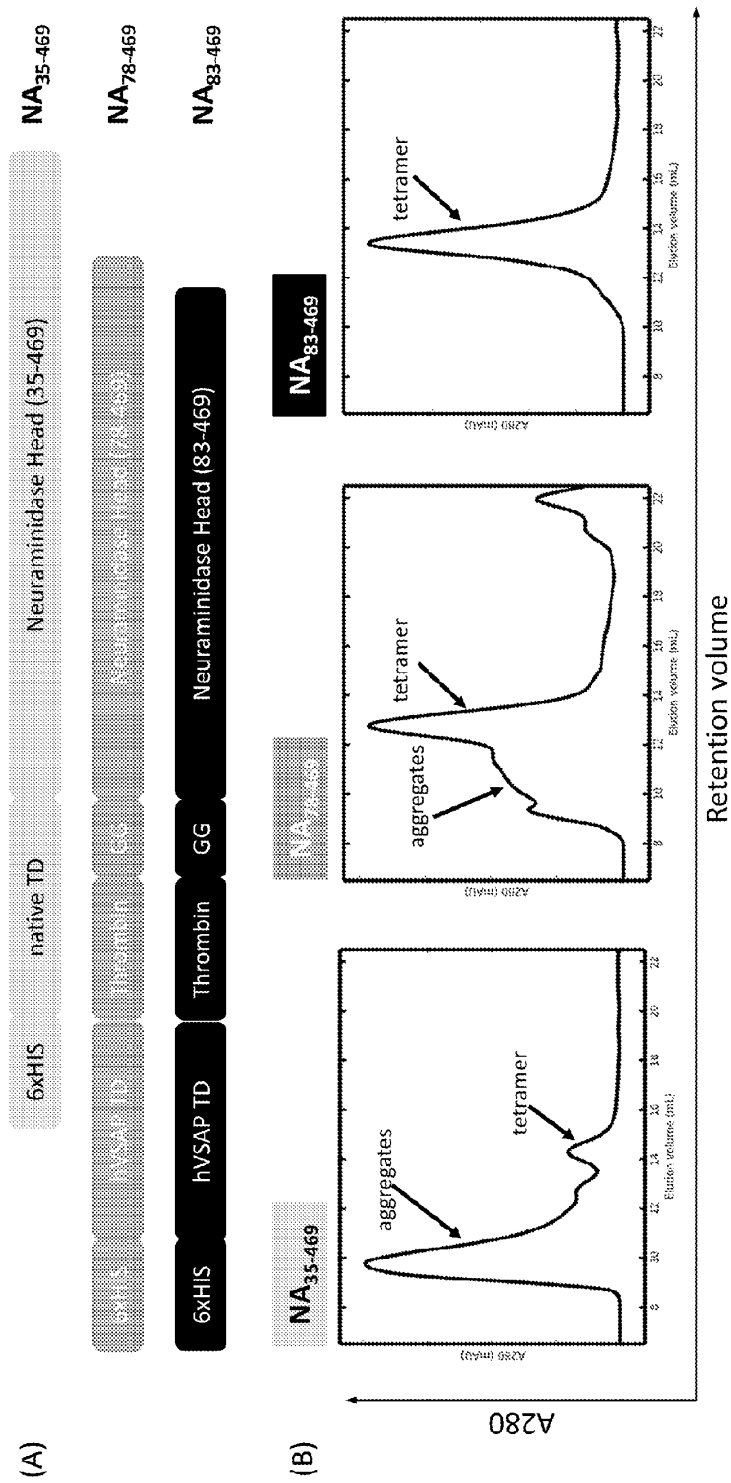




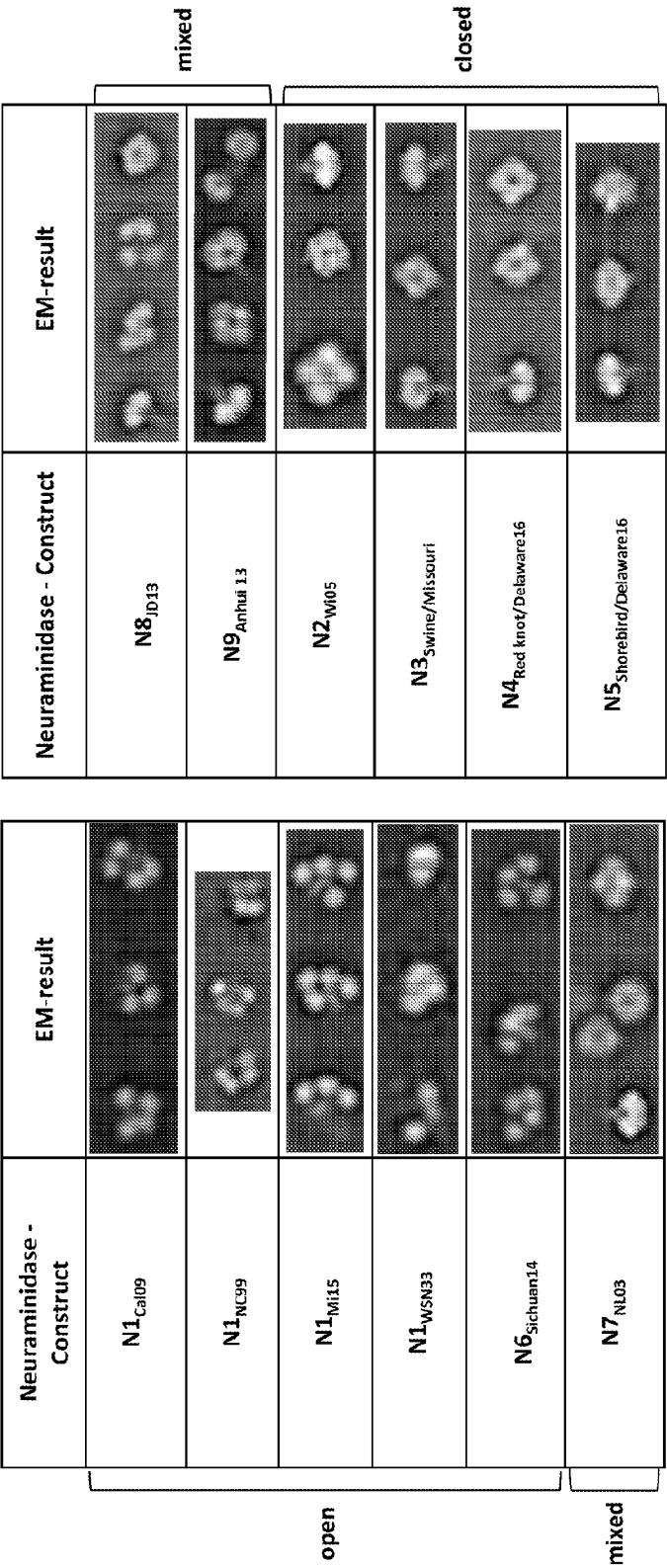


