randomizer The best folding of protein A had a strength of 3.0 and coordinates: [(0, 0, 0), (0, 0, 1), (1, 0, 1), (1, -1, 1), (0, -1, 1), (0, -1, 0), (1, -1, 0), (1, 0, 0)]

randomizer The best folding of protein B1 had a strength of 7.0 and coordinates: [(0, 0, 0), (0, 0, 1), (0, 1, 1), (-1, 1, 1), (-1, 1, 0), (-1, 1, -1), (-1, 2, -1), (-1, 2, 0), (0, 2, 0), (0, 1, 0), (0, 1, -1), (0, 0, -1), (-1,

0, -1), (-1, 0, 0)]

randomizer The best folding of protein B2 had a strength of 8.0 and coordinates: [(0, 0, 0), (0, 0, 1), (0, 0, 2), (0, 1, 2), (1, 1, 2), (1, 0, 2), (1, 0, 1), (1, -1, 1), (2, -1, 1), (2, -1, 2), (2, 0, 2), (2, 0, 1), (2, 1, 1),

(1, 1, 1), (1, 1, 0), (1, 1, -1), (1, 0, -1), (1, 0, 0), (2, 0, 0), (2, 1, 0)]

randomizer The best folding of protein B3 had a strength of 14.0 and coordinates: [(0, 0, 0), (0, 0, 1), (1, 0, 1), (2, 0, 1), (2, 0, 2), (2, -1, 2), (3, -1, 2), (3, 0, 2), (3, 0, 3), (3, -1, 3), (2, -1, 3), (2, 0, 3), (2, 1, 3)

, (2, 2, 3), (3, 2, 3), (3, 2, 2), (4, 2, 2), (4, 2, 3), (5, 2, 3), (5, 1, 3), (4, 1, 3), (4, 1, 4), (3, 1, 4), (3, 1, 3), (3, 1, 2), (3, 1, 1), (3, 1, 0), (4, 1, 0), (4, 1, 1), (4, 1, 2), (5, 1, 2), (5, 0, 2), (4, 0, 2), (4, 0, 3),

(4, -1, 3), (5, -1, 3)]

randomizer The best folding of protein B4 had a strength of 14.0 and coordinates: [(0, 0, 0), (0, 0, 1), (0, -1, 1), (-1, -1, 1), (-1, -2, 1), (-1, -2, 2), (-1, -1, 2), (-1, 0, 2), (-1, 1, 2), (-2, 1, 2), (-2, 0, 2), (-2, 0, 3),

(-1, 0, 3), (0, 0, 3), (0, 0, 2), (1, 0, 2), (1, 0, 1), (1, 1, 1), (1, 1, 0), (1, 0, 0), (2, 0, 0), (2, 1, 0), (2, 1, 1), (2, 0, 1), (2, -1, 1), (1, -1, 1), (1, -1, 0), (0, -1, 0), (-1, -1, 0), (-2, -1, 0), (-3, -1, 0), (-3, -1, -1)

, (-2, -1, -1), (-2, 0, -1), (-2, 1, -1), (-2, 1, 0), (-1, 1, 0), (-1, 0, 0), (-2, 0, 0), (-3, 0, 0), (-4, 0, 0), (-4, 0, 1), (-4, -1, 1), (-3, -1, 1), (-3, 0, 1), (-2, 0, 1), (-1, 0, 1), (-1, 1, 1), (-2, 1, 1), (-2, 2, 1)]

randomizer The best folding of protein C1 had a strength of 23.0 and coordinates: [(0, 0, 0), (0, 0, 1), (1, 0, 1), (2, 0, 1), (2, 1, 1), (2, 1, 0), (1, 1, 0), (1, 0, 0), (1, 0, -1), (0, 0, -1), (-1, 0, -1), (-1, -1, -1), (0, -1

, -1), (1, -1, -1), (2, -1, -1), (2, 0, -1), (2, 0, 0), (2, -1, 0), (1, -1, 0), (1, -2, 0), (2, -2, 0), (2, -3, 0), (1, -3, 0), (1, -3, -1), (1, -3, -2), (1, -4, -2), (1, -4, -1), (2, -4, -1), (2, -3, -1), (2, -3, -2), (2, -4, -2), (

2, -5, -2), (2, -5, -3), (2, -4, -3), (3, -4, -3), (4, -4, -3)]

randomizer The best folding of protein C2 had a strength of 35.0 and coordinates: [(0, 0, 0), (0, 0, 1), (0, -1, 1), (0, -1, 0), (0, -1, -1), (-1, -1, -1), (-1, -1, 0), (-2, -1, 0), (-3, -1, 0), (-3, 0, 0), (-3, 0, 1), (-2, 0, 1

