Strain 27 – SH3-FLS in pSB1A3 w/o primer or RBS

Sequenced: 10-190884405 pg 110 on 2/20/2012: **kept colony 3**

See google doc 2012\_04\_09 Review SH3-FLS stuff for more details.

From VF2:

>SH3-FLS-pSB1A3-c3-VF2\_E12.ab1  
NNNNNNNNNNNNNNNNNNNNATNNNAATAGGCGTATCACGAGGCAGAATTTCAGATAAAAAAAATCCTTAGCTTTCGCTAAGGATGATTTCTGGAATTCGCGGCCGCTTCTAGAGATGCCGCCGCCGGCGCTGCCGCCGAAAAGAAGGAGAGGTAGCGGCGCGATGATCACGGGCGGCGAGCTGGTAGTGCGCACCTTAATCAAGGCGGGTGTTGAGCACCTGTTTGGTCTGCACGGTATCCATATTGACACGATCTTCCAGGCTTGTCTGGACCACGACGTGCCGATTATCGACACTCGTCACGAGGCGGCTGCCGGCCACGCTGCGGAGGGCTACGCTCGTGCCGGTGCGAAACTGGGTGTGGCTTTGGTCACCGCGGGTGGCGGCTTCACTAATGCGGTGACCCCTATTGCGAATGCGTGGCTGGACCGTACGCCGGTCCTGTTTCTGACCGGCAGCGGTGCGCTGCGTGACGACGAAACTAACACCCTGCAAGCGGGTATTGACCAAGTTGCGATGGCAGCGCCGATTACGAAGTGGGCACACCGCGTTATGGCCACCGAGCACATCCCGCGCCTGGTTATGCAGGCAATCCGTGCGGCGCTGAGCGCTCCGCGTGGCCCGGTTTTGTTGGACCTGCCGTGGGATATCCTGATGAACCAAATCGACGAGGACTCTGTCATTATCCCTGACCTGGTGCTGTCCGCACACGGTGCACGCCCGGACCCAGCTGATTTAGATCAGGCCTTGGCTCTGTTGCGCAAAGCAGAACGCCCGGTCATTGTCTTGGGCAGCGAAGCATCGCGCACCGCGCGTAAGACTGCCCTGAGCGCCTTCGTGGCGGCGACGGGTGTTCCGGTTTTCGCAGATTACGAGGGTCTGAGCATGCTGTCTGGTCTGCCTGACGCGATGCGTGGTGGNCTGTGCAGAACCTGTACAGCTTCGCAAAGGCAGATGCGGCGCCGGACCTGGTTCTGATGTTGGGTGCGCGCTTCGGCCTGAATACTGGTCACGGCAGCGGTCAGCTGATCCCGCATAGCGCACAGGTCATTCAGGTTGATCCNNATGCGTGTGAACTGGGNCNN

>SH3-FLS-pSB1A3-c3-VR\_F12.ab1  
NNNNNNNNNNNNNNNANGANNGAGCGCAGCGAGTCAGTGAGCGAGGAAGCCTGCATAACGCGAAGTAATCTTTTCGGTTTTAAAGAAAAAGGGCAGGGTGGTGACACCTTGCCCTTTTTTGCCGGACTGCAGCGGCCGCTACTAGTACTCGAGTCATTACTCCAGGGCGCCAGATTGAAAGTACAGATTTTCGGTGCTACCCGCGAACGGGTCCATACCGATCAGAATCAGTTCTTCAGGTGGAATCGGGTCCAGTGCAACTGCAACGTTGATACAGGCTGGACGGTTGTGGGCCAACGCTTGAGCCAGTGCGGCGGAGAAGCTCTCGACGCTGTCGACGTGGTAGCCATCTGCACCAAATGCCGCTGCAACACCATGATAAGAGCCATTTTCCAGGCGCGTACCCGTAACACGATTCGGACCAACGGCCAGTTGTTGGAAGTGCAGGGTCCAGCCCCAGCTCTGATTATTCATAATGATCACGATCAGCGGCAGCTGCTTGCGAACCAGGGTATCAAACTCGCCGATGCTGTAACCGACGCTACCATCACCGGTGACCAGGATCGTGCGACGACCCGCTTCCAGATCCGCAACTTGTGCACCCAGCGCGGTGCCGAAACCCACACCCATGCTGTTCAGGTAACCGTGGCACAGAAAGCCACCCGGCTTAACGCGAGACATGACTTCCGACAGCCACAGGTAGGTCAGACCACCGTCCGCCACCACGGTCACACCCGCGTCGACGTGTTTAGCGATGACTTGAGATGCGTGGAACGGATGCAACGCGTGTTCCGAGCTGCTCTTTGCCGCAATGCTGGCATAGCGCTCCTGGGCCAGATCAGTCACTTTTGCGCACCAATCACCACGATCTGGCCAGGCAGCATCTTGCGCGGTAGCCTGGGCCAGTGCTTCGATGGTACCACCCACGTCCGCGACGATGCCCAGAGCAATACCCTGCAAACGGCCCAGTTCACACGCATCCGGATCAACCTGAATGANCTGTGCGCTATGCGGGATCAGCTGACCGCTGCCGTGACCAGTATTCAGGCCGAAGCGCGCACCCAANATCNNAANCCAGGNCNN

