

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|-----------------|-----------|----|---------------------------|----------------------------|----------------------------|---------------------------|
| 1 | 1230 | 42 | 0.919 | GAAUCGUUGUAGGU | 14 | 57 | -2.2 | 0 | -20.9 | CGCGAGAAUCGUUGUAGGUUCGCG |
| 2 | 1231 | 42 | 0.869 | AGAAUCGUUGUAGG | 14 | 57 | -2.2 | 0 | -20.8 | GCACGAGAAUCGUUGUAGGCGUGC |
| 3 | 1229 | 35 | 0.859 | AAUCGUUGUAGGUU | 14 | 55 | -1.8 | -0.2 | -18.9 | CCGAAUCGUUGUAGGUUCGG |
| 4 | 84 | 35 | 0.834 | UAAUAGGUUUUGGC | 14 | 55 | 0 | 0 | -19.1 | CGACGUAAUAGGUUUUGGCCGUGC |
| 5 | 83 | 42 | 0.825 | AAUAGGUUUUGGCG | 14 | 58 | -2.7 | 0 | -20.2 | CGACGAAUAGGUUUUGGCCGCGUGC |
| 6 | 76 | 42 | 0.823 | UUUGGCGGAAGUUAU | 14 | 60 | -7.1 | 0 | -21.2 | CGACGUUUGGCCGGAAGUAUCGUGC |
| 7 | 75 | 42 | 0.820 | UUGGCGGAAGUAAU | 14 | 60 | -5.3 | 0 | -21.2 | CGAGCUUGGCCGGAAGUAUUGCUCG |
| 8 | 82 | 50 | 0.818 | AUAGGUUUUGGCGG | 14 | 63 | -2.7 | 0 | -22.6 | CGACGAUAGGUUUUGGCCGCGUGC |
| 9 | 1232 | 42 | 0.816 | GAGAAUCGUUGUAG | 14 | 54 | -2.7 | 0 | -20.4 | GCACGAGAAUCGUUGUAGCGUGC |
| 10 | 1233 | 35 | 0.813 | AGAGAAUCGUUGUA | 14 | 54 | -2.7 | 0 | -19.4 | GCACGAGAGAAUCGUUGUACGUGC |
| 11 | 81 | 50 | 0.809 | UAGGUUUUGGCGGA | 14 | 64 | -4.1 | 0 | -23.4 | CCGGUAGGUUUUGGCCGACCGG |
| 12 | 1234 | 42 | 0.809 | CAGAGAAUCGUUGU | 14 | 56 | -5.8 | 0 | -20.7 | GCACGCAGAGAAUCGUUGUCGUGC |
| 13 | 80 | 50 | 0.802 | AGGUUUUGGCCGAA | 14 | 64 | -5.9 | 0 | -23 | CGACGAGGUUUUGGCCGGAACGUGC |
| 14 | 1228 | 42 | 0.795 | AUCGUUGUAGGUUC | 14 | 57 | -0.2 | 0 | -20.9 | GCACGAUCGUUGUAGGUUCCGUGC |
| 15 | 74 | 50 | 0.795 | UGGCGGAAGUAUUG | 14 | 62 | -2.7 | 0 | -22.9 | CGCGAUGGCCGGAAGUAUUGUCGCG |
| 16 | 1227 | 50 | 0.790 | UCGUUGUAGGUUCC | 14 | 62 | -3.4 | 0 | -23.1 | GCACGUCGUUGUAGGUUCCCGUGC |
| 17 | 1226 | 50 | 0.788 | CGUUGUAGGUUCCA | 14 | 61 | -6.4 | 0 | -22.8 | GCACGCGUUGUAGGUUCCACGUGC |
| 18 | 2585 | 42 | 0.781 | ACGGAAACAGAAAG | 14 | 56 | -1.5 | 0 | -20.2 | CGAGCACGGAAACAGAAAGGCUCG |
| 19 | 854 | 50 | 0.774 | UUAUCUUGGGCACG | 14 | 62 | -2.7 | 0 | -22.9 | CGCGAUUAUCUUGGGCACGUCGCG |
| 20 | 855 | 50 | 0.774 | GUUAUCUUGGGCAC | 14 | 61 | -2.8 | 0 | -23.2 | CCGGUUAUCUUGGGCACCGG |
| 21 | 2812 | 35 | 0.767 | AGCUUGUUAUAGGA | 14 | 57 | -7 | 0 | -20.1 | GCACGAGCUUGUUAUAGGACGUGC |
| 22 | 2233 | 42 | 0.765 | UUUUGGGAAAAGCG | 14 | 57 | -2.7 | 0 | -19.8 | CGCGAUUUUGGGAAAAGCGUCGCG |
| 23 | 2813 | 42 | 0.765 | CAGCUUGUUAUAGG | 14 | 56 | -4.8 | 0 | -20.8 | CGAGCAGCUUGUUAUAGGCUCG |
| 24 | 2811 | 42 | 0.765 | GCUUGUUAUAGGAC | 14 | 57 | -7 | 0 | -21.2 | CGAGGCUUGUUAUAGGACCUCG |
| 25 | 2816 | 35 | 0.760 | UUGCAGCUUGUUAU | 14 | 56 | -5.9 | 0 | -19.5 | GCACGUUGCAGCUUGUUAUCGUGC |
| 26 | 2826 | 35 | 0.758 | GGAUUUUACAUUGC | 14 | 52 | -1.1 | 0 | -18.5 | CGAGGGAUUUUACAUUGCCUCG |
| 27 | 2814 | 42 | 0.758 | GCAGCUUGUUAUAG | 14 | 57 | -5.1 | 0 | -20.9 | GCACGGCAGCUUGUUAUAGCGUGC |
| 28 | 2815 | 35 | 0.758 | UGCAGCUUGUUAUA | 14 | 57 | -5.9 | 0 | -19.9 | GCCGUGCAGCUUGUUAUACGGC |
| 29 | 2586 | 35 | 0.756 | AACGGAAACAGAAA | 14 | 54 | -1.5 | 0 | -18.5 | CGAGCAACGGAAACAGAAAGCUCG |
| 30 | 2823 | 35 | 0.753 | UUUACAUUGCAGC | 14 | 54 | -4.9 | 0 | -18.8 | GCACGUUUUACAUUGCAGCCGUGC |
| 31 | 2822 | 35 | 0.751 | UUUACAUUGCAGCU | 14 | 56 | -4.9 | 0 | -19.5 | GCACGUUUACAUUGCAGCUCGUGC |
| 32 | 2584 | 42 | 0.749 | CGGAAACAGAAAGA | 14 | 56 | -0.9 | 0 | -20.4 | CGAGCCGGAAACAGAAAGAGCUCG |
| 33 | 1235 | 50 | 0.747 | GCAGAGAAUCGUUG | 14 | 59 | -5 | 0 | -22.4 | GCACGGCAGAGAAUCGUUGCGUGC |
| 34 | 399 | 42 | 0.747 | UUGCUGUUGUAGGU | 14 | 61 | -3.6 | -0.9 | -21.8 | GCACGUUGCUGUUGUAGGUCGUGC |
| 35 | 2232 | 50 | 0.744 | UUUGGGAAAAGCGG | 14 | 62 | -2.7 | 0 | -22.2 | CGCGAUUUUGGGAAAAGCGGUCGCG |
| 36 | 72 | 50 | 0.740 | GCGGAAGUAUUGGU | 14 | 63 | -2.7 | 0 | -23 | CGCGAGCGGAAGUAUUGGUUCGCG |
| 37 | 856 | 50 | 0.740 | CGUUAUCUUGGGCA | 14 | 62 | -2.8 | 0 | -22.9 | CGACGCGUUAUCUUGGGCACGUGC |
| 38 | 1638 | 35 | 0.737 | CGGAUAAACUUGUU | 14 | 52 | -2.4 | 0 | -18.1 | GCACGCGGAUAAACUUGUUCGUGC |
| 39 | 2215 | 35 | 0.735 | AGUUUGAAGAGAAG | 14 | 52 | -0.6 | 0 | -18.9 | CGACGAGUUUGAAGAGAAGCGUGC |
| 40 | 2225 | 35 | 0.735 | AAAGCGGAAAAGUU | 14 | 55 | -2.7 | 0 | -18.2 | CCGAAAGCGGAAAAGUUCGG |
| 41 | 2587 | 35 | 0.733 | AAACGGAAACAGAA | 14 | 54 | -1.5 | 0 | -18.5 | CGAGCAAACGGAAACAGAAGCUCG |
| 42 | 2228 | 42 | 0.733 | GGAAAAGCGGAAAA | 14 | 58 | -2.7 | 0 | -20.1 | CGAGCGGAAAAGCGGAAAAGCUCG |
| 43 | 2227 | 42 | 0.733 | GAAAAGCGGAAAAG | 14 | 55 | -2.7 | 0 | -19.4 | CGAGCGAAAAGCGGAAAAGGCUCG |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|-----------------|-----------|----|---------------------------|----------------------------|----------------------------|-----------------------------|
| 44 | 2226 | 35 | 0.733 | AAAAGCGGAAAAGU | 14 | 55 | -2.7 | 0 | -18.2 | CGCCAAAAGCGGAAAAGUGGCG |
| 45 | 2224 | 35 | 0.733 | AAGCGGAAAAGUUU | 14 | 55 | -2.7 | -0.4 | -18.2 | CCGAAGCGGAAAAGUUUCGG |
| 46 | 401 | 42 | 0.733 | UGUUGCUGUUGUAG | 14 | 58 | -2.8 | -0.5 | -21.1 | GCACGUGUUGCUGUUGUAGCGUGC |
| 47 | 400 | 50 | 0.733 | GUUGCUGUUGUAGG | 14 | 61 | -3.6 | -0.9 | -22.8 | GCACGGUUGCUGUUGUAGGCGUGC |
| 48 | 2231 | 50 | 0.726 | UUGGAAAAGCGGA | 14 | 64 | -2.7 | 0 | -23.2 | CCGGUUGGAAAAGCGGACCGG |
| 49 | 2229 | 50 | 0.726 | GGGAAAAGCGGAAA | 14 | 62 | -2.7 | 0 | -22.5 | CGAGCGGAAAAGCGGAAAGCUCG |
| 50 | 1225 | 50 | 0.724 | GUUGUAGGUUCCAC | 14 | 61 | -6.4 | 0 | -23.1 | CCGGUUGUAGGUUCCACCGG |
| 1 | 1230 | 40 | 0.871 | AGAAUCGUUGUAGGU | 15 | 60 | -2.2 | 0 | -22.5 | CGCCAGAAUCGUUGUAGGUGGCG |
| 2 | 1229 | 40 | 0.867 | GAAUCGUUGUAGGUU | 15 | 58 | -2.6 | -0.6 | -21.8 | CGCGAGAAUCGUUGUAGGUUUCGCG |
| 3 | 85 | 33 | 0.843 | GAUAAUAGGUUUUGG | 15 | 53 | 0 | 0 | -19.7 | CGACGGAUAAUAGGUUUUGGCGUCG |
| 4 | 84 | 33 | 0.830 | AUAAUAGGUUUUGGC | 15 | 56 | 0 | 0 | -20.2 | CGACGAUAAUAGGUUUUGGCCGUCG |
| 5 | 75 | 40 | 0.828 | UUUGCGGAAGUAUU | 15 | 61 | -7.1 | 0 | -22.1 | CGACGUUUGCGGAAGUAUUCGUCG |
| 6 | 1231 | 46 | 0.824 | GAGAAUCGUUGUAGG | 15 | 59 | -2.7 | 0 | -23.7 | GCACGGAGAAUCGUUGUAGGCGUGC |
| 7 | 83 | 40 | 0.822 | UAAUAGGUUUUGGCG | 15 | 59 | -2.7 | 0 | -21.5 | CGCGAUAAUAGGUUUUGGCGUCGCG |
| 8 | 82 | 46 | 0.819 | AAUAGGUUUUGGCGG | 15 | 63 | -2.7 | 0 | -23.5 | CGACGAUAGGUUUUGGCGGCGUCG |
| 9 | 1232 | 40 | 0.817 | AGAGAAUCGUUGUAG | 15 | 57 | -2.7 | 0 | -22 | GCACGAGAGAAUCGUUGUAGCGUGC |
| 10 | 1233 | 40 | 0.815 | CAGAGAAUCGUUGUA | 15 | 57 | -5.8 | 0 | -22 | GCACGCAGAGAAUCGUUGUACGUGC |
| 11 | 81 | 46 | 0.813 | AUAGGUUUUGGCGGA | 15 | 65 | -4.1 | 0 | -24.5 | CGACGAUAGGUUUUGGCGGACGUCG |
| 12 | 80 | 46 | 0.806 | UAGGUUUUGGCGGAA | 15 | 65 | -5.9 | 0 | -24.3 | CCGGUAGGUUUUGGCGGAACCGG |
| 13 | 74 | 46 | 0.804 | UUGGCGGAAGUAUUG | 15 | 62 | -5.3 | 0 | -23.8 | CGCGAUUGGCGGAAGUAUUGUCGCG |
| 14 | 1228 | 40 | 0.802 | AAUCGUUGUAGGUUC | 15 | 58 | -2 | -0.3 | -21.8 | GCACGAUCGUUGUAGGUUCCGUGC |
| 15 | 1227 | 46 | 0.796 | AUCGUUGUAGGUUCC | 15 | 62 | -3.4 | 0 | -24.2 | GCACGAUCGUUGUAGGUUCCCGUGC |
| 16 | 1226 | 46 | 0.794 | UCGUUGUAGGUUCCA | 15 | 63 | -6.4 | 0 | -24.7 | GCCGUCGUUGUAGGUUCCACGGC |
| 17 | 73 | 53 | 0.778 | UGGCGGAAGUAUUGG | 15 | 66 | -2.7 | 0 | -26.2 | CGCGAUGGCGGAAGUAUUGGUCGCG |
| 18 | 2812 | 40 | 0.776 | CAGCUUGUUAUAGGA | 15 | 59 | -7 | 0 | -22.7 | GCACGCAGCUUGUUAUAGGACGUGC |
| 19 | 2813 | 46 | 0.774 | GCAGCUUGUUAUAGG | 15 | 62 | -5.1 | 0 | -24.2 | GCACGGCAGCUUGUUAUAGGCGUGC |
| 20 | 2815 | 33 | 0.774 | UUGCAGCUUGUUAUA | 15 | 57 | -5.9 | 0 | -20.8 | GCCGUUGCAGCUUGUUAUACGGC |
| 21 | 2811 | 40 | 0.774 | AGCUUGUUAUAGGAC | 15 | 60 | -7 | 0 | -22.8 | GCACGAGCUUGUUAUAGGACCGUGC |
| 22 | 2824 | 33 | 0.772 | GAUUUUACAUUGCAG | 15 | 52 | -4.5 | 0 | -19.4 | GCACGGAUUUUACAUUGCAGCGUGC |
| 23 | 2814 | 40 | 0.772 | UGCAGCUUGUUAUAG | 15 | 59 | -5.9 | 0 | -22.5 | CGCGAUGCAGCUUGUUAUAGUCGCG |
| 24 | 2823 | 33 | 0.770 | AUUUUACAUUGCAGC | 15 | 55 | -4.9 | 0 | -19.9 | GCACGAUUUUACAUUGCAGCCGUGC |
| 25 | 2585 | 40 | 0.768 | AACGGAAACAGAAAG | 15 | 57 | -1.5 | 0 | -21.1 | CGAGCAACGGAAACAGAAAGGCUCG |
| 26 | 2825 | 33 | 0.768 | GGAUUUUACAUUGCA | 15 | 55 | -2.9 | 0 | -20.1 | GCACGGGAUUUUACAUUGCACGUGC |
| 27 | 2822 | 33 | 0.768 | UUUUACAUUGCAGCU | 15 | 57 | -4.9 | 0 | -20.4 | GCACGUUUUACAUUGCAGCUCGUGC |
| 28 | 2826 | 33 | 0.766 | UGGAUUUUACAUUGC | 15 | 55 | -1.1 | 0 | -20.1 | GCACGUGGAUUUUACAUUGCAGCGUGC |
| 29 | 2232 | 46 | 0.761 | UUUUGGAAAAGCGG | 15 | 62 | -2.7 | 0 | -23.1 | CGCGAUUUUGGAAAAGCGGUCGCG |
| 30 | 854 | 53 | 0.761 | GUUAUCUUGGGCACG | 15 | 64 | -2.8 | 0 | -25.6 | CGACGGUUAUCUUGGGCACGCGUCG |
| 31 | 2215 | 33 | 0.751 | AAGUUUGAAGAGAAG | 15 | 53 | -0.6 | 0 | -19.8 | CGACGAAGUUUGAAGAGAAGCGUCG |
| 32 | 399 | 46 | 0.751 | GUUGCUGUUGUAGGU | 15 | 63 | -3.6 | -0.9 | -24.5 | CGCGAGUUGCUGUUGUAGGUUCGCG |
| 33 | 400 | 46 | 0.751 | UGUUGCUGUUGUAGG | 15 | 63 | -3.6 | -0.9 | -24.4 | GCACGUGUUGCUGUUGUAGGCGUGC |
| 34 | 72 | 53 | 0.748 | GGCGGAAGUAUUGGU | 15 | 67 | -2.7 | 0 | -26.3 | CGCGAGGCGGAAGUAUUGGUUCGCG |
| 35 | 2227 | 46 | 0.748 | GGAAAAGCGGAAAAG | 15 | 60 | -2.7 | 0 | -22.7 | CGAGCGGAAAAGCGGAAAAGGCUCG |
| 36 | 2226 | 40 | 0.748 | GAAAAGCGGAAAAGU | 15 | 58 | -2.7 | 0 | -21.1 | CGCGAGAAAAGCGGAAAAGUUCGCG |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|------------------|-----------|----|--------------------|---------------------|---------------------|----------------------------|
| 37 | 2586 | 33 | 0.744 | AAACGGAAACAGAAA | 15 | 55 | -1.5 | 0 | -19.4 | CGAGCAAACGGAAACAGAAAGCUCG |
| 38 | 2231 | 46 | 0.744 | UUUGGGAAAAGCGGA | 15 | 64 | -2.7 | 0 | -24.1 | CCGGUUUGGGAAAAGCGGACCGG |
| 39 | 2228 | 46 | 0.742 | GGGAAAAGCGGAAAA | 15 | 63 | -2.7 | 0 | -23.4 | CGAGCGGGAAAAGCGGAAAAGCUCG |
| 40 | 2225 | 33 | 0.742 | AAAAGCGGAAAAGUU | 15 | 56 | -2.7 | 0 | -19.1 | CCGAAAAGCGGAAAAGUUCGG |
| 41 | 2584 | 40 | 0.738 | ACGGAACAGAAAGA | 15 | 59 | -1.5 | 0 | -22.1 | CGAGCACGGAAACAGAAAGAGCUCG |
| 42 | 2230 | 46 | 0.738 | UUGGGAAAAGCGGAA | 15 | 64 | -2.7 | 0 | -24.1 | CCGUUGGGAAAAGCGGAACGG |
| 43 | 2224 | 33 | 0.738 | AAAGCGGAAAAGUUU | 15 | 56 | -2.8 | -0.7 | -19.1 | GGAAAGCGGAAAAGUUUCC |
| 44 | 2229 | 46 | 0.735 | UGGAAAAGCGGAAA | 15 | 64 | -2.7 | 0 | -24.1 | CCGGUGGGAAAAGCGGAAACCGG |
| 45 | 1225 | 53 | 0.735 | CGUUGUAGGUUCCAC | 15 | 64 | -6.4 | 0 | -25.5 | GCACGCGUUGUAGGUUCCACCGUGC |
| 46 | 973 | 33 | 0.731 | GGUAGAAUUGUUGA | 15 | 54 | 0 | 0 | -20.2 | GCACGGUAGAAUUGUUGACGUGC |
| 47 | 974 | 33 | 0.729 | UGGUAGAAUUGUUG | 15 | 54 | 0 | 0 | -19.9 | CGCGAUGGUAGAAUUGUUGUCGCG |
| 48 | 855 | 53 | 0.729 | CGUUAUCUUGGGCAC | 15 | 64 | -2.8 | 0 | -25.6 | CGACGCGUUAUCUUGGGCACCGUGC |
| 49 | 853 | 53 | 0.725 | UUAUCUUGGGCACGG | 15 | 66 | -2.7 | 0 | -26.2 | CGCGAUUAUCUUGGGCACGGUCGCG |
| 50 | 972 | 33 | 0.720 | GUAGAAUUGUUGAG | 15 | 52 | 0 | 0 | -19.5 | GCACGGUAGAAUUGUUGAGCGUGC |
| 1 | 85 | 31 | 0.833 | AGAUAAUAGGUUUUGG | 16 | 56 | 0 | 0 | -21.3 | CGACGAGAUAAUAGGUUUUGGCGUGC |
| 2 | 84 | 37 | 0.829 | GAUAAUAGGUUUUGGC | 16 | 59 | 0 | 0 | -23.1 | CGAGGAUAAUAGGUUUUGGCCUCG |
| 3 | 1230 | 43 | 0.829 | GAGAAUCGUUGUAGGU | 16 | 62 | -2.7 | 0 | -25.4 | CGCGAGAGAAUCGUUGUAGGUUCGCG |
| 4 | 1231 | 43 | 0.825 | AGAGAAUCGUUGUAGG | 16 | 62 | -2.7 | 0 | -25.3 | GCACGAGAGAAUCGUUGUAGGCGUGC |
| 5 | 1229 | 37 | 0.825 | AGAAUCGUUGUAGGUU | 16 | 60 | -2.6 | -0.6 | -23.4 | CGCCAGAAUCGUUGUAGGUUGGCG |
| 6 | 83 | 37 | 0.819 | AUAAUAGGUUUUGGCG | 16 | 59 | -2.7 | 0 | -22.6 | CGACGAUAAUAGGUUUUGGCGGUGC |
