

## Supplementary legends

**Table S1.** Dissociation constants ( $K_D$ ) of *A. thaliana* NRP1 interaction with either histones or Cc measured by Surface Plasmon Resonance (SPR).  $K_D$  values were calculated from the fits of SPR curves to the binding models described in Figure S6.

**Figure S1.** Multiple alignment of amino acid sequences of NRP1 (UniProt entry: Q9CA59-1), AtNAP1;1 (UniProt: Q9SZI2-1), AtNAP1;2 (UniProt: Q9ZUP3-1), AtNAP1;3 (UniProt: Q94K07-1) and AtNAP1;4 (UniProt: F4JEI8-1) using Clustal Omega. Sequences are coloured by similarity: fully conserved residue (black), residues with strongly similar properties (light blue) and residues with weakly similar properties (grey).

**Figure S2.** MALDI-TOF MS analyses of H2B, H3 and H4 histones (*X. laevis*), Cc and NRP1 (*A. thaliana*).

**Figure S3. A.** MALDI-TOF MS analyses of the H2A, H2B, H3 and H4 histones (*G. gallus*). **B.** *Left:* SDS-PAGE showing the electrophoretic purity of *A. thaliana* Cc and NRP1 (lanes 2-3), *X. laevis* H2B, H3 and H4 histones (lanes 4-6). *Right:* SDS-PAGE of *G. gallus* H2A-H2B and H3-H4 dimers (lanes 2-3). In both gels, lane 1 indicates protein ladder markers.

**Figure S4.** Far-UV CD spectra of NRP1 (*left*) and *X. laevis* core histones H2B, H3 and H4 (*right*).

**Figure S5.** ITC measurements of interactions of NRP1 with H2B, H3 and H4 isolated core histones, H2A-H2B, H3-H4 and Cc. Thermograms along with the binding isotherms (*top* and *bottom*, respectively) are shown.

**Figure S6.** Analysis of Surface Plasmon Resonance curves. SPR response curves – obtained with 0.1 and 1  $\mu$ M NRP1 analyte and distinct immobilized ligands – are represented by dots. Red lines correspond to a simultaneous, global fit of the two curves to a one-site binding model. Blue lines represent global fits to a multiple-site binding model. Data is representative of a total of 6 injections.

**Figure S7.** Multiple alignment of amino acid sequences of core histones H2A, H2B, H3 and H4 from *X. laevis* (UniProt [respectively]: P06897-1, P02281-1, P02302-1, P62799-1) and *A. thaliana* (UniProt [respectively]: Q8GUH3-1, Q1H5F7-1, B9DGR9-1, P59259-1) using Clustal Omega. Sequences coloured by similarity: fully conserved residue (black), residues with strongly similar properties (light blue) and residues with weakly similar properties (grey).

**Figure S8. A.** Schematic representation of the nucleosome assembly activity of NRP1 by means of plasmid supercoiling assays. **B.** Nucleosome assembly activity by supercoiling assays in presence of isolated NRP1 (lane 3), HeLa core histones (lane 4), Cc (lane 5) or combination of Cc with histones (lane 6) or NRP1 (lane 7). Plasmids previously treated with Topo I. Lane 1 (control) shows supercoiled, untreated DNA plasmid, whereas lane 2 corresponds to DNA plasmid relaxed by Topo I. **C.** MNase assay in presence of isolated HeLa core histones (lane 2),

NRP1 (lane 3), Cc (lane 4) or combination of Cc with histones (lane 5) or NRP1 (lane 6). Plasmid DNA was digested with 30 U/ml MNase. Lane 1 indicates a DNA ladder marker and the size of each band is represented on the left. **D.** 1D  $^1\text{H}$  NMR spectra monitoring Met-88 methyl signal of reduced Cc (13  $\mu\text{M}$ ) in absence (—) or presence of 6.5  $\mu\text{M}$  BSA (—) or 300  $\mu\text{g}$  calf thymus histones (...).

**Figure S9. BiGGER molecular docking of complexes between NRP1 and *A. thaliana* core histones.**

500 solutions of docking for histone:NRP1 complexes. Centres of mass for H2A (green spheres), H2B (purple spheres), H3 (red spheres) and H4 (blue spheres) represented. NRP1 ribbon representations (gold) are shown and arrows indicate the two highest-scoring solutions.

**Figure S10. Differences in line-width ( $\Delta\Delta v_{1/2\text{Binding}}$ ) in  $^{15}\text{N}$  dimension of Cc amide NMR signals upon binding to NRP1.**

$\Delta\Delta v_{1/2\text{Binding}}$  of Cc amide groups were calculated from differences between [ $^1\text{H}$ ,  $^{15}\text{N}$ ] HSQC spectra of free Cc and Cc in Cc:NRP1 complex at a ratio of 1:0.5. Residues exhibiting significant line broadening beyond threshold marked with asterisk. Threshold (dashed line) corresponds to average plus 2-fold the standard deviations ( $\Delta\Delta v_{1/2\text{Binding}} \geq \Delta\Delta v_{1/2\text{Binding}} + 2S_{n-1}$ ).

**Figure S11. Comparison of complexes formed between NRP1 and Cc or core histones.**

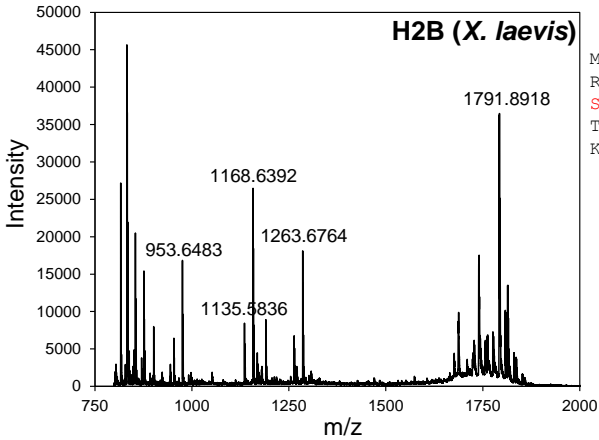
**A.** Ribbon representations for two best models, according to overall score for complex between NRP1 and Cc yielded by NMR-restrained BiGGER molecular docking. NRP1 ribbon representation (gold), Cc (blue) and Cc heme group (red) are shown.

**B-E.** Ribbon representations for two best models according to overall score for complexes between NRP1 and histones H2A (B), H2B (C) H3 (D) or H4 (E) obtained by BiGGER molecular docking. NRP1 ribbon representation (gold), H2A (green), H2B (purple), H3 (red) and H4 (dark blue) are shown. NRP1 is shown in the same orientation as in A.