Figure 2

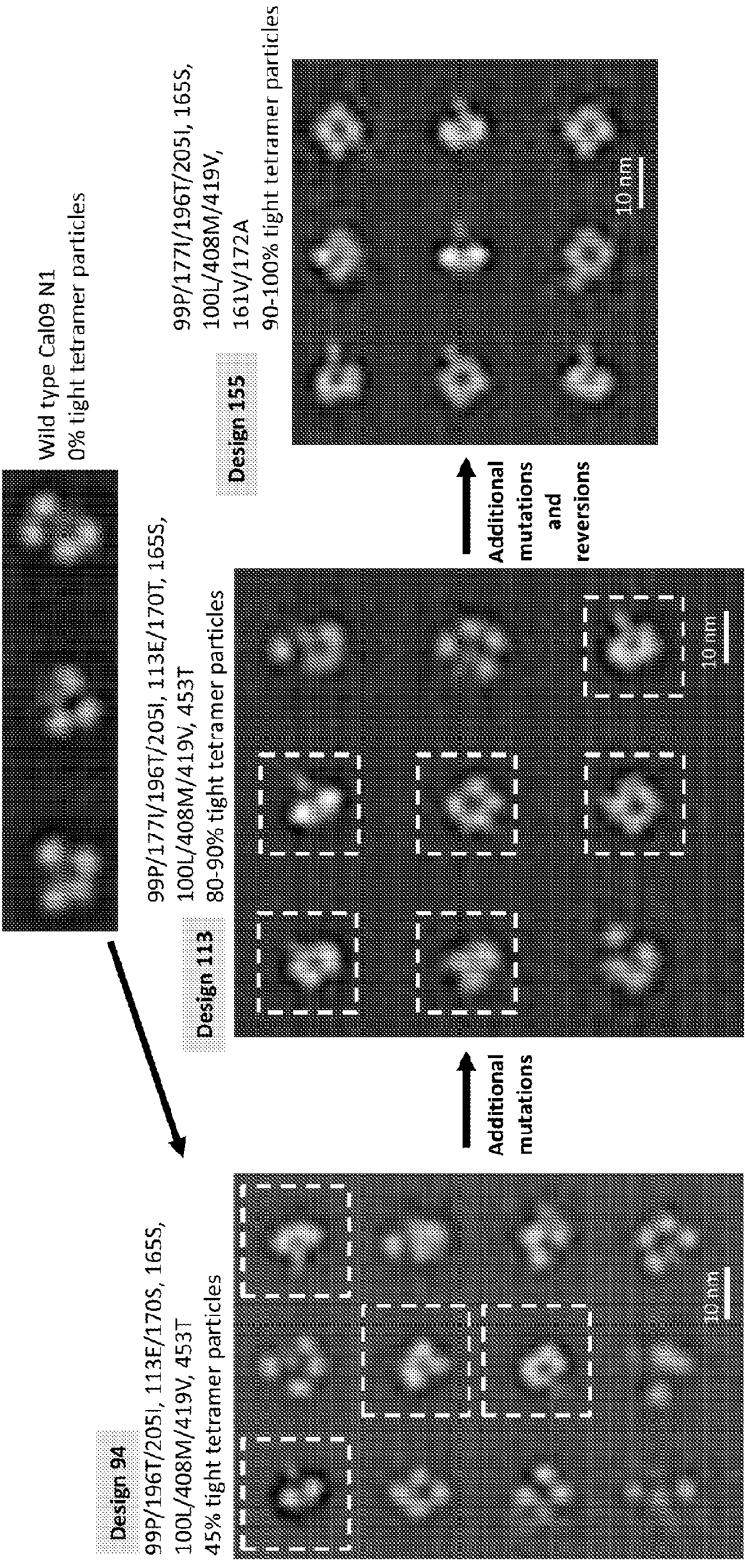


Figure 3

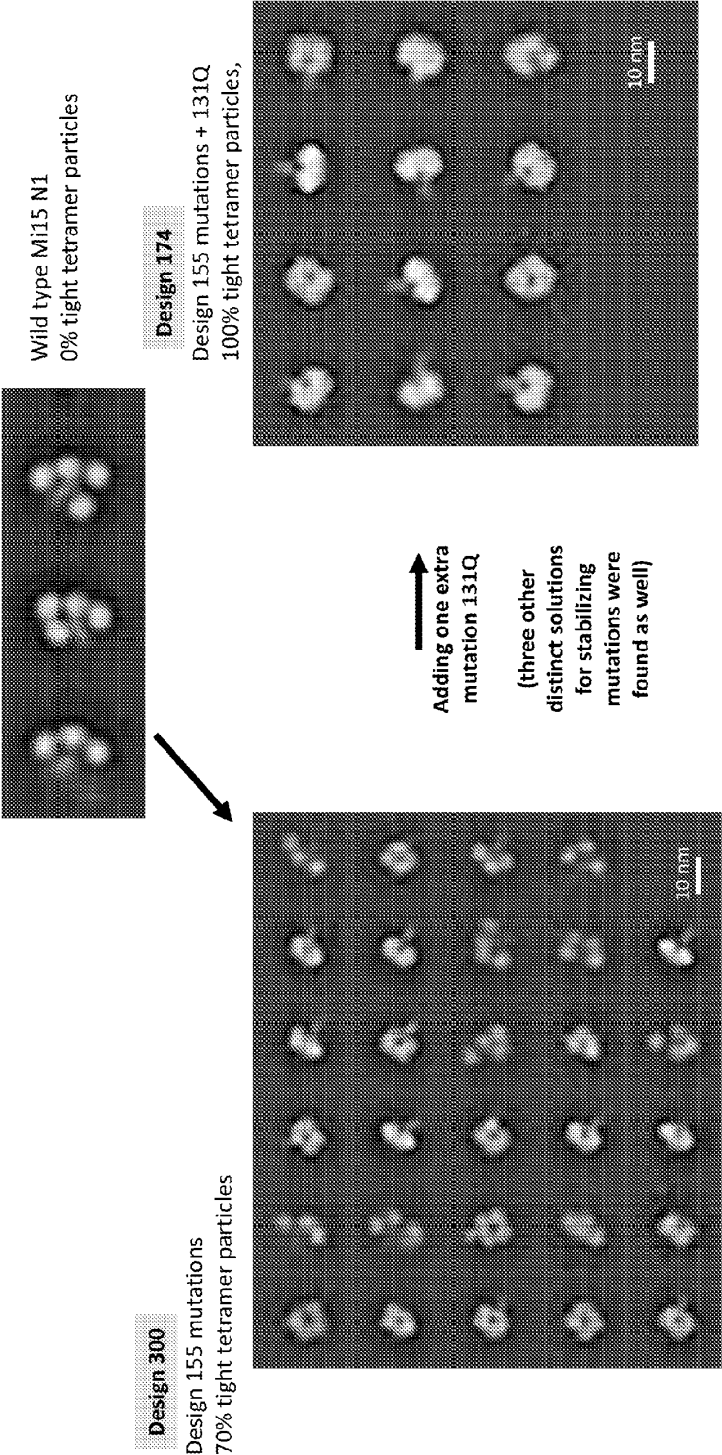