| 7 | 1232 | 43 | 0.819 | CAGAGAAUCGUUGUAG | 16 | 59 | -5.8 | 0 | -24.6 | CGAGCAGAGAAUCGUUGUAGCUCG |
| 8 | 82 | 43 | 0.817 | UAAUAGGUUUUGGCGG | 16 | 64 | -2.7 | 0 | -24.8 | CGCGAUAAUAGGUUUUGGCGGUCGCG |
| 9 | 81 | 43 | 0.815 | AAUAGGUUUUGGCGGA | 16 | 65 | -4.1 | 0 | -25.4 | CGACGAAUAGGUUUUGGCGGACGUGC |
| 10 | 74 | 43 | 0.813 | UUUGGCGGAAGUAUUG | 16 | 63 | -7.1 | 0 | -24.7 | CGCGAUUUGGCGGAAGUAUUGUCGCG |
| 11 | 80 | 43 | 0.810 | AUAGGUUUUGGCGGAA | 16 | 65 | -5.9 | 0 | -25.4 | CGACGAUAGGUUUUGGCGGAACGUGC |
| 12 | 1227 | 43 | 0.802 | AAUCGUUGUAGGUUCC | 16 | 63 | -3.4 | -0.3 | -25.1 | GCACGAAUCGUUGUAGGUUCCCGUGC |
| 13 | 1226 | 43 | 0.798 | AUCGUUGUAGGUUCCA | 16 | 64 | -6.4 | 0 | -25.8 | GCACGAUCGUUGUAGGUUCCACGUGC |
| 14 | 73 | 50 | 0.788 | UUGGCGGAAGUAUUGG | 16 | 66 | -5.3 | 0 | -27.1 | CGCGAUUGGCGGAAGUAUUGGUCGCG |
| 15 | 2813 | 43 | 0.786 | UGCAGCUUGUUAUAGG | 16 | 64 | -5.9 | 0 | -25.8 | CGCGAUGCAGCUUGUUAUAGGUCGCG |
| 16 | 2814 | 37 | 0.786 | UUGCAGCUUGUUAUAG | 16 | 60 | -5.9 | 0 | -23.4 | GCACGUUGCAGCUUGUUAUAGCGUGC |
| 17 | 2812 | 43 | 0.784 | GCAGCUUGUUAUAGGA | 16 | 64 | -7 | 0 | -26.1 | GCACGGCAGCUUGUUAUAGGACGUGC |
| 18 | 2822 | 31 | 0.782 | AUUUUACAUUGCAGCU | 16 | 58 | -4.9 | 0 | -21.5 | CGCCAUUUUACAUUGCAGCUGGCG |
| 19 | 2811 | 43 | 0.782 | CAGCUUGUUAUAGGAC | 16 | 62 | -7 | 0 | -25.4 | GCACGCAGCUUGUUAUAGGACCGUGC |
| 20 | 2823 | 37 | 0.780 | GAUUUUACAUUGCAGC | 16 | 58 | -4.9 | 0 | -22.8 | CGAGGAUUUUACAUUGCAGCCUCG |
| 21 | 2824 | 37 | 0.778 | GGAUUUUACAUUGCAG | 16 | 57 | -4.5 | 0 | -22.7 | GCACGGGAUUUUACAUUGCAGCGUGC |
| 22 | 2826 | 31 | 0.774 | UUGGAUUUUACAUUGC | 16 | 56 | -1.1 | 0 | -21 | GCACGUUGGAUUUUACAUUGCCGUGC |
| 23 | 2825 | 31 | 0.774 | UGGAUUUUACAUUGCA | 16 | 57 | -2.9 | 0 | -21.7 | CCGUGGAUUUUACAUUGCACGG |
| 24 | 399 | 43 | 0.766 | UGUUGCUGUUGUAGGU | 16 | 65 | -3.6 | -0.9 | -26.1 | GCACGUGUUGCUGUUGUAGGUCGUGC |
| 25 | 2226 | 43 | 0.762 | GGAAAAGCGGAAAAGU | 16 | 63 | -2.7 | 0 | -24.4 | CGCGAGGAAAAGCGGAAAAGUUCGCG |
| 26 | 2215 | 31 | 0.760 | AAAGUUUGAAGAGAAG | 16 | 54 | -0.6 | 0 | -20.7 | CGACGAAAGUUUGAAGAGAAGCGUGC |
| 27 | 2231 | 43 | 0.760 | UUUUGGGAAAAGCGGA | 16 | 64 | -2.7 | 0 | -25 | CCGGUUUUGGGAAAAGCGGACCGG |
| 28 | 72 | 50 | 0.758 | UGGCGGAAGUAUUGGU | 16 | 68 | -2.7 | 0 | -27.9 | CGAGCUGGCGGAAGUAUUGGUCGUGC |
| 29 | 2585 | 37 | 0.756 | AAACGGAAACAGAAAG | 16 | 58 | -1.5 | 0 | -22 | CGAGCAAACGGAAACAGAAAGGCUCG |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔGbimol | ΔGunimol | ΔGduplex | Molecular beacon sequence |
|------|-------|-----|----------|-------------------|-----------|----|---------|----------|----------|------------------------------|
| 30 | 2227 | 50 | 0.756 | GGGAAAAGCGGAAAAG | 16 | 65 | -2.7 | 0 | -26 | CGAGCGGGAAAAGCGGAAAAGGCUCG |
| 31 | 2225 | 37 | 0.756 | GAAAAGCGGAAAAGUU | 16 | 58 | -2.7 | 0 | -22 | CGCGAGAAAAGCGGAAAAGUUUCGCG |
| 32 | 2230 | 43 | 0.754 | UUUGGGAAAAGCGGAA | 16 | 64 | -2.7 | 0 | -25 | CCGUUUUGGGAAAAGCGGAACGG |
| 33 | 2229 | 43 | 0.752 | UUGGGAAAAGCGGAAA | 16 | 64 | -2.7 | 0 | -25 | CCGUUGGGAAAAGCGGAAACGG |
| 34 | 2228 | 43 | 0.750 | UGGGAAAAGCGGAAAA | 16 | 64 | -2.7 | 0 | -25 | CCGGUGGGAAAAGCGGAAAACCGG |
| 35 | 1225 | 50 | 0.744 | UCGUUGUAGGUUCCAC | 16 | 66 | -6.4 | 0 | -27.4 | GCACGUCGUUGUAGGUUCCACCGUGC |
| 36 | 2224 | 31 | 0.744 | AAAAGCGGAAAAGUUU | 16 | 56 | -2.8 | -0.7 | -20 | GGAAAAGCGGAAAAGUUUCC |
| 37 | 973 | 31 | 0.738 | UGGUAGAAAUUGUUGA | 16 | 57 | 0 | 0 | -21.8 | GCCGUGGUAGAAAUUGUUGACGGC |
| 38 | 91 | 31 | 0.738 | GACUUAAGAUAAUAGG | 16 | 53 | -5.4 | 0 | -21.3 | CGAGCGACUUAAGAUAAUAGGGCUCG |
| 39 | 2217 | 31 | 0.728 | GAAAAGUUUGAAGAGA | 16 | 54 | -1.4 | 0 | -21 | CGACGAAAAGUUUGAAGAGACGUCG |
| 40 | 2584 | 37 | 0.728 | AACGGAAACAGAAAGA | 16 | 59 | -1.5 | 0 | -23 | CGAGCAACGGAAACAGAAAGAGCUCG |
| 41 | 2815 | 31 | 0.726 | AUUGCAGCUUGUUAUA | 16 | 58 | -5.9 | 0 | -21.9 | GCACGAUUGCAGCUUGUUAUACGUGC |
| 42 | 2810 | 37 | 0.726 | AGCUUGUUUAGGACA | 16 | 62 | -7 | -0.3 | -24.4 | GCACGAGCUUGUUUAGGACACGUGC |
| 43 | 1638 | 31 | 0.724 | UUCGGAAUAAACUUGUU | 16 | 56 | -4.1 | 0 | -20.9 | GCACGUUCGGAAUAAACUUGUUCGUGC |
| 44 | 2821 | 31 | 0.724 | UUUUACAUUGCAGCUU | 16 | 58 | -4.9 | 0 | -21.3 | GCACGUUUUACAUUGCAGCUUCGUGC |
| 45 | 972 | 37 | 0.722 | GGUAGAAAUUGUUGAG | 16 | 57 | 0 | 0 | -22.8 | GCACGGGUAGAAAUUGUUGAGCGUGC |
| 46 | 92 | 31 | 0.716 | GGACUUAAGAUAAUAG | 16 | 53 | -5.4 | 0 | -21.3 | CGAGCGGACUUAAGAUAAUAGGCUCG |
| 47 | 2218 | 37 | 0.714 | GGAAAAGUUUGAAGAG | 16 | 56 | -1.4 | 0 | -22.4 | CGACGGGAAAAGUUUGAAGAGCGUCG |
| 48 | 2214 | 31 | 0.712 | AAGUUUGAAGAGAAGU | 16 | 56 | -0.6 | 0 | -21.5 | CGCCAAGUUUGAAGAGAAGUGGCG |
| 49 | 2223 | 37 | 0.706 | AAAGCGAAAAGUUUG | 16 | 58 | -4.4 | -1.5 | -21.7 | CGACGAAAGCGAAAAGUUUGCGUCG |
| 50 | 398 | 50 | 0.704 | GUUGCUGUUGUAGGUG | 16 | 65 | -3.6 | -0.9 | -27.1 | GCACGGUUGCUGUUGUAGGUGCGUGC |
| 1 | 1230 | 41 | 0.829 | AGAGAAUCGUUGUAGGU | 17 | 64 | -2.7 | 0 | -27 | CGCCAGAGAAUCGUUGUAGGUGGCG |
| 2 | 1231 | 47 | 0.825 | CAGAGAAUCGUUGUAGG | 17 | 63 | -5.8 | 0 | -27.9 | CGAGCAGAGAAUCGUUGUAGGCUCG |
| 3 | 84 | 35 | 0.820 | AGAUAAUAGGUUUUGGC | 17 | 61 | 0 | 0 | -24.7 | CGACGAGAUAAUAGGUUUUGGCCGUCG |
| 4 | 83 | 41 | 0.818 | GAUAAUAGGUUUUGGCG | 17 | 62 | -2.7 | 0 | -25.5 | CGACGGAUAAUAGGUUUUGGCCGCGUCG |
| 5 | 82 | 41 | 0.814 | AUAAUAGGUUUUGGCGG | 17 | 64 | -2.7 | 0 | -25.9 | CGACGAUAAUAGGUUUUGGCCGCGUCG |
| 6 | 81 | 41 | 0.812 | UAAUAGGUUUUGGCGGA | 17 | 65 | -4.1 | 0 | -26.7 | CCGGUAAUAGGUUUUGGCCGGACCGG |
| 7 | 80 | 41 | 0.812 | AAUAGGUUUUGGCGGAA | 17 | 65 | -5.9 | 0 | -26.3 | CGACGAAUAGGUUUUGGCCGGAACGUCG |
| 8 | 1226 | 41 | 0.805 | AAUCGUUGUAGGUUCCA | 17 | 64 | -6.4 | -0.3 | -26.7 | GCACGAAUCGUUGUAGGUUCCACGUGC |
| 9 | 2813 | 41 | 0.799 | UUGCAGCUUGUUUAGG | 17 | 64 | -5.9 | 0 | -26.7 | GCACGUUGCAGCUUGUUUAGGCGUGC |
| 10 | 73 | 47 | 0.797 | UUUGGCGGAAGUUAUGG | 17 | 67 | -7.1 | 0 | -28 | CGCGAUUUGGCGGAAGUUAUGGUCGCG |
| 11 | 2812 | 41 | 0.795 | UGCAGCUUGUUUAGGA | 17 | 65 | -7 | 0 | -27.7 | GCCGUGCAGCUUGUUUAGGACGGC |
| 12 | 2822 | 35 | 0.791 | GAUUUUACAUUGCAGCU | 17 | 60 | -4.9 | 0 | -24.4 | CGCGAGAUUUUACAUUGCAGCUUCGCG |
| 13 | 2811 | 47 | 0.789 | GCAGCUUGUUUAGGAC | 17 | 66 | -7 | 0 | -28.8 | CGAGGCAGCUUGUUUAGGACCUCG |
| 14 | 1229 | 41 | 0.787 | GAGAAUCGUUGUAGGUU | 17 | 62 | -2.7 | -0.6 | -26.3 | CGCGAGAGAAUCGUUGUAGGUUUCGCG |
| 15 | 2823 | 41 | 0.786 | GGAUUUUACAUUGCAGC | 17 | 62 | -4.9 | 0 | -26.1 | CGAGGGAUUUUACAUUGCAGCCUCG |
| 16 | 2824 | 35 | 0.784 | UGGAUUUACAUUGCAG | 17 | 59 | -4.9 | 0 | -24.3 | GCACGUGGAUUUACAUUGCAGCGUGC |
| 17 | 2226 | 47 | 0.769 | GGGAAAAGCGGAAAAGU | 17 | 67 | -2.7 | 0 | -27.7 | CGCGAGGGAAAAGCGGAAAAGUUCGCG |
| 18 | 2230 | 41 | 0.769 | UUUUGGGAAAAGCGGAA | 17 | 64 | -2.7 | 0 | -25.9 | CCGUUUUGGGAAAAGCGGAACGG |
| 19 | 2225 | 41 | 0.769 | GGAAAAGCGGAAAAGUU | 17 | 63 | -2.7 | 0 | -25.3 | CGCGAGGAAAAGCGGAAAAGUUUCGCG |
| 20 | 72 | 47 | 0.769 | UUGGCGGAAGUAUUGGU | 17 | 68 | -5.3 | 0 | -28.8 | CGAGCUUGGCGGAAGUAUUGGUCUCG |
| 21 | 2229 | 41 | 0.767 | UUUGGGAAAAGCGGAAA | 17 | 64 | -2.7 | 0 | -25.9 | GGUUUGGGAAAAGCGGAAACC |
| 22 | 2228 | 41 | 0.765 | UUGGGAAAAGCGGAAAA | 17 | 64 | -2.7 | 0 | -25.9 | CCGUUGGGAAAAGCGGAAAACGG |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|--------------------|-----------|----|---------------------------|----------------------------|----------------------------|------------------------------|
| 23 | 2227 | 47 | 0.763 | UGGGAAAAGCGGAAAAG | 17 | 66 | -2.7 | 0 | -27.6 | CGCGAUGGGAAAAGCGGAAAAGUCGCG |
| 24 | 2224 | 35 | 0.757 | GAAAAGCGGAAAAGUUU | 17 | 59 | -2.8 | -0.7 | -22.9 | CGCGAGAAAAGCGGAAAAGUUUUCGCG |
| 25 | 1225 | 47 | 0.751 | AUCGUUGUAGGUUCCAC | 17 | 66 | -6.4 | 0 | -28.5 | GCACGAUCGUUGUAGGUUCCACCGUGC |
| 26 | 2814 | 35 | 0.740 | AUUGCAGCUUGUUUAG | 17 | 60 | -5.9 | 0 | -24.5 | GCACGAUUGCAGCUUGUUUAGCGUGC |
| 27 | 2810 | 41 | 0.736 | CAGCUUGUUUAGGACA | 17 | 63 | -7 | -0.3 | -27 | GCACGCAGCUUGUUUAGGACACGUGC |
| 28 | 972 | 35 | 0.729 | UGGUAGAAUUGUUGAG | 17 | 59 | 0 | 0 | -24.4 | CGCGAUGGUAGAAUUGUUGAGUCGCG |
| 29 | 71 | 52 | 0.729 | UGGCGGAAGUUAUUGGUG | 17 | 70 | -3.2 | -0.2 | -30.5 | CGCGAUGGCGGAAGUUAUUGGUGUCGCG |
| 30 | 2217 | 35 | 0.725 | GGAAAAGUUUGAAGAGA | 17 | 59 | -1.4 | 0 | -24.3 | CGACGGGAAAAGUUUGAAGAGACGUCG |
| 31 | 91 | 35 | 0.723 | GGACUUAAGAUAAUAGG | 17 | 58 | -5.4 | 0 | -24.6 | CGAGCGGACUUAAGAUAAUAGGGCUCG |
| 32 | 399 | 47 | 0.721 | CUGUUGCUGUUGUAGGU | 17 | 67 | -3.6 | -0.9 | -28.7 | GCACGCUGUUGCUGUUGUAGGUCGUGC |
| 33 | 398 | 47 | 0.721 | UGUUGCUGUUGUAGGUG | 17 | 66 | -3.6 | -0.9 | -28.7 | GCACGUGUUGCUGUUGUAGGUGCGUGC |
| 34 | 2584 | 35 | 0.719 | AAACGGAAACAGAAAGA | 17 | 60 | -1.5 | 0 | -23.9 | CGAGCAAACGGAAACAGAAAGAGCUCG |
| 35 | 2223 | 35 | 0.713 | AAAAGCGGAAAAGUUUG | 17 | 59 | -4.4 | -1.5 | -22.6 | CGACGAAAAGCGGAAAAGUUUGCGUCG |
| 36 | 2585 | 41 | 0.712 | CAAACGGAAACAGAAAG | 17 | 60 | -1.5 | 0 | -24.6 | CGAGCAAACGGAAACAGAAAGCUCG |
| 37 | 973 | 35 | 0.708 | CUGGUAGAAUUGUUGA | 17 | 59 | -5 | 0 | -24.4 | GCACGCUGGUAGAAUUGUUGACGUGC |
| 38 | 1224 | 47 | 0.706 | UCGUUGUAGGUUCCACU | 17 | 67 | -6.4 | 0 | -29 | GCACGUCGUUGUAGGUUCCACUCGUGC |
| 39 | 971 | 35 | 0.704 | GGUAGAAUUGUUGAGA | 17 | 59 | 0 | 0 | -24.7 | GCACGGGUAGAAUUGUUGAGACGUGC |
| 40 | 852 | 52 | 0.693 | GUUAUCUUGGGCACGGU | 17 | 70 | -2.8 | 0 | -30.6 | CGCGAGUUAUCUUGGGCACGGUUCGCG |
| 41 | 2583 | 41 | 0.687 | AACGGAAACAGAAAGAC | 17 | 62 | -1.5 | 0 | -25.7 | CGAGCAACGGAAACAGAAAGACGUCG |
| 42 | 1638 | 35 | 0.687 | CUUCGGAUAAACUUGUU | 17 | 58 | -4.5 | 0 | -23.5 | GCACGCUUCGGAUAAACUUGUUCGUGC |
| 43 | 585 | 47 | 0.687 | UUGUCGUGCAGUGGAAA | 17 | 67 | -5.1 | 0 | -28.6 | CCGUUGUCGUGCAGUGGAAACGG |
| 44 | 1637 | 35 | 0.685 | UUCGGAUAAACUUGUUG | 17 | 58 | -4.1 | 0 | -23.5 | CGCGAUUCGGAUAAACUUGUUGUCGCG |
| 45 | 2820 | 35 | 0.685 | UUUUACAUUGCAGCUUG | 17 | 60 | -4.9 | 0 | -23.9 | GCACGUUUUACAUUGCAGCUUGCGUGC |
| 46 | 584 | 47 | 0.685 | UGUCGUGCAGUGGAAAU | 17 | 67 | -5.1 | 0 | -28.8 | GCACGUGUCGUGCAGUGGAAAUUCGUGC |
| 47 | 405 | 47 | 0.685 | GUGUUGCUGUUGCUGUU | 17 | 67 | -4.1 | -1.1 | -28.4 | CGCGAGUGUUGCUGUUGCUGUUUCGCG |
| 48 | 2809 | 35 | 0.685 | AGCUUGUUUAGGACAA | 17 | 62 | -7 | -1.1 | -25.3 | GCACGAGCUUGUUUAGGACAACGUGC |
| 49 | 92 | 35 | 0.683 | CGGACUUAAGAUAAUAG | 17 | 57 | -5.4 | 0 | -23.7 | CGAGCGGACUUAAGAUAAUAGCUCG |
| 50 | 2815 | 35 | 0.683 | CAUUGCAGCUUGUUUAU | 17 | 60 | -5.9 | 0 | -24.5 | GCACGCAUUGCAGCUUGUUUAUCGUGC |
| 1 | 1230 | 44 | 0.830 | CAGAGAAUCGUUGUAGGU | 18 | 65 | -5.8 | 0 | -29.6 | GCACGCAGAGAAUCGUUGUAGGUCGUGC |
| 2 | 82 | 44 | 0.814 | GAUAAUAGGUUUUGGCGG | 18 | 66 | -2.7 | 0 | -28.8 | CGACGGAUAAUAGGUUUUGGCGGUCG |
| 3 | 84 | 33 | 0.810 | AAGAUAAUAGGUUUUGGC | 18 | 61 | -2.4 | 0 | -25.6 | CGACGAAGAUAAUAGGUUUUGGCCGUCG |
| 4 | 83 | 38 | 0.810 | AGAUAAUAGGUUUUGGCG | 18 | 64 | -2.7 | 0 | -27.1 | CGACGAGAUAAUAGGUUUUGGCGGUCG |
| 5 | 81 | 38 | 0.810 | AUAAUAGGUUUUGGCGGA | 18 | 66 | -4.1 | 0 | -27.8 | CGACGAUAAUAGGUUUUGGCGGACGUCG |
| 6 | 80 | 38 | 0.810 | UAAUAGGUUUUGGCGGAA | 18 | 65 | -5.9 | 0 | -27.6 | CCGGUAAUAGGUUUUGGCGGAACCGG |
| 7 | 2812 | 38 | 0.806 | UUGCAGCUUGUUUAGGA | 18 | 66 | -7 | 0 | -28.6 | GCCGUUGCAGCUUGUUUAGGACGGC |
| 8 | 2811 | 44 | 0.799 | UGCAGCUUGUUUAGGAC | 18 | 67 | -7 | 0 | -30.4 | GCACGUGCAGCUUGUUUAGGACCGUGC |
| 9 | 2822 | 38 | 0.796 | GGAUUUUACAUUGCAGCU | 18 | 64 | -4.9 | 0 | -27.7 | CGCGAGGAUUUUACAUUGCAGCUUCGCG |