**Table S1**

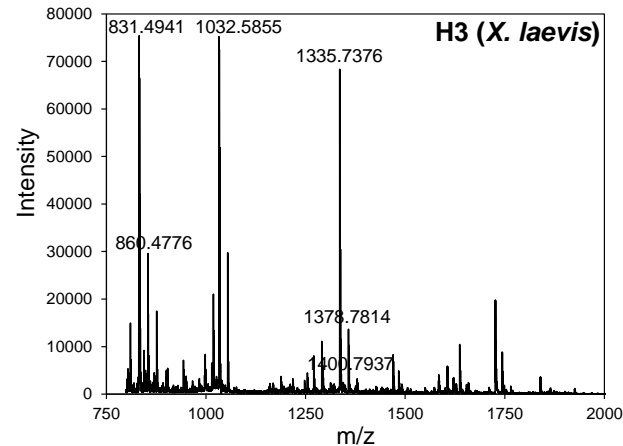
<b>Protein complex</b>	<b><math>K_D</math> (<math>\mu\text{M}</math>)</b>
H2B:NRP1	18.5
H3:NRP1	57.9
H4:NRP1	28.9
H2A-H2B:NRP1	0.51
H3-H4:NRP1	0.74
Cc:NRP1	12.1

NRP1	-----MVA	DKSKKSKIEEK	GEENLEQIDAELVLS	30
AtNAP1;4	MSNEENIKSDNKS	GDSSDLPTIP-	ALDIGAEECDLLAELK	NLT
AtNAP1;2	MSND-----	KDSMNMSDLSTAL	NEDDRAGLVNALK	NKLQNL
AtNAP1;1	MSND-----	KDSFNVSDLTAAL	KDEDDRAGLVNALK	NKLQNL
AtNAP1;3	MSND-----	KDSFNVSDLTSA	LKDEDDRAGLVNALK	NKLQNL
NRP1		TEKLOEIQDDLEK	INEKASDEVLEVEQ	KYNVTRKPVYDKRNEVI
AtNAP1;4		VLFKLDIQVTHDE	LEEKFLAEKSALEAT	YDNLKPLFAKRYEIV
AtNAP1;2		VEFLREIQNQYDE	MEAKFFERAAL	EAKYQKLYQPLYTKRYEIV
AtNAP1;1		VDALRDIQSQHDE	LEAKFREERAIL	EAKYQTLYQPLYVKRYEIV
AtNAP1;3		VEVLEIQGKHDEI	ETKFRERAALEAK	YQKLYQPLYNKRVEIV
NRP1		-----QSTPG	FWMTAFLSHPALGDL	TEEDQKIFKYLNSLEVEDAKD
AtNAP1;4		-----AEKEG	VPNFWLIAMKTNEML	ANETTERDEAALKYLKDIR
AtNAP1;2		EQGEDKSAEEKG	VDFWLIALKNEITA	EETTERDEGALKYLKDIK
AtNAP1;1		DQGEKTAEEKG	VPSFWLTAALKNND	VISEEETTERDEGALKYLK
AtNAP1;3		DQGDEKTAEEKG	VPSFWLTAALKNND	VISEEETTERDEGALILY
NRP1		FFFTSNPFFEDAK	LTKTFTFLEEGTT--	KITATPIKWKKEGKGL
AtNAP1;4		FFFDNSLYFKNS	VLSKTYHVNDE	DGPVLEKVI
AtNAP1;2		FFFDQNPYFKNT	VLTTKTYHMIDE	DEPILEKALGTEIEWY
AtNAP1;1		FFFDTNPYFKNT	VLTTKSYHMIDE	DEPLLEKAMGTEIDWY
AtNAP1;3		FFFDQNPYFKNT	LLTKAYHMIDE	DEPLLEKAMGTEIDWY
NRP1		-----KRALPE	SFFTWF	TDACHKEDAG-----
AtNAP1;4		VNNIPMTKTENC	SFFNF	FKPPEIPEIDEVDDY
AtNAP1;2		KNTKPI	TKTEDCESFFNF	FSPQVPDDD-----
AtNAP1;1		KNTKPI	TKLEDCESFFNF	FSPQVPDED-----
AtNAP1;3		KNAKPI	TKTEDCESFFNF	FNPQVPDDD-----
NRP1		DLWSNPLTYFN	NDADEE-DFDGD	DGDEE-----
AtNAP1;4		KLIIPHAVSWFT	GEALVDEDDSD	DDNDDN-DEKSD-----
AtNAP1;2		KIISHAVSWFT	GEAVEADDLIED	DDD-EIDEDEDEDEDEDE
AtNAP1;1		KIIPRAVSWFT	GEAMEADFEID	DEEDDIDEDEDEDEDE
AtNAP1;3		KIIPHAVSWFT	GEALIEGEEFEI	DNDEDDIDEDEDEDEDE
NRP1		-----		
AtNAP1;4		-----		
AtNAP1;2		QGKSKKKSSAG	HKKAGRSQA-	EGQAGERPPECKQQ
AtNAP1;1		EESKTKKKPSI	GKKGGRSQI	VGEGKQDERPPECKQQ
AtNAP1;3		EVSKTKKKPSV	LHKKGGRPQ	VTD-DQQGERPPECKQQ



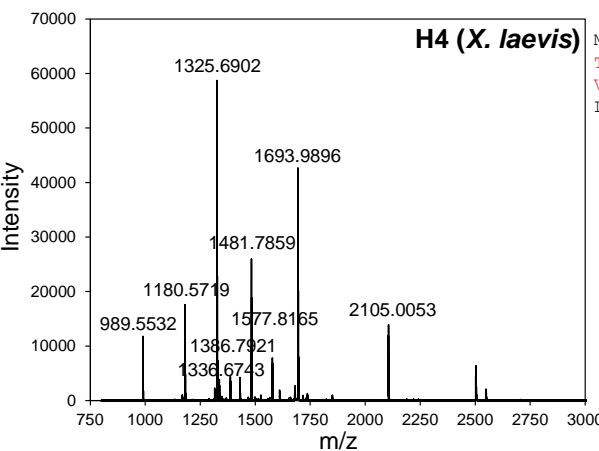
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 TSREIQTAVRLLLPGLGELAKHAVSEGTKAVT  
 KYTSAK

Observed m/z	Peptide
953.6483	LLLPGLGELAK
1135.5836	ESYAIYVYK
1168.6392	QVHPDTGISSK
1263.6764	KESYAIYVYK
1791.8918	AMSIMNSFVNDVFER



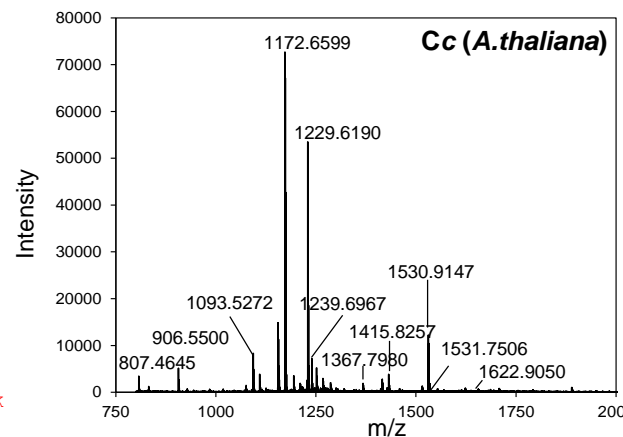
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 SAVMALQEASEAYLVLFEDTNLCAIHAK  
 RVTIMPKDIQLARRIRGERA

Observed m/z	Peptide
831.4941	STELLIR
860.4776	RVTIMPK
1032.5855	YRPGTVLALR
1335.7376	EIAQDFKTDLR
1378.7814	CAPATGGVKKPHR
1400.7937	TIMPKDIQLAR



