

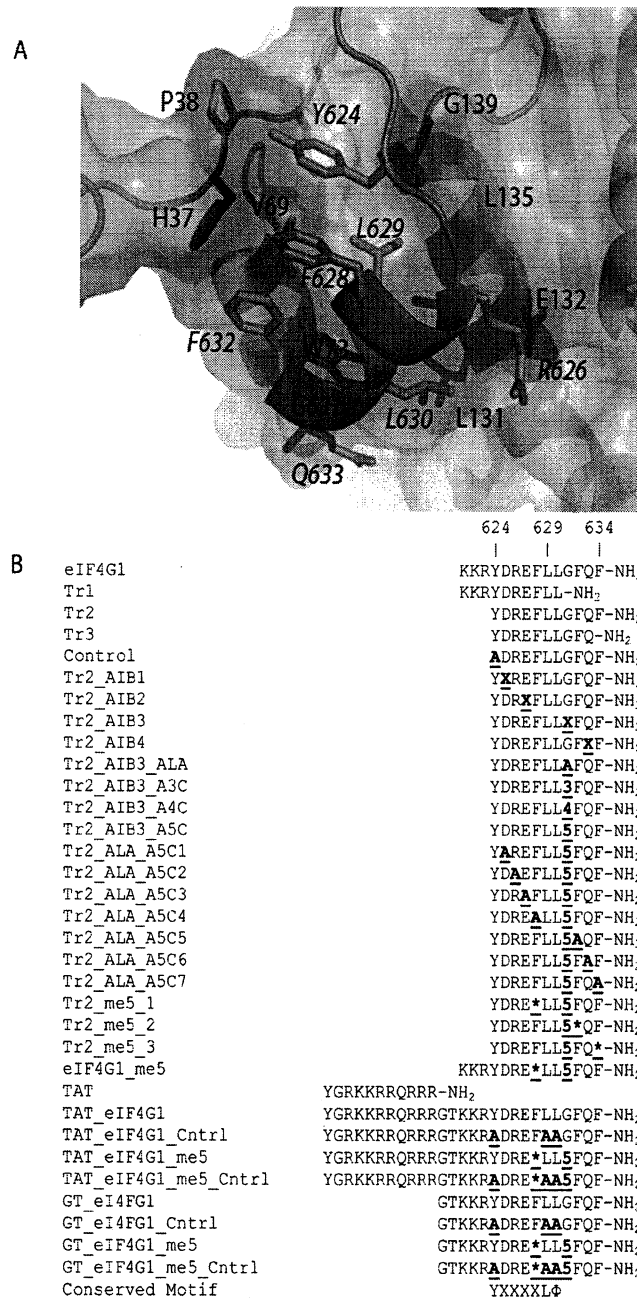


Figure 1

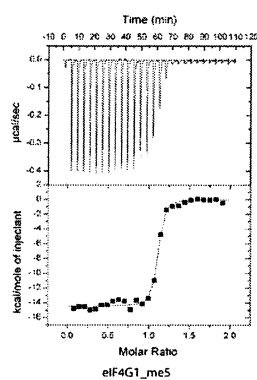
Minimal Motif	ΔT (°C)	Estimated K_d (nM)
eIF4G1	8.7	470
Tr1	1.7*	50160
Tr2	4.2	5960
Tr3	2.25*	35210
Control	0.65*	n/a
AIB scan for sites of helix stabilization		
Tr2_AIB1	1.32	29840
Tr2_AIB2	-	n/a
Tr2_AIB3	5.42	3050
Tr2_AIB4	1.52	25080
Replacement of Glycine by ALA and amino-cycloalkane-1-carboxylic acid derivatives		
Tr2_AIB3_ALA	5.60	2550
Tr2_AIB3_A3C	5.67	2500
Tr2_AIB3_A4C	5.80	2350
Tr2_AIB3_A5C	6.60	1450
Alanine scan of A5C substituted eIF4G1 peptide.		
Tr2_Ala_A5C1	5.02	760
Tr2_Ala_A5C2	2.69	14300
Tr2_Ala_A5C3	4.22	1220
Tr2_Ala_A5C4	3.72	8090
Tr2_Ala_A5C5	3.65	8400
Tr2_Ala_A5C6	6.72	1370
Tr2_Ala_A5C7	5.48	2900
CA methylation of Phe residue 628 dramatically increases the Affinity of Derivative Peptide		
Tr2_me5_1	8.8	360
Tr2_me5_2	NA	n/a
Tr2_me5_3	5.8	2400
Re-addition of the N-terminal to Residues 624-634 generates a High Affinity eIF4G1 peptide derivative		
eIF4G1_me5	14.6	7

