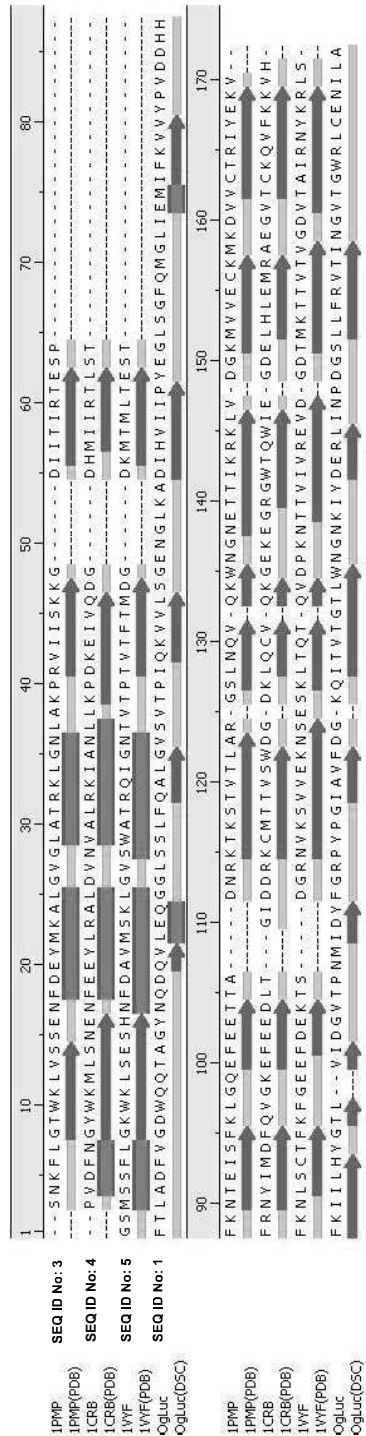
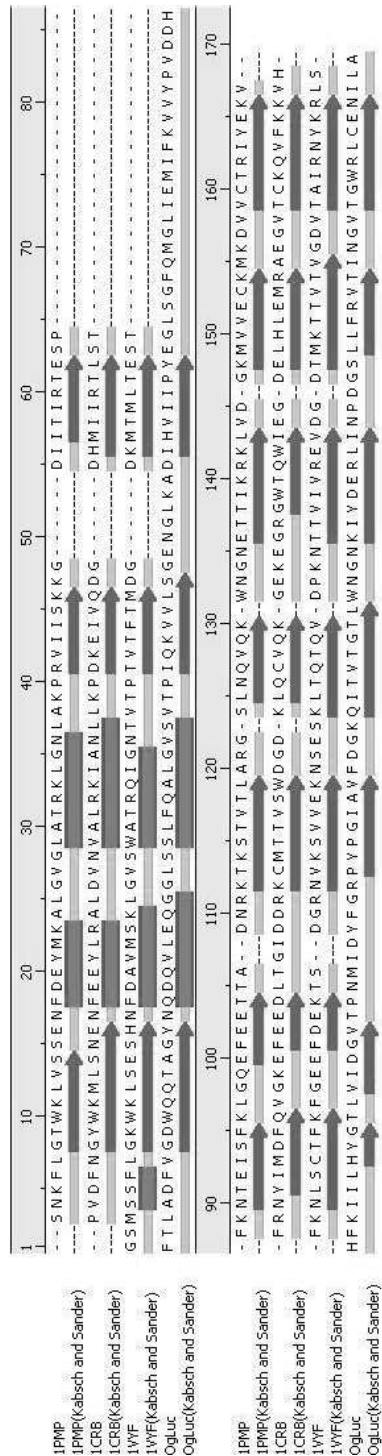


- approximate extent of helix secondary structure elements
- approximate extent of beta-sheet secondary structure elements
- secondary structure other than helix or beta-sheet

Secondary structure alignment #1:



Secondary structure alignment #2:



The sequence motifs centered on the conserved residues of the calycin structural signature can be seen in the alignments. The more highly conserved N-terminal MOTIF1 includes Ogluc residue Trp10, and the less well conserved C-terminal MOTIF2 includes Ogluc residue N166. For alignment #2, the approximate pair-wise percent protein sequence identities are: Ogluc-1PMP 14%, Ogluc-1CRB 9%, and Ogluc-1VVF 15%.

