The structure of the nucleoprotein of Influenza D shows that all *Orthomyxoviridae* nucleoproteins have a similar NP_{CORE}, with or without a NP_{TAIL} for nuclear transport

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Supplementary information

Supplementary Figure 1

Sequence alignment of NP from representative Influenza strains. The sequences used are the same as in Table 1. The figure has been drawn using ESPript [1]. The upper and lower secondary structures correspond to the X-ray structures of D/NP (PDB entry 5N2U) and A/NP (PDB entry 2IQH), respectively. The stars indicate the phosphorylation sites identified for A/NP (closed symbol) and B/NP (open symbol) by Hutchinson *et al.* (red)[2], Li *et al.* (green)[3] and Monda *et al.* (blue)[4].

Supplementary Figure 2

Effect of trimethylamine N-oxide (TMAO) on the folding of D/NP$_{TAIL}$. Far UV-circular dichroism spectra of either D/NP$_{TAIL}$ alone (purple) or in presence of TMAO (0.5 M in yellow, 1M in red, 2M in blue and 3 M in green) were collected. Because of the high background induced by the presence of TMAO around 200 nm, spectra were cut when the voltage (right bottom insert) became too high (> 700 V).

References

1 Robert, X. & Gouet, P. Deciphering key features in protein structures with the new ENDscript server. *Nucleic Acids Res* **42**, W320-324, doi:10.1093/nar/gku316 (2014).

2 Hutchinson, E. C. *et al.* Mapping the phosphoproteome of influenza A and B viruses by mass spectrometry. *PLoS Pathog* **8**, e1002993, doi:10.1371/journal.ppat.1002993 (2012).

3 Li, Y. *et al.* Phosphorylation and dephosphorylation of threonine 188 in nucleoprotein is crucial for the replication of influenza A virus. *Virology* **520**, 30-38, doi:10.1016/j.virol.2018.05.002 (2018).

4 Mondal, A. *et al.* Influenza virus recruits host protein kinase C to control assembly and activity of its replication machinery. *Elife* **6**, doi:10.7554/eLife.26910 (2017).