Figure 2

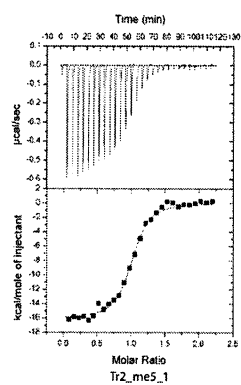
A

Peptides	K_d (nM)	ΔH (kCal mol ⁻¹ K ⁻¹)	$-T\Delta S$ (kCal mol ⁻¹ K ⁻¹)
Tr2	1014.20±65.83	-10.95±0.13	-2.91
Tr2_me5_1	145.99±22.81	-16.07±0.2	-6.89
eIF4G1	147.93±22.81	-9.7±0.05	-0.58
eIF4G1_me5	9.43±2.57	-14.45±0.11	-3.69

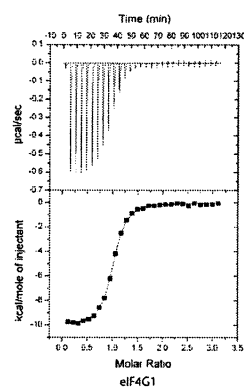
B



C



D



E

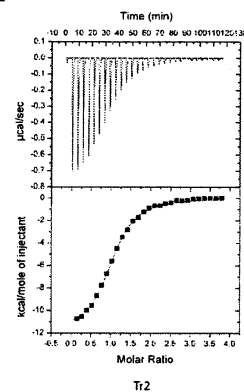


Figure 3

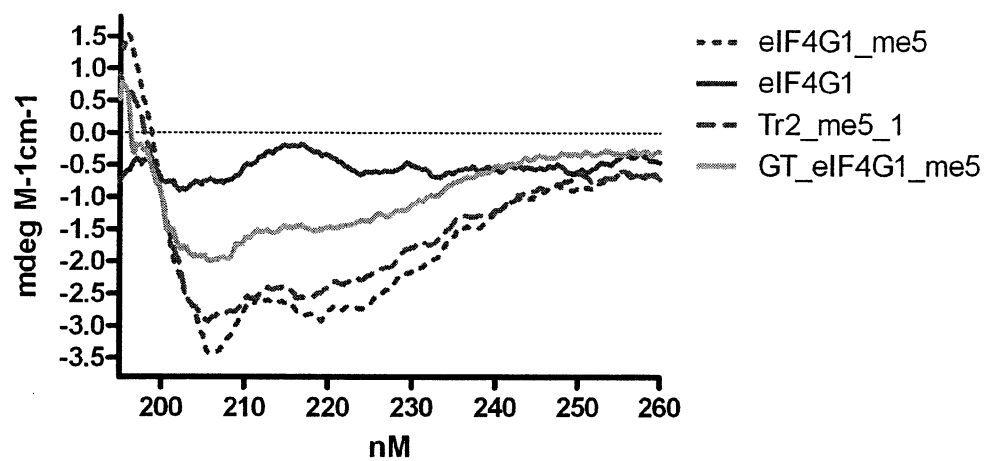


Figure 4A

