Data S1

Protein Sequences

β-galactosidase with Protein A fusion:

MTMITDSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRN**GSGSGSGSGSGSGS**DQQS
AFYEILNMPNLNEEQRNGFIQSLKDDPSQSTNVLGEAKKLNESQ**KALEAQKQKEQ**SEE
ARTDRPSQQLRSLNGEWRFAWFPAPEAVPESWLECDLPEADTVVVPSNWQMHGYDAPI
YTNVTYPITVNPPFVPTENPTGCYSLTFNVDESWLQEGQTRIIFDGVNSAFHLWCNGRW
VGYGQDSRLPSEFDLSAFLRAGENRLAVMVLRWSDGSYLEDQDMWRMSGIFRDVSLL
HKPTTQISDFHVATRFNDDFSRAVLEAEVQMCGELRDYLRVTVSLWQGETQVASGTAP
FGGEIIDERGGYADRVTLRLNVENPKLWSAEIPNLYRAVVELHTADGTLIEAEACDVGF
REVRIENGLLLLNGKPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNAVRCS
HYPNHPLWYTLCDRYGLYVVDEANIETHGMVPMNRLTDDPRWLPAMSERVTRMVQR
DRNHPSVIIWSLGNESGHGANHDALYRWIKSVDPSRPVQYEGGGADTTATDIICPMYAR
VDEDQPFPAVPKWSIKKWLSLPGETRPLILCEYAHAMGNSLGGFAKYWQAFRQYPRLQ
GGFVWDWVDQSLIKYDENGNPWSAYGGDFGDTPNDRQFCMNGLVFADRTPHPALTEA
KHQQQFFQFRLSGQTIEVTSEYLFRHSDNELLHWMVALDGKPLASGEVPLDVAPQGKQ
LIELPELPQPESAGQLWLTVRVVQPNATAWSEAGHISAWQQWRLAENLSVTLPAASHAI
PHLTTSEMDFCIELGNKRWQFNRQSGFLSQMWIGDKKQLLTPLRDQFTRAPLDNDIGVS
EATRIDPNAWVERWKAAGHYQAEAALLQCTADTLADAVLITTAHAWQHQGKTLFISR
KTYRIDGSGQMAITVDVEVASDTPHPARIGLNCQLAQVAERVNWLGLGPQENYPDRLT
AACFDRWDLPLSDMYTPYVFPSENGLRCGTRELNYGPHQWRGDFQFNISRYSQQQLME
TSHRHLLHAEEGTWLNIDGFHMGIGGDDSWSPSVSAEFQLSAGRYHYQLVWCQK

scFv against Protein A:

DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSR
FSGSGSGTDFTLTISSLQPEDFATYYCQQSYSAPRTFGQGTKVEIKR**GGGGSGGGGSGG**
GGSSGGGQVQLVESGGGVVQPGKSLRLSCAASGFTFSGYGMHWVRQAPGKGLEWVA
LISYDESNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVKFYDPTAP
NDYWGQGTLVTVSS

GFP:

MSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPT
LVTTFSYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGD
TLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQ
LADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGITHGMDE
LYK

β-gal with DARPin fusion:

MTMITDSLAVVLQRRDWENPGVTQLNRLAAHPPFASWRN**GSGSGSGSGSGSGS**DLGK
KLLEAARAGQDDEVRILMANGADVNALDRFGLTPLHLAAQRGHLEIVEVLLKCGADVN
AADLWGQTPLHLAATAGHLEIVEVLLKYGADVNALDLIGKTPLHLTAIDGHLEIVEVLL
KHGADVNAQDKFGKTAFDISIDNGNEDLAEINSEEARTDRPSQQLRSLNGEWRFAWFPA
PEAVPESWLECDLPEADTVVVPSNWQMHGYDAPIYTNVTYPITVNPPFVPTENPTGCYS
LTFNVDESWLQEGQTRIIFDGVNSAFHLWCNGRWVGYGQDSRLPSEFDLSAFLRAGEN
RLAVMVLRWSDGSYLEDQDMWRMSGIFRDVSLLHKPTTQISDFHVATRFNDDFSRAVL
EAEVQMCGELRDYLRVTVSLWQGETQVASGTAPFGGEIIDERGGYADRVTLRLNVENP
KLWSAEIPNLYRAVVELHTADGTLIEAEACDVGFREVRIENGLLLLNGKPLLIRGVNRHE
HHPLHGQVMDEQTMVQDILLMKQNNFNAVRCSHYPNHPLWYTLCDRYGLYVVDEANI
ETHGMVPMNRLTDDPRWLPAMSERVTRMVQRDRNHPSVIIWSLGNESGHGANHDALY
RWIKSVDPSRPVQYEGGGADTTATDIICPMYARVDEDQPFPAVPKWSIKKWLSLPGETR
PLILCEYAHAMGNSLGGFAKYWQAFRQYPRLQGGFVWDWVDQSLIKYDENGNPWSAY
GGDFGDTPNDRQFCMNGLVFADRTPHPALTEAKHQQQFFQFRLSGQTIEVTSEYLFRHS
DNELLHWMVALDGKPLASGEVPLDVAPQGKQLIELPELPQPESAGQLWLTVRVVQPNA
TAWSEAGHISAWQQWRLAENLSVTLPAASHAIPHLTTSEMDFCIELGNKRWQFNRQSGF
LSQMWIGDKKQLLTPLRDQFTRAPLDNDIGVSEATRIDPNAWVERWKAAGHYQAEAAL
LQCTADTLADAVLITTAHAWQHQGKTLFISRKTYRIDGSGQMAITVDVEVASDTPHPAR
IGLNCQLAQVAERVNWLGLGPQENYPDRLTAACFDRWDLPLSDMYTPYVFPSENGLRC
GTRELNYGPHQWRGDFQFNISRYSQQQLMETSHRHLLHAEEGTWLNIDGFHMGIGGDD
SWSPSVSAEFQLSAGRYHYQLVWCQK

