

# MarinLit

**A comprehensive database of the literature for  
Marine Natural Products**

**Maintained at the University of Canterbury**

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## Installation of MarinLit Files

The MarinLit files are available for downloading from a web site. Appropriate installation instructions will be included separately with each download.

## Navigation in MarinLit and On-line Help

Often when MarinLit is being used, two or more screens may be visible, but only the last one opened will accept input, permitting return to the previous screen. If an 'inactive' screen is accidentally clicked in, the 'active' screen may disappear behind and further navigation becomes impossible. The 'active' screen may be recovered however by pulling down on the **Windows** menu and selecting the checked item. MarinLit can only be closed by using the **QUIT** button on the **Main Display**. Context-sensitive help is available at all times by using **control-h**.

### The Main Display (home screen)

The screenshot shows the MarinLit main display window. It is divided into several sections:

- BIBLIOGRAPHIC DATA:** Title: Eudistomins C,E,K, and L, potent antiviral compounds containing a novel oxathiazepine ring from the Caribbean tunicate Eudistoma olivaceum. Authors: Rinehart KL, Kobayashi J, Harbour GC, Hughes RG, Mlzsak SA, Scahill TA. Keywords: 2D nmr. Journal: J. Am. Chem. Soc. vol: 106, year: 1984, issue: , pp: 1524 - 1526, links: 2335.
- COMPOUND DATA:** A table with columns: trivial names, #, name, formula, mass, UV  $\lambda_{max}$ , and (log  $\epsilon$ ).
 

trivial names	#	name	formula	mass	UV $\lambda_{max}$	(log $\epsilon$ )
eudistomin	N 1	eudistomin C	C <sub>14</sub> H <sub>16</sub> N <sub>3</sub> O <sub>2</sub> S	369.0147	226	287
			UV in MeOH		(4.37)	(3.90)
	N 2	eudistomin E	C <sub>14</sub> H <sub>16</sub> N <sub>3</sub> O <sub>2</sub> S	369.0147		
	N* 5	eudistomin K	C <sub>14</sub> H <sub>16</sub> N <sub>3</sub> O <sub>3</sub> S	353.0198		
	N 6	eudistomin L	C <sub>14</sub> H <sub>16</sub> N <sub>3</sub> O <sub>3</sub> S	353.0198		
- TAXONOMY DATA:** A table with columns: phylum, class, order, family, genus, species.
 

phylum	class	order	family	genus	species
Chordata	Ascidiacea	Enterogona	Polycitoridae	Eudistoma	olivaceum *

At the bottom, there are navigation buttons: **about Marinlit**, **Article # 18**, **browse**, navigation arrows, **SEARCH**, and **QUIT**.

The screen above is the main display screen of the MarinLit database system.

Click on **about MarinLit** (lower left corner) to see information about this version.

One article is displayed at a time. To view the next article click on **>** and the previous article by clicking **<**. Clicking on **|<** or **>|** will display the first or last article of the database respectively.

To view a specific article click on the article number (lower left). The **Article Selection** screen will appear. To move to any article enter the number required and click on **continue** or press **enter**.

The Article Selection dialog box is titled "Article Select...". It contains the text "Enter Article # to go to" above a text input field. Below the input field are two buttons: "continue" and "cancel".

In the **BIBLIOGRAPHIC DATA** area is the **Keywords** pop-up list. Only the first keyword is displayed but a full pop-up list will appear if you click on this box and hold down the mouse button. The \* next to **Article #**, on the main display, indicates that the files are ordered by article #. If you click on the left end of the **Authors'** field, the files will be ordered alphabetically by first author's name, and a \* next to the **Authors'** field will appear. Click on **Article** (lower left) to reset the order to article #.

