Supporting Materials

Sortase-Mediated Ligation as a Modular Approach for the Covalent Attachment of Proteins to the Exterior of the Bacteriophage P22 Virus-like Particle.

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DNA sequences

CP-LPETG

ATGGCTTTGAACGAAGGTCAAATTGTTACACTGGCGGTAGATGAAATCATCGAAACCATCTCCGCAATC ACTCCAATGGCGCAGAAAGCCAAGAAATACACCCCGCCTGCTGCTTCTATGCAGCGCTCCAGCAATACC ATCTGGATGCCTGTAGAGCAAGAGTCACCCACTCAGGAGGGCTGGGATTTAACTGATAAAGCGACAGG GTTACTGGAACTTAACGTCGCGGTAAACATGGGAGAGCCGGATAACGACTTCTTCCAGTTGCGTGCTGA TGACTTGCGAGACGAAACTGCGTATCGTCGCCGCATCCAGTCTGCCGCTCGCAAGCTGGCGAACAACGT TGAGTTGAAAGTCGCAAACATGGCCGCCGAGATGGGTTCGCTGGTTATCACCTCCCCTGATGCCATCGG CACTAATACCGCAGACGCCTGGAACTTTGTGGCCGACGCAGAAGAAATCATGTTCTCCCGCGAACTTAA CCGCGACATGGGGACATCGTACTTCTTCAACCCTCAGGACTACAAAAAGCGGGTTACGACCTGACCAA GCGTGACATCTTCGGGCGTATTCCTGAAGAAGCATACCGAGATGGCACCATTCAGCGTCAGGTCGCTGG CTTCGATGATGTCNTGCGCTCTCCGAAACTTCCTGTGCTGACCAAATCCACCGCAACTGGCATCACTGTA TCCGGTGCGCAGTCCTTCAAGCCTGTCGCATGGCAACTGGATAACGATGGCAACAAAGTTAACGTTGAT AACCGTTTTGCTACCGTCACCTGTCTGCAACTACCGGCATGAAACGCGGCGACAAAATTTCGTTTGCTG GCGTTAAGTTCCTTGGTCAGATGGCTAAGAACGTACTGGCTCAGGATGCGACTTTCTCCGTAGTCCGCGT TGTTGACGGTACTCATGTTGAAATCACGCCGAAGCCGGTAGCGCTGGATGATGTTTCCCTGTCTCCGGA GCAGCGTGCCTACGCCAACGTTAACACCTCGCTGGCTGATGCAATGGCAGTGAACATTCTGAACGTTAA AGACGCTCGCACTAATGTGTTCTGGGCTGACGATGCTATTCGTATCGTGTCTCAGCCGATTCCGGCTAAC CATGAACTTTTTGCAGGTATGAAAACTACCTCATTCAGCATCCCTGATGTTGGCCTGAACGGTATCTTCGC TACGCAGGGTGATATTTCCACCCTGTCCGGCCTGTGCCGTATTGCGCTGTGGTACGGCGTAAACGCGAC ACGACCGGAGGCAATCGGTGTTGGCCTGCCTGGTCAGACTGCGAGATCTGCAGGCGGCGGAGGTGCCG GAGGAGGTACCCCGGGAAACCGGCGGTAGCTAACTCGAG

*underlined is the flexible peptide spacer used and in yellow highlight is the sortase recognition sequence.

Polyglycine-GFP

ATGGGCGGAGGAGGCAAGGGGGTGAAGGAAGTAATGAAGATCAGTCTGGAGATGGACTGCACTGTTA ACGGCGACAAATTTAAGATCATTGGGGATGGAACAGGAGAACCTTACGAAGGAACACAGACTTTACAT CTTACAGAGAAGGAAGGCAAGCCTCTGACGTTTTCTTTCGATGTATTGACACCAGCATTTCAGTATGGAA ACCGTACATTCACCAAATACCCAGGCAATATACCAGACTTTTTCAAGCAGACCGTTTCTGGTGGCGGGTA

MBP-HAhead (pRK793)

ATGAAAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTGA AGTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAG AGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTG GTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAGCGTTCCAGGACAAGCTGTATC CGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTTGAAGCGTTATC GCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAGAGATCCCGGCGCTGGATAA AGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGTACTTCACCTGGCCGCT GATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTACGACATTAAAGACGTGGGCG CAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCC CGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGG GTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGC TGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAAC CGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACC ATGGAAAACGCCCAGAAAGGTGAAATCATGCCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTG CGTACTGCGGTGATCAACGCCGCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGAC TAATTCGAGCTCGgaaaatctgtactttcaaggtGGCGGCGGTGCAAGCAAGGGCATCGCACCGCTGCAGCTG GGTAAATGCAATATTGCTGGTTGGCTGCTGGGCAACCCGGAATGTGATCCGCTGCTGCCGGTCCGCAGC TGGTCTTATATTGTGGAAAACCCCGAATAGCGAAAACGGTATCTGCTATCCGGGCGATTTCATTGACTACG AAGAACTGCGTGAACAACTGAGCAGCGTGAGCAGCTTTGAACGCTTCGAAATCTTTCCGAAAGAATCAT CGTGGCCGAACCATAATACCAACGGCGTTACGGCGGCCTGTAGCCACGAAGGTAAAAGCAGCTTTTATC GTAATCTGCTGTGGCTGACCGAAAAAGAAGGTAGTTATCCGAAACTGAAGAATTCCTACGTGAACAAAA AGGGCAAGGAAGTTCTGGTCCTGTGGGGTATCCATCACCCGCCGAATAGCAAAGAACAGCAAAACCTG TATCAGAATGAAAACGCGTACGTTAGTGTGGTTACCTCCAATTATAACCGTCGCTTCACGCCGGAAATTG CGGAACGTCCGAAGGTCCGCGATCAAGCCGGTCGTATGAACTATTACTGGACCCTGCTGAAACCGGGC GACACGATTATCTTTGAAGCGAATGGTAACCTGATCGCCCCGATGTACGCGTTCGCCCTGTCACGCGGCT ACCACTAA

