



## AiO, combining DNA/protein programs and oligo-management

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### ABSTRACT

**Summary:** AiO (All in One) is a program for Windows, that combines typical DNA/protein features such as plasmid map drawing, finding of ORFs, translate, backtranslate and high quality printing with a number of databases. These databases allow the management of oligonucleotides, oligonucleotide-manufacturers, restriction enzymes, structural DNA and program users in a multi-user/multi-group environment.

**Availability:** An AiO specific website, with the possibility to download is at: <http://134.99.88.55/aio/>

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**Supplementary Information:** Examples with screen shots—<http://134.99.88.55/aio/>: Manual (in PDF format)—<http://134.99.88.55/aio/manual.pdf>

The program AiO uniquely combines all the features of a DNA/protein program and those of database (DB) management. AiO is a program that, hopefully, can offer the advantages of such a gestalt and runs under Windows on a PC.

AiO is a multi-group/multi-user program that keeps track of who is using it and to which group this user belongs. Every user has her/his own DB with selected oligonucleotide sequences and access to the larger DB of the group (s)he belongs to. Since the ordering of new oligonucleotides can be done within AiO these DBs will be kept up to date automatically.

Other, general DBs are available to every user. An example of such a DB is the restriction enzyme DB. This DB is also automatically updated, albeit in this case by FTP. Furthermore, there are DBs for oligonucleotide manufacturers, scoring tables for proteins, users and structural DNA. This latter DB is used by the 'plasmid map' and 'linear map' programs. It contains the sequence of genes and functionally defined DNAs linked to graphical data. This combination allows the fully automatic recognition of known sequences and their representation in the resulting maps.

All DBs have their own editor included in AiO and changes can be monitored directly.

In AiO multiple files can be opened at the same time. All features of AiO (i.e. translate or map drawing) can be applied to all these open files. The DNA/protein part of the program opens sequence files directly in an editor that is, next to a full text editor, also especially designed for use with DNA files.

Within the editor several basic options can be selected directly, such as; selection of just a part of the sequence, selection of what should be included (restriction enzymes and/or oligonucleotides) and whether the DNA should be treated as a circular or as a linear molecule.

With a few button clicks it is possible to show the DNA sequence, the translation of it, the sites for restriction enzymes and those of the oligonucleotides all in the same figure.

The incorporated DNA programs enable the user to visualize: sequence with sites shown underneath (restriction and/or oligonucleotides), the coordinates of the sites, table of all possible PCR products, the frequency of sites, plasmid maps, linear maps, digests with restriction enzymes (simple, combined and/or partial), digests for plasmid mapping (automatically generated double digests), prediction of gel patterns, ORF finding, translation (just select an ORF by clicking on it), backtranslate and dotplot (Karreman, 1992). All relevant programs offer the choice to incorporate restriction enzymes and/or the oligonucleotides from either their own DB or that of the group. Graphic output is in PostScript and therefore of very high quality. For an overview of the use of several DBs by the various programs see Table 1.

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### REFERENCES

- Karreman, C. (1992) A dotplot program for the Atari ST, for the analysis of DNA and protein sequences. *Comput. Appl. Biosci.*, **8**, 75–77.

**Table 1.** The various DNA programs included into AiO and their use of the DBs.

<b>Programs</b>	<b>R.enzymes</b>	<b>Own oligos</b>	<b>Oligo bank</b>	<b>Structural</b>	<b>Matrix</b>
Sequence & site	+	+	+	-	-
Coordinates	(+)	+	+	-	-
Frequency	+	(+)	(+)	-	-
Plasmid map	+	+	+	+	-
Linear map	+	+	+	+	-
Digest	+	-	-	-	-
Triangle	+	-	-	-	-
ORF	-	-	-	-	-
Translate	+	+	+	-	-
Backtranslate	+	(+)	(+)	-	-
Dotplot	-	-	-	-	+

The DBs on the horizontal axis: R. Enzymes; general accessible DB with restriction enzymes, Own oligos; DB with oligonucleotides that is only accessible for the user, Oligo Bank; DB with all the oligonucleotides of the group, Structural; DB that links sequence data with graphical data, Matrix; homology-scoring tables for proteins.

Most programs have the option to show the sites for restriction enzymes and/or oligonucleotides. The programs that can depict these positions are marked by a '+' in the relevant column. Those programs that are not able to do this are marked with a '-'.

For some programs it makes little sense to show certain kind of sites, to indicate this fact the '+' is in brackets. As an example: it is possible to have a list of all oligos displayed that is ordered according to the frequency of which they will hybridize to the target DNA. As most oligos will be designed to bind uniquely, this list will contain no new information. However, when used with restriction enzymes this programs generates valuable data.

Some DBs are used by only a small number of programs, like the DB for structural DNAs and the homology scoring matrices. A number of DBs are not directly used in DNA related programs and are therefore not shown in this table.