Supporting Information:
Dodecin as carrier protein for immunizations and bioengineering applications

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Abbreviations:
ACP, acyl carrier protein; AB, antibody; BSA, bovine serum albumin; Catcher, small protein fold (SpyCatcher or SnoopCatcher) that binds and reacts with Tag; CDS, coding sequence; CellSig., Cell Signaling Technology; CHIP, C-terminus of heat shock cognate 70 interacting protein; EU, endotoxin units; FMN, riboflavin-5'-phosphate; GFP, green fluorescent protein; GSG, PAS, PAS2 GPAS, GPAS2, PASG, PAS2G, linker systems, see Table 1; HB-EGF, proheparin-binding EGF-like growth factor; HSP, heat shock protein; IPTG, isopropyl-β-D-thiogalactopyranoside; KLH, keyhole limpet hemocyanin; L, Ladder (only used in figures); LAL, *Limulus* amebocyte lysate; Lys., lysate (only used in figures); MAP, multiple antigen peptides; mCHIP, middle fragment of C-terminus of heat shock cognate 70 interacting protein; MG, proteasome inhibitor MG-132; *mm*ACP, *Mus musculus* acyl carrier protein; msfGFP, monomeric superfolder green fluorescent protein; *mt*Dod, *Mycobacterium tuberculosis* dodecin; *mt*Dod(WT), *Mycobacterium tuberculosis* dodecin wild type; OD600, optical density at 600 nm; OE, over expressing cells; RSA, rabbit serum albumin; SCBT, Santa Cruz Biotechnology; *se*ACP, *Saccharopolyspora erythraea* acyl carrier protein; SEC, size exclusion chromatography; Sfp, 4'-phosphopantetheine transferase from *Bacillus subtilis*; Sigma, Sigma-Aldrich; SnpC, SnoopCatcher; SnpT, SnoopTag; SpyC, SpyCatcher; SpyT, SpyTag; SZ, SYNZIP domain; Tag, small peptide sequence that interacts with Catcher's (SpyTag or SnoopTag); TB, terrific broth; TBS, Tris-HCl buffered saline; TBST, Tris-HCl buffered saline with Tween-20; TT, tetanus toxoid; VLP, virus-like particle.

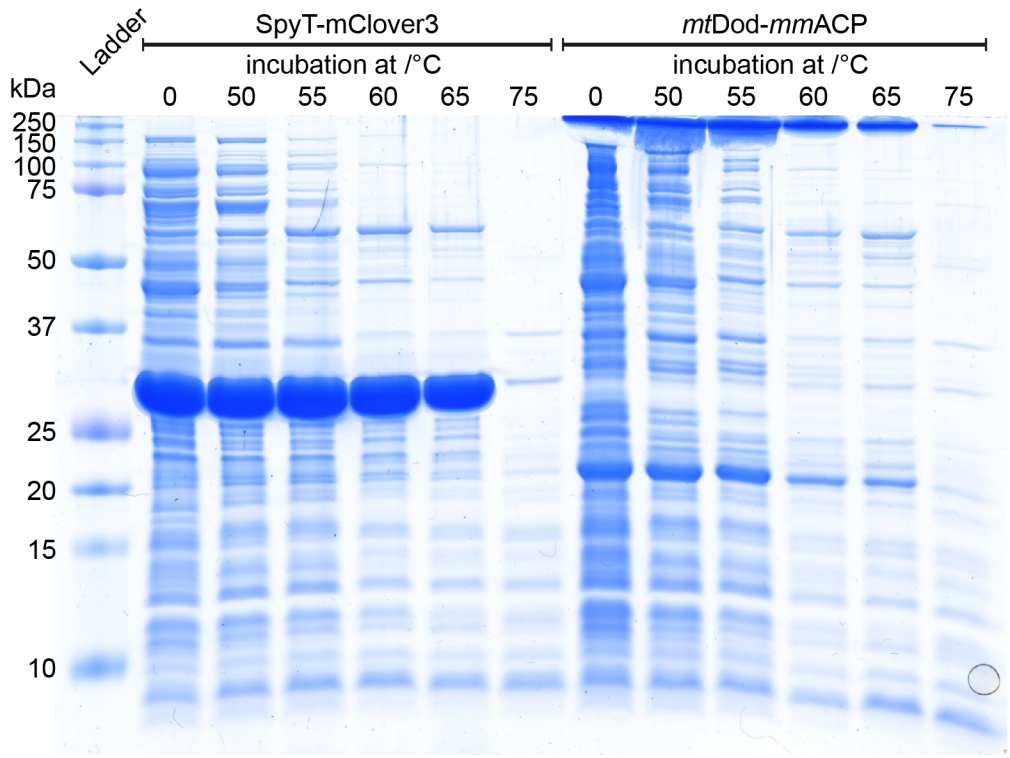

Fig. S1: SDS-PAGE gel of supernatant after heat denaturation of lysate at different temperatures. Standard loading buffer (pH 6.8, 2.5% SDS) was used for sample preparation with 15 min heat treatment (95 °C). Lysate samples were incubated at depicted temperatures for 25 min and aggregated protein was removed by centrifugation (15.000 rcf, 10 min). After centrifugation, for all samples, the same amount of supernatant was mixed with loading buffer, incubated as stated and loaded onto the gel. Left: Bands show heat denaturation of SpyT-mClover3 at different temperatures. At 60 °C, most *E. coli* proteins are aggregated and removed by centrifugation, while SpyT-mClover (thick band above 25 kDa) is still present in high concentration. At 75 °C, also SpyT-mClover is denatured and aggregated, as indicated by the intensity decrease of the respective band. Right: Supernatant samples of heat denaturation of *mt*Dod-*mm*ACP. Since standard loading buffer is not able to denature the dodecamer (only a small fraction of the dodecamer denatures under these conditions), the dodecamer hardly migrated in the gel, as indicated by bands at very top edge of the gel. The band representing the *mt*Dod-*mm*ACP monomer is visible slightly above 20 kDa. At 60 °C, the intensity of the *mt*Dod-*mm*ACP band decreases (best observable for the monomer band slightly above 20 kDa), indicating that *mt*Dod-*mm*ACP starts to precipitate during the heat denaturing step. At 75 °C, only weakly stained bands *mt*Dod-*mm*ACP are visible, showing that most *mt*Dod-*mm*ACP precipitated at this temperature and was removed by centrifugation (see Fig. S7 for SDS-PAGE of the pellet).

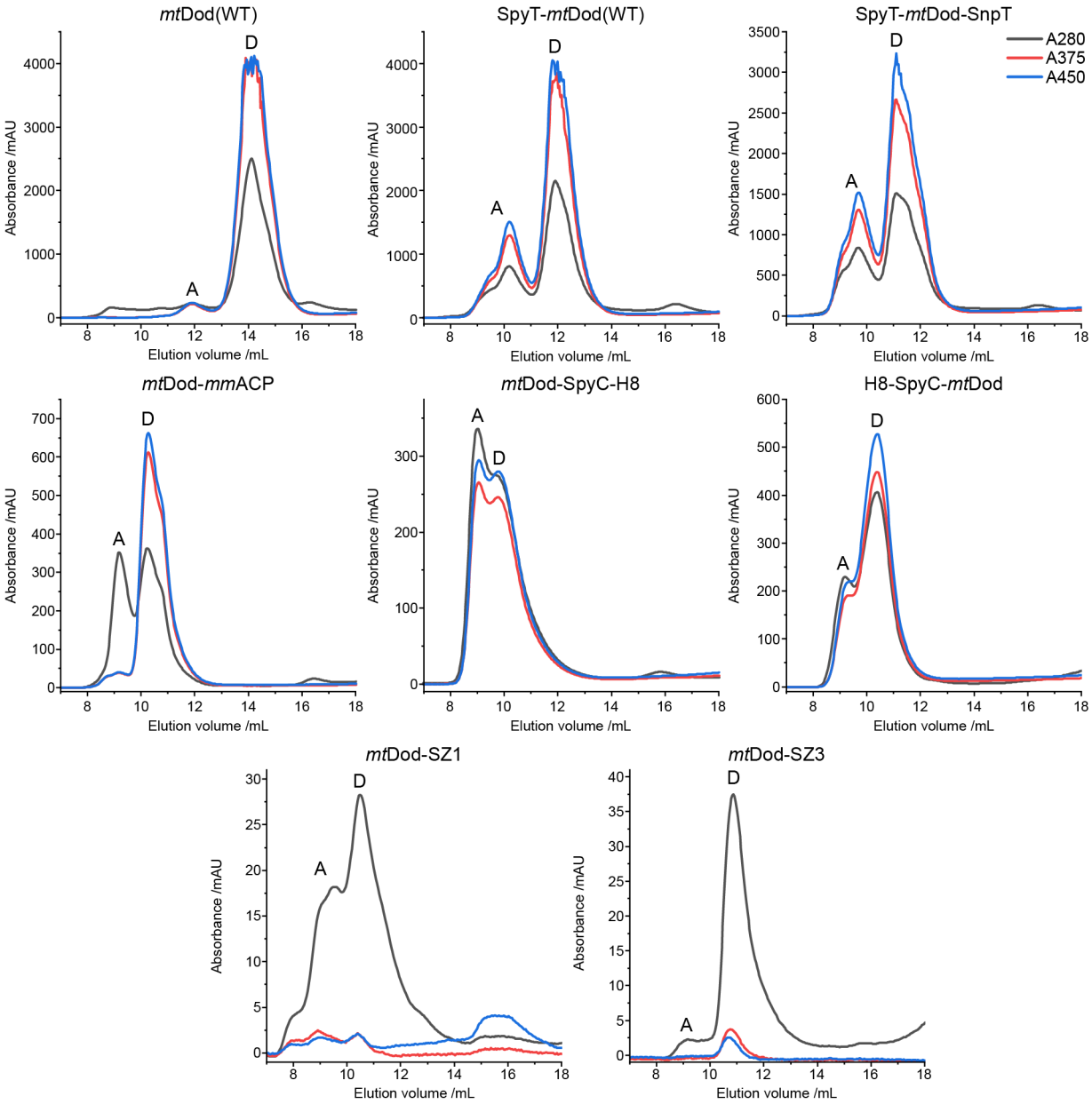

Fig. S2: SEC chromatograms of various *mt*Dod constructs. Column: Superdex 200 increase 10/300. A: Peak/peaks representing aggregates. D: Peak representing the dodecamer. Top row: Example of *mt*Dod constructs purified by the heat denaturation protocol. The second DMSO precipitation step was used to concentrate samples as high as possible (buffer added in small portions, until the pellet was nearly fully dissolved but not completely). Under these high concentrations, some *mt*Dod constructs seem to form aggregates that still bind FMN. Chromatogram of *mt*Dod-*mm*ACP purified by the heat denaturation strategy shows a prominent aggregation peak at about 9 mL. Chromatograms of refolded *mt*Dod SpyC constructs form FMN binding dodecamers, but tend to aggregate (peak at about 9 mL). H8-SpyC-*mt*Dod seems to have lower aggregation tendencies than *mt*Dod-SpyC-H8 (the separation of dodecamer and aggregates was not possible). *Mt*Dod SYNZIP constructs were refolded and purified without additional FMN. The high aggregation tendencies of SYNZIP constructs (especially *mt*Dod-SZ1) made the purification of higher amounts challenging, as samples tended to suddenly precipitate during concentration and filtration at higher concentrations.

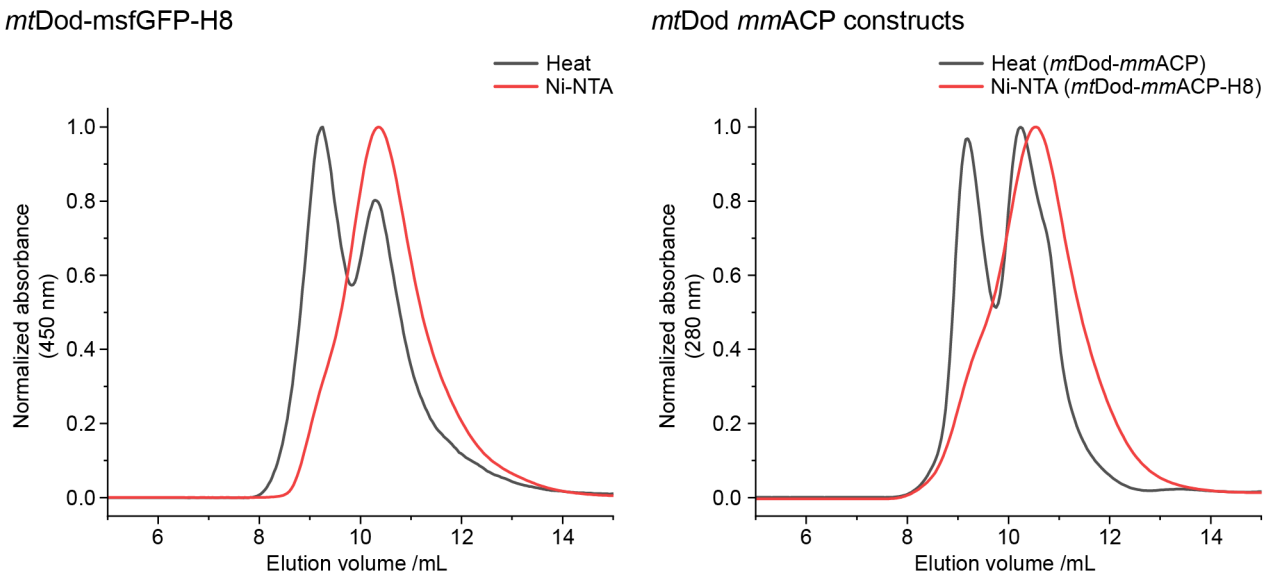

Fig. S3: Comparison of SEC chromatograms of *mt*Dod-msfGFP-H8 and *mt*Dod *mm*ACP constructs purified by Ni-NTA affinity chromatography and/or by heat denaturation. In both cases, the Ni-NTA affinity chromatography purification caused less aggregation. However, dodecameric fractions of *mt*Dod-msfGFP-H8 and *mt*Dod-*mm*ACP could also be received from the heat denaturation protocol.

