

Molecular Coding Format manual

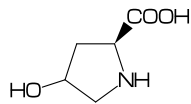
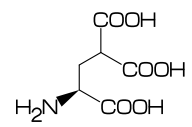
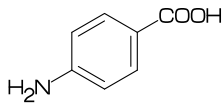
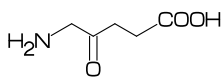
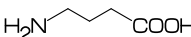
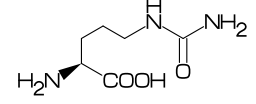
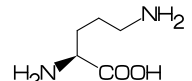
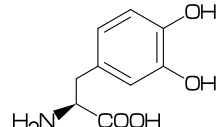
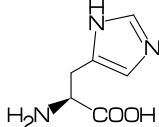
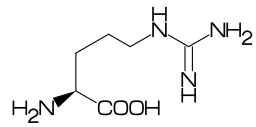
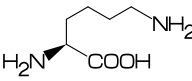
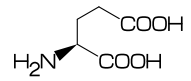
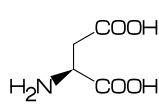
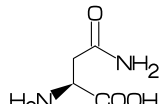
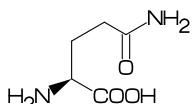
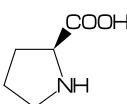
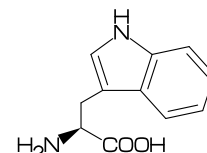
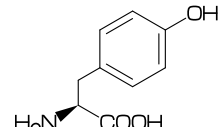
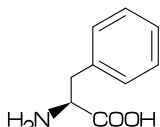
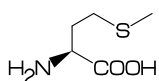
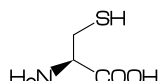
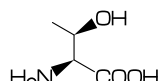
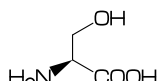
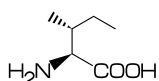
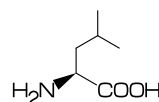
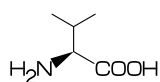
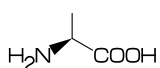
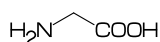
Akira Yamaji

February 25, 2024

mcf2graph version 5.12

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

Suggestion or request mail to: mcf2graph@gmail.com



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1 Introduction

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

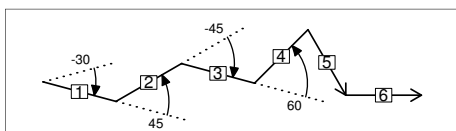
2 MCF syntax

2.1 Make bond

2.1.1 Chain

real number plus (+): counterclockwise
real number minus(-): clockwise
\$n (0<=n<360): absolute angle

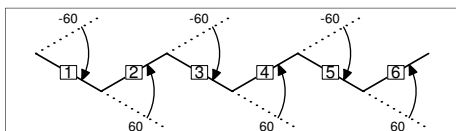
<10,-30,45,-45,60,\$300,\$0



2.1.2 Chain with !,!n

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

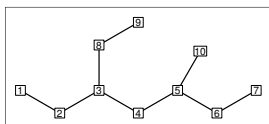
<-30,!6



2.1.3 Jump to atom

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

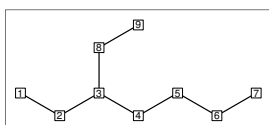
<-30,!6,@3,0,!,@5,-30



2.1.4 Branch bond

\ : 0

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

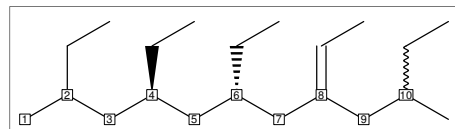


2.1.5 Branch modified bond

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

<30,!8,

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

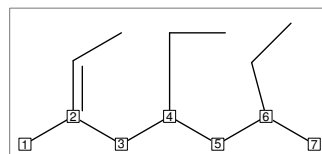


<30,!6,

\~dr,! : 0~dr,!

\^1.5,-90 : 0^1.5,-90

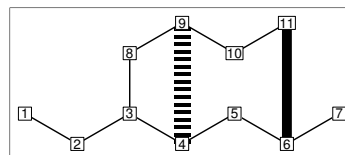
\^15,-60 : 0^15,-60



2.1.6 Connect atom

&n : Connect to An

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

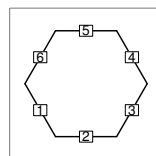


2.1.7 Ring

?n : n membered ring(3<=n<=20)

?6 : <-120,60,60,60,60,60,&1

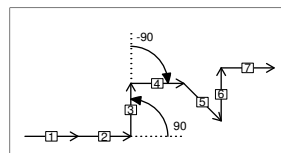
?6



2.1.8 Rotate current angle

<angle : rotate current angle

0,0,<90,0,<-90,0,<\$315,0,<\$90,0,<\$0,0



2.2 Change bond type

2.2.1 Double, triple, wedge, vector

(Double, triple)

a~type : ~~type, a

dm : double middle

dl : double left side

dr : double right side

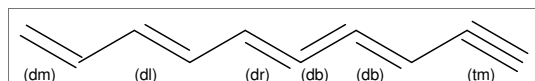
db : double left or right side

tm : triple

!db, !d : !~db / !tm, !t : !~tm

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

<-30, !dm, !, !dl, !, !dr, !d, !d, !, !t



(Wedge, Vector)

wf: wedge forward

wb: wedge backward

zf: hashed(zebra stripe) wedge forward

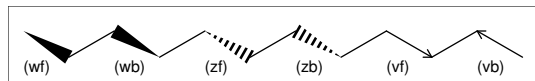
zb: hashed(zebra stripe) wedge backward

vf: vector forward

vb: vector backward

<-30,

!~wf, !, !~wb, !, !~zf, !, !~zb, !, !~vf, !~vb



(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



2.2.2 Over line

si_ : single over line

wf_ : wedge forward over line

wb_ : wedge backward over line

zf_ : hashed wedge forward over line

zb_ : hashed wedge backward over line

bd_ : broad over line

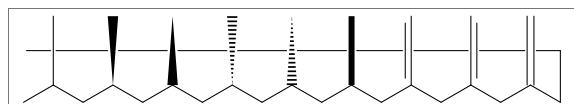
dl_ : double left over line

dr_ : double right over line

dm_ : double 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



2.2.3 Steric ring

wf_r : wedge forward (half width)

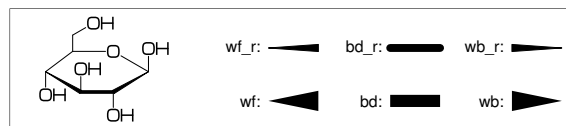
bd_r : broad (half width, rounded)

wb_r : wedge backward (half width)

#1.25, -30~wf_r, 30~bd_r`1, 30~wb_r,

120, 0, 30, &1, ##, #.5, 6~\$90: /!OH,

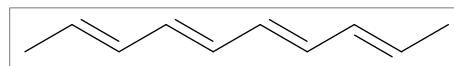
{1~\$-90, 2~\$90, 3~\$-90, 4~\$90}:/OH,



2.2.4 Change multiple bond type

{2, 4, 6, 8'}=dl : 2=dl, 4=dl, 6=dl, 8=dr

<30, !7, {2, 4, 6, 8'}=dl

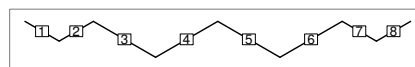


2.3 Change bond length

2.3.1 Chain length

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

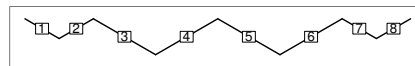
<-30, !2, !4`1.2, !2



#n : bond length=n

: reset bond length

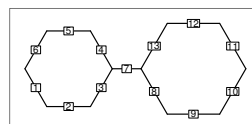
<-30, !2, #1.2, !4, ##, !2



2.3.2 Ring length

?n`length : change ring length

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

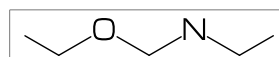


2.4 Change atom

2.4.1 Insert atom

Insert hetero atom

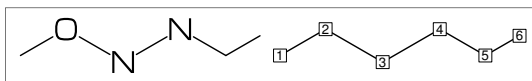
<-30, !2, 0, !2, N, !2



2.4.2 Addressed atom

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

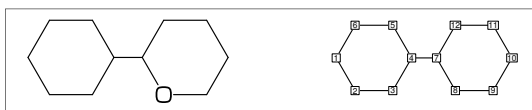
<30,14,2:0,{3,4}:N



2.4.3 Brock address

| : divide brock

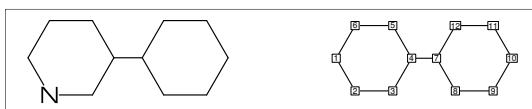
?6,@4,\,|,?6,2:0



2.4.4 Reset brock address

|| : reset brock address

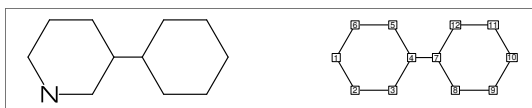
?6,@4,\,|,?6,||,2:N



2.4.5 Absolute address

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

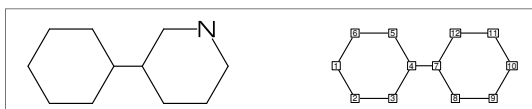
?6,@4,\,|,?6,\$2:N



2.4.6 Relative address

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

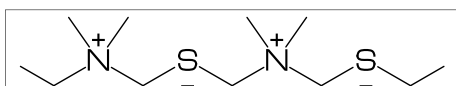
?6,@4,\,?6,-2:N



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_~180



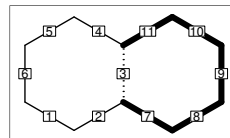
2.5 Fuse ring

(Attached 1 bond)

