

Supplementary data for:

## Interactions of the N- and C-Terminal SH3 Domains of *Drosophila* Drk with the Proline-Rich Peptides from Sos and Dos

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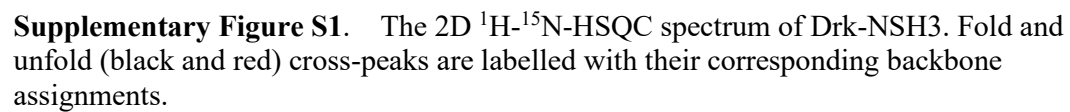
\*Authors to whom correspondence should be addressed.

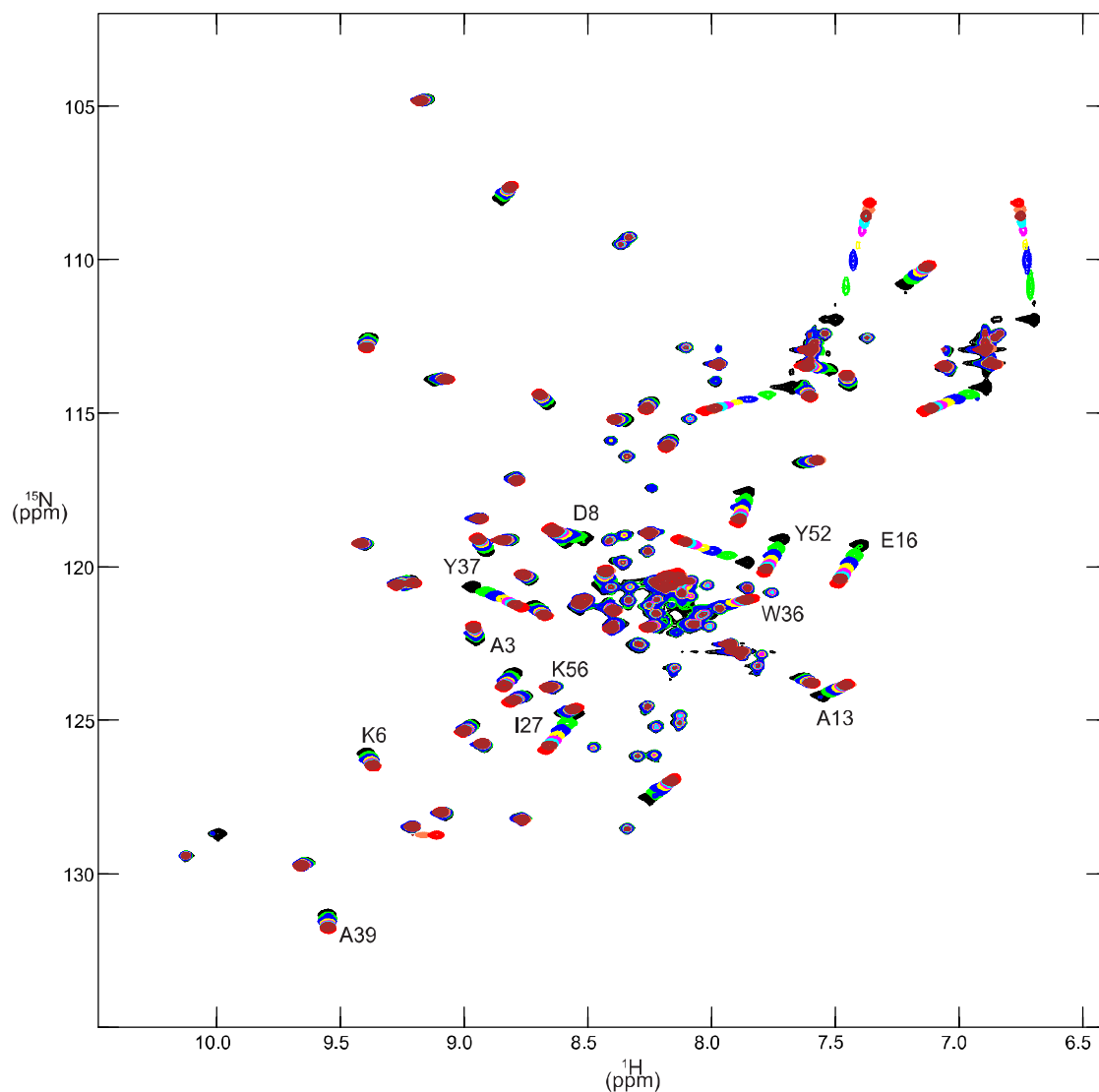