Figure 4

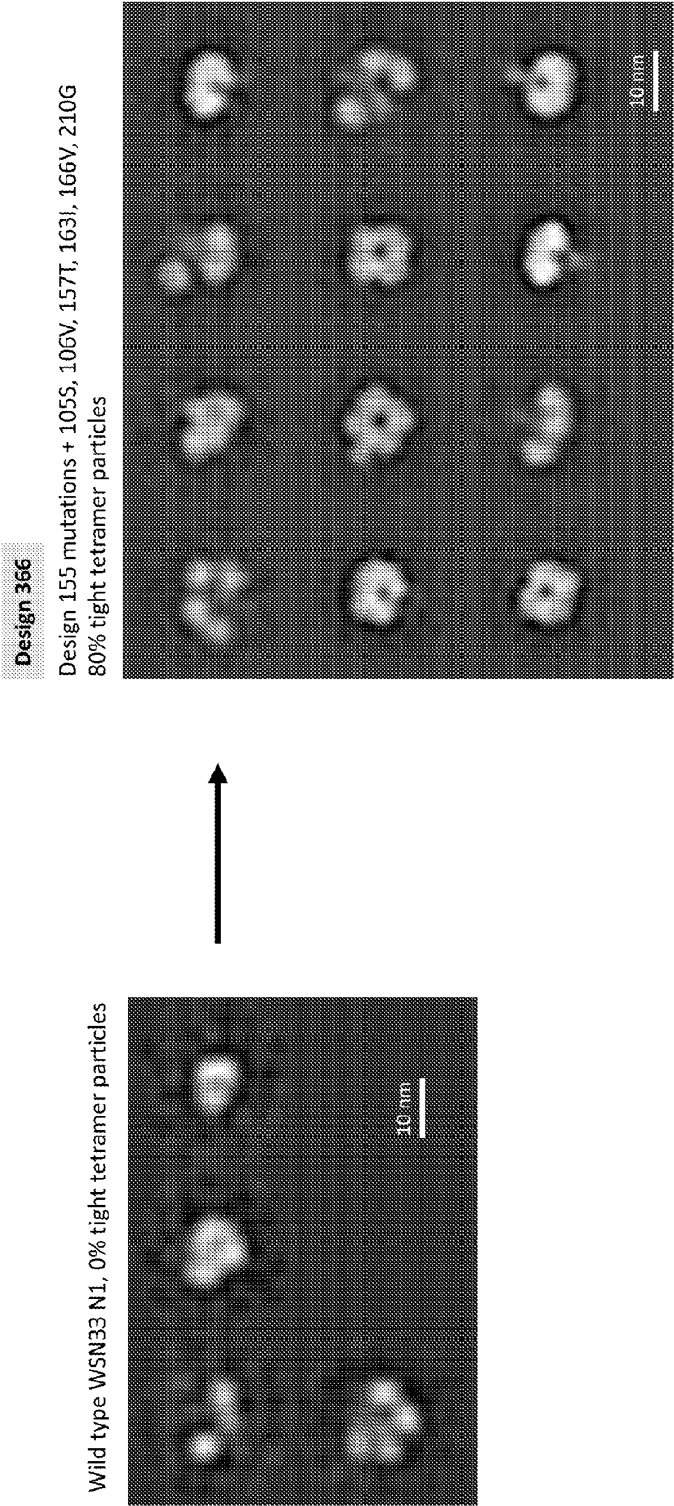


Figure 5

