Supplementary Information

Methods

General

All reagents were purchased from commercial sources and used as received. Solvents were procured from Sigma-Aldrich and used as received. Double-distilled water was obtained from a PURELAB Chorus system (ELGA Veolia). Oligonucleotides for molecular cloning were synthesized by Microsynth (Switzerland). Plasmids were purified with the NucleoSpin plasmid purification kit purchased from Macherey-Nagel (Germany), agarose gel purifications were carried out with the NucleoSpin Gel and PCR Clean-up kit (Macherey-Nagel, Germany). Q5® Site-Directed Mutagenesis kit, restriction enzymes, T4 DNA ligase and Q5 DNA polymerase were purchased from New England Biolabs (NEB, USA). Antibiotics (chloramphenicol, kanamycin, spectinomycin) were purchased from Applichem. GluC endoprotease was purchased from NEB (USA) and sequencing grade trypsin endoprotease was purchased from Promega. Bacteria lysis was done on a Qsonica Q700 sonicator equipped with either a 2 or 12 mm probe. Protino® agarose Ni-NTA resin was purchased from Macherey-Nagel (Germany). LC-MS experiments were performed on a Dionex Ultimate 3000 UHPLC equipped with columns from Phenomenex (USA) and coupled to a mass spectrometer. Mass spectra were acquired on an LTQ Orbitrap XL or Q Exactive (Thermo Fisher Scientific) spectrometer by using heated electrospray ionization

(HESI). LC/MS data was analyzed with the Thermo Xcalibur Qual browser 4.1 (Thermo Fisher Scientific). Data analysis and statistical analysis were done in Microsoft Excel (2016) and Prism 9 (GraphPad).

Bioinformatic analysis

Multiple sequence alignments of PcpY, PlpY, and spliceotide leader sequences were made using MUSCLE in Geneious 7.1.9. Sequences were selected from previously reported precursor predictions,[1] and leader sequences were selected by truncating the sequences at the first double glycine motif in the sequence. Sequences not containing a double glycine motif were excluded from the analysis.

Structure predictions

Protein and protein complex structure predictions were conducted with AlphaFold Version 2.2.0 by providing FASTA files containing the amino acid sequences of the respective proteins.[2,3] AlphaFold2 was accessed in the ETH Euler cluster through a bash script.

Plasmid construction

All plasmids used in this study are listed in Table S2. Protein production plasmids were constructed by Gibson Assembly® Cloning (for genes >100 base pairs) or Q5® site-directed mutagenesis (for genes <100 base pairs) protocol provided by New England Biolabs (USA). Genes encoding for His_6-SUMO-Rha_{core} truncation precursors were ordered from Twist Bioscience as gene fragments with flanking NcoI and BamHI restriction sites and subcloned into pACYCDuet vectors through restriction cloning (NEB). Gene assembly fragments were designed by NEBuilder tool online. Overlapping mutagenic primers were designed by NEBaseChanger tool online. A typical polymerase chain reaction (PCR) (50 µL) contained 20 ng template DNA, 1× Q5 reaction buffer, 200 µM dNTPs, 0.5 µM of each primer (Table S1), and 0.5 u Q5 High-Fidelity DNA Hot-Start Polymerase. The reaction was heated to 98 °C for 45 s followed by 35 cycles of 98 °C for 10 s, X °C for 20 s, and 72 °C for 20 s per kilobase DNA target sequence. The primer annealing temperature X was calculated with the NEB Tm calculator website or the NEBaseChanger (in case of the Q5 site-directed mutagenesis protocol). The resulting PCR amplicons were treated with kinase-ligase-DpnI mix (KLD mix, NEB). Gibson Assembly® was performed with Gibson Assembly Master Mix (New England BioLabs) according to the manufacturer's instructions. DNA was visualized by 1% (w/v) agarose gel electrophoresis supplemented with ethidium bromide and GeneRuler™ 1kb DNA ladder (Thermo Scientific) marker. Plasmids were transformed into chemically competent *E. coli* DH5α strain (Invitrogen) and grown on LB agar containing appropriate antibiotics, then inoculated in corresponding liquid LB media. Plasmids were isolated from fresh overnight cultures and the gene-of-interest was sequence-verified by Microsynth AG (Switzerland). Sequence-verified plasmids were transformed into chemically competent *E. coli* BL21(DE3). All plasmids are under isopropyl-β-D-1-thiogalactopyranoside (IPTG) regulation. pACYCDuet encodes chloramphenicol resistance, pRSFDuet kanamycin resistance, and pCDFDuet spectinomycin resistance.

Protein expression and purification of substrate proteins

A Falcon tube containing 5 mL of LB medium was inoculated with *E. coli* BL21(DE3) cells taken from previously prepared glycerol stocks or from colonies on agar plates and supplemented with the appropriate antibiotics. The culture was shaken at 180 rpm overnight at 37 °C.

On the next day, 100 mL TB medium containing the appropriate antibiotics were inoculated with 1% v/v of this overnight culture and shaken at 37 °C until an OD_{600} of 1.2 to 1.6 was reached, according to previously reported expressions in similar systems.[4] After cooling the cultures at 4 °C for at least 20 min, 1 mM of IPTG was added and the cultures were

incubated on a shaker at 180 rpm at 16 °C for approximately 16 to 20 h. Subsequently, 40 mL from the cultures were centrifuged at 6000 × g for 10 min at 4 °C. The supernatant was discarded, and the cell pellets resuspended in 1 mL NPI-10 buffer. All NPI buffers were supplemented with 10% Glycerol. NPI buffers contain 50 mM NaH_2PO_4, 300 mM NaCl, 5 - 250 mM imidazole (where NPI-X contains X mM imidazole) and are adjusted to pH 8.0.

Cells resuspended in NPI-10 buffer were sonicated for 12 times 10 s, with 10 s of pause in between, at an amplitude of 30% to 40%. A sonication tip with a diameter of 2 mm was used, the resulting suspensions were kept on ice and centrifuged at 21000 × g for 30 min at 4 °C.

The supernatant was transferred to a new tube and 125 µL of Protino® Ni-nitrilotriacetic acid (NTA) Agarose (Macherey-Nagel) was added. The samples were slowly shaken on a rotor at 10 rpm for at least 30 min. An appropriate polypropylene column was prewashed with NPI-10 buffer, the sample added, washed twice with NPI-10 (500 µL), twice with NPI-20 (500 µL), and the protein eluted with NPI-250 (550 µL) and collected. Elution fractions were digested with appropriate endoproteinases. Protein splicing was analyzed by high-resolution LC-MS-MS. Samples were stored at -20 °C for further use.

Protein substrates for *in vitro* reactions were buffer-exchanged with PD MidiTrap G-25 columns (Cytiva) to reaction buffer (50 mM HEPES, 150 mM KCl, 10 % glycerol, pH 8) according to the manufacturer's protocol, frozen with liquid nitrogen and transferred to an anaerobic workstation (UNIIab pro, MBRAUN) for further use.

Time course of modification of His_6-RhaA and His_6-SUMO-Rha_{core} by RhaX and $RhaXA_{leader}$

Protein expressions were set up as described above for His_6-RhaA and His_6-SUMO-Rhacore with either RhaX and $RhaXA_{leader}$ in duplicates. After 4.5 h, 24 h, and 48 h a 10 mL aliquot of the expression cultures was taken and stored at -20 °C until purified as usual. Proteins were digested by trypsin and analyzed by LC-MS to quantify relative conversion and signals of modified and unmodified peptide.

Protein purification and reconstitution of radical SAM enzymes

A Falcon tube containing 10 mL of LB medium was inoculated with *E. coli* BL21(DE3) cells taken from previously prepared glycerol stocks or from single colonies on agar plates and supplemented with the appropriate antibiotics. The culture was shaken at 180 rpm overnight at 37 °C.

On the next day, two Ultrayield® 2.5 L flasks (Thomson) filled with 1 L TB medium containing the appropriate antibiotics were inoculated with 1% v/v of the overnight culture, supplemented with 25 µM $FeCl_3$ and shaken at 37 °C until an OD_{600} of around 1.5 was reached, according to previously reported expressions in similar systems.[4] After cooling the cultures at 4 °C for at least 20 min, 1 mM of IPTG, 25 µM $FeCl_3$, and 300 µM L-Cys were added and the cultures were incubated on a shaker at 180 rpm at 16 °C for approximately 16 to 20 h. Subsequently, the cultures were centrifuged at 6000 × g for 10 min at 4 °C. The supernatant was discarded and the cell pellets resuspended in 4 mL NPI-5 buffer per gram cell pellet. Suspensions were supplemented with cOmplete Protease Inhibitor Cocktail (Roche), 2 mM DTT and 0.5 mg/mL lysozyme (Roth) and incubated at 4 °C for 1 h.

Cells resuspended in NPI-5 buffer were sonicated for 12 times 10 s, with 10 s of pause, at an amplitude of 50% to 70%. A sonication tip with a diameter of 12 mm was used. The resulting suspensions were kept on ice and centrifuged at 18000 × g for 45 min at 4 °C.

The supernatant was transferred to a new tube and 4 mL of cOmplete His-tag purification resin (Roche) was added. The samples were slowly shaken on a rotor at 10 rpm for at least 30 min. Samples were centrifuged at 800 × g for 1

min, the supernatant carefully removed, and the resin resuspended in the same volume of NPI-5. This wash was repeated twice. An appropriate polypropylene column was prewashed with NPI-5 buffer, the sample added, washed twice with NPI-5 (5 column volumes), twice with NPI-20 (1 column volume), and the protein eluted with NPI-250 (three times 1 column volume) and pooled. Elution fractions were concentrated using 30 kDa MWCO Amicon-ULTRA-15 centrifugal filters to a volume of 0.5–1 mL. Samples were supplemented with 5 mM DTT, frozen with liquid nitrogen, and transferred to an anaerobic workstation.

After at least 16 h in an anaerobic environment, samples were buffer-exchanged using PD-10 columns (Cytiva) to reaction buffer (50 mM HEPES, 150 mM KCl, 10 % glycerol, pH 8) following the manufacturer's instructions. Samples were concentrated/diluted to around 250 µM and added with 20 equivalents DTT, 13 equivalents $FeCl_2$, 12 equivalents L-Cys and 1 µM of ecIscS (*E. coli* cysteine desulfurase) and incubated overnight at 4 °C. Samples were then again buffer-exchanged to reaction buffer and concentrated to 250–1000 µM, frozen and stored for further use.

Analytical high-performance liquid chromatography-size exclusion chromatography

Reconstituted SUMO-tagged PcpX (57.7 kDa) or PcpXY (64.1 kDa) were incubated with PcpA (18.3 kDa) and transferred to air-tight vials prior to removal from the anaerobic chamber. Samples of individual components were similarly prepared for comparison, and all samples were separated by HPLC-SEC.

Anaerobic *in vitro* reactions

For anaerobic reactions, N-terminally His_6-tagged ecFldA and ecFpr from the ASKA collection[5] were expressed according to the general protein expression and purification protocol. Elution fractions were concentrated, frozen and transferred to an anaerobic workstation and buffer-exchanged to reaction buffer with PD MidiTrap G-25 (Cytiva) columns.

Anaerobic reactions were carried out as follows: 50 µM splicease (SUMO-PcpX, SUMO-PcpXY or SUMO-$PcpXY_{fusion}$), 0–500 µM SUMO-PcpY, 100 µM PcpA, 20 µM ecFldA, 5 µM ecFpr, 2 mM NADPH, 10 mM DTT and filled with reaction buffer to 50 µL.[6] Reactions were typically carried out at room temperature for 3 h, then removed from the glovebox and directly digested with appropriate proteases and analyzed by LC-MS-MS.

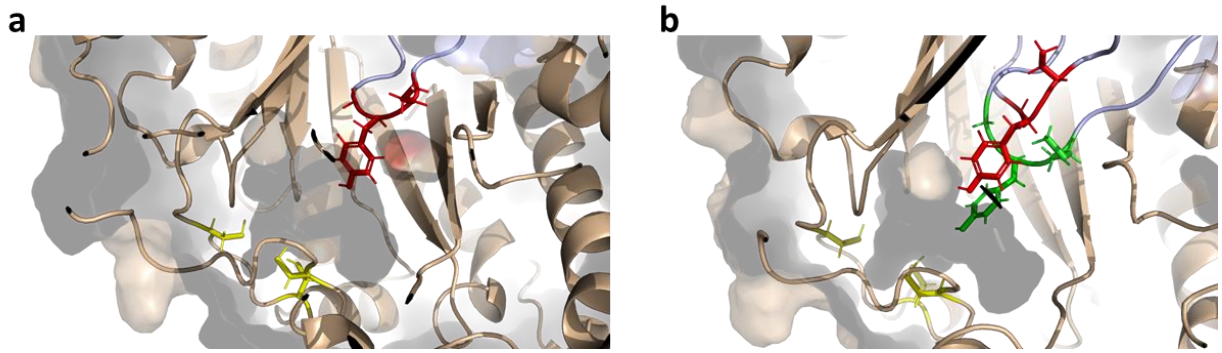
High-resolution mass spectrometry

Mass spectra were acquired on an LTQ Orbitrap XL, Q Exactive, or Ascend Tribrid (Thermo Fisher Scientific, USA) spectrometer by using heated electrospray ionization (HESI). The following method was used for analysis on LC-MS:

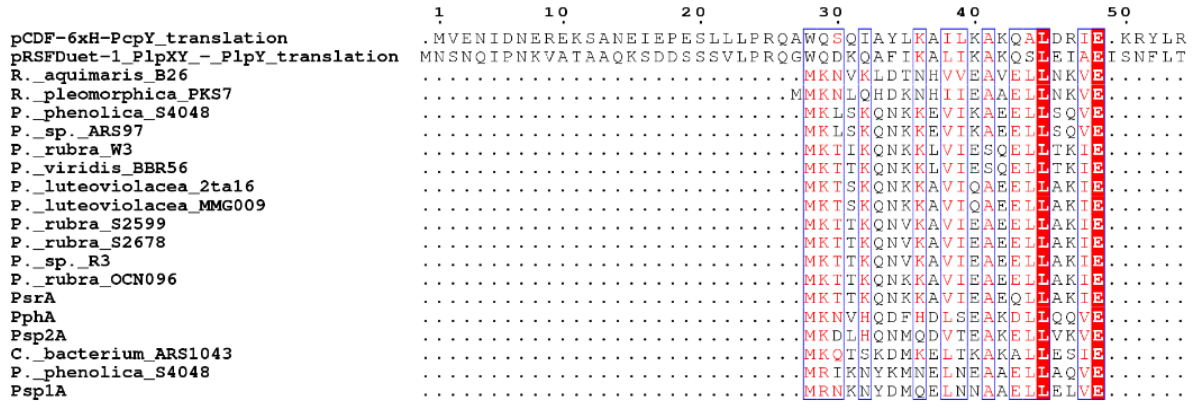
Solvent A: H_2O + 0.1% formic acid; solvent B: MeCN + 0.1% formic acid; column, Phenomenex Kinetex 2.6 µm C18-XB 100 Å (150 × 4.6 mm); flow rate, 0.7 mL/min; gradient: 95:5 A/B for 0.5 min ramped to 5:95 A/B over 20 min).

For MS-MS analysis, a normalized collision energy of 15 to 28 was used, depending on the observed fragmentation properties of peptide fragments. The MS instrument was operated in positive ionization mode at a scan range of 400–2000 *m/z* (or alternatively 700–1500 *m/z*), AGC target 2e5, maximum IT 100 ms and a resolution of 70000 at 400 *m/z*. The spray voltage was set to 5.0 kV, the probe heater temperature to 475 °C, and the capillary temperature to 270 °C. Columns were heated to 50 °C.

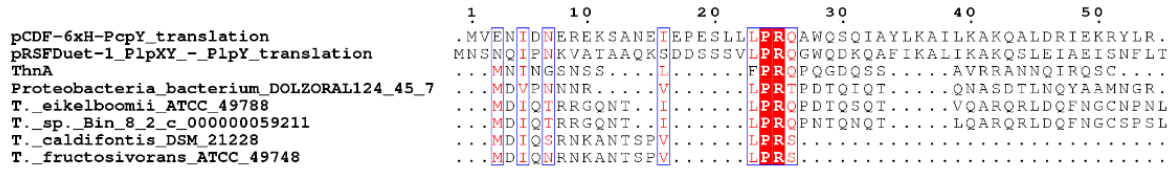
Supplementary Figures and Tables



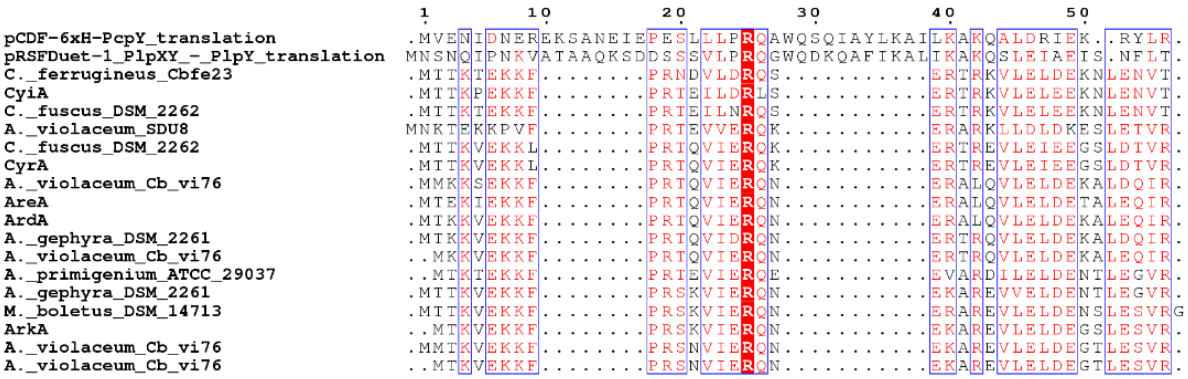
Supplementary Figure S1. a) AlphaFold model of PcpA and SUMO-PcpX with the N-terminal MYG site (red) placed in the putative active site near the putative iron-binding cysteines (yellow). **b**) Structural model of PcpA and SUMO-PcpX with the two MYG sites (red and green) placed in the putative active site near the putative iron-binding cysteines (yellow).



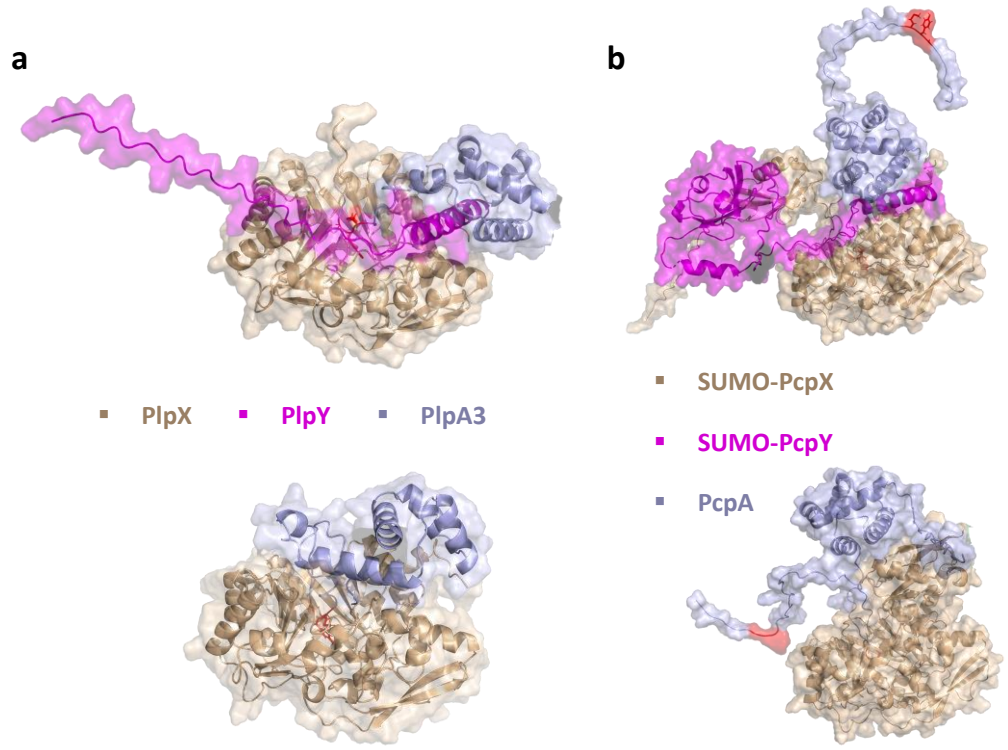
Supplementary Figure S2. Multiple sequence alignment of PcpY, PlpY, and leader sequences of type II spliceotides.[1] R._aquimaris_B26 is the RhaA leader peptide. Sequences were aligned with MUSCLE in Geneious 7.1.9 and the alignment image was generated using ESPript 3.0.[7]



