

Supporting Information

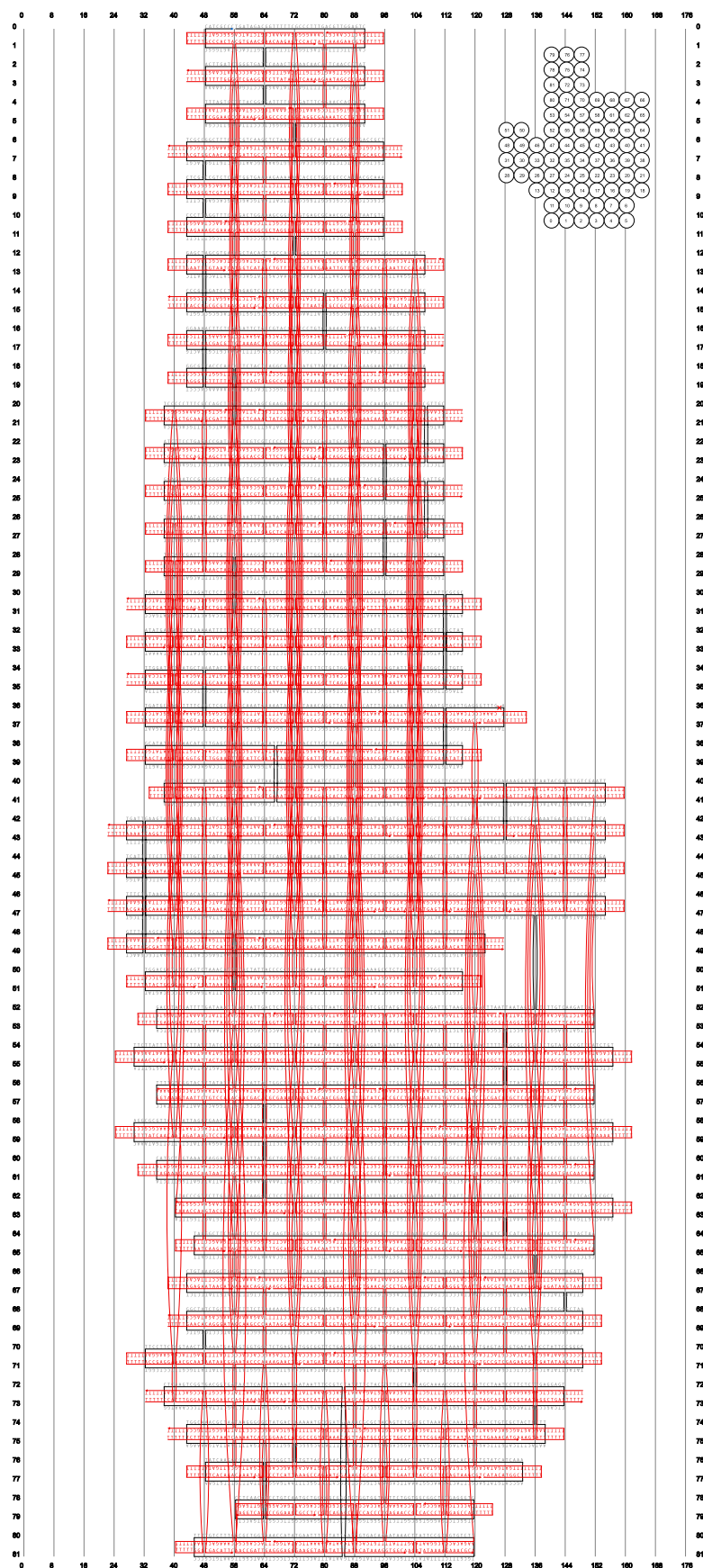
Bai et al. 10.1073/pnas.1215713109

SI Text

The frequency-dependent fall-off of signal power in a cryo-EM reconstruction may be used to estimate the intrinsic variability in the underlying structure. After correcting for the modulation transfer function of the detector, a B-factor sharpening of approximately $-1,000 \text{ \AA}^2$ gave a density map at the core of the object, as expected from the atomic model. This B-factor still comprises various components, among which errors in the rotational and translational assignments and intrinsic variability in the structure are assumed to be the most significant ones. From the tilt-pair validation plot in Fig. S4, we estimated the errors in the rotational assignments to be on the order of 2° . According to Henderson et al. (1) this estimate results in a B-factor component

of $B_{\text{rot}} = (\Delta\Theta D)^2/2200 = \sim 400 \text{ \AA}^2$. On the basis of signal-to-noise considerations, we estimated the errors in the translational assignments to be on the order of ~ 0.5 pixel, or $\sim 1.8 \text{ \AA}$, leading to a B-factor component of $B_{\text{trans}} = 8 \pi^2 (\text{rmsd})^2 = 250 \text{ \AA}^2$. That then leaves a remaining B-factor component for the intrinsic structural variability (at the core of the object) of $B_{\text{structural}} = 1,000 - 400 - 250 = 350 \text{ \AA}^2$, which corresponds to an rmsd in the atom positions of $\sim 2 \text{ \AA}$. The mentioned range of up to 3 \AA in the main text is an attempt to reflect uncertainties in our B-factor estimation and in the empirical calculations related to the orientational errors. Additionally, as mentioned in the main text, the structural variability is larger at the periphery of the object than at its core.