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

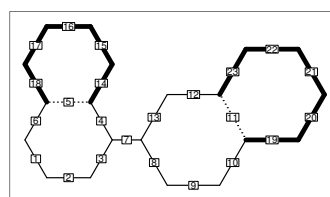
** Bn(n:-999<=n<=4095): bond number

?6,3=?6



** fused ring size depend on
 attached bond length

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

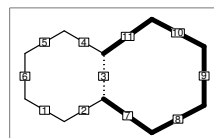


?6,3=?6[13] : fuse ?6[13] at B3

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

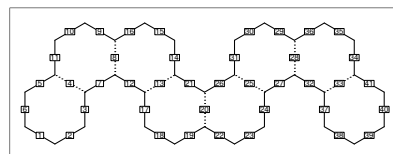
** ?m[n] (5<=m<=8,11<=n<=15)

?6,3=?6[13]



?6,{-3,-4,-4,-2,-2,-4,-4}=?6

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



(Attached 2 bond)

4--11=?6 : fuse 4/6 ring to B11..B4

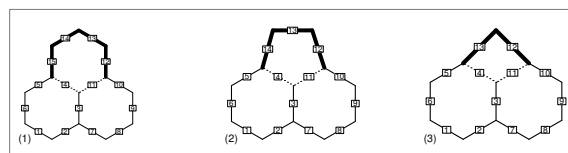
4--11=?5 : fuse 3/5 ring to B11..B4

4--11=?4 : fuse 2/4 ring to B11..B4

1:<30,?6,3=?6,11--4=?6

2:<30,?6,3=?6,11--4=?5

3:<30,?6,3=?6,11--4=?4



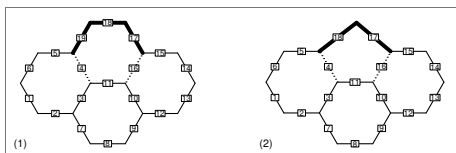
(Attached 3 bond)

16---4=?6 : fuse 3/6 ring to B16..B4

16---4=?5 : fuse 2/5 ring to B16..B4

1:?6,{3,10,16---4}=?6

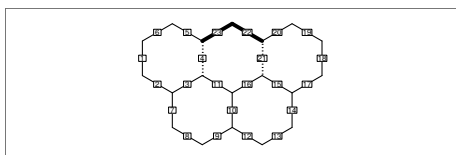
2:?6,{3,10}=?6,16---4=?5



(Attached 4 bond)

21----4=?6 : fuse 2/6 ring to B21..B4

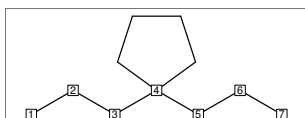
<-30,?6,{3,10,15,21----4}=?6



2.6 Spiro ring

@4,?5 : add ?5 at A4

<30,!6,@4,?5



2.7 Group

2.7.1 Insert group

/ : group start single bond

/_ : methyl

/! : ethyl

/!2 : propyl

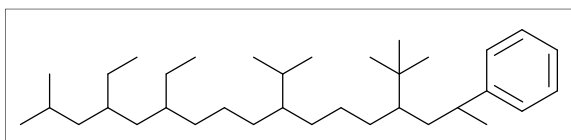
/?! : isopropyl

/??! : tert-butyl

/Ph : phenyl

<30,!/_,!2,/!,!2,/!2,!4,/?!,

!4,/??!,!2,/Ph^-60,!



2.7.2 Insert modified group

// : double (double middle)

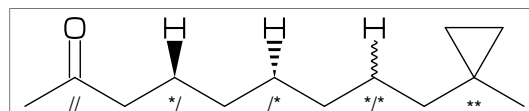
*/ : wedge forward

/* : hashed wedge forward

/ : wave

** : direct

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



~ : change type

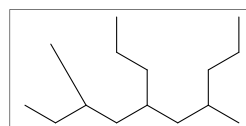
^ : change angle

` : change length

> : change environment

<-30,`^1,!,

/_`^2^30,!2,/!2>lr,!2,/!2>r1,!)

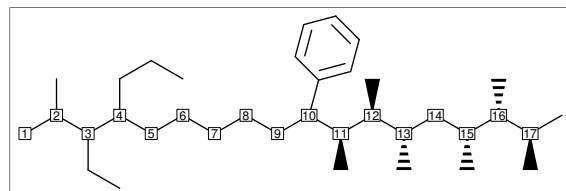


2.7.3 Add group

<30,!17,2/_ ,3:/!,4:/!2,7:/iPr,

8:/tBu,10:/!(Ph^0.6)^-15,

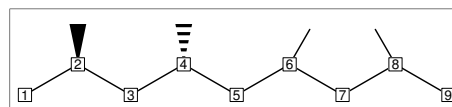
{11,12,13'}:*/_,{15,16,17'}:/*_



2.7.4 Add modified group

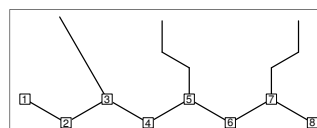
~,^,` : change type,angle,length

<30,!6,{2~wf,4~zf,6^-30,8^\$120}:/_



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

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

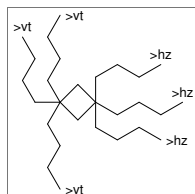


2.8 Chain environment

2.8.1 Horizontal,vertical

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

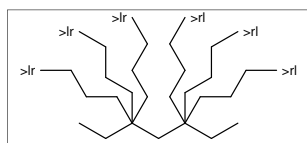
```
?4,  
{3^-90,3^-30,3^90}:/!3>hz,  
{1^-60,1,1^60}:/!3>vt
```



2.8.2 Left-right,right-left

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

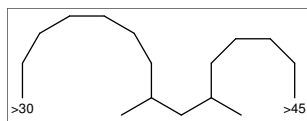
```
<-30,!6,  
{3^-30,3,3^30}:/!3>lr,  
{5^-30,5,5^30}:/!3>rl
```



2.8.3 Rotate fixed angle

>n : rotate n

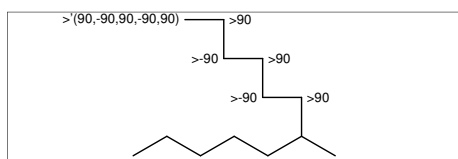
```
<30,!4,  
2:/!6>30, % 2:\,30,30,30,30,30,30  
4:/!4>-45 % 4:\,-45,-45,-45,-45
```



2.8.4 Rotate multiple angle

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

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

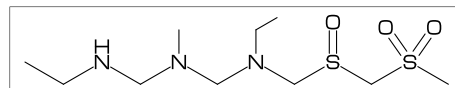


2.9 Miscellaneous

2.9.1 Abbreviated parts

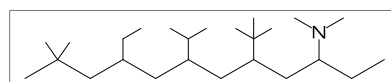
```
NH : N,/H~n1 N? : N,/_  
N?2 : N,/! S?0 : S,//0  
S?0?0 : S,//0^35,/^-35
```

```
<-30,!2,NH,!2,N?,!2,N?2,S?0,!2,S?0?0,!
```



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

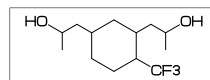
```
<30,!11^1,2:??,4:/!,6:/?!,8:/?!!,10:/N?!
```



2.9.2 Define group,parts

```
^(..) : define group  
``(..)(..) : define group with atoms  
'(..) : define parts
```

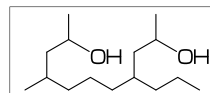
```
CF3:=`("{CF3}") ; % ** group weight =0  
CF3:=``("{CF3}") (C,F,F,F) ;  
** group weight =12(C)+19(F)*3=69  
iBuOH:= '(?! ,OH) ;  
\(<30,?6,{4,6}:/iBuOH,3:/CF3)
```



