

single-stranded scaffold DNA type p4844
0.5 ml at 100 nM

Conc.: 100 nM

Store at -20°C

Vol.: 500 µl

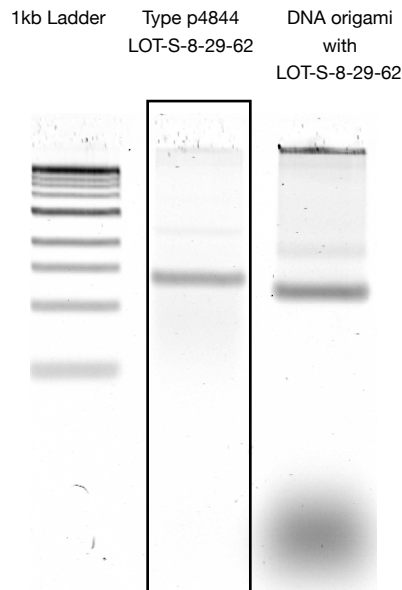
Amount: 50 pmol (75 µg)

Product No.: PRO-S-8-17-2ML-100nM

Lot No.: LOT-S-8-29-62

Description: 50 pmol of single-stranded, circular DNA. The single-stranded viral DNA is isolated from a M13mp18 derivative. M13mp18 is a M13 lac phage vector. Length 4844 bases. See below for the sequence of bases. Volume is sufficient for 25 'standard' (20 nM, 100 µl) DNA origami folding reactions.

Normalised to 100 nM (150 µg/ml) concentration. Dissolved in buffer containing 10 mM TRIS-BASE, 1 mM EDTA. Ready to use for DNA self-assembly experiments. Quality control by agarose gel electrophoresis. Let equilibrate after thawing. Avoid shearing, pipet gently.



Photograph of an GelRed® stained 2% agarose gel on which purified scaffold DNA samples were electrophoresed.



Product sheet

tilibit nanosystems GmbH
Friedenstraße 18
DE 81671 München
Germany
info@tilibit.com



Photograph of an GelRed® stained 2% agarose gel on which purified scaffold DNA samples were electrophoresed.

Exemplary references for usage:

Rothermund, PWK: "Folding DNA to create nanoscale shapes and patterns" -- Nature. 2006 Mar 16; 440(7082):297-302

Douglas, SM; Dietz, H; Liedl, T; Högberg, B; Graf, F; Shih, WM: "Self-assembly of DNA into nanoscale three-dimensional shapes" -- Nature. 2009 May 21; 459(7245):414-418

Detailed usage recipes:

Castro CE, et al: "A primer to scaffolded DNA origami" — Nature Methods. 2011 Mar; 8(3):221-9

Sequence:

