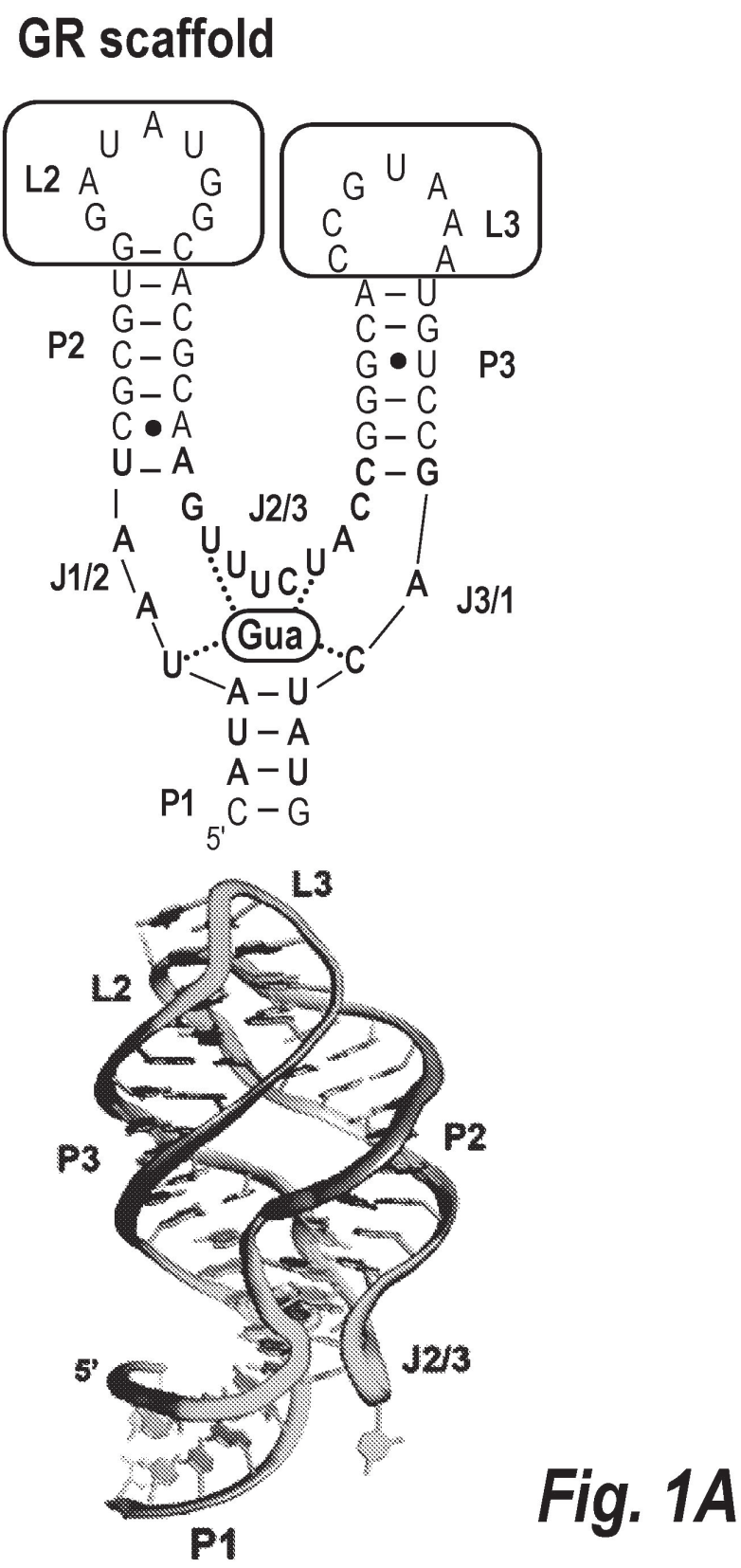


Fig. 1A

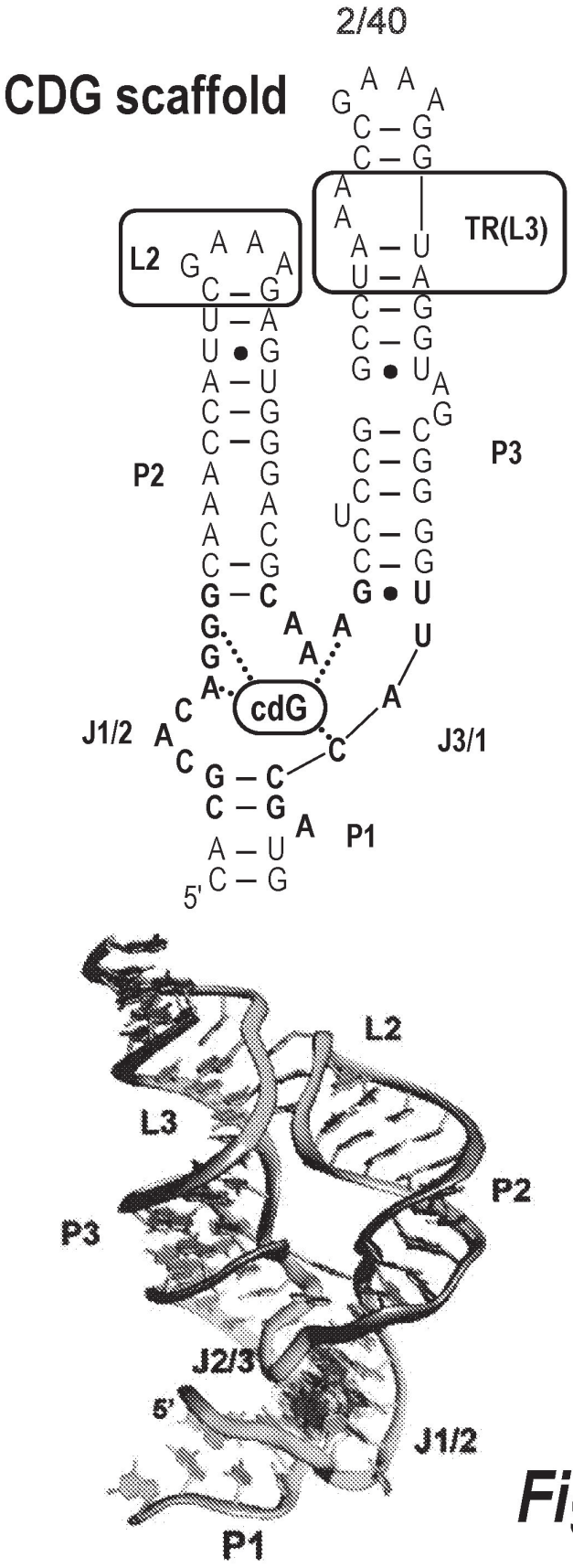

CDG scaffold
L2
TR(L3)
P2
P3
cdG
J1/2
J3/1
P1
5'
L2
L3
P2
P3
J2/3
5'
J1/2
P1

Fig. 1B

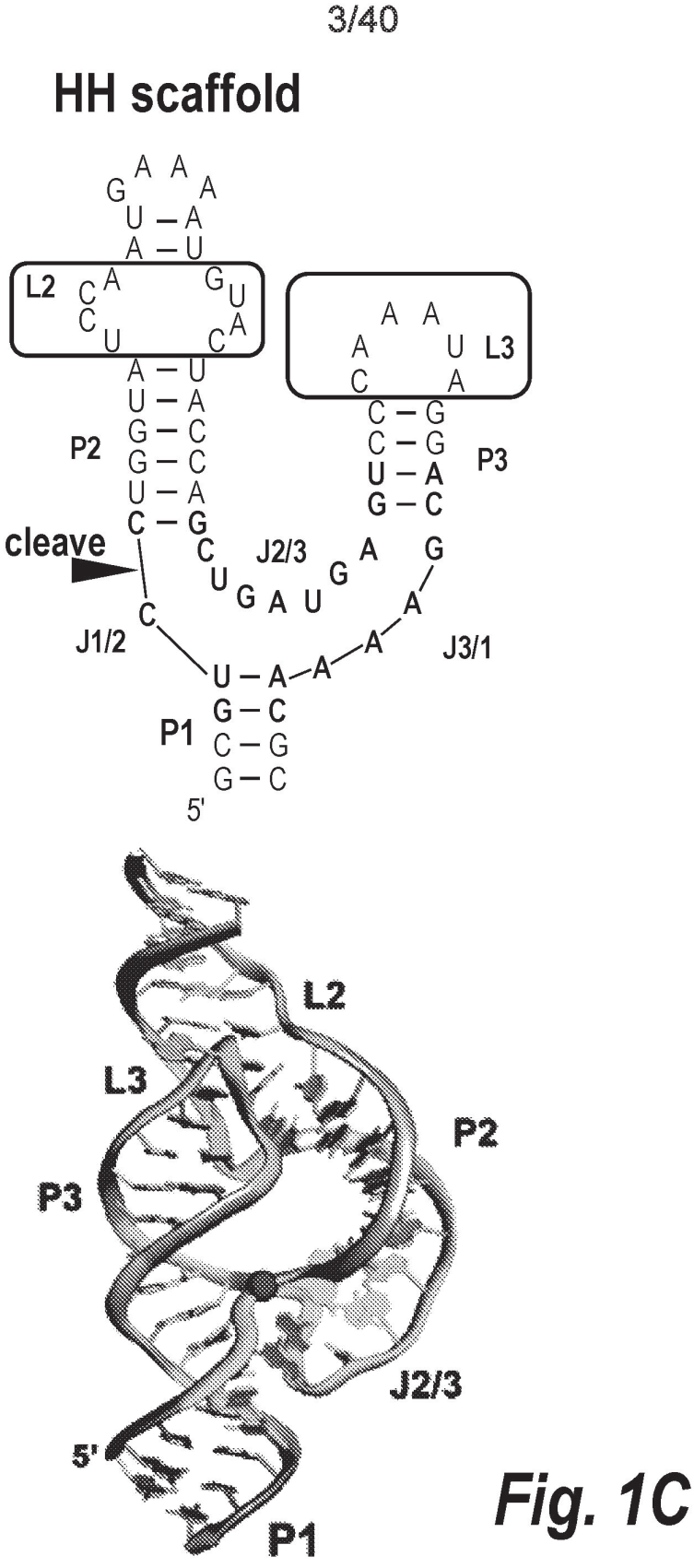

HH scaffold
L2
L3
P2
P3
cleave
J2/3
J1/2
J3/1
P1
5'
L2
L3
P2
P3
J2/3
5'
P1

Fig. 1C

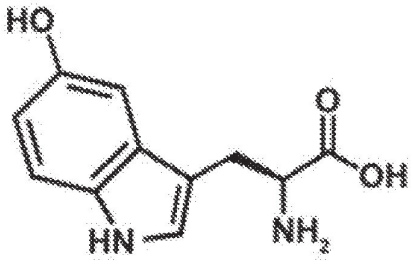


Fig. 2A

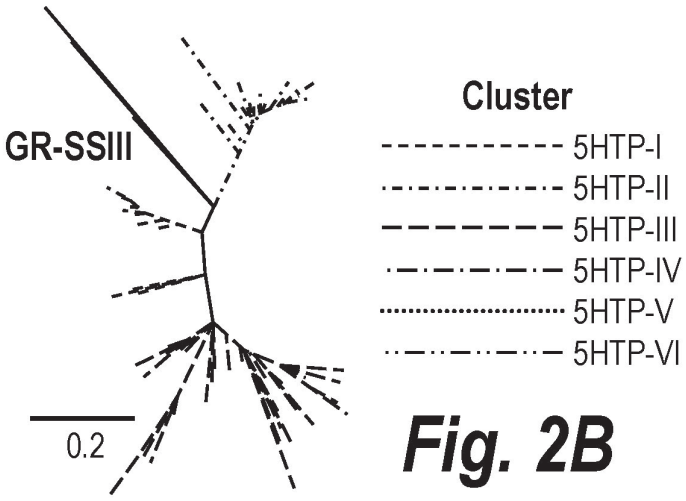


Fig. 2B

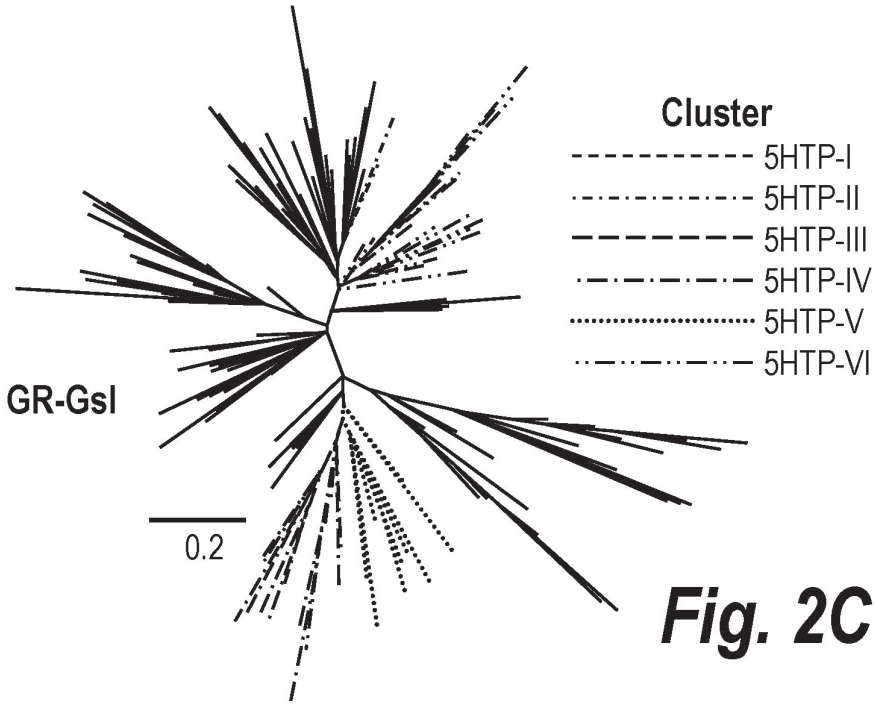


Fig. 2C

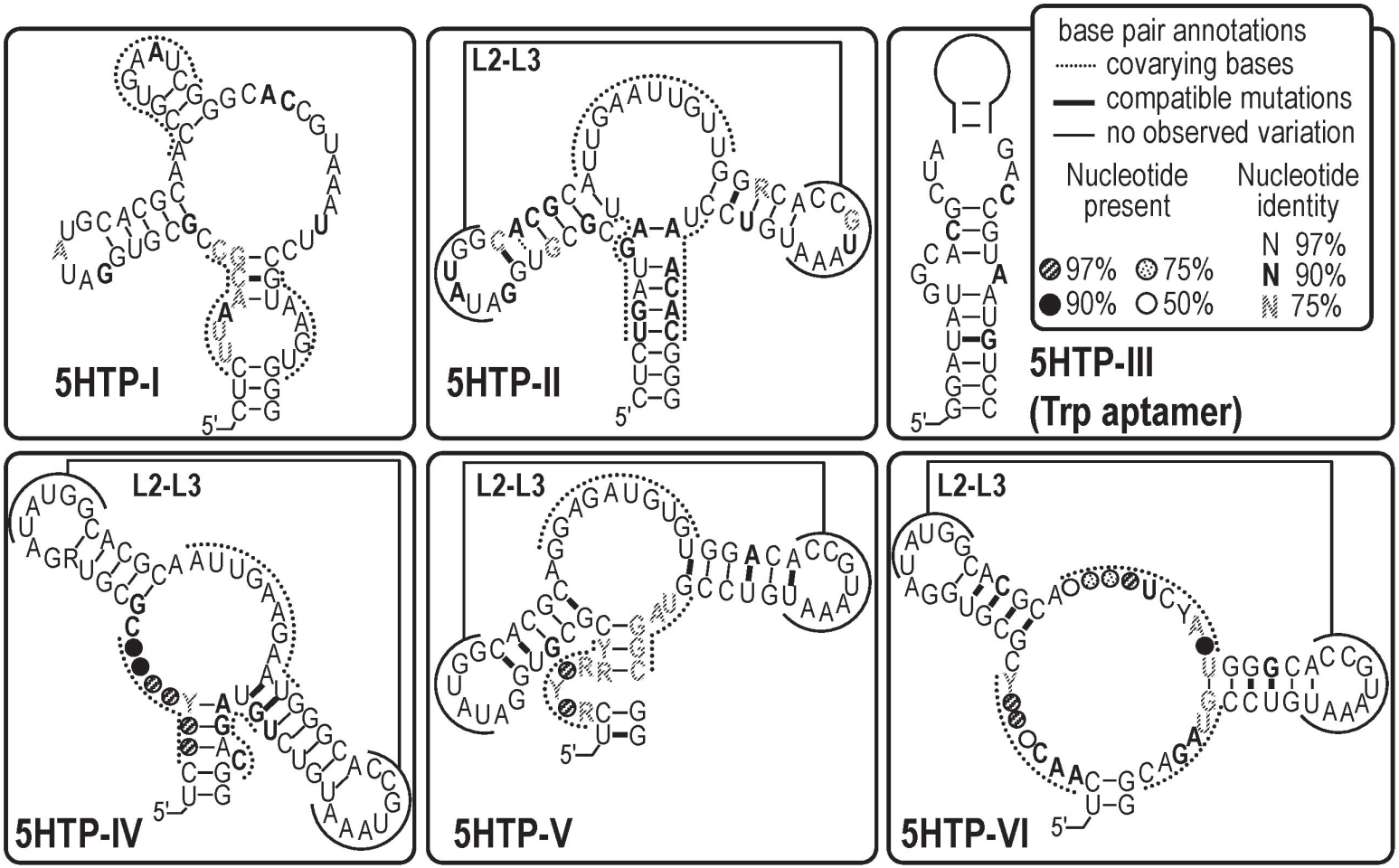

5HTP-I
5HTP-II
L2-L3
5HTP-III
(Trp aptamer)
base pair annotations
covarying bases
compatible mutations
no observed variation
Nucleotide present
Nucleotide identity
97%
75%
90%
50%
N 97%
N 90%
75%
5HTP-IV
5HTP-V
5HTP-VI
5'