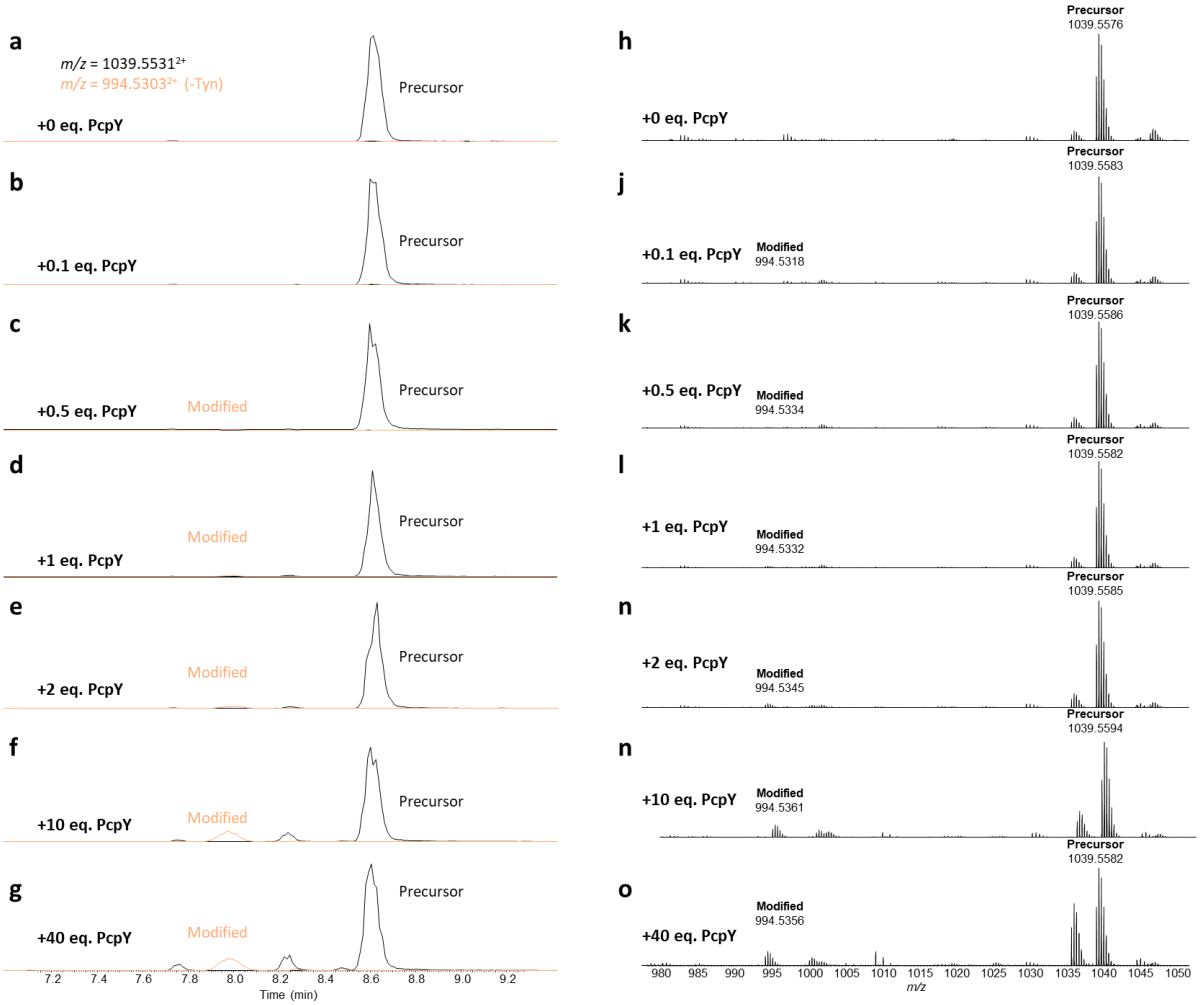
Supplementary Figure S3. Multiple sequence alignment of PcpY, PlpY, and leader sequences of type III spliceotides.[1] Sequences were aligned with MUSCLE in Geneious 7.1.9 and the alignment image was generated using ESPript 3.0.[7]



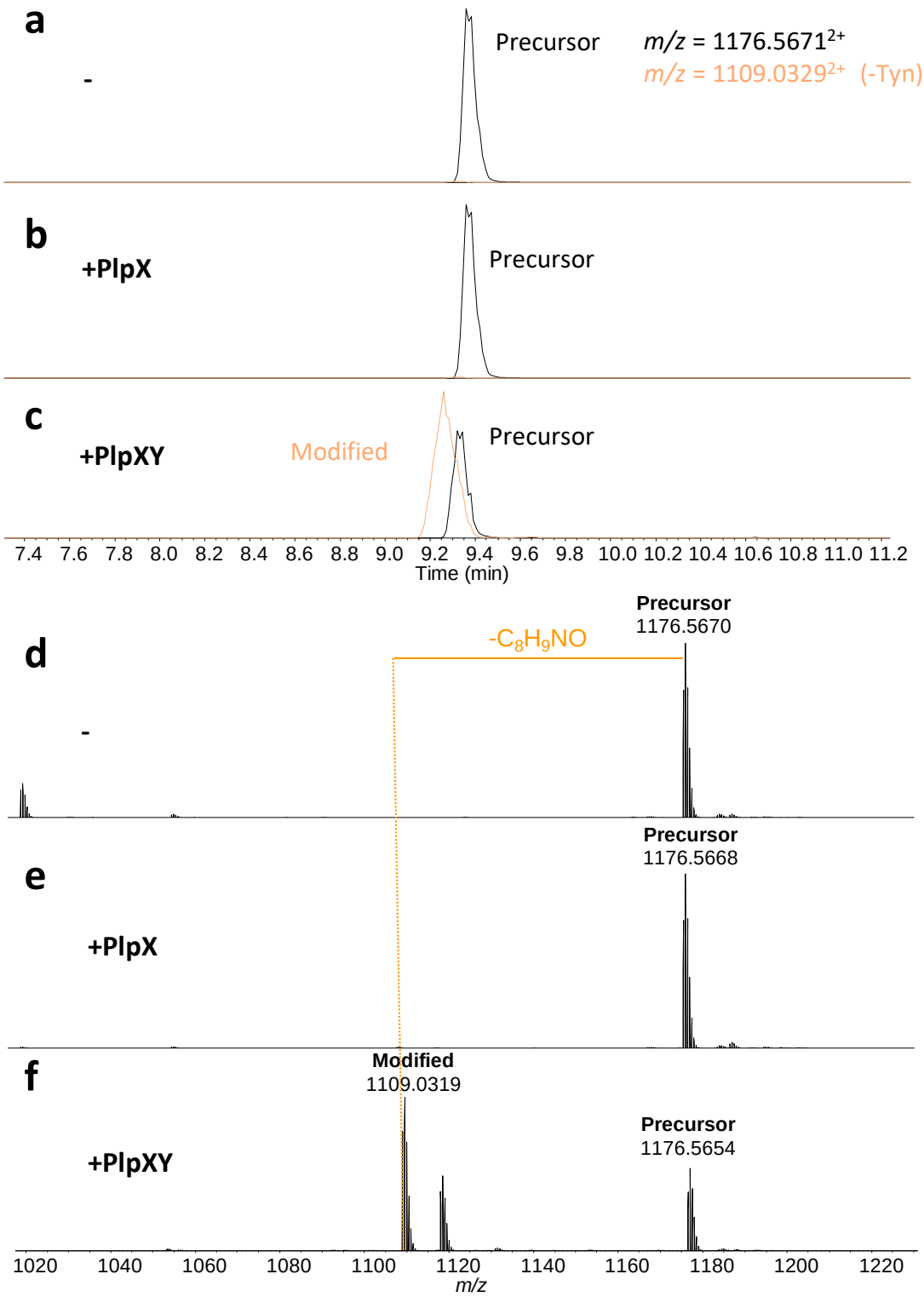
Supplementary Figure S4. Multiple alignment of PcpY, PlpY, and leader sequences of type V spliceotides.[1] Sequences were aligned with MUSCLE in Geneious 7.1.9 and the alignment image was generated using ESPript 3.0.[7]



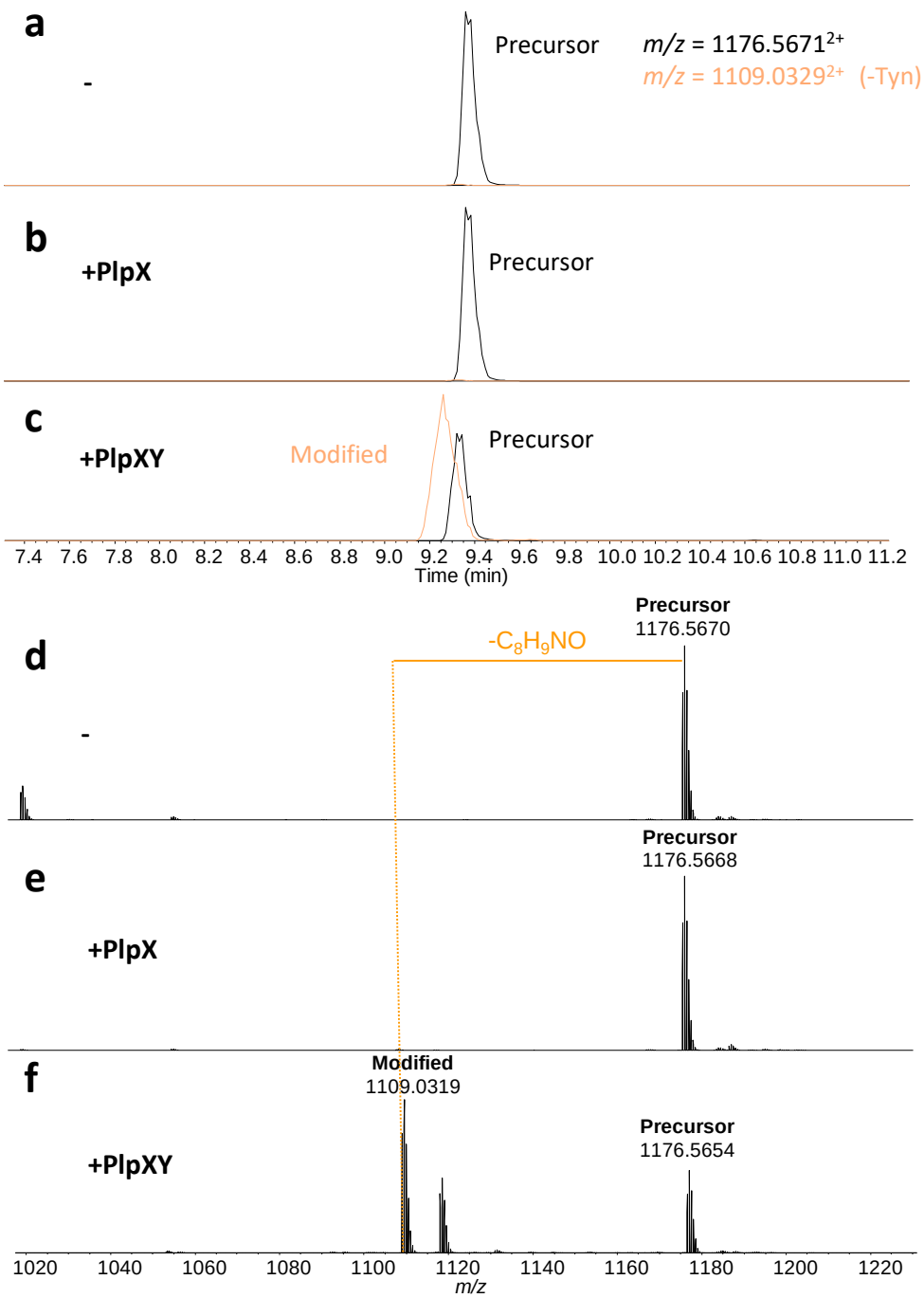
Supplementary Figure S5. a) AlphaFold model of PlpA3 and PlpX in the presence (top) and absence (bottom) of PlpY. Without PlpY, the binding helix is not replaced by PlpA3. **a**) AlphaFold model of PcpA and PcpX in the presence (top) and absence (bottom) of PcpY. Without PcpY, the binding helix is not replaced by PcpA.



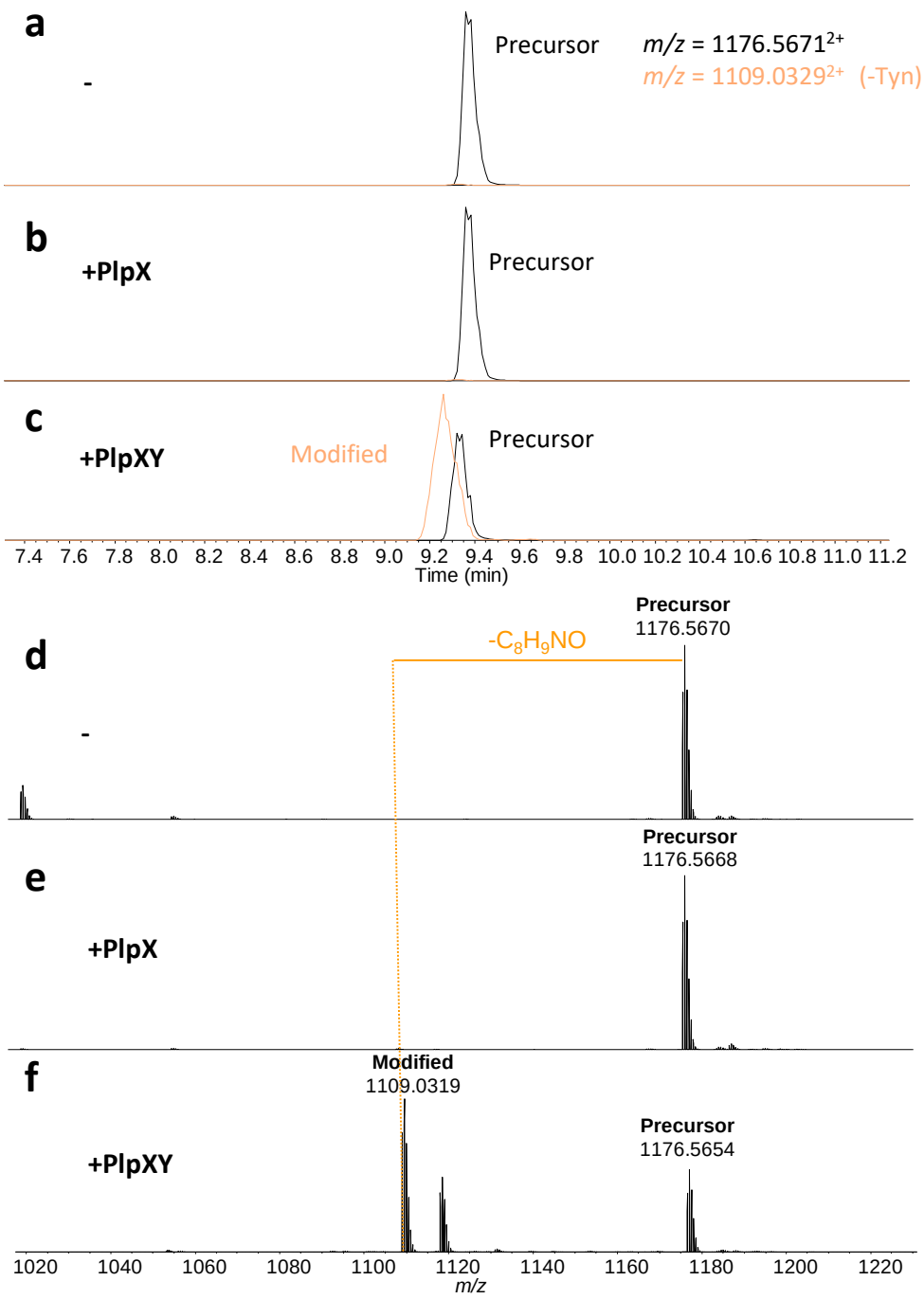
Supplementary Figure S6. LC-MS analysis for His_6-PcpA cleaved with trypsin and GluC to give the peptide fragment LVTAVGGVTGGSGIYGPIQAMYGAVVGDPKPGK. Extracted ion chromatograms for *m/z* 1039.5531 (precursor, $[M+3H]^{3+}$), *m/z* 994.5303 (modified, $[M+3H]^{3+}$) for *in vitro* enzymatic reactions of His_6-PcpA and SUMO-PcpX with 0 (**a**), 0.1 (**b**), 0.5 (**c**), 1 (**d**), 2 (**e**), 10 (**f**), or 40 (**g**) equivalents SUMO-PcpY. Extracted mass spectra for *in vitro* enzymatic reactions of His_6-PcpA and SUMO-PcpX with 0 (**h**), 0.1 (**j**), 0.5 (**k**), 1 (**l**), 2 (**m**), 10 (**n**), or 40 (**o**) equivalents SUMO-PcpY. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



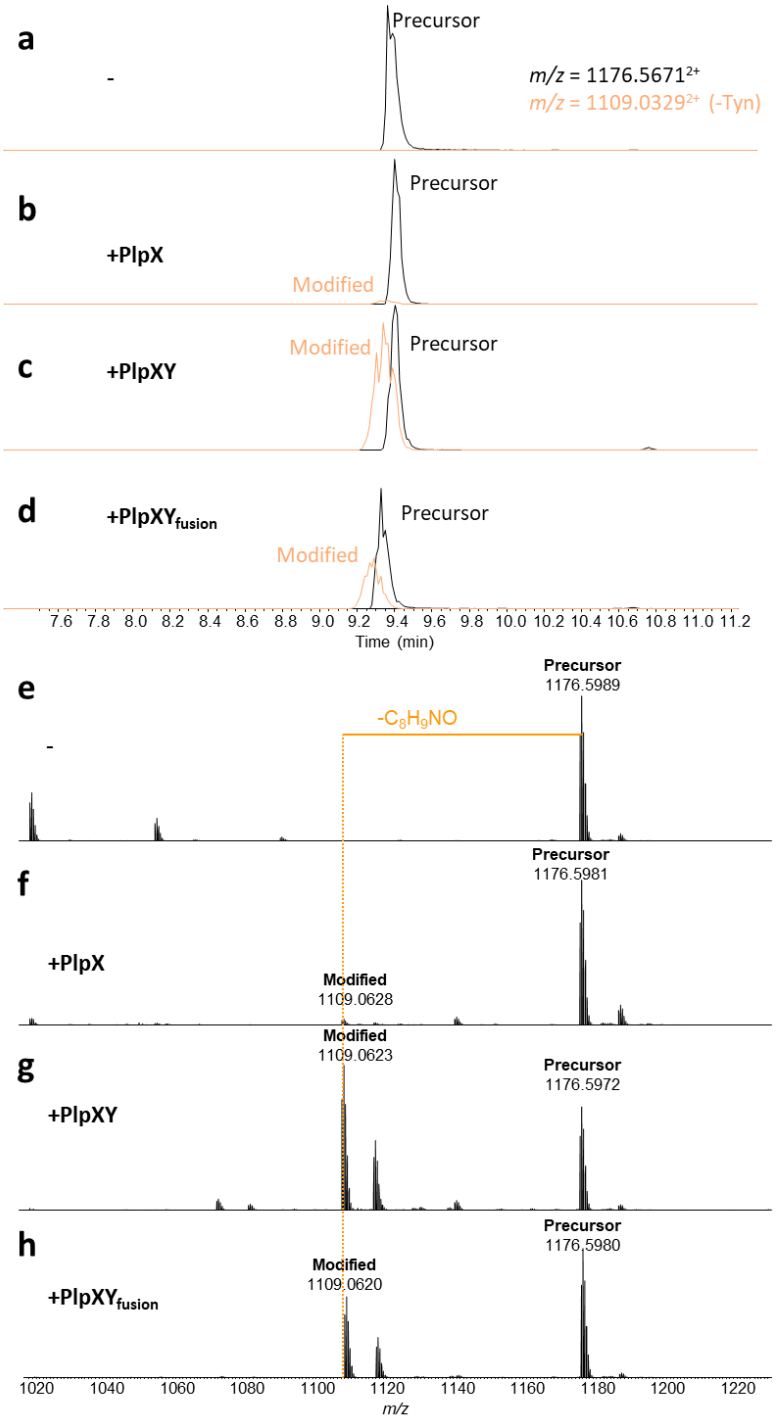
Supplementary Figure S7. LC-MS analysis for His_6-PlpA3 cleaved with trypsin to give the peptide fragment AVAAMYGVVFPWDNEFPWPR. Extracted ion chromatograms for *m/z* 1176.5671 (precursor, $[M+2H]^{2+}$), *m/z* 1109.0329 (modified, $[M+2H]^{2+}$) for **a**) precursor only expression, **b**) precursor + PlpX co-expression, and **c**) precursor + PlpXY co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + PlpX co-expression, and **f**) precursor + PlpXY co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



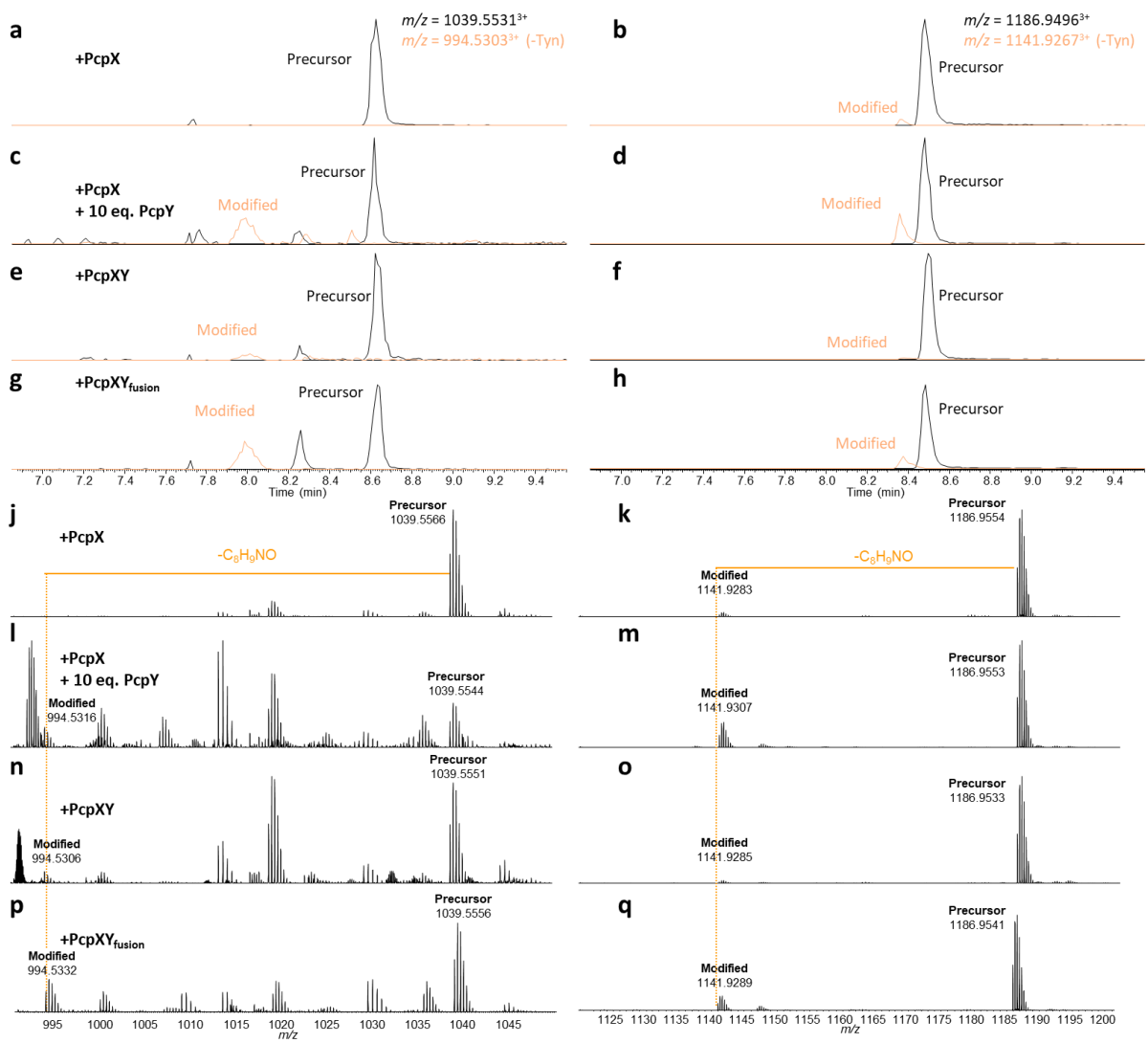
Supplementary Figure S8. LC-MS analysis for His_6-PlpA3-33 cleaved with trypsin to give the peptide fragment AVAAMYGVVFPWDNEFPWPR. Extracted ion chromatograms for *m/z* 1176.5671 (precursor, $[M+2H]^{2+}$), *m/z* 1109.0329 (modified, $[M+2H]^{2+}$) for **a**) precursor only expression, **b**) precursor + PlpX co-expression, and **c**) precursor + PlpXY co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + PlpX co-expression, and **f**) precursor + PlpXY co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



