Supplementary file 1: List of DARPin sequences.

Clone		DNA Sequence	AA Sequence	DARPin ID	DARPin type
27	G2	ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGC TGCTCGTGCTGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTATGG ACTTCACTGGTTACACTCCGCTGCACCTGGCTGCTAAAGAAGGTCACCTGGAAATCGTTGAAGTTCTGC TGAAAACCGGTGCTGACGTTAACGCTATCGACAAACGTGGTAACACTCCGCTGCACCTGGCTGCTTGG CGTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGCGCCGACGTTAACGCTCAGGACGTTTA CGGTACTACTCCGTTCGACCTGGCTGCTTGGGCTGGTAACGAGGACATCGCTGAAGTTCTGCAGAAAG CTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG	MRGSHHHHHHHHGSDLGKKLLEAAR AGQDDEVRILMANGADVNAMDFTGY TPLHLAAKEGHLEIVEVLLKTGADVNAI DKRGNTPLHLAAWRGHLEIVEVLLKHG ADVNAQDVYGTTPFDLAAWAGNEDI AEVLQKAAKLNDYKDDDDK	008-855-2308-A9	N2C
27	H2	ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGC TGCTCGTGCCGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTTGG GACAAACATGGTCATACTCCGCTGCACCTGGCTGCTGCTTGGGGTCACCTGGAAATCGTTGAAGTTCT GTTGAAAACCGGTGCTGACGTTAACGCTCAGGACCAGATGGGTTACACTCCGCTGCACCTGGCTGCTT GGTACGGTCATCTGGAAATCGTTGAAGTTCTGCTGAAGCATGGCGCCGACGTTAACGCTCAGGACAAA TTCGGTAAGACTCCGTTCGACCTGGCTGCTATGGCTGGTAACGAGGACATCGCTGAAGTTCTGCAGAA AGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG	MRGSHHHHHHHHGSDLGKKLLEAAR AGQDDEVRILMANGADVNAWDKHG HTPLHLAAAWGHLEIVEVLLKTGADVN AQDQMGYTPLHLAAWYGHLEIVEVLL KHGADVNAQDKFGKTPFDLAAMAGN EDIAEVLQKAAKLNDYKDDDDK	008-855-2308-B9	N2C
27	B3	ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGC TGCTATCCATGGTCAGCTGGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTACTG ACCTGCAGGGTCATACTCCGCTGCACCTGGCTGCTAAATGGGGTCACCTGGAAATCGTTGAAGTTCTG CTGAAAACCGGTGCTGACGTTAACGCTGAAGACGTTCGTGGTTACACTCCGCTGCACCTGGCTGCTCT GTGGGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGCGCCGACGTTAACGCTCAGGACCGTT GGGGTGAAACTCCGTTCGACCTGGCTGCTTGGTTCGGTAACGAGGACATCGCTGAAGTTCTGCAGAAA GCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG	MRGSHHHHHHHHGSDLGKKLLEAAIH GQLDEVRILMANGADVNATDLQGHT PLHLAAKWGHLEIVEVLLKTGADVNAE DVRGYTPLHLAALWGHLEIVEVLLKHG ADVNAQDRWGETPFDLAAWFGNEDI AEVLQKAAKLNDYKDDDDK	008-855-2308-C11	N2C
27	D3	ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGC TGCTCGTGCTGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTGTTG ACACTTTCGGTTGGACTCCGCTGCACCTGGCTGCTGCTAACGGTCACCTGGAAATCGTTGAAGTTCTGC TGAAAACCGGTGCTGACGTTAACGCTAACGACCAGCGTGGTAACACTCCGCTGCACCTGGCTGCTTGG GACGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGCGCCGACGTTAACGCTCAGGACAACTT CGGTATCACTCCGTTCGACCTGGCTGCTTACCGTGGTAACGAGGACATCGCTGAAGTTCTGCAGAAAG CTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG	MRGSHHHHHHHHGSDLGKKLLEAAR AGQDDEVRILMANGADVNAVDTFGW TPLHLAAANGHLEIVEVLLKTGADVNA NDQRGNTPLHLAAWDGHLEIVEVLLK HGADVNAQDNFGITPFDLAAYRGNED IAEVLQKAAKLNDYKDDDDK	008-855-2309-A6	N2C
27	F3	ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGC TGCTCGTGCTGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTTCTG ACGTTGTTGGTCAGACTCCGCTGCACCTGGCTGCTTGGTCTGGTCACCTGGAAATCGTTGAAGTTCTGC TGAAAACCGGTGCTGACGTTAACGCTGAAGACATGGTTGGTAACACTCCGCTGCACCTGGCTGCTTAC GTTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGGCCGGCGCTGACGTTAACGCTGACGACTTCCG TGGTCGTACTCCGCTGCACCTGGCTGCTTACTACGGTCACCTGGAAATTGTTGAAGTTCTGCTGAAGCA CGGCGCCGACGTTAACGCTCAGGACAAATTCGGTAAGACTCCGTTCGACCTGGCTATCGACAACGGTA ACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAA G	MRGSHHHHHHHHGSDLGKKLLEAAR AGQDDEVRILMANGADVNASDVVGQ TPLHLAAWSGHLEIVEVLLKTGADVNA EDMVGNTPLHLAAYVGHLEIVEVLLKA GADVNADDFRGRTPLHLAAYYGHLEIV EVLLKHGADVNAQDKFGKTPFDLAIDN GNEDIAEVLQKAAKLNDYKDDDDK	008-855-2309-D7	N3C