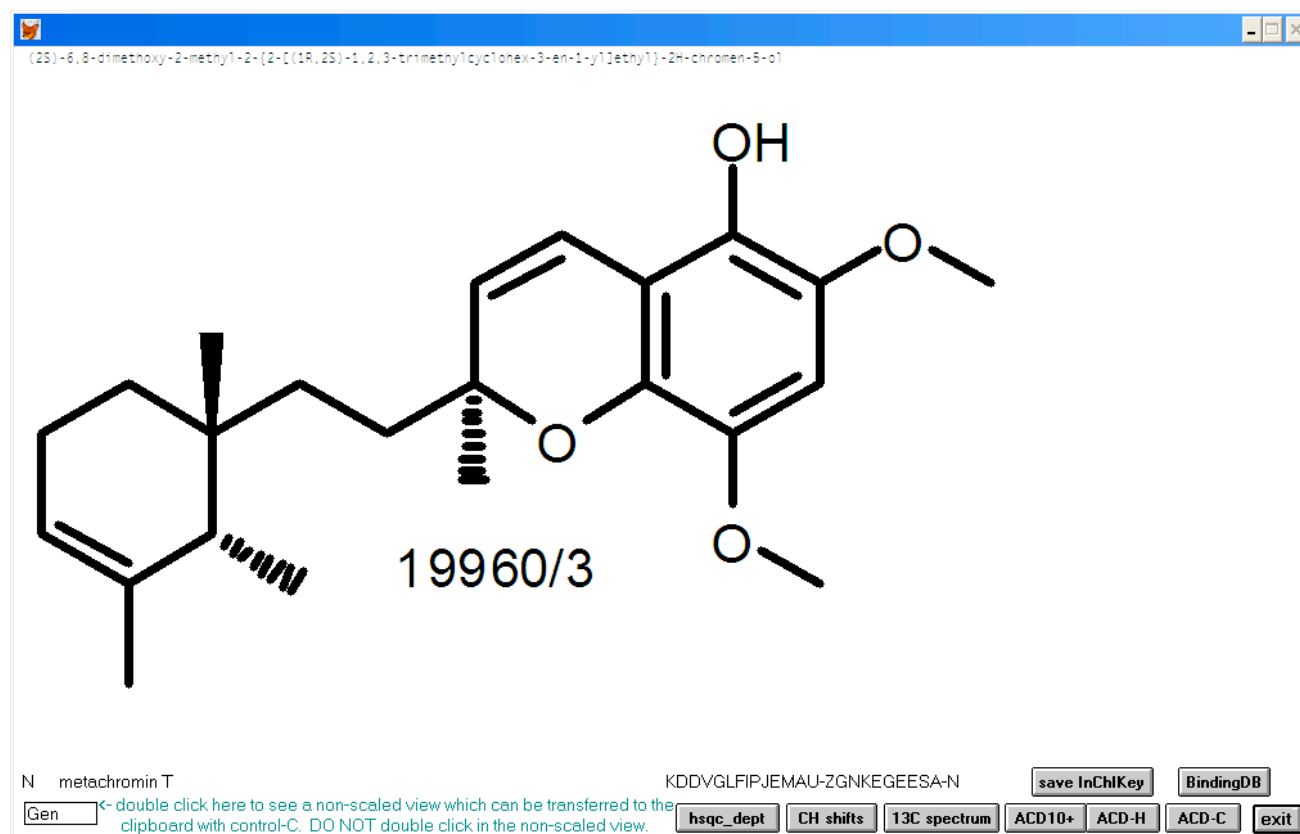
In the **COMPOUND DATA** area, an N (new compound) M (new to marine) or R (revised structure or stereochemistry) preceding each compound listing identifies the status of the compound. The # that follows is the compound number as it appears in the reference, followed by its trivial name (if one has been assigned). An \* next to any of N M or R indicates that the structure for that compound has been revised in a later publication. Access to that publication can be made by double clicking on the number in the **links** box in the **BIBLIOGRAPHIC DATA** section. In the example shown, compound 5 has the status N\* and the structural revision is contained in article # 2335.

In the **TAXONOMY DATA** section, a \* at the end of an entry indicates the specie(s) that have provided any compound(s) with status N or M showing in the **COMPOUND DATA** section. To access the taxonomy primer, click on **taxonomy scheme**. See page 11 of this manual for information on the use of this scheme.

The **browse** or **SEARCH** screens can be accessed by clicking on these words respectively. When in the browse mode, only the first sections of some fields will be visible. To see all of each field, click on the **Browse** item in the menu bar and pull down to **Change**. Pull down again to **Grid** to revert to browse mode.

## Viewing or printing structures

A double click on any one compound number in the **COMPOUND DATA** section will display the structure of that compound (example shown below). Clicking on the box on the bottom left of the screen that appears (the box containing **Gen**) brings up another window from which the structure can be copied to the clipboard for pasting into other applications. One example of this is pasting into Word Pad from where the picture may be sent to a printer.



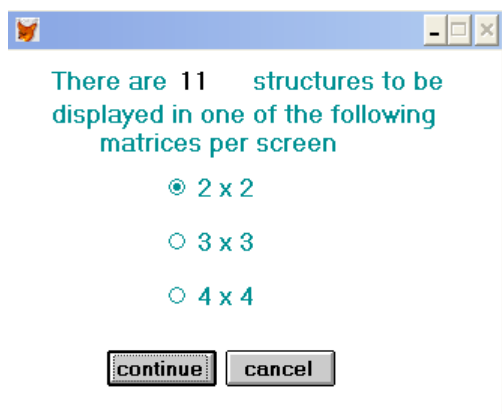
**WARNING:** Do not click in the non-scaled view as this will cause MarinLit to crash (unresolved problem with FoxPro). If you want to copy the structure simply use **control-c**.

The standard InChIKey for the structure is shown. Clicking on **save InChIKey** will store this value for later use in the search process (see later, page 6).

Clicking on **BindingDB** will direct you via the web to [www.bindingdb.org](http://www.bindingdb.org). BindingDB is a public, web-accessible database of measured binding affinities, focusing chiefly on the interactions of proteins considered to be drug-targets with small, drug-like molecules. There are >5,000 compounds in MarinLit that are associated with >7,000 identical or similar compounds in BindingDB. When viewing one of these ~5,000 compounds in MarinLit, you can now access relevant experimental  $K_i$ ,  $K_D$ ,  $IC_{50}$  etc data in BindingDB. Before using this button, ensure that Internet Explorer is activated. (Thanks to Mike Gilson and his team at UCSD for the access to BindingDB.)

If you have subscribed to the ACD/Labs NMR data option, you will also be able to view the calculated  $^{13}\text{C}$  and  $^1\text{H}$  chemical shift data (click on **CH shifts**) and the IUPAC name for the displayed structure. Clicking on  **$^{13}\text{C}$  spectrum** will display a stick spectrum for the  $^{13}\text{C}$  shifts, colour coded according to carbon type. You can also link to the ACD Predictors (provided you have your own copies) to view the spectra and assignments for each compound displayed, as well as the ACD/Labs calculated properties for the compound. Use the **ACD10+** button for access to Predictor versions 10 or later, otherwise use the **ACD-H** or **ACD-C** buttons. The **hsqc\_dept** button accesses a simulated 2D hsqc dept spectrum from the ACD chemical shift data.