2.9.3 Concatenate group,parts

```
a+b : '(a,b)  
/!?!+OH : /'(!?! ,OH)
```

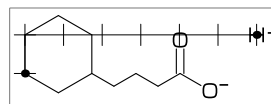
```
<30,!8,{2,6}:/!?!+OH
```



2.9.4 Move position [@]

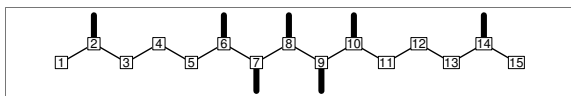
```
@(x,y) : Move l*(x,y) from current position  
@$(x,y) : Move l*(x,y) from origin(@1)  
** l=bond length of ring
```

```
<30,?6,@3,!4,//0,! ,0,n_~60,@$(6,1),H,p_~15
```



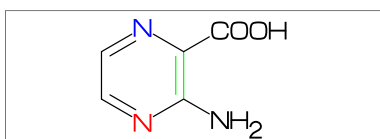
2.9.5 Serial number

```
6:10 : 6,7,8,9,10
<30,!14,{2,6:10,14}:/_~bd_r`0.5
```



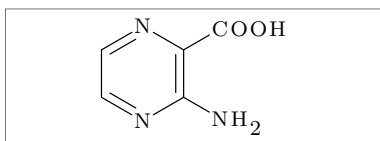
2.9.6 Change color

```
beginfigm
  \(<30,Ph,{2,5}:N,3:/NH2,4:/COOH,
    2:red, 5:blue, 3=green)
endfigm
```



2.9.7 Change font

```
beginfigm
  %-----
  atomfont:="cmr8";
  %-----
  \(<30,Ph,{2,5}:N,3:/NH2,4:/COOH)
endfigm
```

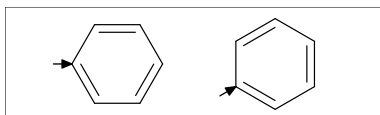


3 Option parameter

3.1 Angle parameter

mangle=0 ** default

```
@(0.2,0.5)\(Ph)
mangle:=30;
@(0.8,0.5)\(Ph)
```

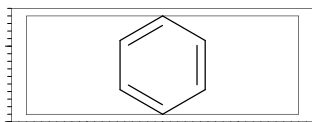


3.2 Size/Ratio parameter

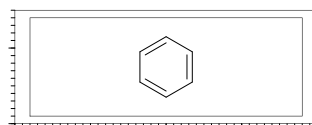
3.2.1 Bond length [|=]

|=(n) : abbreviated form of blength:=n;

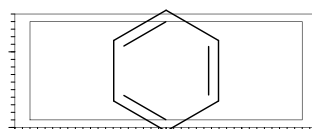
(fit to figure size)
blength=0 ** default



(ratio bond/figure width)
blength=0.1 ** (0<blength<=1)
blength=60mm(width)*0.1=6mm

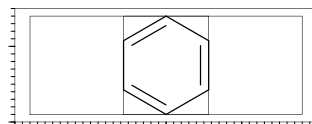


(bond length)
blength=9mm
** (blength>1) ignore msize(w,h)

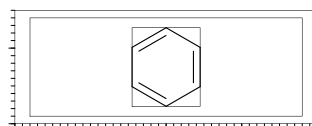


3.2.2 Molecular size

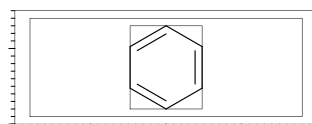
##(1,1) : msize=(1,1) ** default
p : abbreviated form of msize:=p;



##(0.25,1) : msize=(0.25,1)
** msize=(40mm-4mm)*0.25=9mm

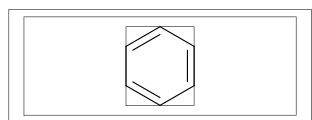


##(11mm,11mm) : msize=(11mm,11mm)

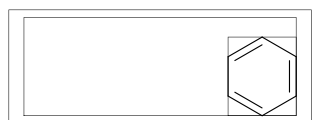


3.2.3 Molecular position

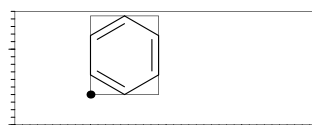
@(0.5,0.5) : mposition=(0.5,0.5) **default



@(1,0) : mposition=(1,0)



@(10mm,4mm) : mposition=(10mm,4mm)

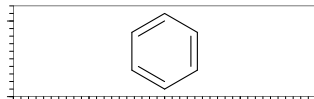


3.3 Size parameter

3.3.1 Figure size [#]

fsize=(figure width,figure height)
** default: (30mm,20mm)
p : abbreviated form of fsize:=p;

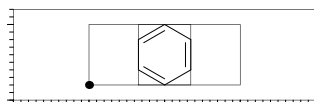
#(40mm,15mm) : fsize=(40mm,15mm)



3.3.2 Figure margin [#@]

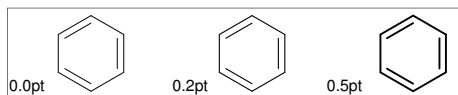
fmargin=(margin left right,top bottom)
** default: (0.4mm,0.4mm)
#@ p : abbreviated form of fmargin:=p;

#@(10mm,2mm) : fmargin=(10mm,2mm)



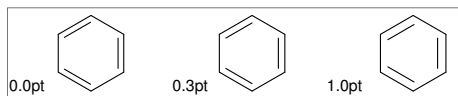
3.3.3 Offset thickness of bond

default: offset_thickness=0.2pt



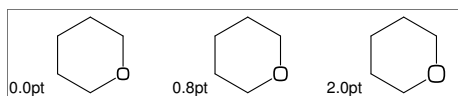
3.3.4 Offset of double bond gap

default: offset_bond_gap=0.3pt



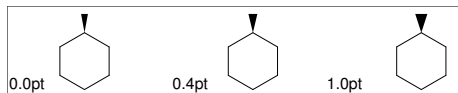
3.3.5 Offset of atom width

default: offset_atom=0.8pt



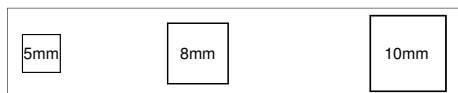
3.3.6 Offset of wedge width

default: offset_wedge=0.4pt



3.3.7 Max bond length [|<]

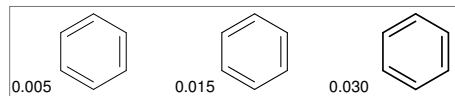
|<(n): abbreviated form of max_blength:=n;
default: max_blength=10mm



3.4 Ratio parameter

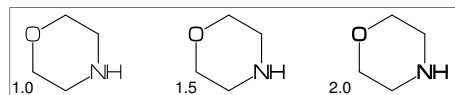
3.4.1 Thickness/bond length

default: ratio_thickness_bond=0.015



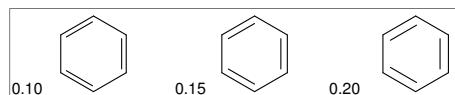
3.4.2 Char/bond thickness

default: ratio_char_bond=1.5



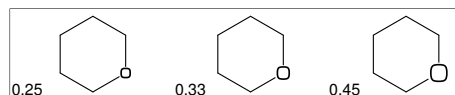
3.4.3 Bond gap/bond length

default: ratio_bondgap_bond= 0.15



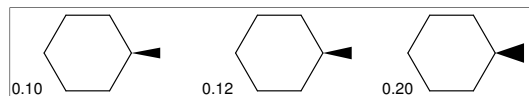
3.4.4 Atom/bond length

default: ratio_atom_bond= 0.36



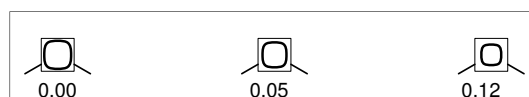
3.4.5 Wedge/bond length

default: ratio_wedge_bond=0.12



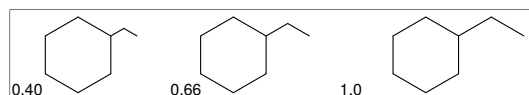
3.4.6 Figure atom gap/atom length

default: ratio_atomgap_atom= 0.050



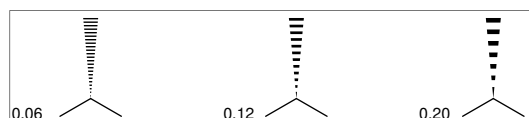
3.4.7 Chain/ring length

default: ratio_chain_ring= 0.66



3.4.8 Hash gap/bond length

default: ratio_hashgap_bond=0.12

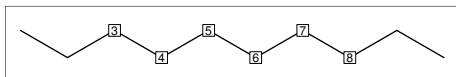


3.5 Drawing mode

3.5.1 Numbering atom

```
sw_numbering=Atom
numbering_start:=3;
numbering_end:=8;
default: sw_numbering=0
```

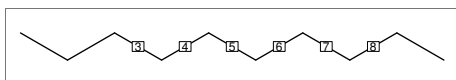
```
sw_numbering:=Atom;
\(<-30,!9)
```



3.5.2 Numbering bond

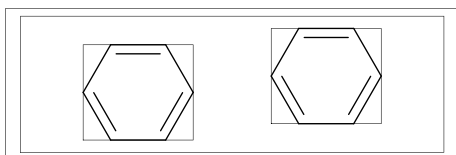
```
sw_numbering=Bond
numbering_start:=3;
numbering_end:=8;
default: sw_numbering=0
```

```
sw_numbering:=Bond;
\(<-30,!9)
```

