

OLIGO PROPERTY SCAN “MOPS” - TUTORIAL

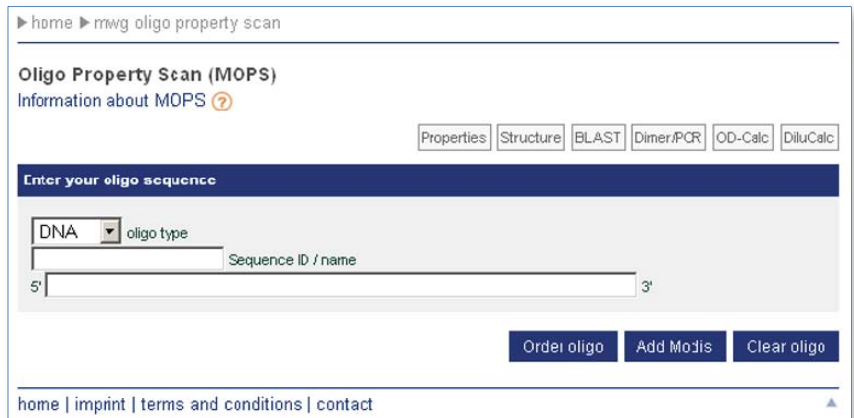
The one-stop solution for quick and easy oligo analysis and calculation

MOPS

Our MOPS is a multifunctional oligo calculation tool, which gives you the option of checking your oligos before you order.

It also facilitates the set up of experiments by calculating the adequate amounts and dilution factors for your oligo solutions.

You can enter DNA as well as RNA sequences and you can attach or insert modifications to your oligos:



home ▶ mwg oligo property scan

Oligo Property Scan (MOPS)
Information about MOPS ?

Properties | Structure | BLAST | Dimer/PCR | OD-Calc | DiluCalc

Enter your oligo sequence

DNA oligo type

Sequence ID / name

5' _____ 3'

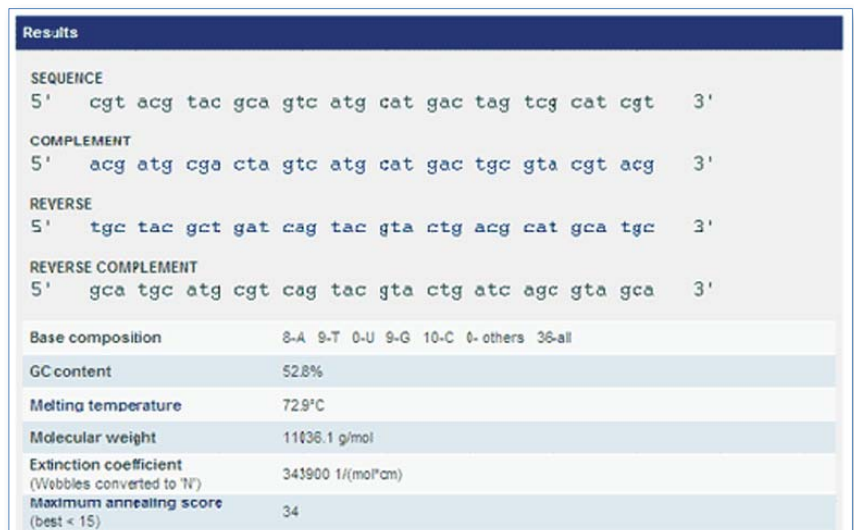
Order oligo | Add Modis | Clear oligo

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Editor and start page

Physical property check

By using “Properties” you ask the system to specify all physical attributes such as GC content, melting temperature (T_m), molecular weight (MW), extinction coefficient and sequence complements of your oligo:



Results

SEQUENCE
5' cgt acg tac gca gtc atg cat gac tag tcg cat cgt 3'

COMPLEMENT
5' acg atg cga cta gtc atg cat gac tgc gta cgt acg 3'

REVERSE
5' tgc tac gct gat cag tac gta ctg acg cat gca tgc 3'

REVERSE COMPLEMENT
5' gca tgc atg cgt cag tac gta ctg atc agc gta gca 3'

Base composition	8-A 9-T 0-U 9-G 10-C 6-others 36-all
GCcontent	52.8%
Melting temperature	72.9°C
Molecular weight	11036.1 g/mol
Extinction coefficient (Webbles converted to 'N')	343900 1/(mol*cm)
Maximum annealing score (best < 15)	34

Physical property result

Secondary structure prediction

By pressing “Structure” the software predicts the secondary structure of DNA oligos by using the mfold program. This program is an adaptation of the mfold package (version 2.3) by Zuker and Jaeger that has been modified to work with the Wisconsin Package.

The RNAfold program (Vienna RNA Package) is used to predict RNA secondary structures.