Fig. 2D

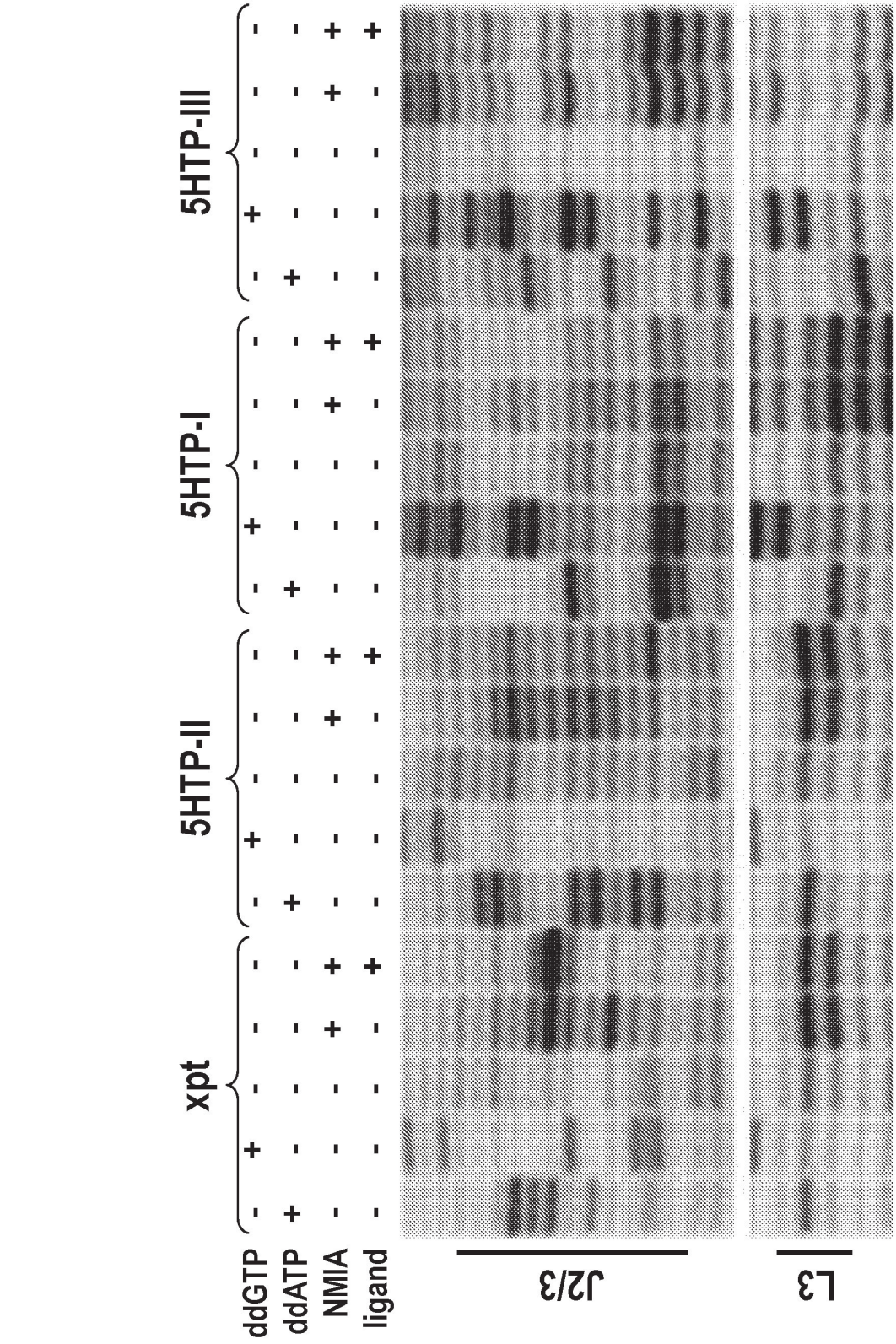


Fig. 3A

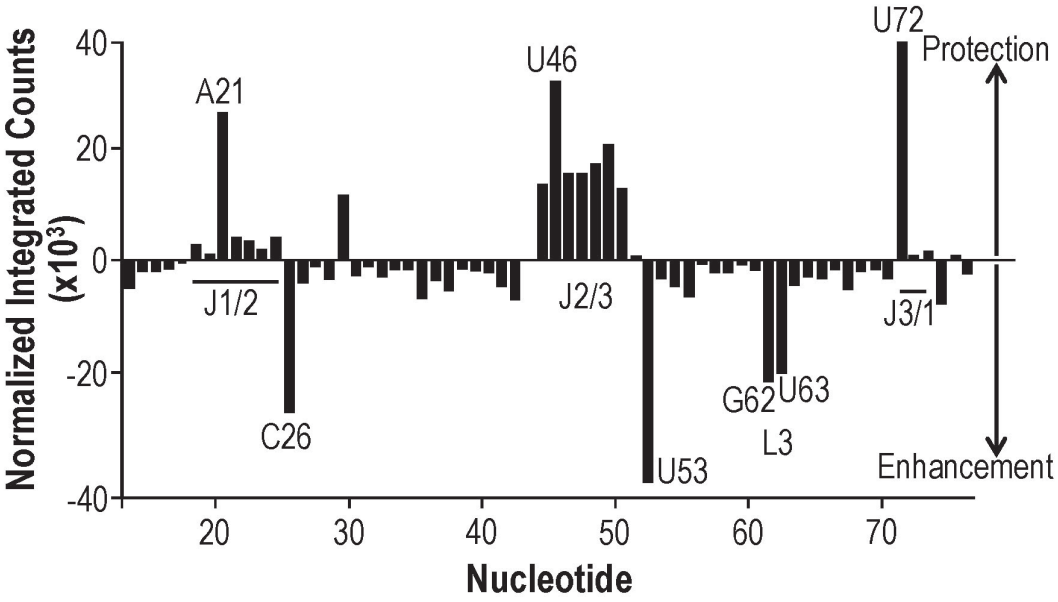

Normalized Integrated Counts (x10³)
40
20
0
-20
-40
A21
U46
U72
Protection
J1/2
J2/3
J3/1
C26
G62
U63
L3
U53
Enhancement
20
30
40
50
60
70
Nucleotide

Fig. 3B

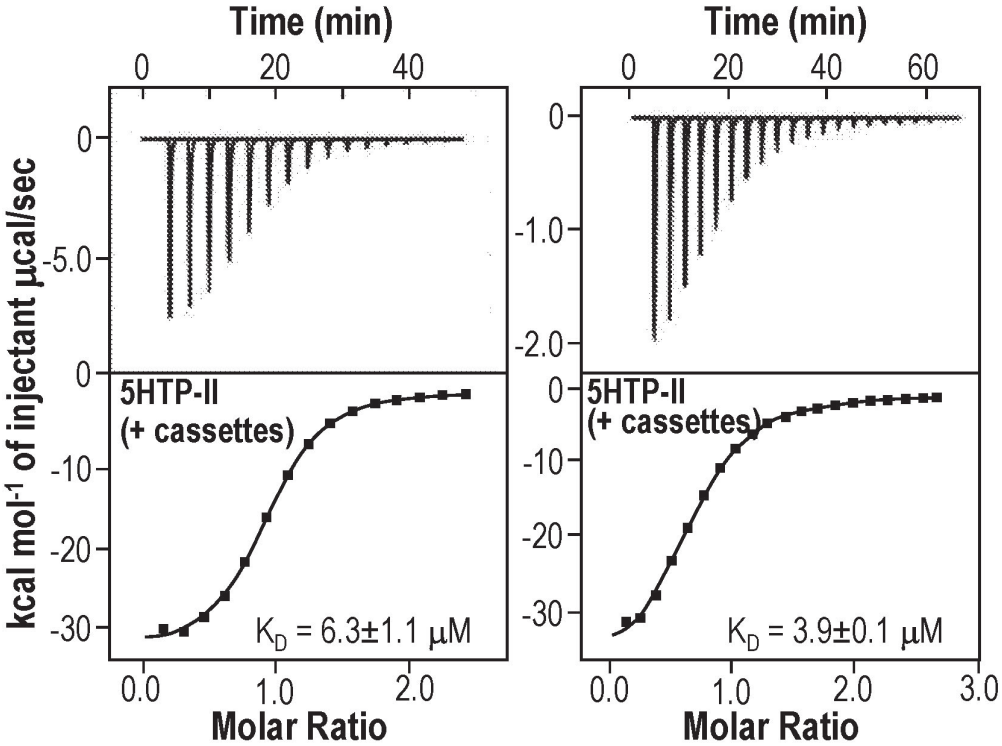

Time (min)
0
20
40
60
kcal mol⁻¹ of injectant µcal/sec
0
-5.0
-1.0
-2.0
5HTP-II
(+ cassettes)
-10
-20
-30
K_D = 6.3±1.1 µM
K_D = 3.9±0.1 µM
0.0
1.0
2.0
3.0
Molar Ratio

Fig. 3C

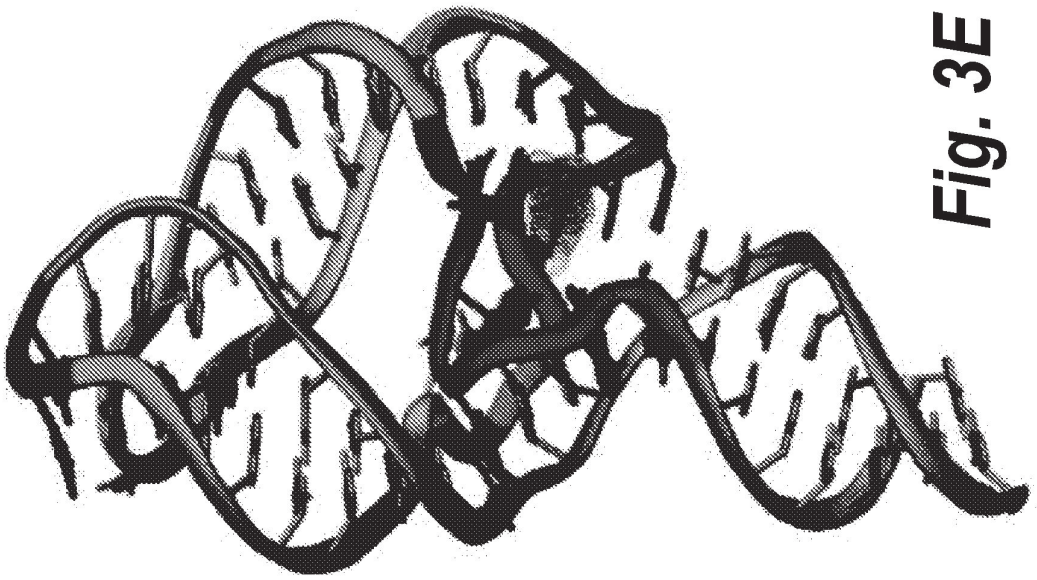


Fig. 3E

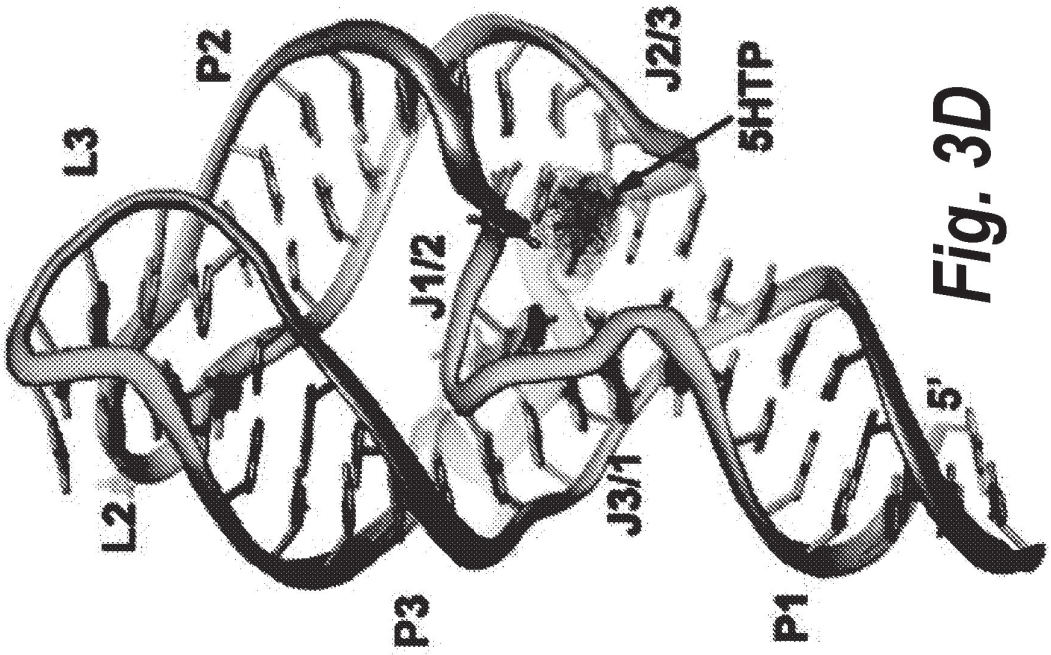


Fig. 3D

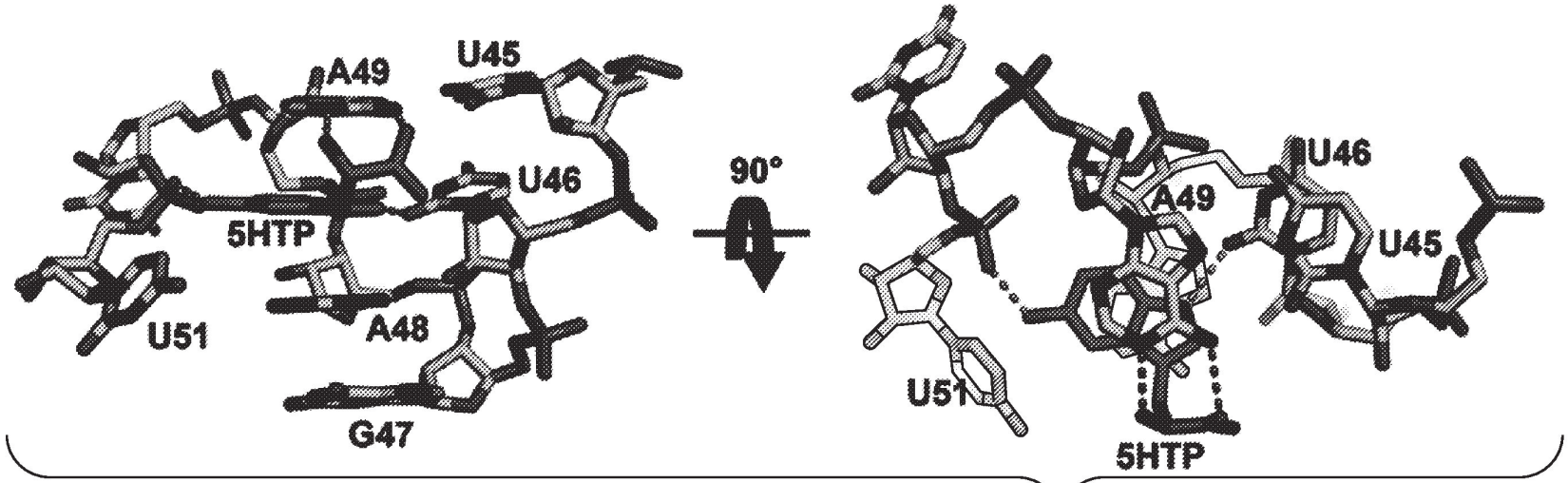

A49
U45
U46
5HTP
U51
A48
G47
90°
U46
A49
U45
U51
5HTP

Fig. 4A

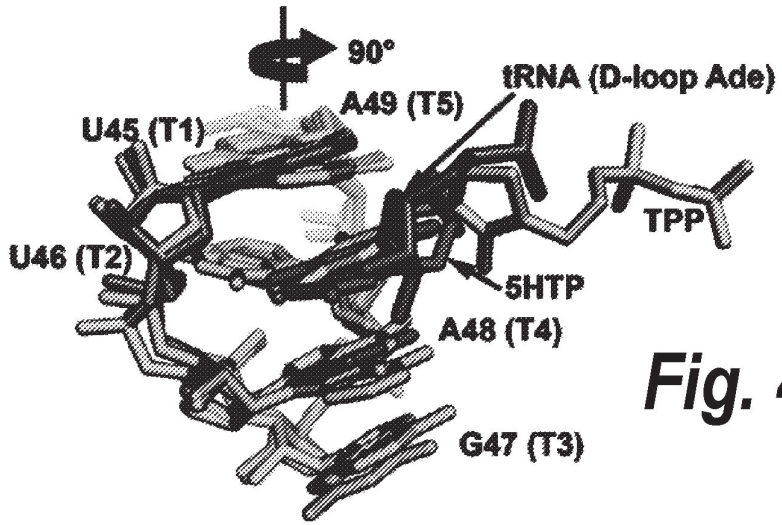

90°
tRNA (D-loop Ade)
A49 (T5)
U45 (T1)
TPP
U46 (T2)
5HTP
A48 (T4)
G47 (T3)