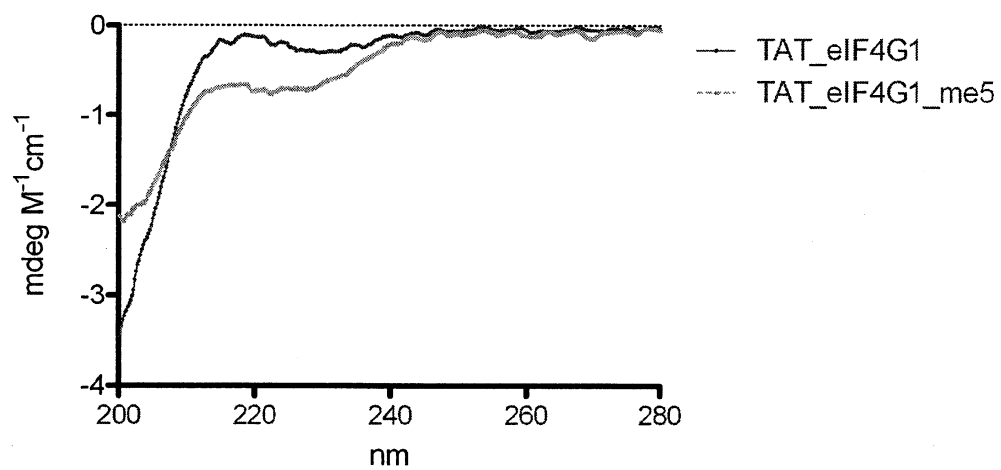


Figure 4B

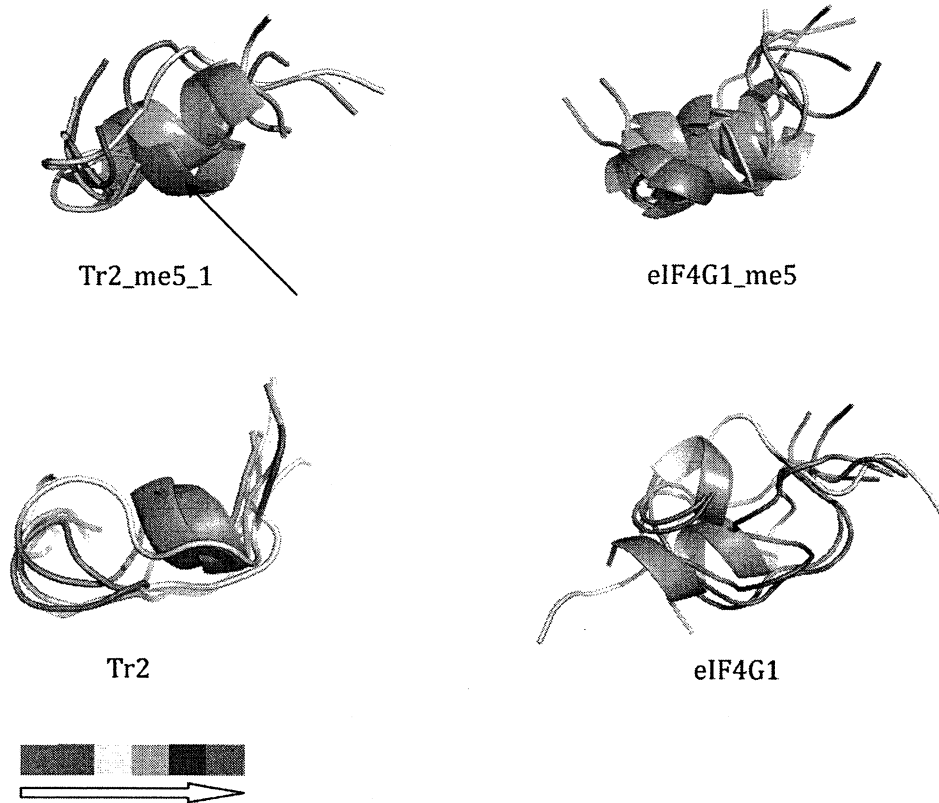


Figure 5

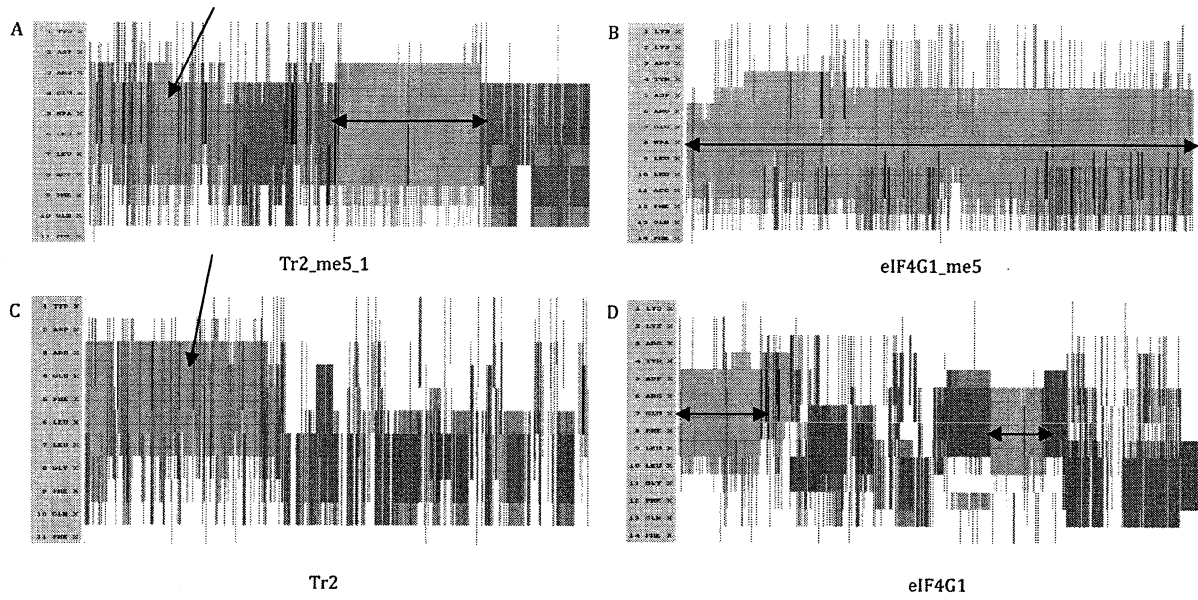
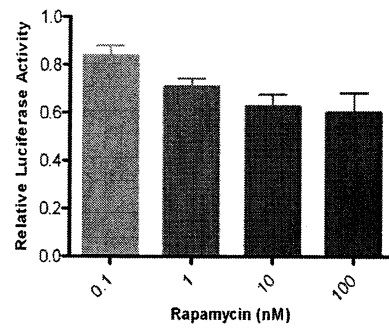
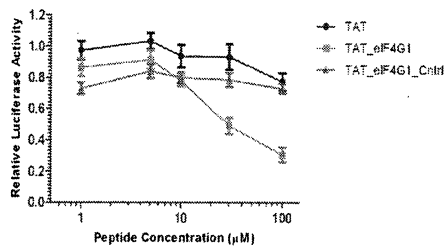


