

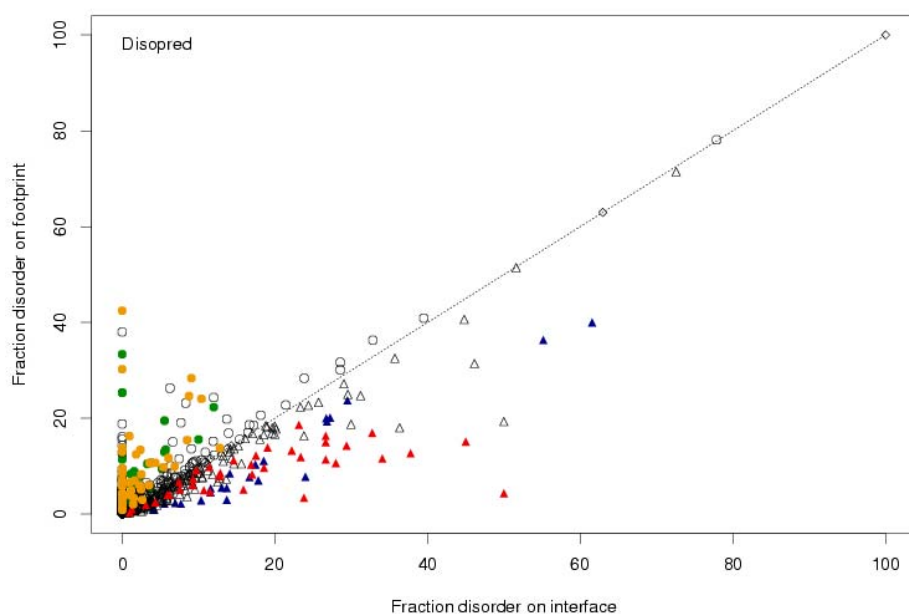
The role of intrinsic disorder in protein binding

Jessica H. Fong and Anna R. Panchenko

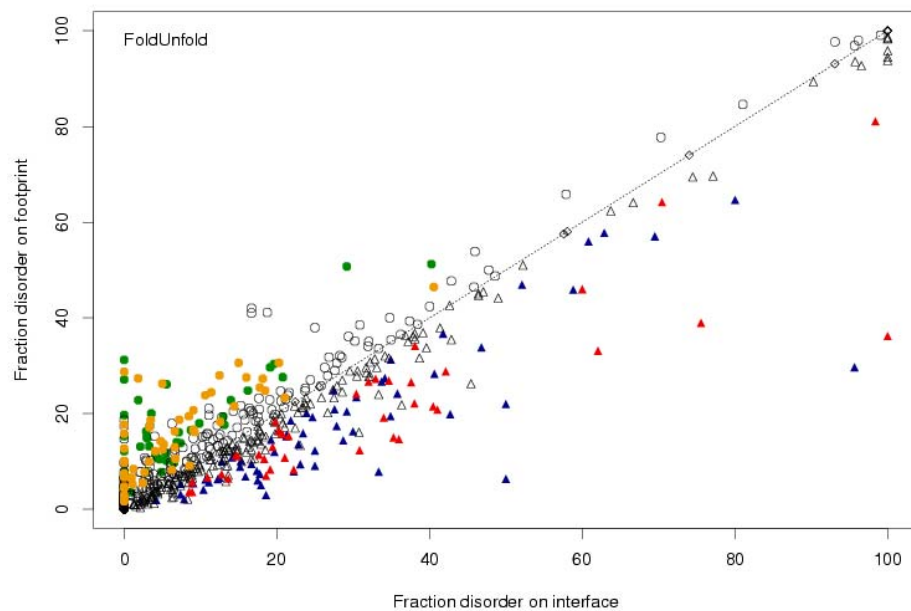
Supplementary Information

Figure S1. Pairwise comparison of average fraction disorder in the footprint, interface, and overlap multibinding interface by three disorder prediction methods. Points with higher, equal, and lower fraction disorder are shown as circles, diamonds, and triangles, respectively. Families with statistically significant bias towards/against disorder on different regions are colored: green or blue, respectively, if significant by one disorder prediction method; or orange or red, respectively, if significant by at least two disorder prediction methods. (A) Footprint vs. interface by Disopred2. (B) Footprint vs. interface by FoldUnfold. (C) Footprint vs. interface by VSL2. (D) Multibinding interface vs. interface by Disopred2. (E) Multibinding interface vs. interface by FoldUnfold. (F) Multibinding interface vs. interface by VSL2.

