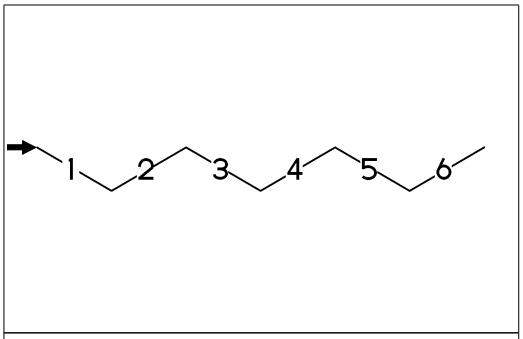
Molecular Coding Format manual

Author : Akira Yamaji Date : February 11, 2016
Located at : http://www.ctan.org/pkg/mcf2graph

Molecular Coding Format(MCF) is new linear notation represent chmical structure diagram. This 'Coding' is named from coding(programing) technique like adressing,grouping,macro,etc. There are no Meta language commands in MCF. mcf2graph.mf(metapost/metafont macro) convert MCF file to graphics file pk font,PNG,SVG,EPS or MDL MOL file(V2000).

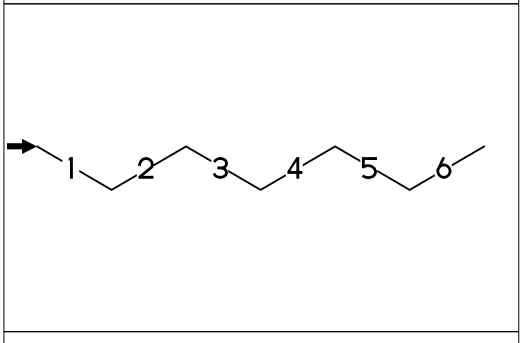
No.1 **Chain(1)**

```
plus(+):anticlockwize,minus(-):clockwize

  <30,-60,60,-60,60,-60,60

  ** bold arrow is default angle and position
```



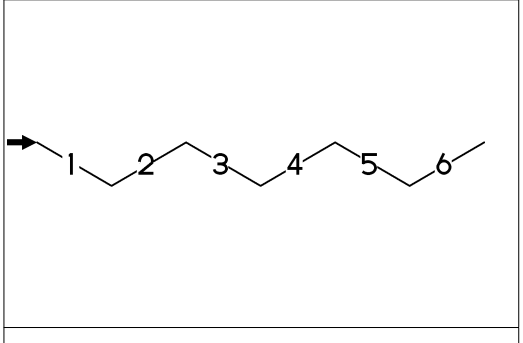
No.2 **Chain(2)**

```
! : take value(60 or -60) depend on
        current angle and enviroment

  <30,!,!,!,!,!,!
```



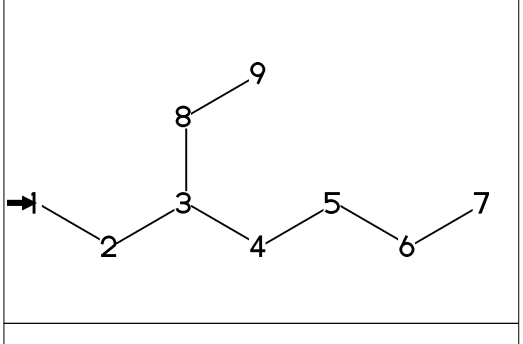
No.3 **Chain(3)**

```
!6 : !,!,!,!, !,!

  <30,!6
```



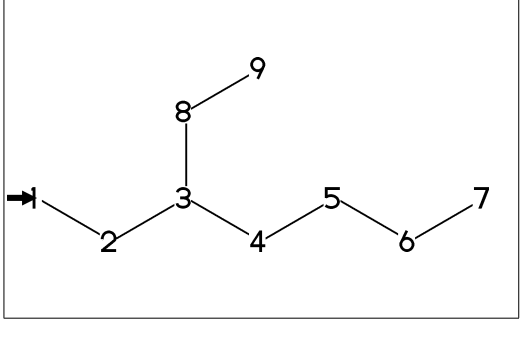
No.4 **Jump to atom**

```
3* : Jump to A3

  <30,!6,3*,0,!
```



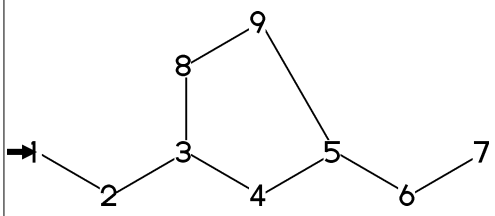
No.5 **Jump to atom and branch bond**

```
3\ : 3*,0

  <30,!6,3\,!
```



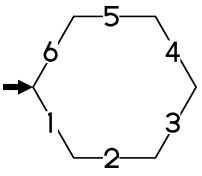
No.6 **Connect bond**

```
&5 : Connect to A5

  <30,!6,3\,!,&5
```



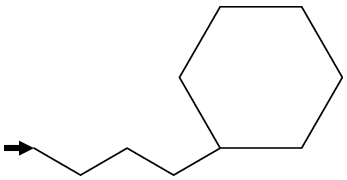
No.7 **Ring**

```
six membered ring

  ?6

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



No.8 **Rotate current angle**

```
<angle : rotate current angle

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

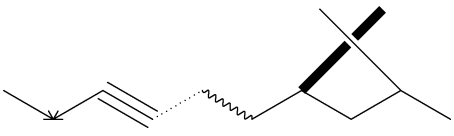


No.9 **Change bond type (1)**

```
~bond : change bond
  dm:double,dl:double left,dr:double right,
  wf:wedge forward,wb:wedge backward,
  zf:wedge dotted,zb:wedge dotted backward

  <30,!~dm,!~dl,!~dr,!~wf,!~wb,!~zf,!~zb
```

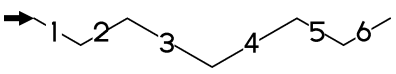
No.10 **Change bond type (2)**

```
  Bn=bond type : change bond type at Bn
  vf:vector forward, vb:vector backward,
  tm:triple, wv:waved, bd:broad single,
  ov:over line

  <30,!9,1=vf,2=vb,3=tm,4=dt,5=wv,
  @(7~bd^-45‘2,9~ov^45‘2)/Me
```