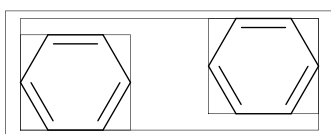


3.5.3 Trimming mode

```
sw_trimming:=0; ** default
##(1,0.7)
@(0.2,0.3)\(Ph) @(0.8,0.7)\(Ph)
```



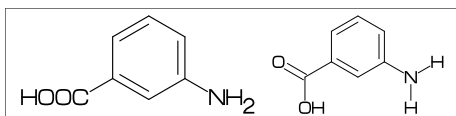
```
sw_trimming:=1;
@(0.2,0.3)\(Ph) @(0.8,0.7)\(Ph)
```



3.5.4 Expand mode

```
** put before input mcf2graph
sw_expand:=1;
input mcf2graph.mp;

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



3.5.5 Abbreviate group

```
** default: sw_abbreviate=Group
```



3.5.6 Abbreviate bond type

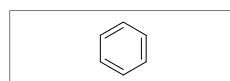
```
** default: sw_abbreviate=Bond
```



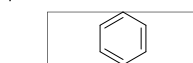
3.6 Frame

3.6.1 Figure frame

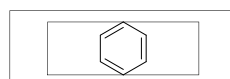
```
** default:sw_frame=0
(Draw figure frame)
fmargin:=(5mm,2mm);
sw_frame=Outside
```



```
(Frame inside margin)
sw_frame=Inside
```

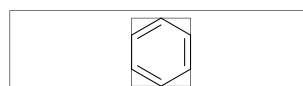


```
(Draw both frame)
sw_frame=Bothside=Inside+Outside
```



3.6.2 Molecular frame

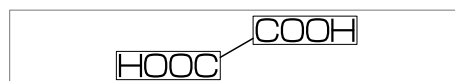
```
sw_frame=Mol
** default:sw_frame=0
```



3.6.3 Atom frame

```
sw_frame=Atom
** default: sw_frame=0
```

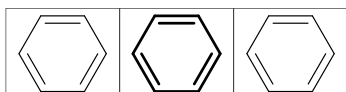
```
\(<30,COOH,! ,COOH)
```



3.7 Parameter setting

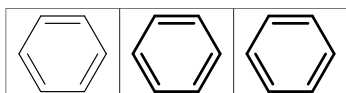
3.7.1 Local parameter setting

```
beginfigm
  \(\Ph)
endfigm
beginfigm
  %-----
  ratio_thickness_bond:=0.05;
  %-----
  \(\Ph)
endfigm
beginfigm
  \(\Ph)
endfigm
```



3.7.2 Global parameter setting

```
beginfigm
  \(\Ph)
endfigm
%-----
ratio_thickness_bond:=0.05;
%-----
beginfigm
  \(\Ph)
endfigm
beginfigm
  \(\Ph)
endfigm
```



4 Command

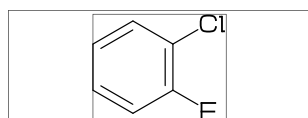
4.1 drawm [\]

(Draw molecule)

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

a: ratio molecular width/figure width
b: ratio molecular height/figure height
c: x axis position
d: y axis position
\(): abbreviated form of drawm()

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



4.2 readm [' ']

```
readm(string1,string2, ...);
** string = mcf code
'(): abbreviated form of readm()
```

(example)

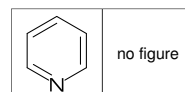
```
'("<30,Ph,{1,2,6}:/0!,{-4,-5}=?7,"
  "{-1,-4,-6}=d1,-2://0,-3:/0!", "
  "@9,\,NH,!,//0,!")
```

4.3 checkm [*]

```
\*(): abbreviated form of checkm()
(immediately compile)
beginfigm \(<30,Ph,2:N) endfigm
```

(check mcf and compile)

```
beginfigm
  '("<30,Ph,2:") % ** '2:' missing arg
  if \*(mc)=0: \(\scantokens(mc)) fi
endfigm
** \*(mc) : error count
```



4.4 getm [\$]

```
getm(number)
** number = numeric
** ucount = molecular data unit count
$(): abbreviated form of getm()
```

```
for i=1 upto ucount:
  beginfigm
    $(i)           % get data unit no=i
    \\             % put figure
  endfigm
endfor
```

```
getm("name"): "name"=string
```

```
beginfigm
  $("Adenine")    % get data EN="Adenine"
  \\              % put figure
endfigm
```

4.5 putm [\\]

putm: put figure
\\ : abbreviated form of putm

```
if op_row>=1: scantokens(op) fi
if mc_row>=1:
  if checkm(mc)=0: drawm(scantokens(mc))
  fi
fi
if ad_row>=1: add(scantokens(ad)) fi
if ex_row>=1: ext(scantokens(ex)) fi
```

4.6 add [++]

(Add label to molecule)

++(): add()

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

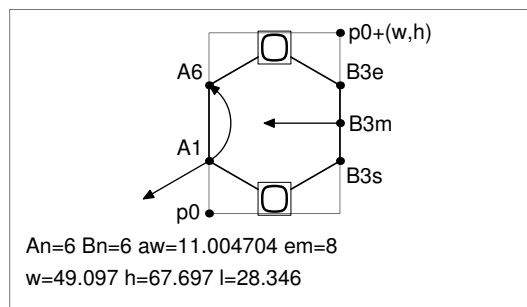
plus : '+' circled
minus : '-' circled
circlediam = 0.6aw (default)
circlepen = 0.2bp (default)

lonenpair r: ':' rotated r
lonenpairdiam = 0.3aw (default)
lonenpairspace = 0.7aw (default)

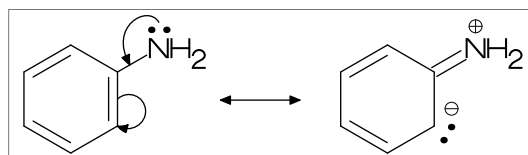
: scaled
<< : rotated
a /* b : point b of a

```
beginfigm
#(70mm,40mm) ##(.91,.9) |<(10mm)
sw_frame:=sw_frame+Atom+Mol;
@(.5,.85)\(<30,?6,{2,5}:0)
++(
defaultscale:=.8;
labeloffset:=.3aw;
dotlabel.lft("p0",p0);
dotlabel.rtl("p0+(w,h)",p0+(w,h));
dotlabel.ulft("A1",A1);
drawarrow A1..A1+__*l<<A1ang;
dotlabel.lrt("B3s",B3s);
dotlabel.rtl("B3m",B3m);
drawarrow B3m..B3m+__*l<<(B3ang+90);
dotlabel.ulft("A6",A6);
drawarrow A1{A1down}..A6;
```

```
dotlabel.rtl("B3e",B3e);
label.rtl("An"&decimal(An)&
" Bn"&decimal(Bn)&
" aw"&decimal(aw)&
" em"&decimal(em),
p0+(-9em,-1.5em));
label.rtl("w"&decimal(w)&
" h"&substring(0,6)of decimal(h)&
" l"&substring(0,6)of decimal(l),
p0+(-9em,-3em));
)
endfigm
```