To view all structures for the current article, click on **all structures** in the main display screen. A screen will appear similar to this one:



**Print** **text file** **Cancel**

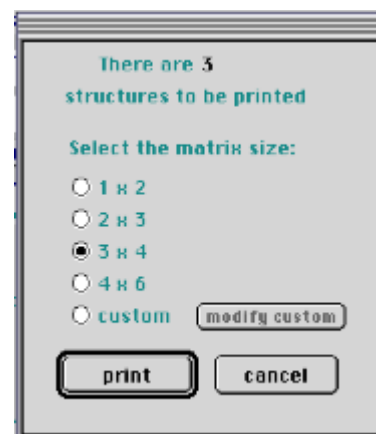
$^{13}\text{C}$  and  $^1\text{H}$  Chemical Shifts for 19960/3  
ACD ID# = 18920  
metachromin T

1	(2)	22.8 ± 3.7	2.01 ± 0.73	2.12 ± 0.73
2	(1)	120.0 ± 4.8	5.29 ± 0.39	
3	(0)	136.2 ± 5.4		
4	(1)	46.7 ± 5.3	1.85 ± 0.73	
5	(0)	33.4 ± 4.1		
6	(2)	33.3 ± 4.1	1.17 ± 0.73	1.32 ± 0.73
7	(3)	22.1 ± 2.5	1.63 ± 0.27	
8	(3)	14.9 ± 2.9	1.03 ± 0.27	
9	(2)	30.4 ± 4.4	1.15 ± 0.45	1.39 ± 0.45
10	(3)	24.8 ± 3.9	0.77 ± 0.27	
11	(2)	34.8 ± 3.1	1.62 ± 0.45	1.70 ± 0.45
12	(0)	78.0 ± 4.1		
14	(1)	130.4 ± 5.4	5.74 ± 0.41	
15	(0)	136.1 ± 4.3		
16	(0)	110.2 ± 3.8		
17	(1)	118.3 ± 5.5	6.56 ± 0.45	
18	(0)	142.1 ± 3.8		
19	(1)	100.5 ± 3.8	6.27 ± 0.41	
20	(0)	140.8 ± 3.8		
21	(0)	131.4 ± 4.4		
22			9.48 ± 4.62	
24	(3)	56.5 ± 1.1	3.82 ± 0.22	
26	(3)	56.6 ± 1.1	3.74 ± 0.22	
27	(3)	26.1 ± 2.9	1.39 ± 0.27	

This screen tells you how many structures there are to display, and allows you to choose between three matrix sizes for the structures display. Eg. a 3x3 matrix will show a maximum of 9 structures on the screen at a time. Once you have made your selection click on **continue** or press return. The structures will now be displayed in the requested matrix.

If there are more structures than will fit on one screen you can flip through screens by clicking on the **next** or **previous** buttons. If the detail of any one structure is unclear because of the size of presentation, then clicking on that structure will enlarge it to a full screen size.

Clicking on **print**, below **all structures**, will generate the interaction shown alongside, from which you may select the matrix size in which the structures will be printed on each page. Setting the custom radio button activates the **modify custom** button. This allows access to the FoxPro Report Generator in which you can design your own custom layout for printing structures. Accessing the **Page Layout** option will permit you to use the Page Setup option for setting paper size etc. Any changes you make to the custom report will be retained for the next use. If you experience trouble with black backgrounds when printing, set your system print dialog box to show 'Color/Greyscale' under 'Color matching'.



## Searching

The main function of the database is, of course, the retrieval of selected data. The following sections describe how searching with a variety of criteria may be achieved, and the results presented.

The following screen allows construction of a search profile, which can include searches on bibliographic, compound, substructure and taxonomic data.

The screenshot shows a window titled "Search Profile" with four main sections:

- BIBLIOGRAPHIC DATA**: A large empty text box with a "clear all" button to its right.
- COMPOUND DATA**: A text box with "AND" and "(AND operations only)" above it.
- TAXONOMY DATA**: A text box with "AND" and "(OR operations only)" above it, and a "do search" button to its right.
- SUBSTRUCTURE**: A text box with "AND" above it. Below the box is a message: "Use ChemOffice to carry out a substructure search. When completed, use the Collect script in Chemfinder to create a results file in tfr.bt. Then use **recover results** to retrieve these results. There are currently 0 structures in the search results file." To the right of this section is a "home screen" button.

Any combination of these four types of information can be searched at the same time. The search profiles for each of the first three areas are generated in separate screens that are accessed by clicking on the respective headings.

The screenshot shows a search profile construction screen for BIBLIOGRAPHIC DATA. The search query is: "Year > 1987 AND "wright" CONTAINED IN Authors AND Keys CONTAINS "2D nmr"".

Below the query, there are three buttons: "Journal", "Key", and "Trivial name".

Below these buttons, there are three columns: "field", "condition", and "match".

Under "field", there is a dropdown menu showing "Authors".

Under "condition", there is a dropdown menu showing "contains".

Under "match", there is a text box containing "wright".

To the right of the "match" text box is an "Add" button.

Below the "Add" button, there are three buttons: "And", "Or", and "Not".

Below these buttons, there are two buttons: "(" and ")".

At the bottom of the screen, there are three buttons: "clear all", "clear last", and "accept".