Figure 6

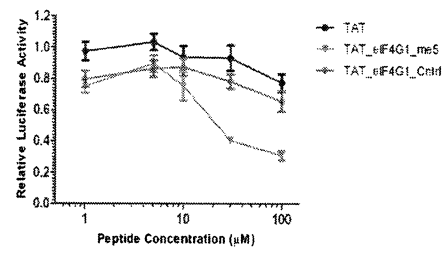
A



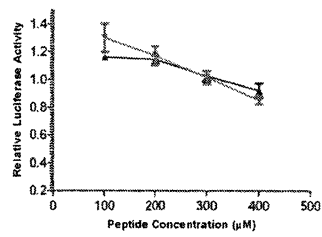
B



C



D



E

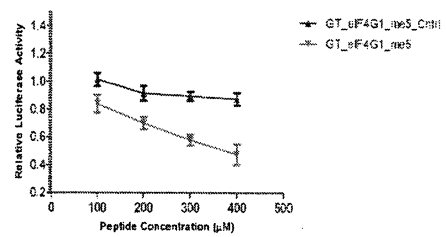


Figure 7

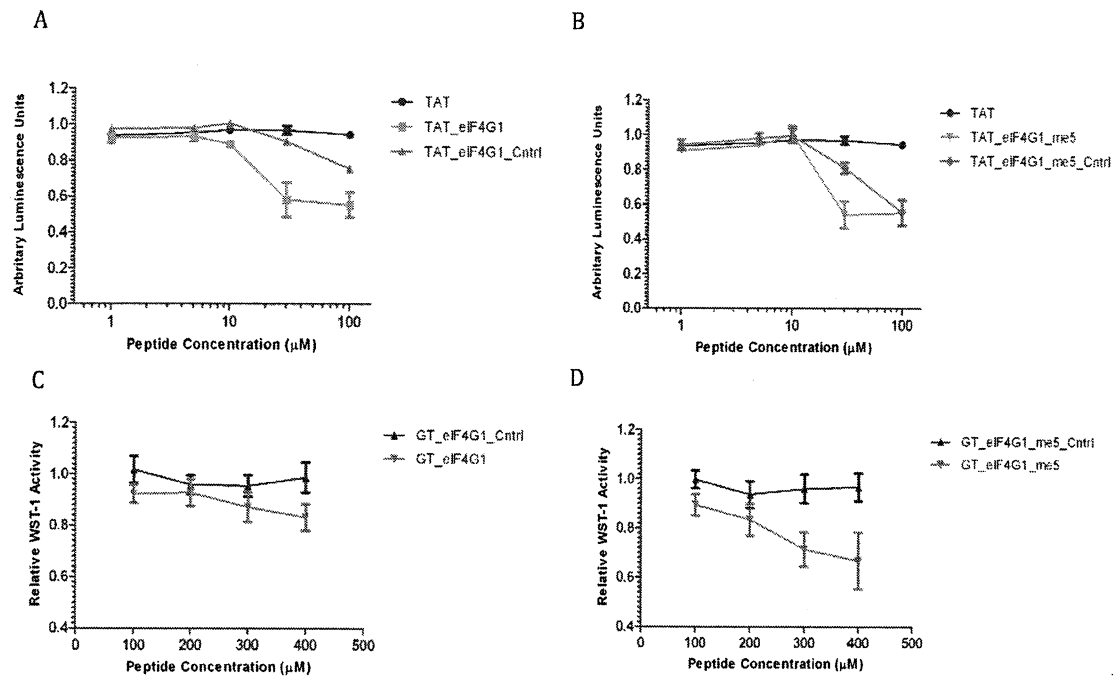


Figure 8

	DMSO 0.1%	GT_eIF4G1_me5 (400μM)	GT_eIF4G1_me5_Cntrl (400μM)
G1 (%)	50.5 ±2.6	47.5±0.9 (p=0.5493)	46.1±2.6 (p=0.3156)
S (%)	8.2± 0.9	2.2±0.1 (p=0.0065)	9.0±0.8 (p=0.4466)
G2 (%)	19.8±0.4	16.9±1.1 (p=0.0606)	27.2±3.6 (p=0.1034)
Sub G1 (%)	15.6±5.2	25.9±2.0 (p=0.0261)	11.1±2.8 (p=0.3967)

Figure 9

	TAT	PBS Mock
G1 (%)	40.1±0.6 (p=0.0013)	35.3±0.8
S (%)	16.8±1.12 (p=0.2077)	15.5±1.1
G2 (%)	13.3±1.3 (p=0.0017)	21.4±1.4
Sub G1 (%)	24.0±0.9 (p=0.1402)	21.8±1.9
	TAT_eIF4G1	TAT_eIF4G1_Cntrl
G1 (%)	34.7±2.8 (p=0.1793)	38.6±3.0
S (%)	5.5±0.2 (p<0.0001)	15.2±1.0
G2 (%)	5.5±0.4 (p=0.0002)	24.8±2.6
Sub G1 (%)	43.4±3.2 (p<0.0001)	15.2±1.0
	TAT_eIF4G1_me5	TAT_eIF4G1_me5_Cntrl
G1 (%)	17.0±0.7 (p<0.0001)	28.5±0.1
S (%)	2.6±0.3 (p<0.0001)	9.1±0.2
G2 (%)	3.2±0.1 (p<0.0001)	15.6±0.3
Sub G1 (%)	71.7±1.0 (p<0.0001)	40.1±0.8