1. Henderson R, et al. (2011) Tilt-pair analysis of images from a range of different specimens in single-particle electron cryomicroscopy. *J Mol Biol* 413(5):1028–1046.



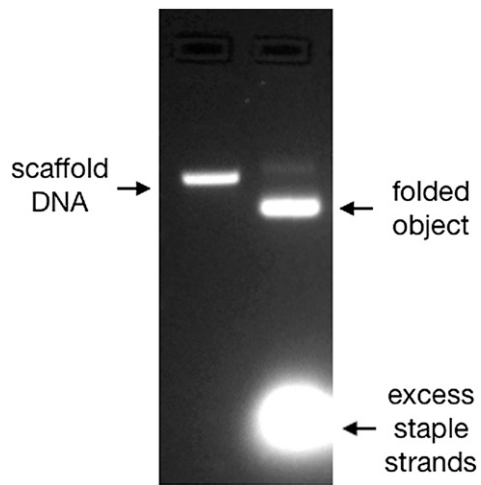


Fig. S2. Gel electrophoretic folding quality assessment. Photograph of an ethidium bromide-stained 2% agarose gel on which reaction products were electrophoresed.

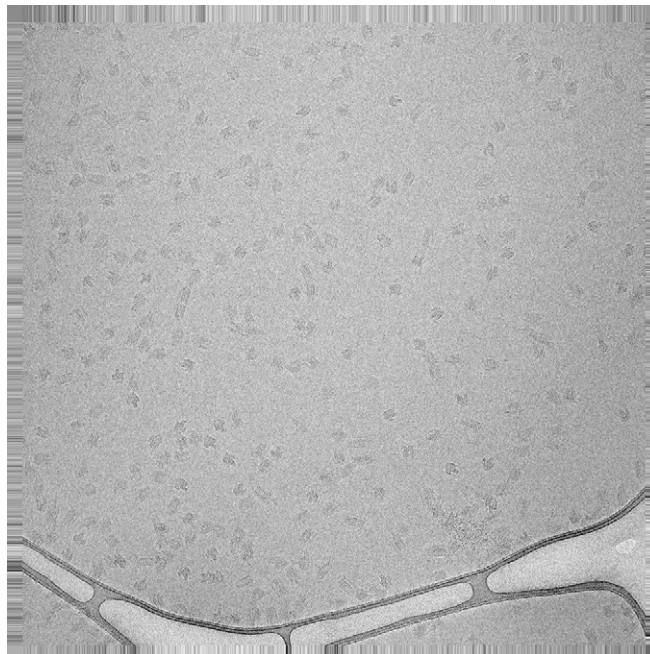


Fig. S3. Exemplary cryo-EM micrograph. The field of view is $1.45\ \mu\text{m} \times 1.45\ \mu\text{m}$.

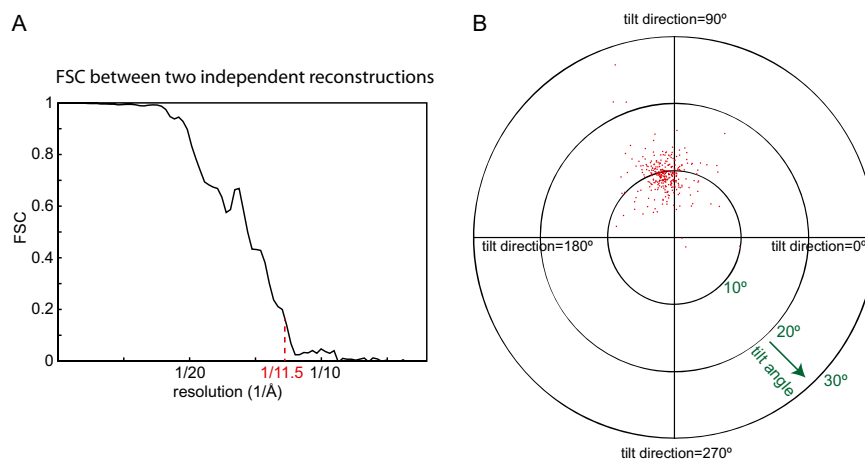


Fig. 54. Quality assessment of the cryo-EM map. (A) Fourier shell correlation (FSC) curve. (B) Tilt-pair validation plot. Note that 32 of the 342 particle pairs had tilt differences larger than 30° and are therefore not depicted.