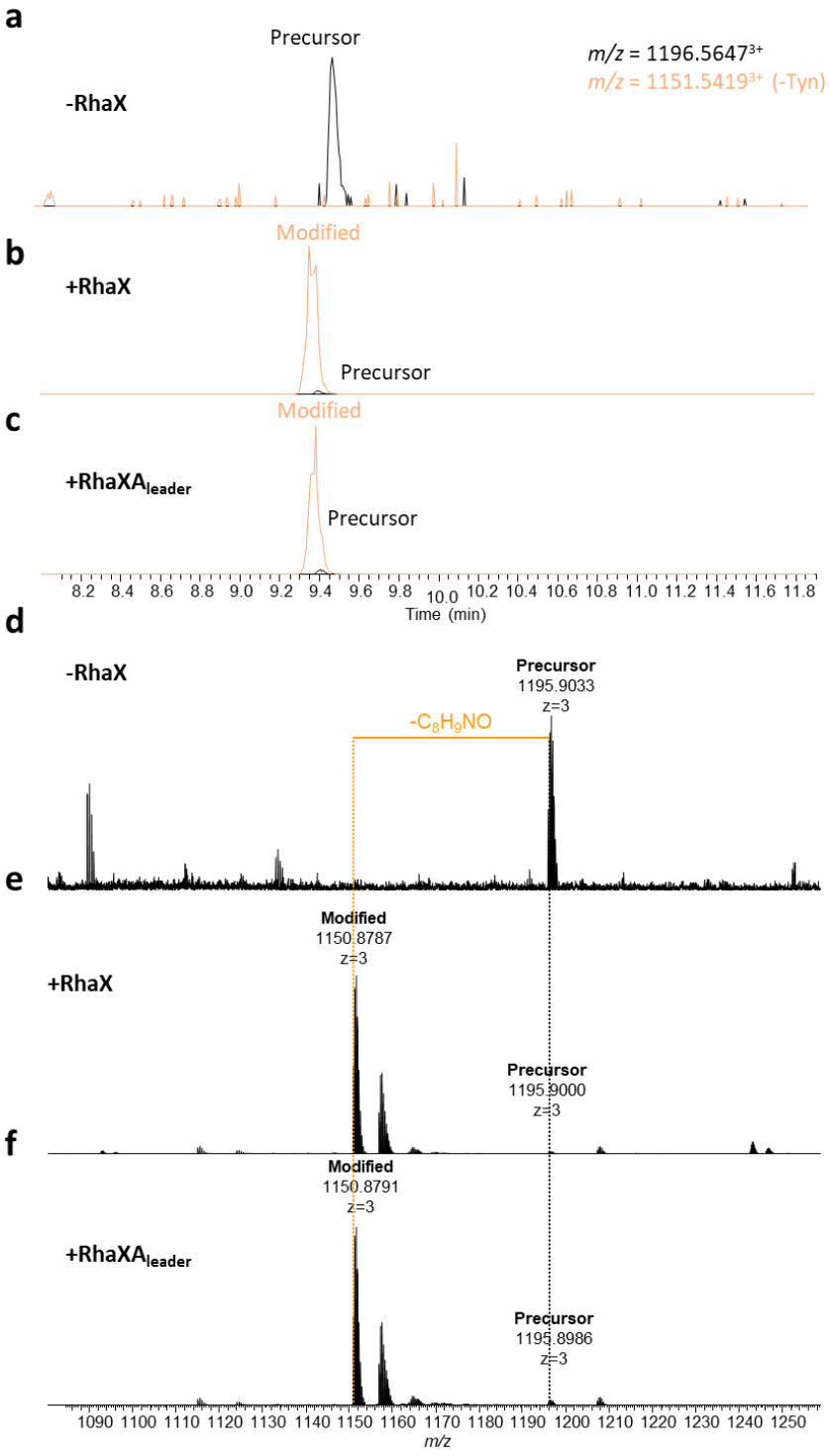
Supplementary Figure S9. LC-MS analysis for His_6-PlpA3-45 cleaved with trypsin to give the peptide fragment AVAAMYGVVFPWDNEFPWPR. Extracted ion chromatograms for *m/z* 1176.5671 (precursor, $[M+2H]^{2+}$), *m/z* 1109.0329 (modified, $[M+2H]^{2+}$) for **a**) precursor only expression, **b**) precursor + PlpX co-expression, and **c**) precursor + PlpXY co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + PlpX co-expression, and **f**) precursor + PlpXY co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



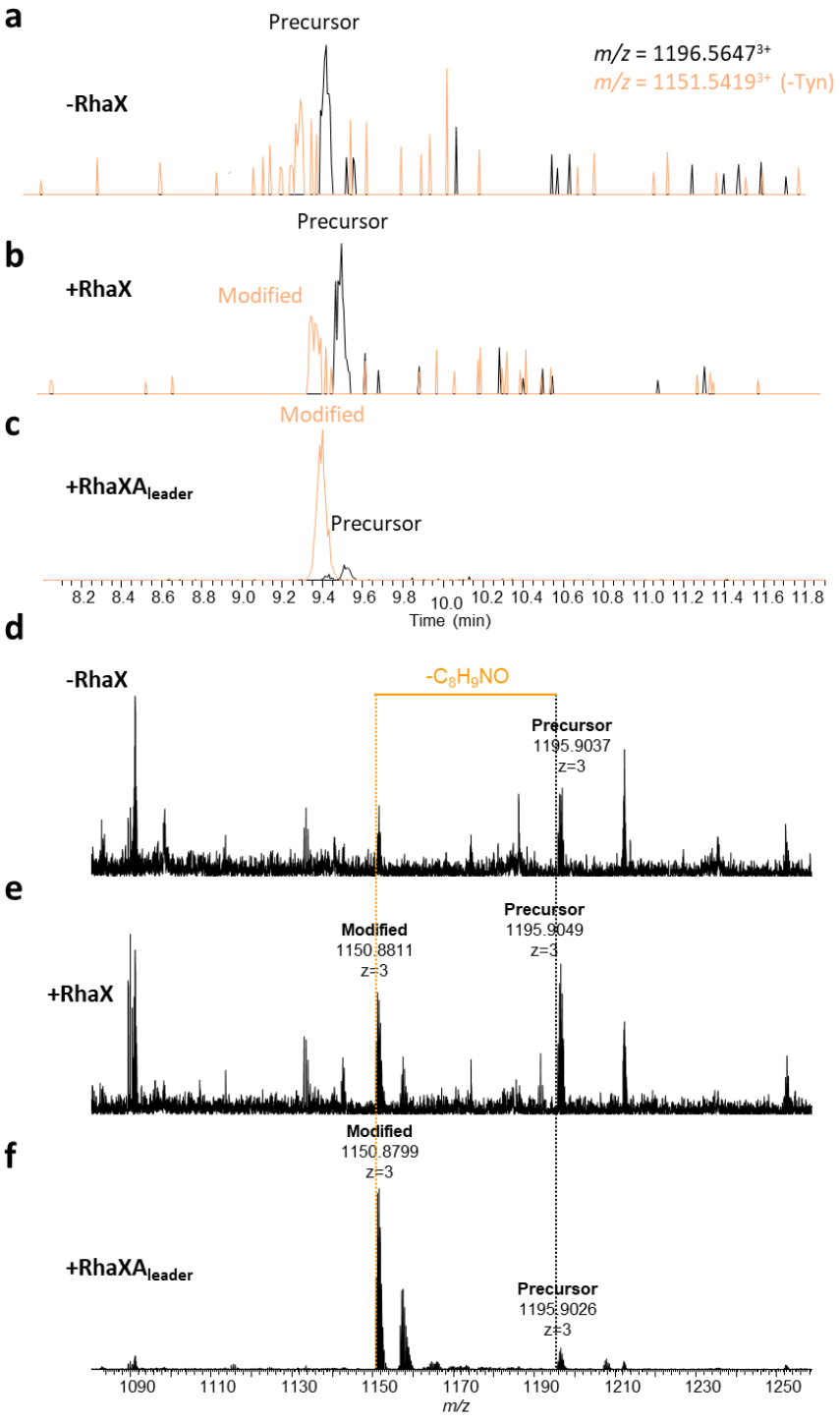
Supplementary Figure S10. LC-MS analysis for His_6-PlpA3 cleaved with trypsin to give the peptide fragment AVAAMYGVVFPWDNEFPWPR. Extracted ion chromatograms for *m/z* 1176.5671 (precursor, $[M+2H]^{2+}$), *m/z* 1109.0329 (modified, $[M+2H]^{2+}$) for **a**) precursor only expression, **b**) precursor + PlpX co-expression, **c**) precursor + PlpXY co-expression, and **d**) precursor + $PlpXY_{fusion}$ co-expression. Extracted mass spectra for **e**) precursor only expression, **f**) precursor + PlpX co-expression, **g**) precursor + PlpXY co-expression, and **h**) precursor + $PlpXY_{fusion}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



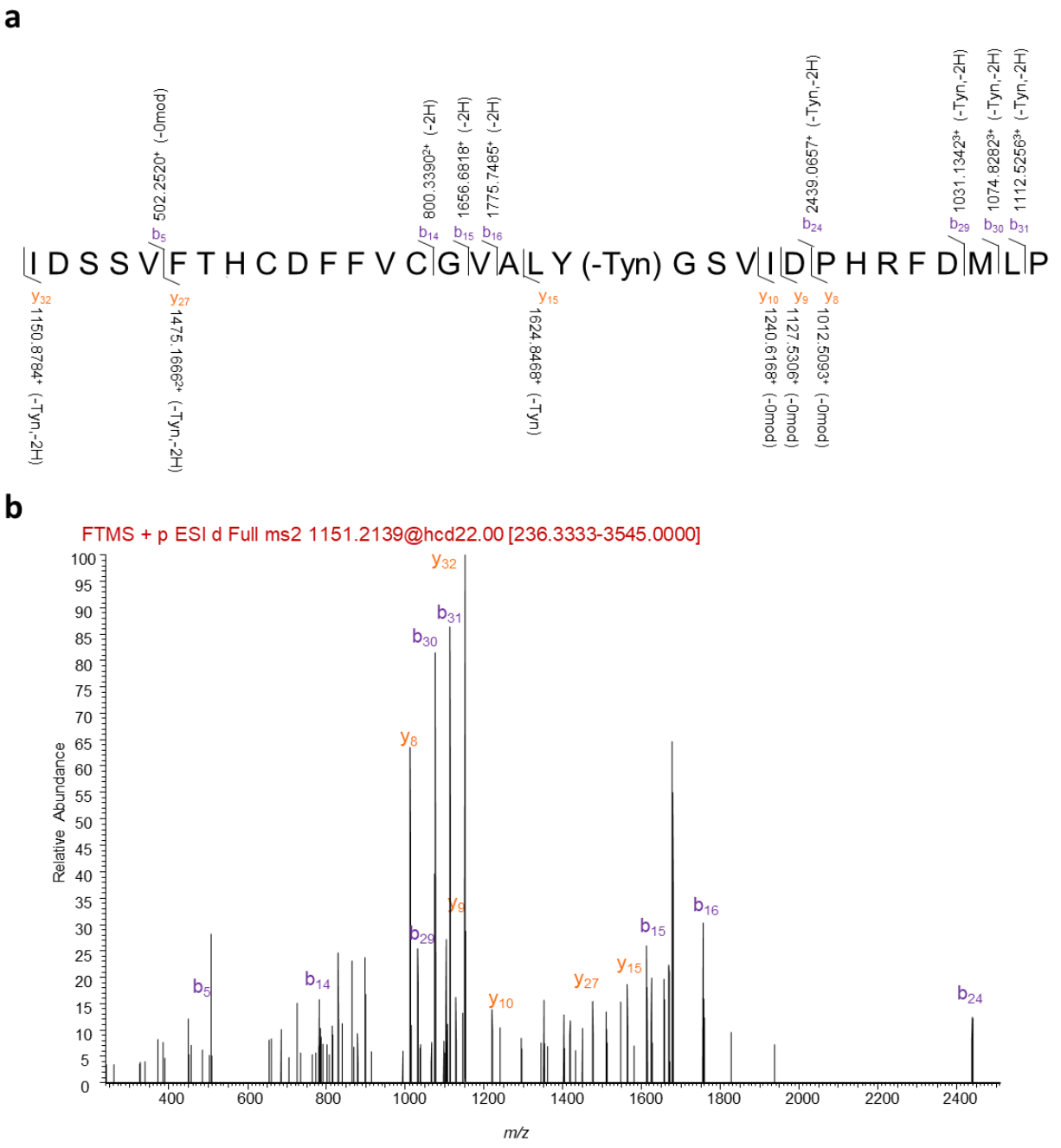
Supplementary Figure S11. LC-MS analysis for His_6-PcpA cleaved with trypsin and GluC to give the peptide fragment LVTAVGGVTGGSGIYGPIQAMYGAVVGDPKPGK (**a**, **c**, **e**, **h**, **j**, **l**, **n**, **p**) or FPSPLPKPSPIPSPWKPPVDVQPMYGVVVSNDS (**b**, **d**, **f**, **h**, **k**, **m**, **o**, **q**). Extracted ion chromatograms for: *m/z* 1039.5531 (precursor, $[M+3H]^{3+}$), *m/z* 994.5303 (modified, $[M+3H]^{3+}$), (**a**, **c**, **e**, **g**, **j**, **l**, **n**, **p**) ; or *m/z* 1186.9496 (precursor, $[M+3H]^{3+}$), *m/z* 1141.9267.5303 (modified, $[M+3H]^{3+}$) (**b**, **d**, **f**, **h**, **k**, **m**, **o**, **q**) for *in vitro* enzymatic reactions of His_6-PcpA and SUMO-PcpX (**a**, **b**), SUMO-PcpX + 10 eq. SUMO-PcpY (**c**, **d**), SUMO-PcpXY (**e**, **f**), or $PcpXY_{fusion}$ (**g**, **h**). Extracted mass spectra for *in vitro* enzymatic reactions of His_6-PcpA and SUMO-PcpX (**j**, **k**), SUMO-PcpX + 10 eq. SUMO-PcpY (**l**, **m**), SUMO-PcpXY (**n**, **o**), or $PcpXY_{fusion}$ (**p**, **q**). "Modified" refers to excision of tyramine ($-C_8H_9NO$).



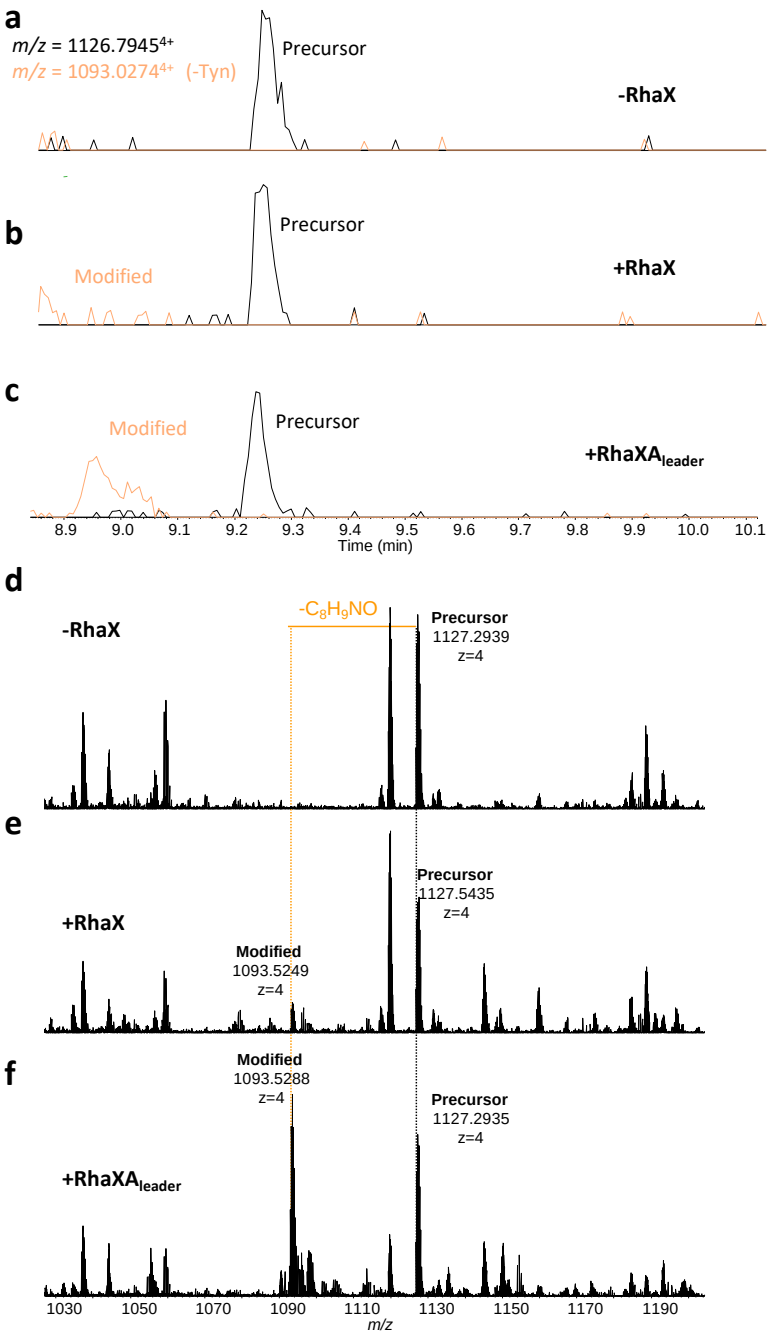
Supplementary Figure S12. LC-MS analysis for His_6-RhaA cleaved with trypsin to give the peptide fragment IDSSVFTHCDFFVCGVALYGSVIDPHRFDMLP. Extracted ion chromatograms for *m/z* 1196.5647 (precursor, $[M+3H]^{3+}$), *m/z* 1151.5419 (modified, $[M+3H]^{3+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



Supplementary Figure S13. LC-MS analysis for His_6-SUMO-$RhaA_{core}$ cleaved with trypsin to give the peptide fragment IDSSVFTHCDFFVCGVALYGSVIDPHRFDMLP. Extracted ion chromatograms for *m/z* 1196.5647 (precursor, $[M+3H]^{3+}$), *m/z* 1151.5419 (modified, $[M+3H]^{3+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).

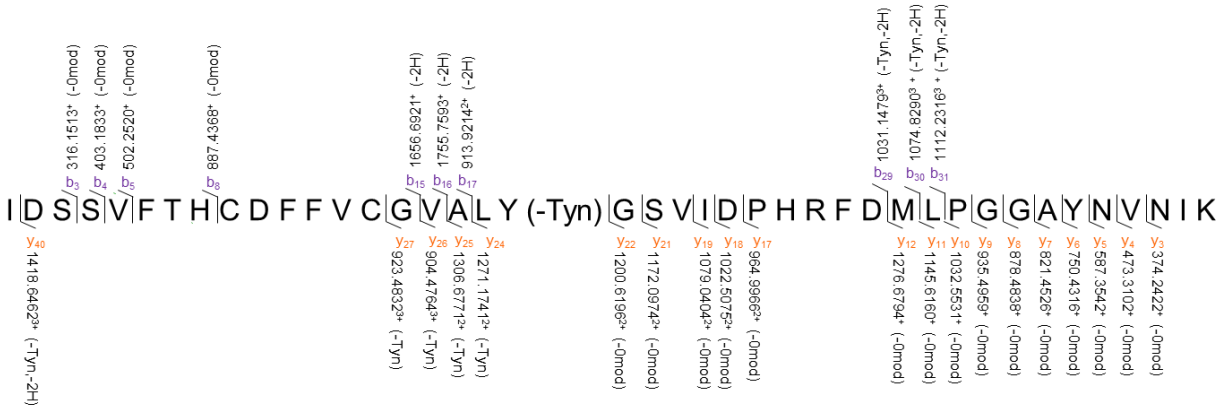


Supplementary Figure S14. Localization of C_8H_9NO loss from His_6-SUMO-$RhaA_{core}$ cleaved with trypsin to give the peptide fragment IDSSVFTHCDFFVCGVALYGSVIDPHRFDMLP. **a**) Summary of observed b (above, purple) and y (below, orange) fragmentation ions. **b**) MS/MS spectrum from parallel reaction monitoring (PRM)-mediated fragmentation (CE 22) from *m/z* 1151.2139 ($[M+3H]^{3+}$) parent ion. Observed b and y ions are indicated as before.

