

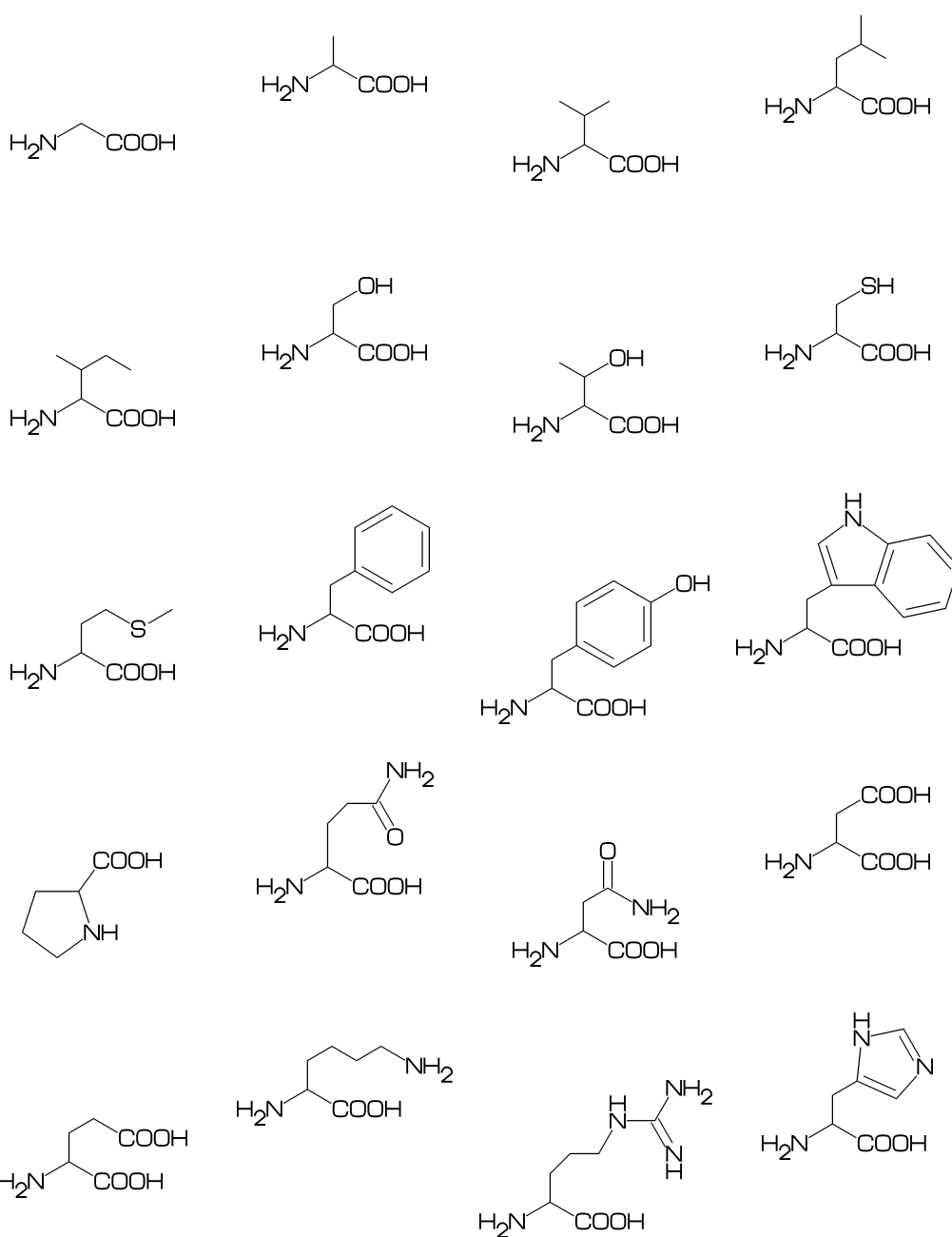
# Molecular Coding Format manual

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Located at <http://www.ctan.org/pkg/mcf2graph>

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# 1 Introduction

Molecular Coding Format(MCF) is new linear notation represent chemical structure diagrams. This 'Coding' is named from coding(programing) technique like addressing,grouping,macro,etc. There are no Meta language commands in MCF. mcf2graph convert MCF file to graphics file pk font,PNG,SVG,EPS or MDL MOL file.

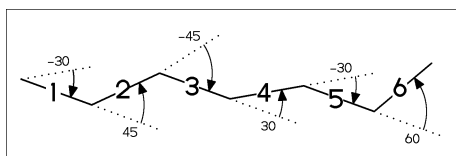
## 2 MCF syntax

### 2.1 Make bond

#### 2.1.1 Chain

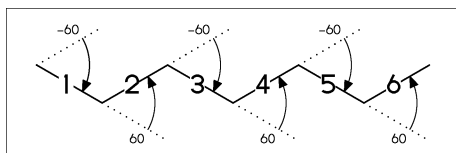
real number plus (+): Counterclockwise  
real number minus(-): Clockwise

<10,-30,45,-45,30,-30,60



! : take value 60 or -60 depend on current angle and enviroment  
!6 : !,!,!,!,!,!

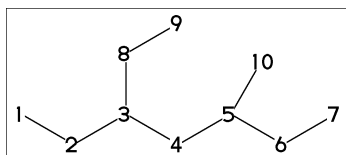
<30,!,!,!,!,!,!  
<30,!6



#### 2.1.2 Jump and branch bond

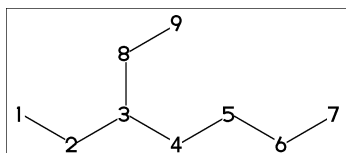
n:@ : Jump to An  
\*\* An: atom number(-999<=n<=4095)

<30,!6,3:@,0,!,5:@,-30



3:\ : 3:@,0

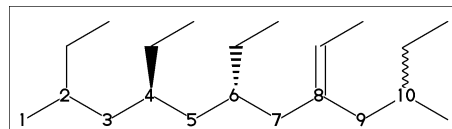
<30,!6,3:\,!



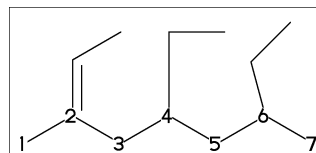
#### 2.1.3 Branch bond

2:\ : 2:@,0  
4:\* \ : 4:@,0~wf  
6:\\* : 6:@,0~zf  
8:\\ : 8:@,0~dm  
10:\* \\* : 10:@,0~wv

<30,!8,  
2:\,!,4:\* \,!,6:\\*,!,8:\\,!,10:\* \\*,!



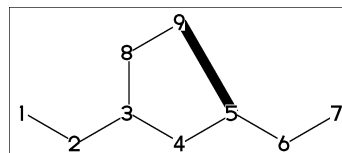
<-30,!6,  
2:\~dr,!, : 2:@,0~dr,!  
4:\'1.5,-90, : 4:@,0'1.5,-90  
6:\^15,-60 : 6:@,0^15,-60



#### 2.1.4 Connect atom

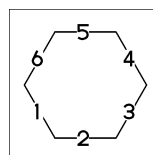
n:# : Connect to An

<30,!6,3:\,!,5~bd:#



#### 2.1.5 Ring

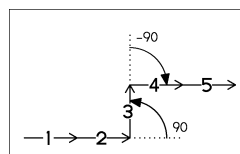
?n : n membered ring(3<=n<=20)  
?6 : <-120,60,60,60,60,60,1:#  
?6



#### 2.1.6 Rotate current angle

<angle : rotate current angle

0,0,<90,0,<-90,0,0,{1,2,3,4,5}=vf

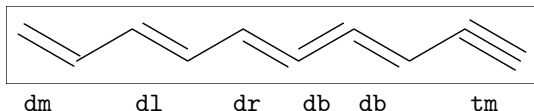


## 2.2 Change bond type

### 2.2.1 Double, triple

a~type : ~type,a  
dm : double middle  
dl : double left side  
dr : double right side  
db : double left or right side  
tm : triple  
!! : !~db / !!! : !~tm

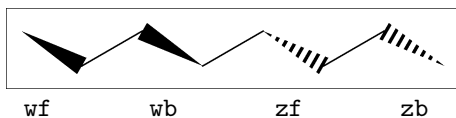
```
<30,!~dm,!~dl,!~dr,!~db,!~db,!~tm  
<30,!~dm,!~dl,!~dr,!! ,!! ,!,!!!
```