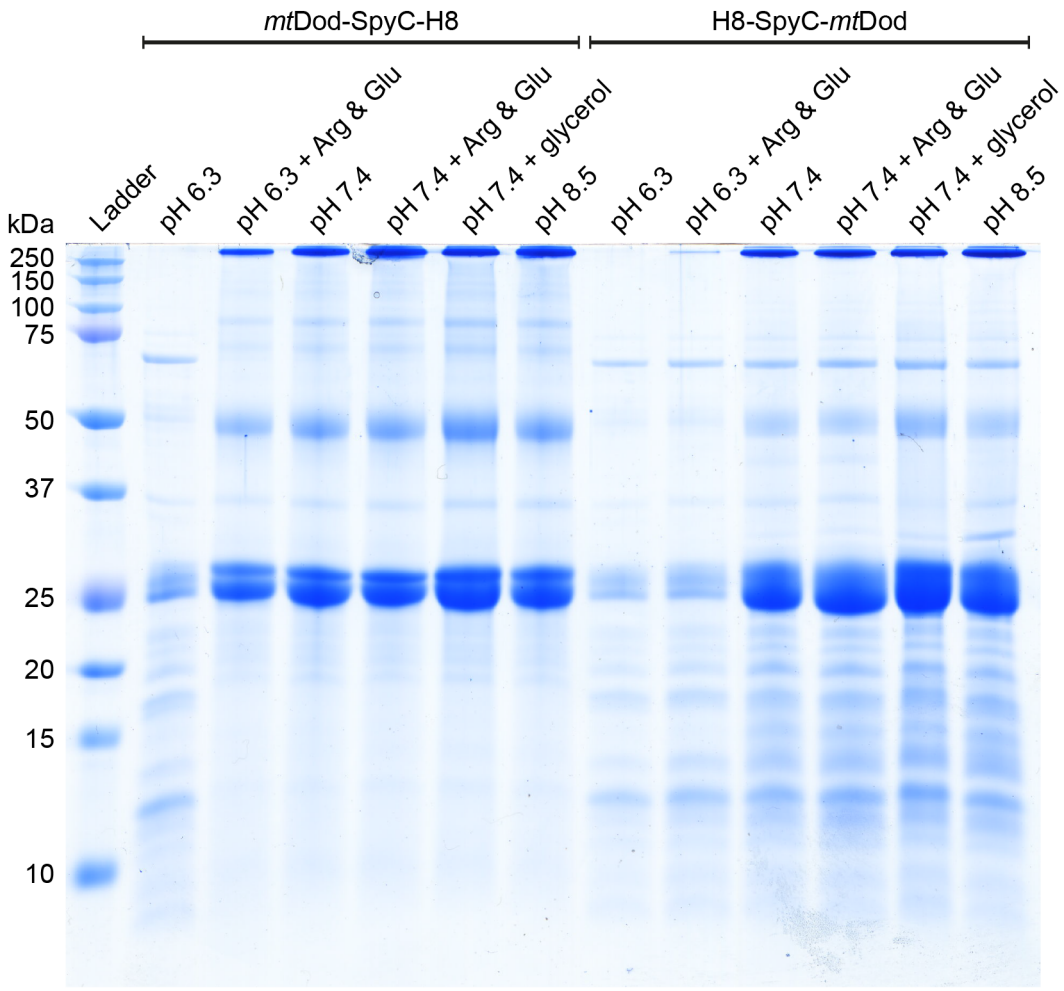

Fig. S4: SDS-PAGE gel of *mt*Dod SpyC constructs refolded under different conditions via dialysis. Acidic loading buffer used for sample preparation contained 50 mM acetic acid, which did not allow a full denaturation of the dodecamer. General buffer solution for refolding (final concentrations): 100 mM NaCl, 25 mM Na_2HPO_4 and 25 mM boric acid. The pH was adjusted to the shown values with HCl or NaOH. Refolding additives were 50 mM arginine and 50 mM glutamic acid (Arg & Glu)[1] and 20% glycerol (glycerol). Except under slightly acidic conditions, refolding of *mt*Dod SpyC constructs is possible. Arginine and glutamic acid seem to be beneficial for refolding (clearly seen for *mt*Dod-SpyC-H8 at pH 6.3). Overall, the best tested condition seems to be pH 7.4 with 20% glycerol (highest band intensity and lowest amount of precipitate was observed).

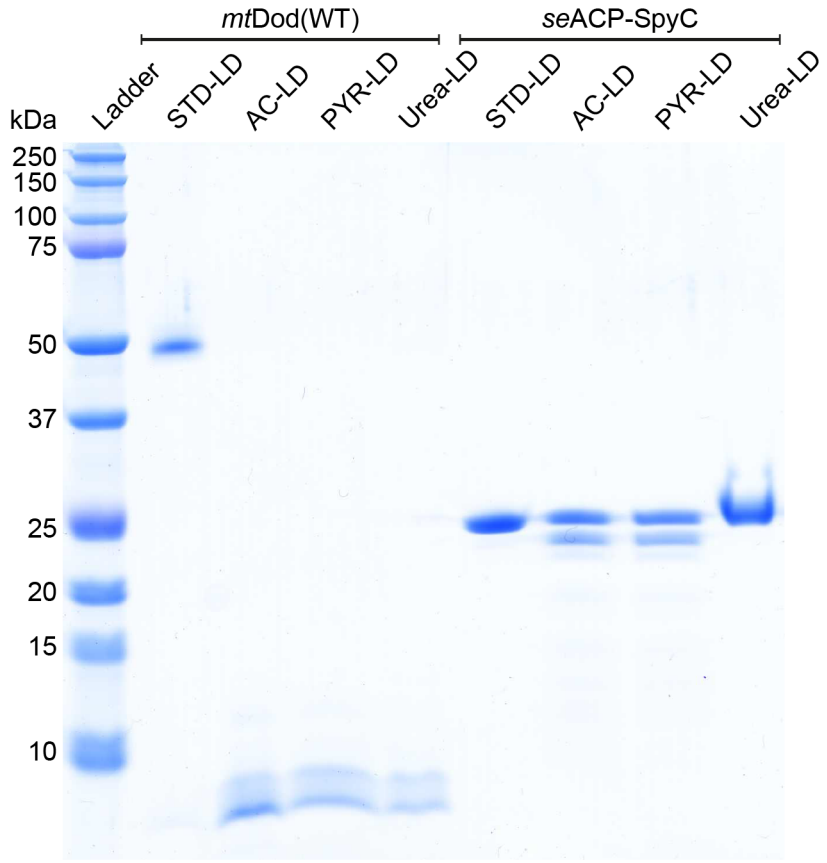

Fig. S5: SDS-PAGE gel for comparison of loading buffers. *Mt*Dod(WT) and *se*ACP-SpyC were used. STD-LD: standard loading buffer (denaturing step conditions: pH 6.8, 2.5% SDS). AC-LD: Acetic acid two-component loading buffer (denaturing step conditions: pH < 5.0, 3.3% SDS). PYR-LD: Pyridine two-component loading buffer (denaturing step conditions: pH < 5.0, 3.3% SDS). Urea-LD: standard loading buffer with 8 M urea (denaturing step conditions: pH 6.8, 2.5% SDS, 8 M Urea). All samples were denatured for 5 min at 95 °C. After denaturation, the second component buffer was added to the two-component loading buffer samples (final pH, SDS and glycerol content as in standard loading buffer). All loading buffers, except the standard loading buffer, are able to denature the *mt*Dod(WT) dodecamer, indicated by the monomer band (below 10 kDa). The smearing double bands seem to be an artefact of this specific SDS-PAGE gel, as also the lower molecular weight bands of the ladder show this phenomenon. The gel shows that the *mt*Dod dodecamer tolerates SDS, as long the conditions do not become too acidic. For seACP-SpyC, the acidic denaturing conditions cause the appearance of a band at lower molecular weight. The formation of this band is also temperature dependent. Heat treatment at 60°C with acidic loading buffer did not cause the formation of double bands (see Fig 5).

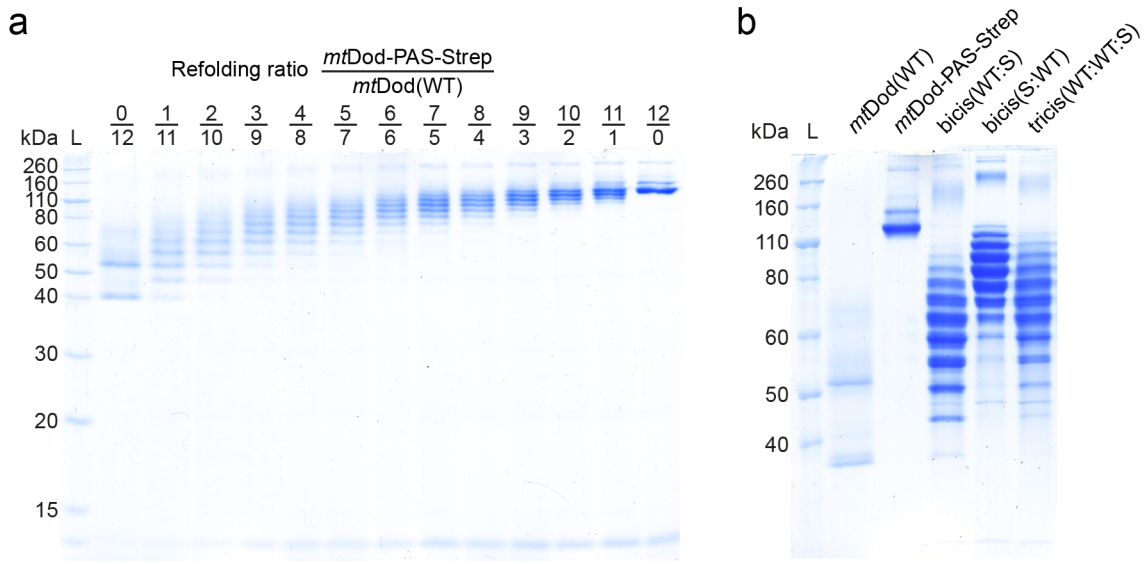

Fig. S6: Uncropped SDS-PAGE gel of Fig. 3. L: Ladder. S: *mt*Dod-PAS-Strep. WT: *mt*Dod(WT). a) Uncropped SDS-PAGE gel of Fig. 3 a. Heterododecamers obtained by refolding *mt*Dod(WT) and mtDod-PAS-Strep at different ratios. Bands below 15 kDa represent the mtDod-PAS-Strep monomer (9916 Da), while *mt*Dod(WT) monomer (7497 Da) migrated through the full gel so that no bands are visible. b) Full length gel image of Fig. 3 b. Heterododecamers formed during polycistronic expression of *mt*Dod(WT) and *mt*Dod-PAS-Strep. Gene order of polycistronic expression vectors given in brackets (bicis: bicistronic(first gene : second gene); tricis: tricistronic(first gene : second gene : third gene). For improved separation of higher molecular weight bands running time was prolonged to about 4 h. The monomers of *Mt*Dod constructs and lower weight proteins migrated through the entire gel so that protein and ladder bands (below 40 kDa) are not visible. The gel is cropped at the right to remove not relevant samples.

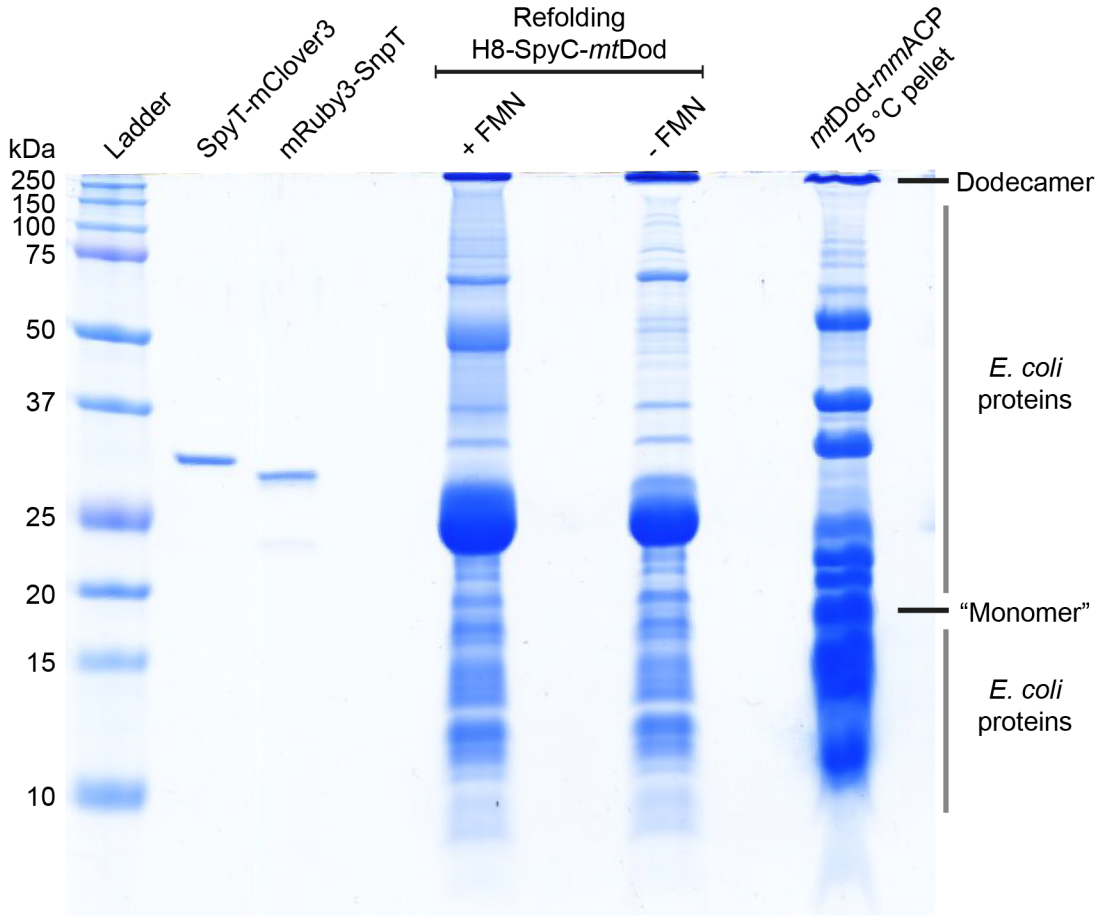

Fig. S7: SDS-PAGE gel of *mt*Dod-*mm*ACP precipitating during heat denaturation and other samples. Standard loading buffer was used to preserve dodecameric species. Right sample: Cytosol containing *mt*Dod-*mm*ACP was incubated at 75 °C for 25 min and aggregated proteins were pelleted by centrifugation (15.000 rcf, 10 min). A small amount of the pellet was dissolved in standard SDS loading buffer at 95 °C (about 15 min) and loaded to the gel. In the stained gel, a strong band at high molecular weight (top of the gel, labelled dodecamer) is visible indicating intact dodecamer of *mt*Dod-*mm*ACP. The potential band representing the monomer of *mt*Dod-*mm*ACP (about 18 kDa) cannot be selected with certainty (most fitting band labelled with "Monomer"). Other bands are the during the heat incubation denatured *E. coli* proteins resolubilized with SDS (grey bar). Other samples: SpyT-Clover-H8 and mRuby3-SnpT: pooled SEC fractions (purified by a heat denaturation based protocol). Refolding H8-SpyC-*mt*Dod: first refolding attempt of H8-SpyC-*mt*Dod in our standard buffer, aggregated protein was removed by centrifugation (15,000 rcf, 10 min).