FIG. 1

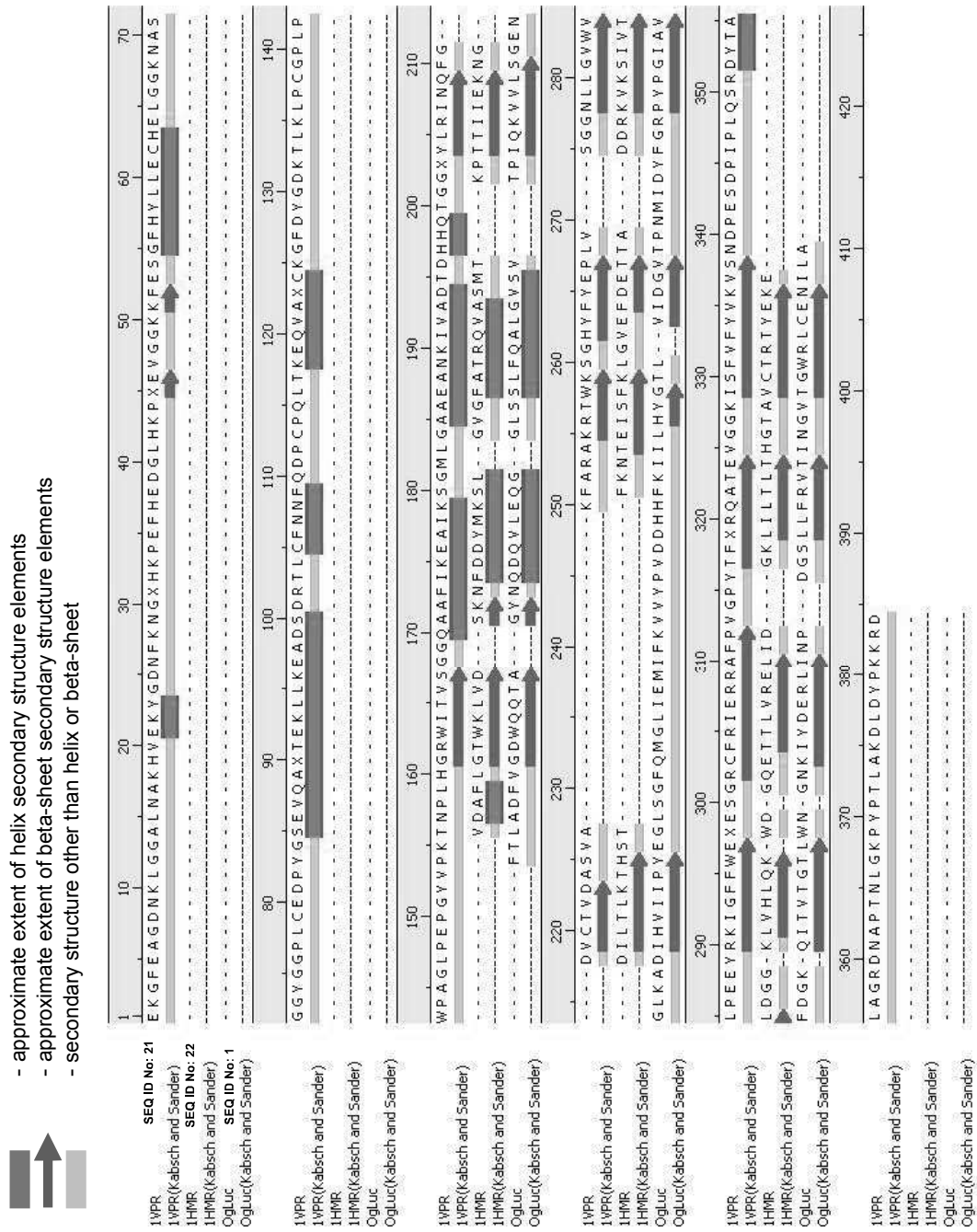


FIG. 2



FIG. 3

Section 1									
	1	10	20	30	40	50	60	70	
SEQ ID NO.:10 True wt protein seq	(1)	MAYSTLFII	ALTAVVTQASSTQKS	NLTFTL	ADFVGDWQQ	TAGYNQDQVLEQG	SSLFQA	LGVS	VTPIQK
SEQ ID NO.:13 Promega wt protein seq	(1)	-----	-----	-----	-----	-----	-----	-----	-----
SEQ ID NO.:15 N166R protein seq	(1)	-----	-----	-----	-----	-----	-----	-----	-----
SEQ ID NO.:25 C1 protein seq	(1)	-----	-----	-----	-----	-----	-----	-----	-----
SEQ ID NO.:27 C1+C2 protein seq	(1)	-----	-----	-----	-----	-----	-----	-----	-----
SEQ ID NO.:23 C1+A4E protein seq	(1)	-----	-----	-----	-----	-----	-----	-----	-----
SEQ ID NO.:29 C1+C2+A4E protein seq	(1)	-----	-----	-----	-----	-----	-----	-----	-----
SEQ ID NO.:31 C1+C3+A4E proteins seq	(1)	-----	-----	-----	-----	-----	-----	-----	-----
SEQ ID NO.:33 Consensus	(1)	-----	-----	-----	-----	-----	-----	-----	-----
Section 2									
	71	80	90	100	110	120	130	140	
True wt protein seq	(71)	VVLSG	ENGLKAD	IHVII	IPYEG	LSGFQMG	LIEMIF	KVVYP	VDDH
Promega wt protein seq	(46)	VVLSG	ENGLKAD	IHVII	IPYEG	LSGFQMG	LIEMIF	KVVYP	VDDH