### 2.2.2 Wedge

wf : wedge forward / wb : wedge backward  
zf : wedge dotted  
zb : wedge dotted backward

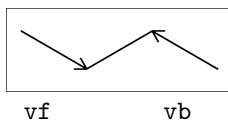
```
<30,!~wf,!~wb,!~zf,!~zb
```



### 2.2.3 Vector

vf:vector forward / vb:vector backward

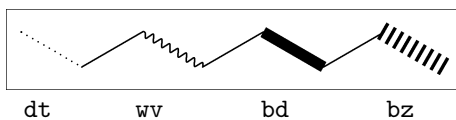
```
<30,!~vf,!~vb
```



### 2.2.4 Dotted, wave

Bn=bond type : change bond type at Bn  
dt : dotted / wv : wave  
bd : broad / bz : broad dotted

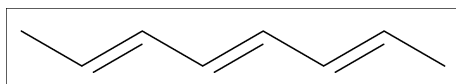
```
<30,!7,1=dt,3=wv,5=bd,7=bz
```



### 2.2.5 Change multiple bond type

```
{2,4,6}=dr : 2=dr,4=dr,6=dr
```

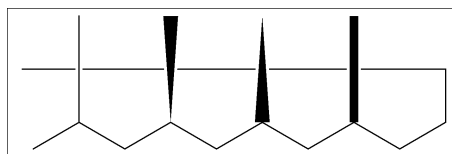
```
<30,!7,{2,4,6}=dr
```



### 2.2.6 Over line

si\_ : single over line  
wf\_ : wedge forward over line  
wb\_ : wedge backward over line  
bd\_ : broad over line

```
<-30,!8,!60,90'8,  
{2~si_,4~wf_,6~wb_,8~bd_}:/_2
```



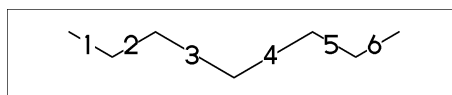
## 2.3 Change bond length

### 2.3.1 Chain length

(!,!n)'length : change length of !,!n

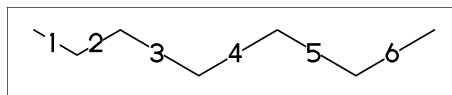
```
<30,!2,!2'1.2,!2
```

```
** !2'1.2 : ''1.2,!2
```



'length : change all bond length after

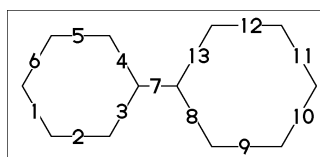
```
<30,!2,'1.2,!4
```



### 2.3.2 Ring length

?n'length : change ring length

```
?6,4:\,?6'1.2
```

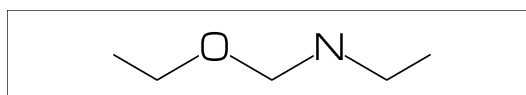


## 2.4 Change atom

### 2.4.1 Insert atom

Insert hetero atom

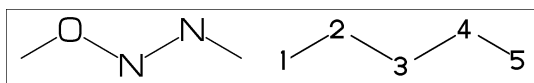
```
<30,!2,0,!2,N,!2
```



## 2.4.2 Addressed atom

2:0 : change A2 C to O  
 {3,4}:N : change A3,A4 C to N

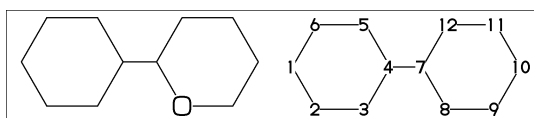
<30,!4,2:0,{3,4}:N



## 2.4.3 Brock address

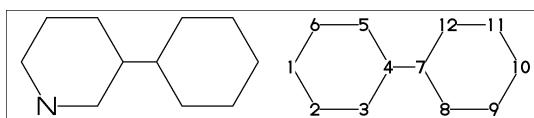
| : divide brock

?6,4:\,|,?6,2:0



|| : reset brock address

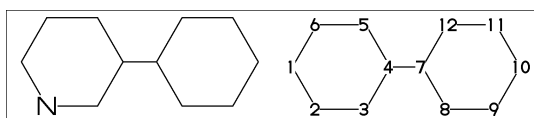
?6,4:\,|,?6,||,2:N



## 2.4.4 Absolute address

\$2:N : change A\$2 C to N  
 \*\* \$n : (1<=n<=3095)

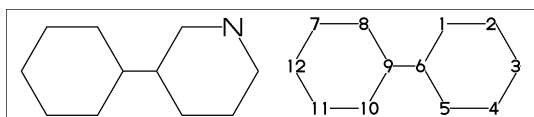
?6,4:\,|,?6,\$2:N



## 2.4.5 Relative address

-2:N : change A(-2) C to N  
 \*\* -n : (1<=n<=999)

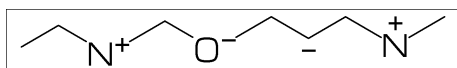
?6,4:\,?6,-2:N



## 2.4.6 Charged atom

N[1]:N+ / O[-1]:O- / A,&"c":A+c

<-30,!2,N[1],!2,O[-1],  
 !2,&"-" ,!2,N,&"+"^180,!

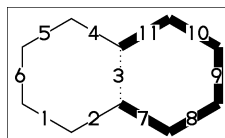


## 2.5 Fuse ring

### 2.5.1 Attached 1 bond

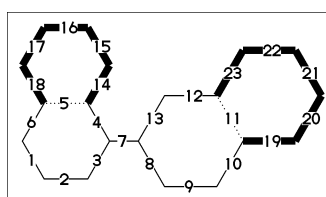
?6,3=?6 : fuse ?6 at B3  
 \*\* Bn(n:-999<=n<=4095): bond number

?6,3=?6



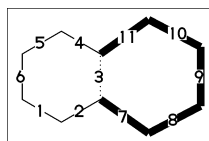
\*\* fused ring size depend on  
 attached bond length

?6,4:\,?6^1.2,5=?6,11=?6

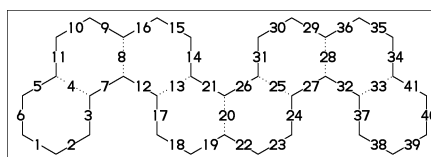


?6,3=?6[13] : fuse ?6[13] at B3  
 ?6[13]: 6 membered ring scaled 13/10  
 \*\* ?m[n] (5<=m<=8,11<=n<=15)

?6,3=?6[13]



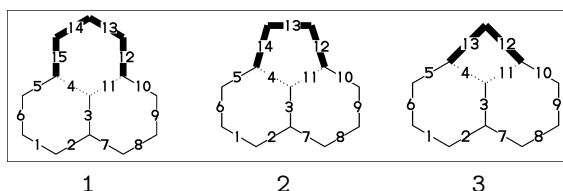
?6,{-3,-4,-4,-2,-2,-4,-4}=?6  
 ?6,{4,8,13,20,25,28,33}=?6



### 2.5.2 Attached 2 bond

(4,11)=?6[4] : fuse 4/6 ring to B11..B4  
 (4,11)=?5[3] : fuse 3/5 ring to B11..B4  
 (4,11)=?4[2] : fuse 2/4 ring to B11..B4  
 \*\* ?m[n] (4<=m<=6,n=m-2)

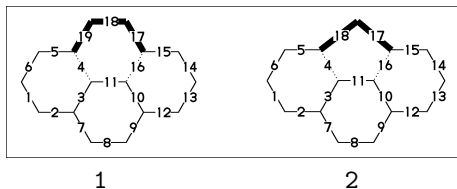
1:MCd(1,.7)( 0,0)(<30,?6,3=?6,(11,4)=?6[4])  
 2:MCd(1,.6)(.54,1)(<30,?6,3=?6,(11,4)=?5[3])  
 3:MCd(1,.6)( 1,0)(<30,?6,3=?6,(11,4)=?4[2])



### 2.5.3 Attached 3 bond

(16,4)=?6[3] : fuse 3/6 ring to B16..B4  
 (16,4)=?5[2] : fuse 2/5 ring to B16..B4  
 \*\* ?m[n] (5<=m<=6,n=m-3)

1:MCd(1,.55)(0,0)(?6,{3,10}=?6,(16,4)=?6[3])  
 2:MCd(1,.55)(1,0)(?6,{3,10}=?6,(16,4)=?5[2])

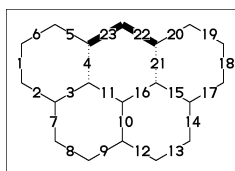


### 2.5.4 Attached 4 bond

(21,4)=?6[2] : fuse 2/6 ring to B21..B4

MCf(<-30,?6,{3,10,15}=?6,(21,4)=?6[2])

\*\* ?m[n] (m=6,n=2)

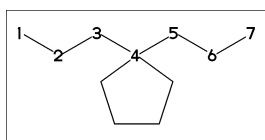


### 2.5.5 Spiro ring

4:@,?5 : add ?5 at A4

<30,!6,4:@,?5

An:@ : jump to An



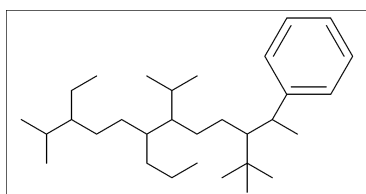
## 2.6 Substituent

### 2.6.1 Insert substituent

/ : single

<30,!/,/Me,!,/Et,!,/Pr,!,/iPr,  
 !3,/tBu,!,/Ph^-30,!