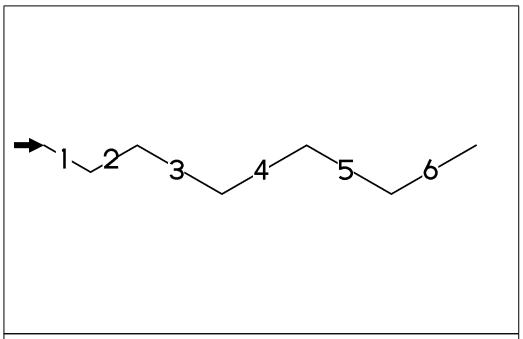
No.11 **Change bond length (1)**

```
Bn‘length : change bond length at Bn

  <30,!2,!2‘1.2,!2
```



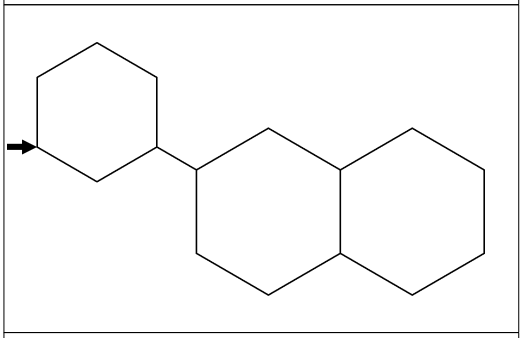
No.12 **Change bond length (2)**

```
‘‘length : change all bond length after

  <30,!2,‘‘1.2,!4
```



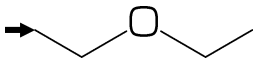
No.13 **Change ring length**

```
?n‘length : change ring length

  <30,?6,3\,?6‘1.2,11=?6
```



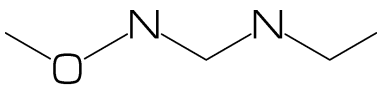
No.14 **Change atom (1)**

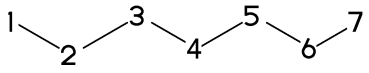
```
Insert hetero atom

  <30,!2,O,!2
```



No.15 **Change atom (2)**

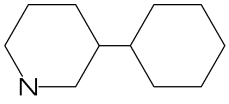
```
2:O : change A2 C to O
@(3,5)N : change  A3,A5 C to N

  <30,!6,2:O,@(3,5)N

** An(-999<=n<=4095): atom number
```

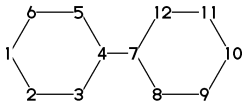




No.16 **Change atom (3)**

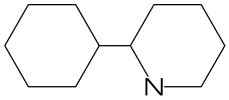
```
2:N : change A2 C to N

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

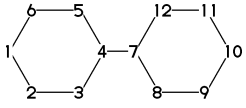




No.17 **Change atom (brock address 1)**

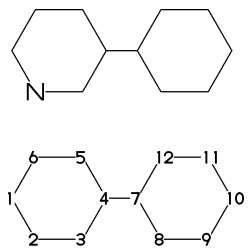
```
|  : divide brock

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





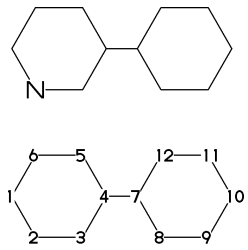
No.18 **Change atom (brock address 2)**

```
|| : reset brock adress

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



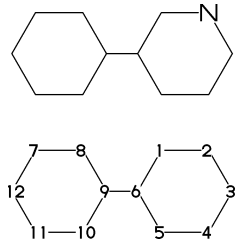
No.19 **Change atom (absolute address)**

```
#2:N : change A#2 C to N

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

** #n : (1<=n<=3095)
```



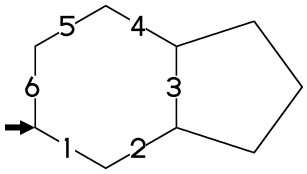
No.20 **Change atom (relative address)**

```
-2:N : change A(-2) C to N

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

** -n : (1<=n<=999)
```



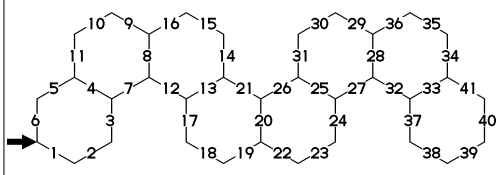
No.21 **Fuse ring (attached 1 bond)**

```
?6,3=?5 : fuse ?5 at B3

  ?6,3=?5

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



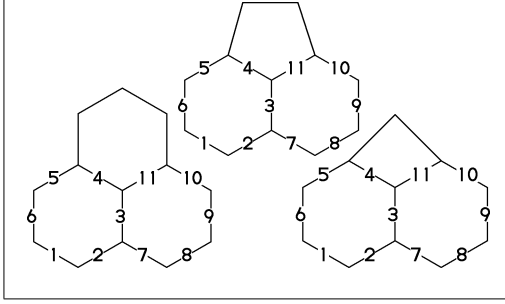
No.22 **Fuse multi ring (attached 1 bond)**

```
?6,$(-3,-4,-4,-2,-2,-4,-4)?6
?6,$(4,8,13,20,25,28,33)?6
```



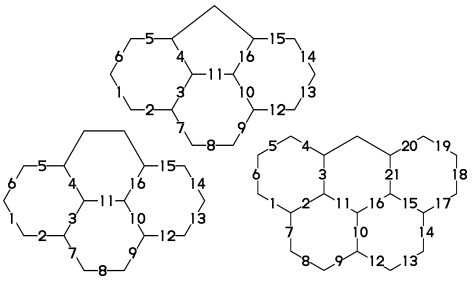
No.23 **Fuse ring (attached 2 bond)**

```
(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

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



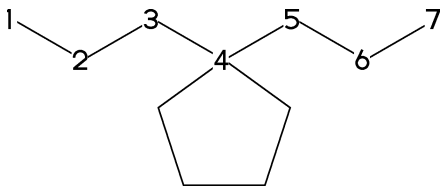
No.24 **Fuse ring (attached 3,4 bond)**

```
(16,4)=?6[3] : fuse 3/6 ring to B16..B4
(16,4)=?5[2] : fuse 2/5 ring to B16..B4
(21,3)=?6[2] : fuse 2/6 ring to B21..B3