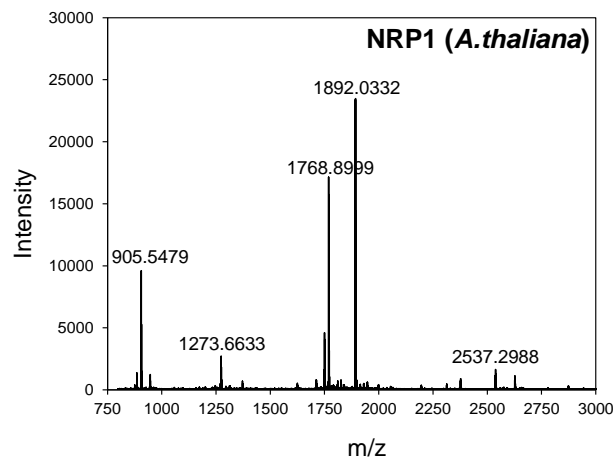
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Observed m/z	Peptide
989.5532	VFLENVIR
1180.5719	ISGLIYEETR
1325.6902	DNIQGITKPAIR
1336.6743	RISGLIYEETR
1386.7921	GVLKVFLENVIR
1481.7859	DNIQGITKPAIRR
1577.8165	ISGLIYEETRGLVK
1693.9896	VLRDNIQGITKPAIR
2105.0053	VFLENVIRDAVYTEHAK



MASFDEAPPGNPKAGEKIFRTKCAQCHT  
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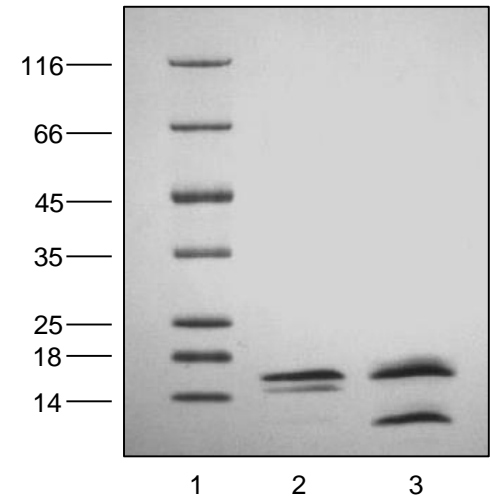
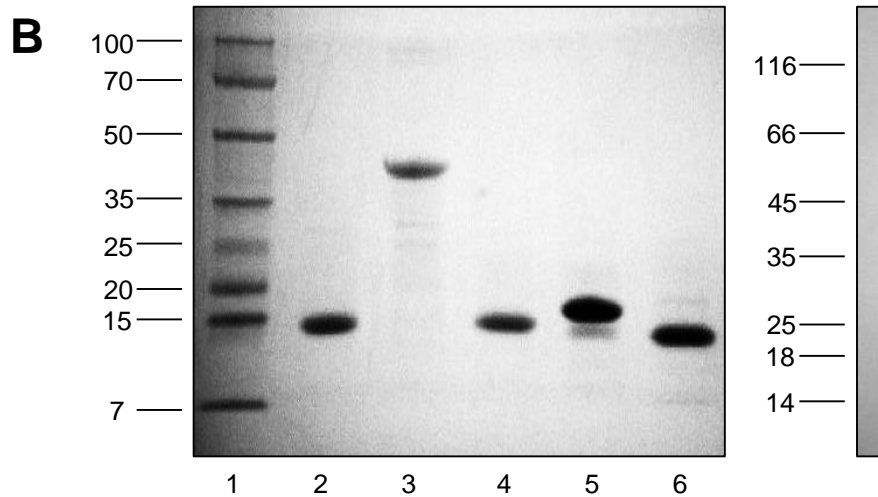
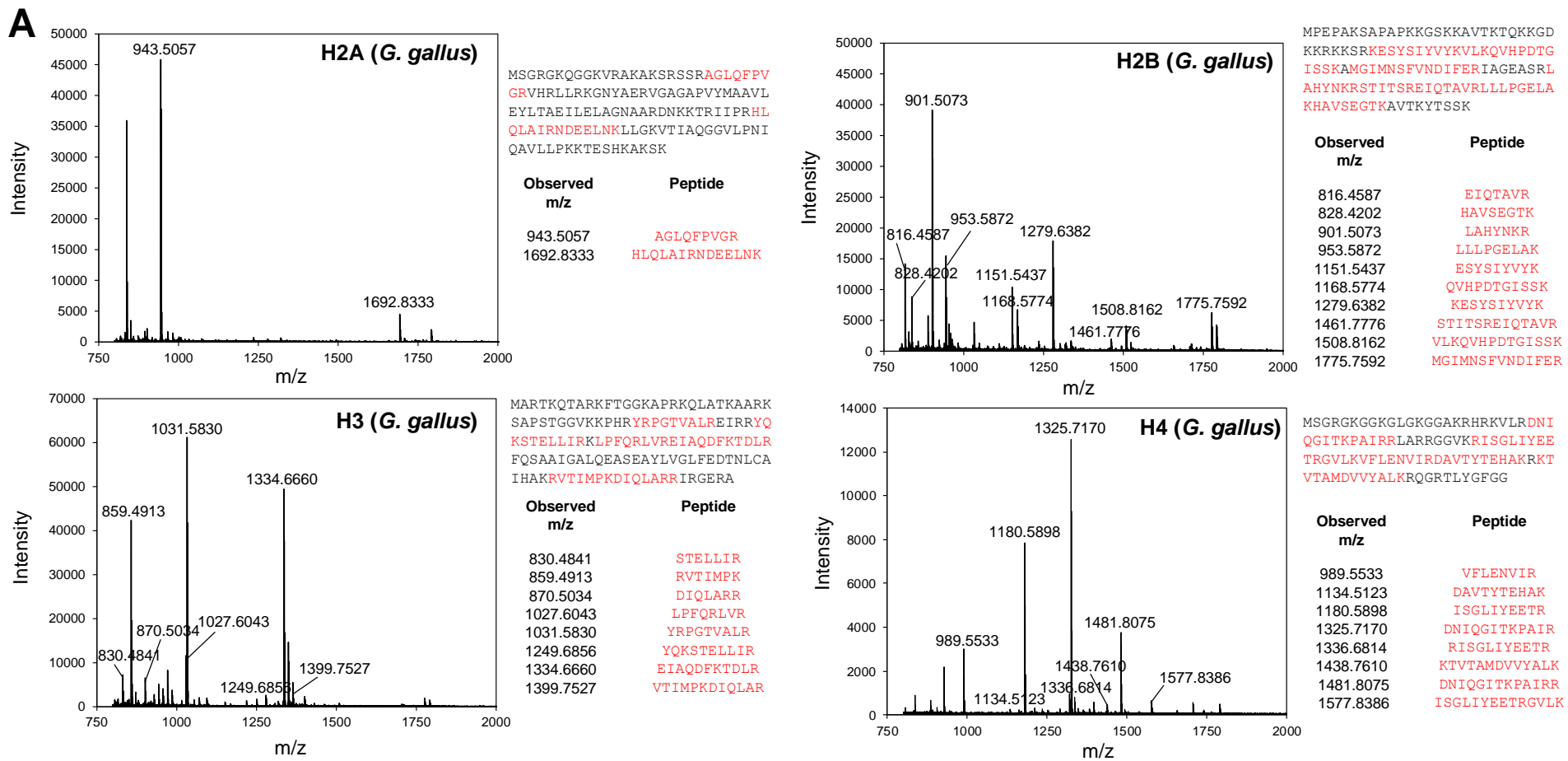
Observed m/z	Peptide
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1093.5272	SMAVNWEET
1172.6599	QGNLNLGFR
1229.6190	ASFDEAPPGNPK
1239.6967	TYDYLLNPK
1367.7980	TYDYLLNPKK
1415.8257	MVFPGLKPKQDR
1530.9147	KPQDRADLIAYLK
1531.7506	QSGTTPGYSYSAANK
1622.9050	GAGHKQGNLNLGFR