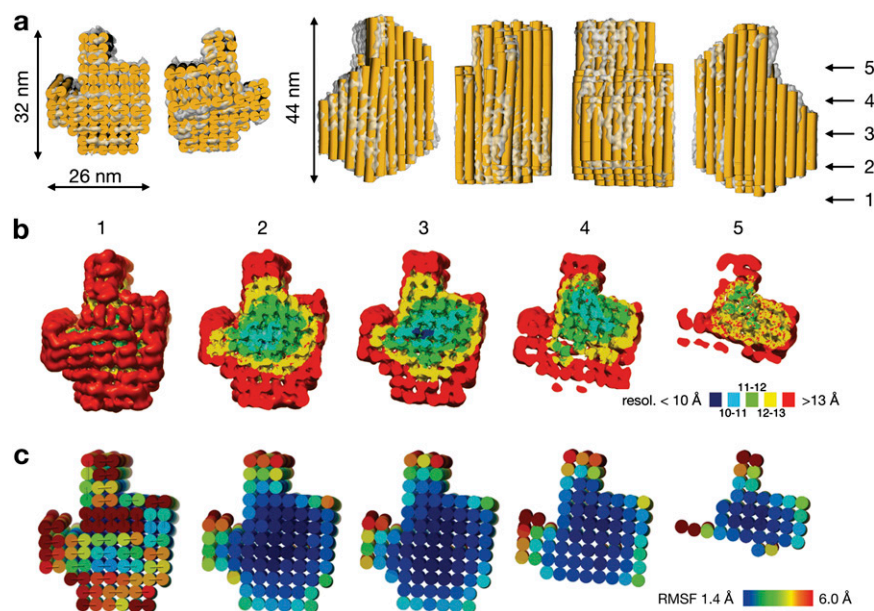


Fig. 55. Comparison of cryo-EM map and CanDo predictions. (A) Cryo-EM map (gray) and CanDo predicted shape (ocre) agree in overall dimensions and twist when assuming a reciprocal twist density of 10.44 bp/turn and an effective helical diameter of 2.6 nm. (B and C) The variation in resolution as estimated in the cryo-EM map (B) and the estimated root mean square fluctuation (rmsf) of the atoms in the shape prediction (C). Cross-sections are shown at five different slices (1–5) through the object, the positions of which are indicated with vertical arrows in A. Note that CanDo does not output a color scale bar for the estimated rmsf values. The scale bar shown reflects that colors are reported to range from dark blue (for an rmsf of 1.4 Å) to dark red (for an rmsf of 6 Å).

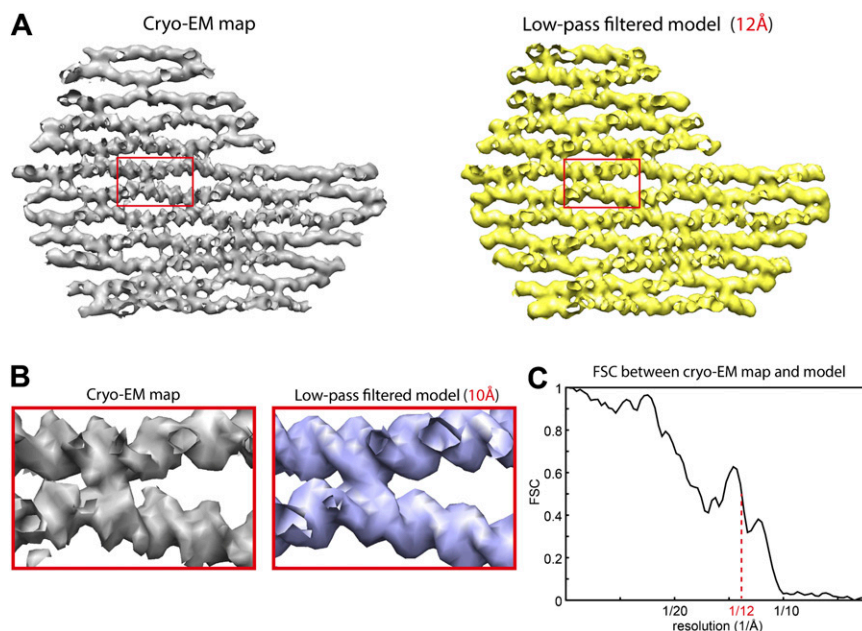


Fig. S6. Quality assessment of the pseudoatomic model. (A) Comparison of a slice (column 4) through the cryo-EM reconstruction and a 12-Å low-pass filtered map obtained from the pseudoatomic model. (B) As in A, but for a close-up of an area at the core of the object and a 10-Å low-pass filtered map obtained from the pseudoatomic model. (C) FSC between the cryo-EM map and the pseudoatomic model.

