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Adjustment of Standing Orders and Search archives

These brief instructions help you with the adjustment of standing orders and stored search archives in the DIMDI ClassicSearch: This enables you to exclude MEDLINE documents from the EMBASE search results when searching in both EMBASE and MEDLINE.

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The manufacturer Elsevier has expanded EMBASE by 2,000 journals with about eight million new documents. As of June 30th 2010, the database includes more than 7,000 journals.

The new entries come from the MEDLINE database of the U.S. National Library of Medicine (NLM). For this reason, standing orders and searches with DIMDI that are carried out simultaneously in both databases may now contain numerous duplicates among the search results.

With DIMDI, you can recognise the new documents in EMBASE by the entry „MEDLINE“ in the "Subunit" (SU) data field. In the DIMDI ClassicSearch, you can search for it by using the command FIND SU=MEDLINE.

To exclude MEDLINE documents from EMBASE for standing orders or in searches, use the search formulation NOT SU=MEDLINE. When carrying out a simultaneous search in MEDLINE and EMBASE, you can reduce your costs by using this search formulation **before** removing the duplicates.

To adjust your standing orders or stored search archive in the DIMDI ClassicSearch, proceed with the following steps:

1. **Starting DIMDI ClassicSearch**
2. **Please note that the following command is only used without opening a database:**

MODIFY SDI= *Name of the standing order/search archive*

- For search archives, you can then directly edit your search steps.
- For standing orders, you now get a selection to edit your search steps and modify the order parameters:
Select the editing of the search archive with **E** (Edit). After that, you can directly edit the search formulations in your standing order.

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3a Command for standing orders and stored search archives that search exclusively in EMBASE:

- Enter the line number of the final search step.
- Exclusion of MEDLINE documents from the final search step using the following command:
FIND formulation of final search step or formulation of search step that is referred to by the CH-DUP command NOT (BASE=EMBASE AND SU=MEDLINE)
- Finally, you can export the revised profile table for verification purposes with **L** (List).
- Now save the search archive with **S** (Save Profile).
- **Result:** The MEDLINE documents are removed from the EMBASE search in the final search step.

3b Command for standing orders and stored search archives that search in several databases (EMBASE and at least MEDLINE):

- Enter the line number of the final search step. If your search contains the command „Check Duplicates“ (CH DUP), enter the line number of the search step here that is referred to by the CH-DUP command.
- Now enter the following command to exclude MEDLINE documents:
FIND formulation of final search step or formulation of search step that is referred to by the CH-DUP command NOT (BASE=EMBASE AND SU=MEDLINE)
- Finally, you can export the revised profile table for verification purposes with **L** (List).
- Now save the search archive with **S** (Save Profile).
- **Result:** The MEDLINE documents are removed from the EMBASE search in the final search step.