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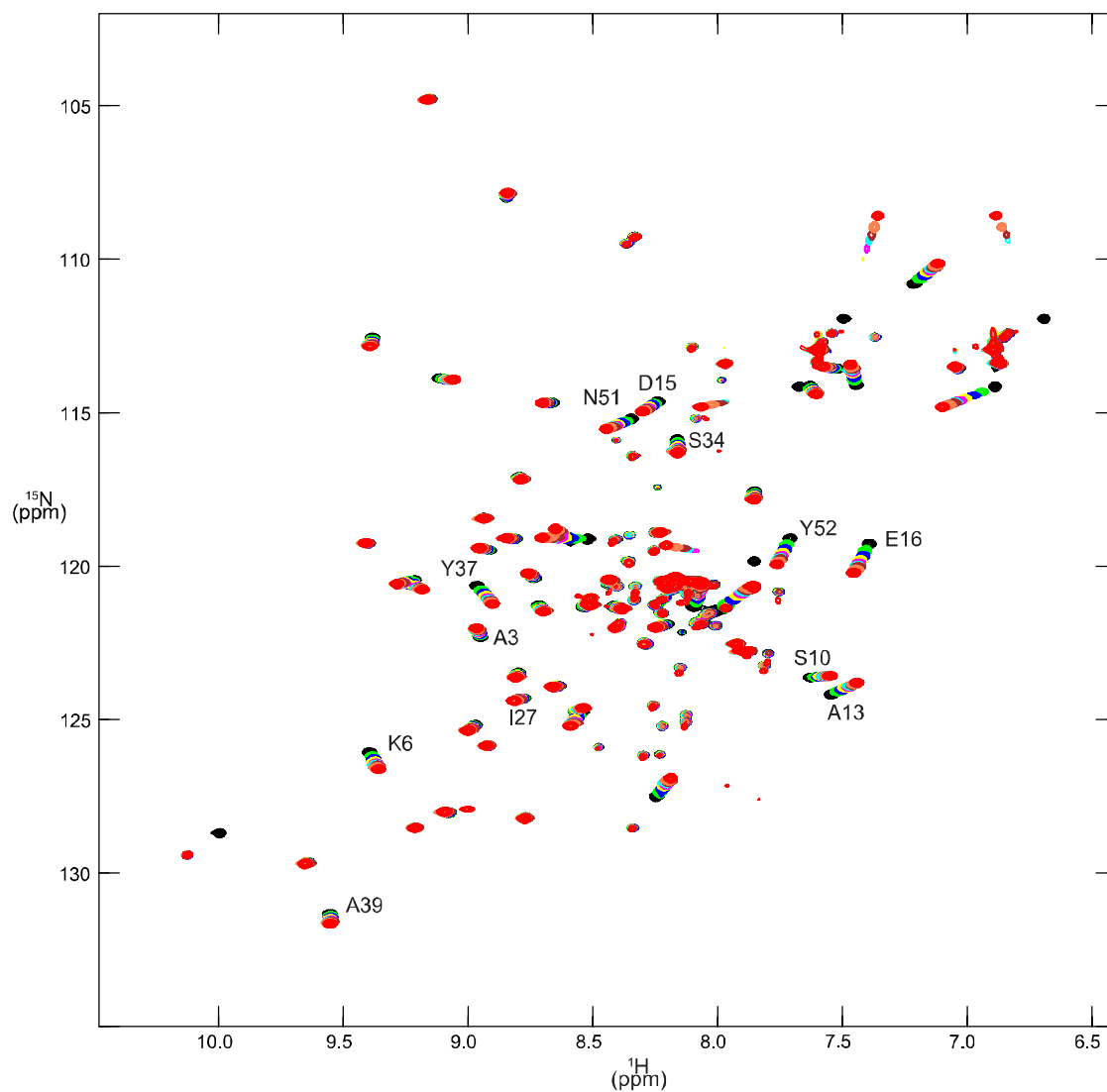
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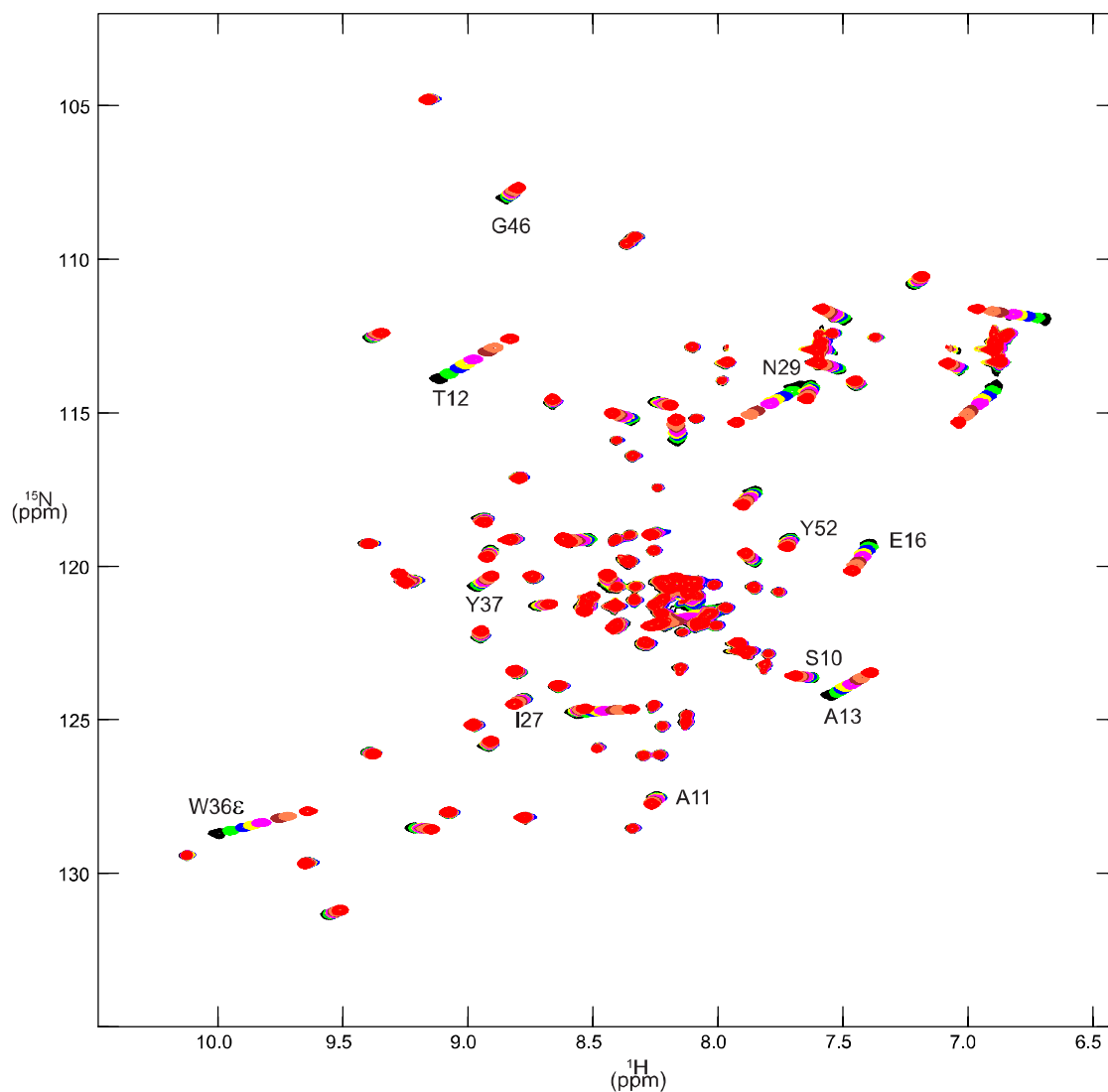