N166R protein seq	(46)	VVLSG	ENGLKAD	IHVII	IPYEG	LSGFQMG	LIEMIF	KVVYP	VDDH
C1 protein seq	(46)	VVLSG	ENGLKAD	IHVII	IPYEG	LSGFQMG	LIEMIF	KVVYP	VDDH
C1+C2 protein seq	(46)	VVLSG	ENGLKAD	IHVII	IPYEG	LSGFQMG	LIEMIF	KVVYP	VDDH
C1+A4E protein seq	(46)	VVLSG	ENGLKAD	IHVII	IPYEG	LSGFQMG	LIEMIF	KVVYP	VDDH
C1+C2+A4E protein seq	(46)	VVLSG	ENGLKAD	IHVII	IPYEG	LSGFQMG	LIEMIF	KVVYP	VDDH
C1+C3+A4E proteins seq	(46)	VVLSG	ENGLKAD	IHVII	IPYEG	LSGFQMG	LIEMIF	KVVYP	VDDH
Consensus	(71)	VVLSG	ENGLKAD	IHVII	IPYEG	LSGFQMG	LIEMIF	KVVYP	VDDH
Section 3									
	141	150	160	170	180	190	200	210	
True wt protein seq	(141)	YPGIA	VF	DKQ	IT	VT	GLW	NGK	IY
Promega wt protein seq	(116)	YPGIA	VF	DKQ	IT	VT	GLW	NGK	IY
N166R protein seq	(116)	YPGIA	VF	DKQ	IT	VT	GLW	NGK	IY
C1 protein seq	(116)	YPGIA	VF	DKQ	IT	VT	GLW	NGK	IY
C1+C2 protein seq	(116)	YPGIA	VF	DKQ	IT	VT	GLW	NGK	IY
C1+A4E protein seq	(116)	YPGIA	VF	DKQ	IT	VT	GLW	NGK	IY
C1+C2+A4E protein seq	(116)	YPGIA	VF	DKQ	IT	VT	GLW	NGK	IY
C1+C3+A4E proteins seq	(116)	YPGIA	VF	DKQ	IT	VT	GLW	NGK	IY
Consensus	(141)	YPGIA	VF	DKQ	IT	VT	GLW	NGK	IY