MCd(1,.55)( 0, 0)(?6,$(3,10)?6,(16,4)=?6[3])
MCd(1,.55)(.43,1)(?6,$(3,10)?6,(16,4)=?5[2])
MCd(1,.53)(1,0)(<30,?6,$(2,10,15)?6,(21,3)=?6[2])
```



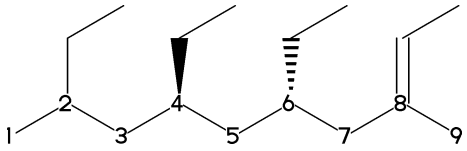
No.25 **Spiro ring**

```
4*,?5 : add ?5(5 membered ring) at A4

<30,!6,4*,?5

An* : jump to An
```



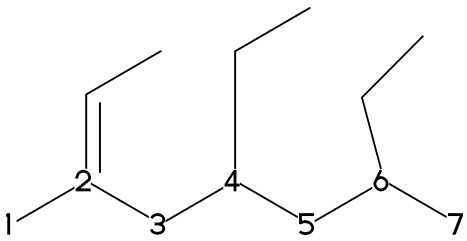
No.26 **Branch bond (1)**

```
2\  : 2*,0     4*\ : 4*,0~wf
6\* : 6*,0~zf  8\\ : 8*,0~dm

MCf(<30,!8,2\,!,4*\,!,6\*,!,8\\,!)
```



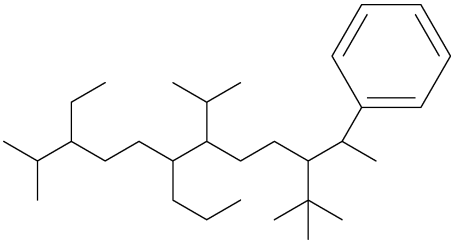
No.27 **Branch bond (2)**

```
2\~dr  : 2*,0~dr
4\‘1.5 : 4*,0‘1.5
6\^15 : 6*,0^15

MCf(<-30,!6,2\~dr,!,4\‘1.5,!,6\^15,-60)
```



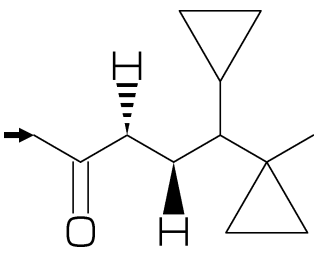
No.28 **Insert substituent(1)**

```
MCf(<30,
!,/Me,!,/Et,!3,/Pr,!,/iPr,!3,/tBu,!,/Ph^-30,!)

** Me:methyl Et:ethyl Pr:propyl iPr:isopropyl
   tBu:tertial buthyl Ph:phenyl
```



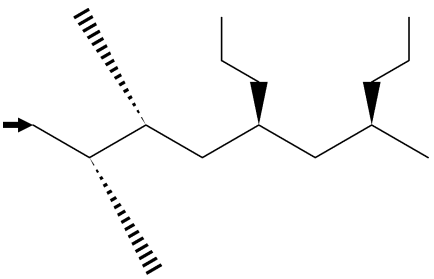
No.29 **Insert substituent(2)**

```
/  : single          // : double
*/ : wedge forward   /* : wedge backward
** : direct

MCf(<30,!,//O,!,/*H,!,*/H,!,/?3,!,**?3,!)
```



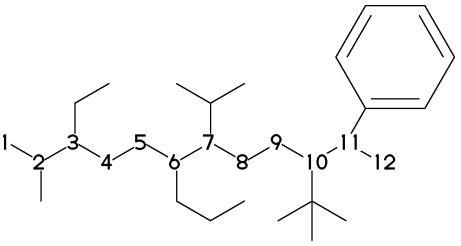
No.30 **Insert substituent(3)**

```
~,^,‘,> : change type,angle,length,enviroment
          of substituent

MCf(<30,!‘1,/Me~zf‘2^30,!‘1,/Me~zf‘2^30,
    !2‘1,*/Pr>lr,!2‘1,*/Pr>rl,!‘1)
```



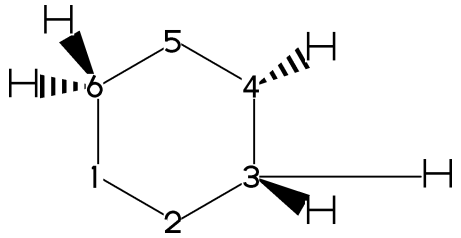
No.31 **Add substituent(1)**

```
sw_numberA:=1; numberA_end:=12;
MCf(<30,!11,
  2:/Me,3:/Et,6:/Pr,7:/iPr,10:/tBu,11:/Ph^-30)
```



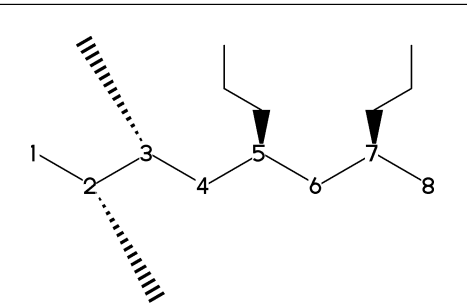
No.32 **Add substituent(2)**

```
~,^,‘,> : change type,angle,length,enviroment
          of substituent

MCf(<30,?6,
    @(3‘2^30,3~wf,4~zf,6~wf^-30,6~zf^30)/H)
```



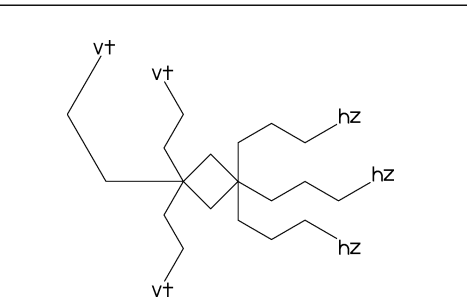
No.33 **Add substituent(3)**