**Supplementary Figure S2.** Overlays of 2D  $^1\text{H}$ - $^{15}\text{N}$  HSQC spectra from multipoint titrations of  $^{15}\text{N}$ -labelled Drk-NSH3 with Sos-S1 (YRAVPPPLPPRR) peptide. The peptide concentration was increased stepwise (the protein: peptide molar ratio of 1:0.25, 1:0.5, 1:0.75, 1:1, 1:1.25, 1:1.5, 1:2, 1:2.5, 1:3, 1:3.5, 1:4, 1:4.5 and 1:8). In this figure, the colour codes of  $^1\text{H}$ - $^{15}\text{N}$  correlation cross-peaks at each titration point, showing the molar ratio of Drk-NSH3: Sos-S1, are as follows: black (1:0); green (1:0.25); blue (1:0.5); yellow (1:0.75); magenta (1:1); cyan (1:1.25); brown (1:1.5); coral (1:2); red (1:4). Cross peaks that showed large chemical shift changes were annotated.

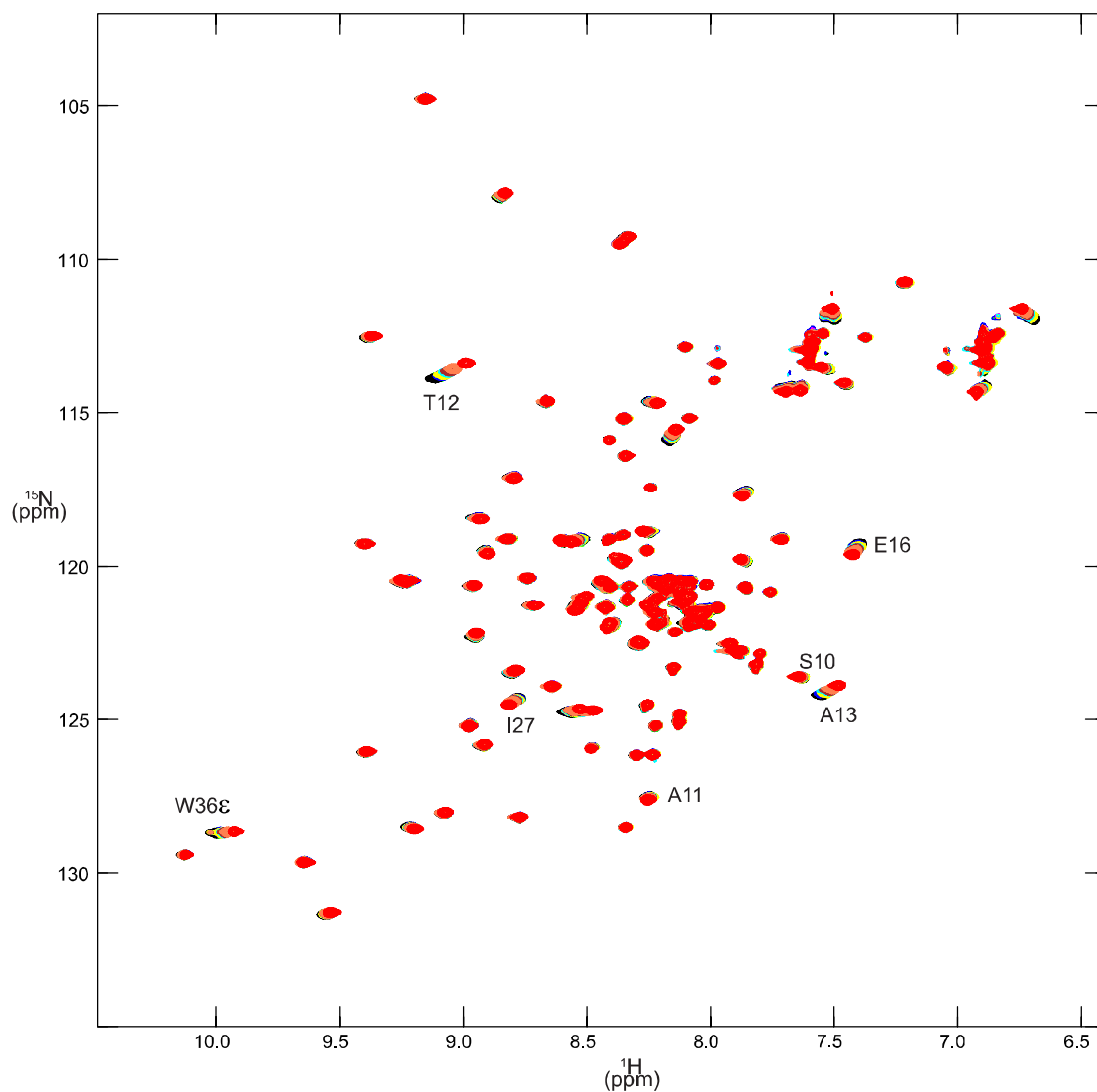


**Supplementary Figure S3.** Overlays of 2D  $^1\text{H}$ - $^{15}\text{N}$  HSQC spectra from multipoint titrations of  $^{15}\text{N}$ -labelled Drk-NSH3 with Sos-S2 (GELSPPPIPPRL) peptide. The peptide concentration was increased stepwise (the protein:peptide molar ratio of 1:0.25, 1:0.5, 1:0.75, 1:1, 1:1.25, 1:1.5, 1:2, 1:2.5, 1:3, 1:3.5, 1:4, 1:4.5 and 1:8). In this figure, the colour codes of  $^1\text{H}$ - $^{15}\text{N}$  correlation cross-peaks at each titration point, showing the molar ratio of Drk-NSH3: Sos-S2, are as follows: black (1:0); green (1:0.25); blue (1:0.5); yellow (1:0.75); magenta (1:1); cyan (1:1.25); brown (1:1.5); coral (1:2); red (1:4). Cross peaks that showed large chemical shift changes were annotated.