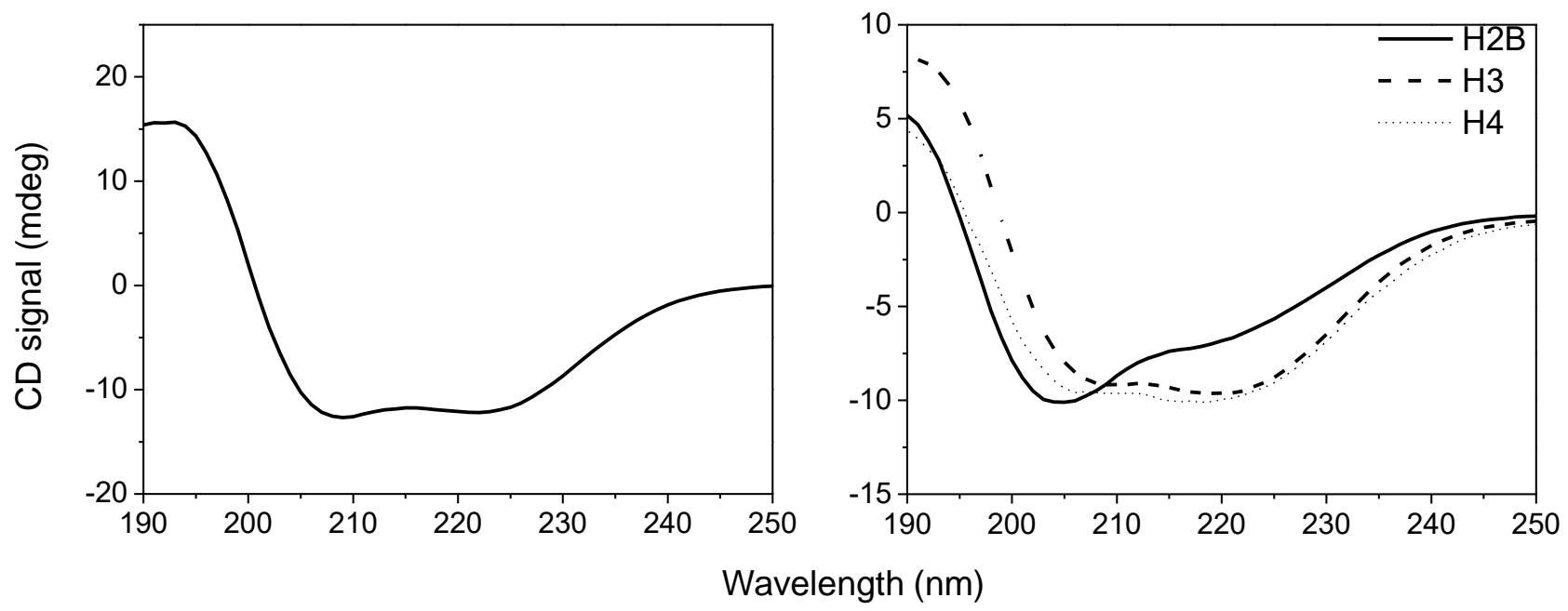
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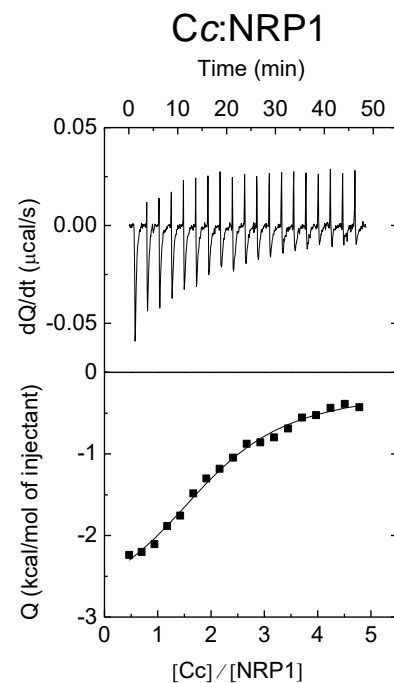
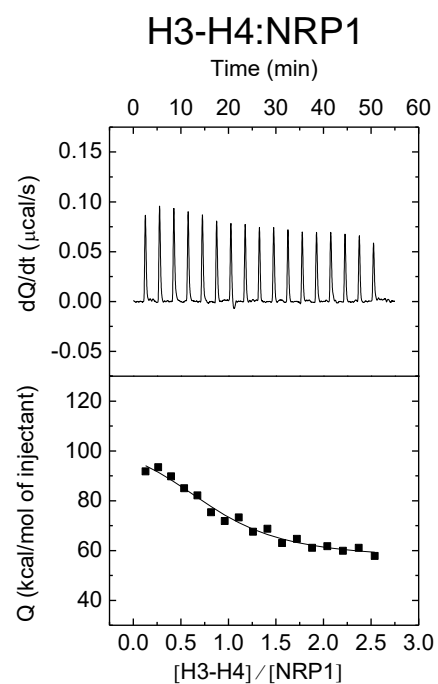
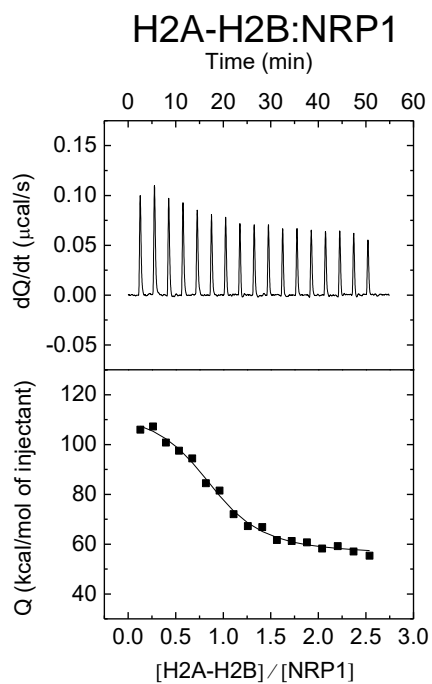
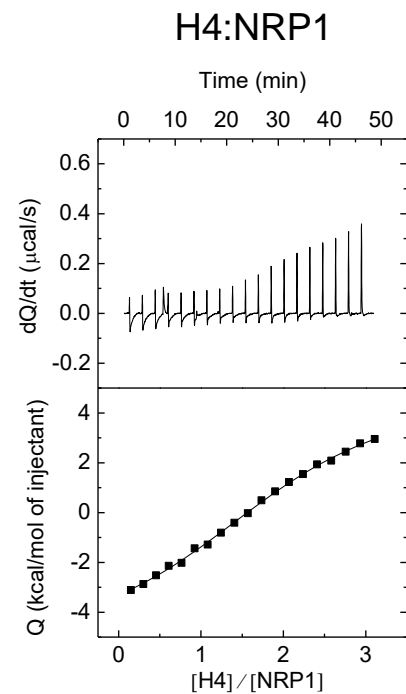
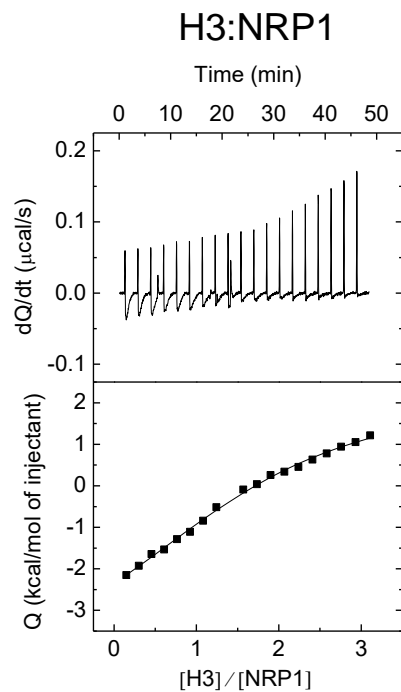
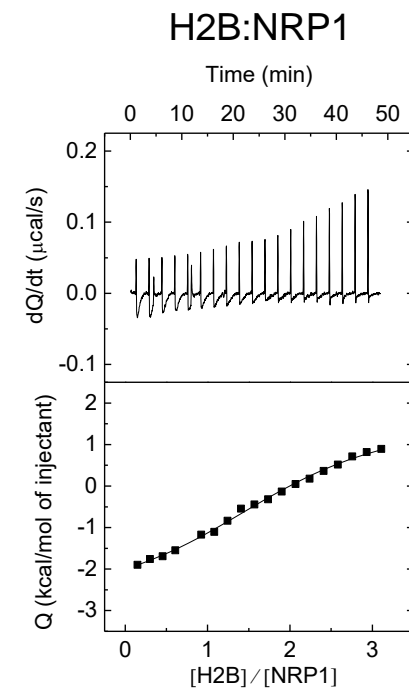
Observed m/z	Peptide
905.5479	KPVYDKR
1273.6633	TFTFLEEGTTK
1768.8999	EDAGDEIHDEVADIK
1892.0332	ASDEVLEVEQKYNVIR
2537.2988	SGYSITFHFTSNPFFEDAKLTK