FIG. 31

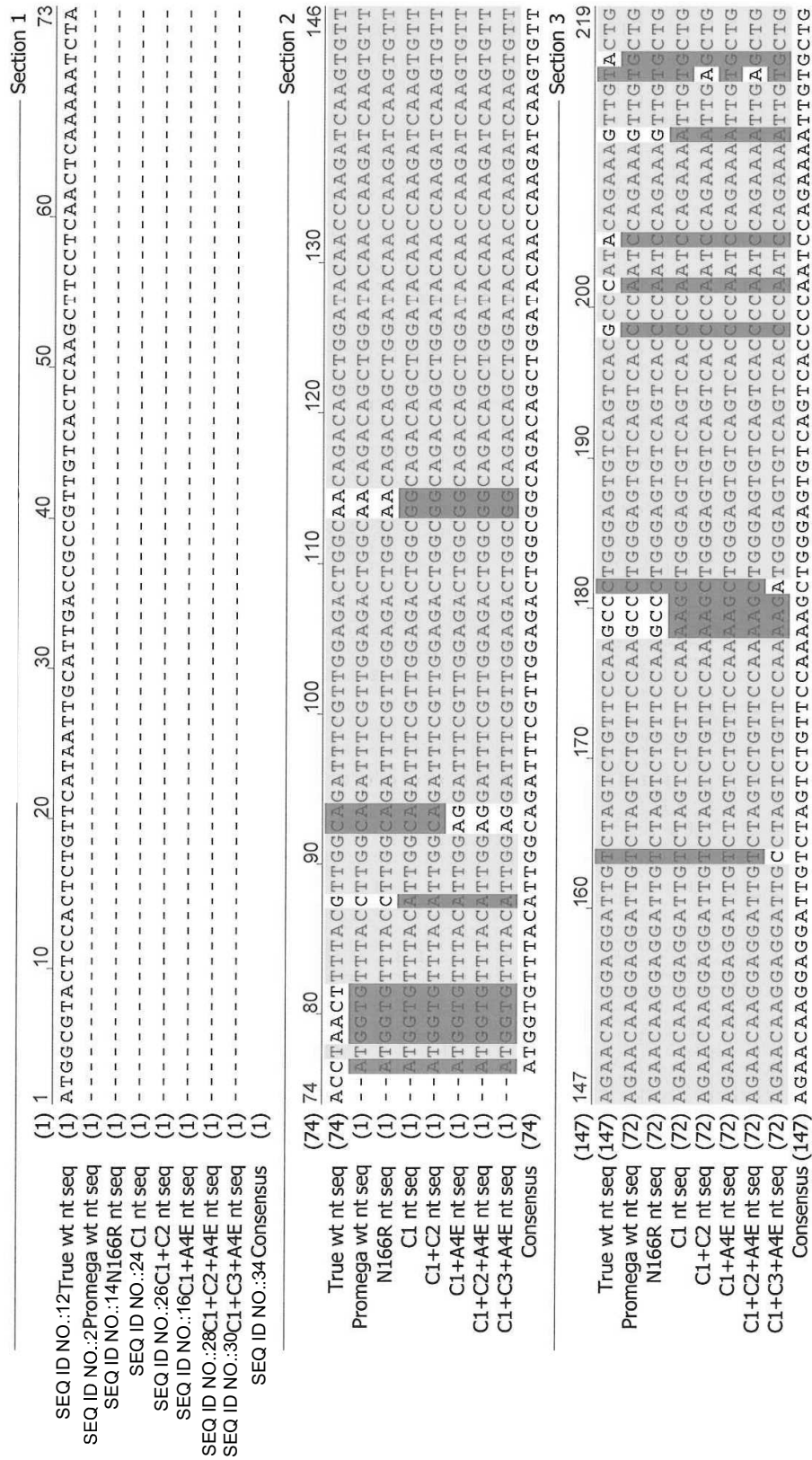


FIG. 32

Section 4									
(220)	220	230	240	250	260	270	280	290	
True wt nt seq (220)	TCTGGGGAGAAATG	GGTTAAAGCTGATATTCATGTCATAA	TACCTTACGAGGGGACTCAGTGGTTTTCAAATGG						
Promega wt nt seq (145)	TCTGGGGAGAAATG	GGTTAAAGCTGATATTCATGTCAT	GATCCTTACGAGGGGACTCAGTGGTTTTCAAATGG						
N166R nt seq (145)	TCTGGGGAGAAATG	GGTTAAAGCTGATATTCATGTCAT	GATCCTTACGAGGGGACTCAGTGGTTTTCAAATGG						
C1 nt seq (145)	TCTGGGGAGAAATG	GGTTAAAGCTGATATTCATGTCAT	GATCCTTACGAGGGGACTCAGTGGTTTTCAAATGG						
C1+C2 nt seq (145)	TCTGGGGAGAAATG	GGTTAAAGCTGATATTCATGTCAT	GATCCTTACGAGGGGACTCAGTGGTTTTCAAATGG						
C1+A4E nt seq (145)	TCTGGGGAGAAATG	GGTTAAAGCTGATATTCATGTCAT	GATCCTTACGAGGGGACTCAGTGGTTTTCAAATGG						
C1+C2+A4E nt seq (145)	TCTGGGGAGAAATG	GGTTAAAGCTGATATTCATGTCAT	GATCCTTACGAGGGGACTCAGTGGTTTTCAAATGG						
C1+C3+A4E nt seq (145)	TCTGGGGAGAAATG	GGTTAAAGCTGATATTCATGTCAT	GATCCTTACGAGGGGACTCAGTGGTTTTCAAATGG						
Consensus (220)	TCTGGGGAGAAATG	GGTTAAAGCTGATATTCATGTCAT	GATCCTTACGAGGGGACTCAGTGGTTTTCAAATGG						
Section 5									
(293)	293	300	310	320	330	340	350	360	
True wt nt seq (293)	GTCTAATTGAAATGATCTTCAAAAGTTGTTT	ACCCCGTGGATGATCATCATTTCAAGATTAT	TCTCCATTATGG						
Promega wt nt seq (218)	GTCTAATTGAAATGATCTTCAAAAGTTGTTT	ACCCCGTGGATGATCATCATTTCAAGATTAT	TCTCCATTATGG						
N166R nt seq (218)	GTCTAATTGAAATGATCTTCAAAAGTTGTTT	ACCCCGTGGATGATCATCATTTCAAGATTAT	TCTCCATTATGG						
C1 nt seq (218)	GTCTAATTGAAATGATCTTCAAAAGTTGTTT	ACCCCGTGGATGATCATCATTTCAAGATTAT	TCTCCATTATGG						