CTTTTCGGGGAAATGTGCGCGGAACCTTGATCGGGCAGTAAAGAGTTCCAACTTTACCATAATGAAATAAGATCACTACCGGGCGTATTTTTGAGTTATCGAGATTTTCAGGAGCTAAGGAAGC
TAAATGGAGAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTGAGGCATTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTCCAGCTGGATATACGGC
CTTTTAAAGACCGTAAGAAAAATAAGCACAAAGTTTATCCGGCCTTTATTCACATCTTGCCCGCCTGATGAATGCTCATCCGGAATTCGTATGGCAATGAAAGACGGTGAGCTGGTATGGGATAGT
GTTACCCCTTGTTACACCGTTTTCCATGAGCAAACTGAAACGTTTTATCGCTCTGGAGTGAATACCAACGACGATTTCCGGCAGTTTTACACATATATTCGCAAGATGTGGCGTGTACGGTGAAACCTG
GCCTATTTCCCTAAAGGGTTTTATGAGAAATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTTACCAAGTTTTGATTTAAACGTGGCCAAATGGCAACATCTTTCGCCCCCGTTTTACCATGGGCAAAAT
TATACGCAAGGCGCAAGGTGCTGATGCCGCTGGCGATTGAGTTTCATCATGCCGTTTTGTATGGCTTCCATGTGGCAGAAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCG
TAATTTGATATCGAGCTCGCTGGACTCCGTGTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGATTTGTTCAGAACCGCTCGGTTGCCGCGGGGCTTTTTATGGTGAGAAATCCAAAGCTCGAGCT
GTCAGACCAAGTTTACTCATATATACTTAGATTGATTTAAACTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTGATAATCTCATGACCAAAATCCCTAACGTGAGTTTTCTGCCACT
GAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTCTGCGCGTAATCTGCTGCTTGCAAAACAAAAAACCCACCGCTACCAGCGGTGGTTTTGTTGCCGGATCAAGAGCTAC
CAACTCTTTTTCCGAAAGTAACCTGGCTCAGCAGAGCGCAGATACCAAACTGTTCTTTAGTGTAGCCGCTAGTTAGGCCACCCACTCAAGAAGCTCTGACACCGCTACATACTCGCTGCTAATCTCT
GTTACCAAGTGGCTGCTGCCAGTGGCGATAAGTGTGTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTGGGCTGAAACGGGGGGTTCTGCACACAGCCAGCTGGAGC
GAACGACCTACACCGAATGAGATACCTACAGCGTGGCTGATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAAGCGGACGGTCCGAAACAGGAGAGCGCAC
GAGGGAGCTTCCAGGGGGGAAACGCTTGGTATCTTTATAGTCCGTGCGGGTTTTCCGCCACTCTGACTTGAAGCGTCTGATTTTTGATGCTCGTCAAGGGGGGCGGAGCCTATG
GAAAACCGCCAGCAACCGGCTTTTTACGGTCTCGGCCTTTTGCTGGCCTTTGCTCAGCAAAATCACTCGAAAGCAAGCTGATAAACCGATAACAATAAGGCTCCTTTGGAGCCTTTTTTTTTGGA
GATTTTCAAGCTGAAAAATATATTCGCAATTCCTTAGTTGTTCTTCTATTCTCACTCCGCTGAAACTGTGAAAGTTGTTAGCAAAACCCATACAGAAAATTCATTACTAACGTCTGGAAGACGA
CAAAACTTTAGATCGTTACCGTAACATGAGGGCTGTCTGTGGAATGCTACAGGCGTTGAGTTTTGACTGGTGACGAAACTCAGTGTACGGTACATGGGTTCTATTGGGCTTGCTATCCCTGAAAAAT
GAGGGTGGTGGCTCTGAGGGTGGCGGTTCTGAGGGTGGCGGTTCTGAGGGTGGCGGTAACCTCCTGAGTACGGGTGATACCTATTCCGGGCTATACTATATCAACCCCTCGACGGCACTTATC
CGCTGGTACTGAGCAAAACCCGCTAATCCTAATCCTTCTTTGAGGAGTCTCAGCCTTAAATACTTTTCAATGTTTCAAGAATAATAGGTTCCGAAATAGGCAGGGGGCATTAACTGTTTATAACGGCACTGT
