

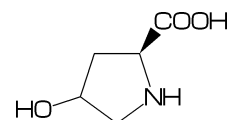
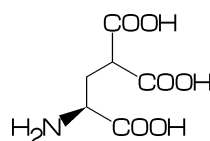
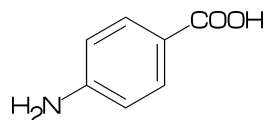
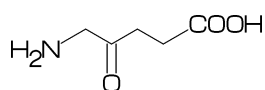
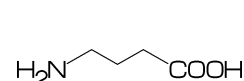
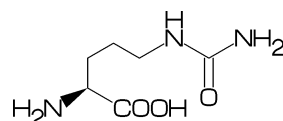
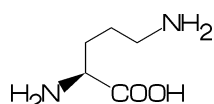
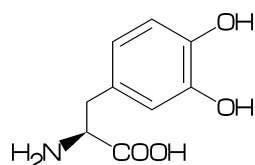
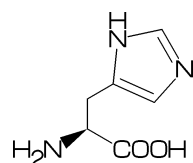
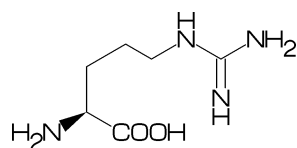
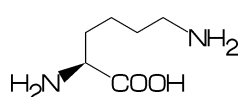
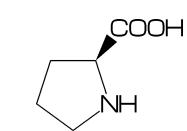
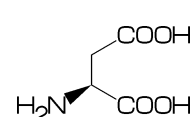
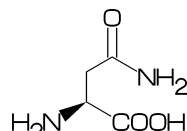
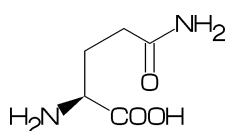
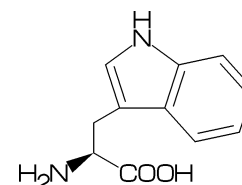
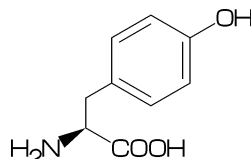
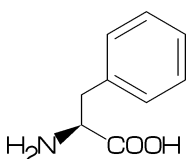
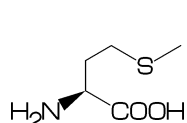
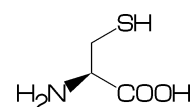
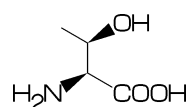
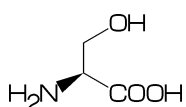
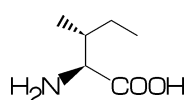
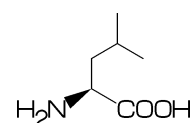
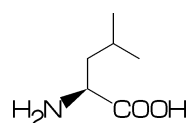
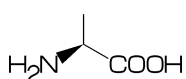
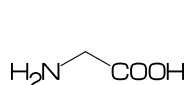
Molecular Coding Format manual

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February 21, 2021

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

Suggestion or request mail to: mcf2graph@gmail.com



Contents

| | | |
|----------|---------------------------------|-----------|
| 1 | Introduction | 3 |
| 2 | MCF syntax | 3 |
| 2.1 | Make bond | 3 |
| 2.1.1 | Chain | 3 |
| 2.1.2 | Chain use !,ln | 3 |
| 2.1.3 | Jump to atom | 3 |
| 2.1.4 | Branch bond | 3 |
| 2.1.5 | Branch modified bond | 3 |
| 2.1.6 | Connect atom | 3 |
| 2.1.7 | Ring | 3 |
| 2.1.8 | Rotate current angle | 3 |
| 2.2 | Change bond type | 4 |
| 2.2.1 | Double,triple | 4 |
| 2.2.2 | Wedge | 4 |
| 2.2.3 | Vector | 4 |
| 2.2.4 | Dotted,wave | 4 |
| 2.2.5 | Change multiple bond type | 4 |
| 2.2.6 | Over line | 4 |
| 2.3 | Change bond length | 4 |
| 2.3.1 | Chain length | 4 |
| 2.3.2 | Ring length | 4 |
| 2.4 | Change atom | 4 |
| 2.4.1 | Insert atom | 4 |
| 2.4.2 | Addressed atom | 5 |
| 2.4.3 | Brock address | 5 |
| 2.4.4 | Reset brock address | 5 |
| 2.4.5 | Absolute address | 5 |
| 2.4.6 | Relative address | 5 |
| 2.4.7 | Charged atom | 5 |
| 2.5 | Fuse ring | 5 |
| 2.5.1 | Attached 1 bond | 5 |
| 2.5.2 | Attached 2 bond | 5 |
| 2.5.3 | Attached 2 bond | 6 |
| 2.5.4 | Attached 4 bond | 6 |
| 2.5.5 | Spiro ring | 6 |
| 2.6 | Group | 6 |
| 2.6.1 | Insert group | 6 |
| 2.6.2 | Insert modified group | 6 |
| 2.6.3 | Add group | 6 |
| 2.6.4 | Add modified group | 6 |
| 2.7 | Chain environment | 7 |
| 2.7.1 | Horizontal,vertical | 7 |
| 2.7.2 | Left-right,right-left | 7 |
| 2.7.3 | Fixed rotate angle | 7 |
| 2.7.4 | Multi rotate angle | 7 |
| 2.8 | Miscellaneous | 7 |
| 2.8.1 | Abbreviated parts | 7 |
| 2.8.2 | Parts definition | 7 |
| 2.8.3 | Parts inline definition | 7 |
| 3 | Option parameter | 8 |
| 3.1 | Angle parameter | 8 |
| 3.2 | Size/Ratio parameter | 8 |
| 3.2.1 | Bond length | 8 |
| 3.2.2 | Molecular size | 8 |
| 3.2.3 | Molecular position | 8 |
| 3.3 | Size parameter | 8 |
| 3.3.1 | Font size | 8 |
| 3.3.2 | Font margin | 8 |
| 3.3.3 | Offset thickness of bond | 8 |
| 3.3.4 | Offset of double bond gap | 8 |
| 3.3.5 | Offset of atom width | 9 |
| 3.3.6 | Offset of wedge width | 9 |
| 3.3.7 | Max bond length | 9 |
| 3.4 | Ratio parameter | 9 |
| 3.4.1 | Thickness/bond length | 9 |
| 3.4.2 | Char/bond thickness | 9 |
| 3.4.3 | Bond gap/bond length | 9 |
| 3.4.4 | Atom/bond length | 9 |
| 3.4.5 | Wedge/bond length | 9 |
| 3.4.6 | Font atom gap/atom length | 9 |
| 3.4.7 | Chain/ring length | 9 |
| 3.4.8 | Zebra gap/bond length | 9 |
| 3.5 | Drawing mode | 9 |
| 3.5.1 | Numbering atom | 9 |
| 3.5.2 | Numbering bond | 10 |
| 3.5.3 | Trimming mode | 10 |
| 3.5.4 | Expand mode | 10 |
| 3.5.5 | Group off mode | 10 |
| 3.5.6 | Single bond mode | 10 |
| 3.6 | Frame | 10 |
| 3.6.1 | Font frame | 10 |
| 3.6.2 | Molecular frame | 10 |
| 3.6.3 | Atom frame | 10 |
| 3.6.4 | Remove indent | 10 |
| 3.7 | Parameter setting | 11 |
| 3.7.1 | Local parameter setting | 11 |
| 3.7.2 | Global parameter setting | 11 |
| 4 | Function | 11 |
| 4.1 | Function MC() | 11 |
| 4.2 | Function MCat() | 11 |
| 4.3 | Function check_mc() | 11 |
| 4.4 | Function add() | 12 |
| 4.5 | Function ext() | 13 |
| 4.5.1 | Local ext() setting | 13 |
| 4.5.2 | Global ext() setting | 13 |
| 5 | MCF example | 14 |
| 5.1 | Luciferin | 14 |
| 5.2 | Colchicine | 14 |
| 5.3 | Paclitaxel | 14 |
| 5.4 | Lycorine | 14 |
| 5.5 | Gibberellin | 14 |
| 5.6 | Quinine | 14 |
| 6 | Example to use mcf2graph | 15 |
| 6.1 | Molecular definition file | 15 |
| 6.2 | Information auxfile output | 16 |
| 6.3 | Report output | 17 |
| 6.4 | MOL file output | 18 |
| 6.5 | LuaTeX file example | 19 |
| 6.6 | LaTeX file example | 20 |

1 Introduction

Molecular Coding Format(MCF) is new linear notation represent chemical structure diagrams. This Coding is named from programing technique such as operator, array, scope, macro, adressing, etc. mcf2graph convert from MCF to pk font, PNG, SVG, EPS, MOL file. It is also able to calculate molecular weight, exact mass, molecular formula.