\*\* Me:methyl(/\_) Et:ethyl(/!)  
 Pr:propyl(/!2) iPr:isopropyl  
 tBu:tertial buthyl Ph:phenyl



### 2.6.2 Insert modified substituent

// : double (double middle)

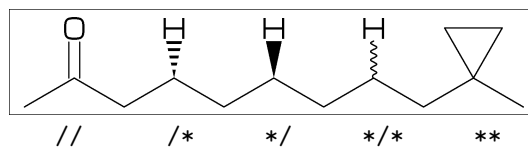
\*/ : wedge forward

/\* : wedge dotted forward

\*/\* : wave

\*\* : direct

<30,!/,/0,!2,/\*H,!2,\*H,!2,\*/\*H,!2,\*\*?3,!



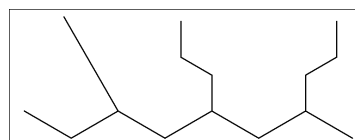
~ : change type

^ : change angle

' : change length

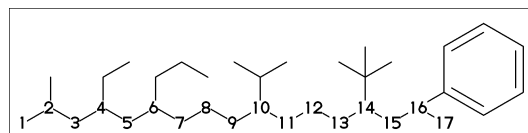
> : change enviroment

<30,'^1,!,  
 /\_'^2^30,!2,!!>lr,!2,!!>r1,!)



### 2.6.3 Add substituent

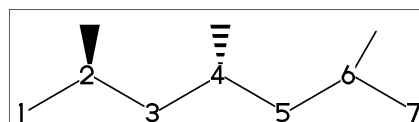
<-30,!17,2:/\_,4:!/!,6:/!2,  
 10:/iPr,14:/tBu,16:/Ph^-60



### 2.6.4 Add modified substituent

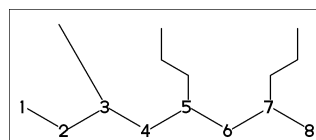
~,^,' : change type,angle,length

<-30,!6,  
 {2~wf,4~zf,6^-30}:/\_



~,^,'> : change angle,length,environment

<30,!7^1,  
 3:/\_'^2^30,5:/!2>lr,7:/!2>r1

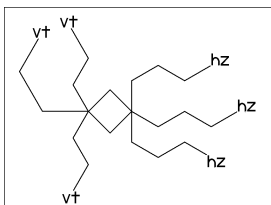


## 2.7 Chain environment

### 2.7.1 Horizontal,vertical

```
>hz : horizontal enviroment (default)
>vt : vertical enviroment
```

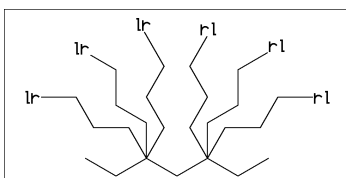
```
?4,{3^-90,3^-30,3^90}:/'(!3,"{hz}")>hz,
{1^-60,1^2,1^60}:/'(!2,"{vt}")>vt
```



### 2.7.2 Left-right,right-left

```
>lr : left-right enviroment
>rl : right-left enviroment
```

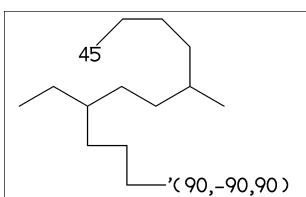
```
<30,!6,
{3^-30,3,3^30}:/'(!3,"{lr}")>lr,
{5^-30,5,5^30}:/'(!3,"{rl}")>rl
```



### 2.7.3 Fixed angle,multi angle

```
>45 : fixed angle enviroment
>'(-90,90,-90) : multi angle enviroment
```

```
<-30,!6,2>45:/'(!3,"{45}"),
{6>'(-90,90,-90)}:/'(!3,"{(-90,90,-90)}")
```

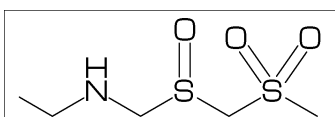


## 2.8 Miscellaneous

### 2.8.1 Change atom and Substituent

```
NH,S0,S00 :
inset hetero atom and substituent
simultaneously
```

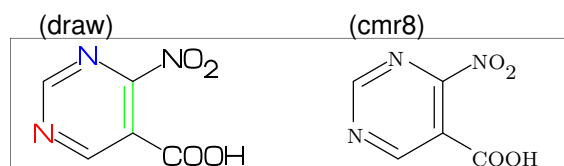
```
<30,!2,NH,! ,S0,! ,S00,!
```



### 2.8.2 Change color, atom font

```
1=green : change color of B1 green
3:red : change color of A3 red
atomfont:="cmr8" : use cmr8 for atom font
```

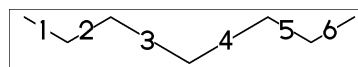
```
defaultfont:="uhvr8r";
defaultsize:=8bp;
Mca(0,0.5)(<30,Ph,{1,5}:N,3:/COOH,4:/NO2,
1:red,5:blue,3=green)
ext(label.urt("(draw)",p0+(0,h));)
atomfont:="cmr8"; % default:"draw"
atomfontsize:=8bp; % default:8bp
Mca(1,0.5)(<30,Ph,{1,5}:N,3:/COOH,4:/NO2)
ext(label.urt("(cmr8)",p0+(0,h));)
```



### 2.8.3 Make block

```
|< : start brock
>| : end brock
|<=n : |<,'n
```

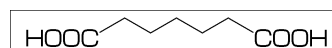
```
<30,!2,|<,'1.2,!2,>|,!2
<30,!2,|<=1.2,!2,>|,!2
```



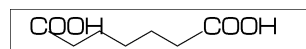
### 2.8.4 Chain start multiple characters

```
if chain start multi charactor string,
use !0 instead of !
```

```
Mcf(<30,COOH,!0,!3,COOH)
```

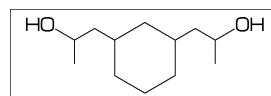


```
Mcf(<30,COOH,!4,COOH)
```

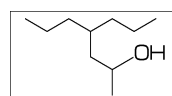


### 2.8.5 User definition

```
user defined substructure
iBuOH:= '(!/_,! ,OH)
<30,?6,{4,6}:/iBuOH
```



```
Insert user defined substructure
<30,!3,/'(!/_,! ,OH),!3
```

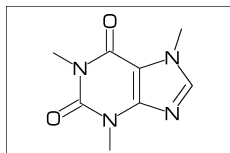


## 3 Option parameter

### 3.1 Size parameter

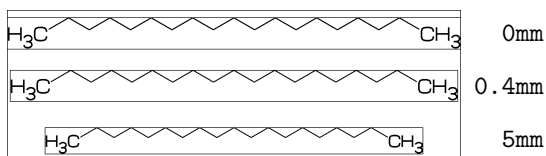
#### 3.1.1 Font size

```
beginfont("EN:Caffeine")  
font_wd:=30mm; %<==font width  
font_ht:=20mm; %<==font height  
MCf(<30,?6,-4=?5,{3,8}=d1,{2,6,7,9}:N,  
{2,6,9}:/_{1,5}://0) endfont
```