**Fig. S2**

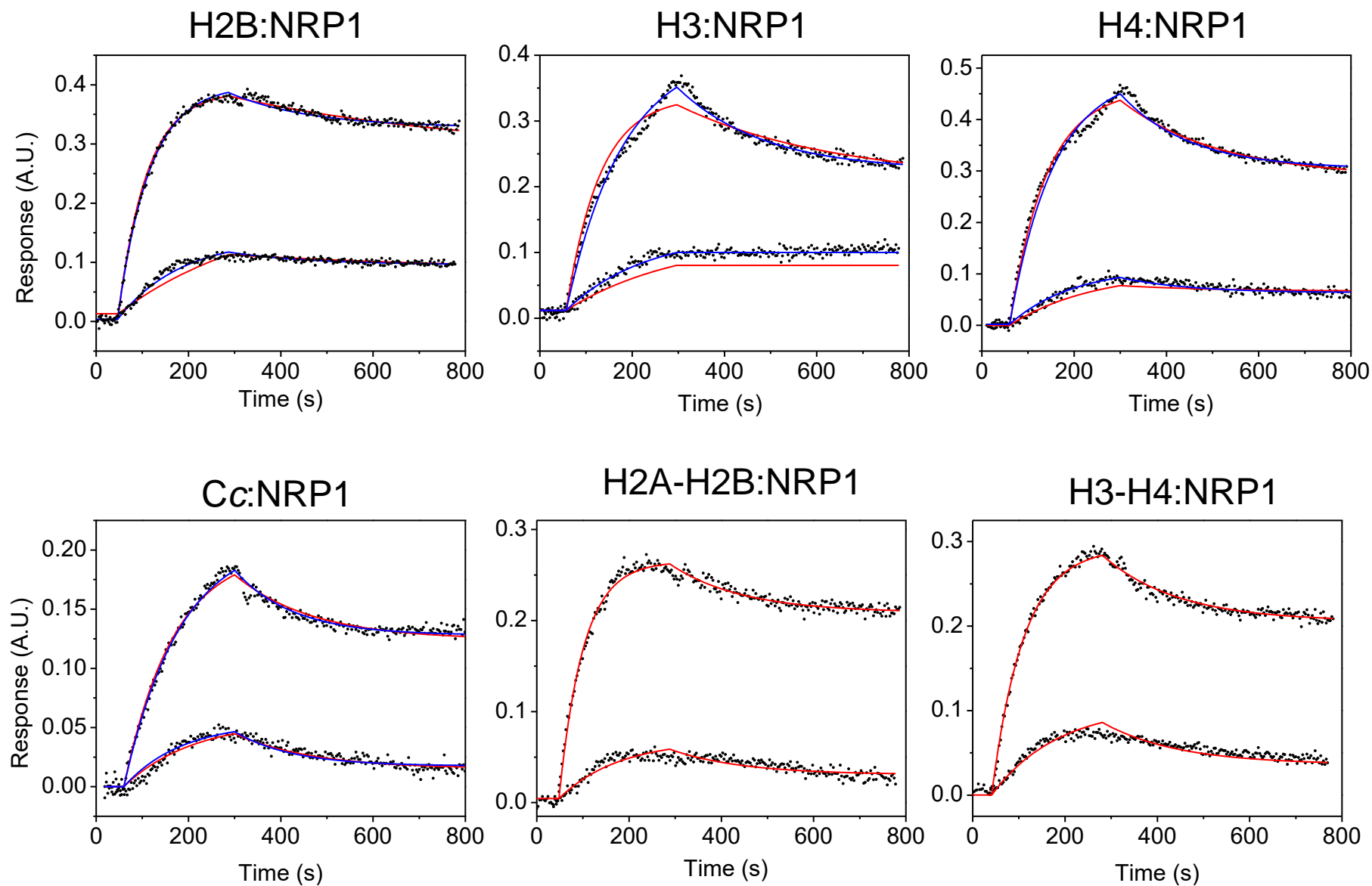


**Fig. S3**

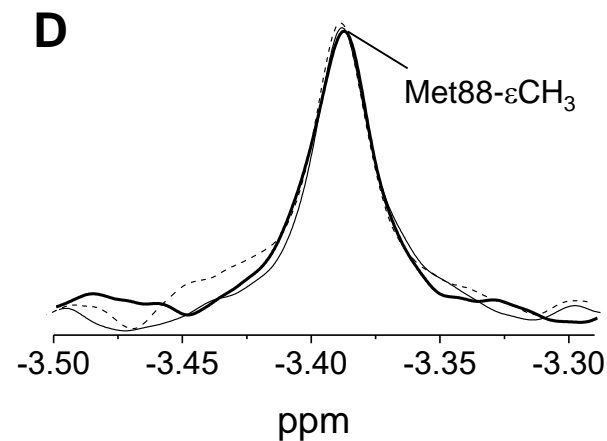