Fig. 4B

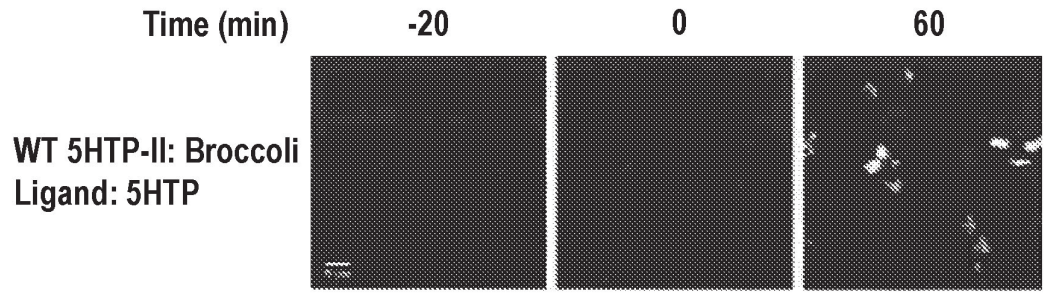


Fig. 5A

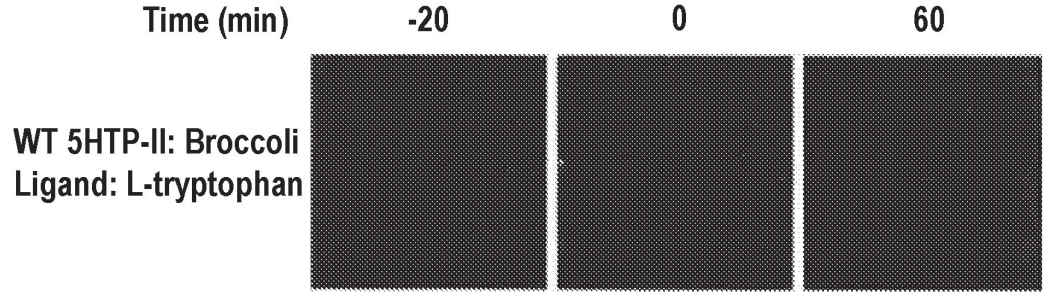


Fig. 5B

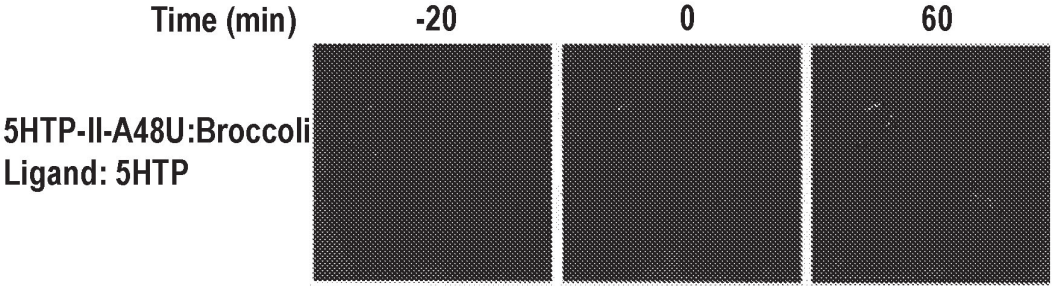


Fig. 5C

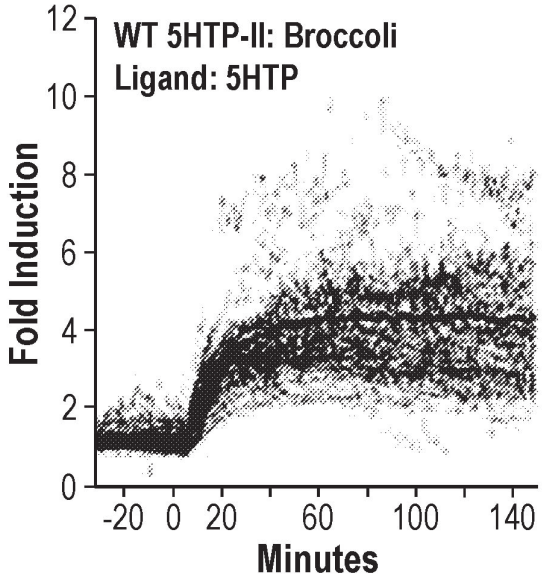


Fig. 5D

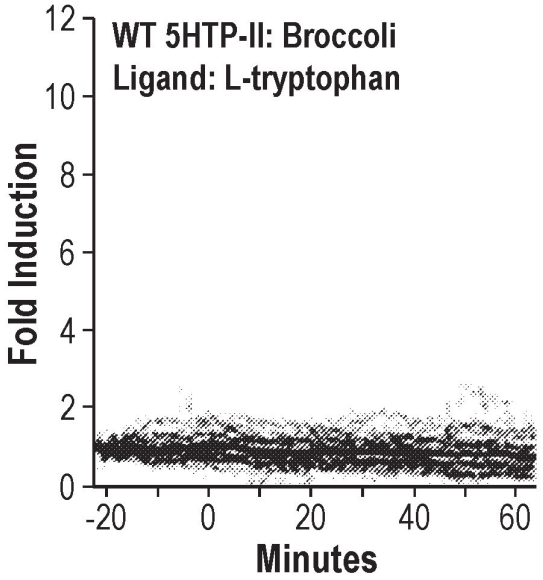


Fig. 5E

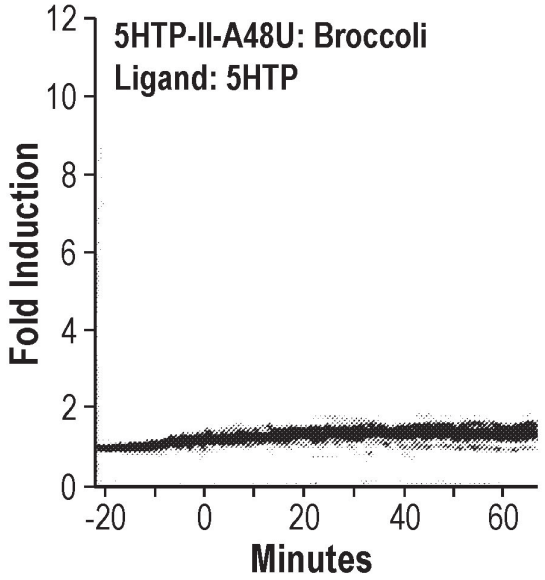


Fig. 5F

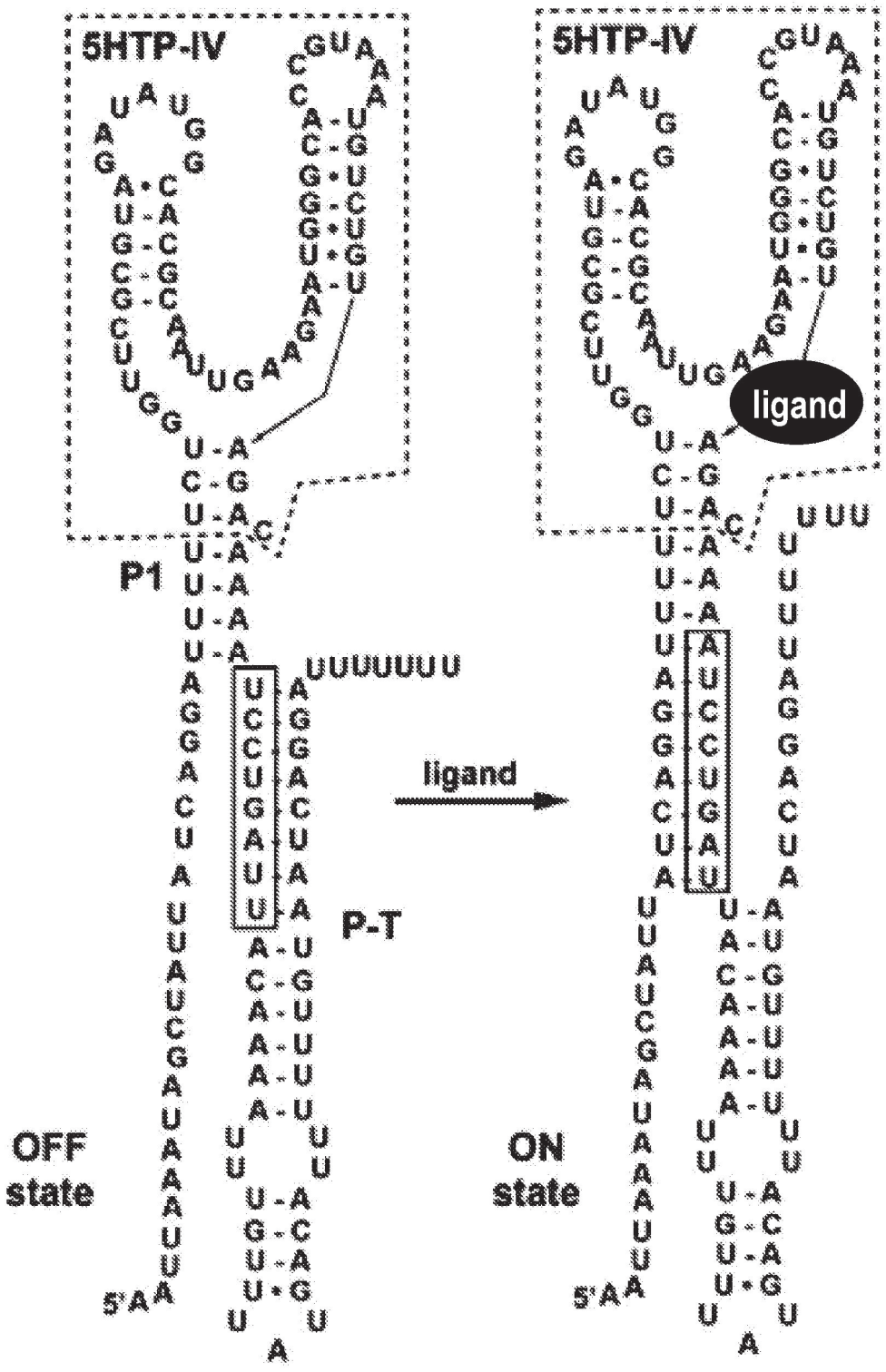


Fig. 6A

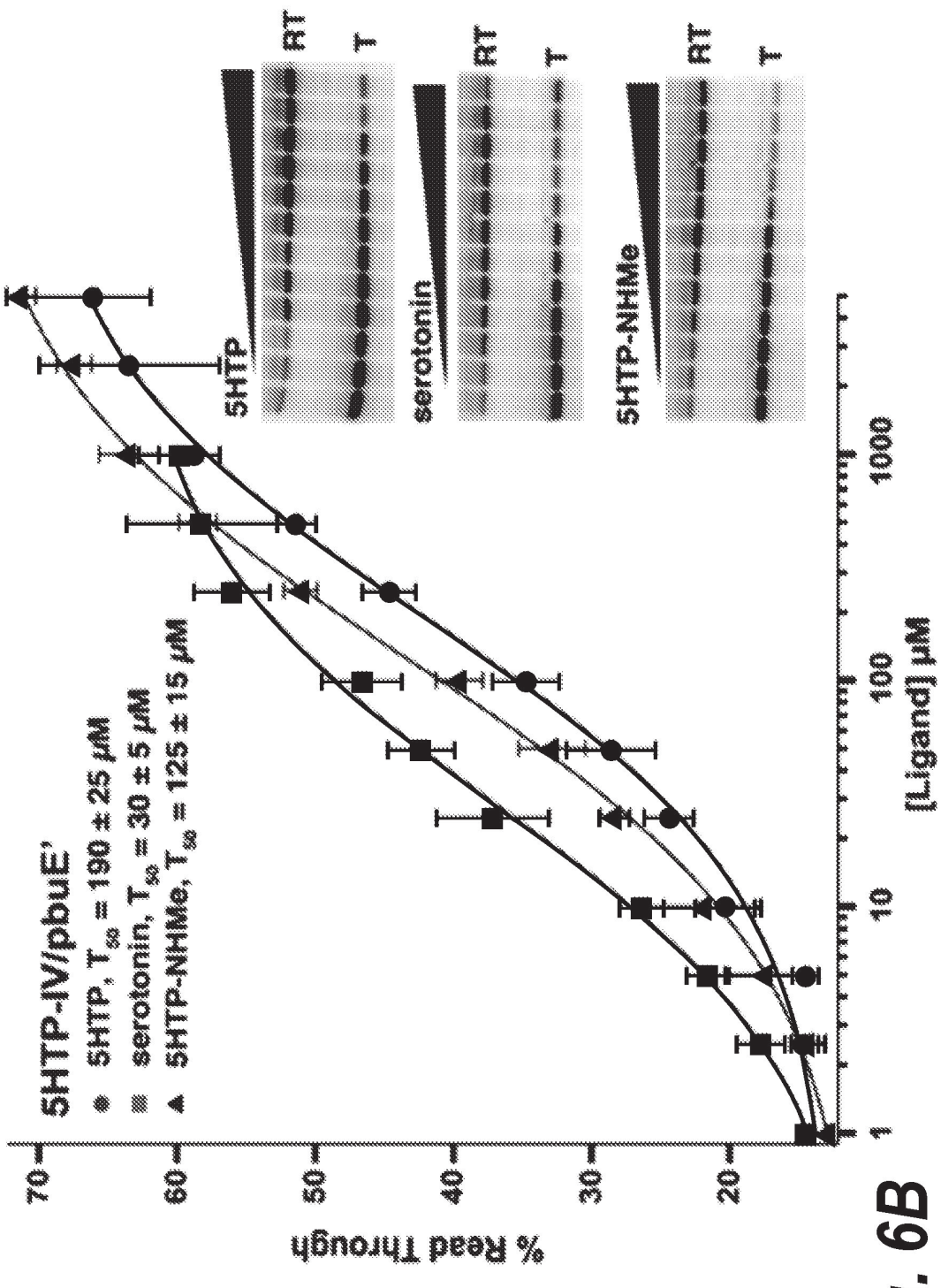

5HTP-IV/pbuE'
5HTP, T50 = 190 ± 25 μM
serotonin, T50 = 30 ± 5 μM
5HTP-NHMe, T50 = 125 ± 15 μM
% Read Through
[Ligand] μM
5HTP
serotonin
5HTP-NHMe
RT
T