C1+C2 nt seq (218)	GTCTAATTGAAATGATCTTCAAAAGTTGTTT	ACCCCGTGGATGATCATCATTTCAAGATTAT	TCTCCATTATGG						
C1+A4E nt seq (218)	GTCTAATTGAAATGATCTTCAAAAGTTGTTT	ACCCCGTGGATGATCATCATTTCAAGATTAT	TCTCCATTATGG						
C1+C2+A4E nt seq (218)	GTCTAATTGAAATGATCTTCAAAAGTTGTTT	ACCCCGTGGATGATCATCATTTCAAGATTAT	TCTCCATTATGG						
C1+C3+A4E nt seq (218)	GTCTAATTGAAATGATCTTCAAAAGTTGTTT	ACCCCGTGGATGATCATCATTTCAAGATTAT	TCTCCATTATGG						
Consensus (293)	GTCTAATTGAAATGATCTTCAAAAGTTGTTT	ACCCCGTGGATGATCATCATTTCAAGATTAT	TCTCCATTATGG						
Section 6									
(366)	366	380	390	400	410	420	430	440	
True wt nt seq (366)	TACACTCGTTT	TTGACGGGTGAACAC	CAACATGATTGACTACTTTGGAAGAC	CCCTTACCC	TGGAATTGCTGTA				
Promega wt nt seq (291)	TACACTCGTTT	TTGACGGGTGAACAC	CAACATGATTGACTACTTTGGAAGAC	CCCTTACCC	TGGAATTGCTGTA				
N166R nt seq (291)	TACACTCGTTT	TTGACGGGTGAACAC	CAACATGATTGACTACTTTGGAAGAC	CCCTTACCC	TGGAATTGCTGTA				
C1 nt seq (291)	TACACTCGTTT	TTGACGGGTGAACAC	CAACATGATTGACTACTTTGGAAGAC	CCCTTACCC	TGGAATTGCTGTA				
C1+C2 nt seq (291)	TACACTCGTTT	TTGACGGGTGAACAC	CAACATGATTGACTACTTTGGAAGAC	CCCTTACCC	TGGAATTGCTGTA				
C1+A4E nt seq (291)	TACACTCGTTT	TTGACGGGTGAACAC	CAACATGATTGACTACTTTGGAAGAC	CCCTTACCC	TGGAATTGCTGTA				
C1+C2+A4E nt seq (291)	TACACTCGTTT	TTGACGGGTGAACAC	CAACATGATTGACTACTTTGGAAGAC	CCCTTACCC	TGGAATTGCTGTA				
C1+C3+A4E nt seq (291)	TACACTCGTTT	TTGACGGGTGAACAC	CAACATGATTGACTACTTTGGAAGAC	CCCTTACCC	TGGAATTGCTGTA				
Consensus (366)	TACACTCGTTT	TTGACGGGTGAACAC	CAACATGATTGACTACTTTGGAAGAC	CCCTTACCC	TGGAATTGCTGTA				