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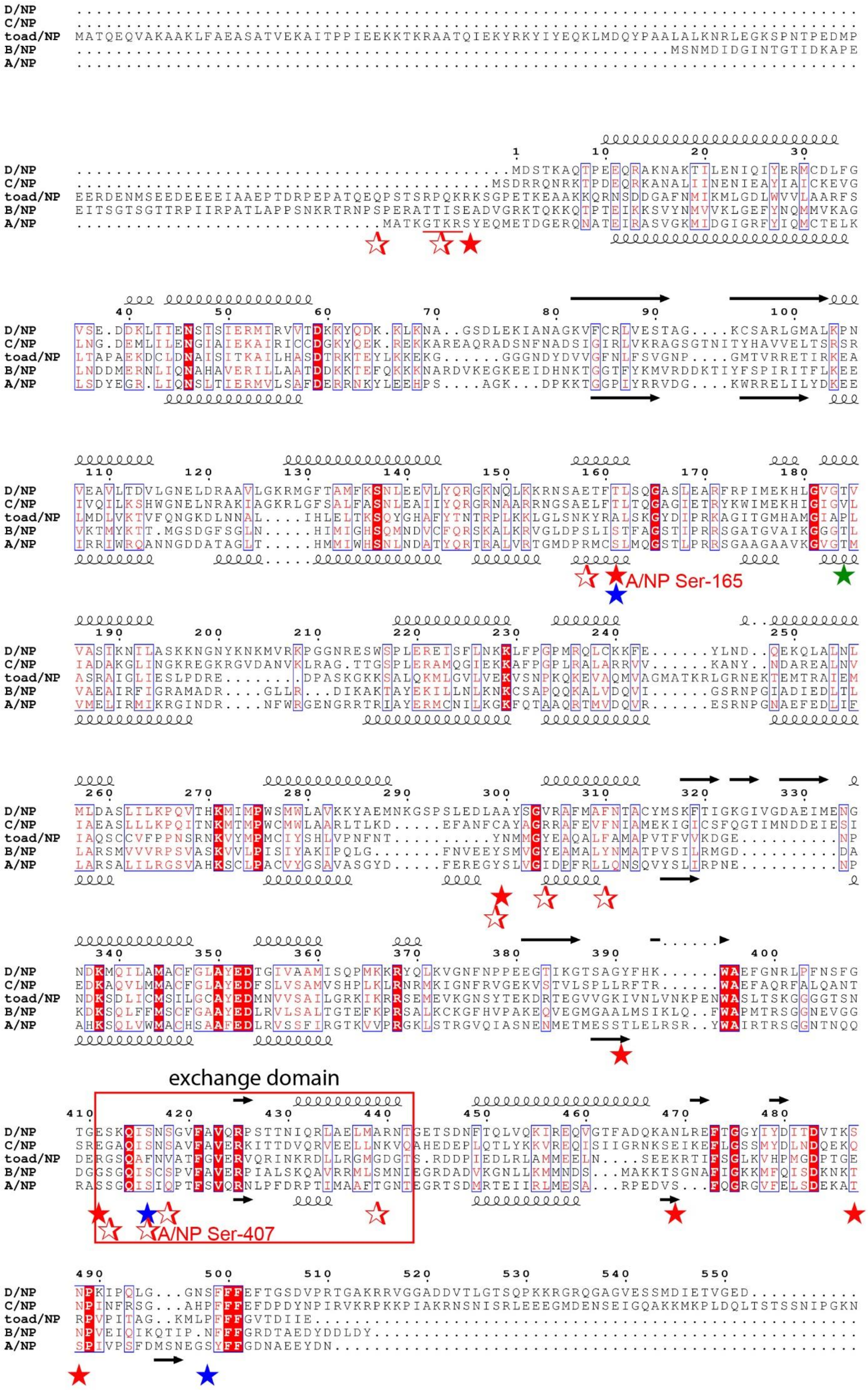
Supplementary Table 1: Crystallographic data collection and structure refinement statistics. Values in parentheses are for highest resolution shell.

Crystal Parameters	D/NP
Data collection	
Beamline	ID30A3 - ESRF
Wavelength (Å)	0.9677
Space group	P1
Cell Dimensions a, b, c (Å)	75.17, 85.17, 103.39
α, β, γ (°)	91.20, 101.94, 101.02
Molecules per asymmetric unit	4
Wilson B-factor (Å^2)	51.4
Resolution (Å)	40 - 2.4 (2.48 - 2.4)
Observed Reflections	191 888 (18 695)
Unique Reflections	87 824 (8 505)
Completeness (%)	91.3 (94.1)
R_{sym} (I)$^{(a)}$ (%)	9.3 (84.7)
$\langle I/\sigma(I)\rangle$	7.78 (1.05)
Model quality indicators	
R_{cryst} (%)	20.2 (21.9)
R_{free} (%)	25.2 (23.8)
Non-hydrogen atoms	14 646
Water atoms	235
Average B-factors (Å^2)	55.7
B-factors per chains (Å^2)	59.8, 54.3, 52.8, 56.3
B-factors water (Å^2)	49.5
Ramachandran favoured / allowed (%)	94.0 / 5.1
rms deviations, bonds (Å) / angles (°)	0.009 / 1.15
Clashscore$^{(b)}$	4.31
MolProbity score$^{(b)}$	2.28

(a) $R_{sym} = \sum_{hkl}\sum_j |I_{hkl,j} - \langle I_{hkl}\rangle| \,/\, \sum_{hkl}\sum_j I_{hkl,j}$

(b) calculated using MolProbity [5]


D/NP
C/NP
toad/NP
B/NP
A/NP
A/NP Ser-165
exchange domain
A/NP Ser-407

Supplementary Figure 2