Fig. 6B

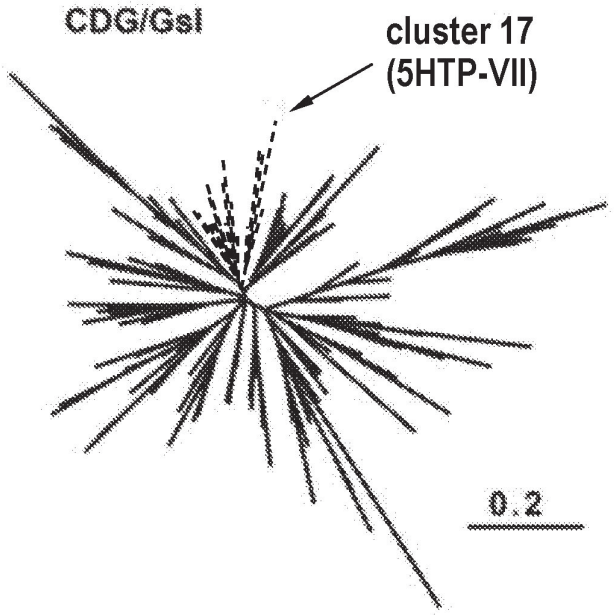


Fig. 7A

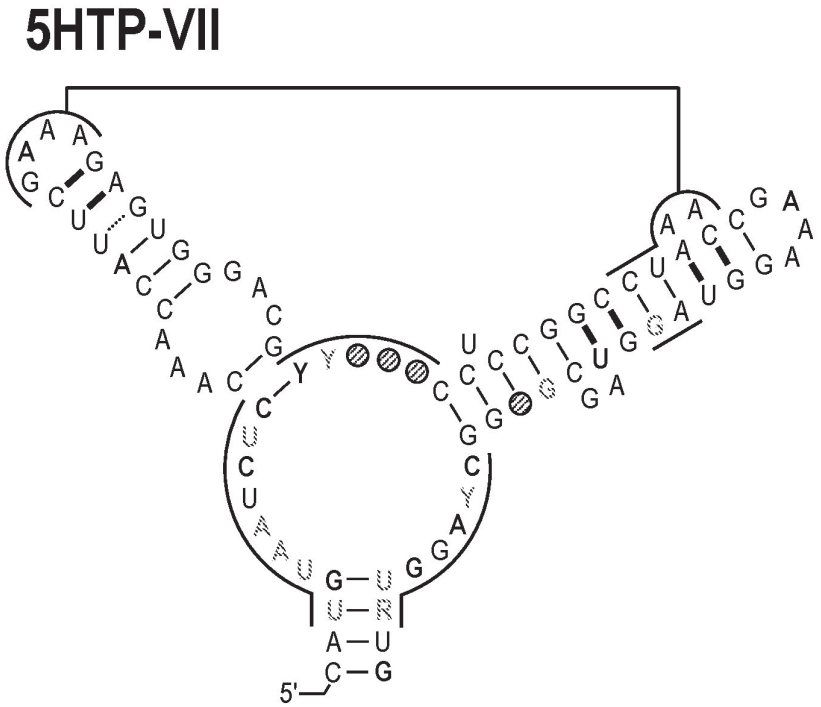


Fig. 7B

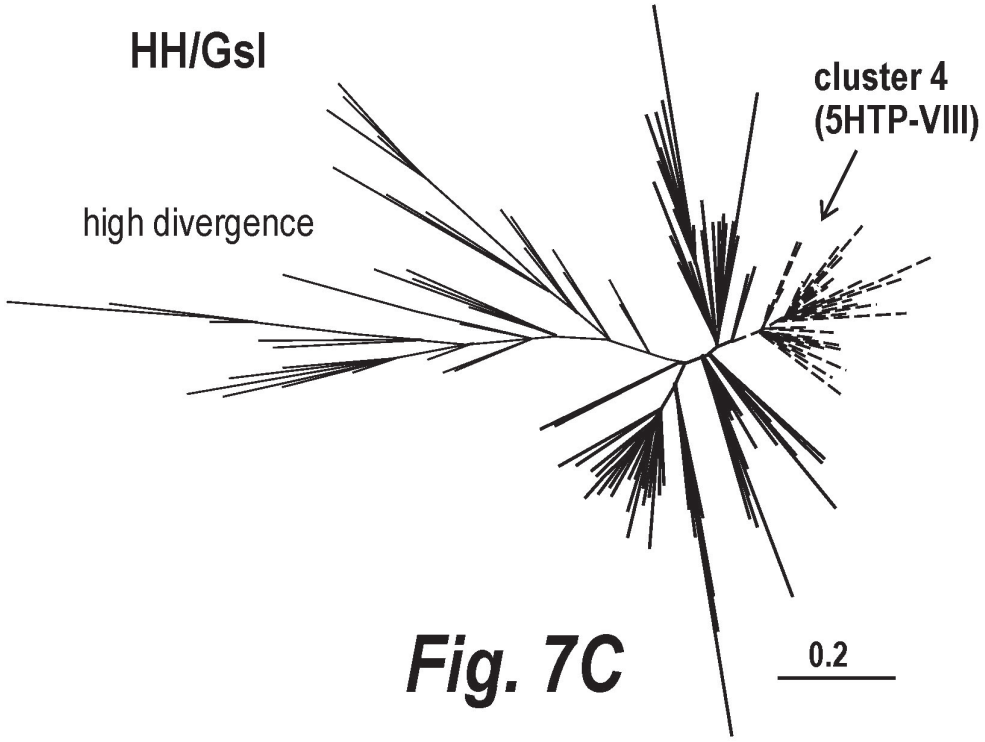


Fig. 7C

5HTP-VIII

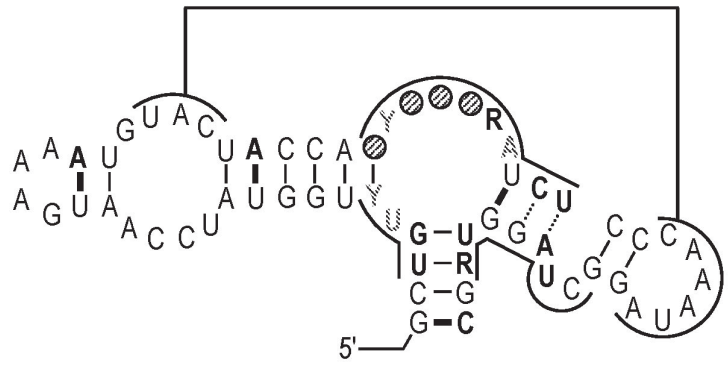


Fig. 7D

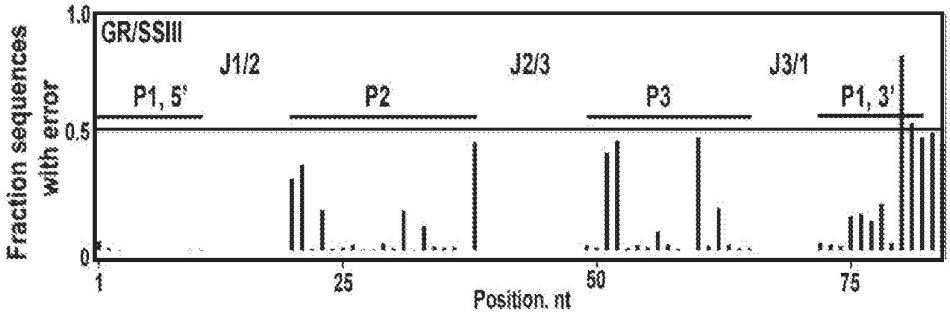


Fig. 8A

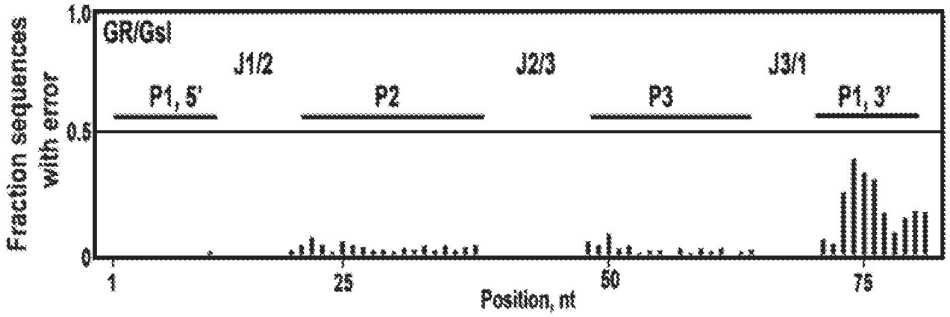


Fig. 8B

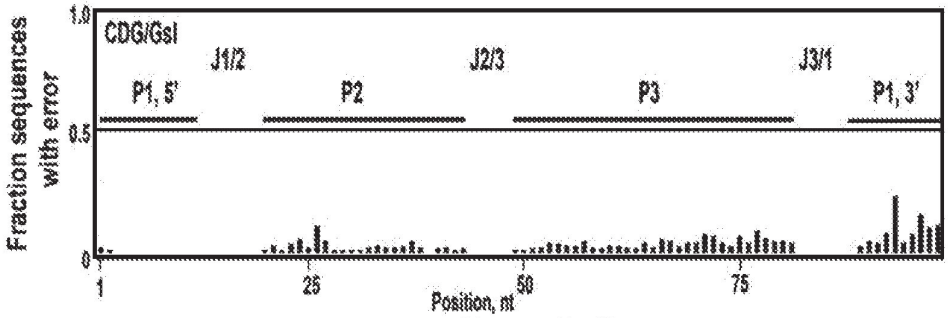


Fig. 8C

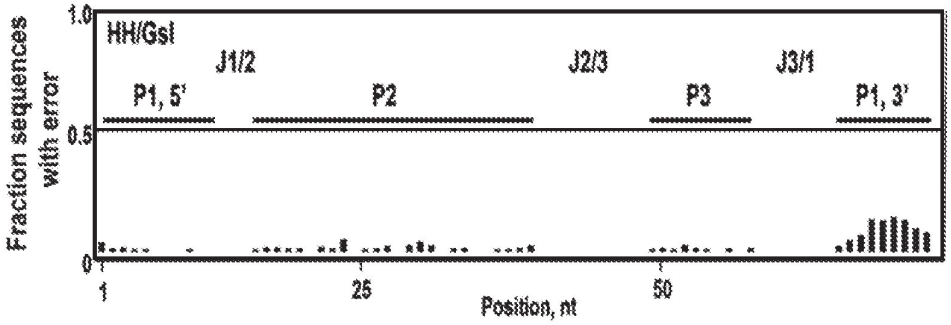


Fig. 8D

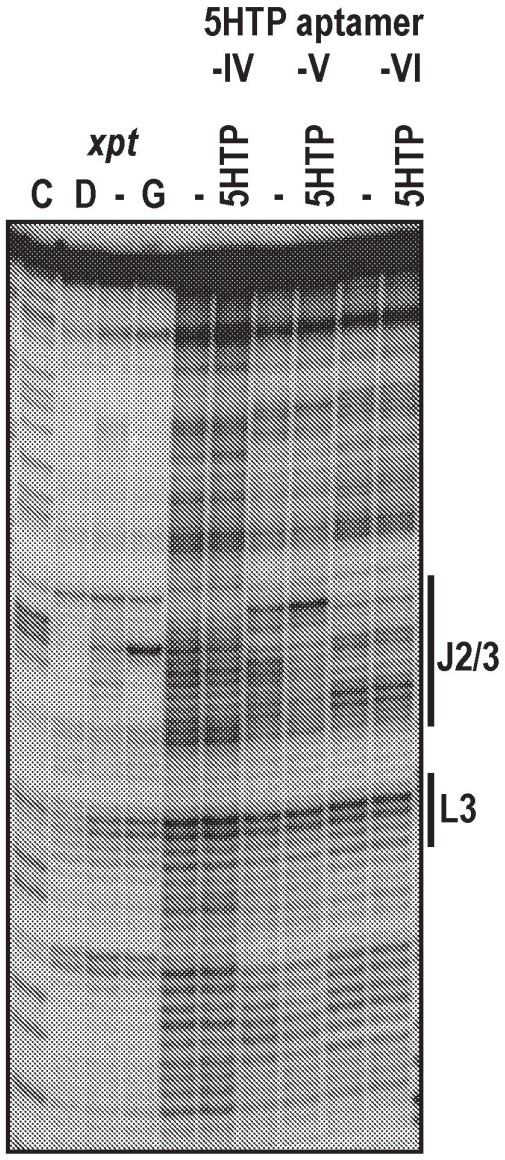


Fig. 9A

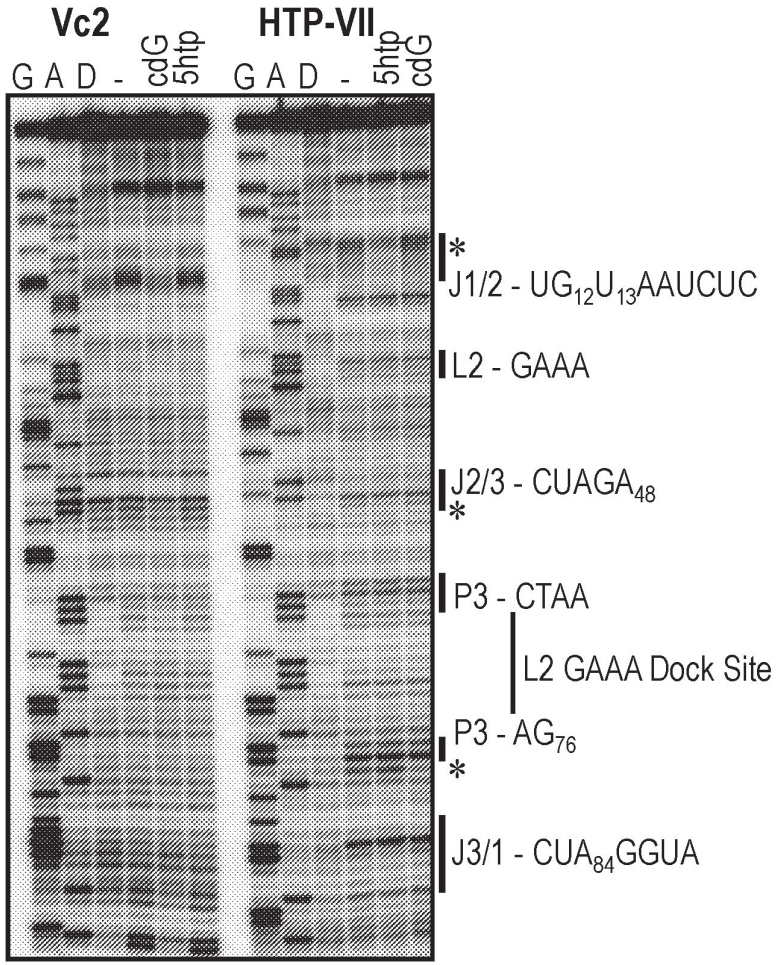

Vc2
HTP-VII
G A D - cdG 5htp
G A D - 5htp cdG
*
J1/2 - UG12U13AAUCUC
L2 - GAAA
J2/3 - CUAGA48
*
P3 - CTAA
L2 GAAA Dock Site
P3 - AG76
*
J3/1 - CUA84GGUA

Fig. 9B

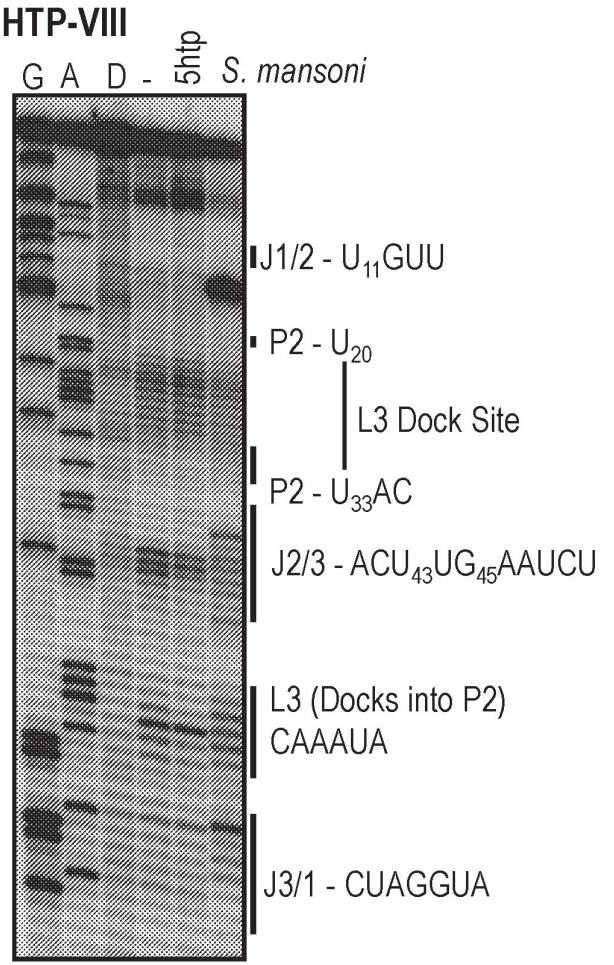

HTP-VIII
G A D - 5htp S. mansoni
J1/2 - U11GUU
P2 - U20
L3 Dock Site
P2 - U33AC
J2/3 - ACU43UG45AAUCU
L3 (Docks into P2)
CAAAUA
J3/1 - CUAGGUA