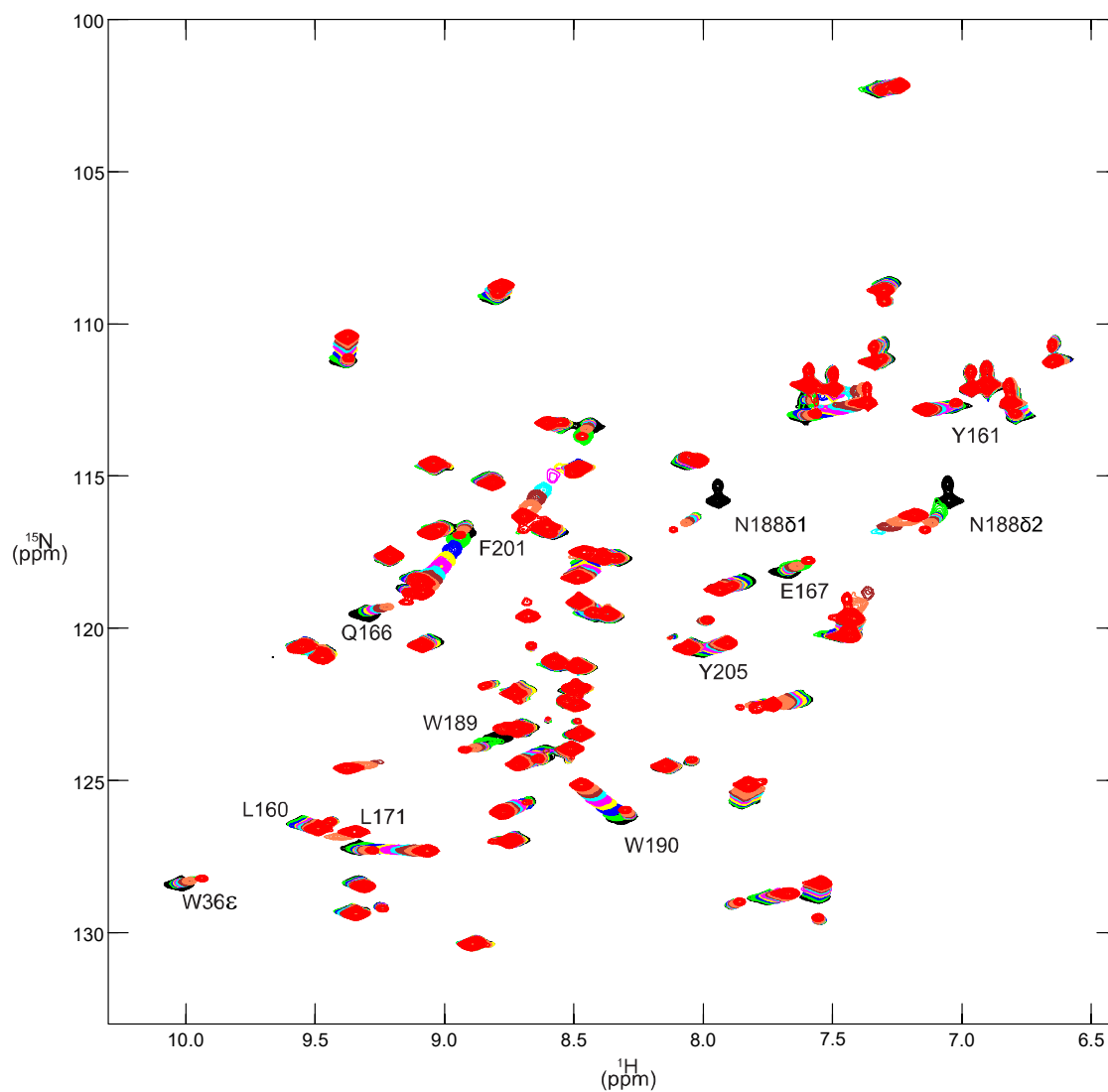




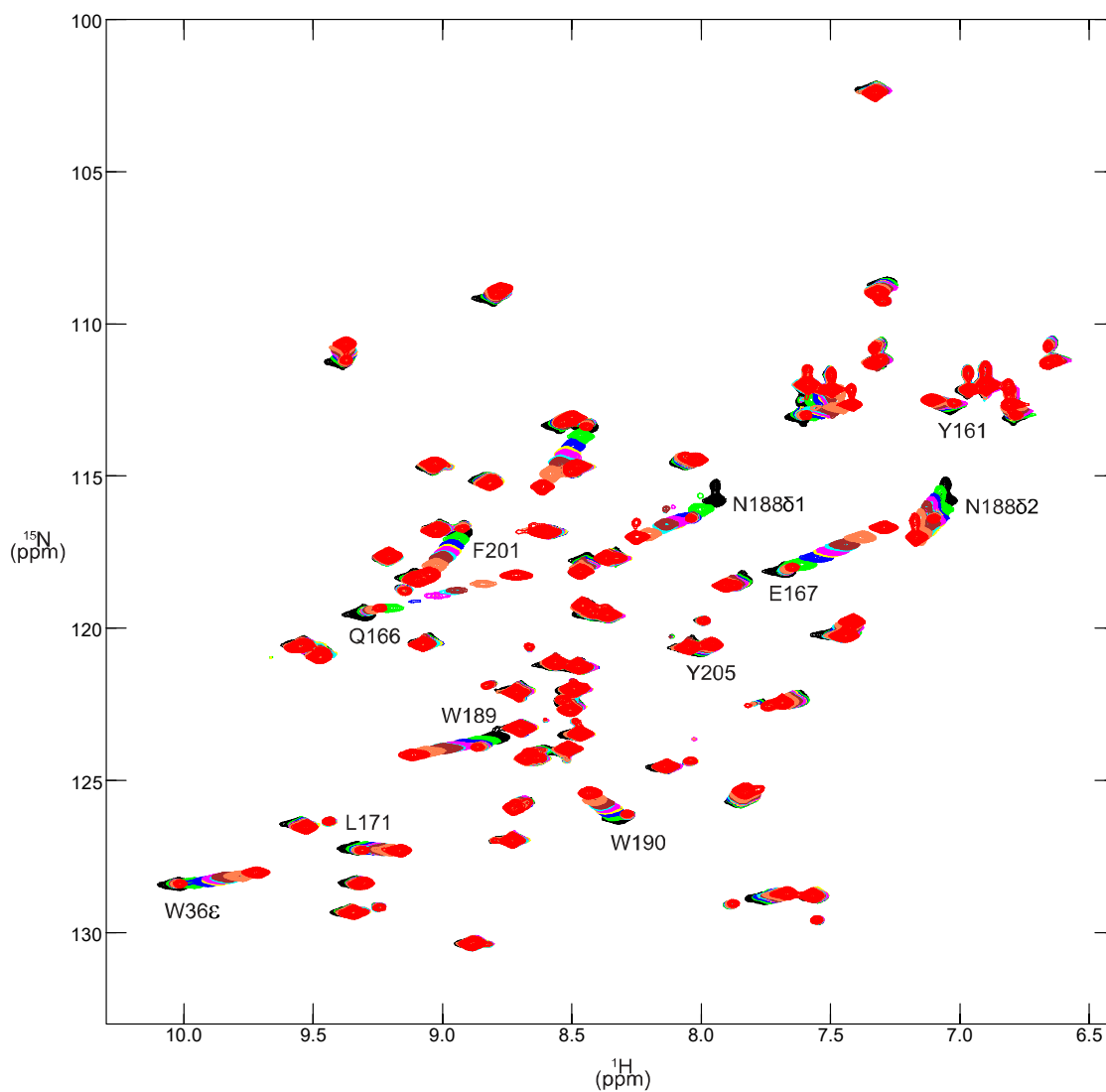
**Supplementary Figure S4.** Overlays of 2D  $^1\text{H}$ - $^{15}\text{N}$  HSQC spectra from multipoint titrations of  $^{15}\text{N}$ -labelled Drk-NSH3 with Dos-S1 (DCPPVNRKCLKPKV) peptide. The peptide concentration was increased stepwise (the protein:peptide molar ratio of 1:0.25, 1:0.5, 1:0.75, 1:1, 1:1.25, 1:1.5, 1:2, 1:2.5, 1:3, 1:3.5, 1:4 and 1:8). In this figure, the colour codes of  $^1\text{H}$ - $^{15}\text{N}$  correlation cross-peaks at each titration point, showing the molar ratio of Drk-NSH3: Dos-S1, are as follows: black (1:0); green (1:0.25); blue (1:0.5); yellow (1:0.75); magenta (1:1); cyan (1:1.25); brown (1:1.5); coral (1:2); red (1:4). Cross peaks that showed large chemical shift changes were annotated.