```
~,^,‘,> : change type,angle,length,enviroment
          of substituent

MCF(<30,!7‘1,
@(2,3)/*Me‘2^30,5:*/Pr>lr,7:*/Pr>rl)
```



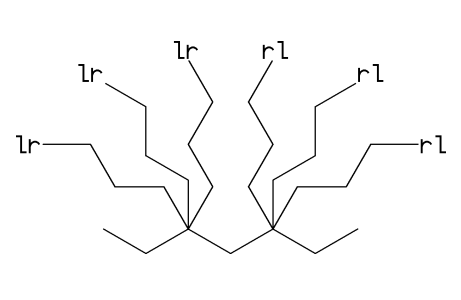
No.34 **Chain strech direction environment (1)**

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

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



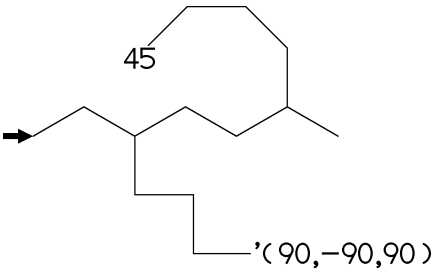
No.35 **Chain strech direction environment (2)**

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

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



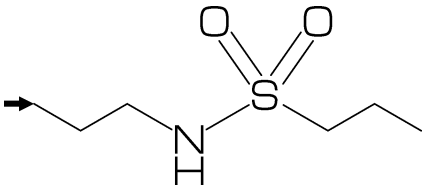
No.36 Chain strech direction environment (3)

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

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



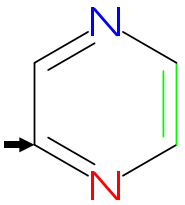
No.37 Change atom and Substituent

```
NH,SOO : inset hetero atom and substituent
         simultaneously

 <30,!3,NH,!,SOO,!3
```



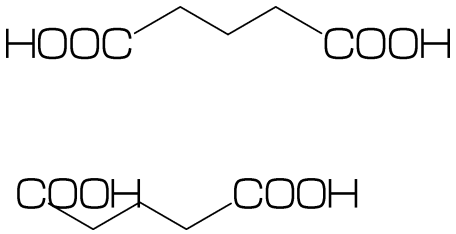
No.38 Change color

```
@(5)green : change color of A5 green
$(3)red :   change color of B3 red

 <30,Ph,@(2,5)N,
        2:red,5:blue,3=green

**  METAFONT ignore color command
```



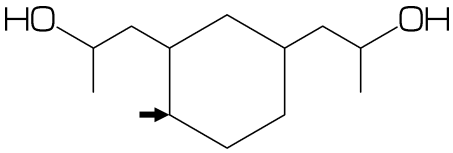
No.39 Chain start multiple characters

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

 MCd( 1,1)(0  ,0.9)(<30,COOH,!0,!3,COOH)

 MCd(.8,1)(0.3,0.1)(<30,COOH,!4,COOH)
```



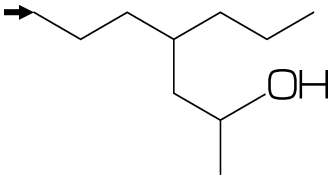
No.40 User definition

```
iBuOH : user defined substructure

 iBuOH:='(!,/Me,!,OH)
 MCf(<30,?6,@(4,6)/iBuOH)
```



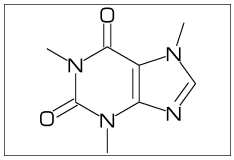
No.41 Inline definition

```
Insert user defined substructure

 <30,!3,/'(!,/Me,!,OH),!3
```



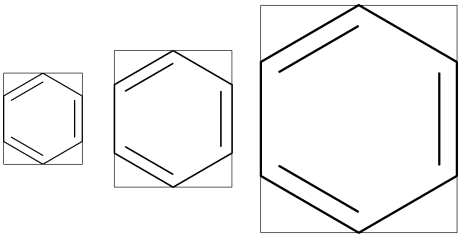
No.42 **Font size**

```
beginfont("EN:Caffeine")
  font_wd#:=30mm#;  %<==font width
  font_ht#:=20mm#;  %<==font height
  sw_font_frame:=1;
  MCf(<30,?6,-4=?5,$(3,8)dl,@(2,6,7,9)N,
     @(2,6,9)/Me,@(1,5)//O)
endfont
```



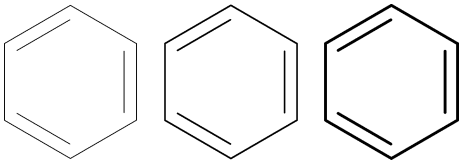
No.43 **Max ratio bond/width length**

```
max_bond_width:=0.10;
MCd(1,1)( 0, .5)(<30,Ph)
max_bond_width:=0.15;   %<<== : default
MCd(1,1)(.33,.5)(<30,Ph)
max_bond_width:=0.25;
MCd(1,1)( 1, .5)(<30,Ph)
```



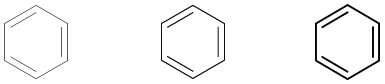
No.44 **Ratio thickness/bond length**

```
ratio_thickness_bond:= 0.005;
MCd(1,.6)(0, .5)(<30,Ph)
ratio_thickness_bond:= 0.015;  %<<==
MCd(1,.6)(.5,.5)(<30,Ph)
ratio_thickness_bond:= 0.030;
MCd(1,.6)(1, .5)(<30,Ph)
```



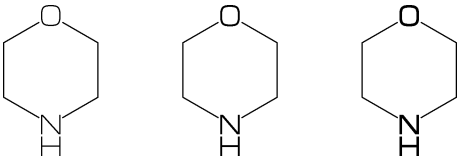
No.45 **Offset thickness of bond**

```
beginfont() offset_thickness#:=0pt#;
MCd(1,.3)(0, .5)(<30,Ph) endfont
beginfont() offset_thickness#:=0.2pt#;  %<<==
MCd(1,.3)(.5,.5)(<30,Ph) endfont
beginfont() offset_thickness#:=0.5pt#;
MCd(1,.3)(1, .5)(<30,Ph) endfont
```



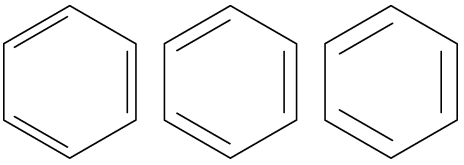
No.46 **Ratio char/bond thickness**

```
ratio_char_bond:=1.0;
MCd(1,.6)(0, .5)(<30,?6,5:O,2:NH)
ratio_char_bond:=1.5; %<<==
MCd(1,.6)(.5,.5)(<30,?6,5:O,2:NH)
ratio_char_bond:=2.0;
MCd(1,.6)(1, .5)(<30,?6,5:O,2:NH)
```



