

Electron-deficient p-benzoyl-L-phenylalanine derivatives increase covalent chemical capture yields for protein-protein interactions

Cassandra M. Joiner^{1,2, ‡}, Meghan E. Breen^{2, ‡}, Anna K. Mapp^{1,2,3*}

1 Department of Chemistry, University of Michigan, 930 N. University, Ann Arbor, MI 48109

2 Life Sciences Institute, University of Michigan, 210 Washtenaw Ave., Ann Arbor, MI 48109

3 Program in Chemical Biology, University of Michigan, 210 Washtenaw Ave., Ann Arbor, MI 48109

Dedication We dedicate this work to Professor Ronald Raines on the occasion of his 60th birthday. The use of physical organic principles to dissect complex biological problems by Professor Raines serves an inspiration.

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ABSTRACT

The photoactivatable amino acid p-benzoyl-L-phenylalanine (pBpa) has been used for the covalent capture of protein-protein interactions (PPIs) *in vitro* and in living cells. However, this technique often suffers from poor photocrosslinking yields due to the low reactivity of the active species. Here we demonstrate that the incorporation of halogenated pBpa analogs into proteins leads to increased crosslinking yields for protein-protein interactions. The analogs can be incorporated into live yeast and upon irradiation capture endogenous PPIs. Halogenated pBpas will extend the scope of PPIs that can be captured and expand the toolbox for mapping PPIs in their native environment.

Keywords: protein-protein interactions, covalent chemical capture, photocrosslinking, p-benzoyl-L-phenylalanine

INTRODUCTION

Transient protein-protein interactions (PPIs) are critical for the precise flow of information in cellular processes, and misregulation of these interactions have been implicated in an array of human diseases.¹⁻⁴ There is great interest in methods to successfully detect and characterize these interactions. This is particularly true because the often short (ns-ps) lifetimes and moderate strengths (micromolar to millimolar dissociation constants) of these PPIs makes them difficult to study in their native environment using traditional biochemical techniques.⁵⁻⁹ With the advance of amber nonsense suppression, photo-activatable unnatural amino acids (UAAs) such as p-benzoyl-L-phenylalanine (pBpa) have been incorporated into proteins and used to capture transient, moderate affinity interactions for mechanistic purposes.¹⁰⁻²⁸ For example, our lab and others have utilized pBpa to interrogate the interactions involved in a variety of different cellular processes, such as those between transcriptional activators and their coactivator binding partners required for transcriptional initiation and those between chaperones and their substrates required for proper protein folding.²⁹⁻³⁴

pBpa is activated for crosslinking through exposure to UV light (350-365 nm). Upon irradiation, the benzophenone carbonyl undergoes an n to π^* transition to form a diradical species, and the triplet state can abstract hydrogen atoms from activated C-H bonds and recombine to form a covalent adduct [Fig. 1(A)]. If an activated C-H bond is not available, the triplet state will relax back to the ground state and can be reactivated.³⁵⁻³⁶ As a result, pBpa undergoes minimal side reactions with solvent, making it particularly useful for in *in vivo*

applications and for interaction surfaces where considerable water is present. However, the low molar absorptivity and quantum yield ($\epsilon_{\max} < 300 \text{ M}^{-1}\text{cm}^{-1}$; $\Phi = 0.05\text{-}0.4$) of pBpa often limits crosslinking yield. For example, significant starting pBpa-containing protein is often observed in experiments (Fig. S1).

Early mechanistic studies of benzophenone suggest that the incorporation of electron-withdrawing groups (EWGs) onto one or more of the aromatic rings decreases the energy barrier for the n to π^* transition and concomitantly increases the rate of hydrogen atom abstraction.³⁵⁻³⁹ Accordingly, we hypothesized that pBpa analogs substituted with electron-withdrawing groups would increase crosslinking yields [Fig. 1(B)]. Here, we demonstrate that halogenated pBpa analogs can be incorporated into live yeast cells using the bioorthogonal *Escherichia coli* tyrosyl tRNA/tRNA synthetase ($\text{tRNA}^{\text{TYR}}_{\text{CUA}}/\text{TyrRS}$) system and can capture *in vivo* transcriptional activator-coactivator PPIs. Additionally, the crosslinking yields for EWG-modified pBpa is substantively enhanced.