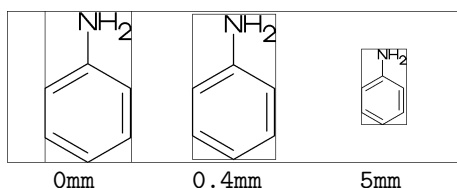
#### 3.1.2 Margin left and right

default: margin\_left\_right=0.4mm



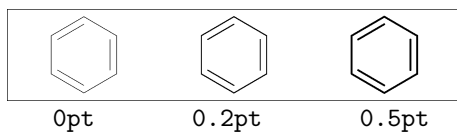
#### 3.1.3 Margin top and bottom

default: margin\_top\_bottom=0.4mm



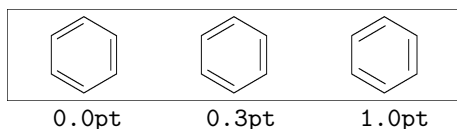
#### 3.1.4 Offset thickness of bond

default: offset\_thickness=0.2pt



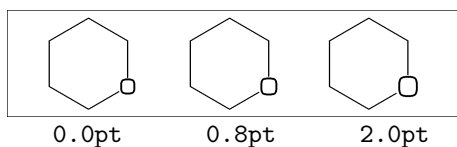
#### 3.1.5 Offset of doublebond gap

default: offset\_bond\_gap=0.3pt



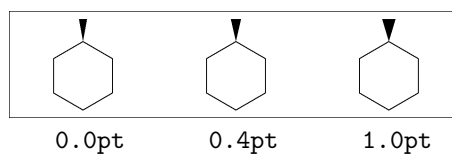
#### 3.1.6 Offset of atom width

default: offset\_atom=0.8pt



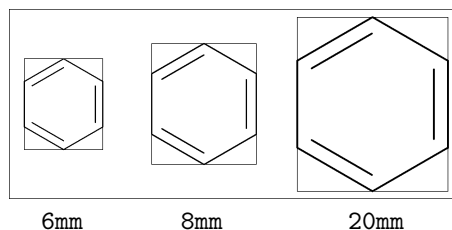
#### 3.1.7 Offset of wedge width

default: offset\_wedge=0.4pt



#### 3.1.8 Max bond length

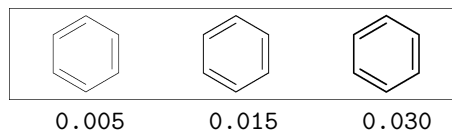
default: max\_bond\_length=10mm



## 3.2 Ratio parameter

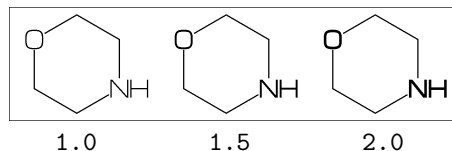
#### 3.2.1 Thickness/bond length

default: ratio\_thickness\_bond=0.015



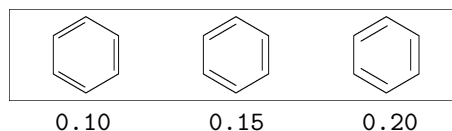
#### 3.2.2 Char/bond thickness

default: ratio\_char\_bond=1.5



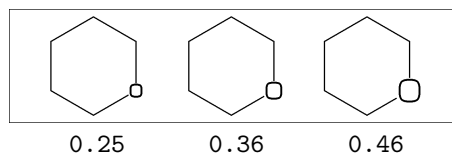
#### 3.2.3 Bondgap/bond length

default: ratio\_bondgap\_bond= 0.15



#### 3.2.4 Atom/bond length

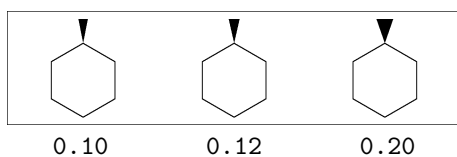
default: ratio\_atom\_bond= 0.36





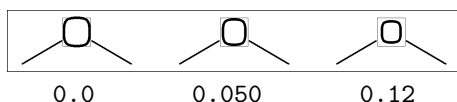
### 3.2.5 Wedge/bond length

default: ratio\_wedge\_bond=0.12



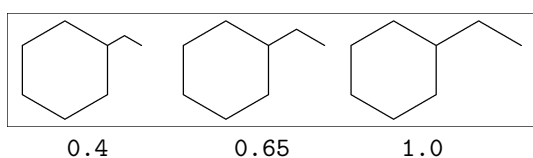
### 3.2.6 Font atom gap/atom length

default: ratio\_atomgap\_atom= 0.050



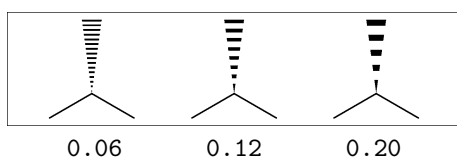
### 3.2.7 Chain/ring length

default: ratio\_chain\_ring= 0.66



### 3.2.8 Zebra gap/bond length

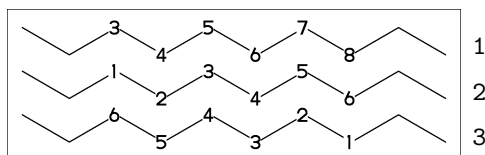
default: ratio\_zebragap\_bond=0.12



## 3.3 Drawing mode

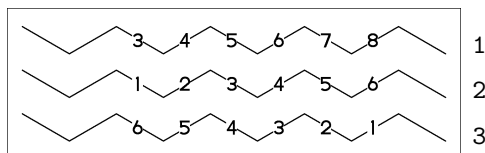
### 3.3.1 Numbering atom

numberA\_start:=3; numberA\_end:=8;  
default: sw\_numberA=0 :  
numberA\_start=1 numberA\_end=4095



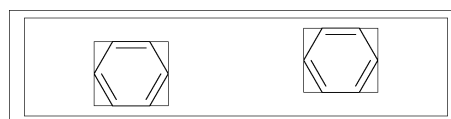
### 3.3.2 Numbering bond

numberB\_start:=3; numberB\_end:=8;  
default: sw\_numberB=0 :  
numberB\_start=1 numberB\_end=4095



### 3.3.3 Clipping mode

```
sw_clip:=0;  
MCd(1,0.7)(0.2,0.3)(Ph)  
MCd(1,0.7)(0.8,0.7)(Ph)  
** default: sw_clip=0
```

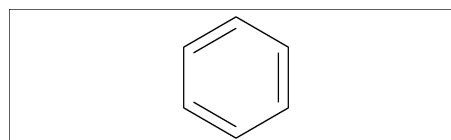


```
sw_clip:=1;  
MCd(1,0.7)(0.2,0.3)(Ph)  
MCd(1,0.7)(0.8,0.7)(Ph)
```

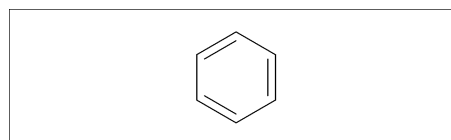


### 3.3.4 Solid mode

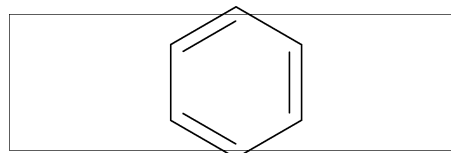
(fit to font size)  
sw\_solid=0    \*\* default



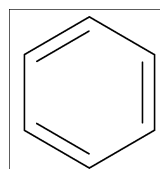
(solid ratio bond/font width)  
sw\_solid:=1;  
ratio\_bond\_width=0.1  
font\_width=60mm  
(bond\_len=60mm\*0.1=6mm)  
\*\* ignore bond\_len



(solid bond length)  
sw\_solid:=2;  
bond\_len=10mm  
\*\* ignore ratio\_bond\_width

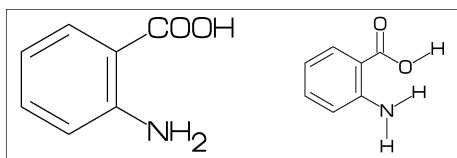


(solid bond length and clip)  
sw\_solid:=2;  
sw\_clip:=1;  
bond\_len=10mm



### 3.3.5 Expand mode

default: sw\_expand=0

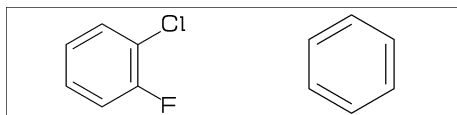


0 :default

1

### 3.3.6 Substituent off mode

default: sw\_subst\_off=0

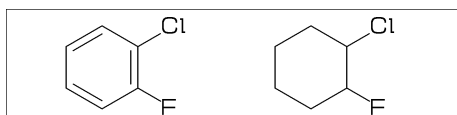


0 :default

1

### 3.3.7 Single bond mode

default: sw\_bond\_single=0



0 :default

1

## 3.4 Frame

### 3.4.1 Font frame

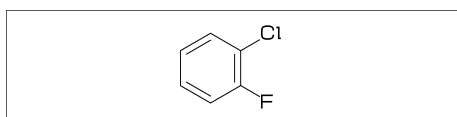
(Draw font frame)

margin\_left\_right:=5mm;

margin\_top\_bottom:=2mm;