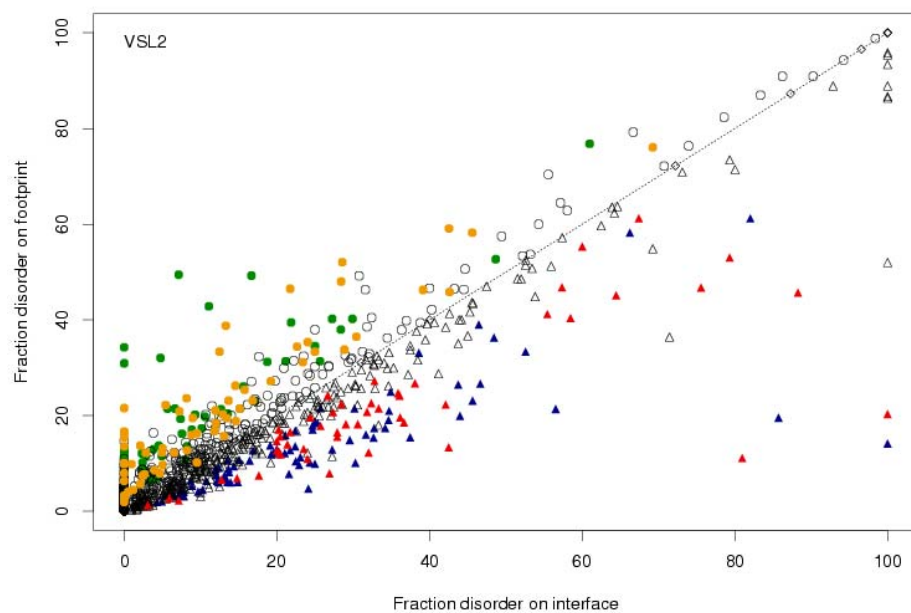
(A)



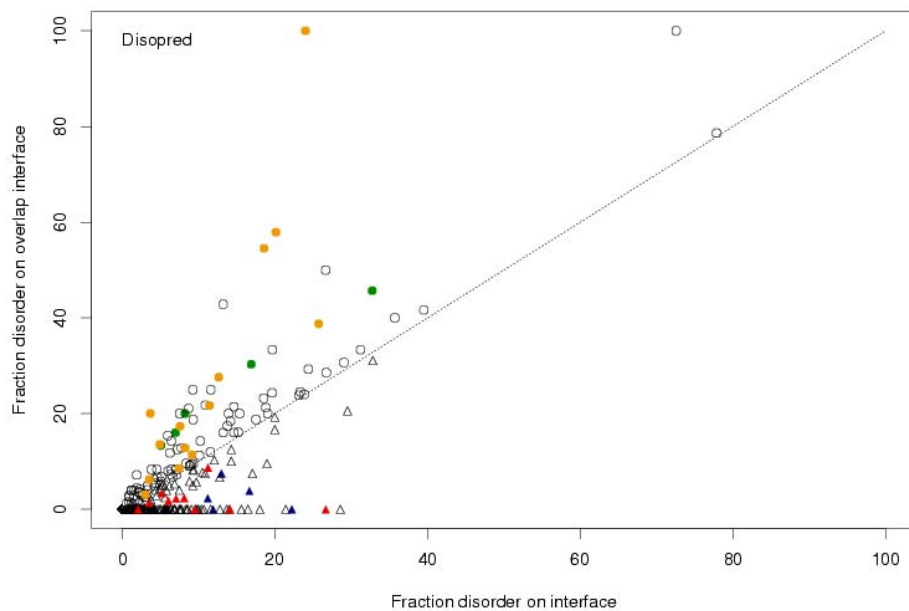
(B)



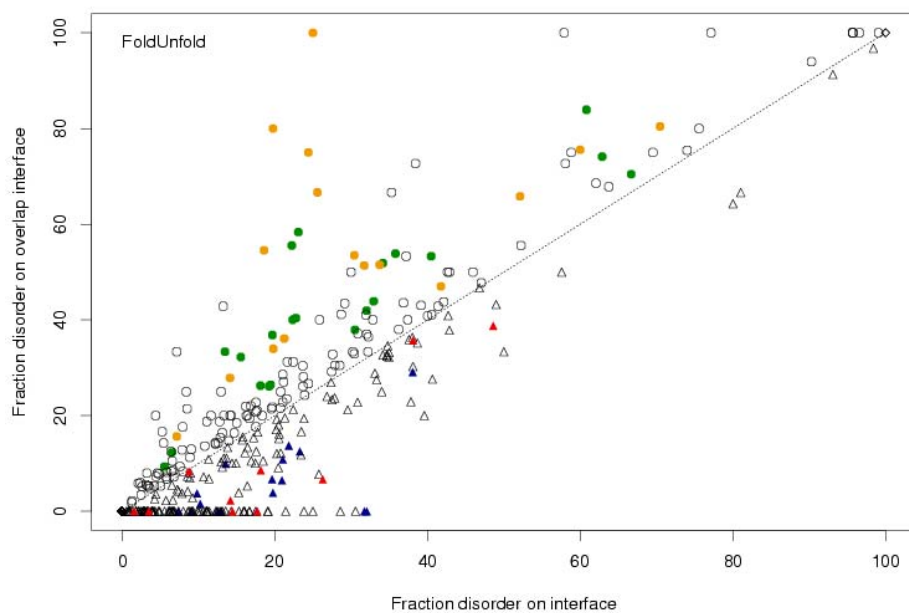
(C)