RESULTS AND DISCUSSION

The design of pBpa analogs containing EWGs was influenced by the crystal structure of the *E. coli* tyrosyl tRNA synthetase that would be used for incorporation.⁴⁰ Examination of the structure suggested that the active site would likely accommodate substituents at the para position of the distal ring, but that meta substituents would be more likely to experience steric

clashes (Fig. S2).⁴¹ Seven mono-substituted pBpa analogs containing halogen moieties (Cl, F, Br, and CF₃) at either the meta or para positions of the benzophenone ring were prepared via an air-tolerant carbonylative Suzuki-Miyaura coupling with mono-substituted boronic acids and 4-iodo-L-phenylalanine [Fig. 1(C)].^{42,43} The substituted pBpa analogs could be accessed with high purity and excellent yields over 5 steps (see Supporting Information). The incorporation of each analog was assessed in live yeast using the *E. coli* tRNA^{TYR}_{CUA}-TyrRS system.⁴⁰ We evaluated the incorporation of each analog into the prototypical Gal4 transcriptional activation domain (TAD) at position 849 which has been well characterized for UAA incorporation.³⁰ Western blotting indicated that all five of the para-substituted analogs were incorporated into LexA-Gal4 at position 849 at levels comparable to pBpa (Fig. 2). As suggested by the crystal structure, substitution at the meta position was not well tolerated and sharp declines in incorporation were observed with substituents larger than fluorine [Fig. 2(C), 2(D)]. Due to the failure of the synthetase to efficiently incorporate the 3-CF₃ Bpa analog, a 3-Br Bpa analog was not prepared for evaluation. These findings are in agreement with previous work by Mehl and others that has demonstrated bioorthogonal tRNA synthetases developed for specific UAAs can incorporate analogs of the cognate UAA without any further mutagenesis to the active site.^{42,44-48} Furthermore, this suggests the flexibility of the pBpa specific synthetase could enable the use of a variety of pBpa analogs, particularly those with substitution at the para position.

With the successful incorporation of the analogs, the modified pBpa analogs were assessed for their function as crosslinkers *in vivo* by examining the well-defined PPI between

Gal4 and its masking protein, Gal80. In yeast, Gal4 interacts with the Gal80 repressor through its TAD under normal glucose conditions.⁴⁹⁻⁵¹ Our lab has previously demonstrated that pBpa incorporated in either the Gal4 TAD or Gal80 can capture this endogenous interaction in live yeast. Because of the high incorporation yields, the 3-F and 4-F Bpa analogs were selected for comparison with pBpa in this model system. Live yeast expressing a LexA+Gal4 fusion construct with the amber mutation at position 849 and a Myc epitope-tagged Gal80 were grown in glucose in the presence of either pBpa or one of the fluorine analogs [Fig. 3(A)]. Live cells were irradiated with UV light to capture all Gal4 binding partners and were then lysed and immunoprecipitated for the LexA DNA binding domain (DBD) to isolate all LexA+Gal4 protein interactions. To fully characterize the crosslinking abilities of the UAAs, a duplex western blotting strategy was used such that both the binding profile of Gal4 (red) and its direct interaction with Gal80 (green) could be observed on the same western blot (Fig. 3). As seen in Figure 3(B), both fluorine-containing pBpa analogs captured Gal4's endogenous binding partners, including the Gal4-Gal80 interaction (yellow). It was not, however, possible to quantitatively determine a change in crosslinking yield in this system. This is likely due to the high affinity of the Gal4•Gal80 complex, which in turn results in high crosslinking yields with even unmodified pBpa.⁴⁹

To quantitate changes in crosslinking yield, we identified an interaction that was more modest in affinity and that also could be easily examined *in vitro*, thus removing additional variables *in vivo* such as changes in degradation rate that could influence any observations. The

moderate affinity interaction between the VP16 TAD and the Med25 subunit of the Mediator complex was used for this quantitation.⁵²⁻⁵³ It has previously been shown that a minimal peptide sequence (441-DFDLMLG-448) within the N-terminal TAD of VP16 is sufficient for interaction with the Med25 activator interaction domain (AcID) and transcriptional activation.⁵⁴⁻⁵⁶ We hypothesized that incorporating pBpa at position F442 would not abrogate binding with Med25 AcID and would enable us to observe changes in crosslinking efficiency for the pBpa analogs.