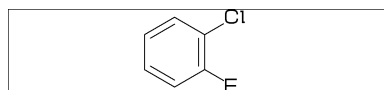
sw\_font\_frame:=1;

MCf(<30,Ph,4:/Cl,3:/F)



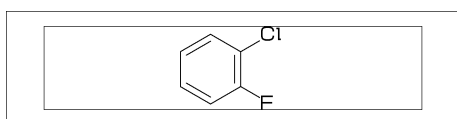
(Draw frame inside margin)

sw\_font\_frame=2



(Draw both frame)

sw\_font\_frame=3

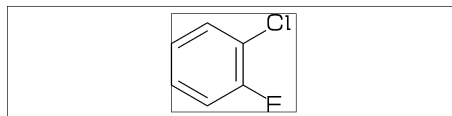


### 3.4.2 Molecular frame

sw\_mol\_frame:=1;

MCd(1,.5)(1,0.5)(<30,Ph,4:/Cl,3:/F)

\*\* default: sw\_mol\_frame=0

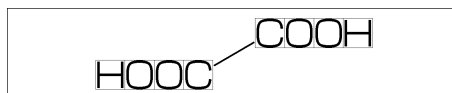


### 3.4.3 Atom frame

sw\_atom\_frame:=1;

MCf(<30,COOH,!0,COOH)

\*\* default: sw\_atom\_frame=0



## 3.5 Local parameter setting

beginfont()

MCf(Ph)

endfont

beginfont()

%-----

ratio\_thickness\_bond:=0.05;

%-----

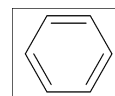
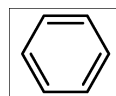
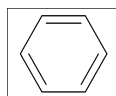
MCf(Ph)

endfont

beginfont()

MCf(Ph)

endfont



## 3.6 Global parameter setting

beginfont()

MCf(Ph)

endfont

%-----

ratio\_thickness\_bond:=0.05;

%-----

beginfont()

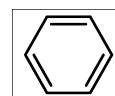
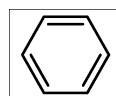
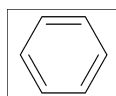
MCf(Ph)

endfont

beginfont()

MCf(Ph)

endfont



## 4 Function

### 4.1 Function MCd()

(Draw molecule)

```
MCd(a,b)(c,d)(...)
```

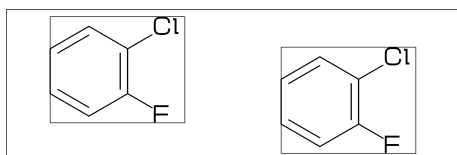
a: ratio molecular width/font width  
b: ratio molecular height/font height  
c: x axis position  
d: y axis position

```
beginfont()
```

```
MCd(1,0.8)(0.2,0.9)(<30,Ph,3:/F,4:/Cl)
```

```
MCd(1,0.8)(0.8,0.1)(<30,Ph,3:/F,4:/Cl)
```

```
endfont
```



### 4.2 Function MCa()

(Draw molecule at (x,y))

```
MCa(a,b)(...) : MCd(1,1)(a,b)(...)
```

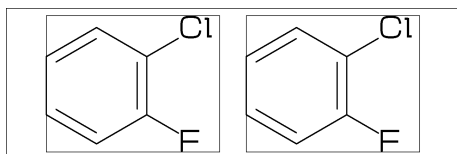
a: x axis position  
b: y axis position

```
beginfont()
```

```
MCa(0.2,0.5)(<30,Ph,3:/F,4:/Cl)
```

```
MCa(0.8,0.5)(<30,Ph,3:/F,4:/Cl)
```

```
endfont
```



### 4.3 Function MCc()

(Draw molecule to center of font)

```
MCc(a,b)(...) : MCd(a,b)(0.5,0.5)(...)
```

a: ratio molecular width/font width  
b: ratio molecular height/font height

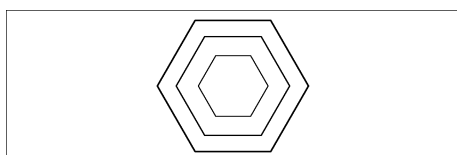
```
beginfont()
```

```
MCc(1,1)(?6)
```

```
MCc(0.75,0.75)(?6)
```

```
MCc(0.5,0.5)(?6)
```

```
endfont
```



### 4.4 Function MCf()

(Draw molecule fit to font size)

```
MCf(...) : MCd(1,1)(0.5,0.5)(...)
```

(Draw molecule fit to font height)

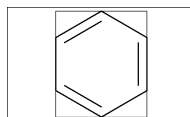
```
beginfont()
```

```
font_wd:=25mm;
```

```
font_ht:=15mm;
```

```
MCf(<30,Ph)
```

```
endfont
```



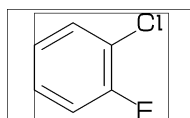
```
beginfont()
```

```
font_wd:=25mm;
```

```
font_ht:=15mm;
```

```
MCf(<90,Ph,3:/F,4:/Cl)
```

```
endfont
```



(Draw molecule fit to font width)

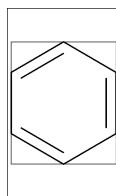
```
beginfont()
```

```
font_wd:=15mm;
```

```
font_ht:=25mm;
```

```
MCf(<30,Ph)
```

```
endfont
```



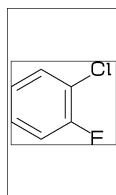
```
beginfont()
```

```
font_wd:=15mm;
```

```
font_ht:=25mm;
```

```
MCf(<30,Ph,3:/F,4:/Cl)
```

```
endfont
```

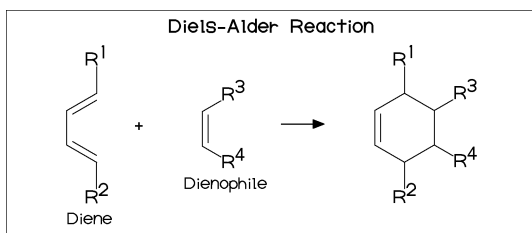


## 4.5 Function EXT()

(Add extra graphic to font)

```
w: font width
h: font height
w0: font width-margin_left_right*2
h0: font height-margin_top_bottom*2
aw: atom font size
em: label font size
p0: x=margin_left_right
    y=margin_top_bottom
n: molecular number
p[m]: molecular origin position
w[m]: molecular width
h[m]: molecular height
ratio_thickness_char:
    pen thickness / char width

%-----
beginfont()
font_wd:=70mm;
font_ht:=30mm;
ratio_bond_width:=0.065;
sw_solid:=1;
%-----
MCd(1,1)(0.1,0.5)
(<-210,60'1,60'1,60'1,{1,3}=d1,
 1:/R1,4:/R2^-60)
ext(defaultscale:=0.6;
  label.bot("Diene",p0+(0.5w,0));)
%-----
MCd(1,1)(0.4,0.5)
(<-30,-60'1,1=d1,1:/R3,2:/R4^60)
ext(defaultscale:=0.6;
  label.bot("Dienophile",p0+(0.5w,0));)
%-----
MCd(1,1)(0.9,0.5)
(<30,?6,6=d1,2:/R2,3:/R4,4:/R3,5:/R1)
%-----
EXT(
 drawarrow (0.52w,0.5h)..(0.6w,0.5h);
 defaultscale:=0.7;
 label("+", (0.25w,0.5h));
 ratio_thickness_char:=0.125;
 label.bot("Diels-Alder Reaction",
 (0.5w,h));
)
%-----
endfont
```