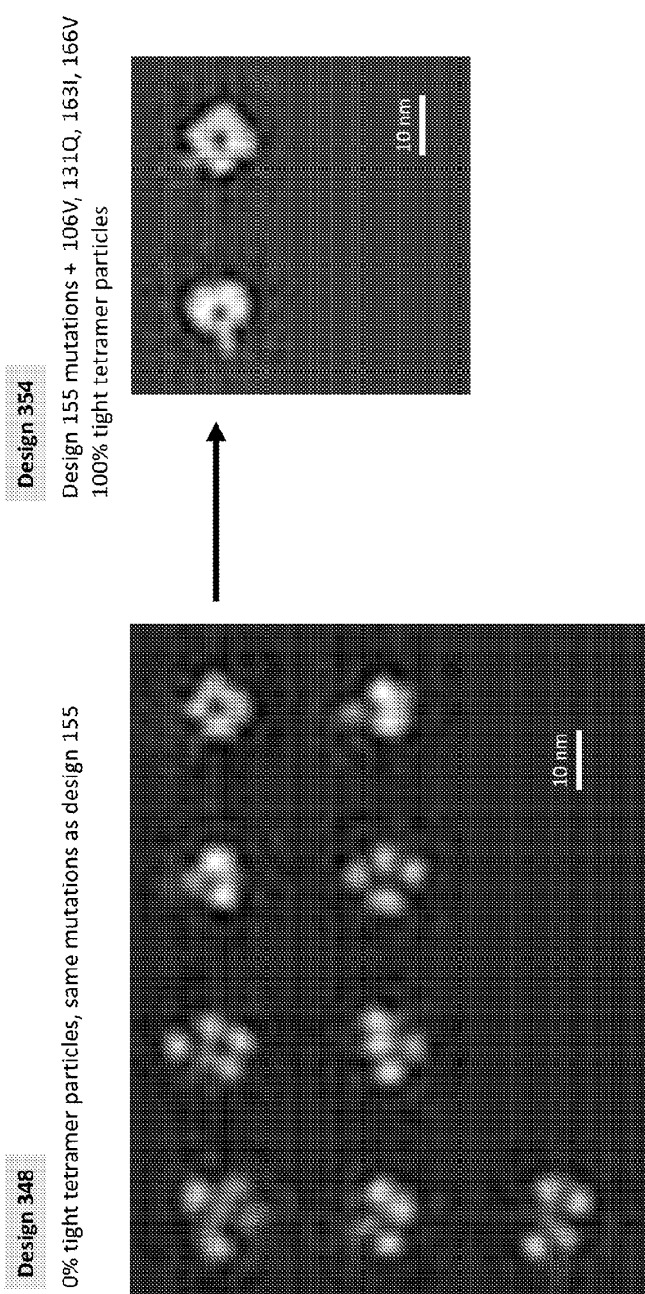


Figure 6

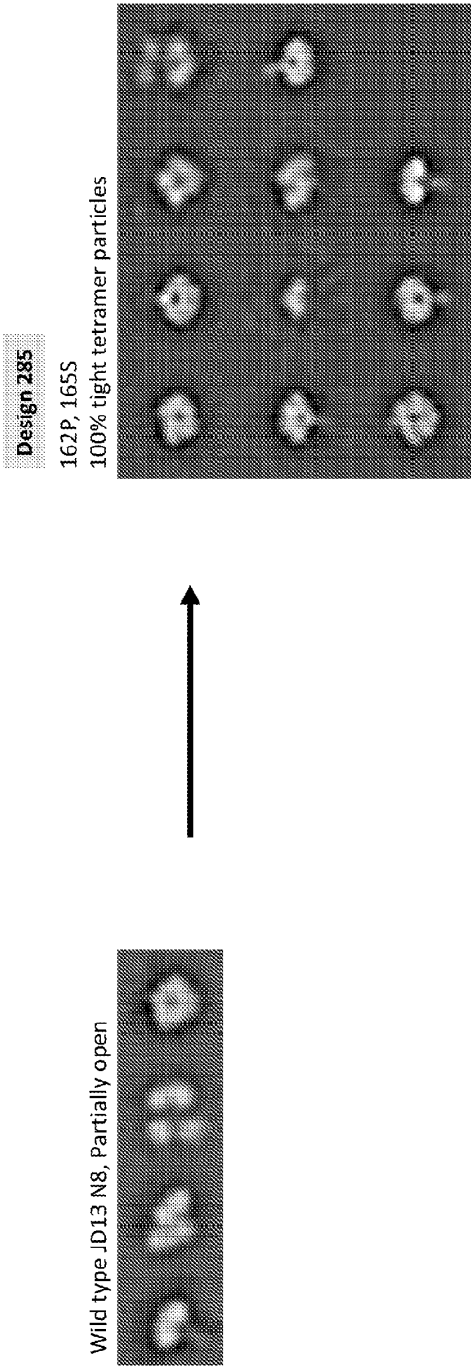