FIG. 32 CONT.

		Section 7									
		(439)	439	450	460	470	480	490	500	511	
True wt nt seq	(439)	TTTGACGGCAAGCAGATCACAGTTACTGGAACTCTGTGGAACGGCAA									
Promega wt nt seq	(364)	TTTGACGGCAAGCAGATCACAGTTACTGGAACTCTGTGGAACGGCAA									
N166R nt seq	(364)	TTTGACGGCAAGCAGATCACAGTTACTGGAACTCTGTGGAACGGCAA									
C1 nt seq	(364)	TTTGACGGCAAGCAGATCACAGTTACTGGAACTCTGTGGAACGGCAA									
C1+C2 nt seq	(364)	TTTGACGGCAAGCAGATCACAGTTACTGGAACTCTGTGGAACGGCAA									
C1+A4E nt seq	(364)	TTTGACGGCAAGCAGATCACAGTTACTGGAACTCTGTGGAACGGCAA									
C1+C2+A4E nt seq	(364)	TTTGACGGCAAGCAGATCACAGTTACTGGAACTCTGTGGAACGGCAA									
C1+C3+A4E nt seq	(364)	TTTGACGGCAAGCAGATCACAGTTACTGGAACTCTGTGGAACGGCAA									
Consensus	(439)	TTTGACGGCAAGCAGATCACAGTTACTGGAACTCTGTGGAACGGCAA									
		Section 8									
		(512)	512	520	530	540	550	560	570	584	
True wt nt seq	(512)	ACCCAGATGGTTCACTCCTCTTCAGAGTTACTATCAATGGAGTCACGGGATGGAGGCTTTCGAGAAC									
Promega wt nt seq	(437)	ACCCAGATGGTTCACTCCTCTTCAGAGTTACTATCAATGGAGTCACGGGATGGAGGCTTTCGAGAAC									
N166R nt seq	(437)	ACCCAGATGGTTCACTCCTCTTCAGAGTTACTATCAATGGAGTCACGGGATGGAGGCTTTCGAGAAC									
C1 nt seq	(437)	ACCCAGATGGTTCACTCCTCTTCAGAGTTACTATCAATGGAGTCACGGGATGGAGGCTTTCGAGAAC									
C1+C2 nt seq	(437)	ACCCAGATGGTTCACTCCTCTTCAGAGTTACTATCAATGGAGTCACGGGATGGAGGCTTTCGAGAAC									
C1+A4E nt seq	(437)	ACCCAGATGGTTCACTCCTCTTCAGAGTTACTATCAATGGAGTCACGGGATGGAGGCTTTCGAGAAC									
C1+C2+A4E nt seq	(437)	ACCCAGATGGTTCACTCCTCTTCAGAGTTACTATCAATGGAGTCACGGGATGGAGGCTTTCGAGAAC									
C1+C3+A4E nt seq	(437)	ACCCAGATGGTTCACTCCTCTTCAGAGTTACTATCAATGGAGTCACGGGATGGAGGCTTTCGAGAAC									
Consensus	(512)	ACCCAGATGGTTCACTCCTCTTCAGAGTTACTATCAATGGAGTCACGGGATGGAGGCTTTCGAGAAC									
		Section 9									
		(585)	585	588							
True wt nt seq	(585)	TGCC									
Promega wt nt seq	(510)	TGCC									
N166R nt seq	(510)	TGCC									
C1 nt seq	(510)	TGCC									
C1+C2 nt seq	(510)	TGCC									
C1+A4E nt seq	(510)	TGCC									
C1+C2+A4E nt seq	(510)	TGCC									
C1+C3+A4E nt seq	(510)	TGCC									
Consensus	(585)	TGCC									

FIG. 32 CONT.