VipA/VipB:

VipA-DARPin fusion:

SKEGSVAPKERINIKYIPATGDAQAEVELPLKTLVVGDFKGHAEQTPLEERATVTVDKN
NFEAVMRESELKITATVKNKLTDDENAELPVELNFKSLADFAPDAVASQVPELKKLIELR
EALVALLLEAARAGQDDECRILMANGADVNALDEVGWTPLHLAAWGHLEIVECLLKN
GADVNAADIDGYTPLHLAAFSGHLEIVEVLLKYGADVNADDQAGFTPLHLAAIFGHLEI
VEVLLKNGADVNAQDKFGKTPRDLAIDNGNEDIAEVL

VipB:

NKSLVDQMLVELDKKISAQMDEILHNSQFQAMESAWRGLKLFVDRTDFRENNKVEILH
VTKDELLEDFEFAPETAQSGLYKHVYSAGYGQFGGEPVGAIIGNYAFTPSTPDMKLLQY
MGALGAMAHAPFISSVGPEFFGIDSFEELPNIKDLKSTFESPKYTKWRSLRESEDARYLG
LTAPRFLLRVPYDPIENPVKSFNYAENVSASHEHYLWGNTAFAFATRLTDSFAKYRWCP
NIIGPQSGGAVEDLPVHVFESMGALQSKIPTEVLITDRKEFELAEEGFIALTMRKGSDNAA
FFSANSIQKPKVFPNTKEGKEAETNYKLGTQLPYMMIINRLAHYVKVLQREQIGAWKER
QDLERELNSWIKQYVADQENPPADVRSRRPLRAARIEVMDVEGNPGWYQVSLSVRPHF
KYMGANFELSLVGRLDQA

TibC DARPin fusion:

MSTLKNTFFITPPDTPTQAGPENIFYDFNDGARVLLPEGKWHVRLLDADSENILFCCDVD
KGWVTSSKKYFVRFRIQVFRQGEETPLLDETLKLKDRPVLISFPTGTLGDLLGWFPYAER
FQSLHKCRLECTMSQDIIDLLAPQYPQIQFSTPDKPRTVAPYATYRVGLYFGGDTNNQPV
DFRKVGFHRSAGYILGVDPREAPVRLDLSAPRVIQEPYVCIATQSTCQAKYWNNGTGWS
EVIAHLKSLGYRVMCIDRDAHYGQGFVWNHIPWGAEDFTGKLPLQERVNLLRHASFFIG
LPSGLSWLAWATRIPVVLISGFSLPNSEFYTPWRVFNSHGCYGCWDDTSLNFDHHDFLW
CPRHKNTDRQFECTRLITGAQVNGVINKLHRSLTEQKALEAQKQKLLEAARAGQDDEC
RILMANGADVNALDEVGWTPLHLAAWGHLEIVECLLKNGADVNAADIDGYTPLHLAA
FSGHLEIVEVLLKYGADVNADDQAGFTPLHLAAIFGHLEIVEVLLKNGADVNAQDKFGK
TPRDLAIDNGNEDIAEVL

Ferritin DARPin fusion cage:

MLKPEMIEKLNEQMNLELYSSLLYQQMSAWCSYHTFEGAAAFLRRHAQEEMTHMQRL
FDYLTDTGNLPRINTVESPFAEYSSLDELFQETYKHEQLITQKINELAHAAMTNQDYPTF
NFLQWYVSEQHEEEKLFKSIIDKLSLAGKSGEGLYFIDKELSTLDTQNLLEAARAGQDDE
CRILMANGADVNALDEVGWTPLHLAAWGHLEIVECLLKNGADVNAADIDGYTPLHLA
AFSGHLEIVEVLLKYGADVNADDQAGFTPLHLAAIFGHLEIVEVLLKNGADVNAQDKFG
KTPRDLAIDNGNEDIAEVL

Artificial cage (EPN-01):

EELFKKHKIVAVLRANSVEEAKKKALAVFLGGVHLIEITFTVPDADTVIKELSFLKEMGA
IIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKKALEAQKSDLGRKLLEAARA
GQDDECRILMANGADVNALDEVGWTPLHLAAWGHLEIVECLLKNGADVNAADIDGYT
PLHLAAFSGHLEIVEVLLKYGADVNADDQAGFTPLHLAAIFGHLEIVEVLLKNGADVNA
QDKFGKTPRDLAIDNGNEDIAEVL**GGGGSGGGGSGGGGSGGGGSGGG**VFYMPGVM
TPTELVKAMKLGHTILKLFPGEVVGPQFVKAMKGPFPNVKFVPTGGVNLDNVCEWFKA
GVLAVGVGSAL VKGTPVEVAEKAKAFVEKIRGCTE

Ribosomal protein L29-PrA fusion:

MGGSHHHHHHGENLYFQSKAKELREKSVEELNTELLNLLREQFNLRMQAASGQLQQSH
LLKQVRRDVARVKTLLNEKKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLA
EAKKLNDA