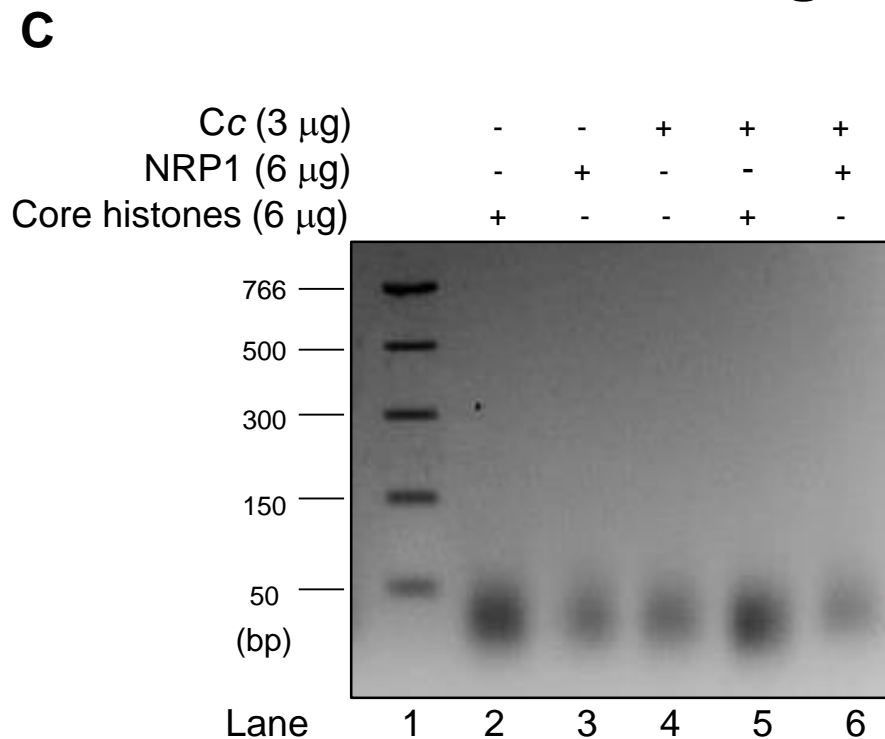
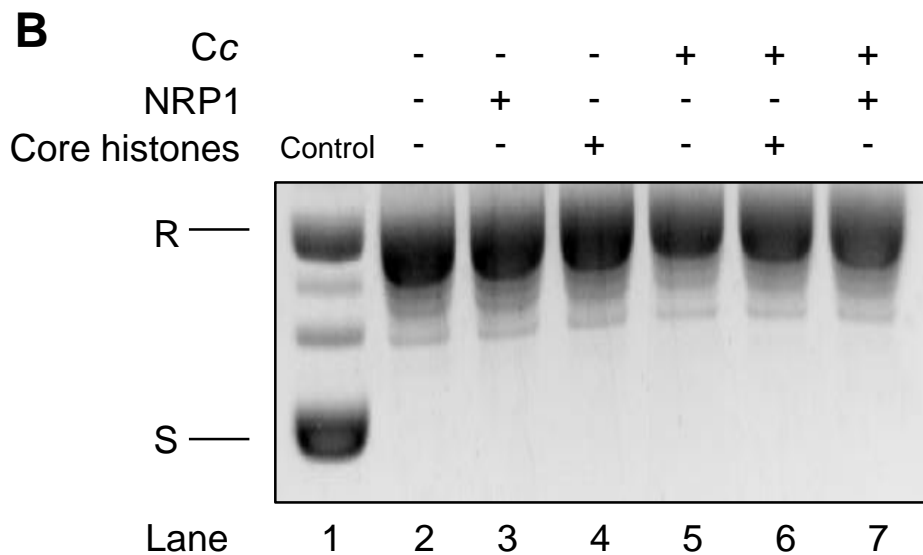
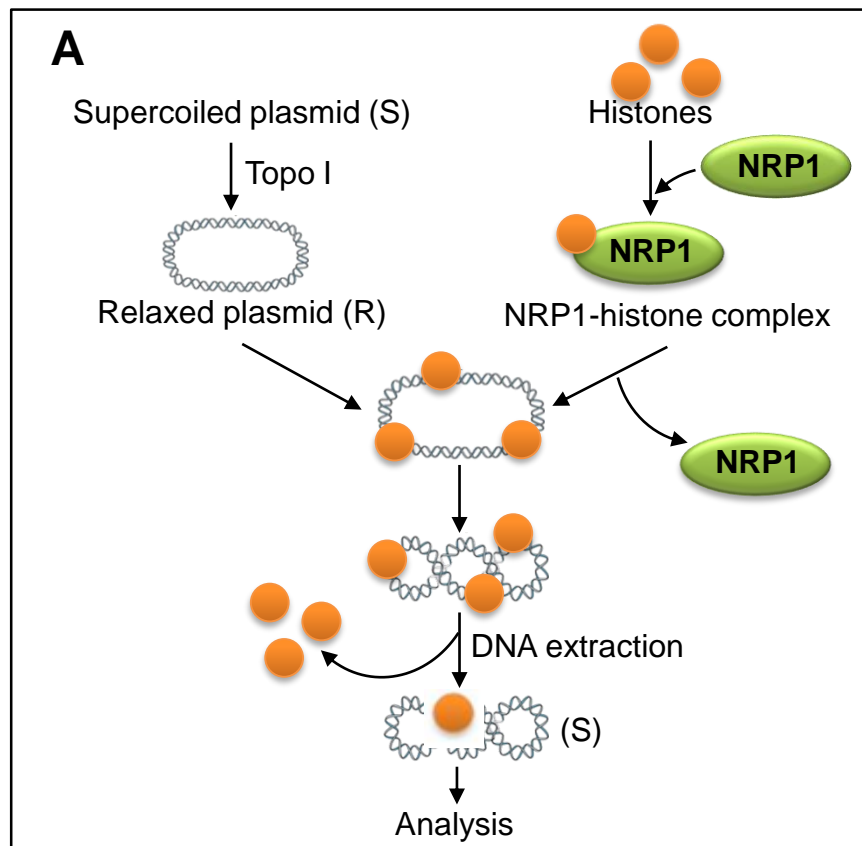