| 10 | 2824 | 33 | 0.790 | UUGGAUUUUACAUUGCAG | 18 | 60 | -5 | 0 | -25.2 | GCACGUUGGAUUUUACAUUGCAGCGUGC |
| 11 | 2823 | 38 | 0.790 | UGGAUUUUACAUUGCAGC | 18 | 64 | -5.1 | 0 | -27.7 | GCACGUGGAUUUUACAUUGCAGCCGUGC |
| 12 | 1229 | 38 | 0.790 | AGAGAAUCGUUGUAGGUU | 18 | 64 | -2.7 | -0.6 | -27.9 | CGCCAGAGAAUCGUUGUAGGUUGGCG |
| 13 | 2229 | 38 | 0.780 | UUUUGGGAAAAGCGGAAA | 18 | 65 | -3.8 | -0.6 | -26.8 | GGUUUUGGGAAAAGCGGAAACC |
| 14 | 2228 | 38 | 0.778 | UUUGGGAAAAGCGGAAAA | 18 | 65 | -2.7 | 0 | -26.8 | GGUUUGGGAAAAGCGGAAACC |
| 15 | 72 | 44 | 0.778 | UUUGGCGGAAGUAUUGGU | 18 | 68 | -7.1 | 0 | -29.7 | CGACGUUUGGCGGAAGUAUUGGUCGUGC |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔGbimol | ΔGunimol | ΔGduplex | Molecular beacon sequence |
|------|-------|-----|----------|---------------------|-----------|----|---------|----------|----------|-------------------------------|
| 16 | 2227 | 44 | 0.776 | UUGGGAAAAGCGGAAAAG | 18 | 66 | -2.7 | 0 | -28.5 | CGCGAUUGGGAAAAGCGGAAAAGUCGCG |
| 17 | 2226 | 44 | 0.774 | UGGGAAAAGCGGAAAAGU | 18 | 68 | -2.7 | 0 | -29.3 | CGAGCUGGGAAAAGCGGAAAAGUCGUCG |
| 18 | 2225 | 44 | 0.774 | GGGAAAAGCGGAAAAGUU | 18 | 67 | -2.7 | 0 | -28.6 | CGCGAGGGAAAAGCGGAAAAGUUUCGCG |
| 19 | 2224 | 38 | 0.769 | GGAAAAGCGGAAAAGUUU | 18 | 63 | -2.8 | -0.7 | -26.2 | CGCGAGGAAAAGCGGAAAAGUUUUCGCG |
| 20 | 1225 | 44 | 0.760 | AAUCGUUGUAGGUUCCAC | 18 | 66 | -6.4 | -0.3 | -29.4 | GCACGAAUCGUUGUAGGUUCCACCGUGC |
| 21 | 2215 | 33 | 0.756 | GAAAAGUUUGAAGAGAAG | 18 | 57 | -1.4 | 0 | -24.5 | CGACGGAAAAGUUUGAAGAGAAGCGUCG |
| 22 | 2813 | 38 | 0.754 | AUUGCAGCUUGUUUAGG | 18 | 64 | -5.9 | 0 | -27.8 | GCACGAUUGCAGCUUGUUUAGGCGUGC |
| 23 | 2821 | 33 | 0.751 | GAUUUUACAUUGCAGCUU | 18 | 61 | -4.9 | 0 | -25.3 | CGCGAGAUUUUACAUUGCAGCUUUCGCG |
| 24 | 2810 | 44 | 0.746 | GCAGCUUGUUUAGGACA | 18 | 67 | -7 | -0.3 | -30.4 | GCACGGCAGCUUGUUUAGGACACGUGC |
| 25 | 71 | 50 | 0.740 | UUGGCGGAAGUAUUGGUG | 18 | 70 | -5.3 | -0.2 | -31.4 | CGCGAUUGGCGGAAGUAUUGGUGUCGCG |
| 26 | 2216 | 33 | 0.738 | GGAAAAGUUUGAAGAGAA | 18 | 59 | -1.4 | 0 | -25.2 | CGACGGGAAAAGUUUGAAGAGAAGCGUCG |
| 27 | 90 | 33 | 0.731 | GGACUUAAGAUAAUAGGU | 18 | 61 | -5.6 | -1 | -26.3 | CGCGAGGACUUAAGAUAAUAGGUUCGCG |
| 28 | 2223 | 38 | 0.728 | GAAAAGCGGAAAAGUUUG | 18 | 61 | -4.4 | -1.5 | -25.5 | CGACGGAAAAGCGGAAAAGUUUGCGUCG |
| 29 | 1224 | 44 | 0.715 | AUCGUUGUAGGUUCCACU | 18 | 68 | -6.4 | 0 | -30.1 | CGCCAUCGUUGUAGGUUCCACUGGCG |
| 30 | 971 | 33 | 0.711 | UGGUAGAAUUGUUGAGA | 18 | 61 | 0 | 0 | -26.3 | GCCGUGGUAGAAUUGUUGAGACGCG |
| 31 | 2820 | 33 | 0.703 | AUUUUACAUUGCAGCUUG | 18 | 60 | -4.9 | 0 | -25 | GCACGAUUUUACAUUGCAGCUUGCGUGC |
| 32 | 584 | 44 | 0.703 | UUGUCGUGCAGUGGAAU | 18 | 67 | -5.1 | 0 | -29.7 | GCACGUUGUCGUGCAGUGGAAUUCGUGC |
| 33 | 972 | 38 | 0.701 | CUGGUAGAAUUGUUGAG | 18 | 61 | -5 | 0 | -27 | CCGCUGGUAGAAUUGUUGAGCGG |
| 34 | 70 | 55 | 0.701 | UGGCGGAAGUAUUGGUGC | 18 | 73 | -6.8 | -0.2 | -33.9 | CGAGCUGGCGGAAGUAUUGGUGCUCG |
| 35 | 2814 | 38 | 0.699 | CAUUGCAGCUUGUUUAG | 18 | 62 | -5.9 | 0 | -27.1 | CGAGCAUUGCAGCUUGUUUAGCUCG |
| 36 | 2809 | 38 | 0.697 | CAGCUUGUUUAGGACAA | 18 | 64 | -7 | -1.1 | -27.9 | GCACGCAGCUUGUUUAGGACAACGUGC |
| 37 | 405 | 50 | 0.695 | GGUGUUGCUGUUGCUGUU | 18 | 70 | -4.1 | -1.1 | -31.7 | CGCGAGGUGUUGCUGUUGCUGUUUCGCG |
| 38 | 91 | 38 | 0.692 | CGGACUUAAGAUAAUAGG | 18 | 61 | -5.4 | 0 | -27 | CGAGCGGACUUAAGAUAAUAGGCUCG |
| 39 | 404 | 50 | 0.692 | GUGUUGCUGUUGCUGUUG | 18 | 68 | -4.1 | -1.1 | -31 | CGAGCGUGUUGCUGUUGCUGUUGGCUCG |
| 40 | 970 | 33 | 0.690 | GGUAGAAUUGUUGAGAU | 18 | 60 | -0.6 | 0 | -25.8 | CGCGAGGUAGAAUUGUUGAGAUUCGCG |
| 41 | 406 | 50 | 0.688 | UGGUGUUGCUGUUGCUGU | 18 | 71 | -4.1 | -1.1 | -32.4 | CGAGCUGGUGUUGCUGUUGCUGUCUCG |
| 42 | 403 | 44 | 0.688 | UGUUGCUGUUGCUGUUGU | 18 | 68 | -4.1 | -1.1 | -30 | GCACGUGUUGCUGUUGCUGUUGUCGUGC |
| 43 | 2217 | 38 | 0.686 | CGGAAAAGUUUGAAGAGA | 18 | 61 | -2.4 | 0 | -26.7 | CGACGCGAAAAGUUUGAAGAGACGUCG |
| 44 | 2222 | 33 | 0.686 | AAAAGCGGAAAAGUUUGA | 18 | 61 | -4.4 | -1.5 | -24.5 | CGACGAAAAGCGGAAAAGUUUGACGUCG |
| 45 | 402 | 44 | 0.685 | GUUGCUGUUGCUGUUGUA | 18 | 67 | -4.1 | -1.1 | -29.7 | GCACGGUUGCUGUUGCUGUUGUACGUGC |
| 46 | 1242 | 44 | 0.683 | GUUAAUCGUCAGCAGAGA | 18 | 65 | -3.3 | 0 | -29.9 | GCACGGUUAUCGUCAGCAGAGACGUGC |
| 47 | 2583 | 38 | 0.681 | AAACGGAAACAGAAAGAC | 18 | 62 | -1.5 | 0 | -26.6 | CGAGCAAACGGAAACAGAAAGACGCUCG |
| 48 | 973 | 38 | 0.681 | GCUGGUAGAAUUGUUGA | 18 | 63 | -5.4 | 0 | -27.8 | GCACGGCUGGUAGAAUUGUUGACGUGC |
| 49 | 1221 | 50 | 0.681 | GUUGUAGGUUCCACUGGU | 18 | 70 | -6.4 | -0.5 | -32.3 | CGCGAGUUGUAGGUUCCACUGGUUCGCG |
| 50 | 1219 | 44 | 0.681 | UGUAGGUUCCACUGGUUA | 18 | 68 | -6.4 | -0.5 | -30.9 | GCCGUGUAGGUUCCACUGGUUACGCG |
| 1 | 81 | 42 | 0.810 | GAUAAUAGGUUUUGGCGGA | 19 | 67 | -4.1 | 0 | -30.7 | CGACGGAUAAUAGGUUUUGGCGGACGUCG |
| 2 | 2811 | 42 | 0.810 | UUGCAGCUUGUUUAGGAC | 19 | 67 | -7 | 0 | -31.3 | GCACGUUGCAGCUUGUUUAGGACCGUGC |
| 3 | 80 | 36 | 0.808 | AUAAUAGGUUUUGGCGGAA | 19 | 66 | -5.9 | 0 | -28.7 | CGACGAUAAUAGGUUUUGGCGGAACGUCG |
| 4 | 82 | 42 | 0.806 | AGAUAAUAGGUUUUGGCGG | 19 | 67 | -2.7 | 0 | -30.4 | CGACGAGAUAAUAGGUUUUGGCGGCGUCG |
| 5 | 84 | 31 | 0.803 | UAAGAUAAUAGGUUUUGGC | 19 | 62 | -4.6 | -0.4 | -26.9 | CGACGUAAGAUAAUAGGUUUUGGCGGUCG |
| 6 | 83 | 36 | 0.801 | AAGAUAAUAGGUUUUGGCG | 19 | 64 | -3.4 | 0 | -28 | CGACGAAGAUAAUAGGUUUUGGCGGUCG |
| 7 | 2822 | 36 | 0.800 | UGGAUUUUACAUUGCAGCU | 19 | 66 | -5.1 | 0 | -29.3 | GCACGUGGAUUUUACAUUGCAGCUCGUGC |
| 8 | 2823 | 36 | 0.796 | UUGGAUUUUACAUUGCAGC | 19 | 64 | -5.1 | 0 | -28.6 | GCACGUUGGAUUUUACAUUGCAGCCGUGC |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|----------------------|-----------|----|--------------------|---------------------|---------------------|--------------------------------|
| 9 | 1229 | 42 | 0.793 | CAGAGAAUCGUUGUAGGUU | 19 | 65 | -5.8 | -0.6 | -30.5 | GCACGCAGAGAAUCGUUGUAGGUUCGUGC |
| 10 | 2228 | 36 | 0.789 | UUUUGGGAAAAGCGGAAA | 19 | 65 | -3.8 | -0.6 | -27.7 | GGUUUUGGGAAAAGCGGAAAACC |
| 11 | 2227 | 42 | 0.788 | UUUGGGAAAAGCGGAAAAG | 19 | 66 | -2.7 | 0 | -29.4 | CGCGAUUUGGGAAAAGCGGAAAAGUCGCG |
| 12 | 2226 | 42 | 0.786 | UUGGGAAAAGCGGAAAAGU | 19 | 68 | -2.7 | 0 | -30.2 | CGAGCUUGGGAAAAGCGGAAAAGUGCUCG |
| 13 | 2225 | 42 | 0.779 | UGGAAAAGCGGAAAAGUU | 19 | 68 | -2.7 | 0 | -30.2 | CGAGCUGGGAAAAGCGGAAAAGUUGCUCG |
| 14 | 2224 | 42 | 0.774 | GGGAAAAGCGGAAAAGUUU | 19 | 67 | -2.8 | -0.7 | -29.5 | CGCGAGGGAAAAGCGGAAAAGUUUCGCG |
| 15 | 2812 | 36 | 0.764 | AUUGCAGCUUGUUAUAGGA | 19 | 66 | -7 | 0 | -29.7 | GCACGAUUGCAGCUUGUUAUAGGACGUGC |
| 16 | 2821 | 36 | 0.757 | GGAUUUUACAUUGCAGCUU | 19 | 64 | -4.9 | 0 | -28.6 | CGCGAGGAUUUUACAUUGCAGCUUUCGCG |
| 17 | 2824 | 31 | 0.754 | UUUGGAUUUUACAUUGCAG | 19 | 60 | -5 | 0 | -26.1 | GCACGUUUGGAUUUUACAUUGCAGCGUGC |
| 18 | 2215 | 36 | 0.752 | GGAAAAGUUUGAAGAGAAG | 19 | 61 | -1.4 | 0 | -27.8 | CGACGGGAAAAGUUUGAAGAGAAGCGUCG |
| 19 | 71 | 47 | 0.750 | UUUGGCGGAAGUAUUGGUG | 19 | 70 | -7.1 | -0.2 | -32.3 | CGCGAUUUGGCGGAAGUAUUGGUGUCGCG |
| 20 | 2223 | 42 | 0.740 | GGAAAAGCGGAAAAGUUUG | 19 | 65 | -4.4 | -1.5 | -28.8 | CGACGGGAAAAGCGGAAAAGUUUGCUCG |
| 21 | 1224 | 42 | 0.725 | AAUCGUUGUAGGUUCCACU | 19 | 68 | -6.4 | -0.3 | -31 | CGCCAUCGUUGUAGGUUCCACUGGCG |
| 22 | 2214 | 31 | 0.723 | GAAAAGUUUGAAGAGAAGU | 19 | 59 | -1.4 | 0 | -26.2 | CGCGAGAAAAGUUUGAAGAGAAGUUCGCG |
| 23 | 2820 | 36 | 0.715 | GAUUUUACAUUGCAGCUUG | 19 | 62 | -4.9 | 0 | -27.9 | GCACGGAUUUUACAUUGCAGCUUGCUCG |
| 24 | 2813 | 42 | 0.715 | CAUUGCAGCUUGUUAUAGG | 19 | 66 | -5.9 | 0 | -30.4 | CGAGCAUUGCAGCUUGUUAUAGGCUCG |
| 25 | 70 | 52 | 0.713 | UUGGCGGAAGUAUUGGUGC | 19 | 73 | -6.8 | -0.2 | -34.8 | CGAGCUUGGCGGAAGUAUUGGUGCGCUCG |
| 26 | 405 | 47 | 0.705 | UGGUGUUGCUGUUGCUGUU | 19 | 71 | -4.1 | -1.1 | -33.3 | CGAGCUGGUGUUGCUGUUGCUGUUGCUCG |
| 27 | 2216 | 36 | 0.701 | CGGAAAAGUUUGAAGAGAA | 19 | 62 | -2.4 | 0 | -27.6 | CGACGCGGAAAAGUUUGAAGAGAACGUCG |
| 28 | 90 | 36 | 0.701 | CGGACUUAAGAUAAUAGGU | 19 | 64 | -5.6 | -1 | -28.7 | CGAGCCGGACUUAAGAUAAUAGGUGCUCG |
| 29 | 404 | 52 | 0.701 | GGUGUUGCUGUUGCUGUUG | 19 | 71 | -4.1 | -1.1 | -34.3 | CGAGCGGUGUUGCUGUUGCUGUUGCUCG |
| 30 | 2222 | 36 | 0.701 | GAAAAGCGGAAAAGUUUGA | 19 | 63 | -4.4 | -1.5 | -27.4 | CGACGGAAAAGCGGAAAAGUUUGACGUCG |
| 31 | 970 | 31 | 0.698 | UGGUAGAAUUGUUGAGAU | 19 | 61 | -0.6 | 0 | -27.4 | GCACGUGGUAGAAUUGUUGAGAUUCGUGC |
| 32 | 403 | 47 | 0.698 | GUGUUGCUGUUGCUGUUGU | 19 | 70 | -4.1 | -1.1 | -32.7 | CGCGAGUGUUGCUGUUGCUGUUGUUCGCG |
| 33 | 399 | 47 | 0.698 | UGCUGUUGCUGUUGUAGGU | 19 | 71 | -4.7 | -1.1 | -33.7 | GCACGUGCUGUUGCUGUUGUAGGUCGUGC |
| 34 | 400 | 47 | 0.698 | UUGCUGUUGCUGUUGUAGG | 19 | 70 | -5.9 | -1.1 | -32.9 | GCACGUUGCUGUUGCUGUUGUAGGCGUGC |
| 35 | 1220 | 47 | 0.696 | GUUGUAGGUUCCACUGGUU | 19 | 70 | -6.4 | -0.5 | -33.2 | CGCGAGUUGUAGGUUCCACUGGUUUCGCG |
| 36 | 1219 | 42 | 0.696 | UUGUAGGUUCCACUGGUUA | 19 | 68 | -6.4 | -0.5 | -31.8 | GCCGUUGUAGGUUCCACUGGUUACGGC |
| 37 | 1218 | 42 | 0.694 | UGUAGGUUCCACUGGUUAA | 19 | 68 | -6.4 | -0.5 | -31.8 | GCCGUGUAGGUUCCACUGGUUACGGC |
| 38 | 402 | 42 | 0.694 | UGUUGCUGUUGCUGUUGUA | 19 | 68 | -4.1 | -1.1 | -31.3 | GCCGUGUUGCUGUUGCUGUUGUACGGC |
| 39 | 1241 | 42 | 0.693 | GUUAAUCGUCAGCAGAGAA | 19 | 65 | -4.3 | 0 | -30.8 | GCACGGUAAUCGUCAGCAGAGAACGUGC |
| 40 | 1685 | 42 | 0.693 | GUUGAUUAGACAGGAGUGU | 19 | 66 | -6.2 | -0.4 | -31.5 | CGCGAGUUGAUUAGACAGGAGUGUUCGCG |
| 41 | 1221 | 52 | 0.693 | CGUUGUAGGUUCCACUGGU | 19 | 72 | -6.4 | -0.5 | -34.7 | GCACGCGUUGUAGGUUCCACUGGUCGUGC |
| 42 | 1236 | 47 | 0.691 | UCGUCAGCAGAGAAUCGUU | 19 | 69 | -4.3 | 0 | -32.9 | GCACGUCGUCAGCAGAGAAUCGUUCGUGC |
| 43 | 401 | 47 | 0.691 | GUUGCUGUUGCUGUUGUAG | 19 | 68 | -5.1 | -1.1 | -32.3 | GCACGGUUGCUGUUGCUGUUGUAGCGUGC |
| 44 | 1684 | 36 | 0.689 | UUGAUUAGACAGGAGUGUA | 19 | 64 | -6.2 | -0.4 | -30.1 | GCCGUUGAUUAGACAGGAGUGUACGGC |
| 45 | 1235 | 52 | 0.689 | CGUCAGCAGAGAAUCGUUG | 19 | 69 | -7.1 | -1.3 | -33.6 | CGAGCGUCAGCAGAGAAUCGUUGCUCG |
| 46 | 1237 | 47 | 0.688 | AUCGUCAGCAGAGAAUCGU | 19 | 69 | -4.3 | 0 | -33.1 | CGCCAUCGUCAGCAGAGAAUCGUGGCG |
| 47 | 1240 | 36 | 0.688 | UUAUCGUCAGCAGAGAAU | 19 | 64 | -4.3 | 0 | -29.2 | GCACGUUAAUCGUCAGCAGAGAAUCGUGC |
| 48 | 1222 | 52 | 0.688 | UCGUUGUAGGUUCCACUGG | 19 | 72 | -6.4 | -0.5 | -34.9 | CGCGAUCGUUGUAGGUUCCACUGGUCGCG |
| 49 | 1238 | 47 | 0.686 | AAUCGUCAGCAGAGAAUCG | 19 | 67 | -4.3 | 0 | -32.3 | GCACGAAUCGUCAGCAGAGAAUCGCGUGC |
| 50 | 971 | 36 | 0.686 | CUGGUAGAAUUGUUGAGA | 19 | 63 | -5 | 0 | -28.9 | GCACGCUUGUAGAAUUGUUGAGACGUGC |
| 1 | 80 | 40 | 0.808 | GAUAAUAGGUUUUGGCGGAA | 20 | 67 | -5.9 | 0 | -31.6 | CGACGGAUAAUAGGUUUUGGCGGAACGUGC |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|----------------------|-----------|----|---------------------------|----------------------------|----------------------------|---------------------------------|
| 2 | 2822 | 35 | 0.805 | UUGGAUUUUACAUUGCAGCU | 20 | 66 | -5.1 | 0 | -30.2 | GCACGUUGGAUUUUACAUUGCAGCUCGUGC |
| 3 | 81 | 40 | 0.803 | AGAUAUUAGGUUUUGGCGGA | 20 | 69 | -4.1 | 0 | -32.3 | CGACGAGAUAAUAGGUUUUGGCGGACGUCG |
| 4 | 82 | 40 | 0.798 | AAGAUAAUAGGUUUUGGCGG | 20 | 67 | -3.4 | 0 | -31.3 | CGACGAAGAUAAUAGGUUUUGGCGGCGUCG |
| 5 | 2227 | 40 | 0.798 | UUUUGGGAAAAGCGGAAAAG | 20 | 66 | -3.8 | -0.6 | -30.3 | CGCGAUUUUGGGAAAAGCGGAAAAGUCGCG |