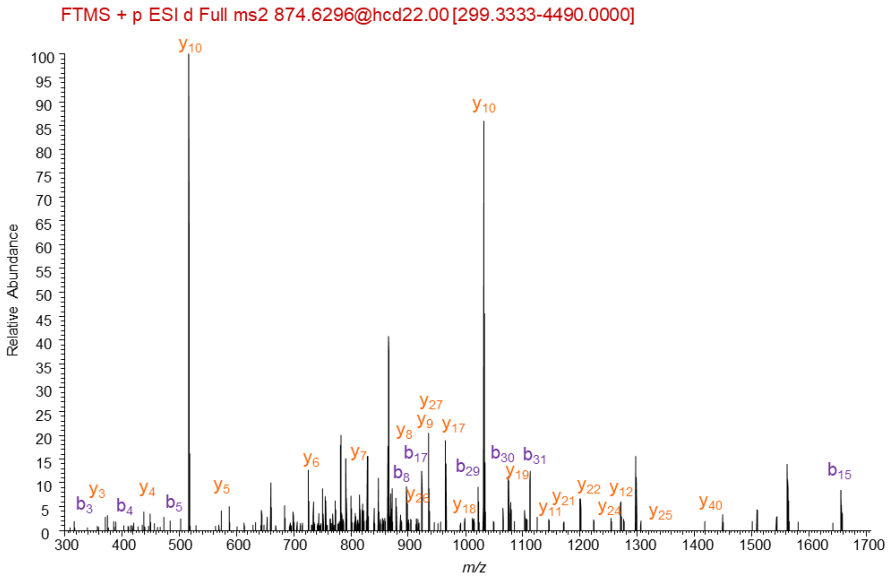


Supplementary Figure S15. LC-MS analysis for His_6-mCherry209-$RhaA_{core}$ cleaved with trypsin to give the peptide fragment IDSSVFTHCDFFVCGVALYGSVIDPHRFDMLPGGAYNVNIK. Extracted ion chromatograms for *m/z* 1126.7945 (precursor, $[M+4H]^{4+}$), *m/z* 1093.0274 (modified, $[M+4H]^{4+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).

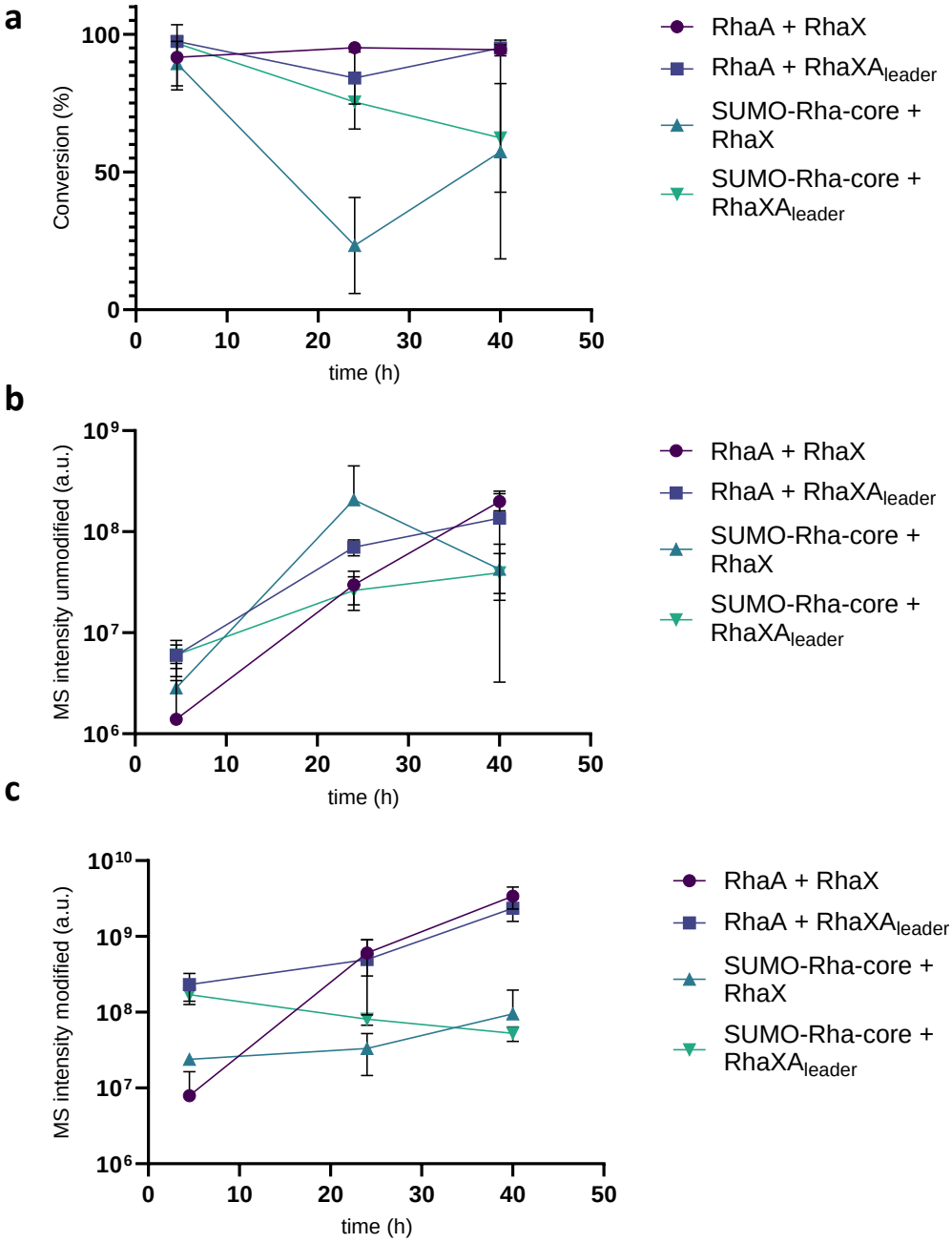
a



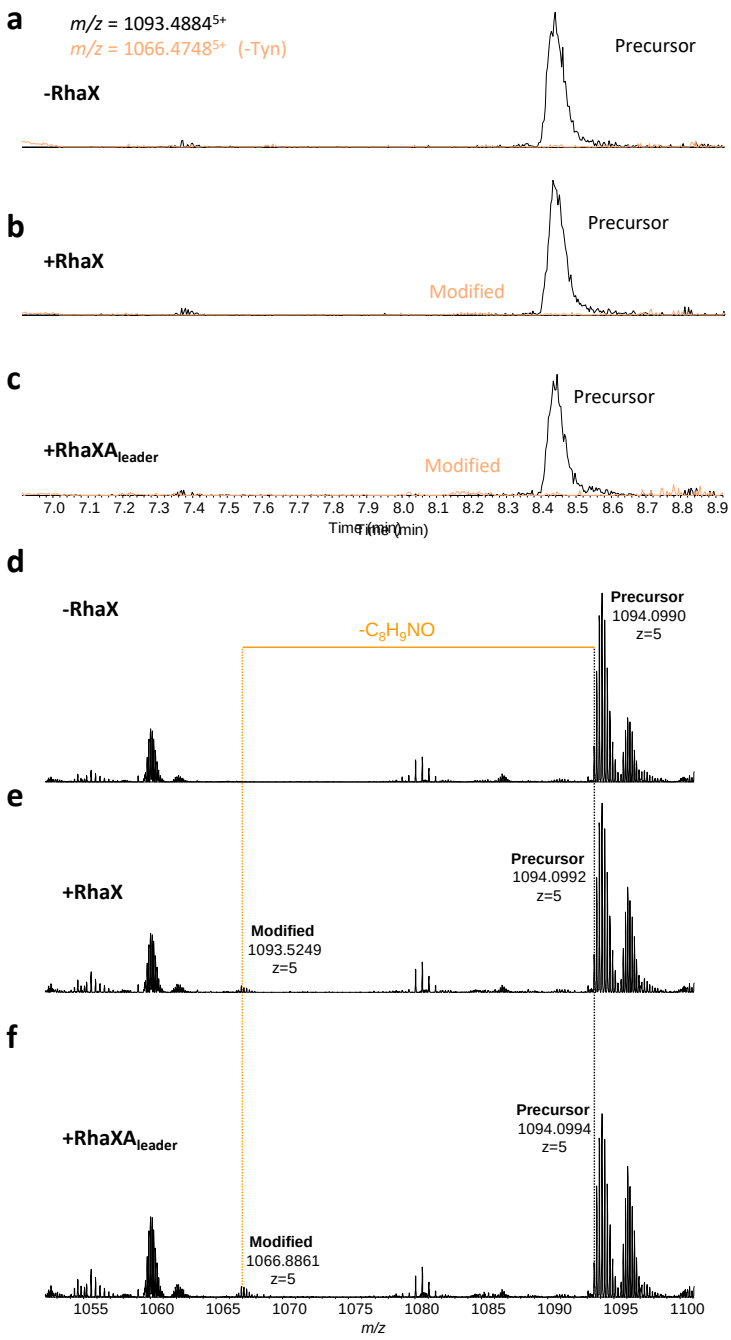
b



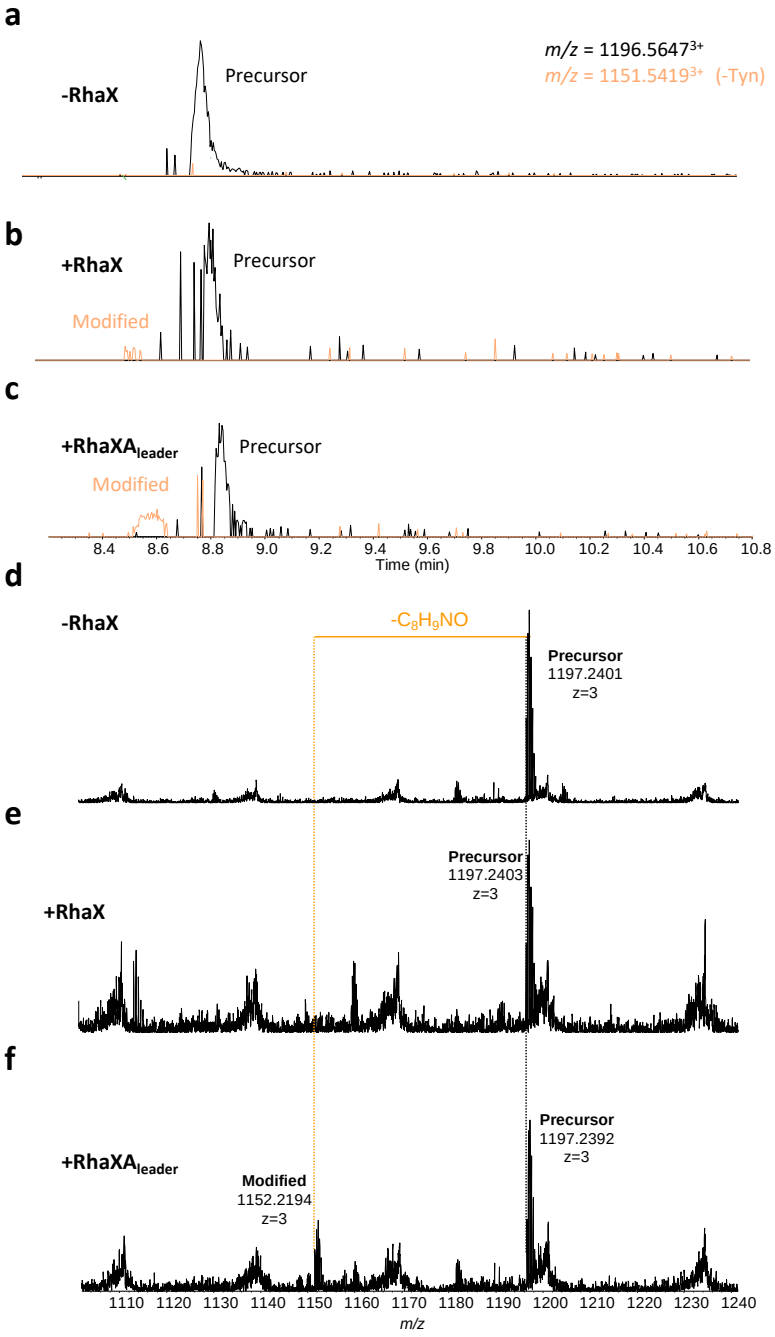
Supplementary Figure S16. Localization of C_8H_9NO loss from His_6-mCherry209-$RhaA_{core}$ cleaved with trypsin to give the peptide fragment DSSVFTHCDFFVCGVALYGSVIDPHRFDMLPGGAYNVNIK. **a**) Summary of observed b (above, purple) and y (below, orange) fragmentation ions. **b**) MS/MS spectrum from parallel reaction monitoring (PRM)-mediated fragmentation (CE 22) from *m/z* 874.6296 ($[M+5H]^{5+}$) parent ion. Observed b and y ions are indicated as before.



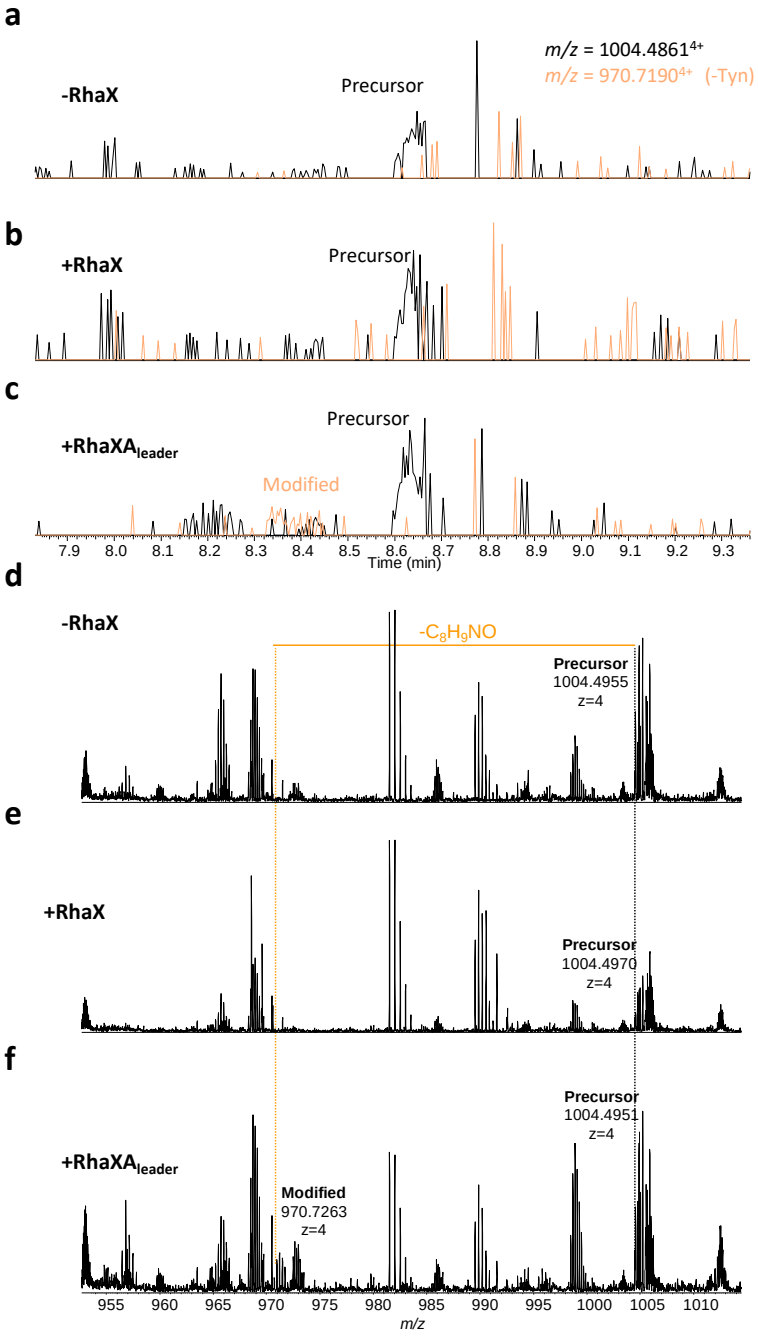
Supplementary Figure S17. LC-MS based conversion (**a**), MS intensities (logarithmic scale) of unmodified (**b,** *m/z* 1196.5647 $[M+3H]^{3+}$), and modified (**c,** *m/z* 1151.5419 $[M+3H]^{3+}$) tryptic peptide fragments of expressions of His_6-RhaA or His_6-SUMO-RhaAcore with RhaX or $RhaXA_{leader}$ purified at 4.5 h, 24 h, and 48 h after induction



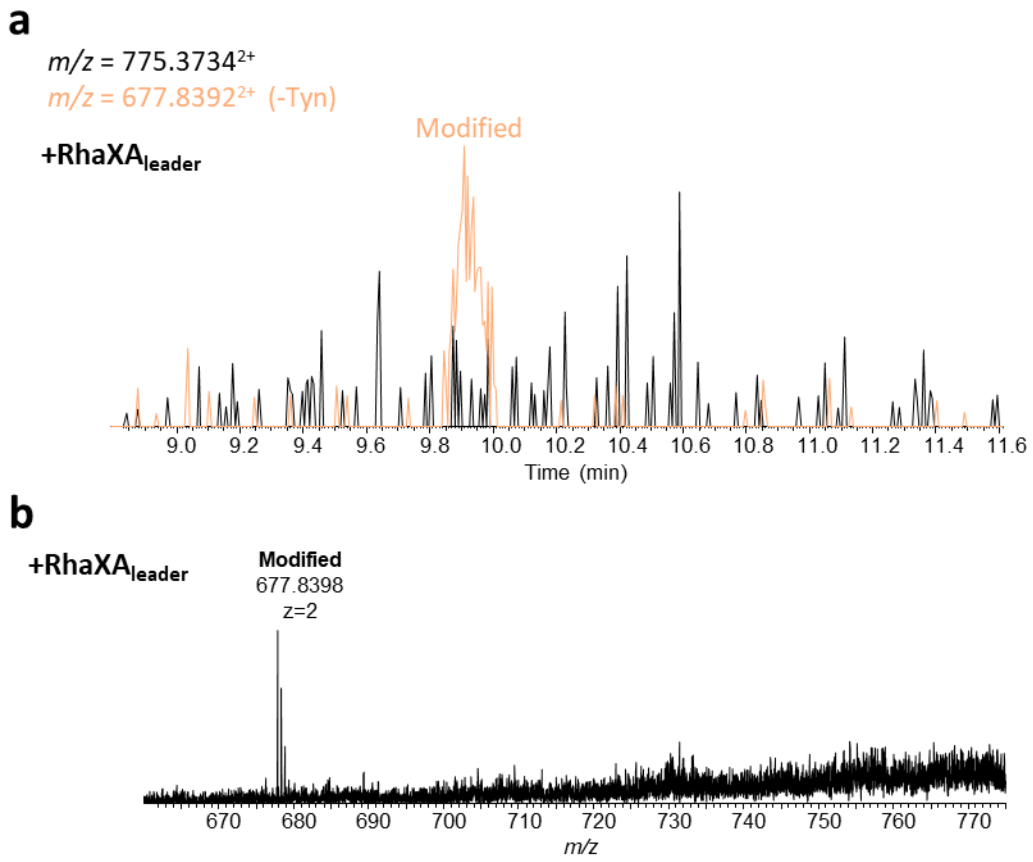
Supplementary Figure S18. LC-MS analysis for His_6-DHFR118-$RhaA_{core}$ cleaved with trypsin to give the peptide fragment IDSSVFTHCDFFVCGVALYG SVIDPHRFDMLPGDTHYPDYEPDDWER. **a**) Extracted ion chromatograms for *m/z* 1093.4884 (precursor, $[M+5H]^{5+}$), *m/z* 1066.4748 (modified, $[M+5H]^{5+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



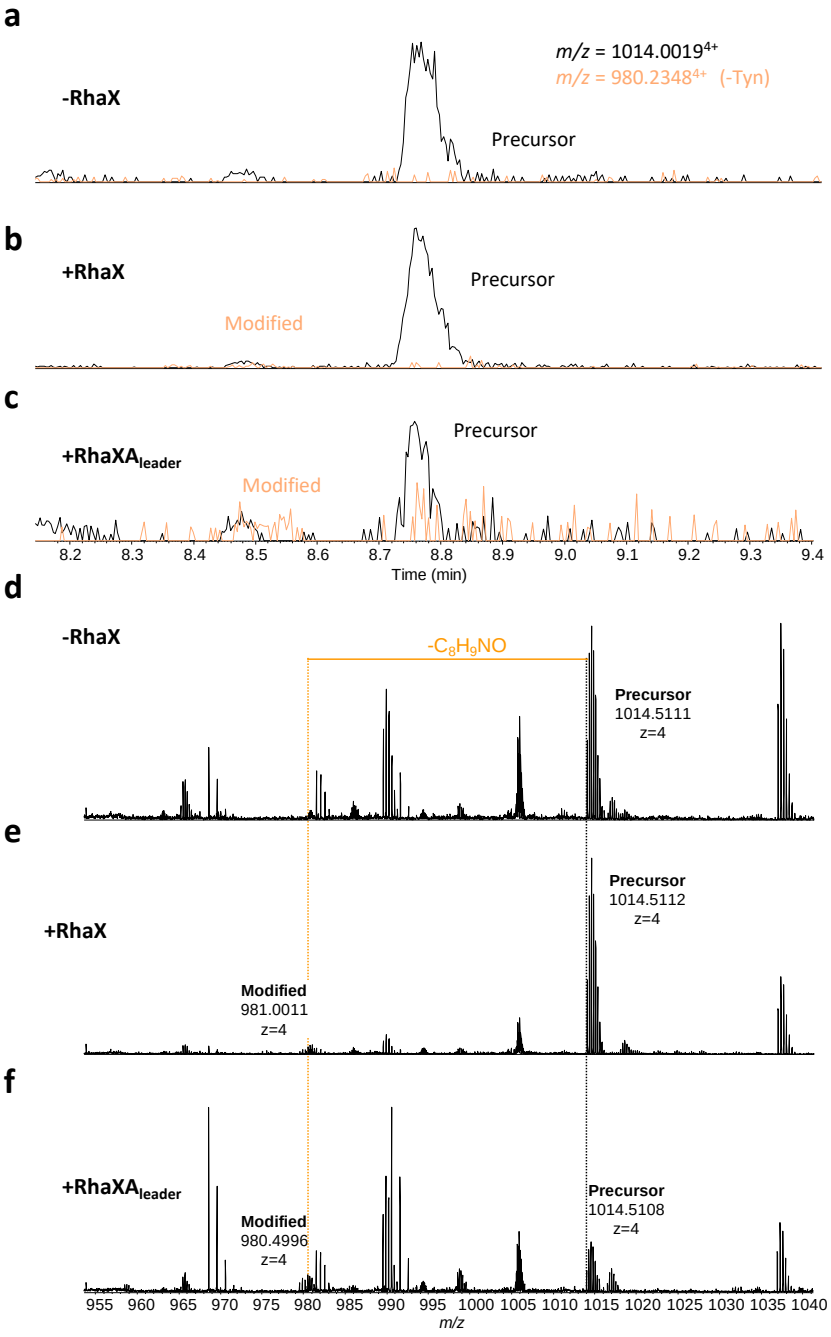
Supplementary Figure S19. LC-MS analysis for His_6-MBP-Cterm-$RhaA_{core}$ cleaved with trypsin to give the peptide fragment IDSSVFTHCDFFVCGVALYGSVIDPHRFDMLP. **a**) Extracted ion chromatograms for *m/z* 1196.5647 (precursor, $[M+3H]^{3+}$), *m/z* 1151.5419 (modified, $[M+3H]^{3+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