To determine the binding affinities, biotinylated UAA-containing VP16 peptides were incubated with Med25 coated plates. Following incubation with streptavidin-HRP and tetramethylbenzidine (TMB) substrate, the plates were read at 450 nm and it was found that the binding affinities of each pBpa analog containing VP16 peptides were minimally weakened (2-3 fold decrease in affinity) compared to the parent pBpa peptide (Fig. S3).^{52,57} These values are in line with the binding affinity of pBpa incorporated VP16 measured by fluorescence polarization (Fig. S4). To evaluate the crosslinking yield, Med25 was incubated with each UAA-containing VP16 peptide at 12.5% of its K_d value to normalize for occupancy. Following 10 minutes of UV irradiation with 365 nm light to covalently capture the interaction, the amount of crosslinked VP16 peptide was quantified by Western blot analysis. As seen in Figure 4, all pBpa analogs gave increased crosslinking yields, and the largest increases were observed with the 3-CF₃ (49-fold increase), 3-Cl (30-fold increase), and 4-CF₃ (23-fold increase) analogs. Similar trends in reactivity for the pBpa analogs were also observed with 1 minute irradiation time (Fig. S5). To

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further validate these results, crosslinking yields were also analyzed via ELISA. The biotinylated VP16 peptides were incubated with Med25 coated plates and irradiated with 365 nm light. Following washing and incubation with streptavidin-HRP, the covalently captured VP16 peptide was visualized by addition of TMB substrate [Fig. S6(A)]. Similar trends in reactivity were observed [Fig. S6(B), S6(C)], although the total increase in crosslinking yield is lower. This can be attributed to higher background to the format of the assay. Taken together, our results support the predicted effect of appending electron withdrawing groups onto the benzophenone framework to decrease the excitation energy gap for the n to π^* transition of the carbonyl oxygen's electrons, thereby increasing the reactivity of the benzophenone core and ultimately increasing the crosslinking yield of the molecule.

CONCLUSION

Although pBpa has been shown to have lower reactivity compared to the other common photocrosslinking groups such as the aryl azides and diazarines, its ability to be reactivated and minimal reactivity with solvent makes it a strong tool for the covalent capture of transient PPIs *in vivo*.¹⁴ Therefore, there was a need to increase the crosslinking yield of pBpa to improve the capture of PPIs and accelerate their characterization. Based on previous studies with benzophenones, we hypothesized that pBpa analogs substituted with electron withdrawing groups would increase crosslinking yields. We synthesized seven mono-substituted pBpa analogs (Fig. 1) and showed that upon irradiation of live yeast expressing UAA-containing LexA+Gal4

we capture Gal4's endogenous binding partners, including its masking protein Gal80. Furthermore, we demonstrated *in vitro* the halogenated pBpa analogs increased crosslinking yields for weak transient interactions. Taken together, we recommend use of the 4-CF₃ analog in cases where increased crosslinking yield is needed as it is incorporated at similar levels to pBpa and produced a 23-fold increase in crosslinking yield.