Figure 10

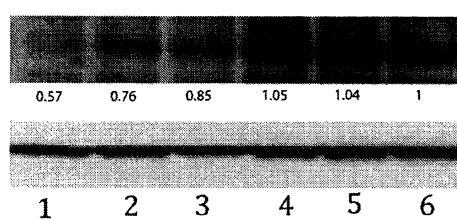


Figure 11

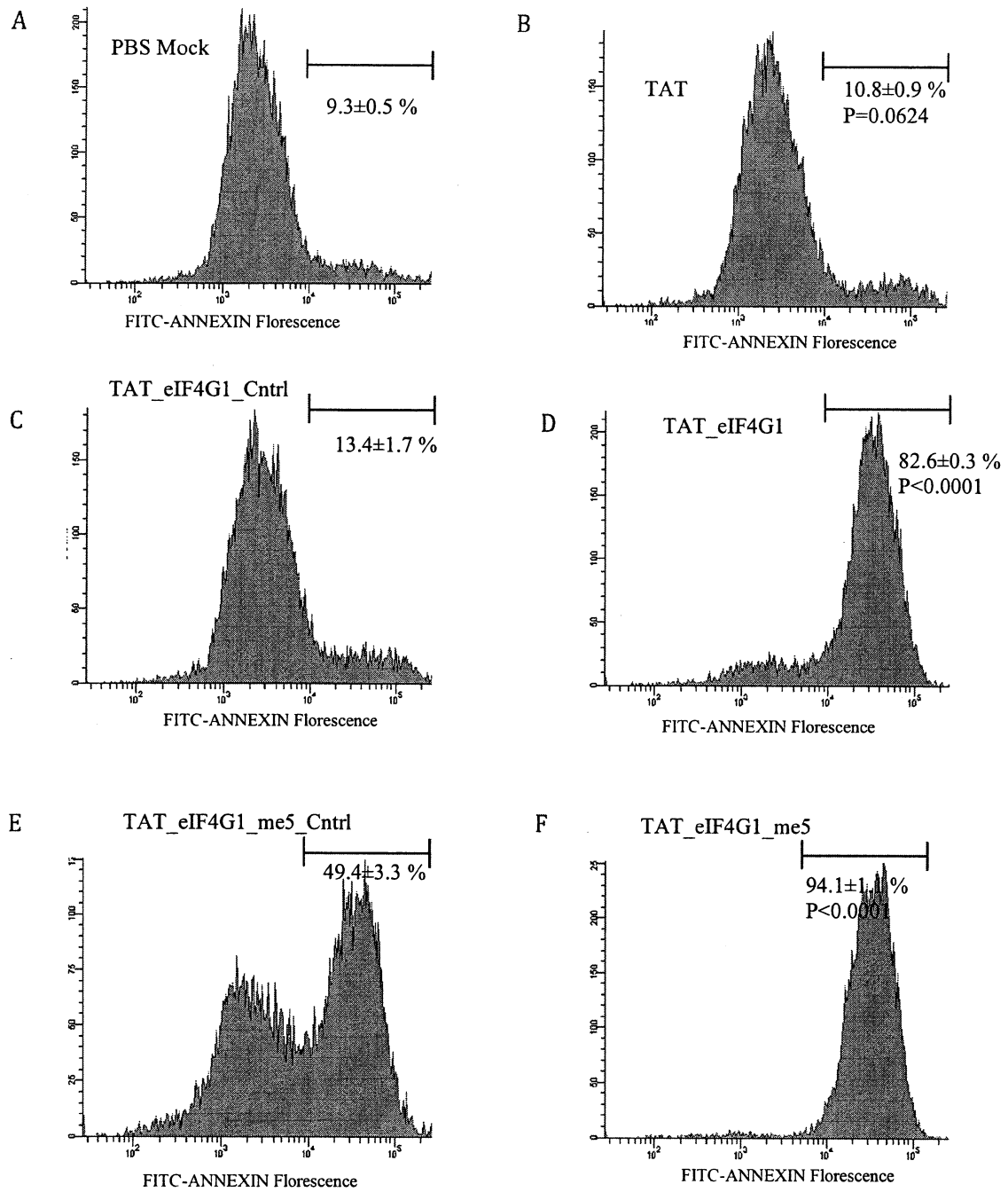


Figure 12

A

Peptides	K_d (nM)	ΔH (kCal mol ⁻¹ K ⁻¹)	ΔS (Cal mol ⁻¹ K ⁻¹)
TAT-eIF4G1	56.18±2.55	-5.52±0.06	15
TAT_eIF4GI_me5	10.17±8.60	-12.39±0.10	-5.69