Fig. 9C

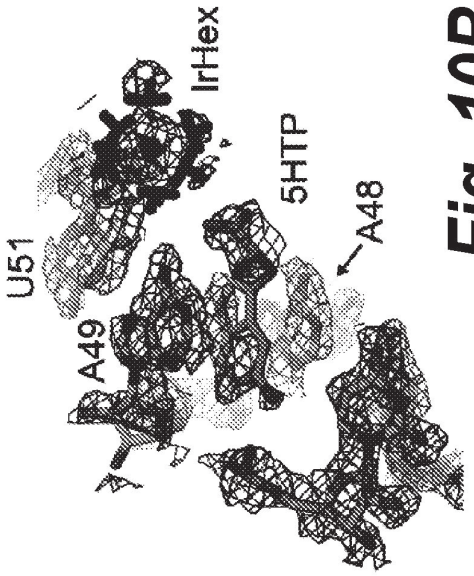


Fig. 10B

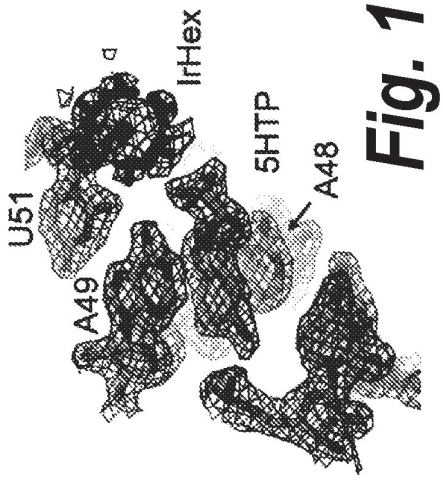


Fig. 10C

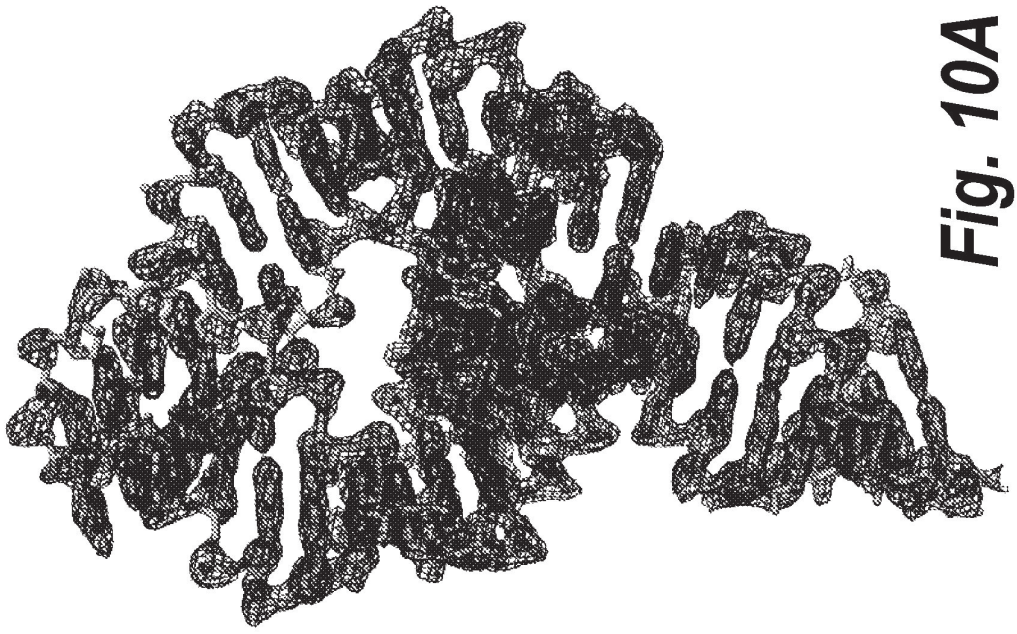


Fig. 10A

5HTP-VIII

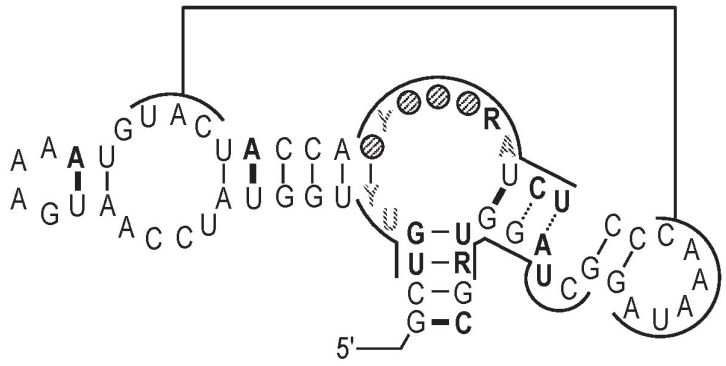


Fig. 11A

T-loop	Pos.	U	C	G	A
	1	**80**	8	0	**9**
	2	27	2	70	0
	3	14	2	16	68
	4	0	0	**32**	**67**
	5	8	0	0	**89**

HTP-VIII	Pos.	U	C	G	A
	1	**62**	3	16	**19**
	2	62	11	13	14
	3	24	10	46	20
	4	5	3	**32**	**60**
	5	0	2	0	**97**

Fig. 11B

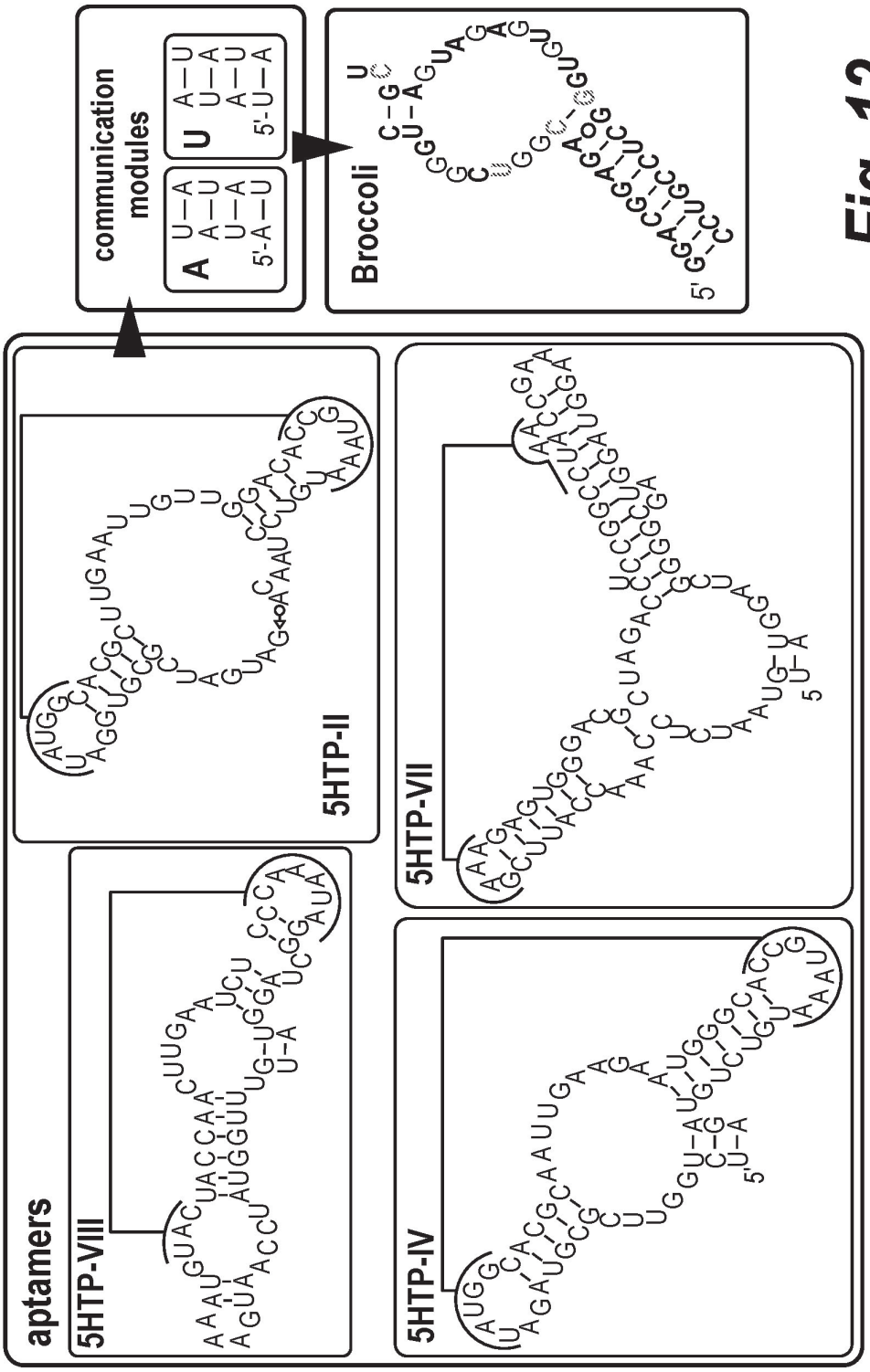

aptamers
5HTP-VIII
5HTP-II
5HTP-IV
5HTP-VII
communication modules
A
U
Broccoli

Fig. 12

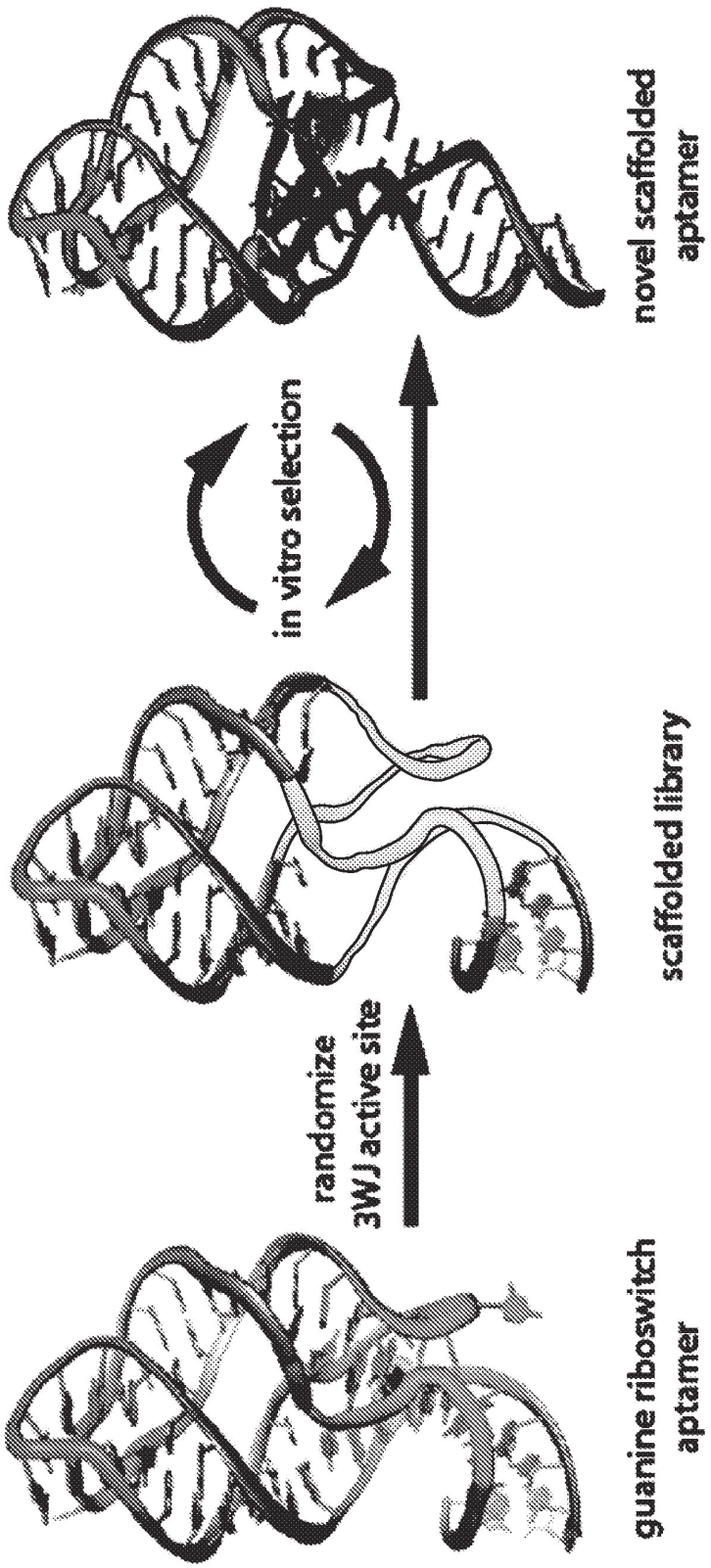
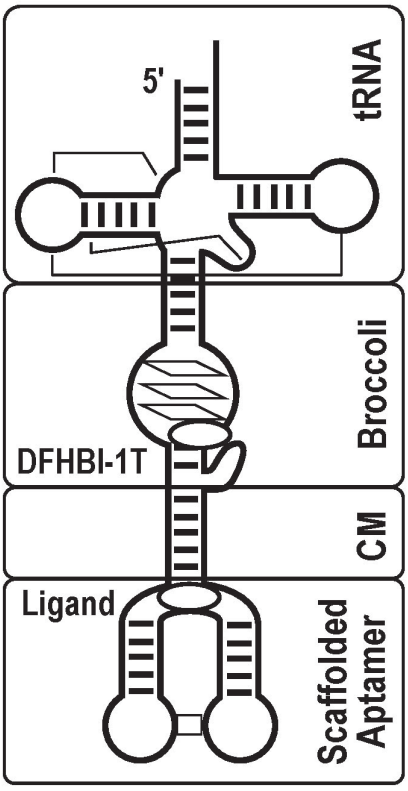

guanine riboswitch aptamer
randomize 3WJ active site
scaffolded library
in vitro selection
novel scaffolded aptamer