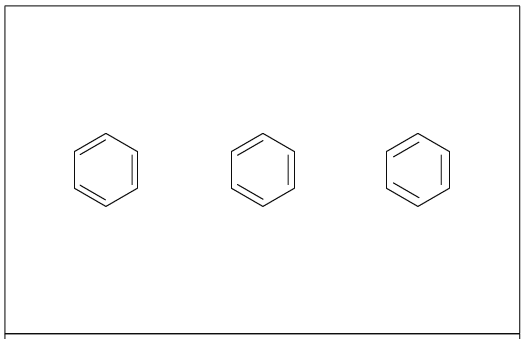
No.47 **Ratio bondgap/bond length**

```
ratio_bondgap_bond:= 0.10;
MCd(1,.6)(0, .5)(<30,Ph)
ratio_bondgap_bond:= 0.15; %<<==
MCd(1,.6)(.5,.5)(<30,Ph)
ratio_bondgap_bond:= 0.20;
MCd(1,.6)(1, .5)(<30,Ph)
```



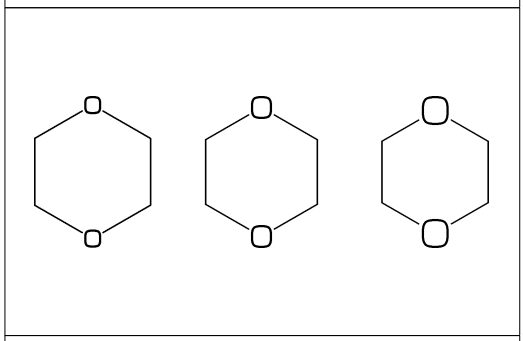
No.48 **Offset of doublebond gap**

```
beginfont() offset_bond_gap#:=0.0pt#;
MCd(1,.3)(0, .5)(<30,Ph) endfont
beginfont() offset_bond_gap#:=0.3pt#; %<<==
MCd(1,.3)(.5,.5)(<30,Ph) endfont
beginfont() offset_bond_gap#:=1.0pt#;
MCd(1,.3)(1, .5)(<30,Ph) endfont
```



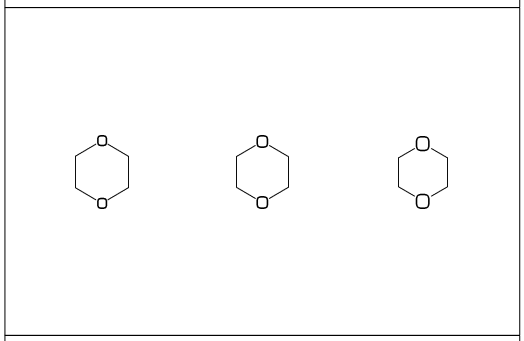
No.49 **Ratio atom/bond length**

```
ratio_atom_bond:= 0.25;
MCd(1,.6)(0, .5)(<30,?6,@(2,5)O)
ratio_atom_bond:= 0.36;  %<<==
MCd(1,.6)(.5,.5)(<30,?6,@(2,5)O)
ratio_atom_bond:= 0.45;
MCd(1,.6)(1, .5)(<30,?6,@(2,5)O)
```



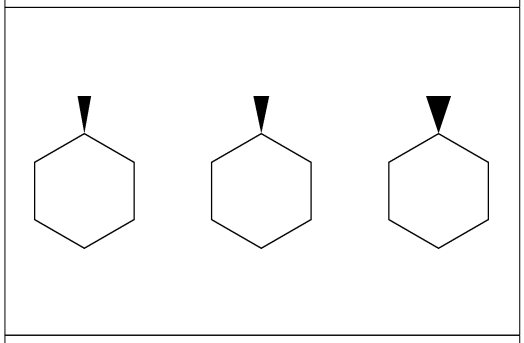
No.50 **Offset of atom width**

```
beginfont() offset_atom#:=0.0pt#;
MCd(1,.3)(0, .5)(<30,Ph,@(2,4,6)N) endfont
beginfont() offset_atom#:=0.8pt#;  %<<==
MCd(1,.3)(.5,.5)(<30,Ph,@(2,4,6)N) endfont
beginfont() offset_atom#:=2.0pt#;
MCd(1,.3)(1, .5)(<30,Ph,@(2,4,6)N) endfont
```



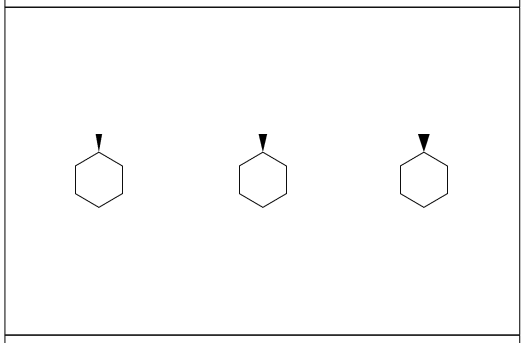
No.51 **Ratio wedge/bond length**

```
ratio_wedge_bond:=0.10;
MCd(1,.6)(0, .5)(<30,?6,5:*/Me)
ratio_wedge_bond:=0.12; %<<==
MCd(1,.6)(.5,.5)(<30,?6,5:*/Me)
ratio_wedge_bond:=0.20;;
MCd(1,.6)(1, .5)(<30,?6,5:*/Me)
```



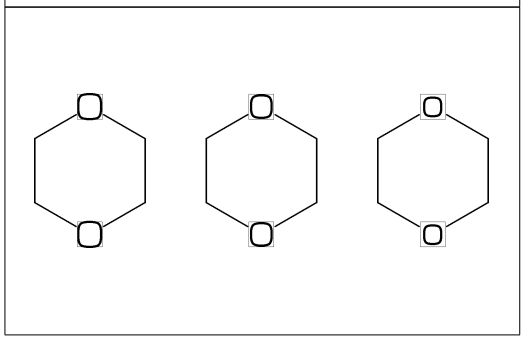
No.52 **Offset of wedge width**

```
beginfont("EN:Offset_wedge")
offset_wedge#:=0.0pt#;
MCd(1,.3)(0, .5)(<30,?6,5:*/Me) endfont
beginfont() offset_wedge#:=0.4pt#;  %<<==
MCd(1,.3)(.5,.5)(<30,?6,5:*/Me) endfont
beginfont() offset_wedge#:=1.0pt#;
MCd(1,.3)(1, .5)(<30,?6,5:*/Me) endfont
```



