

## Supporting Information

### Enzymatic Spin Labeling of Protein N- and C-Termini for Electron Paramagnetic Resonance Spectroscopy

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**Figure S1:** Purification of His-TEV-gp41c-SSSDVC-Thrombin-SUMO

**Figure S2:** X Band CW Fitting

**Figure S3:** Background Subtraction of DEER Data

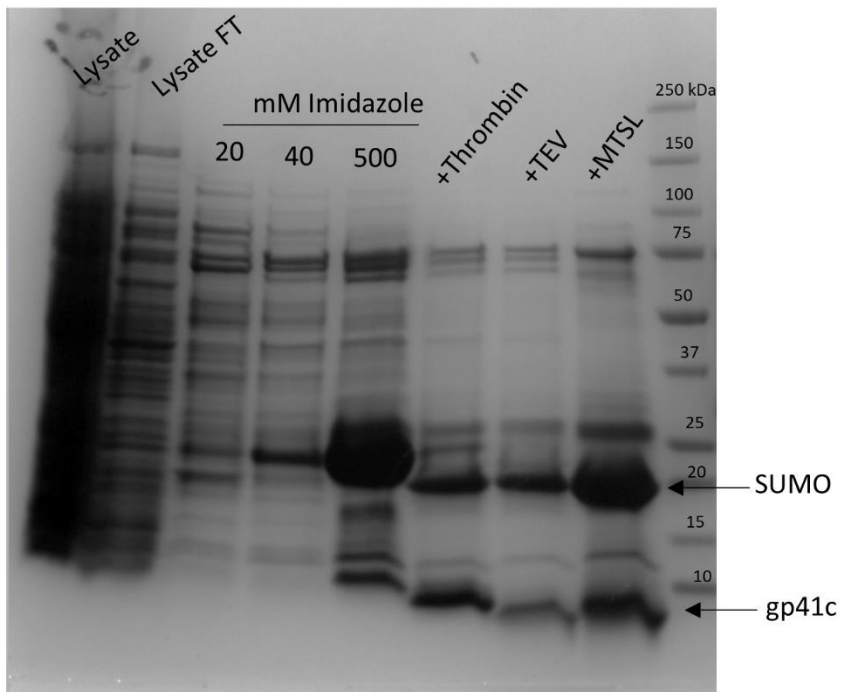
**Figure S4:** DeerLab Analysis of DEER Data

**Figure S5:** CheY/iLOV/CheA DEER with C Terminal Sortase Linkers

**Figure S6:** iLOV DEER With Extended N and C Terminal Linkers

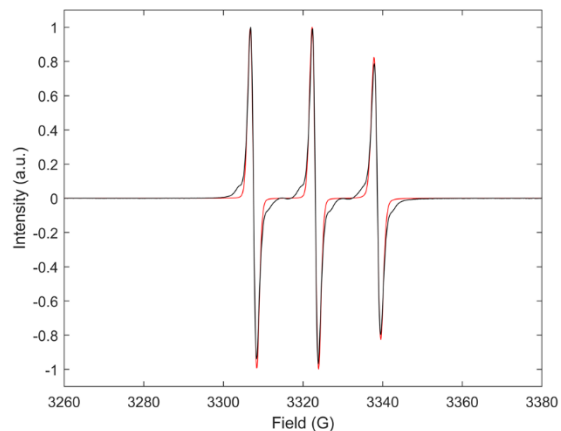
**Figure S7:** Nonreducing SDS-PAGE of CheA-SSSDVC

**DNA Sequences of Expressed Constructs**



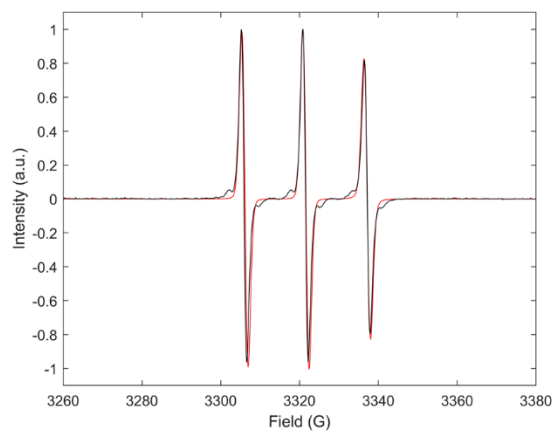
**Figure S1.** Purification of His-TEV-gp41c-SSSDVC-Thrombin-SUMO

