

## **Supplementary information**

### **Chimeragenesis of distantly-related proteins by noncontiguous recombination**

Matthew A. Smith, Philip A. Romero, Timothy Wu, Eric M. Brustad, Frances H. Arnold

Division of Chemistry and Chemical Engineering, California Institute of Technology, Pasadena, CA, 91125, USA.

**Supplementary Table 1** DNA sequence of NcrBgl.

ATGCATCACCACCACCATCACATGAACGTTAAGAAATTC CCAGAAGGCTTCCTGTGGGGCGTTGCGACC  
GCGTCTTACCAGATTGAGGGTTCCCCGCTGGCAGATGGTGC GGGCATGAGCATTGGGCACACCTTTAGC  
CATACCCCGGGTAATGTTAAGAATGGCGATACGGGCGATGTTGCTT GCGACCATTACAATCGTTGGAAA  
GAAGATATTGAGATTATCGAAAAGCTGGGCGTCAAGGCGTACCGCTTCAGCATCTCCTGGCCGCGTATC  
CTGCCGGAAGGCACGGGCCGTGTCAATCAGAAAGGCTGGATTTCTATAACCGCATCATTGACACCCCTG  
CTGGAGAAAGGTATTACCCCGTTTGTCAACCATCTTCCACTGGGATCTGCCGTTTGC GCTGCAACTGAAG  
GGCGGTTTGTGAATCGTGAGATTGCCGATTGGTTCGCAGAGTACAGCCGCGTGCTGTTCGAGA ACTTC  
GGCGACCGTGTCAAGAATTGGATTACCTTTAACGAACCGCTGTGTAGCGCGATTCCGGGTTACGGTTCT  
GGCACGTTTCGCTCCAGGTCGTCAAAGCACGAGCGAGCCGTGGACGGTGGGTCATAACATTC TGGTGGCC  
CACGGTCGTGCGGTCAAGGTCTTTCGTGAAACGGTTAAGGACGGTAAAATCGGTATTGTTCTGAACGGC  
GACTTCACGTACCCGTGGGACGCAGCGGACCCGGCAGACAAAGAGGCCGAGAGCGCCGCTGGAGTTC  
TTCATGCGATGGTTTGCAGACCCGATCTATCTGGCGACTATCCAGCCAGCATGCGTAAGCAGTTGGGT  
GACCGTCTGCCGACCTTTACCCCGGAAGAACGTGCGCTGGTTCACGGTAGCAACGACTTTTACGGTATG  
AACCATTATACCTCGAACTATATCCGCCACCGCTCCAGCCCTGCGTCTGCGGACGATACGGTTGGCAAT  
GTTGATGTGCTGTTTACCAATAAAACAAGGTAAGTGCATTTGGCCCGGAGACTGCGATGCCGTGGCTGCGT  
CCGTGTGCGGCTGGTTTCCGCGACTTCTGGTTTGGATTAGCAAACGTTATGGTTATCCTCCGATCTAT  
GTGACCGAAAATGGTGCGGCCTTCGATGATGTGGTTAGCGAGGATGGTCGCGTTCACGATCAGAATCGT  
ATCGACTACCTGAAAGCATATATCGGTGCAATGGTGACCGCCGTGGAATTGGACGGTGTGAATGTAAAA  
GGTACTTTGTCTGGAGCTTGCTGGATAACTTCGAGTGGGCGGAAGTTACAGCAAGCGTTTTTGGCATC  
GTGTACGTGGATTACAGCACCCAAAAACGCATCGTGAAGGACAGCGGTTATTGGTACTCCAATGTCGTC  
AAAAACAACGGCTTGGAGGACTGA

## Supplementary Table 2 Data collection and refinement statistics for 4GXP

<b>Data collection</b>	
Space group	P 31 1 2
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	115.38, 115.38, 282.54
<i>a</i> , <i>b</i> , <i>g</i> (°)	90.0, 90.0, 120.0
Resolution (Å)	37.8 – 3.0 (3.00 – 3.15)
<i>R</i> <sub>merge</sub>	5.2 (3.8)
<i>I</i> / <i>sI</i>	16.3 (3.3)
Completeness (%)	99.6 (99.6)
Redundancy	4.9 (4.8)
<b>Refinement</b>	
Resolution (Å)	37.4 - 3.0
No. reflections	41124
<i>R</i> <sub>work</sub> / <i>R</i> <sub>free</sub>	0.24/0.29
No. atoms	
Protein	9869
Ligand/ion	-
Water	2
<i>B</i> -factors	
Protein	13.1
Ligand/ion	-
Water	-
R.m.s. deviations	
Bond lengths (Å)	0.014
Bond angles (°)	1.73

\*All data were collected from a single crystal. Values in parentheses are for highest-resolution shell.