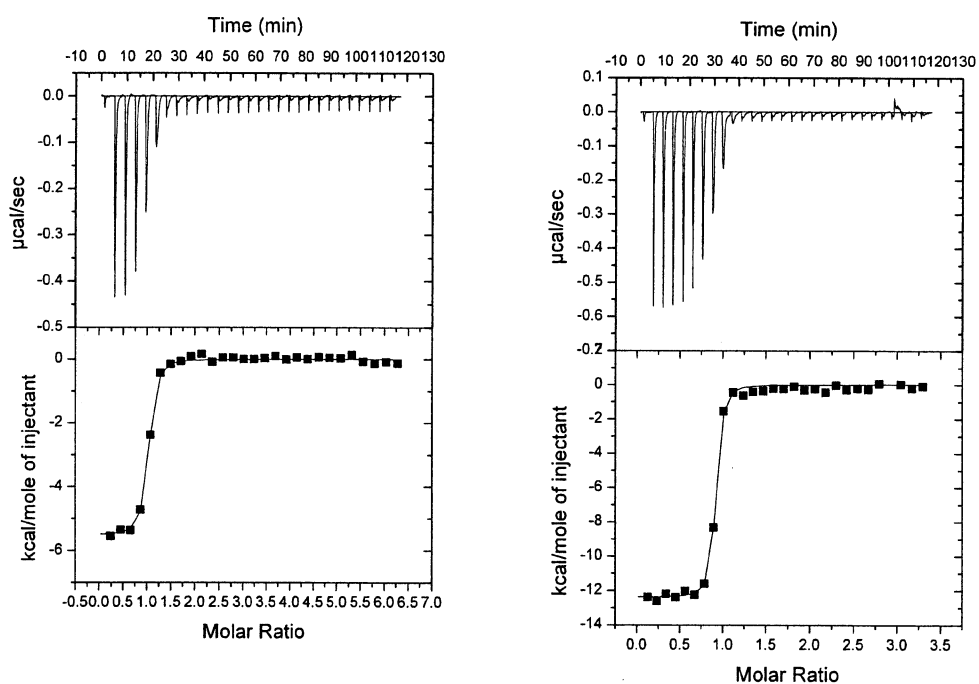
B

Figure 13

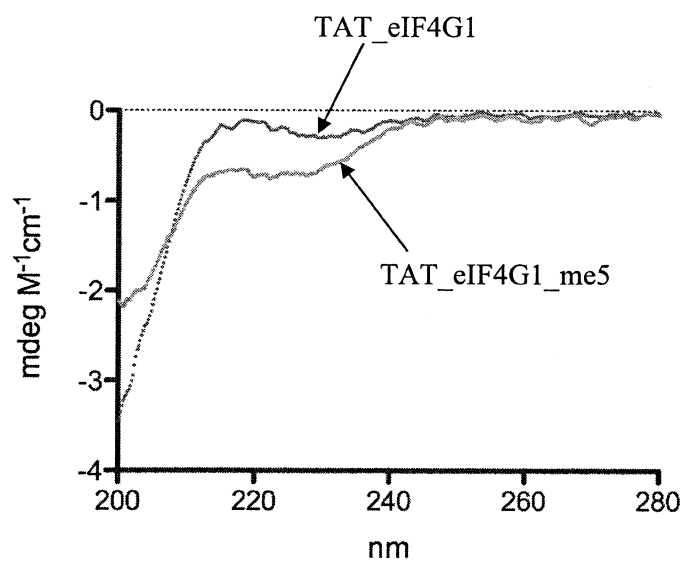


Figure 14

