**Supplementary file 1: List of DARPin sequences.**

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| --- | --- | --- | --- | --- |
| Clone | DNA Sequence | AA Sequence | DARPin ID | DARPin type |
| 27 | G2 | ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGCTGCTCGTGCTGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTATGGACTTCACTGGTTACACTCCGCTGCACCTGGCTGCTAAAGAAGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAAACCGGTGCTGACGTTAACGCTATCGACAAACGTGGTAACACTCCGCTGCACCTGGCTGCTTGGCGTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGCGCCGACGTTAACGCTCAGGACGTTTACGGTACTACTCCGTTCGACCTGGCTGCTTGGGCTGGTAACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG | MRGSHHHHHHHHGSDLGKKLLEAARAGQDDEVRILMANGADVNAMDFTGYTPLHLAAKEGHLEIVEVLLKTGADVNAIDKRGNTPLHLAAWRGHLEIVEVLLKHGADVNAQDVYGTTPFDLAAWAGNEDIAEVLQKAAKLNDYKDDDDK | 008-855-2308-A9 | N2C |
| 27 | H2 | ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGCTGCTCGTGCCGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTTGGGACAAACATGGTCATACTCCGCTGCACCTGGCTGCTGCTTGGGGTCACCTGGAAATCGTTGAAGTTCTGTTGAAAACCGGTGCTGACGTTAACGCTCAGGACCAGATGGGTTACACTCCGCTGCACCTGGCTGCTTGGTACGGTCATCTGGAAATCGTTGAAGTTCTGCTGAAGCATGGCGCCGACGTTAACGCTCAGGACAAATTCGGTAAGACTCCGTTCGACCTGGCTGCTATGGCTGGTAACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG | MRGSHHHHHHHHGSDLGKKLLEAARAGQDDEVRILMANGADVNAWDKHGHTPLHLAAAWGHLEIVEVLLKTGADVNAQDQMGYTPLHLAAWYGHLEIVEVLLKHGADVNAQDKFGKTPFDLAAMAGNEDIAEVLQKAAKLNDYKDDDDK | 008-855-2308-B9 | N2C |
| 27 | B3 | ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGCTGCTATCCATGGTCAGCTGGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTACTGACCTGCAGGGTCATACTCCGCTGCACCTGGCTGCTAAATGGGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAAACCGGTGCTGACGTTAACGCTGAAGACGTTCGTGGTTACACTCCGCTGCACCTGGCTGCTCTGTGGGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGCGCCGACGTTAACGCTCAGGACCGTTGGGGTGAAACTCCGTTCGACCTGGCTGCTTGGTTCGGTAACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG | MRGSHHHHHHHHGSDLGKKLLEAAIHGQLDEVRILMANGADVNATDLQGHTPLHLAAKWGHLEIVEVLLKTGADVNAEDVRGYTPLHLAALWGHLEIVEVLLKHGADVNAQDRWGETPFDLAAWFGNEDIAEVLQKAAKLNDYKDDDDK | 008-855-2308-C11 | N2C |
| 27 | D3 | ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGCTGCTCGTGCTGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTGTTGACACTTTCGGTTGGACTCCGCTGCACCTGGCTGCTGCTAACGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAAACCGGTGCTGACGTTAACGCTAACGACCAGCGTGGTAACACTCCGCTGCACCTGGCTGCTTGGGACGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGCGCCGACGTTAACGCTCAGGACAACTTCGGTATCACTCCGTTCGACCTGGCTGCTTACCGTGGTAACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG | MRGSHHHHHHHHGSDLGKKLLEAARAGQDDEVRILMANGADVNAVDTFGWTPLHLAAANGHLEIVEVLLKTGADVNANDQRGNTPLHLAAWDGHLEIVEVLLKHGADVNAQDNFGITPFDLAAYRGNEDIAEVLQKAAKLNDYKDDDDK | 008-855-2309-A6 | N2C |
| 27 | F3 | ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGCTGCTCGTGCTGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTTCTGACGTTGTTGGTCAGACTCCGCTGCACCTGGCTGCTTGGTCTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAAACCGGTGCTGACGTTAACGCTGAAGACATGGTTGGTAACACTCCGCTGCACCTGGCTGCTTACGTTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGGCCGGCGCTGACGTTAACGCTGACGACTTCCGTGGTCGTACTCCGCTGCACCTGGCTGCTTACTACGGTCACCTGGAAATTGTTGAAGTTCTGCTGAAGCACGGCGCCGACGTTAACGCTCAGGACAAATTCGGTAAGACTCCGTTCGACCTGGCTATCGACAACGGTAACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG | MRGSHHHHHHHHGSDLGKKLLEAARAGQDDEVRILMANGADVNASDVVGQTPLHLAAWSGHLEIVEVLLKTGADVNAEDMVGNTPLHLAAYVGHLEIVEVLLKAGADVNADDFRGRTPLHLAAYYGHLEIVEVLLKHGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLNDYKDDDDK | 008-855-2309-D7 | N3C |
