Supplementary Information

Splice Modulation Synergizes Cell Cycle Inhibition

Kelsey A. Trieger, [†] James J. La Clair, [†] and Michael D. Burkart^{†,*}

[†] Department of Chemistry and Biochemistry, University of California, San Diego, La Jolla, CA 92093-0358, United States

*Correspondence: Michael D. Burkart, Phone: 858-534-5673, e-mail: mburkart@ucsd.edu

Table of Contents

S 1
S2
S3
S4
S5
S6



Supplementary Figure S1. Expanded set of splicing modulators including natural products FD-895 (1a), pladienolide B (1b), herboxidiene (1c), and FR901464 (1d). Structures of clinically-evaluated analogs E7107 (1e) and H3B-8800 (1f) along with clinical-candidate 17S-FD-895 (1g).



Supplementary Figure S2. Roles of polo-like kinase 1 (PLK-1) and aurora kinases (AURK) in the mitotic cycle. Both kinases play an interactive role in regulating each stage of passage through mitosis with effects arising from inhibition or reduced expression of PLK-1 (in red) and aurora kinases (in green).



Supplementary Figure S3. AURKA gene regulation by FD-895. Increasing concentrations of FD-895 led to a decrease in the inclusion of exons 3-7 in AURKA RNA.



Supplementary Figure S4. Splice modulator selectivity. FD-895 (1a) and pladienolide B (1b) reduced AURKA and PLK-1 protein expression in a concentration-dependent manner. 17S-FD-895 (1g) reduced AURKA expression and modestly increased PLK-1 expression. Experiments were conducted in biological triplicate. Statistics were calculated using a standard one-way ANVOA; p-values were represented so that * signifies p<0.05, ** signifies p<0.01, *** signifies p<0.001, and **** signifies p<0.001.



Supplementary Figure S5. Full scale scans of representative western blots used in this manuscript. **a)** Representative western blot used in Figure 3d. **b)** Representative western blot used in Figure 3e. **c)** Representative western blot used in Figure 4c. **d)** Representative western blot used in Figure 4d.

Supplementary Table 1. Sequences of the qPCR primers used in this study.

qPCR primers				
Primer	Location	5' Sequence 3'		
GAPDH-FP	Exon 3	TGGTCACCAGGGCTGCTT		
GAPDH-RP	Exon 4	AGCTTCCCGTTCTCAGCCTT		
AURKA-FP	Intron 2	CCACCTTCGGCATCCTAAT		
AURKA-RP	Intron 2	TCCAAGTGGTGCATATTCC		
AURKB-FP	Intron 2	GGAGAGCTTAAAATTGCAG		
AURKB-RP	Intron 2	TGCAGCTCTTCTGCAGCTC		
PLK1-FP		CTCAACACGCCTCATCCTC		
PLK1-RP		GTGCTCGCTCATGTAATTG		
FP: forward primer; RP reverse primer				

Compounds	Cell Line	GI ₅₀ value (nM)	Standard error (nM)	Confidence interval
1a	HCT116	0.5-1.7	0.1-0.4	0.4-2.6
1a	Caov3	1.6-2.0	0.46-0.59	0.94-3.46
1a	HeLa	3.7-4.5	0.92-1.26	2.16-8.24
2a	HCT116	430.0	440.7	3453.0 - 5231.0
2a + 1 nM 1a	HCT116	517.0	281.0	136.9 - 1886.0
2a + 5 nM 1a	HCT116	0.05	0.05	0.01 - 0.18
2a	Caov3	5500	621	4303 - 6938
2a + 1 nM 1a	Caov3	2800	450	1906 - 3979
2a + 5 nM 1a	Caov3	0.08	0.06	0.01 - 0.22
2a	HeLa	10100	3371	5527 - 20150
2a + 1 nM 1a	HeLa	4000	1084	2368 - 6667
2a + 5 nM 1a	HeLa	0.20	0.10	0.01 - 0.42
2b	HCT116	2100	186	1737 - 2492
2b + 1 nM 1a	HCT116	250.0	35.7	180.3 - 351.6
2b + 5 nM 1a	HCT116	0.05	0.04	0.01 - 0.13
2b	Caov3	6000	402	5233 - 6942
2b + 1 nM 1a	Caov3	900	230	468 - 1765
2b + 5 nM 1a	Caov3	0.07	0.06	0.01 - 0.19
2b	HeLa	19500	4112	13180 - 31166
2b + 1 nM 1a	HeLa	16300	4178	10281 - 28836
2b + 5 nM 1a	HeLa	0.30	0.16	0.01 - 0.74
3a	HCT116	160.0	52.9	67. 0 - 444.6
3a + 1 nM 1a	HCT116	0.90	0.33	0.33 - 2.28
3a + 5 nM 1a	HCT116	0.004	0.002	0.001 - 0.008
3a	Caov3	25.9	9.6	6.2 - 79.8
3a + 1 nM 1a	Caov3	12.8	5.4	1.7 - 48.8
3a + 5 nM 1a	Caov3	0.20	0.05	0.07 - 0.30
3a	HeLa	13200	2662	8927 - 20456
3a + 1 nM 1a	HeLa	10700	2369	7036 - 17217

Supplementary Table 2. Confidence intervals of GI₅₀ values for cytotoxicity studies.*