Through this study, we have expanded our toolbox of chemical probes for capturing challenging PPIs in their native environment. We anticipate that these halogenated pBpa analogs will have additional downstream applications post-crosslinking and isolation. For instance, bromine and chlorine atoms have enabled quantitative proteomic analysis without the need for expensive isotopic labeling systems, such as stable isotope labeling using amino acids in cell culture (SILAC) systems.⁵⁸⁻⁵⁹ Upon MS analysis, the protein targets can be quantified between samples using the specific chlorine or bromine isotopes to accurately identify interaction partners with minimal bias between experimental replicates. The unique isotopic signatures of these halogens could enable the identification of PPIs such as low abundance activator-coactivator interactions that may be drowned out by high abundance proteins and have eluded research efforts for years.⁶⁰ Utilizing the halogenated pBpa analogs developed will more readily facilitate the successful implementation of *in vivo* covalent capture for studying PPIs involved in a variety of biological processes.

MATERIALS AND METHODS

UAA incorporation and expression

LS41 yeast was transformed with pLexA+Gal4 849 TAG-1X Flag or pLexA+Gal4WT-1X Flag and pSNRtRNA-pBpaRS plasmids. Individual colonies were grown in 5 mL SC media containing 2% raffinose, but lacking histidine, tryptophan, and uracil for selection. The cultures were incubated at 30°C with 250 rpm agitation. Following incubation, these cultures were used to inoculate 5 mL cultures of SC media containing 2% raffinose and 2% galactose, with or without 1 mM pBpa/1 mM pBpa EWG analog (dissolved in 50 μ L 1 M NaOH), and 50 μ L 1 M HCl. The cultures were incubated at 30°C with agitation to an OD₆₆₀ of 1.0. Three ODs were isolated, washed with sterile water, and stored at -20°C. The samples were lysed in 10 μ L 4X NuPAGE LDS Sample loading buffer (Invitrogen), 10 μ L 1X lysis buffer (50 mM Tris-Acetate pH 7.9, 100 mM potassium acetate, 20% glycerol, 0.2% Tween20, 2 mM β -mercaptoethanol, and 2 mM magnesium acetate), and 10 μ L 1 M DTT by boiling at 95°C for 10 min. The samples were run on a 3-8% Tris-acetate SDS-PAGE gel and analyzed by Western blot with the anti-Flag (M2) antibody (Sigma Aldrich). Expression levels were quantified using ImageJ and relative levels of LexA-Gal4 protein for each experiment were expressed as follows ((experimental/WT LexA-Gal4)*100).

***In vivo* crosslinking analysis**

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A colony of LexA+Gal4 849 TAG-5X Flag:Gal80-6X Myc was grown in 5 mL SC media containing 2% glucose, but lacking histidine, tryptophan, leucine and uracil for selection. The cultures were incubated at 30°C with 250 rpm agitation. Following incubation, these cultures were used to inoculate 100 mL cultures of SC media containing 2% glucose, with 1 mM pBpa or 1 mM EWG pBpa analog (dissolved in 1 mL 1 M NaOH), and 100 mL 1 M HCl. The cultures were incubated at 30°C with agitation to an OD₆₆₀ of 1.0. For each culture, the cells were isolated by centrifugation and washed with the SC media lacking histidine, tryptophan, and uracil. The cell pellets were resuspended in 2 mL SC media containing 2% glucose and then transferred to small culture dishes and subjected to UV light at 365nm (Eurosolar 15W UV lamp) with cooling for 30 minutes. The cells were isolated by centrifugation and stored at -20°C until lysis. The control samples were washed with 1 mL SC media containing 2% glucose, isolated by centrifugation, and stored at -20°C until lysis.

For lysis, cells were resuspended in 600 µL lysis buffer (50 mM HEPES – KOH pH 7.5, 140 mM NaCl, 1 mM EDTA, 1% Triton X-100, 0.1% Na-Deoxycholate and 2X Complete Mini, EDTA Free Protease Inhibitor (Roche)) and lysed using glass beads by vortexing at 4°C. Subsequently, the lysate was pelleted and the supernatant incubated with anti-LexA antibody (sc-1725, Santa Cruz Biotechnologies) for 2 hours at 4°C for immunoprecipitation. The proteins bound to the antibody were isolated by incubation for 1 hour with 40 µL pre-washed Dynabeads® protein G magnetic beads (ThermoFisher) at 4°C. After immunoprecipitation, the

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beads were washed six times with 1 mL Wash Buffer (10 mM Tris-HCl pH 8.0, 250 mM LiCl, 0.5% NP-40, 0.1% Na-Deoxycholate, and 1 mM EDTA) and stored at -20°C until elution.