### R1-CNGL



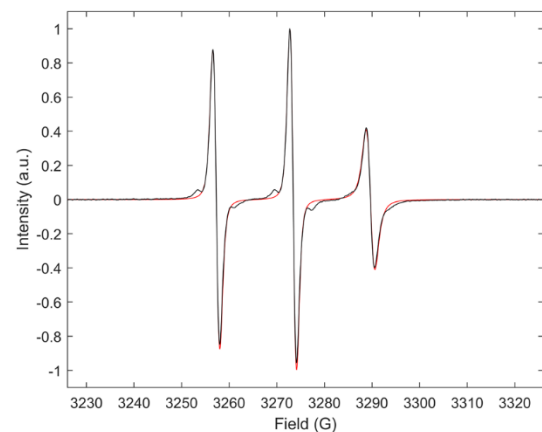
A (MHz)	[2.7453 18.6602 109.5000]
g	[2.00692, 2.00626, 2.00079]
$I_w$ (mT)	0.1841
$T_c$	51 ps

### GGGGC-R1



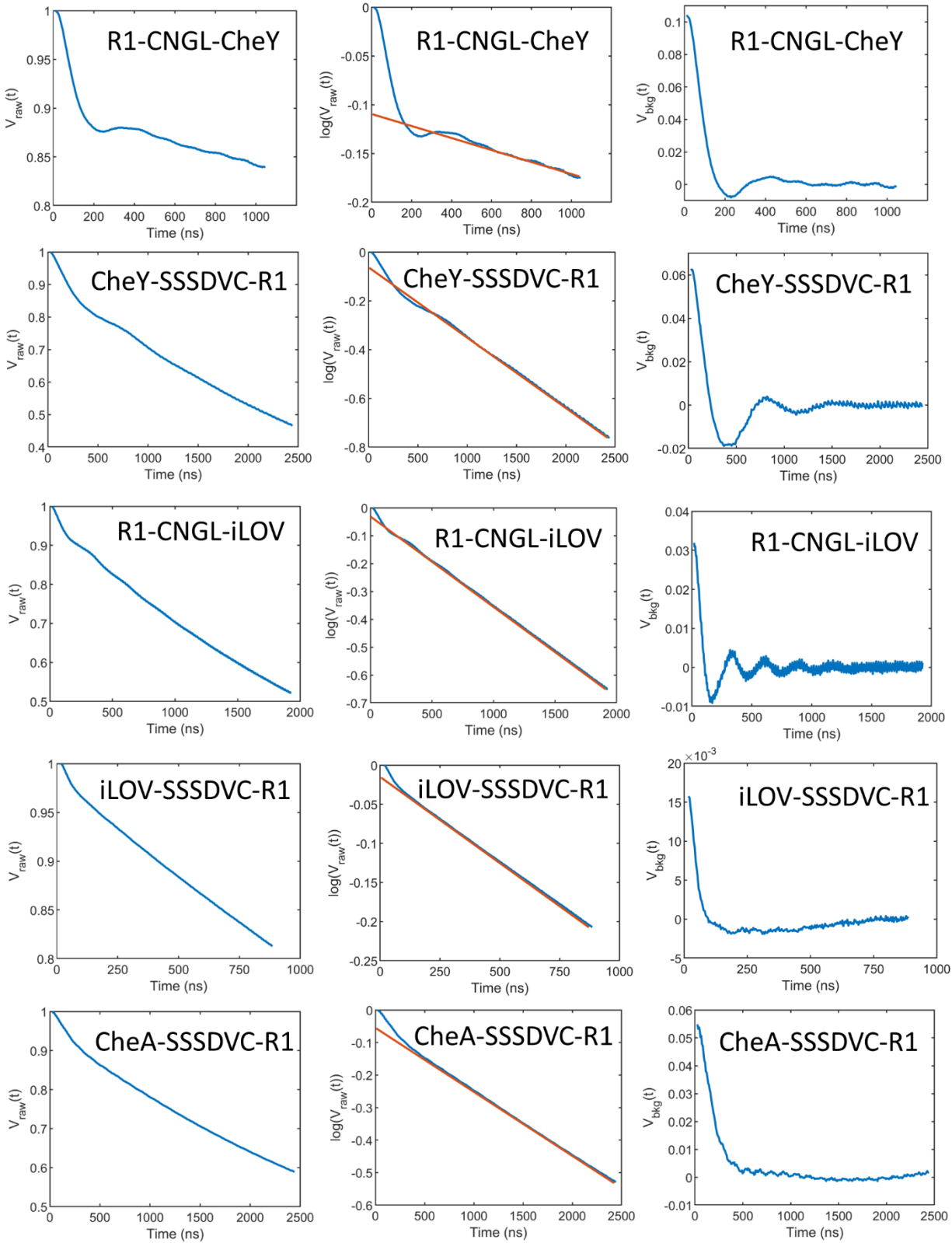
A (MHz)	[2.9578 18.5552 109.116]
g	[2.00667, 2.00582, 2.0009]
$I_w$ (mT)	0.1818
$T_c$	53 ps