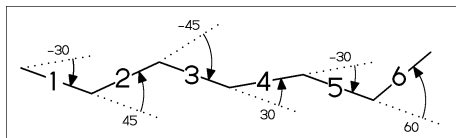
2 MCF syntax

2.1 Make bond

2.1.1 Chain

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

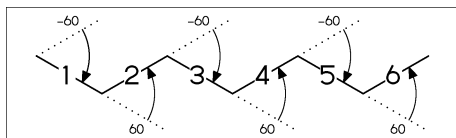
<-10,-30,45,-45,30,-30,60



2.1.2 Chain use !,!n

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

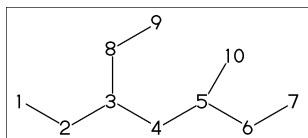
<-30,! ,! ,! ,! ,! ,!
<-30,!6



2.1.3 Jump to atom

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

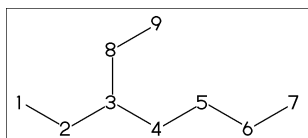
<-30,!6,@3,0,! ,@5,-30



2.1.4 Branch bond

\ : 0

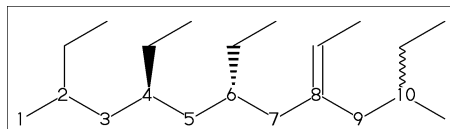
<-30,!6,@3,\,! ,!



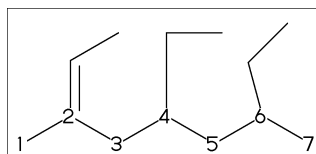
2.1.5 Branch modified bond

\ : 0
*\ : 0~wf
* : 0~zf
\ \ : 0~dm
** : 0~wv

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



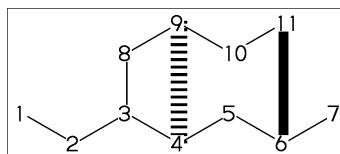
<30,!6,
\~dr,! , : 0~dr,!
\'1.5,-90 : 0'1.5,-90
\^15,-60 : 0^15,-60



2.1.6 Connect atom

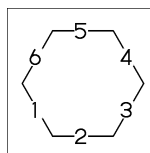
&n : Connect to An

<-30,!6,@3,\,!3,&6~bd,@9,&4~bz



2.1.7 Ring

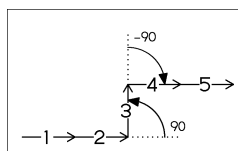
?n : n membered ring(3<=n<=20)
?6 : <-120,60,60,60,60,60,&1
?6



2.1.8 Rotate current angle

<angle : rotate current angle

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

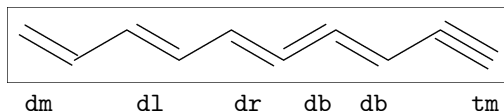


2.2 Change bond type

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

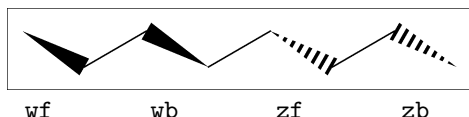
```
<-30,!~dm,!~dl,!~dr,!~db,!~db,!~tm  
<-30,!~dm,!~dl,!~dr,!! ,!! ,!!!
```



2.2.2 Wedge

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

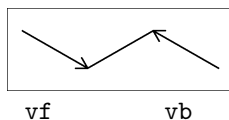
```
<-30,!~wf,!~wb,!~zf,!~zb
```



2.2.3 Vector

vf:vector forward / vb:vector backward

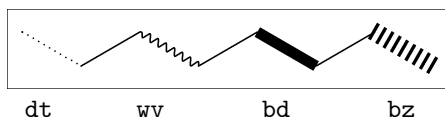
```
<-30,!~vf,!~vb
```



2.2.4 Dotted,wave

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

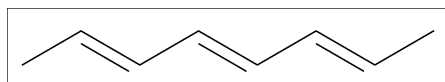
```
<-30,!7,1=dt,3=wv,5=bd,7=bz
```



2.2.5 Change multiple bond type

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

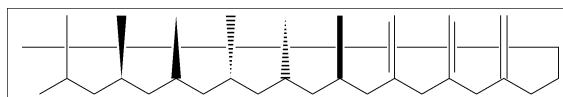
```
<30,!7,{2,4,6}=dr
```



2.2.6 Over line

si_ : single over line
wf_ : wedge forward over line
wb_ : wedge backward over line
zf_ : wedge dotted forward over line
zb_ : wedge dotted backward over line
bd_ : broad over line
dl_ : duble left over line
dr_ : duble right over line
dm_ : duble over line

```
<30,!8,!60,90'18,  
{2~si_,4~wf_,6~wb_,8~zf_,10~zb_,  
12~bd_,14~dl_,16~dr_,18~dm_}:/_ '2
```

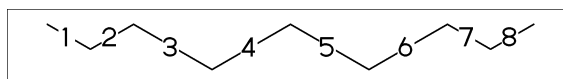


2.3 Change bond length

2.3.1 Chain length

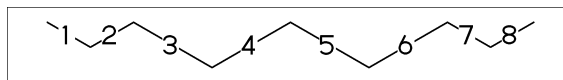
(!,!n)'length : change length of !,!n

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



#n : bond length=n
: reset bond length

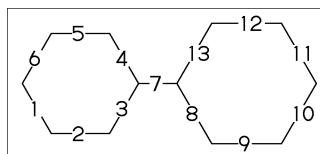
```
<-30,!2,#1.2,!4,##,!2
```



2.3.2 Ring length

?n'length : change ring length

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

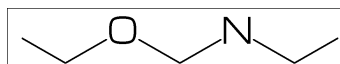


2.4 Change atom

2.4.1 Insert atom

Insert hetero atom

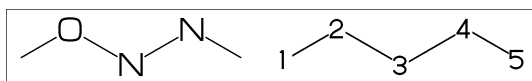
```
<-30,!2,0,!2,N,!2
```



2.4.2 Addressed atom

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

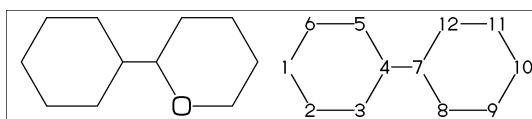
<30,!4,2:0,{3,4}:N



2.4.3 Brock address

| : divide brock

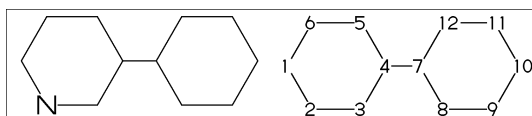
?6,@4,\,|,?6,2:0



2.4.4 Reset brock address

|| : reset brock address

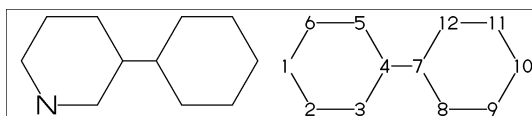
?6,@4,\,|,?6,||,2:N



2.4.5 Absolute address

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

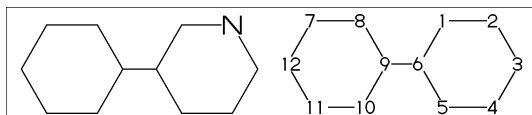
?6,@4,\,|,?6,\$2:N



2.4.6 Relative address

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

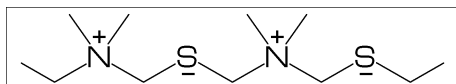
?6,@4,\,?6,-2:N



2.4.7 Charged atom

p_ : positive / n_ : negative

<-30,!2,N,??,p_,!2,S,n_~180,
!6,7:N,7:??,9:S,7:n_,9:n_~180



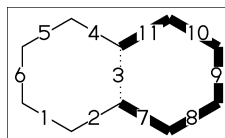
2.5 Fuse ring

2.5.1 Attached 1 bond

?6,3=?6 : fuse ?6 at B3

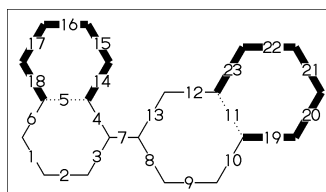
** Bn(n:-999<=n<=4095): bond number

?6,3=?6



** fused ring size depend on
attached bond length

?6,@4,\,?6'1.2,5=?6,11=?6

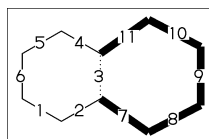


?6,3=?6[13] : fuse ?6[13] at B3

?6[13]: 6 membered ring scaled 13/10

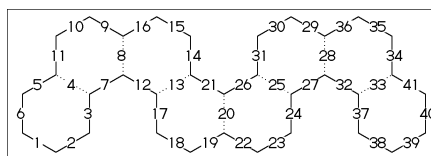
** ?m[n] (5<=m<=8,11<=n<=15)