*lowercase lettering indicates the sequence encoding the TEV protease cleavage site

Protein Sequences

CP-LPETG

MALNEGQIVTLAVDEIIETISAITPMAQKAKKYTPPAASMQRSSNTIWMPVEQESPTQEGWDLTDKATGLLE LNVAVNMGEPDNDFFQLRADDLRDETAYRRRIQSAARKLANNVELKVANMAAEMGSLVITSPDAIGTNTA DAWNFVADAEEIMFSRELNRDMGTSYFFNPQDYKKAGYDLTKRDIFGRIPEEAYRDGTIQRQVAGFDDVXR SPKLPVLTKSTATGITVSGAQSFKPVAWQLDNDGNKVNVDNRFATVTLSATTGMKRGDKISFAGVKFLGQM AKNVLAQDATFSVVRVVDGTHVEITPKPVALDDVSLSPEQRAYANVNTSLADAMAVNILNVKDARTNVFW ADDAIRIVSQPIPANHELFAGMKTTSFSIPDVGLNGIFATQGDISTLSGLCRIALWYGVNATRPEAIGVGLPGQ TAR<u>SAGGGGAGGGTLPETG</u>GS

*underlined is the flexible peptide spacer used and in yellow highlight is the sortase recognition sequence.

Poly-glycine-GFP-6xHis

GGGGKGVKEVMKISLEMDCTVNGDKFKIIGDGTGEPYEGTQTLHLTEKEGKPLTFSFDVLTPAFQYGNRTFTK YPGNIPDFFKQTVSGGGYTWERKMTYEDGGISNVRSDISVKGDSFYYKIHFTGEFPPHGPVMQRKTVKWEP STEVMYVDDKSDGVLKGDVNMALLLKDGRHLRVDFNTSYIPKKKVENMPDYHFIDHRIEILGNPEDKPVKLY ECAVARYSLLPEKNKGSGGLVPRGSGHHHHHH

MBP-Poly-glycine-HA-6xHis pRK793

MKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYA QSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSA LMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAF NKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEG LEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEA LKDAQTNSSS<u>ENLYFQG</u>GGGASKGIAPLQLGKCNIAGWLLGNPECDPLLPVRSWSYIVETPNSENGICYPGDF IDYEELREQLSSVSSFERFEIFPKESSWPNHNTNGVTAACSHEGKSSFYRNLLWLTEKEGSYPKLKNSYVNKKG KEVLVLWGIHHPPNSKEQQNLYQNENAYVSVVTSNYNRRFTPEIAERPKVRDQAGRMNYYWTLLKPGDTIIF EANGNLIAPMYAFALSRGFGSGIITSGSGGLVPRGSGHHHHHH

*underlined portion is the recognition sequence for TEV protease cleavage after residue Q

Cleaved PolyG-HAhead

GGGGASKGIAPLQLGKCNIAGWLLGNPECDPLLPVRSWSYIVETPNSENGICYPGDFIDYEELREQLSSVSSFE RFEIFPKESSWPNHNTGVTAACSHEGKSSFYRNLLWLTEKEGSYPKLKNSYVNKKGKEVLVLWGIHHPPNSKE QQNLYQNENAYVSVVTSNYNRRFTP EIAERPKVRD QAGRMNYYWT LLKPGDTIIF EANGNLIAPM YAFALSRGFGSGIITSGSGG LVPRGSGHHH HHH



Figure S1. Characterization of purified P22-LPETG VLPs, polyG-GFP, and Sortase. A) SDS-PAGE gel of purified P22-LPETG, polyG-GFP, and Sortase. B) Transmission electron microscopy images of the procapsid and expanded shell P22-LPETG VLPs. C) Size exclusion chromatography elution profiles and multiangle light scattering analysis of PC P22-LPETG (red and green) and EX P22-LPETG (blue and purple).





6 hr



22 hr





Figure S2. Sortase mediated ligation of polyG-GFP to PC P22-LPETG. SDS-PAGE gels of samples taken at different time points evaluating ligation reactions conditions of different ratios of Sortase to reactants and polyG-GFP to P22 CP-LPETG.



Figure S3.Evaluation of reaction mixtures and products of cesium chloride purification. A) Sortase mediated ligation reaction mixtures showed more increased turbidity in comparison with non-ligated reaction mixtures. B) SDS-PAGE analysis of protein disks produced from cesium chloride gradient purification contains cross-linked P22-GFP. C) TEM image obtained from the protein disk.



Figure S4. Small angle x-ray scattering of P22-GFP VLP disks and control samples.



Figure S5. Evaluation of the ability to remove free polyG-GFP by dialysis. 50 kDa molecular weight cutoff (MWCO) dialysis tubing was found to retain most of the free polyG-GFP, whereas 100 kDa MWCO dialysis tubing allow exchange and removal of GFP after two exchanges.



Figure S6. Preparation of polyG-HAhead from the MBP-HAhead fusion protein. SDS-PAGE gel analysis for TEV protease (lane 2), MBP-HAhead (lane 3), MBP-HAhead treated with catalytic amount of TEV (lane 4) and purified polyG-HAhead (lane 5). Expected molecular weights are: MBP-HAhead (68.9 kDa), MBP (43.9 kDa), and HAhead (25 kDa).