```
beginfigm
#(60mm,20mm) ##(1,0.85)
%-----
@(0,0)\(<30,Ph,3=d1,4:/NH2)
%-----
++(
labeloffset:=.7aw;
label.top(lone_pair 90,A7);
drawarrow
(A7+up#1.2aw){A7left}
..{B7right}B7/*0.3;
drawarrow
B3m..A3+B2up#1.5aw..{A3down}A3;
)
%-----
@(1,0)\(<30,?6,{1,5}=d1,4://NH2)
%-----
++(
labeloffset:=.7aw;
label.top(plus,A7);
label.rtl(minus,A3);
label(lonenpair A3ang,A3+A3up#.7aw);
)
%-----
** (drawdblarrow (.4w,.4h)..(.55w,.4h);)
%-----
endfigm
```



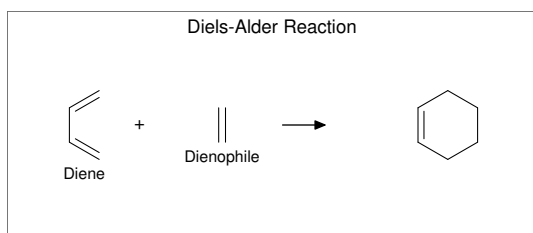
4.7 ext [**]

(Extra label to figure)

```
**(): ext()
w:   figure width
h:   figure height
w0:  figure width-2xpart(fmargi)
h0:  figure 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

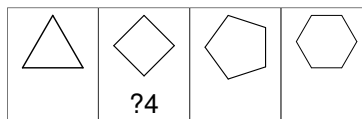
ratio_thickness_char:
pen thickness / char width
%-----
beginfigm
#(70mm,30mm)
|=(0.065)
%-----
@(0.1,0.5)
\(<-210,60`1,60`1,60`1,{1,3}=dl)
++(
  defaultscale:=0.6;
  label.bot("Diene",p0+(0.5w,0));
)
@(0.4,0.5)
\(<-30,-60`1,1=dm)
++(
  defaultscale:=0.6;
  label.bot("Dienophile",p0+(.5w,0));
)
@(0.9,0.5)\(<30,?6,6=dl)
%-----
**(
  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)
            );
)
%-----
endfigm
```



4.7.1 Local ext setting

_s : abbreviated form of EN:=s;

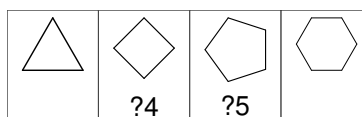
```
beginfigm
_"?3"@(.5,1)\(<30,?3)
endfigm
beginfigm
_"?4"@(.5,1)\(?4)
%-----
** (label.top(EN,(0.5w,0));)
%-----
endfigm
beginfigm
_"?5"@(.5,1)\(?5)
endfigm
beginfigm
_"?6"@(.5,1)\(?6)
endfigm
```



4.7.2 Global ext setting

ext_clear: reset global ext()

```
beginfigm
_"?3"@(.5,1)\(<30,?3)
endfigm
%-----
ext(label.top(EN,(0.5w,0));)
%-----
beginfigm
_"?4"@(.5,1)\(?4)
endfigm
beginfigm
_"?5"@(.5,1)\(?5)
endfigm
%-----
ext_clear;
%-----
beginfigm
_"?6"@(.5,1)\(?6)
endfigm
```

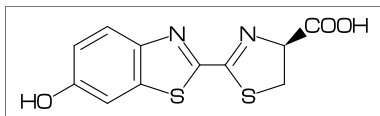


5 Example

5.1 drawm example

(Luciferin)

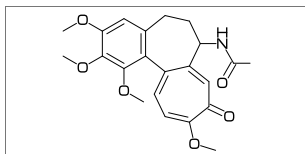
```
beginfigm
  #(50mm,15mm)
  \(<30,Ph,3=?5,@8,\,?5,{9,16}=d1,{9,14}:N,{7,11}:S,1:/OH,-2:*/COOH)
endfigm
```



5.2 readm example

(Colchicine)

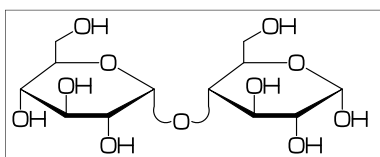
```
beginfigm
  '(
    "<30,Ph,{1,2,6}:/O!,{-4,-5}=?7, ",
    " {-1,-4,-6}=d1,-2://0,-3:/O!, ",
    " 9:/NH!+?0! )"
  #(40mm,20mm) \\
endfigm
```



(Maltose)

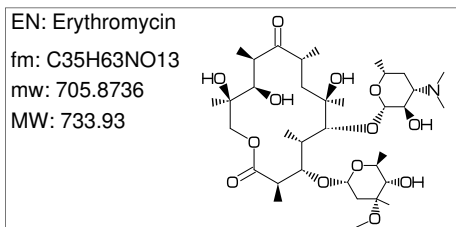
```
(bond type for glycan)
arc_lb : arc left > bottom
arc_br : arc bottom right
```

```
beginfigm
  %"EN:Maltose","MW:342.3",
  '(
    %-----
    "#1.25,-30~wf_r,30~bd_r`1,30~wb_r,120,0,30,&1,##, ",
    "#.5,{1~$-90,2~$90,3~$-90}:/OH,6~$90:/!OH, ",
    "@4,$-50~arc_lb`1,0,$50~arc_br`1,<$0, ",
    "|,#1.25,-30~wf_r,30~bd_r`1,30~wb_r,120,0,30,&1,##, ",
    "#.5,{2~$90,3~$-90,4~$-90}:/OH,6~$90:/!OH )"
    %-----
  #(50mm,20mm) \\
endfigm
```



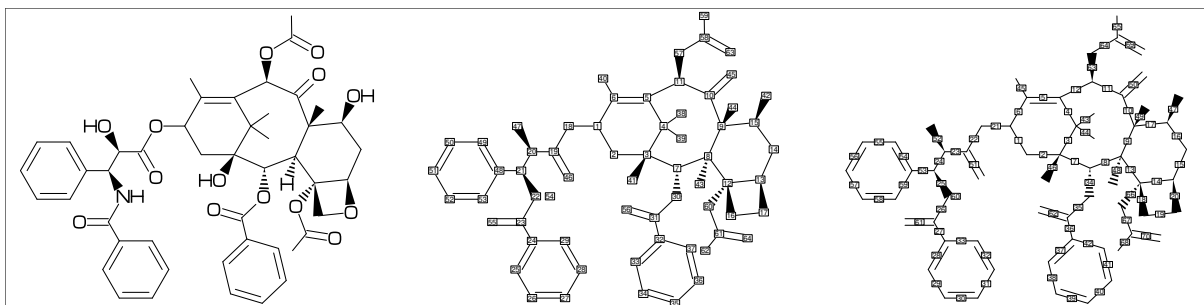
(Erythromycin)

```
beginfigm
  _"Erythromycin" MW="733.93";
  #(60mm,30mm) @(1,0.5)
  '(
  %-----
  "<30,#1,<-120,60,60,60,-60,60,60,-60,60,60,60,-60,60,60,##,&1,      ",
  " 14:0,13:/*Et,{1,9}://0,      ",
  " {2',4,6^-35,8,10',12^35}:/*_,      ",
  " {6^35,11,12^-35}:*/OH,      ",
  " @$3,\*,0,30~zb,|,?6^.7,6:0,#.5,{5~wf,3^35}:/_ ,4:/*OH,3^-35:/*0!,##, ",
  " @$5,\*^30^1.7,0,!~zb,|,?6^.7,6:0,#.5,5:/*_,2:*/OH,3:/*N?!      ")
  %-----
  \\
  ** (defaultscale:=0.8;
    label.lrt("EN: "&EN,(0,h));
    label.lrt("fm: "&fm,(0,h-5mm));
    label.lrt("mw: "&mw,(0,h-9mm));
    label.lrt("MW: "&MW,(0,h-13mm));
  )
endfigm;
```



(Paclitaxel)

```
beginfigm
  % "EN:Paclitaxel","MW:853.918",
  '(
  %-----
  "?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://0,      ",
  " @1,\,0,!//0,!,*OH,!/Ph,60~wf,NH,-60,//0,60,Ph,      ",
  " @7,\*,0,-45,//0,60,Ph,{11>r1,12'^-15>1r}:*/0!+?0!      ")
  %-----
  #(140mm,30mm)
  if \*(mc)=0:
    @(0,0.5)\(scantokens(mc))
    sw_numbering:=Atom;
    @(0.6,0.5)\(scantokens(mc))
    sw_numbering:=Bond;
    @(1,0.5)\(scantokens(mc))
  fi
endfigm;
```



5.3 loadm example

(Example)

```
loadm("CAT=biological","MW>=285","MW<=288","a:EN");
```

(output)