In the **BIBLIOGRAPHIC DATA** section, any of the bibliographic fields can be selected by pulling down on the **field** pop-up menu (initially showing **Article**). A condition can then be chosen in the same manner by pulling down on the **condition** pop-up menu (initially showing **{number} equals**). Enter the match required in the **match** entry box to the right of the **condition** pop-up menu, and click on the **Add** button. Matches specified in this way are not case-sensitive. Any combination of these criteria can be added to the profile using the logical operators shown, which can also be nested using the parentheses provided. Journal or key word criteria can also be added

from pop-up menus. Trivial names associated with an article (not a specific compound) can be selected from a pop-up menu or a partial name can be selected from the **field/condition/match** menus and entry box. The bibliographic search profile can be deleted with the **clear all** button, or sequentially from right to left with the **clear last** button.

As an example, the profile specified in the screen shown above will search for all articles published after 1987, with an author named Wright, that in some way deals with two dimensional NMR. If **clear last** were clicked the condition 'Keys CONTAINS "2D nmr"' would be deleted, and if clicked again the operator 'AND' would be removed, etc.

**COMPOUND DATA** may be searched for by making appropriate entries in the following screen.

The screenshot shows a search interface with the following elements:

- Formula contains:** A text input field with a dropdown menu and an 'and' operator. Below it, a note says '(order is C,H then alphabetical)'. A 'clear formula' button is to the right.
- Mass from:** Two numeric input boxes (0 and 9999) with 'to' between them. A 'clear mass' button is to the right.
- UV maximum:** A numeric input box (0) followed by a plus-minus sign and another numeric input box (5). A 'clear UV' button is to the right.
- Name contains:** A text input field. A 'clear name' button is to the right.
- Number of functional groups:** A text input field. A 'clear groups' button is to the right.
- Functional Group Selection:** A dropdown menu showing 'all C=C', followed by 'from' and 'to' numeric input boxes (0 and 0) and an 'enter' button.
- Status Selection:** A list of radio buttons: 'all types' (selected), 'new', 'new to marine', 'revised', 'new\*', 'new to marine\*', and 'revised\*'.
- 13C shifts:** A numeric input box (0) followed by 'minimum hits for match (0 will require all)'. A 'clear shifts' button is to the right.
- InChIKey:** A text input field. A 'recover last set' button is to the left, and a 'clear InChIKey' button is to the right.
- Bottom Buttons:** 'recover InChIKey', 'accept', and 'clear all'.

Search criteria based on compound data are selected by putting entries into any of the boxes above. AND will be added automatically where needed when the **accept** button is clicked.

Exact or partial formulae can be entered. The chemical symbol does not have to be followed by a number, although it can be; ie C15, As or H32O4 are all valid. Note however the required order - C,H and then alphabetical. Therefore the H32O4 will not succeed if Br is present. Entries are not case sensitive. No more than two formula fragments can be specified per search profile.

The **Mass between** boxes are initially set at 0 and 9999. If the 0 were changed to 350, say, then all compounds with mass > 350 would be located, while if the 0 were left, and the 9999 changed to 400, say, then all compounds with mass < 400 would be found. A narrow range of masses would be located if the 0 were changed to 450 and the 9999 to 470, say. No mass search will be made while 0 and 9999 are present in the selection boxes.

The **UV maximum** boxes are set by default to 0 ± 5, in which condition no UV search will be made. Entering 240 ± 10 will locate any UV maximum between 230 and 250 nm. Additional UV maxima can be included using the **refine uv** option, which will appear in the **Output Selection** screen (see page 9) once the search on the initially chosen UV maximum is completed.

A compound name or part thereof can be entered in the **Name contains** box.

Compounds with a particular status N (new), M (new to marine) or R (revised structure or stereochemistry) can be selected by clicking the appropriate button. Note the N\*, M\* and R\* options for compounds whose structures have been revised or further revised in later articles. The default setting is all compound types.

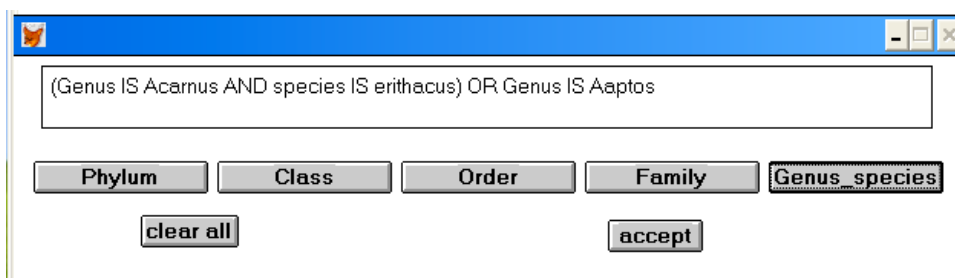
**Functional groups** can be searched for by selecting a number for each type, or a range of numbers for each type. For example, if the <sup>1</sup>H NMR spectrum shows 3 singlet methyl resonances, then select 'singlet methyl' from the functional group selection pull-down menu, and enter 3 into the adjacent 'from' box. Click on **enter**. Unless some

other number is placed in the 'to' box, then 3 will be inserted when the compound search profile is created. If one of these singlet methyls is due to OCH<sub>3</sub>, then place a 1 in the 'from' box adjacent to an 'O-methyl' selection. 'all C-O' includes all alcohols, ethers (counts as 2), esters and lactones (count as 1, on the alkyl side), carboxylic acids etc. 'all C=O' includes ketones, aldehydes, amides, esters etc. 'all C=C' excludes benzene and pyridine ring double bonds. This functional group search is also available with a more extensive range of features and a more convenient selection interface in the **ChemFinder** structure files for MarinLit. See the later section (page 8) on **Searching by Substructure**.