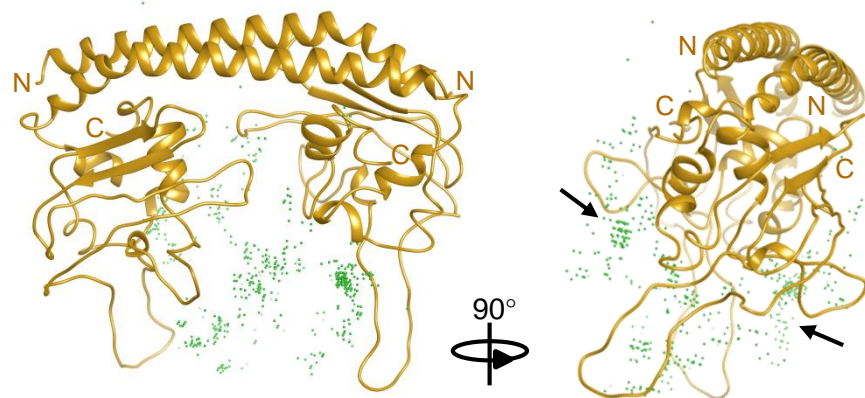
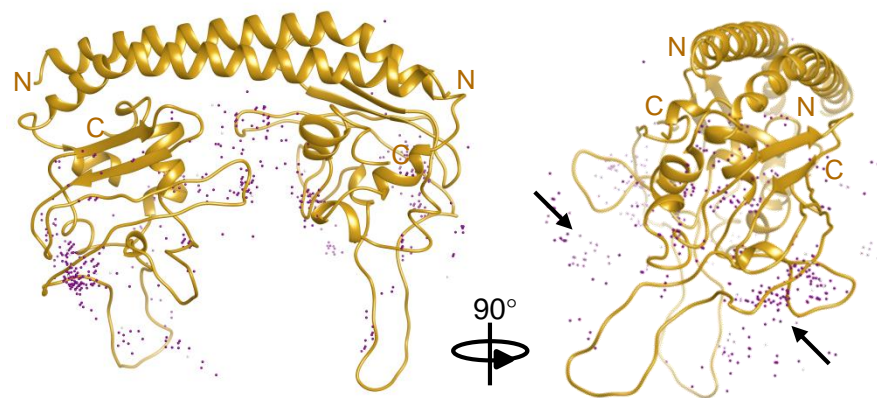
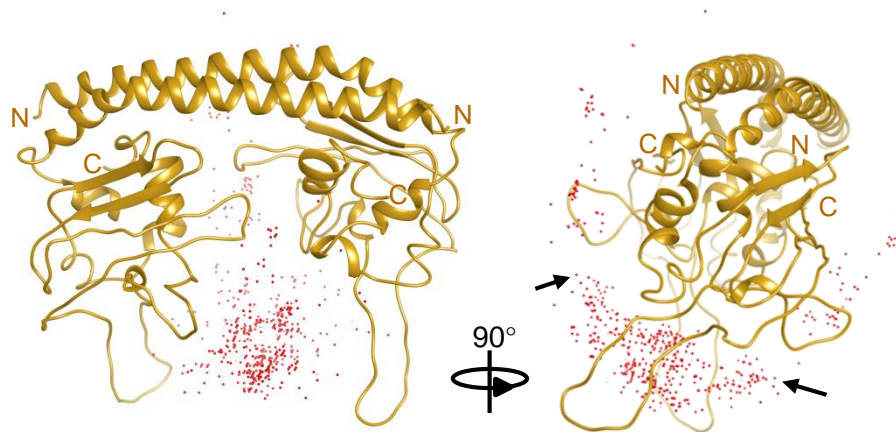
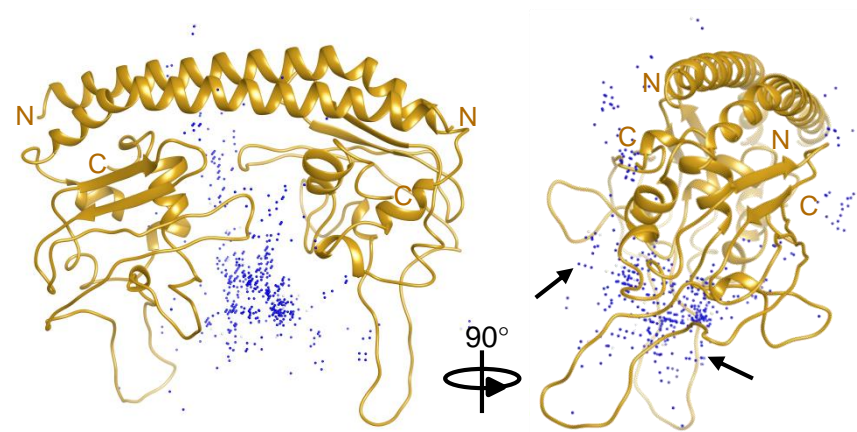