🡪 they pretty much/essentially overlap (there are a few Ns in the region, but it is great.

-----------------------------VF2:

BLASTN 2.2.26+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and

Webb Miller (2000), "A greedy algorithm for aligning DNA

sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: S6ZC1B1X112

Query= SH3-FLS-pSB1A3-c3-VF2\_E12.ab1

Length=1086

Score E

Sequences producing significant alignments: (Bits) Value

lcl|58335 strain 27 1930 0.0

ALIGNMENTS

>lcl|58335 strain 27

Length=3940

Score = 1930 bits (1045), Expect = 0.0

Identities = 1053/1058 (99%), Gaps = 1/1058 (0%)

Strand=Plus/Plus

Query 26 aaTAGGCGTATCACGAGGCAGAATTTCAGATaaaaaaaaTCCTTAGCTTTCGCTAAGGAT 85

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 51 AATAGGCGTATCACGAGGCAGAATTTCAGATAAAAAAAATCCTTAGCTTTCGCTAAGGAT 110

Query 86 GATTTCTGGAATTCGCGGCCGCTTCTAGAGATGCCGCCGCCGGCGCTGCCGCCGAAAAGA 145

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 111 GATTTCTGGAATTCGCGGCCGCTTCTAGAGATGCCGCCGCCGGCGCTGCCGCCGAAAAGA 170

Query 146 AGGAGAGGTAGCGGCGCGATGATCACGGGCGGCGAGCTGGTAGTGCGCACCTTAATCAAG 205

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 171 AGGAGAGGTAGCGGCGCGATGATCACGGGCGGCGAGCTGGTAGTGCGCACCTTAATCAAG 230

Query 206 GCGGGTGTTGAGCACCTGTTTGGTCTGCACGGTATCCATATTGACACGATCTTCCAGGCT 265

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 231 GCGGGTGTTGAGCACCTGTTTGGTCTGCACGGTATCCATATTGACACGATCTTCCAGGCT 290

Query 266 TGTCTGGACCACGACGTGCCGATTATCGACACTCGTCACGAGGCGGCTGCCGGCCACGCT 325

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 291 TGTCTGGACCACGACGTGCCGATTATCGACACTCGTCACGAGGCGGCTGCCGGCCACGCT 350

Query 326 GCGGAGGGCTACGCTCGTGCCGGTGCGAAACTGGGTGTGGCTTTGGTCACCGCGGGTGGC 385

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 351 GCGGAGGGCTACGCTCGTGCCGGTGCGAAACTGGGTGTGGCTTTGGTCACCGCGGGTGGC 410

Query 386 GGCTTCACTAATGCGGTGACCCCTATTGCGAATGCGTGGCTGGACCGTACGCCGGTCCTG 445

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 411 GGCTTCACTAATGCGGTGACCCCTATTGCGAATGCGTGGCTGGACCGTACGCCGGTCCTG 470

Query 446 TTTCTGACCGGCAGCGGTGCGCTGCGTGACGACGAAACTAACACCCTGCAAGCGGGTATT 505

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 471 TTTCTGACCGGCAGCGGTGCGCTGCGTGACGACGAAACTAACACCCTGCAAGCGGGTATT 530

Query 506 GACCAAGTTGCGATGGCAGCGCCGATTACGAAGTGGGCACACCGCGTTATGGCCACCGAG 565

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 531 GACCAAGTTGCGATGGCAGCGCCGATTACGAAGTGGGCACACCGCGTTATGGCCACCGAG 590