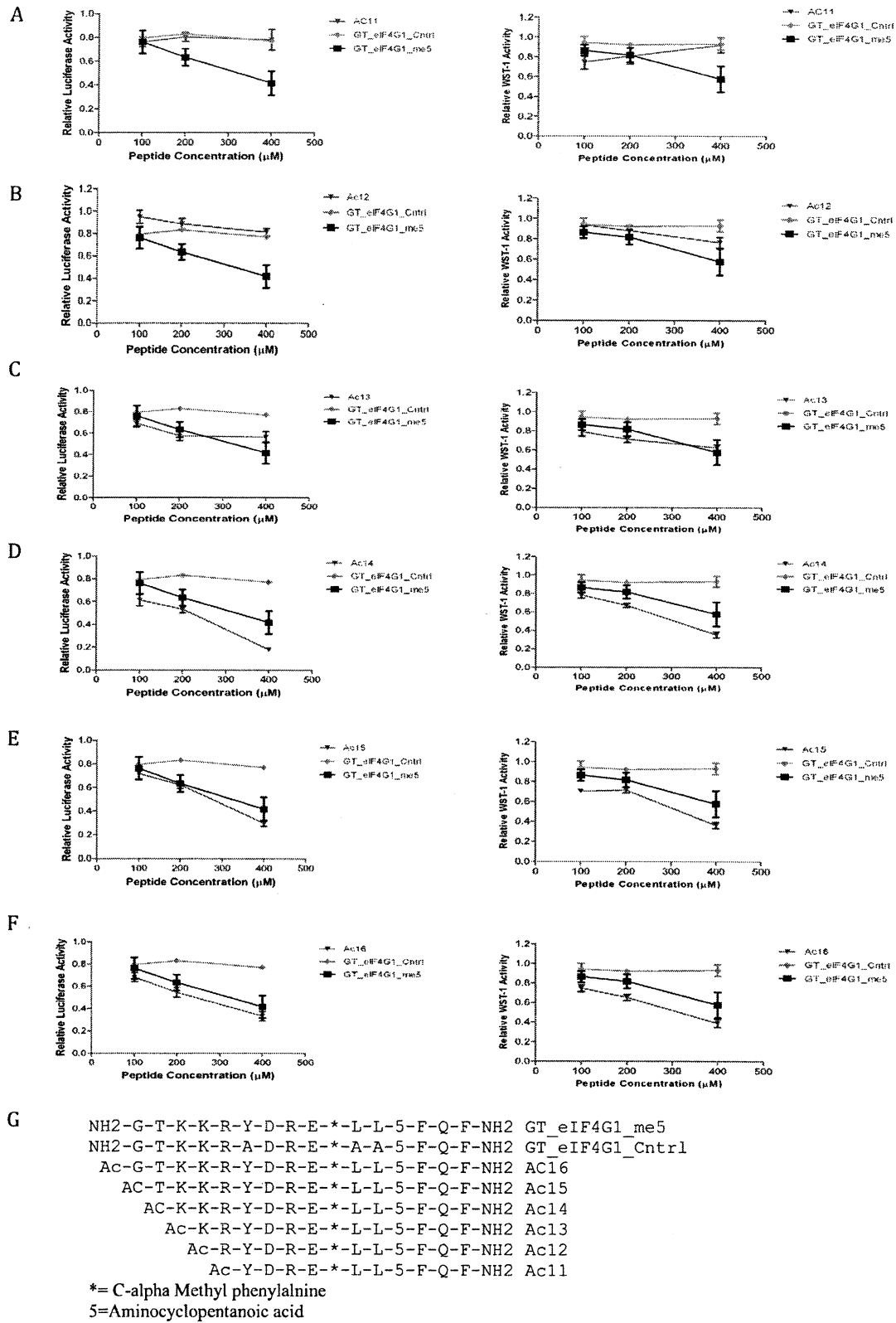


Figure 15

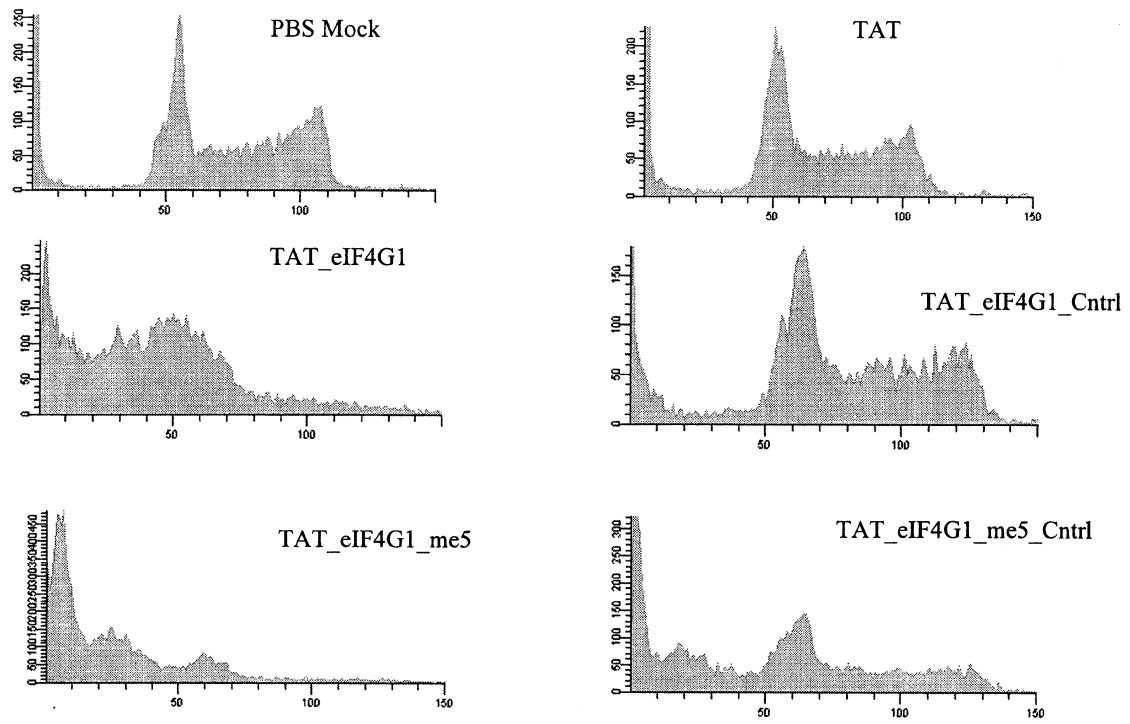


Figure 16