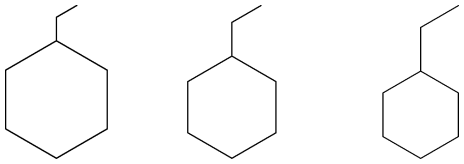
No.53 **Ratio font atom gap/atom length**

```
ratio_atomgap_atom:=0.0;
MCd(1,.6)(0, .5)(<30,?6,@(2,5)O)
ratio_atomgap_atom:=0.050;  %<<==
MCd(1,.6)(.5,.5)(<30,?6,@(2,5)O)
ratio_atomgap_atom:=0.12;
MCd(1,.6)(1, .5)(<30,?6,@(2,5)O)
```



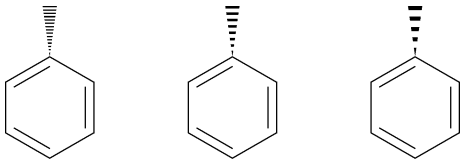
No.54 **Ratio chain/ring length**

```
ratio_chain_ring:= 0.4;
MCd(1,.6)(0, .5)(<30,?6,5:/Et)
ratio_chain_ring:= 0.66; %<<==
MCd(1,.6)(.5,.5)(<30,?6,5:/Et)
ratio_chain_ring:= 1.0;
MCd(1,.6)(1, .5)(<30,?6,5:/Et)
```



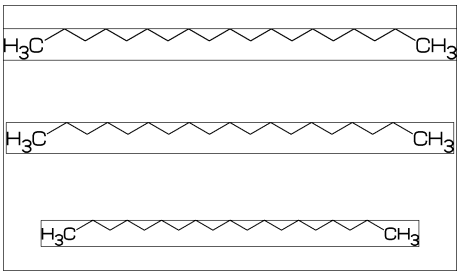
No.55 **Ratio zebra gap/bond length**

```
ratio_zebragap_bond:=0.06;
MCd(1,.6)(0, .5)(<30,Ph,5:/*Me‘1)
ratio_zebragap_bond:=0.12;  %<<==
MCd(1,.6)(.5,.5)(<30,Ph,5:/*Me‘1)
ratio_zebragap_bond:=0.20;
MCd(1,.6)(1, .5)(<30,Ph,5:/*Me‘1)
```



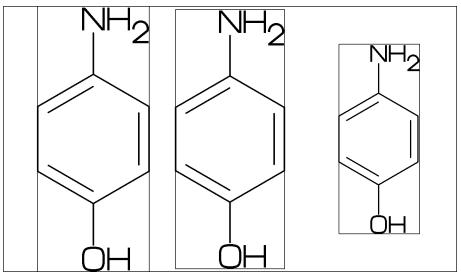
No.56 **Margin left and right**

```
margin_left_right:=0mm;
MCd(1,1)(0.5,0.9)(<30,CH3,!0,!17,CH3)
margin_left_right:=0.4mm;  %<<==
MCd(1,1)(0.5,0.5)(<30,CH3,!0,!17,CH3)
margin_left_right:=5mm;
MCd(1,1)(0.5,0.1)(<30,CH3,!0,!17,CH3)
```



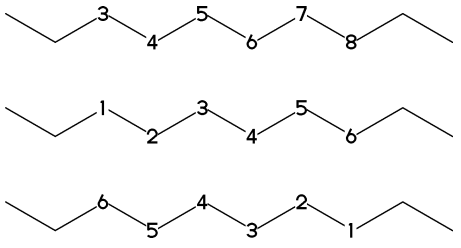
No.57 **Margin top and bottom**

```
margin_top_bottom:=0mm;
MCd(1,1)(0.1,0.5)(<30,Ph,2:/OH,5:/NH2)
margin_top_bottom:=0.4mm;  %<<==
MCd(1,1)(0.5,0.5)(<30,Ph,2:/OH,5:/NH2)
margin_top_bottom:=5mm;
MCd(1,1)(0.9,0.5)(<30,Ph,2:/OH,5:/NH2)
```



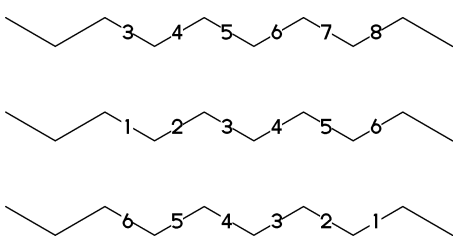
No.58 **Switch Numbering atom**

```
numberA_start:=3; numberA_end:=8;

sw_numberA:=1; MCd(1,1)(.5,.9)(<30,!9)
sw_numberA:=2; MCd(1,1)(.5,.5)(<30,!9)
sw_numberA:=3; MCd(1,1)(.5,.1)(<30,!9)

** default: numberA_start=1 numberA_end=4095
```



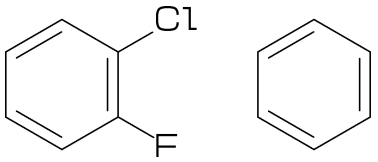
No.59 **Switch Numbering bond**

```
numberB_start:=3; numberB_end:=8;

sw_numberB:=1; MCd(1,1)(.5,.9)(<30,!9)
sw_numberB:=2; MCd(1,1)(.5,.5)(<30,!9)
sw_numberB:=3; MCd(1,1)(.5,.1)(<30,!9)

** default: numberB_start=1 numberB_end=4095
```



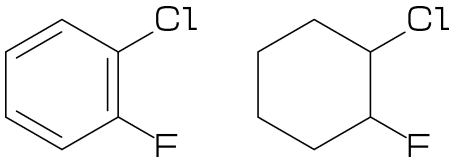
No.60 **Switch substituent off**

```
MCd(1,.6)( 0,0.5)(<30,Ph,4:/Cl,3:/F)
sw_subst_off:=1;
MCd(1,.6)( 1,0.5)(<30,Ph,4:/Cl,3:/F)

** default: sw_subst_off=0
```



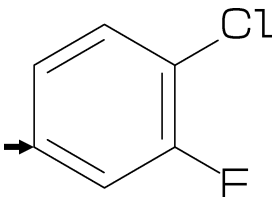
No.61 **Switch all bond single**

```
MCd(1,.6)( 0,0.5)(<30,Ph,4:/Cl,3:/F)
sw_bond_single:=1;
MCd(1,.6)( 1,0.5)(<30,Ph,4:/Cl,3:/F)

** default: sw_bond_single=0
```