| 27 | G4 | ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGCTGCTCGTGCTGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTGAAGACGCTAAAGGTCATACTCCGCTACACCTGGCTGCTTACCTGGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAAACCGGTGCTGACGTTAACGCTTACGACAAACATGGTCATACTCCGCTGCACCTGGCTGCTTCTTGGGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGGCCGGCGCTGACGTTAACGCTTCTGACCATACTGGTCGTACTCCGCTGCACCTGGCTGCTTGGTACGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGGCCGGCGCTGACGTTAACGCTCAGGACAAATTCGGTAAGACTCCGTTCGACCTGGCTATCGACAACGGTAACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG | MRGSHHHHHHHHGSDLGKKLLEAARAGQDDEVRILMANGADVNAEDAKGHTPLHLAAYLGHLEIVEVLLKTGADVNAYDKHGHTPLHLAASWGHLEIVEVLLKAGADVNASDHTGRTPLHLAAWYGHLEIVEVLLKAGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLNDYKDDDDK | 008-855-2310-G12 | N3C |
| 27 | B5 | ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGCTGCTTTCATGGGTCAGCACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTCAGGACAAAGCTGGTCATACTCCGCTGCACCTGGCTGCTCAGATGGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAAACCGGTGCTGACGTTAACGCTTCTGACTGGTACGGTATCACTCCGCTGCACCTGGCTGCTTGGAACGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGCGCCGACGTTAACGCTCAGGACTGGGACGGTAACACTCCGTTCGACCTGGCTGCTATGGTTGGTAACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG | MRGSHHHHHHHHGSDLGKKLLEAAFMGQHDEVRILMANGADVNAQDKAGHTPLHLAAQMGHLEIVEVLLKTGADVNASDWYGITPLHLAAWNGHLEIVEVLLKHGADVNAQDWDGNTPFDLAAMVGNEDIAEVLQKAAKLNDYKDDDDK | 008-855-2311-B9 | N2C |
| 27 | D5 | ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAACCTGCTGGAAGCTGCTGTTCAGGGTCAGGACGACGAAGTTCGTATCCTGATGGCAAACGGTGCTGACGTTAACGCTGAAGACTTCCATGGTCTGACTCCGCTGCACCTGGCTGCTTGGCATGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAAACCGGTGCTGACGTTAACGCTCATGACATGATCGGTTGGACTCCGCTGCACCTGGCTGCTCGTGTTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGGCCGGCGCTGACGTTAACGCTTGGGACACTCGTGGTCGTACTCCGCTGCACCTGGCTGCTTGGGCTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGCGCCGACGTTAACGCTCAGGACAAATTCGGTAAGACTCCGTTCGACCTGGCTATCGACAACGGTAACGAGGACATCGCTGAAGTTCTGCAGAAAGCTGCTAAGCTTAATGACTACAAGGATGACGACGACAAG | MRGSHHHHHHHHGSDLGKNLLEAAVQGQDDEVRILMANGADVNAEDFHGLTPLHLAAWHGHLEIVEVLLKTGADVNAHDMIGWTPLHLAARVGHLEIVEVLLKAGADVNAWDTRGRTPLHLAAWAGHLEIVEVLLKHGADVNAQDKFGKTPFDLAIDNGNEDIAEVLQKAAKLNDYKDDDDK | 008-855-2311-D10 | N3C |
|  | E3\_5 | ATGAGAGGATCGCATCACCATCACCATCACCATCACGGATCCGACCTGGGTAAGAAACTGCTGGAAGCTGCTCGTGCTGGTCAGGACGACGAAGTTCGTATCCTGATGGCTAACGGTGCTGACGTTAACGCTACTGACAATGATGGTTATACTCCGCTGCACCTGGCTGCTTCTAATGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGAACGGTGCTGACGTTAACGCTTCTGACCTTACTGGTATTACTCCGCTGCACCTGGCTGCTGCTACTGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGTGCTGACGTTAACGCTTATGACAATGATGGTCATACTCCGCTGCACCTGGCTGCTAAGTATGGTCACCTGGAAATCGTTGAAGTTCTGCTGAAGCACGGTGCTGACGTTAACGCTCAGGACAAATTCGGTAAGACCGCTTTCGACATCTCCATCGACAACGGTAACGAGGACCTGGCTGAAATCCTGCAAAAGCTTAATGACTACAAGGATGACGACGACAAG | MRGSHHHHHHHHGSDLGKKLLEAARAGQDDEVRILMANGADVNATDNDGYTPLHLAASNGHLEIVEVLLKNGADVNASDLTGITPLHLAAATGHLEIVEVLLKHGADVNAYDNDGHTPLHLAAKYGHLEIVEVLLKHGADVNAQDKFGKTAFDISIDNGNEDLAEILQKLNDYKDDDDK | E3\_5 | N3C |