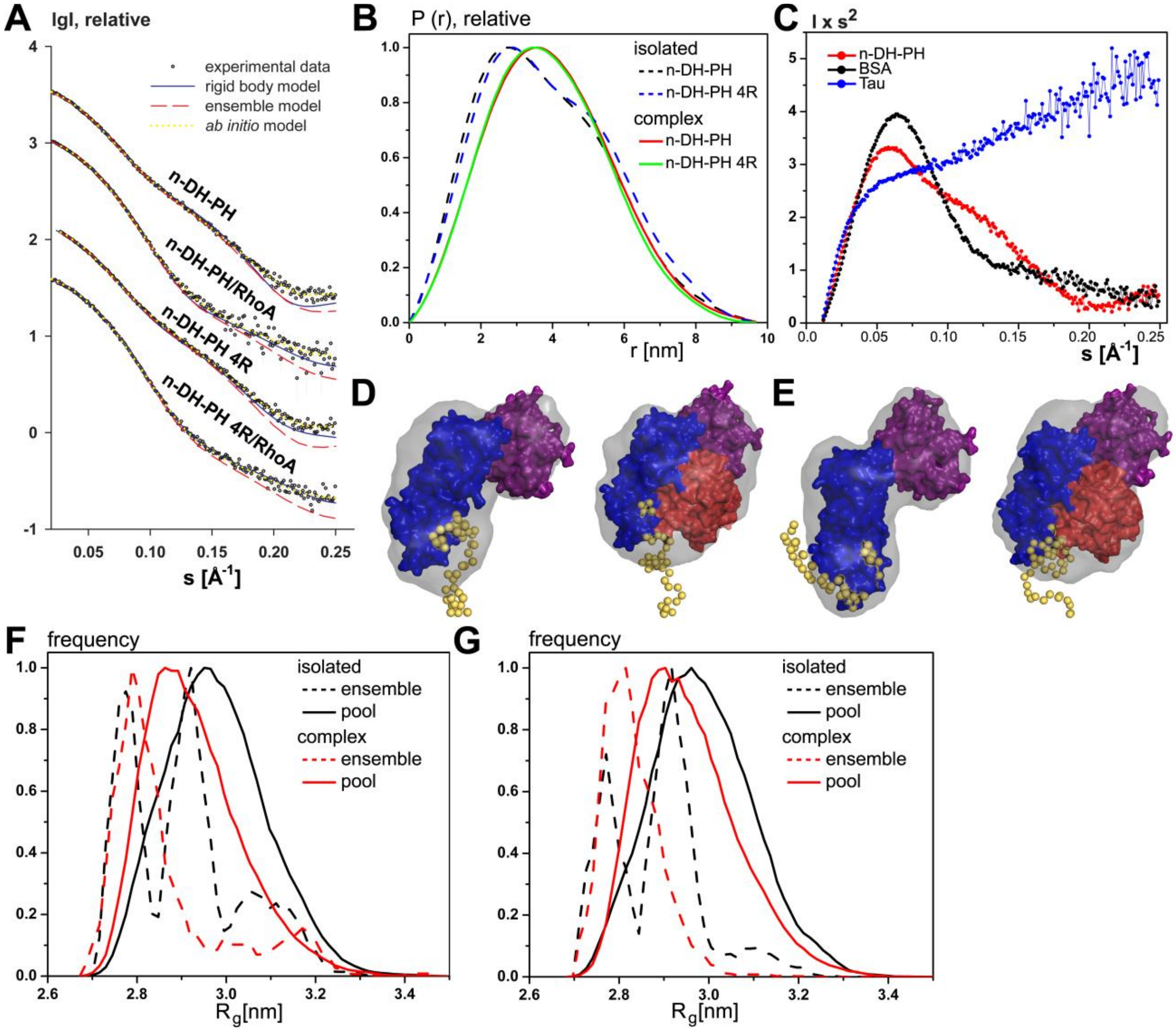
Fig. S2. Summary of SAXS data and models for n-DH-PH constructs. (*A*) Scattering profiles for n-DH-PH fragments. Experimental data, fit to *ab initio*, rigid body, and EOM models are shown as *open circles*, *yellow dotted line*, *blue solid line*, *and red dashed line*, respectively. Plots display the logarithm of the scattering intensity as a function of momentum transfer $s = 4\pi sin(\theta)/\lambda$, where 2θ is the scattering angle and λ is the X-ray wavelength. Experimental SAXS profiles were appropriately displaced along the logarithmic axis for better visualization and overlaid with corresponding fits. (*B*) Distance distribution function, *P(r)*, of isolated n-DH-PH and n-DH-PH 4R (*black and blue dashed lines*, respectively), and n-DH-PH/RhoA complex and n-DH-PH 4R/RhoA (*red and green solid lines*, respectively). (*C*) Comparison of Kratky plots of n-DH-PH (*red circle*), with bovine serum albumin (*black circle*), and protein tau (*blue circle*). (*D*) Rigid body models (BUNCH) superposed onto the *ab initio* models (GASBOR) of isolated n-DH-PH (*left*), and n-DH-PH/RhoA complex (*right*). (*E*) Rigid body models (BUNCH) superposed onto the *ab initio* models (GASBOR) of isolated n-DH-PH 4R (*left*), and n-DH-PH 4R/RhoA complex (*right*). (*F*) Radius of gyration distribution for n-DH-PH. Distributions for pools of models are shown as *black* and *red solid lines*, for the isolated protein and the RhoA complex, respectively. Distributions for selected ensemble of models are shown as *black* and *red dashed lines*, for the isolated protein and the RhoA complex, respectively. (*G*) Radius of gyration distribution for n-DH-PH 4R. Distributions for pools of models are shown as *black* and *red solid lines*, for the isolated protein and the RhoA complex, respectively. Distributions for selected ensemble of models are shown as *black* and *red dashed lines*, for the isolated protein and the RhoA complex, respectively.

Figure S2


A
lgI, relative
experimental data
rigid body model
ensemble model
ab initio model
n-DH-PH
n-DH-PH/RhoA
n-DH-PH 4R
n-DH-PH 4R/RhoA
4
3
2
1
0
-1
0.05
0.10
0.15
0.20
0.25
s [Å^{-1}]
B
P (r), relative
isolated
n-DH-PH
n-DH-PH 4R
complex
n-DH-PH
n-DH-PH 4R
1.0
0.8
0.6
0.4
0.2
0.0
0
2
4
6
8
10
r [nm]
C
I x s^2
n-DH-PH
BSA
Tau
5
4
3
2
1
0
0.00
0.05
0.10
0.15
0.20
0.25
s [Å^{-1}]
D
E
F
frequency
isolated
ensemble
pool
complex
ensemble
pool
1.0
0.8
0.6
0.4
0.2
0.0
2.6
2.8
3.0
3.2
3.4
R$_g$[nm]
G
frequency
isolated
ensemble
pool
complex
ensemble
pool
1.0
0.8
0.6
0.4
0.2
0.0
2.6
2.8
3.0
3.2
3.4
R$_g$[nm]