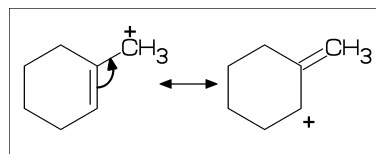


## 4.6 Function ext()

(Add extra graphic to molecule)

```
w: molecular width
h: molecular height
aw: atom font size
em: label font size
p0: origin of molecular structure
l: bond length
An: atom number
A[m]: atom position
A[m]dir: branch direction of A[m]
Bn: bond number
B[m]s: bond start position
B[m]e: bond end position
B[m]: bond position(0.5[B[m]s,B[m]e])
B[m]dir: bond direction

%-----
beginfont()
font_wd:=50mm;
font_ht:=20mm;
%-----
MCd(1,0.7)(0,0.5)(<30,?6,3=d1,4:/CH3)
ext(
 label.top("+",A7);
 drawarrow B3{dir(B3dir-90)}..
 {dir(B7dir+90)}0.4[B7s,B7e];
)
%-----
MCd(1,0.7)(1,0.5)(<30,?6,4://CH3)
ext(
 labeloffset:=0bp;
 label.lrt("+",A3);
)
%-----
EXT(
 drawdblarrow (0.4w,0.5h)..(0.55w,0.5h);
)
%-----
endfont
```



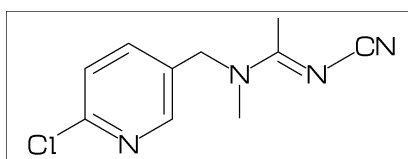
```
label:
defaultfont: label font
defaultfont="draw": draw font
**default defaultfont="draw"
```

```
drawarrow & drawdblarrow:
sw_arrow=0: emulation mode
sw_arrow=1: plain.mp mode
**default sw_arrow=0
```

## 5 MCF example

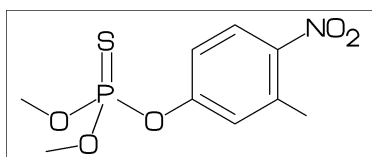
### 5.1 Acetamidrid

<30,Ph,2:N,1:/Cl,  
4:\,!,N,/\_,!,/\_,!!N,!,CN



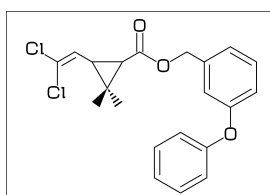
### 5.2 Fenitrothion

<30,!,0,!,P,//S,/O!^160,!,0,!,  
|,Ph,3:/\_,4:/NO2



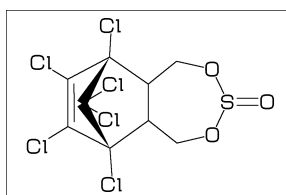
### 5.3 Permethrin

<-30,?3,2^-35:\*/\_-,2^35:/\*\_,  
1:\,!!/,Cl,!,Cl,  
3:\,//0,!,0,!2,Ph,  
-4:\,0,-60,Ph



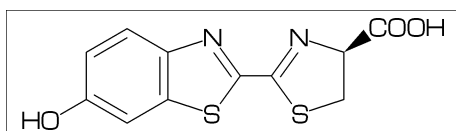
### 5.4 Endosulfan

<26,?7,7=?6[13],11:@,208~wf'1.45,8~wb:#,  
10=d,{3,5}:0,4:S,4://0,  
{8,9,10,11,12^-210,12^-150}:/Cl



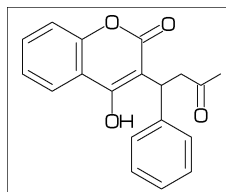
### 5.5 Luciferin

<30,Ph,3=?5,8:\,?5,{9,16}=d1,  
{9,14}:N,{7,11}:S,  
1:/OH,-2:\*/COOH



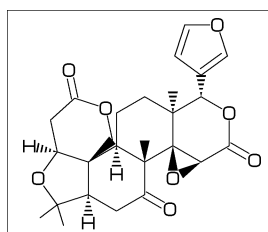
### 5.6 Warfarin

<30,Ph,3=?6,8=d1,  
10:0,7:/OH,9://0,  
8:\,/Ph'1,60,!,//0,!



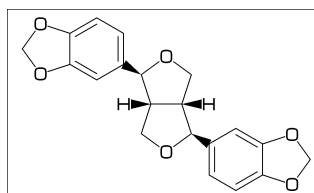
### 5.7 Limonin

<30,?6,{-3,-4}?6,-5=?3,  
-2=wf,-1=wb,6=?5,-4=?6,-5=wf,  
{13,15,17,20}:0,{3,12,21}://0,  
{4~wf^60,8~zf^60,18^35,18^-35}:/\_-,  
{1^60,5^180,16^60}:/\*H,  
14:\\*,|,?5,{1,4}=d1,3:0



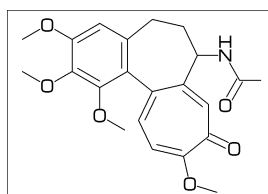
### 5.8 Sesamine

<54,?5,1=?5,  
{4,7}:0,{1^-54,2^54}:\*/H,  
5:\*^-12,Ph,-3=?5,{-1,-3}:0,  
8:\*^-12,Ph,-3=?5,{-1,-3}:0



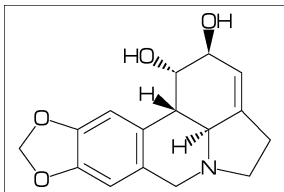
### 5.9 Colchicine

<30,Ph,{1,2,6}:/O!,  
-4=?7,-5=?7,  
{-1,-4,-6}=d1,-2://0,-3:/O!,  
9:\,NH,!,//0,!



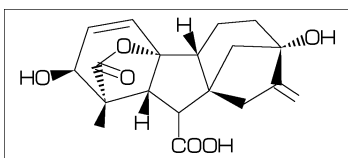
## 5.10 Lycorine

<30, Ph,  
-4=?6, -2=?6, 6=?5, (9, 12)=?5[3],  
13=d1,  
8:N, {15, 17}:0,  
9:/\*H^180, 10:\*/H^60,  
13:\*/OH, 14:/\*OMe



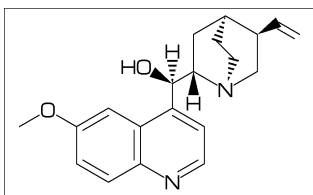
## 5.11 Gibberellin

<18, ?5, 3=?7, 5=?6[12],  
8:@, 160'1.3, 3:#,  
13=d1, 6=wf, 8=wb,  
5:@, 40~zf'1, 0, 60, //0^180, 14~zb:#,  
2:/COOH, 7://\_, 13:\*/OH, 8:\*/OH,  
14:\*/\_, {1, 4}:\*/H^60



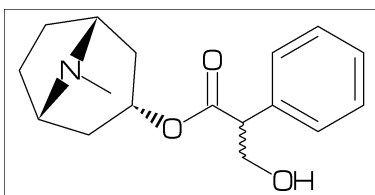
## 5.12 Quinine

<30, Ph, 3=Ph, 7:N, 6:/O!,  
10:\, \*/OH, /H^zf^-60, !,  
|, ?6, 2:N, 1:\*/H^60,  
4:\*!, !!,  
2:@, 165~zf, 60, 5~zb:#



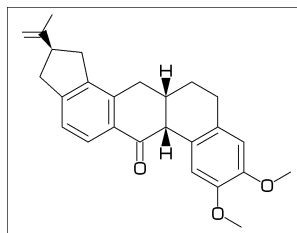
## 5.13 Atoropin

<-30, 0, !, //0, !, !, Ph,  
\$1:@, -120~zb,  
|, ?7, 6:\*^190'1.02, N, /\_, 3~wb:#,  
\$3:\*!, !, OH



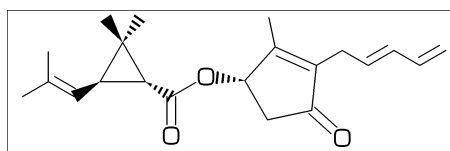
## 5.14 Rotenone

<-60, ?5, {-3, -2, -3, -4}=?6,  
{7, 9, -2, -4}=d1, {3, 17}=dr,  
{2, 13, 16}:0, 10://0, {11^-60, 12^60}:\*/H,  
{-2, -3}:/O!, 1:\*!, /\_, !!