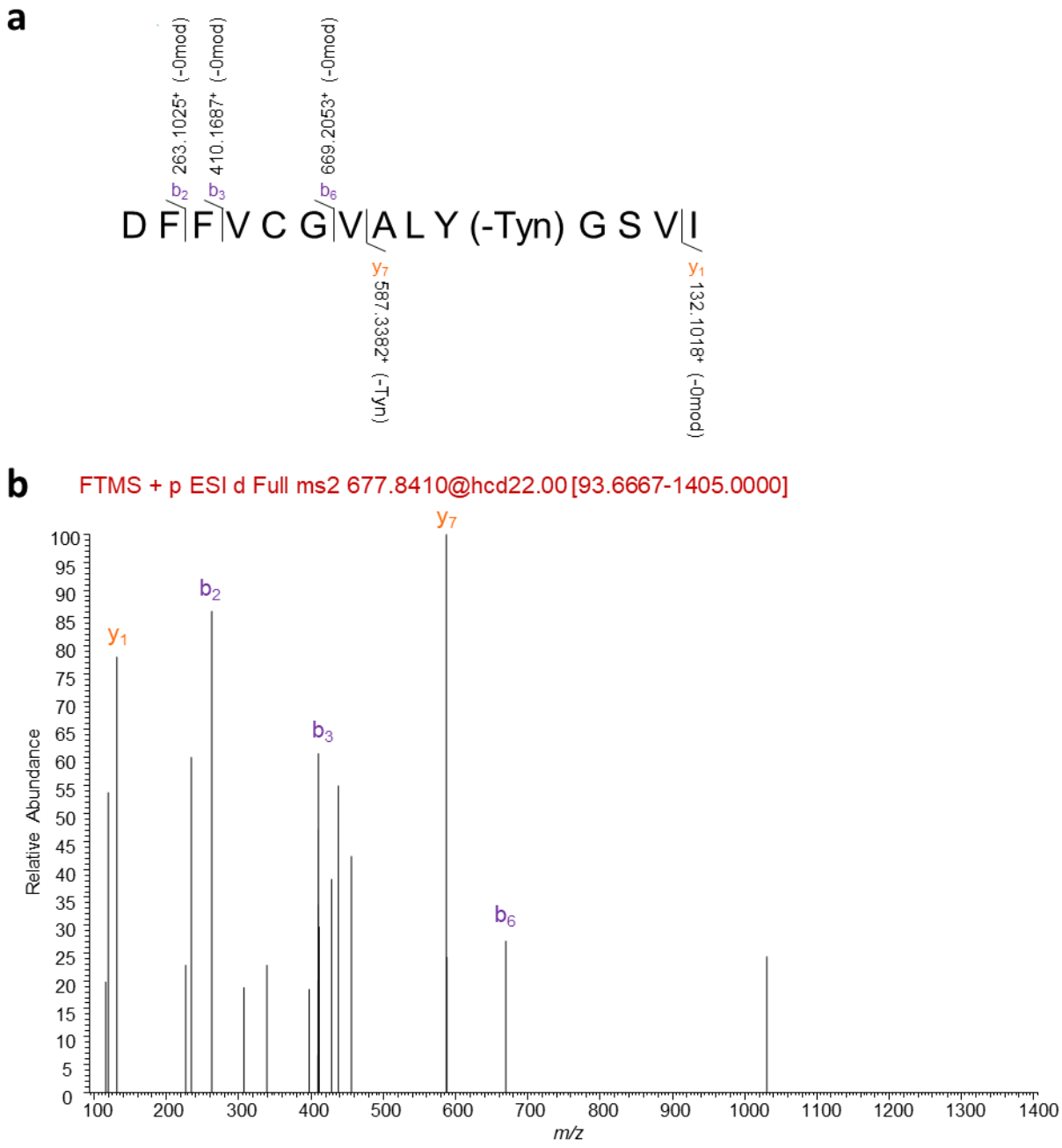
Supplementary Figure S20. LC-MS analysis for His_6-MBP154-$RhaA_{core}$ cleaved with trypsin to give the peptide fragment IDSSVFTHCDFFVCGVALYGSVIDPHRFDMLPALDKSVIDPHRFDMLP. **a**) Extracted ion chromatograms for *m/z* 1004.4861 (precursor, $[M+4H]^{4+}$), *m/z* 970.7190 (modified, $[M+4H]^{4+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



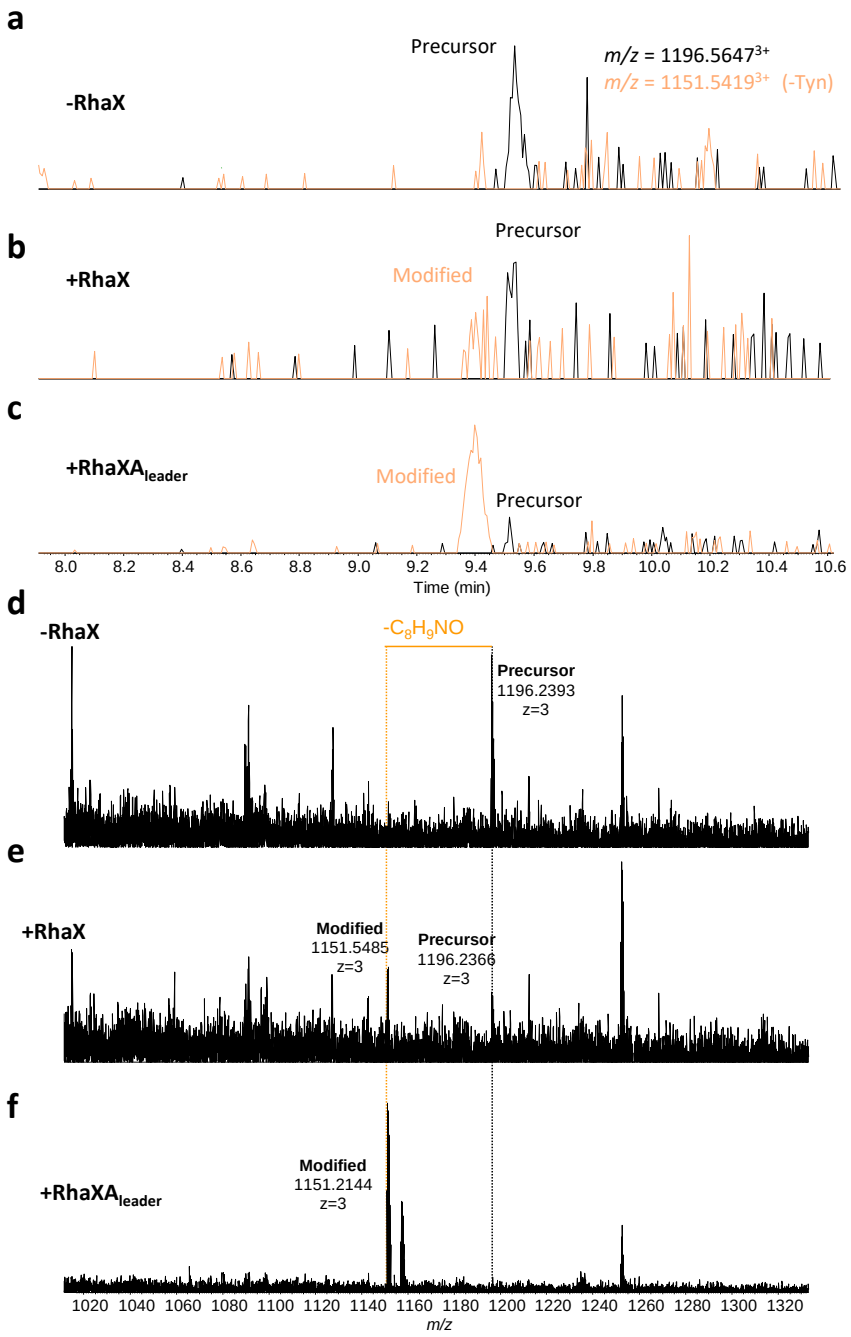
Supplementary Figure S21. LC-MS analysis for DHFR-Nterm-RhaA$_{core}$-His$_6$ cleaved with AspN to give the peptide fragment DFFVCGVALYGSVI. **a**) Extracted ion chromatograms for *m/z* 775.3734 (precursor, $[M+2H]^{2+}$), *m/z* 677.8392 (modified, $[M+2H]^{2+}$) for precursor + RhaXA$_{leader}$ co-expression. **b**) Extracted mass spectra precursor + RhaXA$_{leader}$ co-expression. "Modified" refers to excision of tyramine (-C_8H_9NO).



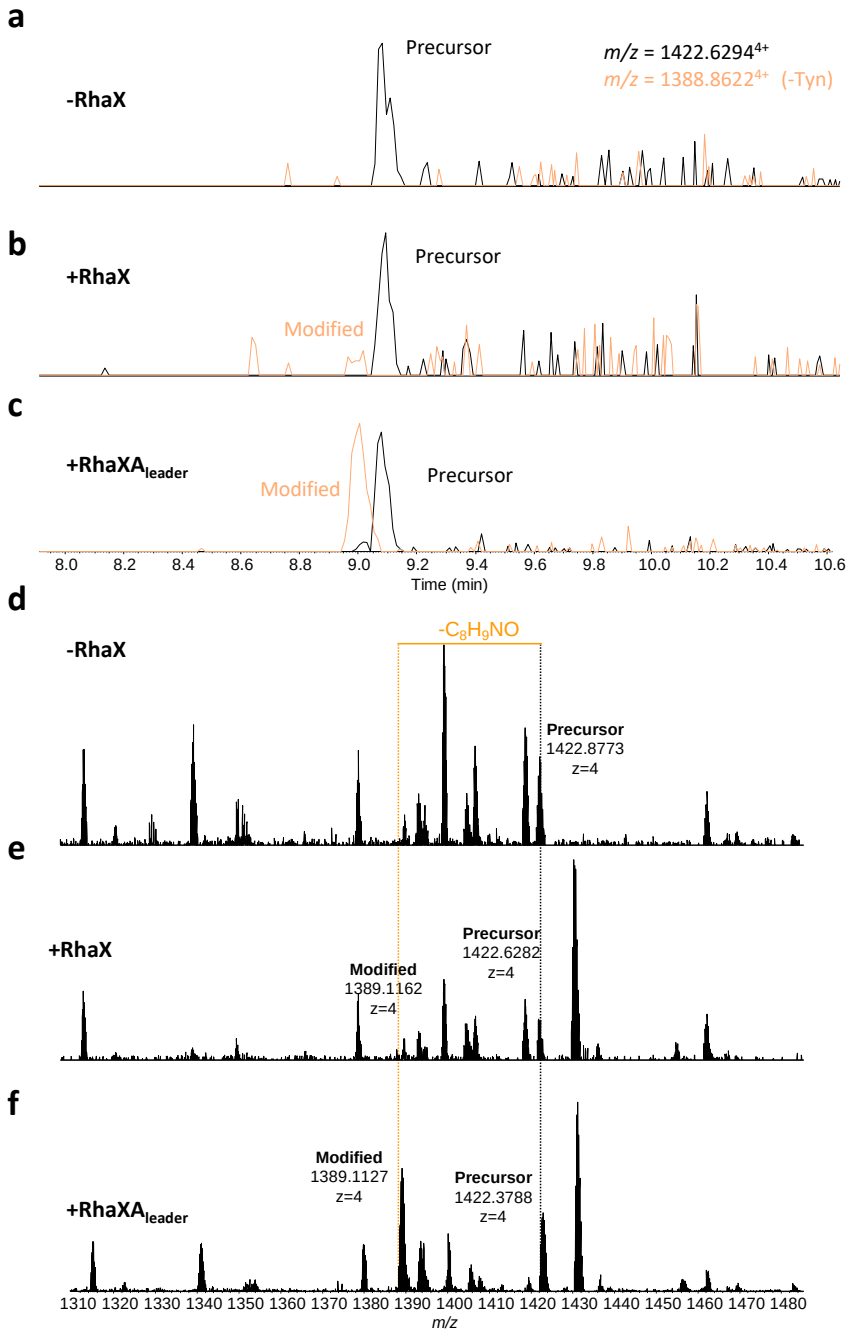
Supplementary Figure S22. LC-MS analysis for His_6-SUMO-Nterm-$RhaA_{core}$ cleaved with trypsin to give the peptide fragment IDSSVFTHCDFFVCGVALYG SVIDPHRFDMLPLVPR. **a**) Extracted ion chromatograms for *m/z* 1014.0019 (precursor, $[M+4H]^{4+}$), *m/z* 980.2348 (modified, $[M+4H]^{4+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



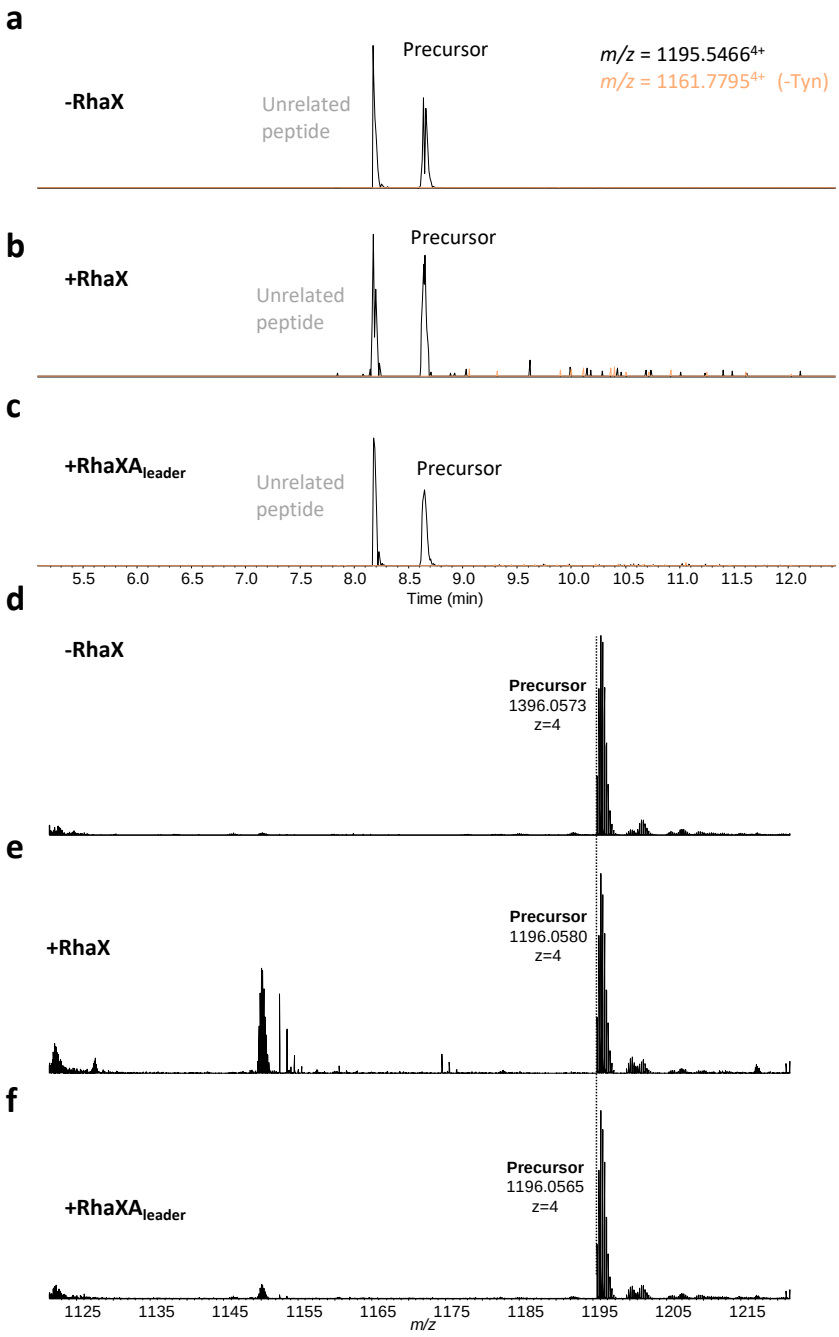
Supplementary Figure S23. Localization of C_8H_9NO loss from His_6-MBP-Cterm-$RhaA_{core}$ cleaved with AspN to give the peptide fragment DFFVCGVALYGSVI. **a**) Summary of observed b (above, purple) and y (below, orange) fragmentation ions. **b**) MS/MS spectrum from parallel reaction monitoring (PRM)-mediated fragmentation (CE 22) from *m/z* 677.8410 ($[M+2H]^{2+}$) parent ion. Observed b and y ions are indicated as before.



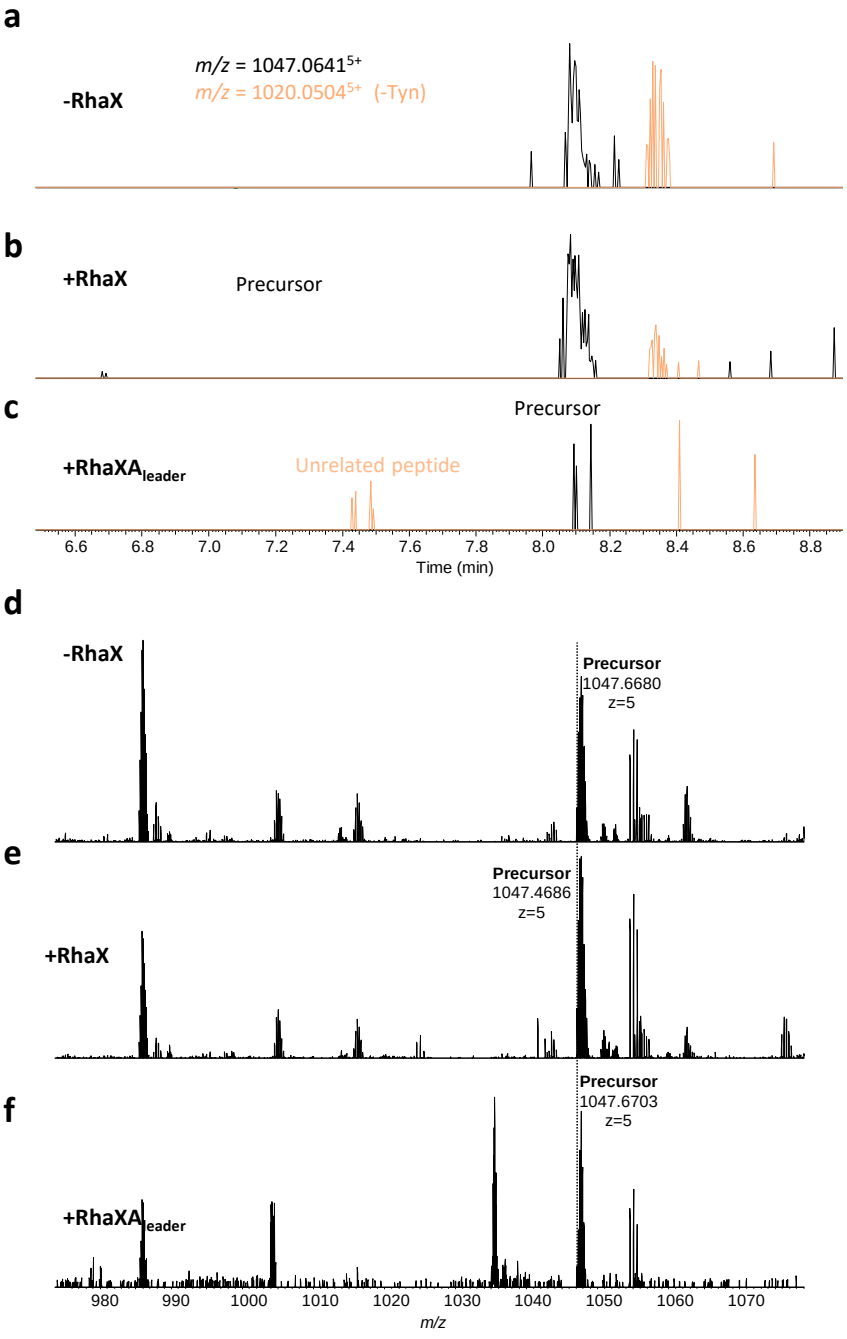
Supplementary Figure S24. LC-MS analysis for His_6-SUMO-$RhaA_{core}$-N8 cleaved with trypsin to give the peptide fragment IDSSVFTHCDFFVCGVALYGSVIDPHRFDMLP. Extracted ion chromatograms for *m/z* 1196.5647 (precursor, $[M+3H]^{3+}$), *m/z* 1151.5419 (modified, $[M+3H]^{3+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