?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

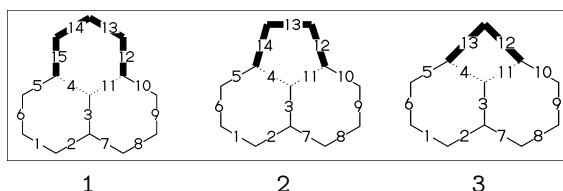
(4,11)=?4[2] : fuse 2/4 ring to B11..B4

** ?m[n] (4<=m<=6,n=m-2)

1:<30,?6,3=?6,(11,4)=?6[4]

2:<30,?6,3=?6,(11,4)=?5[3]

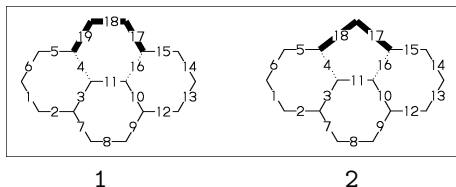
3:<30,?6,3=?6,(11,4)=?4[2]



2.5.3 Attached 2 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:?6,{3,10}=?6,(16,4)=?6[3]
2:?6,{3,10}=?6,(16,4)=?5[2]
```

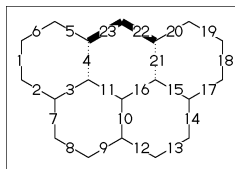


2.5.4 Attached 4 bond

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

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

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

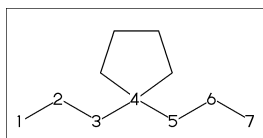


2.5.5 Spiro ring

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

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

```
@An : jump to An
```

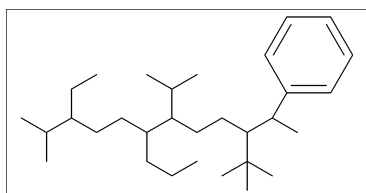


2.6 Group

2.6.1 Insert group

```
/ : single
<-30,!/_,!/,!/,!3,!2,!/,?! ,
!3,/??! ,!/,Ph~30,!
```

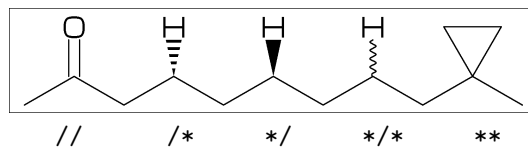
```
** /_ : methyl      /! : ethyl
   /!2 : propyl     /?! : isopropyl
   /?! : tert-butyl /Ph : phenyl
```



2.6.2 Insert modified group

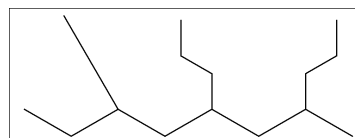
```
// : double (double middle)
/* : wedge forward
/* : wedge dotted forward
/* : wave
** : direct
```

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



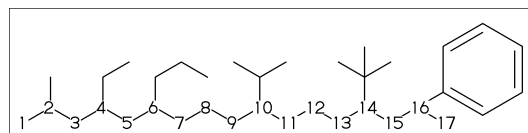
```
~ : change type
^ : change angle
' : change length
> : change environment
```

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



2.6.3 Add group

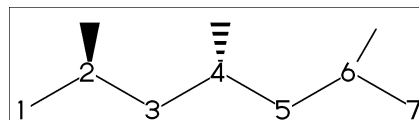
```
<30,!17,2:/_ ,4:/! ,6:/!2 ,
10:/?! ,14:/?! ,16:/Ph~60
```



2.6.4 Add modified group

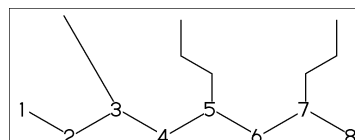
```
~,^,' : change type,angle,length
```

```
<30,!6,
{2~wf,4~zf,6~30}:/_
```



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

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

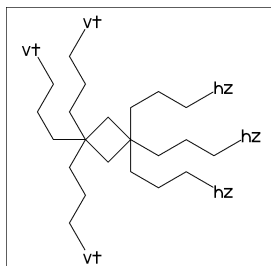


2.7 Chain environment

2.7.1 Horizontal,vertical

>hz : horizontal environment (default)
>vt : vertical environment

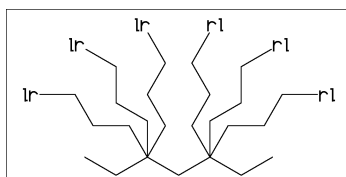
```
?4,  
{3^-90,3^-30,3^90}:/'(!3,"{hz}")>hz,  
{1^-60,1,1^60}:/'(!3,"{vt}")>vt
```



2.7.2 Left-right,right-left

>lr : left-right environment
>rl : right-left environment

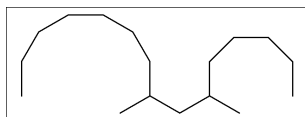
```
<-30,!6,  
{3^-30,3,3^30}:/'(!3,"{lr}")>lr,  
{5^-30,5,5^30}:/'(!3,"{rl}")>rl
```



2.7.3 Fixed rotate angle

>n : rotate n

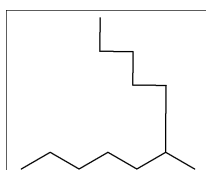
```
<30,!4,  
2:/!6>30, % 2:\,30,30,30,30,30,30  
4:/!4>-45 % 4:\,-45,-45,-45,-45
```



2.7.4 Multi rotate angle

>'(90,-90,...) : rotate 90,-90,...

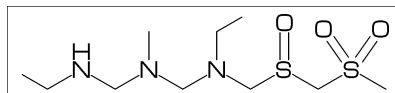
```
<30,!6,6>'(90,-90,90,-90,90):/!5
```



2.8 Miscellaneous

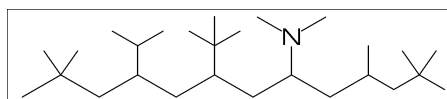
2.8.1 Abbreviated parts

```
NH : N,/H~nl  
N! : N,/_  
N!2 : N,/!  
SO : S,//O  
S00 : S,//O^35,/^-35  
  
<-30,!2,NH,!2,N!,!2,N!2,SO,!2,S00,!2
```



```
?! : /_,!  
?? : /_~35,/_-35  
/?! : isopropyl  
/??! : tert-butyl  
/N?! : dimethylamino
```

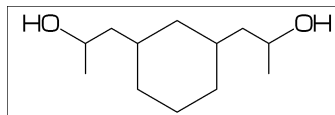
```
<30,!9'1,?!,!2,??,!2,  
2:??,4:/??,6:/??!,8:/N?!
```



2.8.2 Parts definition

'(..) : user defined parts

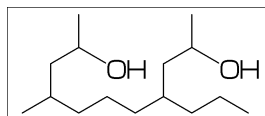
```
iBuOH:='(!,/_,!2,OH);  
MC(<30,!6,{4,6}:/iBuOH)
```



2.8.3 Parts inline definition

