Supporting Information

Selective Immobilization of Fusion Proteins on Polyhydroxyalkanoate Microbeads

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Table S1. Bacterial Strains and Plasmids Used in This Study.

Strain or plasmid	Relevant characteristics	References
***E. coli* strains**		
XL1-Blue	*recA1, endA1, gyrA96, thi, hsdR17, suppE44, relA1, l*$^-$, *lac*$^-$, F'[*proAB lacI*^{q} lacZρM15, Tn*10* (tet)^r]	Strategene[a]
BL21(DE3)	F$^-$ *ompT hsdS*$_B$ (r_B^- m_B^-) *gal dcm* (DE3)	Novagen[b]
Plasmids		
pET-22b(+)	5.5 kb, Ap^r, *T7* promoter, *T7* terminater	Novagen[b]
pTrc99A	4.2 kb, Ap^r; *Trc* promoter	Pharmacia[c]
pEGFP	3.4 kb, Ap^r, *lac* promoter	Clontech[d]
pDsRed2-N1	4.7 kb, Kan^r, CMV promoter	Clontech[d]
pET-EGFP-SBD	6His-EGFP- SBD fusion gene, pET-22b(+) derivative	This study
pET-RFP-SBD	6His-RFP- SBD fusion gene, pET-22b(+) derivative	This study
pTrc-SCVe-SBD	6His-SCVe-SBD fusion gene, pTrc99A derivative	This study

[a]Stratagene Cloning Systems, La Jolla, CA

[b]Novagen, Darmstadt, Germany

[c]Pharmacia Biotech, Uppsala, Sweden

[d]BD Biosciences Clontech, Palo Alto, CA

Table S2. Oligonucleotides Used in Extended PCR for the Synthesis of the SARS-CoV Envelope Sequence.

No.	Sequences (5’ → 3’)
Primer 1	CATGCCATGCCCACCATCACCATCACCATTACTCATTCGTTTCGGAAGAAACAGGTACGTTAATAGTTAA
Primer 2	TAATAGTTAATAGCGTACTTCTTTTTCTTGCTTTCGTGGTATTCTTGCTAGTCACACTAGCCA
Primer 3	TAGTCACACTAGCCATCCTTACTGCGCTTCGATTGTGTGCGTACTGCTGCAATATTGTTAACGTGAG
Primer 4	TATTGTTAACGTGAGTTTAGTAAAACCAACGGTTTACGTCTACTCGCGTGTTAAAAATCTGAACTCT
Primer 5	AAAAATCTGAACTCTTCTGAAGGAGTTCCTGATCTTCTGGTCTAACGGTGACCG
Primer 6	CTTCTGGTCTAACGGTGACCGCCGC
Primer 7	CGGTGACCGCCGCCG
Primer 8	TTAGACCAGAAGATCAGGAACTCCTTCAGAGTTCAGATTTTTAACACGCGAGTAGAC
Primer 9	TTTAACACGCGAGTAGACGTAAACCGTTGGTTTTACTAAACTCACGTTAACAATATTGCAGCAGTACGCACA
Primer 10	GCAGTACGCACACAATCGAAGCGCAGTAAGGATGGCTAGTGTGACTAGCAACAATAC
Primer 11	TAGCAACAATACCACGAAAGCAAGAAAAAGAAGTACGCTATTAACTATTAACGTACC
Primer 12	TATTAACGTACCTGTTTCTTCCGAAACGAATGAGTAGGCATGGCATG
Primer 13	CCCAAGCTTTTATCCACCACCTGACCG

Underlines indicate the restriction enzyme sites.