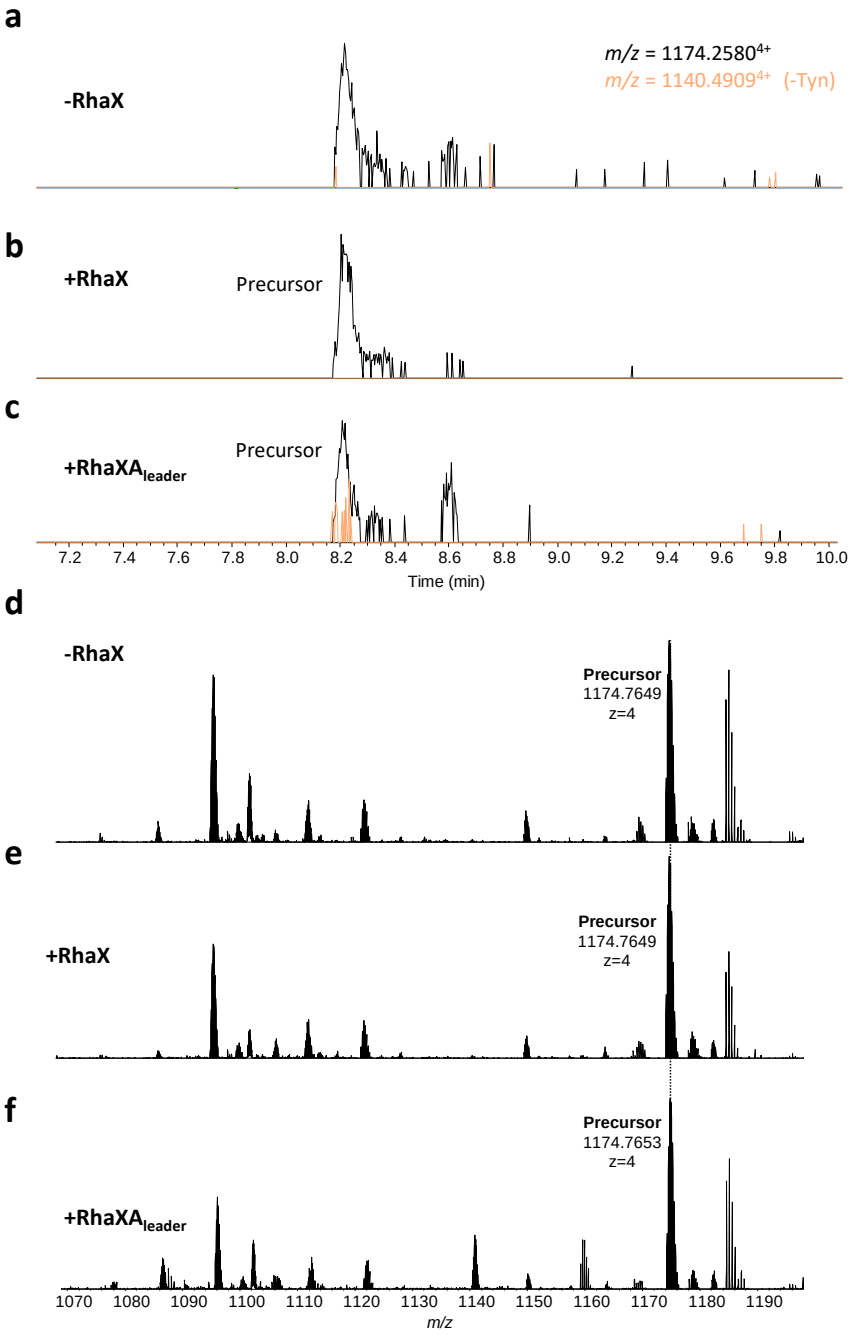
Supplementary Figure S25. LC-MS analysis for His_6-SUMO-$RhaA_{core}$-N24 cleaved with trypsin to give the peptide fragment AEQTPDELEMEDGDEIDAMLHQTGGHHCDFFVCGVALYGSVIDPHRFDMLP. Extracted ion chromatograms for *m/z* 1422.6294 (precursor, $[M+4H]^{4+}$), *m/z* 1388.8622 (modified, $[M+4H]^{4+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



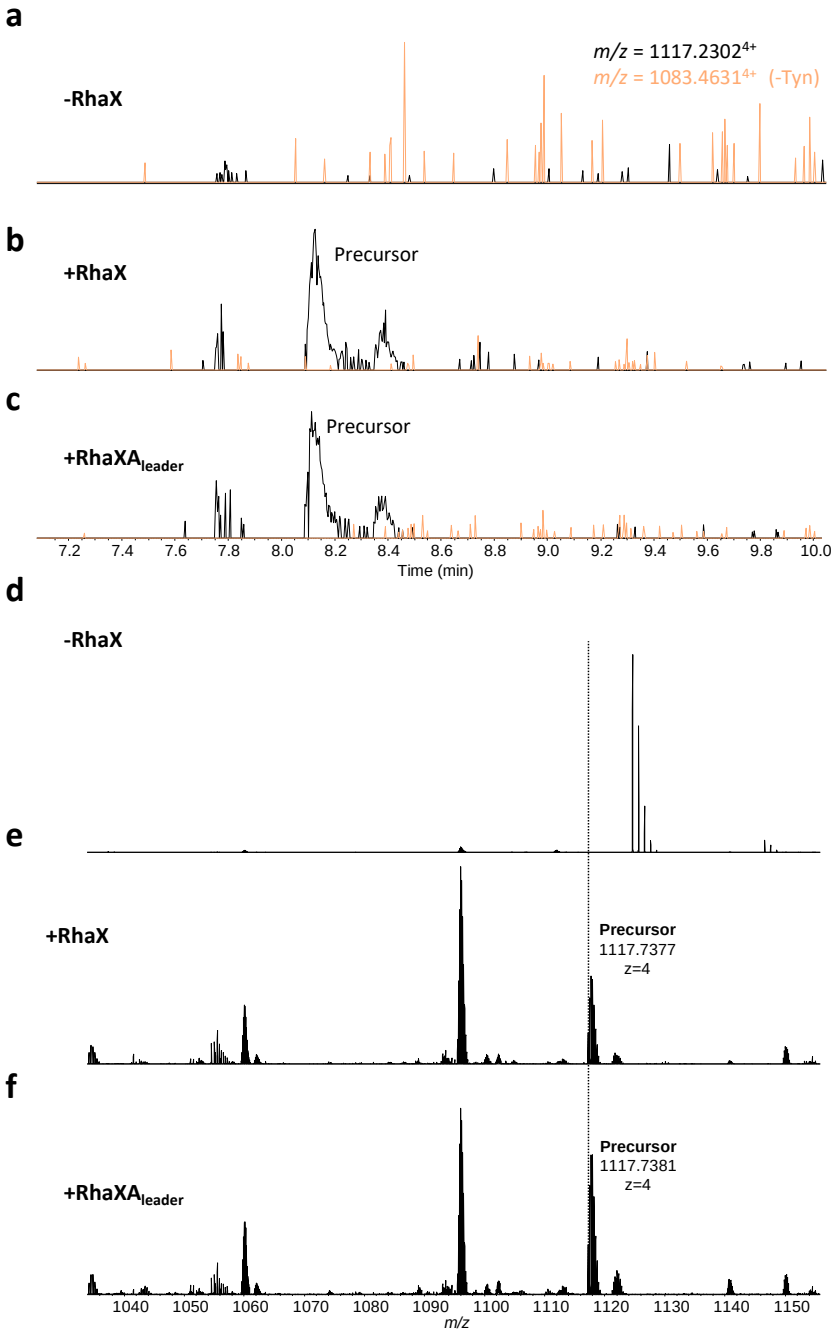
Supplementary Figure S26. LC-MS analysis for His_6-SUMO-$RhaA_{core}$-N32 cleaved with trypsin to give the peptide fragment AEQTPDELEMEDGDEIDAMLHQTGGHVALYGSVIDPHRFDMLP. Extracted ion chromatograms for *m/z* 1195.5466 (precursor, $[M+4H]^{4+}$), *m/z* 1161.7795 (modified, $[M+4H]^{4+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



Supplementary Figure S27. LC-MS analysis for His_6-SUMO-$RhaA_{core}$-N24-C4 cleaved with trypsin to give the peptide fragment AEQTPDELEMEDGDEIDAMLHQTGGHHCDFFVCGVALYGSVIDPHRF. Extracted ion chromatograms for *m/z* 1047.0641 (precursor, $[M+5H]^{5+}$), *m/z* 1020.0504 (modified, $[M+5H]^{5+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



Supplementary Figure S28. LC-MS analysis for His_6-SUMO-$RhaA_{core}$-N24-C8 cleaved with trypsin to give the peptide fragment AEQTPDELEMEDGDEIDAMLHQTGGHHCDFFVCGVALYGSVID. Extracted ion chromatograms for *m/z* 1174.2580 (precursor, $[M+4H]^{4+}$), *m/z* 1140.4909 (modified, $[M+4H]^{4+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).



Supplementary Figure S29. LC-MS analysis for His_6-SUMO-$RhaA_{core}$-N24-C10 cleaved with trypsin to give the peptide fragment AEQTPDELEMEDGDEIDAMLHQTGGHHCDFFVCGVALYGSV. Extracted ion chromatograms for *m/z* 1117.2302 (precursor, $[M+4H]^{4+}$), *m/z* 1083.4631 (modified, $[M+4H]^{4+}$) for **a**) precursor only expression, **b**) precursor + RhaX co-expression, **c**) precursor + $RhaXA_{leader}$ co-expression. Extracted mass spectra for **d**) precursor only expression, **e**) precursor + RhaX co-expression, **f**) precursor + $RhaXA_{leader}$ co-expression. "Modified" refers to excision of tyramine ($-C_8H_9NO$).

Table S1. Primers used in this study.

Name	Sequence (5'-3')
PlpY-PlpA3-N33_plpA3_fwd	TTATCTAAAGAAGAACGCCAACAAC
PlpY-PlpA3-N33_plpA3_rev	GCCGCTGCTGTGATGATG
PlpY-PlpA3-N33_plpy_fwd	ATCATCATCACAGCAGCGGCAACTCTAATCAAATACCAAATAAAG
PlpY-PlpA3-N33_plpy_rev	TGGCGTTCTTCTTTAGATAATGTCAGAAAATTGCTAATTTC
PlpY-PlpA3-N45_plpA3_fwd	TCTGGCTATGATTTCACTGCC
PlpY-PlpA3-N45_plpA3_rev	GCCGCTGCTGTGATGATG
PlpY-PlpA3-N45_plpy_fwd	ATCATCATCACAGCAGCGGCAACTCTAATCAAATACCAAATAAAG
PlpY-PlpA3-N45_plpy_rev	GCAGTGAAATCATAGCCAGATGTCAGAAAATTGCTAATTTC
PcpXYfusion_fwd	ATGGTCGAAAATATAGACAAC
PcpXYfusion _rev	ATCAACTACAGCACCAATC
RhaXY_Cfusion_fwd	GTTGAGGCTGTAGAGCTACTAAACAAAGTTGAATAGCTCGAGTCTGGTAAAG
RhaXY_Cfusion_rev	AACATGGTTTGTATCAAGTTTTACGTTTTTCATGCTGGCTATTGCGATACC
PlpXYfusion_PlpX_fwd	TAACTCGAGTCTGGTAAAG
PlpXYfusion_PlpX_rev	CTTTGCTAAAGCGTAAGC
PlpXYfusion_PlpY_fwd	CTGCTTACGCTTTAGCAAAGATGAACTCTAATCAAATACCAAATAAAG
PlpXYfusion_PlpY_rev	TCTTTACCAGACTCGAGTTATTATGTCAGAAAATTGCTAATTTC
mCherry_Rha_fwd	CTCCTCGGTTTTTACCCACTGTGACTTTTTCGTTTGTGGTGTAGCGCTGTACGGCAGC
mCherry_Rha_rev	TCGATACGCTGACCGGTAGCGTTAATGCCGCCGCCGGGCAGCTG
pACYC_Rha_fwd	GGCGGGATTAACGCTACC
pACYC_Rha_rev	AGGCAACATATCGAAACGATG
MBP_Cterm_fwd	ATCGTTTCGATATGTTGCCTTAATCGTATTGTACACGGC
MBP_Cterm_rev	CCGGTAGCGTTAATCCCGCCCTTTCTGTTCGACTTAAGC
MBP_154_fwd	ATCGTTTCGATATGTTGCCTGCGCTGGATAAAGAACTGAAAG
MBP_154_rev	CCGGTAGCGTTAATCCCGCCCGGGATCTCTTCCCAGGTTTTTG
SUMO_nterm_fwd	ATCGTTTCGATATGTTGCCTTTAGTTCCTCGTGGTTCAG
SUMO_nterm_rev	CCGGTAGCGTTAATCCCGCCACCGCTGCTATGATGATG
DHFR_nterm_fwd	ATCGTTTCGATATGTTGCCTAGCCAGGATCCGGAGAATG
DHFR_nterm_rev	CCGGTAGCGTTAATCCCGCCCATGGTATATCTCCTTATTAAAGTTAAACAAAATTATTTC
DHFR_118_fwd	ATCGTTTCGATATGTTGCCTGGGGATACCCATTATCCG
DHFR_118_rev	CCGGTAGCGTTAATCCCGCCTTCTACTTCGGCGTCAATG

Table S2. Plasmids used in this study.

Plasmid	Description
plpA3/pACYCDuet-1	PlpA3 precursor protein with an N-terminal His_6-tag and a Factor Xa cleavage site under IPTG regulation and with chloramphenicol resistance (from here on referred to as PlpA3 (Morinaka, 2018))
plpXY/pRSFDuet	Splicease PlpX together with its accessory protein PlpY under IPTG regulation and with kanamycin resistance (referred to as PlpXY) (Morinaka, 2018)
sumo-pcpY/pCDF	Accessory protein PcpY with an N-terminal His_6-tag, SUMO-tagged under IPTG regulation and with spectinomycin resistance (referred to as SUMO-PcpY)
sumo-pcpX/pCDF	Splicease PcpX with an N-terminal His_6-tag, SUMO-tagged under IPTG regulation and with spectinomycin resistance (referred to as SUMO-PcpY)
sumo-pcpXY/pCDF	Splicease PcpX with an N-terminal His_6-tag and the accessory protein PcpY, Pcpx is SUMO-tagged under IPTG regulation and with spectinomycin resistance (referred to as SUMO-PcpY)
pcpA/pCDF	PcpA precursor protein with an N-terminal His_6-tag, under IPTG regulation and with spectinomycin resistance (referred to as PcpA (Morinaka, 2018))
plpX/pRSFDuet	Splicease PlpX under IPTG regulation and with kanamycin resistance (referred to as PlpXY)
plpA3-33/pACYCDuet-1	PlpA3 precursor protein with an N-terminal His_6-tag and a Factor Xa cleavage site, the first 33 amino acids replaced by PlpY, under IPTG regulation and with chloramphenicol resistance (from here on referred to as PlpA3-33)
plpA3-45/pACYCDuet-1	PlpA3 precursor protein with an N-terminal His_6-tag and a Factor Xa cleavage site, the first 45 amino acids replaced by PlpY, under IPTG regulation and with chloramphenicol resistance (from here on referred to as PlpA3-45)
plpXYfusion/pRSFDuet	Splicease PlpX fused to its accessory protein PlpY under IPTG regulation and with kanamycin resistance (referred to as PlpXYfusion)
*rhaA/*pACYC	RhaA precursor protein with an N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as RhaA)
*sumo-rhaA/*pACYC	SUMO with C-terminal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as SUMO-RhaAcore)
*sumo-nterm-rhaA/*pACYC	SUMO with N-terminal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as RhaAcore-SUMO)
*mbp-rhaA/*pACYC	MBP with C-terminal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as MBP-RhaAcore)
*mbp-154-rhaA/*pACYC	MBP with internal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as MBP-154-RhaAcore)
*dhfr-118-rhaA/*pACYC	DHFR with internal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as DHFR-118-RhaAcore)
*mCherry-209-rhaA/*pACYC	mCherry with internal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as mCherry-209-RhaAcore)

rhaX/pRSF	Splicease RhaX under IPTG regulation and with kanamycin resistance (referred to as RhaX)
rhaXAleader/pRSF	Splicease RhaX with C-terminal fusion of the RhaA leader under IPTG regulation and with kanamycin resistance (referred to as $RhaXA_{leader}$)
*sumo-rhaA_N8del/*pACYC	SUMO with C-terminal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as SUMO-RhaAcore). Truncation of the cleavage site and core by 8 N-terminal amino acids.
*sumo-rhaA_N24del/*pACYC	SUMO with C-terminal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as SUMO-RhaAcore). Truncation of the cleavage site and core by 24 N-terminal amino acids.
*sumo-rhaA_N32del/*pACYC	SUMO with C-terminal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as SUMO-RhaAcore). Truncation of the cleavage site and core by 32 N-terminal amino acids.
*sumo-rhaA_N24_C4del/*pACYC	SUMO with C-terminal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as SUMO-RhaAcore). Truncation of the cleavage site and core by 24 N-terminal and 4 C-terminal amino acids.
*sumo-rhaA_N24_C8del/*pACYC	SUMO with C-terminal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as SUMO-RhaAcore). Truncation of the cleavage site and core by 24 N-terminal and 8 C-terminal amino acids.
*sumo-rhaA_N24_C10del/*pACYC	SUMO with C-terminal RhaA core and N-terminal His_6-tag under IPTG regulation and with chloramphenicol resistance (from here on referred to as SUMO-RhaAcore). Truncation of the cleavage site and core by 24 N-terminal and 10 C-terminal amino acids.

Table S3. Protein sequences used in this study. The precursor (minimal) core sequence is underlined. Splicease modification sites are shown in bold.

Protein	**Sequence**
His_6-PlpA3	GSSHHHHHHSSGLVPRGSHMSIESAKAFYQRMTDDASFRTPFEAELSKEERQQLIKDSGYDFTAEEW QQAMTEIQAARSNEELNEEELEAIAGRAVAAMYGVVFPWDNEFPWPRWGG
His_6-PlpYA3-33	MGSSHHHHHHSSGNSNQIPNKVATAAQKSDDSSSVLPRQGWQDKQAFIKALIKAKQSLEIAEISNFLTL SKEERQQLIKDSGYDFTAEEWQQAMTEIQAARSNEELNEEELEAIDGRAVAAMYGVVFPWDNEFPWP RWGG
His_6-PlpYA3-45	MGSSHHHHHHSSGNSNQIPNKVATAAQKSDDSSSVLPRQGWQDKQAFIKALIKAKQSLEIAEISNFLT SGYDFTAEEWQQAMTEIQAARSNEELNEEELEAIDGRAVAAMYGVVFPWDNEFPWPRWGG
His_6-PcpA	MGSSHHHHHHSSGENLYFQSHMSSNILEKVKEFFVRLVKDDAFQSQLQNNSIDEVRNILQEAGYIFSK EEFETATIELLDLKERDEFHELTEEELVTAVGGVTGGSGIYGPIQAMYGAVVGDPKPGKDWGWRFPSP LPKPSPIPSPWKPPVDVQPMYGVVVSNDS
His_6-SUMO-PcpX	MGSHHHHHHHSSGLVPRGSASHINLKVKGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLF DGRRLRAEQTPDELEMEDGDEIDAMLHQTGGHMTYRRTSYAVWEITLKCNLACSHCGSRAGHTRAK ELSTQEALDLVRQMADVGIIEVTLIGGEAFLRPDWLQIAEAITKAGMLCSMTTGGYGISLETARKMKAA GIASVSVSIDGLEETHDRLRGRKGSWQAAFKTMSHLREVGIFFGCNTQINRLSAPEFPLIYERIRDAGA RAWQIQLTVPMGRAADNANILLQPYELLDLYPMIARVARRARQEGVQIQPGNNIGYYGPYERLLRGRG SDSEWAFWQGCAAGLSTLGIEADGAIKGCPSLPTSAYTGGNIREHSLREIVEESEQLRFNLGAGTSQG TAHLWGFCQTCEFSELCRGGCTWTAHVFFNRRGNNPYCHHRALFQAEQGIRERVVPKVEAQGLPFD NGEFELIEEPIDAPLPENDPLHFTSDLVQWSASWQEESESIGAVVD
His_6-SUMO-PcpY	MGSHHHHHHHSSGLVPRGSASHINLKVKGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLF DGRRLRAEQTPDELEMEDGDEIDAMLHQTGGHMVENIDNEREKSANEIEPESLLLPRQAWQSQIAYLK AILKAKQALDRIEKRYLR
PcpY	MVENIDNEREKSANEIEPESLLLPRQAWQSQIAYLKAILKAKQALDRIEKRYLR

