USER GUIDE

Clicking the Menagerie button defaults to the General Search mode of the database.

# GENERAL SEARCH

Entry of a term into the search box on the homepage searches all fields for any part of that term. Results are broad but can include non-specific terms. Results can be further refined using COLUMN SEARCH, or downloaded as is in .csv format.

**Note:** The site allows download of a maximum of 5000 rows at once. Searches delivering results greater than this require refinement.

# COLUMN SEARCH

Terms are entered in specific columns and returned data is limited to those studies containing the search term in the selected column. Results can be further refined using action buttons below, or downloaded as is in .csv format.



**Search**: To search within a specific column. All data associated with a query entered into one column is returned.

**Modify last search**: Enter queries into other columns of returned dataset to refine the search.



**Perform Search:** to search following each query

**Omit/Include button**: Use **Include** to return data ***including*** query terms. Use **Omit** to return data ***excluding*** query terms.

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**Extend Found Set:** Will extend dataset by adding all data associated with an entered query term.



**Constrain Found Set:** Will limit dataset by returning only those data associated with an entered query term



**Find all:** This will return you to the original database (**Clear search**) so that you can do another search. Use scroll bar on right to scroll to top of dataset.

**Records Found:** Numerator indicates the number of rows returned. The number of abstracts (unique PMIDs) will be fewer as rows are duplicated to accommodate each returned variable associated with an abstract.

**Download Foundset:** Downloads data in .csv format. A maximum of 5000 rows can be downloaded. Use the Modify Search button to narrow dataset.

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# CONTENT OF THE DATABASE

**PMID, YEAR, TITLE:** Each abstract is identified by a unique PubMed identifier (**PMID**), its year of publication (**YEAR**) and its title (**TITLE**). Each successive column is populated by a term if found as given below. The cell is blank if no term is found.

**SPECIES:** Species (e.g. human, dog) mentioned in the abstract. Related species terms are mapped to a single term (e.g. cats, feline *→* Cat). Undefined species terms e.g. monkey, are mapped to the closest general term e.g. non-human primate.

**MODELS***:* Related terms are mapped to common identifiers (e.g.,1-methyl-4-phenyl-1,2,3,6 tetrahydropyridine and variants *→* MPTP) to facilitate subsequent analysis. Genetic model terms are captured as a group, and distinct models are not identified individually.

**INTERVENTIONS/DISEASE MODIFIER TERM***:* Any pharmaceutical, phytochemical, physical, genetic, behavioral or environmental entities that could alter the PD phenotype. Some imaging terms are also present. Data for this module is collected from the title only.

**INTERVENTION/DISEASE MODIFIER TERM\_ID**: Closely related intervention terms are mapped to a common identifier.

**TERM\_ID SOURCE:** Term identifiers are derived from one of the three sources: Medical Subject Headings (MESH), Unified Medical Language System Metathesaurus (META) or National Center for Biotechnology Information (NCBI) human gene identifiers.

Data can be extracted at either level according to user preference.

**FUNCTIONAL OUTCOME TERM**: These are defined as measurable variables that reflect the eﬀect of an intervention on a living organism (e.g., cognition, motor tests or survival).

**FUNCTIONAL OUTCOME MEASURE USED**: If a functional outcome term was identified in the abstract, this column contains **YES**. If not, it is left blank.

**OVERALL OUTCOME***:* The conclusion of the study (as defined by the authors) regarding the overall potential of the intervention to influence trajectory of the disease. Four categories are used: those with therapeutic promise (POSITIVE), those with adverse effects (NEGATIVE), those with both promising and adverse effects (MIXED) and those in which outcomes are indeterminate (OTHER).

**GENE/PROTEIN TERM***:* Gene or protein terms identified in the abstract.

**GENE/PROTEIN TERM\_ID:** Synonyms for gene terms are mapped to NCBI or META gene identifiers according to species.

Data can be extracted at either level according to user preference.