Fig. 13



CM-2
5' U A
I I
A U

CM-3
5' U A U
I I I
A U A

CM-4
5' U A U A
I I I I
A U A U

CM-5
5' U A U A U
I I I I I
A U A U A

Fig. 14A

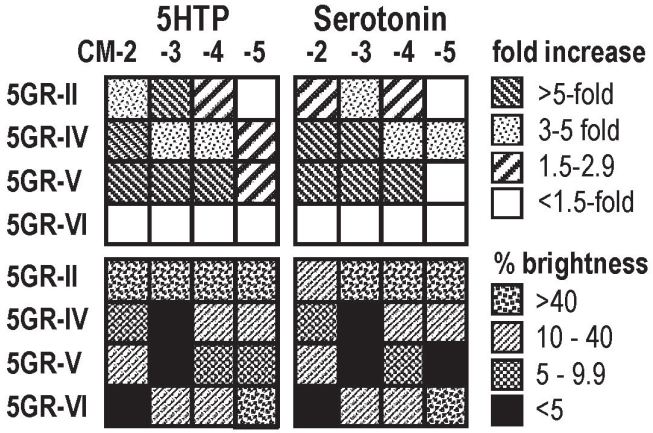


Fig. 14B

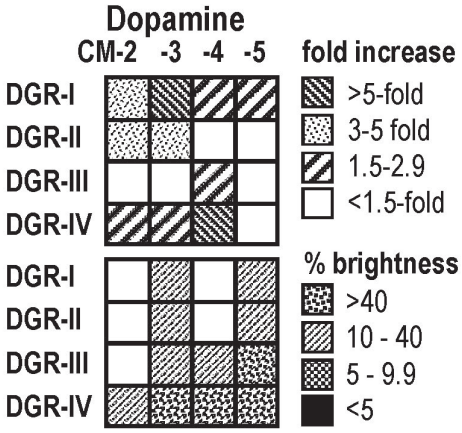


Fig. 14C

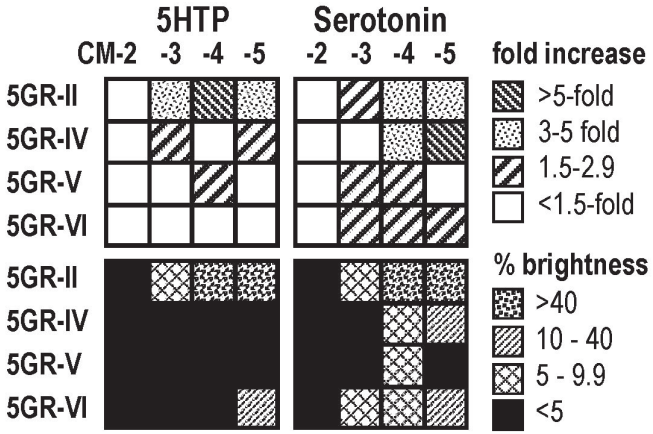


Fig. 14D

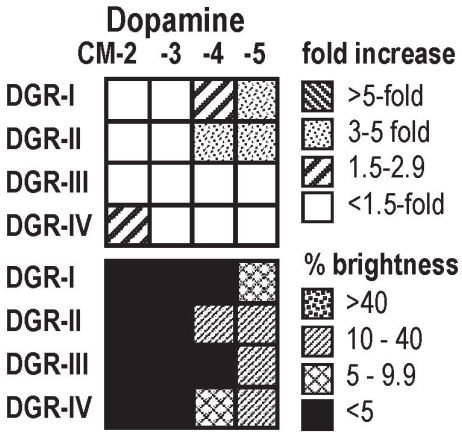


Fig. 14E

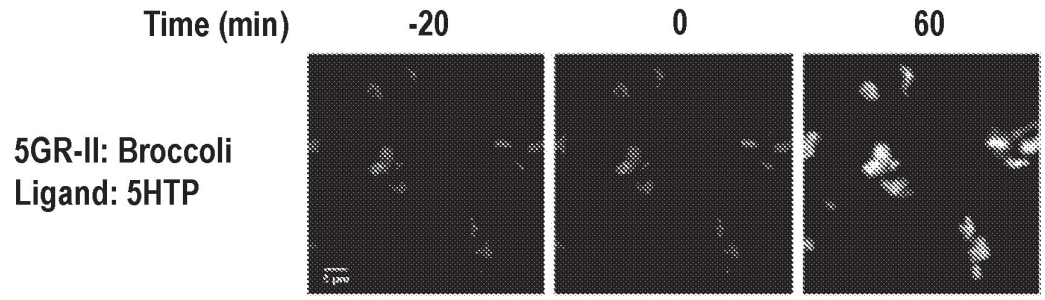


Fig. 15A

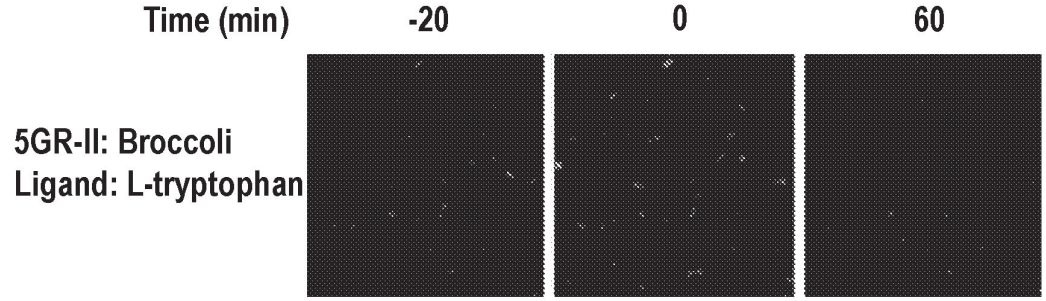


Fig. 15B

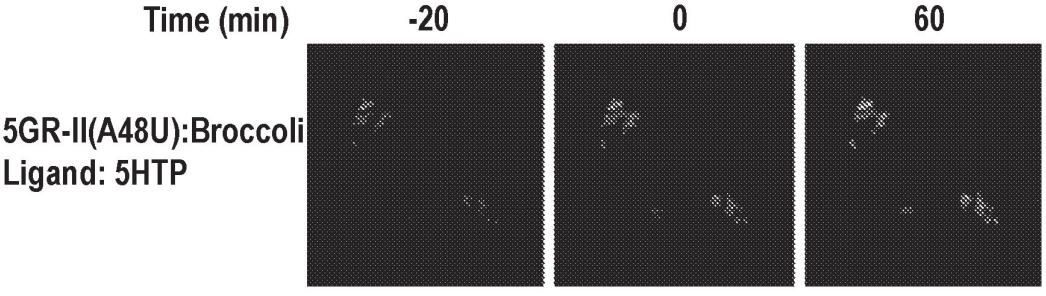


Fig. 15C

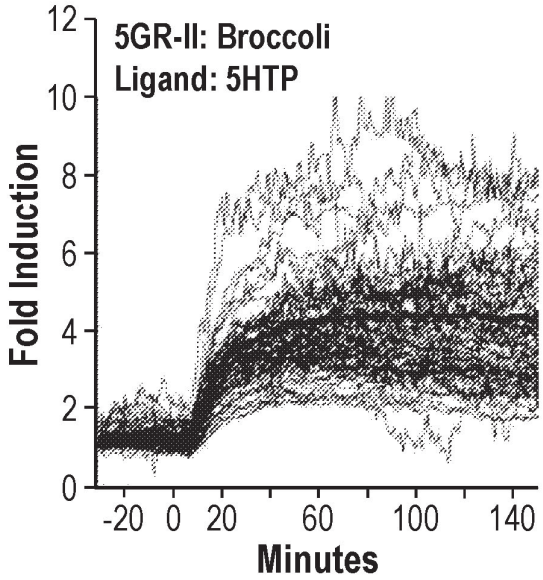


Fig. 15D

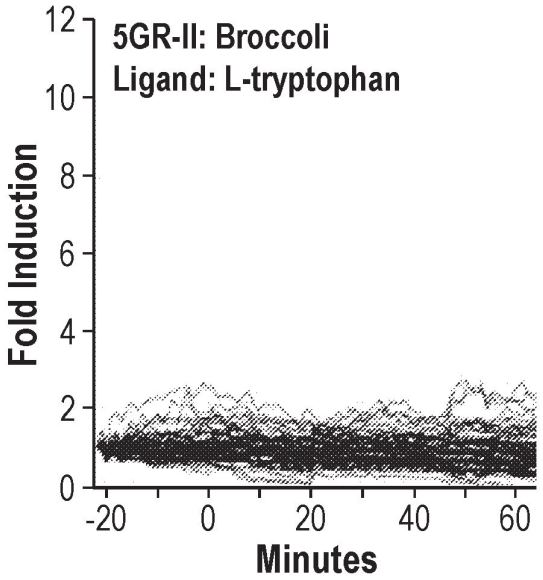


Fig. 15E

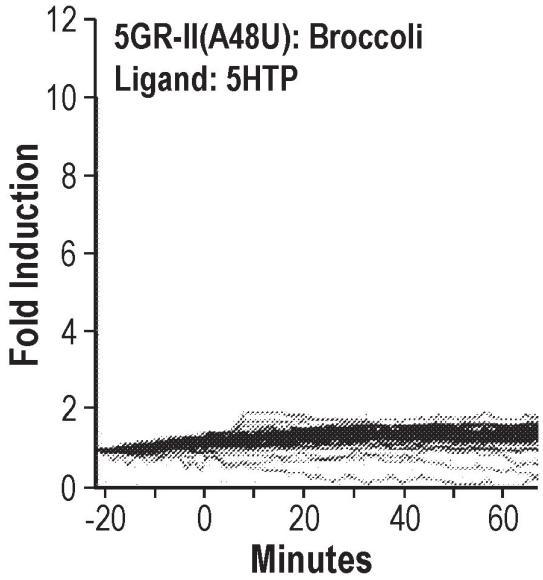


Fig. 15F

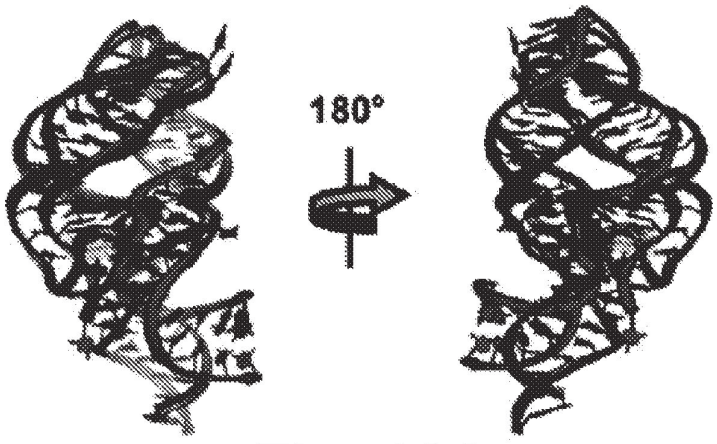


Fig. 16A

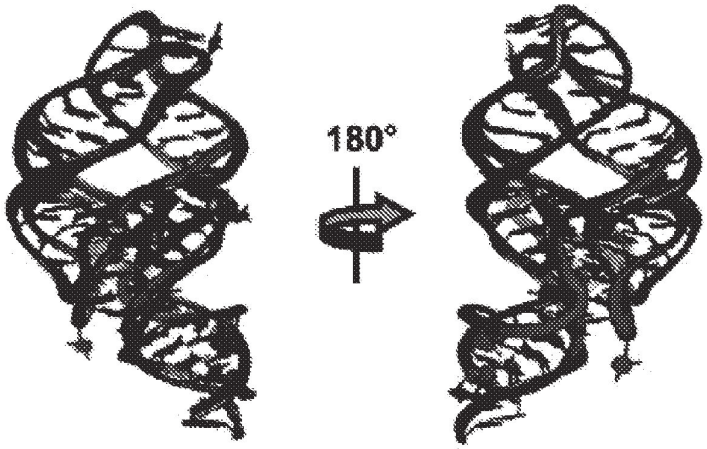


Fig. 16B

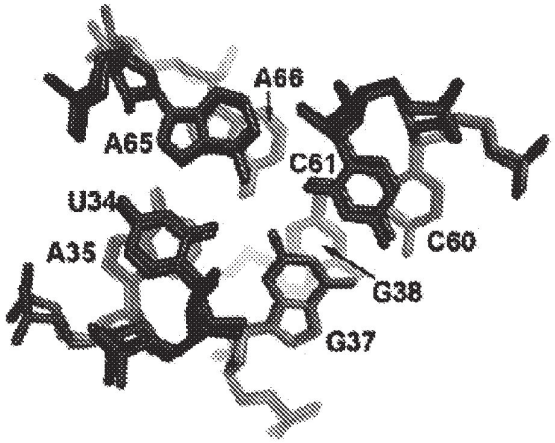


Fig. 16C

Fig. 17A

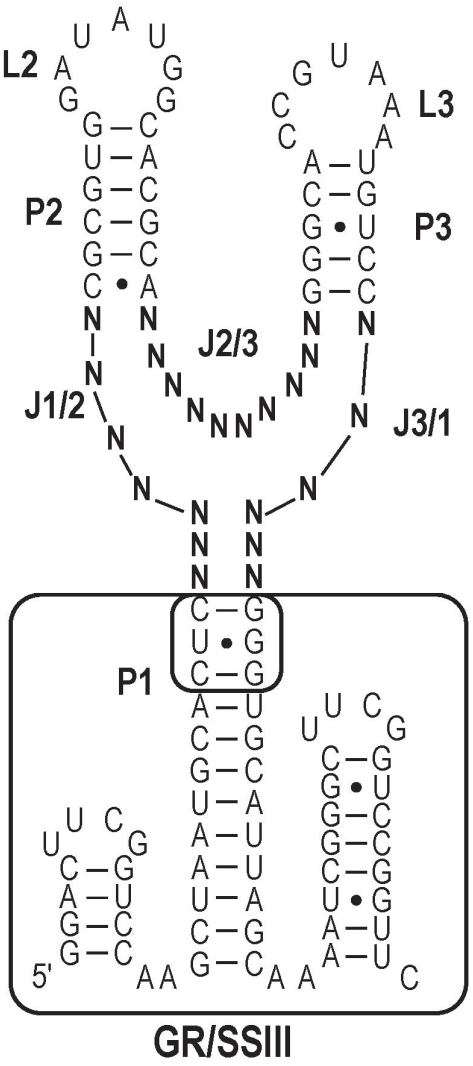
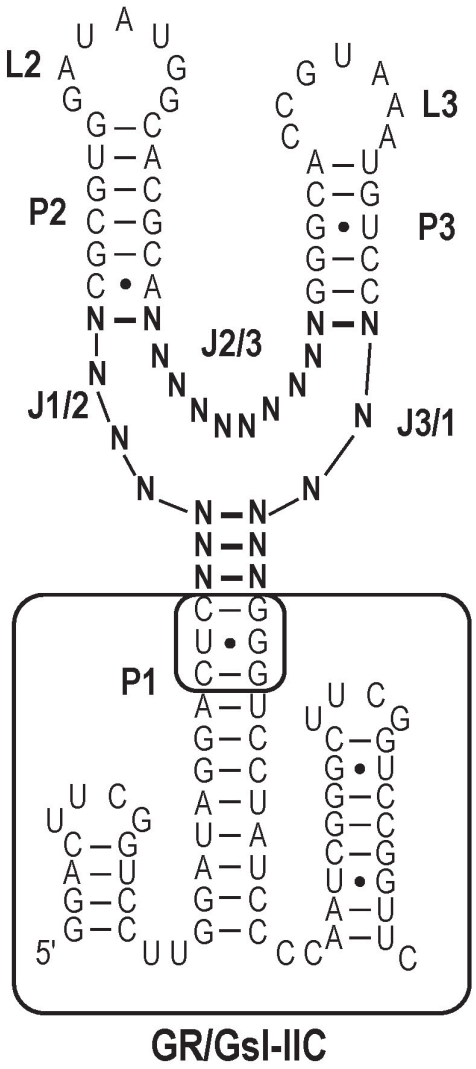
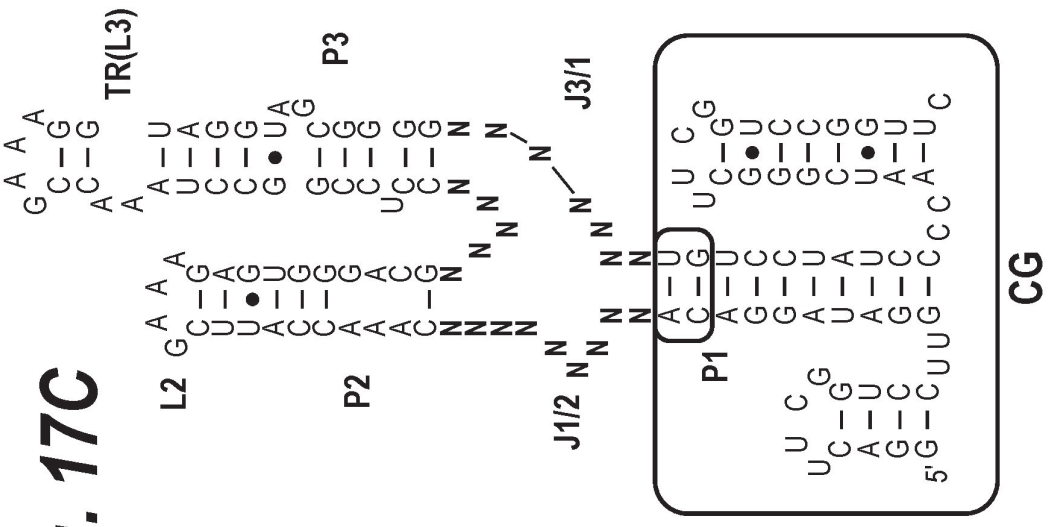
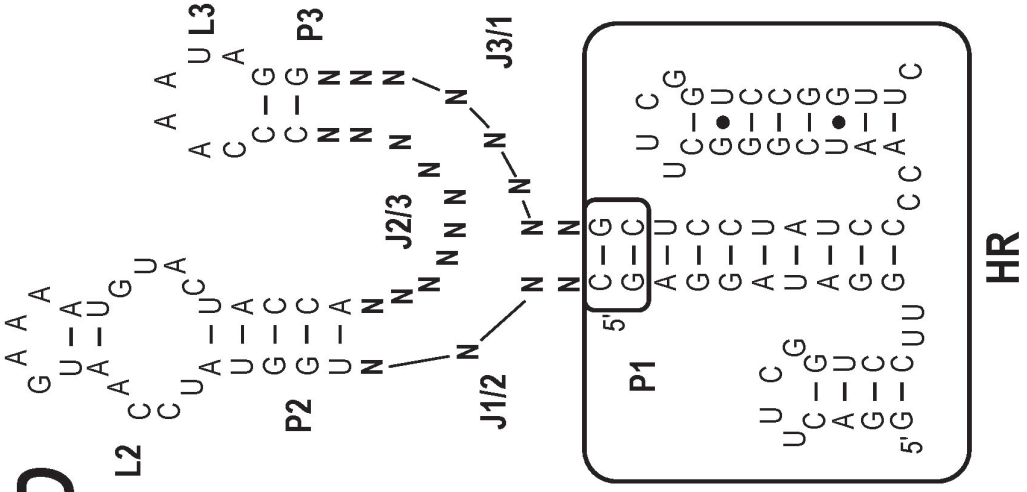


Fig. 17B




Fig. 17C
TR(L3)
L2
P2
P3
J1/2
J3/1
P1
CG


Fig. 17D
L2
L3
P2
P3
J1/2
J2/3
J3/1
P1
HR

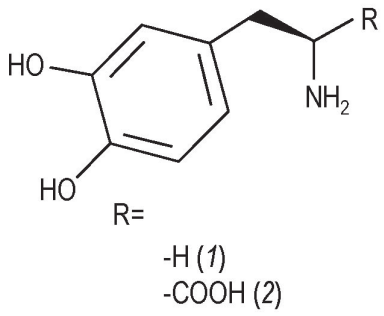


Fig. 18A

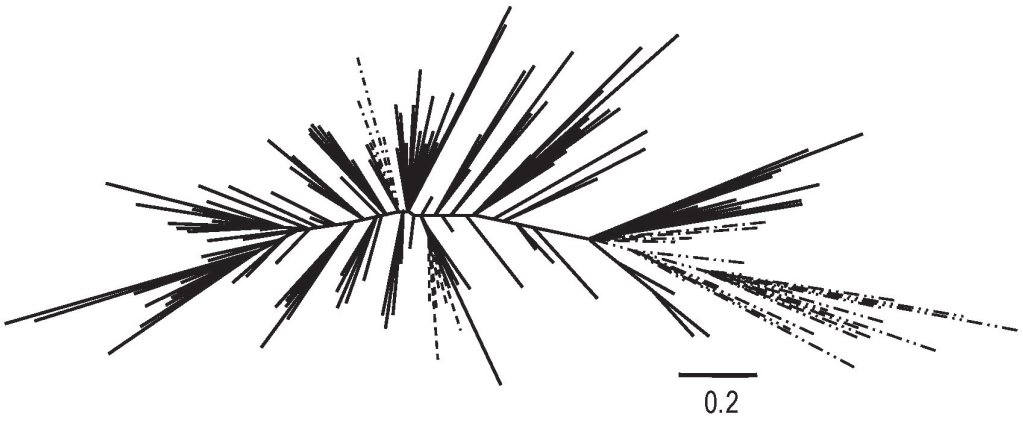
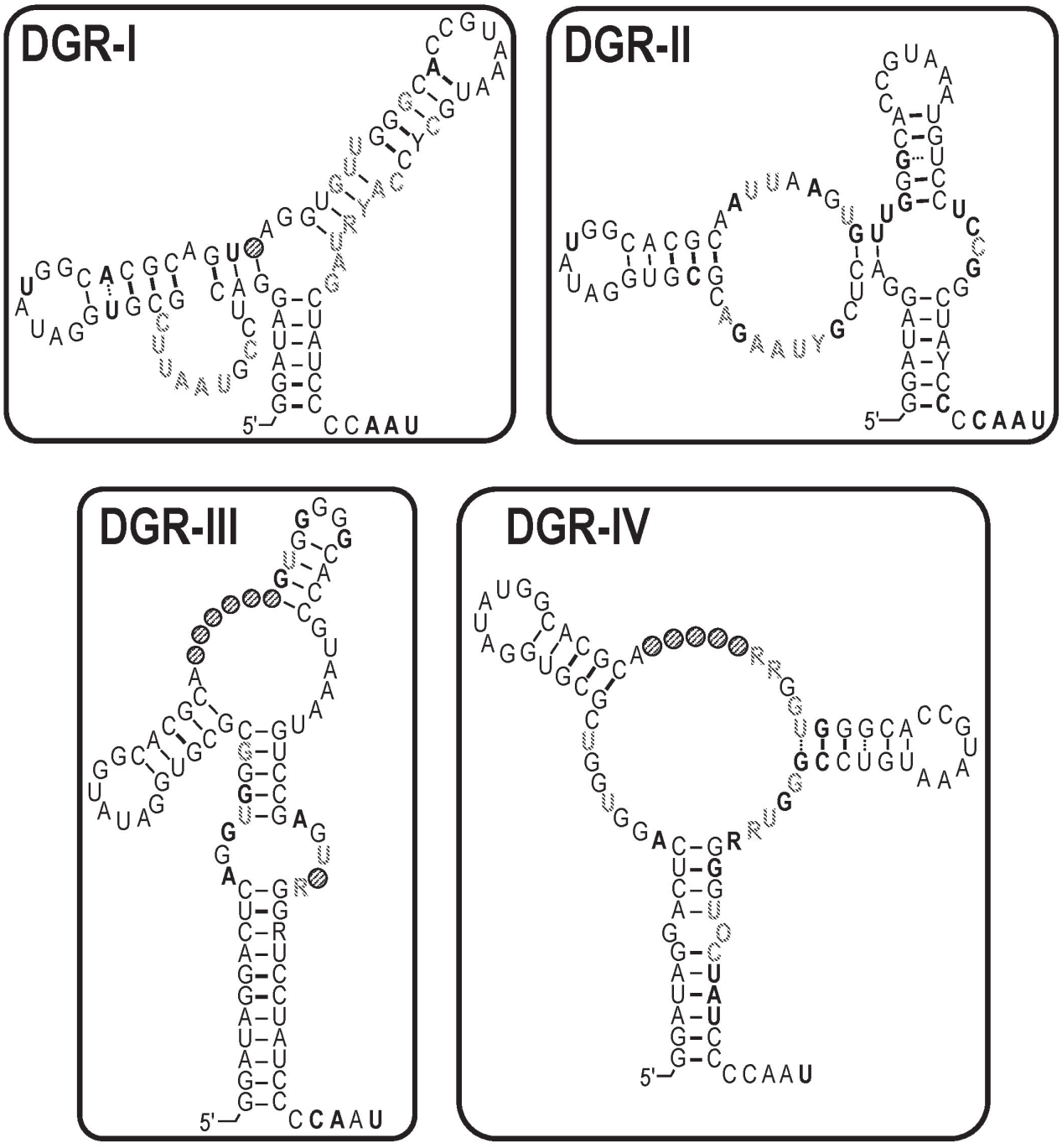