The samples were eluted from the beads by heating at 95°C for 10 minutes in 10 µL NuPAGE 4X LDS Sample Loading Buffer (Invitrogen), 10 µL water, and 10 µL 1M DTT. The samples were run on a 4-15% Mini-PROTEAN® TGX™ pre-cast SDS-PAGE gel (Bio-Rad). The gel was transferred to immobilin PDVF membrane (Millipore) and blocked for 1 hour at room temperature using SuperBlock™ (PBS) Blocking Buffer (ThermoFisher). The membrane was incubated with both mouse anti-Flag (M2) (Sigma Aldrich, F1804) and rabbit anti-cMyc (Sigma Aldrich, C3956) primary antibodies overnight at 4°C. The membrane was washed three times for 10 minutes each with PBS-T (10 mM Na₂HPO₄•7H₂O, 1.7 mM KH₂PO₄, 140 mM NaCl, 3 mM KCl, 0.05% Tween-20, pH 7.4), followed by incubation with anti-mouse 680nm (LI-COR, 926-68072) and anti-rabbit 800nm (LI-COR, 926-32211) secondary antibodies for 1 hour at room temperature. The membrane was washed three times for 10 minutes each with PBS-T, 5 minutes with PBS (10 mM Na₂HPO₄•7H₂O, 1.7 mM KH₂PO₄, 140 mM NaCl, 3 mM KCl, pH 7.4), and visualized using an Azure c600 western blot imager (Azure Biosystems).

***In vitro* crosslinking analysis**

Med25 AcID 6x-His was diluted in binding buffer (25 mM HEPES, 40 mM KCl, 8 mM MgCl₂, 100 mM NaCl, 0.01% Tween-20, pH 7.4) to 22 µM, and biotin labeled VP16 peptides

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were diluted to 25% of their K_d values in binding buffer. Equivalent volumes of Med25 AcID and peptide were incubated at room temperature for 30 minutes in a clear, flat bottom, polystyrene, 96-well plates (Fisherbrand). The solutions were irradiated with UV light at 365nm (Eurosolar 15W UV lamp) with cooling for 10 minutes. 15 μL of each sample was mixed with 5 μL NuPAGE 4X LDS Sample Loading Buffer (Invitrogen) and boiled for 5 minutes. The samples were run on a 4-20% Mini-PROTEAN® TGX™ pre-cast SDS-PAGE gel (Bio-Rad). The gel was transferred to PDVF membrane (Bio-Rad) and blocked for 1 hour at room temperature with SuperBlock™ (PBS) Blocking Buffer (ThermoFisher). The membrane was incubated with 1:100 diluted anti-HIS HRP conjugated antibody (Santa Cruz sc-8036 HRP) for 1 h at room temperature. The membrane was washed three times for 10 minutes each with PBS-T (10 mM Na₂HPO₄•7H₂O, 1.7 mM KH₂PO₄, 140 mM NaCl, 3 mM KCl, 0.05% Tween-20, pH 7.4), and visualized with SuperSignal West Femto ECL substrate (ThermoFisher) using an Azure c600 western blot imager (Azure Biosystems). The membrane was washed three times with PBS-T then stripped by incubating in Restore western blot stripping buffer (ThermoFisher) for 45 minutes at 37°C. The membrane was washed three times with PBS-T then incubated with 1:2000 diluted HRP-conjugated streptavidin (Abcam 7403) for 1 hour at room temperature. The membrane was washed three times for 10 minutes each with PBS-T and visualized with SuperSignal West Femto ECL substrate (ThermoFisher) using an Azure c600 western blot imager (Azure Biosystems). Crosslinking yields were quantified using ImageJ. The relative amount of Med25-VP16 crosslinked product for each sample was normalized based on the

protein levels of Med25 in the HIS-HRP blot. The fold changes were expressed as follows (Med25-VP16 F442UAA crosslinked product / Med25-VP16 F442Bpa crosslinked product)

Supplementary Material

Additional supplemental figures, detailed experimental methods, and compound characterization can be found in the Supporting Information.