* Data from these studies was obtained from and reported in Figure 2

Supplementary Table 3. Combination Index values for cytotoxicity studies.*

Figure	[1a] (nM)	[2a] (nM)	[2b] (nM)	[2b] (nM)	CI value
	1.0	1.0			2.35
2a	1.0	10.0			12.4
	1.0	50.0			28.4
	1.0	100.0			24.5
	1.0	500.0			12.2
	1.0	1,000.0			4.34
	1.0	5,000.0			0.190
	1.0	10,000.0			0.166
	5.0	1.0			0.0605
	5.0	10.0			0.0741
	5.0	50.0			0.0525
20	5.0	100.0			0.0403
Za	5.0	500.0			0.0530
	5.0	1,000.0			0.0681
	5.0	5,000.0			0.627
	5.0	10,000.0			0.833
	1.0	1.0			12,700,000
	1.0	10.0			76,600,000
	1.0	50.0			404,000
21	1.0	100.0			1,600
20	1.0	500.0			1,790,000
	1.0	1,000.0			3,300
	1.0	5,000.0			10.7
	1.0	10,000.0			0.0962
	5.0	1.0			0.000218
	5.0	10.0			0.000329
	5.0	50.0			0.000348
26	5.0	100.0			0.000372
20	5.0	500.0			0.000567
	5.0	1,000.0			0.000810
	5.0	5,000.0			0.00275
	5.0	10,000.0			0.00519
	1.0	1.0			498,000,000
	1.0	10.0			30,400
2c	1.0	50.0			1,790,000
	1.0	100.0			1,790,000
	1.0	500.0			1,790,000
	1.0	1,000.0			76,600,000
	1.0	5,000.0			78.6
	1.0	10,000.0			0.0000407
	5.0	1.0			0.00811
20	5.0	10.0			0.00642
20	5.0	50.0			0.00642
	5.0	100.0			0.0156

	5.0 500.0		0.0157
	5.0 1,000.0		0.00234
	5.0 5,000.0		0.0000237
	5.0 10,000.0		0.0000108
	1.0	1.0	4,580
	1.0	10.0	6.75
	1.0	50.0	2.56
2.1	1.0	100.0	2.30
20	1.0	500.0	0.519
	1.0	1,000.0	0.268
	1.0	5,000.0	0.260
	1.0	10,000.0	0.0409
	5.0	1.0	0.0761
	5.0	10.0	0.0823
	5.0	50.0	0.0686
24	5.0	100.0	0.0787
20	5.0	500.0	0.0769
	5.0	1,000.0	0.0890
	5.0	5,000.0	0.181
	5.0	10,000.0	0.450
	1.0	1.0	587,000
	1.0	10.0	426,000
	1.0	50.0	154,000
2e	1.0	100.0	54,800
20	1.0	500.0	2,090
	1.0	1,000.0	223
	1.0	5,000.0	8.74
	1.0	10,000.0	4.04
	5.0	1.0	0.00242
	5.0	10.0	0.01263
	5.0	50.0	0.00593
2e	5.0	100.0	0.00882
	5.0	500.0	0.0251
	5.0	1,000.0	0.0187
	5.0	5,000.0	0.0123
	5.0	10,000.0	0.0120
	1.0	1.0	307,000,000,000.
2f	1.0	10.0	307,000,000,000.
	1.0	50.0	307,000,000,000.
	1.0	100.0	307,000,000,000.
	1.0	1 000 0	1,108,000,000
	1.0	1,000.0	
	1.0	3,000.0	1,108,000,000.
	1.0	10,000.0	8.53
26	5.0	1.0	0.0244
21	5.0	10.0	0.0344
	5.0	50.0	0.437

	5.0	100.0		0.135
	5.0	500.0		0.0156
	5.0	1,000.0		0.0156
	5.0	5,000.0		0.000324
	5.0	10,000.0		0.0000536
	1.0		1.0	4.03
	1.0		10.0	1.57
	1.0		50.0	1.49
2	1.0		100.0	1.66
2g	1.0		500.0	0.807
	1.0		1,000.0	0.501
	1.0		5,000.0	0.00378
	1.0		10,000.0	0.000414
	5.0		1.0	0.0254
	5.0		10.0	0.00704
	5.0		50.0	0.00415
2.	5.0		100.0	0.00712
2g	5.0		500.0	0.0185
	5.0		1,000.0	0.00472
	5.0		5,000.0	0.0170
	5.0		10,000.0	0.0000336
	1.0		1.0	35,700,000
	1.0		10.0	240,000,000
	1.0		50.0	922,000
21	1.0		100.0	4,470,000
211	1.0		500.0	2,610
	1.0		1,000.0	4,330
	1.0		5,000.0	10.4
	1.0		10,000.0	0.0938
	5.0		1.0	0.000188
	5.0		10.0	0.000412
	5.0		50.0	0.000309
2h	5.0		100.0	0.000295
211	5.0		500.0	0.000447
	5.0		1,000.0	0.000879
	5.0		5,000.0	0.00385
	5.0		10,000.0	0.00455
	1.0		1.0	307,000,000,000
	1.0		10.0	6,140,000
	1.0		50.0	76,600,000
2i	1.0		100.0	76,600,000
21	1.0		500.0	1,790,000
	1.0		1,000.0	307,000,000,000
	1.0		5,000.0	144,000
	1.0		10,000.0	1.59
2i	5.0		1.0	0.0156
<u>1</u>	5.0		10.0	0.0234

5.0		50.0	0.135
5.0		100.0	0.0496
5.0		500.0	0.00811
5.0		1,000.0	0.00811
5.0		5,000.0	0.000142
5.0		10,000.0	0.0000167

*Data from these studies was obtained from and reported in Figure 2