| 6 | 2226 | 40 | 0.797 | UUUGGGAAAAGCGGAAAAGU | 20 | 68 | -2.7 | 0 | -31.1 | CGACGUUUGGGAAAAGCGGAAAAGUCGUCG |
| 7 | 83 | 35 | 0.795 | UAAGAUAAUAGGUUUUGGCG | 20 | 64 | -4.6 | -0.4 | -29.3 | CGCGAUAAAGAUAAUAGGUUUUGGCGUCGCG |
| 8 | 2225 | 40 | 0.790 | UUGGGAAAAGCGGAAAAGUU | 20 | 68 | -2.7 | 0 | -31.1 | CGAGCUUGGGAAAAGCGGAAAAGUUCGUCG |
| 9 | 2224 | 40 | 0.779 | UGGGAAAAGCGGAAAAGUUU | 20 | 68 | -2.8 | -0.7 | -31.1 | CGACGUGGGAAAAGCGGAAAAGUUUCGUCG |
| 10 | 2811 | 40 | 0.769 | AUUGCAGCUUGUUUAGGAC | 20 | 68 | -7 | 0 | -32.4 | GCACGAUUGCAGCUUGUUUAGGACCGUGC |
| 11 | 2821 | 35 | 0.763 | UGGAUUUUACAUUGCAGCUU | 20 | 66 | -5.1 | 0 | -30.2 | GCACGUGGAUUUUACAUUGCAGCUUCGUGC |
| 12 | 2823 | 35 | 0.761 | UUUGGAUUUUACAUUGCAGC | 20 | 64 | -5.1 | 0 | -29.5 | GCACGUUUGGAUUUUACAUUGCAGCCGUGC |
| 13 | 2223 | 45 | 0.747 | GGGAAAAGCGGAAAAGUUUG | 20 | 68 | -4.4 | -1.5 | -32.1 | CGACGGGAAAAGCGGAAAAGUUUGCGUCG |
| 14 | 2812 | 40 | 0.726 | CAUUGCAGCUUGUUUAGGA | 20 | 67 | -7 | 0 | -32.3 | GCACGCAUUGCAGCUUGUUUAGGACGUGC |
| 15 | 70 | 50 | 0.724 | UUUGGCGGAAGUAUUGGUGC | 20 | 73 | -7.1 | -0.2 | -35.7 | CGACGUUUGGCGGAAGUAUUGGUGCCGUCG |
| 16 | 2820 | 40 | 0.723 | GGAUUUUACAUUGCAGCUUG | 20 | 66 | -4.9 | 0 | -31.2 | GCACGGGAUUUUACAUUGCAGCUUCGUGC |
| 17 | 2214 | 35 | 0.721 | GGAAAAGUUUGAAGAGAAGU | 20 | 63 | -1.4 | 0 | -29.5 | CGCGAGGAAAAGUUUGAAGAGAAGUUCGCG |
| 18 | 2215 | 40 | 0.716 | CGGAAAAGUUUGAAGAGAAG | 20 | 63 | -2.4 | 0 | -30.2 | CGAGCGGAAAAGUUUGAAGAGAAGCUCG |
| 19 | 2222 | 40 | 0.715 | GGAAAAGCGGAAAAGUUUGA | 20 | 66 | -4.4 | -1.5 | -30.7 | CGACGGGAAAAGCGGAAAAGUUUGACGUCG |
| 20 | 399 | 45 | 0.713 | UUGCUGUUGCUGUUGUAGGU | 20 | 71 | -5.9 | -1.1 | -34.6 | GCACGUUGCUGUUGCUGUUGUAGGUCGUGC |
| 21 | 1219 | 45 | 0.710 | GUUGUAGGUUCCACUGGUUA | 20 | 70 | -6.4 | -0.5 | -34.5 | GCACGGUUGUAGGUUCCACUGGUUACGUGC |
| 22 | 404 | 50 | 0.710 | UGGUGUUGCUGUUGCUGUUG | 20 | 72 | -4.1 | -1.1 | -35.9 | CGAGCUGGUGUUGCUGUUGCUGUUGGCUCG |
| 23 | 1218 | 40 | 0.708 | UUGUAGGUUCCACUGGUUAA | 20 | 68 | -6.4 | -0.5 | -32.7 | CCGUUGUAGGUUCCACUGGUUACGG |
| 24 | 1220 | 50 | 0.706 | CGUUGUAGGUUCCACUGGUU | 20 | 72 | -6.4 | -0.5 | -35.6 | GCACGCGUUGUAGGUUCCACUGGUUCGUGC |
| 25 | 403 | 50 | 0.706 | GGUGUUGCUGUUGCUGUUGU | 20 | 72 | -4.1 | -1.1 | -36 | CGCGAGGUGUUGCUGUUGCUGUUGUUCGCG |
| 26 | 400 | 50 | 0.706 | GUUGCUGUUGCUGUUGUAGG | 20 | 71 | -5.9 | -1.1 | -35.6 | GCACGGUUGCUGUUGCUGUUGUAGGCGUGC |
| 27 | 402 | 45 | 0.703 | GUGUUGCUGUUGCUGUUGUA | 20 | 69 | -4.1 | -1.1 | -34 | CGAGCGUGUUGCUGUUGCUGUUGUAGCUCG |
| 28 | 1236 | 45 | 0.702 | AUCGUCAGCAGAGAAUCGUU | 20 | 69 | -4.3 | 0 | -34 | CGCCAUCGUCAGCAGAGAAUCGUUGGCG |
| 29 | 1240 | 40 | 0.702 | GUUAAUCGUCAGCAGAGAAU | 20 | 66 | -4.3 | 0 | -31.9 | CGCGAGUAAUCGUCAGCAGAGAAUCGCG |
| 30 | 1684 | 40 | 0.702 | GUUGAUUAGACAGGAGUGUA | 20 | 66 | -6.2 | -0.4 | -32.8 | CGAGCGUUGAUUAGACAGGAGUGUAGCUCG |
| 31 | 1221 | 50 | 0.702 | UCGUUGUAGGUUCCACUGGU | 20 | 73 | -6.4 | -0.5 | -36.6 | GCACGUCGUUGUAGGUUCCACUGGUCGUGC |
| 32 | 1235 | 50 | 0.702 | UCGUCAGCAGAGAAUCGUUG | 20 | 70 | -7.1 | -1.3 | -35.5 | CGCGAUCGUCAGCAGAGAAUCGUUGUCGCG |
| 33 | 1237 | 45 | 0.700 | AAUCGUCAGCAGAGAAUCGU | 20 | 69 | -4.3 | 0 | -34 | CGCCAAUCGUCAGCAGAGAAUCGUGGCG |
| 34 | 401 | 45 | 0.700 | UGUUGCUGUUGCUGUUGUAG | 20 | 69 | -5.1 | -1.1 | -33.9 | GCACGUGUUGCUGUUGCUGUUGUAGCGUGC |
| 35 | 1238 | 45 | 0.698 | UAAUCGUCAGCAGAGAAUCG | 20 | 67 | -4.3 | 0 | -33.6 | CGCGAUAAUCGUCAGCAGAGAAUCGUCGCG |
| 36 | 1239 | 40 | 0.698 | UUAAUCGUCAGCAGAGAAUC | 20 | 65 | -4.3 | 0 | -32.1 | GCACGUUAAUCGUCAGCAGAGAAUCCGUGC |
| 37 | 1683 | 35 | 0.698 | UUGAUUAGACAGGAGUGUAU | 20 | 65 | -6.2 | -0.4 | -31.2 | CGAGCUUGAUUAGACAGGAGUGUAUGCUCG |
| 38 | 1222 | 50 | 0.697 | AUCGUUGUAGGUUCCACUGG | 20 | 72 | -6.4 | -0.5 | -36 | GCACGAUCGUUGUAGGUUCCACUGGCGUGC |
| 39 | 1223 | 45 | 0.695 | AAUCGUUGUAGGUUCCACUG | 20 | 69 | -6.4 | -0.3 | -33.6 | GCACGAAUCGUUGUAGGUUCCACUGCGUGC |
| 40 | 1217 | 40 | 0.690 | UGUAGGUUCCACUGGUUAAA | 20 | 68 | -6.4 | -0.5 | -32.7 | GCCGUGUAGGUUCCACUGGUUAAACGGC |
| 41 | 2819 | 35 | 0.682 | GAUUUUACAUUGCAGCUUGU | 20 | 64 | -5.4 | 0 | -29.6 | CGCGAGAUUUUACAUUGCAGCUUGUUCGCG |
| 42 | 858 | 40 | 0.682 | UUUUCAUCCGUUAUCUUGGG | 20 | 66 | -5.4 | -1.8 | -31.4 | CGCGAUUUUCAUCCGUUAUCUUGGGUCGCG |
| 43 | 2813 | 40 | 0.681 | ACAUUGCAGCUUGUUUAGG | 20 | 68 | -5.9 | 0 | -32.1 | GCACGACAUUGCAGCUUGUUUAGGCGUGC |
| 44 | 2814 | 35 | 0.681 | UACAUUGCAGCUUGUUUAG | 20 | 64 | -6 | 0 | -30.1 | GCACGUACAUUGCAGCUUGUUUAGCGUGC |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|-----------------------|-----------|----|--------------------|---------------------|---------------------|----------------------------------|
| 45 | 857 | 45 | 0.679 | UUUCAUCCGUUAUCUUGGGC | 20 | 69 | -6.5 | -1.9 | -33.9 | CGACGUUUCAUCCGUUAUCUUGGGCCGUCG |
| 46 | 2221 | 35 | 0.677 | GAAAAGCGGAAAAGUUUGAA | 20 | 63 | -4.4 | -1.5 | -28.3 | CGACGGAAAAGCGGAAAAGUUUGAACGUCG |
| 47 | 90 | 35 | 0.676 | ACGGACUUAAGAUAAUAGGU | 20 | 66 | -7.1 | -1 | -30.4 | CCGACGGACUUAAGAUAAUAGGUCGG |
| 48 | 970 | 35 | 0.674 | CUGGUAGAAUUGUUGAGAU | 20 | 63 | -5 | 0 | -30 | GCACGCUGGUAGAAUUGUUGAGAUUCGUGC |
| 49 | 1216 | 40 | 0.673 | GUAGGUUCCACUGGUUAAAA | 20 | 67 | -6.4 | -0.5 | -32 | GCACGGUAGGUUCCACUGGUUAAAACGUGC |
| 50 | 859 | 40 | 0.669 | CUUUUCAUCCGUUAUCUUGG | 20 | 64 | -2.6 | -0.4 | -30.7 | CGAGCUUUUCAUCCGUUAUCUUGGCUCG |
| 1 | 2226 | 38 | 0.806 | UUUUGGGAAAAGCGGAAAAGU | 21 | 68 | -3.8 | -0.6 | -32 | CGACGUUUUGGGAAAAGCGGAAAAGUCGUCG |
| 2 | 80 | 38 | 0.802 | AGAUAAUAGGUUUUGGCGGAA | 21 | 69 | -5.9 | 0 | -33.2 | CGACGAGAUAAUAGGUUUUGGCGGAACGUCG |
| 3 | 2225 | 38 | 0.800 | UUUGGGAAAAGCGGAAAAGUU | 21 | 68 | -2.7 | 0 | -32 | CGACGUUUUGGGAAAAGCGGAAAAGUUCGUCG |
| 4 | 81 | 38 | 0.796 | AAGAUAAUAGGUUUUGGCGGA | 21 | 69 | -4.1 | 0 | -33.2 | CGACGAAGAUAAUAGGUUUUGGCGGACGUCG |
| 5 | 82 | 38 | 0.793 | UAAGAUAAUAGGUUUUGGCGG | 21 | 67 | -4.6 | -0.4 | -32.6 | CGCGAUAAAGAUAAUAGGUUUUGGCGGUCGCG |
| 6 | 83 | 33 | 0.793 | UUAAGAUAAUAGGUUUUGGCG | 21 | 64 | -5 | -0.6 | -30.2 | CGCGAUAAAGAUAAUAGGUUUUGGCGUCGCG |
| 7 | 2224 | 38 | 0.790 | UUGGGAAAAGCGGAAAAGUUU | 21 | 68 | -2.8 | -0.7 | -32 | CGACGUUGGGAAAAGCGGAAAAGUUUCGUCG |
| 8 | 84 | 33 | 0.783 | CUUAAGAUAAUAGGUUUUGGC | 21 | 64 | -5.4 | -0.8 | -30.4 | CGACGCUUAAGAUAAUAGGUUUUGGCCGUCG |
| 9 | 2822 | 33 | 0.771 | UUUGGAUUUUACAUUGCAGCU | 21 | 66 | -5.1 | 0 | -31.1 | GCACGUUUGGAUUUUACAUUGCAGCUCGUGC |
| 10 | 2821 | 33 | 0.770 | UUGGAUUUUACAUUGCAGCUU | 21 | 66 | -5.1 | 0 | -31.1 | GCACGUUGGAUUUUACAUUGCAGCUUCGUGC |
| 11 | 2223 | 42 | 0.753 | UGGGAAAAGCGGAAAAGUUUG | 21 | 69 | -4.4 | -1.5 | -33.7 | CGCGAUGGGAAAAGCGGAAAAGUUUGUCGCG |
| 12 | 2811 | 42 | 0.733 | CAUUGCAGCUUGUUUAGGAC | 21 | 69 | -7 | 0 | -35 | GCACGCAUUGCAGCUUGUUUAGGACCGUGC |
| 13 | 2820 | 38 | 0.730 | UGGAUUUUACAUUGCAGCUUG | 21 | 67 | -5.1 | 0 | -32.8 | GCACGUGGAUUUUACAUUGCAGCUUGCGUGC |
| 14 | 2823 | 33 | 0.730 | UUUUGGAUUUUACAUUGCAGC | 21 | 64 | -5.1 | 0 | -30.4 | GCACGUUUUGGAUUUUACAUUGCAGCCGUGC |
| 15 | 2222 | 42 | 0.722 | GGGAAAAGCGGAAAAGUUUGA | 21 | 69 | -4.4 | -1.5 | -34 | CGACGGGAAAAGCGGAAAAGUUUGACGUCG |
| 16 | 1218 | 42 | 0.720 | GUUGUAGGUUCCACUGGUUAA | 21 | 70 | -6.4 | -0.5 | -35.4 | GCACGGUUGUAGGUUCCACUGGUUAAACGUGC |
| 17 | 399 | 47 | 0.720 | GUUGCUGUUGCUGUUGUAGGU | 21 | 73 | -5.9 | -1.1 | -37.3 | CGCGAGUUGCUGUUGCUGUUGUAGGUUCGCG |
| 18 | 1219 | 47 | 0.719 | CGUUGUAGGUUCCACUGGUUA | 21 | 72 | -6.4 | -0.5 | -36.9 | GCACGCGUUGUAGGUUCCACUGGUUACGUGC |
| 19 | 1220 | 47 | 0.714 | UCGUUGUAGGUUCCACUGGUU | 21 | 73 | -6.4 | -0.5 | -37.5 | GCACGUCGUUGUAGGUUCCACUGGUUCGUGC |
| 20 | 403 | 47 | 0.714 | UGGUGUUGCUGUUGCUGUUGU | 21 | 73 | -4.1 | -1.1 | -37.6 | CGAGCUGGUGUUGCUGUUGCUGUUGUGCUCG |
| 21 | 400 | 47 | 0.714 | UGUUGCUGUUGCUGUUGUAGG | 21 | 72 | -5.9 | -1.1 | -37.2 | GCACGUGUUGCUGUUGCUGUUGUAGGCGUGC |
| 22 | 1236 | 42 | 0.713 | AAUCGUCAGCAGAGAAUCGUU | 21 | 69 | -4.3 | 0 | -34.9 | CCGAAUCGUCAGCAGAGAAUCGUUCGG |
| 23 | 1237 | 42 | 0.711 | UAAUCGUCAGCAGAGAAUCGU | 21 | 69 | -4.3 | 0 | -35.3 | GCACGUAAUCGUCAGCAGAGAAUCGUCGUGC |
| 24 | 1239 | 42 | 0.711 | GUUAAUCGUCAGCAGAGAAUC | 21 | 67 | -4.3 | 0 | -34.8 | CGAGGUUAAUCGUCAGCAGAGAAUCCUCG |
| 25 | 1238 | 42 | 0.711 | UUAUCGUCAGCAGAGAAUCG | 21 | 67 | -4.3 | 0 | -34.5 | CGCGAUUAAUCGUCAGCAGAGAAUCGUCGCG |
| 26 | 402 | 47 | 0.711 | GGUGUUGCUGUUGCUGUUGUA | 21 | 72 | -4.4 | -1.1 | -37.3 | CGAGCGGUGUUGCUGUUGCUGUUGUAGCUCG |
| 27 | 1235 | 47 | 0.711 | AUCGUCAGCAGAGAAUCGUUG | 21 | 70 | -7.1 | -1.3 | -36.6 | GCACGAUCGUCAGCAGAGAAUCGUUGCGUGC |
| 28 | 1683 | 38 | 0.710 | GUUGAUUAGACAGGAGUGUAU | 21 | 67 | -6.2 | -0.4 | -33.9 | CGCGAGUUGAUUAGACAGGAGUGUAUUCGCG |
| 29 | 401 | 47 | 0.708 | GUGUUGCUGUUGCUGUUGUAG | 21 | 71 | -5.1 | -1.1 | -36.6 | CGAGCGUGUUGCUGUUGCUGUUGUAGGCUCG |
| 30 | 1217 | 38 | 0.704 | UUGUAGGUUCCACUGGUUAAA | 21 | 68 | -6.4 | -0.5 | -33.6 | CCGUUGUAGGUUCCACUGGUUAAAACGG |
| 31 | 2818 | 33 | 0.697 | GAUUUUACAUUGCAGCUUGUU | 21 | 64 | -6 | 0 | -30.5 | CGCGAGAUUUUACAUUGCAGCUUGUUUCGCG |
| 32 | 2813 | 38 | 0.696 | UACAUUGCAGCUUGUUUAGG | 21 | 68 | -6 | 0 | -33.4 | GCACGUACAUUGCAGCUUGUUUAGGCGUGC |
| 33 | 2814 | 33 | 0.696 | UUACAUUGCAGCUUGUUUAG | 21 | 65 | -6 | 0 | -31 | GCACGUUACAUUGCAGCUUGUUUAGCGUGC |
| 34 | 2213 | 33 | 0.693 | GGAAAAGUUUGAAGAGAAGUU | 21 | 63 | -1.4 | 0 | -30.4 | CGCGAGGAAAAGUUUGAAGAGAAGUUUCGCG |
| 35 | 2812 | 38 | 0.693 | ACAUUGCAGCUUGUUUAGGA | 21 | 69 | -7 | 0 | -34 | GCACGACAUUGCAGCUUGUUUAGGACGUGC |
| 36 | 2819 | 38 | 0.691 | GGAUUUUACAUUGCAGCUUGU | 21 | 67 | -5.4 | 0 | -32.9 | CGCGAGGAUUUUACAUUGCAGCUUGUUCGCG |
| 37 | 2221 | 38 | 0.691 | GGAAAAGCGGAAAAGUUUGAA | 21 | 66 | -4.4 | -1.5 | -31.6 | CGACGGGAAAAGCGGAAAAGUUUGAACGUCG |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|------------------------|-----------|----|--------------------|---------------------|---------------------|-----------------------------------|
| 38 | 2214 | 38 | 0.688 | CGGAAAAGUUUGAAGAGAAGU | 21 | 65 | -2.4 | 0 | -31.9 | CGACGCGGAAAAGUUUGAAGAGAAGUCGUCG |
| 39 | 1216 | 38 | 0.687 | UGUAGGUUCCACUGGUUAAAA | 21 | 68 | -6.4 | -0.5 | -33.6 | GCCGUGUAGGUUCCACUGGUUAAAACGGC |
| 40 | 857 | 42 | 0.687 | UUUUCAUCCGUUAUCUUGGGC | 21 | 69 | -6.5 | -1.9 | -34.8 | CGACGUUUUCAUCCGUUAUCUUGGGCCGUCG |
| 41 | 2215 | 42 | 0.684 | GCGGAAAAGUUUGAAGAGAAG | 21 | 67 | -2.8 | 0 | -33.6 | CGACGCGGAAAAGUUUGAAGAGAAGCGUCG |
| 42 | 2220 | 38 | 0.680 | GAAAAGCGGAAAAGUUUGAAG | 21 | 64 | -4.4 | -1.5 | -30.9 | CGACGAAAAGCGGAAAAGUUUGAAGCGUCG |
| 43 | 398 | 47 | 0.679 | UUGCUGUUGCUGUUGUAGGUG | 21 | 72 | -5.9 | -1.1 | -37.2 | GCACGUUGCUGUUGCUGUUGUAGGUGCGUGC |
| 44 | 404 | 52 | 0.676 | CUGGUGUUGCUGUUGCUGUUG | 21 | 73 | -4.1 | -1.1 | -38.5 | CGAGCUGGUGUUGCUGUUGCUGUUGCUCG |
| 45 | 2216 | 38 | 0.674 | AGCGAAAAGUUUGAAGAGAA | 21 | 67 | -2.8 | 0 | -32.6 | CGACGAGCGGAAAAGUUUGAAGAGAACGUCG |
| 46 | 858 | 42 | 0.674 | CUUUUCAUCCGUUAUCUUGGG | 21 | 67 | -5.4 | -1.8 | -34 | CGAGCUUUUCAUCCGUUAUCUUGGGCUCG |
| 47 | 856 | 42 | 0.674 | UUUCAUCCGUUAUCUUGGGCA | 21 | 70 | -6.5 | -1.9 | -35.5 | GCCGUUUUCAUCCGUUAUCUUGGGCACGGC |
| 48 | 1240 | 38 | 0.671 | AGUUAUCGUCAGCAGAGAAU | 21 | 67 | -4.3 | 0 | -33.5 | CGCCAGUUAUCGUCAGCAGAGAAUGGCG |
| 49 | 1684 | 42 | 0.670 | CGUUGAUUAGACAGGAGUGUA | 21 | 68 | -6.2 | -0.4 | -35.2 | CGAGCCGUUGAUUAGACAGGAGUGUAGCUCG |
| 50 | 1215 | 38 | 0.670 | GUAGGUUCCACUGGUUAAAAU | 21 | 68 | -6.4 | -0.5 | -33.1 | CGCGAGUAGGUUCCACUGGUUAAAAUUCGCG |