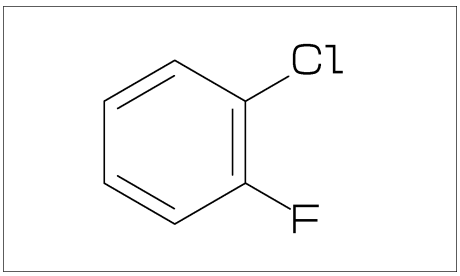
No.62 **Switch start vector**

```
sw_start_vector:=1;

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

** default: sw_start_vector=0
```



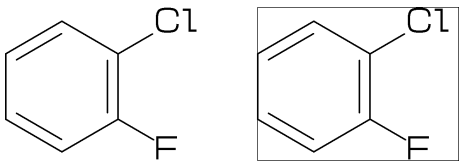
No.63 **Switch font frame**

```
sw_font_frame:=1;

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

** default: sw_font_frame=0
```



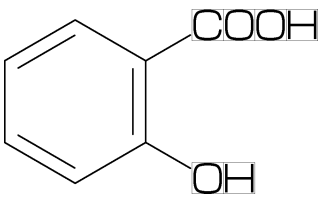
No.64 **Switch molecular frame**

```
MCd(1,.6)(0,0.5)(<30,Ph,4:/Cl,3:/F)
sw_mol_frame:=1;
MCd(1,.6)(1,0.5)(<30,Ph,4:/Cl,3:/F)

** default: sw_mol_frame=0
```



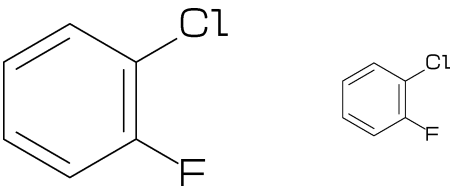
No.65 **Switch atom frame**

```
sw_atom_frame:=1;

MCf(<30,Ph,4:/COOH,3:/OH)

** default: sw_atom_frame=0
```



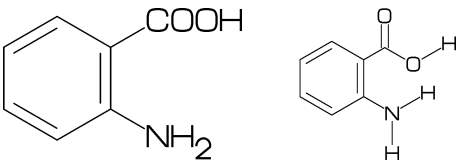
No.66 **Switch solid mode**

```
MCd(1,.8)( 0,0.5)(<30,Ph,4:/Cl,3:/F)
sw_solid:=1; ratio_bond_width:=0.08;
MCd(1,.8)( 1,0.5)(<30,Ph,4:/Cl,3:/F)

** default: sw_solid=0
```



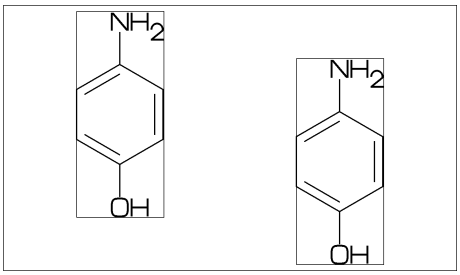
No.67 **Switch Expand**

```
MCd(1,.6)(0,0.5)(<30,Ph,4:/COOH,3:/NH2)
sw_expand:=1;
MCd(1,.6)(1,0.5)(<30,Ph,4:/COOH,3:/NH2)

** default: sw_expand=0
```



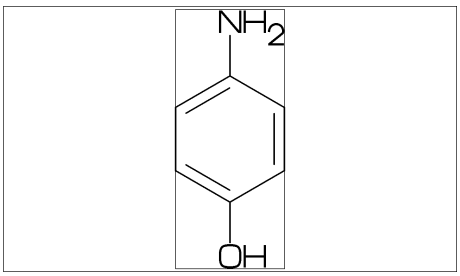
No.68 **Function MCd (draw)**

```
MCd(a,b)(c,d)(...)
  a: ratio molecular width/font width
  b: ratio molecular hight/font hight
  c: x axis position  d:y axis position

MCd(1,0.8)(0.2,0.9)(<30,Ph,2:/OH,5:/NH2)
MCd(1,0.8)(0.8,0.1)(<30,Ph,2:/OH,5:/NH2)
```



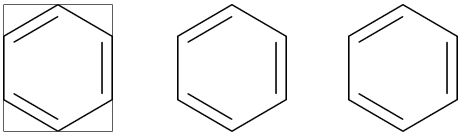
No.69 **Function MCf (fit draw)**

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

sw_font_frame:=1;  sw_mol_frame:=1;

MCf(<30,Ph,2:/OH,5:/NH2)
```



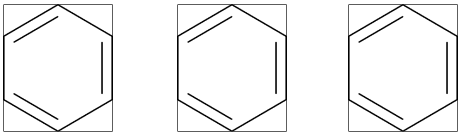
No.70 **Local setting**

```
beginfont("NO:1")
  sw_mol_frame:=1; % <<== Local setting
  MCd(1,.5)(0.0,0.5)(<30,Ph) endfont
beginfont("NO:2")
  MCd(1,.5)(0.5,0.5)(<30,Ph) endfont
beginfont("NO:3")
  MCd(1,.5)(1.0,0.5)(<30,Ph) endfont
```



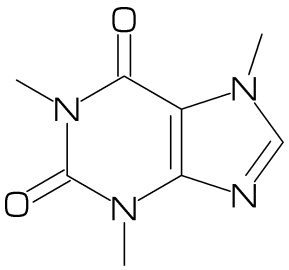
No.71 **Global setting**

```
sw_mol_frame:=1; % <<== Global setting
beginfont("NO:1")
  MCd(1,.5)(0.0,0.5)(<30,Ph) endfont
beginfont("NO:2")
  MCd(1,.5)(0.5,0.5)(<30,Ph) endfont
beginfont("NO:3")
  MCd(1,.5)(1.0,0.5)(<30,Ph) endfont
```



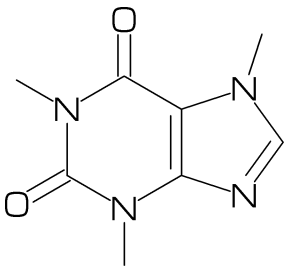
No.72 **Output molecular infomation**

