to-batch reliability. Standard wobbles are free of charge – even at the 3'-end!

Special mixtures

(specially defined ratio of bases)

These mixtures are manually prepared according to customers' orders and are available at a small extra fee. They are extremely useful for long stretches of random sequences, experiments requiring high batch-to-batch uniformity or to over- or under-represent one or more bases in a degenerate site (e.g., equimolar N wobble or special M wobble with 17.5% A and 82,5% C).

Easily order wobbles via the web:

www.thermo.com/oligos

or via email:

sales.oligos@thermo.com

by indicating the required wobble bases in the IUB Code.

When ordering special mixtures, please denote the percentage of bases for the required mixtures.

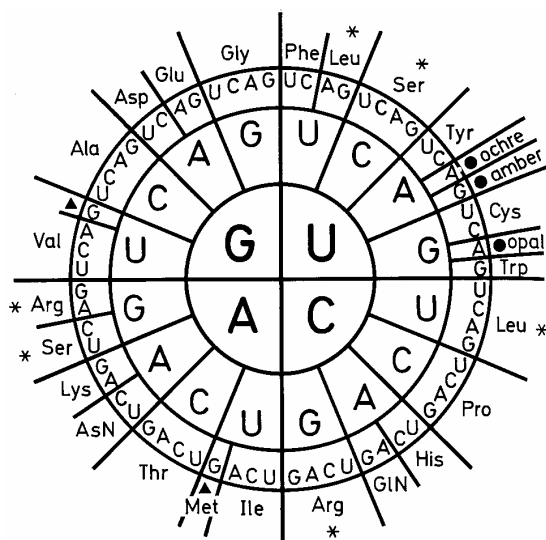
For oligos with longer stretches of wobbles, it is important to order the correct synthesis scale so all possible oligonucleotide sequences are represented in the product at least once. However, we recommend that you choose a scale where each sequence is theoretically present with a minimum of 50-100 molecules. Please refer to the table below for example calculations for random sequences N₂₀ and N₂₅.

Synthesis Scale	Random Sequence	Different sequence possibilities	Guaranteed amount [nmol]	No. of molecules present	Theoretical presence of each single sequence
0,02	N ₂₀	1,1 * 10 ¹²	9	5,4 * 10 ¹⁵	5.000
	N ₂₅	1,1 * 10 ¹⁵	7	4,2 * 10 ¹⁵	4
0,04	N ₂₀	1,1 * 10 ¹²	18	1,1 * 10 ¹⁶	10.000
	N ₂₅	1,1 * 10 ¹⁵	15	9,0 * 10 ¹⁵	8
0,2	N ₂₀	1,1 * 10 ¹²	47	2,8 * 10 ¹⁶	25.000
	N ₂₅	1,1 * 10 ¹⁵	37	2,2 * 10 ¹⁶	20
1	N ₂₀	1,1 * 10 ¹²	137	8,3 * 10 ¹⁶	75.000
	N ₂₅	1,1 * 10 ¹⁵	110	6,6 * 10 ¹⁶	60
10	N ₂₀	1,1 * 10 ¹²	1400	8,4 * 10 ¹⁷	750.000
	N ₂₅	1,1 * 10 ¹⁵	1100	6,6 * 10 ¹⁷	600

IUB Code:

IUB	Coding for	IUB	Coding for	IUB	Coding for
A	Adenine				
C	Cytosine	M	A and C	V	A and G and C
G	Guanine	R	A and G	H	A and C and T
T	Thymine	W	G and C	D	A and G and T
U	Uridine	S	C and T	B	G and T and C
I	Inosine	Y	C and T		any of four bases possible
		K	G and T	N	A and G and C and T

Codon sun:



TI-OL07-1104

Please note:

Purifying oligonucleotides with multiple wobbles by PAGE purification is not recommended. This will lead to narrowing the oligonucleotide pool. It is not possible to calculate melting temperatures or molecular weights for oligonucleotides with mixed bases because those oligonucleotides represent a mixture of different individual molecules. When performing PCR using degenerate primers, it might be necessary to increase primer concentration, as only a small part of the primer pool represents the 100% complement to the target.

Contact us:

Thermo Electron GmbH

Sedanstrasse 18

89077 Ulm

Germany

phone

+49 (0)731 93579 290

fax

+49 (0)731 93579 291

email

services.biopolymers@thermo.com

web page

www.thermo.com/biopolymers

2004 Thermo Electron Corporation.

All rights reserved.