```
* jobname=mcf_exa_soc
* numbersystem=double
* output report file
* file name=mcf_exa_soc-report.txt)
* mcf_template 2023.05.07
* Input  : main_lib.mcf [525]
* Output : ucount [4]
* Filter(1): CAT =biological
* Filter(2): MW >= 285
* Filter(3): MW <= 288
* Sort key : EN (ascending)
[1]:Luteolin
[2]:Lycorine
[3]:Morphine
[4]:Piperine )

row[1] [1]="CAT:biological;EN:Luteolin;MW:286.24;EXA:-"
row[1] [2]=":"
row[1] [3]="<30,Ph,3=?6,9=d1,10:0,7://0,@9,\,Ph,{2,6,14,15}:/OH"
row[1] [4]=":"
row[2] [1]="CAT:biological;EN:Lycorine;MW:287.315;EXA:1"
row[2] [2]=":"
row[2] [3]="<30,Ph,{-4,-2}=?6,{6,9--12}=?5,13=d1,8:N,{15,17}:0,"
row[2] [4]="{9'^180,10^60}:*/H,{13,14}:'*/OH"
row[2] [5]=":"
row[3] [1]="CAT:biological;EN:Morphine;MW:285.343;EXA:1"
row[3] [2]=":"
row[3] [3]="<30,Ph,{2,-4}=?6,1---12=?5,-1:0,-1=zb,"
row[3] [4]="@7,60~wf`0.75,70~si_`1.3,45,N!,&9~wb,15=d1,6:/OH,8^180:*/H,12:/*OH"
row[3] [5]=":"
row[4] [1]="CAT:biological;EN:Piperine;MW:285.343;EXA:1"
row[4] [2]=":"
row[4] [3]="<30,Ph,-1=?5,{-1,-3}:0,@4,\,!d,!,!d,!,//0,!,?6,-6:N"
row[4] [4]=":"
```

(sw_comment)

```
sw_comment=1:

row[1] [1]="%-----"
row[1] [2]="CAT:biological;EN:Luteolin;MW:286.24;EXA:-"
row[1] [3]=":"
row[1] [4]="<30,Ph,3=?6,9=d1,10:0,7://0,@9,\,Ph,{2,6,14,15}:/OH"
row[1] [5]=":"

** default sw_comment=0
```

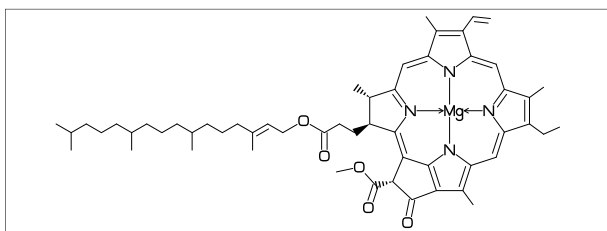
(Tag)

J	: jobname	CAT	: category
EN	: english name	JN	: japanese name
FM	: formula from data	MW	: molecular weight from data
MI	: monoisotopic mass from data	USE	: the use

5.4 getm example

(Chlorophyll a)

```
beginfigm
  $("Chlorophyll a")
  sw_output:=Fig+Calc+Mcode;
  #(80mm,30mm)
  \scantokens(mc)
  VerbatimTeX("\gdef\EN{"&EN&"}\gdef\MW{"&MW&"}");
  VerbatimTeX("\gdef\mw{"&mw&"}\gdef\fm{"&fm&"}");
endfigm
\end{mplibcode}
\verbatiminput{temp-mc.aux}          %%% input temp-mc.aux %%%
{\tt ** EN:\EN \quad mw:\MW \quad MW:\mw \quad fm:\fm}%
```

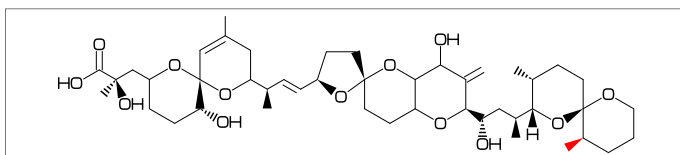


```
<-36,#1,?5,@3,\,54,?5,@-2,\,54,?5,@-2,\,54,?5,@-2,\,&5,@6,22,70,&8,##,
{4,6,8,10,14,16,18,21,23,27}=d1,@4,\`1.48~vf,Mg,&17~vb,@11,&27,@27,&23,
{4,11,17,23}:N,{1~zf,9,15,21}:/_ ,14:!/ ,20:!/d,25:/*?0!+0!,26:?0,
@2,*\^-6,!2,?0!,0!2,!d,|,!13,{1,5,9,13}:/_
```

```
** EN:Chlorophyll a mw:893.509 MW:893.4889 fm:C55H72MgN4O5
```

(Dinophysistoxin-1)

```
beginfigm
  $("Okadaic acid")
  ' (" ,38:*/_ ,65=red")          %%% add methyl group (color red) %%%
  sw_output:=Fig+Calc+Mcode;      %%% output temp-mc.aux %%%
  _"Dinophysistoxin-1" #(90mm,20mm)
  MW:="819";
  if \*(mc)=0: \scantokens(mc)
    VerbatimTeX("\gdef\EN{"&EN&"}\gdef\MW{"&MW&"}");
    VerbatimTeX("\gdef\mw{"&mw&"}\gdef\fm{"&fm&"}");
  fi
endfigm;
\end{mplibcode}
\verbatiminput{temp-mc.aux}          %%% input temp-mc.aux %%%
{\tt ** EN:\EN \quad mw:\MW \quad MW:\mw \quad fm:\fm}%
```

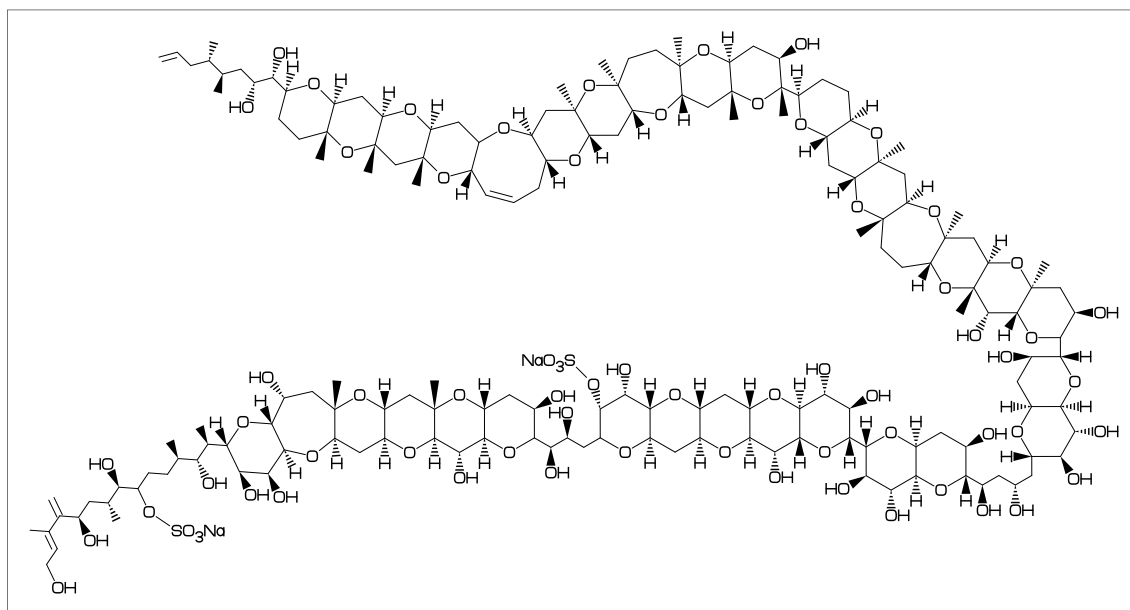


```
<30,?6,@4,?6,@-4,\,!3,<-12,?5,@-3,<-12,?6,-3=?6,@-3,*\,!3,
?6,@-4,?6,@6,\,!,/*_^-40,*/OH^20,!,?0!,OH,
3=wb,11=d1,15=dr,17=wf,19=wf,38=wb,{5,7,16,24,25,33,42}:0,
32:*/H^60,10:/_ ,{12,31,37'}:*/_ ,27://_ ,28:/OH,{3,29}:/*OH
,38:*/_ ,65=red
```