### gp41c-SSSDVC-R1

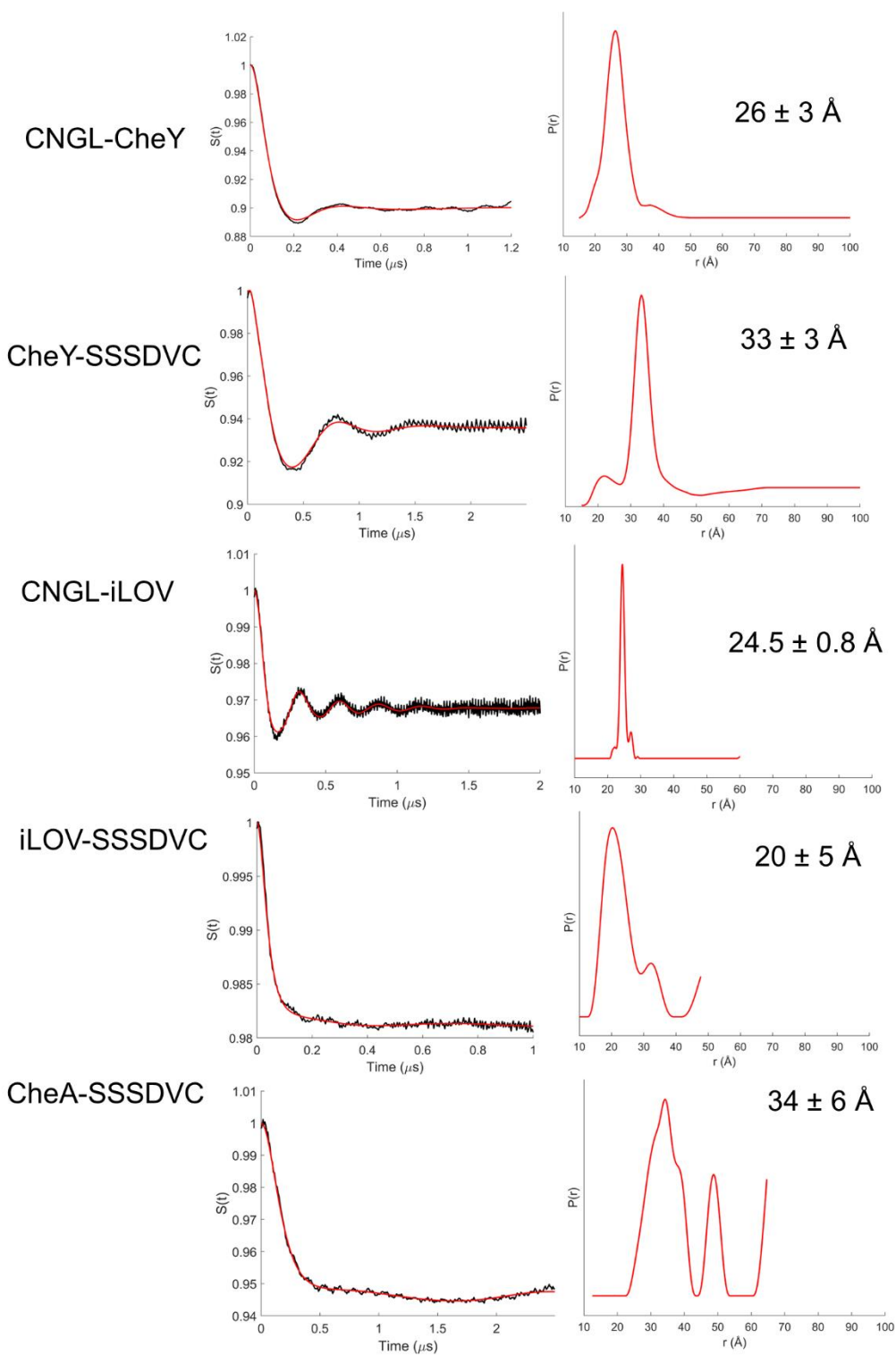


A (MHz)	[1.9604 22.5518 111.8470]
g	[2.00664, 2.00830, 2.00182]
$I_w$ (mT)	0.1331
$T_c$	255 ps

**Figure S 2:** Fitting of CW Spectra using EasySpin. Experimental spectra are shown in black, with fits in red. A represents the principal values of the hyperfine interaction tensor, g represents the principal values of the g tensor,  $I_w$  gives the FWHM of the Gaussian broadened linewidth and  $T_c$  is the rotational correlation time.

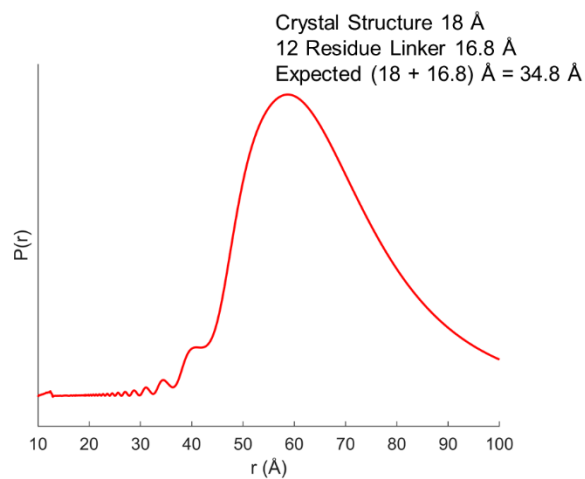
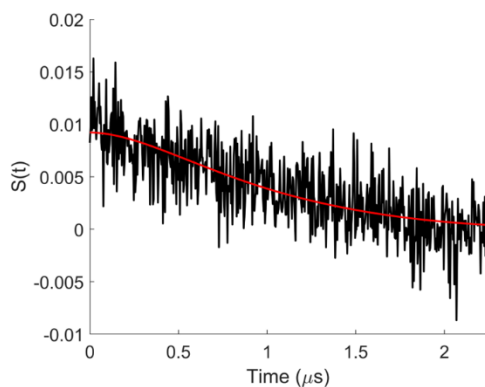


**Figure S 3.** Background Subtraction for Select DEER Spectra. For iLOV samples, higher background was observed likely due to blue light irradiation reducing a significant portion of nitroxides present in the sample. Additionally, we have observed increased background for NSQ radicals measuring at 60 K ( $T_2$  maximum  $\sim 150$  K). For intein labelled samples, background is due to free gp41c-SSSDVC-R1 in solution; low molecular weight proteins (10-15 kDa) are difficult to separate from gp41c-SSSDVC-R1 in size exclusion chromatography.