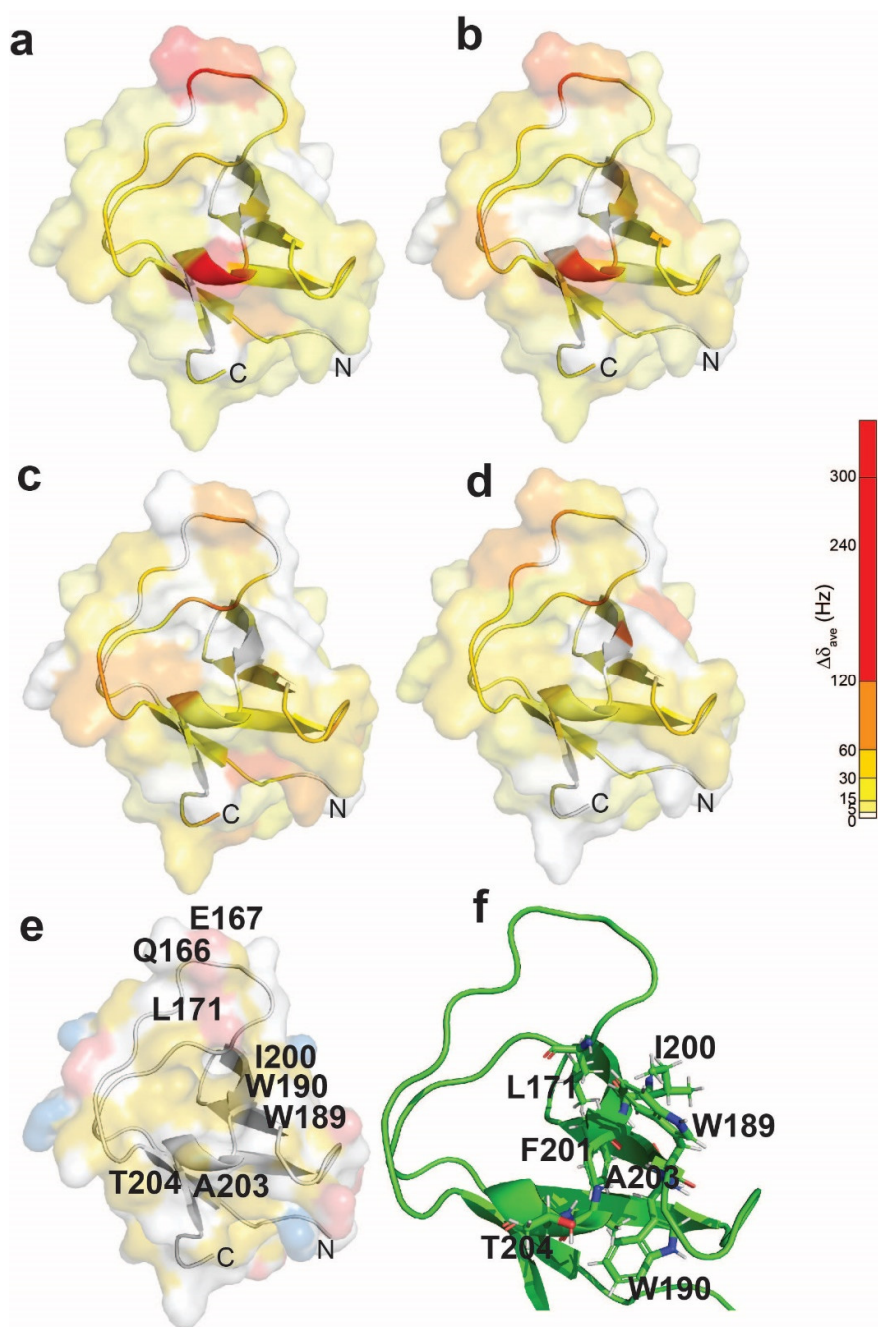
**Supplementary Figure S5.** Overlays of 2D  $^1\text{H}$ - $^{15}\text{N}$  HSQC spectra from multipoint titrations of  $^{15}\text{N}$ -labelled Drk-NSH3 with Dos-S2 (GPPSVDRKCKPNA) peptide. The peptide concentration was increased stepwise (the protein:peptide molar ratio of 1:0.25, 1:0.5, 1:0.75, 1:1, 1:1.25, 1:1.5, 1:2, 1:2.5, 1:3, 1:3.5, 1:4 and 1:8). In this figure, the colour codes of  $^1\text{H}$ - $^{15}\text{N}$  correlation cross-peaks at each titration point, showing the molar ratio of Drk-NSH3: Dos-S2, are as follows: black (1:0); green (1:0.25); blue (1:0.5); yellow (1:0.75); magenta (1:1); cyan (1:1.25); brown (1:1.5); coral (1:2); red (1:4). Cross peaks that showed large chemical shift changes were annotated.



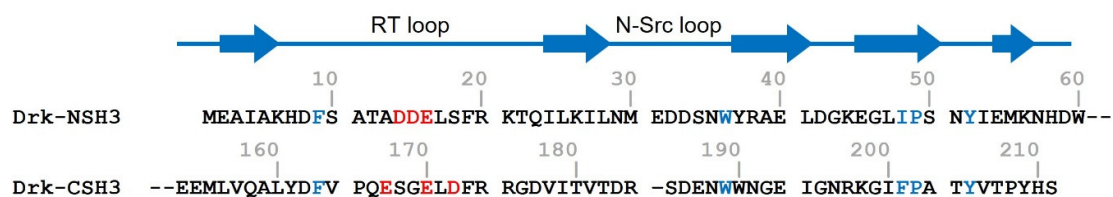
**Supplementary Figure S6.** Overlays of 2D  $^1\text{H}$ - $^{15}\text{N}$  HSQC spectra from multipoint titrations of  $^{15}\text{N}$ -labelled Drk-CNSH3 with Dos-S1 (DCPPVNRKLKPKV) peptide. The peptide concentration was increased stepwise (the protein:peptide molar ratio of 1:0.25, 1:0.5, 1:0.75, 1:1, 1:1.25, 1:1.5, 1:2, 1:2.5, 1:3, 1:3.5, 1:4 and 1:8). In this figure, the colour codes of  $^1\text{H}$ - $^{15}\text{N}$  correlation cross-peaks at each titration point, showing the molar ratio of Drk-CNSH3: Dos-S1, are as follows: black (1:0); green (1:0.25); blue (1:0.5); yellow (1:0.75); magenta (1:1); cyan (1:1.25); brown (1:1.5); coral (1:2); red (1:4). Cross peaks that showed large chemical shift changes were annotated.