Figure 7

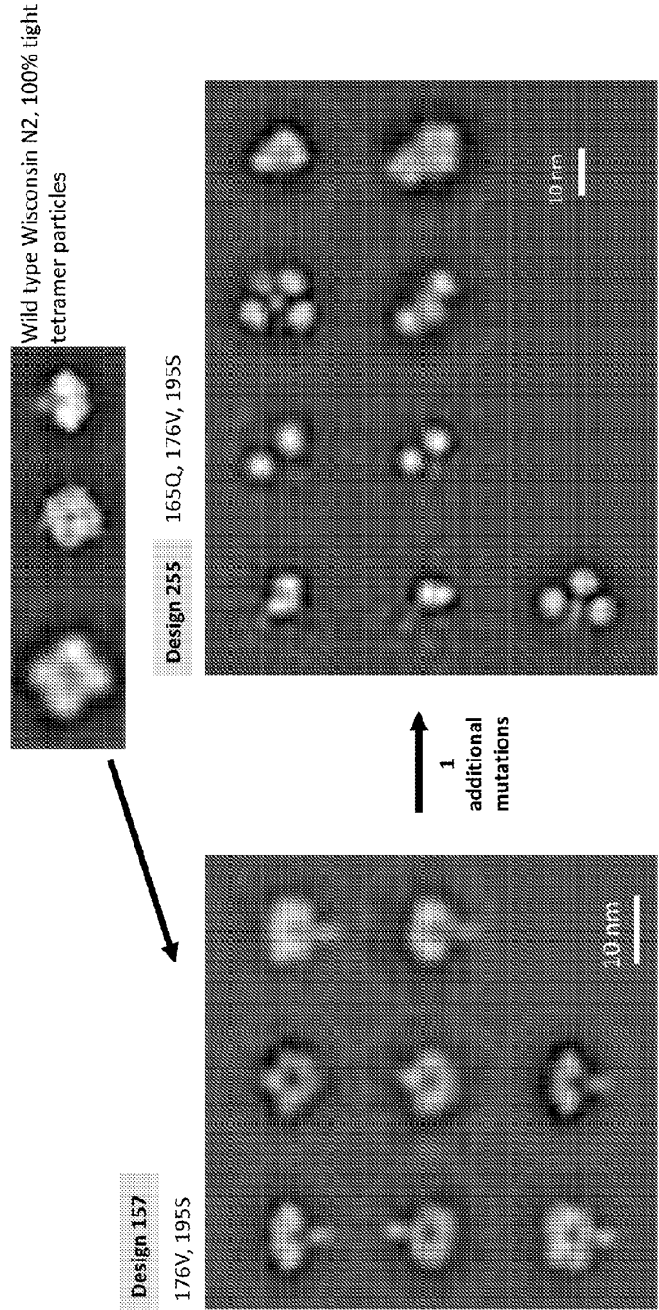


Figure 8

Comparison of SEQ ID NO:1 (Query) with a different N1 sequence (Sbjct) that contains one insertion (SEQ ID NO: 98 & 99)