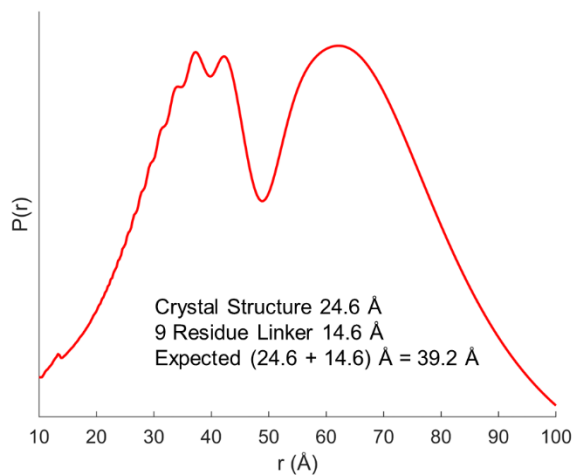
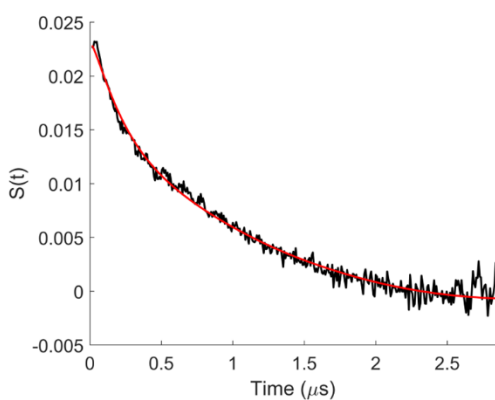


**Figure S 4.** DEER Spectra of select samples analyzed using DEER Analysis with Tikhonov Regularization. For all samples, a homogeneous (3 dimension) background subtraction was used. The regularization parameter  $\alpha$  was chosen using the AIC criteria option in DEER Analysis.

CheY-LPGTGGGGGC-R1 (Sortase)  