Enter your oligo sequence

DNA oligo type

My Oligo Sequence ID / name

5' |act gactga ctg act gac tga ctg act gac tg| 3' - 32 bases

Order oligo | Add Modis | Clear oligo

minimum free energy: 1.8 kcal/mol
maximum stack length: 1

ACTGACTGACTGACTGACTGACTGACTG
...(.....)

Visualisation of secondary structure

BLASTn analysis

This functionality aligns your sequence against the human, mouse and rat Refseq mRNA database. A comprehensive BLASTn report is provided online:

```
Blast Results

BLASTN 2.2.13 [Nov-27-2005]

Reference: Aaron E. Darling, Lucas Carey, and Wu-chun Feng,
"The design, implementation, and evaluation of mpiBLAST."
In Proceedings of The 4th International Conference on Linux Clusters:
The HPC Revolution, June 24-26 2003, San Jose, CA

Query= thistoolisgreat
      (14 letters)

Database: /database/mpidb/refseq_mouse_mrna
          36,068 sequences; 83,597,831 total letters

Sequences producing significant alignments:

          Score   E
          (bits) Value
NM_001081300 Mus musculus teashirt zinc finger family member 1 (...   28  0.52
NM_001025581 Mus musculus potassium voltage gated channel, Shaw-rel...  24  8.2
NM_001081048 Mus musculus solute carrier family 25 (mitochondria...  24  8.2

>NM_001081300 Mus musculus teashirt zinc finger family member 1 (Tshz1), mRNA.
      Length = 5814

      Score = 28.2 bits (14), Expect = 0.52
      Identities = 14/14 (100%)
      Strand = Plus / Minus

Query: 1      gactgacgtacgtg 14
          |||
Sbjct: 4139 gactgacgtacgtg 4126

>NM_001025581 Mus musculus potassium voltage gated channel, Shaw-related
```

BLASTn report

Dimer formation

The dimer formation check tests your oligo against itself or another oligo for dimer formation.

```
maximum annealing score (opt. <= 14): 10
maximum stack size : 4
5'      GACTGACGTACGTG
      |||
3' TAGCTCAGGACT
```

Result of a dimer formation check

PCR viability check

The PCR check performs a PCR viability check for a primer pair.

```
Results PCR check
5' ACGACGACGACG.....GCAGCAGCAGCA 3'
forward primer
5' ACG ACG ACG ACG 3' - 12 bases
maximum 3' annealing score (best < 9): 6 ✓
maximum annealing score (best < 15): 6 ✓
reverse primer
5' ACG ACG ACG ACG 3' - 12 bases
maximum 3' annealing score (best < 9): 6 ✓
maximum annealing score (best < 15): 6 ✓
forward/reverse primer
maximum 3' annealing score (best < 9): 6 ✓
maximum annealing score (best < 15): 6 ✓
difference tm (best < 3): 0.0 °C ✓
Recommendation
This primer pair can be recommended for use in PCR.
```

Result of a PCR viability check

OD Calculation

With "OD-Calc" you can calculate the optical density (OD), mass, amount and molecular weight (MW) of your oligo for specific experimental conditions.

Additionally you can decipher the appropriate oligo synthesis scale you need for your experiments.

Sequence

5' CAG TCA TGC AGT CAG TCA GAC TCG TAC GAC TGC GTA CG 3'

Experimental settings

number of experiments 10

amount/experiment 50 pmole

concentration* 0 ng/µl

OD 0.2

final amount 500.00 pmole

molecular weight 11663.5 g/mol

* required if amount per experiment is given in gram

Clear form Submit

Result of yield calculation

Dilution Calculation

With "Dilu-Calc" you are able to determine how much volume you need to dilute an oligo stock solution of higher concentration down to a specific lower concentration.

This application also supports different units for concentration and volume.

DiluCalc

This tool is designed to determine how much volume is needed to dilute an oligo stock solution of higher concentration down to a lower concentration. Stock volume and the final volume (default 100 µl) can be defined as well.

Sequence

5' tag tca tgc agt cag tca gac tgc tac gac tgc gta cg 3'

Dilution settings

Stock Concentration* 100 µM (pmole/µl)

Stock Volume 100 µl

Final Concentration* 10 µM (pmole/µl)

Final Volume 100 µl

Molecular weight** 11663.5 g/mol

* mandatory ** required if one of the concentrations is given in (n.p.s)g/µl

Result

To get a 100 µl 10 µM (pmole/µl) solution, mix 10.0 µl of 100 µM (pmole/µl) oligo stock with 90.0 µl of water or buffer

Clear form Submit

Result of dilution calculation

Feel Free to Contact Us

We invite you to send us your request using our online request form at www.eurofindna.com, by email or contact us directly by phone.



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