

```

material = dna
#
# target structures
#
structure substratea = U5 D18 (U5 U2 D16 (U5 U2 D16+))
structure substrateb = D16 (U2 U5 D18 (U5 +))
structure helpera = U6 U32
structure helperb = U16 U6
structure trigger = U18 U5
structure complexa = D5 D18 + U5 U2 D16 ( U5 U2 D16+) U18
structure complexb = D5 D18 (U5 U2 U16 U5 U2 U16+)
structure byproducta = D6 D32 + U12
structure complexc = D5 D18 + D5 D18 ( D5D18 (+ U18 U5) + U18 U5 )
structure complexd = D5 D2 D16 + D5 D2 D16 ( D5 D2 D16(+ U2U16 D16 (+)U2U5) + U2U16 D16
(+)U2U5 )

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#
# sequence domains
#
domain a = N5
domain b = N2
domain c = N10
domain d = N6
domain z = N16
domain e = N18
domain f = N5
domain g = N2
domain h = N16
domain i = N12
domain j = N6
domain k = N18

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

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

```

strand A = a b z f g h f g h  
strand B = h\* h\* e\*  
strand C = z b a h\* g\* f\*  
strand D = g h z\*  
strand E = d h h  
strand F = z j\*  
strand G = z\* 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  
complexc.seq = G A C C  
complexd.seq = G A D C D C

#  
# prevent sequence patterns  
#  
prevent = AAAA, CCCC, GGGG, UUUU, KKKKKK, MMMMMM, RRRRRR, SSSSSS, WWWWWW, YYYYYY