C term to Cys81 (MTSL)



iLOV-LPGTGGGGGC-R1 (Sortase)  
FMN to CT



CheA-LPGTGGGGGC-R1 (Sortase)  
CT to CT

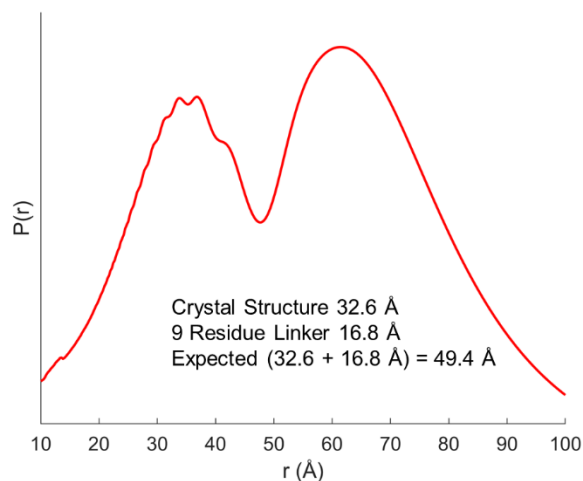
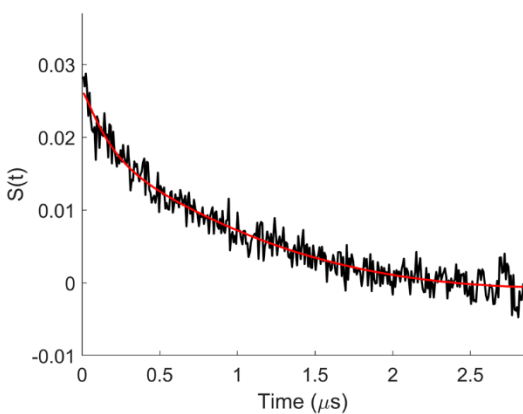
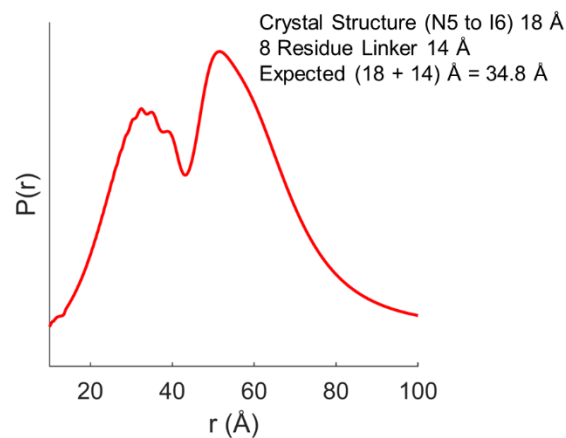
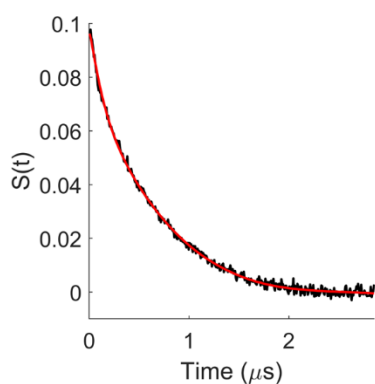
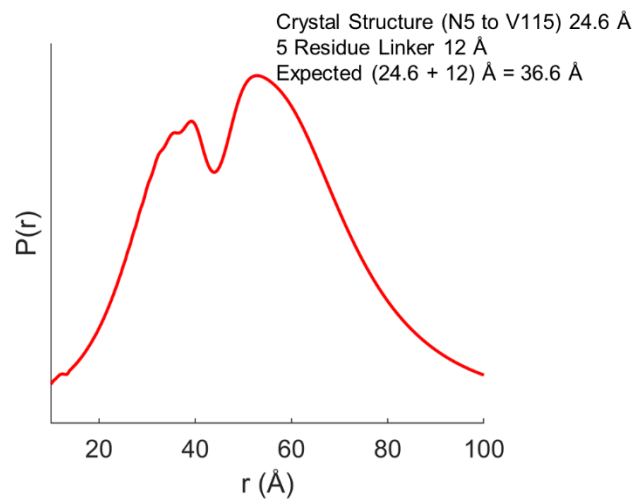
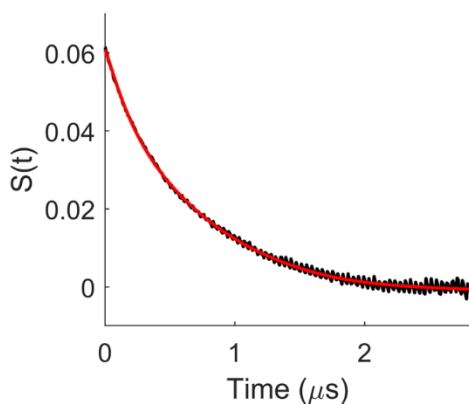