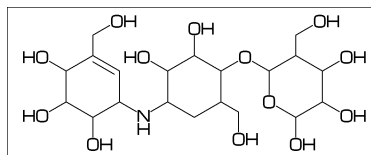
## 5.15 Pyrethrin I

<30, ?3, {3^35~wf, 3^-35~zf}:/\_,  
1:\*!, !!, iPr, 2:\\*, //0, !, 0, -36~zb, |,  
?5, -2=d, -1:/\_, -3://0, -2\, 14, {-1, -3}=d1



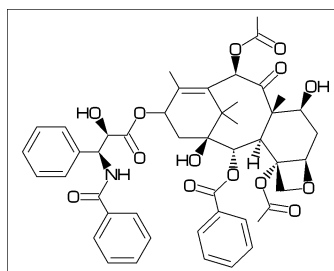
## 5.16 Validamycin

<30, ?6, {5, 6}:/OH, 3:/!OH>r1,  
\$4:\, 0, -60, |, ?6, 2:0, {3, 4, 5}:/OH, 6:/!OH,  
\$1:\, NH, !, |, ?6, 2=d1, {4, 5, 6}:/OH, 3:/!OH



## 5.17 Paclitaxel

?6, 5=d, 3:@, |<=1, 36, 45, 45, 45, >|, \$5:#,  
-4=?6, -4=?4, -1=wb, -3=wf, -1:0, ||,  
{4^35, 4^-35, 6}:/\_, {3^-60, 15}:\*/OH,  
8:/\*H^-60, 9:\*/\_ ^60, 10://0,  
1:\, 0, !, //0, !, \*/OH, !, /Ph,  
60~wf, NH, -60, //0, 60, Ph,  
7:\\*, 0, -45, //0, 60, Ph, 11:\*!, 0, -60, //0, 60,  
12:\\*^-15, 0, 60, //0, -60



## 6 Example to use mcf2graph

### 6.1 Molecular definition file

```
%-----  
input mcf2graph.mf;                                % input macro  
%-----  
sw_auxout:=1;          % aux(information) file output on > Gloval setting  
font_wd:=60mm;        % font width >  
font_ht:=40mm;        % font height >  
var3:="cal_MW"; tag3:="cMW"; > AUX file table  
var4:="cal_FM"; tag4:="cFM"; >  
%% sw_report:=1; > Report output  
%% sw_MOLout:=1; > MOL file output  
outputformat:="png"; hppp:=vppp:=0.1; > PNG output  
outputtemplate:="%j-%3c.png"; >  
%-----  
beginfont("NO:1","EN:Ampicillin") > begin font(information)  
  MCF(<45,?4,2:N,2=?5,-1:S, > begin MCF (1)  
    {3^45,4^-45}:/*H,1://O^15,5:/*COOH^-18, >  
    {6^35,6^-35}:/_ , >  
    4:@,75,NH,! ,//O,! ,/*NH,! ,Ph) > end MCF  
endfont > end font  
%-----  
beginfont("NO:2","EN:Cholesterol") > begin font(information)  
  MCF(<30,?6,{-4,-2}=?6,-4=?5,7=d1, > begin MCF (2)  
    1:*/OH,{4,12}:*/_ ^60,9:*/H^60, >  
    10:/*H^180,{11,-1}:/*H^-60, >  
    -1:@,17,/*_ ,!4,/_ ,!) > end MCF  
endfont > end font  
%-----  
beginfont("NO:3","EN:Limonin") > begin font(information)  
  MCF(<30,?6,{-3,-4}=?6, > begin MCF (3)  
    -5=?3,-2=wf,-1=wb,6=?5,-4=?6,-5=wf, >  
    {13,15,17,20}:0,{3,12,21}://O, >  
    {4~wf^60,8~zf^60,18^35,18^-35}:/_ , >  
    {1^60,5^180,16^60}:/*H, >  
    14:\*,| ,?5,{1,4}=d1,3:0) > end MCF  
endfont > end font  
%-----  
beginfont("NO:4","EN:beta-carotene") > begin font(information)  
  MCF(<30,?6,3=d1,{3,5^35,5^-35}:/_ , > begin MCF (4)  
    4:\,| ,!18,{1,3,5,7,9,11,13,15,17}=dr, >  
    {3,7,12,16}:/_ , >  
    | ,?6,6=d1,{6,2^35,2^-35}:/_ ) > end MCF  
endfont > end font  
%-----  
beginfont("NO:5","EN:Gibberellin A3"); > begin font(information)  
  MCF(<18,?5,3=?7,5=?6[12], > begin MCF (5)  
    8:@,160'1.3,3:#,13=d1,6=wf,8=wb, >  
    5:@,40~zf'1,0,60,//O^180,14~zb:#, >  
    2:/COOH,7://_ ,13:*/OH,8:/*OH, >  
    14:*/_ ,{1^60,4^60}:*/H) > end MCF  
endfont; > end font  
%-----  
bye
```

## 6.2 Information auxfile output

(Insert option parameter setting)

```
sw_auxout:=1;
** default : sw_auxout=0
```

(Command line)

```
>mpost -s ahandle=0 FILENAME (molecular definition file)
```

(Source)

```
beginfont("EN:Ampicillin")(...)
beginfont("EN:Cholesterol")(...)
beginfont("EN:Limonin")(...)
beginfont("EN:beta-Carotene")(...)
beginfont("EN:Gibberellin A3")(...)
```

(Setting)

```
tag1:="F"; var1:="jobname"; * default output
tag2:="C"; var2:="char_num"; * default output
tag3:="cMW"; var3:="calc_weight";
tag4:="cFM"; var4:="calc_formula";
```

(Output)

(sw\_auxfix=0)

```
F:mcf_man_soc;C:1;cMW:349.40462;cFM:C16H19N3O4S;EN:Ampicillin
F:mcf_man_soc;C:2;cMW:386.6532;cFM:C27H46O;EN:Cholesterol
F:mcf_exa_soc;C:3;cMW:470.5113;cFM:C26H30O8;EN:Limonin
F:mcf_exa_soc;C:4;cMW:536.8722;cFM:C40H56;EN:beta-Carotene
F:mcf_exa_soc;C:5;cMW:346.3742;cFM:C19H22O6;EN:Gibberellin A3
```

(sw\_auxfix=1)

```
F;C;cMW;cFM;EN
mcf_man_soc;1;349.40462;C16H19N3O4S;Ampicillin
mcf_man_soc;2;386.6532;C27H46O;Cholesterol
mcf_exa_soc;3;470.5113;C26H30O8;Limonin
mcf_exa_soc;4;536.8722;C40H56;beta-Carotene
mcf_exa_soc;5;346.3742;C19H22O6;Gibberellin A3
```

(aux\_delimiter:="/");

```
F:mcf_man_soc/C:1/cMW:349.40462/cFM:C16H19N3O4S/EN:Ampicillin
F:mcf_man_soc/C:2/cMW:386.6532/cFM:C27H46O/EN:Cholesterol
F:mcf_exa_soc/C:3/cMW:470.5113/cFM:C26H30O8/EN:Limonin
F:mcf_exa_soc/C:4/cMW:536.8722/cFM:C40H56/EN:beta-Carotene
F:mcf_exa_soc/C:5/cMW:346.3742/cFM:C19H22O6/EN:Gibberellin A3
```

(Tag)

```
F : filename
C : char number
NO : serial number
EN : english name
JN : japanese name
FM : formula from literature data
MW : molecular weight from literature data
USE : the use
cMW : molecular weight calculated
cMI : monoisotopic mass calculated
cFM : molecular formula calculated
```



### 6.3 Report output

(Insert option parameter setting)

```
sw_report:=1;
** default : sw_report=0
```

(Command line)

```
>mpost -s ahangle=0 -s ahlength=2 FILENAME (molecular definition file)
```