| 1 | 2225 | 36 | 0.809 | UUUUGGGAAAAGCGGAAAAGUU | 22 | 68 | -3.8 | -0.6 | -32.9 | CGACGUUUUGGGAAAAGCGGAAAAGUUCGUCG |
| 2 | 2224 | 36 | 0.799 | UUUGGGAAAAGCGGAAAAGUUU | 22 | 68 | -2.8 | -0.7 | -32.9 | CGACGUUUUGGGAAAAGCGGAAAAGUUUCGUCG |
| 3 | 80 | 36 | 0.795 | AAGAUAAUAGGUUUUGGCGGAA | 22 | 69 | -5.9 | 0 | -34.1 | CGACGAAGAUAAUAGGUUUUGGCGAACGUCG |
| 4 | 81 | 36 | 0.790 | UAAGAUAAUAGGUUUUGGCGGA | 22 | 69 | -4.6 | -0.4 | -34.5 | CCGUAAGAUAAUAGGUUUUGGCGGACCGG |
| 5 | 82 | 36 | 0.790 | UUAAGAUAAUAGGUUUUGGCGG | 22 | 68 | -5 | -0.6 | -33.5 | CGCGAUUAAAGAUAAUAGGUUUUGGCGGUCGCG |
| 6 | 83 | 36 | 0.777 | CUUAAGAUAAUAGGUUUUGGCG | 22 | 66 | -5.4 | -0.8 | -32.8 | CGAGCUUAAGAUAAUAGGUUUUGGCGCUCG |
| 7 | 84 | 31 | 0.770 | ACUUAAGAUAAUAGGUUUUGGC | 22 | 65 | -5.4 | -0.8 | -32.1 | CGACGACUUAAGAUAAUAGGUUUUGGCCGUCG |
| 8 | 2223 | 40 | 0.764 | UUGGGAAAAGCGGAAAAGUUUG | 22 | 69 | -4.4 | -1.5 | -34.6 | CGCGAUUGGGAAAAGCGGAAAAGUUUGUCGCG |
| 9 | 2822 | 31 | 0.740 | UUUUGGAUUUUACAUUGCAGCU | 22 | 66 | -5.1 | 0 | -32 | GCACGUUUUGGAUUUUACAUUGCAGCUCGUGC |
| 10 | 2821 | 31 | 0.739 | UUUGGAUUUUACAUUGCAGCUU | 22 | 66 | -5.1 | 0 | -32 | GCACGUUUUGGAUUUUACAUUGCAGCUUCGUGC |
| 11 | 2820 | 36 | 0.738 | UUGGAUUUUACAUUGCAGCUUG | 22 | 67 | -5.1 | 0 | -33.7 | GCACGUUGGAUUUUACAUUGCAGCUUGCUGUC |
| 12 | 1218 | 45 | 0.729 | CGUUGUAGGUUCCACUGGUUAA | 22 | 72 | -6.4 | -0.5 | -37.8 | GCACGCGUUGUAGGUUCCACUGGUUAAACGUGC |
| 13 | 2222 | 40 | 0.729 | UGGGAAAAGCGGAAAAGUUUGA | 22 | 70 | -4.4 | -1.5 | -35.6 | CCGUGGGAAAAGCGGAAAAGUUUGACCGG |
| 14 | 399 | 45 | 0.727 | UGUUGCUGUUGCUGUUGUAGGU | 22 | 73 | -5.9 | -1.1 | -38.9 | GCACGUGUUGCUGUUGCUGUUGUAGGUCGUGC |
| 15 | 1219 | 45 | 0.726 | UCGUUGUAGGUUCCACUGGUUA | 22 | 73 | -6.4 | -0.5 | -38.8 | GCCGUCGUUGUAGGUUCCACUGGUUACGGC |
| 16 | 1238 | 45 | 0.723 | GUUAAUCGUCAGCAGAGAAUCG | 22 | 69 | -4.3 | 0 | -37.2 | GCACGGUUAUCGUCAGCAGAGAAUCGCGUGC |
| 17 | 1237 | 40 | 0.723 | UUAUCGUCAGCAGAGAAUCGU | 22 | 69 | -4.3 | 0 | -36.2 | GCACGUUAAUCGUCAGCAGAGAAUCGUCGUGC |
| 18 | 1236 | 40 | 0.723 | UAAUCGUCAGCAGAGAAUCGUU | 22 | 69 | -4.3 | 0 | -36.2 | GCACGUAAUCGUCAGCAGAGAAUCGUUCGUGC |
| 19 | 400 | 50 | 0.721 | GUGUUGCUGUUGCUGUUGUAGG | 22 | 73 | -5.9 | -1.1 | -39.9 | CGAGCGUGUUGCUGUUGCUGUUGUAGGGCUCG |
| 20 | 1235 | 45 | 0.721 | AAUCGUCAGCAGAGAAUCGUUG | 22 | 70 | -7.1 | -1.3 | -37.5 | GCACGAAUCGUCAGCAGAGAAUCGUUGCGUGC |
| 21 | 402 | 45 | 0.718 | UGGUGUUGCUGUUGCUGUUGUA | 22 | 73 | -4.6 | -1.1 | -38.9 | GCCGUGGUGUUGCUGUUGCUGUUGUACGGC |
| 22 | 1217 | 40 | 0.716 | GUUGUAGGUUCCACUGGUUAAA | 22 | 70 | -6.4 | -0.5 | -36.3 | GCACGGUUGUAGGUUCCACUGGUUAAACGUGC |
| 23 | 401 | 50 | 0.716 | GGUGUUGCUGUUGCUGUUGUAG | 22 | 73 | -5.7 | -1.1 | -39.9 | CGAGCGGUGUUGCUGUUGCUGUUGUAGGCUCG |
| 24 | 2817 | 31 | 0.711 | GAUUUUACAUUGCAGCUUGUUA | 22 | 64 | -6 | 0 | -31.8 | GCACGGAUUUUACAUUGCAGCUUGUUAACGUGC |
| 25 | 2813 | 36 | 0.710 | UUACAUUGCAGCUUGUUAUAGG | 22 | 68 | -6 | 0 | -34.3 | GCACGUUACAUUGCAGCUUGUUAUAGGCGUGC |
| 26 | 2814 | 31 | 0.710 | UUUACAUUGCAGCUUGUUAUAG | 22 | 65 | -6 | 0 | -31.9 | GCACGUUUACAUUGCAGCUUGUUAUAGCGUGC |
| 27 | 2812 | 36 | 0.707 | UACAUUGCAGCUUGUUAUAGGA | 22 | 69 | -7 | 0 | -35.3 | GCCGUACAUUGCAGCUUGUUAUAGGACGGC |
| 28 | 2818 | 36 | 0.705 | GGAUUUUACAUUGCAGCUUGUU | 22 | 67 | -6 | 0 | -33.8 | CGCGAGGAUUUUACAUUGCAGCUUGUUUCGCG |
| 29 | 2823 | 31 | 0.701 | UUUUUGGAUUUUACAUUGCAGC | 22 | 65 | -5.1 | 0 | -31.3 | GCACGUUUUUGGAUUUUACAUUGCAGCCGUGC |
| 30 | 2811 | 40 | 0.701 | ACAUUGCAGCUUGUUAUAGGAC | 22 | 70 | -7 | 0 | -36.7 | GCACGACAUUGCAGCUUGUUAUAGGACCGUGC |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|-------------------------|-----------|----|--------------------|---------------------|---------------------|------------------------------------|
| 31 | 2819 | 36 | 0.699 | UGGAUUUUACAUUGCAGCUUGU | 22 | 68 | -5.4 | 0 | -34.5 | GCACGUGGAUUUUACAUUGCAGCUUGUCGUGC |
| 32 | 1216 | 36 | 0.699 | UUGUAGGUUCCACUGGUUAAAA | 22 | 68 | -6.4 | -0.5 | -34.5 | CCGUUGUAGGUUCCACUGGUUAAAACGG |
| 33 | 2221 | 40 | 0.699 | GGAAAAGCGGAAAAGUUUGAA | 22 | 69 | -4.4 | -1.5 | -34.9 | CGACGGGAAAAGCGGAAAAGUUUGAACGUCG |
| 34 | 2220 | 40 | 0.694 | GGAAAAGCGGAAAAGUUUGAAG | 22 | 68 | -4.4 | -1.5 | -34.2 | CGACGGGAAAAGCGGAAAAGUUUGAAGCGUCG |
| 35 | 2215 | 40 | 0.689 | AGCGGAAAAGUUUGAAGAGAAG | 22 | 68 | -2.8 | 0 | -35.2 | CGACGAGCGGAAAAGUUUGAAGAGAAGCGUCG |
| 36 | 398 | 50 | 0.688 | GUUGCUGUUGCUGUUGUAGGUG | 22 | 73 | -5.9 | -1.1 | -39.9 | GCACGGUUGCUGUUGCUGUUGUAGGUGCGUGC |
| 37 | 1215 | 36 | 0.683 | UGUAGGUUCCACUGGUUAAAAU | 22 | 69 | -6.4 | -0.5 | -34.7 | GCACGUGUAGGUUCCACUGGUUAAAAUCGUGC |
| 38 | 1239 | 40 | 0.682 | AGUUAUCGUCAGCAGAGAAUC | 22 | 68 | -4.3 | 0 | -36.4 | GCACGAGUUAUCGUCAGCAGAGAAUCCGUGC |
| 39 | 2216 | 36 | 0.682 | AAGCGGAAAAGUUUGAAGAGAA | 22 | 67 | -3.6 | -1.1 | -33.5 | CGACGAAGCGGAAAAGUUUGAAGAGAACGUCG |
| 40 | 403 | 50 | 0.682 | CUGGUGUUGCUGUUGCUGUUGU | 22 | 74 | -4.1 | -1.1 | -40.2 | CGAGCCUGGUGUUGCUGUUGCUGUUGUCUCG |
| 41 | 2219 | 36 | 0.682 | GAAAAGCGGAAAAGUUUGAAGA | 22 | 66 | -4.4 | -1.5 | -32.8 | CGACGAAAAGCGGAAAAGUUUGAAGACGUCG |
| 42 | 856 | 40 | 0.682 | UUUUCAUCCGUUAUCUUGGGCA | 22 | 70 | -6.5 | -1.9 | -36.4 | GCCGUUUUCAUCCGUUAUCUUGGGCACGGC |
| 43 | 1682 | 40 | 0.680 | GUUGAUUAGACAGGAGUGUAUG | 22 | 68 | -6.2 | -0.4 | -36.5 | CGAGCGUUGAUUAGACAGGAGUGUAUGGCUCG |
| 44 | 1683 | 40 | 0.679 | CGUUGAUUAGACAGGAGUGUAU | 22 | 69 | -6.2 | -0.4 | -36.3 | CGAGCCGUUGAUUAGACAGGAGUGUAUGCUCG |
| 45 | 857 | 45 | 0.679 | CUUUUCAUCCGUUAUCUUGGGC | 22 | 71 | -6.5 | -1.9 | -37.4 | CGACGCUUUUCAUCCGUUAUCUUGGGCCGUCG |
| 46 | 2217 | 36 | 0.674 | AAAGCGGAAAAGUUUGAAGAGA | 22 | 67 | -4.4 | -1.5 | -33.5 | CGACGAAAGCGGAAAAGUUUGAAGAGACGUCG |
| 47 | 2218 | 36 | 0.672 | AAAAGCGGAAAAGUUUGAAGAG | 22 | 66 | -4.4 | -1.5 | -32.5 | CGACGAAAAGCGGAAAAGUUUGAAGAGCGUCG |
| 48 | 855 | 45 | 0.670 | UUUCAUCCGUUAUCUUGGGCAC | 22 | 72 | -6.5 | -1.9 | -38.2 | CGACGUUUUCAUCCGUUAUCUUGGGCACCGUCG |
| 49 | 2212 | 31 | 0.667 | GGAAAAGUUUGAAGAGAAGUUU | 22 | 63 | -3 | 0 | -31.3 | CGCGAGGAAAAGUUUGAAGAGAAGUUUCGCG |
| 50 | 858 | 40 | 0.667 | UCUUUCAUCCGUUAUCUUGGG | 22 | 69 | -5.4 | -1.8 | -35.9 | CGCGAUCUUUCAUCCGUUAUCUUGGGUCGCG |
| 1 | 2224 | 34 | 0.808 | UUUUGGGAAAAGCGGAAAAGUUU | 23 | 68 | -7 | -0.7 | -33.8 | CGACGUUUUGGGAAAAGCGGAAAAGUUUCGUCG |
| 2 | 80 | 34 | 0.790 | UAAGAUAAUAGGUUUUGGCGGAA | 23 | 69 | -5.9 | -0.4 | -35.4 | CCGGUAAGAUAAUAGGUUUUGGCGGAACCGG |
| 3 | 81 | 34 | 0.788 | UUAAGAUAAUAGGUUUUGGCGGA | 23 | 69 | -5 | -0.6 | -35.4 | CCGGUUAAGAUAAUAGGUUUUGGCGGACCGG |
| 4 | 82 | 39 | 0.776 | CUUAAGAUAAUAGGUUUUGGCGG | 23 | 69 | -5.4 | -0.8 | -36.1 | CGAGCUUAAGAUAAUAGGUUUUGGCGGCUCG |
| 5 | 2223 | 39 | 0.774 | UUUGGGAAAAGCGGAAAAGUUUG | 23 | 69 | -5.4 | -1.5 | -35.5 | CGCGAUUUGGGAAAAGCGGAAAAGUUUGUCGCG |
| 6 | 83 | 34 | 0.764 | ACUUAAGAUAAUAGGUUUUGGCG | 23 | 67 | -5.4 | -0.8 | -34.5 | CGACGACUUAAGAUAAUAGGUUUUGGCGGUCG |
| 7 | 2222 | 39 | 0.741 | UUGGGAAAAGCGGAAAAGUUUGA | 23 | 70 | -4.4 | -1.5 | -36.5 | CCGGUUGGGAAAAGCGGAAAAGUUUGACCGG |
| 8 | 1218 | 43 | 0.735 | UCGUUGUAGGUUCCACUGGUUAA | 23 | 73 | -6.4 | -0.5 | -39.7 | GCCGUCGUUGUAGGUUCCACUGGUUAAACGGC |
| 9 | 1237 | 43 | 0.734 | GUUAUCGUCAGCAGAGAAUCGU | 23 | 70 | -4.3 | 0 | -38.9 | CGCGAGUUAUCGUCAGCAGAGAAUCGUUCGCG |
| 10 | 1236 | 39 | 0.734 | UUAUCGUCAGCAGAGAAUCGUU | 23 | 69 | -4.3 | 0 | -37.1 | GCACGUUAUCGUCAGCAGAGAAUCGUUCGUGC |
| 11 | 399 | 47 | 0.734 | GUGUUGCUGUUGCUGUUGUAGGU | 23 | 75 | -5.9 | -1.1 | -41.6 | CGCGAGUGUUGCUGUUGCUGUUGUAGGUUCGCG |
| 12 | 1235 | 43 | 0.731 | UAAUCGUCAGCAGAGAAUCGUUG | 23 | 70 | -7.1 | -1.3 | -38.8 | CGCGAUAAUCGUCAGCAGAGAAUCGUUGUCGCG |
| 13 | 1217 | 43 | 0.724 | CGUUGUAGGUUCCACUGGUUAAA | 23 | 72 | -6.4 | -0.5 | -38.7 | GCACGCGUUGUAGGUUCCACUGGUUAAAACGUGC |
| 14 | 2813 | 34 | 0.722 | UUUCAUUGCAGCUUGUUAUAGG | 23 | 68 | -6 | 0 | -35.2 | GCACGUUUACAUUGCAGCUUGUUAUAGGCGUGC |
| 15 | 2812 | 34 | 0.719 | UUACAUUGCAGCUUGUUAUAGGA | 23 | 69 | -7 | 0 | -36.2 | GCCGUUACAUUGCAGCUUGUUAUAGGACGGC |
| 16 | 2817 | 34 | 0.718 | GGAUUUUACAUUGCAGCUUGUUA | 23 | 67 | -6 | 0 | -35.1 | GCACGGGAUUUUACAUUGCAGCUUGUUAACGUGC |
| 17 | 2811 | 39 | 0.714 | UACAUUGCAGCUUGUUAUAGGAC | 23 | 70 | -7 | 0 | -38 | GCACGUACAUUGCAGCUUGUUAUAGGACCGUGC |
| 18 | 2818 | 34 | 0.712 | UGGAUUUACAUUGCAGCUUGUU | 23 | 68 | -6 | 0 | -35.4 | GCACGUGGAUUUACAUUGCAGCUUGUUCGUGC |
| 19 | 1216 | 39 | 0.711 | GUUGUAGGUUCCACUGGUUAAAA | 23 | 70 | -6.4 | -0.5 | -37.2 | GCACGGUUGUAGGUUCCACUGGUUAAAACGUGC |
| 20 | 2820 | 34 | 0.710 | UUUGGAUUUACAUUGCAGCUUG | 23 | 67 | -5.1 | 0 | -34.6 | GCACGUUUGGAUUUACAUUGCAGCUUGCGUGC |
| 21 | 2819 | 34 | 0.708 | UUGGAUUUACAUUGCAGCUUGU | 23 | 68 | -5.4 | 0 | -35.4 | GCACGUUGGAUUUACAUUGCAGCUUGUCGUGC |
| 22 | 2221 | 39 | 0.707 | UGGAAAAGCGGAAAAGUUUGAA | 23 | 70 | -4.4 | -1.5 | -36.5 | CCGGUGGGAAAAGCGGAAAAGUUUGAACCGG |
| 23 | 2220 | 43 | 0.701 | GGAAAAGCGGAAAAGUUUGAAG | 23 | 70 | -4.4 | -1.5 | -37.5 | CGACGGGAAAAGCGGAAAAGUUUGAAGCGUCG |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔGbimol | ΔGunimol | ΔGduplex | Molecular beacon sequence |
|------|-------|-----|----------|--------------------------|-----------|----|---------|----------|----------|-------------------------------------|
| 24 | 1215 | 34 | 0.696 | UUGUAGGUUCCACUGGUUAAAAU | 23 | 69 | -6.4 | -0.5 | -35.6 | GCACGUUGUAGGUUCCACUGGUUAAAAUCGUGC |
| 25 | 2215 | 39 | 0.696 | AAGCGGAAAAGUUUGAAGAGAAG | 23 | 68 | -3.6 | -1.1 | -36.1 | CGACGAAGCGGAAAAGUUUGAAGAGAAGCGUCG |
| 26 | 398 | 47 | 0.696 | UGUUGCUGUUGCUGUUGUAGGUG | 23 | 74 | -5.9 | -1.1 | -41.5 | GCACGUGUUGCUGUUGCUGUUGUAGGUGCGUGC |
| 27 | 1238 | 43 | 0.694 | AGUUAUUCGUCAGCAGAGAAUCG | 23 | 70 | -4.3 | 0 | -38.8 | GCACGAGUUAUUCGUCAGCAGAGAAUCGCGUGC |
| 28 | 2219 | 39 | 0.694 | GGAAAAGCGGAAAAGUUUGAAGA | 23 | 69 | -4.4 | -1.5 | -36.1 | CGACGGGAAAAGCGGAAAAGUUUGAAGACGUCG |
| 29 | 402 | 47 | 0.687 | CUGGUGUUGCUGUUGCUGUUGUA | 23 | 74 | -6.7 | -1.1 | -41.5 | CGAGCCUGGUGUUGCUGUUGCUGUUGUAGCUCG |
| 30 | 2216 | 34 | 0.687 | AAAGCGGAAAAGUUUGAAGAGAA | 23 | 67 | -4.4 | -1.5 | -34.4 | CGACGAAAGCGGAAAAGUUUGAAGAGAACGUCG |
| 31 | 2218 | 39 | 0.684 | GAAAAGCGGAAAAGUUUGAAGAG | 23 | 67 | -4.4 | -1.5 | -35.4 | CGACGAAAAGCGGAAAAGUUUGAAGAGCGUCG |
| 32 | 2217 | 34 | 0.682 | AAAAGCGGAAAAGUUUGAAGAGA | 23 | 67 | -4.4 | -1.5 | -34.4 | CGACGAAAAGCGGAAAAGUUUGAAGAGACGUCG |
| 33 | 1214 | 39 | 0.677 | UGUAGGUUCCACUGGUUAAAAUC | 23 | 70 | -6.4 | -0.5 | -37.6 | GCACGUGUAGGUUCCACUGGUUAAAAUCGUGC |
| 34 | 855 | 43 | 0.677 | UUUUCAUCCGUUAUCUUGGGCAC | 23 | 72 | -6.5 | -1.9 | -39.1 | CGACGUUUUCAUCCGUUAUCUUGGGCACCGUCG |
| 35 | 856 | 43 | 0.675 | CUUUUCAUCCGUUAUCUUGGGCA | 23 | 71 | -6.5 | -1.9 | -39 | CGACGCUUUUCAUCCGUUAUCUUGGGCACGUCG |
| 36 | 857 | 43 | 0.672 | UCUUUCAUCCGUUAUCUUGGGC | 23 | 71 | -6.5 | -1.9 | -39.3 | CGACGUCUUUCAUCCGUUAUCUUGGGCCGUCG |
| 37 | 854 | 47 | 0.666 | UUUCAUCCGUUAUCUUGGGCACG | 23 | 73 | -6.5 | -1.9 | -40.6 | CGCGAUUUUCAUCCGUUAUCUUGGGCACGUCGCG |
| 38 | 2214 | 39 | 0.665 | AGCGGAAAAGUUUGAAGAGAAGU | 23 | 70 | -2.8 | 0 | -36.9 | CGCCAGCGGAAAAGUUUGAAGAGAAGUGGCG |
| 39 | 397 | 47 | 0.658 | GUUGCUGUUGCUGUUGUAGGUGA | 23 | 74 | -6.1 | -1.5 | -41.8 | GCACGGUUGCUGUUGCUGUUGUAGGUGACGUGC |
| 40 | 1239 | 43 | 0.655 | GAGUUAUUCGUCAGCAGAGAAUC | 23 | 69 | -4.3 | 0 | -39.3 | CCGGAGUUAUUCGUCAGCAGAGAAUCCGG |
| 41 | 1684 | 39 | 0.654 | UUCGUUGAUUAGACAGGAGUGUA | 23 | 69 | -6.5 | -0.4 | -38 | GCCGUUCGUUGAUUAGACAGGAGUGUACGGC |