```
** EN:Dinophysistoxin-1 mw:819 MW:819.0294 fm:C45H70O13
```

(Maitotoxin)

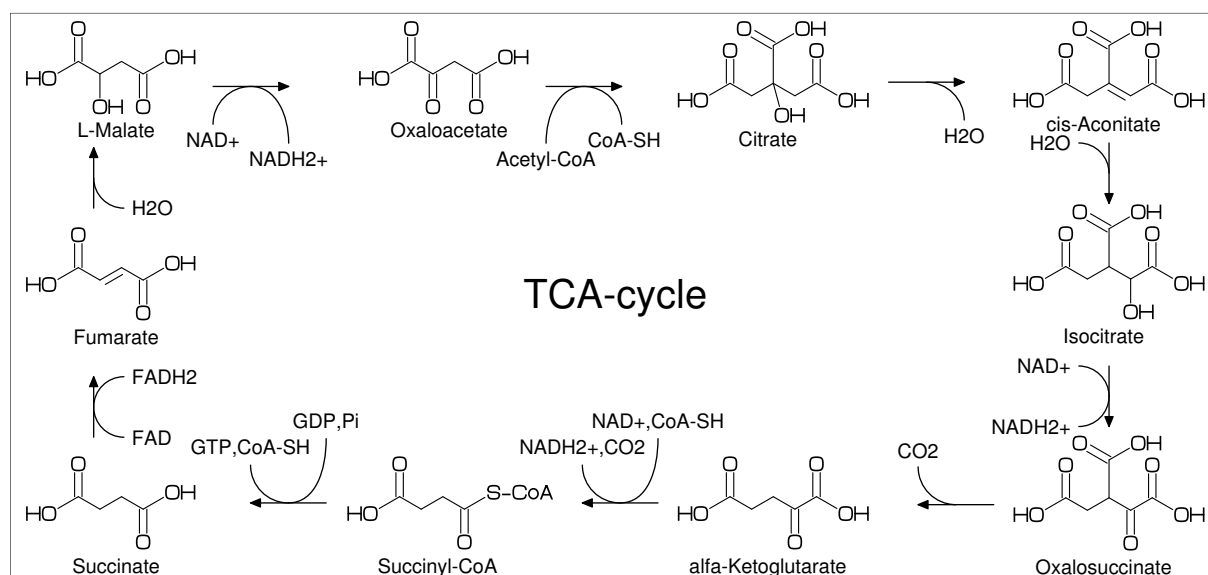
```
%-----  
\begin{mplibcode}  
  beginfigm  
    $("Maitotoxin") #(150mm,80mm) #@ (3mm,3mm)  
    sw_output:=Fig+Calc+Mcode;          %%% output temp-mc.aux %%%  
    sw_frame:=Outside;  
    if *(mc)=0: \ (scantokens(mc))  
      VerbatimTeX("\gdef\EN{"&EN&"}\gdef\MW{"&MW&"}");  
      VerbatimTeX("\gdef\mw{"&mw&"}\gdef\fm{"&fm&"}");  
    fi  
  endfigm  
\end{mplibcode}  
\verbatiminput{temp-mc.aux}             %%% input temp-mc.aux %%%  
{\tt ** EN:\EN \quad mw:\MW \quad MW:\mw \quad fm:\fm}%  
%-----
```



```
<55.8,?6,-4=?7 ,{-4,-3,-3,-3}=?6,@-3,\,!3,?6,{-4,-3,-3,-3}=?6,@-3,\,?6,-3=?6,  
@-3,\,!3,60,<-30,?6,-3=?6,@-3,30,<30,?6,{-3,-3}=?6,-3=?7,{-4,-3,-3}=?6,  
@-2,\,?6,-3=?6,-3=?7,{-3,-3}=?6,-3=?8,-3=d1,{-5,-3,-3,-3}=?6,  
{5,7,15,16,23,24,32,40,41,48,49,58,59,72,73,82,83,90,91,99,  
100,107,113,114,122,123,130,131,140,141,148,149}:0,  
{1^60,2,26,28,29,51,54,61,63,68,75^60,78,109}:*/OH,  
{11,20,35,45,52,55,65,69,86}:/*OH,  
{3,8,13,17,21,33,38,42,56,70,84,92,101,106,111,128,138,142,146,150}:/*H^-60,  
{4,14,22,34,39,43,47',57',71',81,89,98,102,116,121,125,129,133}:*/H^60,  
{6,46,50,53,60,67,74}:*/H^-60,  
{9,18,85,93,112,139,143,147}:*/_^-60^1,{80,88,97,108',115,120,124}:*/_^-60^1,  
@6,\,|,!11,60~dr,-60,60,OH,{2',7,10}:*/OH,{1,3,8'}:*/_ ,11://_ ,12:/_ ,  
@6,\,0,30,S03Na,  
@$36,-45~zf,0,30,S03Na,  
@$150,\,|,!7,{1,2}:*/OH,4:*/_ ,5:/*_ ,7=d1
```

```
** EN:Maitotoxin mw:3425.86 MW:3425.856 fm:C164H256Na2O68S2
```

5.5 User define parts example



```

beginfigm
#(160mm,75mm) |<(5mm)
COOH:='(//0,! ,OH); % define COOH
HOCO:='(OH,! ,//0,); % define HOCO
S_CoA:='("{S-CoA}"); % define S_CoA
@(0.33, 1)\(<30,HOCO,! ,//0,!2,COOH) % Oxaloacetate
@(0.66, 1)\(<30,HOCO,!4,COOH,@-4`1,\,COOH,4:/OH^-165) % Citrate
@(1, 1)\(<30,HOCO,!2,!-dr,! ,COOH,@-4`1,\,COOH) % cis-Aconitate
@(1, 0.58)\(<30,HOCO,!4,COOH,@-4,\`1,COOH,5:/OH) % Isocitrate
@(1, 0.05)\(<30,HOCO,!3,//0,! ,COOH,@-4,\`1,COOH) % Oxalosuccinate
@(0.66,0.05)\(<30,HOCO,!3,//0,! ,COOH) % alpha-Ketoglutarate
@(0.33,0.05)\(<30,HOCO,!3,//0,! ,S_CoA) % Succinyl-CoA
@(0, 0.05)\(<30,HOCO,!3,COOH) % Succinate
@(0, 0.55)\(<30,HOCO,! ,!-dr,! ,COOH) % Fumarate
@(0, 1)\(<30,HOCO,!3,COOH,3:/OH) % L-Malate
ext(
defaultfont:="uhvr8r"; defaultscale:=0.75;
ext_setup;
save dx; pair dx; dx:=(12mm,0);
label.bot("Oxaloacetate",p1+dx); label.bot("Citrate",p2+dx);
label.bot("cis-Aconitate",p3+dx); label.bot("Isocitrate",p4+dx);
label.bot("Oxalosuccinate",p5+dx); label.bot("alpha-Ketoglutarate",p6+dx);
label.bot("Succinyl-CoA",p7+dx); label.bot("Succinate",p8+dx);
label.bot("Fumarate",p9+dx); label.bot("L-Malate",p10+dx);
sw_label_emu:=1;
ext_setup;
r_arrow(10mm)( 0)(p1+( 1.1w1, 0.3h1))("Acetyl-CoA",1.5)(" CoA-SH",1);
r_arrow(10mm)( 0)(p2+( 1.1w2, 0.4h2))("",0)("H2O",1);
r_arrow( 8mm)(270)(p3+( 0.5w3,-0.4h3))("H2O",1)("",0);
r_arrow( 8mm)(270)(p4+( 0.5w4,-0.4h4))("NAD+",1)("NADH2+",1);
r_arrow(10mm)(180)(p5+( -0.1w5, 0.4h5))("",0)("CO_2_",1);
r_arrow(10mm)(180)(p6+( -0.1w6, 0.5h6))("NAD+,CoA-SH",1.7)("NADH2+,CO2",1);
r_arrow(10mm)(180)(p7+( -0.1w7, 0.5h7))("GDP,Pi",1.7)("GTP,CoA-SH",1);
r_arrow( 8mm)( 90)(p8+( 0.4w8, 1.2h8))("FAD",1)("FADH2",1);
r_arrow( 8mm)( 90)(p9+( 0.4w9, 1.2h9))("H2O",1)("",0);
r_arrow(10mm)( 0)(p10+( 1.1w10,0.3h10))("NAD+",1)("NADH2+",1.5);
defaultscale:=1.5;
label("TCA-cycle",(0.5w,0.5h));
)
endfigm

```

6 Example to use mcf2graph

6.1 MetaPost souce file