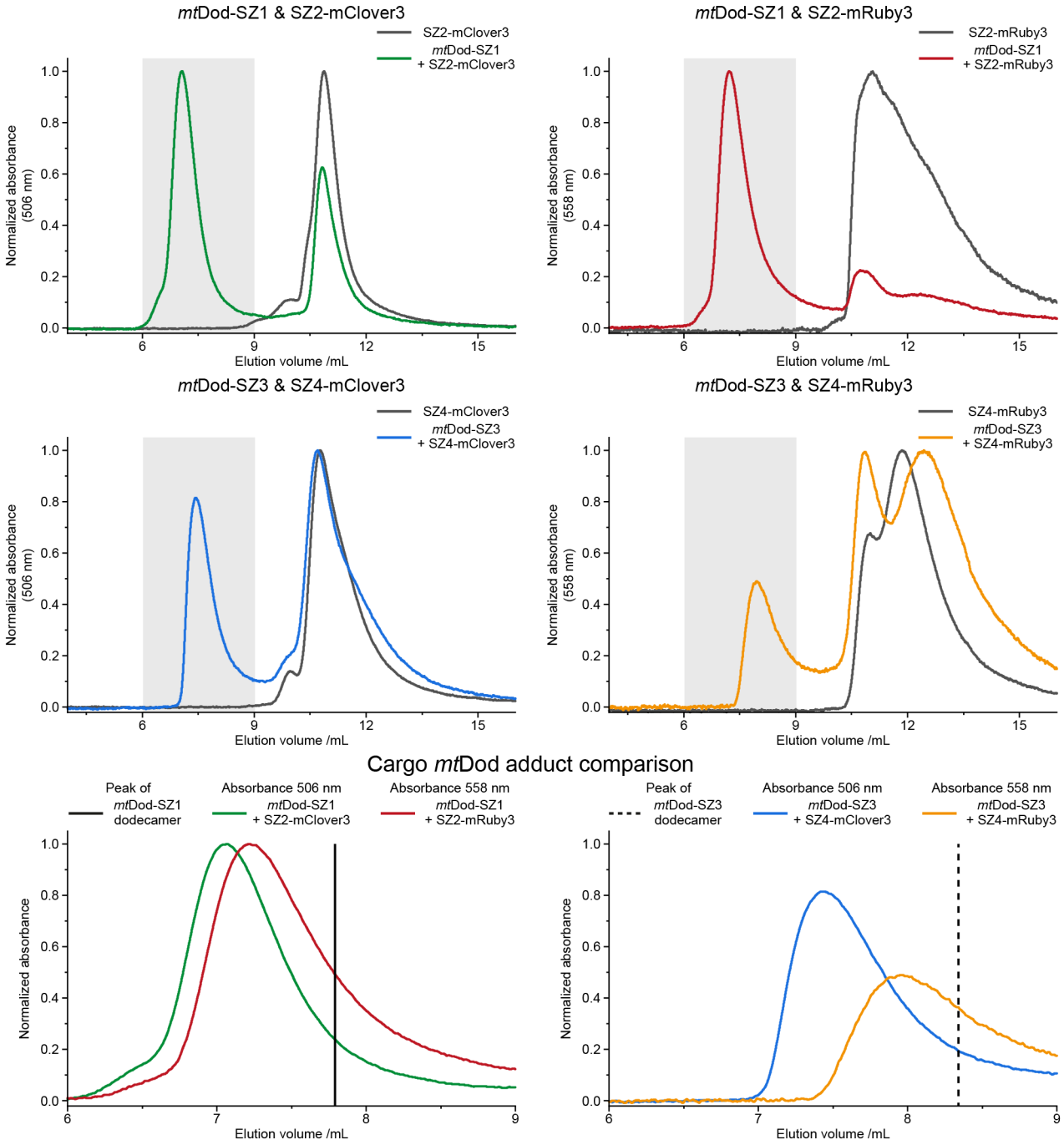

Fig. S8: HPLC-SEC chromatograms of *mt*Dod SYNZIP constructs and SYNZIP fluorescence protein constructs. Chromophore absorption of mRuby3 or mClover3 constructs was measured to observe the formation of high molecular weight species. Peaks of the formed adducts (grey highlighted areas) are overlaid in the bottom row. For comparison, elution volumes of the SYNZIP *mt*Dod constructs are shown as a straight (*mt*Dod-SZ1) or dashed (*mt*Dod-SZ3) line (based on absorbance at 280 nm). While for all combinations adduct species were observed, there is a clear difference in dodecamer to cargo composition. The SZ1-SZ2 pair overall performed better than the SZ3-SZ4 pair. For adduct formation, equimolar amounts of carrier and cargo (67 µM) were used and first incubated at 37 °C for 1 h and then on ice for 1 h. Single protein samples were treated the same way. As reaction buffer and running buffer, the standard dodecin buffer (300 mM NaCl, 5 mM $MgCl_2$ and 20 mM Tris-HCl (pH 7.4) was used. Samples were filtered (0.22 µm) and 8 µL were loaded. Runs were performed at 0.3 mL/min and 22 °C. Used column: bioZen 1.8 µm SEC-3 (300 × 4.6 mm, Phenomenex). Absorbance at 280 nm, 375 nm, 506 nm and 558 nm was measured.

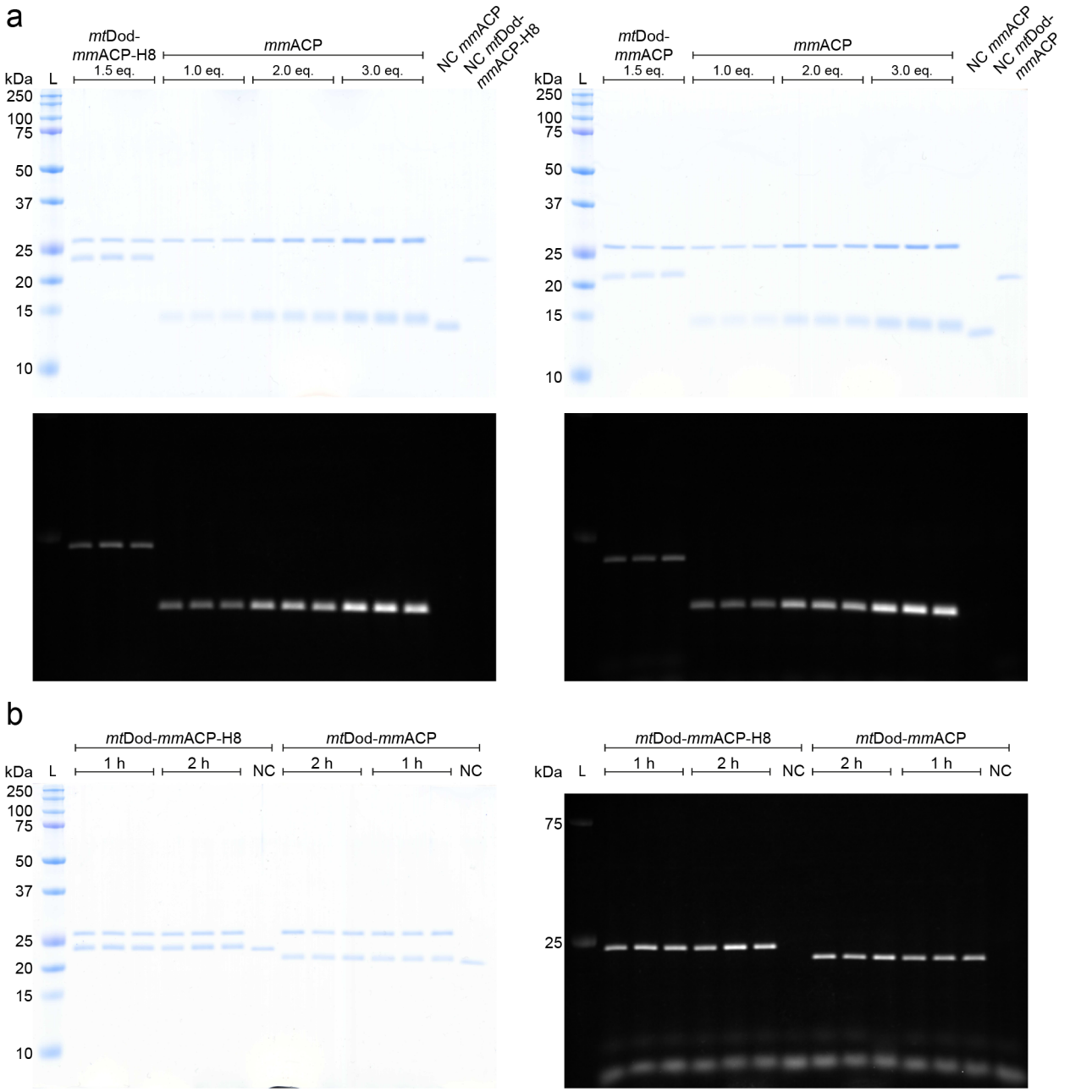

Fig. S9: Uncropped SDS-PAGE gels of the modification of *mt*Dod-*mm*ACP and *mt*Dod-*mm*ACP-H8 by Sfp. a) Coomassie stained gels at top, fluorescence images at the bottom. b) (left panel) Coomassie stained gels, (right) fluorescence images. At the bottom of the gel, free fluorophore is observable. In a) no free fluorophore is visible, because of the shorter exposure time used for the images

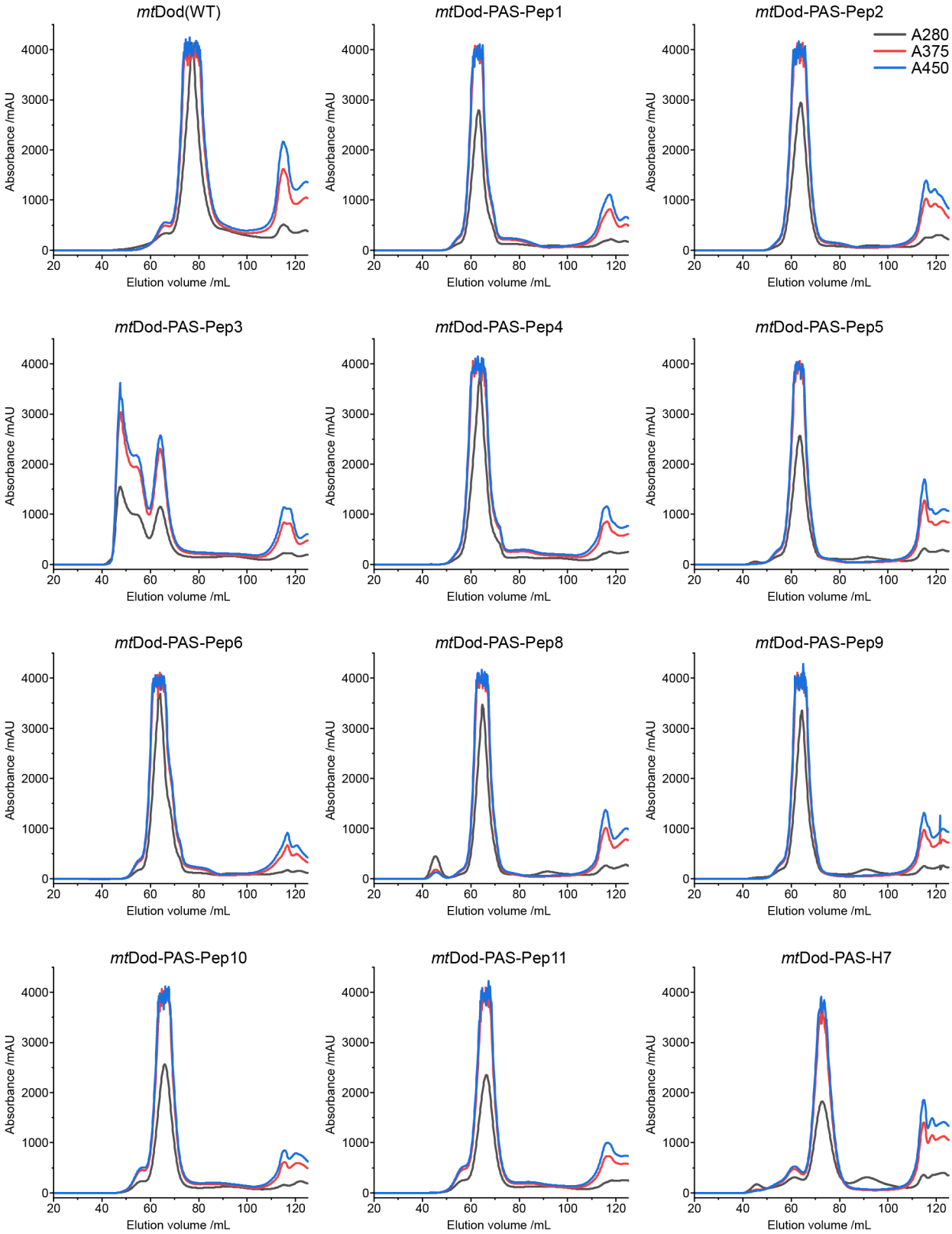

Fig. S10: SEC chromatograms of *mt*Dod-PAS-Pep constructs, *mt*Dod-PAS-H7 and *mt*Dod(WT). Used column: Superdex 200 16/60 pg column. Except for *mt*Dod-PAS-Pep3, only minor amounts of aggregates are visible. At about 117 mL, unbound FMN is eluting.