| 42 | 1682 | 43 | 0.652 | CGUUGAUUAGACAGGAGUGUAUG | 23 | 69 | -6.2 | -0.4 | -38.9 | CGAGCGUUGAUUAGACAGGAGUGUAUGCUCG |
| 43 | 1683 | 39 | 0.651 | UCGUUGAUUAGACAGGAGUGUAU | 23 | 70 | -6.2 | -0.4 | -38.2 | CGAGCUCGUUGAUUAGACAGGAGUGUAUGCUCG |
| 44 | 1681 | 39 | 0.651 | GUUGAUUAGACAGGAGUGUAUGU | 23 | 69 | -6.6 | -0.4 | -38.2 | CGCGAGUUGAUUAGACAGGAGUGUAUGUUCGCG |
| 45 | 858 | 43 | 0.641 | GUCUUUCAUCCGUUAUCUUGGG | 23 | 70 | -5.4 | -1.8 | -38.6 | CGACGGUCUUUCAUCCGUUAUCUUGGGCGUCG |
| 46 | 2212 | 34 | 0.640 | CGGAAAAGUUUGAAGAGAAGUUU | 23 | 66 | -3 | 0 | -33.7 | CGACGCGGAAAAGUUUGAAGAGAAGUUUCGUCG |
| 47 | 90 | 34 | 0.640 | UUCACGGACUUAAGAUAAUAGGU | 23 | 68 | -7.1 | -1 | -35.8 | CGAGCUUCACGGACUUAAGAUAAUAGGUGCUCG |
| 48 | 966 | 34 | 0.638 | UGGUAGAAUUGUUGAGAUGCUU | 23 | 68 | -4.6 | 0 | -35.9 | GCACGUGGUAGAAUUGUUGAGAUGCUUCGUGC |
| 49 | 2213 | 39 | 0.635 | GCGGAAAAGUUUGAAGAGAAGUU | 23 | 69 | -2.8 | 0 | -36.2 | CGCGAGCGGAAAAGUUUGAAGAGAAGUUUCGCG |
| 50 | 91 | 34 | 0.624 | UUUCACGGACUUAAGAUAAUAGG | 23 | 67 | -5.4 | 0 | -35 | CGCGAUUUCACGGACUUAAGAUAAUAGGUCGCG |
| 1 | 80 | 33 | 0.788 | UUAAGAUAAUAGGUUUUGGCGGAA | 24 | 69 | -5.9 | -0.6 | -36.3 | CCGUUAAGAUAAUAGGUUUUGGCGGAACGG |
| 2 | 2223 | 37 | 0.784 | UUUUGGGAAAAGCGGAAAAGUUUG | 24 | 69 | -7 | -1.5 | -36.4 | CGCGAUUUUGGGAAAAGCGGAAAAGUUUGUCGCG |
| 3 | 81 | 37 | 0.774 | CUUAAGAUAAUAGGUUUUGGCGGA | 24 | 70 | -5.4 | -0.8 | -38 | CGACGCUUAAGAUAAUAGGUUUUGGCGGACGUCG |
| 4 | 82 | 37 | 0.763 | ACUUAAGAUAAUAGGUUUUGGCGG | 24 | 70 | -5.4 | -0.8 | -37.8 | CGACGACUUAAGAUAAUAGGUUUUGGCGGCGUCG |
| 5 | 2222 | 37 | 0.751 | UUUGGAAAAGCGGAAAAGUUUGA | 24 | 70 | -5.4 | -1.5 | -37.4 | CCGGUUUGGAAAAGCGGAAAAGUUUGACCGG |
| 6 | 1236 | 41 | 0.743 | GUUAAUCGUCAGCAGAGAAUCGUU | 24 | 70 | -4.3 | 0 | -39.8 | CGCGAGUUAUUCGUCAGCAGAGAAUCGUUUCGCG |
| 7 | 1235 | 41 | 0.741 | UUAUUCGUCAGCAGAGAAUCGUUG | 24 | 70 | -7.1 | -1.3 | -39.7 | CGCGAUUAAUUCGUCAGCAGAGAAUCGUUGUCGCG |
| 8 | 2813 | 33 | 0.734 | UUUUACAUUGCAGCUUGUUAUAGG | 24 | 68 | -6 | 0 | -36.1 | GCACGUUUUACAUUGCAGCUUGUUAUAGGCGUGC |
| 9 | 2812 | 33 | 0.731 | UUUACAUUGCAGCUUGUUAUAGGA | 24 | 69 | -7 | 0 | -37.1 | GCCGUUUACAUUGCAGCUUGUUAUAGGACGGC |
| 10 | 1217 | 41 | 0.730 | UCGUUGUAGGUUCCACUGGUUAAA | 24 | 72 | -6.4 | -0.5 | -40.6 | GCCGUCGUUGUAGGUUCCACUGGUUAAACGGC |
| 11 | 2816 | 33 | 0.728 | GGAUUUUACAUUGCAGCUUGUUAU | 24 | 68 | -6 | 0 | -36.2 | CGCGAGGAUUUACAUUGCAGCUUGUUAUUCGCG |
| 12 | 2811 | 37 | 0.726 | UUACAUUGCAGCUUGUUAUAGGAC | 24 | 70 | -7 | 0 | -38.9 | GCACGUUACAUUGCAGCUUGUUAUAGGACCGUGC |
| 13 | 2817 | 33 | 0.724 | UGGAUUUACAUUGCAGCUUGUUA | 24 | 68 | -6 | 0 | -36.7 | GCCGUGGAUUUACAUUGCAGCUUGUUAACGGC |
| 14 | 2818 | 33 | 0.720 | UUGGAUUUACAUUGCAGCUUGUU | 24 | 68 | -6 | 0 | -36.3 | GCACGUUGGAUUUACAUUGCAGCUUGUUCGUGC |
| 15 | 1216 | 41 | 0.719 | CGUUGUAGGUUCCACUGGUUAAAA | 24 | 72 | -6.4 | -0.5 | -39.6 | GCACGCGUUGUAGGUUCCACUGGUUAAACGUGC |
| 16 | 2221 | 37 | 0.719 | UUGGAAAAGCGGAAAAGUUUGAA | 24 | 70 | -4.4 | -1.5 | -37.4 | CCGUUGGAAAAGCGGAAAAGUUUGAACGG |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|----------------------------|-----------|----|--------------------|---------------------|---------------------|--------------------------------------|
| 17 | 2220 | 41 | 0.708 | UGGAAAAGCGGAAAAGUUUGAAG | 24 | 71 | -4.4 | -1.5 | -39.1 | CGCGAUGGGAAAAGCGGAAAAGUUUGAAGUCGCG |
| 18 | 1215 | 37 | 0.707 | GUUGUAGGUUCCACUGGUUAAAAU | 24 | 70 | -6.4 | -0.5 | -38.3 | CGCGAGUUGUAGGUUCCACUGGUUAAAAUUCGCG |
| 19 | 1237 | 41 | 0.706 | AGUUAAUCGUCAGCAGAGAAUCGU | 24 | 71 | -4.3 | 0 | -40.5 | CGCCAGUUAAUCGUCAGCAGAGAAUCGUGGCG |
| 20 | 398 | 50 | 0.703 | GUGUUGCUGUUGCUGUUGUAGGUG | 24 | 75 | -5.9 | -1.1 | -44.2 | CGAGCGUGUUGCUGUUGCUGUUGUAGGUGGCG |
| 21 | 2219 | 41 | 0.702 | GGGAAAAGCGGAAAAGUUUGAAGA | 24 | 71 | -4.4 | -1.5 | -39.4 | CGACGGGAAAAGCGGAAAAGUUUGAAGACGUCG |
| 22 | 2215 | 37 | 0.700 | AAAGCGGAAAAGUUUGAAGAGAAG | 24 | 68 | -4.4 | -1.5 | -37 | CGACGAAAGCGGAAAAGUUUGAAGAGAAGCGUCG |
| 23 | 2218 | 41 | 0.696 | GGAAAAGCGGAAAAGUUUGAAGAG | 24 | 70 | -4.4 | -1.5 | -38.7 | CGACGGGAAAAGCGGAAAAGUUUGAAGAGCGUCG |
| 24 | 2217 | 37 | 0.694 | GAAAAGCGGAAAAGUUUGAAGAGA | 24 | 68 | -4.4 | -1.5 | -37.3 | CGACGAAAAGCGGAAAAGUUUGAAGAGACGUCG |
| 25 | 2216 | 33 | 0.694 | AAAAGCGGAAAAGUUUGAAGAGAA | 24 | 67 | -4.4 | -1.5 | -35.3 | CGACGAAAAGCGGAAAAGUUUGAAGAGAACGUCG |
| 26 | 1214 | 37 | 0.690 | UUGUAGGUUCCACUGGUUAAAAUC | 24 | 70 | -6.4 | -0.5 | -38.5 | GCACGUUGUAGGUUCCACUGGUUAAAAUCGUCG |
| 27 | 2820 | 33 | 0.684 | UUUUGGAUUUUACAUUGCAGCUUG | 24 | 67 | -5.1 | 0 | -35.5 | GCACGUUUUGGAUUUUACAUUGCAGCUUGCGUCG |
| 28 | 2819 | 33 | 0.683 | UUUGGAUUUUACAUUGCAGCUUGU | 24 | 68 | -5.4 | 0 | -36.3 | GCACGUUUUGGAUUUUACAUUGCAGCUUGCGUCG |
| 29 | 854 | 45 | 0.673 | UUUUCAUCCGUUAUCUUGGGCACG | 24 | 73 | -6.5 | -1.9 | -41.5 | CGCGAUUUUCAUCCGUUAUCUUGGGCACGUCGCG |
| 30 | 2214 | 37 | 0.672 | AAGCGGAAAAGUUUGAAGAGAAGU | 24 | 70 | -3.6 | -1.1 | -37.8 | CGCCAAGCGGAAAAGUUUGAAGAGAAGUGGCG |
| 31 | 855 | 45 | 0.671 | CUUUUCAUCCGUUAUCUUGGGCAC | 24 | 73 | -6.5 | -1.9 | -41.7 | CGACGCUUUUCAUCCGUUAUCUUGGGCACCGUCG |
| 32 | 1238 | 45 | 0.668 | GAGUUAUCGUCAGCAGAGAAUCG | 24 | 71 | -4.3 | 0 | -41.7 | GCACGGAGUUAUCGUCAGCAGAGAAUCGCGUCG |
| 33 | 856 | 41 | 0.668 | UCUUUCAUCCGUUAUCUUGGGCA | 24 | 72 | -6.5 | -1.9 | -40.9 | GCCGUCUUUCAUCCGUUAUCUUGGGCACGGC |
| 34 | 397 | 45 | 0.667 | UGUUGCUGUUGCUGUUGUAGGUGA | 24 | 75 | -6.1 | -1.5 | -43.4 | GCCGUGUUGCUGUUGCUGUUGUAGGUGACGGC |
| 35 | 1683 | 37 | 0.663 | UUCGUUGAUUAGACAGGAGUGUAU | 24 | 69 | -6.5 | -0.4 | -39.1 | CGAGCUUCGUUGAUUAGACAGGAGUGUAUCGUCG |
| 36 | 857 | 45 | 0.647 | GUCUUUCAUCCGUUAUCUUGGGC | 24 | 73 | -6.5 | -1.9 | -42 | CGAGGUCUUUCAUCCGUUAUCUUGGGCCUCG |
| 37 | 2213 | 37 | 0.642 | AGCGGAAAAGUUUGAAGAGAAGUU | 24 | 70 | -2.8 | 0 | -37.8 | CGCCAGCGGAAAAGUUUGAAGAGAAGUUGGCG |
| 38 | 90 | 33 | 0.634 | UUUCACGGACUUAAGAUAAUAGGU | 24 | 68 | -7.1 | -1 | -36.7 | CGAGCUUUCACGGACUUAAGAUAAUAGGUGCUCG |
| 39 | 1684 | 37 | 0.629 | UUUCGUUGAUUAGACAGGAGUGUA | 24 | 69 | -6.5 | -0.8 | -38.9 | GCCGUUUCGUUGAUUAGACAGGAGUGUACGGC |
| 40 | 1239 | 45 | 0.629 | CGAGUUAUCGUCAGCAGAGAAUC | 24 | 71 | -6.3 | -0.9 | -41.7 | GCACGCGAGUUAUCGUCAGCAGAGAAUCGUGC |
| 41 | 1682 | 41 | 0.626 | UCGUUGAUUAGACAGGAGUGUAUG | 24 | 70 | -6.2 | -0.4 | -40.8 | CGCGAUCGUUGAUUAGACAGGAGUGUAUGUCGCG |
| 42 | 1681 | 41 | 0.625 | CGUUGAUUAGACAGGAGUGUAUGU | 24 | 71 | -6.6 | -0.4 | -40.6 | CGAGCCGUUGAUUAGACAGGAGUGUAUGUCGUCG |
| 43 | 858 | 45 | 0.622 | GGUCUUUCAUCCGUUAUCUUGGG | 24 | 72 | -5.4 | -1.8 | -41.9 | CGACGGGUCUUUCAUCCGUUAUCUUGGGCGUCG |
| 44 | 966 | 37 | 0.621 | CUGGUAGAAUUGUUGAGAUGCUU | 24 | 69 | -5 | 0 | -38.5 | GCACGCUUGUAGAAUUGUUGAGAUGCUUCGUCG |
| 45 | 578 | 45 | 0.621 | UUGUCGUCAGUGGAAAUGGAUUG | 24 | 73 | -5.1 | -0.3 | -42.1 | CGCGAUUGUCGUCAGUGGAAAUGGAUUGUCGCG |
| 46 | 91 | 33 | 0.618 | UUUUCACGGACUUAAGAUAAUAGG | 24 | 67 | -5.4 | 0 | -35.9 | CGCGAUUUUCACGGACUUAAGAUAAUAGGUCGCG |
| 47 | 2211 | 33 | 0.618 | CGGAAAAGUUUGAAGAGAAGUUUU | 24 | 66 | -5 | -0.7 | -34.6 | CGACGCGGAAAAGUUUGAAGAGAAGUUUUCGUCG |
| 48 | 2212 | 37 | 0.614 | GCGGAAAAGUUUGAAGAGAAGUUU | 24 | 69 | -3 | 0 | -37.1 | CGCGAGCGGAAAAGUUUGAAGAGAAGUUUUCGCG |
| 49 | 965 | 37 | 0.614 | UGGUAGAAUUGUUGAGAUGCUUC | 24 | 69 | -4.6 | 0 | -38.8 | GCACGUGGUAGAAUUGUUGAGAUGCUUCCGUCG |
| 50 | 860 | 37 | 0.613 | UUGGUCUUUCAUCCGUUAUCUUG | 24 | 68 | -4 | -0.2 | -37.8 | CGCGAUUGGUCUUUCAUCCGUUAUCUUGUCGCG |
| 1 | 2222 | 36 | 0.761 | UUUUGGGAAAAGCGGAAAAGUUUGA | 25 | 70 | -7 | -1.5 | -38.3 | CCGUUUUGGGAAAAGCGGAAAAGUUUGACCGG |
| 2 | 1235 | 44 | 0.750 | GUUAAUCGUCAGCAGAGAAUCGUUG | 25 | 71 | -7.1 | -1.3 | -42.4 | GCACGGUUAUCGUCAGCAGAGAAUCGUUGCGUCG |
| 3 | 2813 | 32 | 0.745 | AUUUUACAUUGCAGCUUGUUUAUAGG | 25 | 68 | -6 | 0 | -37.2 | GCACGAUUUUACAUUGCAGCUUGUUUAUAGGCGUCG |
| 4 | 2814 | 32 | 0.742 | GAUUUUACAUUGCAGCUUGUUUAUAG | 25 | 66 | -6 | 0 | -36.8 | GCACGGAUUUUACAUUGCAGCUUGUUUAUAGCGUCG |
| 5 | 2812 | 32 | 0.742 | UUUUACAUUGCAGCUUGUUUAUAGGA | 25 | 69 | -7 | 0 | -38 | GCCGUUUUUACAUUGCAGCUUGUUUAUAGGACGGC |
| 6 | 2815 | 32 | 0.738 | GAUUUUACAUUGCAGCUUGUUUAUA | 25 | 68 | -6 | 0 | -37.5 | GCACGGAUUUUUACAUUGCAGCUUGUUUAUACGUCG |
| 7 | 2811 | 36 | 0.737 | UUUACAUUGCAGCUUGUUUAUAGGAC | 25 | 70 | -7 | 0 | -39.8 | GCACGUUUACAUUGCAGCUUGUUUAUAGGACCGUCG |
| 8 | 2816 | 32 | 0.734 | UGGAUUUUACAUUGCAGCUUGUUUAU | 25 | 69 | -6 | 0 | -37.8 | GCACGUGGAUUUUACAUUGCAGCUUGUUUAUCGUCG |
| 9 | 2817 | 32 | 0.732 | UUGGAUUUUACAUUGCAGCUUGUUA | 25 | 68 | -6 | 0 | -37.6 | GCCGUUGGAUUUUACAUUGCAGCUUGUUACGGC |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|----------------------------|-----------|----|--------------------|---------------------|---------------------|--------------------------------------|
| 10 | 2221 | 36 | 0.730 | UUUGGGAAAAGCGGAAAAGUUUGAA | 25 | 70 | -5.4 | -1.5 | -38.3 | CCGUUUGGGAAAAGCGGAAAAGUUUGAACGG |
| 11 | 1216 | 40 | 0.725 | UCGUUGUAGGUUCCACUGGUUAAAA | 25 | 72 | -6.4 | -0.5 | -41.5 | GCCGUCGUUGUAGGUUCCACUGGUUAAAACGGC |
| 12 | 2220 | 40 | 0.720 | UUGGGAAAAGCGGAAAAGUUUGAAG | 25 | 71 | -4.4 | -1.5 | -40 | CGCGAUUGGGAAAAGCGGAAAAGUUUGAAGUCGCG |
| 13 | 1236 | 40 | 0.716 | AGUUAUCGUCAGCAGAGAAUCGUU | 25 | 71 | -4.3 | 0 | -41.4 | CGCCAGUUAUCGUCAGCAGAGAAUCGUUGGCG |
| 14 | 1215 | 40 | 0.715 | CGUUGUAGGUUCCACUGGUUAAAAU | 25 | 72 | -6.4 | -0.5 | -40.7 | GCACGCGUUGUAGGUUCCACUGGUUAAAUCGUGC |
| 15 | 2219 | 40 | 0.708 | UGGGAAAAGCGGAAAAGUUUGAAGA | 25 | 72 | -4.4 | -1.5 | -41 | CCGGUGGGAAAAGCGGAAAAGUUUGAAGACCGG |
| 16 | 2215 | 36 | 0.706 | AAAAGCGGAAAAGUUUGAAGAGAAG | 25 | 68 | -4.4 | -1.5 | -37.9 | GCACGAAAAGCGGAAAAGUUUGAAGAGAAGCGUCG |
| 17 | 2217 | 40 | 0.705 | GGAAAAGCGGAAAAGUUUGAAGAGA | 25 | 71 | -4.4 | -1.5 | -40.6 | GCACGGGAAAAGCGGAAAAGUUUGAAGAGACGUCG |
| 18 | 2216 | 36 | 0.705 | GAAAAGCGGAAAAGUUUGAAGAGAA | 25 | 68 | -4.4 | -1.5 | -38.2 | GCACGGAAAAGCGGAAAAGUUUGAAGAGAACGUCG |
| 19 | 2218 | 44 | 0.703 | GGGAAAAGCGGAAAAGUUUGAAGAG | 25 | 72 | -4.4 | -1.5 | -42 | GCACGGGAAAAGCGGAAAAGUUUGAAGAGCGUCG |
| 20 | 1214 | 40 | 0.701 | GUUGUAGGUUCCACUGGUUAAAAUC | 25 | 71 | -6.4 | -0.5 | -41.2 | CGAGGUUGUAGGUUCCACUGGUUAAAUCUCG |
| 21 | 2818 | 32 | 0.695 | UUUGGAUUUUACAUUGCAGCUUGUU | 25 | 68 | -6 | 0 | -37.2 | GCACGUUUGGAUUUUACAUUGCAGCUUGUUCGUGC |
| 22 | 1237 | 44 | 0.680 | GAGUUAUCGUCAGCAGAGAAUCGU | 25 | 72 | -4.3 | 0 | -43.4 | CGCGAGAGUUAUCGUCAGCAGAGAAUCGUUCGCG |
| 23 | 2214 | 36 | 0.677 | AAAGCGGAAAAGUUUGAAGAGAAGU | 25 | 70 | -4.4 | -1.5 | -38.7 | CGCCAAAGCGGAAAAGUUUGAAGAGAAGUGGCG |
| 24 | 397 | 48 | 0.675 | GUGUUGCUGUUGCUGUUGUAGGUGA | 25 | 76 | -6.1 | -1.5 | -46.1 | CGAGCGUGUUGCUGUUGCUGUUGUAGGUGAGCUCG |
| 25 | 854 | 48 | 0.667 | CUUUUCAUCCGUUAUCUUGGGCACG | 25 | 74 | -6.5 | -1.9 | -44.1 | CGAGCUUUUCAUCCGUUAUCUUGGGCACGCUCG |
| 26 | 855 | 44 | 0.665 | UCUUUCAUCCGUUAUCUUGGGCAC | 25 | 73 | -6.5 | -1.9 | -43.6 | CGACGUCUUUCAUCCGUUAUCUUGGGCACCGUCG |
| 27 | 2820 | 32 | 0.661 | UUUUUGGAUUUUACAUUGCAGCUUG | 25 | 67 | -5.1 | 0 | -36.4 | GCACGUUUUUGGAUUUUACAUUGCAGCUUGCGUGC |
| 28 | 2819 | 32 | 0.659 | UUUUGGAUUUUACAUUGCAGCUUGU | 25 | 68 | -5.4 | 0 | -37.2 | GCACGUUUUUGGAUUUUACAUUGCAGCUUGUCGUGC |
| 29 | 2213 | 36 | 0.650 | AAGCGGAAAAGUUUGAAGAGAAGUU | 25 | 70 | -3.6 | -1.1 | -38.7 | CCGAAGCGGAAAAGUUUGAAGAGAAGUUCGG |
| 30 | 1238 | 48 | 0.643 | CGAGUUAUCGUCAGCAGAGAAUCG | 25 | 73 | -6.3 | -0.9 | -44.1 | GGCGAGUUAUCGUCAGCAGAGAAUCGCC |