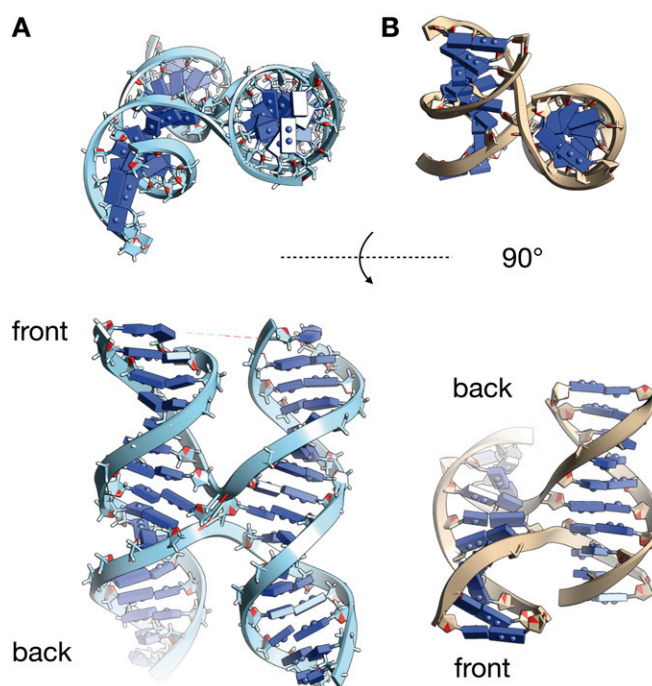


Fig. S7. Holliday junction conformation. (A) A typical Holliday junction in our structure (row 4, columns 4 and 5, base pairs 72–87). (B) Protein Data Bank ID code 1DCW. Both structures are depicted as ribbon-slab models. (Upper) The right helix in both junctions is pointing normally into the figure plane. (Lower) The right helix in both junctions is parallel to the figure plane.