```
<30,!2, /'(!,/_,!2,OH),  
!4,/'(!,/_,!2,OH),!3
```

```
<30,!8,{2,6}:/'(!,/_,!2,OH)
```



3 Option parameter

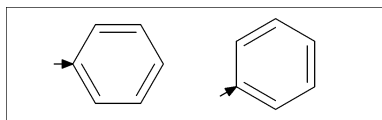
3.1 Angle parameter

mangle=0 ** default

MCat(0.2,0.5)(Ph)

mangle:=30;

MCat(0.8,0.5)(Ph)

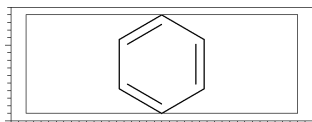


3.2 Size/Ratio parameter

3.2.1 Bond length

(fit to font size)

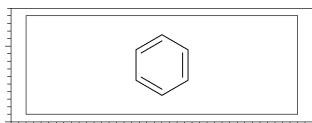
blength=0 ** default



(ratio bond/font width)

blength=0.1 ** (0<blength<=1)

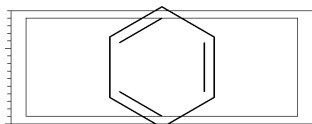
blength=60mm(width)*0.1=6mm



(bond length)

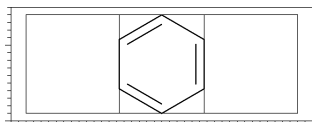
blength=9mm

** (blength>1) ignore msize(w,h)



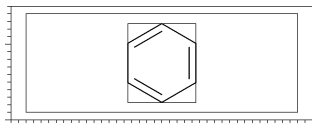
3.2.2 Molecular size

msize=(1,1) ** default

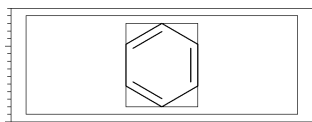


msize=(0.25,1)

msize=40mm-4mm*0.25=9mm

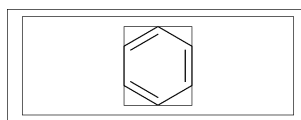


msize=(11mm,11mm)



3.2.3 Molecular position

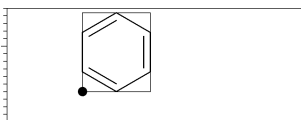
mposition=(0.5,0.5) ** default



mposition=(1,0)



mposition=(10mm,4mm)



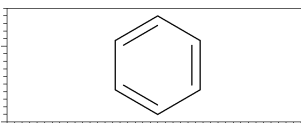
3.3 Size parameter

3.3.1 Font size

fsize=(font width,font height)

** default: (30mm,20mm)

fsize=(40mm,15mm)

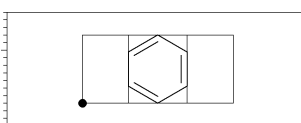


3.3.2 Font margin

fmargin=(margin left right,top bottom)

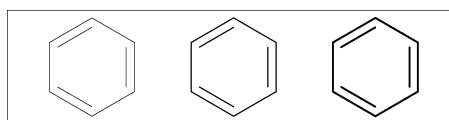
** default: (0.4mm,0.4mm)

fmargin=(10mm,2mm)



3.3.3 Offset thickness of bond

default: offset_thickness=0.2pt



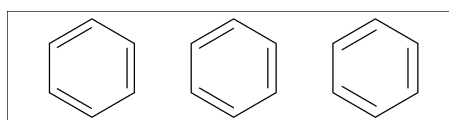
0pt

0.2pt

0.5pt

3.3.4 Offset of double bond gap

default: offset_bond_gap=0.3pt



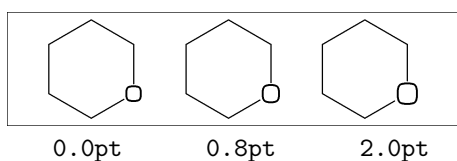
0.0pt

0.3pt

1.0pt

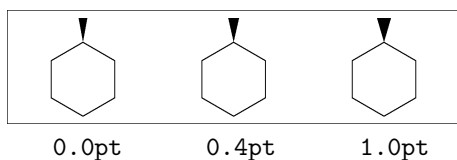
3.3.5 Offset of atom width

default: `offset_atom=0.8pt`



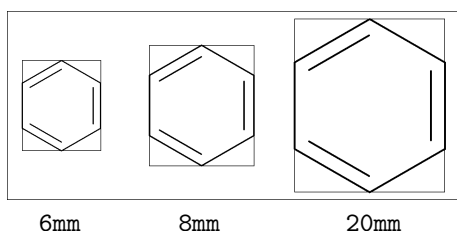
3.3.6 Offset of wedge width

default: `offset_wedge=0.4pt`



3.3.7 Max bond length

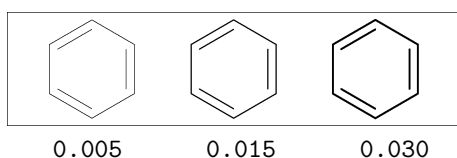
default: `max_blength=10mm`



3.4 Ratio parameter

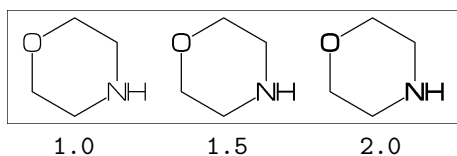
3.4.1 Thickness/bond length

default: `ratio_thickness_bond=0.015`



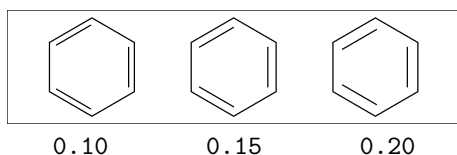
3.4.2 Char/bond thickness

default: `ratio_char_bond=1.5`



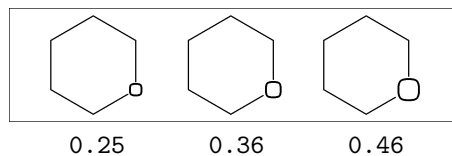
3.4.3 Bond gap/bond length

default: `ratio_bondgap_bond= 0.15`



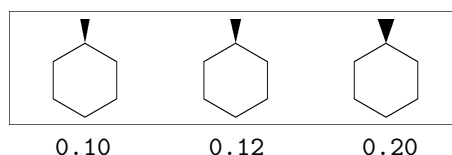
3.4.4 Atom/bond length

default: `ratio_atom_bond= 0.36`



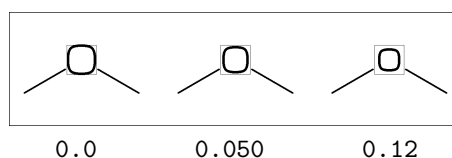
3.4.5 Wedge/bond length

default: `ratio_wedge_bond=0.12`



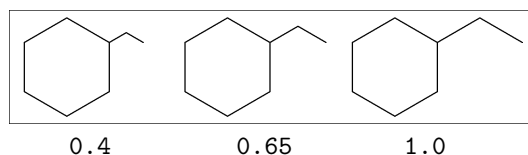
3.4.6 Font atom gap/atom length

default: `ratio_atomgap_atom= 0.050`



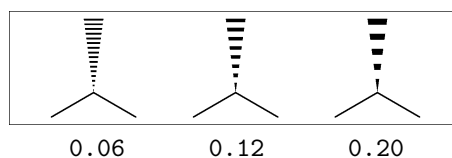
3.4.7 Chain/ring length

default: `ratio_chain_ring= 0.66`



3.4.8 Zebra gap/bond length

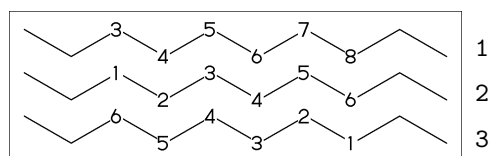
default: `ratio_zebragap_bond=0.12`



3.5 Drawing mode

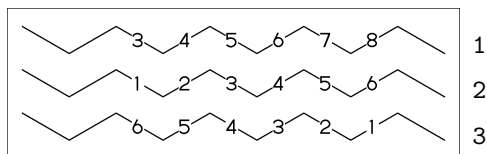
3.5.1 Numbering atom

`numberA_start:=3; numberA_end:=8;`
default: `sw_numberA=0 :`
`numberA_start=1 numberA_end=4095`



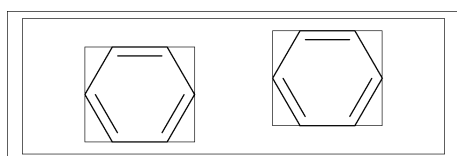
3.5.2 Numbering bond