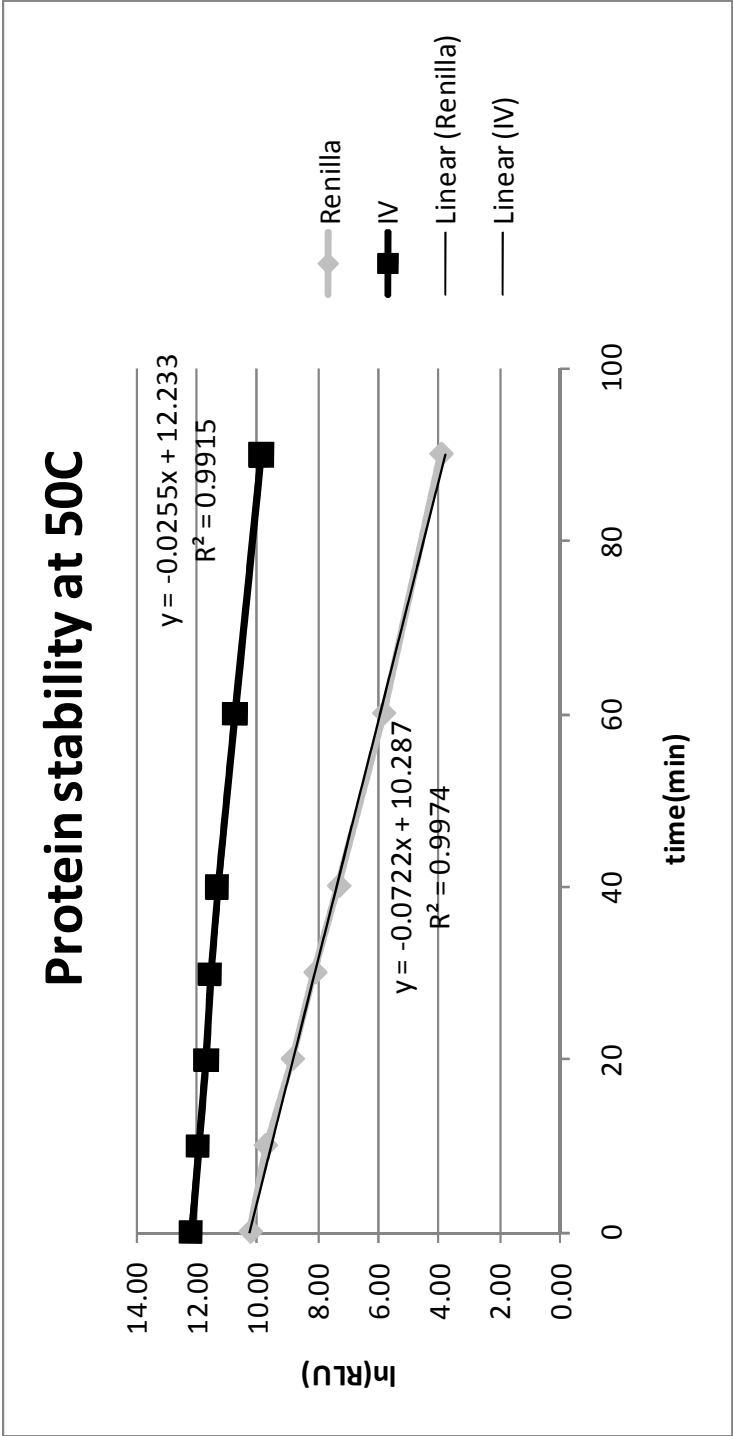


FIG. 34B

Sample	1/2 life (min)
Renilla	9.6
IV	27.2