If an InChIKey has been saved from an earlier structure display, this may be transferred into this screen with the **recover InChIKey** button. Removing all the characters in this key following and including the first – will permit searching for all compounds with the same planar structure as that from which the InChIKey was obtained. InChIKey values may also be entered manually.

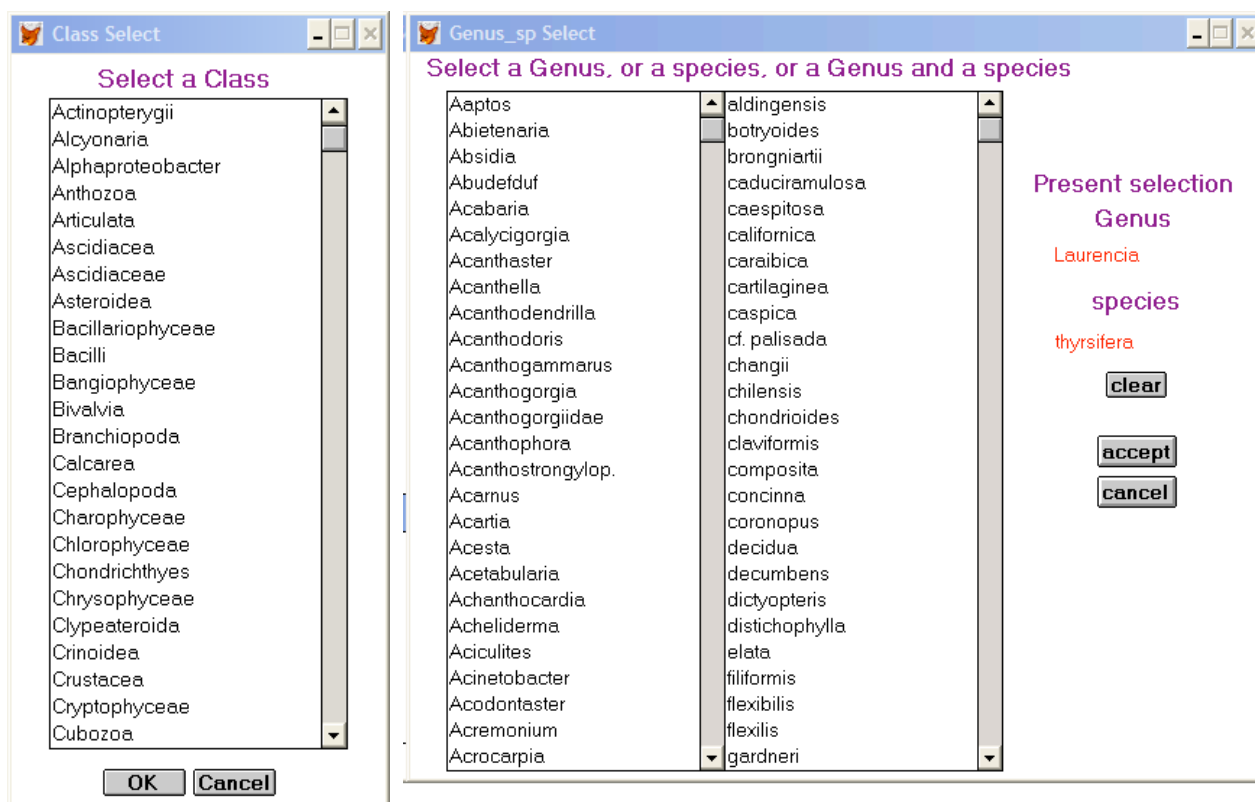
<sup>13</sup>C and <sup>1</sup>H chemical shift data are provided for all compounds. These data are provided by ACD/Labs. For some compounds, the data are actual, but for most they are calculated by ACD/Labs. Patterns of <sup>13</sup>C shifts may be searched for by entering x1,y1,x2,y2, .... where x is an integer shift value and y is the number of attached Hs. If y is not known, enter x1,,x2,,.... For example, 125,1,205,0,134,,42,2. A minimum number of hits may be specified for obtaining a match, for example if 8 shift values are entered, 6 may be entered as the minimum number of matches required. A 0 for minimum hits will require all shifts to be matched. Where the data are calculated, a range of 'reliability' is included, so that an entered value of 120 would be matched by 118+/-3. The minimum range is +/- 2.5, even for actual data. **NOTE:** this feature is only available if the ACD/Labs database file has been subscribed to with MarinLit. However, the data are always included for the first 100 articles, so that this option can be tried out on the limited data set.

In the **TAXONOMY DATA** section, any combination of taxonomic criteria can also be added, but in this case OR will be included automatically, except for the case of **Genus AND species**. To select a taxonomic criterion click on any of the buttons, and a selection screen will appear. As an example the **Class Select** screen is shown on the next page.



To select an item you can scroll using the scroll bar on the right of the screen, or alternatively you can type the first few letters of the name you require. When you have found the item that you want you can select it by double clicking with the mouse, or clicking once to highlight the selection and then pressing the **enter** key or clicking on **OK**.

Also shown on the next page is the **Genus\_sp Select** screen. This is a little different in that both the Genus and species are selected from the same screen. This screen enables you to select either a genus, a species, or a genus and species for searching. You can select by double clicking on the required genus and/or species. If you make a mistake or change your mind you can click on the **clear** button. **accept** will add your selection to the search profile, and **cancel** will take you back to the search profile screen without adding your selection. In the example below, the organism *Laurencia thysifera* is about to be selected.