```
numberB_start:=3; numberB_end:=8;
default: sw_numberB=0 :
    numberB_start=1 numberB_end=4095
```

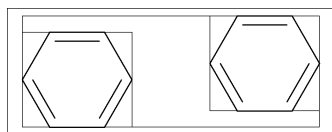


3.5.3 Trimming mode

```
sw_trimming:=0; ** default
msize:=(1,0.7);
MCat(0.2,0.3)(Ph)
MCat(0.8,0.7)(Ph)
```

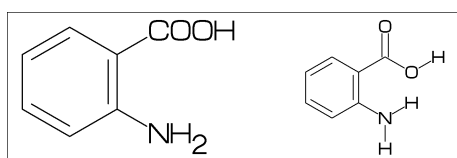


```
sw_trimming:=1;
MCat(0.2,0.3)(Ph)
MCat(0.8,0.7)(Ph)
```



3.5.4 Expand mode

```
MCat(0, .5)(<30,Ph,4:/COOH,3:/NH2)
sw_expand:=1;
MCat(1, .5)(<30,Ph,4:/COOH,3:/NH2)
** default: sw_expand=0
```



3.5.5 Group off mode

```
** default: sw_group_off=0
```



3.5.6 Single bond mode

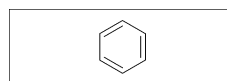
```
** default: sw_single=0
```



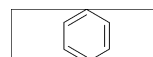
3.6 Frame

3.6.1 Font frame

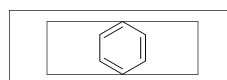
```
(Draw font frame)
fmargin:=(5mm,2mm);
sw_fframe=1
```



```
(Frame inside margin)
sw_fframe=2
```



```
(Draw both frame)
sw_fframe=3
```

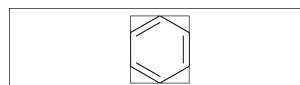


```
(Small dot at corner)
sw_fframe=4
```



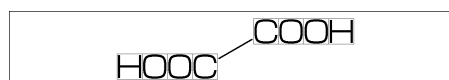
3.6.2 Molecular frame

```
sw_mframe=1 ** default:sw_mframe=0
```



3.6.3 Atom frame

```
sw_aframe=1 ** default: sw_aframe=0
MC(<30,COOH,! ,COOH)
```



3.6.4 Remove indent

```
** default sw_indent_off=0
beginfont(" : Ph ",
    " : ,{1,4}:N ",
    " : ,{2,3}:/_ ")
endfont
```

```
mc1=" Ph"
mc2=" ,{1,4}:N"
mc3=" ,{2,3}:/_ "
```

```
sw_indent_off=1
```

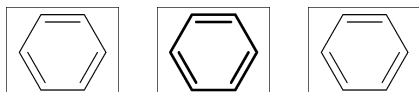
```
mc1="Ph"
mc2=" ,{1,4}:N"
mc3=" ,{2,3}:/_ "
```

```
mc="Ph,{1,4}:N,{2,3}:/_ " ** 0 or 1
```

3.7 Parameter setting

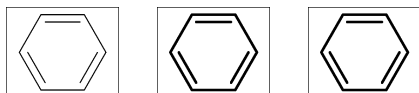
3.7.1 Local parameter setting

```
beginfont()
  MC(Ph)
endfont
beginfont()
  %-----
  ratio_thickness_bond:=0.05;
  %-----
  MC(Ph)
endfont
beginfont()
  MC(Ph)
endfont
```



3.7.2 Global parameter setting

```
beginfont()
  MC(Ph)
endfont
%-----
ratio_thickness_bond:=0.05;
%-----
beginfont()
  MC(Ph)
endfont
beginfont()
  MC(Ph)
endfont
```



4 Function

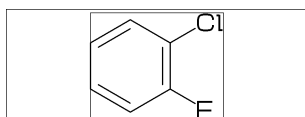
4.1 Function MC()

(Draw molecule)

```
msize=(a,b)      **default (1,1)
mposition=(c,d)   **default (0.5,0.5)
```

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

```
beginfont()
  MC(<30,Ph,3:/F,4:/Cl)
endfont
```



4.2 Function MCat()

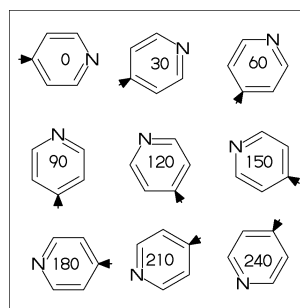
(Draw molecule at mposition)

MCat(c,d)(...) :

mposition:=(c,d); MC(...)

c: x axis position d: y axis position

```
defaultsize:=5bp;
fsize:=(40mm,40mm); fmargin:=(3mm,3mm);
blength:=0.1; sw_fframe:=1;
mangle:=0;
for i=1 step -0.5 until 0:
  for j=0 step 0.5 until 1:
    MCat(j,i)(Ph,4:N)
    add(drawarrow((A1+A1up**aw)..A1);
        label(decimal(mangle),
            p0+(0.5w,0.5h));
    )
    mangle:=mangle+30;
  endfor
endfor
```



4.3 Function check_mc()

(immediately compile)

```
beginfont("EN:Pyridine")
  MC(Ph,<30,2:N)
endfont
```

(check mcf and compile)

```
beginfont("EN:Pyridine",":<30,Ph,2:N")
  if check_mc(mc)=0: MC(scantokens(mc)) fi
endfont
```

```
** error in mcf check_mc(mc)=1
beginfont("EN:Pyridine",":<30,Ph,2):N")
  if check_mc(mc)=0: MC(scantokens(mc)) fi
endfont
```



check_mc(mc)=0 check_mc(mc)>=1

4.4 Function add()

(Add 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]ang: branch angle of A[m]
A[m]up: dir A[m]ang
A[m]left: dir A[m]ang+90
A[m]right: dir A[m]ang-90
A[m]down: dir A[m]ang+180

Bn: bond number
B[m]: bond(path)
B[m]s: bond start position
B[m]m: bond middle position
B[m]e: bond end position
B[m]ang: bond angle
B[m]up: dir B[m]ang
B[m]left: dir B[m]ang+90
B[m]right: dir B[m]ang-90
B[m]down: dir B[m]ang+180

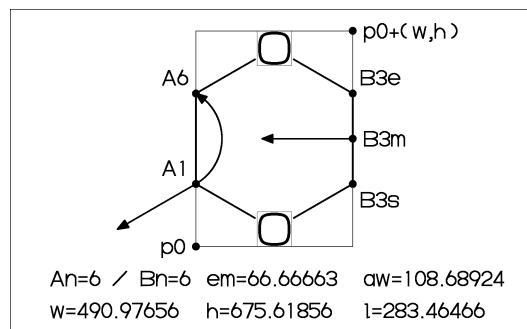
plus : '+' circled
minus : '-' circled
circlediam = 0.6aw (default)
circlepen = 0.2bp (default)

lonpair r: ':' rotated r
lonpairdiam = 0.3aw (default)
lonpairspace = 0.7aw (default)

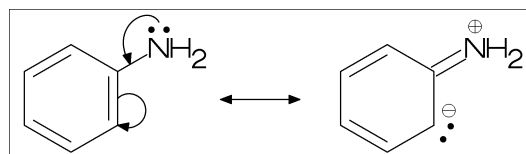
** : scaled
<< : rotated
a /* b : point b of a

```
beginfont("EN:add() 1")
fsize:=(75mm,45mm);
sw_aframe:=sw_mframe:=1;
max_blength:=12mm;
msize:=(.91,.85);
MCat(.5,.8)(<30,?6,{2,5}:0)
%-----
add(
  defaultscale:=.8;
  labeloffset:=.3aw;
  dotlabel.lft("p0",p0);
  dotlabel.rtl("p0+(w,h)",p0+(w,h));
  dotlabel.ulft("A1",A1);
  drawarrow A1..A1+(1,0)<<(A1ang);
  dotlabel.lrt("B3s",B3s);
  dotlabel.rtl("B3m",B3m);
  drawarrow B3m..B3m+(1,0)<<(B3ang+90);
```