(D)



(E)



(F)

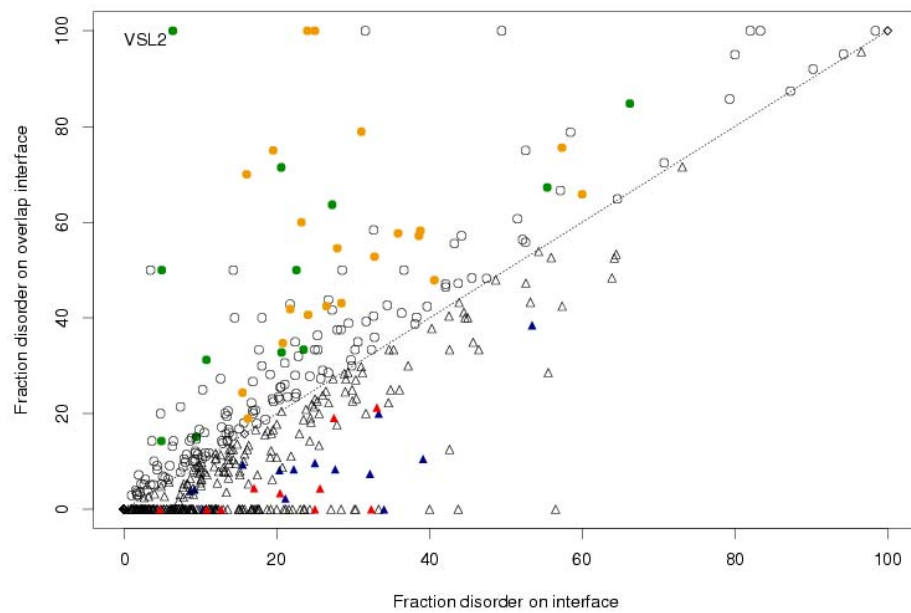


Table S1. Families with significant bias of disorder towards footprint, interface, or multibinding interface for at least two prediction methods (Disopred2: D, FoldUnfold: F, VSL2: V), and the number of domain-domain interactions observed in our dataset. The family name and CDD accession are taken from the representative structure for that family in our dataset.

Family name	Domain (CDD accession)	# Ints	Bias on interface over footprint	Bias on footprint over interface	Bias on interface over multi-binding interface	Bias on multi-binding interface over interface
FruK_PfkB_like	cd01164	5	F,V			
PRK05382	PRK05382	3		D,V	F	
PRK12276	PRK12276	1		D,V	F	
NrfA	COG3303	1		D,F		
rve	pfam00665	1		F,V		
FBPase	cd00354	7		F		D,V
Flavokinase_C	cd02064	14	V			
INB	smart00187	18	F		F,V	
PRK09448	PRK09448	7				F,V
PBPe	smart00079	6		F,V		
CASc	cd00032	4	D,V		D,V	
Asparaginase	cd00411	6	F		F,V	
PRK05679	PRK05679	2	D,V			D,V
NOS_oxygenase_euk	cd00795	1	D,V	F		D,V
DHFR	cd00209	4		V		D,V
PRK10437	PRK10437	3		D,F,V		
14-3-3	pfam00244	1	D,V			
ZnMc_serralysin_like	cd04277	15	F			
pgi	PRK00179	1	D,F,V			
Lyase_I	cd01334	4	D,F		F	
Chorismate_bind	pfam00425	4		D,F,V	F	
proteasome_alpha_type_6	cd03754	13	F		D,V	
PRK11556	PRK11556	1		D,V		
PAP2_acid_phosphatase	cd03397	3		F,V		
ALBUMIN	cd00015	5	V			
FGF	smart00442	4				D
GHB	smart00068	1	F,V			