), (-2, 0, 0), (-2, 0, -1), (-1, 0, -1), (0, 0, -1), (0, 1, -1), (1, 1, -1), (1, 0, -1), (1, -1, -1), (1, -1, 0), (1, 0, 0), (2, 0, 0), (2, 0, -1), (2, -1, -1), (2, -2, -1), (2, -2, 0), (2, -1, 0), (2, -1, 1), (1, -1, 1), (1, 0, 1),

(1, 1, 1), (1, 1, 2), (1, 0, 2), (0, 0, 2), (0, 0, 3)]

randomizer The best folding of protein C3 had a strength of 28.0 and coordinates: [(0, 0, 0), (0, 0, 1), (0, -1, 1), (-1, -1, 1), (-1, -1, 0), (-1, 0, 0), (-1, 0, -1), (-1, 0, -2), (0, 0, -2), (0, -1, -2), (0, -2, -2), (0, -2, -

3), (0, -2, -4), (0, -1, -4), (-1, -1, -4), (-1, 0, -4), (-2, 0, -4), (-2, 0, -3), (-1, 0, -3), (-1, 1, -3), (-1, 1, -4), (0, 1, -4), (0, 0, -4), (0, 0, -3), (0, -1, -3), (1, -1, -3), (2, -1, -3), (2, -1, -4), (2, -2, -4), (2, -2, -3

), (2, -2, -2), (1, -2, -2), (1, -2, -3), (1, -3, -3), (1, -4, -3), (0, -4, -3), (0, -3, -3), (0, -3, -2), (-1, -3, -2), (-1, -3, -3), (-1, -2, -3), (-1, -1, -3), (-1, -1, -2), (-1, -2, -2), (-2, -2, -2), (-3, -2, -2), (-3, -2, -3),

(-2, -2, -3), (-2, -1, -3), (-3, -1, -3)]

randomizer The best folding of protein C4 had a strength of 26.0 and coordinates: [(0, 0, 0), (0, 0, 1), (-1, 0, 1), (-1, -1, 1), (0, -1, 1), (0, -1, 2), (0, -1, 3), (0, 0, 3), (0, 0, 2), (0, 1, 2), (0, 1, 1), (1, 1, 1), (1, 0,

1), (2, 0, 1), (2, 0, 2), (2, 0, 3), (3, 0, 3), (3, 1, 3), (2, 1, 3), (2, 1, 2), (2, 2, 2), (2, 2, 3), (2, 3, 3), (1, 3, 3), (1, 2, 3), (1, 2, 2), (1, 1, 2), (1, 0, 2), (1, -1, 2), (1, -2, 2), (1, -2, 3), (0, -2, 3), (0, -2, 2), (-1,

-2, 2), (-2, -2, 2), (-3, -2, 2), (-3, -1, 2), (-4, -1, 2), (-4, -2, 2), (-5, -2, 2), (-6, -2, 2), (-6, -2, 3), (-6, -2, 4), (-6, -1, 4), (-6, -1, 3), (-5, -1, 3), (-5, -2, 3), (-5, -3, 3), (-5, -3, 2), (-4, -3, 2)]

Folded all the proteins using the randomizer algorithm.

fragment-randomizer The best folding of protein A had a strength of 3.0 and coordinates: [(-1, -1, 0), (-1, 0, 0), (0, 0, 0), (0, -1, 0), (0, -1, -1), (0, -1, -2), (-1, -1, -2), (-1, -1, -1)]

fragment-randomizer The best folding of protein B1 had a strength of 7.0 and coordinates: [(26, -23, -13), (27, -23, -13), (27, -22, -13), (26, -22, -13), (26, -22, -12), (26, -23, -12), (26, -23, -11), (27, -23, -11), (27, -22,

-11), (27, -22, -12), (27, -23, -12), (27, -24, -12), (27, -24, -13), (26, -24, -13)]

fragment-randomizer The best folding of protein B2 had a strength of 11.0 and coordinates: [(9, 10, -5), (9, 10, -4), (8, 10, -4), (7, 10, -4), (7, 10, -5), (8, 10, -5), (8, 10, -6), (7, 10, -6), (7, 9, -6), (7, 9, -7), (8, 9, -

7), (8, 9, -6), (9, 9, -6), (9, 9, -5), (8, 9, -5), (8, 8, -5), (8, 8, -4), (8, 9, -4), (7, 9, -4), (7, 9, -5)]

fragment-randomizer The best folding of protein B3 had a strength of 18.0 and coordinates: [(14, 23, -1), (14, 24, -1), (15, 24, -1), (16, 24, -1), (17, 24, -1), (17, 25, -1), (17, 25, 0), (17, 24, 0), (17, 24, 1), (17, 25, 1),