```
dotlabel.ulft("A6",A6);
drawarrow A1{A1down}..A6;
dotlabel.urtr("B3e",B3e);
label.rtl("An"&decimal(An)&" / "&
  "Bn"&decimal(Bn),p0+(-w,-1.5em));
label.rtl("aw"&decimal(aw),p0+(w,-1.5em));
label.rtl("em"&decimal(em),p0+(0,-1.5em));
label.rtl("w"&decimal(w),p0+(-w,-3em));
label.rtl("h"&decimal(h),p0+(0,-3em));
label.rtl("l"&decimal(l),p0+(w,-3em));
)
endfont
```



```
beginfont("EN:add() 2")
fsize:=(60mm,20mm);
msize:=(1,0.85);
%-----
MCat(0,0)(<30,Ph,3=d1,4:/NH2)
%-----
add(
  labeloffset:=.7aw;
  label.top(lonpair 90,A7);
  drawarrow
    (A7+up**1.2aw){A7left}
    ..{B7right}B7/*0.3;
  drawarrow
    B3m..A3+B2up**1.5aw..{A3down}A3;
)
%-----
MCat(1,0)(<30,?6,{1,5}=d1,4://NH2)
%-----
add(
  labeloffset:=.7aw;
  label.top(plus,A7);
  label.urtr(minus,A3);
  label(lonpair A3ang,A3+A3up**1.7aw);
)
%-----
ext(drawdblarrow (.4w,.4h)..(.55w,.4h);)
%-----
endfont
```



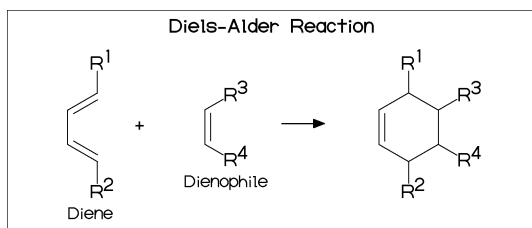
4.5 Function ext()

(Extra graphic to font)

```
w:      font width
h:      font height
w0:     font width-2xpart(fmargi)
h0:     font height-2ypart(fmargi)
aw:     atom font size
em:     label font size
p0:     fmargi

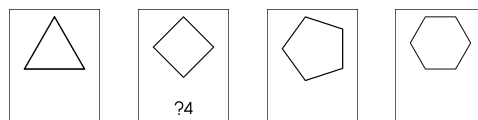
n:      molecular number
p[m]:   molecular origin position
w[m]:   molecular width
h[m]:   molecular height

ratio_thickness_char:
    pen thickness / char width
%-----
beginfont()
    fsize:=(70mm,30mm);
    blength:=0.065;
%-----
MCat(0.1,0.5)(
    <-210,60'1,60'1,60'1,{1,3}=d1,
    1:/R1,4:/R2~-60
)
add(
    defaultscale:=0.6;
    label.bot("Diene",p0+(0.5w,0));
)
MCat(0.4,0.5)(
    <-30,-60'1,1=d1,1:/R3,2:/R4^60
    add(defaultscale:=0.6;
    label.bot("Dienophile",p0+(.5w,0));
)
MCat(0.9,0.5)(
    <30,?6,6=d1,2:/R2,3:/R4,4:/R3,5:/R1
)
%-----
ext(
    drawarrow (.52w,.5h)..(.6w,.5h);
    defaultscale:=0.7;
    label("+",(0.25w,0.5h));
    ratio_thickness_char:=0.125;
    label.bot("Diels-Alder Reaction",
        (.5w,h));
)
%-----
endfont
```



4.5.1 Local ext() setting

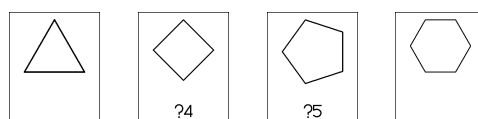
```
beginfont("EN:?3")
    fsize:=(12mm,15mm);
    MCat(0.5,1)(<30,?3)
endfont
beginfont("EN:?4")
    fsize:=(12mm,15mm);
    MCat(0.5,1)(?4)
%-----
ext(label.top(inf_EN,(0.5w,0));)
%-----
endfont
beginfont("EN:?5")
    fsize:=(12mm,15mm);
    MCat(0.5,1)(?5)
endfont
beginfont("EN:?5")
    fsize:=(12mm,15mm);
    MCat(0.5,1)(?6)
endfont
```



4.5.2 Global ext() setting

ext_clear: reset global ext()

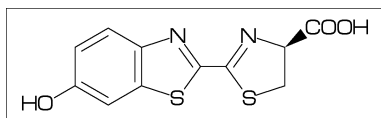
```
beginfont("EN:?3")
    fsize:=(12mm,15mm);
    MCat(0.5,1)(<30,?3)
endfont
%-----
ext(label.top(inf_EN,(0.5w,0));)
%-----
beginfont("EN:?4")
    fsize:=(12mm,15mm);
    MCat(0.5,1)(?4)
endfont
beginfont("EN:?5")
    fsize:=(12mm,15mm);
    MCat(0.5,1)(?5)
endfont
%-----
ext_clear;
%-----
beginfont("EN:?6")
    fsize:=(12mm,15mm);
    MCat(0.5,1)(?6)
endfont
```



5 MCF example

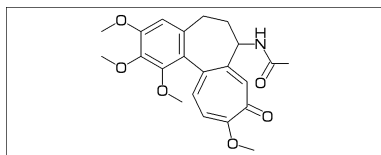
5.1 Luciferin

```
beginfont("EN:Luciferin","MW:280.33",
%-----
": <30,Ph,3=?5,@8,\,?5,{9,16}=d1,    ",
": {9,14}:N,{7,11}:S,1:/OH,-2:*/COOH ")
%-----
fsize:=(50mm,20mm);
if check_mc(mc)=0: MC(scantokens(mc)) fi
endfont
```



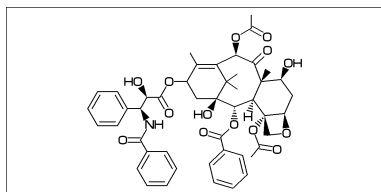
5.2 Colchicine

```
beginfont("EN:Colchicine","MW:385.41",
%-----
": <30,Ph,{1,2,6}:/O!,-4=?7,-5=?7,    ",
": {-1,-4,-6}=d1,-2://O,-3:/O!,      ",
": @9,\,NH,!,//O,!                    ")
%-----
fsize:=(50mm,20mm);
if check_mc(mc)=0: MC(scantokens(mc)) fi
endfont
```



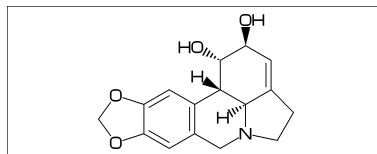
5.3 Paclitaxel

```
beginfont("EN:Paclitaxel","MW:853.91",
%-----
": ?6,5=d1,@3,#1,36,45,45,45,45,##,    ",
": &.$5",                                ",
": -4=?6,-4=?4,-1=wb,-3=wf,-1:0,||,    ",
": 4:??,6:/_,{3~-60,15}:*/OH,          ",
": 8:/*H~-60,"                          ",
": 9:*/_~60,10://O,                     ",
": @1,\,0,!,//O,!,*/*OH,!/,Ph,60~wf,   ",
": NH,-60,//O,60,Ph,                    ",
": @7,\*,0,-45,//O,60,Ph,               ",
": @11,\*,0,-60,//O,60,                 ",
": @12,\*~-15,0,60,//O,-60              ")
%-----
fsize:=(50mm,25mm);
if check_mc(mc)=0: MC(scantokens(mc)) fi
endfont
```



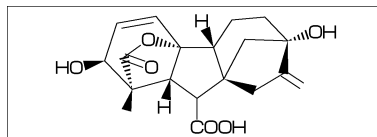
5.4 Lycorine