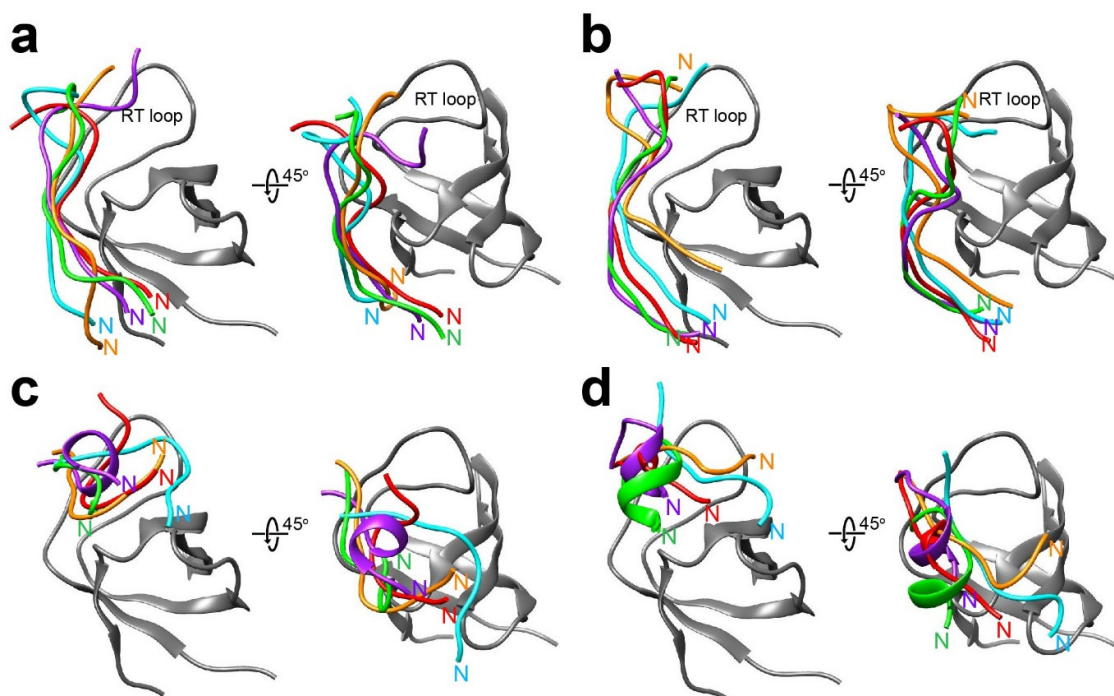
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**Supplementary Figure S8.** Chemical shift perturbation upon the titration with Sos-S1 (a), Sos-S2 (b), Dos-S1 (c), and Dos-S2 (d) represented on the solution structure of Drk-CSH3 (PDB ID: 7Y4N). Figures S9a and S9b were created from the data obtained in our previous study[1]. The residues which were affected during the titration (with the protein:peptide mixing ratio of 1:8) are shown with a colour gradation from white (the lowest) to red (the highest). (e) The residues which showed significant chemical shift perturbations are indicated on the protein surface with the colour-coding according to the hydrophobicity (yellow) and the electrostatic potential (negative: red and positive: blue). (f) The sidechains of these residues are also shown.



**Supplementary Figure S9.** Sequence comparison of Drk-NSH3 with the Drk-CSH3. The residues involved in the hydrophobic PRM-binding interface (blue) and the negatively charged residues in the RT loop (red) are indicated.



**Supplementary Figure S10.** The models of the interactions of Drk-CSH3 with the “longer” Dos-S1 (DCPPVNRKCLKPKV) (**a**) and Dos-S2 (GPPSVDRKCKPNA) (**b**), which are compared with the results of docking simulations with the “shorter” Dos-S1 (PPVNRKCLKP) (**c**) and Dos-S2 (PSVDRKCKP) (**d**) performed previously[1]. The top five structures with the lowest energy are presented for each, in which the positions of the N-terminal of the peptides are indicated.

1. Sayeesh, P. M.; Ikeya, T.; Sugawara, H.; Watanabe, R.; Mishima, M.; Inomata, K.; Ito, Y., Insight into the C-terminal SH3 domain mediated binding of *Drosophila* Drk to Sos and Dos. *Biochemical and Biophysical Research Communications* **2022**, 625, 87-93.