```
beginfont() sw_info_weight:=sw_info_formula:=1;
MCf(...) endfont
%% Output to mcf_man_soc-info.aux %%
\INFO{{F:mcf_man_soc}{C:82}{MWc:194.19174}
      {FMc:C8H10N4O2}}%
MWc:calculated molecular weight
FMc:calculated molecular formula
```



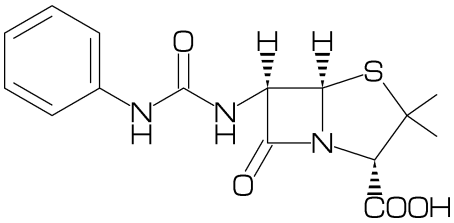
No.73 **Output additional infomation**

```
beginfont("EN:Caffeine","CAS:58-08-2")
MCf(...) endfont
%% Output to mcf_man_soc-info.aux %%
\INFO{{F:mcf_man_soc}{C:83}{EN:Caffeine}
     {CAS:58-08-2}}%
*F:filename *C:char number EN:molecular name
CAS:CAS number *:default output
```



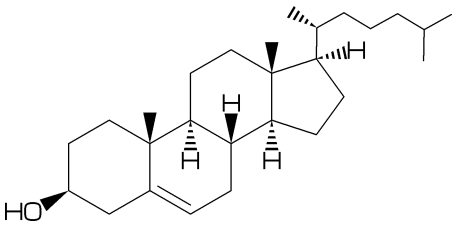
No.74 **Example(1) Ampicillin**

```
<45,?4,2:N,2=?5,-1:S,
@(3^45,4^-45)/*H,1://O^15,
5:/*COOH^-18,@(6^35,6^-35)/Me,
4\^75,NH,!,//O,!,NH,!,Ph
```



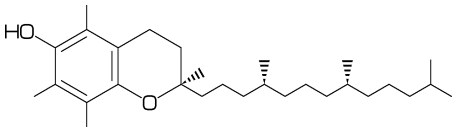
No.75 **Example(2) Cholesterol**

```
<30,?6,$(-4,-2)?6,-4=?5,7=dl,
1:*/OH,@(4,12)*/Me^60,9:*/H^60,
10:/*H^180,@(11,-1)/*H^-60,
-1\^17,/*Me,!4,/Me,!,
```



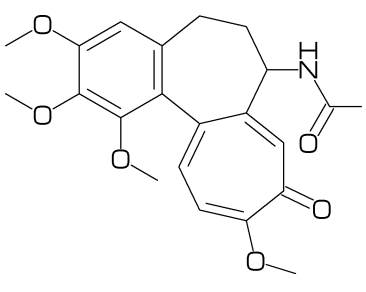
No.76 **Example(3) alfa-Tocopherol**

```
<30,Ph,3=?6,
7:O,@(1,2,5)/Me,8:/*Me^60,6:/OH,
8\,|,!12,@(4,8)/*Me,12:/Me
```



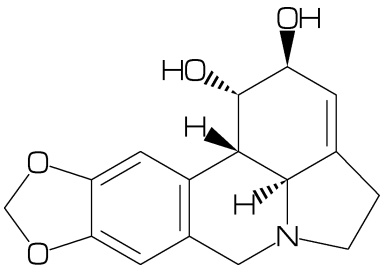
No.77 **Example(4) Colchicine**

```
<30,Ph,@(1,2,6)/OMe,|,-4=?7,
|,-5=?7,$(-1,-4,-6)dl,-2://O,-3:/OMe,
#9\,NH,!,//O,!
```



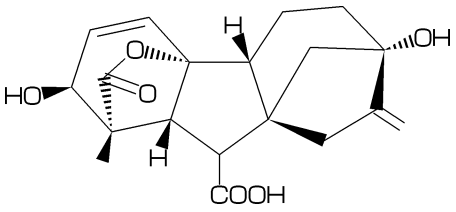
No.78 **Example(5) Lycorine**

```
<30,Ph,-4=?6,-2=?6,6=?5,(9,12)=?5[3],
13=dl,8:N,@(15,17)O,
9:/*H^180,10:*/H^60,13:*/OH,14:/*OH
```



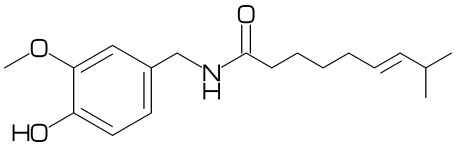
No.79 **Example(6) Gibberellin**

```
<12,?6'1.3,3=?5,9=?7,12\^160'1.6,&8,
4\^155~zf'1.2,O,55,//O^180'1,&2~zb,
5=dl,11=wf,13=wb,
7:/COOH,11://Me,1:*/OH,12:/*OH,2:*/Me,
@(3^-60,9^60)*/H
```



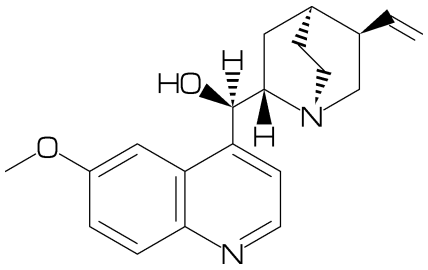
No.80 **Example(7) Capsaicin**

```
<30,Ph,
1:/OH,6:/OMe,4\,!,NH,!,//O,
|,!8,-3=dr,-1:/Me
```



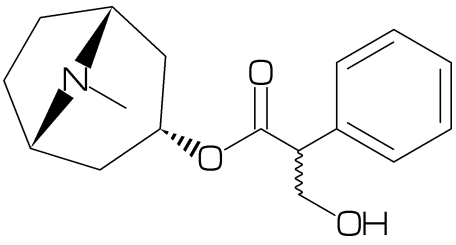
No.81 **Example(8) Quinine**

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



No.82 **Example(9) Atoropin**

```
<-30,O,!,//O,!,!,Ph,
#1\~zb^-120,
|,?7'1.1,6*\^190'1.25,N,/Me,&3~wb,
#3\~wv,!,OH
```



No.83 **Example(10) Paclitaxel**

```
?6,5=d,3*,{,''1,36,45,45,45,45,},&#5,
-4=?6,-4=?4,-1=wb,-3=wf,-1:O,||,
@(4^35,4^-35,6)/Me,@(3^-60,15)*/OH,
8:/*H^-60,9:*/Me^60,10://O,
1\,O,!,//O,!,*/OH,!,/Ph,
60~wf,NH,-60,//O,60,Ph,
7\*,O,-45,//O,60,Ph,11*\,O,-60,//O,60,
12\*^-15,O,60,//O,-60
```