His_6-SUMO-PcpXYfusion	MGSHHHHHHHSSGLVPRGSASHINLKVKGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLF DGRRLRAEQTPDELEMEDGDEIDAMLHQTGGHMTYRRTSYAVWEITLKCNLACSHCGSRAGHTRAK ELSTQEALDLVRQMADVGIIEVTLIGGEAFLRPDWLQIAEAITKAGMLCSMTTGGYGISLETARKMKAA GIASVSVSIDGLEETHDRLRGRKGSWQAAFKTMSHLREVGIFFGCNTQINRLSAPEFPLIYERIRDAGA RAWQIQLTVPMGRAADNANILLQPYELLDLYPMIARVARRARQEGVQIQPGNNIGYYGPYERLLRGRG SDSEWAFWQGCAAGLSTLGIEADGAIKGCPSLPTSAYTGGNIREHSLREIVEESEQLRFNLGAGTSQG TAHLWGFCQTCEFSELCRGGCTWTAHVFFNRRGNNPYCHHRALFQAEQGIRERVVPKVEAQGLPFD NGEFELIEEPIDAPLPENDPLHFTSDLVQWSASWQEESESIGAVVDMVENIDNEREKSANEIEPESLLL PRQAWQSQIAYLKAILKAKQALDRIEKRYLR
PlpX	MTKKYRRVSYAVWEITLKCNLACSHCGSRAGQARTKELSTEEAFNLVRQLADVGIKEVTLIGGEAFMR SDWLEIAKAVTEAGMICGMTTGGFGVSLETARKMKEAGIKTVSVSIDGGIPETHDRQRGKKGAWHSAF RTMSHLKEVGIYFGCNTQINRLSASEFPIIYERIRDAGARAWQIQLTVPMGNAADNADMLLQPYELLDIY PMLARVAKRAKQEGVRIQAGNNIGYYGPYERLLRGSDEWTFWQGCGAGLNTLGIEADGKIKGCPSLP TAAYTGGNIRDRPLREIVEQTEELKFNLKAGTEQGTDHMWGFCKTCEFAELCRGGCSWTAHVFFDRR GNNPYCHHRALKQAQKDIRERFYLKVKAKGNPFDNGEFVIIEEPFNAPLPENDLLHFNSDHIQWPENW QNSESAYALAK
PlpY	MNSNQIPNKVATAAQKSDDSSSVLPRQGWQDKQAFIKALIKAKQSLEIAEISNFLT
$PlpXY_{fusion}$	MTKKYRRVSYAVWEITLKCNLACSHCGSRAGQARTKELSTEEAFNLVRQLADVGIKEVTLIGGEAFMR SDWLEIAKAVTEAGMICGMTTGGFGVSLETARKMKEAGIKTVSVSIDGGIPETHDRQRGKKGAWHSAF RTMSHLKEVGIYFGCNTQINRLSASEFPIIYERIRDAGARAWQIQLTVPMGNAADNADMLLQPYELLDIY PMLARVAKRAKQEGVRIQAGNNIGYYGPYERLLRGSDEWTFWQGCGAGLNTLGIEADGKIKGCPSLP TAAYTGGNIRDRPLREIVEQTEELKFNLKAGTEQGTDHMWGFCKTCEFAELCRGGCSWTAHVFFDRR GNNPYCHHRALKQAQKDIRERFYLKVKAKGNPFDNGEFVIIEEPFNAPLPENDLLHFNSDHIQWPENW QNSESAYALAK*MNSNQIPNKVATAAQKSDDSSSVLPRQGWQDKQAFIKALIKAKQSLEIAEISNFLT*
His_6-RhaA	MGSSHHHHHHSQDPMKNVKLDTNHVVEAVELLNKVEGGINATGQRIDSSVFTHCDFFVCGVALYGSV IDPHRFDMLP
RhaX	MTSLANSGIKLRHRQTYAVWEITLKCNLACSHCGSRAGDSRVNELSTSEALDLVQQMAELGIEDVSLIG GEAFLRPDWLIIAAEITRLGMNANMTTGGYGISRGTAKRMKEAGISNVSVSVDGLEATHDKLRGKLGA WQQCFKTIEHLRAVGINVGCNTQINKHSATELPMLYQQLVQHGVSAWQIQLTVPMGNAVEHNAMLLQ PYELLELYPVLAYLSKRGRKDKLMVQPGNNIGYFGPYERLLREPISRHRDFAFFRGCGAGINTIGIEAD GKVKGCPSLPSEQYTGGNIRERSLRDIYENSKELRFNDINKPEDVTAHMWGDCASCEYAKVCRAGCS WTAHVFFGRRGNNPYCHHRALKKAVLGKMERFYLKTPAAGQPFDHGVFELVEEQIKPFDPMDPAHFS IAQTQFPAEWLAEEPDLQKSLMLERSMLMLQYVESGIVKQADSPWFDPAKREAIKQGIAIAS
$RhaXA_{leader}$	MTSLANSGIKLRHRQTYAVWEITLKCNLACSHCGSRAGDSRVNELSTSEALDLVQQMAELGIEDVSLIG GEAFLRPDWLIIAAEITRLGMNANMTTGGYGISRGTAKRMKEAGISNVSVSVDGLEATHDKLRGKLGA WQQCFKTIEHLRAVGINVGCNTQINKHSATELPMLYQQLVQHGVSAWQIQLTVPMGNAVEHNAMLLQ PYELLELYPVLAYLSKRGRKDKLMVQPGNNIGYFGPYERLLREPISRHRDFAFFRGCGAGINTIGIEAD GKVKGCPSLPSEQYTGGNIRERSLRDIYENSKELRFNDINKPEDVTAHMWGDCASCEYAKVCRAGCS WTAHVFFGRRGNNPYCHHRALKKAVLGKMERFYLKTPAAGQPFDHGVFELVEEQIKPFDPMDPAHFS IAQTQFPAEWLAEEPDLQKSLMLERSMLMLQYVESGIVKQADSPWFDPAKREAIKQGIAIAS*MKNVKL DTNHVVEAVELLNKVE*
His_6-SUMO-Rha_{core}	MGSHHHHHHHSSGLVPRGSASHINLKVKGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLF DGRRLRAEQTPDELEMEDGDEIDAMLHQTGGHMASMTGGQGGINATGQRIDSSVFTHCDFFVCGVA LYGSVIDPHRFDMLP
His_6-mCherry209-Rha_{core}	VSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQ FMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPS DGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGGGINAT GQRIDSSVFTHCDFFVCGVALYGSVIDPHRFDMLPGGAYNVNIKLDITSHNEDYTIVEQYERAEGRHST GGMDELYKELKLRS
His_6-DHFR118-$RhaA_{core}$	MGSSHHHHHHSQDPENAMPWNLPADLAWVKRNTLNKPVIMGRHTWESIGRPLPGRKNIILSSQPGTD DRVTWVKSVDEAIAACGDVPEIMVIGGGRVYEQLLPKAQKLYLTHIDAEVEGGINATGQRIDSSVFTHC DFFVCGVALYGSVIDPHRFDMLPGDTHYPDYEPDDWERVFSEYHDADAQNSHSYCYEILERRGSRSH HHHHH
His_6-MBP-Cterm-$RhaA_{core}$	MGSSHHHHHHSSGLVPRGSHNKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKF PQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIY NKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDN AGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQ PSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATME

	NAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTNSSSNNNNNNNNNNLGIEGLYFQ SGSEFELGAPAGRQACGRIMLKSNRKGGINATGQRIDSSVFTHCDFFVCGVALYGSVIDPHRFDMLP
His_6-MBP154-$RhaA_{core}$	MGSSHHHHHHSSGLVPRGSHNKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKF PQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIY NKDLLPNPPKTWEEIPGGINATGQRIDSSVFTHCDFFVCGVALYGSVIDPHRFDMLPALDKELKAKGKS ALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAE AAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLEN YLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAA SGRQTVDEALKDAQTNSSSNNNNNNNNNNLGIEGLYFQSGSEFELGAPAGRQACGRIMLKSNRK
DHFR-Nterm-$RhaA_{core}$-His_6	MGGINATGQRIDSSVFTHCDFFVCGVALYGSVIDPHRFDMLPQDPENAMPWNLPADLAWVKRNTLNK PVIMGRHTWESIGRPLPGRKNIILSSQPGTDDRVTWVKSVDEAIAACGDVPEIMVIGGGRVYEQLLPKA QKLYLTHIDAEVEGDTHYPDYEPDDWERVFSEYHDADAQNSHSYCYEILERRGSRSHHHHHH
His_6-SUMO-Nterm-$RhaA_{core}$	MGSHHHHHHHSSGGGINATGQRIDSSVFTHCDFFVCGVALYGSVIDPHRFDMLPLVPRGSASHINLKV KGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLFDGRRLRAEQTPDELEMEDGDEIDAMLH QTGG
His_6-SUMO-Rha_{core}-N8	MGSHHHHHHHSSGLVPRGSASHINLKVKGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLF DGRRLRAEQTPDELEMEDGDEIDAMLHQTGGHGGINATGQRIDSSVFTHCDFFVCGVALYGSVIDPH RFDMLP
His_6-SUMO-Rha_{core}-N24	MGSHHHHHHHSSGLVPRGSASHINLKVKGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLF DGRRLRAEQTPDELEMEDGDEIDAMLHQTGGHHCDFFVCGVALYGSVIDPHRFDMLP
His_6-SUMO-Rha_{core}-N32	MGSHHHHHHHSSGLVPRGSASHINLKVKGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLF DGRRLRAEQTPDELEMEDGDEIDAMLHQTGGHVALYGSVIDPHRFDMLP
His_6-SUMO-Rha_{core}-N24C4	MGSHHHHHHHSSGLVPRGSASHINLKVKGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLF DGRRLRAEQTPDELEMEDGDEIDAMLHQTGGHHCDFFVCGVALYGSVIDPHRF
His_6-SUMO-Rha_{core}-N24C8	MGSHHHHHHHSSGLVPRGSASHINLKVKGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLF DGRRLRAEQTPDELEMEDGDEIDAMLHQTGGHHCDFFVCGVALYGSVID
His_6-SUMO-Rha_{core}-N24C10	MGSHHHHHHHSSGLVPRGSASHINLKVKGQDGNEVFFRIKRSTQLKKLMNAYCDRQSVDMTAIAFLF DGRRLRAEQTPDELEMEDGDEIDAMLHQTGGHHCDFFVCGVALYGSV

Table S4. Nucleotide sequences encoding for protein sequences used in this study.

Encoded Protein	**Nucleotide Sequence**
His_6-PlpA3	ATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATATGT CTATTGAAAGTGCAAAAGCTTTTTACCAAAGAATGACCGATGATGCATCCTTTCGCACACCATTTG AAGCAGAATTATCTAAAGAAGAACGCCAACAACTAATTAAAGACTCTGGCTATGATTTCACTGCCG AGGAATGGCAGCAAGCGATGACAGAAATTCAAGCTGCTAGGTCTAATGAGGAATTGAATGAAGAA GAACTTGAAGCGATCGCAGGTGGTGCTGTAGCAGCAATGTATGGCGTAGTTTTTCCTTGGGATAA TGAATTTCCTTGGCCTAGGTGGGGGGGATAA
His_6-PlpYA3-33	ATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCAACTCTAATCAAATACCAAATAAAGTA GCCACAGCAGCTCAAAAATCAGATGATTCCAGCTCGGTTTTACCTCGTCAGGGTTGGCAAGACAA GCAAGCTTTTATCAAAGCATTAATTAAAGCAAAACAAAGTTTAGAAATTGCTGAAATTAGCAATTTT CTGACATTATCTAAAGAAGAACGCCAACAACTAATTAAAGACTCTGGCTATGATTTCACTGCCGAG GAATGGCAGCAAGCGATGACAGAAATTCAAGCTGCTAGGTCTAATGAGGAATTGAATGAAGAAGA ACTTGAAGCGATCGATGGTCGTGCTGTAGCAGCAATGTATGGCGTAGTTTTTCCTTGGGATAATG AATTTCCTTGGCCTAGGTGGGGGGGATAA
His_6-PlpYA3-45	ATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCAACTCTAATCAAATACCAAATAAAGTA GCCACAGCAGCTCAAAAATCAGATGATTCCAGCTCGGTTTTACCTCGTCAGGGTTGGCAAGACAA GCAAGCTTTTATCAAAGCATTAATTAAAGCAAAACAAAGTTTAGAAATTGCTGAAATTAGCAATTTT CTGACATCTGGCTATGATTTCACTGCCGAGGAATGGCAGCAAGCGATGACAGAAATTCAAGCTGC TAGGTCTAATGAGGAATTGAATGAAGAAGAACTTGAAGCGATCGATGGTCGTGCTGTAGCAGCAA TGTATGGCGTAGTTTTTCCTTGGGATAATGAATTTCCTTGGCCTAGGTGGGGGGGATAA
His_6-PcpA	ATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCGAGAATCTCTACTTCCAGTCACATAT GTCCTCAAATATCTTAGAAAAAGTCAAAGAGTTTTTTGTCAGGCTAGTTAAAGATGACGCTTTCCAA TCTCAACTTCAAAATAATTCAATCGACGAAGTTAGAAACATCTTACAAGAAGCTGGCTATATTTTCT CAAAAGAAGAATTTGAGACAGCTACGATTGAGCTACTCGATTTAAAAGAACGAGACGAATTTCACG AACTGACAGAAGAAGAGTTAGTGACAGCCGTTGGTGGGGTGACTGGGGGTAGCGGGATCTACGG ACCCATTCAGGCAATGTACGGAGCAGTGGTAGGAGATCCCAAGCCCGGTAAGGATTGGGGTTGG

	CGCTTTCCAAGTCCGTTACCAAAGCCATCACCCATACCTTCTCCCTGGAAGCCGCCAGTTGACGT GCAGCCGATGTATGGGGTAGTTGTCTCAAACGATTCATAA
His_6-SUMO-PcpX	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTTTAGTTCCTCGTGGTTCAGCTAGCCA CATCAACCTGAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCC AGCTGAAGAAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTC CTGTTCGATGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCG ACGAGATTGATGCCATGCTGCATCAGACCGGTGGCCATATGACTTATCGCAGAACCAGTTATGCC GTTTGGGAAATTACCCTAAAGTGTAATTTAGCCTGTAGTCACTGCGGTTCGCGAGCGGGACATAC CAGGGCTAAGGAACTCTCGACACAAGAGGCTCTCGATCTCGTCCGGCAGATGGCGGACGTAGGG ATTATAGAGGTGACGTTGATTGGCGGCGAGGCATTTCTTCGTCCAGACTGGCTGCAAATTGCAGA GGCTATTACTAAGGCGGGGATGCTATGCAGTATGACGACTGGCGGCTATGGCATTTCGCTGGAG ACGGCGCGTAAAATGAAGGCAGCAGGCATCGCTTCGGTTTCGGTTTCCATTGATGGGCTCGAAG AAACCCACGATCGCCTGCGGGGAAGAAAAGGCTCCTGGCAAGCTGCTTTTAAGACTATGAGCCA CCTGCGAGAAGTCGGGATTTTCTTTGGCTGCAACACCCAAATCAACCGTCTTTCTGCGCCGGAAT TTCCCCTCATTTACGAACGCATTCGCGACGCTGGCGCTAGGGCTTGGCAAATTCAGCTAACCGTA CCGATGGGAAGGGCAGCAGACAATGCCAATATTCTGCTGCAACCTTACGAGTTACTAGATCTCTA CCCAATGATAGCCCGCGTAGCCCGTCGGGCACGGCAAGAAGGCGTTCAGATCCAGCCTGGAAAC AATATTGGTTATTATGGTCCTTACGAACGGCTCTTACGGGGACGAGGAAGCGATAGCGAATGGGC ATTTTGGCAGGGTTGCGCTGCCGGACTCTCAACCTTGGGAATCGAGGCAGACGGCGCAATTAAG GGGTGTCCTTCACTGCCAACTTCGGCTTACACCGGCGGAAACATTCGAGAGCATTCGCTGCGGG AGATCGTTGAAGAATCAGAGCAACTACGTTTCAATCTCGGCGCGGGAACGTCCCAGGGAACTGCT CATCTGTGGGGGTTCTGCCAAACCTGCGAGTTTTCAGAACTGTGTCGTGGGGGCTGCACTTGGA CTGCCCACGTTTTCTTCAACCGTCGAGGAAACAACCCTTACTGCCATCACCGGGCGCTCTTTCAA GCAGAGCAAGGCATTCGGGAGCGCGTCGTTCCTAAAGTAGAGGCGCAGGGACTACCTTTTGACA ATGGGGAATTCGAGCTAATTGAAGAGCCGATTGATGCTCCTTTACCAGAAAACGATCCCCTGCATT TTACATCCGATCTCGTCCAGTGGTCGGCAAGCTGGCAGGAAGAATCCGAGTCGATTGGTGCTGTA GTTGATTAA
His_6-SUMO-PcpY	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTTTAGTTCCTCGTGGTTCAGCTAGCCA CATCAACCTGAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCC AGCTGAAGAAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTC CTGTTCGATGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCG ACGAGATTGATGCCATGCTGCATCAGACCGGTGGCCATATGGTCGAAAATATAGACAACGAGCGA GAGAAATCGGCAAATGAAATCGAGCCAGAATCTCTCCTATTGCCCCGTCAAGCTTGGCAAAGTCA AATTGCCTATCTAAAAGCGATTTTGAAAGCCAAACAAGCTCTAGATCGAATAGAAAAAAGGTATTT GCGTTAA
PcpY	ATGGTCGAAAATATAGACAACGAGCGAGAGAAATCGGCAAATGAAATCGAGCCAGAATCTCTCCT ATTGCCCCGTCAAGCTTGGCAAAGTCAAATTGCCTATCTAAAAGCGATTTTGAAAGCCAAACAAGC TCTAGATCGAATAGAAAAAAGGTATTTGCGTTAA
His_6-SUMO-PcpXYfusion	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTTTAGTTCCTCGTGGTTCAGCTAGCCA CATCAACCTGAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCC AGCTGAAGAAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTC CTGTTCGATGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCG ACGAGATTGATGCCATGCTGCATCAGACCGGTGGCCATATGACTTATCGCAGAACCAGTTATGCC GTTTGGGAAATTACCCTAAAGTGTAATTTAGCCTGTAGTCACTGCGGTTCGCGAGCGGGACATAC CAGGGCTAAGGAACTCTCGACACAAGAGGCTCTCGATCTCGTCCGGCAGATGGCGGACGTAGGG ATTATAGAGGTGACGTTGATTGGCGGCGAGGCATTTCTTCGTCCAGACTGGCTGCAAATTGCAGA GGCTATTACTAAGGCGGGGATGCTATGCAGTATGACGACTGGCGGCTATGGCATTTCGCTGGAG ACGGCGCGTAAAATGAAGGCAGCAGGCATCGCTTCGGTTTCGGTTTCCATTGATGGGCTCGAAG AAACCCACGATCGCCTGCGGGGAAGAAAAGGCTCCTGGCAAGCTGCTTTTAAGACTATGAGCCA CCTGCGAGAAGTCGGGATTTTCTTTGGCTGCAACACCCAAATCAACCGTCTTTCTGCGCCGGAAT TTCCCCTCATTTACGAACGCATTCGCGACGCTGGCGCTAGGGCTTGGCAAATTCAGCTAACCGTA CCGATGGGAAGGGCAGCAGACAATGCCAATATTCTGCTGCAACCTTACGAGTTACTAGATCTCTA CCCAATGATAGCCCGCGTAGCCCGTCGGGCACGGCAAGAAGGCGTTCAGATCCAGCCTGGAAAC AATATTGGTTATTATGGTCCTTACGAACGGCTCTTACGGGGACGAGGAAGCGATAGCGAATGGGC ATTTTGGCAGGGTTGCGCTGCCGGACTCTCAACCTTGGGAATCGAGGCAGACGGCGCAATTAAG GGGTGTCCTTCACTGCCAACTTCGGCTTACACCGGCGGAAACATTCGAGAGCATTCGCTGCGGG AGATCGTTGAAGAATCAGAGCAACTACGTTTCAATCTCGGCGCGGGAACGTCCCAGGGAACTGCT CATCTGTGGGGGTTCTGCCAAACCTGCGAGTTTTCAGAACTGTGTCGTGGGGGCTGCACTTGGA CTGCCCACGTTTTCTTCAACCGTCGAGGAAACAACCCTTACTGCCATCACCGGGCGCTCTTTCAA GCAGAGCAAGGCATTCGGGAGCGCGTCGTTCCTAAAGTAGAGGCGCAGGGACTACCTTTTGACA