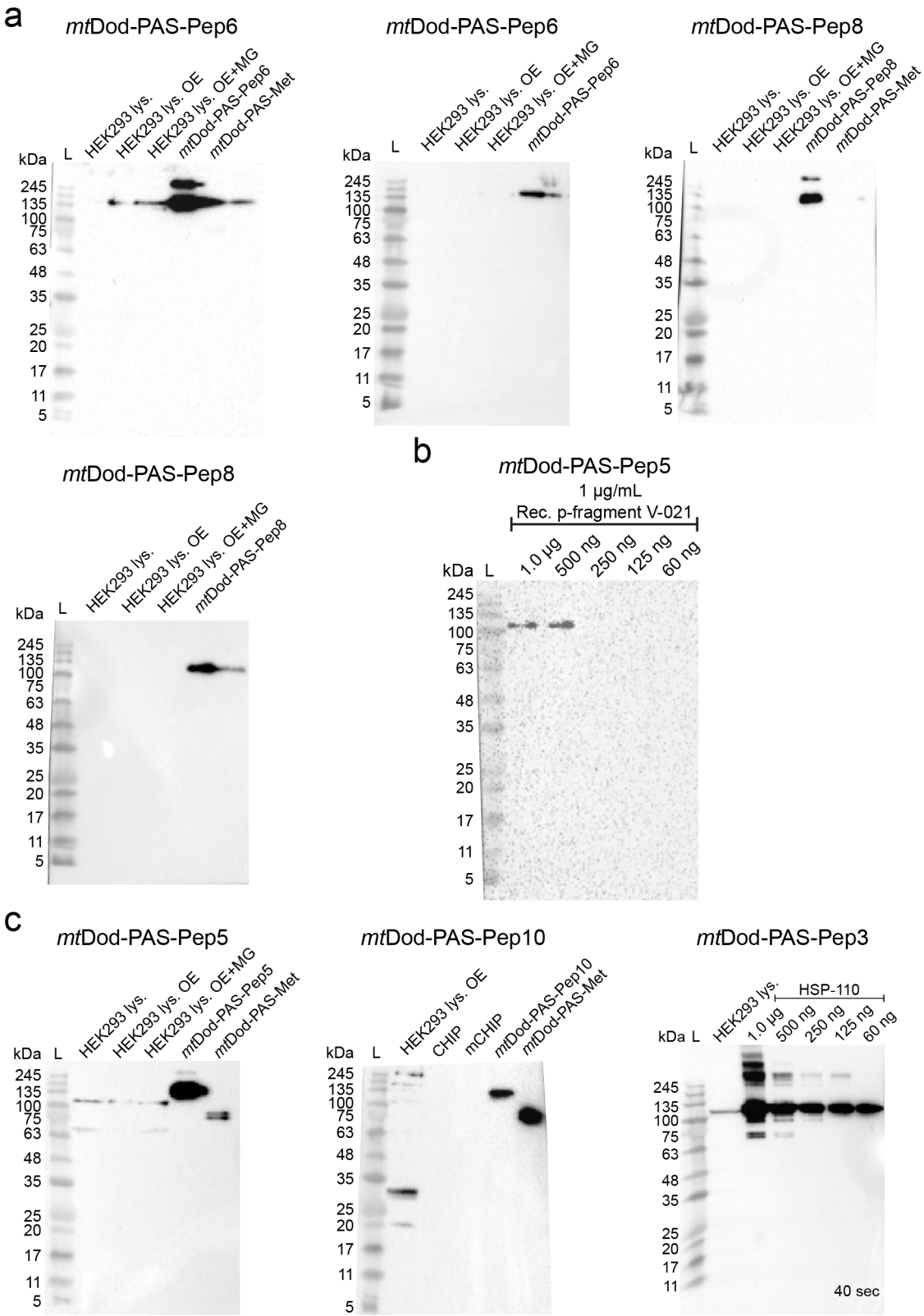

Fig. S11: Additional western blots for class assignment. L: Ladder. Lys.: Lysate. OE: protein overexpressing cells. MG: proteasome inhibitor MG-132 added. mCHIP: fragment of CHIP. a) Western blots of "class 3"ABs. Both ABs seem not to recognize *mt*Dod-PAS-Met (band expected at about 75 kDa) b) Western blot with ABs derived from *mt*Dod-PAS-Pep5. Bands were observed after an exposure time of about 300 sec. c) Uncropped western blots of Fig. 8 a.

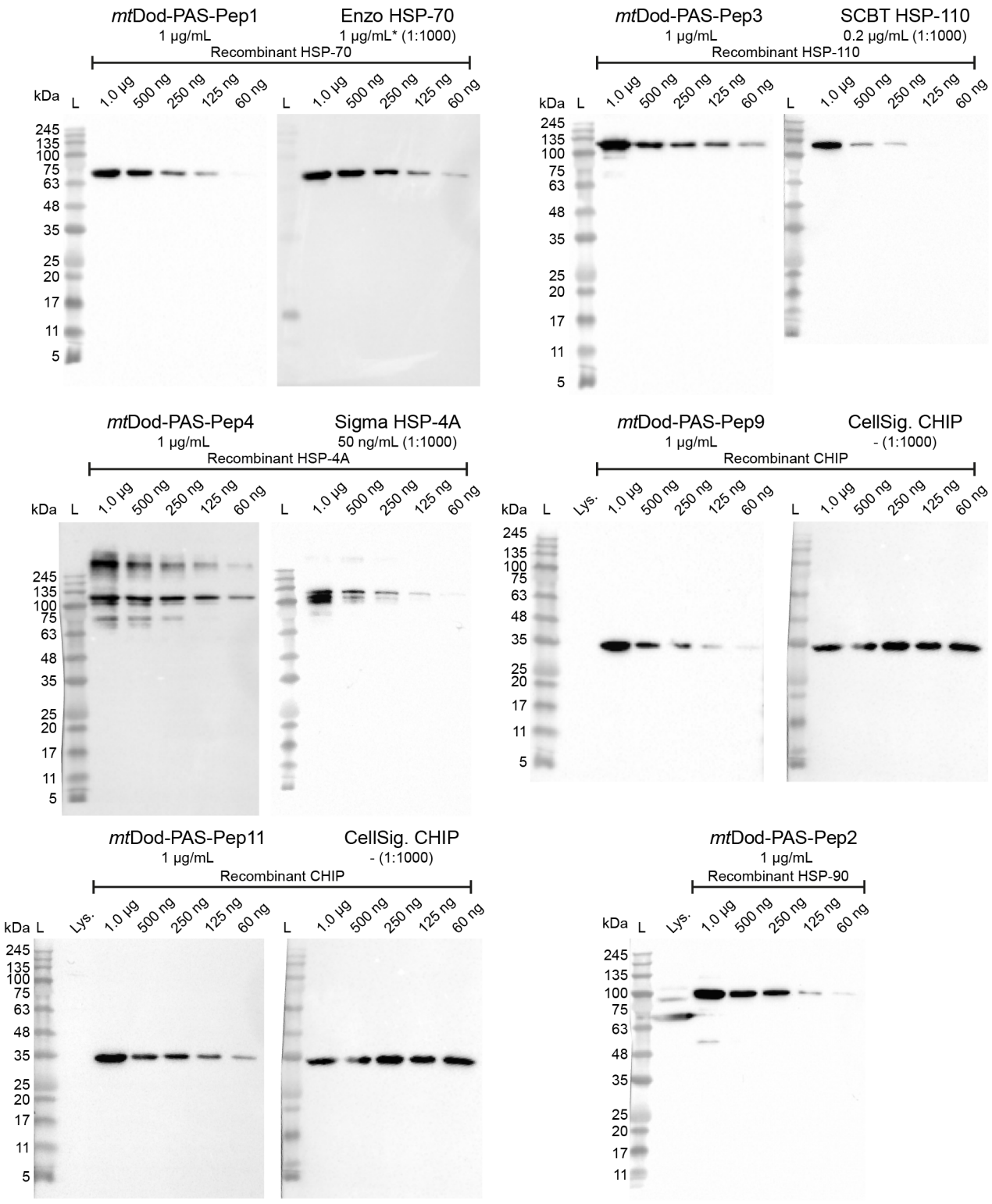

Fig. S12: Uncropped western blots of Fig 8 b. L: Ladder. Lys.: Lysate.

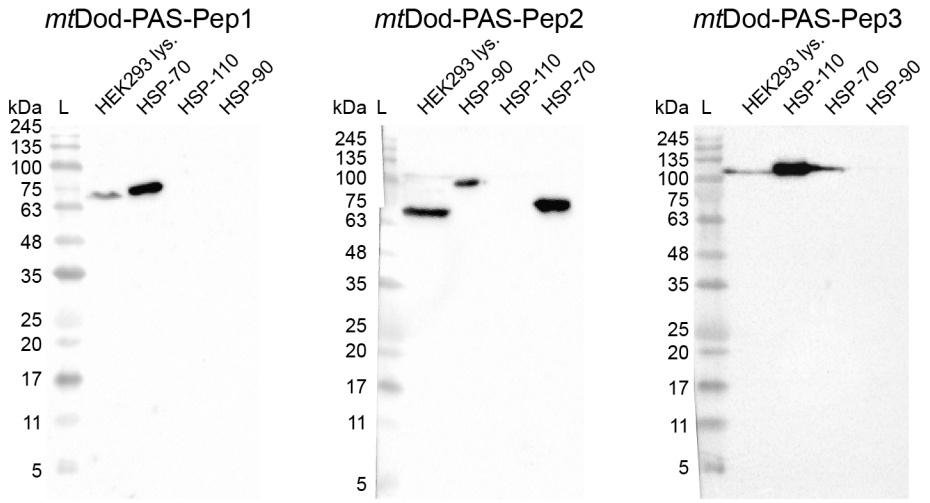

Fig. S13: Western blots of HSP recognizing ABs in comparison. L: Ladder. ABs derived from *mt*Dod-PAS-Pep2 (designed for HSP-90) recognizes also HSP-70. AB derived from *mt*Dod-PAS-Pep1 and *mt*Dod-PAS-Pep3 recognize only the protein of interest (HSP-90 and HSP-110, respectively).

Table S1: Table of encoding sequences for all constructs used in this study, except recombinant proteins used in western blotting. All plasmids used for expression were based on a pET22b vector backbone (*lacI* coding sequence, ampicillin resistance, pBR322 origin and f1 origin). Sequences encoding mClover3, mRuby3, SpyC and SnpC were cloned from vectors obtained from Addgene (Plasmid: #74252, pKanCMV-mClover3-mRuby3[2]; Plasmid: #72324, pET28a SpyCatcher-SnoopCatcher[3]). For the polycistronic constructs, spacer DNA sequences between stop codon of the previous gene and the +42 upstream bases of the next gene (based on the pET22b vector and an added restriction side) were designed with EGNAS (version 1158, to minimize secondary structures).[4] These spacer regions were used for cloning (annealing area for In-Fusion HD Cloning (TaKaRa Bio Europe)). Amino acid sequences of linkers and restriction sites are highlighted in yellow.

