

```

material = dna
temperature = 25.0
#
# target structures
#
structure substrateA = U5 D18 (U5 U2 D16 (U5 U2 D16 (U5 U2 D16+)))
structure substrateB = D16 (U2 U5 D18 (U5 +))
structure helperA = U6 U32 U14
structure helperB = U14 U6
structure trigger = U18 U5
structure complexA = D5 D18 + U5 U2 D16 ( U5 U2 D16 (U5 U2 D16+)) U18
structure complexB = D5 D18 (U5 U2 U16 U5 U2 U16 U5 U2 U16+)
structure byproductA = D6 D32 D14 (+ U2) U12
structure complexD = D5 D18 + D5 D18 ( D5 D18 (+ U18 U5)+ U5 U18) + U18 U5)
structure complexC = D5 D2 D16 + D5 D2 D16 ( D5 D2 D16(D5 D2 D16(+ U2U16 D16 (+)U2U5) +
U2U16 D16 (+)U2U5 ) + U2U16 D16 (+)U2U5 )
structure byproductB = D14 D6 (+ U12) U2

```

```

#
# sequence domains
#
domain a = N5
domain b = N2
domain c = N10
domain d = N6
domain z1 = N2
domain z2 = N14
domain e = N18
domain f = N5
domain g = N2
domain h = N10
domain i1 = N4
domain i2 = N2
domain j = N6
domain k = N18

```

```

#
# match constraint
#
# match z = cd
# match e = bz

```

```

#

```

```
# strands (optional, used for threading sequence information
# and for displaying results)
```

```
#
```

```
strand A = a b z1 z2 f g h i1 i2 f g h i1 i2 f g h i1 i2
```

```
strand B = i2* i1* h* i2* i1* h* i2* i1* h* e*
```

```
strand C = z1 z2 b a i2* i1* h* g* f*
```

```
strand D = g h i1 i2 z2* z1*
```

```
strand E = d h i1 i2 h i1 i2 h i1
```

```
strand F = z2 i2* i1*
```

```
strand G = z2* z1* b* a*
```

```
#
```

```
# thread strand sequence information onto target structures
```

```
#
```

```
substrateA.seq = A B
```

```
substrateB.seq = C D
```

```
helperA.seq = E
```

```
helperB.seq = F
```

```
trigger.seq = G
```

```
complexA.seq = G A B
```

```
complexB.seq = A G
```

```
byproductA.seq = E B
```

```
complexD.seq = G A C C C
```

```
complexC.seq = G A D C D C D C
```

```
byproductB.seq = F D
```

```
#
```

```
#target testtubes
```

```
#
```

```
tube tubeinitial = substrateA substrateB helperA helperB
```

```
tubeinitial.maxsize = 2
```

```
tube tubestep1 = complexA substrateB helperB
```

```
tubestep1.maxsize = 2
```

```
tube tubestep2 = complexB byproductA
```

```
tubestep2.maxsize = 2
```

```
tube tubestep3 = complexC byproductA helperA
```

```
tubestep3.maxsize = 2
```

```
tube tubestep4 = complexD byproductB byproductA
```

```
tubestep4.maxsize = 2
```

```
#
```

```
# prevent sequence patterns
```

```
#
```

```
prevent = AAAA, CCCC, GGGG, UUUU, KKKKKK, MMMMMM, RRRRRR, SSSSSS, WWWWWW, YYYYYY
```