## Searching by Substructure

Switch to the ChemFinder application in ChemOffice by double clicking on the **marinlit.cfw** file in the **mlitcf8** directory. Carry out a substructure search in the MarinLit ChemFinder files, and then select **collect** from the **Scripts** menu. This will create a text file **tfr.txt**. Return to the substructure search screen in MarinLit, and click on **recover results**. You will be asked to locate the file **tfr.txt**, the location of which will depend on how you opened the ChemFinder application. For example, if you had opened ChemFinder by double clicking on **marinlit.cfw** in the **mlitcf8** directory, then the **tfr.txt** file will appear in that directory.

SUBSTRUCTURE AND

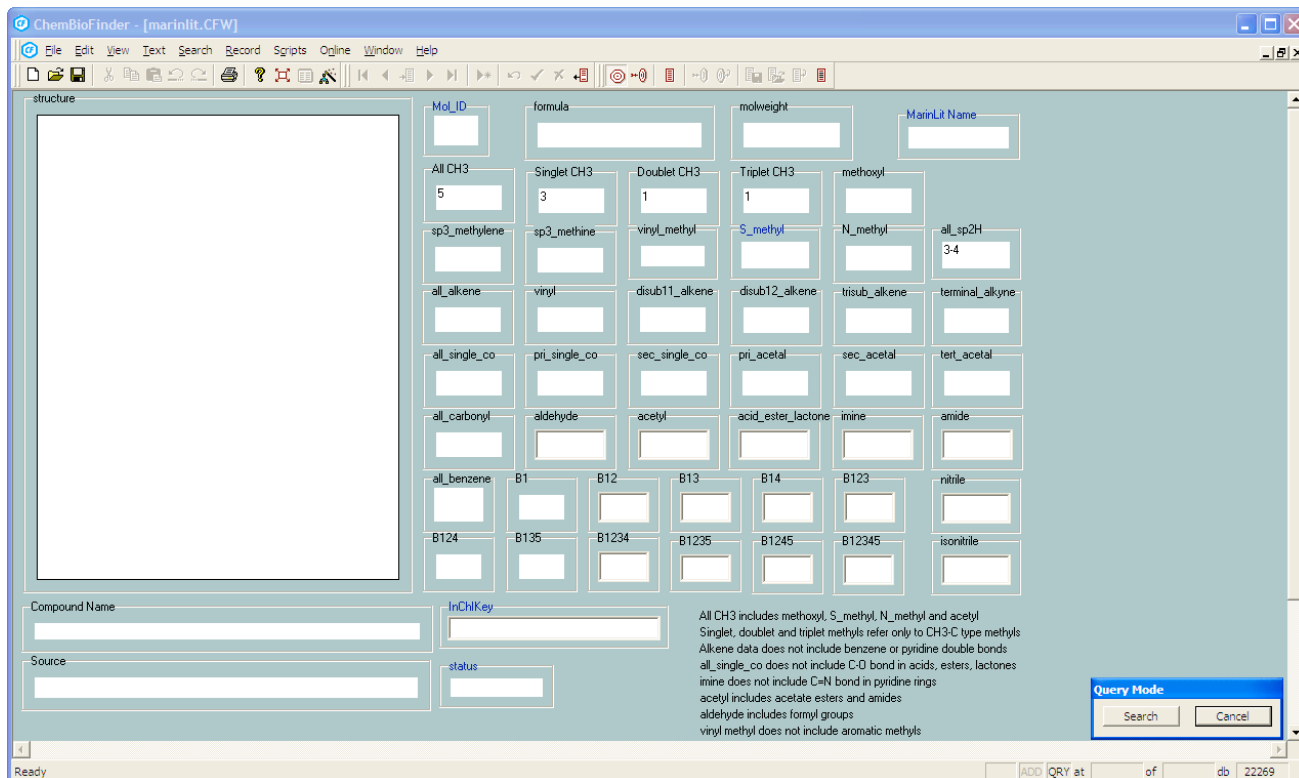
Use ChemOffice to carry out a substructure search. When completed, use the Collect script in Chemfinder to create a results file in tfr.txt.

Then use **recover results** to retrieve these results.

There are currently 4 structures in the search results file.

As noted earlier, the ChemFinder MarinLit file may also be used to set up a functional group search more conveniently than from within the **COMPOUND DATA** selection window. The results from such a search will be contained in the **tfr.txt** file that can be recovered into MarinLit to become part of the total search profile required. Selecting functional groups by this method can be done with or without a substructure being constructed in ChemFinder.

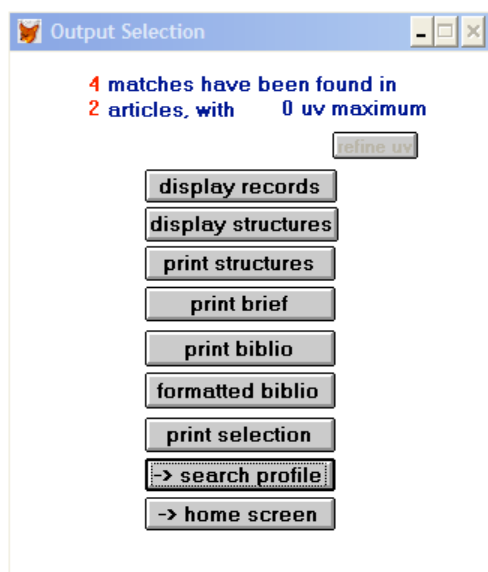
The following example shows a selection being made of 5 methyl groups, of which 3 are singlets, 1 is doublet and 1 is triplet, together with 3-4 sp<sup>2</sup> Hs. This profile gave 19 hits.