```
%-----
input mcf2graph;                                > input main macro
%-----
sw_output:=Info;    % aux(information) file output on > global setting
%%sw_output:=Report;    > report output
%%sw_output:=MOL2000;    > MOL file output
#(60mm,40mm);    % (figure width,figure height)    >
outputformat:="png"; hppp:=vppp:=0.1;    > PNG output
outputtemplate:="c%3c-%{EN_}.png";    >
%-----
beginfigm
  % EN:Ampicillin MW:349.405
  \(<45,?4,-3=?5,2:N,7:S,    > immediately compile
    3^45:/*H,1://O^15,5:/*COOH^-18,6:??,
    @4,*\^15,NH,! ,//O,! ,/*NH2,! ,Ph)    >
endfigm    >
%-----
beginfigm
  % EN:Cholesterol MW:386.65
  '(    > read Mcode
  "<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
  \\    > put figure
endfigm    >
%-----
loadm("EN<>");    > load all unit
beginfigm
  $("Adenine")    > get EN=Adenine
  \\    > ** put figure
endfigm    >
%-----
beginfigm
  $(4)    > select No.4
  \\    > put figure
endfigm    >
%-----
for i=1 upto ucount:    > figure count
  beginfigm
    $(i)    > select No.i
    \\    > put figure
  endfigm
endfor
%-----
bye
```

6.2 Molecular library file

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% molecular library file   main_lib.mcf   by Akira Yamaji   2022.10.10
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% tag1:var1;tag2:var2;tag3:var3   ....
% first character of line "%" comment out
% first character of line ":" start MCF
% first character of line ";" stop MCF
% first character of line "=" start parameter setting
% first character of line "*" start ext(...)
% first character of line "+" start add(...)
% CAT = Category,EN = Name,MW = Molecular weight
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
CAT:-;EN:-;MW:0;EXA:-
=
  sw_frame:=Atom;
:
<30,?6,3=?5,{1,3,5,9}=d1,{2,6,9}:N,5:/NH2,7:NH
*
  defaultscale:=.5;
  label.bot(decimal(fig_num)&" "&EN,(.5w,0));
+
  defaultscale:=.3;
  label.bot("A2",A2) withcolor red;
  label.top("A6",A6) withcolor red;
  label.top("A9",A9) withcolor red;
;
%=====
CAT:biological;EN:Adenine;MW:135.13;EXA:1
:
<30,?6,3=?5,{1,3,5,9}=d1,{2,6,9}:N,5:/NH2,7:NH
;
%-----
CAT:biological;EN:Guanine;MW:151.13;EXA:1
:
<30,?6,3=?5,{1,3,9}=d1,{2,9}:N,{6,7}:NH,5://0,1:/NH2
;
%-----
CAT:biological;EN:Cytosine;MW:111.10;EXA:1
:
<30,?6,{4,6}=d1,4:N,3://0,2:NH,5:/NH2
;
%-----
CAT:biological;EN:Thymine;MW:126.11;EXA:1
:
<30,?6,3=d1,{2,6}:NH,{1,5}://0,4:/_
;
%-----
CAT:biological;EN:Uracil;MW:112.09;EXA:1
:
<30,?6,6=d1,{3,5}://0,{2,4}:NH
;
%== Amino acid =====
CAT:biological;EN:Glycine;MW:75.07;EXA:-
:
<30,NH2,!2,COOH
;
%-----
```

6.3 MCF aux file output

(Option parameter setting)

```
sw_output:=Mcode;          %% output 'temp-mc.aux'
```

(Command line)

```
>mpost -s ahlength=3 FILENAME (sw_output=Info+Mcode)
```

(Output mcf file)

```
sw_output=Mcode           %% file name = 'temp-mc.aux'
```

(result)

```
<30,?6,3=?5,{1,3,5,9}=d1,{2,6,9}:N,5:/NH2,7:NH
```

(Output library file)

```
sw_output=Info+Mcode      %% file name = 'jobname-lib.aux'
```

(result)

```
CAT:biological;EN:Adenine;MW:135.13;EXA:1
```

```
:
```

```
<30,?6,3=?5,{1,3,5,9}=d1,{2,6,9}:N,5:/NH2,7:NH
```

```
;
```

(LuaLaTeX example)

```
%-----  
%% "EN:Vancomycin  
\begin{mplibcode}  
  beginfigm  
    sw_output:=Mcode;      %%% output temp-mc.aux %%%  
  endfigm;  
\end{mplibcode}  
%-----  
\verbatiminput{temp-mc.aux}  
%-----
```

(result)

```
file name = 'temp-mc.aux'
```

```
<30,?6,@4,?6,@-4,\,!3,<-12,?5,@-3,<-12,?6,-3=?6,@-3,*\,!3,  
?6,@-4,?6,@6,\,!/*Me^-40,*OH^20,!//0,!1,OH,  
3=wb,11=d1,15=dr,17=wf,19=wf,38=wb,{5,7,16,24,25,33,42}:0,  
32:*/H^60,10:/Me,{12,31}:*/_ ,27://_ ,37:/*_ ,28:/OH,{3,29}:/*OH
```

6.4 Report output

(Option parameter setting)

```
sw_output:=Report;          %% file name = 'jobname-report.aux'
```

(Command line)

```
>mpost -s ahlength=7 FILENAME
```

(Output)

```
=====
No[5],Name<Cytosine>,Category<biological>,File<main_lib.mcf>
-----
<30,?6,{4,6}=db,4:N,3://0,2:NH,5:/NH2
-----
Row[1],Length[37],Block[7],Code pair[59],Warning[0]
-----
=[1] :[4] ?[1] <[1]
-----
Width[30.92419],Height[42.36527], Shift x[-1.77635],Shift y[-12.9921]
Bond length[11.33855],Atom size[4.881881]
-----
Atom[9],Bond[9],Ring[1],Hide H[2]
< NO. ><atom(s) >( x axis , y axis )<bond><hideH><chg>
A1 C ( 0 , 0 ) 3 1
A2 N ( 1 , -1 ) 3
A3 C ( 2 , 0 ) 4
A4 N ( 2 , 1 ) 3
A5 C ( 1 , 1 ) 4
A6 C ( 0 , 1 ) 3 1
A7 O ( 3 , 0 ) 2
A8 H ( 1 , -1 ) 1
A9 NH2 ( 1 , 2 ) 1
-----
< NO. >< bond (sdt)><angle +( +- )><length ( pt )>
B1 1 -> 2 ( 1 ) 330 ( -30) 1 ( 11)
B2 2 -> 3 ( 1 ) 30 ( 30) 1 ( 11)
B3 3 -> 4 ( 1 ) 90 ( 90) 1 ( 11)
B4 4 -> 5 ( 2 ) 150 ( 150) 1 ( 11)
B5 5 -> 6 ( 1 ) 210 ( -150) 1 ( 11)
B6 6 -> 1 ( 2 ) 270 ( -90) 1 ( 11)
B7 3 -> 7 ( 2 ) 330 ( -30)0.660000 ( 7)
B8 2 -> 8 ( 1 ) 270 ( -90)0.359999 ( 4)
B9 5 -> 9 ( 1 ) 90 ( 90)0.660000 ( 7)
-----
<atom>( atom wt ) [ mi wt ] < cnt > < sum wt > [ sum mi wt ]
C ( 12.0107) [ 12 ] * 4 48.0428 [ 48 ]
H (1.0079400) [1.0078250] * 5 5.03969 [5.0391251611]
N ( 14.0067) [14.003074] * 3 42.0200 [42.009222013]
O ( 15.9994) [15.994914] * 1 15.9994 [15.994914619]
Molecular Weight [Mono Isotopic] = 111.1019 [ 111.043261]
-----
Weight Calc: 111.1019 - Input: 111.10 = 0.0019999
Formula Calc: C4H5N3O
=====
```

6.5 MOL file output

(Option parameter setting)

```
sw_output:=MOL2000; % MOL(V2000)
sw_output:=MOL3000; % MOL(V3000)
```

(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 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
```

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
```


6.6 LuaTeX file example

```

\documentclass{article}
\usepackage{luamplib}%
\usepackage[T1]{fontenc}%
\usepackage{textcomp}%
\mplibcodeinherit{enable}%
\mplibverbatim{enable}%
\mplibnumbersystem{double}%
\begin{mplibcode}
\end{mplibcode}
\begin{document}
\noindent%
%-----
\begin{mplibcode}
  input mcf2graph;
  sw_output:=Fig;
  max_blength:=4.5mm;
  defaultfont:="uhvr8r";
  defaultsize:=8bp;
  defaultscale:=1;
  %-----
  EN:="Limonin";
  MW="470.51";
  beginfigm
    #(50mm,50mm)
    '(
    %-----
    "<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          "
    %-----
    \\\
  endfigm
\end{mplibcode}\\
%-----
\begin{mplibcode}
  EN:="beta-carotene";
  MW:="536.87";
  beginfigm
    #(80mm,50mm)
    '(
    %-----
    "<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}:/_        "
    %-----
    \\\
  endfigm
\end{mplibcode}\\
%-----
\end{document}

```

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