Table S1. Sequence information

Start	End	Sequence	Length (nt)
0[79]	22[78]	CAAAGGGCGGGTGCCTCGCTCACTGCTTAATGTTGCATGCGGTCACGTTG	50
1[78]	23[77]	ATTGTTGTTCCGGCCAACCAAGGTTGGTGCACAGCGACAGGAAGCCGGA	48
3[43]	14[38]	TTTTTTTTTTGGGTGAGACGGGCGAGTTTTTTTTTAAAGGGTCGTGCCGAGGATCCCCGGGTTTTT	67
3[78]	21[74]	AGCGAAATCGCCTGGCCCTTGCCCCAGAGTAAATAACATCACTT	45
4[69]	16[86]	AAAATCAGCCCCCGGCAGGCGAAAATCCTGACGCTGGTTGAGAGAGGG	48
5[62]	6[38]	GGCCCGTAAAGCACTAAATTTTTTTTTTTCGGAACCGGAAAGCCGGCGATTTTT	54
6[100]	8[82]	TTTTTAGCGGTCCTTTTTTTTTTTTTGATGGTGGTTCAATAGCCCTTGGGC	51
7[38]	22[54]	TTTTTACGTGGCAACAGCTGAGAAGTTTTCTTTTTTTTTTTCAGTCACGACGTTGT	56
8[81]	32[82]	GCGCGGGGACGCTGCTTCGCGCTACAGCTTTCATAGGAATTGCGG	48
9[90]	10[86]	AGGCGGTTTTTTTTTTTTTTGCGTAGAGTTTTTTTTTATAGGTTGAGTAAAGAACTT	58
10[52]	13[53]	AACCTAAGGGTTTTTTTTTAAAGAAAGCGAAAGGTCACGCTAGCTCTTTTTTTTTTGAATTCGTAAT	67
10[85]	30[86]	GCGTTGAATGAGTGTAAGTGTAATTGTTAAGGAAGATGATAATCATG	48
12[65]	3[77]	AACCCGCCGCGCCCGCTTAAATGAATCAGTTTGGCCTTATAAATCAAA	48
12[109]	32[106]	TTTAACTCGCTCTTTTTTTTTTTGAAATGGATCACCATCAACTGTTTTTTTTTATAGCAAAACAT	66
13[54]	51[45]	CAAAACGTTAAACCTAGCTTGAGAGATCTGGAGCTCATTGAATCCCCCTCGAATCG	56
14[61]	10[53]	ACTCTAAGCTGCATTCCAGTCGCGTGAACCGTCTATCAGGGCGATTTTTTTTTTTGCCACTAGGA	67
15[38]	33[53]	TTTTTTACCGCGCGTAAACAACCCGAAATTTTTTAAAAATCTGAGT	48
15[62]	1[77]	CAGTGAGCGGAGCGGGCGCTAGGGCGAAAAACCAACAAGAGTCCACT	48
16[85]	44[86]	ATTTTATCCTCGTTCTGTGCATCTGGTGTAGCACCAGCACTCAGAGCAA	48
16[111]	36[106]	TTTTTAACCAGAGGAATTTTTTTTTTAAACGCTCCATCACCTCATTAG	48
18[64]	20[53]	GAGTAGAAGGTTGGGTAACGCCTTTTTTTTTTAGGGTGTTTTATCCA	48
18[93]	37[81]	TCTTTTGATTAGTAAGAGTCTGTGGCGATCCCAGGCAACAATAACCCA	48
20[52]	56[54]	GCTGGCAGCTTTCGCGCGAGCAACACCGCTCCTGATTTAGAACCTGA	47
20[61]	2[43]	ATTACGAATCAGTGCAGAACTCTGATTGCCTTCACCAGGTCGAGGTATACCCAAATCAAGTTTTTT	67
20[116]	41[106]	TTTTTGCAACGCTAGTTTGACATATCTTTTTTTTTTTGGTCAGTTGGCACC	52
21[48]	59[53]	GCGATTAAATAGCTCAACTGGAAGTCTTTTGATCTATTATACCATCTAGTCCTG	54
21[75]	60[86]	GCTGGTAATATCCGAATTGAGCCAATTCTAGGTCAGGAAAAAGATGC	47
22[53]	52[54]	ATCGGCCGGCGGATTCAGTATTGGCAAAGAGATGATGATTAACAATAA	48
22[65]	5[61]	GACTTCTGGTCGGTACGACGCCACCATTTAGAGCTTGACGGCTAAAG	48
22[77]	63[73]	CCAGTCTGAGAGCTGTTTAGCATTGCATCATTAGAGAAA	40
23[46]	64[54]	GCCGAAAGGGTACGGTGTCTATGTTTTGCGGATGGCTTAGAGCTT	44
23[78]	64[82]	AAGGTGCGGGGTTGATTCAAGGTTACTTTAGGAGCACTAACGTTTTTA	48
23[102]	21[116]	TTAGGAGGCCCAAATTAACCGTTTTTTTTTTTTTGACGCCATTTTTTTT	47
24[69]	4[70]	AATGTGATGGGATACTGCAGGTACGGCAGTTTTTCTTCTTACC	48
24[77]	60[86]	CAACATAATAAAGCGAAGATAATTGACGTGATGATGGCATCGGAAGT	48
24[89]	0[80]	GCCAGGGCGCCGGAAGCAAGCTAACTTTTTTTTTTTCACATTAAGTGTTTTTTTTTTGA	68
24[116]	42[106]	TTTTTTCAATCGTTGTACCAACCTAATTTTTTTTTTAACTCGCCATTAAGATTTTCGAGCGG	63
26[57]	24[78]	GTTGGTCATAGCTGTTCCTGTGTGAAAAGCCTGTTTTAACCAT	44
26[77]	56[78]	TATAAGCAAAAGGGGAAGCCTTTTTTAATATTCAATCATATGCGGG	48
26[97]	25[116]	ACAAAATAATATACGAGGCTACTATGGTTTTTTTTTTTGTCTTTGACGCTTTTT	55
27[90]	12[110]	CCATCACCAAAACCTCCGCTCACAATTCACACTTTTTTT	40
28[80]	46[78]	GGCCAACAGATACGTGGTAATGCCGGGAAGAAG	35
28[105]	47[101]	CGATTAGTCTTTAATTTTTTTTTTTGCGCGAATATGATAACGGAACGACGAGAAACACCA	68
30[61]	31[45]	CTATTTATGTCAATCCCTTCTGAAACAGAGAATCGATCCTGAG	44
30[85]	51[73]	ATAAATCACAGACACCACATTCACCTAATGAT	32
31[27]	32[46]	TTTTTGGTCATTGGAATTTTTTTTTTTCGGTAATCGTAATATTTTGTGCAATGCTT	55
31[46]	46[22]	AGCTACAAAAAGAACTGTTGTGAATTACCTTATAGAAATTTTT	44
31[91]	28[106]	TTTTTGAATGGCTACCAGTAAATTGGCAGATTACCATTTTTTTTTTGTGACA	53
32[45]	56[35]	TAGAACAATTACATAACAAACAATCATAATAGTACCGACAAA	43
32[81]	51[93]	GATGAGAAAGGTAAATTGAAATCTACAAAAGAAGAGCAACACTATCAT	48
32[105]	58[110]	TATGTGAGTGAAGTTACAAGCCAACGATTTAACATAAATTGTAA	44
33[38]	45[41]	AATTATTTTTTTTTTAAATTCGCATTCGGAATTCACAGGCAATAGCATTAGG	52
33[54]	51[63]	AATTTAATCAGCTCATTAATGTTTAAATAAATAAAGGAAT	42
35[27]	36[42]	TTTTTTAATCATTCCTTTTTTTTTTTGTGGGAACAACCTCAGGAAATAGTAGTGAAAA	59
36[41]	65[53]	GGTACCCTGAAAGAGGTCTAAACCAATTATTTTTTTTTTAAATCAAGAT	48
36[93]	9[89]	AATGGTAGCGCCATATCGTAACAGAATCAGCACGTATAAG	40
36[105]	65[116]	ATAGACTTCAACCAGACCACCGCGCTCCGGTATCTAACGAGCGTCT	47
37[58]	15[61]	GCAACATGAGGCGGTGACCGTAAGCGAGTACCACCA	36
37[82]	80[80]	GCAGCAGATTATCAAAACAGATAGGCAGATTATACAAGACCTAACTATATGTATCAATAG	62
37[122]	56[118]	CAAAATTTTTTTTTTTTTTCAACCCCTCAATCATGCTGAACACCAGAAGAGGTTTAAAT	59
38[92]	7[100]	GAAAGAGAACAATGTTGGGAACCATCAGGATTAAAGTTGCAGCATTTTT	50
40[39]	21[47]	ATTTTTTTTTTTTTTAAATATGCTTTTTTTTTTAACTAAAGGATTTTTTTTTTGTGCTGCAAG	64
40[61]	14[62]	TTGCTCTTCATTCCCATTTGGGCGGCACCGCGACGAGTAAACGCG	48