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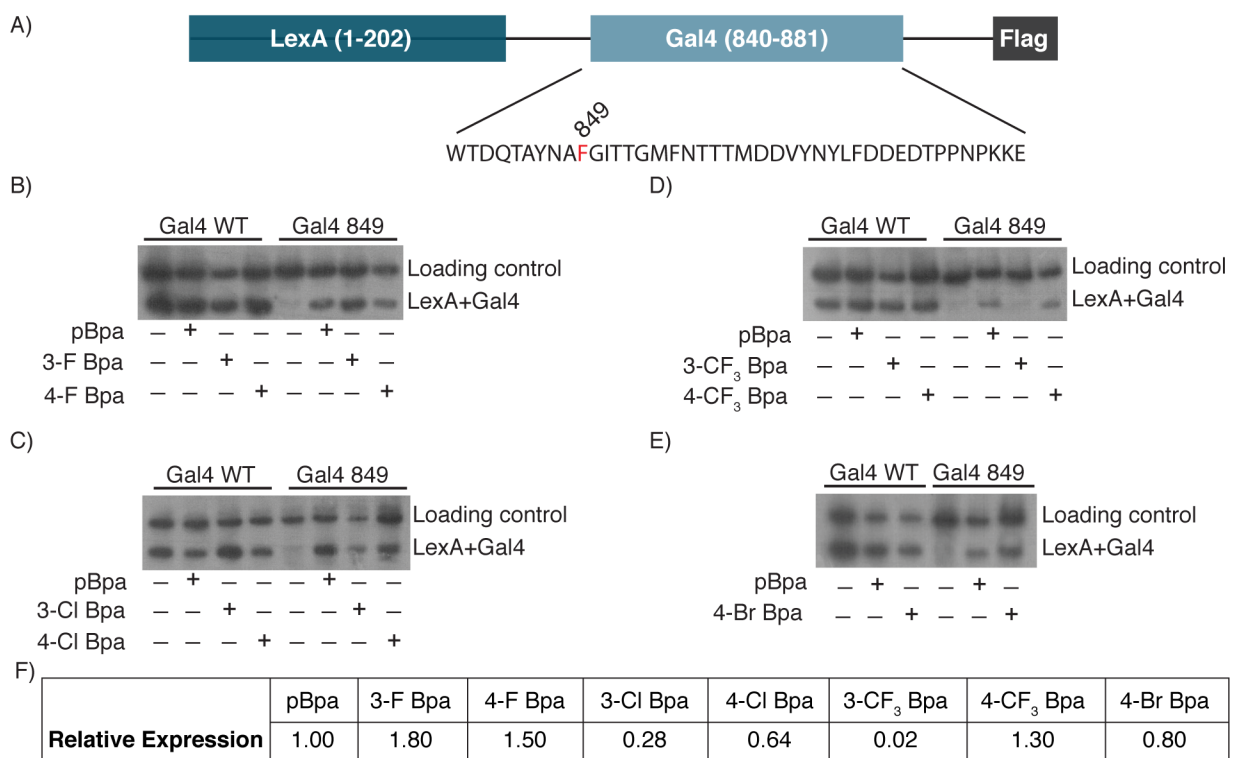
Figure Legends

Figure 1. (A) Covalent chemical capture mechanism of pBpa. Upon irradiation with 365 nm UV light, pBpa reversibly forms a diradical species. If an activated C-H bond is available, hydrogen atom abstraction followed by radical recombination will yield the crosslinked adduct. (B) A series of pBpa analogs with halogen substituents either meta or para to the carbonyl group were prepared. (C) Synthesis of halogenated pBpa analogs. Full experimental details and compound characterization can be found in the Supporting Information.