(Output)

```
-----
Molecular name = Nicotine
Warnings = 0 / Expanded command = 40
Width * Height = 49.57332 * 41.37605
Shift width * height = 0 * -9.07253
Bond length = 12.75589 Atom size = 5.38914
Atom count= 12 Bond count= 13 Ring count= 2 Hide H count= 14
-----
< NO. >( x axis , y axis )< atom >< bond >< hide_H >
A1 ( 0 , 0 ) C 3 1
A2 ( 0.866 , -0.5 ) N 3
A3 ( 1.732 , 0 ) C 3 1
A4 ( 1.732 , 1 ) C 4
A5 ( 0.866 , 1.5 ) C 3 1
A6 ( 0 , 1 ) C 3 1
A7 ( 2.304 , 1.33 ) C 3 1
A8 ( 3.217 , 0.923 ) N 3
A9 ( 3.886 , 1.666 ) C 2 2
A10 ( 3.386 , 2.532 ) C 2 2
A11 ( 2.408 , 2.325 ) C 2 2
A12 ( 3.399 , 0.067 ) C 1 3
-----
< NO. >< bond (sdt)><angle + ( +- )><length ( pt )>
B1 1 -> 2 ( 2) 330 ( -30) 1 ( 12.76)
B2 2 -> 3 ( 1) 30 ( 30) 1 ( 12.76)
B3 3 -> 4 ( 2) 90 ( 90) 1 ( 12.76)
B4 4 -> 5 ( 1) 150 ( 150) 1 ( 12.76)
B5 5 -> 6 ( 2) 210 ( -150) 1 ( 12.76)
B6 6 -> 1 ( 1) 270 ( -90) 1 ( 12.76)
B7 4 -> 7 ( 1) 30 ( 30) 0.66 ( 8.42)
B8 7 -> 8 ( 1) 336 ( -24) 1 ( 12.76)
B9 8 -> 9 ( 1) 48 ( 48) 1 ( 12.76)
B10 9 -> 10 ( 1) 120 ( 120) 1 ( 12.76)
B11 10 -> 11 ( 1) 192 ( -168) 1 ( 12.76)
B12 11 -> 7 ( 1) 264 ( -96) 1 ( 12.76)
B13 8 -> 12 ( 1) 282 ( -78) 0.66 ( 8.42)
-----
<atom>( atom wt ) [ mi wt ] < cnt > < sum wt > [ sum mi wt ]
C ( 12.0107) [ 12 ] * 10 = 120.10696 [ 120 ]
H ( 1.00793) [ 1.00783 ] * 14 = 14.11108 [ 14.10959 ]
N ( 14.0067) [ 14.00307 ] * 2 = 28.0134 [ 28.00613 ]
Molecular Weight [Mono Isotopic] = 162.2314 [ 162.11572 ]
-----
Weight Calc: 162.2314 / Input: 162.23 / weight gap= 0.00145
Fomula Calc: C10H14N2 / Input:
=====
```

## 6.4 MOL file output

(Insert option parameter setting)

```
sw_mol_out:=1; (V2000)
sw_mol_out:=2; (V3000)
** default : sw_mol_out=0
```

(Command line)

```
>mpost -s ahangle=3 FILENAME (molecular definition file) V2000
>mpost -s ahangle=4 FILENAME (molecular definition file) V3000
```

(Output)

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
-MCFtoMOL- EN:Caffeine

14 15 0 0 0 0 0 0 0 0999 V2000
      0      0      0 C  0 0 0 0
  0.86603    -0.5      0 N  0 0 0 0
  1.73206      0      0 C  0 0 0 0
  1.73206      1      0 C  0 0 0 0
  0.86603     1.5      0 C  0 0 0 0
      0      1      0 N  0 0 0 0
  2.6831   -0.30902    0 N  0 0 0 0
  3.27089      0.5      0 C  0 0 0 0
  2.6831    1.30902    0 N  0 0 0 0
  0.86603   -1.36383    0 C  0 0 0 0
 -0.76894    1.44394    0 C  0 0 0 0
 -0.76894   -0.44394    0 D  0 0 0 0
  0.86603    2.36383    0 D  0 0 0 0
  2.95299    2.1396     0 C  0 0 0 0
  1  2  1  0      0  0
  2  3  1  0      0  0
  3  4  2  0      0  0
  4  5  1  0      0  0
  5  6  1  0      0  0
  6  1  1  0      0  0
  3  7  1  0      0  0
  7  8  2  0      0  0
  8  9  1  0      0  0
  9  4  1  0      0  0
  2 10  1  0      0  0
  6 11  1  0      0  0
  1 12  2  0      0  0
  5 13  2  0      0  0
  9 14  1  0      0  0
M  END
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
```

## 6.5 LuaTeX file example

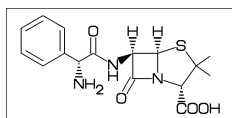
```
%-----  
\documentclass{article}  
\usepackage{luamplib}%  
\mplibcodeinherit{enable}%  
\mplibverbatim{enable}%  
\everymplib{if unknown Ph1:  
    input mcf2graph.mf;  
    mp_log_name:="temp-info.aux";  
    sw_auxout:=1;  
    fi}%  
%-----  
\begin{document}  
\noindent%  
%-----  
\begin{mplibcode}  
    font_wd:=50mm; font_ht:=50mm;  
    beginfont("NO:2","EN:Limonin","MW:470.51")  
    MCF(<30,  
        ?6,{-3,-4}=?6,  
        -5=?3,-2=wf,-1=wb,6=?5,-4=?6,-5=wf,  
        {13,15,17,20}:0,{3,12,21}://0,  
        {4~wf^60,8~zf^60,18^35,18^-35}:/_,  
        {1^60,5^180,16^60}:/*H,  
        14:\*,|,?5,{1,4}=d1,3:0  
    )  
    endfont  
\end{mplibcode}\\  
%-----  
\begin{mplibcode}  
    font_wd:=80mm; font_ht:=50mm;  
    beginfont("NO:3","EN:beta-carotene","MW:536.87")  
    MCF(<30,  
        ?6,3=d1,{3,5^35,5^-35}:/_,  
        4:\,|,!18,{1,3,5,7,9,11,13,15,17}=dr,  
        {3,7,12,16}:/_,  
        |,?6,6=d1,{6,2^35,2^-35}:/_  
    )  
    endfont  
\end{mplibcode}\\  
%-----  
\begin{mplibcode}  
    font_wd:=50mm; font_ht:=50mm;  
    beginfont("NO:4","EN:Gibberellin A3","MW:346.37");  
    MCF(<18,?5,3=?7,5=?6[12],  
        8:@,160'1.3,3:#,13=d1,6=wf,8=wb,  
        5:@,40~zf'1,0,60,//0^180,14~zb:#,  
        2:/COOH,7://_,13:*/OH,8:/*OH,  
        14:*/_,{1^60,4^60}:/*H  
    )  
endfont;  
\end{mplibcode}\\  
%-----  
\end{document}  
%-----
```

## 6.6 LaTeX file example

```
%-----  
\documentclass[a4paper]{article}  
\usepackage{graphicx}  
\pagestyle{empty}  
\makeatletter%  
%-----  
\def\@F{F}\def\@C{C}\def\@EN{EN}\def\@NO{NO}\def\@MW{MW}\def\@FMc{FMc}%  
\def\@fst@param#1:#2;{#1}\def\@sec@param#1:#2;{#2}%  
\def\mol@sel#1{%  
\if#1empty\relax\else%  
  \edef\@tag{\expandafter\@fst@param#1;}%  
  \edef\@var{\expandafter\@sec@param#1;}%  
  \ifx\@tag\@F\edef\MOLfile{\@var}\fi%  
  \ifx\@tag\@C\edef\MOLchar{\@var}\fi%  
  \ifx\@tag\@EN\edef\MOLnameE{\@var}\fi%  
  \ifx\@tag\@NO\edef\MOLnum{\@var}\fi%  
  \ifx\@tag\@MW\edef\CALmw{\@var}\fi%  
  \ifx\@tag\@FMc\edef\CALfm{\@var}\fi%  
\fi}%  
\def\put@char{%  
  \begin{picture}(84,42)%  
    \put(0,38){\bf [MOLnum]\MOLnameE{ }\small\tt/FM:\CALfm/MW:\CALmw}%  
    \put(10,0){\font\@strufont=\MOLfile\relax%  
      \hbox{\@strufont\char\MOLchar}}%  
  \end{picture}%  
\def\INFO#1{\@for\@temp=#1\do{\mol@sel\@temp}\put@char}%  
\makeatother  
%-----  
\begin{document}  
\unitlength=1mm%  
\INFO{F:mcf_man_soc,C:134,NO:1,cMW:349.40462,cFM:C16H19N3O4S,EN:Ampicillin}%  
\INFO{F:mcf_man_soc,C:135,NO:2,cMW:386.6532,cFM:C27H46O,EN:Cholesterol}%  
\end{document}  
%-----
```

### [1]Ampicillin

FM:C16H19N3O4S MW:349.40462



### [2]Cholesterol

FM:C27H46O MW:386.6532