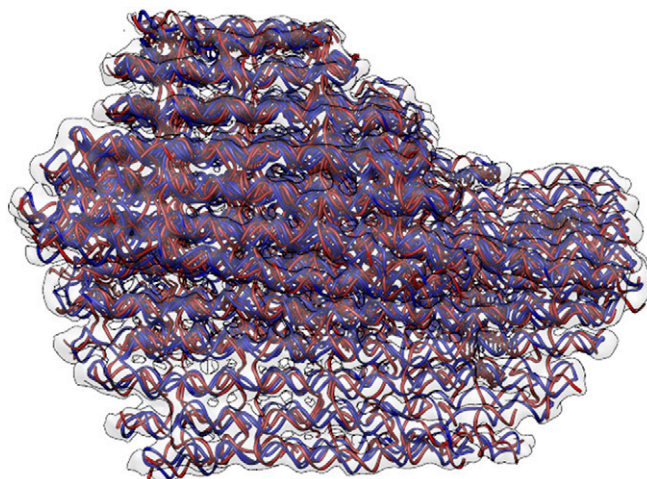
Table S1. Cont.

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41[152]	60[146]	AACTTTTTTTTTTAATTCGACAACCTTTTAAACATCGC	38
42[65]	18[65]	ATCAAAGCGGTATATTTTATATAACACCTCTTCGTATCGGCCTTGCCCT	49
42[105]	66[106]	AACTTTGAGGTGCAGGGATTTCTTAATAATTTTAAAGTCAGATTTAT	48
43[22]	23[45]	TTTTTAAATCAGGTCTTTGGCATCATTTTTTTTTTATTCTACTGATTTTTTTTTTCGCACTCCA	66
43[98]	18[94]	CCCGAAACATTTCGGTAGATTTGCGCAACTATTACCGCTAGCAATACT	48
43[131]	65[151]	CGAACGTTATTAATCGTATTATAAACAACTGAATTTTGTCTCTTTCCAGACG	53
43[152]	56[146]	GTTTTTTTTTTTTTGTAGTAACATTTACCTTTTGAGGCG	38
44[85]	71[73]	TTATTCGGAAACAGTTAGATTAAGACGCTGTTATATAATTTAATGGGG	48
45[42]	62[40]	AAGGGTGTTTGGATATAGATAAATTTACGAGCATGTTTTTTTTTTAGAAACCAATCAACGGGTAT	66
45[58]	26[58]	CATATCCAAAAGAAATTAGCAACGCAAGGAGTTAAATCTAAATT	44
45[142]	67[137]	AGATCATTTTTTCCATTACGCATAACGACAATGTAGAAAGGAG	44
45[152]	54[138]	ACATTTTTTTTTTTCGGGAGAACTCATTACCGTAATCTTGACAAGAACTGACCTTGACAG	62
46[77]	24[70]	CTTGAGATGGTTAAATTACCTTATTTCAAATTAAGCTA	40
47[22]	33[37]	TTTTTACGAGACAAAATTCCTCATATTTTTTTTTTATTTTA	42
47[94]	28[81]	AAAACGAGTAGCCGAGAGTTCTAGCGAAAAGCCTAAAAGGGACATTCT	49
47[102]	17[111]	TATGACCTGAAATCGGTCTGGCCTTACCTACATTTGACGAGAGCGGGAGCTATTTTT	58
47[114]	71[109]	TAACCTTCCCTTAGAATCCTTGCCAATCGCATATTTTAAAGTACC	44
47[130]	57[141]	AACTCGTCCGGATATAATAACGGACTGACCAGACGGTCACTTACT	44
47[152]	47[129]	CAATTTTTTTTTTATCAACGTAACAAAGCTGCTCATTCACTA	42
48[34]	30[27]	CTTTAACTTTTTTTTTTAGTTTCGCGATTTTGGCTATCATTTTT	44
48[61]	26[78]	ACGCCAACCTGAAAGCGTAAGAAGATAGAACATAGTACCCCGGTTG	48
48[127]	50[110]	TTTTTAGGTAGAAAGATTCATCAGTACCAGACGACGATTTTTTTTTTTTAAAAAC	54
50[109]	31[90]	CAAAATAGCGAGAGGCTTTTGCCTTAATAATAGGAATAATA	41
51[46]	48[35]	TCGACTGGATAGCGTCCATTTTTTTTTTATACTGCGAAATG	41
51[64]	12[66]	TACGAGGCCAGATACAAGGACGTTGAGAGGGTTAAAGATTCAAATATTAGCTCATTGCTGGC	62
51[74]	48[62]	AGTAAGTTTTGCCAGAGGGGTAATAGTAATACCAGTCTA	40
51[94]	26[98]	AACCTCGTTTTGAGATTAACGAACCTTCAACCCAGTCAAATTTATTT	48
52[53]	54[42]	TTTATCAAAATCATAGGTCTTTTTTTTTTTTGGAGACTACCTATAAGG	48
52[65]	22[66]	GTTTTAGTATTACCTGAGAAAATTATAACAGAGGGTGCACGTGAGGG	48