TACTCAAGGCACTGACCCGTTAAACTTATTACAGTACACTCCTGTATCATCAAAGCCATGTATGACGCTTACTGGAACGGTAAATTCAGAGACTGCGCTTCCATTCGGCTTTAATGAGGATC
CATTCTGTTGTGAATCAAGGCCAATGCTGACCTGCCTCAACTCCTGCTCAATGCTGGCGGGGCTCTGGTGGTGGTTCTGGTGGCGGCTCTGAGGGTGGGCTCTGAGGGTGGCGTTCT
GAGGGTGGCGGCTCTGAGGGAGGGGTTCCGGTGGTGGCTCTGGTTCCGGTGAATTTGATTGAAAAGATGGCAAAACCGCTAATAAGGGGGCTATGACCGAAAATGCCGATGAAAACCGGCTACAGTCT
GACGCTAAAGGCAAACTGATTCTGTGCTACTGATTACGGTGTGCTATCGATGGTTTTTATTGGTGAACGTTTTCCGGCCTTGTCAATGGTAATGGTGTACTGGTGAATTTGCTGGCTCTAATCCCAATG
GCTCAAGTCGGTGACCGGTGATAATTCACCTTAAATGAATAATTCOCGTCAATATTTACCTTCCCTCCCTCAATCGGTTGAATGTGGGCTTTTTGCTTTGGCGCTGGTAAACCATATGAATTTCTATTGATGT
GACAAAATAAATCTATCCGTGGTGTCTTTGGCTTTCTTTATATGTTGCCACCTTTATGATGATTTTCTACGTTTGTAAACATACTGCGTAATAAGGAGTCTTAATCATGCCAGTCTTTTGGGTAAAGTAA
TAAGGAGCTTAACTCCTACTTTCATACGCCACCGCACAGACTTCAATGACCACGTATCTGAGACTCCTTTGAAACTGACTACTCCAGCTCCATCAACAATCTTGAAGAAAGTTCTATCCGATCAGGGTATCGC
GAGTCTTAGCGTAGCCAACTGCTGGCCGTAGCGTCTACTTAAACGGAAGAAGGGTGAAGCTGCCACAGAAAATAAATTAATTAATTTGTAAGACAAGTTAGTATGGTAAATACTGGCTTAGTCT
GCGGGAACTTAGCCATACGACTTGGTTGCCTATCGTTACAGCGTACGACCCGTTACCAATCGCATTTGCGATGCAGATAACAACCTCGGACGAAGTAACCACGGAGTATCCTATCTTACGAGTGT
TATTTCTATTATAAAGTGCAATGGCAGGGGGTGTGCGGGTATACTAAACGTAATAAGGGATTACCATGAAGGTAATGTTTCAAGGACAACCTCTGTGATTTGGCTTAGGATAGCGGAAAAACTGCGGTATGTG
GTACCGAATGGTGTGGAAGACCGTAGTGTGCTGCTTTAAGTTTTCTGCGGTTGCTGGATGAGAATTAATAAGGGCCCTCAGATGCCATCTGGTGTACTGTTTATGGAGAGGAGGGTCTCCAGGT
GACGTGCCGTGGCGCCGATGAGTCAAAAGGCACAAGCAGAAAATCATATGACTATGGCCGCTGAATCCCCGTCACGAACCGGTAGCATCAACCCAGTTGACAGCTTCTGACCTTCCAACACT
TAACAGGCCAGCGTAGGGCGCTTCCACAGTCCCTAAGAGCCAAACCTCTAGTGGGGGCTGACCCAGAGTTCCCTCGGATCGCTGAGCGCCCTGTAGCGGGCATTAAAGCGCGGGGTGTG
GTGGTTACGCGCAGCTGACCGCTACACTGCCAGCGCCCTAGCGCCGCTCCTTCCGTTTTCTCCCTCCTTTCTCGCCACGTTCCGCGGCTTTCCCGTCAAGCTCAAAATCGGGGCTCCTT
TAGGGTCCGATTTAGTGTCTTACGGCACCTCGACCCCAAAAACTTGATAGGGTGTGGTTACAGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTT
TAATAGTGGACTCTTTGCCAAACTGGAACAACACTCAACCTATCTCGGTCGAAGTCTATTAGCCTAGCTCCTTGGCCCTTTTTGTGAAACAAATTTTATCGAAAAGAACTCGAGCAATCCCAACT
GCTCTCGTACTTTGGTTACACACGCTTTGGTCACTCGTTCCGCCATACAGACATTTGACGCCCGCATGCTCGGGAACATCCGCTGTCGGCAAAAGCCGCTGAGCGATTCAATACCCGACTCC
CGGGGCATAACGGCTAATCGGACGACGCTCGCGTAGGTTGAGGTGATCTTTCCGAGAAGCTATATAGTACGGCTCCGACCAAGATACCGGTTGACTGATAATGATGGCGACCCCTGCCTTAT
GCAACGACACCGCGAGGCTCGCAAGGAATTTCTTGATCATTCCGTTCTACATAGAGATTTACTCGACGGTCCACTACCTGTACAATCTAACTACGTTTACGTTGTAAGCGTGAGACGATACCTGGCT