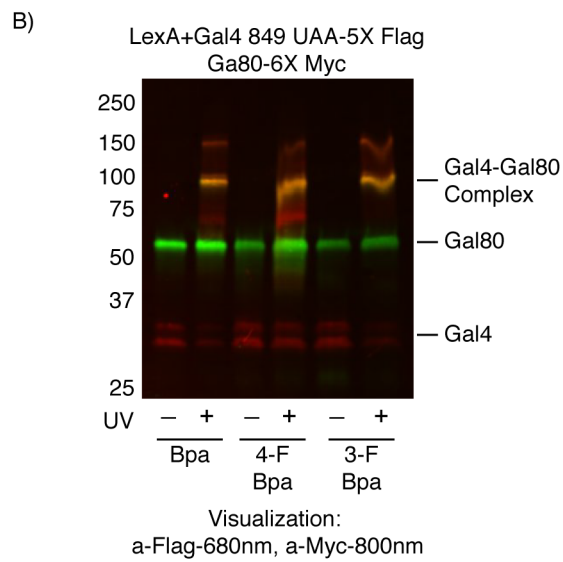
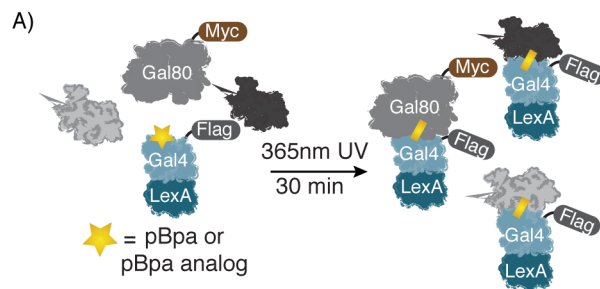
Figure 2. *In vivo* incorporation of Halo-Bpa analogs. (A) Position 849 was mutated to the amber stop codon (TAG) for UAA incorporation within the LexA+Gal4 chimeric transcriptional activator. A C-terminal Flag tag was appended for visualization. (B-E) Incorporation of the Halo-Bpa analogs into LexA+Gal4 849TAG in the presence or absence of 1 mM UAA. Loading control is an endogenous yeast protein that consistently comes out with Flag visualization. (F) Relative expression levels of the Halo-Bpa analogs compared to pBpa. Expression levels of LexA+Gal4 849UAA mutants relative to LexA+Gal4 WT were quantified by using ImageJ.

Figure 3. LexA+Gal4 849UAA *in vivo* crosslinking. (A) Experimental scheme of *in vivo* covalent chemical capture of Gal4 binding partners. (B) 3-F and 4-F Bpa capture Gal4's endogenous binding partners (red) and the Gal4-Gal80 interaction (yellow) when irradiated with UV light.

Figure 4. VP16 (441-448) F442UAA *in vitro* crosslinking. Each Halo-Bpa analog had increased crosslinking yield for the Med25-VP16 adduct compared to pBpa upon UV irradiation. (A) Western blot visualization of 6XHis+Med25:Biotin+VP16 F442UAA *in vitro* crosslinking. Crosslinked adducts visualized with Streptavidin-HRP and Med25 loading visualized with anti-HIS-HRP antibody. (B) Relative fold change in Halo-Bpa crosslinking yields compared to pBpa from 6XHis+Med25:Biotin+VP16 F442UAA western blot. The yields are an average of two replicates. Crosslinking yields were quantified using ImageJ. The relative amount of Med25-VP16 crosslinked adducts for each sample was normalized based on the protein levels of Med25 in the HIS-HRP blot. The fold changes were expressed as follows (Med25-VP16 F442UAA crosslinked product / Med25-VP16 F442Bpa crosslinked product).