```
beginfont("EN:Lycorine","MW:287.31")
%-----
": 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:/*OH                        ")
%-----
fsize:=(50mm,20mm);
if check_mc(mc)=0: MC(scantokens(mc)) fi
endfont
```



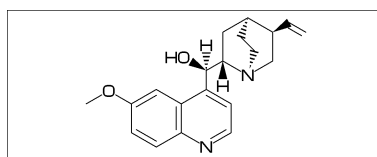
5.5 Gibberellin

```
beginfont("EN:Gibberellin A3","MW:346.37");
%-----
": <18,?5,3=?7,5=?6[12],@8,160'1.3,&3,  ",
": 13=d1,6=wf,8=wb,                        ",
": @5,40~zf'1,0,50,//O^180,&14~zb,        ",
": 2:/COOH,7://_,13:*/OH,8:/*OH,          ",
": 14:*/_,{1,4}:*/H^60                     ")
%-----
fsize:=(50mm,18mm);
if check_mc(mc)=0: MC(scantokens(mc)) fi
endfont
```



5.6 Quinine

```
beginfont("EN:Quinine","MW:324.42")
%-----
": <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                      ")
%-----
fsize:=(50mm,20mm);
if check_mc(mc)=0: MC(scantokens(mc)) fi
endfont
```



6 Example to use mcf2graph

6.1 Molecular definition file

```
%-----
input mcf2graph.mf;                                     % input macro
%-----
sw_aux_out:=1;      % aux(information) file output on > Global setting
fsize:=(60mm,40mm); % (font width,font height)      >
tag1:="F";          > AUX file table
tag2:="C";          >
tag3:="mw";         >
tag4:="fm";         >
%%% sw_rep_out:=1;  > Report output
%%% sw_mol_out:=1;  > MOL file output
outputformat:="png"; hppp:=vppp:=0.1;               > PNG output
outputtemplate:="%j-%3c.png";                       >
%-----
beginfont("EN:Ampicillin","MW:349.405",              > information
%-----
": <45,?4,-3=?5,2:N,7:S,                             ", >
": 3^45:/*H,1://0^15,5:/*COOH^-18,6:??, ", > mc1
": @4,*\^15,NH,! ,//0,! ,/*NH2,! ,Ph          ") > mc2
%----- > mc3
if check_mc(mc)=0: MC(scantokens(mc)) fi > mc=mc1&mc2&mc3
endfont > end font
%-----
beginfont("EN:Cholesterol","MW:386.65",              >information
%-----
": <30,?6,{-4,-2}=?6,-4=?5,7=d1, ", > mc1
": 10:/*H^180,11:/*H^-60,17:/*H^-54, ", > mc2
": {4,12}:*/_ ^60, ", > mc3
": @-1,18,/*_,-60,!3,?! ") > mc4
%----- >
if check_mc(mc)=0: MC(scantokens(mc)) fi > mc=mc1&mc2&mc3
endfont > end font
%-----
beginfont("EN:Limonin", > information
%-----
": <30,?6,{-3,-4}=?6, ", > mc1
": -5=?3,-2=wf,-1=wb,6=?5,-4=?6,-5=wf, ", > mc2
": {13,15,17,20}:0,{3,12,21}://0, ", > mc3
": {4~wf^60,8~zf^60,18^35,18^-35}:/_, ", > mc4
": {1^60,5^180,16^60}:/*H, ", > mc5
": @14,\*,| ,?5,{1,4}=d1,3:0) ") > mc6
%----- >
if check_mc(mc)=0: MC(scantokens(mc)) fi > mc=mc1 - mc6
endfont > end font
%-----
beginfont("EN:beta-carotene", > information
%-----
": <30,?6,3=d1,{3,5^35,5^-35}:/_, ", > mc1
": @4,\,| ,!18,{1,3,5,7,9,11,13,15,17}=dr, ", > mc2
": {3,7,12,16}:/_, ", > mc3
": | ,?6,6=d1,2:??,6:/_) ") > mc4
%----- >
if check_mc(mc)=0: MC(scantokens(mc)) fi > mc=mc1 - mc4
endfont > end font
%-----
bye
```

6.2 Information auxfile output

(Insert option parameter setting)

```
sw_aux_out=1 : tag1:var1;tag2:var2
sw_aux_out=2 : tag1;tag2 var1;var2
** default : sw_aux_out=0
```

(Command line)

```
>mpost -s ahlength=1 FILENAME (sw_aux_out=1)
>mpost -s ahlength=2 FILENAME (sw_aux_out=2)
```

(Source)

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

(Setting)

```
tag1:="F"; tag2:="C"; tag3:="mw"; tag4:="fm"; tag5:="EN";
```

(Output)

(sw_aux_out=1)

```
F:mcf_man_soc;C:1;mw:349.40462;fm:C16H19N3O4S;EN:Ampicillin
F:mcf_man_soc;C:2;mw:386.6532;fm:C27H46O;EN:Cholesterol
F:mcf_exa_soc;C:3;mw:470.5113;fm:C26H30O8;EN:Limonin
F:mcf_exa_soc;C:4;mw:536.8722;fm:C40H56;EN:beta-Carotene
```

(sw_aux_out=2)

```
F;C;mw;fm
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
```

(aux_delimiter="/")

```
F:mcf_man_soc/C:1/mw:349.40462/fm:C16H19N3O4S/EN:Ampicillin
F:mcf_man_soc/C:2/mw:386.6532/fm:C27H46O/EN:Cholesterol
F:mcf_exa_soc/C:3/mw:470.5113/fm:C26H30O8/EN:Limonin
F:mcf_exa_soc/C:4/mw:536.8722/fm:C40H56/EN:beta-Carotene
```

(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
MI  : monoisotopic mass from literature data
USE : the use
mw  : molecular weight calculated
mi  : monoisotopic mass calculated
fm  : molecular formula calculated
w   : font width
h   : font height
```


6.3 Report output

(Insert option parameter setting)

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

(Command line)

```
>mpost -s ahlength=3 FILENAME
```

(Output)

```
-----  
Molecular name = Nicotine  
Warnings = 0 / Command count= 44  
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. ><atom(s) >( x axis , y axis )<bond><hideH><chg>  
A1 C ( 0 , 0 ) 3 1  
A2 N ( 0.866 , -0.5 ) 3  
A3 C ( 1.732 , 0 ) 3 1  
A4 C ( 1.732 , 1 ) 4  
A5 C ( 0.866 , 1.5 ) 3 1  
A6 C ( 0 , 1 ) 3 1  
A7 C ( 2.304 , 1.33 ) 3 1  
A8 N ( 3.217 , 0.923 ) 3  
A9 C ( 3.886 , 1.666 ) 2 2  
A10 C ( 3.386 , 2.532 ) 2 2  
A11 C ( 2.408 , 2.325 ) 2 2  
A12 C ( 3.399 , 0.067 ) 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  
Formula Calc: C10H14N2 / Input:  
=====
```

6.4 MOL file output

(Insert option parameter setting)