27	G4	ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGC TGCTCGTGCTGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTGAAG ACGCTAAAGGTCATACTCCGCTACACCTGGCTGCTTACCTGGGTCACCTGGAAATCGTTGAAGTTCTGC TGAAAACCGGTGCTGACGTTAACGCTTACGACAAACATGGTCATACTCCGCTGCACCTGGCTGCTTCTT GGGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGGCCGGCGCTGACGTTAACGCTTCTGACCATACT GGTCGTACTCCGCTGCACCTGGCTGCTTGGTACGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGGC CGGCGCTGACGTTAACGCTCAGGACAAATTCGGTAAGACTCCGTTCGACCTGGCTATCGACAACGGTA ACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAA G	MRGSHHHHHHHHGSDLGKKLLEAAR AGQDDEVRILMANGADVNAEDAKGH TPLHLAAYLGHLEIVEVLLKTGADVNAY DKHGHTPLHLAASWGHLEIVEVLLKAG ADVNASDHTGRTPLHLAAWYGHLEIV EVLLKAGADVNAQDKFGKTPFDLAIDN GNEDIAEVLQKAAKLNDYKDDDDK	008-855-2310-G12	N3C
27	B5	ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGC TGCTTTCATGGGTCAGCACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTCAGG ACAAAGCTGGTCATACTCCGCTGCACCTGGCTGCTCAGATGGGTCACCTGGAAATCGTTGAAGTTCTG CTGAAAACCGGTGCTGACGTTAACGCTTCTGACTGGTACGGTATCACTCCGCTGCACCTGGCTGCTTG GAACGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGCGCCGACGTTAACGCTCAGGACTGG GACGGTAACACTCCGTTCGACCTGGCTGCTATGGTTGGTAACGAGGACATCGCTGAAGTTCTGCAGAA AGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG	MRGSHHHHHHHHGSDLGKKLLEAAF MGQHDEVRILMANGADVNAQDKAG HTPLHLAAQMGHLEIVEVLLKTGADVN ASDWYGITPLHLAAWNGHLEIVEVLLK HGADVNAQDWDGNTPFDLAAMVGN EDIAEVLQKAAKLNDYKDDDDK	008-855-2311-B9	N2C
27	D5	ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAACCTGCTGGAAGC TGCTGTTCAGGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTGAA GACTTCCATGGTCTGACTCCGCTGCACCTGGCTGCTTGGCATGGTCACCTGGAAATCGTTGAAGTTCTG CTGAAAACCGGTGCTGACGTTAACGCTCATGACATGATCGGTTGGACTCCGCTGCACCTGGCTGCTCG TGTTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGGCCGGCGCTGACGTTAACGCTTGGGACACTC GTGGTCGTACTCCGCTGCACCTGGCTGCTTGGGCTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAG CACGGCGCCGACGTTAACGCTCAGGACAAATTCGGTAAGACTCCGTTCGACCTGGCTATCGACAACGG TAACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGAC AAG	MRGSHHHHHHHHGSDLGKNLLEAAV QGQDDEVRILMANGADVNAEDFHGL TPLHLAAWHGHLEIVEVLLKTGADVNA HDMIGWTPLHLAARVGHLEIVEVLLKA GADVNAWDTRGRTPLHLAAWAGHLE IVEVLLKHGADVNAQDKFGKTPFDLAI DNGNEDIAEVLQKAAKLNDYKDDDDK	008-855-2311-D10	N3C
	E3_5	ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGC TGCTCGTGCTGGTCAGGACGACGAAGTTCGTATCCTGATGGCTAACGGTGCTGACGTTAACGCTACTG ACAATGATGGTTATACTCCGCTGCACCTGGCTGCTTCTAATGGTCACCTGGAAATCGTTGAAGTTCTGC TGAAGAACGGTGCTGACGTTAACGCTTCTGACCTTACTGGTATTACTCCGCTGCACCTGGCTGCTGCTA CTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGTGCTGACGTTAACGCTTATGACAATGAT GGTCATACTCCGCTGCACCTGGCTGCTAAGTATGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCA CGGTGCTGACGTTAACGCTCAGGACAAATTCGGTAAGACCGCTTTCGACATCTCCATCGACAACGGTA ACGAGGACCTGGCTGAAATCCTGCAAAAGCTTAATGACTACAAGGATGACGACGACAAG	MRGSHHHHHHHHGSDLGKKLLEAAR AGQDDEVRILMANGADVNATDNDGY TPLHLAASNGHLEIVEVLLKNGADVNA SDLTGITPLHLAAATGHLEIVEVLLKHG ADVNAYDNDGHTPLHLAAKYGHLEIVE VLLKHGADVNAQDKFGKTAFDISIDNG NEDLAEILQKLNDYKDDDDK	E3_5	N3C