Fig. 18B

Fig. 18C



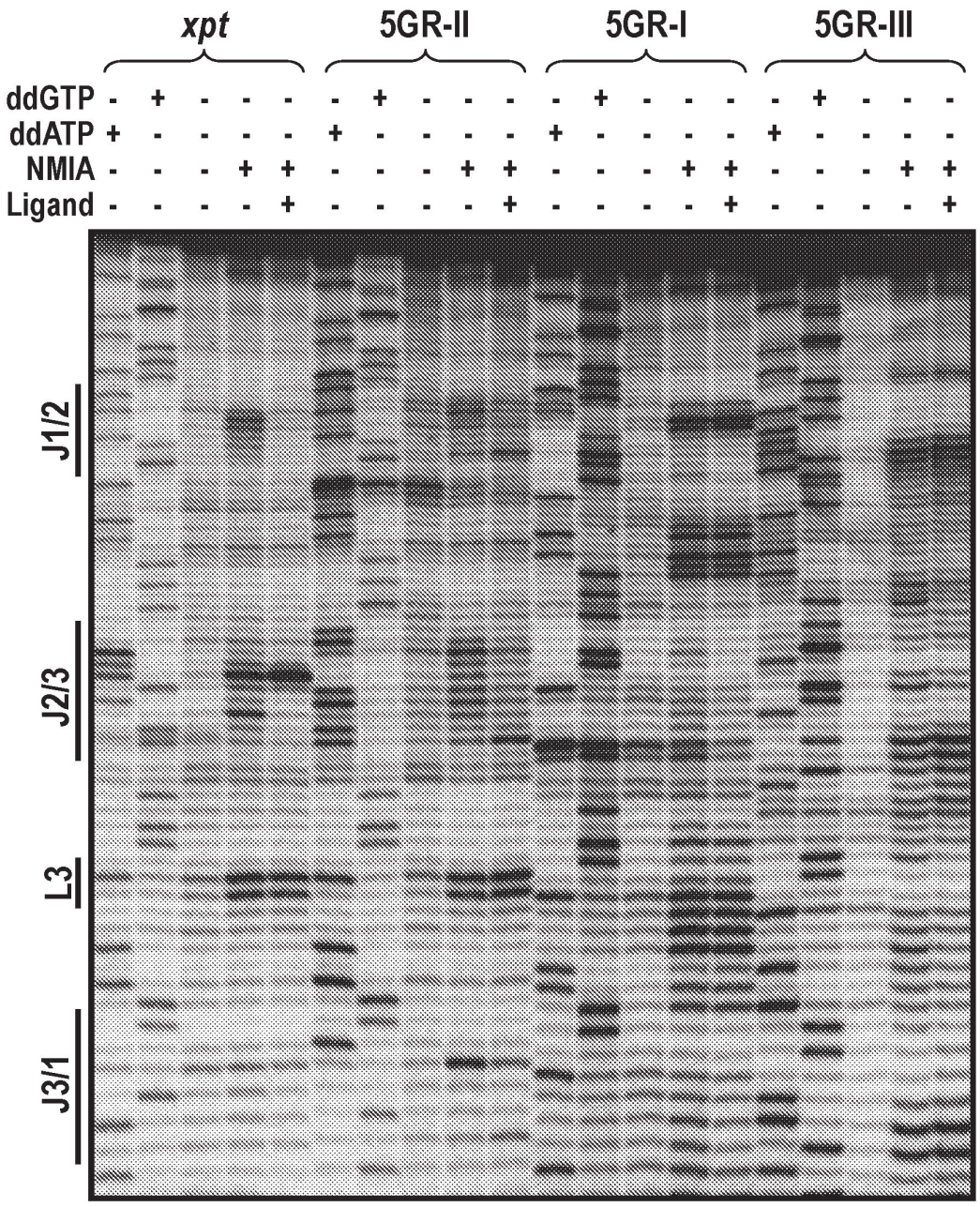


Fig. 19

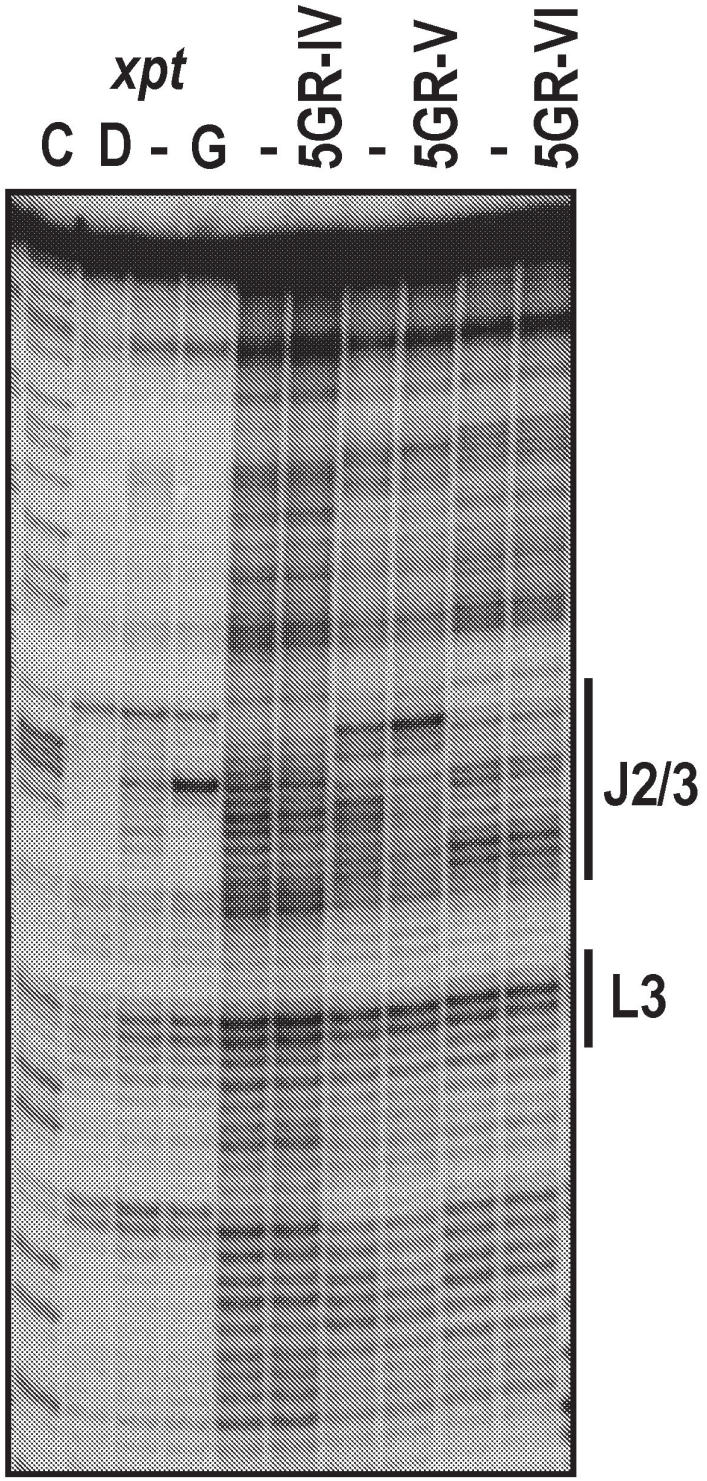


Fig. 20

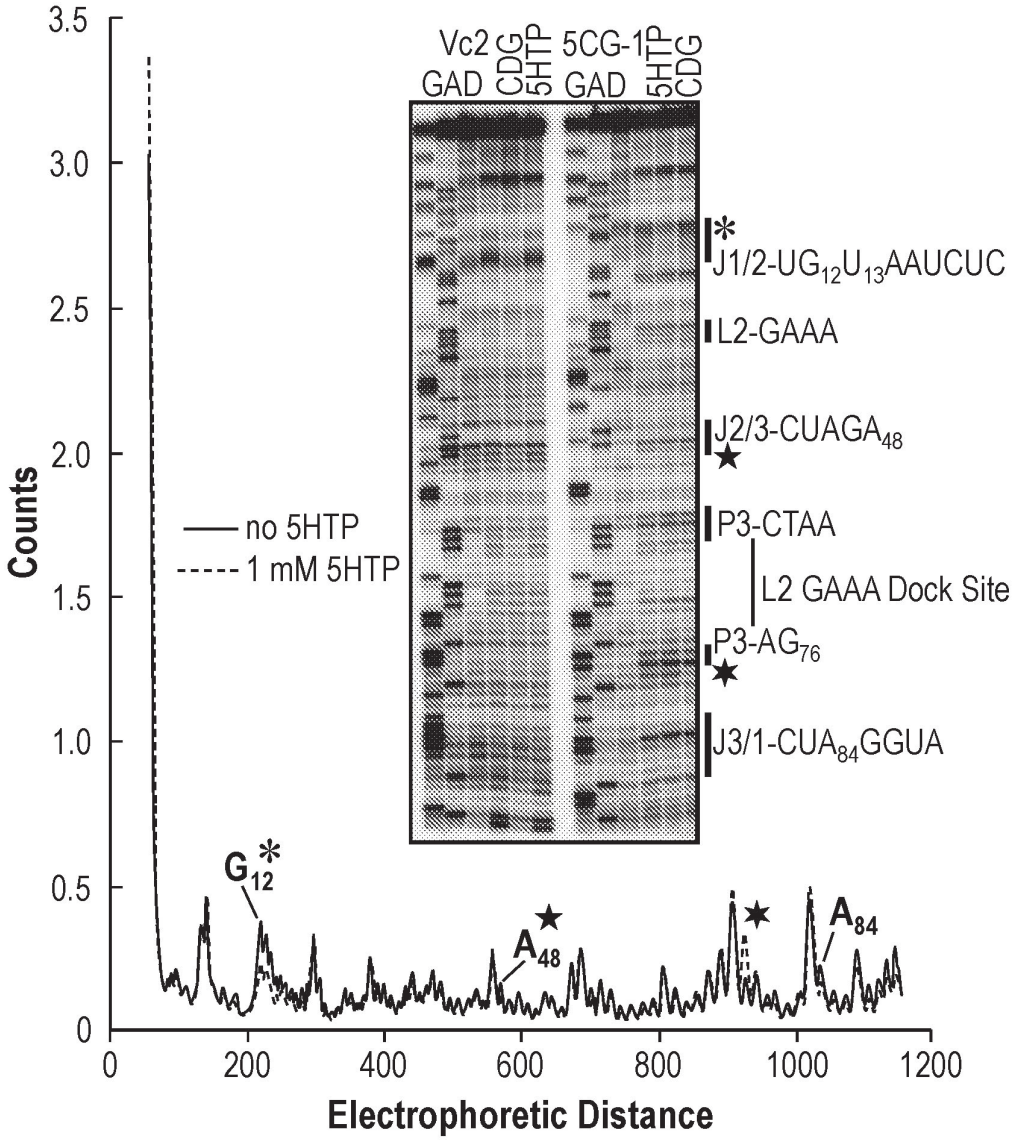

Vc2
GAD
CDG
5HTP
5CG-1P
GAD
5HTP
CDG
J1/2-UG12U13AAUCUC
L2-GAAA
J2/3-CUAGA48
P3-CTAA
L2 GAAA Dock Site
P3-AG76
J3/1-CUA84GGUA
no 5HTP
1 mM 5HTP
Counts
Electrophoretic Distance
G12
A48
A84
0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
0
200
400
600
800
1000
1200

Fig. 21

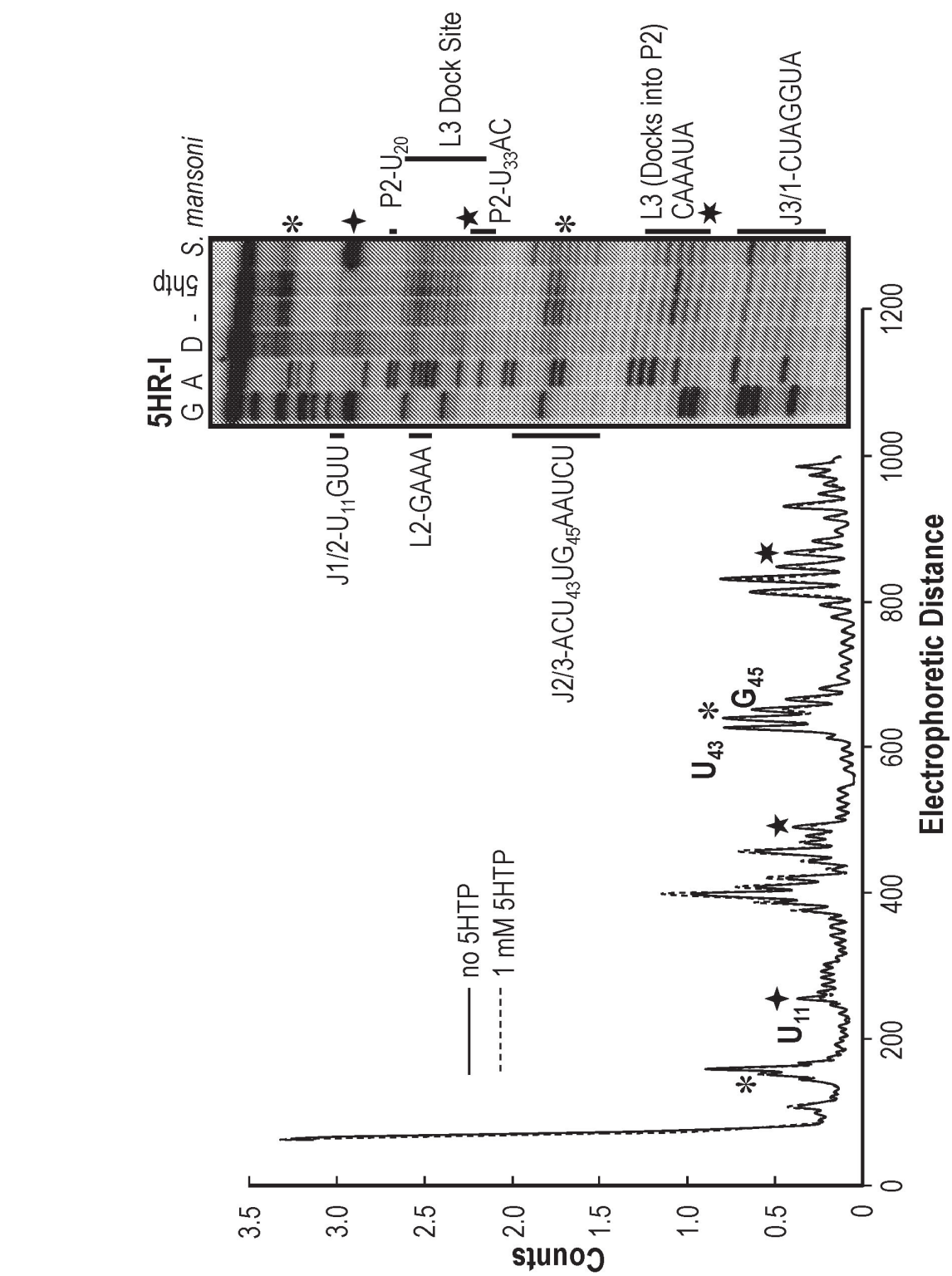

5HR-I
G A D - 5htp S. mansoni
J1/2-U11GUU
L2-GAAA
J2/3-ACU43UG45AAUCU
P2-U20
L3 Dock Site
P2-U33AC
L3 (Docks into P2)
CAAAUA
J3/1-CUAGGUA
no 5HTP
1 mM 5HTP
U11
U43
G45
Counts
Electrophoretic Distance
0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
200
400
600
800
1000
1200