52[101]	23[101]	AACATACAGTATAAAATCGCGAATTGCGTAAAATACCATCTAAAGATGGAAATTCGCCA	60
52[125]	49[127]	TAATTTTGCTTCTGTGAATAAGGCTTGCCCAACATTATTACTTTTT	46
53[120]	45[141]	GAACGCGATAGGCTGGCGCTATTAGGAACCGAATTCGCCTGAATATACAGTAAC	54
54[41]	74[38]	CGAACGCAATAAGTTACCTTTGGGAATTAGAGCCTTAGCGTTTGCCATTTTT	52
54[57]	30[62]	CGAAAGCCTGCAATAGTGTTTCATTTGATTTCACCTGTGTAGGAG	44
54[137]	73[148]	ACTGATATAAGTATATTTTTTTTTTGCCCGGAATAGGTAGGCTGAGTTTTT	51
55[38]	34[27]	GATCAAGAAAAATGATTTTTTTTTTCCATATGAATAATACATCCAATTTTT	51
56[53]	72[32]	ATATAATACTAGAATGTGATAATTTTAAACCAAGACAAAAATTTTTTTTTTGGGACCGACTTGAGTTTTT	70
56[77]	67[65]	CATTTTAAAGTACACAGCGATTCCCATGTATACCGAAGCCCTTTTTGA	48
56[93]	27[89]	GTAATTAATAAAGACAGAGGCGATAAAGCTTAATACTTCG	40
56[117]	81[105]	CGCCATCTCAACAGTTTCAAATAAGACAAAAAGACACCACGGAATAAT	48
56[145]	53[151]	CAACTTTGAAAGAGGTTTTTTTTTTTACAGATGAACGGTCATCAAGA	46
57[35]	42[22]	GGTAAAGTAATTCGCTAATGCAGAACGCGCTTTTTTTTTTTGTTTATCAACATATACTTCAATCATTTTT	71
57[142]	68[136]	TAACGAAGGCACAGCCCTCATAGTTTTTTTTTTTAGCCCCACAAG	46
58[109]	65[97]	GAATACGTACAAACAGCAAGAAACAATGAACCCCTGAATCAGTTGTA	48
58[117]	81[119]	AGGCAAGTCGAAATGAGGTTTAGCGGATAATAGCGGGGAAACGCA	46
58[125]	47[113]	AACGAACCTTTTCAAATTGAGACGTCAGATGATTGCTTTGAATACCAA	48
59[54]	81[55]	AACATGTTTCATGTCCAGACTCATTTTAATAACGGTCACCGTCCGACATTC	50
60[77]	66[62]	CACCTGTATCGGTAGGCTCCATTAGACGGTGTAAACGTCAAAAAATG	48
60[85]	70[82]	GGGATCCGAGGGTATTGACCCACGGAGATCCCTCA	36
60[89]	24[90]	TTTAAGAGGAATATTCCTAATGAAAAGAACGAACATGGGCGCCCTGTA	48
60[133]	64[146]	GATATAGATTTTGCAATCCTTTGATTTAGAAGTATTAGACTTTACATTAGTA	52
60[145]	57[151]	CCAAACGGGTAAAAATTTTTTTTTTACGTAATGCCACTGCCGGAAC	46
61[98]	38[93]	GGTGAAGTTAAAGGGAATCATTGGAAGCAAGATTAGAGAATCAACAGTT	49
63[70]	20[62]	GCGTACCTTTTGAATATTCTAAATATAATGCTGAACCTCAAACT	44
63[74]	67[89]	GCGTTGAACCTCCAGCTACAATTTTATCCGATTTTGAAGATTAAAC	48
64[53]	68[38]	GAAGCCGTACCGCATTCGAAGAATAATCGGTAAGCAGATAGCCTTTTT	48
64[81]	69[93]	GCTTTATTTTCAAAAAATATCAGCAGCTATCTCCGTAACACTGAGT	48
64[145]	61[151]	AATTTCAACAGTTTCTTTTTTTTTTACGGGAGTGAGAAACAACAAC	46
65[54]	67[55]	TAGCAGCCTTACAGTTTTTTTTTTTAGAGATAACATA	38
65[98]	36[94]	CCAACGTCTAAGAACGCGAGGCACTAATAACTCCAACGCGAACGACA	48

Table S1. Cont.