Construct ***mt*Dod-peptides**	DNA sequence T7 promotor to T7 terminator (CDS uppercase)	Amino acid sequence (linker)
*mt*Dod(WT)	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCTGActcgagcacca ccaccaccaccactgagatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataacta gcataacccctggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDS*
*mt*Dod-GSG-Lys	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGGGGG GTGGCGGCAGTGGTGGCGGCGGTAAATGAGGTGACTCTCTGTCTTGGCTGCTGCGTC TGCTGAACTgagatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagc ataacccctggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLEGGGGSGGGG K*
*mt*Dod-PAS-Met	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCATGTGAggatcccaccaccaccaccaccactgag atccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataacccctggggcc tctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SM*
*mt*Dod-SpyT	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCGGTGGCAGCGGTGCACATATCGTCAT GGTTGATGCGTACAAACCGACCAAATGAggatcccaccaccaccaccaccactgagatccggctgctaac aaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataacccctggggcctctaaacgggtctt gaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SGGSGAHIVMVDAYKPTK*
SpyT-*mt*Dod	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGGCACATATCGTCATGGTTGATGCGTACAAACCGACCAAAGGTGGCAGC GGTTCTCCAGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCAGCAATCACACCTACCGA GTGATCGAGATCGTCGGGACCTCGCCCGACGGCGTCGACGCGGCAATCCAGGGCGG TCTGGCCCGAGCTGCGCAGACCATGCGCGCGCTGGACTGGTTCGAAGTACAGTCAAT TCGAGGCCACCTGGTCGACGGAGCGGTCGCGCACTTCCAGGTGACTATGAAAGTCGG CTTCCGCCTGGAGGATTCCTGActcgagcaccaccaccaccaccactgagatccggctgctaacaaagcccg aaaggaagctgagttggctgctgccaccgctgagcaataactagcataacccctggggcctctaaacgggtcttgaggggttttt tg	MAHIVMVDAYKPTKGGSGSPAAPAPAS PASSNHTYRVIEIVGTSPDGVDAAIQGGL ARAAQTMRALDWFEVQSIRGHLVDGAV AHFQVTMKVGFRLEDS*
*mt*Dod-PAS2-SpyT	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGTCTCCGGCACCGTCTGCGCCAGCTGCATC TCCAGCAGCGGGTGGCAGCGGTGCACATATCGTCATGGTTGATGCGTACAAACCGAC CAAATGAggatcccaccaccaccaccaccactgagatccggctgctaacaaagcccgaaaggaagctgagttggctgct gccaccgctgagcaataactagcataacccctggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SPAPSAPAASPAAGGSGAHIVMVDAYKP TK*
SpyT-PAS2-*mt*Dod	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGGCACATATCGTCATGGTTGATGCGTACAAACCGACCAAAGGTGGCAGC GGTTCTCCAGCTGCGCCTGCTCCGGCAAGCCCTGCGTCTCCGGCACCGTCTGCGCCA GCTGCATCTCCAGCAGCGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCT CGCCCGACGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACC ATGCGCGCGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGA GCGGTCGCGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCTGAc tcgagcaccaccaccaccaccactgagatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctga gcaataactagcataacccctggggcctctaaacgggtcttgaggggtttttg	MAHIVMVDAYKPTKGGSGSPAAPAPAS PASPAPSAPAASPAASNHTYRVIEIVGTS PDGVDAAIQGGLARAAQTMRALDWFEV QSIRGHLVDGAVAHFQVTMKVGFRLED S*

SpyT-*mt*Dod-SnpT	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGGCACATATCGTCATGGTTGATGCGTACAAACCGACCAAAGGTGGCAGC GGTTCTCCAGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCAGCAATCACACCTACCGA GTGATCGAGATCGTCGGGACCTCGCCCGACGGCGTCGACGCGGCAATCCAGGGCGG TCTGGCCCGAGCTGCGCAGACCATGCGCGCGCTGGACTGGTTCGAAGTACAGTCAAT TCGAGGCCACCTGGTCGACGGAGCGGTCGCGCACTTCCAGGTGACTATGAAAGTCGG CTTCCGCCTGGAGGATTCCTCTCCAGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCGG TGGCAGCGGTGGCAAACTGGGCGATATTGAATTTATTAAAGTGAACAAAGGCTATTGAg gatcccaccaccaccaccaccactgagatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctga gcaataactagcataaccccttggggcctctaaacgggtcttgaggggtttttg	MAHIVMVDAYKPTKGGSGSPAAPAPAS PASSNHTYRVIEIVGTSPDGVDAAIQGGL ARAAQTMRALDWFEVQSIRGHLVDGAV AHFQVTMKVGFRLEDSSPAAPAPASPA SGGSGGKLGDIEFIKVNKGY*
SnpT-*mt*Dod-SpyT	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGGGCAAACTGGGCGATATTGAATTTATTAAAGTGAACAAAGGCTATGGT GGCAGCGGTTCTCCAGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCAGCAATCACACC TACCGAGTGATCGAGATCGTCGGGACCTCGCCCGACGGCGTCGACGCGGCAATCCAG GGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCGCGCTGGACTGGTTCGAAGTACAG TCAATTCGAGGCCACCTGGTCGACGGAGCGGTCGCGCACTTCCAGGTGACTATGAAA GTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCCAGCTGCGCCTGCTCCGGCAAGC CCTGCGAGCGGTGGCAGCGGTGCACATATCGTCATGGTTGATGCGTACAAACCGACC AAATGAggatcccaccaccaccaccaccactgagatccggctgctaacaaagcccgaaaggaagctgagttggctgctg ccaccgctgagcaataactagcataaccccttggggcctctaaacgggtcttgaggggtttttg	MGKLGDIEFIKVNKGYGGSGSPAAPAPA SPASSNHTYRVIEIVGTSPDGVDAAIQGG LARAAQTMRALDWFEVQSIRGHLVDGA VAHFQVTMKVGFRLEDSLESPAAPAPAS PASGGSGAHIVMVDAYKPTK*
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*mt*Dod-PAS-H7	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCCACCACCACCACCACCACCACTGAgat ccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataaccccttggggcctc taaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SHHHHHHH*
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*mt*Dod-PAS-Pep2	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCCCGCTGGAAGGCGATGACGATACCAG CCGCATGGAAGAAGTGGATTGAgatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccacc gctgagcaataactagcataaccccttggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SPLEGDDDTSRMEEVD*
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*mt*Dod-PAS-Pep4	cccgcgaaattaatacgactcactatagggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCGTGCCGAGCGACAGCGATAAGAAACT GCCGGAAATGGATATTGATTGAgatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccacc gctgagcaataactagcataaccccttggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SVPSDSDKKLPEMDID*
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*mt*Dod-PAS-Pep6	cccgcgaaattaatacgactcactatagggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCGAACAGAGCACCGGCCAGAAACGCC CGCTGAAGAACGATGAACTGTGAgatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccac cgctgagcaataactagcataaccccttggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SEQSTGQKRPLKNDEL*
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*mt*Dod-PAS-Pep8	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCCTGGTGACCGGCGAAAGCCTGGAACA GCTGCGCCGCGGCCTGGCGTGAgatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccac cgctgagcaataactagcataacccctttggggcctctaaacgggtcttgaggggttttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SLVTGESLEQLRRGLA*
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poly-cistronic constructs	DNA sequence T7 promotor to T7 terminator (CDS uppercase, spacer sequence)	Amino acid sequence (linker)
bici (*mt*Dod(WT); *mt*Dod-PAS-StrepII)	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCTGAcggtttgaaacc ttccgaggagaattcaataattttgtttaactttaagaaggagatatacatATGAGCAATCACACCTACCGAGTGA TCGAGATCGTCGGGACCTCGCCCGACGGCGTCGACGCGGCAATCCAGGGCGGTCTG GCCCGAGCTGCGCAGACCATGCGCGCGCTGGACTGGTTCGAAGTACAGTCAATTCGA GGCCACCTGGTCGACGGAGCGGTCGCGCACTTCCAGGTGACTATGAAAGTCGGCTTC CGCCTGGAGGATTCCCTCGAGTCTCCAGCTGCGCCTGCTCCGGCAAGCCCTGCGAGC TGGAGCCACCCGCAGTTCGAAAAATGAgaatcgcgattcaccatggtgggatccgatccggctgctaacaaa gcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataacccctttggggcctctaaacgggtcttgag gggttttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDS* & MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SWSHPQFEK*
bici (*mt*Dod-PAS-StrepII; *mt*Dod(WT))	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCTGGAGCCACCCGCAGTTCGAAAAATG AcggtttgaaaccttccgaggaagaattcaataattttgtttaactttaagaaggagatatacatATGAGCAATCACACCT ACCGAGTGATCGAGATCGTCGGGACCTCGCCCGACGGCGTCGACGCGGCAATCCAGG GCGGTCTGGCCCGAGCTGCGCAGACCATGCGCGCGCTGGACTGGTTCGAAGTACAGT CAATTCGAGGCCACCTGGTCGACGGAGCGGTCGCGCACTTCCAGGTGACTATGAAAG TCGGCTTCCGCCTGGAGGATTCCTGAgaatcgcgattcaccatggtgggatccgatccggctgctaacaaag cccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataacccctttggggcctctaaacgggtcttgagg ggttttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SWSHPQFEK* & MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDS*
tricis (*mt*Dod(WT); *mt*Dod(WT); *mt*Dod-PAS-StrepII)	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCTGAcggtttgaaacc ttccgaggagaattcaataattttgtttaactttaagaaggagatatacatATGAGCAATCACACCTACCGAGTGA TCGAGATCGTCGGGACCTCGCCCGACGGCGTCGACGCGGCAATCCAGGGCGGTCTG GCCCGAGCTGCGCAGACCATGCGCGCGCTGGACTGGTTCGAAGTACAGTCAATTCGA GGCCACCTGGTCGACGGAGCGGTCGCGCACTTCCAGGTGACTATGAAAGTCGGCTTC CGCCTGGAGGATTCCTGAacctgtatcgatgcagctaggaagcttaataattttgtttaacttaagaaggagatatac atATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGACGGCGT CGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCGCGCTGG ACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCGCGCACTT CCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCCAGCTGCG CCTGCTCCGGCAAGCCCTGCGAGCTGGAGCCACCCGCAGTTCGAAAAATGAgaatcgcga ttcaccatggtgggatccgatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataact agcataacccctttggggcctctaaacgggtcttgaggggttttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDS* & MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDS* & MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SWSHPQFEK
***mt*Dod-proteins**	DNA sequence T7 promotor to T7 terminator (CDS uppercase)	Amino acid sequence (linker)

*mt*Dod-*mm*ACP	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCGACGGGGACACCCAGAGGGATCTGG TGAAAGCTGTAGCACACATCCTAGGCATCCGAGACCTCGCAGGTATTAACCTGGACAG CACGCTGGCAGACCTCGGCCTGGACTCGCTCATGGGTGTGGAAGTTCGTCAGATCCT GGAACGAGAACACGATCTGGTGCTGCCCATGCGTGAGGTGCGGCAGCTCACGCTGCG GAAACTTCAGGAAATGTCCTCCAAGACTGACTCGGCTACTGACACGACAGCCCCCTGA gatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataacccctggggc ctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SDGDTQRDLVKAVAHILGIRDLAGINLDS TLADLGLDSLMGVEVRQILEREHDLVLP MREVRQLTLRKLQEMSSKTDSATDTTAP *
*mt*Dod-*mm*ACP-H8	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCGACGGGGACACCCAGAGGGATCTGG TGAAAGCTGTAGCACACATCCTAGGCATCCGAGACCTCGCAGGTATTAACCTGGACAG CACGCTGGCAGACCTCGGCCTGGACTCGCTCATGGGTGTGGAAGTTCGTCAGATCCT GGAACGAGAACACGATCTGGTGCTGCCCATGCGTGAGGTGCGGCAGCTCACGCTGCG GAAACTTCAGGAAATGTCCTCCAAGACTGACTCGGCTACTGACACGACAGCCCCCCTC GAGCATCATCACCACCACCACCACCACTGAgatccggctgctaacaaagcccgaaaggaagctgagttg gctgctgccaccgctgagcaataactagcataacccctggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SDGDTQRDLVKAVAHILGIRDLAGINLDS TLADLGLDSLMGVEVRQILEREHDLVLP MREVRQLTLRKLQEMSSKTDSATDTTAP LEHHHHHHHH*
*mt*Dod-msfGFP-H8	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCGTGAGCAAGGGCGAGGAGCTGTTCAC CGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAG CGTGCGCGGCGAGGGCGAGGGCGATGCCACCAACGGCAAGCTGACCCTGAAGTTCAT CTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTA CGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAG TCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTCCTTCAAGGACGACGGC ACCTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATC GAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAG TACAACTTCAACAGCCACAACGTCTATATCACGGCCGACAAGCAGAAGAACGGCATCA AGGCGAACTTCAAGATCCGCCACAACGTCGAGGACGGCAGCGTGCAGCTCGCCGACC ACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACT ACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGG TCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTCGAGC ATCATCACCACCACCACCACCACTGAtgagatccggctgctaacaaagcccgaaaggaagctgagttggctg ctgccaccgctgagcaataactagcataacccctggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SVSKGEELFTGVVPILVELDGDVNGHKF SVRGEGEGDATNGKLTLKFICTTGKLPV PWPTLVTTLTYGVQCFSRYPDHMKQHD FFKSAMPEGYVQERTISFKDDGTYKTRA EVKFEGDTLVNRIELKGIDFKEDGNILGH KLEYNFNSHNVYITADKQKNGIKANFKIR HNVEDGSVQLADHYQQNTPIGDGPVLL PDNHYLSTQSKLSKDPNEKRDHMVLLEF VTAAGITLGMDELEHHHHHHHH*
*mt*Dod-SpyC-H8*	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCGCTATGGTGGACACCCTGTCGGGCCT CTCTAGTGAACAGGGGCAAAGCGGCGATATGACTATCGAAGAAGATAGTGCTACCCAT ATTAAATTCTCAAAACGTGATGAGGACGGCAAAGAGTTAGCTGGTGCAACTATGGAGTT GCGTGATTCATCTGGTAAAACTATTAGTACATGGATTTCAGATGGACAAGTGAAAGATTT CTACCTGTATCCAGGAAAATATACATTTGTCGAAACCGCAGCACCAGACGGTTATGAGG TAGCAACTGCTATTACCTTTACAGTTAATGAGCAAGGTCAGGTTACTGTAAATGGCAAA GCAACTAAAGGTGACGCTCATATTCTCGAGCATCATCACCACCACCACCACCACTGAgat ccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataacccctggggcctc taaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SAMVDTLSGLSSEQGQSGDMTIEEDSA THIKFSKRDEDGKELAGATMELRDSSGK TISTWISDGQVKDFYLYPGKYTFVETAAP DGYEVATAITFTVNEQGQVTVNGKATKG DAHILEHHHHHHHH*
H8-SpyC-*mt*Dod	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGCATCATCACCACCACCACCATCACGGTTCTGCTATGGTGGACACCCTG TCGGGCCTCTCTAGTGAACAGGGGCAAAGCGGCGATATGACTATCGAAGAAGATAGTG CTACCCATATTAAATTCTCAAAACGTGATGAGGACGGCAAAGAGTTAGCTGGTGCAACT ATGGAGTTGCGTGATTCATCTGGTAAAACTATTAGTACATGGATTTCAGATGGACAAGT GAAAGATTTCTACCTGTATCCAGGAAAATATACATTTGTCGAAACCGCAGCACCAGACG GTTATGAGGTAGCAACTGCTATTACCTTTACAGTTAATGAGCAAGGTCAGGTTACTGTA AATGGCAAAGCAACTAAAGGTGACGCTCATATTTCTCCAGCTGCGCCTGCTCCGGCAA GCCCTGCGAGCAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCG ACGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGC GCGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTC GCGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCTGActcgagcacc accaccaccaccactgagatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataact agcataacccctggggcctctaaacgggtcttgaggggtttttg	MHHHHHHHHGSAMVDTLSGLSSEQGQ SGDMTIEEDSATHIKFSKRDEDGKELAG ATMELRDSSGKTISTWISDGQVKDFYLY PGKYTFVETAAPDGYEVATAITFTVNEQ GQVTVNGKATKGDAHISPAAPAPASPAS SNHTYRVIEIVGTSPDGVDAAIQGGLARA AQTMRALDWFEVQSIRGHLVDGAVAHF QVTMKVGFRLEDS*
*mt*Dod-SZ1	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCAATCTAGTCGCTCAGCTAGAGAACGA AGTAGCATCATTAGAGAATGAAAACGAAACCTTGAAAAAGAAGAATCTACACAAAAAGG ATCTTATAGCCTACCTAGAAAAGGAAATTGCTAACTTAAGGAAAAAGATTGAGGAATGAg gatcccaccaccaccaccaccactgagatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctga gcaataactagcataacccctggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SNLVAQLENEVASLENENETLKKKNLHK KDLIAYLEKEIANLRKKIEE*
*mt*Dod-SZ3	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTCGAGTCTCC AGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCAACGAAGTTACAACACTTGAGAATGAC GCTGCCTTTATCGAAAATGAAAATGCTTATCTAGAAAAAGAGATAGCACGTTTGAGAAA GGAGAAAGCAGCATTGAGAAATAGACTGGCACACAAAAAGTGAggatcccaccaccaccaccac cactgagatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataacccct tggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SNEVTTLENDAAFIENENAYLEKEIARLR KEKAALRNRLAHKK*