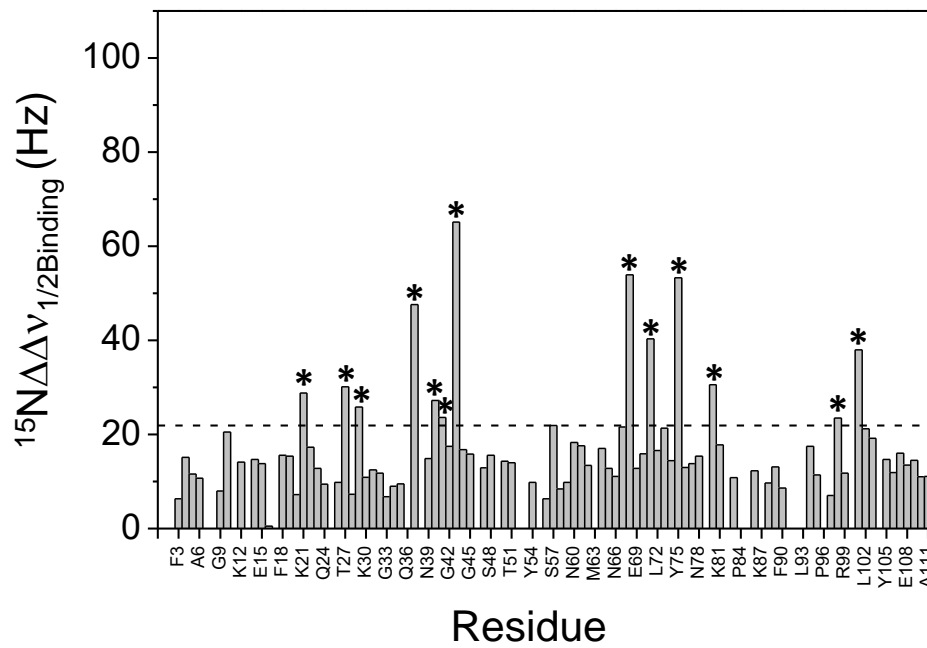


**Fig. S6**

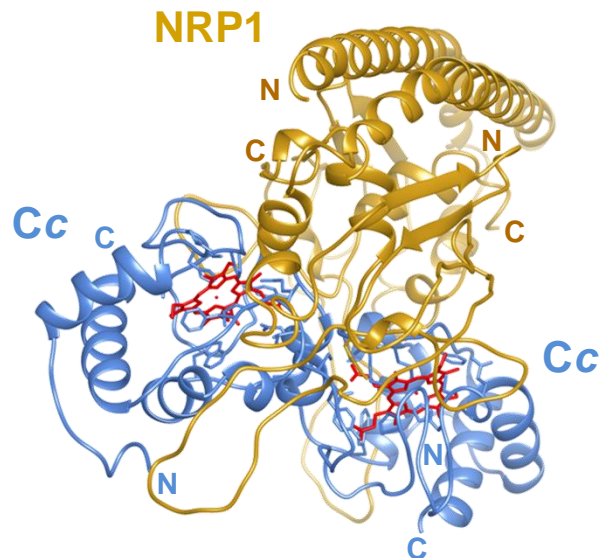
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	<i>Arabidopsis thaliana</i>	MSGRGKGGKAKTKGKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVMEYLA	59
	<i>Xenopus laevis</i>	AETLELAGNAARDNKKTRII PRHLQLAVRNDEELNKLKLGVTIAQGGVLPNIQSVLLPKK	120
	<i>Arabidopsis thaliana</i>	AEVLELAGNAARDNKKTRII PRHLQLAIRNDEELNKLKLSGVTIAQGGVLPNIQAVLLPKK	119
	<i>Xenopus laevis</i>	TESAKSAKSK----- 130	
	<i>Arabidopsis thaliana</i>	TSA PVTSSAPKSGKSSSQSQEY 141	
H2B	<i>Xenopus laevis</i>	-----MPEP-AKSAPAPKKGSKKAVTKT-QKKGKRRKSRKESYAI	40
	<i>Arabidopsis thaliana</i>	MAKADKKPAEKKPAEKTAAEPAAAAEKKPKAGKKLPKEPAGAGDKKRRSKKNVE TYKI	60
	<i>Xenopus laevis</i>	YVYKVLKQVHPDTGISSKAMSIMNSFVNDVFERIAGEASRLAHYNKRSTIITSREIQTAVR	100
	<i>Arabidopsis thaliana</i>	YIFKVLKQVHPDIDGISSKAMGIMNSFINDIFEKLAGESSKRLARYNKKPTIITSREIQTAVR	120
	<i>Xenopus laevis</i>	LLLPGELAKHAVSEGTKAVTKYTSAK 126	
	<i>Arabidopsis thaliana</i>	LVLPGELAKHAVSEGTKAVTKETSS- 145	
H3	<i>Xenopus laevis</i>	MARTKQTARKSTGGKAPRKQLVTKAAKCAPATGGVKKPHRYRPGTVALREIRRYQKSTE	60
	<i>Arabidopsis thaliana</i>	MARTKQTARKSTGGKAPRKQLATKAARKSAPITGGVKKPHRYRPGTVALREIRRYQKSTE	60
	<i>Xenopus laevis</i>	LLIRKLPFQRLVREIAQDFKTDLRFQRSAVMALQEASEAYLVALFEDTNLCAIHAKRVTI	120
	<i>Arabidopsis thaliana</i>	LLIRKLPFQRLVREIAQDFKTDLRFQSHAVLALQEAAEAYLVGLFEDTNLCAIHAKRVTI	120
	<i>Xenopus laevis</i>	MPKDIQLARRIGERA 136	
	<i>Arabidopsis thaliana</i>	MPKDIQLARRIGERA 136	
H4	<i>Xenopus laevis</i>	MSGRGKGGKGLGKGGAKRHRKVLDRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGLVK	60
	<i>Arabidopsis thaliana</i>	MSGRGKGGKGLGKGGAKRHRKVLDRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGLVK	60
	<i>Xenopus laevis</i>	VFLENVIRDAVITYTEHAKRKTVTAMDVVYALKRQRTLYGFGG 103	
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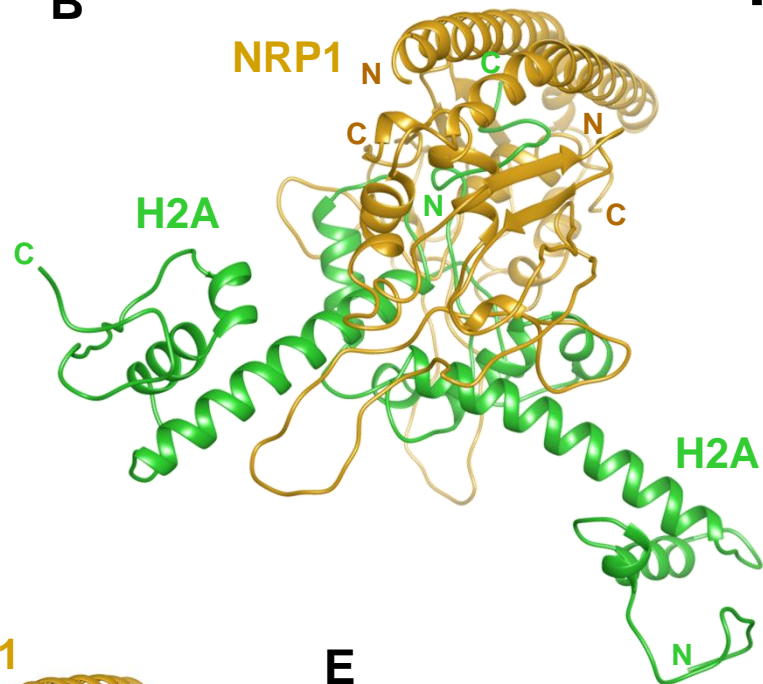
**H2A:NRP1****H2B:NRP1****H3:NRP1****H4:NRP1**



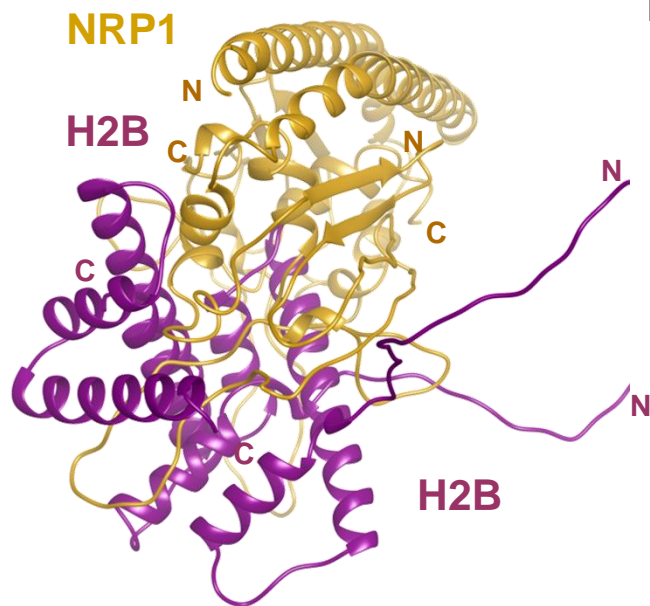
A



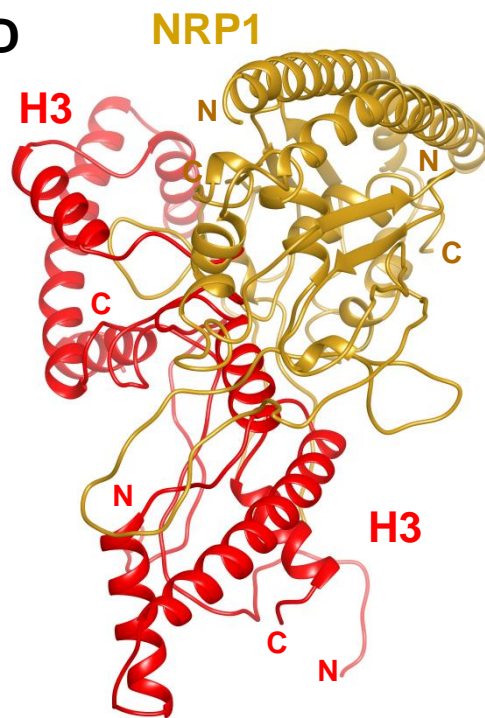
B



C



D



E