Query 566 CACATCCCGCGCCTGGTTATGCAGGCAATCCGTGCGGCGCTGAGCGCTCCGCGTGGCCCG 625

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 591 CACATCCCGCGCCTGGTTATGCAGGCAATCCGTGCGGCGCTGAGCGCTCCGCGTGGCCCG 650

Query 626 GTTTTGTTGGACCTGCCGTGGGATATCCTGATGAACCAAATCGACGAGGACTCTGTCATT 685

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 651 GTTTTGTTGGACCTGCCGTGGGATATCCTGATGAACCAAATCGACGAGGACTCTGTCATT 710

Query 686 ATCCCTGACCTGGTGCTGTCCGCACACGGTGCACGCCCGGACCCAGCTGATTTAGATCAG 745

||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||

Sbjct 711 ATCCCTGACCTGGTGCTGTCCGCACACGGTGCACGCCCGGATCCAGCTGATTTAGATCAG 770

Query 746 GCCTTGGCTCTGTTGCGCAAAGCAGAACGCCCGGTCATTGTCTTGGGCAGCGAAGCATCG 805

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 771 GCCTTGGCTCTGTTGCGCAAAGCAGAACGCCCGGTCATTGTCTTGGGCAGCGAAGCATCG 830

Query 806 CGCACCGCGCGTAAGACTGCCCTGAGCGCCTTCGTGGCGGCGACGGGTGTTCCGGTTTTC 865

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 831 CGCACCGCGCGTAAGACTGCCCTGAGCGCCTTCGTGGCGGCGACGGGTGTTCCGGTTTTC 890

Query 866 GCAGATTACGAGGGTCTGAGCATGCTGTCTGGTCTGCCTGACGCGATGCGTGGTGGNCTG 925

|||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||

Sbjct 891 GCAGATTACGAGGGTCTGAGCATGCTGTCTGGTCTGCCTGACGCGATGCGTGGTGGCCTG 950

Query 926 -TGCAGAACCTGTACAGCTTCGCAAAGGCAGATGCGGCGCCGGACCTGGTTCTGATGTTG 984

|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 951 GTGCAGAACCTGTACAGCTTCGCAAAGGCAGATGCGGCGCCGGACCTGGTTCTGATGTTG 1010

Query 985 GGTGCGCGCTTCGGCCTGAATACTGGTCACGGCAGCGGTCAGCTGATCCCGCATAGCGCA 1044

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1011 GGTGCGCGCTTCGGCCTGAATACTGGTCACGGCAGCGGTCAGCTGATCCCGCATAGCGCA 1070

Query 1045 CAGGTCATTCAGGTTGATCCNNATGCGTGTGAACTGGG 1082

|||||||||||||||||||| ||||||||||||||||

Sbjct 1071 CAGGTCATTCAGGTTGATCCGGATGCGTGTGAACTGGG 1108

-----------------------------VR:

BLASTN 2.2.26+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and

Webb Miller (2000), "A greedy algorithm for aligning DNA

sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: S6ZK7HNR113

Query= SH3-FLS-pSB1A3-c3-VR\_F12.ab1

Length=1083

Score E

Sequences producing significant alignments: (Bits) Value

lcl|3301 strain 27 1927 0.0

ALIGNMENTS

>lcl|3301 strain 27

Length=3939

Score = 1927 bits (1043), Expect = 0.0

Identities = 1052/1058 (99%), Gaps = 1/1058 (0%)

Strand=Plus/Minus

Query 22 GAGCGCAGCGAGTCAGTGAGCGAGGAAGCCTGCATAACGCGAAGTAATCTTTTCGGTTTT 81

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 2050 GAGCGCAGCGAGTCAGTGAGCGAGGAAGCCTGCATAACGCGAAGTAATCTTTTCGGTTTT 1991

Query 82 AAAGAAAAAGGGCAGGGTGGTGACACCTTGCCCTTTTTTGCCGGACTGCAGCGGCCGCTA 141

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1990 AAAGAAAAAGGGCAGGGTGGTGACACCTTGCCCTTTTTTGCCGGACTGCAGCGGCCGCTA 1931

Query 142 CTAGTACTCGAGTCATTACTCCAGGGCGCCAGATTGAAAGTACAGATTTTCGGTGCTACC 201

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1930 CTAGTACTCGAGTCATTACTCCAGGGCGCCAGATTGAAAGTACAGATTTTCGGTGCTACC 1871

Query 202 CGCGAACGGGTCCATACCGATCAGAATCAGTTCTTCAGGTGGAATCGGGTCCAGTGCAAC 261

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1870 CGCGAACGGGTCCATACCGATCAGAATCAGTTCTTCAGGTGGAATCGGGTCCAGTGCAAC 1811