Score	Expect	Method	Identities	Positives	Gaps
693 bits(1789)	0.0	Compositional matrix adjust	324/388(84%)	355/388(91%)	1/388(0%)
Query	83	VNLAGNSLCPVSGMAIVKSDSVYKSGQVFIKREFFIEGKFLKCTFFFLQGALLND	142		
Sbjct	1	VNLAGNSLCPVSGMAIVKSDSVYKSGQVFIKREFFIEGKFLKCTFFFLQGALLND	60		
Query	143	KHSGTINRSGPTATLMSQCIKGEVPSFINSKPTASVANSASACEDG+LIGLQGFDRWA	292		
Sbjct	61	KHSGTINRSGPTATLMSQCIKGEVPSFINSKPTASVANSASACEDG+LIGLQGFDRWA	120		
Query	203	VAVLYNGIITDTIKSWRNILATQESACVNGSCFTVMTDPSNGQASYKIFRIERK	262		
Sbjct	121	VAVLYNGIITDTIKSWRNILATQESACVNGSCFTVMTDPSNGQASYKIFRIERK	180		
Query	263	IVKSDNRNAPVHYECCSCYFD+VCDNRWNGSNRPVWPFQMLSYQIGYICGVF	322		
Sbjct	181	IVKSDNRNAPVHYECCSCYFD+VCDNRWNGSNRPVWPFQMLSYQIGYICGVF	240		
Query	323	GVFPNDGSCGVSFGANGVYKPTVYKNGVNIQPKYKISGRGKPTMTDPSNGQ	382		
Sbjct	241	GVFPNDGSCGVSFGANGVYKPTVYKNGVNIQPKYKISGRGKPTMTDPSNGQ	300		
Query	383	TDHNSIKQDIKGVNWSGVSSFPVQHEFLQGLDINPCFWYEL+BC P+EN TINTSGS	441		
Sbjct	301	TDHNSIKQDIKGVNWSGVSSFPVQHEFLQGLDINPCFWYEL+BC P+EN TINTSGS	360		
Query	442	SIFCGVNSDTGVNSWFDGAELEPTIDK	469		
Sbjct	361	SIFCGVNSDTGVNSWFDGAELEPTIDK	388		

Comparison of SEQ ID NO:1 (Query) with a different N1 sequence (Sbjct) that contains multiple deletions (SEQ ID NO: 96 & 97)

Score	Expect	Method	Identities	Positives	Gaps
734 bits(1896)	0.0	Compositional matrix adjust	353/387(91%)	371/387(95%)	5/387(1%)
Query	83	VNLAGNSLCPVSGMAIVKSDSVYKSGQVFIKREFFIEGKFLKCTFFFLQGALLND	142		
Sbjct	1	VNLAGNSLCPVSGMAIVKSDSVYKSGQVFIKREFFIEGKFLKCTFFFLQGALLND	60		
Query	143	KHSGTINRSGPTATLMSQCIKGEVPSFINSKPTASVANSASACEDG+LIGLQGFDRWA	282		
Sbjct	61	KHSGTINRSGPTATLMSQCIKGEVPSFINSKPTASVANSASACEDG+LIGLQGFDRWA	120		
Query	203	VAVLYNGIITDTIKSWRNILATQESACVNGSCFTVMTDPSNGQASYKIFRIERK	262		
Sbjct	121	VAVLYNGIITDTIKSWRNILATQESACVNGSCFTVMTDPSNGQASYKIFRIERK	180		
Query	263	IVKSDNRNAPVHYECCSCYFD+VCDNRWNGSNRPVWPFQMLSYQIGYICGVF	322		
Sbjct	181	IVKSDNRNAPVHYECCSCYFD+VCDNRWNGSNRPVWPFQMLSYQIGYICGVF	216		
Query	323	GVFPNDGSCGVSFGANGVYKPTVYKNGVNIQPKYKISGRGKPTMTDPSNGQ	382		
Sbjct	237	GVFPNDGSCGVSFGANGVYKPTVYKNGVNIQPKYKISGRGKPTMTDPSNGQ	296		
Query	383	TDHNSIKQDIKGVNWSGVSSFPVQHEFLQGLDINPCFWYEL+BC P+EN TINTSGS	442		
Sbjct	237	TDHNSIKQDIKGVNWSGVSSFPVQHEFLQGLDINPCFWYEL+BC P+EN TINTSGS	358		
Query	443	SIFCGVNSDTGVNSWFDGAELEPTIDK	469		
Sbjct	356	SIFCGVNSDTGVNSWFDGAELEPTIDK	382		

Figure 9