	ATGGGGAATTCGAGCTAATTGAAGAGCCGATTGATGCTCCTTTACCAGAAAACGATCCCCTGCATT TTACATCCGATCTCGTCCAGTGGTCGGCAAGCTGGCAGGAAGAATCCGAGTCGATTGGTGCTGTA GTTGATTAAATGGTCGAAAATATAGACAACGAGCGAGAGAAATCGGCAAATGAAATCGAGCCAGA ATCTCTCCTATTGCCCCGTCAAGCTTGGCAAAGTCAAATTGCCTATCTAAAAGCGATTTTGAAAGC CAAACAAGCTCTAGATCGAATAGAAAAAAGGTATTTGCGTTAA
PlpX	ATGACTAAAAAATACAGACGAGTTAGTTATGCAGTTTGGGAAATTACCTTGAAATGCAATCTAGCTT GTAGTCACTGTGGTTCGAGAGCAGGGCAGGCAAGAACCAAGGAACTATCTACAGAAGAAGCTTTT AATCTGGTTCGGCAACTAGCCGATGTAGGAATCAAAGAGGTTACTCTAATCGGTGGCGAAGCCTT TATGCGCTCTGATTGGCTAGAAATTGCCAAGGCTGTTACTGAGGCAGGGATGATCTGCGGTATGA CTACAGGTGGATTTGGTGTCAGTTTGGAAACTGCCAGAAAAATGAAAGAAGCTGGAATTAAAACA GTTTCTGTATCTATCGATGGTGGCATACCAGAAACCCACGATCGCCAGCGAGGGAAAAAAGGTGC TTGGCATTCTGCTTTTAGAACCATGAGCCATCTAAAAGAAGTCGGCATCTATTTTGGCTGCAATAC CCAGATAAACCGTTTATCTGCCTCTGAATTCCCAATAATTTACGAACGAATAAGGGACGCTGGAGC AAGAGCTTGGCAGATTCAATTAACTGTACCTATGGGTAATGCGGCAGATAATGCAGACATGTTATT GCAACCATACGAACTATTAGATATTTATCCCATGTTAGCTCGTGTTGCTAAACGAGCTAAACAGGA AGGTGTTCGCATACAGGCGGGAAATAATATTGGCTATTATGGCCCTTATGAAAGACTGCTGCGTG GTAGTGATGAATGGACATTTTGGCAGGGTTGCGGAGCGGGTTTAAATACCTTGGGTATCGAAGCT GATGGCAAAATTAAAGGTTGTCCTTCTTTACCTACGGCTGCTTATACGGGCGGTAATATCCGCGAT CGCCCTTTAAGAGAAATAGTCGAACAGACTGAAGAGCTTAAATTTAATCTGAAGGCTGGGACTGAA CAGGGCACAGACCACATGTGGGGATTTTGTAAAACCTGTGAATTTGCTGAACTCTGTCGAGGTGG TTGTTCTTGGACGGCTCATGTCTTCTTTGATCGCCGTGGGAATAATCCCTACTGCCATCATCGTGC TTTGAAACAGGCACAAAAAGACATCAGAGAAAGATTCTATTTAAAAGTAAAAGCAAAAGGGAATCC TTTTGATAATGGGGAATTTGTCATTATAGAAGAACCTTTCAACGCACCTTTGCCAGAGAACGATTT GCTTCATTTTAATAGCGATCACATTCAGTGGCCAGAAAACTGGCAAAATTCTGAATCTGCTTACGC TTTAGCAAAGTAA
PlpY	ATGAACTCTAATCAAATACCAAATAAAGTAGCCACAGCAGCTCAAAAATCAGATGATTCCAGCTCG GTTTTACCTCGTCAGGGTTGGCAAGACAAGCAAGCTTTTATCAAAGCATTAATTAAAGCAAAACAA AGTTTAGAAATTGCTGAAATTAGCAATTTTCTGACATAA
$PlpXY_{fusion}$	ATGACTAAAAAATACAGACGAGTTAGTTATGCAGTTTGGGAAATTACCTTGAAATGCAATCTAGCTT GTAGTCACTGTGGTTCGAGAGCAGGGCAGGCAAGAACCAAGGAACTATCTACAGAAGAAGCTTTT AATCTGGTTCGGCAACTAGCCGATGTAGGAATCAAAGAGGTTACTCTAATCGGTGGCGAAGCCTT TATGCGCTCTGATTGGCTAGAAATTGCCAAGGCTGTTACTGAGGCAGGGATGATCTGCGGTATGA CTACAGGTGGATTTGGTGTCAGTTTGGAAACTGCCAGAAAAATGAAAGAAGCTGGAATTAAAACA GTTTCTGTATCTATCGATGGTGGCATACCAGAAACCCACGATCGCCAGCGAGGGAAAAAAGGTGC TTGGCATTCTGCTTTTAGAACCATGAGCCATCTAAAAGAAGTCGGCATCTATTTTGGCTGCAATAC CCAGATAAACCGTTTATCTGCCTCTGAATTCCCAATAATTTACGAACGAATAAGGGACGCTGGAGC AAGAGCTTGGCAGATTCAATTAACTGTACCTATGGGTAATGCGGCAGATAATGCAGACATGTTATT GCAACCATACGAACTATTAGATATTTATCCCATGTTAGCTCGTGTTGCTAAACGAGCTAAACAGGA AGGTGTTCGCATACAGGCGGGAAATAATATTGGCTATTATGGCCCTTATGAAAGACTGCTGCGTG GTAGTGATGAATGGACATTTTGGCAGGGTTGCGGAGCGGGTTTAAATACCTTGGGTATCGAAGCT GATGGCAAAATTAAAGGTTGTCCTTCTTTACCTACGGCTGCTTATACGGGCGGTAATATCCGCGAT CGCCCTTTAAGAGAAATAGTCGAACAGACTGAAGAGCTTAAATTTAATCTGAAGGCTGGGACTGAA CAGGGCACAGACCACATGTGGGGATTTTGTAAAACCTGTGAATTTGCTGAACTCTGTCGAGGTGG TTGTTCTTGGACGGCTCATGTCTTCTTTGATCGCCGTGGGAATAATCCCTACTGCCATCATCGTGC TTTGAAACAGGCACAAAAAGACATCAGAGAAAGATTCTATTTAAAAGTAAAAGCAAAAGGGAATCC TTTTGATAATGGGGAATTTGTCATTATAGAAGAACCTTTCAACGCACCTTTGCCAGAGAACGATTT GCTTCATTTTAATAGCGATCACATTCAGTGGCCAGAAAACTGGCAAAATTCTGAATCTGCTTACGC TTTAGCAAAGATGAACTCTAATCAAATACCAAATAAAGTAGCCACAGCAGCTCAAAAATCAGATGA TTCCAGCTCGGTTTTACCTCGTCAGGGTTGGCAAGACAAGCAAGCTTTTATCAAAGCATTAATTAA AGCAAAACAAAGTTTAGAAATTGCTGAAATTAGCAATTTTCTGACATAATAA
His_6-RhaA	ATGGGCAGCAGCCATCACCATCATCACCACAGCCAGGATCCGATGAAAAACGTAAAACTTGATAC AAACCATGTTGTTGAGGCTGTAGAGCTACTAAACAAAGTTGAAGGCGGGATTAACGCTACCGGTC AGCGTATCGACTCCTCGGTTTTTACCCACTGTGACTTTTTCGTTTGTGGTGTAGCGCTGTACGGCA GCGTAATTGATCCTCATCGTTTCGATATGTTGCCTTAA
RhaX	ATGACATCGCTTGCAAACTCCGGCATTAAACTCCGACACCGCCAAACCTATGCTGTATGGGAAAT CACCCTAAAATGCAATCTGGCTTGCAGCCATTGTGGTTCGAGGGCAGGCGATTCACGTGTAAACG AGCTGAGTACCAGCGAGGCGCTGGATCTGGTGCAGCAAATGGCTGAGCTTGGTATCGAGGATGT TTCTCTGATCGGCGGTGAGGCATTTTTGCGACCAGACTGGTTAATTATTGCTGCAGAAATTACCCG TCTTGGCATGAATGCCAACATGACGACCGGGGGCTACGGGATATCACGCGGTACGGCAAAACGG ATGAAAGAAGCGGGTATCAGTAACGTTTCGGTATCGGTAGATGGCCTTGAGGCTACGCACGATAA

	GCTACGTGGTAAGCTGGGTGCCTGGCAGCAATGTTTTAAGACGATAGAACATTTACGCGCCGTGG GGATCAATGTTGGCTGCAATACGCAGATCAACAAGCACTCCGCTACCGAGTTGCCCATGTTGTAT CAGCAATTAGTCCAGCATGGCGTGTCGGCCTGGCAGATACAGCTTACCGTACCAATGGGCAATG CGGTAGAGCATAACGCTATGTTGCTGCAGCCTTACGAGCTACTGGAGTTATATCCAGTGCTGGCG TATCTGTCTAAACGCGGCCGTAAGGATAAACTTATGGTGCAGCCGGGTAATAACATCGGTTACTTT GGTCCGTACGAGCGCCTGTTGCGGGAGCCGATTTCCCGTCACCGCGACTTTGCGTTTTTCCGCG GCTGTGGTGCGGGCATAAATACCATAGGCATAGAAGCGGACGGCAAAGTAAAAGGTTGCCCTTCT TTACCTTCCGAGCAATACACTGGCGGTAATATCCGTGAACGTAGCTTGCGCGATATTTATGAAAAC AGTAAAGAGCTACGATTTAACGATATCAATAAGCCTGAAGATGTCACGGCCCATATGTGGGGCGA TTGCGCAAGTTGTGAATACGCCAAGGTCTGCCGCGCTGGCTGCAGTTGGACAGCTCATGTCTTTT TTGGTCGGCGCGGGAATAACCCTTATTGCCATCACCGGGCATTGAAGAAAGCCGTGCTGGGCAA GATGGAGCGTTTTTACCTGAAAACGCCTGCTGCCGGCCAGCCATTTGACCATGGTGTGTTTGAAC TGGTTGAGGAGCAGATTAAGCCATTTGACCCGATGGACCCGGCACACTTTAGTATTGCCCAAACA CAGTTTCCAGCTGAGTGGTTGGCGGAAGAACCTGATCTGCAGAAAAGCCTTATGCTGGAGAGAAG TATGCTGATGCTGCAGTACGTTGAAAGCGGTATAGTCAAACAGGCCGACTCGCCATGGTTTGATC CCGCTAAGCGTGAGGCGATAAAACAGGGTATCGCAATAGCCAGCTAG
$RhaXA_{leader}$	ATGACATCGCTTGCAAACTCCGGCATTAAACTCCGACACCGCCAAACCTATGCTGTATGGGAAAT CACCCTAAAATGCAATCTGGCTTGCAGCCATTGTGGTTCGAGGGCAGGCGATTCACGTGTAAACG AGCTGAGTACCAGCGAGGCGCTGGATCTGGTGCAGCAAATGGCTGAGCTTGGTATCGAGGATGT TTCTCTGATCGGCGGTGAGGCATTTTTGCGACCAGACTGGTTAATTATTGCTGCAGAAATTACCCG TCTTGGCATGAATGCCAACATGACGACCGGGGGCTACGGGATATCACGCGGTACGGCAAAACGG ATGAAAGAAGCGGGTATCAGTAACGTTTCGGTATCGGTAGATGGCCTTGAGGCTACGCACGATAA GCTACGTGGTAAGCTGGGTGCCTGGCAGCAATGTTTTAAGACGATAGAACATTTACGCGCCGTGG GGATCAATGTTGGCTGCAATACGCAGATCAACAAGCACTCCGCTACCGAGTTGCCCATGTTGTAT CAGCAATTAGTCCAGCATGGCGTGTCGGCCTGGCAGATACAGCTTACCGTACCAATGGGCAATG CGGTAGAGCATAACGCTATGTTGCTGCAGCCTTACGAGCTACTGGAGTTATATCCAGTGCTGGCG TATCTGTCTAAACGCGGCCGTAAGGATAAACTTATGGTGCAGCCGGGTAATAACATCGGTTACTTT GGTCCGTACGAGCGCCTGTTGCGGGAGCCGATTTCCCGTCACCGCGACTTTGCGTTTTTCCGCG GCTGTGGTGCGGGCATAAATACCATAGGCATAGAAGCGGACGGCAAAGTAAAAGGTTGCCCTTCT TTACCTTCCGAGCAATACACTGGCGGTAATATCCGTGAACGTAGCTTGCGCGATATTTATGAAAAC AGTAAAGAGCTACGATTTAACGATATCAATAAGCCTGAAGATGTCACGGCCCATATGTGGGGCGA TTGCGCAAGTTGTGAATACGCCAAGGTCTGCCGCGCTGGCTGCAGTTGGACAGCTCATGTCTTTT TTGGTCGGCGCGGGAATAACCCTTATTGCCATCACCGGGCATTGAAGAAAGCCGTGCTGGGCAA GATGGAGCGTTTTTACCTGAAAACGCCTGCTGCCGGCCAGCCATTTGACCATGGTGTGTTTGAAC TGGTTGAGGAGCAGATTAAGCCATTTGACCCGATGGACCCGGCACACTTTAGTATTGCCCAAACA CAGTTTCCAGCTGAGTGGTTGGCGGAAGAACCTGATCTGCAGAAAAGCCTTATGCTGGAGAGAAG TATGCTGATGCTGCAGTACGTTGAAAGCGGTATAGTCAAACAGGCCGACTCGCCATGGTTTGATC CCGCTAAGCGTGAGGCGATAAAACAGGGTATCGCAATAGCCAGCATGAAAAACGTAAAACTTGAT ACAAACCATGTTGTTGAGGCTGTAGAGCTACTAAACAAAGTTGAATAG
His_6-SUMO-Rha_{core}	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTTTAGTTCCTCGTGGTTCAGCTAGCCA CATCAACCTGAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCC AGCTGAAGAAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTC CTGTTCGATGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCG ACGAGATTGATGCCATGCTGCATCAGACCGGTGGCCATATGGCTAGCATGACTGGTGGACAGGG CGGGATTAACGCTACCGGTCAGCGTATCGACTCCTCGGTTTTTACCCACTGTGACTTTTTCGTTTG TGGTGTAGCGCTGTACGGCAGCGTAATTGATCCTCATCGTTTCGATATGTTGCCTTGACAAAT
His_6-mCherry109-Rha_{core}	ATGGGCAGCAGCCATCACCATCATCACCACAGCCAGGATCCGGTGAGCAAGGGCGAGGAGGATA ACATGGCCATCATCAAGGAGTTCATGCGCTTCAAGGTGCACATGGAGGGCTCCGTGAACGGCCA CGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGCCAAGCT GAAGGTGACCAAGGGTGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCTCAGTTCATGTAC GGCTCCAAGGCCTACGTGAAGCACCCCGCCGACATCCCCGACTACTTGAAGCTGTCCTTCCCCG AGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAGG ACTCCTCCCTGCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGCACCAACTTCCCCTC CGACGGCCCCGTAATGCAGAAGAAGACCATGGGCTGGGAGGCCTCCTCCGAGCGGATGTACCC CGAGGACGGCGCCCTGAAGGGCGAGATCAAGCAGAGGCTGAAGCTGAAGGACGGCGGCCACTA CGACGCTGAGGTCAAGACCACCTACAAGGCCAAGAAGCCCGTGCAGCTGCCCGGCGGCGGCAT TAACGCTACCGGTCAGCGTATCGACTCCTCGGTTTTTACCCACTGTGACTTTTTCGTTTGTGGTGT AGCGCTGTACGGCAGCGTAATTGATCCTCATCGTTTCGATATGTTGCCTGGGGGAGCCTACAACG TCAACATCAAGTTGGACATCACCTCCCACAACGAGGACTACACCATCGTGGAACAGTACGAACGC

	GCCGAGGGCCGCCACTCCACCGGCGGCATGGACGAGCTGTACAAGGAATTGAAGCTTAGATCTT GA
His_6-DHFR118- $RhaA_{core}$	ATGGGCAGCAGCCATCACCATCATCACCACAGCCAGGATCCGGAGAATGCCATGCCATGGAATC TGCCTGCTGATCTTGCGTGGGTGAAACGCAATACCCTGAACAAACCGGTTATCATGGGGCGCCAT ACCTGGGAAAGCATTGGCCGTCCTTTGCCAGGTCGGAAGAACATCATCCTGAGCAGTCAACCGG GCACAGATGACCGTGTCACGTGGGTCAAATCCGTGGATGAAGCGATTGCAGCATGTGGCGATGT TCCGGAGATCATGGTGATTGGCGGAGGTCGCGTATACGAACAGCTGTTACCGAAAGCGCAGAAA CTCTATCTGACTCACATTGACGCCGAAGTAGAAGGCGGGATTAACGCTACCGGTCAGCGTATCGA CTCCTCGGTTTTTACCCACTGTGACTTTTTCGTTTGTGGTGTAGCGCTGTACGGCAGCGTAATTGA TCCTCATCGTTTCGATATGTTGCCTGGGGATACCCATTATCCGGACTATGAACCCGACGATTGGG AACGCGTGTTTAGCGAGTATCACGATGCTGATGCCCAGAACTCGCATTCGTACTGCTACGAGATT CTGGAACGTCGTGGTTCACGCTCTCACCATCATCACCACCATTAA
His_6-MBP-Cterm- $RhaA_{core}$	ATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATAATA AAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAA GTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGA AGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACC GCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGAC AAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGC TGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAG AGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCA AGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACG GCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCT GGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTT TAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGC AAAGTGAATTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGG CGTGCTGAGCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAA AACTATCTGCTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGC GCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACTATGGAAAACGCCC AGAAAGGTGAAATCATGCCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCG GTGATCAACGCCGCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATT CGAGCTCGAACAACAACAACAATAACAATAACAACAACCTCGGGATCGAGGGACTGTACTTCCAG TCAGGATCCGAATTCGAGCTCGGCGCGCCTGCAGGTCGACAAGCTTGCGGCCGCATAATGCTTA AGTCGAACAGAAAGGGCGGGATTAACGCTACCGGTCAGCGTATCGACTCCTCGGTTTTTACCCAC TGTGACTTTTTCGTTTGTGGTGTAGCGCTGTACGGCAGCGTAATTGATCCTCATCGTTTCGATATG TTGCCTTAA
His_6-MBP154- $RhaA_{core}$	ATGGGCAGCAGCCATCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATAATA AAATCGAAGAAGGTAAACTGGTAATCTGGATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAA GTCGGTAAGAAATTCGAGAAAGATACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGA AGAGAAATTCCCACAGGTTGCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACC GCTTTGGTGGCTACGCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGAC AAGCTGTATCCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGC TGTTGAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAG AGATCCCGGGCGGGATTAACGCTACCGGTCAGCGTATCGACTCCTCGGTTTTTACCCACTGTGAC TTTTTCGTTTGTGGTGTAGCGCTGTACGGCAGCGTAATTGATCCTCATCGTTTCGATATGTTGCCT GCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAACCTGCAAGAACCGT ACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAAACGGCAAGTAC GACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCGGGTCTGACCTTCCTGGTTGACC TGATTAAAAACAAACACATGAATGCAGACACCGATTACTCCATCGCAGAAGCTGCCTTTAATAAAG GCGAAACAGCGATGACCATCAACGGCCCGTGGGCATGGTCCAACATCGACACCAGCAAAGTGAA TTATGGTGTAACGGTACTGCCGACCTTCAAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGA GCGCAGGTATTAACGCCGCCAGTCCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTG CTGACTGATGAAGGTCTGGAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGT CTTACGAGGAAGAGTTGGCGAAAGATCCACGTATTGCCGCCACTATGGAAAACGCCCAGAAAGGT GAAATCATGCCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAA CGCCGCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG AACAACAACAACAATAACAATAACAACAACCTCGGGATCGAGGGACTGTACTTCCAGTCAGGATC CGAATTCGAGCTCGGCGCGCCTGCAGGTCGACAAGCTTGCGGCCGCATAATGCTTAAGTCGAAC AGAAAGTAA
DHFR-Nterm- $RhaA_{core}$-His_6	ATGGGCGGGATTAACGCTACCGGTCAGCGTATCGACTCCTCGGTTTTTACCCACTGTGACTTTTT CGTTTGTGGTGTAGCGCTGTACGGCAGCGTAATTGATCCTCATCGTTTCGATATGTTGCCTCAGG

	ATCCGGAGAATGCCATGCCATGGAATCTGCCTGCTGATCTTGCGTGGGTGAAACGCAATACCCTG AACAAACCGGTTATCATGGGGCGCCATACCTGGGAAAGCATTGGCCGTCCTTTGCCAGGTCGGA AGAACATCATCCTGAGCAGTCAACCGGGCACAGATGACCGTGTCACGTGGGTCAAATCCGTGGA TGAAGCGATTGCAGCATGTGGCGATGTTCCGGAGATCATGGTGATTGGCGGAGGTCGCGTATAC GAACAGCTGTTACCGAAAGCGCAGAAACTCTATCTGACTCACATTGACGCCGAAGTAGAAGGGGA TACCCATTATCCGGACTATGAACCCGACGATTGGGAACGCGTGTTTAGCGAGTATCACGATGCTG ATGCCCAGAACTCGCATTCGTACTGCTACGAGATTCTGGAACGTCGTGGTTCACGCTCTCACCAT CATCACCACCATTAA
His_6-SUMO- Nterm-$RhaA_{core}$	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTGGCGGGATTAACGCTACCGGTCAGC GTATCGACTCCTCGGTTTTTACCCACTGTGACTTTTTCGTTTGTGGTGTAGCGCTGTACGGCAGCG TAATTGATCCTCATCGTTTCGATATGTTGCCTTTAGTTCCTCGTGGTTCAGCTAGCCACATCAACCT GAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCCAGCTGAAG AAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTCCTGTTCGA TGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCGACGAGATT GATGCCATGCTGCATCAGACCGGTGGC
His_6-SUMO- Rha_{core}-N8	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTTTAGTTCCTCGTGGTTCAGCTAGCCA CATCAACCTGAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCC AGCTGAAGAAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTC CTGTTCGATGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCG ACGAGATTGATGCCATGCTGCATCAGACCGGTGGCCATGGCGGGATTAACGCTACCGGTCAGCG TATCGACTCCTCGGTTTTTACCCACTGTGACTTTTTCGTTTGTGGTGTAGCGCTGTACGGCAGCGT AATTGATCCTCATCGTTTCGATATGTTGCCT
His_6-SUMO- Rha_{core}-N24	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTTTAGTTCCTCGTGGTTCAGCTAGCCA CATCAACCTGAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCC AGCTGAAGAAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTC CTGTTCGATGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCG ACGAGATTGATGCCATGCTGCATCAGACCGGTGGCCATCACTGTGACTTTTTCGTTTGTGGTGTA GCGCTGTACGGCAGCGTAATTGATCCTCATCGTTTCGATATGTTGCCT
His_6-SUMO- Rha_{core}-N32	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTTTAGTTCCTCGTGGTTCAGCTAGCCA CATCAACCTGAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCC AGCTGAAGAAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTC CTGTTCGATGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCG ACGAGATTGATGCCATGCTGCATCAGACCGGTGGCCATGTAGCGCTGTACGGCAGCGTAATTGAT CCTCATCGTTTCGATATGTTGCCT
His_6-SUMO- Rha_{core}-N24C4	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTTTAGTTCCTCGTGGTTCAGCTAGCCA CATCAACCTGAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCC AGCTGAAGAAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTC CTGTTCGATGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCG ACGAGATTGATGCCATGCTGCATCAGACCGGTGGCCATCACTGTGACTTTTTCGTTTGTGGTGTA GCGCTGTACGGCAGCGTAATTGATCCTCATCGTTTC
His_6-SUMO- Rha_{core}-N24C8	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTTTAGTTCCTCGTGGTTCAGCTAGCCA CATCAACCTGAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCC AGCTGAAGAAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTC CTGTTCGATGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCG ACGAGATTGATGCCATGCTGCATCAGACCGGTGGCCATCACTGTGACTTTTTCGTTTGTGGTGTA GCGCTGTACGGCAGCGTAATTGAT
His_6-SUMO- Rha_{core}-N24C10	ATGGGTAGCCACCACCACCACCATCATCATAGCAGCGGTTTAGTTCCTCGTGGTTCAGCTAGCCA CATCAACCTGAAGGTGAAAGGCCAGGATGGCAACGAGGTGTTCTTCCGCATTAAACGCTCAACCC AGCTGAAGAAGCTGATGAACGCGTACTGCGATCGTCAGAGCGTGGATATGACCGCAATTGCGTTC CTGTTCGATGGTCGTCGTTTACGTGCAGAACAAACCCCGGACGAACTGGAAATGGAAGATGGCG ACGAGATTGATGCCATGCTGCATCAGACCGGTGGCCATCACTGTGACTTTTTCGTTTGTGGTGTA GCGCTGTACGGCAGCGTA

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