Once all the criteria have been entered, initiate a search with **do search**. Any conditions specified in the Bibliographic, Compound and/or Taxonomy selection windows will be included in the search profile along with the substructure and/or functional groups selected in ChemFinder.

## Selecting Search Result Output

When a search is completed, the **Output Selection** screen will appear.



At the top of this screen you are shown the number of records that matched the search profile and the number of articles that contained matching records. You may notice that sometimes the number of matches is greater than the number of articles, which is due to multiple compound matches in one or more articles. This screen allows you to select in what manner the results of a search will be viewed. **display records** shows the results in the same manner as the home screen display. If a UV maximum was selected in the search criteria, the **refine uv** button will be active. This feature allows up to three more UV criteria to be searched for amongst the matches from the first search. You can enter a new maximum, or alternatively reduce or enlarge the range of previous criteria.

Structures from matching articles can be viewed or printed. Clicking on **display structures** or **print structures** will take you to matrix selection screens as described in the Main display section earlier in this manual.

**-> search profile** will take you back one screen to the Search Profile generator, while **-> home screen** will take you back to the main MarinLit display.

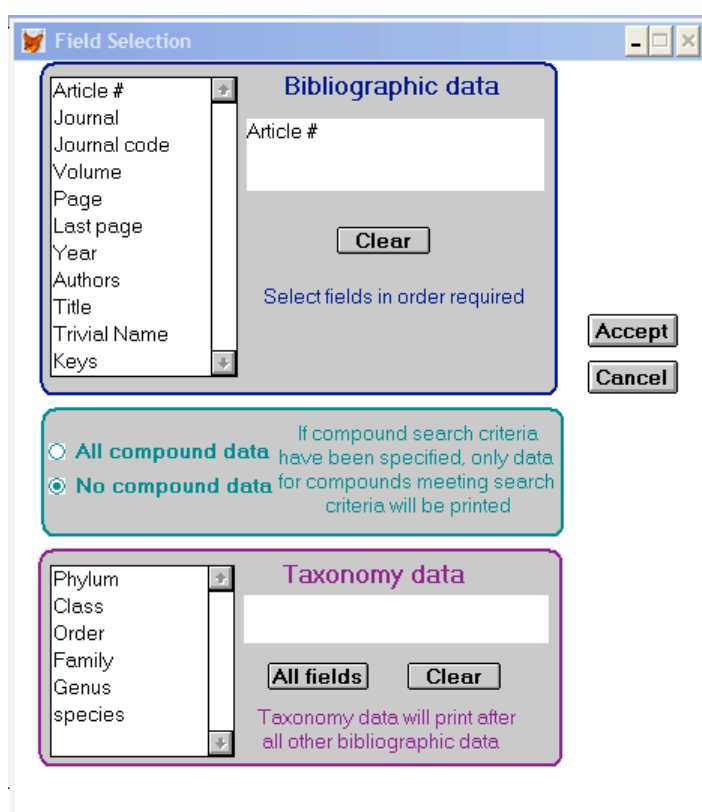
## Printing of Search Results

Hard copy of results can be obtained through four options; **print structures** (see above), **print brief**, **print biblio** or **print selection**.

**Print brief** gives a printout with one line per article of selected bibliographic data. The fields that are printed by this option are: Article #, Journal code (CAS CODEN), Volume, First page, Last page, Year and a truncated Title. For a more descriptive printout choose **print biblio**, which prints: Article #, Journal, Volume, First page, Last page, Year, Authors and Title.

**Formatted biblio** creates a text file with the bibliographic data formatted as required by a particular journal. The present selections are for ACS, RSC or Tetrahedron. Choosing any other journal type will output in CAS format. This CAS file can be read into EndNote using the CAS filter. The text file will need to be edited for embolding and italicising as appropriate. Some Authors names will not format correctly, so a careful check should be made of the results.

For a custom printout **print selection** allows you to choose any combination of the MarinLit fields to print. The **Field Selection** screen (see below) allows you to choose which fields from records with matching search results you would like to print.

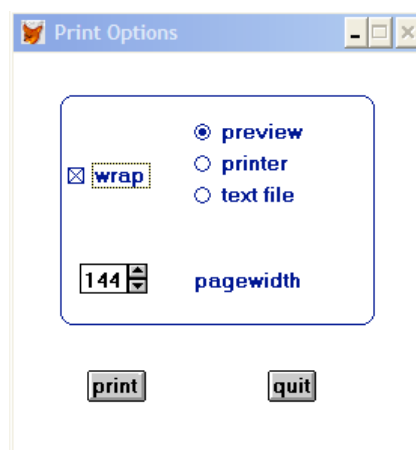


To select fields from the bibliographic data, double click on the required field names in the order required. Article # will appear as a default first field but if desired, it can be cleared by clicking on the **Clear** button first.

There are two options for compound data printout; **all data**, or **no data**. These are selected by clicking on the buttons on the middle left.

Taxonomy data to be printed can be selected, field by field, in the order required, or **All fields** can be selected by clicking on that button. The taxonomy selections can also be cleared independently of the bibliographic field selection.

Once you have the desired field selection click on **Accept** to commence printing procedures. The following screen will appear:



This screen is the same one that is

displayed after clicking on **print brief** or **print biblio**. It allows selection of the output device, either to the screen (preview), to the current printer, or to a text file. Once you have made one selection you can also make another without leaving this screen. For example, you can choose preview before sending the results to the printer so as to check that everything is in order. The wrap button allows you to choose whether there will be wrapping within fields, and you can set the pagewidth (in characters) to suit your printer.