Figure S 5: CheY/iLOV/CheA DEER with C Terminal Sortase Linkers

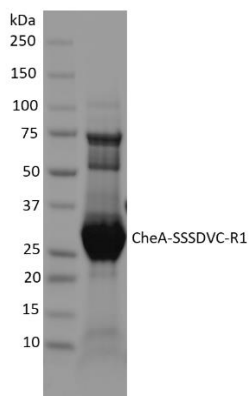
R1-CNGL-(MIGTIEK)-iLOV  
NT to FMN\*



iLOV-(GSDHV)-SSSDVC-R1  
CT to FMN\*



**Figure S 6.** DEER spectroscopy of iLOV with Extended Linkers. Residues indicated in parenthesis have been added compared to the samples shown in Figure 4.



**Figure S 7.** Nonreducing SDS-PAGE of CheA-SSSDVC-R1 (28kDa).



## DNA Sequences of Constructs

### OaAEP1 (C243A) TEV-His in pET28a

ATGGGCAGCAGCCATCATCATCATCACAGCAGCGGCCTGGTGCCGCGCGGCAGCCATATGGCTAGCATGACT  
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GCGAAGAACAGATGGCGGAAGCGGCGAGCCAGGCGTGCGCGAGCATTCCGCTCGAGCACCACCACCACCAC

### His-TEV-gp41c-SSSDVCG-Thrombin-SUMO in pET28a

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GGAGGATAACGATATTATTGAGGCTCACAGAGAACAGATTGGTGGTTATCCGTATGATGTGCCGGATTATGCG

### His-TEV-L-CheY-gp41n in pET28a

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His-iLOV(Q489D)-gp41n in pET28a

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His-TEV-L-iLOV(Q489D)-gp41n in pET28a

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ATCACCTGGAAGACGGTAAAGAGATCATCTGCTCTGAAGAACACCTGTTCCCGACCCAGACCGGTGAAATGAAC  
ATCTCTGGTGGTCTCAAAGAGGGTATGTGCCTGTACGTTAAAGAA

His-TEV-L-CheA-GP41N

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GAGGGTATGTGCCTGTACGTAAAGAA

His-TEV-L-CheA-LPGTGGS

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