(18, 25, 1), (19, 25, 1), (19, 24, 1), (19, 23, 1), (18, 23, 1), (18, 24, 1), (18, 24, 0), (18, 23, 0), (17, 23, 0), (17, 23, -1), (16, 23, -1), (16, 22, -1), (16, 22, 0), (16, 23, 0), (16, 24, 0), (15, 24, 0), (15, 25, 0), (16, 25,

0), (16, 25, 1), (16, 24, 1), (16, 23, 1), (16, 23, 2), (17, 23, 2), (17, 23, 1), (17, 22, 1), (17, 22, 0)]

fragment-randomizer The best folding of protein B4 had a strength of 29.0 and coordinates: [(-4, 1, -7), (-4, 0, -7), (-4, 0, -6), (-4, 1, -6), (-5, 1, -6), (-5, 1, -7), (-6, 1, -7), (-6, 1, -8), (-6, 1, -9), (-5, 1, -9), (-5, 1

, -8), (-5, 0, -8), (-5, 0, -9), (-6, 0, -9), (-6, 0, -8), (-7, 0, -8), (-7, 0, -7), (-6, 0, -7), (-5, 0, -7), (-5, 0, -6), (-5, -1, -6), (-4, -1, -6), (-4, -1, -7), (-5, -1, -7), (-5, -1, -8), (-5, -2, -8), (-4, -2, -8), (-4, -1, -8

), (-4, -1, -9), (-4, -1, -10), (-5, -1, -10), (-5, 0, -10), (-5, 1, -10), (-4, 1, -10), (-4, 0, -10), (-4, 0, -9), (-4, 1, -9), (-4, 1, -8), (-4, 0, -8), (-3, 0, -8), (-3, 0, -7), (-3, -1, -7), (-3, -1, -8), (-3, -1, -9), (-3, 0, -9

), (-3, 1, -9), (-3, 1, -8), (-2, 1, -8), (-2, 0, -8), (-2, 0, -7)]

stuck! [(-2, 11, 13), (-2, 12, 13), (-3, 12, 13), (-3, 13, 13), (-3, 13, 12), (-4, 13, 12), (-4, 13, 13), (-4, 12, 13), (-5, 12, 13), (-5, 12, 14), (-4, 12, 14), (-4, 11, 14), (-4, 11, 13), (-4, 11, 12), (-4, 11, 11), (-3, 11, 11),

(-3, 11, 12), (-3, 12, 12), (-4, 12, 12), (-5, 12, 12), (-5, 11, 12), (-5, 11, 11), (-5, 10, 11), (-4, 10, 11), (-3, 10, 11), (-2, 10, 11), (-2, 11, 11), (-2, 12, 11), (-3, 12, 11), (-4, 12, 11), (-5, 12, 11), (-6, 12, 11), (-6, 12,

10), (-5, 12, 10), (-4, 12, 10), (-4, 11, 10)] : [(-2, 11, 13), (-2, 12, 13), (-3, 12, 13), (-3, 13, 13), (-3, 13, 12), (-4, 13, 12), (-4, 13, 13), (-4, 12, 13), (-5, 12, 13), (-5, 12, 14), (-4, 12, 14), (-4, 11, 14), (-4, 11, 13),

(-4, 11, 12), (-4, 11, 11), (-3, 11, 11), (-3, 11, 12), (-3, 12, 12), (-4, 12, 12), (-5, 12, 12), (-5, 11, 12), (-5, 11, 11), (-5, 10, 11), (-4, 10, 11), (-3, 10, 11), (-2, 10, 11), (-2, 11, 11), (-2, 12, 11), (-3, 12, 11), (-4, 12,

11), (-5, 12, 11), (-6, 12, 11), (-6, 12, 10), (-5, 12, 10), (-4, 12, 10), (-4, 11, 10)]

fragment-randomizer The best folding of protein C1 had a strength of 35.0 and coordinates: [(-9, 8, -3), (-8, 8, -3), (-7, 8, -3), (-7, 7, -3), (-6, 7, -3), (-6, 7, -4), (-6, 8, -4), (-6, 8, -3), (-5, 8, -3), (-5, 9, -3), (-6, 9

, -3), (-7, 9, -3), (-7, 9, -2), (-7, 8, -2), (-7, 7, -2), (-6, 7, -2), (-5, 7, -2), (-5, 8, -2), (-6, 8, -2), (-6, 8, -1), (-6, 7, -1), (-6, 6, -1), (-5, 6, -1), (-5, 7, -1), (-5, 8, -1), (-4, 8, -1), (-4, 8, -2), (-4, 8, -3), (-4,