| 31 | 1682 | 40 | 0.639 | UUCGUUGAUUAGACAGGAGUGUAUG | 25 | 70 | -6.5 | -0.4 | -41.7 | CGCGAUUCGUUGAUUAGACAGGAGUGUAUGUCGCG |
| 32 | 1683 | 36 | 0.639 | UUUCGUUGAUUAGACAGGAGUGUAU | 25 | 69 | -6.5 | -0.8 | -40 | CGAGCUUUCGUUGAUUAGACAGGAGUGUAUGCUCG |
| 33 | 90 | 32 | 0.628 | UUUUCACGGACUUAAGAUAAUAGGU | 25 | 68 | -7.1 | -1 | -37.6 | CGAGCUUUUCACGGACUUAAGAUAAUAGGUGCUCG |
| 34 | 857 | 48 | 0.628 | GGUCUUUUCAUCCGUUAUCUUGGGC | 25 | 75 | -6.5 | -1.9 | -45.3 | CGAGGGUCUUUUCAUCCGUUAUCUUGGGCCUCG |
| 35 | 859 | 40 | 0.623 | UUGGUCUUUUCAUCCGUUAUCUUGG | 25 | 71 | -6 | -1.7 | -41.1 | CGCGAUUGGUCUUUUCAUCCGUUAUCUUGGUCGCG |
| 36 | 2212 | 36 | 0.622 | AGCGGAAAAGUUUGAAGAGAAGUUU | 25 | 70 | -3 | 0 | -38.7 | CGCCAGCGGAAAAGUUUGAAGAGAAGUUUGGCG |
| 37 | 567 | 48 | 0.619 | GUGGAAAUGGAUUGCCCGUCAGUUU | 25 | 76 | -6 | -2.1 | -45.4 | CGCGAGUGGAAAUGGAUUGCCCGUCAGUUUUCGCG |
| 38 | 566 | 44 | 0.617 | UGGAAAUGGAUUGCCCGUCAGUUUU | 25 | 75 | -7.3 | -2.1 | -43.6 | GCACGUGGAAAUGGAUUGCCCGUCAGUUUUCGUGC |
| 39 | 91 | 32 | 0.613 | UUUUUCACGGACUUAAGAUAAUAGG | 25 | 67 | -5.4 | 0 | -36.8 | CGCGAUUUUUCACGGACUUAAGAUAAUAGGUCGCG |
| 40 | 568 | 48 | 0.608 | AGUGGAAAUGGAUUGCCCGUCAGUU | 25 | 77 | -6 | -2.1 | -46.1 | CGCCAGUGGAAAUGGAUUGCCCGUCAGUUGGCG |
| 41 | 1239 | 48 | 0.606 | CCGAGUUAUCGUCAGCAGAGAAUC | 25 | 73 | -6.3 | -1.3 | -45 | GCACGCCGAGUUAUCGUCAGCAGAGAAUCGUGC |
| 42 | 1684 | 40 | 0.606 | CUUUCGUUGAUUAGACAGGAGUGUA | 25 | 70 | -7.4 | -1.9 | -41.5 | CGAGCCUUCGUUGAUUAGACAGGAGUGUAUGCUCG |
| 43 | 966 | 40 | 0.605 | GCUGGUAGAAAUUGUUGAGAUGCUU | 25 | 72 | -5.4 | 0 | -41.9 | CGCGAGCUGGUAGAAAUUGUUGAGAUGCUUUCGCG |
| 44 | 92 | 32 | 0.601 | CUUUUUCACGGACUUAAGAUAAUAG | 25 | 65 | -5.4 | 0 | -36.1 | CCGCUUUUUCACGGACUUAAGAUAAUAGCGG |
| 45 | 1681 | 40 | 0.601 | UCGUUGAUUAGACAGGAGUGUAUGU | 25 | 72 | -6.6 | -0.4 | -42.5 | CGAGCUCGUUGAUUAGACAGGAGUGUAUGUCUCG |
| 46 | 965 | 40 | 0.599 | CUGGUAGAAAUUGUUGAGAUGCUUC | 25 | 70 | -5 | 0 | -41.4 | GCACGUCUGGUAGAAAUUGUUGAGAUGCUUCCGUGC |
| 47 | 860 | 40 | 0.597 | CUUGGUCUUUUCAUCCGUUAUCUUG | 25 | 69 | -4 | -0.2 | -40.4 | CGAGCUUGGUCUUUUCAUCCGUUAUCUUGCUCG |
| 48 | 578 | 48 | 0.597 | GUUGUCGUCAGUGGAAAUGGAUUG | 25 | 74 | -5.7 | -0.3 | -44.8 | GCACGGUUGUCGUCAGUGGAAAUGGAUUGCGUGC |
| 49 | 967 | 40 | 0.595 | UGCUGGUAGAAAUUGUUGAGAUGCU | 25 | 72 | -7.4 | 0 | -42.6 | GCACGUCUGGUAGAAAUUGUUGAGAUGCUCGUGC |
| 50 | 2211 | 36 | 0.595 | GCGGAAAAGUUUGAAGAGAAGUUUU | 25 | 69 | -6.1 | -0.7 | -38 | CGCGAGCGGAAAAGUUUGAAGAGAAGUUUUCGCG |
| 1 | 2813 | 34 | 0.752 | GAUUUUACAUUGCAGCUUGUUAUAGG | 26 | 69 | -6 | 0 | -40.1 | GCACGGAUUUUACAUUGCAGCUUGUUAUAGGCGUGC |
| 2 | 2814 | 34 | 0.747 | GGAUUUUACAUUGCAGCUUGUUAUAG | 26 | 69 | -6 | 0 | -40.1 | GCACGGGAUUUUACAUUGCAGCUUGUUAUAGCGUGC |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG bimol | ΔG unimol | ΔG duplex | Molecular beacon sequence |
|------|-------|-----|----------|-----------------------------|-----------|----|-----------------|------------------|------------------|---------------------------------------|
| 3 | 2811 | 34 | 0.747 | UUUUACAUUGCAGCUUGUUUAGGAC | 26 | 70 | -7 | 0 | -40.7 | GCACGUUUUACAUUGCAGCUUGUUUAGGACCGUGC |
| 4 | 2221 | 34 | 0.741 | UUUUGGGAAAAGCGGAAAAGUUUGAA | 26 | 70 | -7 | -1.5 | -39.2 | CCGUUUUGGGAAAAGCGGAAAAGUUUGAACGG |
| 5 | 2220 | 38 | 0.731 | UUUGGGAAAAGCGGAAAAGUUUGAAG | 26 | 71 | -5.4 | -1.5 | -40.9 | CGCGAUUUUGGGAAAAGCGGAAAAGUUUGAAGUCGCG |
| 6 | 1235 | 42 | 0.723 | AGUUAUUCGUCAGCAGAGAAUCGUUG | 26 | 72 | -7.1 | -1.3 | -44 | GCACGAGUUAUUCGUCAGCAGAGAAUCGUUGCGUGC |
| 7 | 1215 | 38 | 0.721 | UCGUUGUAGGUUCCACUGGUUAAAAU | 26 | 72 | -6.4 | -0.5 | -42.6 | GCACGUCGUUGUAGGUUCCACUGGUUAAAAUCGUGC |
| 8 | 2219 | 38 | 0.720 | UUGGGAAAAGCGGAAAAGUUUGAAGA | 26 | 72 | -4.4 | -1.5 | -41.9 | CCGGUUGGGAAAAGCGGAAAAGUUUGAAGACCGG |
| 9 | 2215 | 38 | 0.716 | GAAAAGCGGAAAAGUUUGAAGAGAAG | 26 | 69 | -4.4 | -1.5 | -40.8 | CGACGGAAAAGCGGAAAAGUUUGAAGAGAAGCGUGC |
| 10 | 2216 | 38 | 0.715 | GGAAAAGCGGAAAAGUUUGAAGAGAA | 26 | 71 | -4.4 | -1.5 | -41.5 | CGACGGGAAAAGCGGAAAAGUUUGAAGAGAAGCGUGC |
| 11 | 2217 | 42 | 0.711 | GGGAAAAGCGGAAAAGUUUGAAGAGA | 26 | 73 | -4.4 | -1.5 | -43.9 | CGACGGGGAAAAGCGGAAAAGUUUGAAGAGACGUGC |
| 12 | 2218 | 42 | 0.710 | UGGGAAAAGCGGAAAAGUUUGAAGAG | 26 | 73 | -4.4 | -1.5 | -43.6 | CGCGAUGGGAAAAGCGGAAAAGUUUGAAGAGUCGCG |
| 13 | 1214 | 42 | 0.708 | CGUUGUAGGUUCCACUGGUUAAAAUC | 26 | 72 | -6.4 | -0.5 | -43.6 | GCACGCGUUGUAGGUUCCACUGGUUAAAAUCCGUGC |
| 14 | 1236 | 42 | 0.691 | GAGUUAUUCGUCAGCAGAGAAUCGUU | 26 | 72 | -4.3 | 0 | -44.3 | CGCGAGAGUUAUUCGUCAGCAGAGAAUCGUUUCGCG |
| 15 | 2214 | 34 | 0.684 | AAAAGCGGAAAAGUUUGAAGAGAAGU | 26 | 70 | -4.4 | -1.5 | -39.6 | CGCCAAAAGCGGAAAAGUUUGAAGAGAAGUGGCG |
| 16 | 854 | 46 | 0.661 | UCUUUUCAUCCGUUAUCUUGGGCACG | 26 | 75 | -6.5 | -1.9 | -46 | CGCGAUCUUUUCAUCCGUUAUCUUGGGCACGUCGCG |
| 17 | 2213 | 34 | 0.656 | AAAGCGGAAAAGUUUGAAGAGAAGUU | 26 | 70 | -4.4 | -1.5 | -39.6 | CCGAAAGCGGAAAAGUUUGAAGAGAAGUUCGG |
| 18 | 1237 | 46 | 0.655 | CGAGUUAUUCGUCAGCAGAGAAUCGU | 26 | 74 | -6.3 | -1.2 | -45.8 | GCACGCGAGUUAUUCGUCAGCAGAGAAUCGUCGUGC |
| 19 | 2212 | 34 | 0.630 | AAGCGGAAAAGUUUGAAGAGAAGUUU | 26 | 70 | -3.8 | -1.1 | -39.6 | CCGAAGCGGAAAAGUUUGAAGAGAAGUUCGG |
| 20 | 567 | 46 | 0.623 | AGUGGAAAUGGAUUGCCCGUCAGUUU | 26 | 77 | -6 | -2.1 | -47 | CGCCAGUGGAAAUGGAUUGCCCGUCAGUUUGGCG |
| 21 | 566 | 46 | 0.623 | GUGGAAAUGGAUUGCCCGUCAGUUUU | 26 | 76 | -7.3 | -2.1 | -46.3 | CGCGAGUGGAAAUGGAUUGCCCGUCAGUUUUUCGCG |
| 22 | 1238 | 50 | 0.620 | CCGAGUUAUUCGUCAGCAGAGAAUCG | 26 | 75 | -6.3 | -1.3 | -47.4 | CGAGCCGAGUUAUUCGUCAGCAGAGAAUCGCUCG |
| 23 | 1682 | 38 | 0.617 | UUUCGUUGAUUAGACAGGAGUGUAUG | 26 | 70 | -6.5 | -0.8 | -42.6 | CGCGAUUUCGUUGAUUAGACAGGAGUGUAUGUCGCG |
| 24 | 1683 | 38 | 0.617 | CUUUCGUUGAUUAGACAGGAGUGUAU | 26 | 71 | -7.4 | -1.9 | -42.6 | CGAGCCUUCGUUGAUUAGACAGGAGUGUAUGCUCG |
| 25 | 1681 | 38 | 0.614 | UUCGUUGAUUAGACAGGAGUGUAUGU | 26 | 71 | -6.6 | -0.4 | -43.4 | CGAGCUUCGUUGAUUAGACAGGAGUGUAUGUCUCG |
| 26 | 91 | 34 | 0.610 | CUUUUUCACGGACUUAAGAUAAUAGG | 26 | 68 | -5.4 | 0 | -39.4 | CGAGCUUUUUCACGGACUUAAGAUAAUAGGCUCG |
| 27 | 859 | 42 | 0.608 | CUUGGUCUUUUCAUCCGUUAUCUUGG | 26 | 72 | -6 | -1.7 | -43.7 | CGAGCUUGGUCUUUUCAUCCGUUAUCUUGGCUCG |
| 28 | 2211 | 34 | 0.603 | AGCGGAAAAGUUUGAAGAGAAGUUUU | 26 | 70 | -6.1 | -0.7 | -39.6 | CGCCAGCGGAAAAGUUUGAAGAGAAGUUUUGGCG |
| 29 | 966 | 38 | 0.600 | UGCUGGUAGAAUUGUUGAGAUGC UU | 26 | 72 | -7.4 | 0 | -43.5 | GCACGUGCUGGUAGAAUUGUUGAGAUGC UUUCGUGC |
| 30 | 92 | 34 | 0.591 | GCUUUUUCACGGACUUAAGAUAAUAG | 26 | 68 | -5.4 | 0 | -39.5 | CGACGGCUUUUUCACGGACUUAAGAUAAUAGCGUCG |
| 31 | 1239 | 46 | 0.586 | UCCGAGUUAUUCGUCAGCAGAGAAUC | 26 | 74 | -6.3 | -1.3 | -46.9 | GCACGUCCGAGUUAUUCGUCAGCAGAGAAUCCGUGC |
| 32 | 965 | 42 | 0.584 | GCUGGUAGAAUUGUUGAGAUGC UU | 26 | 72 | -5.4 | 0 | -44.8 | CGAGGCUGGUAGAAUUGUUGAGAUGC UUCCUCG |
| 33 | 860 | 42 | 0.584 | CCUUGGUCUUUUCAUCCGUUAUCUUG | 26 | 72 | -4.1 | -0.2 | -43.7 | CGAGCCUUGGUCUUUUCAUCCGUUAUCUUGCUCG |
| 34 | 964 | 42 | 0.576 | CUGGUAGAAUUGUUGAGAUGC UU | 26 | 72 | -5 | 0 | -44.7 | GCACGCUUGGUAGAAUUGUUGAGAUGC UUCCCGUGC |
| 35 | 548 | 34 | 0.571 | UCAGUUUUCGAUUAUCACUCUUGAUG | 26 | 67 | -4.6 | 0 | -40.4 | CGCGAUCAGUUUUCGAUUAUCACUCUUGAUGUCGCG |
| 36 | 861 | 38 | 0.569 | UCCUUGGUCUUUUCAUCCGUUAUCUU | 26 | 72 | -4.3 | -0.2 | -43 | CGACGUCCUUGGUCUUUUCAUCCGUUAUCUUCGUGC |
| 37 | 2574 | 42 | 0.568 | AACGGAAACAGAAAGACGAAAUCGC | 26 | 72 | -4.3 | 0 | -42.5 | GCAGCAACGGAAACAGAAAGACGAAAUCGCGCUGC |
| 38 | 1019 | 53 | 0.567 | CGGGGCUGUAGAUGUUGAUGGGUACU | 26 | 80 | -7.4 | 0 | -51.7 | GCACGCGGGGCUGUAGAUGUUGAUGGGUACUCGUGC |
| 39 | 963 | 38 | 0.567 | UGGUAGAAUUGUUGAGAUGC UU | 26 | 72 | -6.8 | -1.6 | -43.7 | GGUGGUAGAAUUGUUGAGAUGC UUCCACC |
| 40 | 549 | 34 | 0.565 | GUCAGUUUUCGAUUAUCACUCUUGAU | 26 | 68 | -6.2 | 0 | -40.5 | CGCGAGUCAGUUUUCGAUUAUCACUCUUGAUUCGCG |
| 41 | 93 | 34 | 0.562 | CGCUUUUUCACGGACUUAAGAUAAUA | 26 | 69 | -5.4 | 0 | -39.3 | CGACGCGCUUUUUCACGGACUUAAGAUAAUACGUCG |
| 42 | 2575 | 38 | 0.560 | AAACGGAAACAGAAAGACGAAAUCG | 26 | 69 | -3.1 | 0 | -40 | GCAGCAAACGGAAACAGAAAGACGAAAUCGGCUGC |
| 43 | 1017 | 53 | 0.558 | GGGUCUGUAGAUGUUGAUGGGUACUGG | 26 | 79 | -7.2 | 0 | -51.9 | GCACGGGGCUGUAGAUGUUGAUGGGUACUGGGCUGC |
| 44 | 439 | 42 | 0.553 | GGAUUAUAGUUGCUCUCGAUGAUGG | 26 | 72 | -5.1 | 0 | -45.4 | GCACGGGAUUAUAGUUGCUCUCGAUGAUGGGCUGC |
| 45 | 1240 | 42 | 0.553 | AUCCGAGUUAUUCGUCAGCAGAGAAU | 26 | 73 | -6.3 | -1.3 | -45.1 | CCGAUCCGAGUUAUUCGUCAGCAGAGAAUCGG |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG bimol | ΔG unimol | ΔG duplex | Molecular beacon sequence |
|------|-------|-----|----------|-----------------------------|-----------|----|-----------------|------------------|------------------|--|
| 46 | 438 | 38 | 0.552 | GAUUAUAGUUGCUCUCGAUGAUGGU | 26 | 71 | -6.4 | 0 | -43.8 | CGCGAGAUUAUAGUUGCUCUCGAUGAUGGUUCGCG |
| 47 | 863 | 38 | 0.551 | UAUCCUUGGUCUUUUAUCCGUUAUC | 26 | 71 | -4.3 | -0.2 | -42.9 | CGACGUAUCCUUGGUCUUUUAUCCGUUAUCGUCG |
| 48 | 547 | 38 | 0.550 | CAGUUUUCGAUUAUCACUCUUGAUGC | 26 | 69 | -4.1 | 0 | -41.9 | GCACGCAGUUUUCGAUUAUCACUCUUGAUGCCGUGC |
| 49 | 546 | 34 | 0.550 | AGUUUUCGAUUAUCACUCUUGAUGCU | 26 | 69 | -4.1 | -0.1 | -40.9 | CCGAGUUUUCGAUUAUCACUCUUGAUGCUCGG |
| 50 | 862 | 38 | 0.548 | AUCCUUGGUCUUUUAUCCGUUAUCU | 26 | 72 | -4.3 | -0.2 | -43.2 | CGCCAUCCUUGGUCUUUUAUCCGUUAUCUGGCG |
| 1 | 2812 | 33 | 0.759 | GAUUUACAUUGCAGCUUGUUUAUAGGA | 27 | 70 | -7 | 0 | -42 | GCACGGAUUUUACAUUGCAGCUUGUUUAUAGGACGUGC |
| 2 | 2813 | 37 | 0.756 | GAUUUACAUUGCAGCUUGUUUAUAGG | 27 | 71 | -6 | 0 | -43.4 | GCACGGGAUUUACAUUGCAGCUUGUUUAUAGGCGUGC |
| 3 | 2811 | 33 | 0.756 | AUUUACAUUGCAGCUUGUUUAUAGGAC | 27 | 70 | -7 | 0 | -41.8 | GCACGAUUUACAUUGCAGCUUGUUUAUAGGACCGUGC |
| 4 | 2814 | 33 | 0.751 | UGGAUUUACAUUGCAGCUUGUUUAUAG | 27 | 70 | -6 | 0 | -41.7 | GCACGUGGAUUUACAUUGCAGCUUGUUUAUAGCGUGC |
| 5 | 2220 | 37 | 0.741 | UUUUGGGAAAAGCGGAAAAGUUUGAAG | 27 | 71 | -7 | -1.5 | -41.8 | CGCGAUUUUGGGAAAAGCGGAAAAGUUUGAAGUCGCG |
| 6 | 2219 | 37 | 0.730 | UUUGGGAAAAGCGGAAAAGUUUGAAGA | 27 | 72 | -5.4 | -1.5 | -42.8 | CCGGUUUGGGAAAAGCGGAAAAGUUUGAAGACCGG |
| 7 | 2215 | 40 | 0.725 | GGAAAAGCGGAAAAGUUUGAAGAGAAG | 27 | 72 | -4.4 | -1.5 | -44.1 | CGACGGGAAAAGCGGAAAAGUUUGAAGAGAAGCGUCG |
| 8 | 2216 | 40 | 0.720 | GGGAAAAGCGGAAAAGUUUGAAGAGAA | 27 | 73 | -4.4 | -1.5 | -44.8 | CGACGGGGAAAAGCGGAAAAGUUUGAAGAGAACGUCG |
| 9 | 2218 | 40 | 0.720 | UUGGGAAAAGCGGAAAAGUUUGAAGAG | 27 | 73 | -4.4 | -1.5 | -44.5 | CGCGAUUGGGAAAAGCGGAAAAGUUUGAAGAGUCGCG |
| 10 | 2217 | 40 | 0.717 | UGGGAAAAGCGGAAAAGUUUGAAGAGA | 27 | 74 | -4.4 | -1.5 | -45.5 | CCGGUGGGAAAAGCGGAAAAGUUUGAAGAGACCGG |
| 11 | 1214 | 40 | 0.714 | UCGUUGUAGGUUCCACUGGUUAAAUC | 27 | 73 | -6.4 | -0.5 | -45.5 | GCACGUCGUUGUAGGUUCCACUGGUUAAAUCGUGC |
| 12 | 1235 | 44 | 0.699 | GAGUUAUCGUCAGCAGAGAAUCGUUG | 27 | 73 | -7.1 | -1.3 | -46.9 | GCACGGAGUUAUCGUCAGCAGAGAAUCGUUGCGUGC |
| 13 | 2214 | 37 | 0.694 | GAAAAGCGGAAAAGUUUGAAGAGAAGU | 27 | 71 | -4.4 | -1.5 | -42.5 | CGCGAGAAAAGCGGAAAAGUUUGAAGAGAAGUUCGCG |
| 14 | 1236 | 44 | 0.667 | CGAGUUAUCGUCAGCAGAGAAUCGUU | 27 | 73 | -6.3 | -1.2 | -46.7 | GCACGCGAGUUAUCGUCAGCAGAGAAUCGUUCGUGC |
| 15 | 2213 | 33 | 0.663 | AAAAGCGGAAAAGUUUGAAGAGAAGUU | 27 | 70 | -4.4 | -1.5 | -40.5 | CCGAAAAGCGGAAAAGUUUGAAGAGAAGUUCGG |
| 16 | 2212 | 33 | 0.637 | AAAGCGGAAAAGUUUGAAGAGAAGUUU | 27 | 70 | -4.6 | -1.5 | -40.5 | GGAAAGCGGAAAAGUUUGAAGAGAAGUUUCC |