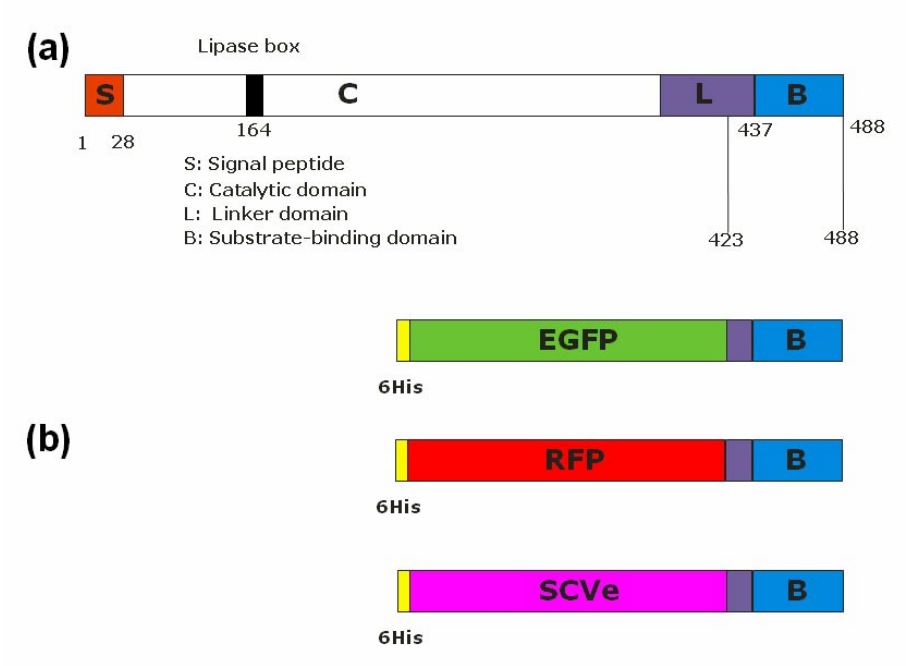

Figure S1. Domain structures of PHA depolymerase from *A. faecalis* T1 (a) and fusion strategy for EGFP-SBD, RFP-SBD and SCVe-SBD genes fused to the six histidine DNA (b). The numbers in (a) are the positions of amino acids in *A. faecalis* T1 PHA depolymerase.

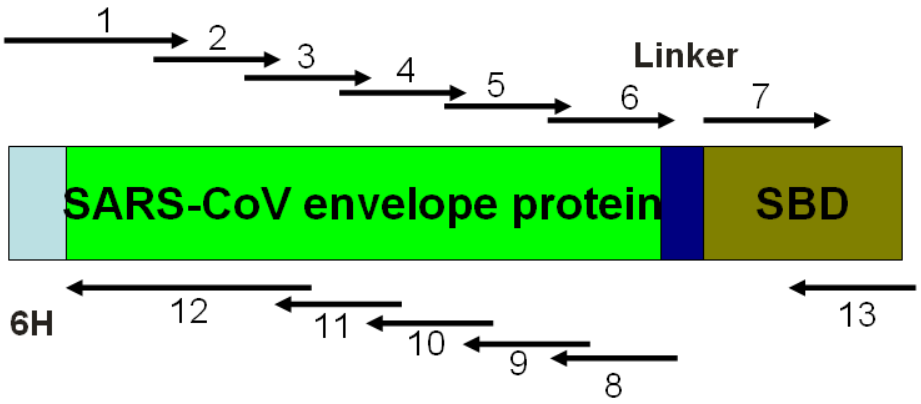

Figure S2. Schematic diagram for overlapping PCR of SARS envelope protein fused to the SBD gene and six histidine DNA.

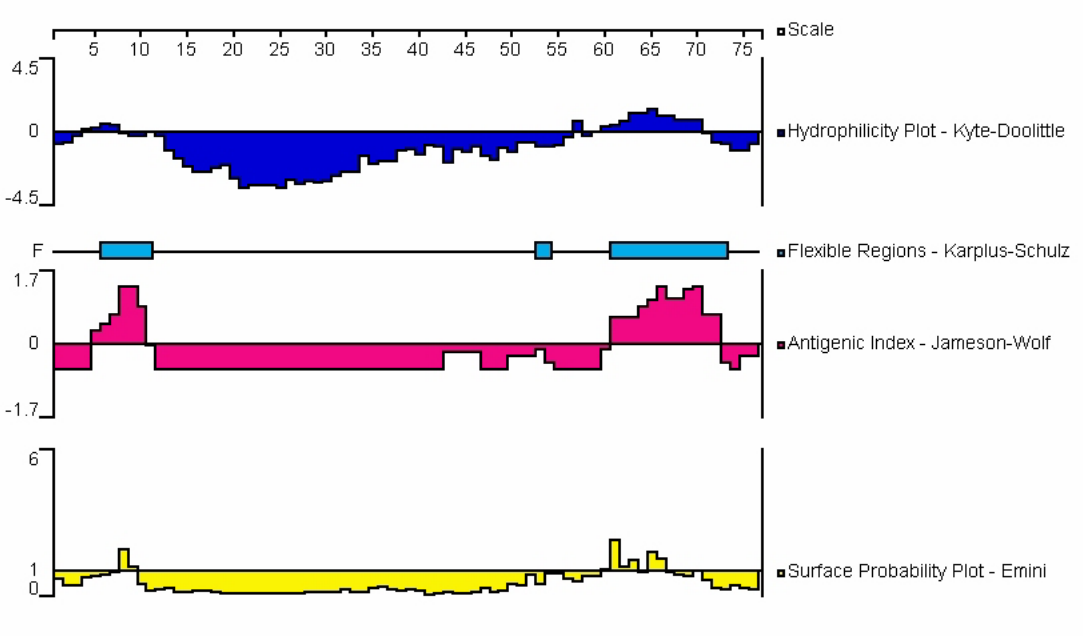

Figure S3. Analysis of SARS-CoV envelope protein. The hydrophilicity, flexible region, antigenicity, and surface probability of SARS-CoV envelope protein were calculated by Kyte-Doolittle plots, Karplus-Schulz prediction, Jameson-Wolf prediction, and Emini prediction, respectively.