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

(Command line)

```
>mpost -s ahlength=5  FILENAME      % MOL(V2000)
>mpost -s ahlength=6  FILENAME      % MOL(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 O  0  0  0  0
  0.86603    2.36383      0 O  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}%
\usepackage[T1]{fontenc}%
\usepackage{textcomp}%
\mplibcodeinherit{enable}%
\mplibverbatim{enable}%
\mplibnumbersystem{double}%
\everymplib{%
  if unknown Ph1: input mcf2graph.mf; fi
  sw_calc:=1; sw_fframe:=4; max_blength:=4.5mm;
  defaultfont:="uhvr8r"; defaultsize:=8bp; defaultscale:=1;
}%
\begin{document}
\noindent%
%-----
\begin{mplibcode}
  fsize:=(50mm,50mm);
  beginfont("N0:1","EN:Limonin","MW:470.51",
    %-----
    ": <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 ")
    %-----
  if check_mc(mc)=0: MC(scantokens(mc)) fi
  endfont
\end{mplibcode}\\
%-----
\begin{mplibcode}
  fsize:=(80mm,50mm);
  beginfont("N0:2","EN:beta-carotene","MW:536.87",
    %-----
    ": <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}:/_ ")
    %-----
  if check_mc(mc)=0: MC(scantokens(mc)) fi
  endfont
\end{mplibcode}\\
%-----
\begin{mplibcode}
  fsize:=(50mm,50mm);
  beginfont("N0:3","EN:Gibberellin A3","MW:346.37",
    %-----
    ": <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 ")
    %-----
  if check_mc(mc)=0: MC(scantokens(mc)) fi
  endfont;
%-----
\end{mplibcode}\\
\end{document}

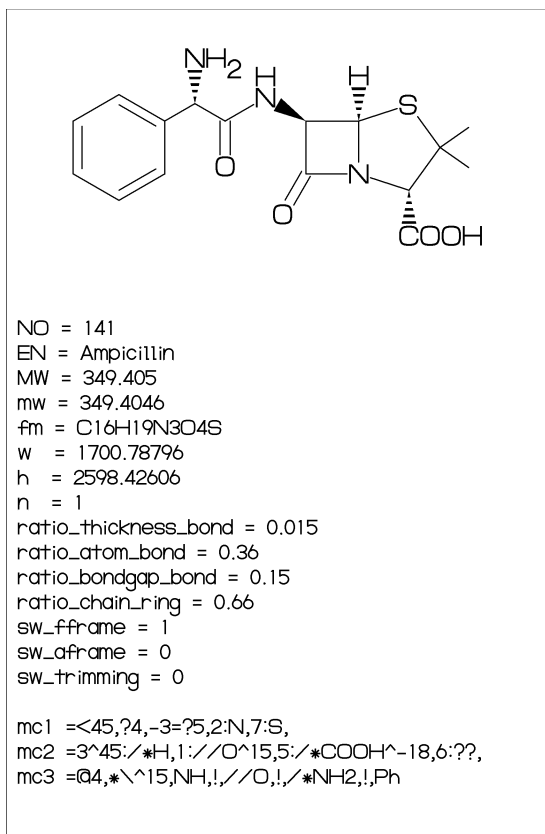
```

6.6 LaTeX file example

```
%-----
\documentclass[a4paper]{article}
\usepackage{graphicx}
%-----
\usepackage{mcf_setup}
%-----
\pagestyle{empty}
\makeatletter%
%-----
\def\put@char{%
  \begin{picture}(84,42)%
    \put(0,38){\bf [MOLnum]\EN{ } \small\tt/FM:\fm/MW:\mw}%
    \put(10,0){\font\@strufont=\File\relax%
      \hbox{\@strufont\char\Char}}}%
  \end{picture}%
}%
\def\INFO#1{\@for\@temp:=#1\do{\tag@var\@temp}\put@char}%
\makeatother
%-----
\begin{document}
\unitlength=1mm%
\INFO{F:mcf_man_soc,C:141,NO:1,mw:349.40462,fm:C16H19N3O4S,EN:Ampicillin}%
\INFO{F:mcf_man_soc,C:142,NO:2,mw:386.6532,fm:C27H46O,EN:Cholesterol}%
\end{document}
%-----
```

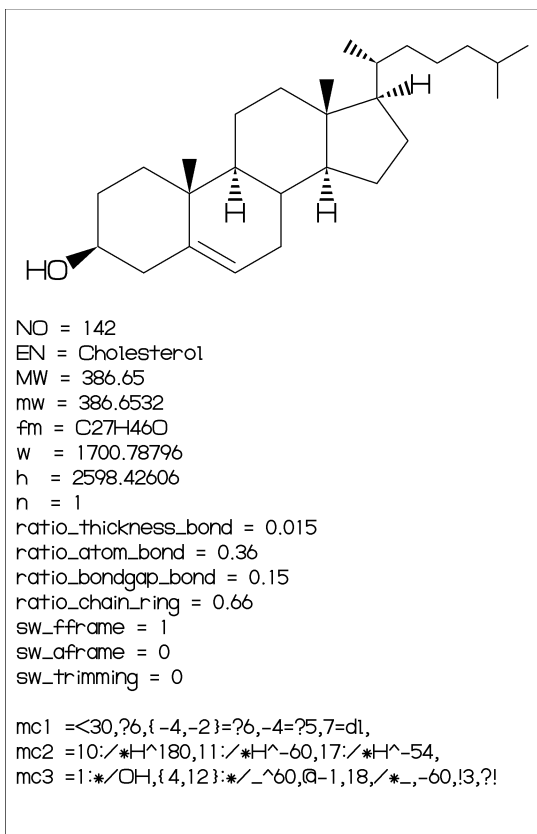
[1]Ampicillin

FM:C16H19N3O4S MW:349.40462



[2]Cholesterol

FM:C27H46O MW:386.6532



Index

!, 3
!!, 4
!!!, 4
, 7
**, 6, 12
*/, 6
/, 6
*\, 3
**, 3
/, 6
/*, 6, 12
//, 6
:, 5
?, 3
?!, 7
??, 7
??!, 7
@, 3
#, 4
##, 4
\$, 5
&, 3
~, 3, 6
~, 3, 4, 6
~~, 4
\, 3
*, 3
\\, 3
|, 5
||, 5
>, 3, 7
>>, 12
<, 6
' , 3, 4, 6

A[], 12
A[]ang, 12
A[]down, 12
A[]left, 12
A[]right, 12
A[]up, 12
add(), 12
An, 12
aux_delimiter, 16
aw, 12, 13

B[], 12
B[]ang, 12
B[]down, 12
B[]e, 12
B[]left, 12
B[]m, 12
B[]right, 12
B[]s, 12
B[]up, 12
bd, 4
bd_, 4
beginfont(), 11

blength, 8
Bn, 12
bz, 4

C, 16
check_mc(), 11, 14
circlediam, 12
circlepen, 12

db, 4
defaultscale, 12, 13
dl, 4
dl_, 4
dm, 4
dm_, 4
dr, 4
dr_, 4
dt, 4

em, 12, 13
EN, 16
endfont, 11
ext(), 13
ext_clear, 13

F, 16
FM, 16
fm, 16
fmarg, 8
fsize, 8

h, 12, 16
h0, 13
hz, 7

JN, 16

l, 12
labeloffset, 12
lonpair, 12
lonpairdiam, 12
lonpairspace, 12
lr, 7

mangle, 8
max_blength, 9
MC(), 11
MCat(), 11
mcf2graph.mf, 15
mcf_setup.sty, 20
MI, 16
mi, 16
minus, 12
mposition, 8
msize, 8
MW, 16
mw, 16

n, 13

| | |
|--------------------------|--------|
| N!, 7 | wf_, 4 |
| N!2, 7 | wv, 4 |
| N?!, 7 | |
| NH, 7 | zb, 4 |
| NO, 16 | zb_, 4 |
| numberA, 9 | zf, 4 |
| numberA_end, 9 | zf_, 4 |
| numberA_start, 9 | |
| numberB, 10 | |
| numberB_end, 10 | |
| numberB_start, 10 | |
| offset_atom, 9 | |
| offset_bond_gap, 8 | |
| offset_thickness, 8 | |
| offset_wedge, 9 | |
| p0, 12 | |
| Ph, 6 | |
| plus, 12 | |
| ratio_atom_bond, 9 | |
| ratio_atomgap_atom, 9 | |
| ratio_bondgap_bond, 9 | |
| ratio_chain_ring, 9 | |
| ratio_char_bond, 9 | |
| ratio_thickness_bond, 9 | |
| ratio_thickness_char, 13 | |
| ratio_wedge_bond, 9 | |
| ratio_zebragap_bond, 9 | |
| rl, 7 | |
| si_, 4 | |
| S0, 7 | |
| S00, 7 | |
| sw_aframe, 10 | |
| sw_aux_out, 15 | |
| sw_expand, 10 | |
| sw_fframe, 10 | |
| sw_group_off, 10 | |
| sw_indent_off, 10 | |
| sw_mframe, 10 | |
| sw_mol_out, 18 | |
| sw_rep_out, 17 | |
| sw_single, 10 | |
| sw_trimming, 10 | |
| tag, 15 | |
| tm, 4 | |
| USE, 16 | |
| var, 15 | |
| vb, 4 | |
| vf, 4 | |
| vt, 7 | |
| w, 12, 16 | |
| w0, 13 | |
| wb, 4 | |
| wb_, 4 | |
| wf, 4 | |