| 17 | 1237 | 48 | 0.633 | CCGAGUUAUCGUCAGCAGAGAAUCGU | 27 | 76 | -6.3 | -1.6 | -49.1 | GCACGCCGAGUUAUCGUCAGCAGAGAAUCGUCGUGC |
| 18 | 566 | 44 | 0.626 | AGUGGAAUGGAUUGCCCGUCAGUUUU | 27 | 76 | -7.3 | -2.1 | -47.9 | CGCCAGUGGAAUGGAUUGCCCGUCAGUUUUGGCG |
| 19 | 90 | 33 | 0.620 | CUUUUUCACGGACUUAAGAUAAUAGGU | 27 | 69 | -7.1 | -1 | -41.1 | CGAGCCUUUUUCACGGACUUAAGAUAAUAGGUGCUCG |
| 20 | 2211 | 33 | 0.612 | AAGCGGAAAAGUUUGAAGAGAAGUUUU | 27 | 70 | -6.1 | -1.1 | -40.5 | CCGAAGCGGAAAAGUUUGAAGAGAAGUUUUCGG |
| 21 | 91 | 37 | 0.600 | GCUUUUUCACGGACUUAAGAUAAUAGG | 27 | 71 | -5.4 | 0 | -42.8 | CGACGGCUUUUUCACGGACUUAAGAUAAUAGGCGUGC |
| 22 | 1238 | 48 | 0.600 | UCCGAGUUAUCGUCAGCAGAGAAUCG | 27 | 75 | -6.3 | -1.3 | -49.3 | CGCGAUCCGAGUUAUCGUCAGCAGAGAAUCGUCGCG |
| 23 | 1682 | 40 | 0.596 | CUUUCGUUGAUUAGACAGGAGUGUAUG | 27 | 71 | -7.4 | -1.9 | -45.2 | CGAGCUUUCGUUGAUUAGACAGGAGUGUAUGCUCG |
| 24 | 859 | 44 | 0.595 | CCUUGGUCUUUUAUCCGUUAUCUUGG | 27 | 74 | -6 | -1.7 | -47 | CCGCCUUGGUCUUUUAUCCGUUAUCUUGGCGG |
| 25 | 1681 | 37 | 0.594 | UUUCGUUGAUUAGACAGGAGUGUAUGU | 27 | 71 | -6.6 | -0.8 | -44.3 | CGAGCUUUCGUUGAUUAGACAGGAGUGUAUGUGCUCG |
| 26 | 965 | 40 | 0.581 | UGCUGGUAGAAAUUGUUGAGAUGCUUC | 27 | 73 | -7.4 | 0 | -46.4 | GCACGUGCUGGUAGAAAUUGUUGAGAUGCUUCCGUGC |
| 27 | 860 | 40 | 0.577 | UCCUUGGUCUUUUAUCCGUUAUCUUG | 27 | 72 | -4.3 | -0.2 | -45.6 | CGCGAUCCUUGGUCUUUUAUCCGUUAUCUUGUCGCG |
| 28 | 92 | 37 | 0.575 | CGCUUUUUCACGGACUUAAGAUAAUAG | 27 | 70 | -5.4 | 0 | -41.9 | CGAGCGCUUUUUCACGGACUUAAGAUAAUAGCUCG |
| 29 | 2574 | 40 | 0.569 | AAACGGAAACAGAAAGACGAAAUCGCG | 27 | 72 | -4.3 | 0 | -43.4 | GCAGCAAACGGAAACAGAAAGACGAAAUCGCGCUGC |
| 30 | 1239 | 44 | 0.566 | AUCCGAGUUAUCGUCAGCAGAGAAUC | 27 | 74 | -6.3 | -1.3 | -48 | GCACGAUCCGAGUUAUCGUCAGCAGAGAAUCGUGC |
| 31 | 862 | 37 | 0.564 | UAUCCUUGGUCUUUUAUCCGUUAUCU | 27 | 72 | -4.3 | -0.2 | -44.5 | CGACGUAUCCUUGGUCUUUUAUCCGUUAUCUCGUGC |
| 32 | 964 | 44 | 0.563 | GCUGGUAGAAAUUGUUGAGAUGCUUCC | 27 | 74 | -5.4 | 0 | -48.1 | CGAGGCUUGUAGAAAUUGUUGAGAUGCUUCCUCG |
| 33 | 861 | 37 | 0.562 | AUCCUUGGUCUUUUAUCCGUUAUCUU | 27 | 72 | -4.3 | -0.2 | -44.1 | CGCCAUCCUUGGUCUUUUAUCCGUUAUCUUGGCG |
| 34 | 547 | 37 | 0.558 | UCAGUUUUCGAUUAUCACUCUUGAUGC | 27 | 70 | -4.6 | 0 | -43.8 | GCACGUCAGUUUUCGAUUAUCACUCUUGAUGCCGUGC |
| 35 | 863 | 37 | 0.557 | AUAUCCUUGGUCUUUUAUCCGUUAUC | 27 | 71 | -4.3 | -0.2 | -44 | CGACGAUAUCCUUGGUCUUUUAUCCGUUAUCGUGC |
| 36 | 546 | 37 | 0.557 | CAGUUUUCGAUUAUCACUCUUGAUGCU | 27 | 70 | -4.4 | -0.4 | -43.5 | GCACGCAGUUUUCGAUUAUCACUCUUGAUGCUCGUGC |
| 37 | 1240 | 40 | 0.556 | AAUCCGAGUUAUCGUCAGCAGAGAAU | 27 | 73 | -6.3 | -1.3 | -46 | CGCAAUCCGAGUUAUCGUCAGCAGAGAAUGGCG |
| 38 | 545 | 37 | 0.554 | AGUUUUCGAUUAUCACUCUUGAUGCUC | 27 | 70 | -4.1 | -0.2 | -43.8 | CGACGAGUUUUCGAUUAUCACUCUUGAUGCUCGUGC |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|--------------------------------|-----------|----|--------------------|---------------------|---------------------|---|
| 39 | 963 | 40 | 0.554 | CUGGUAGAAAUUGUUGAGAUGCUCUCCA | 27 | 73 | -6.8 | -1.6 | -46.3 | GCACGCUGGUAGAAAUUGUUGAGAUGCUCUCCACGUGC |
| 40 | 438 | 40 | 0.553 | GGAUUAUAGUUGCUCUCGAUGAUGGU | 27 | 73 | -6.4 | 0 | -47.1 | CGCGAGGAUAUAUAGUUGCUCUCGAUGAUGGUUCGCG |
| 41 | 544 | 40 | 0.552 | GUUUUCGAUAUUCACUCUUGAUGCUCG | 27 | 71 | -5.4 | -1.2 | -44.6 | CGACGGUUUUCGAUAUUCACUCUUGAUGCUCGCGUCG |
| 42 | 437 | 40 | 0.551 | GAUAUAUAGUUGCUCUCGAUGAUGGUC | 27 | 72 | -7 | -0.2 | -46.7 | CCGGAUAUAUAGUUGCUCUCGAUGAUGGUCCGG |
| 43 | 864 | 37 | 0.550 | GAUAUCCUUGGUCUUUUCAUCCGUUAU | 27 | 71 | -6.5 | -0.2 | -44 | CGCGAGUAUCCUUGGUCUUUUCAUCCGUUAUUCGCG |
| 44 | 2573 | 44 | 0.547 | AACGGAAACAGAAAGACGAAAUCGCG | 27 | 73 | -4.3 | 0 | -44.9 | GCAGCAACGGAAACAGAAAGACGAAAUCGCGGUCG |
| 45 | 1019 | 51 | 0.546 | UCGGGGCUGUAGAUGUUGAUGGGUACU | 27 | 80 | -7.4 | 0 | -53.6 | GCACGUCGGGGCUGUAGAUGUUGAUGGGUACUCGUGC |
| 46 | 549 | 37 | 0.545 | CGUCAGUUUUCGAUAUUCACUCUUGAU | 27 | 69 | -6.8 | 0 | -42.9 | GCACGCGUCAGUUUUCGAUAUUCACUCUUGAUCGUGC |
| 47 | 2575 | 40 | 0.539 | CAAACGGAAACAGAAAGACGAAAUCG | 27 | 70 | -3.1 | 0 | -42.6 | CGAGCAAACGGAAACAGAAAGACGAAAUCGUCG |
| 48 | 439 | 44 | 0.533 | CGGAUAUAUAGUUGCUCUCGAUGAUGG | 27 | 74 | -5.1 | 0 | -47.8 | CGAGCGGAUAUAUAGUUGCUCUCGAUGAUGGUCG |
| 49 | 2572 | 48 | 0.526 | ACGGAAACAGAAAGACGAAAUCGCGC | 27 | 76 | -5.7 | 0 | -47.4 | GCAGCACGGAAACAGAAAGACGAAAUCGCGCGCUCG |
| 50 | 1241 | 40 | 0.526 | UAAUCCGAGUUAUUCGUCAGCAGAGAA | 27 | 73 | -6.3 | -1.3 | -46.2 | GCCGUAAUCCGAGUUAUUCGUCAGCAGAGAACGGC |
| 1 | 2812 | 35 | 0.763 | GGAUUUUACAUUGCAGCUUGUUUAUAGGA | 28 | 72 | -7 | 0 | -45.3 | GCACGGGAUUUUACAUUGCAGCUUGUUUAUAGGACGUGC |
| 2 | 2811 | 35 | 0.763 | GAUUUUACAUUGCAGCUUGUUUAUAGGAC | 28 | 71 | -7 | 0 | -44.7 | CGAGGAUUUUACAUUGCAGCUUGUUUAUAGGACCUCG |
| 3 | 2813 | 35 | 0.760 | UGGAUUUUACAUUGCAGCUUGUUUAUAGG | 28 | 72 | -6 | 0 | -45 | GCACGUGGAUUUUACAUUGCAGCUUGUUUAUAGGCGUGC |
| 4 | 2814 | 32 | 0.757 | UUGGAUUUUACAUUGCAGCUUGUUUAUAG | 28 | 70 | -6 | 0 | -42.6 | GCACGUUGGAUUUUACAUUGCAGCUUGUUUAUAGCGUGC |
| 5 | 2219 | 35 | 0.740 | UUUUGGGAAAAGCGGAAAAGUUUGAAGA | 28 | 72 | -7 | -1.5 | -43.7 | CCGGUUUUGGGAAAAGCGGAAAAGUUUGAAGACCGG |
| 6 | 2215 | 42 | 0.730 | GGGAAAAGCGGAAAAGUUUGAAGAGAAG | 28 | 74 | -4.4 | -1.5 | -47.4 | CGACGGGAAAAGCGGAAAAGUUUGAAGAGAAGCGUGC |
| 7 | 2218 | 39 | 0.730 | UUUGGGAAAAGCGGAAAAGUUUGAAGAG | 28 | 73 | -5.4 | -1.5 | -45.4 | CGCGAUUUGGGAAAAGCGGAAAAGUUUGAAGAGUCGCG |
| 8 | 2217 | 39 | 0.727 | UUGGGAAAAGCGGAAAAGUUUGAAGAGA | 28 | 73 | -4.4 | -1.5 | -46.4 | CCGGUUGGGAAAAGCGGAAAAGUUUGAAGAGACCGG |
| 9 | 2216 | 39 | 0.726 | UGGGAAAAGCGGAAAAGUUUGAAGAGAA | 28 | 73 | -4.4 | -1.5 | -46.4 | CCGGUGGGAAAAGCGGAAAAGUUUGAAGAGAACCGG |
| 10 | 2214 | 39 | 0.704 | GGAAAAGCGGAAAAGUUUGAAGAGAAGU | 28 | 73 | -4.4 | -1.5 | -45.8 | CGCGAGGAAAAGCGGAAAAGUUUGAAGAGAAGUUCGCG |
| 11 | 2213 | 35 | 0.674 | GAAAAGCGGAAAAGUUUGAAGAGAAGUU | 28 | 70 | -4.4 | -1.5 | -43.4 | CGCGAGAAAAGCGGAAAAGUUUGAAGAGAAGUUUCGCG |
| 12 | 1236 | 46 | 0.645 | CCGAGUUAUUCGUCAGCAGAGAAUCGUU | 28 | 75 | -6.3 | -1.6 | -50 | GCACGCCGAGUUAUUCGUCAGCAGAGAAUCGUUCGUGC |
| 13 | 2212 | 32 | 0.644 | AAAAGCGGAAAAGUUUGAAGAGAAGUUU | 28 | 70 | -4.6 | -1.5 | -41.4 | GGAAAAGCGGAAAAGUUUGAAGAGAAGUUUCC |
| 14 | 2211 | 32 | 0.619 | AAAGCGGAAAAGUUUGAAGAGAAGUUUU | 28 | 70 | -6.2 | -1.5 | -41.4 | GGAAAGCGGAAAAGUUUGAAGAGAAGUUUCC |
| 15 | 1237 | 46 | 0.613 | UCCGAGUUAUUCGUCAGCAGAGAAUCGU | 28 | 76 | -6.3 | -1.6 | -51 | GCACGUCCGAGUUAUUCGUCAGCAGAGAAUCGUCGUGC |
| 16 | 90 | 35 | 0.609 | GCUUUUUCACGGACUUAAGAUAAUAGGU | 28 | 72 | -7.1 | -1 | -44.5 | CGCGAGCUUUUUCACGGACUUAAGAUAAUAGGUUCGCG |
| 17 | 859 | 42 | 0.588 | UCCUUGGUCUUUUCAUCCGUUAUCUUGG | 28 | 74 | -6 | -1.7 | -48.9 | CGCGAUCCUUGGUCUUUUCAUCCGUUAUCUUGGUCGCG |
| 18 | 91 | 39 | 0.584 | CGCUUUUUCACGGACUUAAGAUAAUAGG | 28 | 72 | -5.4 | 0 | -45.2 | CGAGCGCUUUUUCACGGACUUAAGAUAAUAGGCUCG |
| 19 | 1238 | 46 | 0.581 | AUCCGAGUUAUUCGUCAGCAGAGAAUCG | 28 | 75 | -6.3 | -1.3 | -50.4 | GCACGAUCCGAGUUAUUCGUCAGCAGAGAAUCGCGUGC |
| 20 | 861 | 35 | 0.576 | UAUCCUUGGUCUUUUCAUCCGUUAUCUU | 28 | 72 | -4.3 | -0.2 | -45.4 | CGACGAUCCUUGGUCUUUUCAUCCGUUAUCUUCGUGC |
| 21 | 1681 | 39 | 0.575 | CUUUCGUUGAUUAGACAGGAGUGUAUGU | 28 | 72 | -7.4 | -1.9 | -46.9 | CGAGCCUUCGUUGAUUAGACAGGAGUGUAUGUCUCG |
| 22 | 860 | 39 | 0.569 | AUCCUUGGUCUUUUCAUCCGUUAUCUUG | 28 | 73 | -4.3 | -0.2 | -46.7 | CGACGAUCCUUGGUCUUUUCAUCCGUUAUCUUGCGUGC |
| 23 | 862 | 35 | 0.569 | AUAUCCUUGGUCUUUUCAUCCGUUAUCU | 28 | 72 | -4.3 | -0.2 | -45.6 | CGCCAUAUCCUUGGUCUUUUCAUCCGUUAUCUGGCG |
| 24 | 1239 | 42 | 0.568 | AAUCCGAGUUAUUCGUCAGCAGAGAAUC | 28 | 74 | -6.3 | -1.3 | -48.9 | GCACGAAUCCGAGUUAUUCGUCAGCAGAGAAUCCGUGC |
| 25 | 546 | 35 | 0.565 | UCAGUUUUCGAUAUUCACUCUUGAUGCUCU | 28 | 71 | -4.6 | -0.4 | -45.4 | GCACGUCAGUUUUCGAUAUUCACUCUUGAUGCUCGUGC |
| 26 | 863 | 39 | 0.562 | GAUAUCCUUGGUCUUUUCAUCCGUUAUC | 28 | 72 | -6.5 | -0.5 | -46.9 | GGGAUAUCCUUGGUCUUUUCAUCCGUUAUCCC |
| 27 | 545 | 39 | 0.561 | CAGUUUUCGAUAUUCACUCUUGAUGCUC | 28 | 71 | -5 | -0.7 | -46.4 | GCACGCAGUUUUCGAUAUUCACUCUUGAUGCUCGUGC |
| 28 | 544 | 39 | 0.561 | AGUUUUCGAUAUUCACUCUUGAUGCUCG | 28 | 72 | -5.4 | -1.2 | -46.2 | CGACGAGUUUUCGAUAUUCACUCUUGAUGCUCGCGUGC |
| 29 | 964 | 42 | 0.560 | UGCUGGUAGAAAUUGUUGAGAUGCUCUCC | 28 | 75 | -7.4 | 0 | -49.7 | GCACGUGCUGGUAGAAAUUGUUGAGAUGCUCUCCGUGC |
| 30 | 437 | 42 | 0.552 | GGAUUAUAUAGUUGCUCUCGAUGAUGGUC | 28 | 74 | -7 | -0.2 | -50 | CGAGGGAUAUAUAGUUGCUCUCGAUGAUGGUCCUCG |
| 31 | 2574 | 42 | 0.548 | CAAACGGAAACAGAAAGACGAAAUCGCG | 28 | 73 | -4.3 | 0 | -46 | GCAGCCAAACGGAAACAGAAAGACGAAAUCGCGCUCG |

| Rank | Base# | %GC | ss-count | Probe sequence | probe len | Tm | ΔG_{bimol} | ΔG_{unimol} | ΔG_{duplex} | Molecular beacon sequence |
|------|-------|-----|----------|-------------------------------|-----------|----|--------------------|---------------------|---------------------|---|
| 32 | 2573 | 42 | 0.548 | AAACGGAAACAGAAAGACGAAAUCGCG | 28 | 73 | -4.3 | 0 | -45.8 | GCAGCAAACGGAAACAGAAAGACGAAAUCGCGGCUGC |
| 33 | 963 | 42 | 0.543 | GCUGGUAGAAUUGUUGAGAUGCUUCCA | 28 | 75 | -6.8 | -1.6 | -49.7 | GCACGGCUGGUAGAAUUGUUGAGAUGCUUCCACGUGC |
| 34 | 1547 | 42 | 0.539 | UGUUAGAAUCGGCACCAAUCGCAUUAUG | 28 | 75 | -4.9 | -0.6 | -48.4 | CGCGAUGUUAGAAUCGGCACCAAUCGCAUUAUGUCGCG |
| 35 | 1240 | 39 | 0.538 | UAAUCCGAGUUAUCGUCAGCAGAGAAU | 28 | 73 | -6.3 | -1.3 | -47.3 | GCACGUAAUCCGAGUUAUCGUCAGCAGAGAAUCGUGC |
| 36 | 438 | 42 | 0.533 | CGGAUAUAUAGUUGCUCUCGAUGAUGGU | 28 | 75 | -6.4 | 0 | -49.5 | GCACGCGGAUAUAUAGUUGCUCUCGAUGAUGGUCGUGC |
| 37 | 864 | 39 | 0.533 | CGAUAUCCUUGGUCUUUUCAUCCGUUUAU | 28 | 72 | -7.1 | -0.2 | -46.4 | CGACGCGAUAUCCUUGGUCUUUUCAUCCGUUUAUCGUGC |
| 38 | 2572 | 46 | 0.528 | AACGGAAACAGAAAGACGAAAUCGCGC | 28 | 76 | -5.7 | 0 | -48.3 | GCAGCAACGGAAACAGAAAGACGAAAUCGCGCGCUGC |
| 39 | 549 | 39 | 0.525 | CCGUCAGUUUUCGAUAUUCACUCUUGAU | 28 | 72 | -6.8 | 0 | -46.2 | GCACGCCGUCAGUUUUCGAUAUUCACUCUUGAUCGUGC |
| 40 | 2575 | 42 | 0.522 | GCAAACGGAAACAGAAAGACGAAAUCG | 28 | 73 | -3.1 | 0 | -46 | GCAGCGCAAACGGAAACAGAAAGACGAAAUCGGCUGC |
| 41 | 2082 | 32 | 0.521 | GACAGCGAAAAAUUGAGAAGUUUAAAUC | 28 | 67 | -4 | -0.2 | -41.1 | CCGGACAGCGAAAAAUUGAGAAGUUUAAAUCCGG |
| 42 | 439 | 42 | 0.516 | ACGGAUAUAUAGUUGCUCUCGAUGAUGG | 28 | 75 | -5.2 | 0 | -49.5 | GCACGACGGAUAUAUAGUUGCUCUCGAUGAUGGCGUGC |
| 43 | 2084 | 32 | 0.516 | CAGACAGCGAAAAAUUGAGAAGUUUAAA | 28 | 68 | -3.3 | -0.2 | -41.3 | GCACGCAGACAGCGAAAAAUUGAGAAGUUUAAAACGUGC |
| 44 | 364 | 46 | 0.510 | UUGGUGGAAAUCUGAGUGGACGAGAAGA | 28 | 76 | -6.7 | 0 | -52.1 | GCCGUUGGUGGAAAUCUGAGUGGACGAGAAGACGGC |
| 45 | 1546 | 42 | 0.508 | GUUAGAAUCGGCACCAAUCGCAUUAUGU | 28 | 75 | -4.9 | -0.6 | -48.5 | CGCGAGUUAGAAUCGGCACCAAUCGCAUUAUGUCGCG |
| 46 | 1241 | 42 | 0.508 | GUAUCCGAGUUAUCGUCAGCAGAGAA | 28 | 74 | -6.3 | -1.3 | -48.9 | GCACGGUAAUCCGAGUUAUCGUCAGCAGAGAACGUGC |
| 47 | 2576 | 39 | 0.507 | UGCAAACGGAAACAGAAAGACGAAAUC | 28 | 72 | -4.1 | 0 | -45.2 | GCAGCUGCAAACGGAAACAGAAAGACGAAAUCGCGCUGC |
| 48 | 551 | 46 | 0.503 | GCCCGUCAGUUUUCGAUAUUCACUCUUG | 28 | 75 | -4.5 | 0 | -49.9 | GCACGGCCCGUCAGUUUUCGAUAUUCACUCUUGCGUGC |
| 49 | 1159 | 35 | 0.503 | CUCUUCAUUAUGUUCAUGCCGUUAAAUG | 28 | 70 | -5.2 | 0 | -43.7 | CGAGCUCUUCAUUAUGUUCAUGCCGUUAAAUGCUCG |
| 50 | 1160 | 32 | 0.503 | UCUCUUCAUUAUGUUCAUGCCGUUAAAU | 28 | 70 | -5.2 | 0 | -43 | CGACGUCUCUUCAUUAUGUUCAUGCCGUUAAAUCGUGC |