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66[61]	37[57]	AAAATAGTTGCTATCCTTATCACTCATCGAATAATATCGTCAGAAGCAATATAACT	56
66[105]	60[90]	CCCAATCCAAATAAGAAACTGAATCTAAAATCTCCATCGTAGCCGCTT	48
66[121]	37[121]	CACAGAGCCTAAGGAATTAGCAAACTCTCGGTGCGTTTAAATAAGAAACCTT	52
67[56]	45[57]	AAAACAGGAAGAAAAGCTGTCTTTATAAACACAAAGAAAATAATAAGAAC	50
67[66]	40[62]	AGCGCAAAAGGAGCTTTGCACCCGACTTGCAGGAGGTTTTAATTGCAA	48
67[90]	56[94]	TGAACAATAGCAATTGCTTTCACTCATCTGCAACGGCAT	40
67[138]	66[122]	AGATAAGTAACCTTTTTTTTTTGATCTAAAGTTTGTAGTTACAAAATAAA	48
68[135]	41[121]	AATTGAGTAATATCAGAACAACTAAATTTGCCCTGTATGGAGATATAGCA	50
69[38]	54[58]	TTTTTGAACACAGGGATAGCAAGCCCCACCACCCGACGACAACCGAC	48
69[94]	47[93]	TTAACCGCCATTGTATCACATCTTCTATTCTACGCGATAGCTACATA	48
69[114]	52[126]	CAACGCCTGTAGCAGTACTCAGCCGCGACCGAAAACCTTAGGGCTTAT	48
70[81]	79[77]	GATAAGACTCATAGACGGATATTCATGAGCCGCCGCCAGCATCGCCTC	48
71[74]	76[86]	CATGATACCGCCACGCACCATTAACATTAGTTTCATCGTAAACAGTGT	48
71[110]	75[117]	AGGTACCGCCACCAATGAAACCATCGAAGTTTGCCCTATT	40
71[122]	43[130]	GCCGTCGAGAGGGTCAGGCGCATGCTCCATATCATAAGTGAGGAAGGCGGAACAGCC	57
72[148]	71[121]	TTTTTACTCCTCAATTTTTTTTTTTTAAAGCAGTAGCGACAGAAATCATAGCAGCATTAGGATGT	63
73[32]	55[37]	TTTTTCCAAGAAGGAATTTTTTTTTTACCAGGATTAATAAGAATTTTTTTTTTAAACACCG	64
73[62]	52[66]	ATGTGAATTAATAACCAACCGCGCTCCGGCTTAGGTTGGGAGAAGA	48
73[70]	63[69]	TACCTCAGAGAATAGGAAATACCAAGCTTTAATTCAGCAGCGGAACAA	48
74[89]	52[102]	GTCAAGGCCGCGTAGAACTTATTACTTGTACAAAATGCTGATGCAAAATA	52
75[38]	77[61]	TTTTTCTTTTCATAATCCCTTGATATTTTTTTTTTTCACAAACAAATA	50
75[98]	61[97]	TGCCATTAGCAAGAAACGTCACCCTCAGCGTCACCACTAAACGA	48
75[118]	78[106]	ATGAGTGACAGAGCCACTTTTTTTTTTTCACCCCTCAGAGCCG	42
75[132]	60[134]	AAGTAGAGAAGGACCGTAATGTATCACCTTCCACAGACCAACCTAGTTGCGCCC	54
76[85]	75[97]	GCCTTGTCAGAGCCGCCACCCCTCAGAACCGACCAGAACC	40
77[62]	80[66]	AAACGATTGGAATAACACGGTTGAGGAACCGATTGAGGGAGGTATGGT	48
77[84]	81[101]	GAAAGCGCAGTCCGGGGTCATAATGCCCCACCACCAACATAAAGGTGGCA	50
77[122]	75[131]	CATACATGGCTTTTTTTTTTTTTTGTATGATACAGTCTGAAACATGA	46
78[105]	74[90]	CCCCACCCTCTGGTAATAAGTTTAACTCGAATTTCAGACTGTAGCGC	48
79[56]	73[69]	CAGGTCAGACCGGAAGTACAGGACGGAACACATTAAGCACCAG	46
79[78]	73[61]	CCAGTAACAGGAGCCACCTCCTCATTTGGTCATAGCCCCCTTAAGCAAA	48
80[65]	42[66]	TTAAAGAACTTTTGAATCGCGAAACCGAGCCAGAAAGACAGCAATTC	48
80[79]	77[83]	AAAATTCAGAAGGTAATAATTTTGGCCGTAGCATTTTCAAGCCAGAATG	52
81[102]	43[97]	ACAGTTTATTGCAGTATGGTTAATTTTCGCCTGAACGCCAACTACAGAGGTTATCATCAG	60
81[106]	77[121]	ATAAAATTTTGCTCTTTTCGGAACCTTAGCGTACCGTTCCAGTAAGCGT	48

The table lists the sequences of the 163 “staple” DNA oligonucleotides that form the object in addition to the M13mp18 scaffold DNA strand. “Start” and “End” refer to the location of 5' and 3' termini in the strand routing scheme (Fig. S1). The first number indicates the helix number; the second number (between square brackets) indicates the nt position within that helix.



Movie S1. The reconstructed cryo-EM density map (gray) is shown in gray, the pseudoatomic model in blue (scaffold strand) and red (staple strands).

[Movie S1](#)