Supplementary Material (ESI) for Molecular BioSystems

This journal is (c) The Royal Society of Chemistry, 2010

HELICc	cd00079	7	D,F,V		D	
KISc_KIF1A_KIF1B	cd01365	2	F	D,V		
PLAT_PL	cd01759	2	D,F,V			D
PIPKc	smart00330	1	D,V			
Calpain_III	pfam01067	1	D,F			
catalase_peroxidase	cd00649	3	D,V	F	D	
Ring_hydroxyl_A	pfam00848	4	D	V		D,V
GlyRS_anticodon	cd00858	6		F,V		V
GlyRS-like_core	cd00774	21		D		D
PARP	pfam00644	1		D,F		
RuBisCO_large	pfam00016	8		D		
Asp	pfam00026	2		D,F,V		
Sod_Fe_N	pfam00081	6	F		F,V	
Hormone_1	pfam00103	2	D,F,V		D,F	
E1-E2_ATPase	pfam00122	4				
RIP	pfam00161	3		D,F		
Ribosomal_S4	pfam00163	1		D,F		
Catalase	pfam00199	5	F,V			
Orn_DAP_Arg_deC	pfam00278	3		D,V		
BluB	cd02145	1		F,V		
GHMP_kinases_N	pfam00288	1	D,F,V			
PRK00737	PRK00737	3			V	
Molybdopterin	pfam00384	8		F,V		
DNA_pol_A	pfam00476	3	F,V			
Flavi_glycoprot	pfam00869	5		F	F,V	
Tissue_fac	pfam01108	4	F,V			
Globin	pfam00042	9				D
RNase_PH	pfam01138	6	V		D,V	
Cu_amine_oxid	pfam01179	9	D,V		D,F,V	
Inos-1-P_synth	pfam01658	2		D,F,V		
Terpene_synth	pfam01397	1		F,V		
Peptidase_M41	pfam01434	1	D,F,V			
Transglut_core	pfam01841	3	D		D,V	
Cytochrom_C1	pfam02167	7		V		F,V
Lyase_8	pfam02278	2		F,V		
Seryl_tRNA_N	pfam02403	2		D,F		
PRK02256	PRK02256	3	F,V		F	
DNA_pol3_beta_3	pfam02768	2	D,F,V			
Semialdhyde_dhC	pfam02774	6			D,F	
Transket_pyr	pfam02779	5		D,V		
RuBisCO_large_N	pfam02788	5		D,F,V		F

Supplementary Material (ESI) for Molecular BioSystems

This journal is (c) The Royal Society of Chemistry, 2010

Chal_sti_synt_C	pfam02797	4		D,F,V		D,F
STAT_bind	pfam02864	2		D,V		
Ldh_1_C	pfam02866	4		F,V		
MurB_C	pfam02873	1	F,V			
ATP-synt_ab_N	pfam02874	3		D,F,V		
PARP_reg	pfam02877	1		D,F		
SRP54_N	pfam02881	1		D,F		
TetR_C	pfam02909	3			D,F,V	
Formyl_trans_C	pfam02911	1		F,V	D,F,V	
FAD_binding_7	pfam03441	1		D,V		
petB	CHL00070	9		D,V		F,V
PRK10518	PRK10518	3	F		F,V	D
PUD	pfam03714	1		F,V	F,V	D
PRCH	pfam03967	3		V		F,V
SPOUT_MTase	pfam02590	1		D,F		F,V
RNA_pol_Rpb1_1	pfam04997	11		D,F		
Peptidase_M16_C	pfam05193	5			D,V	F
groEL	PRK00013	5				F,V
iPGM_N	pfam06415	1	F,V			
FtsH_ext	pfam06480	1	D,V			
Myotub-related	pfam06602	1		D,F,V	V	
RIBOc	smart00535	1		D,V		
FERM_M	pfam00373	15	F,V		V	
PDZ_serine_protease	cd00987	6	F,V		F	V
A2M_N_2	pfam07703	1	D,F			
Plug	pfam07715	1	D,F			
lamB	PRK09360	1		F,V		
PRK12677	PRK12677	3	D,F,V		D,V	
IMD	pfam08397	1		D,F,V		
PepX_C	pfam08530	3		D,F		
GCV_T_C	pfam08669	3	D,F			
TR_THY	smart00095	4		D,F		
PTPc	cd00047	6		D,F,V		
PRK07157	PRK07157	1		F,V		
Transpeptidase	pfam00905	5	F,V			
PRK08292	PRK08292	5	F,V			
PRK11883	PRK11883	9	F,V			
PRK05716	PRK05716	9	F,V			
Rep_fac-A_3	pfam08661	10	F		F	
TMADH_HD_FMN	cd02929	33	F,V		F,V	