SZ1-*mt*Dod	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAATCTAGTCGCTCAGCTAGAGAACGAAGTAGCATCATTAGAGAATGAA AACGAAACCTTGAAAAAGAAGAATCTACACAAAAAGGATCTTATAGCCTACCTAGAAAA GGAAATTGCTAACTTAAGGAAAAAGATTGAGGAATCTCCAGCTGCGCCTGCTCCGGCA AGCCCTGCGAGCAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCC GACGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCG CGCGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCGCGCACTTCCAGGTG CGCGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCTGAggatccca ccaccaccaccaccactgagatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaata actagcataaccccttggggcctctaaacgggtcttgaggggtttttg	MNLVAQLENEVASLENENETLKKKNLHK KDLIAYLEKEIANLRKKIEESPAAPAPASP ASSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDS*
SZ3-*mt*Dod	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAACGAAGTTACAACACTTGAGAATGACGCTGCCTTTATCGAAAATGAAA ATGCTTATCTAGAAAAAGAGATAGCACGTTTGAGAAAGGAGAAAGCAGCATTGAGAAAT AGACTGGCACACAAAAAGTCTCCAGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCAGC AATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGACGGCGTCGACGCG GCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCGCGCTGGACTGGTTC GAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCGCGCACTTCCAGGTG ACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCTGAggatcccaccaccaccaccactgagatc cggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataaccccttggggcctct aaacgggtcttgaggggtttttg	MNEVTTLENDAAFIENENAYLEKEIARLR KEKAALRNRLAHKKSPAAPAPASPASSN HTYRVIEIVGTSPDGVDAAIQGGLARAAQ TMRALDWFEVQSIRGHLVDGAVAHFQV TMKVGFRLEDS*
*mt*Dod-*se*ACP**	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCAATCACACCTACCGAGTGATCGAGATCGTCGGGACCTCGCCCGA CGGCGTCGACGCGGCAATCCAGGGCGGTCTGGCCCGAGCTGCGCAGACCATGCGCG CGCTGGACTGGTTCGAAGTACAGTCAATTCGAGGCCACCTGGTCGACGGAGCGGTCG CGCACTTCCAGGTGACTATGAAAGTCGGCTTCCGCCTGGAGGATTCCCTcgagTCTCCA GCTGCGCCTGCTCCGGCAAGCCCTGCGAGCCGCGTAGACGAGATCGAGGACAAGTTG GGAAACTATATCCGCAGGCACCTGCTGACTGAGGACCCTCCAGAGGAATTCACTTACT CCACCGCCCTCTTCGGCGATGGGGTGCTGGATTCGCTCCGGCTGGCGATGCTGATCA ACTTCATCCGCAACGAGCTGGCCGTGGAGATCCCGTACGAGCACGTGAACCGGGACG ACTTCCACGATGTGCACACTATCGCCAAGATGGTGGTCGGCCTGTCGAGCGAAGCGAA ACTCGAGCATCATCACCACCACCACCACCACTGAgatccggctgctaacaaagcccgaaaggaagct gagttggctgctgccaccgctgagcaataactagcataaccccttggggcctctaaacgggtcttgaggggtttttg	MSNHTYRVIEIVGTSPDGVDAAIQGGLA RAAQTMRALDWFEVQSIRGHLVDGAVA HFQVTMKVGFRLEDSLESPAAPAPASPA SRVDEIEDKLGNYIRRHLLTEDPPEEFTY STALFGDGVLDSLRLAMLINFIRNELAVEI PYEHVNRDDFHDVHTIAKMVVGLSSEAK LEHHHHHHHH*
non-dodecin *constructs*	DNA sequence T7 promotor to T7 terminator (CDS uppercase)	Amino acid sequence (linker)
SpyT-*se*ACP	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGGCACATATCGTCATGGTTGATGCGTACAAACCGACCAAAGGTGGCAGC GGTTCTCCAGCTGCGCCTGCTCCGGCAAGCCCTGCGAGCCGCGTAGACGAGATCGAG GACAAGTTGGGAAACTATATCCGCAGGCACCTGCTGACTGAGGACCCTCCAGAGGAAT TCACTTACTCCACCGCCCTCTTCGGCGATGGGGTGCTGGATTCGCTCCGGCTGGCGAT GCTGATCAACTTCATCCGCAACGAGCTGGCCGTGGAGATCCCGTACGAGCACGTGAAC CGGGACGACTTCCACGATGTGCACACTATCGCCAAGATGGTGGTCGGCCTGTCGAGC GAAGCGAAACTCGAGCATCATCACCACCACCACCACCACTGAgatccggctgctaacaaagcccg aaaggaagctgagttggctgctgccaccgctgagcaataactagcataaccccttggggcctctaaacgggtcttgaggggttttt tg	MAHIVMVDAYKPTKGGSGSPAAPAPAS PASRVDEIEDKLGNYIRRHLLTEDPPEEF TYSTALFGDGVLDSLRLAMLINFIRNELA VEIPYEHVNRDDFHDVHTIAKMVVGLSS EAKLEHHHHHHHH*
*se*ACP-SpyC	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGCGCGTAGACGAGATCGAGGACAAGTTGGGAAACTATATCCGCAGGCA CCTGCTGACTGAGGACCCTCCAGAGGAATTCACTTACTCCACCGCCCTCTTCGGCGAT GGGGTGCTGGATTCGCTCCGGCTGGCGATGCTGATCAACTTCATCCGCAACGAGCTG GCCGTGGAGATCCCGTACGAGCACGTGAACCGGGACGACTTCCACGATGTGCACACT ATCGCCAAGATGGTGGTCGGCCTGTCGAGCGAAGCGAAAGGTGGCAGCGGTGCTATG GTGGACACCCTGTCGGGCCTCTCTAGTGAACAGGGGCAAAGCGGCGATATGACTATC GAAGAAGATAGTGCTACCCATATTAAATTCTCAAAACGTGATGAGGACGGCAAAGAGTT AGCTGGTGCAACTATGGAGTTGCGTGATTCATCTGGTAAAACTATTAGTACATGGATTT CAGATGGACAAGTGAAAGATTTCTACCTGTATCCAGGAAAATATACATTTGTCGAAACC GCAGCACCAGACGGTTATGAGGTAGCAACTGCTATTACCTTTACAGTTAATGAGCAAGG TCAGGTTACTGTAAATGGCAAAGCAACTAAAGGTGACGCTCATATTCTCGAGCATCATC ACCACCACCACCACCACTGAgatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgct gagcaataactagcataaccccttggggcctctaaacgggtcttgaggggtttttgctgaaag	MRVDEIEDKLGNYIRRHLLTEDPPEEFTY STALFGDGVLDSLRLAMLINFIRNELAVEI PYEHVNRDDFHDVHTIAKMVVGLSSEAK GGSGAMVDTLSGLSSEQGQSGDMTIEE DSATHIKFSKRDEDGKELAGATMELRDS SGKTISTWISDGQVKDFYLYPGKYTFVE TAAPDGYEVATAITFTVNEQGQVTVNGK ATKGDAHILEHHHHHHHH*
mClover3-SnpC	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGG TCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTCCGCGGCGAGGGCGAG GGCGATGCCACCAACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTG CCCGTGCCCTGGCCCACCCTCGTGACCACCTTCGGCTACGGCGTGGCCTGCTTCAGC CGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTCTTTCAAGGACGACGGTACCTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTTCAACAGCCACTA CGTCTATATCACGGCCGACAAGCAGAAGAACTGCATCAAGGCTAACTTCAAGATCCGC CACAACGTTGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCC ATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCCATCAGTCCAAG CTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACC GCCGCCGGCATTACCCATGGCATGGATGAACTGTATAAAGGTGGCAGCGGTAGCGGT AGCGGCAAGCCGCTGCGTGGTGCCGTGTTTAGCCTGCAGAAACAGCATCCCGACTAT CCCGATATCTATGGCGCGATTGATCAGAATGGGACCTATCAAAATGTGCGTACCGGCG AAGATGGTAAACTGACCTTTAAGAATCTGAGCGATGGCAAATATCGCCTGTTTGAAAAT AGCGAACCCGCTGGCTATAAACCGGTGCAGAATAAGCCGATTGTGGCGTTTCAGATTG TGAATGGCGAAGTGCGTGATGTGACCAGCATTGTGCCGCAGGATATTCCGGCTACATA TGAATTTACCAACGGTAAACATTATATCACCAATGAACCGATACCGCCGAAACTCGAGC ATCATCACCACCACCACCACCACTGAgatccggctgctaacaaagcccgaaaggaagctgagttggctgctg ccaccgctgagcaataactagcataaccccttggggcctctaaacgggtcttgaggggtttttgctgaaag	MVSKGEELFTGVVPILVELDGDVNGHKF SVRGEGEGDATNGKLTLKFICTTGKLPV PWPTLVTTFGYGVACFSRYPDHMKQHD FFKSAMPEGYVQERTISFKDDGTYKTRA EVKFEGDTLVNRIELKGIDFKEDGNILGH KLEYNFNSHYVYITADKQKNCIKANFKIR HNVEDGSVQLADHYQQNTPIGDGPVLL PDNHYLSHQSKLSKDPNEKRDHMVLLE FVTAAGITHGMDELYKGGSGSGSGKPL RGAVFSLQKQHPDYPDIYGAIDQNGTYQ NVRTGEDGKLTFKNLSDGKYRLFENSEP AGYKPVQNKPIVAFQIVNGEVRDVTSIVP QDIPATYEFTNGKHYITNEPIPPKLEHHH HHHHH*