**NOTE:** as with all print operations in MarinLit, difficulty may be experienced on some computers as not all systems have printer drivers that are compatible with the FoxPro software. If the output selected is text, then output should be made to a text file that can then be opened in another application such as Word for then printing. If you create a text file, you will be asked to select the directory in which it is to be saved, and to give the file a name.

# Taxonomy Features

## Taxonomy Scheme

The taxonomy entries in MarinLit, particularly at the Phylum level, are being progressively realigned to be consistent with the schema of the Catalogue of Life ([www.catalogueoflife.com](http://www.catalogueoflife.com)). In this screen you can view taxonomy connections and build a taxonomy tree, working from anywhere in the taxonomy hierarchy. Double clicking on any Phylum will display all Classes, Orders, Families, and Genera belonging to that phylum, each in alphabetical order. Species are not shown, as they would be too numerous. At any point the screen can be changed back to its original display by clicking on **reset**.

To work from the other end, double click on a genus. The Family, Order, Class and Phylum to which that genus belongs will be displayed, as well as all species in the database that belong to that genus. If you double click on a species the numbers of all articles involving that organism will be displayed. Clicking on any article number will show the title of that article.

Phylum	Class	Order	Family	Genus	Species
Mollusca	Gastropoda	Nudibranchia	Chromodorididae	Chromodoris	cavae
Actinobacteria	Actinobacteria	Aciculata	Acanthaceae	Aaptos	annulata
Annelida	Actinopterygii	Acoela	Acanthasteridae	Abietenaria	cavae
Arthropoda	Alcyonaria	Acrosiphonales	Acanthochitonidae	Absidia	elisabethina
Ascomycota	Alphaproteobacter	Actinaria	Acanthogorgiidae	Abudefduf	funerea
Bacillariophyta	Anthozoa	Actiniaria	Acamiidae	Acabaria	geminus
Bacteroidetes	Articulata	Actinomycetales	Acartiidae	Acalycigorgia	glenei
Basidiomycota	Asciacea	Agelasida	Acmaeidae	Acanthaster	glenei
Brachiopoda	Astroidea	Alcyonacea	Acrochaetiaceae	Acanthella	hamiltoni
Bryozoa	Bacillariophyceae	Alismatales	Acroporidae	Acanthocardia	inopinata
Chloroflexi	Bacilli	Alteromonadales	Acrosiphoniaceae	Acanthodendrilla	inornata
Chlorophyta	Bangiophyceae	Amphidiscophora	Acrotylaceae	Acanthodoris	lochi
Chordata	Bivalvia	Amphinomida	Actiniidae	Acanthogammarus	luteorosea
Ciliophora	Branchiopoda	Amphipoda	Adapedonta	Acanthogorgia	macfarlandi
Cnidaria	Calcarea	Anaspidae	Aeolidacea	Acanthogorgiidae	maridadius
Cryptophyta	Calcaronea	Anaspidea	Aequoreidae	Acanthophora	marislae
Ctenophora	Cephalopoda	Anguilliformes	Agavaceae	Acanthostromylop.	norrisi
Cyanobacteria	Charophyceae	Antipatharia	Agelasidae	Acanthostylotella	
Dinophyta	Chloroflexi	Aplysiacea	Aglaidae	Acanthus	
Echinodermata	Chlorophyceae	Apodida	Aglaopheniidae	Acanus	
Euglenozoa	Chondrichthyes	Archaeogastropoda	Aiptasiidae	Acartia	2830
Euryarchaeota	Chrysophyceae	Architaenioglossa	Alariaceae	Acesta	4458
Firmicutes	Ciliatea	Arhynchobdellida	Alcanivoraceae	Acetabularia	5938
Haptophyta	Clypeateroidea	Arthrosporae	Alcyonidiidae	Acheliderma	
	Crinoidea	Ascoglossa	Alcyoniidae	Achlionice	
	Crustacea	Asparagales	Aldisidae	Aciculites	
	Cryptophyceae	Aspidochirotida	Aliciidae	Acinetobacter	
	Cubozoa	Astrophorida	Alteromonadaceae	Acodontaster	
	Cyanophyceae	Axinellida	Alvinellidae	Acremonium	

This feature can also be accessed from any of the intermediate groupings (eg class, order, family).

The example above shows a screen where the Genus *Chromodoris* was selected. Then the species *cavae* was selected to give the numbers of the articles appearing in MarinLit which deal with *Chromodoris cavae*.

At any point in the selection process a taxonomy tree can be created by clicking on **build tree**. This tree shows the connections between Phyla, Classes, Orders, Families, Genera and Species in the selection(s) you have made.

Some of the operations in this screen may be slow.

## Selecting Taxonomy Tree Output

If the build tree option has been chosen, then this screen permits selection of the manner in which the taxonomy tree will be displayed. You can display it on the screen, print it, or create a text file on disk simply by clicking on the appropriate button.

## Errors

There is no guarantee that the MarinLit program is absolutely free of errors, as not all combinations of the search capabilities may have been exercised. However, if an unrecoverable error should occur, diagnostic information will be reported to the screen. It would be most helpful if you could send a note if this happens (<mailto:john.blunt@canterbury.ac.nz>), stating what you were trying to do, and what diagnostic information appeared.

It would also be appreciated that you communicate any errors in the data that you encounter – these can then be fixed for the next update.