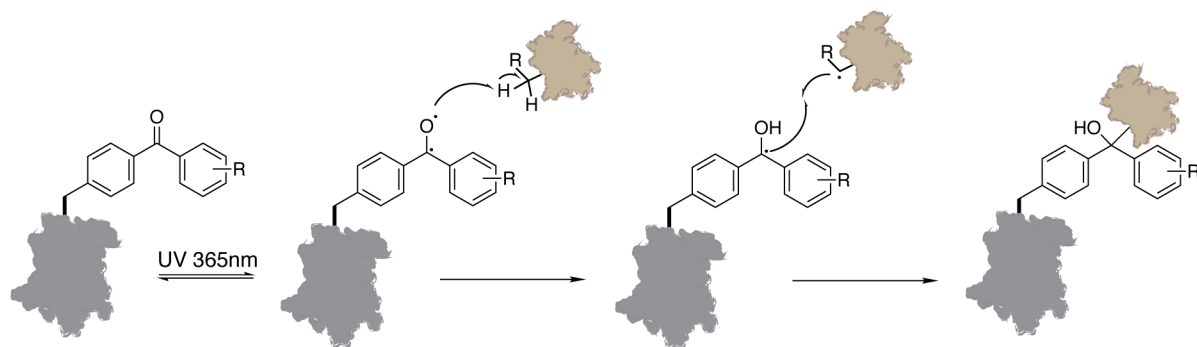


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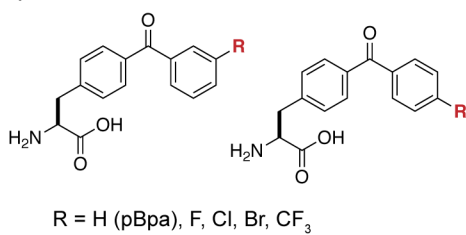


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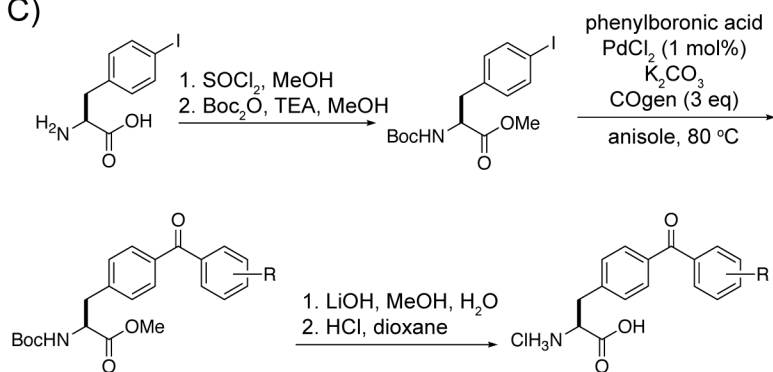
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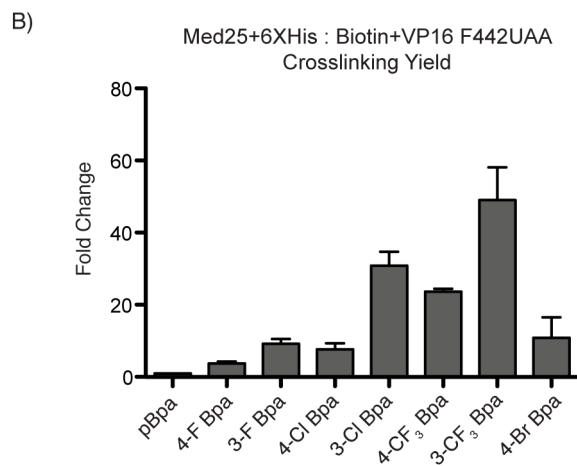
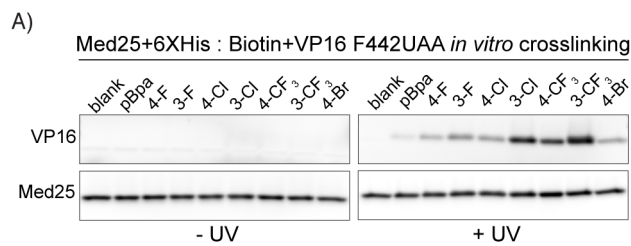
B)



C)



PRO_3621_HaloBpa_Figure 1_Joineretal.tif



PRO_3621_HaloBpa_Figure 4_Joineretal.tif