Fig. 22

In vitro selection	
GR/SSIII library template[a]	GCGCGCGAATTCTAATACGACTCACTATAGGACTTC GGTCCAAGCTAATGCACTCNNNNNNNCGCGTGGAT ATGGCACGCANNNNNNNNNNGGGCACCGTAAATGT CCNNNNNNGGGTGCATTAGCAAAATCGGGCTTCGG TCCGGTTC
GR/GsI library template	GCGCGCGAATTCTAATACGACTCACTATAGGACTTC GGTCCTTGGATAGGACTCNNNNNNNCGCGTGGATA TGGCACGCANNNNNNNNNNGGGCACCGTAAATGTC CNNNNNNGGGTCCTATCCCCAATCGGGCTTCGGTC CGGTTC
CDG/GsI library template	GCGCGCGAATTCTAATACGACTCACTATAGGACTTC GGTCCTTGGATAGGACANNNNNNNNNNCAAACCATTC GAAAGAGTGGGACGNNNNNCCTCCGGCCTAAACCG AAAGGTAGGTAGCGGGGNNNNNNNNTGTCCTATCCC CAATCGGGCTTCGGTCCGGTTC
HH/GsI library template	GCGCGCGAATTCTAATACGACTCACTATAGGACTTC GGTCCTTGGATAGGAGCNNNNTGGTATCCAATGAAA ATGTACTACCANNNNNNNNNNCCCAAATAGGNNNNN NNGCTCCTATCCCCAATCGGGCTTCGGTCCGGTTC
T7 site appending primer	GCGCGCGAATTCTAATACGACTCACTATAGGACTTC GGTCCAAGCTAATGCACTC
RT-PCR primer	GAACCGGACCGAAGCCCG
High throughput sequencing	
HTS reverse sequencing primer, GR/SSIII	CAAGCAGAAGACGGCATACGAGATGTCGTGTAGCC TAGTCAGTCAGCCGAACCGGACCGAAGCCCG
HTS reverse sequencing primer, GR/GsI	CAAGCAGAAGACGGCATACGAGATTGGTCAACGATA AGTCAGTCAGCCGAACCGGACCGAAGCCCG
HTS reverse sequencing primer, CDG/GsI	CAAGCAGAAGACGGCATACGAGATATCACCAGGTGT AGTCAGTCAGCCGAACCGGACCGAAGCCCG
HTS reverse sequencing primer, HH/GsI	CAAGCAGAAGACGGCATACGAGATGCTGTACGGATT AGTCAGTCAGCCGAACCGGACCGAAGCCCG
Forward sequencing primer	AATGATACGGCGACCACCGAGATCTACACTATGGTA ATTGTGCGCGCGAATTCTAATACGACTCACTATAG
RT primer	AGTCAGTCAGCCGAACCGGACCGAAGCCCG
Indexing primer	CGGGCTTCGGTCCGGTTCGGCTGACTGACT
Crystallization	
5GR-II	GGACACTCTGATGATCGCGTGGATATGGCACGCATT GAATTGTTGGACACCGTAAATGTCCTAACACGTGTC CA
Isothermal titration calorimetry	
5GR-I aptamer[b]	GGAGCTAATGCACTCTTAACGCCGCGTGGATATGCA CGCAACCGTGAATCGGGCACCGTAAATTCCGTAAGT GGGTGCATTAGC
5GR-II aptamer	GGCACTCTGATGATCGCGTGGATATGGCACGCATT GAATTGTTGGACACCGTAAATGTCCTAACACGGGTG CC
5GR-III aptamer	GGAGCTAATGCACTCCCATTTTCCGTGGATATGGCA CGCTACCGATGTTGGGACCGTAATGTCCATTACGG GTGCATTAGC
5GR-IV aptamer	GGATAGGACTCTCTGGTTCGCGTAGATATGGCACGC AATTGAAGAATGGGCACCGTAAATGTCTGTAGACGG

Fig. 23

	GTCCTATCC
5GR-V aptamer	GGATAGGACTCATTCGGCCGCGTGGATATGGCACG CAGGAGATGTGTGGACACCGTAAATGTCCGTAGGC GGGTCCTATCC
5GR-VI aptamer	GGATAGGACTCAACATCTCGCGTGGATATGGCACG CAGACTTCCAGTGGGCACCGTAAATGTCCGTAGACG GGTCCTATCC
5CG-VII aptamer	GGATAGGACATGTAATCTCCAAACCATTCGAAAGAG TGGGACGCTAGACCTCCGGCCTAAACCGAAAGGTA GGTAGCGGGGCTAGGTATGTCCTATCC
5HR-VIII aptamer	GGATAGGAGCTGTTTGGTATCCAATGAAAATGTACT ACCAACTTGAATCTCCCAAATAGGCTAGGTAGCTCC TATCC
SHAPE chemical probing	
5GR-I, SHAPE	GGACTTCGGTCCAAGCTAATGCACTCTTAACGCCGC GTGGATATGCACGCAACCGTGAATCGGGCACCGTA AATTCCGTAAGTGGGTGCATTAGCAATCGATCCGGT TCGCCGGATCCAAATCGGGCTTCGGTCCGGTTC
5GR-II, SHAPE	GGACTTCGGTCCAAGCTAATGCACTCTGATGATCGC GTGGATATGGCACGCATTGAATTGTTGGACACCGTA AATGTCCTAACACGGGTGCATTAGCAATCGATCCGG TTCGCCGGATCCAAATCGGGCTTCGGTCCGGTTC
5GR-III, SHAPE	GGACTTCGGTCCAAGCTAATGCACTCCCATTTTCCG TGGATATGGCACGCTACCGATGTTGGGACCGTAAT GTCCATTACGGGTGCATTAGCAAAATCGATCCGGTT CGCCGGATCCAAATCGGGCTTCGGTCCGGTTC
5GR-IV, SHAPE	GGACTTCGGTCCTTGGATAGGACTCTCTGGTTCGC GTAGATATGGCACGCAATTGAAGAATGGGCACCGTA AATGTCTGTAGACGGGTCCTATCCAATCGGGCTTCG GTCCGGTTC
5GR-V, SHAPE	GGACTTCGGTCCTTGGATAGGACTCATTCGGCCGC GTGGATATGGCACGCAGGAGATGTGTGGACACCGT AAATGTCCGTAGGCGGGTCCTATCCAATCGGGCTTC GGTCCGGTTC
5GR-VI, SHAPE	GGACTTCGGTCCTTGGATAGGACTCAACATCTCGCG TGGATATGGCACGCAGACTTCCAGTGGGCACCGTA AATGTCCGTAGACGGGTCCTATCCAATCGGGCTTCG GTCCGGTTC
5CG-I, SHAPE	GGACTTCGGTCCTTGGATAGGACATGTAATCTCCAA ACCATTCGAAAGAGTGGGACGCTAGACCTCCGGCC TAAACCGAAAGGTAGGTAGCGGGGCTAGGTATGTC CTATCCAATCGGGCTTCGGTCCGGTTC
5HR-I, SHAPE	GGACTTCGGTCCTTGGATAGGAGCTGTTTGGTATCC AATGAAAATGTACTACCAACTTGAATCTCCCAAATAG GCTAGGTAGCTCCTATCCAATCGGGCTTCGGTCCG GTTC
*Broccoli sensors**	
5GR-II/CM-2	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACCG GTCGCGTCTTAGATGATCGCGTGGATATGGCACGCAT TGAATTGTTGGACACCGTAAATGTCCTAACATTCCA GTAGAGTGTGGCGTCCGCGGGTCCAGGGTTCAAGT CCCTGTTCGGGCGCCA
5GR-II/CM-3	GCCCGGATAGCTCAGTCGGTAGCGCAGCGGAGACCG GTCGCGTCTTAGATGATCGCGTGGATATGGCACGCA TTGAATTGTTGGACACCGTAAATGTCCTAACATTCC

Fig. 23

(Continued)

	GAGTAGAGTGTGGGCTCCGCGGGTCCAGGGTTCAA GTCCCTGTTCGGGCGCCA
5GR-II/CM-4	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATAGCTGATCGCGTGGATATGGCACGC ATTGAATTGTTGGACACCGTAAATGTCCTAACA ATA TCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGGTTC AAGTCCCTGTTCGGGCGCCA
5GR-II/CM-5	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATATGATGATCGCGTGGATATGGCACG CATTGAATTGTTGGACACCGTAAATGTCCTAACA TA TATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGGTT CAAGTCCCTGTTCGGGCGCCA
5GR-IV/CM-2	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATCTGGTTCGCGTAGATATGGCACGCA ATTGAAGAATGGGCACCGTAAATGTCTGTAGAC ATC GAGTAGAGTGTGGGCTCCGCGGGTCCAGGGTTCAA GTCCCTGTTCGGGCGCCA
5GR-IV/CM-3	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATCTGGTTCGCGTAGATATGGCACGC AATTGAAGAATGGGCACCGTAAATGTCTGTAGAC ATA TCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGGTTC AAGTCCCTGTTCGGGCGCCA
5GR-IV/CM-4	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATATCTGGTTCGCGTAGATATGGCACG CAATTGAAGAATGGGCACCGTAAATGTCTGTAGAC A TATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGGT TCAAGTCCCTGTTCGGGCGCCA
5GR-IV/CM-5	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATATCTGGTTCGCGTAGATATGGCAC GCAATTGAAGAATGGGCACCGTAAATGTCTGTAGAC ATATATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGG GTTCAAGTCCCTGTTCGGGCGCCA
5GR-V/CM-2	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTAATTCGGCCGCGTGGATATGGCACGCA GGAGATGTGTGGACACCGTAAATGTCCGTAGGC TA CGAGTAGAGTGTGGGCTCCGCGGGTCCAGGGTTCA AGTCCCTGTTCGGGCGCCA
5GR-V/CM-3	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATATTCGGCCGCGTGGATATGGCACGC AGGAGATGTGTGGACACCGTAAATGTCCGTAGGC T ATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGGTT CAAGTCCCTGTTCGGGCGCCA
5GR-V/CM-4	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATAATTCGGCCGCGTGGATATGGCACG CAGGAGATGTGTGGACACCGTAAATGTCCGTAGGC T ATATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGG TTCAAGTCCCTGTTCGGGCGCCA
5GR-V/CM-5	GCCCGGATAGCTCAGTCCGTAGAGCAGCGGAGACG GTCGGGTCTATATATTCGGCCGCGTGGATATGGCAC GCAGGAGATGTGTGGACACCGTAAATGTCCGTAGGC ATATATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGG GTTCAAGTCCCTGTTCGGGCGCCA
5GR-VI/CM-2	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTAAACATCTCGCGTGGATATGGCACGCA GACTTCCAGTGGGCACCGTAAATGTCCGTAGAC TA

Fig. 23

(Continued)

	CGAGTAGACTGTGGGCTCCGCGGGTCCAGGGTTCA AGTCCCTGTTCGGGCGCCA
DGR-VI/CM-3	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTATAACATCTCGCGTGGATATGGCACGC AGACTTCCAGTGGGCACCGTAAATGTCCGTAGAC ATCGAGTAGACTGTGGGCTCCGCGGGTCCAGGGTT CAAGTCCCTGTTCGGGCGCCA
DGR-VI/CM-4	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTATAACATCTCGCGTGGATATGGCACG CAGACTTCCAGTGGGCACCGTAAATGTCCGTAGAC ATATCGAGTAGACTGTGGGCTCCGCGGGTCCAGGG TTCAAGTCCCTGTTCGGGCGCCA
DGR-VI/CM-5	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTATAACATCTCGCGTGGATATGGCAC GCAGACTTCCAGTGGGCACCGTAAATGTCCGTAGAC ATATCGAGTAGACTGTGGGCTCCGCGGGTCCAGG GTTCAAGTCCCTGTTCGGGCGCCA
DGR-I/CM-2	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTAGACTCCGTAATTCGCGTGGATATGGC ACGCAGTCAGGTGTTGGGCACCGTAAATGTCCCACA TAGATCGAGTAGACTGTGGGCTCCGCGGGTCCAG GGTTCAAGTCCCTGTTCGGGCGCCA
DGR-I/CM-3	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTATGACTCCGTAATTCGCGTGGATATGG CACGCAGTCAGGTGTTGGGCACCGTAAATGTCCCAC ATAGATCGAGTAGACTGTGGGCTCCGCGGGTCCA GGGTTCAAGTCCCTGTTCGGGCGCCA
DGR-I/CM-4	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTATAGACTCCGTAATTCGCGTGGATATG GCACGCAGTCAGGTGTTGGGCACCGTAAATGTCCCA CATAGATATCGAGTAGACTGTGGGCTCCGCGGGTC CAGGGTTCAAGTCCCTGTTCGGGCGCCA
DGR-I/CM-5	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTATATGACTCCGTAATTCGCGTGGATAT GGCACGCAGTCAGGTGTTGGGCACCGTAAATGTCCC ACATAGATATCGAGTAGACTGTGGGCTCCGCGGGG TCCAGGGTTCAAGTCCCTGTTCGGGCGCCA
DGR-II/CM-2	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTAGACTCCGTAATTCGCGTGGATATGGC ACGCAGTAAGGTATTGGGCACCGTAAATGTCCATAT GTATCGAGTAGACTGTGGGCTCCGCGGGTCCAGG GTTCAAGTCCCTGTTCGGGCGCCA
DGR-II/CM-3	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTAGACTCCGTAATTCGCGTGGATATGG CACGCAGTAAGGTATTGGGCACCGTAAATGTCCATA TGTATCGAGTAGACTGTGGGCTCCGCGGGTCCAG GGTTCAAGTCCCTGTTCGGGCGCCA
DGR-II/CM-4	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTATAGACTCCGTAATTCGCGTGGATATG GCACGCAGTAAGGTATTGGGCACCGTAAATGTCCAT ATGTATATCGAGTAGACTGTGGGCTCCGCGGGTCC AGGGTTCAAGTCCCTGTTCGGGCGCCA
DGR-II/CM-5	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGACACG GTCGGGTCTATATGACTCCGTAATTCGCGTGGATAT GGCACGCAGTAAGGTATTGGGCACCGTAAATGTCCA

Fig. 23

(Continued)

	TATGTATATCGAGTAGAGTGTGGGCTCCGCGGGT CCAGGGTTCAAGTCCCTGTTCGGGCGCCA
DGR-III/CM-2	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTAAGGTGGGCGCGTGGATATGGCACGC ATGTTTGGTGGGGGCACCGTAAATGTCCGAGTTA TCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGGTTC AAGTCCCTGTTCGGGCGCCA
DGR-III/CM-3	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGCTCTATAGGTGGGCGCGTGGATATGGCACG CATGTTTGGTGGGGGCACCGTAAATGTCCGAGTTA TATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGGT TCAAGTCCCTGTTCGGGCGCCA
DGR-III/CM-4	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATAAGGTGGGCGCGTGGATATGGCAC GCATGTTTGGTGGGGGCACCGTAAATGTCCGAGTTA TATATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGG GTTCAAGTCCCTGTTCGGGCGCCA
DGR-III/CM-5	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATATAGGTGGGCGCGTGGATATGGCAC GCATGTTTGGTGGGGGCACCGTAAATGTCCGAGTTA ATATATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGG GTTCAAGTCCCTGTTCGGGCGCCA
DGR-IV/CM-2	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTAAGGTGGTCGCGTGGATATGGCACGC ATAATAGAGGTGGGCACCGTAAATGTCCGGGTAA TCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGGTTC AAGTCCCTGTTCGGGCGCCA
DGR-IV/CM-3	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATAGGTGGTCGCGTGGATATGGCACG CATAATAGAGGTGGGCACCGTAAATGTCCGGGTAA TATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGGT TCAAGTCCCTGTTCGGGCGCCA
DGR-IV/CM-4	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATATAGGTGGTCGCGTGGATATGGCACG CATAATAGAGGTGGGCACCGTAAATGTCCGGGTAA ATATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGGG TTCAAGTCCCTGTTCGGGCGCCA
DGR-IV/CM-5	GCCCGGATAGCTCAGTCGGTAGAGCAGCGGAGACG GTCGGGTCTATATAGGTGGTCGCGTGGATATGGCAC GCATAATAGAGGTGGGCACCGTAAATGTCCGGGTAA ATATATCGAGTAGAGTGTGGGCTCCGCGGGTCCAGG GTTCAAGTCCCTGTTCGGGCGCCA

Fig. 23

(Continued)