SpyT-mClover3	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGGCACATATCGTCATGGTTGATGCGTACAAACCGACCAAAGGTGGCAGC GGTTCTGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAG CTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTCCGCGGCGAGGGCGAGGGCGA TGCCACCAACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGT GCCCTGGCCCACCCTCGTGACCACCTTCGGCTACGGCGTGGCCTGCTTCAGCCGCTA CCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTC CAGGAGCGCACCATCTCTTTCAAGGACGACGGTACCTACAAGACCCGCGCCGAGGTG AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAG GAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTTCAACAGCCACTACGTCT ATATCACGGCCGACAAGCAGAAGAACTGCATCAAGGCTAACTTCAAGATCCGCCACAA CGTTGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGG CGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCCATCAGTCCAAGCTGAG CAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGC CGGCATTACCCATGGCATGGATGAACTGTATAAAcTCGAGCATCATCACCACCACCACC ACCACTGAgatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcata acccctggggcctctaaacgggtcttgaggggttttttg	MAHIVMVDAYKPTKGGSGSVSKGEELFT GVVPILVELDGDVNGHKFSVRGEGEGD ATNGKLTLKFICTTGKLPVPWPTLVTTFG YGVACFSRYPDHMKQHDFFKSAMPEGY VQERTISFKDDGTYKTRAEVKFEGDTLV NRIELKGIDFKEDGNILGHKLEYNFNSHY VYITADKQKNCIKANFKIRHNVEDGSVQL ADHYQQNTPIGDGPVLLPDNHYLSHQSK LSKDPNEKRDHMVLLEFVTAAGITHGMD ELYKLEHHHHHHHH*
SZ2-mRuby3	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGGCCAGAAATGCATACTTAAGGAAAAAGATTGCTAGATTGAAAAAGGAC AACTTACAATTAGAAAAGAGATGAGCAAAATCTTGAAAAAGATCATTGCCAATTTGAGAGAT GAAATCGCCAGACTTGAAAATGAGGTGGCCTCTCATGAACAAGGTGGCAGCGGTGTGT CTAAGGGCGAAGAGCTGATCAAGGAAAATATGCGTATGAAGGTGGTCATGGAAGGTTC GGTCAACGGCCACCAATTCAAATGCACAGGTGAAGGAGAAGGCAGACCGTACGAGGG AGTGCAAACCATGAGGATCAAAGTCATCGAGGGAGGACCCCTGCCATTTGCCTTTGAC ATTCTTGCCACGTCGTTCATGTATGGCAGCCGTACCTTTATCAAGTACCCGGCCGACAT CCCTGATTTCTTTAAACAGTCCTTTCCTGAGGGTTTTACTTGGGAAAGAGTTACGAGATA CGAAGATGGTGGAGTCGTCACCGTCACGCAGGACACCAGCCTTGAGGATGGCGAGCT CGTCTACAACGTCAAGGTCAGAGGGGTAAACTTTCCCTCCAATGGTCCCGTGATGCAG AAGAAGACCAAGGGTTGGGAGCCTAATACAGAGATGATGTATCCAGCAGATGGTGGTC TGAGAGGATACACTGACATCGCACTGAAAGTTGATGGTGGTGGCCATCTGCACTGCAA CTTCGTGACAACTTACAGGTCAAAAAAGACCGTCGGGAACATCAAGATGCCCGGTGTC CATGCCGTTGATCACCGCCTGGAAAGGATCGAGGAGAGTGACAATGAAACCTACGTAG TGCAAAGAGAAGTGGCAGTTGCCAAATACAGCAACCTTGGTGGTGGCATGGACGAGCT GTACAAGCTCGAGCATCATCACCACCACCACCACCACTGAgatccggctgctaacaaagcccgaa aggaagctgagttggctgctgccaccgctgagcaataactagcataaccccttggggcctctaaacgggtcttgaggggttttttg	MARNAYLRKKIARLKKDNLQLERDEQNL EKIIANLRDEIARLENEVASHEQGGSGVS KGEELIKENMRMKVVMEGSVNGHQFKC TGEGEGRPYEGVQTMRIKVIEGGPLPFA FDILATSFMYGSRTFIKYPADIPDFFKQSF PEGFTWERVTRYEDGGVVTVTQDTSLE DGELVYNVKVRGVNFPSNGPVMQKKTK GWEPNTEMMYPADGGLRGYTDIALKVD GGGHLHCNFVTTYRSKKTVGNIKMPGV HAVDHRLERIEESDNETYVVQREVAVAK YSNLGGGMDELYKLEHHHHHHHH*
SZ2-mClover3	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGGCCAGAAATGCATACTTAAGGAAAAAGATTGCTAGATTGAAAAAGGAC AACTTACAATTAGAAAAGAGATGAGCAAAATCTTGAAAAAGATCATTGCCAATTTGAGAGAT GAAATCGCCAGACTTGAAAATGAGGTGGCCTCTCATGAACAAGGTGGCAGCGGTGTGA GCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGC GACGTAAACGGCCACAAGTTCAGCGTCCGCGGCGAGGGCGAGGGCGATGCCACCAA CGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCC CACCCTCGTGACCACCTTCGGCTACGGCGTGGCCTGCTTCAGCCGCTACCCCGACCA CATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCG CACCATCTCTTTCAAGGACGACGGTACCTACAAGACCCGCGCCGAGGTGAAGTTCGAG GGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGC AACATCCTGGGGCACAAGCTGGAGTACAACTTCAACAGCCACTACGTCTATATCACGG CCGACAAGCAGAAGAACTGCATCAAGGCTAACTTCAAGATCCGCCACAACGTTGAGGA CGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCC CGTGCTGCTGCCCGACAACCACTACCTGAGCCATCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGCATTACC CATGGCATGGATGAACTGTATAAACTCGAGCATCATCACCACCACCACCACCACTGAgat ccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataaccccttggggcctc taaacgggtcttgaggggttttttg	MARNAYLRKKIARLKKDNLQLERDEQNL EKIIANLRDEIARLENEVASHEQGGSGVS KGEELFTGVVPILVELDGDVNGHKFSVR GEGEGDATNGKLTLKFICTTGKLPVPWP TLVTTFGYGVACFSRYPDHMKQHDFFK SAMPEGYVQERTISFKDDGTYKTRAEVK FEGDTLVNRIELKGIDFKEDGNILGHKLE YNFNSHYVYITADKQKNCIKANFKIRHNV EDGSVQLADHYQQNTPIGDGPVLLPDN HYLSHQSKLSKDPNEKRDHMVLLEFVTA AGITHGMDELYKLEHHHHHHHH*
SZ4-mRuby3	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGCAGAAAGTGGCTGAATTGAAAAACAGAGTTGCTGTTAAACTTAACAGAA ATGAACAATTGAAAAACAAGGTAGAAGAGTTGAAAAACCGTAATGCTTACCTGAAAAAC GAACTGGCTACATTAGAAAATGAAGTCGCCAGATTGGAGAACGATGTTGCTGAAGGTG GCAGCGGTGTGTCTAAGGGCGAAGAGCTGATCAAGGAAAATATGCGTATGAAGGTGGT CATGGAAGGTTCGGTCAACGGCCACCAATTCAAATGCACAGGTGAAGGAGAAGGCAGA CCGTACGAGGGAGTGCAAACCATGAGGATCAAAGTCATCGAGGGAGGACCCCTGCCA TTTGCCTTTGACATTCTTGCCACGTCGTTCATGTATGGCAGCCGTACCTTTATCAAGTAC CCGGCCGACATCCCTGATTTCTTTAAACAGTCCTTTCCTGAGGGTTTTACTTGGGAAAG AGTTACGAGATACGAAGATGGTGGAGTCGTCACCGTCACGCAGGACACCAGCCTTGAG GATGGCGAGCTCGTCTACAACGTCAAGGTCAGAGGGGTAAACTTTCCCTCCAATGGTC CCGTGATGCAGAAGAAGACCAAGGGTTGGGAGCCTAATACAGAGATGATGTATCCAGC AGATGGTGGTCTGAGAGGATACACTGACATCGCACTGAAAGTTGATGGTGGTGGCCAT CTGCACTGCAACTTCGTGACAACTTACAGGTCAAAAAAGACCGTCGGGAACATCAAGAT GCCCGGTGTCCATGCCGTTGATCACCGCCTGGAAAGGATCGAGGAGAGTGACAATGA AACCTACGTAGTGCAAAGAGAAGTGGCAGTTGCCAAATACAGCAACCTTGGTGGTGGC ATGGACGAGCTGTACAAGCTCGAGCATCATCACCACCACCACCACCACTGAgatccggctg ctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataaccccttggggcctctaaacgg gtcttgaggggttttttg	MQKVAELKNRVAVKLNRNEQLKNKVEE LKNRNAYLKNELATLENEVARLENDVAE GGSGVSKGEELIKENMRMKVVMEGSVN GHQFKCTGEGEGRPYEGVQTMRIKVIE GGPLPFAFDILATSFMYGSRTFIKYPADI PDFFKQSFPEGFTWERVTRYEDGGVVT VTQDTSLEDGELVYNVKVRGVNFPSNG PVMQKKTKGWEPNTEMMYPADGGLRG YTDIALKVDGGGHLHCNFVTTYRSKKTV GNIKMPGVHAVDHRLERIEESDNETYVV QREVAVAKYSNLGGGMDELYKLEHHHH HHHH*
SZ4-mClover3	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGCAGAAAGTGGCTGAATTGAAAAACAGAGTTGCTGTTAAACTTAACAGAA ATGAACAATTGAAAAACAAGGTAGAAGAGTTGAAAAACCGTAATGCTTACCTGAAAAAC GAACTGGCTACATTAGAAAATGAAGTCGCCAGATTGGAGAACGATGTTGCTGAAGGTG GCAGCGGTGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTC GAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTCCGCGGCGAGGGCGAGGG CGATGCCACCAACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCC CGTGCCCTGGCCCACCCTCGTGACCACCTTCGGCTACGGCGTGGCCTGCTTCAGCCG CTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTAC GTCCAGGAGCGCACCATCTCTTTCAAGGACGACGGTACCTACAAGACCCGCGCCGAG GTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTC AAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTTCAACAGCCACTAC GTCTATATCACGGCCGACAAGCAGAAGAACTGCATCAAGGCTAACTTCAAGATCCGCC ACAACGTTGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCA TCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCCATCAGTCCAAGC TGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCG CCGCCGGCATTACCCATGGCATGGATGAACTGTATAAACTCGAGCATCATCACCACCA CCACCACCACTGAgatccggctgctaacaaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataac tagcataaccccttggggcctctaaacgggtcttgaggggttttttg	MQKVAELKNRVAVKLNRNEQLKNKVEE LKNRNAYLKNELATLENEVARLENDVAE GGSGVSKGEELFTGVVPILVELDGDVNG HKFSVRGEGEGDATNGKLTLKFICTTGK LPVPWPTLVTTFGYGVACFSRYPDHMK QHDFFKSAMPEGYVQERTISFKDDGTYK TRAEVKFEGDTLVNRIELKGIDFKEDGNI LGHKLEYNFNSHYVYITADKQKNCIKANF KIRHNVEDGSVQLADHYQQNTPIGDGPV LLPDNHYLSHQSKLSKDPNEKRDHMVLL EFVTAAGITHGMDELYKLEHHHHHHHH*

*mm*ACP	cccgcgaaattaatacgactcactataggggaattgtgagcggataacaattcccctctagaaataattttgtttaactttaagaag gagatatacatATGAGCGCTTGGAGCCACCCGCAGTTCGAAAAAGGCGCCGGGGACGGGG ACACCCAGAGGGATCTGGTGAAAGCTGTAGCACACATCCTAGGCATCCGAGACCTCGC AGGTATTAACCTGGACAGCACGCTGGCAGACCTCGGCCTGGACTCGCTCATGGGTGT GGAAGTTCGTCAGATCCTGGAACGAGAACACGATCTGGTGCTGCCCATGCGTGAGGT GCGGCAGCTCACGCTGCGGAAACTTCAGGAAATGTCCTCCAAGACTGACTCGGCTACT GACACGACAGCCCCCCTCGAGCATCATCACCACCACCACCACTGAgatccggctgctaa caaagcccgaaaggaagctgagttggctgctgccaccgctgagcaataactagcataaccccttggggcctctaaacgggtctt gaggggtttttg	MSAWSHPQFEKGAGDGDTQRDLVKAV AHILGIRDLAGINLDSTLADLGLDSLMGV EVRQILEREHDLVLPMREVRQLTLRKLQ EMSSKTDSATDTTAPLEHHHHHHHH*
Sfp	tcataaaaaatttatttgctttgtgagcggataacaattataatagattcaattgtgagcggataacaatttcacacagaattctgcag acggaggatctagaATGAAGATTTACGGAATTTATATGGACCGCCCGCTTTCACAGGAAGAAA ATGAACGGTTCATGACTTTCATATCACCTGAAAAACGGGAGAAATGCCGGAGATTTTAT CATAAAGAAGATGCTCACCGCACCCTGCTGGGAGATGTGCTCGTTCGCTCAGTCATAA GCAGGCAGTATCAGTTGGACAAATCCGATATCCGCTTTAGCACGCAGGAATACGGGAA GCCGTGCATCCCTGATCTTCCCGACGCTCATTTCAACATTTCTCACTCCGGCCGCTGG GTCATTGGTGCGTTTGATTCACAGCCGATCGGCATAGATATCGAAAAAACGAAACCGAT CAGCCTTGAGATCGCCAAGCGCTTCTTTTCAAAAACAGAGTACAGCGACCTTTTAGCAA AAGACAAGGACGAGCAGACAGACTATTTTTATCATCTATGGTCAATGAAAGAAAGCTTT ATCAAACAGGAAGGCAAAGGCTTATCGCTCCCGCTTGATTCCTTTTCAGTGCGCCTGCA TCAGGACGGACAAGTATCCATTGAGCTTCCGGACAGCCATTCCCCATGCTATATCAAAA CGTATGAGGTCGATCCCGGCTACAAAATGGCTGTATGCGCCGCACACCCTGATTTCCC CGAGGATATCACAATGGTCTCGTACGAAGAGCTTTTAAGATCTCATCACCATCACCATC ACTAAgcttaattagctgagcttggactcctgttgatagatccagtaatgacctcagaactccatctggatttgttcagaacgctc	MKIYGIYMDRPLSQEENERFMTFISPEKR EKCRRFYHKEDAHRTLLGDVLVRSVISR QYQLDKSDIRFSTQEYGKPCIPDLPDAH FNISHSGRWVIGAFDSQPIGIDIEKTKPIS LEIAKRFFSKTEYSDLLAKDKDEQTDYFY HLWSMKESFIKQEGKGLSLPLDSFSVRL HQDGQVSIELPDSHSPCYIKTYEVDPGY KMAVCAAHPDFPEDITMVSYEELLRSHH HHHH*

Table S2: Amino acid sequence of proteins from which the peptide sequences were selected for the *mt*Dod-PAS-Pep constructs. Selected peptide sequences highlighted in red.