8, -4), (-5, 8, -4), (-5, 7, -4), (-4, 7, -4), (-4, 7, -3), (-5, 7, -3), (-5, 6, -3), (-5, 6, -2)]

fragment-randomizer The best folding of protein C2 had a strength of 57.0 and coordinates: [(-2, -4, 14), (-2, -5, 14), (-2, -5, 13), (-2, -4, 13), (-2, -3, 13), (-3, -3, 13), (-3, -4, 13), (-3, -4, 14), (-3, -5, 14), (-4, -5, 1

4), (-4, -5, 15), (-3, -5, 15), (-2, -5, 15), (-2, -5, 16), (-3, -5, 16), (-4, -5, 16), (-4, -4, 16), (-4, -3, 16), (-4, -3, 15), (-4, -4, 15), (-3, -4, 15), (-2, -4, 15), (-2, -4, 16), (-3, -4, 16), (-3, -3, 16), (-3, -2, 16), (-3,

-2, 15), (-3, -3, 15), (-3, -3, 14), (-2, -3, 14), (-2, -3, 15), (-2, -2, 15), (-1, -2, 15), (-1, -3, 15), (-1, -4, 15), (-1, -4, 14)]

fragment-randomizer The best folding of protein C3 had a strength of 47.0 and coordinates: [(-7, 2, 5), (-6, 2, 5), (-6, 3, 5), (-7, 3, 5), (-7, 3, 6), (-6, 3, 6), (-5, 3, 6), (-4, 3, 6), (-4, 2, 6), (-5, 2, 6), (-5, 1, 6), (-5,

1, 7), (-6, 1, 7), (-7, 1, 7), (-7, 2, 7), (-7, 2, 8), (-7, 1, 8), (-6, 1, 8), (-5, 1, 8), (-4, 1, 8), (-4, 1, 7), (-4, 2, 7), (-5, 2, 7), (-5, 3, 7), (-5, 3, 8), (-5, 3, 9), (-5, 2, 9), (-5, 2, 8), (-6, 2, 8), (-6, 2, 7), (-6, 3, 7

(-5, 2, 7), (-5, 3, 7), (-5, 3, 8), (-5, 3, 9), (-5, 2, 9), (-5, 2, 8), (-6, 2, 8), (-6, 2, 7), (-6, 3, 7), (-7, 3, 7), (-8, 3, 1, 6), (-6, 1, 5), (-6, 0, 5), (-7, 0, 5), (-7, 0, 6), (-6, 0, 6), (-5, 0, 6), (-5, 0, 7), (-6, 0, 7)]

7), (-8, 3, 6), (-8, 2, 6), (-8, 2, 5), (-8, 1, 5), (-7, 1, 5), (-7, 1, 6), (-7, 2, 6), (-6, 2, 6), (-6, 1, 6), (-6, 1, 5), (-6,, (2, 6, 1), (1, 6, 1), (1, 5, 1), (1, 5, 0), (2, 5, 0), (3, 5, 0), (4, 5, 0), (4, 6, 0), (4, 6, 1), (4,

0, 5), (-7, 0, 5), (-7, 0, 6), (-6, 0, 6), (-5, 0, 6), (-5, 0, 7), (-6, 0, 7)] (3, 3, 0), (2, 3, 0), (2, 4, 0), (3, 4, 0), (4, 4, 0), (5, 4, 0), (5, 5, 0), (5, 6, 0), (5, 6, -1), (5,7

fragment-randomizer The best folding of protein C4 had a strength of 50.0 and coordinates: [(3, 7, 0), (3, 6, 0), (2, 6, 0), (5, 6, 2), (5, 5, 2), (4, 5, 2), (4, 5, 1), (5, 5, 1)]

, (2, 6, 1), (1, 6, 1), (1, 5, 1), (1, 5, 0), (2, 5, 0), (3, 5, 0), (4, 5, 0), (4, 6, 0), (4, 6, 1), (4, 6, 2), (3, 6, 2), (3, 6

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2, 4, 0), (3, 4, 0), (4, 4, 0), (5, 4, 0), (5, 5, 0), (5, 6, 0), (5, 6, -1), (5, 7, -1), (5, 7, 0), (4, 7, 0), (4, 8, 0), (4, 8,

1), (4, 8, 2), (4, 7, 2), (3, 7, 2), (3, 7, 1), (4, 7, 1), (5, 7, 1), (5, 6, 1), (5, 6, 2), (5, 5, 2), (4, 5, 2), (4, 5, 1), (5

, 5, 1)]

Folded all the proteins using the fragment-randomizer algorithm.