Query 262 TGCAACGTTGATACAGGCTGGACGGTTGTGGGCCAACGCTTGAGCCAGTGCGGCGGAGAA 321

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1810 TGCAACGTTGATACAGGCTGGACGGTTGTGGGCCAACGCTTGAGCCAGTGCGGCGGAGAA 1751

Query 322 GCTCTCGACGCTGTCGACGTGGTAGCCATCTGCACCAAATGCCGCTGCAACACCATGATA 381

||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||

Sbjct 1750 GCTCTCGACGCTGTCGACGTGGTAGCCATCTGCACCAAACGCCGCTGCAACACCATGATA 1691

Query 382 AGAGCCATTTTCCAGGCGCGTACCCGTAACACGATTCGGACCAACGGCCAGTTGTTGGAA 441

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1690 AGAGCCATTTTCCAGGCGCGTACCCGTAACACGATTCGGACCAACGGCCAGTTGTTGGAA 1631

Query 442 GTGCAGGGTCCAGCCCCAGCTCTGATTATTCATAATGATCACGATCAGCGGCAGCTGCTT 501

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1630 GTGCAGGGTCCAGCCCCAGCTCTGATTATTCATAATGATCACGATCAGCGGCAGCTGCTT 1571

Query 502 GCGAACCAGGGTATCAAACTCGCCGATGCTGTAACCGACGCTACCATCACCGGTGACCAG 561

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1570 GCGAACCAGGGTATCAAACTCGCCGATGCTGTAACCGACGCTACCATCACCGGTGACCAG 1511

Query 562 GATCGTGCGACGACCCGCTTCCAGATCCGCAACTTGTGCACCCAGCGCGGTGCCGAAACC 621

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1510 GATCGTGCGACGACCCGCTTCCAGATCCGCAACTTGTGCACCCAGCGCGGTGCCGAAACC 1451

Query 622 CACACCCATGCTGTTCAGGTAACCGTGGCACAGAAAGCCACCCGGCTTAACGCGAGACAT 681

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1450 CACACCCATGCTGTTCAGGTAACCGTGGCACAGAAAGCCACCCGGCTTAACGCGAGACAT 1391

Query 682 GACTTCCGACAGCCACAGGTAGGTCAGACCACCGTCCGCCACCACGGTCACACCCGCGTC 741

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1390 GACTTCCGACAGCCACAGGTAGGTCAGACCACCGTCCGCCACCACGGTCACACCCGCGTC 1331

Query 742 GACGTGTTTAGCGATGACTTGAGATGCGTGGAACGGATGCAACGCGTGTTCCGAGCTGCT 801

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1330 GACGTGTTTAGCGATGACTTGAGATGCGTGGAACGGATGCAACGCGTGTTCCGAGCTGCT 1271

Query 802 CTTTGCCGCAATGCTGGCATAGCGCTCCTGGGCCAGATCAGTCACTTTTGCGCACCAATC 861

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1270 CTTTGCCGCAATGCTGGCATAGCGCTCCTGGGCCAGATCAGTCACTTTTGCGCACCAATC 1211

Query 862 ACCACGATCTGGCCAGGCAGCATCTTGCGCGGTAGCCTGGGCCAGTGCTTCGATGGTACC 921

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1210 ACCACGATCTGGCCAGGCAGCATCTTGCGCGGTAGCCTGGGCCAGTGCTTCGATGGTACC 1151

Query 922 ACCCACGTCCGCGACGATGCCCAGAGCAATACCCTGCAAACGGCCCAGTTCACACGCATC 981

||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Sbjct 1150 ACCCACGTCCGCGACGATGCCCAGAGCAATACCCTGCAAACGGCCCAGTTCACACGCATC 1091

Query 982 CGGATCAACCTGAATGANCTGTGCGCTATGCGGGATCAGCTGACCGCTGCCGTGACCAGT 1041

||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||

Sbjct 1090 CGGATCAACCTGAATGACCTGTGCGCTATGCGGGATCAGCTGACCGCTGCCGTGACCAGT 1031

Query 1042 ATTCAGGCCGAAGCGCGCACCCAANATCNNAANCCAGG 1079

|||||||||||||||||||||||| ||| || |||||

Sbjct 1030 ATTCAGGCCGAAGCGCGCACCCAACATCAGAA-CCAGG 994