Construct & peptide	Identifier & name	Amino acid sequence (peptide)
*mt*Dod-PAS-Pep1 PKGGSGSGPTIEEVD	AAD21816.1 HSP70-1 [Homo sapiens]	MAKAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTVFDAKRLIGRKF GDPVVQSDMKHWPFQVINDGDKPKVQVSYKGDTKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQ RQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRTGKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDF DNRLVNHFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEELCSDLFR STLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAILMGDKSENV QDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPP APRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVSAKNALES YAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELEQVCNPIISGLYQGAGGPGPG GFGAQGPKGGSGSGPTIEEVD
*mt*Dod-PAS-Pep2 PLEGDDDTSRMEEVD	NP_001017963.2 heat shock protein HSP90-alpha isoform 1 [Homo sapiens]	MPPCSGGDGSTPPGPSLRDRDCPAQSAEYPRDRLDPRPGSPSEASSPPFLRSRAPVNWYQEKAQVFLWHLMVS GSTTLLCLWKQPFHVSAFPVTASLAFRQSQGAGQHLYKDLQPFILLRLLMPEETQTQDQPMEEEEVETFAFQAEIA QLMSLIINTFYSNKEIFLRELISNSSDALDKIRYESLTDPSKLDSGKELHINLIPNKQDRTLTIVDTGIGMTKADLINNLGT IAKSGTKAFMEALQAGADISMIGQFGVGFYSAYLVAEKVTVITKHNDDEQYAWESSAGGSFTVRTDTGEPMGRGTK VILHLKEDQTEYLEERRIKEIVKKHSQFIGYPITLFVEKERDKEVSDDEAEEKEDKEEEKEKEEKESEDKPEIEDVGSD EEEEKKDGDKKKKKKKIKEKYIDQEELNKTKPIWTRNPDDITNEEYGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALL FVPRRAPFDLFENRKKKNNIKLYVRRVFIMDNCEELIPEYLNFIRGVVDSEDLPLNISREMLQQSKILKVIRKNLVKKC LELFTELAEDKENYKKFYEQFSKNIKLGIHEDSQNRKKLSELLRYYTSASGDEMVSLKDYCTRMKENQKHIYYITGET KDQVANSAFVERLRKHGLEVIYMIEPIDEYCVQQLKEFEGKTLVSVTKEGLELPEDEEEKKKQEEKKTKFENLCKIMK DILEKKVEKVVVSNRLVTSPCCIVTSTYGWTANMERIMKAQALRDNSTMGYMAAKKHLEINPDHSIIETLRQKAEAD KNDKSVKDLVILLYETALLSSGFSLEDPQTHANRIYRMIKLGLGIDEDDPTADDTSAAVTEEMPPLEGDDDTSRMEE VD
*mt*Dod-PAS-Pep3 ECYPNEKNSVNMDLD	NP_006635.2 heat shock protein 105 kDa isoform 1 [Homo sapiens]	MSVVGLDVGSQSCYIAVARAGGIETIANEFSDRCTPSVISFGSKNRTIGVAAKNQQITHANNTVSNFKRFHGRAFND PFIQKEKENLSYDLVPLKNGGVGIKVMYMGEEHLFSVEQITAMLLTKLKETAENSLKKPVTDCVISVPSFFTDAERRS VLDAAQIVGLNCLRLMNDMTAVALNYGIYKQDLPSLDEKPRIVVFVDMGHSAFQVSACAFNKGKLKVLGTAFDPFLG GKNFDEKLVEHFCAEFKTKYKLDAKSKIRALLRLYQECEKLKKLMSSNSTDLPLNIECFMNDKDVSGKMNRSQFEEL CAELLQKIEVPLYSLLEQTHLKVEDVSAVEIVGGATRIPAVKERIAKFFGKDISTTLNADEAVARGCALQCAILSPAFKV REFSVTDAVPFPISLIWNHDSEDTEGVHEVFSRNHAAPFSKVLTFLRRGPFELEAFYSDPQGVPYPEAKIGRFVVQN VSAQKDGEKSRVKVKVRVNTHGIFTISTASMVEKVPTEENEMSSEADMECLNQRPPENPDTDKNVQQDNSEAGTQ PQVQTDAQQTSQSPPSPELTSEENKIPDADKANEKKVDQPPEAKKPKIKVVNVELPIEANLVWQLGKDLLNMYIETE GKMIMQDKLEKERNDAKNAVEEYVYEFRDKLCGPYEKFICEQDHQNFLRLLTETEDWLYEEGEDQAKQAYVDKLE ELMKIGTPVKVRFQEAEERPKMFEELGQRLQHYAKIAADFRNKDEKYNHIDESEMKKVEKSVNEVMEWMNNVMNA QAKKSLDQDPVVRAQEIKTKIKELNNTCEPVVTQPKPKIESPKLERTPNGPNIDKKEEDLEDKNNFGAEPPHQNGEC YPNEKNSVNMDLD
*mt*Dod-PAS-Pep4 VPSDSDKKLPEMDID	EAW62295.1 heat shock 70kDa protein 4, isoform CRA_b [Homo sapiens]	MSVVGIDLGFQSCYVAVARAGGIETIANEYSDRCTPACISFGPKNRSIGAAAKSQVISNAKNTVQGFKRFHGRAFSD PFVEAEKSNLAYDIVQLPTGLTGIKVTYMEEERNFTTEQVTAMLLSKLKETAESVLKKPVVDCVVSVPCFYTDAERR SVMDATQIAGLNCLRLMNETTAVALAYGIYKQDLPALEEKPRNVVFVDMGHSAYQVSVCAFNRGKLKVLATAFDTT LGGRKFDEVLVNHFCEEFGKKYKLDIKSKIRALLRLSQECEKLKKLMSANASDLPLSIECFMNDVDVSGTMNRGKFL EMCNDLLARVEPPLRSVLEQTKLKKEDIYAVEIVGGATRIPAVKEKISKFFGKELSTTLNADEAVTRGCALQCAILSPA FKVREFSITDVVPYPISLRWNSPAEEGSSDCEVFSKNHAAPFSKVLTFYRKEPFTLEAYYSSPQDLPYPDPAIEKMQ VDQEEPHVEEQQQQTPAENKAESEEMETSQAGSKDKKMDQPPQAKKAKVKTSTVDLPIENQLLWQIDREMLNLYI ENEGKMIMQDKLEKERNDAKNAVEEYVYEMRDKLSGEYEKFVSEDDRNSFTLKLEDTENWLYEDGEDQPKQVYV DKLAELKNLGQPIKIRFQESEERPKLFEELGKQIQQYMKIISSFKNKEDQYDHLDAADMTKVEKSTNEAMEWMNNKL NLQNKQSLTMDPVVKSKEIEAKIKELTSTCSPIISKPKPKVEPPKEEQKNAEQNGPVDGQGDNPGPQAAEQGTDTA VPSDSDKKLPEMDID
*mt*Dod-PAS-Pep5 DSSQHTKSSGEMEVD	NP_055093.2 heat shock 70 kDa protein 4L isoform 1 [Homo sapiens]	MSVVGIDLGFLNCYIAVARSGGIETIANEYSDRCTPACISLGSRTRAIGNAAKSQIVTNVRNTIHGFKKLHGRSFDDPI VQTERIRLPYELQKMPNGSAGVKVRYLEEERPFAIEQVTGMLLAKLKETSENALKKPVADCVISIPSFFTDAERRSV MAAAQVAGLNCLRLMNETTAVALAYGIYKQDLPPLDEKPRNVVFIDMGHSAYQVLVCAFNKGKLKVLATTFDPYLG GRNFDEALVDYFCDEFKTKYKINVKENSRALLRLYQECEKLKKLMSANASDLPLNIECFMNDLDVSSKMNRAQFEQ LCASLLARVEPPLKAVMEQANLQREDISSIEIVGGATRIPAVKEQITKFFLKDISTTLNADEAVARGCALQCAILSPAFK VREFSITDLVPYSITLRWKTSFEDGSGECEVFCKNHPAPFSKVITFHKKEPFELEAFYTNLHEVPYPDARIGSFTIQNV FPQSDGDSSKVKVKVRVNIHGIFSVASASVIEKQNLEGDHSDAPMETETSFKNENKDNMDKMQVDQEEGHQKCHA EHTPEEEIDHTGAKTKSAVSDKQDRLNQTLKKGKVKSIDLPIQSSLCRQLGQDLLNSYIENEGKMIMQDKLEKERND AKNAVEEYVYDFRDRLGTVYEKFITPEDLSKLSAVLEDTENWLYEDGEDQPKQVYVDKLQELKKYGQPIQMKYMEH EERPKALNDLGKKIQLVMKVIEAYRNKDERYDHLDPTEMEKVEKCISDAMSWLNSKMNAQNKLSLTQDPVVKVSEI VAKSKELDNFCNPIIYKPKPKAEVPEDKPKANSEHNGPMDGQSGTETKSDSTKDSSQHTKSSGEMEVD
*mt*Dod-PAS-Pep6 EQSTGQKRPLKNDEL	XP_005271449.1 hypoxia up-regulated protein 1 isoform X1 [Homo sapiens]	MADKVRRQRPRRRVCWALVAVLLADLLALSDTLAVMSVDLGSESMKVAIVKPGVPMEIVLNKESRRKTPVIVTLKE NERFFGDSAASMAIKNPKATLRYFQHLLGKQADNPHVALYQARFPEHELTFDPQRQTVHFQISSQLQFSPEEVLGM VLNYSRSLAEDFAEQPIKDAVITVPVFFNQAERRAVLQAARMAGLKVLQLINDNTATALSYGVFRRKDINTTAQNIMF YDMGSGSTVCTIVTYQMVKTKEAGMQPQLQIRGVGFDRTLGGLEMELRLRERLAGLFNEQRKGQRAKDVRENPR AMAKLLREANRLKTVLSANADHMAQIEGLMDDVDFKAKVTRVEFEELCADLFERVPGPVQQALQSAEMSLDEIEQV ILVGGATRVPRVQEVLLKAVGKEELGKNINADEAAAMGAVYQAAALSKAFKVKPFVVRDAVVYPILVEFTREVEEEP GIHSLKHNKRVLFSRMGPYPQRKVITFNRYSHDFNFHINYGDLGFLGPEDLRVFGSQNLTTVKLKGVGDSFKKYPD YESKGIKAHFNLDESGVLSLDRVESVFETLVEDSAEEESTLTKLGNTISSLFGGGTTPDAKENGTDTVQEEEESPAE GSKDEPGEQVELKEEAEAPVEDGSQPPPPEPKGDATPEGEKATEKENGDKSEAQKPSEKAEAGPEGVAPAPEGE KKQKPARKRRMVEEIGVELVVLDLPDLPEDKLAQSVQKLQDLTLRDLEKQERERKAANSLEAFIFETQDKLYQPEYQE VSTEEQREEISGKLSAASTWLEDEGVGATTVMLKEKLAELRKLCQGLFFRVEERKKWPERLSALDNLLNHSSMFLK GARLIPEMDQIFTEVEMTTLEKVINETWAWKNATLAEQAKLPATEKPVLLSKDIEAKMMALDREVQYLLNKAKFTKP RPRPKDKNGTRAEPPLNASASDQGEKVIPPAGQTEDAEPISEPEKVETAGSEPGDTEPLELGGPGAEPEQKEQST GQKRPLKNDEL
*mt*Dod-PAS-Pep8 LVTGESLEQLRRGLA	sp|Q09118.1|HBEGF_CHLAE	MKLLPSVVLKLLLAAVLSALVTGESLEQLRRGLAAGTSNPDPSTGSTDQLLRLGGGRDRKVRDLQEADLDLLRVTL SSKPQALATPSKEEHGKRKKKGKGLGKKRDPCLRKYKDFCIHGECKYVKELRAPSCICHPGYHGERCHGLSLPVE NRLYTYDHTTILAVVAVVLSSVCLLVIVGLLMFRYHRRGGYDVENEEKVKLGMTNSH
*mt*Dod-PAS-Pep9 MKGKEEKEGGARLGA	NP_005852.2 E3 ubiquitin-protein ligase CHIP isoform a [Homo sapiens]	MKGKEEKEGGARLGAGGGSPEKSPSAQELKEQGNRLFVGRKYPEAAACYGRAITRNPLVAVYYTNRALCYLKMQ QHEQALADCRRALELDGQSVKAHFFLGQCQLEMESYDEAIANLQRAYSLAKEQRLNFGDDIPSALRIAKKKRWNSI EERRIHQESELHSYLSRLIAAERERELEECQRNHEGDEDDSHVRAQQACIEAKHDKYMADMDELFSQVDEKRKKR DIPDYLCGKISFELMREPCITPSGITYDRKDIEEHLQRVGHFDPVTRSPLTQEQLIPNLAMKEVIDAFISENGWVEDY
*mt*Dod-PAS-Pep10 EERRIHQESE	NP_005852.2 E3 ubiquitin-protein ligase CHIP isoform a [Homo sapiens] Pos. 151-160	MKGKEEKEGGARLGAGGGSPEKSPSAQELKEQGNRLFVGRKYPEAAACYGRAITRNPLVAVYYTNRALCYLKMQ QHEQALADCRRALELDGQSVKAHFFLGQCQLEMESYDEAIANLQRAYSLAKEQRLNFGDDIPSALRIAKKKRWNSI EERRIHQESELHSYLSRLIAAERERELEECQRNHEGDEDDSHVRAQQACIEAKHDKYMADMDELFSQVDEKRKKR DIPDYLCGKISFELMREPCITPSGITYDRKDIEEHLQRVGHFDPVTRSPLTQEQLIPNLAMKEVIDAFISENGWVEDY
*mt*Dod-PAS-Pep11 NHEGDEDDSH	NP_005852.2 E3 ubiquitin-protein ligase CHIP isoform a [Homo sapiens] Pos. 183-192	MKGKEEKEGGARLGAGGGSPEKSPSAQELKEQGNRLFVGRKYPEAAACYGRAITRNPLVAVYYTNRALCYLKMQ QHEQALADCRRALELDGQSVKAHFFLGQCQLEMESYDEAIANLQRAYSLAKEQRLNFGDDIPSALRIAKKKRWNSI EERRIHQESELHSYLSRLIAAERERELEECQRNHEGDEDDSHVRAQQACIEAKHDKYMADMDELFSQVDEKRKKR DIPDYLCGKISFELMREPCITPSGITYDRKDIEEHLQRVGHFDPVTRSPLTQEQLIPNLAMKEVIDAFISENGWVEDY

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